

The Book of OHDSI Korea

OHDSI-Korea

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서문

이 책은 관찰 보건 데이터 과학 및 정보학 (Observational Health Data Sience and Informatics : OHDSI) 공동작업에 대한 내용을 담고있다. OHDSI 커뮤니티에 의해 작성된 이 책은 OHDSI 관련 모든 지식의 중앙저장소 역할을 담당하고자 쓰여졌으며 오픈소스 개발 도구들을 통해 커뮤니티에 의해 관리되는 생명력있는 문서로 계속 진화하고 있다. 또한 ohdsi-korea.github.io/TheBookOfOhdsiKorea/에서 온라인으로 항상 최신 버전의 책을 무료로 받아 볼 수 있으며 실물로 구입을 원할 경우 Amazon 등에서 구입이 가능하다.

이 책의 목표

이 책은 OHDSI 관련 모든 지식의 중앙저장소 역할을 담당하고자 쓰여졌으며 OHDSI 커뮤니티, OHDSI 데이터 기준과 OHDSI 도구들에 중점을 두었다. OHDSI의 초보자와 숙련자 모두를 위해 현실적으로 필요 이론과 사용방법에 대한 교육을 제공하는 실용적인 부분에 목표를 두고 있다. 이 책을 읽은 뒤 당신은 OHDSI란 무엇인가, 또한 그 여정에 어떻게 동참할 것인가에 관하여 이해하게 될 것이다. 또한 공통 데이터 모델(CDM)과 표준화된 용어들이 무엇인지, 이러한 것들이 관찰 보건 데이터 베이스의 표준화에 어떻게 사용되는지 알게 될 것이다. 이 데이터에 대해 Clinical characterization, Population-level estimation, Population-level prediction, 이 3 가지 주요 이용 사례들을 배우게 될 것이다. 이 책을 통해 이 3가지 활동을 지원하는 OHDSI의 오픈 소스 도구와 사용법에 대해 익히게 될 것이다. 데이터 품질, 임상적 타당성, 소프트웨어 타당성, 방법의 타당성 등에 관한 chapter들에서 CDM에서 생성된 근거들의 품질을 어떻게 확립했는지를 설명할 것이다. 마지막으로, 분산 연구망에서 이러한 연구들을 실행하기 위해 OHDSI를 어떻게 사용하는지를 배우게 될 것이다.

이 책의 구성

이 책은 5개의 주요 섹션으로 정리되어있다:

- I) OHDSI 커뮤니티
- II) 획일적 데이터 표현
- III) 데이터 분석
- IV) 근거 품질
- V) OHDSI 연구

각각의 섹션은 다수의 chapter로 구성되어 있으며 각각의 chapter는 아래의 순서대로 해당 chapter에 맞게 구성되어 있다: 도입, 이론, 실행, 요약, 예제.

기여자

각각의 chapter는 해당 chapter를 이끈 주요 작성자들을 표기하고 있다. 그러나 주요 작성자 외에도 이 책을 완성하는데 기여를 한 많은 사람들이 있으며 아래의 기여자들에게 감사를 표한다:

Hamed Abedtash	Mustafa Ascha	Mark Beno
Clair Blacketer	David Blatt	Brian Christian
Gino Cloft	Frank DeFalco	Sara Dempster
Jon Duke	Sergio Eslava	Clark Evans
Thomas Falconer	George Hripcak	Vojtech Huser
Mark Khayter	Greg Klebanov	Kristin Kostka
Bob Lanese	Wanda Lattimore	Chun Li
David Madigan	Sindhoosha Malay	Harry Menegay
Akihiko Nishimura	Ellen Palmer	Nirav Patil
Jose Posada	Nicole Pratt	Dani Prieto-Alhambra
Christian Reich	Jenna Reps	Peter Rijnbeek
Patrick Ryan	Craig Sachson	Izzy Saridakis
Paola Saroufim	Martijn Schuemie	Sarah Seager
Anthony Sena	Sunah Song	Matt Spotnitz
Marc Suchard	Joel Swerdel	Devin Tian
Don Torok	Kees van Bochove	Mui Van Zandt
Erica Voss	Kristin Waite	Mike Warfe
Jamie Weaver	James Wiggins	Andrew Williams
Seng Chan You		

소프트웨어 버전

이 책의 많은 부분은 OHDSI의 오픈소스 소프트웨어를 다루고 있으며 이 소프트웨어는 시간이 지나면서 계속 진화해 나갈 것이다. 개발자들은 사용들에게 일관되고 안정적인 경험을 제공하고자 최선을 다할 것이다, 시간이 지나면서 소프트웨어의 개선으로 인해 불가피하게 이 책의 내용이 더이상 맞지 않는 경우가 발생할 것이다. 이를 보완하기 위해 커뮤니티는 온라인 버전을 통해 변화를 계속 업데이트할 예정이며 새로운 에디션의 실물 책을 출간할 예정이다. 이 책이 쓰여진 버전의 소프트웨어 버전은 아래를 참고하면 된다 :

- ACHILLES: version 1.6.6
- ATLAS: version 2.7.3
- EUNOMIA: version 1.0.0
- Methods Library packages: 테이블 참조 1

Table 1: Versions of packages in the Methods Library used in this book.

Package	Version
CaseControl	1.6.0
CaseCrossover	1.1.0
CohortMethod	3.1.0
Cyclops	2.0.2
DatabaseConnector	2.4.1
EmpiricalCalibration	2.0.0
EvidenceSynthesis	0.0.4
FeatureExtraction	2.2.4
MethodEvaluation	1.1.0
ParallelLogger	1.1.0
PatientLevelPrediction	3.0.6
SelfControlledCaseSeries	1.4.0
SelfControlledCohort	1.5.0
SqlRender	1.6.2



Figure 1:

라이선스

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이 책이 쓰여진 과정

이 책은 bookdown 패키지를 사용한 RMarkdown으로 쓰여졌다. 온라인 버전은 지속적 통합 시스템인 “travis”를 통해서 <https://github.com/OHDSI-Korea/TheBookOfOhdsiKorea>의 저장소를 사용해 자동작성 되었다. 이러한 온라인 버전은 정기적으로 스냅샷 형식으로 저장되며 이렇게 저장된 파일을 “에디션”이라 표기한다. 이 에디션들의 실물 책자들은 아마존에서 구입이 가능하다.

Part I

The OHDSI Community

Chapter 1

The OHDSI Community

Chapter leads: Patrick Ryan & George Hripcsak

함께 모이면 시작되고, 함께 지내면 진보하고, 함께 일하면 성공한다. -
헨리 포드

1.1 데이터에서 근거로의 여정 (The Journey from Data to Evidence)

의료 연구 기관 및 사설 의료 기관, 규제 기관 및 의료 제품 제조업체, 보험 회사 및 정책 기관, 그리고 환자와 의료 제공자 간의 모든 상호관계를 포함하는 전 세계 보건 의료의 어느 곳에서나 공통적인 과제가 있다. 어떻게 우리가 과거에서 배운 것을 토대로 미래를 위해 더 나은 결정을 내릴 수 있을 것인가?

10년이 넘도록, 많은 사람들이 **보건의료 체계 학습** (learning healthcare system)의 비전에 대해서 논의해 왔다. “그것은, 환자와 의료 제공자의 협력적인 보건 의료 선택에 있어 최상의 근거를 생성하고 적용하기 위함입니다. 또한 환자 치료의 자연스러운 발전을 도모하고, 보건의료의 혁신, 질, 안전 및 가치를 보장하기 위함입니다.”(Olsen et al., 2007) 이 원대한 계획의 주요한 요소는 일상적인 임상 치료 과정에서 수집된 환자 수준 (patient-level) 데이터를 분석하여 **실세계 근거** (real-world evidence) 를 생성할 수 있으며, 의료 시스템에 전파되어 실제의 임상에 정보를 제공 할 수 있으리라는 흥미로운 전망에 있다. 의학 연구소 (Institute of Medicine)의 근거 중심 의학 원탁회 (Roundtable on Evidence-Based Medicine) 가 발간한 2007년 보고서에서 “2020년까지 90%의 임상 결정이 정확하고, 시기 적절하고, 최신의 임상 정보에 의해 뒷받침 될 것이며, 그것은 가능한 최선의 근거를 반영할 것이다.”라고 예측했다.(Olsen et al., 2007) 비록 여러가지면에서 엄청난 발전이 있었지만, 우리는 여전히 이 위대한 열망에는 한참 미치지 못하고 있다.

무엇때문인가? 부분적으로는 환자 수준의 데이터에서 신뢰할만한 근거까지의 여정이 몹시 고되기 때문일 것이다. 데이터로부터 근거를 생성하는데에는 정해진 하나의 길이 없으며, 어떠한 지도도 그 길을 안내해주지 않는다. 사실, “데이터 (data)” 가

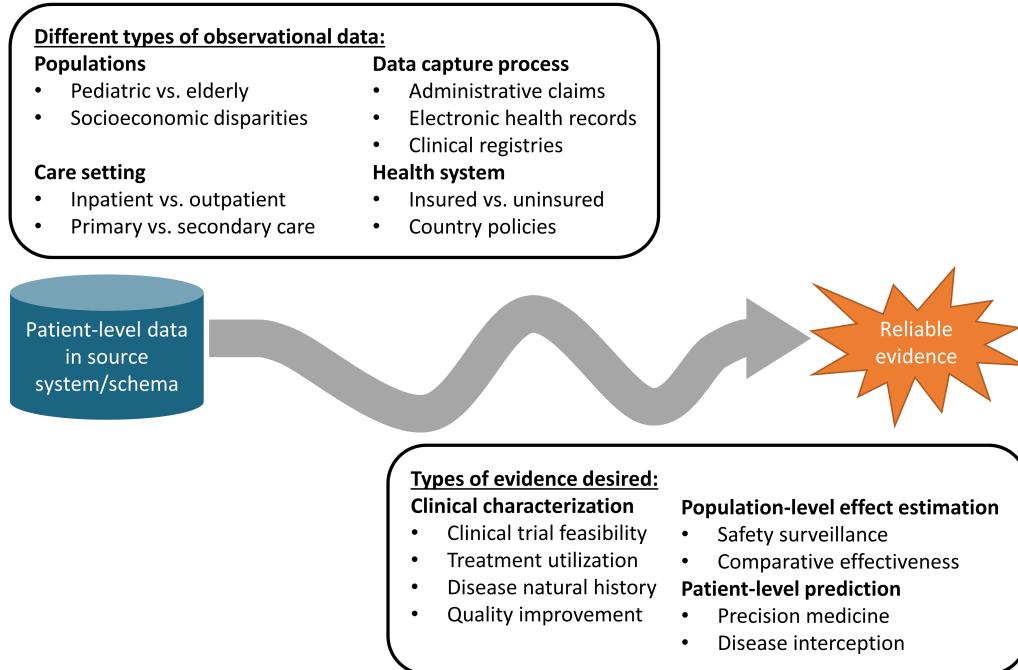


Figure 1.1: The journey from data to evidence

무엇인지, 그리고 “근거 (evidence)”가 무엇인지에 대한 통일된 관념도 존재하지 않는다.

원본 시스템에서 다양한 환자 수준의 데이터를 수집하는 여러 유형의 관찰 데이터 베이스 (observational database)가 있다. 이 데이터베이스는 서로 다른 의료 시스템 내부의 인구, 치료 설정 및 데이터 수집 프로세스의 이질성만큼 다양하다. 의사 결정에 도움이 될 수 있는 다양한 유형의 근거가 있으며, 환자 특성 분석 (clinical characterization), 인구 수준 추정 (population-level estimation) 및 환자 수준 예측 (patient-level prediction)으로 분류할 수 있다. 모집단 수준 영향 추정 및 환자 수준 예측의 분석 사용 사례로 분류 할 수 있습니다. 출발지 (원본 데이터) 및 원하는 목적지 (근거)와는 별도로, 여정을 수행하는 데 필요한 광범위한 임상, 과학 및 기술 역량들은 문제를 더욱 복잡하게 만든다. 보험 청구나 진료 과정이 데이터로 수집되면서 보건 정책이나 보험 환급과 관련된 행동 동기들로 인해 데이터 수집 및 정제 과정에서 발생할 수 있는 편향을 비롯하여, 환자와 의료 제공자간의 접점으로부터 원본 데이터가 발생하는 전반적인 과정에 대한 철저한 이해도 필요하다. 임상적 의문을 관련 해답을 도출하는 데 적합한 관찰 연구 설계으로 변환하기 위해선 역학 원칙과 통계적 방법을 숙지해야 한다. 수백만 명의 환자의 수년간의 종적 추적에 걸친 수십억 건의 임상 관찰을 가진 데이터셋에 대해 계산적으로 효율적인 데이터 과학 알고리즘을 구현하고 실행할 수 있는 기술적 능력 역시 필요하다. 관찰형 연구 통해 습득한 내용을 다른 종류의 근거와 통합하고, 이 새로운 지식이 건강 정책 및 임상 관행에 어떤 영향을 미칠지 결정하기 위해 임상 지식 또한 필요하다. 따라서, 한 개인이 데이터에서 근거를 성공적으로 만들어 내는 데 필요한 기술과 자원을 모두 보유하는 것은 매우 드문 일이다. 그보다는 이용 가능한 최선의 데이터를 가장 적

절한 방법으로 분석하여 모든 이해당사자들이 의사결정 과정에 신뢰하고 사용할 수 있는 근거를 생산하는, 데이터에서 근거까지의 이 여정을 위해서는 보통 여러 개인과 조직의 협력이 필요하다.

1.2 오몹 (**Observational Medical Outcomes Partnership, OMOP**)

협력 관찰형 연구 모델로써 주목할만한 예시로 오몹 (*Observational Medical Outcomes Partnership, OMOP*)이 있었다. 오몹은 미국의 식품의약국 (FDA)이 주관하고, 미국 국립 보건원 (National Institutes of Health) 관리하에 학술 연구자 및 보건 데이터 파트너와 협력하는 제약 회사의 컨소시엄으로 구성되었으며, 관찰형 보건의료 데이터를 이용하여 능동적 의료 제품 안전성 감시의 발전을 꾀하는 민관 협력체였다. (Stang et al., 2010) OMOP은 다수의 이해관계자 간의 거버넌스 구조를 확립했고, 다수의 청구자료 및 전자 의무 기록 데이터베이스에 적용하여 진정한 약물 안전성 연관성과 거짓 양성 소견을 식별할 수 있는 대안적인 역학 설계 및 통계 방법의 성능을 경험적으로 검증하는 일련의 방법론적 실험을 설계하였다. 분산되어 있는 관찰형 데이터 베이스를 통해 연구릴 진행함에 있어 기술적인 난제를 인식하고, 연구진들은 데이터의 구조, 내용 및 용어를 표준화하여 하나의 통계 분석 코드가 모든 데이터 파트너에서 사용될 수 있도록, OMOP 공통 데이터 모델 (Common Data Model, CDM) 을 설계하였다. (Overhage et al., 2012) OMOP 실험은 공통 데이터 모델과 표준화된 어휘를 확립하는 것이 가능하다는 것을 증명했다. 이는 서로 다른 관리 설정으로부터, 다른 용어 체계를 통해 다른 데이터 유형을 수용하고 하여 기관 간 협업과 효율적인 분석을 용이하게 할 수 있는 방식으로 구현되었다.

OMOP는 처음부터 연구 설계, 데이터 표준, 분석 코드, 경험적 결과 등 모든 작업 제품을 공공에 배포하여 투명성을 증진하고, OMOP가 수행하고 있는 연구에 대한 신뢰도를 쌓을 뿐 아니라, 또한 다른 이들의 연구 목적을 위하여 발전할 수 있도록 개방형 과학 (open science) 정책을 채택하였다. OMOP의 원래 초점은 약물 안전성이었지만, OMOP-CDM은 의료 처치와 보건 시스템 정책의 비교 효과성을 포함한 확대된 분석 사용 사례를 지원하기 위해 지속적으로 발전했다.

비록 OMOP이 대규모의 경험적 실험을 완성하는 데 성공하였고, (Ryan et al., 2012, 2013b) 방법론적인 혁신을 만들고, (Schuemie et al., 2014) 관찰형 데이터를 이용하여 안정성에 관련되어 의사결정에 유용한 지식 생성을 위한 적절한 방법론을 제시하였지만, (Madigan et al., 2013b,a) 이제 OMOP의 유산은 OHDSI 커뮤니티의 형성에 동기를 부여한 자극과 개방형 과학 원칙을 조기에 채택한 것으로 더 기억될 수 있다.

OMOP 프로젝트가 FDA의 능동 감시에 도움을 줄 숭 있는 관찰론적 연구를 완료하고 종료된 이후, 사람들은 OMOP 여정의 끝이, 새로운 여정의 시작이 되어야 된다고 생각했다. OMOP의 방법론적 연구가 관찰 데이터에서 생성되는 근거의 품질을 명시적으로 개선할 수 있는 과학적 모범 사례에 대한 가시적 통찰력을 제공함에도 불구하고, 그러한 모범 사례의 채택은 느렸다. 몇 가지 장애물들을 있었는데, 1) 방법론적의 혁신 이전에 관찰형 데이터 품질에 대한 근본적인 우려 2) 방법론적 문제와 해결책에 대한 불충분한 개념적 이해 3) 개별 데이터 파트너의 로컬 환경 내에서 솔루션을 독립적으로 구현할 수 없다는 점 4) 이러한 접근방식이 그들의 관심 임상

문제에 적용 가능한지에 대한 불확실성 등이었다. 이러한 모든 장애물에 대한 하나의 공통된 실마리는 한 사람만이 스스로 변화를 만드는 데 필요한 모든 것을 가지고 있지는 않지만, 여러 사람이 협력하면 이러한 문제들을 극복할 수 있다는 것이었다.

- 기초 데이터 품질에 대한 신뢰도를 높이며 구조, 콘텐츠 및 의미론의 일관성을 촉진하여 표준화된 분석이 가능하도록 개방형 커뮤니티의 (open community) 데이터 구조, 어휘 및 추출 변환 적재 (Extract-Transform-Load, ETL)의 표준 규약 구축을 위한 협업
- 약물 안전성 연구 외에도 clinical characterization, population-level effect estimation, patient-level prediction을 위한 보다 광범위한 모범 사례 (best practice)을 확립하기 위한 협업. 방법론적 연구를 통해 입증된 과학적 모범 사례 구현을 코드화하고 연구자들이 쉽게 채택할 수 있는 오픈 소스 분석 소프트웨어 개발에 대한 협업.
- 데이터에서 근거로의 여정을 인도해줄, 주요한 보건 문제에 대한 공동체 공통의 질문에 대한 임상적 적용에 대한 협업

이러한 통찰을 통해, 오딧세이 (OHDSI)가 태어났다.

1.3 개방형 협업 공동체로서의 오딧세이 (OHDSI as an Open-Science Collaborative)

OHDSI (Observational Health data Sciences and Informatics, 오딧세이)는 보다 더 나은 의료 결정과 더 나은 보건 관리를 촉진할 수 있는 과학적 근거를 공동으로 생성하도록 함으로써 보건 수준을 향상시키는 것을 목표로 하는 개방형 과학 공동체다. (Hripcsak et al., 2015) OHDSI는 관찰 건강 데이터의 적절한 사용에 대한 과학적 모범 사례를 확립하기 위한 방법론적 연구를 수행하고, 이러한 연구방법론을 일관되고 투명하며 재현 가능한 솔루션으로 코드화하는 오픈 소스 분석 소프트웨어를 개발하여, 보건의료 정책 및 환자 치료에 도움이 될 수 있는 임상적 근거를 마련하는데에 적용할 수 있도록 노력한다.

1.3.1 OHDSI의 사명 (Our Mission)

참여 공동체의 상호협력 하에 의료 발전을 촉진하는 근거를 생성하는 능력을 부여 한다.

To improve health by empowering a community to collaboratively generate the evidence that promotes better health decisions and better care.

1.3.2 OHDSI의 이상 (Our Vision)

의료 빅데이터의 분석을 통해 세계에 건강과 질병에 대한 포괄적인 이해를 제공한다.

A world in which observational research produces a comprehensive understanding of health and disease.

1.3.3 OHDSI의 핵심 가치 (Our Objectives)

- 혁신성 **Innovation**: 우리는 적극적으로 의료 빅데이터 분석 및 연구에 대한 혁신적인 방법론과 접근법을 찾고 격려한다.

Observational research is a field which will benefit greatly from disruptive thinking. We actively seek and encourage fresh methodological approaches in our work.

- 재현성 **Reproducibility**: 우리는 보건 증진을 위하여 정확하고, 재현 가능하며, 잘 보정된 근거를 찾도록 노력한다.

Accurate, reproducible, and well-calibrated evidence is necessary for health improvement.

- 공동체 정신 **Community**: 우리는 모든 참여자들을 환영하며 동등하게 우리의 활동에 참여할 수 있도록 돕는다.

Everyone is welcome to actively participate in OHDSI, whether you are a patient, a health professional, a researcher, or someone who simply believes in our cause.

- 개방성 **Openness**: 우리는 의사 결정 과정의 투명성을 지향하며, 우리의 진보 및 우리가 생성한 방법론, 소프트웨어, 근거를 가능한 공개적으로 접근 가능하게 한다.

We strive to make all our community's proceeds open and publicly accessible, including the methods, tools and the evidence that we generate.

- 협력 정신 **Collaboration**: 우리는 참여자들의 실제적 요구를 우선적으로 다루고, 그것을 위해 공동으로 노력한다.

We work collectively to prioritize and address the real world needs of our community's participants.

- 선행의 정신 **Beneficence**: 우리는 고통 받는 환자를 비롯하여 참여자 및 참여기관의 권리를 보호하기 위해 노력한다.

We seek to protect the rights of individuals and organizations within our community at all times.

1.4 오딧세이의 진척 (*OHDSI's Progress*)

OHDSI는 2014년 설립된 이래 성장을 지속하여 컴퓨터 과학, 역학, 통계, 생물 의학 정보학, 보건 정책 및 임상 의학 등 다양한 분야를 대표하는 학계, 의료 제품 산업, 규제 기관, 정부, 보험자, 기술 제공자, 의료 시스템, 임상의사 및 환자 집단 2,500명 이상의 다양한 이해관계자이 온라인 포럼에서 활동하고 있다. OHDSI 협력체로써 자발적으로 보고한 기관 및 데이터베이스의 리스트는 OHDSI 웹사이트에서 확인할



Figure 1.2: Map of OHDSI collaborators as of August, 2019

수 있다.¹ 오딧세이 협력 지도 (Figure 1.2) 는 폭넓은 국제 공동체로써의 다양성을 상기시킨다.

OHDSI는 OMOP-CDM이라는 개방형 공동체 데이터 표준 기반으로 2019년 8월 기준으로 20여개국, 100개 이상의 의료 데이터베이스들로 구성된 분산형 연구망 (distributed research network, DRN)을 구축했다. 분산형 연구망이란 환자 수준의 데이터를 개인이나 조직 간에 공유할 필요가 없다는 것을 의미한다. 분산연구망에서는, 데이터를 기관 폐쇄망 안에 두고 연구자는 프로토콜 형태의 분석코드/프로그램을 공유한다. 데이터 파트너들은 연구자의 요청에 따라 기관 안에서 연구 프로토콜을 실행해 자동으로 생성되는 요약 집합정보(평균, 합, 표준편차, 오즈비, 위험도 등)만 연구자에게 회신하는 방식으로, 연구자는 폐쇄망 안에 있는 환자의 개별 정보를 보거나 취득하지 않는다. OHDSI 분산망에서 각 데이터 파트너는 환자 수준 데이터의 사용에 대한 완전한 자율성을 유지하고, 각 기관의 데이터 거버넌스 정책을 지속적으로 준수한다.

OHDSI 개발자 커뮤니티는 3가지의 사용 사례를 지원하기 위해 OMOP CDM 위에 다음 3가지의 강력한 오픈 소스 분석 소프트웨어 라이브러리를 구축하였다.

- 1) Clinical characterization: 질병의 자연 경과, 치료 행태 및 질 향상을 위한 임상 특성 분석
- 2) Population-level effect estimation: 의약품 안전성 감시 및 비교 효과 연구에 서의 인과성 분석
- 3) Patient-level prediction: 머신러닝 알고리즘을 활용한 정밀 의학 또는 의료 개입

¹<https://www.ohdsi.org/who-we-are/collaborators/>

OHDSI 개발자들은 또한 OMOP CDM의 채택, 데이터 품질 평가, OHDSI 네트워크 연구의 촉진을 지원하는 애플리케이션을 개발했다. 이러한 소프트웨어에는 R과 Python에 내장된 백엔드 통계 패키지 및 HTML과 Javascript로 개발된 프론트엔드 웹 어플리케이션이 포함된다. 모든 OHDSI 소프트웨어들은 오픈 소스 정책을 채택하여 Github을 통해 공개된다.²

오픈 소스 소프트웨어들과 함께, OHDSI의 개방형 과학 공동체적 접근은 관찰형 연구의 발전을 가능하게 했다. 첫번째 OHDSI 네트워크 연구는 당뇨, 우울증, 고혈압의 3가지 만성 질병에 대한 치료 패턴을 분석하는 것이었다. PNAS(Proceedings of the National Academy of Science)에 출판된 연구는, 그 때까지 수행된 최대 규모의 관찰형 연구로써 11개의 데이터베이스에서 2억 5천만명의 환자 데이터를 이용하여 이전에 보고된 적 없는 치료 패턴의 지역적 차이 및 환자별 치료선택에 대한 이질성에 대해 발표하였다. (Hripcsak et al., 2016) OHDSI는 교란변수를 통제하는 새로운 통계적 방법론을 제시하였고, (Tian et al., 2018) 인과성 검증 능력에 대해 검증하였고, (Schuemie et al., 2018a) 이러한 방법론을 뇌전증 약제의 개별 안전성 연구 (Duke et al., 2017) 및 당뇨병의 이차 약제의 비교 효과 연구 (Vashisht et al., 2018) 및 우울증 치료의 대규모 비교 효과 연구 (Schuemie et al., 2018b)에 활용하였다. OHDSI 공동체는 또한 관찰형 보건의료 데이터의 머신러닝 알고리즘을 활용 프레임워크를 구축 (Reps et al., 2018) 하여 다양한 치료 분야에 활용하였다. (Johnston et al., 2019; Cepeda et al., 2018; Reps et al., 2019)

1.5 Collaborating in OHDSI

OHDSI는 근거를 생성하기 위해 협업을 강화하는 것을 목표로 하는 공동체인데, OHDSI 참가자가 된다는 것은 무엇을 의미하는가? 만약 당신이 OHDSI의 사명을 믿고 데이터에서 근거에 이르는 여성의 어디든지 기여를 하는 데 관심이 있다면, OHDSI는 당신을 위한 공동체가 될 수 있다. OHDSI 참가자는 보건 의료 데이터에 접근이 가능하고, 이를 활용해 의학적 근거를 생성하고 싶은 개인일 수 있다. OHDSI 참가자는 과학적 모범 사례를 수립하고 대안적 접근법을 평가하는 데 관심이 있는 방법론 연구자일 수 있다. OHDSI 참가자는 OHDSI의 타 연구자들이 사용할 수 있는 도구를 만들기 위해 프로그래밍 기술을 적용하는 데 관심이 있는 소프트웨어 개발자일 수 있다. OHDSI 참가자는 중요한 의학보건학적 질문을 가지고 있고 논문 발표 등을 통해 그러한 질문들에 대한 근거를 보다 더 큰 의료 커뮤니티에 제공하고자 하는 임상 연구자일 수 있다. OHDSI 참가자는 공공 보건을 위해 이러한 공통적인 사명과 가치를 믿고 해당 지역의 공동체가 OHDSI 관련 교육과 심포지엄 개최를 포함하여, 그 임무를 지속할 수 있도록 자원을 제공하는 개인 또는 단체일 수도 있다. 당신의 배경이나 소속과 관계없이, OHDSI는 개개인이 공동의 목적을 위해 함께 일할 수 있는 공동체가 되기를 추구하고 있으며, 각 개인이 공동으로 의료 서비스를 발전시킬 수 있는 기여를 하고 있다. 이 여성에 함께하고 싶다면, 챕터 2 (“Where To Begin”)를 통해 어떻게 시작하는 지 배울 수 있다.

²<https://github.com/OHDSI>



Figure 1.3: OHDSI International Symposium 2017 in Korea



Figure 1.4: OHDSI International Symposium 2017 in Korea

1.6 한국 오딧세이의 역사

아주대학교 박래웅 교수가 아주대 병원의 전자의무기록을 이용하여 2014년 OMOP-CDM 도입을 시작하였고, 2015년 첫 연례 심포지엄에서 활용 결과를 발표하면서 한국의 OHDSI 참여가 시작되었다. 이후 계속적으로 한국에서 OMOP-CDM, OHDSI 전파를 위해 노력하였고, 2016년부터는 최초로 국제 OHDSI committee에서 개별 국가를 위한 포럼 Korean chapter을 개설하고, 한국의 OHDSI 참여를 독려하였다. 첫 한국 국제 오딧세이 심포지엄은 2017년 3월 아주대학교에서 튜토리얼, 리더십 미팅을 포함하여 3일간 개최되었다.

한국 OHDSI 네트워크에 참여를 희망하는 병원 관계자들과 함께 2017년 3월 7일 첫번째 리더십 미팅을 가진 후 현재까지 2달마다 전국의 의과대학/병원을 순회하며 한국 OHDSI 리더십 미팅을 개최하며 OHDSI 전파 및 상호 협력을 꾀하고 있다.



Figure 1.5: Tutorial in the OHDSI International Symposium 2017

1.7 Summary



- OHDSI의 사명은 참여 공동체의 상호협력 하에 의료 발전을 촉진하는 근거를 생성하는 능력을 부여하는 것이다.
- OHDSI의 이상은 혁신성, 재현성, 공동체 정신, 개방성, 협력 정신, 선행의 정신을 바탕으로 의료 빅데이터의 분석을 통해 세계에 건강과 질병에 대한 포괄적인 이해를 제공하는 것이다.
- OHDSI 참가자들은 개방형 공동체로서의 데이터 표준, 방법론 연구, 오픈 소스 분석 소프트웨어 개발 및 임상적 적용을 통해 데이터로부터 근거로의 여정을 발전시키고자 노력한다.

Chapter 2

Where to Begin

Chapter leads: Hamed Abedtash & Kristin Kostka

“A journey of a thousand miles begins with a single step.” - Lao Tzu

The OHDSI community represents a mosaic of stakeholders across academia, industry and government-entities. Our work benefits a range of individuals and organizations, including patients, providers, and researchers, as well as health care systems, industry, and government agencies. This benefit is achieved by improving both the quality of healthcare data analytics as well as the usefulness of healthcare data to these stakeholders. We believe observational research is a field which benefits greatly from disruptive thinking. We actively seek and encourage fresh methodological approaches in our work.

2.1 Join the Journey

Everyone is welcome to actively participate in OHDSI, whether you are a patient, a health professional, a researcher, or someone who simply believes in our cause. OHDSI maintains an inclusive membership model. To become an OHDSI collaborator requires no membership fee. Collaboration is as simple as raising a hand to be included in the yearly OHDSI membership count. Involvement is entirely at-will. A collaborator can have any level of contribution within the community, ranging from someone who attends weekly community calls to leading network studies or OHDSI working groups. Collaborators do not have to be data holders to be considered active members of the community. The OHDSI community aims to serve data holders, researchers, health care providers and patients & consumers alike. A record of collaborator profiles are maintained and periodically updated on the OHDSI website. Membership is fostered via OHDSI community calls, workgroups and regional chapters.

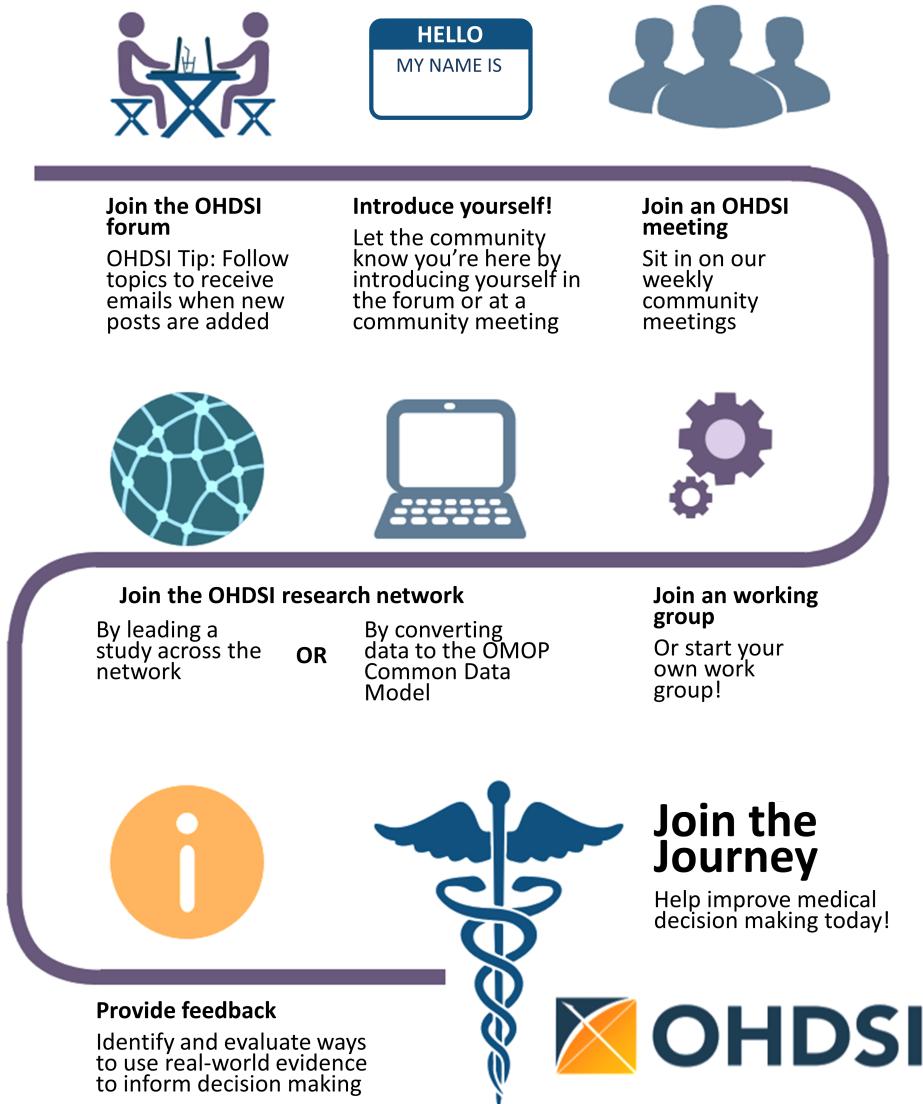


Figure 2.1: Join the journey - How to become an OHDSI collaborator.

2.1.1 OHDSI Forums

The OHDSI Forums¹ is an online discussion site where OHDSI Community Collaborators can hold conversations in the form of posted messages. The forums consist of a tree-like directory structure. The top end is “Categories”. The forums can be divided into categories for the relevant discussions. Under the categories are sub-forums and these sub-forums can further have more sub-forums. The topics (commonly called threads) come under the lowest level of sub-forums and these are the places under which forums members can start their discussions or posts.

In the OHDSI forums, you can find categories of content including:

- **General:** for general discussion about the OHDSI community and how to get involved
- **Implementers:** for discussion about how to implement the Common Data Model and OHDSI analytics framework in your local environment
- **Developers:** for discussion around open-sourced development of OHDSI applications and other tools that leverage the OMOP CDM
- **Researchers:** for discussion around CDM-based research, including evidence generation, collaborative research, statistical methods and other topics of interest to the OHDSI Research Network
- **CDM Builders:** for discussion of ongoing CDM development, including requirements, vocabulary, and technical aspects
- **Vocabulary Users:** for discussion around vocabulary content
- **Regional Chapters (e.g. Korea, China, Europe):** for regional discussions in their native languages related to local OMOP implementations and OHDSI community activities

To begin posting your own topics, you will need to sign up for an account. Once you have a forums account, you are encouraged to introduce yourself on the General Topic under the thread called “Welcome to OHDSI! - Please introduce yourself”. You are invited to reply and 1) Introduce yourself and tell us a bit about what you do and 2) Let us know how you’d like to help out in the community (ex. software development, run studies, write research papers, etc). Now you are on your OHDSI Journey! From here, you are encouraged to join in the discussion. The OHDSI Community encourages using the Forums as your way to ask questions, discuss new ideas and collaborate.



You can select topics to “watch.” What this means is whenever a new post is added in a topic you’re watching, you will receive an email and be able to reply to the post directly through your email. Watch the general thread to receive details about upcoming meeting agendas, collaboration opportunities and have the weekly OHDSI digest delivered directly to your inbox!

¹<http://forum.ohdsi.org>

2.1.2 OHDSI Events

OHDSI regularly holds in-person events to provide opportunities for collaborators to learn from each other and connect to foster future collaborations. These events are communicated on the OHDSI website, and are free for anyone interested in attending.

OHDSI Symposia are scientific conferences, held annually in US, Europe, and Asia, where collaborators can present their latest research through plenary talks, poster presentations, and software demonstrations. OHDSI Symposia provide a great venue for networking and to learn about the most recent progress across the community. OHDSI Symposia are generally accompanied by OHDSI tutorials, taught by fellow OHDSI collaborators as the course faculty, which provide community newcomers the opportunity for hands-on engagement on topics around data standards and analysis best practices. These tutorials are generally video-recorded and made available on the OHDSI website after the events for those who can't make it in person.

OHDSI Collaborator face-to-face events are smaller fora which are typically centered on a problem of shared interest to focus on during the time together. Past events have included a phenotype hack-a-thon, and data quality hack-a-thon, and open-source software documentation-a-thon. OHDSI has hosted multiple Study-a-thon events, where the goal of the multi-day session is to collaborate as a team on a particular research question by designing and implementing an appropriate observational analysis, executing the study across the OHDSI network, and synthesizing the evidence for public dissemination. In all of these events, there is a shared desire to solve a common problem but also a shared interest in providing a welcoming environment that encourages learning and continuous improvement on the process of collaborative problem-solving.

Learn more about the power of the OHDSI Community. Explore past symposiums, face-to-face meetings and watch OHDSI tutorials by visiting the OHDSI Past Events section on the OHDSI website. Past Events is updated regularly to archive community events.

2.1.3 OHDSI Community Calls

OHDSI Community Calls are a weekly opportunity to spotlight ongoing activity within the OHDSI community. Held every Tuesday from 12-1pm ET, these teleconferences are a time for the OHDSI community to come together to share recent developments and recognize the accomplishments of individual collaborators, working groups and the community as a whole. Each week's meeting is recorded, and presentations are archived in the OHDSI website resources.

All OHDSI Collaborators are welcome to participate in this weekly teleconference and encouraged to propose topics for community discussion. OHDSI Community Calls can be a forum to share research findings, present and seek feedback for active

works-in-progress, demonstrate open-source software tools under development, debate community best practices for data modeling and analytics, and brainstorm future collaborative opportunities for grants/publications/conference workshops. If you are a Collaborator with a topic for an upcoming OHDSI Collaborator meeting, you are invited to post your thoughts on the OHDSI Forums.

As a newcomer to the OHDSI community, it is encouraged to add this call series to your calendar to get acquainted with what is happening across the OHDSI network. If you would like to join an OHDSI call, please consult the OHDSI wiki. Community call topics vary from week-to-week. You can also consult the OHDSI Weekly Digest on the OHDSI forum for more information on weekly presentation topics. Newcomers are invited to introduce themselves on their first call and tell the community about themselves, their background and what brought them to OHDSI.

2.1.4 OHDSI Workgroups

OHDSI has a variety of ongoing projects lead by workgroup teams. Each workgroup has its own leadership team which determine the project's objectives, goals and artifacts to be contributed to the community. Workgroup participation is open to all who have an interest in contributing to the project objectives and goals. Workgroups may be long-standing, strategic objectives or short-term projects to accomplish a specific need in the community. Workgroup meeting cadence is determined by the project leadership and will vary from group to group. A list of the active workgroups is maintained on the OHDSI Wiki.

Table 2.1 provides a quick reference to active OHDSI workgroups. You are encouraged to join a call and learn more.

Table 2.1: Notable OHDSI Workgroups

Workgroup Name	Objective	Target Audience
Atlas & WebAPI	Atlas and WebAPI are part of the OHDSI open-source software architecture that aim to provide standardized analytic capabilities built on the foundation of the OMOP Common Data Model.	Java & JavaScript developers aiming to contribute to the open-source Atlas/WebAPI platform
CDM & Vocabulary	To continue to develop the OMOP Common Data Model for the purpose of systematic, standardized and large-scale analytics applied to clinical patient data. To improve the quality of the Standardized Vocabularies by increasing their coverage of international coding systems and clinical aspects of patient care in order to support the standardized analytics developed by other working groups.	Any who has an interest in improving the OMOP Common Data Model and Standardized Vocabularies to meet all needs and use cases

Workgroup Name	Objective	Target Audience
Genomics	Expand the OMOP CDM to incorporate genomic data from patients. The group will define a CDM-compatible schema that can store information for genetic variants from various sequencing process.	Open to all
Population Level	Develop scientific methods for observational research leading to population level estimates of effects that are accurate, reliable, and reproducible, and facilitate the use of these methods by the community.	Open to all
Natural Language Processing	To promote the use of textual information from Electronic Health Records (EHRs) for observational studies under the OHDSI umbrella. To facilitate this objective, the group will develop methods and software that can be implemented to utilize clinical text for studies by the OHDSI community.	Open to all

Workgroup Name	Objective	Target Audience
Patient-Level Prediction	<p>establish a standardized process for developing accurate and well-calibrated patient-centered predictive models that can be utilized for multiple outcomes of interest and can be applied to observational healthcare data from any patient subpopulation of interest</p>	Open to all
Gold Standard Phenotype Library	<p>To enable members of the OHDSI community to find, evaluate, and utilize community-validated cohort definitions for research and other activities</p>	Open to all with an interest in curation and validation of phenotypes

Workgroup Name	Objective	Target Audience
FHIR Workgroup	To establish the padmap for the OHDSI FHIR integration and to make recommendations to the broader community for leveraging the FHIR implementation and data in EHR community for the OHDSI-based observation studies and for disseminating the OHDSI data and research results through the FHIR-based tools and APIs.	Open to all with an interest in interoperability
GIS	Expand the OMOP CDM and leverage OHDSI tools so that patients' environmental exposure histories can be related to their clinical phenotypes	Open to all with an interest in health-related geographic attributes
Clinical Trials	Understand clinical trial use cases where the OHDSI platform & ecosystem can aid trials in any aspect, and assist in driving updates in OHDSI tools to support.	Open to all with an interest in clinical trials

Workgroup Name	Objective	Target Audience
THEMIS	The objective of THEMIS is to develop standard conventions, above and beyond the OMOP CDM conventions, to ensure ETL protocols designed at each OMOP site are of highest quality, reproducible and efficient.	
Metadata	Our goal is to define & a standard process	Open to all
Annotations	for storing human- and machine-authored metadata and annotations in the Common Data Model to ensure researchers can consume and create useful data artifacts about observational data sets.	
Patient Generated Health Data (PGHD)	The goal of this WG would be developing ETL conventions, integration process with clinical data, and analytic process for PGHD, which is generated through Smart Phone/App/Wearable devices.	Open to all

Workgroup Name	Objective	Target Audience
Women of OHDSI	To provide a forum for women within the OHDSI community to come together and discuss challenges they face as women working in science, technology, engineering and mathematics (STEM). We aim to facilitate discussions where women can share their perspectives, raise concerns, propose ideas on how the OHDSI community can support women in STEM, and ultimately inspire women to become leaders within the community and their respective fields.	Open to all who identify with this mission

Workgroup Name	Objective	Target Audience
Steering Committee	To uphold OHDSI's mission vision and values by ensuring all OHDSI activities and events are aligned with the needs of our growing community. In addition, the group serves as an advisory group for the OHDSI coordinating center based at Columbia by providing guidance for OHDSI's future direction.	Leaders within the community

2.1.5 OHDSI Regional Chapters

An OHDSI regional chapter represents a group of OHDSI collaborators located in a geographic area who wish to hold local networking events and meetings to address problems specific to their geographic location. Today, OHDSI regional chapters include OHDSI in Europe², OHDSI in South Korea³ and OHDSI in China.⁴ If you would like to set-up an OHDSI regional chapter in your region, you may do so by following the OHDSI regional chapter process outlined on the OHDSI website.

2.1.6 OHDSI Research Network

Many OHDSI collaborators are interested in converting their data into the OMOP Common Data Model. The OHDSI research network represents a diverse, global community of observational databases that have undergone Extract-Transform-Load (ETL) processes to become OMOP compliant. If your journey in the OHDSI community includes transforming data, there are numerous community resources available to aid you in your journey including tutorials on the OMOP CDM and Vocabularies, freely available tools to assist with conversion, and workgroups targeting specific domains or types of data conversions. The OHDSI collaborators

²<https://www.ohdsi-europe.org/>

³<http://forums.ohdsi.org/c/For-collaborators-wishing-to-communicate-in-Korean>

⁴<https://ohdsichina.org/>

are encouraged to utilize the OHDSI forum to discuss and troubleshoot challenges that arise during CDM conversions.

2.2 Where You Fit In

By now, you may be wondering: *where do I fit into the OHDSI Community?*

I am a clinical researcher looking to start a study. If you are a clinical researcher interesting in using the OHDSI Research Network to answer a specific question – maybe even publish a paper – you’re in the right place. You can start by posting your idea to the OHDSI Researchers Topic on the OHDSI Forum. This will help you connect with researchers of similar interest. OHDSI loves to publish and has many resources available to expedite turning your research question into an analysis and a paper. You can find more information in Chapters 11, 12, and 13.

I want to read and consume the information the OHDSI community is produce. Whether you’re a patient, a practicing clinician or subject matter expertise in healthcare, OHDSI wants to provide you with high quality evidence to help you better understand health outcomes. Maybe it’s been a while since you have written code. Maybe you never program. You have a place in this community. We call you an *evidence consumer* – you are the individuals who are turning OHDSI research into action. You are sifting through to know what evidence OHDSI has generated and is generating, possibly also wanting to suggest questions relevant for you. We welcome you to join the discussion. Start asking questions on the OHDSI Forum. Attend Community Calls and hear about the latest research. Attend the OHDSI Symposiums and Face-to-Face Meetings to engage directly with the community. Your questions are an important part of the OHDSI community. Speak up and help us learn more about what evidence you are searching for!

I work in a healthcare leadership role. I may be a data owner and/or represent one. I am evaluating the utility of the OMOP CDM and OHDSI analytical tools for my organization. As an administrator/leader of an organization, you may have heard about OHDSI and are curious to know the OMOP CDM could work for your use cases. You may start by looking through OHDSI Past Events materials to see the body of research. You may join a Community Call and simply listen in. You may also find that Chapter 7 (Data Analytics Use Cases) helps you understand the kind of research the OMOP CDM and OHDSI analytics tools can enable. The OHDSI Community is here for you in your journey. Don’t be afraid to speak up and ask for examples if you have specific areas you’re interested in. More than 200 organizations around the world are collaborating in OHDSI, there’s plenty of success stories to help showcase the value of this community.

I am a database administrator looking to ETL/convert my institution’s data to the OMOP CDM. Choosing to “OMOP” your data is a novel and

worthwhile undertaking. If you’re just starting out on your ETL process, consult the OHDSI Community ETL Tutorial Slides or sign-up for the next offering at an upcoming OHDSI Symposium. Consider dialing into the THEMIS workgroup calls and engaging the OHDSI Forum with your questions. You will find a wealth of knowledge in the community who are interested in helping your successful implementation of the OMOP CDM. Don’t be shy!

I am a biostatistician and/or methods developer interested in contributing to the OHDSI tool stack. You’re savvy in R. You know how to commit to Git. Most of all, you’re eager to bring your expertise to the OHDSI Methods Library and further develop these methodologies. You’ll want to start by joining either the Population-Level Estimation or Patient Level Prediction workgroup calls to hear more about current community priorities. As you’re using the OHDSI tools, you can also file Issues under the respective GitHub repo (e.g. if it is a SQL Render package problem, you would file under the GitHub Repo for OHDSI/SqlRender). We welcome your contributions!

I am a software developer interested in building a tool that complements the OHDSI tool stack. Welcome to the community! As part of the OHDSI mission, our tools are open source and governed under Apache licenses. You are welcome to develop solutions that complement the OHDSI tool stack. Feel free to join a workgroup and pitch your ideas. Please be mindful that OHDSI is heavily invested in open-science and open collaboration. Proprietary algorithms and software solutions are welcome but are not the main focus of our software development efforts.

I am a consultant looking to advise the OHDSI Community. Welcome to the community! Your expertise is valuable and appreciated. You are welcome to promote your services on the OHDSI Forum, as appropriate. You’re invited to join us at OHDSI Tutorials and consider giving back by contributing your expertise in the Symposium proceedings and OHDSI face-to-face meetings throughout the year.

I am a student looking to learn more about OHDSI. You’re in the right place! Consider joining an OHDSI Community Call and introducing yourself. You are encouraged to delve into the OHDSI tutorials, attend OHDSI Symposia and face-to-face meetings to learn more about the methods and tools the OHDSI community offers. If you have a specific research interest, let us know by posting in the Researcher topic on the OHDSI Forum. Many organizations offer OHDSI sponsored research opportunities (e.g. post-Doc, research fellowships). The OHDSI Forum will give you the latest information on these opportunities and more.

2.3 Summary



- Getting started in the OHDSI Community is as easy as saying hello!
- Post on the **OHDSI Forum** and join a Community Call.
- Post your research or ETL questions to the OHDSI Forum.

Chapter 3

Open Science

Chapter lead: Kees van Bochove

From the inception of the OHDSI community, the goal was to establish an international collaborative by building on open-science values, such as the use of open-source software, public availability of all conference proceedings and materials, and transparent, open-access publication of generated medical evidence. But what exactly is open-science? And how could OHDSI build an open-science or open-data strategy around medical data, which is very privacy-sensitive and typically not open for good reasons? Why is it so important to have reproducibility of analysis, and how does the OHDSI community aim to achieve this? These are some of the questions that we touch on in this chapter.

3.1 Open Science

The term ‘open science’ has been used since the nineties, but it really gained traction in the 2010s, during the same period OHDSI was born. Wikipedia (Wikipedia, 2019a) defines it as “the movement to make scientific research (including publications, data, physical samples, and software) and its dissemination accessible to all levels of an inquiring society, amateur or professional,” and goes on to state that it is typically developed through collaborative networks. Although the OHDSI community never positioned itself explicitly as an ‘open-science’ collective or network, the term is frequently used to explain the driving concepts and principles behind OHDSI. For example, in 2015, Jon Duke presented OHDSI as “An Open Science Approach to Medical Evidence Generation,”¹ and in 2019, the EHDEN consortium’s introductory webinar hailed the OHDSI network approach as “21st Century Real World Open Science.”² Indeed, as we shall see in this chapter, many of the practices of open-science can be found in today’s OHDSI community. One

¹https://www.ohdsi.org/wp-content/uploads/2014/07/ARM-OHDSI_Duke.pdf

²<https://www.ehdeneu/webinars/>

could argue that the OHDSI community is a grassroots open-science collective driven by a shared desire for improving the transparency and reliability of medical evidence generation.

Open-science or “Science 2.0” (Wikipedia, 2019b) approaches mean to address a number of perceived problems within the current scientific practice. Information technology has led to an explosion of data generation and analysis methods, and for individual researchers, it is very hard to keep up with all literature published in their area of expertise. This holds even more true for medical doctors who have a practice to run as their day job, but still need to keep abreast of the latest medical evidence. In addition, there is growing concern that many experiments may suffer from poor statistical designs, publication bias, p-hacking and similar statistical problems, and are hard to reproduce. The traditional method of correcting these concerns, peer review of published articles, often fails to identify and tackle these problems. The special 2018 Nature edition on “Challenges in irreproducible research”³ includes several examples of this. A group of authors attempting to apply systematic peer review on the articles in their field found that, for various reasons, it was very hard to get the errors they identified rectified. Experiments that have a flawed design to begin with are especially hard to correct. In the words of Ronald Fisher: “To consult the statistician after an experiment is finished is often merely to ask him to conduct a post mortem examination. He can perhaps say what the experiment died of.” (Wikiquote, 2019) The authors encountered common statistical problems such as poor randomization designs leading to false conclusions about statistical significance, miscalculations in meta-analyses, and inappropriate baseline comparisons. (Allison et al., 2016) Another paper from the same collection, taking experiences from physics as an example, argues that it is critical to not only provide access to the underlying data, but also to publish and properly document the data processing and analysis scripts to achieve full reproducibility. (Chen et al., 2018)

The OHDSI community addresses these challenges in its own way, and it puts significant emphasis on the importance of generating medical evidence at scale. As stated in Schuemie et al. (2018b), while the current paradigm “centers on generating one estimate at a time using a unique study design with unknown reliability and publishing (or not) one estimate at a time,” the OHDSI community “advocates for high-throughput observational studies using consistent and standardized methods, allowing evaluation, calibration and unbiased dissemination to generate a more reliable and complete evidence base.” This is achieved by a combination of a network of medical data sources that map their data to the OMOP common data model, open source analytics code that can be used and verified by all, and large-scale baseline data such as the condition occurrences published at howoften.org. In the following paragraphs, concrete examples are provided and the open-science approach of OHDSI is detailed further using the four principles of Open Standards, Open Source, Open Data and Open Discourse as a guide. The chapter is concluded

³<https://www.nature.com/collections/prbfkwmwvz>

with a brief reference to the FAIR principles and outlook for OHDSI from an open-science perspective.

3.2 Open-Science in Action: the Study-a-Thon

A recent development in the community is the emergence of ‘study-a-thons’: short, concentrated face-to-face gatherings of a multidisciplinary group of scientists aimed at answering an important, clinically relevant research question using the OMOP data model and the OHDSI tools. A nice example is the 2018 Oxford study-a-thon, which is explained in an EHDEN webinar⁴ that provides a walkthrough of the process and also highlights the openly available results. In the period leading up to the study-a-thon, the participants propose medically relevant research questions to study, and one or more research questions are selected to study during the study-a-thon itself. Data is provided through participants that have access to patient-level data in OMOP format and are able to run queries on these data sources. Much of the actual study-a-thon time is devoted to discussing the statistical approach (see also chapter 2), the suitability of the data sources, the results which are interactively produced and the follow-up questions that are inevitably raised by these results. In the case of the Oxford study-a-thon, the questions centered around studying adverse post-surgical effects of different knee replacement methods, and the results were published interactively during the study-a-thon using the OHDSI forums and tools (see chapter 8). The OHDSI tools such as ATLAS facilitate rapid creation, exchange, discussion and tests of cohort definitions, which greatly speeds up the initial process of achieving consensus on problem definition and choice of methods. Thanks to the usage of the OMOP Common Data Model by the involved data sources and the availability of the OHDSI open source patient level prediction packages 13, it was possible to create a prediction model for 90-day post-operative mortality in one day, and validate the model externally in several large data sources the day after. The study-a-thon also resulted in a traditional scholarly paper (Development and validation of patient-level prediction models for adverse outcomes following total knee arthroplasty, Ross Williams, Daniel Prieto-Alhambra et al., manuscript in preparation), which took months to process through peer review. But the fact that the analysis scripts and results for several healthcare databases covering hundreds of millions of patient records were conceived, produced and published from scratch within a week illustrates the fundamental improvements OHDSI can bring to medical science, reducing the turnaround time for evidence to become available from months to days.

3.3 Open Standards

A very significant community resource that is maintained in the OHDSI community is the OMOP Common Data Model (see chapter 4) and associated Standardized

⁴<https://youtu.be/X5yuoJoL6xs>

Vocabularies (see chapter 5). The model itself is scoped to capture observational healthcare data, and it was originally meant to analyze associations between exposures such as drugs, procedures, devices, etc., and outcomes such as conditions and measurements. It has been extended for various analysis use cases (see also 7). However, harmonizing healthcare data worldwide from a wide variety of coding systems, healthcare paradigm and different types of healthcare sources requires a massive amount of ‘mappings’ between source codes and their closest standardized counterparts. The OMOP Standardized Vocabulary is further described in chapter 7 and includes mappings from hundreds of medical coding systems that are used worldwide, and is browsable through the OHDSI Athena tool. By providing these vocabularies and mappings as a freely available community resource, OMOP and the OHDSI community make a significant contribution to healthcare data analytics and is, by several accounts, the most comprehensive model for this purpose, representing approximately 1.2 billion healthcare records worldwide.⁵ (Garza et al., 2016)

3.4 Open Source

Another key resource the OHDSI community provides are open source programs. These can be divided in several categories, such as the helper tools to map data to OMOP (see chapter 6), the OHDSI Methods Library which contain a powerful suite of commonly used statistical methods, open source code for published observational studies, and ATLAS, Athena and other infrastructure-related software which underpins the OHDSI ecosystem (see chapter 8). From an open-science perspective, one of the most important resources is the code for the actual execution of studies, such as studies from the OHDSI Research Network (see chapter 20). In turn, these programs leverage the fully open source OHDSI stack, which can be inspected, reviewed and contributed to via GitHub. For example, network studies often build on the Methods Library, which ensures a consistent re-use of statistical methods across analytical use cases. See chapter 17 for a more detailed overview of how the use of and collaboration on open source software in OHDSI ultimately underpins the quality and reliability of the generated evidence.

3.5 Open Data

Because of the privacy-sensitive nature of healthcare data, fully open, comprehensive patient-level datasets are typically not available. However, it is possible to leverage OMOP mapped datasets to publish important aggregated data and results sets, such as the earlier mentioned <http://howoften.org> and other public result sets that are published to <http://data.ohdsi.org>. Also, the OHDSI community provides simulated datasets such as SynPUF for testing and development purposes, and the OHDSI Research Network (see 20) can be leveraged to run studies in a network of

⁵<https://www.ema.europa.eu/en/events/common-data-model-europe-why-which-how>

available datasources that have mapped their data to OMOP. In order to make the mapping between the source data and the OMOP CDM transparent, it is encouraged for data sources to re-use the OHDSI ETL or ‘mapping’ tools and publish their mapping code as open source as well.

3.6 Open Discourse

Open standards, open source and open data are great assets, but left by themselves, they will not impact medical practice. Key to the open-science practice and impact of OHDSI is the implementation of medical evidence generation and the translation of the science to medical practice. The OHDSI community has several annual OHDSI Symposia, held in the United States, Europe, and Asia as well as dedicated communities of practice in, amongst others, China and Korea. These symposia discuss the advancements in statistical methods, data and software tooling, the standardized vocabularies, and all other aspects of the OHDSI open source community. The OHDSI forums⁶ and wiki⁷ facilitate thousands of researchers worldwide in practicing observational research. The community calls⁸ and the code, issues and pull requests in Github⁹ constantly evolve the open-community assets such as code and the CDM, and in the OHDSI Network Studies, global observational research is practiced in an open and transparent way using hundreds of millions of patient records worldwide. Openness and open discourse is encouraged throughout the community, and this very book is written via an open process facilitated by the OHDSI wiki, community calls and a GitHub repository.¹⁰ It needs to be stressed however that without all the OHDSI collaborators, the processes and tools would be empty shells. Indeed, one could argue that the true value of the OHDSI community is with its members, who share a vision of improving health through collaborative and open-science, as discussed in Chapter 1.

3.7 OHDSI and the FAIR Guiding Principles

3.7.1 Introduction

This last paragraph of the chapter takes a look at the current state of the OHDSI community and tooling, using the FAIR Data Guiding Principles published in Wilkinson et al. (2016).

⁶<https://forums.ohdsi.org>

⁷<https://www.ohdsi.org/web/wiki>

⁸<https://www.ohdsi.org/web/wiki/doku.php?id=projects:overview>

⁹<https://github.com/ohdsi>

¹⁰<https://github.com/OHDSI/TheBookOfOhdsi>

3.7.2 Findability

Any healthcare database that is mapped to OMOP and used for analytics should, from a scientific perspective, persist for future reference and reproducibility. The use of persistent identifiers for OMOP databases is not yet widespread, partly because these databases are often contained behind firewalls and on internal networks and not necessarily connected to the internet. However, it is entirely possible to publish summaries of the databases as a descriptor record that can be referenced for e.g. citation purposes. This method is followed in for example the EMIF catalog¹¹, which provides a comprehensive record of the database in terms of data-gathering purpose, sources, vocabularies and terms, access control mechanisms, license, consents, etc. (Oliveira et al., 2019) This approach is further developed in the IMI EHDEN project.

3.7.3 Accessibility

Accessibility of OMOP mapped data through an open protocol is typically achieved through the SQL interface, which combined with the OMOP CDM provides a standardized and well-documented method for accessing OMOP data. However, as discussed above, OMOP sources are often not directly available over the internet for security reasons. Creating a secure worldwide healthcare data network that is accessible for researchers is an active research topic and operational goal of projects like IMI EHDEN. However, results of analyses in multiple OMOP databases, as shown through OHDSI initiatives such as LEGEND and <http://howoften.org>, can be openly published.

3.7.4 Interoperability

Interoperability is arguably the strong suit of the OMOP data model and OHDSI tooling. In order to build a strong network of medical data sources worldwide which can be leveraged for evidence generation, achieving interoperability between healthcare data sources is key, and this is achieved through the OMOP model and Standardized Vocabularies. However, by sharing cohort definitions and statistical approaches, the OHDSI community goes beyond code mapping and also provides a platform to build an interoperable understanding of the analysis methods for healthcare data. Since healthcare systems such as hospitals are often the source of record for OMOP data, the interoperability of the OHDSI approach could be further enhanced by alignment with operational healthcare interoperability standards such as HL7 FHIR, HL7 CIMI and openEHR. The same is true for alignment with clinical interoperability standards such as CDISC and biomedical ontologies. Especially in areas such as oncology, this is an important topic, and the Oncology Working Group and Clinical Trials Working Group in the OHDSI community provide good examples of forums where these issues are actively discussed. In terms of references to other data and specifically ontology terms,

¹¹<https://emif-catalogue.eu>

ATLAS and OHDSI Athena are important tools, as they allow the exploration of the OMOP Standardized Vocabularies in the context of other available medical coding systems.

3.7.5 Reusability

The FAIR principles around reusability focus on important issues such as the data license, provenance (clarifying how the data came in existence) and the link to relevant community standards. Data licensing is a complicated topic, especially across jurisdictions, and it would fall outside of the scope of this book to cover it extensively. However, it is important to state that if you intend for your data (e.g. analysis results) to be freely used by others, it is good practice to explicitly provide these permissions via a data license. This is not yet a common practice for most data that can be found on the internet, and the OHDSI community is unfortunately not an exception here. Concerning the data provenance of OMOP databases, potential improvements exist for making meta-data available in an automated way, including, for example, CDM version, Standardized Vocabularies release, custom code lists, etc. The OHDSI ETL tools do not currently produce this information automatically, but working groups such as the Data Quality Working Group and Metadata Working Group actively work on these. Another important aspect is the provenance of the underlying databases itself; it is important to know if a hospital or GP information system was replaced or changed, and when known data omissions or other data issues occurred historically. Exploring ways to attach this metadata systematically in the OMOP CDM is the domain of the Metadata Working Group.



- The OHDSI community can be seen as an open-science community that is actively pursuing the interoperability and reproducibility of medical evidence generation.
- It also advocates a paradigm shift from single study and single estimate medical research to large-scale systematic evidence generation, where facts such as baseline occurrence are known and the evidence focuses on statistically estimating the effects of interventions and treatments from real world healthcare sources.

Part II

Uniform Data Representation

Chapter 4

공통 데이터 모델

챕터 책임자: *Clair Blacketer*

관찰 데이터는 환자가 의료 혜택을 받는 동안 어떤 일들이 일어나는지를 보여준다. 전 세계적으로 점점 더 많은 수의 환자에 대한 데이터가 빅 데이터라고 불리는 형태로 수집 및 저장되고 있다. 이러한 수집의 목적은 다음과 같은 세 가지로 설명할 수 있다. (i) 직접적으로 (많은 경우에 설문 조사 및 레지스트리 정보를 활용한) 연구를 용이하게 하기 위해, (ii) 의료 행위 수행을 지원하기 위해 (이를 보통 EHR - Electronic Health Records이라고 함), 또는 (iii) 의료비 지불 관리를 위함 (청구 데이터). 세 가지 목적 모두 임상 연구에 보편적으로 사용되고, 아래 두 항목은 이차적인 목적으로 사용하는 데이터로 사용되며, 모두 일반적으로 고유한 내용의 형식 및 인코딩으로 이루어져 있다.

관찰형 의료 데이터 (Observational healthcare data)에 공통 데이터 모델이 필요한 이유는 무엇일까?

일차적인 목적에 의해 모든 임상적인 사건들을 동일하게 포착하는 관찰형 데이터베이스 (Observational database)는 없다. 따라서, 여러 다른 데이터 출처에서 연구 결과를 도출하고 데이터를 포착하는 과정에서 발생하는 잠재적인 치우침 (bias)의 영향을 이해하기 위해 이를 비교 및 대조해야 한다. 또한 통계적 검증력을 갖춘 결론을 도출하려면 많은 수의 관찰 환자가 필요하다. 이는 여러 데이터 출처를 동시에 평가하고 분석해야 할 필요성을 설명한다. 그러기 위해서는 데이터를 공통 데이터 표준 (common data standard)으로 화합할 필요가 있다. 게다가 환자 데이터는 높은 수준의 보안이 필요하다. 기존에 그래왔듯이 분석을 목적으로 하는 데이터 추출은 엄격한 데이터 사용 계약 및 복잡한 접근 제어 방식이 필요하다. 공통 데이터 표준은 추출 단계를 생략하고 기본 환경의 데이터에 대해 표준화된 분석을 실행할 수 있도록 하여 이러한 필요성을 줄여 줄 수 있다- 분석을 위한 데이터가 아닌 데이터를 위한 분석적 접근(the analytic comes to the data instead of the data to the analytic).

이러한 표준은 공통 데이터 모델 (Common Data Model, CDM)에 의해 제공된다. CDM은 표준화된 내용을 기반으로(5장 참조) 연구 방법들이 효과적으로 비교 가능하고 재현 가능한 결과를 얻을 수 있게 체계적으로 응용될 수 있도록 한다. 이 장에서는

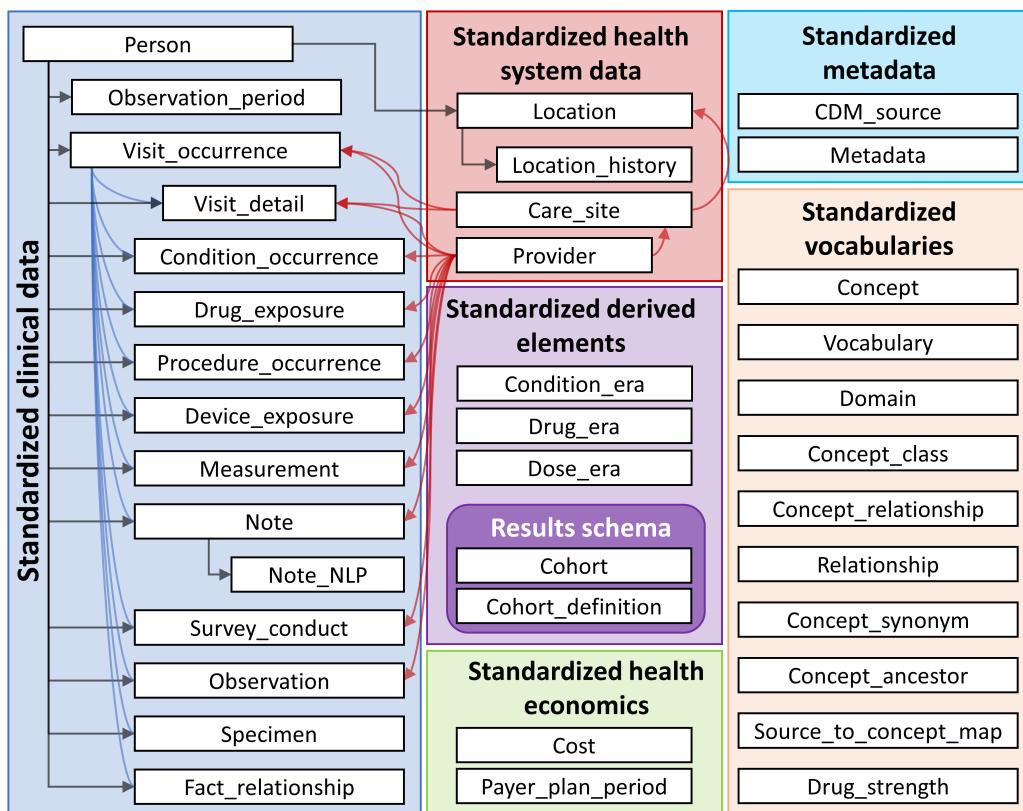


Figure 4.1: CDM 6.0 버전의 모든 테이블에 대한 개요. 테이블 간의 모든 관계가 묘사되어 있는 것은 아니다.

데이터의 모델을 비롯한 디자인, 규칙 및 테이블 선택에 대한 논의를 제공하고자 한다.

CDM내의 모든 테이블에 대한 개요를 Figure 4.1에서 살펴볼 수 있다.

4.1 설계 원리

CDM은 다음과 같은 전형적인 관찰 연구 목적에 최적화되어 있다.

- 특정한 의료 행위의 개입(약물 노출, 시술(procedure), 의료 정책 변경 등)이 있거나 의료 관련 결과(질환, 시술(procedure), 기타 약물 노출에 대한)를 포함하는 환자 집단 확인.
- 인구 통계학적 정보, 질병의 자연사, 의료 서비스 전달, 활용 및 비용, 병적 상태, 치료 및 치료 과정 등과 같은 다양한 매개 변수에 대한 환자 집단의 특성 확인.
- 개별 환자에서 결과들의 발생 예측 - 13장 참고,
- 앞서 설명한 의료 행위의 개입들이 인구에 미치는 영향 추정 - 12장 참고,

이러한 목표를 달성하기 위해서 CDM의 개발은 다음과 같은 설계 요소를 따른다:

- **목적에 대한 적합성:** CDM은 의료 서비스 제공자 혹은 지불인의 운영 요구를 해결하기 위한 목적 보다는 분석에 최적화된 방식으로 구성된 데이터를 제공하는 것을 목표로 한다.
- **데이터 보호:** 이름, 생년월일 등 환자의 신원 및 안전을 위협할 수 있는 모든 데이터는 제한되어 있다. 영아에 대한 연구를 위한 정확한 생년 월일과 같은 보다 자세한 정보가 명시적으로 필요한 경우에는 예외가 가능하다.
- **도메인 설계:** 도메인은 개인 중심 관계형 데이터 모델(person-centric relational data model)로 모델링 되며 각 기록마다 개인의 신원과 날짜 정보가 최소한으로 수집된다. 여기서 관계형 데이터 모델은 데이터가 기본 키와 외래 키로 연결된 테이블의 모음으로 표현되는 모델이다.
- **도메인의 이론적 근거:** 개체-관계 모델(entity-relationship model)에서 도메인은 분석 이용 사례가 있는지 (예를 들면, 질환(conditions)) 그리고 달리 적용 가능한 방안이 없는 특정한 속성(attributes)이 있는지에 따라 식별되고 별도로 정의된다. 다른 모든 데이터는 개체-속성-값 구조(entity-attribute-value structure)의 Observation 테이블에 관찰 데이터로 보존될 수 있다.
- **표준화된 어휘:** 기록들의 내용을 표준화하기 위해, CDM은 모든 필수적이고 적절한 표준 건강 관리 개념(concept)을 포함하는 표준화된 어휘에 의존한다.
- **기존 어휘 재사용:** 이러한 개념은 국립 의학 도서관, 재향 군인 담당 부서, 질병 통제 및 예방 센터 등과 같은 국가 및 산업 표준화 또는 용어 정의 주도 기관이나 협회에서 활용되기도 한다.
- **원본 코드 유지 관리:** 모든 코드가 표준화된 어휘에 매핑(mapping)되어 있더라도 정보가 소실되지 않도록 원본 코드도 저장한다.
- **기술 중립성:** CDM에는 특정한 기술을 필요로 하지 않는다. Oracle, SQL Server 등과 같은 관계형 데이터베이스 또는 SAS 분석 데이터 세트로 구현될 수 있다.
- **확장성:** CDM은 데이터 처리 및 계산 분석에 최적화되어 있기 때문에 수 억 명에 이르는 데이터베이스와 수십 억 건에 달하는 임상 관찰을 비롯한 데이터 베이스의 크기가 다양한 원천 데이터를 수용할 수 있다.
- **이전 버전과의 호환성:** 이전 CDM로부터의 모든 변경 사항은 github 저장소 (<https://github.com/OHDSI/CommonDataModel>)에 명확하게 서술되어 있다. CDM의 이전 버전은 현재 버전을 이용해 쉽게 만들 수 있으며, 이전에 있었던 정보는 손실되지 않는다.

4.2 데이터 모델 규칙

CDM에 채택된 많은 암시적 혹은 명시적인 규칙이 있다. CDM에 관련한 메소드 개발자들은 이러한 규칙들을 이해하고 있어야 한다.

4.2.1 모델의 일반적인 규칙

CDM은 “개인 중심”모델로서, 모든 임상적인 사건에 대한 테이블이 PERSON 테이블에 연결되어 있다. 시작 날짜 및 기타 날짜 정보들과 더불어 이는 모든 의료 관련 사건에 대해 각 사람별로 종적 관찰이 가능하도록 한다. 이러한 규칙들의 예외 사항은 다양한 도메인의 사건들에 직접 연결되는 표준화된 의료 체계의 데이터

테이블들이다.

4.2.2 스키마의 일반적인 규칙

스키마 또는 데이터베이스의 사용자는 읽기 전용 테이블과 읽기/쓰기 테이블을 분리할 수 있다. 임상 사건 및 어휘 테이블은 “CDM” 스키마에 저장되어 있으며 최종 사용자 또는 분석 도구에서는 읽기 전용으로 이용된다. 웹 기반 도구 및 최종 사용자에 의해 조작될 필요가 있는 테이블은 “결과” 스키마에 저장된다. “결과” 스키마의 두 테이블은 COHORT와 COHORT_DEFINITON이다. 이 테이블들은 10 장에 자세히 설명되어 있는 것처럼 사용자가 정의할 수 있는 관심 그룹을 설명하기 위한 것이다. 이는 런타임 동안에 테이블이 작성될 수 있음을, 즉 코호트가 COHORT 테이블에 저장될 수 있다는 것을 의미한다. 모든 사용자를 위한 읽기-쓰기 스키마는 단 하나뿐이므로, 여러 사용자 접근이 어떻게 구성되고 제어되는지는 CDM의 구현에 달려 있다.

4.2.3 데이터 테이블의 일반적인 규칙

CDM은 플랫폼에 비의존적이다. 데이터 유형은 일반적으로 ANSI SQL 데이터 유형(VARCHAR, INTEGER, FLOAT, DATE, DATETIME, CLOB)을 사용하여 정의된다. VARCHAR에서만 정밀도가 제공된다. 이는 필요한 최소 문자열 길이를 반영하지만 구체적인 CDM 인스턴스화 내에서 확장될 수 있다. CDM은 날짜 및 날짜시간 형식을 규정하지 않는다. CDM에 대한 표준 쿼리는 로컬 인스턴스 및 날짜/시간 구성에 따라 달라질 수 있다.

참고: 데이터 모델 자체는 플랫폼에 독립적이지만, 데이터 모델과 함께 작동하도록 구축된 여러 도구는 특정 사양이 요구된다. 이에 대한 자세한 내용은 8장을 참조.

4.2.4 도메인의 일반적인 규칙

서로 다른 성격의 사건들은 도메인에 정리되어 있다. 이러한 사건들은 도메인별로 테이블과 필드에 저장되고, 표준화된 어휘에 정의되어 있는 대로 도메인별 표준 Concept으로 표현된다(5.2.3 참조). 각 표준 Concept에 고유한 도메인 할당이 되는데, 이는 어떤 테이블에 기록되는지를 정의한다. 정확한 도메인 할당이 커뮤니티 내에서 항상 논의의 대상이 되지만, 엄격한 도메인-테이블-필드간 대응 규칙은 어떤 코드나 Concept에 대해서도 항상 모호한 위치는 없음을 보장한다. 예를 들어, 증상 및 진단 Concept은 Condition 도메인에 속하며 Condition_OCCURRENCE 테이블의 CONDITION_CONCEPT_ID로 기록된다. 소위 말하는 시술약품은 일반적으로 원천 데이터의 Procedure 테이블에 Procedure 코드로 기록된다. CDM에서 이러한 정보들은 매핑된 표준 Concept이 약물 도메인에 할당 되어있기 때문에 DRUG_EXPOSURE 테이블에서 찾을 수 있다. 표 4.1과 같이 총 30개의 도메인이 있다.

Table 4.1: 각 도메인에 속하는 표준 Concept의 수.

Concept Count	Domain ID	Concept Count	Domain ID
1731378	Drug	183	Route

Concept Count	Domain ID	Concept Count	Domain ID
477597	Device	180	Currency
257000	Procedure	158	Payer
163807	Condition	123	Visit
145898	Observation	51	Cost
89645	Measurement	50	Race
33759	Spec Anatomic Site	13	Plan Stop Reason
17302	Meas Value	11	Plan
1799	Specimen	6	Episode
1215	Provider Specialty	6	Sponsor
1046	Unit	5	Meas Value Operator
944	Metadata	3	Spec Disease Status
538	Revenue Code	2	Gender
336	Type Concept	2	Ethnicity
194	Relationship	1	Observation Type

4.2.5 Concept을 통한 내용의 표현

CDM 데이터의 테이블에서는 각 정보의 내용이 완전히 정규화되어 Concept으로 표현된다. Concept은 CONCEPT 테이블의 외래 키 역할을 하는 각각의 CONCEPT_ID 값이 할당되어 사건 테이블에 저장되며, 모든 CDM의 인스턴스들은 Concept에 대한 참고 자료로써 공통 데이터 모델과 함께 상호운용의 핵심 메커니즘이자 OHDSI 연구 네트워크의 기반인 동일한 CONCEPT 테이블을 사용한다. 표준 Concept이 없거나 식별되지 않는 경우에는 CONCEPT_ID가 존재하지 않는 Concept 이거나 알 수 없음 또는 매핑이 불가능함을 의미하는 0으로 설정된다.

CONCEPT 테이블의 정보들은 각각의 Concept에 대한 상세 정보(이름, 도메인, 클래스 등)를 포함하고 있다. Concepts, Concept Relationships, Concept Ancestors 및 다른 Concept과 관련 있는 정보들은 표준화된 용어에 포함되어 있다(5장 참조).

4.2.6 필드 명명 규칙

모든 테이블의 변수명은 하나의 규칙을 따른다:

Table 4.2: 필드 명 규칙.

Notation	Description
[Event]_ID	각 행의 고유 식별자로, 사건 테이블간 관계를 설정하는 외래 키 역할을 한다. 예를 들어 PERSON_ID는 각 개인을 고유하게 식별한다. VISIT_OCCURRENCE_ID는 방문을 고유하게 식별한다.

Notation	Description
[Event]_CONCEPT_ID	CONCEPT 참고 테이블의 표준 Concept에 대한 외래 키. 이는 모든 표준화된 분석에 기본 기반이 되는 사건의 주요 표현이다. 예를 들어 CONDITION_CONCEPT_ID = 31967에는 SNOMED Concept인 “Nausea”에 대한 참조 값을 포함하고 있다.
[Event]_SOURCE_CONCEPT_ID	CONCEPT 참고 테이블의 행에 대한 외래 키. 이 Concept은 원본 값(아래)과 동등하며, 이때 [EVENT_CONCEPT_ID]와 동일한 표준 개념이거나 또 다른 비-표준 concept일 수 있다. 예를 들어, Condition_SOURCE_CONCEPT_ID = 45431665는 독해용 용어의 “Nausea” 개념을 나타내며, 유사한 CONDITION_CONCEPT_ID는 표준 SNOMED-CT concept으로 31967이다. 표준 Concept만이 사건의 의미를 모호하지 않게 표현하므로 표준 분석에 응용 시 상호 운용성이 없는 원본 개념을 사용하는 것은 바람직하지 않다.
[Event]_TYPE_CONCEPT_ID	표준화된 용어를 표준화되어 있고 원본 정보의 출처를 나타내는 CONCEPT 참고 테이블의 행에 대한 외래 키. 이는 사건의 유형이나 concept의 유형을 나타내는 것이 아니라 이 기록을 생성한 메커니즘에 대한 정보를 수집하는 것을 의미한다. 예를 들면, DRUG_TYPE_CONCEPT_ID는 이 기록이 약국에서의 처방 (“Pharmacy dispensing”)으로부터 발생하였는지 혹은 전자 처방 신청서 (“Prescription written”)로부터 발생하였는지를 구분한다.
[Event]_SOURCE_VALUE	이 사건이 원천 데이터에 표현되어 있는 방식을 쓰여진 그대로의 코드 혹은 자유 텍스트 문자열이다. 이 원본 값들은 데이터 원본간에 통일되어 있지 않으므로 표준 분석 방식에 사용하는 것은 좋지 않다. 예를 들면, CONDITION_SOURCE_VALUE는 ICD-9 코드 787.02에 점을 제외하고 “78702”라는 기록을 포함할 수 있다.

4.2.7 concept과 원본 값과의 차이

많은 테이블이 원본 값, 원본 concept, 표준 concept으로 다양한 위치에 동일한 정보를 포함하고 있다.

- **Source Values** 은 원천 데이터에서의 사건 기록의 본래의 표현이다. 이는

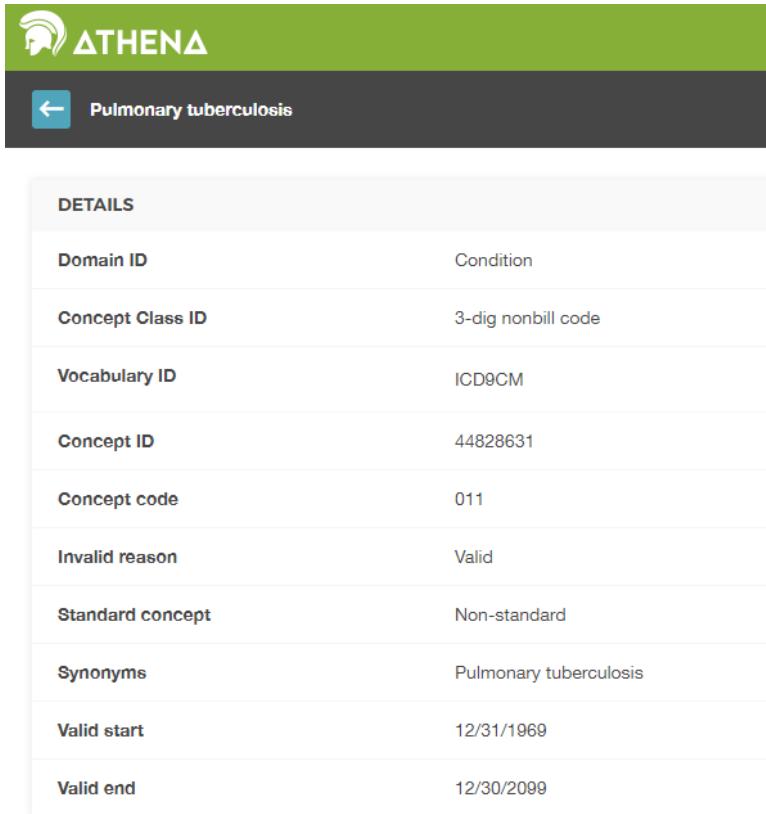
ICD9CM, NDC 또는 Read와 같은 널리 사용되는 공공 도메인의 코딩 시스템이나 CPT4, GPI 또는 MedDRA와 같이 독점적인 코딩 시스템, 혹은 남성은 M 여성은 F와 같이 원천 데이터에서만 사용되는 제한된 어휘의 코드일 수 있다. 또한 표준화 및 제어되지 않은 짧은 자유 텍스트 문구 일 수도 있다. 원본 값은 데이터 테이블의 [Event] _SOURCE_VALUE 필드에 저장됩니다. concept은 임상적 요소의 의미를 일반화하는 CDM 특이적인 개체이다. 대부분의 concept은 이미 의료계에 존재하는 공개되었거나 독점적인 코딩 체계를 기반으로 하고 있지만, 일부는 새롭게 생성되었다 (CONCEPT_CODE는 “OMOP”으로부터 시작됨). concept은 모든 도메인에 걸쳐 고유한 ID를 가지고 있다.

- **Concepts** 은 임상적 요소의 의미를 일반화하는 CDM 특이적인 개체이다. 대부분의 concept은 이미 의료계에 존재하는 공개되었거나 독점적인 코딩 체계를 기반으로 하고 있지만, 일부는 새롭게 생성되었다 (CONCEPT_CODE는 “OMOP”으로부터 시작됨). concept은 모든 도메인에 걸쳐 고유한 ID를 가지고 있다.
- **Source Concepts** 은 원 자료에서 사용된 코드를 나타내는 concept이다. 원본 concept은 OMOP기반의 concept이 아니라 기존에 존재하는 공개되었거나 독점적인 코딩 체계만을 위해 사용한다. 원본 concept은 데이터 테이블의 [Event] _SOURCE_CONCEPT_ID 필드에 저장된다.
- **Standard Concepts** 은 모든 데이터 베이스에서 고유하게 임상적인 개체의 의미를 정의하는 데에 사용되고 원본에서 사용한 코딩 체계와는 독립적인 concept이다. 표준 concept은 일반적으로 이미 공개되어 있거나 독점적인 용어 원본에서 가져온다. 표준 concept과 동일한 의미를 가진 비 표준 concept은 표준 용어의 표준 concept에 매핑되어 있다. 표준 concept은 데이터 테이블의 [Event] _CONCEPT_ID 필드에서 참조된다.

원본 값은 편의 및 품질 보증 (Quality Assurance, QA) 목적으로만 제공된다. 여기에는 특정 데이터 원본의 맥락에서만 의미 있는 정보가 포함될 수 있다. 원본 값이나 원본 concept을 사용하는 것은 선택사항이지만, 원본 데이터가 코딩 시스템을 사용하는 경우 **강력하게 권장된다**. 하지만 표준 concept의 경우 **필수 사항**이다. 이 표준 concept을 필수적으로 사용하면 모든 CDM 인스턴스가 동일한 언어를 사용할 수 있다. 예를 들면 “Pulmonary Tuberculosis” (TB, Figure 4.2)의 condition은 TB에 대한 ICD9CM 코드가 011임을 나타낸다.

문맥이 없으면, 코드 011은 UB04 언어의 “Hospital Inpatient (Including Medicare Part A)”로 해석되거나, DRG 용어의 “Nervous System Neoplasms without Complications, Comorbidities”로 해석될 수 있다. 이것이 원본과 표준 모두의 concept ID가 중요한 이유이다. 011인 ICD9CM 코드를 나타내는 CONCEPT_ID 값은 44828631이다. 이는 ICD9CM을 UBO4 및 DRG와 구별한다. ICD9CM의 TB 원본 concept은 그림 4.3과 같이 “OMOP (Non-standard to Standard Map)”관계를 통해 SNOMED 어휘에서 표준 concept 253954로 매핑된다. 표준 SNOMED 개념을 참조하는 모든 연구가 지원되는 모든 원본 코드를 포함할 수 있도록 Read, ICD10, CIEL 및 MeSH 코드에도 동일한 매핑 관계가 존재한다.

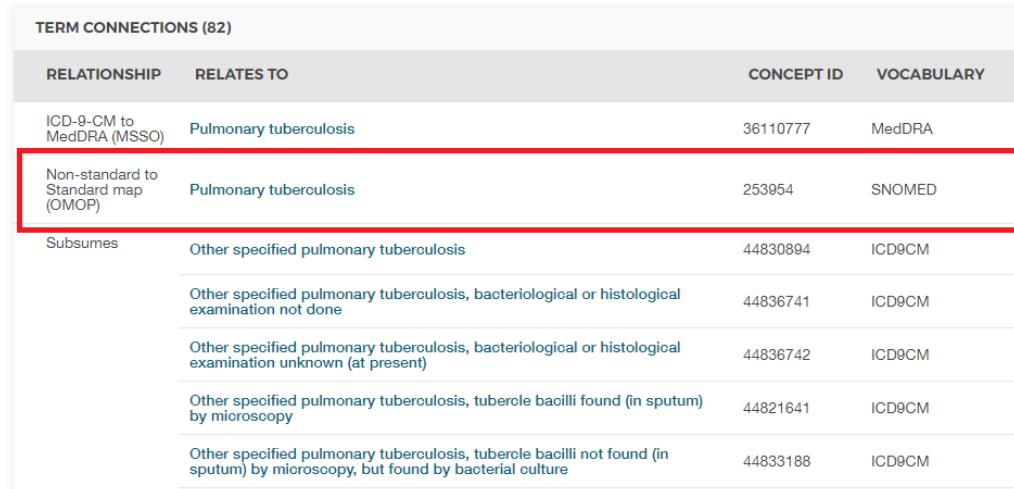
표준 concept과 원본 concept의 관계를 보여주는 예가 표4.7에 나와있다.



The screenshot shows the ATHENA interface for viewing the details of a medical concept. The top bar is green with the ATHENA logo. Below it, a dark bar displays a back arrow icon and the text "Pulmonary tuberculosis". The main area is titled "DETAILS" and contains a table with the following data:

Domain ID	Condition
Concept Class ID	3-dig nonbill code
Vocabulary ID	ICD9CM
Concept ID	44828631
Concept code	011
Invalid reason	Valid
Standard concept	Non-standard
Synonyms	Pulmonary tuberculosis
Valid start	12/31/1969
Valid end	12/30/2099

Figure 4.2: Pulmonary Tuberculosis의 ICD9CM 코드



This table displays term connections between ICD-9-CM and SNOMED codes for Pulmonary tuberculosis. The rows are categorized by relationship type.

TERM CONNECTIONS (82)			
RELATIONSHIP	RELATES TO	CONCEPT ID	VOCABULARY
ICD-9-CM to MedDRA (MSSO)	Pulmonary tuberculosis	36110777	MedDRA
Non-standard to Standard map (OMOP)	Pulmonary tuberculosis	253954	SNOMED
Subsumes	Other specified pulmonary tuberculosis	44830894	ICD9CM
	Other specified pulmonary tuberculosis, bacteriological or histological examination not done	44836741	ICD9CM
	Other specified pulmonary tuberculosis, bacteriological or histological examination unknown (at present)	44836742	ICD9CM
	Other specified pulmonary tuberculosis, tubercle bacilli found (in sputum) by microscopy	44821641	ICD9CM
	Other specified pulmonary tuberculosis, tubercle bacilli not found (in sputum) by microscopy, but found by bacterial culture	44833188	ICD9CM

Figure 4.3: Pulmonary Tuberculosis의 SNOMED 코드

4.3 표준화된 CDM 테이블

DM에는 16개의 임상 사건 테이블, 10개의 어휘 테이블, 2개의 메타데이터 테이블, 4개의 보건 시스템 데이터 테이블, 2개의 보건 경제학 데이터 테이블, 3개의 표준화된 파생 요소 및 2개의 결과 스키마 테이블이 포함되어 있다. 이 테이블들은 CDM Wiki에 전체 명시되어 있다.¹

이러한 테이블들이 실제로 어떻게 사용되는지를 설명하기 위해, 한 사람의 데이터를 이 장의 나머지 부분에서 걸쳐 공통으로 사용할 것이다.

4.3.1 실행 예제: 자궁내막증

자궁내막증은 보통 여성의 자궁 안쪽에서 발견되는 세포가 신체 다른 곳에서 생겨나는 고통스러운 질환이다. 심한 경우는 불임, 장, 방광 문제를 일으킬 수 있다. 해당 섹션에서는 한 환자의 이 질병에 대한 경험과 이 질병이 공통 데이터 모델로 어떻게 표현되는지를 상세하게 설명하고자 한다.



나는 이 고통스러운 여정의 모든 과정마다 내가 얼마만큼의 고통을 받고 있는지를 모두에게 납득시켜야 했다.

Lauren은 수년 동안 자궁 내막증 증상을 겪어 왔다. 그러나 진단을 받기 전에 난소에서 낭종이 파열되었다. Lauren에 대한 자세한 내용은 <https://www.endometriosis-uk.org/laurens-story>에서 확인할 수 있다.

4.3.2 PERSON 테이블

Lauren에 대해서 우리가 알고 있는 것은?

- 그녀는 36세 여성이다
- 그녀의 생년월일은 1982년 3월 12일이다
- 그녀는 백인이다
- 그녀는 영국인이다

이를 염두에 두면 PERSON 테이블을 다음과 같이 나타낼 수 있다:

¹<https://github.com/OHDSI/CommonDataModel/wiki>

Table 4.3: PERSON 테이블.

Column name	Value	Explanation
PERSON_ID	1	PERSON_ID는 원본에서 직접적으로 생성되거나 빌드 과정의 일부분으로 생성된 정수여야 한다.
GENDER_CONCEPT_ID	8532	여성을 의미하는 concept ID는 8532이다.
YEAR_OF_BIRTH	1982	
MONTH_OF_BIRTH	3	
DAY_OF_BIRTH	12	
BIRTH_DATETIME	1982-03-12 00:00:00	시간을 정확히 알 수 없는 경우 자정으로 한다.
DEATH_DATETIME		
RACE_CONCEPT_ID	8527	백인을 의미하는 concept ID는 8527이다. 영국인이라는 민족성은 4093769이다. 둘 다 해당할 경우 전자를 활용한다. 민족성은 ETHNICITY_CONCEPT_ID가 아닌 인종의 일부로써 여기에 저장된다.
ETHNICITY_CONCEPT_ID	8003564	이는 히스패닉을 다른 사람들과 구분하기 위해 사용되는 전형적인 미국식 표기법이다. 이 경우 영국인인 민족성은 RACE_CONCEPT_ID에 저장된다. 미국 이외의 지역에서는 사용되지 않는다. 38003564는 “히스패닉이 아님”을 나타낸다.
LOCATION_ID		주소는 알려져 있지 않다.
PROVIDER_ID		일차 진료 제공자는 알려져 있지 않다.
CARE_SITE		일차 진료 장소는 알려져 있지 않다.
PERSON_SOURCE_1	1	대부분 PERSON_ID 와 동일 하지만 일반적으로 이는 원본 데이터에서의 그녀의 식별자가 될 것이다.
VALUE		
GENDER_SOURCE_F		원본에 나타난 성별에 대한 값이 여기에 저장되어 있다.
VALUE		
GENDER_SOURCE_O	0	원본의 성별에 대한 값이 OHDSI에서 지원하는 코딩 체계를 사용한 경우 해당 concept이 여기에 해당한다. 예를 들어, 그녀의 성별이 원본에서 “sex-F”이고 PCORNet 어휘 concept에 있다고 언급되어 있다면 44814665이 이 필드에 입력될 것이다.
CONCEPT_ID		
RACE_SOURCE_WHITE	white	인종 값이 원본에 있는대로 여기에 저장된다.
VALUE		

Column name	Value	Explanation
RACE_SOURCE_CONCEPT_ID	0	GENDER_CONCEPT_ID와 같은 원리 적용.
ETHNICITY_SOURCE_english VALUE		민족성 값이 원본에 나와 있는대로 여기에 저장된다.
ETHNICITY_SOURCE_0 CONCEPT_ID		GENDER_SOURCE_CONCEPT_ID 와 같은 원리 적용.

4.3.3 OBSERVATION_PERIOD 테이블

OBSERVATION_PERIOD 테이블은 최소한 환자의 인구통계, 질환, 시술 및 약물이 원본 시스템에 기록되는 시간을 민감성과 특수성을 고려하여 합리적인 예상을 통해 정의하도록 설계되었다. 보험 데이터의 경우 일반적으로 환자의 등록 시기이다. 대부분의 의료 시스템이 어떤 의료 기관이나 제공업체를 방문할지 결정해두지 않기 때문에 전자 건강 기록(EHR)에서는 더욱 까다롭다. 차선책으로서 시스템의 첫 번째 기록은 관측 기간의 시작일로 간주되고 최신 기록은 종료일로 간주된다.

Lauren의 Observation Period은 어떻게 정의될까?

표 4.4에 나타난 Lauren의 정보가 EHR 시스템에 기록되었다고 가정하자. 그녀의 Observation period에서 얻어진 방문기록은 다음과 같다:

Table 4.4: Lauren의 의료 기관 방문.

Encounter ID	Start date	Stop date	Type
70	2010-01-06	2010-01-06	outpatient
80	2011-01-06	2011-01-06	outpatient
90	2012-01-06	2012-01-06	outpatient
100	2013-01-07	2013-01-07	outpatient
101	2013-01-14	2013-01-14	ambulatory
102	2013-01-17	2013-01-24	inpatient

방문기록을 기반으로 했을 때 그녀의 OBSERVATION_PERIOD 테이블은 다음과 같을 것이다:

Table 4.5: OBSERVATION_PERIOD 테이블.

Column name	Value	Explanation
OBSERVATION_PERIOD_ID	1	이는 일반적으로 테이블의 각 기록에 대한 고유 식별자를 생성하는 자동으로 생성되는 값이다.

Column name	Value	Explanation
PERSON_ID	1	PERSON 테이블에서 Laura의 기록에 대한 외래 키이며 PERSON을 OBSERVATION_PERIOD 테이블에 연결한다.
OBSERVATION_PERIOD	2010-01-06	이는 기록상 그녀의 가장 처음 방문했을 때 시작 날짜이다.
START_DATE		
OBSERVATION_PERIOD	2013-01-24	이는 기록상 그녀의 가장 마지막 방문했을 때 마지막 날짜이다.
END_DATE		
PERIOD_TYPE_	44814725	concept의 클래스가 “Obs Period Type” 인 어휘에서 가장 좋은 선택은 44814724이며, 이는 “의료 관련 방문 기간(Period covering healthcare encounters)”을 나타냅니다.
CONCEPT_ID		

4.3.4 VISIT_OCCURRENCE

VISIT_OCCURRENCE에서는 환자의 의료 시스템에 방문한 정보에 대해 저장되어 있다. OHDSI 언어내에서 이를 Visit이라고 하며 주요한 사건로 간주한다. 의료 서비스가 제공될 수 있는 다양한 환경을 나타내는 광범위한 계층 구조를 가진 12 가지 주요 방문 카테고리가 있다. 가장 일반적인 Visit 기록은 입원(inpatient), 외래(outpatient), 응급실(emergency department) 및 비-의료 기관방문(non-medical institution Visits)이다.

Lauren의 방문을 Visit으로 어떻게 표현할 수 있을까?

예를 들어 VISIT_OCCURRENCE 테이블의 표 4.4의 입원 환자 방문을 나타내어 보자.

Table 4.6: VISIT_OCCURRENCE 테이블.

Column name	Value	Explanation
VISIT_OCCURRENCE_ID	514	이는 일반적으로 테이블의 각 기록에 대한 고유 식별자를 생성하는 자동으로 생성되는 값이다.
PERSON_ID	1	PERSON 테이블에서 Laura의 기록에 대한 외래 키이며 PERSON을 VISIT_OCCURRENCE에 연결한다.
VISIT_CONCEPT_ID	9201	입원 환자 방문을 나타내는 외래 키는 9201이다.
VISIT_START_DATE	2013-01-17	Visit의 시작 날짜.
VISIT_START_DATETIME	2013-01-17 00:00:00	Visit의 날짜와 시간. 시간을 알 수 없기 때문에 자정으로 나타낸다.

Column name	Value	Explanation
VISIT_END_DATE	2013-01-24	Visit의 종료 날짜. 일일 방문이라면 이 값이 시작 날짜와 동일해야 한다.
VISIT_END_DATETIME	2013-01-24 00:00:00	Visit의 종료 날짜와 시간. 시간을 알 수 없기 때문에 자정으로 나타낸다.
VISIT_TYPE_ CONCEPT_ID	32035	이는 방문 기록의 보험 청구, 병원 청구, EHR 기록과 같은 제공처에 대한 정보를 제공한다. 해당 예에서는 방문 기록이 EHR과 유사하므로 concept ID 32035 (“Visit derived from EHR encounter record”)이 사용되었다.
PROVIDER_ID*	NULL	방문 기록에 해당 제공자와 관련된 ID가 있을 경우 이 필드에 기록한다. 이는 PROVIDER 테이블의 PROVIDER_ID 필드의 내용이어야 한다.
CARE_SITE_ID	NULL	방문 기록에 치료 제공 장소와 관련된 ID가 있을 경우 이 필드에 기록한다. 이는 CARE_SITE 테이블의 CARE_SITE_ID 필드의 내용이어야 한다.
VISIT_SOURCE_ VALUE	inpatient	출처에 나와 있는 방문 값 그대로 여기에 입력한다. Lauren의 데이터에는 존재하지 않는다.
VISIT_SOURCE_ CONCEPT_ID	0	출처의 방문 값이 OHDSI에서 통용되는 용어를 사용하여 코딩 되어 있는 경우 원본 코드를 나타내는 CONCEPT_ID 값을 여기에 넣는다. Lauren의 데이터에는 존재하지 않는다.
ADMITTED_FROM_ CONCEPT_ID	0	환자가 어디에서부터 입원해 왔는지 알 수 있는 경우 이를 나타내는 concept을 포함하고 있다. 이 concept은 “Visit”的 도메인을 가지고 있어야 한다. 예를 들어 만약 환자가 집에서 병원으로 입원한 경우 8536 (“Home”)값일 것이다.
ADMITTED_FROM_ SOURCE_CONCEPT_ID	NULL	환자가 어디에서부터 입원해 왔는지를 나타내는 원본 값이다. 위의 예를 활용하면 여기에는 “Home”이 들어가야 한다.

Column name	Value	Explanation
DISCHARGE_TO_CONCEPT_ID	0	환자가 어디로 퇴원 되었는지 알 수 있는 경우 이를 나타내는 concept을 나타낸다. 이 concept은 “Visit” 도메인을 가지고 있어야 한다. 예를 들면, 만약 환자가 보조 생활 시설로 보내졌을 경우 concept ID는 8615 (“Assisted Living Facility”)일 것이다.
DISCHARGE_TO_SOURCE_VALUE	0	환자가 퇴원 한 곳을 나타내는 원본 값이다. 위의 예를 활용하면 “보조 생활 시설”이 된다.
PRECEDING_VISIT_OCCURRENCE_ID	NULL	현재 Visit의 바로 이전의 방문을 나타낸다. ADMITTED_FROM_CONCEPT_ID와 달리 Visit Concept이 아닌 실제 Visit Occurrence 기록에 연결된다. 또한 Visit Occurrence에 따른 기록은 없으며 Visit Occurrence는 이 필드를 통해서만 연결되어 있다.

- 환자는 입원하는 경우와 마찬가지로 한번 방문하는 동안 여러 의료 제공자와 상호 작용할 수 있다. 이러한 상호작용은 VISIT_DETAIL 테이블에 기록될 수 있다. 이 장에서는 자세히 다루지 않지만 CDM wiki에서 VISIT_DETAIL 테이블에 대한 자세한 내용을 확인할 수 있다.

4.3.5 CONDITION_OCCURRENCE

CONDITION_OCCURRENCE 테이블의 기록은 제공자가 관찰하거나 환자가 보고한 상태의 진단, 징후 또는 증상이다.

Lauren의 condition은 무엇일까?

그녀의 예로 돌아가자면 그녀는 다음과 같이 말한다:

3년 정도 전쯤 그 동안 매우 통증이 심했던 월경이 점점 더 고통스러워지고 있다는 것을 알아챘다. 나는 내 결장 바로 옆에서 날카롭게 쑤시는 통증을 느끼기 시작했고 꼬리뼈와 아랫골반 부위가 따갑고 부풀어 오르는 것을 느꼈다. 내 월경이 너무 고통스러워져서 일을 한달에 하루 이틀 쉬었다. 진통제가 가끔 고통을 줄여 주긴 했지만 보통은 그렇지 않았다.

월경통이라고 하는 고통스러운 월경 경련의 SNOMED 코드는 266599000이다. 표 4.7은 CONDITION_OCCURRENCE 테이블에 어떻게 표시되는지를 보여준다:

Table 4.7: CONDITION_OCCURRENCE 테이블.

Column name	Value	Explanation
CONDITION_OCCURRENCE_ID	964	이는 일반적으로 테이블의 각 기록에 대한 고유 식별자를 생성하는 자동으로 생성되는 값이다.
PERSON_ID	1	이는 PERSON 테이블에서 Laura의 기록에 대한 외래 키이며 PERSON을 CONDITION_OCCURRENCE에 연결한다.
CONDITION_CONCEPT_ID	194696	SNOMED 코드 266599000을 나타내는 외래 키: 194696.
CONDITION_START_DATE	2010-01-06	Condition의 인스턴스가 기록된 날짜이다.
CONDITION_START_DATETIME	2010-01-06 00:00:00	Condition의 인스턴스가 기록된 날짜 및 시간이다. 시간을 알 수 없으므로 자정으로 입력한다.
CONDITION_END_DATE	NULL	이는 인스턴스가 종료된 것으로 여겨지는 날짜지만 거의 기록되지 않는다.
CONDITION_END_DATETIME	NULL	Condition의 인스턴스가 종료된 것으로 여겨지는 날짜 및 시간이 알려져 있을 경우 입력한다.
CONDITION_TYPE_CONCEPT_ID	32020	이 열은 기록의 출처, 즉 보험 청구, 병원 청구 기록, EHR 기록 등에서 얻어졌다는 정보를 제공하기 위한 것이다. 해당 예에서는 방문 기록이 EHR과 유사하기 때문에 concept 32020 (“EHR encounter diagnosis”)을 사용한다. 이 필드에 있는 concept은 “Condition Type” 용어에 있는 것이여야 한다.
CONDITION_STATUS_0_CONCEPT_ID		상황에 대해 알려진 것이 있을 경우 입력한다. 예를 들어, concept ID에 4203942가 사용되었을 경우 Condition이 인정된 진단명일 수 있다.
STOP_REASON	NULL	Condition이 더 이상 존재하지 않는 이유가 알려져 있으면 원본 데이터에 있는대로 입력한다.
PROVIDER_ID	NULL	만약 condition 기록에 진단의 제공자가 수록되어 있으면 해당 제공자의 ID를 이 필드에 입력한다. 이는 방문 시 제공자를 나타내는 PROVIDER 테이블의 PROVIDER_ID의 내용이어야 한다.

Column name	Value	Explanation
VISIT_OCCURRENCE_509_ID		Condition이 진단되었을 당시 Visit 값 (VISIT_OCCURRENCE 테이블의 VISIT_OCCURRENCE_ID에 대한 외래 키).
CONDITION_SOURCE_266599000_VALUE		Conditions을 나타내는 원래의 원본 값. Lauren의 월경 곤란의 사례에서는 해당 Condition에 대한 SNOMED 코드가 여기에 저장되고 코드를 나타내는 Concept은 CONDITION_SOURCE_CONCEPT_ID로 이동했으며 이로부터 매핑된 표준 Concept은 CONDITION_CONCEPT_ID 필드에 저장된다.
CONDITION_SOURCE_194696_CONCEPT_ID		원본의 질환 값이 OHDSI에서 활용하는 용어로 코드화되어 있을 경우 그 값을 나타내는 concept ID를 여기에 입력한다. 월경 곤란의 예에서는 그 원본 값이 SNOMED 코드 194696으로 코드를 나타내는 Concept은 194696이다. 이 경우에서는 CONDITION_CONCEPT_ID 영역과 같은 값이다.
CONDITION_STATUS_0_SOURCE_VALUE		원본의 질환의 상태 값이 OHDSI에서 지원하는 방식으로 코드화 되어 있을 경우 해당 concept을 여기에 입력한다.

4.3.6 DRUG_EXPOSURE

DRUG_EXPOSURE 테이블은 환자에 신체에 약물을 투여하고자 한 의도나 실제 투여에 대한 기록을 수집한다. 의약품에는 처방전이 필수적인 의약품과 처방전 없이 구입할 수 있는 의약품, 백신 및 고분자의 생물학적 제제를 포함한다. 약물 노출은 주문, 처방된 처방전, 약품 조제, 절차적 등록, 기타 환자가 보고한 정보와 같은 임상적인 사건에서 유추된다.

Lauren의 약물 노출은 어떻게 나타낼 수 있을까?

월경 곤란 통증을 완화하기 위해 Lauren은 2010년 1월 6일 방문하여 375mg Acetaminophen (일명 Paracetamol, 미국 NDC 코드 69842087651) 경구 제제 60알을 30일치 받았다. 이는 DRUG_EXPOSURE 테이블에서 다음과 같이 나타난다:

Table 4.8: DRUG_EXPOSURE 테이블.

Column name	Value	Explanation
DRUG_EXPOSURE_ID	1001	이는 일반적으로 테이블의 각 기록에 대한 고유 식별자를 생성하는 자동으로 생성되는 값이다.
PERSON_ID	1	PERSON 테이블에서 Laura의 기록에 대한 외래 키이며 PERSON을 DRUG_EXPOSURE에 연결한다.
DRUG_CONCEPT_ID	1127433	의약품에 대한 개념. 아세트 아미노펜에 대한 NDC 코드는 Concept 1127433으로 표시되는 RxNorm 코드 313782에 매핑된다.
DRUG_EXPOSURE_START_DATE	2010-01-06	약물에 노출되기 시작한 날짜.
DRUG_EXPOSURE_START_DATETIME	2010-01-06 00:00:00	약물에 노출되기 시작한 날짜 및 시각. 알 수 없을 경우 자정을 입력
DRUG_EXPOSURE_END_DATE	2010-02-05	약물 노출이 종료되는 날짜. 서로 다른 출처에서 알려져 있는 날짜나 추정된 날짜 일 수 있으며 환자가 약물에 노출 지속된 날짜의 마지막 날을 의미한다. 해당 사례에서는 Lauren이 30일 동안 제공받았음을 알기에 이 날짜가 추론될 수 있다.
DRUG_EXPOSURE_END_DATETIME	2010-02-05 00:00:00	약물 노출 종료 날짜 및 시간. DRUG_EXPOSURE_END_DATE와 비슷한 규칙이 적용된다. 알 수 없을 경우 자정을 입력.
VERBATIM_END_DATE	NULL	원본에서 실제 종료 날짜를 명시한 경우, 환자가 전체 날짜에 약물에 노출되었다고 가정하여 유추되어 결정된다.
DRUG_TYPE_CONCEPT_ID	38000177	해당 열은 보험 청구, 처방 기록 등에서 비롯된 기록의 출처에 대한 정보를 제공하기 위해 작성이 되었다. 이 예에서는 Concept 38000177 ("Prescription written")이 사용되었다.
STOP_REASON	NULL	T약물 투여가 중단된 이유. 요법 완료, 변경 제거 등이 이유에 포함된다. 이 정보가 수집되는 경우는 거의 없다.

Column name	Value	Explanation
REFILLS	NULL	대다수의 나라에서 처방 시스템의 일부인 초기 처방 이후 자동 재조제 횟수. 초기 처방은 세지 않고 NULL로 시작한다. Lauren의 아세트아미노펜의 경우 재조제되지 않았으므로 NULL이다.
QUANTITY	60	최초 처방전 또는 조제 기록에 기록된 약물의 양.
DAY_S_SUPPLY	30	처방 된 약의 투여 일수.
SIG	NULL	최초 처방전 또는 조제 기록에 기록된 미국 처방 시스템의 용기에 인쇄된 약 처방전의 지침 (“signetur”). 약물 지침은 CDM에서 아직 표준화되지 않았으며 표기된 그대로 입력된다.
ROUTE_CONCEPT_ID	4132161	이 Concept은 환자의 약물 투여 경로를 나타낸다. Lauren은 아세트아미노펜을 경구 복용하였으므로, Concept ID 4132161을 사용하였다.
LOT_NUMBER	NULL	제조업체로부터의 특정 수량 또는 의약품에 할당된 식별자. 이 정보는 거의 수집되지 않는다.
PROVIDER_ID	NULL	약품 기록에 처방자에 대한 정보가 있으면 해당 공급자의 ID가 해당 영역에 들어간다. 이때 PROVIDER 테이블의 PROVIDER_ID를 사용한다.
VISIT_OCCURRENCE_ID	509	약물 처방 시 VISIT_OCCURRENCE 테이블에 대한 외래 키.
VISIT_DETAIL_ID	NULL	약물 처방 시 VISIT_DETAIL 테이블에 대한 외래 키.
DRUG_SOURCE_VALUE	69842087651	원본 데이터에 나와있는 의약품의 원본 코드. Lauren의 예에서 NDC 코드가 저장된다.
DRUG_SOURCE_CONCEPT_ID	750264	이는 약물의 원본 값을 나타내는 Concept이다. 750264 Concept은 “Acetaminophen 325 MG Oral Tablet”의 NDC 코드를 나타낸다.
ROUTE_SOURCE_VALUE	NULL	원본에 나와 있는 그대로의 등록 경로를 나타낸다.

4.3.7 PROCEDURE_OCCURRENCE

PROCEDURE_OCCURRENCE 테이블에는 의료 서비스 제공자가 진단 또는 치료 목적으로 환자에게 주문하거나 시행한 활동 또는 과정에 대한 기록이 포함되어

있다. Procedure는 다양한 수준의 표준화를 통해 다양한 형태로 여러 데이터 출처에 존재한다. 예를 들면 다음과 같다:

- 수행된 시술을 포함한 의료 서비스에 대한 청구의 일부로 시술 코드가 포함하는 의료 청구.
- 발주 정보로부터 시술에 대한 정보를 수집하는 전자 의무 기록.

Lauren이 받은 시술은 무엇일까?

Lauren의 설명에서 2013년 1월 14일에 4x5cm 낭종을 왼쪽 난소 초음파를 통해 확인했다는 것을 알 수 있다. PROCEDURE_OCCURRENCE 테이블에 나타내는 방법은 다음과 같다:

Table 4.9: PROCEDURE_OCCURRENCE 테이블.

Column name	Value	Explanation
PROCEDURE_OCCURRENCE_ID	1277	이는 일반적으로 테이블의 각 기록에 대한 고유 식별자를 생성하는 자동으로 생성되는 값이다.
PERSON_ID	1	PERSON 테이블에서 Laura의 기록에 대한 외래 키이며 PERSON을 PROCEDURE_OCCURRENCE에 연결한다.
PROCEDURE_CONCEPT_ID	4127451	골반 초음파에 대한 SNOMED 처치 코드는 304435002이고, Concept 4127451로 나타낼 수 있다.
PROCEDURE_DATE	2013-01-14	처치가 시행된 날짜.
PROCEDURE_DATETIME	2013-01-14 00:00:00	처치가 시행된 날짜 및 시각. 시간을 알 수 없는 경우 자정으로 입력한다.
PROCEDURE_TYPE_CONCEPT_ID	38000275	해당 열은 보험 청구, EHR내의 발주 기록과 같은 처치 기록의 출처에 대한 정보를 제공하기 위한 것이다. 해당 예제에서 Concept ID 38000275 (“EHR order list entry”)이 EHR 기록으로부터의 처치 기록으로 사용된다.
MODIFIER_CONCEPT_ID		이는 처치에 대한 한정어를 나타내는 Concept Id를 위한 부분이다. 예를 들어, 기록에 CPT4의 처치가 양측에서 수행되었다고 한다면 concept ID 42739579 (“Bilateral procedure”)가 사용되는 것이다.
QUANTITY	0	발주 또는 등록된 처치의 수. 수량이 누락되거나 숫자 0 또는 1일 경우 모두 같은 뜻이다.

Column name	Value	Explanation
PROVIDER_ID	NULL	처치 기록에 제공자가 기록되어 있으면, 제공자의 ID를 이 영역에 입력한다. 이는 PROVIDER 테이블에 있는 PROVIDER_ID의 외래 키 여야만 한다.
VISIT_OCCURRENCE_740_ID		처치가 실행된 방문 정보 (VISIT_OCCURRENCE 테이블의 VISIT_OCCURRENCE_ID로 표시됨)를 알 수 있을 경우 입력한다.
VISIT_DETAIL_ID	NULL	처치가 실행된 방문에 대한 세부 사항 (VISIT_DETAIL 테이블의 VISIT_DETAIL_ID로 표시됨)이 있을 경우 입력한다.
PROCEDURE_SOURCE_304435002_VALUE		원본 데이터에 있는 그대로의 처치에 대한 코드 및 정보.
PROCEDURE_SOURCE_1127451_CONCEPT_ID		처치의 원본 값을 나타내는 Concept.
MODIFIER_SOURCE_NULL_VALUE		원본 데이터에 나타난 그대로의 원본 코드에 대한 한정어.

4.4 부가 정보

이 장에서는 데이터 표현 방법의 예로 CDM에서 사용할 수 있는 일부 테이블만을 다룬다. 자세한 정보는 위키 사이트²에서 참고할 수 있다.

4.5 요약



- CDM은 광범위한 관찰 연구 활동을 지원하도록 설계되었다.
- CDM은 개인 중심 모델입니다.
- CDM은 데이터 구조를 표준화할뿐만 아니라 표준화된 어휘를 통해 내용 표현을 표준화한다.
- 완벽히 추적이 가능하도록 원본 코드가 CDM에 유지된다.

²<https://github.com/OHDSI/CommonDataModel/wiki>

4.6 예제

전제 조건

첫번째 연습에서는 앞에서 설명한 CDM테이블을 확인해야 하며, ATHENA³ 또는 ATLAS⁴를 통해 용어에 있는 Concept을 찾아야 할 것이다.

Exercise 4.1. John은 1974 년 8 월 4 일에 태어난 흑인 남자이다. 이 정보를 인코딩하는 PERSON 테이블 항목을 정의하라.

Exercise 4.2. John은 2015 년 1 월 1 일에 현재 이용하는 보험에 등록했다. 그의 보험 데이터베이스의 데이터는 2019 년 7 월 1 일에 추출되었다. 이 정보를 인코딩하는 OBSERVATION_PERIOD 테이블 항목을 정의하라.

Exercise 4.3. John은 2019 년 5 월 1 일에 Ibuprofen 200 MG Oral 정제 (NDC 코드 : 76168009520)를 30 일간 투여하도록 처방되었다. 이 정보를 인코딩하는 DRUG_EXPOSURE 테이블 항목을 정의하라.

전제 조건

해당 마지막 세 연습 문제에서는 8.4.5 부분에 설명된 것과 같이 R,R-Studio 그리고 Java가 설치되었다고 가정한다. SqlRender, DatabaseConnector 및 Eunomia 패키지가 요구되고 아래 내용을 통해 설치할 수 있다:

```
install.packages(c("SqlRender", "DatabaseConnector", "devtools"))
devtools::install_github("ohdsi/Eunomia", ref = "v1.0.0")
```

Eunomia 패키지는 로컬 R 세션 내에서 실행될 CDM의 가상 데이터 세트를 제공한다. 연결 세부 사항은 아래 내용을 통하여 얻을 수 있다:

```
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
```

CDM 데이터 베이스 스키마는 “main”이다.

Exercise 4.4. SQL과 R을 사용하여 “Gastrointestinal hemorrhage” (concept ID 192671) 질환의 모든 기록을 검색한다.

Exercise 4.5. SQL과 R을 사용하여 원본 코드로 “Gastrointestinal hemorrhage” 질환의 모든 기록을 검색한다. 이 데이터베이스는 ICD-10을 사용하며 관련 ICD-10 코드는 “K92.2”이다.

Exercise 4.6. SQL과 R을 사용하여 PERSON_ID가 61 인 사람의 관찰 기간을 검색하라.

³<http://athena.ohdsi.org/>

⁴<http://atlas-demo.ohdsi.org>

답변은 부록 E.1에서 확인 할 수 있다.

Chapter 5

Standardized Vocabularies

Chapter leads: Christian Reich & Anna Ostropolets

The OMOP Standardized Vocabularies, often referred to simply as “the Vocabulary”, are a foundational part of the OHDSI research network, and an integral part of the Common Data Model (CDM). They allow standardization of methods, definitions and results by defining the content of the data, paving the way for true remote (behind the firewall) network research and analytics. Usually, finding and interpreting the content of observational healthcare data, whether it is structured data using coding schemes or laid down in free text, is passed all the way through to the researcher, who is faced with a myriad of different ways to describe clinical events. OHDSI requires harmonization not only to a standardized format, but also to a rigorous standard content.

In this chapter we first describe the main principles of the Standardized Vocabularies, their components, and the relevant rules, conventions and some typical situations, all of which are necessary to understand and utilizing this foundational resource. We also point out where the support of the community is required to continuously improve it.

5.1 Why Vocabularies, and Why Standardizing

Medical vocabularies go back to the Bills of Mortality in medieval London to manage outbreaks of the plague and other diseases (see Figure 5.1).

Since then, the classifications have greatly expanded in size and complexity and spread into other aspects of healthcare, such as procedures and services, drugs, medical devices, etc. The main principles have remained the same: they are controlled vocabularies, terminologies, hierarchies or ontologies that some healthcare communities agree upon for the purpose of capturing, classifying and analyzing patient data. Many of these vocabularies are maintained by public and government

1660.

A General BILL for this present Year,

Ending the 11th Day of December 1660.

**According to the Report made to the King's most excellent Majesty,
By the Company of Parish Clerks of LONDON, &c.**

DISEASES and CASUALTIES.

A	Bortive and Stillborn	421	Flox and Small Pox	—	1523	Palsy	—	—	17
	Aged	909	Found dead in the Streets,	{	2	Plague	—	—	36
	Ague and Fever	—	Fields, &c.	{		Plurify	—	—	12
	Apoplexy and Suddenly	91	French Pox	—	51	Quinify and sore Throat	—	—	21
	Blasted and Planet	—	Gout	—	4	Rickets	—	—	44
	Bleeding and bloody Issue	7	Grief	—	13	Rising of the Lights	—	—	210
	Bloody Flux, Scowring, and Flux	346	Griping in the Guts	—	253	Rupture	—	—	12
	Burnt and Scalded	6	Hanged and made away them-selves	{	11	Scurvy	—	—	82
	Cancer, Gangrene and Fistula	63	Head-ach and Headmouldshot	—	35	Shot	—	—	7
	Canker, fore Mouth and Thrush	73	Jaundies	—	102	Shingles	—	—	1
	Childbed	—	Imposthume	—	105	Sores, Ulcers, broken and bruised Limbs	{	61	
	Chrisomes and Infants	858	Killed by several Accidents	—	55	Spleen	—	—	7
	Cold, Cough and Hiccough	33	King's Evil	—	28	Spotted Fever and Purples	—	—	368
	Colick and Wind	—	Lethargy	—	6	Starved	—	—	7
	Consumption and Tisick	2982	Livergrown	—	8	Strangury	—	—	22
	Convulsion	—	Lunatick and Frenzy	—	14	Stopping of the Stomach	—	—	186
	Cut of the Stone and Stone	46	Megrims	—	5	Surfeit	—	—	202
	Dropfy and Tympany	646	Measles	—	6	Swine Pox	—	—	2
	Drowned	—	Mother	—	1	Teeth and Worms	—	—	839
	Executed	—	Murthered	—	7	Vomiting	—	—	8
	Falling Sickness	—	Overlaid and Starved at Nurse	—	46	Wen	—	—	1

Figure 5.1: 1660 London Bill of Mortality, showing the cause of death for deceased inhabitants using a classification system of 62 diseases known at the time.

agencies with a long-term mandate for doing so. For example, the World Health Organization (WHO) produces the International Classification of Disease (ICD) with the recent addition of its 11th revision (ICD11). Local governments create country-specific versions, such as ICD10CM (USA), ICD10GM (Germany), etc. Governments also control the marketing and sale of drugs and maintain national repositories of such certified drugs. Vocabularies are also used in the private sector, either as commercial products or for internal use, such as electronic health record (EHR) systems or for medical insurance claim reporting.

As a result, each country, region, healthcare system and institution tends to have their own classifications that would most likely only be relevant where it is used. This myriad of vocabularies prevents interoperability of the systems they are used in. Standardization is the key that enables patient data exchange, unlocks health data analysis on a global level and allows systematic and standardized research, including performance characterization and quality assessment. To address that problem, multinational organizations have sprung up and started creating broad standards, such as the WHO mentioned above and the Standard Nomenclature of Medicine (SNOMED) or Logical Observation Identifiers Names and Codes (LOINC). In the US, the Health IT Standards Committee (HITAC) recommends the use of SNOMED, LOINC and the drug vocabulary RxNorm as standards to the National Coordinator for Health IT (ONC) for use in a common platform for nationwide health information exchange across diverse entities.

OHDSI developed the OMOP CDM, a global standard for observational research. As part of the CDM, the OMOP Standardized Vocabularies are available for two main purposes:

- Common repository of all vocabularies used in the community
- Standardization and mapping for use in research

The Standardized Vocabularies are available to the community free of charge and **must be used** for OMOP CDM instance **as its mandatory reference table**.

5.1.1 Building the Standardized Vocabularies

All vocabularies of the Standardized Vocabularies are consolidated into the same common format. This relieves the researchers from having to understand and handle multiple different formats and life-cycle conventions of the originating vocabularies. All vocabularies are regularly refreshed and incorporated using the Pallas system.¹ It is built and run by the OHDSI Vocabulary Team, which is part of the overall OMOP CDM Workgroup. If you find mistakes please report and help improve our resource by posting in either the OHDSI Forums² or CDM Github page.³

¹<https://github.com/OHDSI/Vocabulary-v5.0>

²<https://forums.ohdsi.org>

³<https://github.com/OHDSI/CommonDataModel/issues>

5.1.2 Access to the Standardized Vocabularies

In order to obtain the Standardized Vocabularies, you do not have to run Pallas yourself. Instead, you can download the latest version from ATHENA⁴ and load it into your local database. ATHENA also allows faceted search of the Vocabularies.

To download a zip file with all Standardized Vocabularies tables select all the vocabularies you need for your OMOP CDM. Vocabularies with Standard Concepts (see Section 5.2.6) and very common usage are preselected. Add vocabularies that are used in your source data. Vocabularies that are proprietary have no select button. Click on the “License required” button to incorporate such a vocabulary into your list. The Vocabulary Team will contact you and request you demonstrate your license or help you connect to the right folks to obtain one.

5.1.3 Source of Vocabularies: Adopt Versus Build

OHDSI generally prefers adopting existing vocabularies, rather than de-novo construction, because (i) many vocabularies have already been utilized in observational data in the community, and (ii) construction and maintenance of vocabularies is complex and requires the input of many stakeholders over long periods of time to mature. For that reason, dedicated organizations provide vocabularies, which are subject to a life-cycle of generation, deprecation, merging and splitting (see Section 5.2.10). Currently, OHDSI only produces internal administrative vocabularies like Type Concepts (e.g. condition type concepts). The only exception is RxNorm Extension, a vocabulary covering drugs that are only used outside the United States (see Section 5.6.9).

5.2 Concepts

All clinical events in the OMOP CDM are expressed as concepts, which represent the semantic notion of each event. They are the fundamental building blocks of the data records, making almost all tables fully normalized with few exceptions. Concepts are stored in the CONCEPT table (see Figure 5.2).

This system is meant to be **comprehensive**, i.e. there are enough concepts to cover any event relevant to the patient’s healthcare experience (e.g. conditions, procedures, exposures to drug, etc.) as well as some of the administrative information of the healthcare system (e.g. visits, care sites, etc.).

5.2.1 Concept IDs

Each concept is assigned a concept ID to be used as a primary key. This meaningless integer ID, rather than the original code from the vocabulary, is used to record data in the CDM event tables.

⁴<http://athena.ohdsi.org>

CONCEPT_ID	313217	Primary key
CONCEPT_NAME	Atrial fibrillation	English description
DOMAIN_ID	Condition	Domain
VOCABULARY_ID	SNOMED	Vocabulary
CONCEPT_CLASS_ID	Clinical Finding	Class in vocabulary
STANDARD_CONCEPT	S	Standard, Source of Classification
CONCEPT_CODE	49436004	Code in vocabulary
VALID_START_DATE	01-Jan-1970	Valid during time interval
VALID_END_DATE	31-Dec-2099	
INVALID_REASON		

Figure 5.2: Standard representation of vocabulary concepts in the OMOP CDM. The example provided is the CONCEPT table record for the SNOMED code for Atrial Fibrillation.

5.2.2 Concept Names

Each concept has one name. Names are always in English. They are imported from the source of the vocabulary. If the source vocabulary has more than one name, the most expressive is selected and the remaining ones are stored in the CONCEPT_SYNONYM table under the same CONCEPT_ID key. Non-English names are recorded in CONCEPT_SYNONYM as well, with the appropriate language concept ID in the LANGUAGE_CONCEPT_ID field. The name is 255 characters long, which means that very long names get truncated and the full-length version recorded as another synonym, which can hold up to 1000 characters.

5.2.3 Domains

Each concept is assigned a domain in the DOMAIN_ID field, which in contrast to the numerical CONCEPT_ID is a short case-sensitive unique alphanumeric ID for the domain. Examples of such domain identifiers are “Condition,” “Drug,” “Procedure,” “Visit,” “Device,” “Specimen,” etc. Ambiguous or pre-coordinated (combination) concepts can belong to a combination domain, but Standard Concepts (see Section 5.2.6) are always assigned a singular domain. Domains also direct to which CDM table and field a clinical event or event attribute is recorded. Domain assignments are an OMOP-specific feature done during vocabulary ingestion using a heuristic laid out in Pallas. Source vocabularies tend to combine codes of mixed domains, but to a varying degree (see Figure 5.3).

The domain heuristic follows the definitions of the domains. These definitions are derived from the table and field definitions in the CDM (see Chapter 4). The heuristic is not perfect; there are grey zones (see Section 5.6 “Special Situations”).

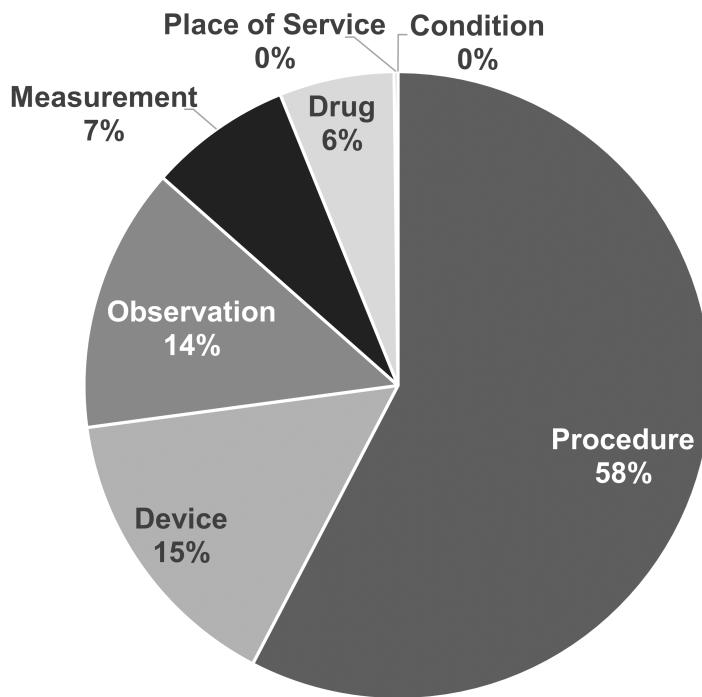


Figure 5.3: Domain assignment in procedure vocabularies CPT4 and HCPCS. By intuition, these vocabularies should contain codes and concepts of a single domain, but in reality they are mixed.

If you find concept domains assigned incorrectly please report and help improve the process through a Forums or CDM issue post.

5.2.4 Vocabularies

Each vocabulary has a short case-sensitive unique alphanumeric ID, which generally follows the abbreviated name of the vocabulary, omitting dashes. For example, ICD-9-CM has the vocabulary ID “ICD9CM”. There are 111 vocabularies currently supported by OHDSI, of which 78 are adopted from external sources, while the rest are OMOP-internal vocabularies. These vocabularies are typically refreshed at a quarterly schedule. The source and the version of the vocabularies is defined in the VOCABULARY reference file.

5.2.5 Concept Classes

Some vocabularies classify their codes or concepts, denoted through their case-sensitive unique alphanumerical IDs. For example, SNOMED has 33 such concept classes, which SNOMED refers to as “semantic tags”: clinical finding, social context, body structure, etc. These are vertical divisions of the concepts. Others, such as MedDRA or RxNorm, have concept classes classifying horizontal levels in their stratified hierarchies. Vocabularies without any concept classes, such as HCPCS, use the vocabulary ID as the Concept Class ID.

Table 5.1: Vocabularies with or without horizontal and vertical sub-classification principles in concept class.

Concept class sub- division principle	Vocabulary
Horizontal	all drug vocabularies, ATC, CDT, Episode, HCPCS, HemOnc, ICDs, MedDRA, OSM, Census
Vertical	CIEL, HES Specialty, ICDO3, MeSH, NAACCR, NDFRT, OPCS4, PCORNET, Plan, PPI, Provider, SNOMED, SPL, UCUM
Mixed	CPT4, ISBT, LOINC
None	APC, all Type Concepts, Ethnicity, OXMIS, Race, Revenue Code, Sponsor, Supplier, UB04s, Visit

Horizontal concept classes allow you to determine a specific hierarchical level. For example, in the drug vocabulary RxNorm the concept class “Ingredient” defines

the top level of the hierarchy. In the vertical model, members of a concept class can be of any hierarchical level from the top to the very bottom.

5.2.6 Standard Concepts

One concept representing the meaning of each clinical event is designated the Standard. For example, MESH code D001281, CIEL code 148203, SNOMED code 49436004, ICD9CM code 427.31 and Read code G573000 all define “Atrial fibrillation” in the condition domain, but only the SNOMED concept is Standard and represents the condition in the data. The others are designated non-standard or source concepts and mapped to the Standard ones. Standard Concepts are indicated through an “S” in the STANDARD_CONCEPT field. And only these Standard Concepts are used to record data in the CDM fields ending in “_CONCEPT_ID“.

5.2.7 Non-Standard Concepts

Non-standard concepts are not used to represent the clinical events, but they are still part of the Standardized Vocabularies, and are often found in the source data. For that reason, they are also called “source concepts”. The conversion of source concepts to Standard Concepts is a process called “mapping” (see Section 5.3.1). Non-standard concepts have no value (NULL) In the STANDARD_CONCEPT field.

5.2.8 Classification Concepts

These concepts are not Standard, and hence cannot be used to represent the data. But they are participating in the hierarchy with the Standard Concepts, and can therefore be used to perform hierarchical queries. For example, querying for all descendants of MedDRA code 10037908 (not visible for users who have not obtained a MedDRA license, see Section 5.1.2 for access restrictions) will retrieve the Standard SNOMED concept for Atrial Fibrillation (see Section 5.4 for hierarchical queries using the CONCEPT_ANCESTOR table) - see Figure 5.4.

The choice of concept designation as Standard, non-standard and classification is typically done for each domain separately at the vocabulary level. This is based on the quality of the concepts, the built-in hierarchy and the declared purpose of the vocabulary. Also, not all concepts of a vocabulary are used as Standard Concepts. The designation is separate for each domain, each concept has to be active (see Section 5.2.10) and there might be an order of precedence if more than one concept from different vocabularies compete for the same meaning. In other words, there is no such a thing as a “standard vocabulary.” See Table 5.2 for examples.

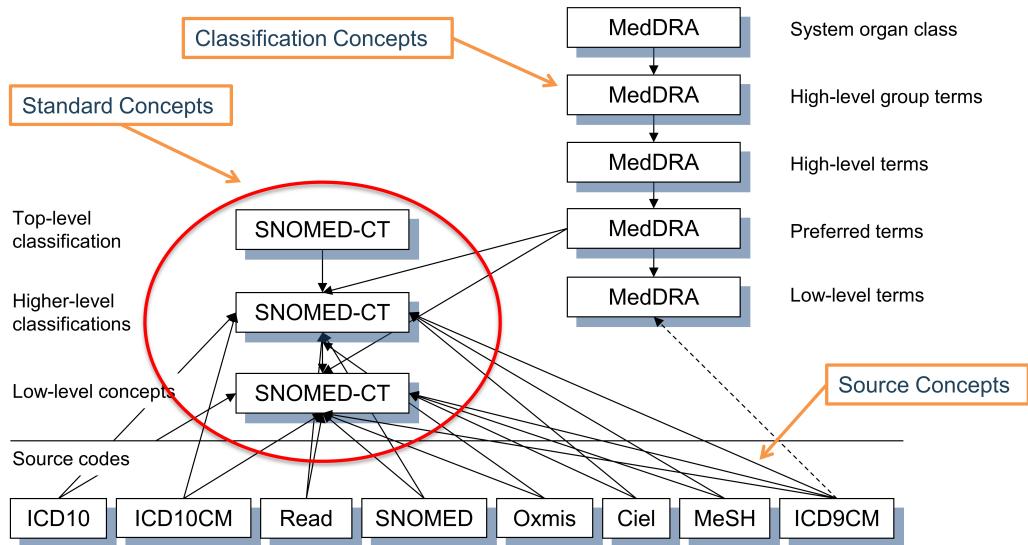


Figure 5.4: Standard, non-standard source and classification concepts and their hierarchical relationships in the condition domain. SNOMED is used for most standard condition concepts (with some oncology-related concepts derived from ICDO3), MedDRA concepts are used for hierarchical classification concepts, and all other vocabularies contain non-standard or source concepts, which do not participate in the hierarchy.

Table 5.2: List of vocabularies to utilize for Standard/non-standard/classification concept assignments.

Domain	for Standard Concepts	for source concepts	for classification concepts
Condition	SNOMED, ICDO3	SNOMED Veterinary	MedDRA
Procedure	SNOMED, CPT4, HCPCS, ICD10PCS, ICD9Proc, OPCS4	SNOMED Veterinary, HemOnc, NAACCR	None at this point
Measurement	SNOMED, LOINC	SNOMED Veterinary, NAACCR, CPT4, HCPCS, OPCS4, PPI	None at this point

Domain	for Standard Concepts	for source concepts	for classification concepts
Drug	RxNorm,	HCPSCS, CPT4,	ATC
	RxNorm	HemOnc,	
	Extension, CVX	NAAACCR	
Device	SNOMED	Others, currently not normalized	None at this point
Observation	SNOMED	Others	None at this point
Visit	CMS Place of Service, ABMT, NUCC	SNOMED, HCPSCS, CPT4, UB04	None at this point

5.2.9 Concept Codes

Concept codes are the identifiers used in the source vocabularies. For example, ICD9CM or NDC codes are stored in this field, while the OMOP tables use the concept ID as a foreign key into the CONCEPT table. The reason is that the name space overlaps across vocabularies, i.e. the same code can exist in different vocabularies with completely different meanings (see Table 5.3)

Table 5.3: Concepts with identical concept code 1001, but different vocabularies, domains and concept classes.

Concept ID	Concept Code	Concept Name	Domain ID	Vocabulary ID	Concept Class
35803438	1001	Granulocyte colony-stimulating factors	Drug	HemOnc	Component Class
35942070	1001	AJCC TNM Clin T	Measurement	NAACCR	NAACCR Variable
1036059	1001	Antipyrine	Drug	RxNorm	Ingredient
38003544	1001	Residential Treatment - Psychiatric	Revenue Code	Revenue Code	Revenue Code
43228317	1001	Aceprometazine maleate	Drug	BDPM	Ingredient
45417187	1001	Brompheniramine Maleate, 10 mg/mL injectable solution	Drug	Multum	Multum

Concept ID	Concept Code	Concept Name	Vocabulary Domain ID	Vocabulary ID	Concept Class
45912144	1001	Serum	Specimen	CIEL	Specimen

5.2.10 Life-Cycle

Vocabularies are rarely permanent corpora with a fixed set of codes. Instead, codes and concepts are added and get deprecated. The OMOP CDM is a model to support longitudinal patient data, which means it needs to support concepts that were used in the past and might no longer be active, as well as supporting new concepts and placing them into context. There are three fields in the CONCEPT table that describe the possible life-cycle statuses: VALID_START_DATE, VALID_END_DATE, and INVALID_REASON. Their values differ depending on the concept life-cycle status:

- **Active or new concept**
 - Description: Concept in use.
 - VALID_START_DATE: Day of instantiation of concept, if that is not known day of incorporation of concept in Vocabularies, if that is not known 1970-1-1.
 - VALID_END_DATE: Set to 2099-12-31 as a convention to indicate “Might become invalid in an undefined future, but active right now”.
 - INVALID_REASON: NULL
- **Deprecated Concept with no successor**
 - Description: Concept inactive and cannot be used as Standard (see Section 5.2.6).
 - VALID_START_DATE: Day of instantiation of concept, if that is not known day of incorporation of concept in Vocabularies, if that is not known 1970-1-1.
 - VALID_END_DATE: Day in the past indicating deprecation, or if that is not known day of vocabulary refresh where concept in vocabulary went missing or set to inactive.
 - INVALID_REASON: “D”
- **Upgraded Concept with successor**
 - Description: Concept inactive, but has defined successor. These are typically concepts which went through de-duplication.
 - VALID_START_DATE: Day of instantiation of concept, if that is not known day of incorporation of concept in Vocabularies, if that is not known 1970-1-1.
 - VALID_END_DATE: Day in the past indicating an upgrade, or if that is not known day of vocabulary refresh where the upgrade was included.
 - INVALID_REASON: “U”
- **Reused code for another new concept**
 - Description: The vocabulary reused the concept code of this deprecated

concept for a new concept.

- VALID_START_DATE: Day of instantiation of concept, if that is not known day of incorporation of concept in Vocabularies, if that is not known 1970-1-1.
- VALID_END_DATE: Day in the past indicating deprecation, or if that is not known day of vocabulary refresh where concept in vocabulary went missing or set to inactive.
- INVALID_REASON: “R”

In general, concept codes are not reused. But there are a few vocabularies that deviate from this rule, in particular HCPCS, NDC and DRG. For those, the same concept code appears in more than one concept of the same vocabulary. Their CONCEPT_ID value stays unique. These reused concept codes are marked with an “R” in the INVALID_REASON field, and the VALID_START_DATE to VALID_END_DATE period should be used to distinguish concepts with the same concept codes.

5.3 Relationships

Any two concepts can have a defined relationship, regardless of whether the two concepts belong to the same domain or vocabulary. The nature of the relationships is indicated in its short case-sensitive unique alphanumeric ID in the RELATIONSHIP_ID field of the CONCEPT_RELATIONSHIP table. Relationships are symmetrical, i.e. for each relationship an equivalent relationship exists, where the content of the fields CONCEPT_ID_1 and CONCEPT_ID_2 are swapped, and the RELATIONSHIP_ID is changed to its opposite. For example, the “Maps to” relationship has an opposite relationship “Mapped from.”

CONCEPT_RELATIONSHIP table records also have life-cycle fields RELATIONSHIP_START_DATE, RELATIONSHIP_END_DATE and INVALID_REASON. However, only active records with INVALID_REASON = NULL are available through ATHENA. Inactive relationships are kept in the Pallas system for internal processing only. The RELATIONSHIP table serves as the reference with the full list of relationship IDs and their reverse counterparts.

5.3.1 Mapping Relationships

These relationships provide translations from non-standard to Standard concepts, supported by two relationship ID pairs (see Table 5.4).

Table 5.4: Type of mapping relationships.

Relationship ID pair	Purpose
“Maps to” and “Mapped from”	Mapping to Standard Concepts. Standard Concepts are mapped to themselves, non-standard concepts to Standard Concepts. Most non-standard and all Standard Concepts have this relationship to a Standard Concept. The former are stored in *_SOURCE_CONCEPT_ID, and the latter in the *_CONCEPT_ID fields. Classification concepts are not mapped.
“Maps to value” and “Value mapped from”	Mapping to a concept that represents a Value to be placed into the VALUE_AS_CONCEPT_ID fields of the MEASUREMENT and OBSERVATION tables.

The purpose of these mapping relationships is to allow a crosswalk between equivalent concepts to harmonize how clinical events are represented in the OMOP CDM. This is a main achievement of the Standardized Vocabularies.

“Equivalent concepts” means it carries the same meaning, and, importantly, the hierarchical descendants cover the same semantic space. If an equivalent concept is not available and the concept is not Standard, it is still mapped, but to a slightly broader concept (so-called “up-hill mappings”). For example, ICD10CM W61.51 “Bitten by goose” has no equivalent in the SNOMED vocabulary, which is generally used for standard condition concepts. Instead, it is mapped to SNOMED 217716004 “Peck by bird,” losing the context of the bird being a goose. Up-hill mappings are only used if the loss of information is considered irrelevant to standard research use cases.

Some mappings connect a source concept to more than one Standard Concept. For example, ICD9CM 070.43 “Hepatitis E with hepatic coma” is mapped to both SNOMED 235867002 “Acute hepatitis E” as well as SNOMED 72836002 “Hepatic Coma.” The reason for this is that the original source concept is a pre-coordinated combination of two conditions, hepatitis and coma. SNOMED does not have that combination, which results in two records written for the ICD9CM record, one with each mapped Standard Concept.

Relationships “Maps to value” have the purpose of splitting of a value for OMOP CDM tables following an entity-attribute-value (EAV) model. This is typically the case in the following situations:

- Measurements consisting of a test and a result value
- Personal or family disease history
- Allergy to substance
- Need for immunization

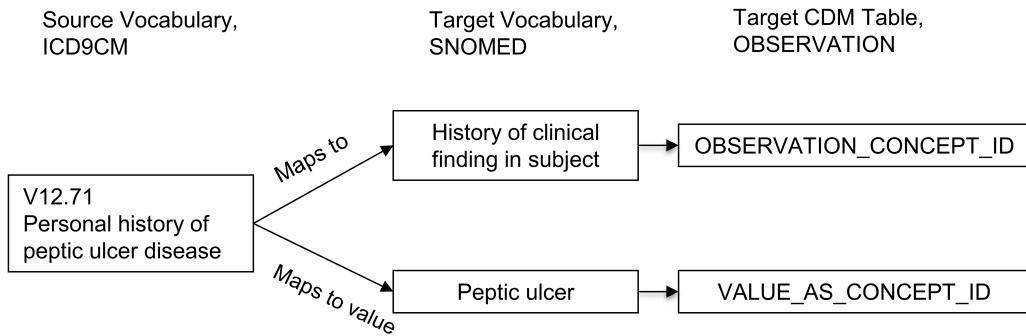


Figure 5.5: One-to-many mapping between source concept and Standard Concepts. A pre-coordinated concept is split into two concepts, one of which is the attribute (here history of clinical finding) and the other one is the value (peptic ulcer). While "Maps to" relationship will map to concepts of the measurement or observation domains, the 'Maps to value' concepts have no domain restriction.

In these situations, the source concept is a combination of the attribute (test or history) and the value (test result or disease). The "Maps to" relationship maps this source to the attribute concept, and the "Maps to value" to the value concept. See Figure 5.5 for an example.

Mapping of concepts is another central feature of the OMOP Standardized Vocabularies provided for free and supporting the efforts of the community conducting Network Studies. Mapping relationships are derived from external sources or maintained manually by the Vocabulary Team. This means they are not perfect. If you find wrong or objectionable mapping relationships it is crucial that you report and help improve the process through a Forums or CDM issue post.

A more detailed description of mapping conventions can be found in the OHDSI Wiki.⁵

5.3.2 Hierarchical Relationships

Relationships which indicate a hierarchy are defined through the "Is a" - "Subsumes" relationship pair. Hierarchical relationships are defined such that the child concept has all the attributes of the parent concept, plus one or more additional attributes or a more precisely defined attribute. For example, SNOMED 49436004 "Atrial fibrillation" is related to SNOMED 17366009 "Atrial arrhythmia" through a "Is a" relationship. Both concepts have an identical set of attributes except the type of arrhythmia, which is defined as fibrillation in one but not the other. Concepts can have more than one parent and more than one child concept. In this example, SNOMED 49436004 "Atrial fibrillation" is also an "Is a" to SNOMED 40593004 "Fibrillation."

⁵<https://www.ohdsi.org/web/wiki/doku.php?id=documentation:vocabulary:mapping>

5.3.3 Relationships Between Concepts of Different Vocabularies

These relationships are typically of the type “Vocabulary A - Vocabulary B equivalent”, which is either supplied by the original source of the vocabulary or is built by the OHDSI Vocabulary team. They may serve as approximate mappings but often times are less precise than the better curated mapping relationships. High-quality equivalence relationships (such as “Source - RxNorm equivalent”) are always duplicated by “Maps to” relationship.

5.3.4 Relationships Between Concepts of the Same Vocabulary

Internal vocabulary relationships are usually supplied by the vocabulary provider. Full descriptions can be found in the vocabulary documentation under the individual vocabulary at the OHDSI Wiki.⁶

Many of these define relationships between clinical events and can be used for information retrieval. For example, disorders of the urethra can be found by following the “Finding site of” relationship (see Table 5.5):

Table 5.5: “Finding site of” relationship of the “Urethra,” indicating conditions that are situated all in the this anatomical structure.

CONCEPT_ID_1	CONCEPT_ID_2
4000504 “Urethra part”	36713433 “Partial duplication of urethra”
4000504 “Urethra part”	433583 “Epispadias”
4000504 “Urethra part”	443533 “Epispadias, male”
4000504 “Urethra part”	4005956 “Epispadias, female”

The quality and comprehensiveness of these relationships varies depending on the quality in the original vocabulary. Generally, vocabularies that are used to draw Standard Concepts from, such as SNOMED, are chosen for the reason of their better curation and therefore tend to have higher quality internal relationships as well.

5.4 Hierarchy

Within a domain, standard and classification concepts are organized in a hierarchical structure and stored in the CONCEPT_ANCESTOR table. This allows querying and retrieving concepts and all their hierarchical descendants. These descendants have the same attributes as their ancestor, but also additional or more defined ones.

⁶<https://www.ohdsi.org/web/wiki/doku.php?id=documentation:vocabulary>

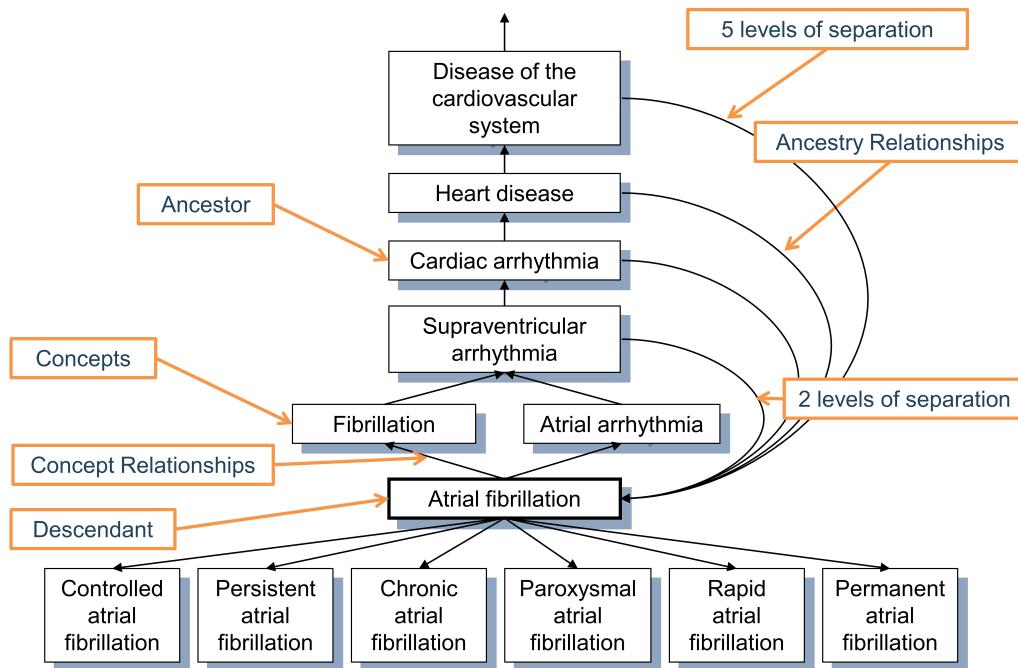


Figure 5.6: Hierarchy of the condition “Atrial fibrillation.” First degree ancestry is defined through “Is a” and “Subsumes” relationships, while all higher degree relations are inferred and stored in the CONCEPT_ANCESTOR table. Each concept is also its own descendant with both levels of separation equal to 0.

The CONCEPT_ANCESTOR table is built automatically from the CONCEPT_RELATIONSHIP table traversing all possible concepts connected through hierarchical relationships. These are the “Is a” - “Subsumes” pairs (see Figure 5.6), and other relationships connecting hierarchies across vocabularies. The choice whether a relationship participates in the hierarchy constructor is defined for each relationship ID by the flag DEFINES_ANCESTRY in the RELATIONSHIP reference table.

The ancestral degree, or the number of steps between ancestor and descendant, is captured in the MIN_LEVELS_OF_SEPARATION and MAX_LEVELS_OF_SEPARATION fields, defining the shortest or longest possible connection. Not all hierarchical relationships contribute equally to the levels-of-separation calculation. A step counted for the degree is determined by the IS_HIERARCHICAL flag in the RELATIONSHIP reference table for each relationship ID.

At the moment, a high-quality comprehensive hierarchy exists only for two domains: drug and condition. Procedure, measurement and observation domains are only partially covered and in the process of construction. The ancestry is particularly useful for the drug domain as it allows browsing all drugs with a given ingredient

or members of drug classes irrespective of the country of origin, brand name or other attributes.

5.5 Internal Reference Tables

DOMAIN_ID, VOCABULARY_ID, CONCEPT_CLASS_ID (all in CONCEPT records) and CONCEPT_RELATIONSHIP_ID (in CONCEPT_RELATIONSHIP) are all controlled by their own vocabularies. They are defined in the four reference tables DOMAIN, VOCABULARY, CONCEPT_CLASS and RELATIONSHIP, containing the *_ID fields as primary keys, a more detailed *_NAME field and a *_CONCEPT_ID field with a reference back to the CONCEPT table, which contains a concept for each of the reference table records. The purpose of these duplicate records is to support an information model allowing for automatic navigation engines.

The VOCABULARY table also contains the VOCABULARY_REFERENCE and VOCABULARY_VERSION fields referring to the source and version of the original vocabulary. The RELATIONSHIP table has the additional fields DEFINES_ANCESTRY, IS_HIERARCHICAL and REVERSE_RELATIONSHIP_ID. The latter defines the counter relationship ID for a pair of relationships.

5.6 Special Situations

5.6.1 Gender

Gender in the OMOP CDM and Standardized Vocabularies denotes the biological sex at birth. Often, questions are posed how to define alternative genders. These use cases have to be covered through records in the OBSERVATION table, where the self-defined gender of a person is stored (if the data asset contains such information).

5.6.2 Race and Ethnicity

These follow the definitions of how the US government defines this. Ethnicity is a differentiation of Hispanic or non-Hispanic populations, which can have any race. Race is divided into the common 5 top races, which have ethnicities as their hierarchical descendants. Mixed races are not included.

5.6.3 Diagnostic Coding Schemes and OMOP Conditions

Commonly used coding schemes such as ICD-9 or ICD-10 define more or less well-defined diagnoses based on a proper diagnostic work-up. The condition domain is not identical with this semantic space, but partially overlapping. For example, conditions also contain signs and symptoms that are recorded before a

diagnosis is derived, and ICD codes contain concepts that belong to other domains (e.g. procedures).

5.6.4 Procedure Coding Systems

Similarly, coding schemes like HCPCS and CPT4 are thought to be listings of medical procedures. In reality, they are more like a menu of justifications for payment for medical service. Many of these services are subsumed under the procedure domain, but many concepts fall outside this realm.

5.6.5 Devices

Device concepts have no standardized coding scheme that could be used to source Standard Concepts. In many source data, devices are not even coded or contained in an external coding scheme. For this same reason, there is currently no hierarchical system available.

5.6.6 Visits and Services

Visits concepts define the nature of healthcare encounters. In many source systems they are called Place of Service, denoting some organization or physical structure, such as a hospital. In others, they are called services. These also differ between countries, and their definition is hard to obtain. Care sites are often specializing on one of few visits (XYZ Hospital), but still should not be defined by them (even in XYZ hospital patients might encounter non-hospital visits).

5.6.7 Providers and Specialties

Any human provider is defined in the provider domain. These can be medical professionals such as doctors and nurses, but also non-medical providers like optometrists or shoemakers. Specialties are descendants of the provider “Physician.” Care Sites cannot carry a specialty, even though they are often defined by the specialty of their main staff (“Surgical department”).

5.6.8 Therapeutic Areas With Special Requirements

The Standardized Vocabularies cover all aspects of healthcare in a comprehensive fashion. However, some therapeutic areas have special needs and require special vocabularies. Examples are oncology, radiology, and genomics. Special OHDSI Working Groups develop these extensions. As a result, the OMOP Standardized Vocabularies constitutes an integrated system, where concepts from different origins and purposes all reside in the same domain-specific hierarchies.

5.6.9 Standard Concepts in the Drug Domain

Many concepts of the drug domain are sourced from RxNorm, a publicly available vocabulary produced by the US National Library of Medicine. However, drugs

outside the US may or may not be covered, depending on whether or not the combination of ingredient, form and strength is marketed in the US. Drugs that are not on the US market are added by the OHDSI Vocabulary Team under a vocabulary called RxNorm Extension, which is the only large domain vocabulary produced by OHDSI.

5.6.10 Flavors of NULL

Many vocabularies contain codes about absence of information. For example, of the five gender concepts 8507 “Male,” 8532 “Female,” 8570 “Ambiguous,” 8551 “Unknown,” and 8521 “Other”, only the first two are Standard, and the other three are source concepts with no mapping. In the Standardized Vocabularies, there is no distinction made why a piece of information is not available; it might be because of an active withdrawal of information by the patient, a missing value, a value that is not defined or standardized in some way, or the absence of a mapping record in CONCEPT_RELATIONSHIP. Any such concept is not mapped, which corresponds to a default mapping to the Standard Concept with the concept ID = 0.

5.7 Summary



- All events and administrative facts are represented in the OMOP Standardized Vocabularies as concepts, concept relationships, and concept ancestor hierarchy.
- Most of these are adopted from existing coding schemes or vocabularies, while some of them are curated de-novo by the OHDSI Vocabulary Team.
- All concepts are assigned a domain, which controls where the fact represented by the concept is stored in the CDM.
- Concepts of equivalent meaning in different vocabularies are mapped to one of them, which is designated the Standard Concept. The others are source concepts.
- Mapping is done through the concept relationships “Maps to” and “Maps to value”.
- There is an additional class of concepts called classification concepts, which are non-standard, but in contrast to source concepts they participate in the hierarchy.
- Concepts have a life-cycle over time.
- Concepts within a domain are organized into hierarchies. The quality of the hierarchy differs between domains, and the completion of the hierarchy system is an ongoing task.
- You are strongly encouraged to engage with the community if you believe you found a mistake or inaccuracy.

5.8 Exercises

Prerequisites

For these first exercises you will need to look up concepts in the Standardized Vocabularies, which can be done through ATHENA⁷ or ATLAS.⁸

Exercise 5.1. What is the Standard Concept ID for “Gastrointestinal hemorrhage”?

Exercise 5.2. Which ICD-10CM codes map to the Standard Concept for “Gastrointestinal hemorrhage”? Which ICD-9CM codes map to this Standard Concept?

Exercise 5.3. What are the MedDRA preferred terms that are equivalent to the Standard Concept for “Gastrointestinal hemorrhage”?

Suggested answers can be found in Appendix E.2.

⁷<http://athena.ohdsi.org/>

⁸<http://atlas-demo.ohdsi.org>

Chapter 6

추출 변환 적재

챕터 작성자 : *Clair Blacketer & Erica Voss*

6.1 서론

원천 데이터에서 OMOP 공통 데이터 모델(Common Data Model, CDM)을 얻기 위해서는 추출, 변환, 적재(Extract Transform Load, ETL) 절차가 필요하다. 이 절차는 데이터를 CDM으로 재구축 과정이며, 표준용어로의 매핑, SQL 코드들을 이용한 자동화된 절차로 이루어지게 된다. ETL 절차는 원천 데이터가 갱신될 때마다 언제든지 재수행 가능하게끔 반복 가능하게 구축하는 것이 중요하다.

ETL을 진행한다는 것은 많은 일들을 필요로 한다. 몇 년 동안의 과정을 통해 우리는 4가지 단계들로 이루어진 최상의 단계들을 개발하였다.

1. 데이터 전문가와 CDM 전문가가 함께 ETL을 설계할 것.
2. 의학 지식이 있는 사람들이 코드 매핑을 작업할 것.
3. 기술자가 ETL을 수행할 것.
4. 모든 사람이 질 관리에 참여할 것.

이 챕터에서 우리는 각 단계들을 세부적으로 살펴볼 것이다. 각 절차들을 보조하기 위해 다양한 도구들이 OHDSI 커뮤니티에 의해 개발되어왔고, 이 도구들에 대해서도 다룰 것이다. 마지막으로 CDM과 ETL의 유지에 관해 이야기하며 마무리할 것이다.

6.2 1단계 : ETL 설계

ETL 설계와 ETL 수행을 명확하게 분리하는 것은 중요하다. ETL을 설계하는 것은 원천 데이터와 CDM 모두에 대한 넓은 지식을 필요로 한다. 반대로 ETL을 수행할 때는 ETL을 기술적인 측면에서 효율적으로 수행하는 방법에 대해 기술 전문가들에게 의존하게 된다. 만약 동시에 두 가지 모두를 진행하려 한다면, 전체적인 그림에 집중할 때보다 세부적인 사항에서 막히게 될 가능성성이 높다.

두 가지의 밀접하게 연관된 도구들이 ETL 설계를 위해 개발되었다: 흰 토끼 (White Rabbit), 모자 속 토끼 (Rabbit-in-a-Hat)

6.2.1 흰 토끼 (White Rabbit)

ETL 절차를 시작하기 위해서는 테이블, 필드, 내용을 포함한 데이터에 대한 이해가 필요하다. 하단의 링크에 White Rabbit에 대한 정보가 기록되어 있다. White Rabbit은 장기적인 보건의료 데이터베이스의 OMOP CDM으로의 ETL 작업 준비를 도와주기 위한 소프트웨어이다. White Rabbit은 데이터를 탐색하고 ETL 설계를 시작하기 위한 필수적인 정보들에 대한 보고서를 생성해준다. 모든 소스 코드와 설치 방법 뿐만 아니라 설명서는 깃헙(Github)에서 확인 가능하다.¹

범위와 목표

White Rabbit의 주요 기능은 원천 데이터에 대한 탐색을 수행하고, 테이블, 필드, 필드값들에 대한 세부적인 정보를 제공하는 것이다. 원천 데이터는 comma-separated 텍스트 파일일 수도 있고, 데이터베이스(MySQL, SQL Server, Oracle, PostgreSQL, Microsoft APS, Microsoft Access, Amazon RedShift)에 적재되어 있을 수도 있다. 탐색 과정에서 Rabbit-In-a-Hat 도구와 함께 쓴다면 ETL을 설계할 때 참고할 수 있는 보고서를 생성할 수 있다. White Rabbit은 다른 표준 데이터 프로파일링 도구들과는 달리 개인 식별 정보(Personally Identifiable Information, PII)가 결과 데이터 파일에서 보여지는 것을 방지한다.

절차 개요

원천 데이터를 탐색하기 위해 소프트웨어를 사용하는 일반적인 순서:

1. 로컬 컴퓨터에서의 결과를 내보낼 작업 폴더를 설정.
2. 데이터베이스 혹은 CSV 텍스트 파일과의 연결 및 연결 확인.
3. 탐색 대상 테이블 선택 및 탐색.
4. White Rabbit의 원천 데이터에 대한 정보 생성 및 내보내기.

작업 폴더 설정

White Rabbit 어플리케이션의 다운로드 및 설치 이후, 처음으로 할 일은 작업 폴더를 설정하는 것이다. White Rabbit이 생성하는 모든 파일들은 설정한 로컬 폴더에 생성될 것이다. 그림 6.1에서 보여지는 “Pick Folder” 버튼을 사용하여 탐색 문서들이 저장될 로컬 환경을 탐색할 수 있다.

데이터베이스 연결

White Rabbit은 구분된 텍스트 파일들과 데이터베이스를 지원한다. 다양한 필드들에 대한 필요 항목들의 설명을 보려면 마우스를 올려야 한다. 더욱 자세한 설명은 설명서에서 확인할 수 있다.

¹<https://github.com/OHDSI/WhiteRabbit>.

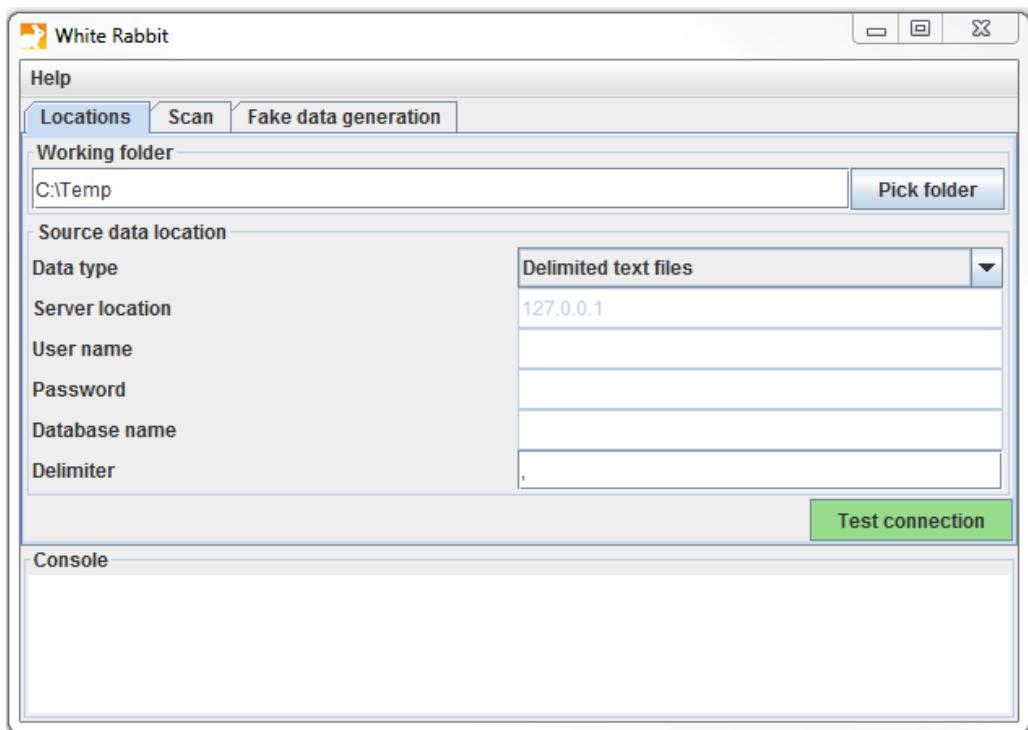


Figure 6.1: The "Pick Folder" button allows the specification of a working folder for the White Rabbit application.

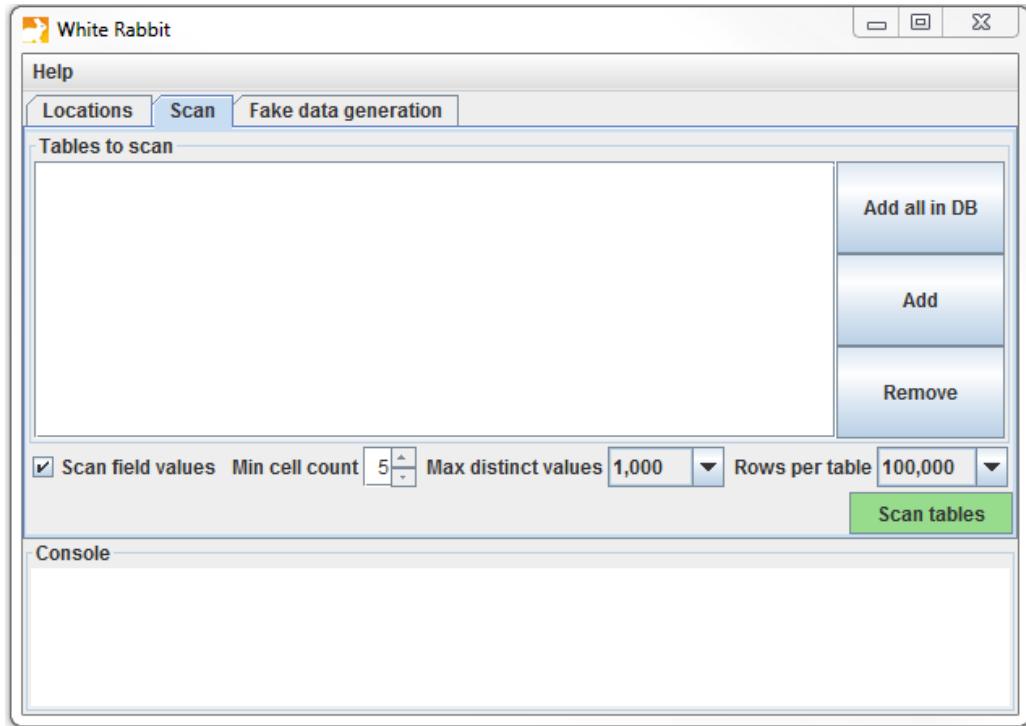


Figure 6.2: White Rabbit Scan tab.

데이터베이스의 테이블 탐색

데이터베이스에 연결한 이후에는 데이터베이스에 적재되어있는 테이블들을 탐색할 수 있다. 탐색 과정은 ETL을 설계하는데 도움을 되는 원천 데이터에 대한 정보를 담은 보고서를 생성할 수 있다. 그림 6.2에 보이는 Scan 탭의 “Add” (Ctrl + mouse click) 버튼을 눌러서 선택된 원천 데이터베이스의 각 테이블들을 선택하거나, “Add all in DB” 누름으로써 모든 테이블들을 자동적으로 선택할 수 있다.

탐색에 사용될 몇 가지 옵션들:

- “Scan field values” 는 열에 어떠한 값들을 나타나는지 보고싶을때 사용한다.
- “Min cell count” 는 필드값을 탐색할 때 쓰이는 옵션이다. 기본값은 5로 설정되어 있으며, 이는 원천 데이터에서 5번 이상으로 나타나는 값들은 보고서에 나타내지 않는 것을 의미한다. 각 데이터셋들은 각각의 고유한 규칙에 따라 minimal cell count가 정해져야할 것이다.
- “Rows per table” 는 필드값을 탐색할 때 쓰이는 옵션이다. 기본값으로 White Rabbit은 테이블에서 무작위로 100,000개의 행렬을 선택하여 탐색할 것이다.

모든 옵션들이 설정된 이후에는 “Scan tables”을 누르면 된다. 탐색이 완료된 이후에는 보고서가 작업 폴더에 생성될 것이다.

The screenshot shows a software interface for a database scan report. At the top, there's a navigation bar with tabs: Overview, dbo.allergies, dbo.carepla ..., and a search bar. The main area is a grid table with columns labeled A through G. Rows 1 through 8 show data for the 'dbo.allergies' table, and rows 9 through 18 show data for the 'dbo.careplans' table. The 'Overview' tab is currently selected.

	A	B	C	D	E	F	G
1	Table	Field	Type	Max length	N rows	N rows checked	Fraction empty
2	dbo.allergies	start	date	10	3184	3184	0
3	dbo.allergies	stop	date	10	3184	3184	0.725188442
4	dbo.allergies	patient	varchar	36	3184	3184	0
5	dbo.allergies	encounter	varchar	36	3184	3184	0
6	dbo.allergies	code	varchar	9	3184	3184	0
7	dbo.allergies	description	varchar	24	3184	3184	0
8							
9	dbo.careplans	id	varchar	36	30199	30199	0
10	dbo.careplans	start	date	10	30199	30199	0
11	dbo.careplans	stop	date	10	30199	30199	0.057849598
12	dbo.careplans	patient	varchar	36	30199	30199	0
13	dbo.careplans	encounter	varchar	36	30199	30199	0
14	dbo.careplans	code	varchar	15	30199	30199	0
15	dbo.careplans	description	varchar	62	30199	30199	0
16	dbo.careplans	reasoncode	varchar	9	30199	30199	0.050796384
17	dbo.careplans	reasondescription	varchar	56	30199	30199	0.050796384
18							

Figure 6.3: Example overview tab from a scan report.

The screenshot shows a small table with two columns, A and B. Column A contains the header 'Sex' and four data rows. Column B contains the header 'Frequency' and four data rows. Row 4 is highlighted with a red background and contains the text 'List truncated...'. The table has a light gray background and thin black borders.

	A	B
1	Sex	Frequency
2		2 61491
3		1 35401
4	List truncated...	

Figure 6.4: Example values for a single column.

탐색 보고서의 이해

탐색이 완료된 이후에는 선택된 작업 폴더에 엑셀 파일이 생성될 것이며, 엑셀 파일에는 스캔한 각 테이블에 대한 하나의 탭과 개요 탭이 생성된다. 개요 탭은 탐색한 모든 테이블들이며, 각 테이블의 필드, 각 필드의 데이터 타입, 필드의 최대 길이, 테이블의 행의 수, 탐색한 행의 수, 그리고 얼마나 많은 필드들이 비어있었는지 보여준다. 그림 6.3은 개요 탭의 예시를 보여준다.

각 테이블들의 탭들은 각각의 필드, 필드의 값들, 그리고 값들의 빈도를 나타낸다. 각 원천 테이블의 컬럼들은 엑셀에서 두 개의 컬럼들로 생성된다. 하나는 탐색 시 설정한 “Min cell count” 보다 큰 값들의 고유한 값을 보여준다. 만약 고유한 값 목록이 잘려있다면, 목록의 마지막 값은 “List truncated” 가 될 것이다; 이는 하나 혹은 그 이상의 값들이 “Min cell count” 보다 작은 고유한 값이 있음을 나타낸다. 각각의 고유한 값 옆에는 빈도를 나타내는 두 번째 컬럼이 있다(표본에서 값이 발생하는 횟수). 이 두 컬럼들(고유한 값과 빈도 수)은 작업책(workbook)의 프로파일링된 테이블의 모든 원천 변수들에 대해 반복되서 나타난다.

보고서는 원천 데이터에 무엇이 있는지를 강조함으로써 데이터를 이해하는데 강력한 도움을 준다. 예를 들면, 그림 6.4에 나타난 결과가 탐색된 테이블 중 하나인

“Sex”에 반환될 경우, 우리는 각각 61,491번과 35,401번 나타난 공통된 값들(1과 2)이 있음을 알 수 있다. White Rabbit은 1을 남성으로, 2를 여성으로 정의하지는 않을 것이다; 데이터 소유자가 일반적으로 원천 시스템에 고유한 원천 코드를 정의해야 한다. 하지만 이 두 가지 값(1 & 2)들은 데이터에 있는 유일한 값들이 아니기 때문에 우리는 잘린 목록을 확인해야한다. 이 값들은 (“Min cell count” 정의에 따라) 매우 낮은 빈도로 나타나게 되고, 종종 부정확하거나 매우 의심스러운 값들로 표현된다. ETL 수행을 계획할 때 우리는 높은 빈도의 성별 개념으로써 1과 2만 다루는 것이 아니라, 컬럼에 존재하는 낮은 빈도의 값들도 고려해야한다. 예를 들어 만약 낮은 빈도의 성별들이 “NULL”일 경우 ETL 진행 시 이러한 데이터에 대해 어떻게 처리할 것인지 확실히 해야한다.

6.2.2 모자 속 토끼 (Rabbit-In-a-Hat)

White Rabbit과 함께 우리는 원천 데이터에 대한 분명한 그림을 그릴 수 있다. 또한 우리는 CDM에 대한 전체 명세서를 알고 있다. 이제 우리는 하나에서 다른 하나로 넘어갈 로직을 정의해야한다. 이 설계 활동은 원천 데이터와 CDM 모두에 대한 온전한 지식을 요구한다. White Rabbit 소프트웨어와 함께 사용되는 Rabbit-in-a-Hat 도구는 명확하게 이 분야의 전문가들을 위해 개발되었다. 일반적으로 ETL 설계팀은 회의실에 같이 앉아 Rabbit-in-a-Hat을 프로젝터 화면으로 같이 보면서 작업을 한다. 첫 번째로 테이블 간의 매핑은 협력적으로 결정될 수 있으며, 그 후에는 필드 간의 매핑이 설계되는 동시에 어떤한 값들을 변환시킬지 로직을 정의할 수 있다.

범위와 목표

Rabbit-In-a-Hat은 White Rabbit의 탐색 문서들을 읽고 나타내기 위해 설계되었다. White Rabbit은 원천 데이터에 대한 정보를 생성하는반면, Rabbit-In-a-Hat은 그 정보를 사용하고 그래픽 사용자 인터페이스를 통하여 사용자들로 하여금 원천 데이터의 테이블과 컬럼들을 CDM으로 연결시켜끔 해준다. Rabbit-In-a-Hat은 ETL 절차에 대한 문서를 생성해주지만 ETL을 위한 코드는 생성하지 않는다.

절차 개요

소프트웨어를 이용한 ETL 문서 생성을 위한 일반적인 순서:

1. WhiteRabbit의 탐색 완료 결과.
2. 탐색 결과 확인; 인터페이스가 원천 테이블들과 CDM 테이블들을 보여줌.
3. 원천 테이블들의 정보와 상응하는 CDM 테이블들의 연결.
4. CDM 테이블에 상응하는 각 원천 테이블들에 대해서 세부적인 원천 컬럼과 CDM 컬럼의 연결을 정의.
5. Rabbit-In-a-Hat 작업을 저장하고 MS 워드 문서로 내보내기.

ETL 로직 작성

일단 Rabbit-In-a-Hat 내의 White Rabbit 탐색 보고서를 확인한다면, 원천 데이터를 OMOP CDM으로 변환하는 설계와 로직 작성은 시작할 준비가 된다. 하나의 예시

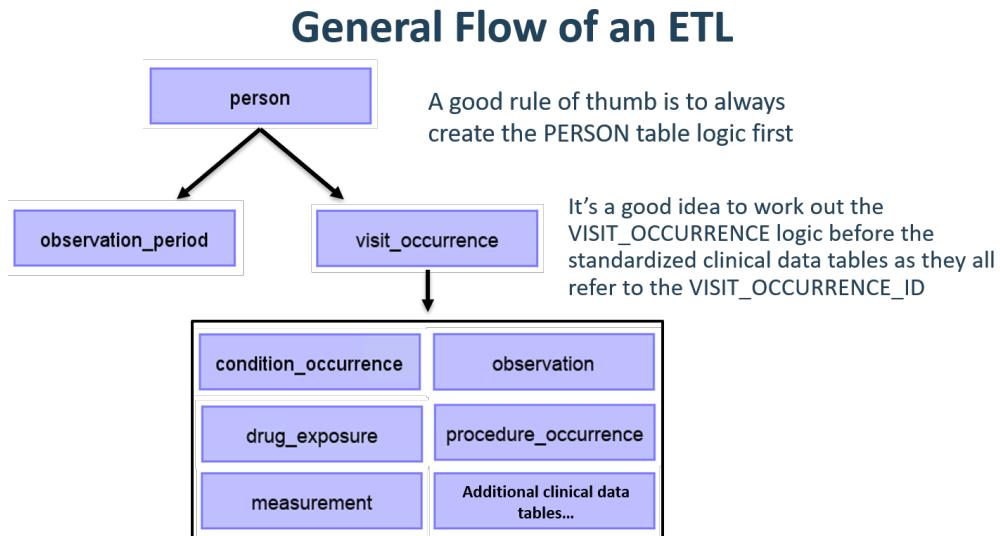


Figure 6.5: General flow of an ETL and which tables to map first.

로써 하단의 챕터들에서 Synthea² 데이터베이스의 일부 테이블들의 변환을 보여줄 것이다.

ETL의 일반적인 흐름

CDM이 사람 중심의 모델이기 때문에 PERSON 테이블 먼저 매핑을 시작하는 것이 좋다. 모든 임상적 사건과 관련있는 테이블들(CONDITION_OCCURRENCE, DRUG_EXPOSURE, PROCEDURE_OCCURRENCE 기타 등.)은 PERSON 테이블의 person_id를 참조하기에 PERSON 테이블에 대한 로직을 먼저 작성하는 것이 나중을 위해 좋다. PERSON 테이블을 변환한 다음에는 OBSERVATION_PERIOD를 변환하는 것이 좋은 선택이다. CDM 데이터베이스의 각 사람들은 최소한 하나의 OBSERVATION_PERIOD를 가져야하고, 일반적으로 한 사람에 대한 모든 사건들은 이 관측시기 내에 맞춰지게 된다. PERSON과 OBSERVATION_PERIOD 테이블들이 완료되면 보통 PROVIDER, CARE_SITE, 그리고 LOCATION과 같은 디멘션 테이블(dimensional table)들이 다음 대상이 된다. 임상 테이블 이전에 마지막으로 로직을 작성해야하는 테이블은 VISIT_OCCURRENCE이다. 한 사람의 환자로써의 여성에서 대부분의 사건들이 방문할 때 발생하기 때문에 종종 모든 ETL 과정에서 가장 복잡하고 중요한 부분이기도 하다. 일단 이 테이블들이 완료되면 어떤 CDM 테이블들 어떤 순서대로 매핑할지는 선택하기 나름이다.

CDM 변환 과정에서 종종 중간 테이블들을 만들 필요가 있을 수 있다. 올바른 VISIT_OCCURRENCE_ID들을 해당 사건들에 부여하거나 아니면 원천 코드를 표준 코드로 매핑하는 경우들일 수도 있다(이 단계는 종종 매우 느리게 진행된다).

²Synthea™ is a patient generator that aims to model real patients. Data are created based on parameters passed to the application. The structure of the data can be found here: <https://github.com/synthetichealth/synthea/wiki>.

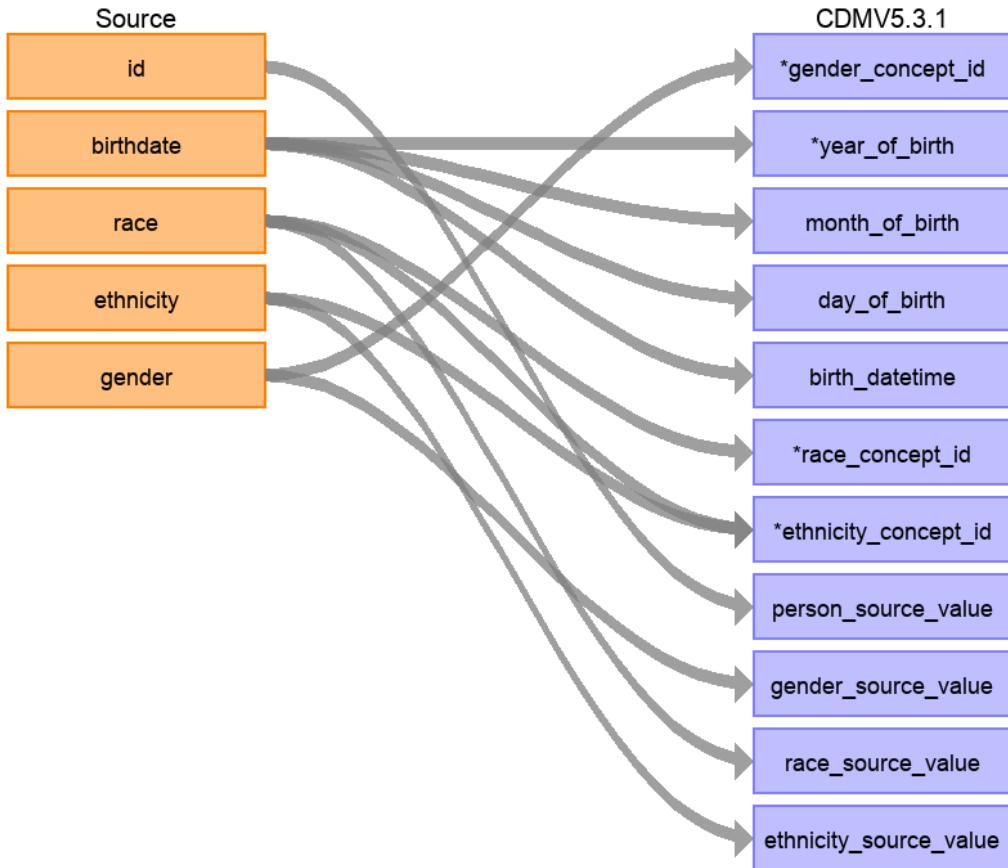


Figure 6.6: Mapping of Synthea Patients table to CDM PERSON table.

중간 테이블들은 100% 허용되고 장려된다. 하지만 이러한 중간 테이블들이 변환이 완료된 이후에도 남아있거나 사용되는 것은 장려되지 않는다.

매핑 예시: PERSON 테이블

Synthea 데이터 구조에서 환자 테이블은 20개의 열들을 갖고 있지만 그림 6.6에서 보이는 것처럼 모든 열들이 PERSON 테이블에 필요한 것은 아니다. 이런 일은 매우 흔한 일이고 문제가 되지 않는다. 이 예시에서는 환자 이름, 운전면허번호, 여권 번호 등 Synthea의 환자 테이블의 많은 데이터 포인트들이 CDM PERSON 테이블에 사용되지 않는 것을 알 수 있다.

하단의 표 6.1는 Synthea의 환자 테이블이 CDM PERSON 테이블로 변환되는 로직을 보여준다. ‘Destination Field’는 CDM 데이터의 어디에 매핑되는지를 나타낸다. ‘Source field’는 원천 테이블(예시에서는 환자 테이블)의 어느 열에서 CDM의 열로 변하는지 나타낸다. 마지막으로, ‘Logic & comments’는 로직에 대한 설명을 의미한다.

Table 6.1: ETL logic to convert the Synthea Patients table to CDM PERSON table.

Destination Field	Source field	Logic & comments
PERSON_ID		Autogenerate. The PERSON_ID will be generated at the time of implementation. This is because the id value from the source is a varchar value while the PERSON_ID is an integer. The id field from the source is set as the PERSON_SOURCE_VALUE to preserve that value and allow for error-checking if necessary.
GENDER_CONCEPT_ID	gender	When gender = 'M' then set GENDER_CONCEPT_ID to 8507, when gender = 'F' then set to 8532. Drop any rows with missing/unknown gender. These two concepts were chosen as they are the only two standard concepts in the gender domain. The choice to drop patients with unknown genders tends to be site-based, though it is recommended they are removed as people without a gender are excluded from analyses.
YEAR_OF_BIRTH	birthdate	Take year from birthdate
MONTH_OF_BIRTH	birthdate	Take month from birthdate
DAY_OF_BIRTH	birthdate	Take day from birthdate
BIRTH_DATETIME	birthdate	With midnight as time 00:00:00. Here, the source did not supply a time of birth so the choice was made to set it at midnight.
RACE_CONCEPT_ID	race	When race = 'WHITE' then set as 8527, when race = 'BLACK' then set as 8516, when race = 'ASIAN' then set as 8515, otherwise set as 0. These concepts were chosen because they are the standard concepts belonging to the race domain that most closely align with the race categories in the source.

Destination Field	Source field	Logic & comments
ETHNICITY_CONCEPT_ID	race ethnicity	When race = 'HISPANIC', or when ethnicity in ('CENTRAL_AMERICAN', 'DOMINICAN', 'MEXICAN', 'PUERTO_RICAN', 'SOUTH_AMERICAN') then set as 38003563, otherwise set as 0. This is a good example of how multiple source columns can contribute to one CDM column. In the CDM ethnicity is represented as either Hispanic or not Hispanic so values from both the source column race and source column ethnicity will determine this value.
LOCATION_ID		
PROVIDER_ID		
CARE_SITE_ID		
PERSON_SOURCE_ID		
VALUE		
GENDER_SOURCE_gender		
VALUE		
GENDER_SOURCE_CONCEPT_ID		
RACE_SOURCE_race		
VALUE		
RACE_SOURCE_CONCEPT_ID		
ETHNICITY_SOURCE_VALUE	ethnicity	In this case the ETHNICITY_SOURCE_VALUE will have more granularity than the ETHNICITY_CONCEPT_ID.
ETHNICITY_SOURCE_CONCEPT_ID		

Synthea 데이터의 CDM으로의 변환에 대한 더 자세한 설명은 전체 명세서를 참고 하면 된다.³

³<https://ohdsi.github.io/ETL-Synthea/>

6.3 2 단계: 코드 매핑 생성

점점 더 많은 원천 코드들이 OMOP 용어에 추가되어지고 있다. 이것은 CDM으로 변환된 데이터의 코딩 체계가 이미 CDM에 포함되거나 매핑되었을 수도 있다는 것을 의미한다. OMOP Vocabulary의 VOCABULARY 테이블을 통해 어떤 용어들이 포함되었는지 확인할 수 있다. 비표준인 원천 코드들(e.g. ICD-10CM codes)에서 표준용어들(e.g. SNOMED codes)로의 매핑을 확인하려면 CONCEPT_RELATIONSHIP 테이블 내의 relationship_id = “Maps to” 인 값들을 찾으면 확인할 수 있다. 예를 들면 ICD-10CM 코드 ‘I21’ (“Acute Myocardial Infarction”)의 표준용어 ID를 확인하기 위해 다음과 같은 SQL을 사용할 수 있다:

```
SELECT concept_id_2 standard_concept_id
FROM concept_relationship
INNER JOIN concept source_concept
  ON concept_id = concept_id_1
WHERE concept_code = 'I21'
  AND vocabulary_id = 'ICD10CM'
  AND relationship_id = 'Maps to';
```

STANDARD_CONCEPT_ID
312327

하지만 가끔은 원천 데이터가 Vocabulary에 없는 코딩 시스템을 사용할 수도 있다. 이러한 경우에는 원천 코딩 시스템의 Standard Concept으로의 매핑을 정의하여야 한다. 하지만 원천 코딩 시스템에 많은 수의 용어들이 있을 경우 코드 매핑이 어려울 수도 있다. 이를 쉽게 진행하기 위한 몇 가지 참고사항들이 있다.

- 가장 높은 빈도의 코드들에 집중하라. 절대 쓰이지 않는 코드나 거의 안 쓰이는 코드들은 실제 연구에서도 안 쓰이기 때문에 많은 노력을 들여서 매핑을 진행할 필요가 없다.
- 가능하면 기존의 정보들을 활용하라. 예를 들어서 많은 국가 약물 코딩 시스템은 이미 ATC로 매핑되어있다. 비록 ATC가 많은 목적에 대해 세부적으로 부합하지는 않지만, ATC와 RxNorm의 관계를 통해 어떤 RxNorm 코드들이 사용되는지 추측할 수는 있다.
- 우사기(Usagi)를 사용하라.

6.3.1 우사기(Usagi)

우사기(Usagi)는 코드 매핑의 절차를 도와주는 도구이다. Usagi는 코드 설명의 단어 유사도에 기반하여 매핑을 추천할 수 있다. 만약 원천 코드가 외국어로만 확인 가능하다면, Google Translate⁴를 통해 종종 해당 용어들의 훌륭한 영어 번역을 확인할 수 있다. Usagi는 사용자들로 하여금 자동 추천이 정확하지 않을 경우 적절한 목표

⁴<https://translate.google.com/>

개념을 찾을 수 있도록 하고 있다. 최종적으로 사용자는 어떤 매핑이 ETL에 사용될 수 있는지 지정할 수 있다. Usagi는 GitHub⁵를 통해 사용할 수 있다.

범위와 목표

매핑이 필요한 원천 코드들은 Usagi로 불러올 수 있다(만약 코드들이 영어가 아닐 경우, 추가적으로 번역된 열들이 필요하다). 단어 유사도 접근법은 원천 코드와 Vocabulary 개념들을 연결시키기 위해 필요하다. 하지만 이러한 코드 연결은 수동적으로 검토해야하고, Usagi는 이를 수행하기 위한 인터페이스를 제공한다. Usagi는 Vocabulary에 Standard인 concept들만을 제안한다.

절차 개요

소프트웨어를 사용하기 위한 일반적인 순서:

1. 원천 시스템(“원천 코드”)로부터 Vocabulary concepts들로의 매핑을 진행하고 싶은 코드들을 올림.
2. Usagi 단어 유사도 접근법을 이용하여 Vocabulary concepts들로의 매핑을 진행.
3. Usagi 인터페이스를 활용하여 제안된 매핑을 확인하고 필요할 경우 개선.
4. 매핑 결과를 Vocabulary의 SOURCE_TO_CONCEPT_MAP으로 내보냄.

Usagi로의 원천 코드 가져오기

원천 시스템에서 CSV나 엑셀(.xlsx) 파일로 원천 코드들을 내보낸다. 이 때 파일은 원천 코드와 영어 코드 설명에 대한 열들이 있어야하지만, 추가적인 정보들 역시 더해질 수 있다(e.g. 약물 용량, 번역되었을 경우 원래 언어로의 코드 설명). 게다가 원천 코드에 대한 정보 뿐만 아니라, 어떤 코드를 먼저 매핑해야 할지 정하는데 도움이 되기 때문에 빈도 역시 포함되었는 것이 좋다(e.g. 1,000개의 원천 코드를 가져올 수 있지만, 100개만 실제 시스템에 정말로 사용되는 경우). 만약 원천 코드가 영어로의 번역이 필요할 경우, Google Translate이 도움이 될 수 있다.

참고: 원천 코드는 도메인(domain)에 의해 분류되어야하며, 하나의 파일로 묶여서는 안됨.

파일로부터 원천 코드를 Usagi로 올린다 -> 코드 메뉴를 가져온다. 여기서 “Import codes ...”는 그림 6.7과 같이 보일 것이다. 이 그림에서 원천 코드 용어들은 네덜란드어이고, 영어로 번역되어있다. Usagi는 표준용어로의 매핑을 위해 영어 번역을 이용할 것이다.

“Column mapping” 부분(왼쪽 아래)은 Usagi로 하여금 불러온 테이블을 어떻게 사용할 것인지 정하는 단계이다. 만약 마우스를 끌어다 놓으면, 각 컬럼들을 정의하는 팝업창이 나타날 것이다. Usagi는 원천 코드를 Vocabulary concept 코드에 연결시키는 정보로써 “Additional info” 컬럼을 사용하지 않을 것이다; 하지만 이 추가적인 정보는 개인이 원천 코드 매핑을 검토하는데 도움을 줄 수 있기에 포함되어야 한다.

⁵<https://github.com/OHDSI/Usagi>

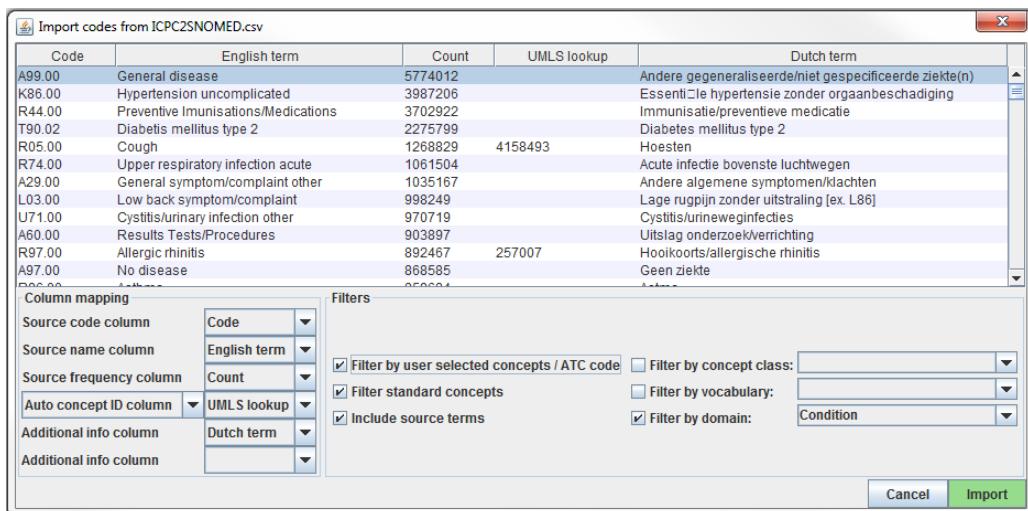


Figure 6.7: Usagi source code input screen.

마지막으로 “Filters” 부분(아래 오른쪽)에서 Usagi로 매핑할 때의 몇 가지 제한을 설정할 수 있다. 예를 들어 그림 6.7에서 사용자는 Condition 도메인에만 원천 코드를 매핑하고 있다. 기본적으로 Usagi는 Standard Ceoncepts에만 매핑을 진행하지만, 만약 “Filter standard concepts” 옵션이 아닐 경우, Usagi는 Classification Concepts 또한 검토할 것이다. 마우스를 다른 필터에 올려놓으면 해당 필터에 대한 추가적인 정보가 나타날 것이다.

한 가지 특별한 필터는 “Filter by automatically selected concepts / ATC code”이다. 만약 검색에 조건을 걸어야 한다면, 자동 concept ID로 표시되는 컬럼(세미콜론으로 구분)에 CONCEPT_ID 목록이나 ATC 코드를 제공하여 하면 된다. 예를 들어 약물의 경우 이미 각 약들에 ATC 코드가 이미 할당되어 있을 수 있다. 비록 ATC 코드가 하나의 RxNorm 약물 코드로 인지되지 않더라도, Vocabulary의 ATC 코드 한정으로 검색을 제한하는데 도와줄 수 있다. ATC 코드를 사용하려면 다음 절차를 따르면 된다:

1. 컬럼 매핑 부분에서, “Auto concept ID column”을 “ATC column”로 바꾸어라.
2. 컬럼 매핑 부분에서, ATC 코드가 포함된 열을 “ATC column”으로 선택하여라.
3. “Filter by user selected concepts / ATC code” 필터를 눌러라.

또한 ATC 코드 이외의 다른 것들로도 조건을 설정할 수 있다. 위의 그림 예시에서 보여지듯이 우리는 UMLS의 부분 매핑을 이용하여 Usagi의 검색을 설정하였다. 이런 경우에는 “Auto concept ID column”을 사용하여야 한다.

일단 모든 설정을 마치고 나면, “Import” 버튼을 눌러서 파일을 불러와야한다. 파일 불러오기를 할 때 단어 유사도 알고리즘을 이용하여 원천 코드를 매핑하기 때문에 대략 몇 분 정도 소요될 수 있다.

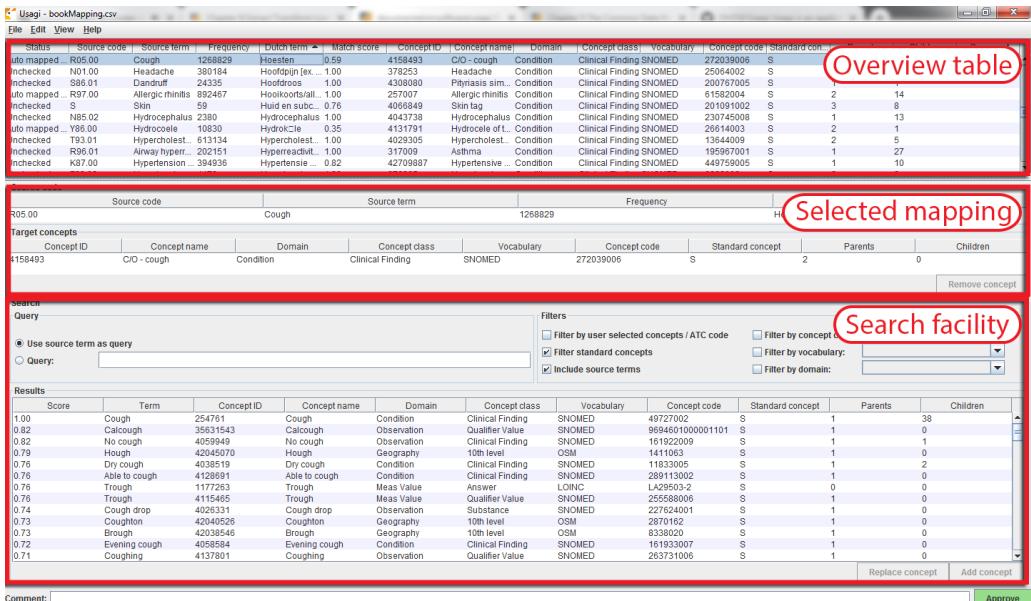


Figure 6.8: Usagi source code input screen.

원천 코드의 Vocabulary Concept 매핑 검토

일단 원천 코드의 파일을 불러오면, 매핑 절차가 시작된다. 그림 6.8에서 Usagi 화면이 3가지 주요 기능으로 구분된 것을 확인할 수 있다: 개요 테이블, 선택된 매핑 테이블, 검색 기능. 이 때, 오른 클릭을 하여 어떤 테이블에 대해서도 컬럼들을 선택하여 숨기거나 가려서 시각적 복잡성을 줄일 수 있다는 것을 참고하면 된다.

제안된 매핑의 승인

“Overview Table”은 현재의 원천 코드의 매핑을 보여준다. 원천 코드를 불러온 직후, 검색 설정과 단어 유사도를 기반으로 자동으로 생성되고 제안되는 매핑을 포함하고 있다. 그림 6.8에서 나타나듯이, 사용자가 검색 옵션을 Condition으로 설정했기에 네덜란드어 Condition 코드의 영어 이름은 Condition 도메인의 표준용어로 매핑되는 것을 볼 수 있다. Usagi는 원천 코드 기술서의 컨셉 이름과 동의어를 비교함으로써 최적의 매칭을 수행한다. 사용자가 “Include source terms”를 선택하였기 때문에 Usagi는 vocabulary의 특정 코드로 매핑되는 모든 원천 코드의 이름과 동의어까지 검토하게 된다. 만약 Usagi가 매핑을 진행할 수 없을 경우, CONCEPT_ID = 0 으로 매핑될 것이다.

코딩 시스템에 익숙한 사람이 원천 코드의 표준 용어로의 매핑을 도와주는 것이 권장된다. 각 개인은 “Overview Table” 탭에서 각 코드에 대하여 Usagi가 권장하는 매핑을 받아들이거나 아니면 새로운 매핑을 선택하는 작업을 하게 된다. 예를 들어 그림 6.8에서 우리는 네덜란드어 “Hoesten”가 영어 “Cough”로 번역되는 것을 볼 수 있다. Usagi는 “Cough”를 사용하고 Vocabulary 개념 “4158493-C/O - cough”로 매핑을 한다. 이 때의 매핑에 대하여 매칭 점수는 0.58(매칭 점수는 일반적으로 0

에서 1의 값을 가짐)이였고, 이는 Usagi가 이 네덜란드어에 대하여 SNOMED에 대해 매핑한 결과에 대해 확실하게 제시하기 어렵다는 것을 의미한다. 이 예시에서는 해당 매핑 결과에 동의하였고, 화면의 하단 우측의 “Approve” 버튼을 클릭함으로써 승인하였다.

새로운 매핑의 탐색

Usagi가 제시해주는 매핑에 대하여 사용자가 새로운 매핑을 찾거나 아니면 컨셉이 없도록(CONCEPT_ID = 0) 하는 경우들도 있을 것이다. 그럼 6.8의 예시를 통해 네덜란드어 “Hoesten”가 영어 “Cough”로 번역되는 것을 확인할 수 있었다. Usagi의 제안은 UMLS에서 파생된 매핑으로 제한되기에, 그 결과가 적합하지 않을 수도 있다. 검색 기능을 통해서 실제 용어 자체 혹은 검색 상자 쿼리를 이용해서 다른 컨셉들을 찾을 수 있다.

메뉴얼 검색 상자를 이용할 때, Usagi는 구조화된 검색 쿼리를 지원하지 않고 fuzzy search를 한다는 것을 기억하여야 한다. 그리고 현재까지는 AND나 OR과 같은 Boolean 연산자에 대해서는 검색을 지원하지 않고 있다.

“Cough”에 대해서 더 나은 매핑을 찾는다고 가정해보자. 검색 기능의 오른편 쿼리 부분에 Vocabulary 검색을 할 때 결과를 정리해주는 기능을 제공하는 필터 부분이 있다. 이러한 경우에는 우리는 표준 용어만을 찾아야 하며, 표준 용어에 매핑되는 코드의 이름과 동의어를 기반으로 검색할 수 있다.

이러한 검색 기준을 적용한다면 “254761-Cough”과 같은 코드를 찾을 수 있으며, 이는 네덜란드어의 코드 매핑에 적합한 용어일 수도 있다. 이를 적용하기 위해 “Selected Source Code” 업데이트의 “Replace concept” 버튼을 누르고, “Approve” 버튼을 누르면 된다. 또한 “Add concept” 버튼이 있는데, 이는 하나의 원천 코드에 대한 다수의 표준 용어 개념 매핑을 할 수 있게 해준다(e.g. 일부 원천 코드들은 표준 용어와는 달리 다양한 질병들을 함께 포함하고 있을 수 있다).

개념 정보

적절한 개념을 찾아 매핑을 하려 할 때, 컨셉의 “social life”을 고려하는 것은 중요하다. 개념의 의미는 계층 구조에서의 위치에 따라 부분적으로 의존적일 수 있으며, 종종 계층적 지위와 거의 혹은 전혀 상관없고 대상 컨셉으로도 적절하지 않은 “orphan concepts”들도 있다. Usagi는 각 개념에 대해 얼마나 많은 부모, 자식 개념들이 있는지 알려주기도 하고, ALT + C를 누르거나 위쪽 메뉴바의 view -> Concept을 누르면 더 자세한 정보를 볼 수 있게 해준다.

그림 6.9은 개념 정보 패널을 보여준다. 개념의 일반적인 정보부터, 부모, 자식, 그리고 다른 원천 코드들과의 정보도 보여준다. 사용자는 이 패널을 이용해서 계층 구조를 탐색할 수 있고, 다른 목표 컨셉을 정할 수도 있다.

모든 코드가 끝날 때까지 코드를 따라 이 절차를 진행하면 된다. 화면의 맨 위의 원천 코드 목록에서, 열 머리글 별로 코드들을 정렬할 수 있다. 종종 최빈도부터 최저빈도의 코드까지 살펴보는 것을 권장한다. 화면의 하단 왼쪽 편에는 매핑을 허용한 코드들의 개수, 그리고 그에 따라 얼마나 많은 코드들이 발생했는지를 확인할 수 있다.

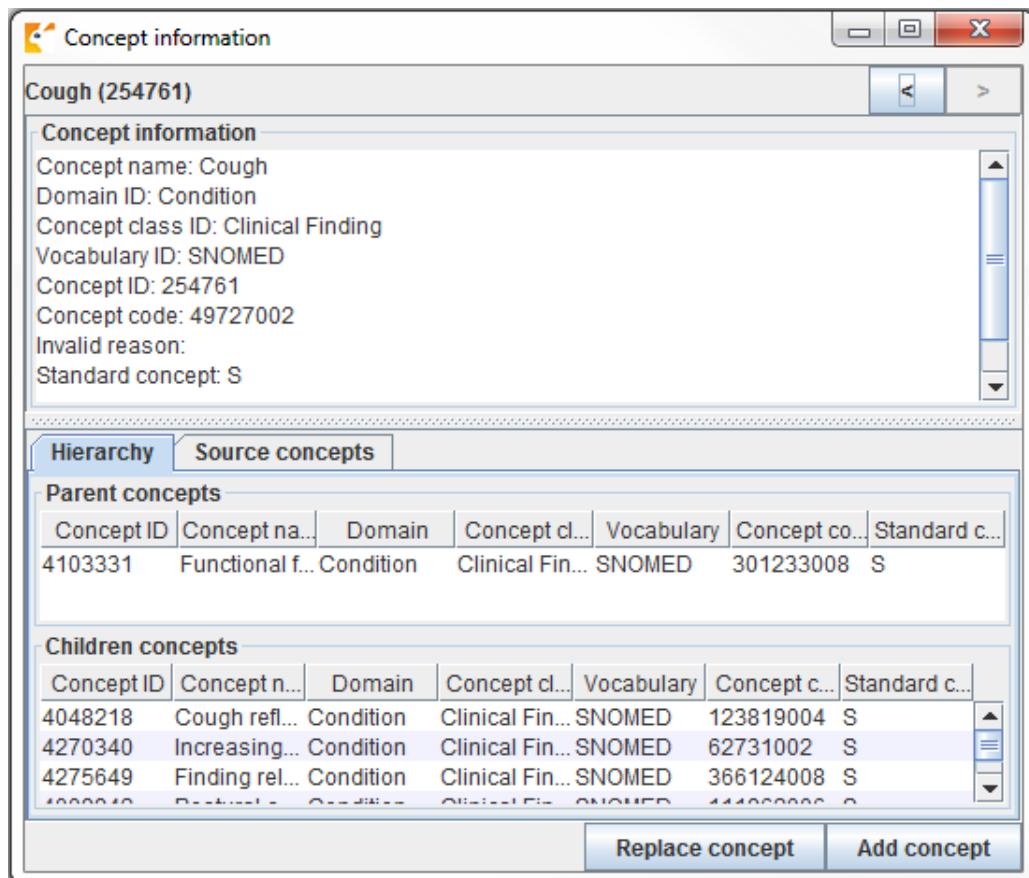


Figure 6.9: Usagi concept information panel.

또한 매핑 결정에 대한 설명을 추가하여 문서화 시에 사용할 수도 있다.

최적의 절차

- 코딩 스키마에 경험이 있는 사람이 할 것
- “Overview Table”的 컬럼들을 컬럼 이름을 눌러서 정렬할 수 있다. “Match Score”를 눌러서 정렬하는 것이 중요할 수도 있다; Usagi가 가장 확실하게 제안하는 매핑 코드들을 검토하면 많은 코드들이의 작업이 빠르게 끝날 수도 있다. 그리고 빈도가 높은 단어와 낮은 단어들에 쓰이는 노력이 각각 다르기 때문에 “Frequency”로 정렬해서 작업하는 것도 중요하다.
- CONCEPT_ID= 0으로 매핑하는 것도 괜찮지만, 어떤 코드들은 최적의 매핑 코드들이 없을 수도 있고, 어떤 것들은 단지 마땅한 코드들이 없어서 일 수도 있다.
- 특히 부모 계층과 자녀 계층에 대해서는 개념의 내용을 고려하는 것이 중요하다.

Usagi 매핑 내보내기

일단 USAGI를 통해 매핑을 생성하였으면, 이를 사용하기 가장 좋은 방법은 매핑을 내보낸 다음 Vocabulary의 SOURCE_TO_CONCEPT_MAP 테이블에 추가하는 것이다.

매핑을 내보내기 위해서는, File -> Export source_to_concept_map으로 가면 된다. 이 때 어느 SOURCE_VOCABULARY_ID를 이용할 것인지 묻는 팝업창이 나타나는데 짧은 식별자를 입력하면 된다. Usagi는 입력된 식별자를 이용할 것이다. SOURCE_VOCABULARY_ID가 SOURCE_TO_CONCEPT_MAP 테이블의 특정 매핑을 식별할 수 있게끔 할 수 있다.

SOURCE_VOCABULARY_ID를 선택한 후에는, 내보낼 CSV 파일의 이름과 파일 경로를 입력하게 된다. 내보내는 CSV 파일의 구조는 SOURCE_TO_CONCEPT_MAP 테이블과 동일하다. 이 매핑은 Vocabulary의 SOURCE_TO_CONCEPT 테이블로 추가될 수 있다. 그리고 앞선 단계에서 정의한 SOURCE_VOCABULARY_ID를 정의하는 VOCABULARY 테이블에 단일 행으로 추가하는 것이 좋다. 마지막으로, “Approved” 상태인 매핑들만을 CSV 파일로 내보내는 것이 중요하다; 매핑을 내보내기 위해서는 USAGI에서 매핑을 완료해야만 한다.

Usagi 매핑 업데이트

매핑은 종종 한 번에 끝나지 않는다. 원천 코드가 추가되는 식으로 데이터가 업데이트 되거나 용어가 정기적으로 업데이트되면 매핑 또한 업데이트 되어야 할 것이다.

원천 코드가 업데이트될 때는 다음과 같은 단계들을 따르는 것이 좋다:

1. 새로운 원천 코드 파일을 불러온다.
2. 파일을 고른다 -> 이전의 매핑을 적용시키고, 예전의 Usagi 매핑 파일을 선택 한다.
3. 이전의 매핑 파일에서 매핑되지 않았던 코드들을 식별하고, 새롭게 매핑한다.

용어가 업데이트 되면 아래의 단계를 따른다:

1. Athena에서 새로운 용어 파일들을 다운받는다.
2. Usagi 인덱스를 새로 빌딩한다(Help -> Rebuild index).
3. 매핑 파일을 연다.
4. 새로운 용어 버전에 따라 표준 용어가 아닌 코드들을 식별하여 적절한 목표 컨셉들을 찾는다.

6.4 3 단계: ETL 수행

일단 설계와 코드 매핑이 완료된다면, ETL 절차는 소프트웨어를 통해 수행 가능하다. ETL이 설계될 때, CDM과 원천 데이터 둘 다에 대해 잘 아는 사람이 참여하기를 권장하였다. 마찬가지로 ETL이 수행될 때도, 데이터(특히 빅데이터)와 ETL 수행 경험이 있는 사람이 참여하는 것이 바람직하다. 즉, 이건 그룹 외부의 기술 전문가를 고용하거나 초청하여 ETL 수행을 시키는 것일 수도 있다. 또한 이건 한 번에 끝나는 작업이 아니라는 점을 참고하기 바란다. 그렇기에 앞으로는 ETL 수행 및 유지에 일정 시간 이상을 할애할 수 있는 사람이나 팀이 있는 것이 좋을 것이다(6.7에서 더 명확히 설명할 것이다).

수행은 각 기관에 따라 다양한 양상을 보이며 특히 인프라, 데이터베이스의 크기, ETL의 복잡성, 기술 전문가의 능력 등의 요소에 따라 많이 달라진다. 많은 요소들에 따라 달라지기 때문에 OHDSI는 ETL을 수행하기 위한 최선의 방법에 대한 공식적인 권고를 하고 있지 않다. 그 동안 많은 그룹들이 SQL builders, SAS, C#, Java, Kettle들을 사용해왔다. 각각 장점들과 단점들이 있었고, 그 어느 것도 이러한 기술에 익숙한 사람이 없으면 아무것도 사용할 수 없었다.

각각 다른 ETL의 예시들 (복잡성에 따라 정렬됨):

- ETL-Synthea - SQL을 이용한 Synthea 데이터베이스 변환
- <https://github.com/OHDSI/etl-synthea>
- ETL-CDMBuilder - 다수의 데이터베이스를 변환하기 위해 고안된 .NET application
- <https://github.com/OHDSI/etl-cdmbuilder>
- ETL-LambdaBuilder - AWS lamda 기능을 이용한 빌더
- <https://github.com/OHDSI/etl-lambdabuilder>

그동안 많은 시도들이 있었지만, ‘ultimate’한 사용자 친화적인 ETL 도구를 개발하는데에는 포기했다. 항상 많은 경우에 이러한 도구들은 ETL 작업의 80%까지는 잘 수행하지만, 남은 20%에 있어서는 원천 데이터베이스에 따라 low-level에서의 코드 작성이 필요하다.

일단 기술 전문가가 수행할 준비가 된다면, ETL 설계 문서가 그들과 공유되어야 한다. 문서에는 수행을 시작할만한 충분한 정보가 있어야하지만, 항상 개발자들이 개발 과정 중에 ETL 설계자들에게 질문할 수 있는 환경 역시 마련되어있어야한다. ETL 설계자들에게는 로직이 명확해 보일지라도 CDM이나 데이터에 친숙하지 않은 수행자들에게는 명확하지 않아 보일 수도 있다. 그렇기에 수행 단계는 팀으로써 수행하여야 한다. 설계자들과 수행자들 모두 로직이 올바르게 작동한다고 동의할 때까지,

둘 사이에서 CDM 생성과 검증을 수행하는 것으로 간주한다.

6.5 4 단계: 질 관리

추출, 변환, 적재의 절차 수행을 위해서 질 관리는 반복적으로 수행된다. 질 관리의 전형적인 패턴은 로직 작성 -> 로직 수행 -> 로직 검증 -> 로직 수정 및 작성 이다. CDM을 검증하기 위한 많은 방법들이 있지만, 아래의 단계들은 몇 년간의 ETL 수행을 통해 OHDSI 내부에서 권고하는 단계들이다.

- ETL 설계 문서, 컴퓨터 코드, 코드 매핑을 검토하라. 어느 누구라도 실수를 할 수 있기 때문에, 항상 한 명 이상이 다른 사람이 어떤 작업을 수행하고 있는지 검토해야한다.
- 컴퓨터 코드의 가장 큰 문제점은 원천 데이터의 원천 코드가 표준 용어에 어떻게 매핑되었는지에 따라 나타나는 경향이 있는 것이다. 특히 NDC처럼 날짜와 관련있을 경우에 매핑이 더욱 어려울 수 있다. 원천 용어가 항상 적절한 개념으로 변환되도록 매핑이 수행되는 부분을 두 번씩 봐야한다.
- 원천 데이터와 목표 데이터의 표본으로로써 한 사람의 모든 정보를 수작업으로 비교하라.
- 여러 개의 기록을 갖고 있는 한 사람의 데이터를 살펴보는 것이 큰 도움이 될 수 있다. 한 사람의 기록을 추적함으로써 CDM 데이터가 로직에 따라 기대했던 결과와 다른 경우들을 발견해낼 수도 있다.
- 원천 데이터와 목표 데이터의 전체 수를 비교하라.
- 특정 문제들을 어떻게 해결하는지 설명하기에 따라 몇 가지 차이점들이 있을 수 있다. 예를 들면, 연구자들에 따라 성별이 NULL로 기록된 사람들을 어차피 연구에 포함되지 않기 때문에 삭제하기로 결정할 수도 있다. 그리고 CDM에서의 방문이나 원천 데이터에서의 방문이 다르게 구성될 수도 있다. 따라서 CDM과 원천 데이터의 총합을 비교할 때는 이러한 차이점들 발생할 수 있다는 것을 예상하고 설명할 수 있어야한다.
- 해당 CDM 버전에 대해 수행된 기준의 연구를 수행해본다.
- 비록 시간이 많이 들겠지만, 원천 데이터와 CDM 버전에 따른 큰 차이점들을 확인하기에 좋은 방법이다.
- ETL에서 다뤄야하는 원천 데이터들의 패턴을 따라하기 위한 단위 검정(Unit Test)을 작성하라. 예를 들어 만약 ETL 명세에서 성별 정보가 없는 환자들을 없애야 한다고 명시한다면, 성별이 없는 환자들에 대한 단위 검정을 작성하고 수행자가 처리하는 방안을 평가하라.
- 단위 검정은 ETL 변환의 정확도와 질을 평가하기 위한 편리한 방법이다. 보통은 변환하고자 하는 원천 데이터의 작은 표본을 사용한다. 데이터셋의 각 사람이나 기록은 ETL 문서에 기록된대로 로직의 특정 부분들로 검정해야한다. 이 방법을 쓴다면 issue를 파악하거나 로직 실패를 확인하기에 좋다. 작은 사이즈는 컴퓨터 코드가 훨씬 빠르고 여러 번 시행하기에도 좋고 에러를 빨리 확인하는데에도 좋다.

ETL의 관점에서 고차원의 질 관리 접근법도 있다. 데이터 질 관리에 대한 더 구체적인 노력은 OHDSI에서 진행되고 있으며, 챕터 15를 확인해주기 바란다.

6.6 ETL 협약과 THEMIS

많은 그룹들이 데이터를 CDM으로 변환함에 따라 구체적인 협약의 필요성이 명확해졌다. 예를 들어 만약 한 사람의 기록에서 출생년도가 없을 경우의 ETL은 어떻게 할 것인가? CDM의 목적은 보건의료 데이터의 표준화이지만 만약 모든 그룹이 데이터의 특정 시나리오를 각각 다르게 다룬다면 network를 통해 systematically하게 데이터를 다루는 것이 더욱 어려워질 것이다.

OHDSI 공동체는 CDM의 일관성을 증진시키기 위해 협약 문서 작성을 시작하였다. OHDSI가 동의하는 이러한 협약의 정의에 대해서는 CDM wiki를 통해 확인 가능하다.⁶ 각 CDM 테이블들은 ETL 설계시 참고될 수 있는 고유의 협약들을 가지고 있다. ETL을 설계할 때 이 협약들을 참고한다면 OHDSI와 동일한 일관성을 가질 수 있게끔 설계 디자인 결정을 내리게끔 도와줄 수 있다.

발생가능한 모든 데이터 시나리오에 대해서 어떻게 다뤄야할지에 대한 문서를 작성하는 것은 불가능하지만, OHDSI working group을 통해 공통적인 시나리오들을 문서화하는 것은 가능하다. THEMIS⁷는 협약들을 모으고, 명시하고, 공동체에 조언을 나눈 다음, 마지막으로 CDM wiki에 완성된 문서를 공개하는 일을 하는 각 개인들로 구성되어 있다. Themis는 고대 그리스의 질서, 공정함, 법, 자연법, 관습을 관장하는 티타니스로 이 그룹에 적합해보인다. ETL을 수행할 때, 만약 특정 시나리오에 대해 어떻게 할지 모르겠다면, THEMIS는 OHDSI 포럼에 질문을 남기기를 권장한다.⁸ 대부분의 경우 질문에 대해 community의 다른 사람들 역시 고민하고 있을 수 있다. THEMIS는 이런 토론들과 work group 미팅과 대면 토론들을 통하여 어떤 협약들이 문서화될 필요가 있는지 알려주고는 한다.

6.7 CDM과 ETL의 유지

ETL을 설계하고, 매핑을 만들고, ETL을 수행하고, 질 관리 검증들을 만드는 것은 절대 쉽지 않다. 안타깝게도, 여기서 끝이 아니다. 첫 번째 CDM이 만들어진 후 지속적으로 이어지는 ETL 유지의 과정이 있다. 유지를 요구하는 몇몇 공통되는 trigger들은 다음과 같다: 원천 데이터의 변화, ETL 상의 bug, 새로운 OMOP Vocabulary의 출시. ETL 수행에 새용되는 소프트웨어, 예시 검정들과 질 관리.

보건의료 데이터들은 종종 영원이 바뀌고는 한다. 새로운 데이터의 출시(e.g. 데이터에 새로운 열의 추가). 기존에 존재하지 않았던 새로운 환자 시나리오의 출현(e.g. 출생 전에 사망이 기록되어있는 새로운 환자). 데이터에 대한 이해도의 상승(e.g. 입원 아동 환자의 출생 기록이 청구 과정으로 인해 외래에서 발견). 원천 데이터의 모든 변경 사항에 대해서는 아니지만, 최소한 ETL 절차를 망가뜨리는 변경 사항들은 다루어야만 할 것이다.

만약 bugs들이 발견된다면 역시 다루어야 할 것이다. 하지만 모든 bugs들이 동일하게 생성되는 것은 아니라는 것을 염두해 두어야한다. 예를 들어 COST 테이블에서 cost 한 자릿수에서 반올림 되었다고 가정해보자(원천 데이터에서 \$3.82이 CDM에서는

⁶<https://github.com/OHDSI/CommonDataModel/wiki>.

⁷<https://github.com/OHDSI/Themis>

⁸<http://forums.ohdsi.org/>

\$4.00이 됨). 만약 이 데이터를 사용하는 주요 연구자들이 환자 약물 노출과 진단들에 대한 characterizations을 주로 한다면, 이는 별로 중요하지 않으며 향후 해결하면 된다. 만약 이 데이터를 사용하는 주요 연구자들 중 보건경제학자들이 있다면, 이는 즉시 해결해야되는 주요 문제가 될 것이다.

OMOP Vocabulary 역시 원천 데이터처럼 지속적으로 변화한다. 사실 Vocabulary는 한 달 안에도 용어들이 업데이트 됨에 따라 여러 개의 버전들을 가질 수 있다. 각 CDM은 특정 Vocabulary 버전 기반으로 운영되며, 새로운 Vocabulary 버전에 작동할 때 원천 코드들이 표준 용어로의 매핑 정도에 따라 다른 결과를 만들 수도 있다. Vocabulary들 간의 차이는 미미할 수도 있지만, Vocabulary가 새로 나올 때마다 CDM을 새로 만드는 것은 불필요하다. 하지만, 일 년에 한두 번 정도 새로 출시된 Vocabulary 기반으로 CDM을 재가공하는 것은 좋을 수 있다. ETL 코드 자체를 새로 업데이트해야 할 정도로 새로운 버전의 Vocabulary가 나오는 일은 매우 드물다.

CDM 또는 ETL의 유지를 하게끔 하는 마지막 trigger는 공통 데이터 모델 자체의 업데이트이다. 공동체가 커져감에 따라 새로운 데이터의 필요성이 커지고, 이는 CDM의 추가적인 데이터로 이끌게 된다. 이는 이전의 CDM에 없었던 데이터가 새로운 버전의 CDM에 들어갈 수 있는 것을 의미한다. CDM 구조의 변화는 잘 생기지 않지만 충분히 가능한 일이다. 예를 들어 CDM은 원래의 DATE 필드에서 DATETIME 필드로 적용해갔고, 이는 ETL 절차에서 에러를 발생시킬 수 있는 일이다. CDM 버전은 자주 출시되지 않고, 각 기관은 데이터를 옮길 때 결정할 수 있다.

6.8 ETL에 대한 마지막 생각

ETL 절차는 여러 가지 이유로 완전히 통달하기 어려운 절차인데 단순히 최소한 각각의 고유한 원천 데이터에 대해 작업하고 있을 뿐만이 아니라 “one-size-fits-all” 방안을 만드는 것이 어려워지고 있다. 하지만, 수년간 시도에서 배운 몇 가지 교훈들이 있다.

- 80/20 규칙. 피할 수만 있다면 너무 많은 시간을 원천 코드의 개념으로의 수동 매핑에 많은 시간을 할애하지 말아라. 데이터의 상당수를 차지하는 원천 코드들을 매핑하는 것이 이상적이다. 이건 시작하기에 충분할 것이고, 실제 사용 예시에 기반하여 남은 코드들도 다룰 수 있다.
- 연구 질에 맞지 않는 데이터를 잃어버리는 것은 괜찮다. 이런 기록들은 분석을 시작하기 전에 결국은 버려지게 되고, 우리는 대신 ETL 절차에서 삭제할 뿐이다.
- CDM은 유지를 필요로 한다. 단순히 ETL을 완료했다는 것은 두 번 다시 손대지 않는 것을 의미하는 것은 아니다. 원천 데이터는 변할 수도 있고, 코드에 bug가 있을 수도 있고, 새로운 용어가 나오거나 CDM에 업데이트가 있을 수 있다. 이러한 변화에 대비하고 ETL을 최신 상태로 유지하기 위해 자원을 할당하는 것이 필요하다.
- OHDSI CDM으로 시작하는 것을 돋고, 데이터베이스의 변환을 수행하거나 분석 도구를 사용하기 위해 Implementers Forum에 방문해주길 바란다.⁹

⁹<https://forums.ohdsi.org/c/implementers>

6.9 요약



- ETL을 위해 접근하는 일반적으로 다음과 같은 동의되는 절차들이 있다,
- 데이터 전문가와 CDM 전문가가 함께 ETL을 설계한다.
- 의료 지식이 있는 사람들이 코드 매핑을 진행한다.
- 기술 전문가가 ETL을 수행한다.
- 모든 사람들이 질 관리에 참여한다.
- 이러한 단계들을 돋기 위해 OHDSI 공동체에서 무료로 사용 가능한 도구들을 개발하였다.
- 많은 ETL 예시들이 있으며, 가이드로 삼을만한 협약들이 있다.

6.10 예제

Exercise 6.1. 다음 ETL 절차들을 올바른 단계로 정렬하시요:

- 가) 데이터 전문가와 CDM 전문가가 함께 ETL을 설계한다. 나) 기술 전문가가 ETL을 수행한다. 다) 의료 지식이 있는 사람들이 코드 매핑을 진행한다. 라) 모든 사람들이 질 관리에 참여한다.

Exercise 6.2. 선택한 OHDSI 자원을 활용하여, 테이블 6.3의 PERSON 기록에서 나타나는 4가지 문제들을 발견하시오(공간 상 축약된 형태의 표):

Table 6.3: A PERSON table.

Column	Value
PERSON_ID	A123B456
GENDER_CONCEPT_ID	8532
YEAR_OF_BIRTH	NULL
MONTH_OF_BIRTH	NULL
DAY_OF_BIRTH	NULL
RACE_CONCEPT_ID	0
ETHNICITY_CONCEPT_ID	8527
PERSON_SOURCE_VALUE	A123B456
GENDER_SOURCE_VALUE	F
RACE_SOURCE_VALUE	WHITE
ETHNICITY_SOURCE_VALUE	NONE PROVIDED

Exercise 6.3. VISIT_OCCURRENCE 기록들을 만들어보자. Synthea에 대한 예시로직이 다음과 같이 있다: PATIENT, START, END에 따라 오름차순으로 데이터를

Data Output Explain Messages Notifications Query History					
	id character varying (1000)	start date	stop date	patient character varying (1000)	encounterclass character varying (1000)
1	12	2004-09-26	2004-09-27	11	inpatient
2	13	2004-09-27	2004-09-30	11	inpatient

Figure 6.10: Example source data.

정렬하라. 그 다음 PERSON_ID 별로, 하나의 기록의 END 시간과 다음 기록의 START 시간의 차이가 1일 이하인 기록들을 하나로 만들어준다. 각 통합된 입원 환자 기록들은 하나의 입원 환자 방문으로 간주되며, 다음과 같이 설정된다:

- MIN(START) as VISIT_START_DATE
- MAX(END) as VISIT_END_DATE
- “IP” as PLACE_OF_SERVICE_SOURCE_VALUE

만약 아래와 같은 그림 6.10의 방문 기록들이 원천 데이터라고 가정한다면, CDM에서의 VISIT_OCCURRENCE 기록은 어떻게 보여질 것인가?

예시 답안은 Appendix E.3에서 확인할 수 있다.

Part III

Data Analytics

Chapter 7

데이터 분석 이용 사례

Chapter lead: David Madigan

OHDSI는 실세계 헬스케어 데이터 (일반적으로 보험청구 또는 의무기록 데이터베이스)로부터 믿을만한 근거를 만들어내는데 초점을 맞춰 왔다. OHDSI가 관심을 가져온 이용 사례들은 크게 3개의 카테고리로 구분된다:

- 특성 분석
- 인구 수준 추정
- 환자 수준 예측

본 장에서는 각 카테고리들에 대해 설명한다. 모든 이용 사례들에 있어서, 생성된 근거들은 데이터 자체가 가지고 있는 한계를 이어 받는다는 점을 유념하라. 이 한계들에 대해서는 이 책의 “근거의 질” 챕터에서 다루고 있다. (챕터 14 - 18)

7.1 특성 분석

특성 분석은 다음과 같은 질문에 답변을 시도한다.

그들에게 무슨 일이 발생했는가?

우리는 데이터를 이용하여 코호트 또는 전체 데이터베이스 내 환자들과 헬스케어의 특성을 묻는 질문에 답할 수 있으며, 시간이 경과함에 따라 이 특성들이 어떻게 변화하는지 알 수 있다.

데이터는 다음과 같은 질문들에 답을 제공할 수 있다:

- 심방세동으로 새 진단을 받은 환자들 중 얼마나 많은 사람이 와파린을 처방 받는가?
- 고관절 치환술을 받은 환자들의 평균 연령은 어떻게 되는가?
- 65세 이상 환자들 중 폐렴 발생률은 얼마나 되는가?

일반적인 특성 분석 질문들은 다음과 같이 표현된다:

- 얼마나 많은 환자들이...?
- 얼마나 자주...?
- 환자들 중 어느 정도의 비율이...?
- ... 검사에 대한 결과값의 분포가 어떠한가?
- ... 질병을 가진 환자들의 당화혈색소(HbA1c) 수준이 어떠한가?
- ... 환자들에 대한 검사 결과값이 어떠한가?
- 환자가 ...에 노출되는 평균 노출 기간은 얼마인가?
- ...의 시간 경과에 따른 트렌드는 무엇인가?
- 이 환자들이 사용하는 다른 약들이 무엇인가?
- 수반되는 치료법들이 무엇인가?
- ...에 대한 충분한 케이스들이 있는가?
- ...에 대한 연구X가 실행 가능한가?
- ...에 대한 인구통계학적 특징은 무엇인가?
- ...의 위험인자들이 무엇인가? (특정 위험인자가 구분된다면, 이는 예측이 아닌 추정에 해당함)
- ...의 예측요인들이 무엇인가?

그리고 원하는 결과값은 다음과 같다:

- 건수 또는 퍼센트
- 평균
- 기술 통계값
- 발병률
- 유병율
- 코호트
- 규칙 기반 표현형
- 약물 사용
- 질병의 자연 경과
- 이행
- 동반질환 프로필
- 치료 경로
- 치료 요법

7.2 인구 수준 추정

데이터가 한정된 범위까지는 헬스케어 개입의 효과에 대한 인과적 추론들을 제공할 수 있다

무엇이 인과 효과들인가?

우리는 행동의 결과를 이해하기 위해 인과 효과를 파악하고자 한다. 예를 들어, 우리가 어떤 치료법을 사용하기로 결정했다면, 이것이 앞으로 우리에게 무슨 변화를 일으킬까?

데이터는 다음과 같은 질문들에 답을 줄 수 있다:

- 새로 심방세동으로 진단받은 환자들에 있어서, 치료 시작한지 1년 내에 와파린이 다비가트란보다 주요 출혈을 더 일으키는가?
- 메트포르민이 설사에 미치는 인과 효과가 연령에 따라 다른가?

일반적인 인구 수준 효과 추정 질문들은 다음과 같이 표현된다:

- ...의 효과는 무엇인가?
- 내가 개입한다면 어떻게 될까...?
- 어떤 치료가 더 효과가 좋을까?
- X가 Y에 미치는 위험이 무엇일까?
- ... 이벤트 발생에 걸리는 시간이 얼마나 될까?

그리고 원하는 결과값은 다음과 같다:

- 상대 위험도
- 발생 위험비
- 승산비
- 평균 치치 효과
- 인과 관계
- 연관 관계
- 상관 관계
- 안전성 감시
- 비교 효과

7.3 환자 수준 예측

데이터베이스에 쌓인 환자 건강 이력을 기반으로, 우리는 미래에 발생할 건강 이벤트에 대해 환자 수준의 예측을 할 수 있다.

나에게 무슨 일이 발생할까?

데이터는 다음과 같은 질문에 답을 제공할 수 있다:

- 주요 우울증으로 새롭게 진단 받은 특정 환자가 진단받은지 1년 안에 자살을 시도할 확률이 얼마나 되는가?
- 심방세동으로 새롭게 진단 받은 특정 환자가, 와파린으로 치료를 시작한지 1년 안에 허혈성 뇌졸중을 겪을 확률이 얼마나 되는가?

일반적인 환자 수준 예측에 대한 질문들은 다음과 같이 표현된다:

- 이 환자가 ... 할 가능성이 얼마나 되는가?
- ...에 대한 후보자들이 누구인가?

그리고 원하는 결과값은 다음과 같다:

- 개인에 대한 확률
- 예측 모델
- 높은/낮은 위험군
- 확률론적 표현형

인구 수준 추정과 환자 수준 예측은 어느 정도 중복된다. 예를 들어, 예측을 위한 중요한 이용사례는 특정 환자의 결과에 약물 A가 처방되었다고 예측하고 약물 B가 처방된 것과 동일한 결과가 나타나는지 예측하는 것이다. 실제로 이 약들 중 하나(약물 A이라고 하자)를 처방 받았고, 약물 A의 예상되는 결과가 실제로 일어나는지를 살펴봤다고 가정해 보자. 약물 B는 처방되지 않았고 치료 B 이후의 결과는 관찰된 적이 없으므로 예측은 할 수 있더라도 사실과 다를 수 있다. 이러한 각각의 예측 작업은 환자 수준 예측에 속한다. 그러나 두 결과의 차이(또는 비율)는 단위 수준의 인과적 효과이며, 인과적 영향 추정 방법을 사용하여 추정해야 한다.



사람들은 예측모델을 인과모델로 잘못 해석하는 자연스러운 경향이 있다. 그러나 예측 모델은 인과성이 아닌 상관성만을 보여줄 수 있다. 예를 들자면, 당뇨병이 심근경색의 강한 예측변수이기 때문에, 당뇨병 약의 사용이 심근경색의 강한 예측변수일 수 있다. 그러나 이것이 당뇨병 약 복용을 중단하는 것이 심근경색을 막는다는 것을 의미하는 것은 아니다!

7.4 고혈압 이용 사례 예

당신은 고혈압의 1차 요법으로서 ACE 억제제 단일요법과 타이아자이드 이뇨제 단일요법이 급성 심근경색과 혈관부종에 미치는 영향을 연구하는데 관심이 있는 연구자이다. 당신은 OHDSI 연구에 기반하여 인구 수준 추정 연구질문을 도출했지만, 먼저 관심을 가지고 있는 특정 치료에 대한 특성을 어떻게 분석할 것인지 해결해야 한다.

7.4.1 특성 분석 질문

급성 심근경색은 고혈압 환자들에게 일어날 수 있는 심혈관계 합병증으로, 고혈압에 대한 효과적인 치료로 이 위험을 줄여야 한다. 혈관부종은 희귀하지만 잠재적으로 심각한 ACE 억제제의 알려진 부작용이다. 당신은 관심 약제(ACE 억제제와 타이아자이드 이뇨제)들에 노출된 코호트 (챕터 10 참고)들을 생성하는 것으로부터 연구를 시작한다. 노출된 환자들의 인구통계학적 정보, 병적 상태, 병용 약물 등 기저 특성을 파악하기 위하여 특성 분석 (챕터 11 참고) 을 수행한다. 또한 이 노출 환자 내에서 분석하고자 하는 결과가 얼마나 발생하는지 추정하는 또 다른 특성 분석을 수행한다. 그리고, 당신은 ‘얼마나 자주 1) 급성 심근경색과 2) 혈관부종이 ACE 억제제와 타이아자이드 이뇨제에 노출된 기간 동안 발생하는가?’를 묻게 된다. 이러한 특성 분석은 인구 수준 추정 연구 수행의 실현 가능성을 판단하게 하고, 두 치료군이 비교 가능한지를 평가하게 하며, 환자들이 받는 치료에 예측되는 위험 요소들을 파악할 수 있게 한다.

7.4.2 인구 수준 추정 질문

인구 수준 효과 추정 연구 (챕터 12 참고) 는 ACE 억제제와 타이아자이드 이뇨제가 급성 심근경색과 혈관부종에 미치는 상대 위험을 추정한다. 더 나아가, 진료군과 음성대조군 분석을 통해 평균 치료 효과에 대해 믿을 수 있는 추정치를 도출했는지 평가한다.

7.4.3 환자 수준 예측 질문

당신은 노출의 인과적 영향 여부와 상관없이, 가장 위험한 결과에 처한 환자들을 알아내고자 할 수 있다. 이것은 환자 수준 예측 (챕터 13 참고) 의 문제이다. ACE 억제제를 처음 사용하는 환자들 중 치료 시작한지 1년 동안 급성 심근경색 발병 위험이 가장 높은 환자들을 평가하는 예측 모델을 개발한다고 생각해 보아라. 이 모델을 통해 우리는 처음으로 ACE 처방을 받은 환자의 병력에서 관찰된 사건을 바탕으로, 향후 1년 동안 급성 심근경색을 겪을 가능성을 예측할 수 있다.

7.5 관찰 연구의 한계

OHDSI 데이터베이스가 답변을 제공할 수 없는 중요한 헬스케어 질문들이 많이 존재한다. 아래 질문들이 이에 해당한다:

- 위약과 비교한 치료의 인과 효과. 때때로 치료의 인과 효과를 위약 치료가 아닌 비치료와 비교하여 분석하는 것은 가능하다.
- 처방전 없이 구입할 수 있는 의약품과 관련된 모든 것
- 많은 결과와 다른 변수들이 거의 기록되지 않음. 사망률, 행동 결과, 라이프 스타일 및 사회-경제적 지위와 같은 것들이 이에 포함된다.
- 환자는 건강이 좋지 않을 때만 의료 시스템을 이용하는 경향이 있기 때문에, 치료의 이점을 측정하는 것이 쉽지 않다.

7.5.1 잘못된 데이터

OHDSI 데이터베이스에 기록된 임상 데이터는 의료 현실과 차이가 있을 수 있다. 예를 들어, 환자가 심근 경색을 경험한 적이 없어도 환자의 기록에 심근 경색 코드가 포함되어 있을 수 있다. 마찬가지로 검사 값이 잘못되었거나 시술에 대한 잘못된 코드가 데이터베이스에 저장되었을 수도 있다. 15와 16 챕터는 이와 같은 이슈들을 다루고 있으며, 모범 사례를 통해 이러한 문제들을 최대한 식별하고 수정하고자 한다. 그럼에도 불구하고, 잘못된 데이터는 필연적으로 어느 정도까지 존재할 수 밖에 없으며, 분석의 타당성을 약화시킬 수 있다. 매우 많은 문헌들이 데이터 오류들을 처리하기 위한 통계적 추론 조정에 초점을 맞추고 있다. - 예: Fuller (2009) 참조

7.5.2 결측 데이터

OHDSI 데이터베이스에서의 결측은 감지하기 어려운 문제점들을 낳는다. 데이터베이스에 기록되어야 하는 건강 이벤트(예: 처방, 검사 값 등)가 기록되지 않은 것, 그것이 “결측”이다. 통계 문헌들은 “임의의 완전 결측”, “임의의 결측”, “임의가 아닌 결측”과 같은 결측 유형들과 이러한 유형들을 다루는 복잡한 방법론들을 구별하고 있다. Perkins et al. (2017) 가 이 주제에 대한 유용한 입문서를 제공한다.

7.6 요약



- 관찰 연구의 이용 사례들은 크게 3개의 카테고리로 구분된다.
- **특성 분석**은 “그들에게 무슨 일이 발생했는가?”라는 질문에 답하는 것을 목적으로 한다.
- **인구 수준 추정**은 “인과적 영향이 무엇인가?”라는 질문에 답하는 것을 목적으로 한다.
- **환자 수준 예측**은 “나에게 무엇이 일어날까?”라는 질문에 답하는 것을 목적으로 한다.
- 예측 모델은 인과 모델이 아니다; 강한 예측변수에 대한 개입이 결과에 영향을 미칠 것이라고 믿을 근거가 없다.
- 헬스케어 관찰 데이터를 이용하여 연구할 수 없는 질문들도 있다.

7.7 연습문제

Exercise 7.1. 다음 질문들은 어떤 사용 사례 카테고리에 해당하는가?

1. 비스테로이드 약물에 최근 노출되었던 환자들이 위장관 출혈을 겪을 비율을 계산하라.
2. 기저 특성을 기반으로 특정 환자가 차년도에 위장관 출혈을 겪을 확률을 계산 하라.
3. 셀레콕시브와 비교하여 디클로페낙이 위장관 출혈에 미치는 위험을 추정하라.

Exercise 7.2. 당신은 디클로페낙이 위장관 출혈에 미치는 위험을 비노출(위약)의 경우와 비교하여 추정하고자 한다. 이와 같은 연구가 헬스케어 관찰 데이터를 이용하여 수행 가능한가?

정답은 부록 E.4에서 확인할 수 있다.

Chapter 8

OHDSI Analytics Tools

Chapter leads: Martijn Schuemie & Frank DeFalco

OHDSI offers a wide range of open source tools to support various data-analytics use cases on observational patient-level data. What these tools have in common is that they can all interact with one or more databases using the Common Data Model (CDM). Furthermore, these tools standardize the analytics for various use cases; Rather than having to start from scratch, an analysis can be implemented by filling in standard templates. This makes performing analysis easier, and also improves reproducibility and transparency. For example, there appear to be a near-infinite number of ways to compute an incidence rate, but these can be specified in the OHDSI tools with a few choices, and anyone making those same choices will compute incidence rates the same way.

In this chapter we first describe various ways in which we can choose to implement an analysis, and what strategies the analysis can employ. We then review the various OHDSI tools and how they fit the various use cases.

8.1 Analysis Implementation

Figure 8.1 shows the various ways in which we can choose to implement a study against a database using the CDM.

There are three main approaches to implementing a study. The first is to write custom code that does not make use of any of the tools OHDSI has to offer. One could write a de novo analysis in R, SAS, or any other language. This provides the maximum flexibility, and may in fact be the only option if the specific analysis is not supported by any of our tools. However, this path requires a lot of technical skill, time, and effort, and as the analysis increases in complexity it becomes harder to avoid errors in the code.

The second approach involves developing the analysis in R, and making use of

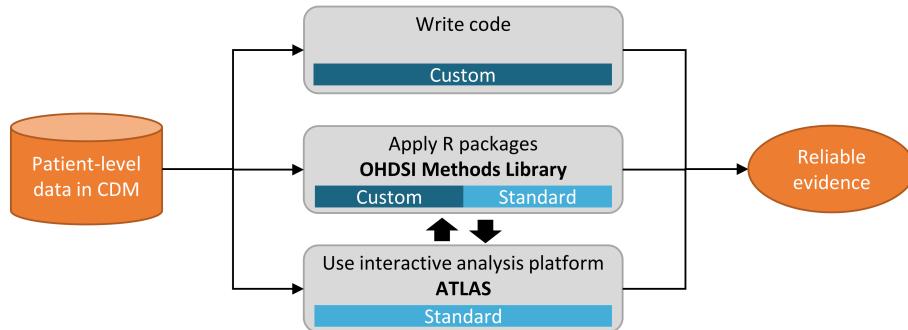


Figure 8.1: Different ways to implement an analysis against data in the CDM.

the packages in the OHDSI Methods Library. At a minimum, one could use the SqlRender and DatabaseConnector packages described in more detail in Chapter 9 that allow the same code to be executed on various database platforms, such as PostgreSQL, SQL Server, and Oracle. Other packages such as CohortMethod and PatientLevelPrediction offer R functions for advanced analytics against the CDM that can be called on in one's code. This still requires a lot of technical expertise, but by re-using the validated components of the Methods Library we can be more efficient and less prone to error than when using completely custom code.

The third approach relies on our interactive analysis platform ATLAS, a web-based tool that allows non-programmers to perform a wide range of analyses efficiently. ATLAS makes use of the Methods Libraries but provides a simple graphical interface to design analyses and in many cases generate the necessary R code to run the analysis. However, ATLAS does not support all options available in the Methods Library. While it is expected that the majority of studies can be performed through ATLAS, some studies may require the flexibility offered by the second approach.

ATLAS and the Methods Library are not independent. Some of the more complicated analytics that can be invoked in ATLAS are executed through calls to the packages in the Methods Library. Similarly, cohorts used in the Methods Library are often designed in ATLAS.

8.2 Analysis Strategies

In addition to the strategy used to implement our analysis against the CDM, for example through custom coding or use of standard analytic code in the Methods Library, there are also multiple strategies for using those analytic techniques to generate evidence. Figure 8.2 highlights three strategies that are employed in OHDSI.

The first strategy views every analysis as a single individual study. The analysis must be pre-specified in a protocol, implemented as code, executed against the

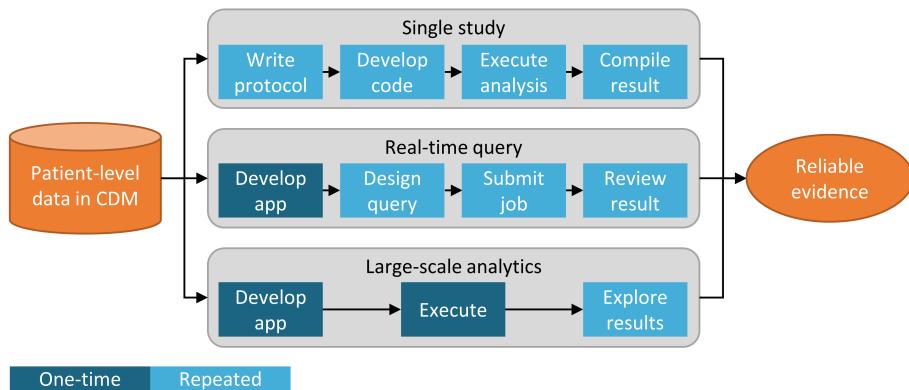


Figure 8.2: Strategies for generating evidence for (clinical) questions.

data, after which the result can be compiled and interpreted. For every question, all steps must be repeated. An example of such an analysis is the OHDSI study into the risk of angioedema associated with levetiracetam compared with phenytoin. (Duke et al., 2017) Here, a protocol was first written, analysis code using the OHDSI Methods Library was developed and executed across the OHDSI network, and results were compiled and disseminated in a journal publication.

The second strategy develops an application that allows users to answer a specific class of questions in real time or near-real time. Once the application has been developed, users can interactively define queries, submit them, and view the results. An example of this strategy is the cohort definition and generation tool in ATLAS. This tool allows users to specify cohort definitions of varying complexity, and execute the definition against a database to see how many people meet the various inclusion and exclusion criteria.

The third strategy similarly focuses on a class of questions, but then attempts to exhaustively generate all the evidence for the questions within the class. Users can then explore the evidence as needed through a variety of interfaces. One example is the OHDSI study into the effects of depression treatments. (Schuemie et al., 2018b) In this study all depression treatments are compared for a large set of outcomes of interest across four large observational databases. The full set of results, including 17,718 empirically calibrated hazard ratios along with extensive study diagnostics, is available in an interactive web app.¹

8.3 ATLAS

ATLAS is a free, publicly available, web-based tool developed by the OHDSI community that facilitates the design and execution of analyses on standardized, patient-level, observational data in the CDM format. ATLAS is deployed as a web

¹<http://data.ohdsi.org/SystematicEvidence/>

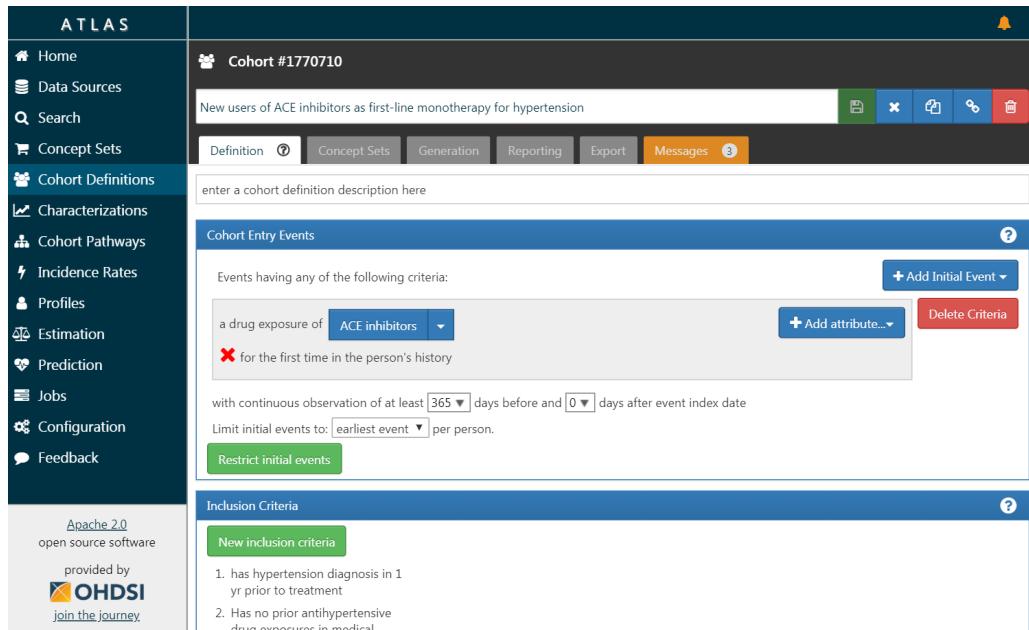


Figure 8.3: ATLAS user interface.

application in combination with the OHDSI WebAPI and is typically hosted on Apache Tomcat. Performing real time analyses requires access to the patient-level data in the CDM and is therefore typically installed behind an organization’s firewall. However, there is also a public ATLAS², and although this ATLAS instance only has access to a few small simulated datasets, it can still be used for many purposes including testing and training. It is even possible to fully define an effect estimation or prediction study using the public instance of ATLAS, and automatically generate the R code for executing the study. That code can then be run in any environment with an available CDM without needing to install ATLAS and the WebAPI.

A screenshot of ATLAS is provided in Figure 8.3. On the left is a navigation bar showing the various functions provided by ATLAS:

Data Sources Data sources provides the capability review descriptive, standardized reporting for each of the data sources that you have configured within your Atlas platform. This feature uses the large-scale analytics strategy: all descriptives have been pre-computed. Data sources is discussed in Chapter 11.

Vocabulary Search Atlas provides the ability to search and explore the OMOP standardized vocabulary to understand what concepts exist within those vocabularies and how to apply those concepts in your standardized analysis against your data sources. This feature is discussed in Chapter 5.

²<http://www.ohdsi.org/web/atlas>

Concept Sets Concept sets provides the ability to create collections of logical expressions that can be used to identify a set of concepts to be used throughout your standardized analyses. Concept sets provide more sophistication than a simple list of codes or values. A concept set is comprised of multiple concepts from the standardized vocabulary in combination with logical indicators that allow a user to specify that they are interested in including or excluding related concepts in the vocabulary hierarchy. Searching the vocabulary, identifying the set of concepts, and specifying the logic to be used to resolve a concept set provides a powerful mechanism for defining the often obscure medical language used in analysis plans. These concept sets can be saved within ATLAS and then used throughout your analysis as part of cohort definitions or analysis specifications.

Cohort Definitions Cohort definitions is the ability to construct a set of persons who satisfy one or more criteria for a duration of time and these cohorts can then serve as the basis of inputs for all of your subsequent analyses. This feature is discussed in Chapter 10.

Characterizations Characterizations is an analytic capability that allows you to look at one or more cohorts that you've defined and to summarize characteristics about those patient populations. This feature uses the real-time query strategy, and is discussed in Chapter 11.

Cohort Pathways Cohort pathways is an analytic tool that allows you to look at the sequence of clinical events that occur within one or more populations. This feature uses the real-time query strategy, and is discussed in Chapter 11.

Incidence Rates Incidence rates is a tool that allows you to estimate the incidence of outcomes within target populations of interest. This feature uses the real-time query strategy, and is discussed in Chapter 11.

Profiles Profiles is a tool that allows you to explore an individual patients longitudinal observational data to summarize what is going on within a given individual. This feature uses the real-time query strategy.

Population Level Estimation Estimation is a capability to allow you to define a population level effect estimation study using a comparative cohort design whereby comparisons between one or more target and comparator cohorts can be explored for a series of outcomes. This feature can be said to implement the real-time query strategy, as no coding is required, and is discussed in Chapter 12.

Patient Level Prediction Prediction is a capability to allow you to apply machine learning algorithms to conduct patient level prediction analyses whereby you can predict an outcome within any given target exposures. This feature can be said to implement the real-time query strategy, as no coding is required, and is discussed in Chapter 13.

Jobs Select the Jobs menu item to explore the state of processes that are running through the WebAPI. Jobs are often long running processes such as generating a cohort or computing cohort characterization reports.

Configuration Select the Configuration menu item to review the data sources that have been configured in the source configuration section.

Feedback The Feedback link will take you to the issue log for Atlas so that you can log a new issue or to search through existing issues. If you have ideas for new features or enhancements, this is also a place note these for the development community.

8.3.1 Security

ATLAS and the WebAPI provide a granular security model to control access to features or data sources within the overall platform. The security system is built leveraging the Apache Shiro library. Additional information on the security system can be found in the online WebAPI security wiki.³

8.3.2 Documentation

Documentation for ATLAS can be found online in the ATLAS GitHub repository wiki.⁴ This wiki includes information on the various application features as well as links to online video tutorials.

8.3.3 How to Install

Installation of ATLAS is done in combination with the OHDSI WebAPI. Installation guides for each component are available online in the ATLAS GitHub repository Setup Guide⁵ and WebAPI GitHub repository Installation Guide.⁶

8.4 Methods Library

The OHDSI Methods Library is the collection of open source R packages shown in Figure 8.4.

The packages offer R functions that together can be used to perform a complete observational study, starting from data in the CDM, and resulting in estimates and supporting statistics, figures, and tables. The packages interact directly with observational data in the CDM, and can be used simply to provide cross-platform compatibility to completely custom analyses as described in Chapter 9, or can provide advanced standardized analytics for population characterization (Chapter 11), population-level effect estimation (Chapter 12), and patient-level prediction (Chapter 13). The Methods Library supports best practices for use of observational data and observational study design as learned from previous and ongoing research, such as transparency, reproducibility, as well as measuring of

³<https://github.com/OHDSI/WebAPI/wiki/Security-Configuration>

⁴<https://github.com/OHDSI/ATLAS/wiki>

⁵<https://github.com/OHDSI/Atlas/wiki/Atlas-Setup-Guide>

⁶<https://github.com/OHDSI/WebAPI/wiki/WebAPI-Installation-Guide>

Prediction and estimation methods	Cohort Method New-user cohort studies using large-scale regression for propensity and outcome models	Self-Controlled Case Series Self-Controlled Case Series analysis using few or many predictors, includes splines for age and seasonality.	Self-Controlled Cohort A self-controlled cohort design, where time preceding exposure is used as control.
	Patient Level Prediction Build and evaluate predictive models for user-specified outcomes, using a wide array of machine learning algorithms.	Case-control Case-control studies, matching controls on age, gender, provider, and visit date. Allows nesting of the study in another cohort.	Case-crossover Case-crossover design including the option to adjust for time-trends in exposures (so-called case-time-control).
Method characterization	Empirical Calibration Use negative control exposure-outcome pairs to profile and calibrate a particular analysis design.	Method Evaluation Use real data and established reference sets as well as simulations injected in real data to evaluate the performance of methods.	Evidence Synthesis Combining study diagnostics and results across multiple sites.
Supporting packages	Database Connector Connect directly to a wide range of database platforms, including SQL Server, Oracle, and PostgreSQL.	Sql Render Generate SQL on the fly for the various SQL dialects.	Cyclops Highly efficient implementation of regularized logistic, Poisson and Cox regression.
	ParallelLogger Support for parallel computation with logging to console, disk, or e-mail.	Feature Extraction Automatically extract large sets of features for user-specified cohorts using data in the CDM.	

Figure 8.4: Packages in the OHDSI Methods Library.

the operating characteristics of methods in a particular context and subsequent empirical calibration of estimates produced by the methods.

The Methods Library has already been used in many published clinical studies (Boland et al., 2017; Duke et al., 2017; Ramcharran et al., 2017; Weinstein et al., 2017; Wang et al., 2017; Ryan et al., 2017, 2018; Vashisht et al., 2018; Yuan et al., 2018; Johnston et al., 2019), as well as methodological studies. (Schuemie et al., 2014, 2016; Reps et al., 2018; Tian et al., 2018; Schuemie et al., 2018a,b; Reps et al., 2019) The validity of the implementations of methods in the Methods library is described in Chapter 17.

8.4.1 Support for Large-Scale Analytics

One key feature incorporated in all packages is the ability to efficiently run many analyses. For example, when performing population-level estimation, the Cohort-Method package allows for computing effect-size estimates for many exposures and outcomes, using various analysis settings, and the package will automatically choose the optimal way to compute all the required intermediary and final data sets. Steps that can be re-used, such as extraction of covariates, or fitting a propensity model that is used for one target-comparator pair but multiple outcomes, will be executed only once. Where possible, computations will take place in parallel to maximize the use of computational resources.

This computational efficiency allows for large-scale analytics, answering many questions at once, and is also essential for including control hypotheses (e.g. negative controls) to measure the operating characteristics of our methods, and perform empirical calibration as described in Chapter 18.

8.4.2 Support for Big Data

The Methods Library is also designed to run against very large databases and be able to perform computations involving large amounts of data. This achieved in three ways:

1. Most data manipulation is performed on the database server. An analysis usually only requires a small fraction of the entire data in the database, and the Methods Library, through the SqlRender and DatabaseConnector packages, allows for advanced operations to be performed on the server to preprocess and extract the relevant data.
2. Large local data objects are stored in a memory-efficient manner. For the data that is downloaded to the local machine, the Methods Library uses the ff package to store and work with large data objects. This allows us to work with data much larger than fits in memory.
3. High-performance computing is applied where needed. For example, the Cyclops package implements a highly efficient regression engine that is used throughout the Methods Library to perform large-scale regressions (large

number of variables, large number of observations) that would not be possible to fit otherwise.

8.4.3 Documentation

R provides a standard way to document packages. Each package has a *package manual* that documents every function and data set contained in the package. All package manuals are available online through the Methods Library website⁷, through the package GitHub repositories, and for those packages available through CRAN they can be found in CRAN. Furthermore, from within R the package manual can be consulted by using the question mark. For example, after loading the DatabaseConnector package, typing the command `?connect` brings up the documentation on the “connect” function.

In addition to the package manual, many packages provide *vignettes*. Vignettes are long-form documentation that describe how a package can be used to perform certain tasks. For example, one vignette⁸ describes how to perform multiple analyses efficiently using the CohortMethod package. Vignettes can also be found through the Methods Library website, through the package GitHub repositories, and for those packages available through CRAN they can be found in CRAN.

8.4.4 System Requirements

Two computing environments are relevant when discussing the system requirements: The database server, and the analytics workstation.

The database server must hold the observational healthcare data in CDM format. The Methods Library supports a wide array of database management systems including traditional database systems (PostgreSQL, Microsoft SQL Server, and Oracle), parallel data warehouses (Microsoft APS, IBM Netezza, and Amazon RedShift), as well as Big Data platforms (Hadoop through Impala, and Google BigQuery).

The analytics workstation is where the Methods Library is installed and run. This can either be a local machine, such as someone’s laptop, or a remote server running RStudio Server. In all cases the requirements are that R is installed, preferably together with RStudio. The Methods Library also requires that Java is installed. The analytics workstation should also be able to connect to the database server, specifically, any firewall between them should have the database server access ports opened the workstation. Some of the analytics can be computationally intensive, so having multiple processing cores and ample memory can help speed up the analyses. We recommend having at least four cores and 16 gigabytes of memory.

⁷<https://ohdsi.github.io/MethodsLibrary>

⁸<https://ohdsi.github.io/CohortMethod/articles/MultipleAnalyses.html>



Figure 8.5: Downloading R from CRAN.

8.4.5 How to Install

Here are the steps for installing the required environment to run the OHDSI R packages. Four things need to be installed:

1. **R** is a statistical computing environment. It comes with a basic user interface that is primarily a command-line interface.
2. **RTools** is a set of programs that is required on Windows to build R packages from source.
3. **RStudio** is an IDE (Integrated Development Environment) that makes R easier to use. It includes a code editor, debugging and visualization tools. Please use it to obtain a nice R experience.
4. **Java** is a computing environment that is needed to run some of the components in the OHDSI R packages, for example those needed to connect to a database.

Below we describe how to install each of these in a Windows environment.



In Windows, both R and Java come in 32-bit and 64-bits architectures. If you install R in both architectures, you **must** also install Java in both architectures. It is recommended to only install the 64-bit version of R.

Installing R

1. Go to <https://cran.r-project.org/>, click on “Download R for Windows”, then “base”, then click the Download link indicated in Figure 8.5.
2. After the download has completed, run the installer. Use the default options everywhere, with two exceptions: First, it is better not to install into program files. Instead, just make R a subfolder of your C drive as shown in Figure 8.6. Second, to avoid problems due to differing architectures between R and Java, disable the 32-bit architecture as shown in Figure 8.7.

Once completed, you should be able to select R from your Start Menu.

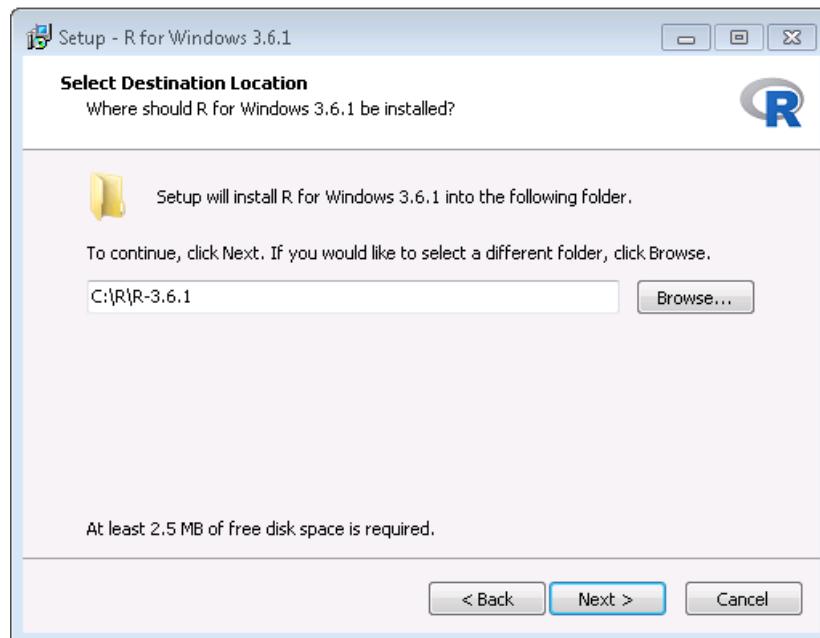


Figure 8.6: Settings the destination folder for R.

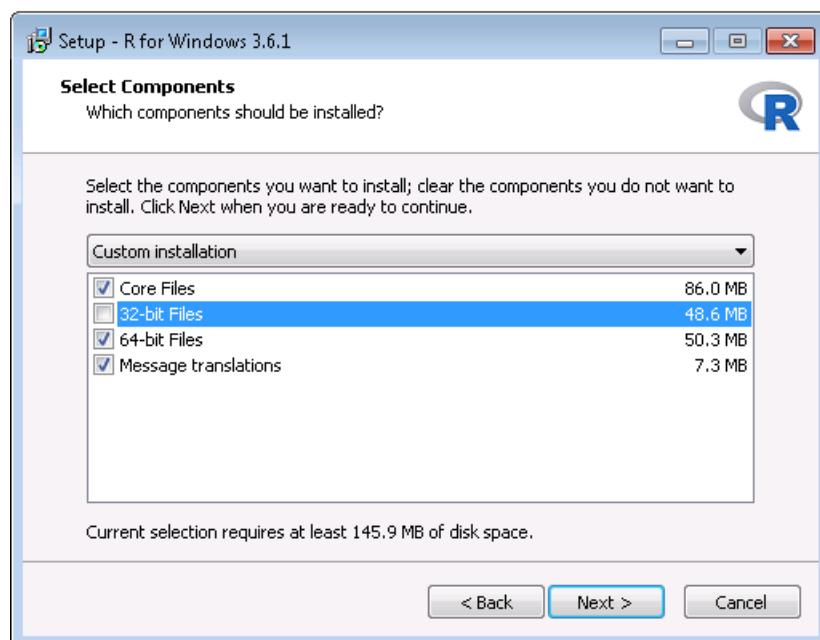


Figure 8.7: Disabling the 32-bit version of R.

Installers for Supported Platforms

Installers		Size	Date	MD5
RStudio 1.2.1335 - Windows 7+ (64-bit)		126.9 MB	2019-04-08	d0e2470f1
RStudio 1.2.1335 - Mac OS X 10.12+ (64-bit)		121.1 MB	2019-04-08	6c570b0e2
RStudio 1.2.1335 - Ubuntu 14/Debian 8 (64-bit)		92.2 MB	2019-04-08	c1b07d051

Figure 8.8: Downloading RStudio.

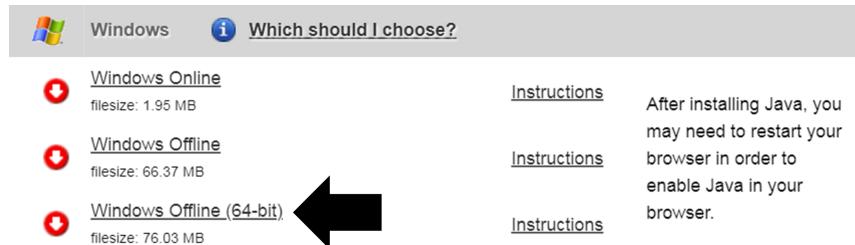


Figure 8.9: Downloading Java.

Installing RTools

1. Go to <https://cran.r-project.org/>, click on “Download R for Windows”, then “Rtools”, and select the very latest version of RTools to download.
2. After downloading has completed run the installer. Select the default options everywhere.

Installing RStudio

1. Go to <https://www.rstudio.com/>, select “Download RStudio” (or the “Download” button under “RStudio”), opt for the free version, and download the installer for Windows as shown in Figure 8.8.
2. After downloading, start the installer, and use the default options everywhere.

Installing Java

1. Go to <https://java.com/en/download/manual.jsp>, and select the Windows 64-bit installer as shown in Figure 8.9. If you also installed the 32-bit version of R, you *must* also install the other (32-bit) version of Java.
2. After downloading just run the installer.

Verifying the Installation

You should now be ready to go, but we should make sure. Start RStudio, and type

```
install.packages("SqlRender")
library(SqlRender)
translate("SELECT TOP 10 * FROM person;", "postgresql")

## [1] "SELECT * FROM person LIMIT 10;"
```

This function uses Java, so if all goes well we know both R and Java have been installed correctly!

Another test is to see if source packages can be built. Run the following R code to install the `CohortMethod` package from the OHDSI GitHub repository:

```
install.packages("drat")
drat::addRepo("OHDSI")
install.packages("CohortMethod")
```

8.5 Deployment Strategies

Deploying the entire OHDSI tool stack, including ATLAS and the Methods Library, in an organization is a daunting task. There are many components with dependencies that have to be considered, and configurations to set. For this reason, two initiatives have developed integrated deployment strategies that allow the entire stack to be installed as one package, using some forms of virtualization: Broadsea and Amazon Web Services (AWS).

8.5.1 Broadsea

Broadsea⁹ uses Docker container technology.¹⁰ The OHDSI tools are packaged along with dependencies into a single portable binary file called a Docker Image. This image can then be run on a Docker engine service, creating a virtual machine with all the software installed and ready to run. Docker engines are available for most operating systems, including Microsoft Windows, MacOS, and Linux. The Broadsea Docker image contains the main OHDSI tools, including the Methods Library and ATLAS.

8.5.2 Amazon AWS

Amazon has prepared two environments that can be instantiated in the AWS cloud computing environment with a click of the button: OHDSI-in-a-Box¹¹ and OHDSIonAWS.¹²

⁹<https://github.com/OHDSI/Broadsea>

¹⁰<https://www.docker.com/>

¹¹<https://github.com/OHDSI/OHDSI-in-a-Box>

¹²<https://github.com/OHDSI/OHDSIonAWS>

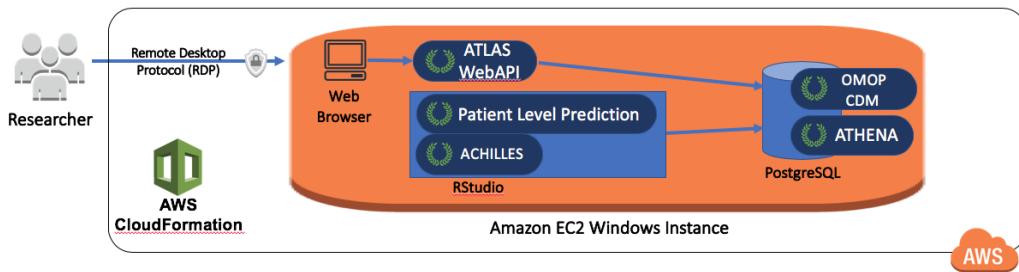


Figure 8.10: The Amazon Web Services architecture for OHDSI-in-a-Box.

OHDSI-in-a-Box is specifically created as a learning environment, and is used in most of the tutorials provided by the OHDSI community. It includes many OHDSI tools, sample data sets, RStudio and other supporting software in a single, low cost Windows virtual machine. A PostgreSQL database is used to store the CDM and also to store the intermediary results from ATLAS. The OMOP CDM data mapping and ETL tools are also included in OHDSI-in-a-Box. The architecture for OHDSI-in-a-Box is depicted in Figure 8.10.

OHDSIonAWS is a reference architecture for enterprise class, multi-user, scalable and fault tolerant OHDSI environments that can be used by organizations to perform their data analytics. It includes several sample datasets and can also automatically load your organization's real healthcare data. The data is placed in the Amazon Redshift database platform, which is supported by the OHDSI tools. Intermediary results of ATLAS are stored in a PostgreSQL database. On the front end, users have access to ATLAS and to RStudio through a web interface (leveraging RStudio Server). In RStudio the OHDSI Methods Library has already been installed, and can be used to connect to the databases. The automation to deploy OHDSIonAWS is open-source, and can be customized to include your organization's management tools and best practices. The architecture for OHDSIonAWS is depicted in Figure 8.11.

8.6 Summary



- We can perform analyses against data in the CDM by
 - * writing custom code
 - * writing code that uses the R packages in the OHDSI Methods Library
 - * using the interactive analysis platform ATLAS
- OHDSI tools use different analysis strategies
 - * Single studies
 - * Real-time queries
 - * Large-scale analytics

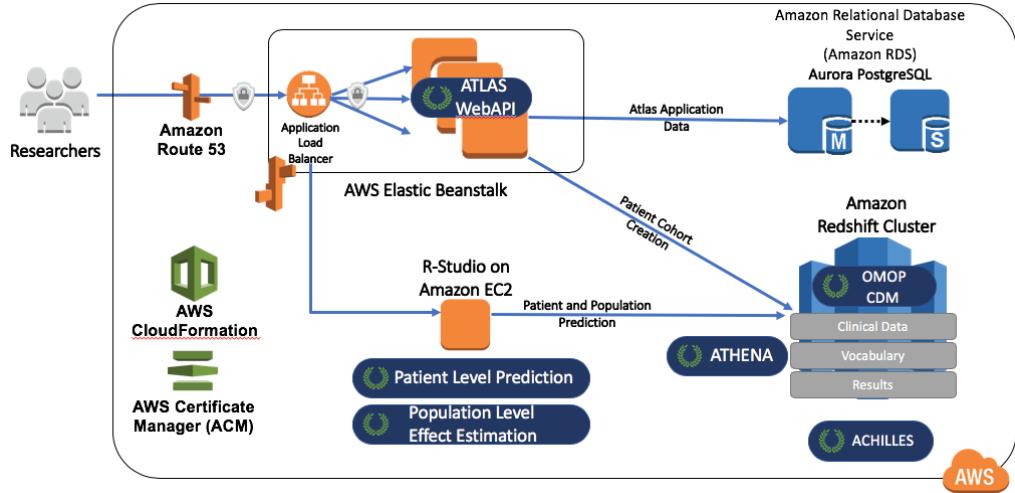


Figure 8.11: The Amazon Web Services architecture for OHDSI on AWS.

- The majority of OHDSI analytics tool are embedded in
 - * The interactive analysis platform ATLAS
 - * The OHDSI Methods Library R packages
- Several strategies exist facilitating the deployment of the OHDSI tools.

Chapter 9

SQL and R

Chapter leads: Martijn Schuemie & Peter Rijnbeek

The Common Data Model (CDM) is a relational database model (all data is represented as records in tables that have fields), which means that the data will typically be stored in a relational database using a software platform like PostgreSQL, Oracle, or Microsoft SQL Server. The various OHDSI tools such as ATLAS and the Methods Library work by querying the database behind the scene, but we can also query the database directly ourselves if we have appropriate access rights. The main reason to do this is to perform analyses that currently are not supported by any existing tool. However, directly querying the database also comes with greater risk of making mistakes, as the OHDSI tools are often designed to help guide the user to appropriate analysis of the data. Direct queries do not provide such guidance.

The standard language for querying relational databases is SQL (Structured Query Language), which can be used both to query the database as well as to make changes to the data. Although the basic commands in SQL are indeed standard, meaning the same across software platforms, each platform has its own dialect, with subtle changes. For example, to retrieve the top 10 rows of the PERSON table on SQL Server, one would type:

```
SELECT TOP 10 * FROM person;
```

Whereas the same query on PostgreSQL would be:

```
SELECT * FROM person LIMIT 10;
```

In OHDSI, we would like to be agnostic to the specific dialect a platform uses; we would like to ‘speak’ the same SQL language across all OHDSI databases. For this reason OHDSI developed the SqlRender package, an R package that can translate

from one standard dialect to any of the supported dialects that will be discussed later in this chapter. This standard dialect - **OHDSI SQL** - is mainly a subset of the SQL Server SQL dialect. The example SQL statements provided throughout this chapter will all use OHDSI SQL.

Each database platform also comes with its own software tools for querying the database using SQL. In OHDSI we developed the DatabaseConnector package, one R package that can connect to many database platforms. DatabaseConnector will also be discussed later in this chapter.

So although one can query a database that conforms to the CDM without using any OHDSI tools, the recommended path is to use the DatabaseConnector and SqlRender packages. This allows queries that are developed at one site to be used at any other site without modification. R itself also immediately provides features to further analyze the data extracted from the database, such as performing statistical analyses and generating (interactive) plots.

In this chapter we assume the reader has a basic understanding of SQL. We first review how to use SqlRender and DatabaseConnector. If the reader does not intend to use these packages these sections can be skipped. In Section 9.3 we discuss how to use SQL (in this case OHDSI SQL) to query the CDM. The following section highlights how to use the OHDSI Standardized Vocabulary when querying the CDM. We highlight the QueryLibrary, a collection of commonly-used queries against the CDM that is publicly available. We close this chapter with an example study estimating incidence rates, and implement this study using SqlRender and DatabaseConnector.

9.1 SqlRender

The SqlRender package is available on CRAN (the Comprehensive R Archive Network), and can therefore be installed using:

```
install.packages("SqlRender")
```

SqlRender supports a wide array of technical platforms including traditional database systems (PostgreSQL, Microsoft SQL Server, SQLite, and Oracle), parallel data warehouses (Microsoft APS, IBM Netezza, and Amazon RedShift), as well as Big Data platforms (Hadoop through Impala, and Google BigQuery). The R package comes with a package manual and a vignette that explores the full functionality. Here we describe some of the main features.

9.1.1 SQL Parameterization

One of the functions of the package is to support parameterization of SQL. Often, small variations of SQL need to be generated based on some parameters. SqlRender

offers a simple markup syntax inside the SQL code to allow parameterization. Rendering the SQL based on parameter values is done using the `render()` function.

Substituting Parameter Values

The @ character can be used to indicate parameter names that need to be exchanged for actual parameter values when rendering. In the following example, a variable called `a` is mentioned in the SQL. In the call to the `render` function the value of this parameter is defined:

```
sql <- "SELECT * FROM concept WHERE concept_id = @a;"  
render(sql, a = 123)
```

```
## [1] "SELECT * FROM concept WHERE concept_id = 123;"
```

Note that, unlike the parameterization offered by most database management systems, it is just as easy to parameterize table or field names as values:

```
sql <- "SELECT * FROM @x WHERE person_id = @a;"  
render(sql, x = "observation", a = 123)
```

```
## [1] "SELECT * FROM observation WHERE person_id = 123;"
```

The parameter values can be numbers, strings, booleans, as well as vectors, which are converted to comma-delimited lists:

```
sql <- "SELECT * FROM concept WHERE concept_id IN (@a);"  
render(sql, a = c(123, 234, 345))
```

```
## [1] "SELECT * FROM concept WHERE concept_id IN (123,234,345);"
```

If-Then-Else

Sometimes blocks of codes need to be turned on or off based on the values of one or more parameters. This is done using the `{Condition} ? {if true} : {if false}` syntax. If the *condition* evaluates to true or 1, the *if true* block is used, else the *if false* block is shown (if present).

```
sql <- "SELECT * FROM cohort {@x} ? {WHERE subject_id = 1}"  
render(sql, x = FALSE)
```

```
## [1] "SELECT * FROM cohort "
```

```
render(sql, x = TRUE)

## [1] "SELECT * FROM cohort WHERE subject_id = 1"
```

Simple comparisons are also supported:

```
sql <- "SELECT * FROM cohort {@x == 1} ? {WHERE subject_id = 1};"
render(sql, x = 1)
```

```
## [1] "SELECT * FROM cohort WHERE subject_id = 1;"
```

```
render(sql, x = 2)
```

```
## [1] "SELECT * FROM cohort ;"
```

As well as the IN operator:

```
sql <- "SELECT * FROM cohort {@x IN (1,2,3)} ? {WHERE subject_id = 1};"
render(sql, x = 2)
```

```
## [1] "SELECT * FROM cohort WHERE subject_id = 1;"
```

9.1.2 Translation to Other SQL Dialects

Another function of the SqlRender package is to translate from OHDSI SQL to other SQL dialects. For example:

```
sql <- "SELECT TOP 10 * FROM person;"
translate(sql, targetDialect = "postgresql")
```

```
## [1] "SELECT * FROM person LIMIT 10;"
```

The `targetDialect` parameter can have the following values: “oracle”, “postgresql”, “pdw”, “redshift”, “impala”, “netezza”, “bigquery”, “sqlite”, and “sql server”.



There are limits to what SQL functions and constructs can be translated properly, both because only a limited set of translation rules have been implemented in the package, but also some SQL features do not have an equivalent in all dialects. This is the primary reason why OHDSI SQL was developed as its own, new SQL dialect. However, whenever possible we have kept to the SQL Server syntax to avoid reinventing the wheel.

Despite our best efforts, there are quite a few things to consider when writing OHDSI SQL that will run without error on all supported platforms. In what follows we discuss these considerations in detail.

Functions and Structures Supported By Translate

These SQL Server functions have been tested and were found to be translated correctly to the various dialects:

Table 9.1: Functions supported by translate.

Function	Function	Function
ABS	EXP	RAND
ACOS	FLOOR	RANK
ASIN	GETDATE	RIGHT
ATAN	HASHBYTES*	ROUND
Avg	ISNULL	ROW_NUMBER
CAST	ISNUMERIC	RTRIM
CEILING	LEFT	SIN
CHARINDEX	LEN	SQRT
CONCAT	LOG	SQUARE
COS	LOG10	STDEV
COUNT	LOWER	SUM
COUNT_BIG	LTRIM	TAN
DATEADD	MAX	UPPER
DATEDIFF	MIN	VAR
DATEFROMPARTS	MONTH	YEAR
DATETIMEFROMPARTS	NEWID	
DAY	PI	
EOMONTH	POWER	

* Requires special privileges on Oracle. Has no equivalent on SQLite.

Similarly, many SQL syntax structures are supported. Here is a non-exhaustive list of expressions that we know will translate well:

```
-- Simple selects:  
SELECT * FROM table;  
  
-- Selects with joins:  
SELECT * FROM table_1 INNER JOIN table_2 ON a = b;  
  
-- Nested queries:  
SELECT * FROM (SELECT * FROM table_1) tmp WHERE a = b;
```

```
-- Limiting to top rows:  
SELECT TOP 10 * FROM table;  
  
-- Selecting into a new table:  
SELECT * INTO new_table FROM table;  
  
-- Creating tables:  
CREATE TABLE table (field INT);  
  
-- Inserting verbatim values:  
INSERT INTO other_table (field_1) VALUES (1);  
  
-- Inserting from SELECT:  
INSERT INTO other_table (field_1) SELECT value FROM table;  
  
-- Simple drop commands:  
DROP TABLE table;  
  
-- Drop table if it exists:  
IF OBJECT_ID('ACHILLES_analysis', 'U') IS NOT NULL  
    DROP TABLE ACHILLES_analysis;  
  
-- Drop temp table if it exists:  
IF OBJECT_ID('tempdb..#cohorts', 'U') IS NOT NULL  
    DROP TABLE #cohorts;  
  
-- Common table expressions:  
WITH cte AS (SELECT * FROM table) SELECT * FROM cte;  
  
-- OVER clauses:  
SELECT ROW_NUMBER() OVER (PARTITION BY a ORDER BY b)  
    AS "Row Number" FROM table;  
  
-- CASE WHEN clauses:  
SELECT CASE WHEN a=1 THEN a ELSE 0 END AS value FROM table;  
  
-- UNIONs:  
SELECT * FROM a UNION SELECT * FROM b;  
  
-- INTERSECTIONS:  
SELECT * FROM a INTERSECT SELECT * FROM b;  
  
-- EXCEPT:  
SELECT * FROM a EXCEPT SELECT * FROM b;
```

String Concatenation

String concatenation is one area where SQL Server is less specific than other dialects. In SQL Server, one would write `SELECT first_name + ' ' + last_name AS full_name FROM table`, but this should be `SELECT first_name || ' ' || last_name AS full_name FROM table` in PostgreSQL and Oracle. SqlRender tries to guess when values that are being concatenated are strings. In the example above, because we have an explicit string (the space surrounded by single quotation marks), the translation will be correct. However, if the query had been `SELECT first_name + last_name AS full_name FROM table`, SqlRender would have had no clue the two fields were strings, and would incorrectly leave the plus sign. Another clue that a value is a string is an explicit cast to VARCHAR, so `SELECT last_name + CAST(age AS VARCHAR(3)) AS full_name FROM table` would also be translated correctly. To avoid ambiguity altogether, it is probably best to use the `CONCAT()` function to concatenate two or more strings.

Table Aliases and the AS Keyword

Many SQL dialects allow the use of the `AS` keyword when defining a table alias, but will also work fine without the keyword. For example, both these SQL statements are fine for SQL Server, PostgreSQL, RedShift, etc.:

```
-- Using AS keyword
SELECT *
FROM my_table AS table_1
INNER JOIN (
    SELECT * FROM other_table
) AS table_2
ON table_1.person_id = table_2.person_id;

-- Not using AS keyword
SELECT *
FROM my_table table_1
INNER JOIN (
    SELECT * FROM other_table
) table_2
ON table_1.person_id = table_2.person_id;
```

However, Oracle will throw an error when the `AS` keyword is used. In the above example, the first query will fail. It is therefore recommended to not use the `AS` keyword when aliasing tables. (Note: we can't make SqlRender handle this, because it can't easily distinguish between table aliases where Oracle doesn't allow `AS` to be used, and field aliases, where Oracle requires `AS` to be used.)

Temp Tables

Temp tables can be very useful to store intermediate results, and when used correctly can dramatically improve performance of queries. On most database platforms temp tables have very nice properties: they're only visible to the current user, are automatically dropped when the session ends, and can be created even when the user has no write access. Unfortunately, in Oracle temp tables are basically permanent tables, with the only difference that the data inside the table is only visible to the current user. This is why, in Oracle, SqlRender will try to emulate temp tables by

1. Adding a random string to the table name so tables from different users will not conflict.
2. Allowing the user to specify the schema where the temp tables will be created.

For example:

```
sql <- "SELECT * FROM #children;"  
translate(sql, targetDialect = "oracle", oracleTempSchema = "temp_schema")
```

```
## [1] "SELECT * FROM temp_schema.mv47tbl7children ;"
```

Note that the user will need to have write privileges on `temp_schema`.

Also note that because Oracle has a limit on table names of 30 characters. **Temp table names are only allowed to be at most 22 characters long**, because else the name will become too long after appending the session ID.

Furthermore, remember that temp tables are not automatically dropped on Oracle, so you will need to explicitly TRUNCATE and DROP all temp tables once you're done with them to prevent orphan tables accumulating in the Oracle temp schema.

Implicit Casts

One of the few points where SQL Server is less explicit than other dialects is that it allows implicit casts. For example, this code will work on SQL Server:

```
CREATE TABLE #temp (txt VARCHAR);  
  
INSERT INTO #temp  
SELECT '1';  
  
SELECT * FROM #temp WHERE txt = 1;
```

Even though `txt` is a `VARCHAR` field and we are comparing it with an integer, SQL Server will automatically cast one of the two to the correct type to allow the comparison. In contrast, other dialects such as PostgreSQL will throw an error when trying to compare a `VARCHAR` with an `INT`.

You should therefore always make casts explicit. In the above example, the last statement should be replaced with either

```
SELECT * FROM #temp WHERE txt = CAST(1 AS VARCHAR);
```

or

```
SELECT * FROM #temp WHERE CAST(txt AS INT) = 1;
```

Case Sensitivity in String Comparisons

Some DBMS platforms such as SQL Server always perform string comparisons in a case-insensitive way, while others such as PostgreSQL are always case sensitive. It is therefore recommended to always assume case-sensitive comparisons, and to explicitly make comparisons case-insensitive when unsure about the case. For example, instead of

```
SELECT * FROM concept WHERE concep_class_id = 'Clinical Finding'
```

it is preferred to use

```
SELECT * FROM concept WHERE LOWER(concep_class_id) = 'clinical finding'
```

Schemas and Databases

In SQL Server, tables are located in a schema, and schemas reside in a database. For example, `cdm_data.dbo.person` refers to the `person` table in the `dbo` schema in the `cdm_data` database. In other dialects, even though a similar hierarchy often exists they are used very differently. In SQL Server, there is typically one schema per database (often called `dbo`), and users can easily use data in different databases. On other platforms, for example in PostgreSQL, it is not possible to use data across databases in a single session, but there are often many schemas in a database. In PostgreSQL one could say that the equivalent of SQL Server's database is the schema.

We therefore recommend concatenating SQL Server's database and schema into a single parameter, which we typically call `@databaseSchema`. For example, we could have the parameterized SQL

```
SELECT * FROM @databaseSchema.person
```

where on SQL Server we can include both database and schema names in the value: `databaseSchema = "cdm_data.dbo"`. On other platforms, we can use the same

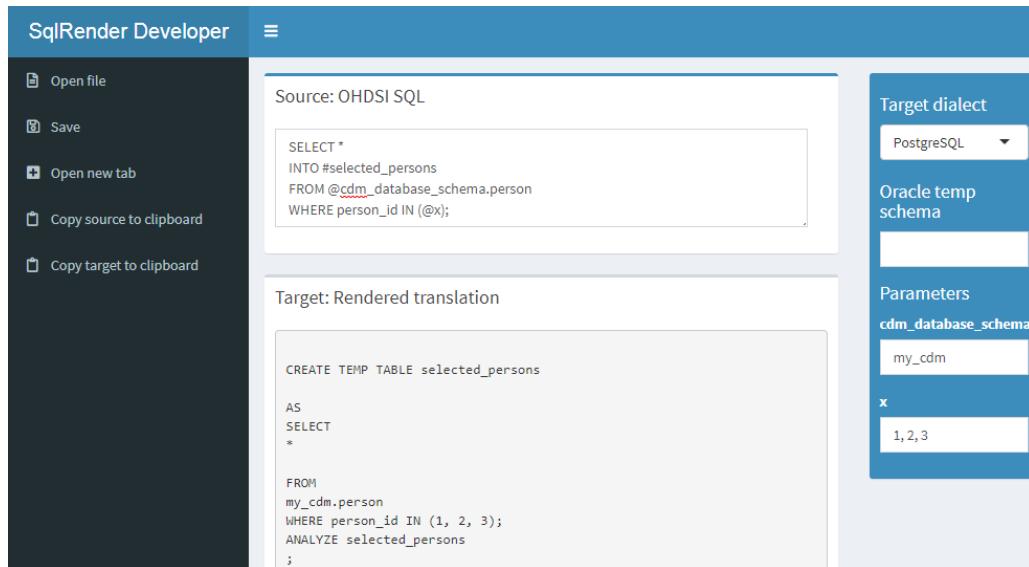


Figure 9.1: The SqlDeveloper Shiny app.

code, but now only specify the schema as the parameter value: `databaseSchema = "cdm_data"`.

The one situation where this will fail is the `USE` command, since `USE cdm_data.dbo;` will throw an error. It is therefore preferred not to use the `USE` command, but always specify the database / schema where a table is located.

Debugging Parameterized SQL

Debugging parameterized SQL can be a bit complicated. Only the rendered SQL can be tested against a database server, but changes to the code should be made in the parameterized (pre-rendered) SQL.

A Shiny app is included in the `SqlRender` package for interactively editing source SQL and generating rendered and translated SQL. The app can be started using:

```
launchSqlRenderDeveloper()
```

That will open the default browser with the app shown in Figure 9.1. The app is also publicly available on the web.¹

In the app you can enter OHDSI SQL, select the target dialect as well as provide values for the parameters that appear in your SQL, and the translation will automatically appear at the bottom.

¹<http://data.ohdsi.org/SqlDeveloper/>

9.2 DatabaseConnector

DatabaseConnector is an R package for connecting to various database platforms using Java's JDBC drivers. The DatabaseConnector package is available on CRAN (the Comprehensive R Archive Network), and can therefore be installed using:

```
install.packages("DatabaseConnector")
```

DatabaseConnector supports a wide array of technical platforms including traditional database systems (PostgreSQL, Microsoft SQL Server, SQLite, and Oracle), parallel data warehouses (Microsoft APS, IBM Netezza, and Amazon RedShift), as well as Big Data platforms (Hadoop through Impala, and Google BigQuery). The package already contains most drivers, but because of licensing reasons the drivers for BigQuery, Netezza and Impala are not included but must be obtained by the user. Type `?jdbcDrivers` for instructions on how to download these drivers. Once downloaded, you can use the `pathToDriver` argument of the `connect`, `dbConnect`, and `createConnectionDetails` functions.

9.2.1 Creating a Connection

To connect to a database a number of details need to be specified, such as the database platform, the location of the server, the user name, and password. We can call the `connect` function and specify these details directly:

```
conn <- connect(dbms = "postgresql",
                 server = "localhost/postgres",
                 user = "joe",
                 password = "secret",
                 schema = "cdm")
```

```
## Connecting using PostgreSQL driver
```

See `?connect` for information on which details are required for each platform. Don't forget to close any connection afterwards:

```
disconnect(conn)
```

Note that, instead of providing the server name, it is also possible to provide the JDBC connection string if this is more convenient:

```
connString <- "jdbc:postgresql://localhost:5432/postgres"
conn <- connect(dbms = "postgresql",
                connectionString = connString,
                user = "joe",
```

```
    password = "secret",
    schema = "cdm")
```

```
## Connecting using PostgreSQL driver
```

Sometimes we may want to first specify the connection details, and defer connecting until later. This may be convenient for example when the connection is established inside a function, and the details need to be passed as an argument. We can use the `createConnectionDetails` function for this purpose:

```
details <- createConnectionDetails(dbms = "postgresql",
                                    server = "localhost/postgres",
                                    user = "joe",
                                    password = "secret",
                                    schema = "cdm")
conn <- connect(details)
```

```
## Connecting using PostgreSQL driver
```

9.2.2 Querying

The main functions for querying database are the `querySql` and `executeSql` functions. The difference between these functions is that `querySql` expects data to be returned by the database, and can handle only one SQL statement at a time. In contrast, `executeSql` does not expect data to be returned, and accepts multiple SQL statements in a single SQL string.

Some examples:

```
querySql(conn, "SELECT TOP 3 * FROM person")
```

```
##   person_id gender_concept_id year_of_birth
## 1          1              8507      1975
## 2          2              8507      1976
## 3          3              8507      1977
```

```
executeSql(conn, "TRUNCATE TABLE foo; DROP TABLE foo;")
```

Both functions provide extensive error reporting: When an error is thrown by the server, the error message and the offending piece of SQL are written to a text file to allow better debugging. The `executeSql` function also by default shows a progress bar, indicating the percentage of SQL statements that has been executed. If those attributes are not desired, the package also offers the `lowLevelQuerySql` and `lowLevelExecuteSql` functions.

9.2.3 Querying Using Ffdf Objects

Sometimes the data to be fetched from the database is too large to fit into memory. As mentioned in Section 8.4.2, in such a case we can use the `ff` package to store R data objects on file, and use them as if they are available in memory. `DatabaseConnector` can download data directly into ffd objects:

```
x <- querySql.ffdf(conn, "SELECT * FROM person")
```

`x` is now an ffd object.

9.2.4 Querying Different Platforms Using the Same SQL

The following convenience functions are available that first call the `render` and `translate` functions in the `SqlRender` package: `renderTranslateExecuteSql`, `renderTranslateQuerySql`, `renderTranslateQuerySql.ffdf`. For example:

```
x <- renderTranslateQuerySql(conn,
                             sql = "SELECT TOP 10 * FROM @schema.person",
                             schema = "cdm_synpuf")
```

Note that the SQL Server-specific ‘TOP 10’ syntax will be translated to for example ‘LIMIT 10’ on PostgreSQL, and that the SQL parameter `@schema` will be instantiated with the provided value ‘`cdm_synpuf`’.

9.2.5 Inserting Tables

Although it is also possible to insert data in the database by sending SQL statements using the `executeSql` function, it is often more convenient and faster (due to some optimization) to use the `insertTable` function:

```
data(mtcars)
insertTable(conn, "mtcars", mtcars, createTable = TRUE)
```

In this example, we’re uploading the `mtcars` data frame to a table called ‘`mtcars`’ on the server, which will be automatically created.

9.3 Querying the CDM

In the following examples we use OHDSI SQL to query a database that adheres to the CDM. These queries use `@cdm` to denote the database schema where the data in CDM can be found.

We can start by just querying how many people are in the database:

```
SELECT COUNT(*) AS person_count FROM @cdm.person;
```

PERSON_COUNT
26299001

Or perhaps we're interested in the average length of an observation period:

```
SELECT AVG(DATEDIFF(DAY,
                     observation_period_start_date,
                     observation_period_end_date) / 365.25) AS num_years
FROM @cdm.observation_period;
```

NUM_YEARS
1.980803

We can join tables to produce additional statistics. A join combines fields from multiple tables, typically by requiring specific fields in the tables to have the same value. For example, here we join the PERSON table to the OBSERVATION_PERIOD table on the PERSON_ID fields in both tables. In other words, the result of the join is a new table-like set that has all the fields of the two tables, but in all rows the PERSON_ID fields from the two tables must have the same value. We can now for example compute the maximum age at observation end by using the OBSERVATION_PERIOD_END_DATE field from the OBSERVATION_PERIOD table together with the year_of_birth field of the PERSON table:

```
SELECT MAX(YEAR(observation_period_end_date) -
           year_of_birth) AS max_age
FROM @cdm.person
INNER JOIN @cdm.observation_period
  ON person.person_id = observation_period.person_id;
```

MAX_AGE
90

A much more complicated query is needed to determine the distribution of age at the start of observation. In this query, we first join the PERSON to the OBSERVATION_PERIOD table to compute age at start of observation. We also compute the ordering for this joined set based on age, and store it as order_nr.

Because we want to use the result of this join multiple times, we define it as a common table expression (CTE) (defined using `WITH ... AS`) that we call “ages,” meaning we can refer to ages as if it is an existing table. We count the number of rows in ages to produce “n,” and then for each quantile find the minimum age where the `order_nr` is smaller than the fraction times n. For example, to find the median we use the minimum age where $order_nr < .50 * n$. The minimum and maximum age are computed separately:

```
WITH ages
AS (
    SELECT age,
           ROW_NUMBER() OVER (
               ORDER BY age
           ) order_nr
    FROM (
        SELECT YEAR(observation_period_start_date) - year_of_birth AS age
        FROM @cdm.person
        INNER JOIN @cdm.observation_period
            ON person.person_id = observation_period.person_id
        ) age_computed
    )
SELECT MIN(age) AS min_age,
       MIN(CASE
           WHEN order_nr < .25 * n
               THEN 9999
           ELSE age
           END) AS q25_age,
       MIN(CASE
           WHEN order_nr < .50 * n
               THEN 9999
           ELSE age
           END) AS median_age,
       MIN(CASE
           WHEN order_nr < .75 * n
               THEN 9999
           ELSE age
           END) AS q75_age,
       MAX(age) AS max_age
    FROM ages
CROSS JOIN (
    SELECT COUNT(*) AS n
    FROM ages
    ) population_size;
```

MIN_AGE	Q25_AGE	MEDIAN_AGE	Q75_AGE	MAX_AGE
0	6	17	34	90

More complex computations can also be performed in R instead of using SQL. For example, we can get the same answer using this R code:

```
sql <- "SELECT YEAR(observation_period_start_date) -
        year_of_birth AS age
FROM @cdm.person
INNER JOIN @cdm.observation_period
    ON person.person_id = observation_period.person_id;"
age <- renderTranslateQuerySql(conn, sql, cdm = "cdm")
quantile(age[, 1], c(0, 0.25, 0.5, 0.75, 1))

##   0%   25%   50%   75% 100%
##     0     6    17    34    90
```

Here we compute age on the server, download all ages, and then compute the age distribution. However, this requires millions of rows of data to be downloaded from the database server, and is therefore not very efficient. You will need to decide on a case-by-case basis whether a computation is best performed in SQL or in R.

Queries can use the source values in the CDM. For example, we can retrieve the top 10 most frequent condition source codes using:

```
SELECT TOP 10 condition_source_value,
       COUNT(*) AS code_count
FROM @cdm.condition_occurrence
GROUP BY condition_source_value
ORDER BY -COUNT(*);
```

CONDITION_SOURCE_VALUE	CODE_COUNT
4019	49094668
25000	36149139
78099	28908399
319	25798284
31401	22547122
317	22453999
311	19626574
496	19570098
I10	19453451
3180	18973883

Here we grouped records in the CONDITION_OCCURRENCE table by values of the CONDITION_SOURCE_VALUE field, and counted the number of records in each group. We retrieve the CONDITION_SOURCE_VALUE and the count, and reverse-order it by the count.

9.4 Using the Vocabulary When Querying

Many operations require the vocabulary to be useful. The Vocabulary tables are part of the CDM, and are therefore available using SQL queries. Here we show how queries against the Vocabulary can be combined with queries against the CDM. Many fields in the CDM contain concept IDs which can be resolved using the CONCEPT table. For example, we may wish to count the number of persons in the database stratified by gender, and it would be convenient to resolve the GENDER_CONCEPT_ID field to a concept name:

```
SELECT COUNT(*) AS subject_count,
       concept_name
  FROM @cdm.person
 INNER JOIN @cdm.concept
    ON person.gender_concept_id = concept.concept_id
 GROUP BY concept_name;
```

SUBJECT_COUNT	CONCEPT_NAME
14927548	FEMALE
11371453	MALE

A very powerful feature of the Vocabulary is its hierarchy. A very common query looks for a specific concept *and all of its descendants*. For example, imagine we wish to count the number of prescriptions containing the ingredient ibuprofen:

```
SELECT COUNT(*) AS prescription_count
  FROM @cdm.drug_exposure
 INNER JOIN @cdm.concept_ancestor
    ON drug_concept_id = descendant_concept_id
 INNER JOIN @cdm.concept ingredient
    ON ancestor_concept_id = ingredient.concept_id
 WHERE LOWER(ingredient.concept_name) = 'ibuprofen'
   AND ingredient.concept_class_id = 'Ingredient'
   AND ingredient.standard_concept = 'S';
```

PRESCRIPTION_COUNT
26871214

Select a query

Group	Name
["drug exposure"]	All
drug exposure	DEX01 Counts of persons with any number of exposures to a certain drug
drug exposure	DEX02 Counts of persons taking a drug, by age, gender, and year of exposure
drug exposure	DEX03 Distribution of age, stratified by drug
drug exposure	DEX04 Distribution of gender in persons taking a drug
drug exposure	DEX05 Counts of drug records for a particular drug
drug exposure	DEX06 Counts of distinct drugs in the database
drug exposure	DEX07 Maximum number of drug exposure events per person over some time period

Query Description

DEX01: Counts of persons with any number of exposures to a certain drug

Description

This query is used to count the persons with at least one exposures to a certain drug (drug_concept_id). See vocabulary queries for obtaining valid drug_concept_id values. The input to the query is a value (or a comma-separated list of values) of a drug_concept_id. If the input is omitted, all drugs in the data table are summarized.

Query

The following is a sample run of the query. The input parameters are highlighted in blue.

```
SELECT
    c.concept_name,
    drug_concept_id,
    COUNT(person_id) AS num_persons
FROM cdm.drug_exposure
INNER JOIN cdm.concept c
ON drug_concept_id = c.concept_id
WHERE domain_id = 'Drug'
```

Figure 9.2: QueryLibrary: a library of SQL queries against the CDM.

9.5 QueryLibrary

QueryLibrary is a library of commonly-used SQL queries for the CDM. It is available as an online application² shown in Figure 9.2, and as an R package.³

The purpose of the library is to help new users learn how to query the CDM. The queries in the library have been reviewed and approved by the OHDSI community. The query library is primarily intended for training purposes, but it is also a valuable resource for experienced users.

The QueryLibrary makes use of SqlRender to output the queries in the SQL dialect of choice. Users can also specify the CDM database schema, vocabulary database schema (if separate), and the Oracle temp schema (if needed), so the queries will be automatically rendered with these settings.

²<http://data.ohdsi.org/QueryLibrary>

³<https://github.com/OHDSI/QueryLibrary>

9.6 Designing a Simple Study

9.6.1 Problem Definition

Angioedema is a well-known side-effect of ACE inhibitors (ACEi). Slater et al. (1988) estimate the incidence rate of angioedema in the first week of ACEi treatment to be one case per 3,000 patients per week. Here we seek to replicate this finding, and stratify by age and gender. For simplicity, we focus on one ACEi: lisinopril. We thus answer the question

What is the rate of angioedema in the first week following lisinopril treatment initiation, stratified by age and gender?

9.6.2 Exposure

We'll define exposure as first exposure to lisinopril. By first we mean no earlier exposure to lisinopril. We require 365 days of continuous observation time prior to the first exposure.

9.6.3 Outcome

We define angioedema as any occurrence of an angioedema diagnosis code during an inpatient or emergency room (ER) visit.

9.6.4 Time-At-Risk

We will compute the incidence rate in the first week following treatment initiation, irrespective of whether patients were exposed for the full week.

9.7 Implementing the Study Using SQL and R

Although we are not bound to any of the OHDSI tool conventions, it is helpful to follow the same principles. In this case, we will use SQL to populate a cohort table, similarly to how the OHDSI tools work. The COHORT table is defined in the CDM, and has a predefined set of fields that we will also use. We first must create the COHORT table in a database schema where we have write access, which likely is not the same as the database schema that holds the data in CDM format.

```
library(DatabaseConnector)
conn <- connect(dbms = "postgresql",
                 server = "localhost/postgres",
                 user = "joe",
                 password = "secret")
cdmDbSchema <- "cdm"
cohortDbSchema <- "scratch"
cohortTable <- "my_cohorts"
```

```

sql <- "
CREATE TABLE @cohort_db_schema.@cohort_table (
    cohort_definition_id INT,
    cohort_start_date DATE,
    cohort_end_date DATE,
    subject_id BIGINT
);
"
renderTranslateExecuteSql(conn, sql,
    cohort_db_schema = cohortDbSchema,
    cohort_table = cohortTable)

```

Here we have parameterized the database schema and table names, so we can easily adapt them to different environments. The result is an empty table on the database server.

9.7.1 Exposure Cohort

Next we create our exposure cohort, and insert it into our COHORT table:

```

sql <- "
INSERT INTO @cohort_db_schema.@cohort_table (
    cohort_definition_id,
    cohort_start_date,
    cohort_end_date,
    subject_id
)
SELECT 1 AS cohort_definition_id,
    cohort_start_date,
    cohort_end_date,
    subject_id
FROM (
    SELECT drug_era_start_date AS cohort_start_date,
        drug_era_end_date AS cohort_end_date,
        person_id AS subject_id
    FROM (
        SELECT drug_era_start_date,
            drug_era_end_date,
            person_id,
            ROW_NUMBER() OVER (
                PARTITION BY person_id
                ORDER BY drug_era_start_date
            ) order_nr
    FROM @cdm_db_schema.drug_era
    WHERE drug_concept_id = 1308216 -- Lisinopril
) ordered_exposures
WHERE order_nr = 1
"

```

```

) first_era
INNER JOIN @cdm_db_schema.observation_period
ON subject_id = person_id
    AND observation_period_start_date < cohort_start_date
    AND observation_period_end_date > cohort_start_date
WHERE DATEDIFF(DAY,
    observation_period_start_date,
    cohort_start_date) >= 365;
"

renderTranslateExecuteSql(conn, sql,
    cohort_db_schema = cohortDbSchema,
    cohort_table = cohortTable,
    cdm_db_schema = cdmDbSchema)

```

Here we use the DRUG_ERAS table, a standard table in the CDM that is automatically derived from the DRUG_EXPOSURE table. The DRUG_ERAS table contains eras of continuous exposure at the ingredient level. We can thus search for lisinopril, and this will automatically identify all exposures to drugs containing lisinopril. We take the first drug exposure per person, and then join to the OBSERVATION_PERIOD table, and because a person can have several observation periods we must make sure we only join to the period containing the drug exposure. We then require at least 365 days between the OBSERVATION_PERIOD_START_DATE and the COHORT_START_DATE.

9.7.2 Outcome Cohort

Finally, we must create our outcome cohort:

```

sql <- "
INSERT INTO @cohort_db_schema.@cohort_table (
    cohort_definition_id,
    cohort_start_date,
    cohort_end_date,
    subject_id
)
SELECT 2 AS cohort_definition_id,
    cohort_start_date,
    cohort_end_date,
    subject_id
FROM (
    SELECT DISTINCT person_id AS subject_id,
        condition_start_date AS cohort_start_date,
        condition_end_date AS cohort_end_date
    FROM @cdm_db_schema.condition_occurrence
    INNER JOIN @cdm_db_schema.concept_ancestor
        ON condition_concept_id = descendant_concept_id

```

```

        WHERE ancestor_concept_id = 432791 -- Angioedema
    ) distinct_occurrence
INNER JOIN @cdm_db_schema.visit_occurrence
    ON subject_id = person_id
    AND visit_start_date <= cohort_start_date
    AND visit_end_date >= cohort_start_date
WHERE visit_concept_id IN (262, 9203,
    9201) -- Inpatient or ER;
"

```

```

renderTranslateExecuteSql(conn, sql,
    cohort_db_schema = cohortDbSchema,
    cohort_table = cohortTable,
    cdm_db_schema = cdmDbSchema)

```

Here we join the CONDITION_OCCURRENCE table to the CONCEPT_ANCESTOR table to find all occurrences of angioedema or any of its descendants. We use DISTINCT to make sure we only select one record per day, as we believe multiple angioedema diagnoses on the same day are more likely to be the same occurrence rather than multiple angioedema events. We join these occurrences to the VISIT_OCCURRENCE table to ensure the diagnosis was made in and inpatient or ER setting.

9.7.3 Incidence Rate Calculation

Now that our cohorts are in place, we can compute the incidence rate, stratified by age and gender:

```

sql <- "
WITH tar AS (
    SELECT concept_name AS gender,
        FLOOR((YEAR(cohort_start_date) -
            year_of_birth) / 10) AS age,
        subject_id,
        cohort_start_date,
        CASE WHEN DATEADD(DAY, 7, cohort_start_date) >
            observation_period_end_date
        THEN observation_period_end_date
        ELSE DATEADD(DAY, 7, cohort_start_date)
        END AS cohort_end_date
    FROM @cohort_db_schema.@cohort_table
    INNER JOIN @cdm_db_schema.observation_period
        ON subject_id = observation_period.person_id
        AND observation_period_start_date < cohort_start_date
        AND observation_period_end_date > cohort_start_date
    INNER JOIN @cdm_db_schema.person
        ON subject_id = person.person_id
"

```

```

        INNER JOIN @cdm_db_schema.concept
            ON gender_concept_id = concept_id
        WHERE cohort_definition_id = 1 -- Exposure
    )
SELECT days.gender,
    days.age,
    days,
    CASE WHEN events IS NULL THEN 0 ELSE events END AS events
FROM (
    SELECT gender,
        age,
        SUM(DATEDIFF(DAY, cohort_start_date,
            cohort_end_date)) AS days
    FROM tar
    GROUP BY gender,
        age
) days
LEFT JOIN (
    SELECT gender,
        age,
        COUNT(*) AS events
    FROM tar
    INNER JOIN @cohort_db_schema.@cohort_table angioedema
        ON tar.subject_id = angioedema.subject_id
        AND tar.cohort_start_date <= angioedema.cohort_start_date
        AND tar.cohort_end_date >= angioedema.cohort_start_date
    WHERE cohort_definition_id = 2 -- Outcome
    GROUP BY gender,
        age
) events
ON days.gender = events.gender
    AND days.age = events.age;
"

```

```

results <- renderTranslateQuerySql(conn, sql,
    cohort_db_schema = cohortDbSchema,
    cohort_table = cohortTable,
    cdm_db_schema = cdmDbSchema,
    snakeCaseToCamelCase = TRUE)

```

We first create “tar,” a CTE that contains all exposures with the appropriate time-at-risk. Note that we truncate the time-at-risk at the OBSERVATION_PERIOD_END_DATE. We also compute the age in 10-year bins, and identify the gender. The advantage of using a CTE is that we can use the same set of intermediate results several times in a query. In this case we use it to count the total amount of time-at-risk, as well as the number of angioedema events that occur during the time-at-risk.

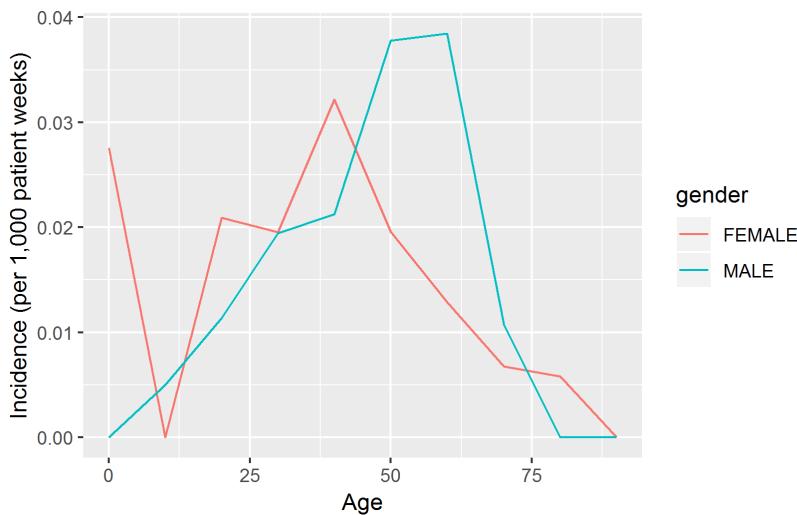
We use `snakeCaseToCamelCase = TRUE` because in SQL we tend to use `snake_case` for field names (because SQL is case-insensitive), whereas in R we tend to use `camelCase` (because R is case-sensitive). The `results` data frame column names will now be in `camelCase`.

With the help of the `ggplot2` package we can easily plot our results:

```
# Compute incidence rate (IR) :
results$ir <- 1000 * results$events / results$days / 7

# Fix age scale:
results$age <- results$age * 10

library(ggplot2)
ggplot(results, aes(x = age, y = ir, group = gender, color = gender)) +
  geom_line() +
  xlab("Age") +
  ylab("Incidence (per 1,000 patient weeks)")
```



9.7.4 Clean Up

Don't forget to clean up the table we created, and to close the connection:

```
sql <- "
TRUNCATE TABLE @cohort_db_schema.@cohort_table;
DROP TABLE @cohort_db_schema.@cohort_table;
"
renderTranslateExecuteSql(conn, sql,
  cohort_db_schema = cohortDbSchema,
  cohort_table = cohortTable)
```

```
disconnect(conn)
```

9.7.5 Compatibility

Because we use OHDSI SQL together with DatabaseConnector and SqlRender throughout, the code we reviewed here will run on any database platform supported by OHDSI.

Note that for demonstration purposes we chose to create our cohorts using hand-crafted SQL. It would probably have been more convenient to construct cohort definition in ATLAS, and use the SQL generated by ATLAS to instantiate the cohorts. ATLAS also produced OHDSI SQL, and can therefore easily be used together with SqlRender and DatabaseConnector.

9.8 Summary



- **SQL** (Structured Query Language) is a standard language for querying databases, including those that conform to the Common Data Model (CDM).
- Different database platforms have different SQL dialects, and require different tools to query them.
- The **SqlRender** and **DatabaseConnector** R packages provide a unified way to query data in the CDM, allowing the same analysis code to be run in different environments without modification.
- By using R and SQL together we can implement custom analyses that are not supported by the OHDSI tools.
- The **QueryLibrary** provides a collection of re-usable SQL queries for the CDM.

9.9 Exercises

Prerequisites

For these exercises we assume R, R-Studio and Java have been installed as described in Section 8.4.5. Also required are the SqlRender, DatabaseConnector, and Eunomia packages, which can be installed using:

```
install.packages(c("SqlRender", "DatabaseConnector", "devtools"))
devtools::install_github("ohdsi/Eunomia", ref = "v1.0.0")
```

The Eunomia package provides a simulated dataset in the CDM that will run inside your local R session. The connection details can be obtained using:

```
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
```

The CDM database schema is “main”.

Exercise 9.1. Using SQL and R, compute how many people are in the database.

Exercise 9.2. Using SQL and R, compute how many people have at least one prescription of celecoxib.

Exercise 9.3. Using SQL and R, compute how many diagnoses of gastrointestinal hemorrhage occur during exposure to celecoxib. (Hint: the concept ID for gastrointestinal hemorrhage is 192671.)

Suggested answers can be found in Appendix E.5.

Chapter 10

Defining Cohorts

Chapter lead: Kristin Kostka

Observational health data, also referred to *real world data*, are the data related to patient health status and/or the delivery of health care routinely collected from a variety of sources. As such, OHDSI data stewards (OHDSI collaborators who maintain data in CDM for their sites) may capture data from a number of sources including Electronic Health Records (EHR), health insurance claims and billing activities, product and disease registries, patient-generated data including in home-use settings, and data gathered from other sources that can inform on health status, such as mobile devices. As these data were not collected for research purposes, the data may not explicitly capture the clinical data elements we are interested in.

For example, a health insurance claims database is designed to capture all care provided for some condition (e.g. angioedema) so the associated costs can appropriately be reimbursed, and information on the actual condition is captured only as part of this aim. If we wish to use such observational data for research purposes, we will often have to write some logic that uses *what is captured in the data* to infer *what we are really interested in*. In other words, we often need to create a cohort using some definition of how a clinical event manifests. Thus, if we want to identify angioedema events in an insurance claims database, we may define logic requiring an angioedema diagnose code recorded in an emergency room setting, to distinguish from claims that merely describe follow-up care for some past angioedema occurrence. Similar considerations may apply for data captured during routine healthcare interactions logged in an EHR. As data are being used for a secondary purpose, we must be cognizant of what each database was originally designed to do. Each time we design a study, we must think through the nuances of how our cohort exists in a variety of healthcare settings.

The chapter serves to explain what is meant by creating and sharing cohort definitions, the methods for developing cohorts, and how to build your own cohorts

using ATLAS or SQL.

10.1 What Is a Cohort?

In OHDSI research, we define a cohort as a set of persons who satisfy one or more inclusion criteria for a duration of time. The term cohort is often interchanged with the term *phenotype*. Cohorts are used throughout OHDSI analytical tools and network studies as the primary building blocks for executing a research question. For instance, in a study aiming to predict the risk of angioedema in a group of people initiation ACE inhibitors, we define two cohorts: the outcome cohort (angioedema), and the target cohort (people initiating ACE inhibitors). An important aspect of cohorts in OHDSI is that they are typically defined independently from the other cohorts in the study, thus allowing re-use. For example, in our example the angioedema cohort would identify all angioedema events in the population, including those outside the target population. Our analytics tools will take the intersection of these two cohorts when needed at analysis time. The advantage of this is that the same angioedema cohort definition can now also be used in other analyses, for example an estimation study comparing ACE inhibitors to some other exposure. Cohort definitions can vary from study to study depending on the research question of interest.



A cohort is a set of persons who satisfy one or more inclusion criteria for a duration of time.

It is important to realize that this definition of a cohort used in OHDSI might differ from that used by others in the field. For example, in many peer-reviewed scientific manuscripts, a cohort is suggested to be analogous to a code set of specific clinical codes (e.g. ICD-9/ICD-10, NDC, HCPCS, etc). While code sets are an important piece in assembling a cohort, a cohort is not defined by code set. A cohort requires specific logic for how to use the code set for the criteria (e.g. is it the first occurrence of the ICD-9/ICD-10 code? any occurrence?). A well-defined cohort specifies how a patient enters a cohort and how a patient exits a cohort.

There are unique nuances to utilizing OHDSI's definition of a cohort, including:

- One person may belong to multiple cohorts
- One person may belong to the same cohort for multiple different time periods
- One person may not belong to the same cohort multiple times during the same period of time
- A cohort may have zero or more members

There are two main approaches to constructing a cohort:

1. **Rule-based cohort definitions** use explicit rules to describe when a patient is in the cohort. Defining these rules typically relies heavily on the domain

expertise of the individual designing the cohort to use their knowledge of the therapeutic area of interest to build rules for cohort inclusion criteria.

2. **Probabilistic cohort definitions** use a probabilistic model to compute a probability between 0 and 100% of the patient being in the cohort. This probability can be turned into a yes-no classification using some threshold, or in some study designs can be used as is. The probabilistic model is typically trained using machine learning (e.g. logistic regression) on some example data to automatically identify the relevant patient characteristics that are predictive.

The next sections will discuss these approaches in further detail.

10.2 Rule-Based Cohort Definitions

A rule-based cohort definition begins with explicitly stating one or more inclusion criteria (e.g. “people with angioedema”) in a specific duration of time (e.g. “who developed this condition within the last 6 months”).

The standard components we use to assemble these criteria are:

- **Domain:** The CDM domain(s) where the data are stored (e.g. “Procedure Occurrence”, “Drug Exposure”) define the type of clinical information and the allowable concepts that can be represented inside that CDM table. Domains are discussed in more detail in Section 4.2.4.
- **Concept set:** A data-agnostic expression that defines one or more Standard Concepts encompassing the clinical entity of interest. These concept sets are interoperable across different observational health data as they represent the standard terms the clinical entity maps to in the Vocabulary. Concept sets are discussed in Section 10.3.
- **Domain-specific attribute:** Additional attributes related to the clinical entity of interest (E.g. DAYS_SUPPLY for a DRUG_EXPOSURE, or VALUE_AS_NUMBER or RANGE_HIGH for a MEASUREMENT.)
- **Temporal logic:** The time intervals within which the relationship between an inclusion criteria and an event is evaluated (E.g. Indicated condition must occur during 365 days prior to or on exposure start.)

As you are building your cohort definition, you may find it helpful to think of Domains analogous to building blocks (see Figure 10.1) that represent cohort attributes. If you are confused about allowable content in each domain, you can always refer to the Common Data Model chapter (Chapter 4) for help.

When creating a cohort definition, you need to ask yourself the following questions:

- *What initial event defines the time of cohort entry?*
- *What inclusion criteria are applied to the initial events?*
- *What defines the time of cohort exit?*



Figure 10.1: Building Blocks of Cohort definitions.

Cohort entry event: The cohort entry event (initial event) defines the time when people enter the cohort, called the **cohort index date**. A cohort entry event can be any event recorded in the CDM such as drug exposures, conditions, procedures, measurements and visits. Initial events are defined by the CDM domain where the data are stored (e.g. PROCEDURE_OCCURRENCE, DRUG_EXPOSURE, etc), the concept sets built to identify the clinical activity (e.g. SNOMED codes for conditions, RxNorm codes for drugs) as well as any other specific attributes (e.g. age at occurrence, first diagnosis/procedure/etc, specifying start and end date, specifying visit type or criteria, days supply, etc). The set of people having an entry event is referred to as the **initial event cohort**.

Inclusion criteria: Inclusion criteria are applied to the initial event cohort to further restrict the set of people. Each inclusion criterion is defined by the CDM domain(s) where the data are stored, concept set(s) representing the clinical activity, domain-specific attributes (e.g. days supply, visit type, etc), and the temporal logic relative to the cohort index date. Each inclusion criterion can be evaluated to determine the impact of the criteria on the attrition of persons from the initial event cohort. The **qualifying cohort** is defined as all people in the initial event cohort that satisfy all inclusion criteria.

Cohort exit criteria: The cohort exit event signifies when a person no longer qualifies for cohort membership. Cohort exit can be defined in multiple ways such as the end of the observation period, a fixed time interval relative to the initial entry event, the last event in a sequence of related observations (e.g. persistent drug exposure) or through other censoring of observation period. Cohort exit strategy will impact whether a person can belong to the cohort multiple times during different time intervals.



In the OHDSI tools there is no distinction between inclusion and exclusion criteria. All criteria are formulated as inclusion criteria. For example, the exclusion criterium “Exclude people with prior hypertension” can be formulated as the inclusion criterium “Include people with 0 occurrences of prior hypertension”.

10.3 Concept Sets

A concept set is an expression representing a list of concepts that can be used as a reusable component in various analyses. It can be thought of as a standardized, computer-executable equivalent of the code lists often used in observational studies. A concept set expression consists of a list of concepts with the following attributes:

- **Exclude:** Exclude this concept (and any of its descendants if selected) from the concept set.
- **Descendants:** Consider not only this concept, but also all of its descendants.
- **Mapped:** Allow to search for non-standard concepts.

For example, a concept set expression could contain two concepts as depicted in Table 10.1. Here we include concept 4329847 (“Myocardial infarction”) and all of its descendants, but exclude concept 314666 (“Old myocardial infarction”) and all of its descendants.

Table 10.1: An example concept set expression.

Concept Id	Concept Name	Excluded	Descendants	Mapped
4329847	Myocardial infarction	NO	YES	NO
314666	Old myocardial infarction	YES	YES	NO

As shown in Figure 10.2, this will include “Myocardial infarction” and all of its descendants except “Old myocardial infarction” and its descendants. In total, this concept set expression implies nearly a hundred Standard Concepts. These Standard Concepts in turn reflect hundreds of source codes (e.g. ICD-9 and ICD-10 codes) that may appear in the various databases.

10.4 Probabilistic Cohort Definitions

Rule-based cohort definitions are a popular method for assembling cohort definitions. However, assembling necessary expert consensus to create a study cohort can be prohibitively time consuming. Probabilistic cohort design is an alternative, machine-driven method to expedite the selection of cohort attributes. In this approach, supervised machine learning allows a phenotyping algorithm to learn

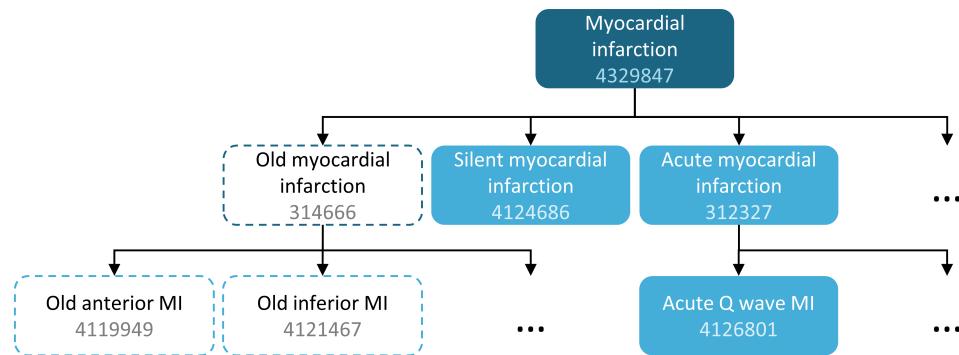


Figure 10.2: A concept set including "Myocardial infarction" (with descendants), but excluding "Old myocardial infarction" (with descendants).

from a set of labeled examples (cases) of what attributes contribute to cohort membership. This algorithm can then be used to better ascertain the defining characteristics of a phenotype and what trade-offs occur in overall study accuracy when choosing to modify phenotype criteria.

An example of applying this approach on data in the CDM is the APHRODITE (Automated PHenotype Routine for Observational Definition, Identification, Training and Evaluation) R-package¹. This package provides a cohort building framework that combines the ability of learning from imperfectly labeled data. (Banda et al., 2017)

10.5 Cohort Definition Validity

When you are building a cohort, you should consider which of these is more important to you: *finding all the eligible patients?* versus *Getting only the ones you are confident about?*

Your strategy to construct your cohort will depend on the clinical stringency of how your expert consensus defines the disease. This is to say, the right cohort design will depend on the question you're trying to answer. You may opt to build a cohort definition that uses everything you can get, uses the lowest common denominator so you can share it across OHDSI sites or is a compromise of the two. It is ultimately at the researcher's discretion what threshold of stringency is necessary to adequately study the cohort of interest.

As mentioned at the beginning of the chapter, a cohort definition is an attempt to infer something we would like to observe from the data that is recorded. This begs the question how well we succeeded in that attempt. In general, the validation of a rule-based cohort definition or probabilistic algorithm can be thought of as a test of the proposed cohort compared to some form of "gold standard" reference

¹<https://github.com/OHDSI/Aphrodite>

(e.g. manual chart review of cases). This is discussed in detail in Chapter 16 (“Clinical Validity”).

10.5.1 OHDSI Gold Standard Phenotype Library

To assist the community in the inventory and overall evaluation of existing cohort definitions and algorithms, the OHDSI Gold Standard Phenotype Library (GSPL) Workgroup was formed. The purpose of the GSPL workgroup is to develop a community-backed phenotype library from rules-based and probabilistic methods. The GSPL enable members of the OHDSI community to find, evaluate, and utilize community-validated cohort definitions for research and other activities. These “gold standard” definitions will reside in a library, the entries of which are held to specific standards of design and evaluation. For additional information related to the GSPL, consult the OHDSI workgroup page.² Research within this workgroup includes APHRODITE (Banda et al., 2017) and the PheEvaluator tool (Swerdel et al., 2019), discussed in the prior section, as well as work done to share the Electronic Medical Records and Genomics eMERGE Phenotype Library across the OHDSI network (Hripcsak et al., 2019). If phenotype curation is your interest, consider contributing to this workgroup.

10.6 Defining a Cohort for Hypertension

We begin to practice our cohort skills by putting together a cohort definition using a rule-based approach. In this example, we want to find *patients who initiate ACE inhibitors monotherapy as first-line treatments for hypertension*

With this context in mind, we are now going to build our cohort. As we go through this exercise, we will approach building our cohort similar to standard attrition chart. Figure 10.3 shows the logical framework for how we want to build this cohort.

You can build a cohort in the user interface of ATLAS or you can write a query directly against your CDM. We will briefly discuss both in this chapter.

10.7 Implementing a Cohort Using ATLAS

To begin in ATLAS, click on the  **Cohort Definitions** module. When the module loads, click on “New cohort”. The next screen you will see will be an empty cohort definition. Figure 10.4 shows what you will see on your screen.

Before you do anything else, you are encouraged to change the name of the cohort from “New Cohort Definition” to your own unique name for this cohort. You may opt for a name like “New users of ACE inhibitors as first-line monotherapy for hypertension”.

²<https://www.ohdsi.org/web/wiki/doku.php?id=projects:workgroups:gold-library-wg>

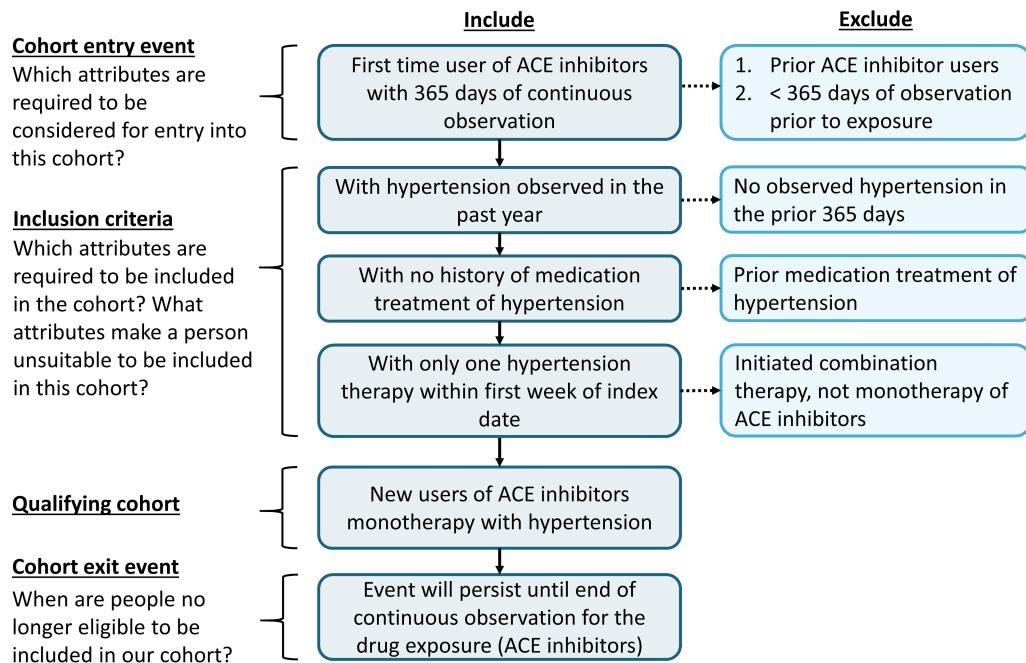


Figure 10.3: Logical Diagram of Intended Cohort

The screenshot shows the 'New Cohort Definition' interface. The top navigation bar includes tabs for 'Definition', 'Concept Sets', 'Generation', 'Reporting', and 'Export'. A large text input field is labeled 'enter a cohort definition description here'. Below this, the 'Cohort Entry Events' section contains fields for specifying the number of days before and after the event index date, and a button to 'Add Initial Event'. The 'Inclusion Criteria' section includes a 'New inclusion criteria' button and a note about limiting qualifying events per person.

Figure 10.4: New Cohort Definition

The screenshot shows the ATLAS Cohort builder interface. At the top, there's a header bar with a user icon, the text "Cohort #1771427", and several buttons: Definition (with a question mark icon), Concept Sets, Generation, Reporting, and Export. To the right of these are icons for saving, deleting, and other functions. Below the header is a search bar containing the placeholder text "enter a cohort definition description here". The main area is titled "Cohort Entry Events" and contains the following text: "Events having any of the following criteria:" followed by a dropdown menu set to "0" days before and "0" days after event index. Below this is a note: "Limit initial events to: earliest event ▾ per person." A green button labeled "Restrict initial events" is visible. To the right of this section is a sidebar with a "Add Initial Event" button and a list of options: Add Condition Era (Find patients with specific diagnosis era), Add Condition Occurrence (Find patients with specific diagnoses), Add Death (Find patients based on death), Add Device Exposure (Find patients based on device exposure), Add Dose Era (Find patients with dose eras), Add Drug Era (Find patients with exposure to drugs over time), and Add Drug Exposure (Find patients with exposure to specific drugs or drug classes). Below the "Cohort Entry Events" section is another section titled "Inclusion Criteria" with a "New inclusion criteria" button. At the bottom is a "Cohort Exit" section with a "Limit qualifying events to: earliest event ▾ per person." button.

Figure 10.5: Adding an Initial Event



ATLAS will not allow two cohorts to have the same exact names. ATLAS will give you a pop-up error message if you choose a name already used by another ATLAS cohort.

Once you have chosen a name, you can save the cohort by clicking

10.7.1 Initial Event Criteria

Now we can proceed with defining the initial cohort event. You will click “Add initial event”. You now have to pick which domain you are building a criteria around. You may ask yourself, “how do I know which domain is the initial cohort event?” Let’s figure that out.

As we see in Figure 10.5, ATLAS provides descriptions below each criteria to help you. If we were building a CONDITION_OCCURRENCE based criteria, our question would be looking for patients with a specific diagnosis. If we were building a DRUG_EXPOSURE based criteria, our question would be looking for patients with a specific drug or drug class. Since we want to find patients who initiate ACE inhibitors monotherapy as first-line treatments for hypertension, we want to choose a DRUG_EXPOSURE criteria. You may say, “but we also care about hypertension as a diagnosis”. You are correct. Hypertension is another criterion we will build. However, the cohort start date is defined by the initiation of the ACE inhibitor treatment, which is therefore the initial event. The diagnosis of hypertension is what we call an *additional qualifying criteria*. We will return to

The screenshot shows the 'Cohort Entry Events' interface. At the top, it says 'Events having any of the following criteria:' followed by a question mark icon. Below this, there is a search bar with the placeholder 'a drug exposure of' and a dropdown menu showing 'Any Drug'. To the right of the search bar are three buttons: '+ Add Initial Event', '+ Add attribute...', and 'Delete Criteria'. Further down, it says 'with continuous observation of at least [0] days before and [0] days after event index date'. Below that, it says 'Limit initial events to: earliest event per person.' A green button labeled 'Restrict initial events' is at the bottom left.

Figure 10.6: Defining a Drug Exposure

this once we build this criteria. We will click “Add Drug Exposure”.

The screen will update with your selected criteria but you are not done yet. As we see in Figure 10.6, ATLAS does not know what drug we are looking for. We need to tell ATLAS which concept set is associated to ACE inhibitors.

10.7.2 Defining the Concept Set

You will need to click to open the dialogue box that will allow you to retrieve a concept set to define ACE Inhibitors.

Scenario 1: You Have Not Built a Concept Set

If you have not assembled your concept sets to apply to your criteria, you will need to do so before you move forward. You may build a concept set within the cohort definition by navigating to the “Concept set” tab and clicking “New Concept Set”. You will need to rename the concept set from “Unnamed Concept Set” to a name of your choosing. From there you can use the module to look for clinical concepts that represent ACE inhibitors (Figure 10.7).

When you have found terms that you would like to use to define this drug exposure, you can select the concept by clicking on . You can return to your cohort definition by using the left arrow in the top left of Figure 10.7. You can refer back to Chapter 5 (Standardized Vocabularies) on how to navigate the vocabularies to find clinical concepts of interest.

Figure 10.8 shows our concept set expression. We selected all ACE inhibitor ingredients we are interested in, and include all their descendants, thus including all drugs that contain any of these ingredients. We can click on “Included concepts” to see all 21,536 concepts implied by this expression, or we can click on “Included Source Codes” to explore all source codes in the various coding systems that are implied.

♫ EXAMPLE: new users of ACE inhibitors as first-line mono-therapy for hypertension ► ACE Inhibitors												
Q Search												
Search		Import										
ace inhibitors												
Advanced Options												
Column visibility		Copy		CSV		Show	15 ▾	entries				
								Filter: <input type="text"/>				
Showing 1 to 9 of 9 entries												
Vocabulary	Id	Code	Name	Class	RC	DRC	Domain	Vocabulary				
ATC (6)	21601784	C09AA	ACE inhibitors, plain	ATC 4th	0	507,772	Drug	ATC				
Multilex (1)	21601783	C09A	ACE INHIBITORS, PLAIN	ATC 3rd	0	507,772	Drug	ATC				
VA Class (1)	21601802	C09BA	ACE inhibitors and diuretics	ATC 4th	0	10,982	Drug	ATC				
LOINC (1)	21601801	C09B	ACE INHIBITORS, COMBINATIONS	ATC 3rd	0	10,982	Drug	ATC				
ATC 4th (4)												

Figure 10.7: Searching the Vocabulary - ACE Inhibitors

Concept Set Expression									Included Concepts 21536	Included Source Codes	Export	Import
Name:												
ACE Inhibitors												
Show 25 ▾ entries												
Showing 1 to 15 of 15 entries												
Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped					
1335471	18867	benazepril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1340128	1998	Captopril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
19050216	21102	Cilazapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1341927	3827	Enalapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1342001	3829	Enalaprilat	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1363749	50166	Fosinopril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
19122327	60245	imidapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1308216	29046	Lisinopril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1310756	30131	moexipril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1373225	54552	Perindopril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1331235	35208	quinapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1334456	35296	Ramipril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
19040051	36908	spirapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
1342439	38454	trandolapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					
19102107	39990	zofenopril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>					

Figure 10.8: A concept set containing ACE inhibitor drugs.

Import Concept Set From Repository...

Filter Repository Concept Sets: ace inhibitors				
Show 10 entries		Created	Modified	Author
Id	Title			
1794480	[OHDSI EU 2019] Excluded concepts of ACE inhibitors or Thiazide diuretics	03/28/2019 11:04 AM	03/28/2019 11:04 AM	anonymous
963	ACE Inhibitors			anonymous
3268	COPY OF: ACE Inhibitors			anonymous
99283	Ace Inhibitors			anonymous
142965	PheKB ACE-I ACE inhibitors			anonymous

Showing 1 to 5 of 5 entries (filtered from 11,667 total entries)

Previous **1** Next

Figure 10.9: Importing a Concept Set from ATLAS Repository

Scenario 2: You Have Already Built a Concept Set

If you have already created a concept set and saved it in ATLAS, you can click to “Import Concept Set”. A dialogue box will open that will be prompt you to find your concept in the concept set repository of your ATLAS as shown in Figure 10.9. In the example figure the user is retrieving concept sets stored in ATLAS. The user typed in the name given to this concept set “ace inhibitors” in the right hand search. This shortened the concept set list to only concepts with matching names. From there, the user can click on the row of the concept set to select it. (Note: the dialogue box will disappear once you have selected a concept set.) You will know this action is successful when the Any Drug box is updated with the name of the concept set you selected.

10.7.3 Additional Initial Event Criteria

Now that you’ve attached a concept set, you are not done yet. Your question is looking for new users or the first time in someone’s history they are exposed to ACE inhibitors. This translates to the *first exposure* of ACE inhibitors in the patient’s record. To specify this, you need to click “+Add attribute”. You will want to select the “Add first exposure criteria”. Notice, you could specify other attributes of a criteria you build. You could specify an attribute of age at occurrence, the date of occurrence, gender or other attributes related to the drug. Criteria available for selection will look different for each domain.

From there, the window will automatically close. Once selected, this additional attribute will show up in the same box as the initial criteria (see Figure 10.10).



The current design of ATLAS may confuse some. Despite its appearance, the **X** is not intended to mean “No”. It is an actionable feature to allow the user to delete the criteria. If you click **X**, this criteria will go away. Thus,

The screenshot shows the 'Cohort Entry Events' section of the ATLAS software. At the top, there's a blue header bar with a question mark icon. Below it, a white form area starts with 'Events having any of the following criteria:' followed by a dropdown menu showing 'ACE inhibitors'. To the right of the dropdown are three buttons: '+ Add Initial Event', '+ Add attribute...', and 'Delete Criteria'. Below the dropdown, a note says 'X for the first time in the person's history'. Further down, it says 'with continuous observation of at least 365 days before and 0 days after event index date'. There's also a note about limiting initial events to the earliest event per person. At the bottom left is a green button labeled 'Restrict initial events'.

Figure 10.10: Setting the required continuous observation before the index date.

you need to leave the criteria with the **X** to keep the criteria active.

Now you have built an initial qualifying event. To ensure you are capturing the first observed drug exposure, you will want to add a look-back window to know that you are looking at enough of the patient's history to know what comes first. It is possible that a patient with a short observation period may have received an exposure elsewhere that we do not see. We cannot control this but we can mandate a minimum amount of time the patient must be in the data prior to the index date. You can do this by adjusting the continuous observation drop downs. You could also click the box and type in a value to these windows. We will require 365 days of continuous observation prior to the initial event. You will update your observation period to: *with continuous observation of 365 days before*, as shown in Figure 10.10. This look-back window is the discretion of your study team. You may choose differently in other cohorts. This creates, as best as we are able, a minimum period of time we see the patient to ensure we are capturing the first record. This criteria is about prior history and does not involve time after the index event. Therefore, we require 0 days after the index event. Our qualifying event is the first-ever use of ACE inhibitors. Thus, we limit initial events to the “earliest event” per person.

To further explain how this logic comes together, you can think about assembling patient timelines.

In Figure 10.11, each line represents a single patient that may be eligible to join the cohort. The filled in stars represent a time the patient fulfills the specified criteria. As additional criteria is applied, you may see some stars are a lighter shade. This means that these patients have other records that satisfy the criteria but there is another record that proceeds that. By the time we get to the last criteria, we are looking at the cumulative view of patients who have ACE inhibitors for the first time and have 365 days prior to the first-time occurrence. Logically, limiting to the initial event is redundant though it is helpful to maintain our explicit logic in

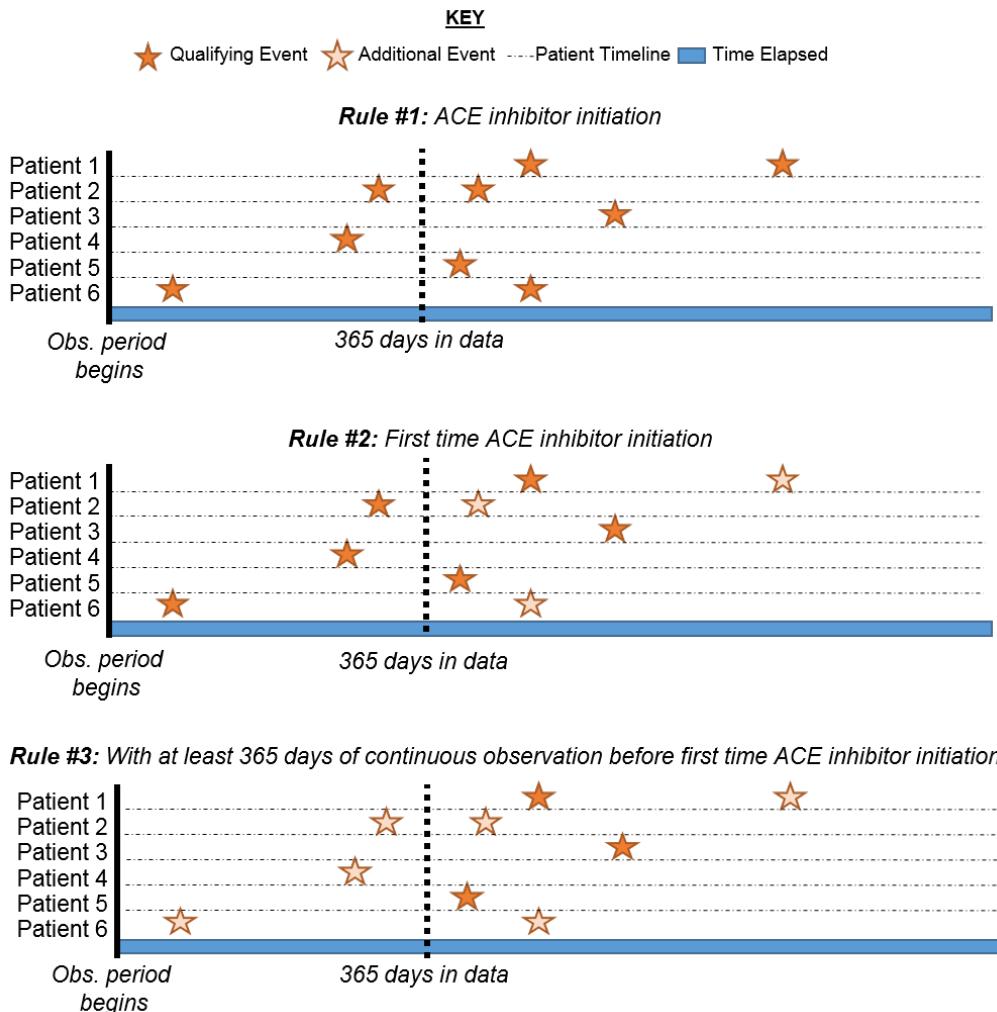


Figure 10.11: Explaining patient eligibility by criteria applied

every selection we make. When you are building your own cohorts, you may opt to engage the Researchers section of the OHDSI Forum to get a second opinion on how to construct your cohort logic.

10.7.4 Inclusion Criteria

Once we have specified a cohort entry event, you could proceed to one of two places to add your additional qualifying events: “Restrict initial events” and “New inclusion criteria”. The fundamental difference between these two options is what interim information you want ATLAS to serve back to you. If you add additional qualifying criteria into the Cohort Entry Event box by selecting “Restrict initial events”, when you choose to generate a count in ATLAS, you will only get back the number of people who meet ALL of these criteria. If you opt to add criteria into the “New inclusion criteria”, you will get an attrition chart to show you how many patients are lost by applying additional inclusion criteria. It is highly encouraged to utilize the Inclusion Criteria section so you can understand the impact of each rule on the overall success of the cohort definition. You may find a certain inclusion criteria severely limits the number of people who end up in the cohort. You may choose to relax this criterion to get a larger cohort. This will ultimately be at the discretion of the expert consensus assembling this cohort.

You will now want to click “New inclusion criteria” to add a subsequent piece of logic about membership to this cohort. The functionality in this section is identical to the way we discussed building cohort criteria above. You may specific the criteria and add specific attributes. Our first additional criteria is to subset the cohort to only patients: *With at least 1 occurrence of hypertension disorder between 365 and 0 days after index date (first initiation of an ACE inhibitor)*. You will click “New inclusion criteria” to add a new criteria. You should name your criteria and, if desired, put a little description of what you are looking for. This is for your own purposes to recall what you build – it will not impact the integrity of the cohort you are defining.

Once you have annotated this new criteria, you will click on the “+Add criteria to group” button to build your actual criteria for this rule. This button functions similar to the “Add Initial Event” except we are no longer specifying an initial event. We could add multiple criteria to this – which is why it specifies “add criteria to group”. An example would be if you have multiple ways of finding a disease (e.g. logic for a CONDITION_OCCURRENCE, logic using a DRUG_EXPOSURE as a proxy for this condition, logic for using a MEASUREMENT as a proxy for this condition). These would be separate domains and require different criteria but can be grouped into one criteria looking for this condition. In this case, we want to find a diagnosis of hypertension so we “Add condition occurrence”. We will follow similar steps as we did with the initial event by attaching a concept set to this record. We also want to specify the event starts between 365 days before and 0 days after the index date (the occurrence of the first ACE inhibitor use). Now check your logic against Figure 10.12.

Inclusion Criteria

New inclusion criteria

has hypertension diagnosis in 1 yr prior to treatment

1. has hypertension diagnosis in 1 yr prior to treatment

enter an inclusion rule description

having all of the following criteria:

+ Add criteria to group... ▾

with at least 1 using all occurrences of:
a condition occurrence of Hypertensive disorder + Add attribute...
where event starts between 365 days Before and 0 days After index start date add additional constraint
 restrict to the same visit occurrence
 allow events from outside observation period

Delete Criteria

Limit qualifying events to: earliest event per person.

Figure 10.12: Additional Inclusion criteria 1

Inclusion Criteria

New inclusion criteria

Has no prior antihypertensive drug exposures in medical history

1. has hypertension diagnosis in 1 yr prior to treatment

2. Has no prior antihypertensive drug exposures in medical history

enter an inclusion rule description

having all of the following criteria:

+ Add criteria to group... ▾

with exactly 0 using all occurrences of:
a drug exposure of Hypertension drugs + Add attribute...
where event starts between All days Before and 1 days Before index start date add additional constraint
 restrict to the same visit occurrence
 allow events from outside observation period

Delete Criteria

Limit qualifying events to: earliest event per person.

Figure 10.13: Additional Inclusion Criteria 2

You will then want to add another criterion to look for patients: *with exactly 0 occurrences of hypertension drugs ALL days before and 1 day before index start date (no exposure to HT drugs before an ACE inhibitor)*. This process begins as we did before by clicking the “New inclusion criteria” button, adding your annotations to this criterion and then clicking “+Add criteria to group”. This is a DRUG_EXPOSURE so you will click “Add Drug Exposure”, attach a concept set for hypertensive drugs, and will specify ALL days before and 0 days after the index date. Make sure to confirm you have *exactly 0* occurrence selected. Now check your logic against Figure 10.13.

You may be confused why “having no occurrences” is coded as “exactly 0 occurrences.” This is a nuance of how ATLAS consumes knowledge. ATLAS only consumes inclusion criteria. You must use logical operators to indicate when you want the absence of a specific attribute such as: “Exactly 0.” Over time you will

The screenshot shows the ATLAS Inclusion Criteria interface. A green box highlights the third criterion: "Is only taking ACE as monotherapy, with no concomitant combination treatments". To the right, there is a text input field containing the rule description: "Is only taking ACE as monotherapy, with no concomitant combination treatments". Below this is a dropdown menu set to "all" and a button "+ Add criteria to group...". Further down, there is a detailed configuration section for this criterion, including fields for "with exactly 1 using distinct occurrences of: a drug era of Hypertension drugs" and "where event starts between 0 days Before and 7 days After index start date add additional constraint". A checkbox "allow events from outside observation period" is also present. At the bottom left, there is a note: "Limit qualifying events to: earliest event per person.".

Figure 10.14: Additional Inclusion Criteria 3

become more familiar with the logical operators available in ATLAS criteria.

Lastly, you will want to add another criterion to look for patients: *with exactly 1 occurrence of hypertension drugs between 0 days before and 7 days after index start date AND can only start one HT drug (an ACE inhibitor)*. This process begins as we did before by clicking the “New inclusion criteria” button, adding your annotations to this criterion and then clicking “+Add criteria to group”. This is a DRUG_EXPOSURE so you will click “Add Drug Exposure”, attach a concept set for hypertensive drugs, and will specify 0 days before and 7 days after the index date. Now check your logic against Figure 10.14.

10.7.5 Cohort Exit Criteria

You have now added all of your qualifying inclusion criteria. You must now specify your cohort exit criteria. You will ask yourself, “when are people no longer eligible to be included in this cohort?” In this cohort, we are following new-users of a drug exposure. We want to look at continuous observation period as it relates to the drug exposure. As such, the exit criterion is specified to follow for the entirety of the continuous drug exposure. If there is a subsequent break in the drug exposure, the patient will exit the cohort at this time. We do this as we cannot determine what happened to the person during the break in the drug exposure. We can also set a criteria on the persistence window to specify an allowable gap between drug exposures. In this case, our experts leading this study concluded that a maximum of 30 days between exposure records is allowable when inferring the era of persistence exposure.

Why are gaps allowed? In some data sets, we see only portions of clinical interactions. Drug exposures, in particular, may represent a dispense of a prescription that can cover a certain period of time. Thus, we allow a certain amount of time between drug exposures as we know the patient may logically still have access to the initial drug exposure because the unit of dispense exceeded one day.

Event Persistence:
Event will persist until: end of a continuous drug exposure ▾

Continuous Exposure Persistence:
Specify a concept set that contains one or more drugs. A drug era will be derived from all drug exposure events for any of the drugs within the concept set, using the specified persistence window as a maximum allowable gap in days between successive exposure events and adding a specified surveillance window to the final exposure event. If no exposure event end date is provided, then an exposure event end date is inferred to be event start date + days supply in cases when days supply is available or event start date + 1 day otherwise. This event persistence assures that the cohort end date will be no greater than the drug era end date.

Concept set containing the drug(s) of interest: ACE Inhibitors ▾

- Persistence window: allow for a maximum of 30 days between exposure records when inferring the era of persistence exposure
- Surveillance window: add 0 days to the end of the era of persistence exposure as an additional period of surveillance prior to cohort exit.

Censoring Events:
Exit Cohort based on the following criteria: + Add Censoring Event ▾

No censoring events selected.

Figure 10.15: Cohort Exit Criteria

We can configure this by selecting the Event will persist “end of a continuous drug exposure”. We then will add our persistence window to “allow for a maximum of 30 days” and append the concept set for “ACE inhibitors”. Now check your logic against Figure 10.15.

In the case of this cohort, there are no other censoring events. However, you may build other cohorts where you need to specify this criteria. You would proceed similarly to the way we have added other attributes to this cohort definition. You have now successfully finished creating your cohort. Make sure to hit the button. Congratulations! Building a cohort is the most important building block of answering a question in the OHDSI tools. You can now use the “Export” tab to share your cohort definition to other collaborators in the form of SQL code or JSON files to load into ATLAS.

10.8 Implementing the Cohort Using SQL

Here we describe how to create the same cohort, but using SQL and R. As discussed in Chapter 9, OHDSI provides two R packages, called `SqlRender` and `DatabaseConnector`, which together allow writing SQL code that can be automatically translated and executed against a wide variety of database platforms.

For clarity, we will split the SQL into several chunks, each chunk generating a temp table that is used in the next. This is likely not the most computationally efficient way to do it, but it is easier to read than a single very long statement.

10.8.1 Connecting to the Database

We first need to tell R how to connect to the server. We use the `DatabaseConnector` package, which provides a function called `createConnectionDetails`. Type `?createConnectionDetails` for the specific settings required for the various database management systems (DBMS). For example, one might connect to a PostgreSQL database using this code:

```
library(CohortMethod)
connDetails <- createConnectionDetails(dbms = "postgresql",
                                         server = "localhost/ohdsi",
                                         user = "joe",
                                         password = "supersecret")

cdmDbSchema <- "my_cdm_data"
cohortDbSchema <- "scratch"
cohortTable <- "mycohorts"
```

The last three lines define the `cdmDbSchema`, `cohortDbSchema`, and `cohortTable` variables. We will use these later to tell R where the data in CDM format live, and where the cohorts of interest have to be created. Note that for Microsoft SQL Server, database schemas need to specify both the database and the schema, so for example `cdmDbSchema <- "my_cdm_data.dbo"`.

10.8.2 Specifying the Concepts

For readability we will define the concept IDs we need in R, and pass them to the SQL:

```
aceI <- c(1308216, 1310756, 1331235, 1334456, 1335471, 1340128, 1341927,
         1342439, 1363749, 1373225)

hypertension <- 316866

allHtDrugs <- c(904542, 907013, 932745, 942350, 956874, 970250, 974166,
                 978555, 991382, 1305447, 1307046, 1307863, 1308216,
                 1308842, 1309068, 1309799, 1310756, 1313200, 1314002,
                 1314577, 1317640, 1317967, 1318137, 1318853, 1319880,
                 1319998, 1322081, 1326012, 1327978, 1328165, 1331235,
                 1332418, 1334456, 1335471, 1338005, 1340128, 1341238,
                 1341927, 1342439, 1344965, 1345858, 1346686, 1346823,
                 1347384, 1350489, 1351557, 1353766, 1353776, 1363053,
                 1363749, 1367500, 1373225, 1373928, 1386957, 1395058,
                 1398937, 40226742, 40235485)
```

10.8.3 Finding First Use

We will first find first use of ACE inhibitors for each patient:

```
conn <- connect(connectionDetails)

sql <- "SELECT person_id AS subject_id,
    MIN(drug_exposure_start_date) AS cohort_start_date
  INTO #first_use
  FROM @cdm_db_schema.drug_exposure
  INNER JOIN @cdm_db_schema.concept_ancestor
    ON descendant_concept_id = drug_concept_id
  WHERE ancestor_concept_id IN (@ace_i)
  GROUP BY person_id;"

renderTranslateExecuteSql(conn,
    sql,
    cdm_db_schema = cdmDbSchema,
    ace_i = aceI)
```

Note that we join the DRUG_EXPOSURE table to the CONCEPT_ANCESTOR table to find all drugs that contain an ACE inhibitor.

10.8.4 Require 365 Days of Prior Observation

Next, we require 365 of continuous prior observation by joining to the OBSERVATION_PERIOD table:

```
sql <- "SELECT subject_id,
    cohort_start_date
  INTO #has_prior_obs
  FROM #first_use
  INNER JOIN @cdm_db_schema.observation_period
    ON subject_id = person_id
    AND observation_period_start_date <= cohort_start_date
    AND observation_period_end_date >= cohort_start_date
  WHERE DATEADD(DAY, 365, observation_period_start_date) < cohort_start_date;"

renderTranslateExecuteSql(conn, sql, cdm_db_schema = cdmDbSchema)
```

10.8.5 Require Prior Hypertension

We require a hypertension diagnosis in the 365 days prior:

```
sql <- "SELECT DISTINCT subject_id,
    cohort_start_date
  INTO #has_ht
```

```

FROM #has_prior_obs
INNER JOIN @cdm_db_schema.condition_occurrence
  ON subject_id = person_id
    AND condition_start_date <= cohort_start_date
    AND condition_start_date >= DATEADD(DAY, -365, cohort_start_date)
INNER JOIN @cdm_db_schema.concept_ancestor
  ON descendant_concept_id = condition_concept_id
WHERE ancestor_concept_id = @hypertension,"

renderTranslateExecuteSql(conn,
                        sql,
                        cdm_db_schema = cdmDbSchema,
                        hypertension = hypertension)

```

Note that we `SELECT DISTINCT`, because else if a person has multiple hypertension diagnoses in their past, we would create duplicate cohort entries.

10.8.6 No Prior Treatment

We require no prior exposure to any hypertension treatment:

```

sql <- "SELECT subject_id,
            cohort_start_date
INTO #no_prior_ht_drugs
FROM #has_ht
LEFT JOIN (
  SELECT *
  FROM @cdm_db_schema.drug_exposure
  INNER JOIN @cdm_db_schema.concept_ancestor
    ON descendant_concept_id = drug_concept_id
  WHERE ancestor_concept_id IN (@all_ht_drugs)
) ht_drugs
  ON subject_id = person_id
    AND drug_exposure_start_date < cohort_start_date
WHERE person_id IS NULL;"

renderTranslateExecuteSql(conn,
                        sql,
                        cdm_db_schema = cdmDbSchema,
                        all_ht_drugs = allHtDrugs)

```

Note that we use a left join, and only allow rows where the `person_id`, which comes from the `DRUG_EXPOSURE` table is `NULL`, meaning no matching record was found.

10.8.7 Monotherapy

We require there to be only one exposure to hypertension treatment in the first seven days of the cohort entry:

```
sql <- "SELECT subject_id,
  cohort_start_date
INTO #monotherapy
FROM #no_prior_ht_drugs
INNER JOIN @cdm_db_schema.drug_exposure
  ON subject_id = person_id
    AND drug_exposure_start_date >= cohort_start_date
    AND drug_exposure_start_date <= DATEADD(DAY, 7, cohort_start_date)
INNER JOIN @cdm_db_schema.concept_ancestor
  ON descendant_concept_id = drug_concept_id
WHERE ancestor_concept_id IN (@all_ht_drugs)
GROUP BY subject_id,
  cohort_start_date
HAVING COUNT(*) = 1;"

renderTranslateExecuteSql(conn,
  sql,
  cdm_db_schema = cdmDbSchema,
  all_ht_drugs = allHtDrugs)
```

10.8.8 Cohort Exit

We have now fully specified our cohort except the cohort end date. The cohort is defined to end when the exposure stops, allowing for a maximum 30-day gap between subsequent exposures. This means we need to not only consider the first drug exposure, but also subsequent drug exposures to ACE inhibitors. The SQL for combining subsequent exposures into eras can be highly complex. Luckily, standard code has been defined that can efficiently create eras. (This code was written by Chris Knoll, and is often referred to within OHDSI as ‘the magic’). We first create a temp table containing all exposures we wish to merge:

```
sql <- "
SELECT person_id,
  CAST(1 AS INT) AS concept_id,
  drug_exposure_start_date AS exposure_start_date,
  drug_exposure_end_date AS exposure_end_date
INTO #exposure
FROM @cdm_db_schema.drug_exposure
INNER JOIN @cdm_db_schema.concept_ancestor
  ON descendant_concept_id = drug_concept_id
WHERE ancestor_concept_id IN (@ace_i);"
renderTranslateExecuteSql(conn,
```

```
sql,
cdm_db_schema = cdmDbSchema,
ace_i = aceI)
```

We then run the standard code for merging sequential exposures:

```
sql <- "
SELECT ends.person_id AS subject_id,
       ends.concept_id AS cohort_definition_id,
       MIN(exposure_start_date) AS cohort_start_date,
       ends.era_end_date AS cohort_end_date
INTO #exposure_era
FROM (
    SELECT exposure.person_id,
           exposure.concept_id,
           exposure.exposure_start_date,
           MIN(events.end_date) AS era_end_date
      FROM #exposure exposure
     JOIN (
--cteEndDates
        SELECT person_id,
               concept_id,
               DATEADD(DAY, - 1 * @max_gap, event_date) AS end_date
          FROM (
            SELECT person_id,
                   concept_id,
                   event_date,
                   event_type,
                   MAX(start_ordinal) OVER (
                     PARTITION BY person_id ,concept_id ORDER BY event_date,
                                         event_type ROWS UNBOUNDED PRECEDING
                     ) AS start_ordinal,
                   ROW_NUMBER() OVER (
                     PARTITION BY person_id, concept_id ORDER BY event_date,
                                         event_type
                     ) AS overall_ord
          FROM (
-- select the start dates, assigning a row number to each
            SELECT person_id,
                   concept_id,
                   exposure_start_date AS event_date,
                   0 AS event_type,
                   ROW_NUMBER() OVER (
                     PARTITION BY person_id, concept_id ORDER BY exposure_start_date
                     ) AS start_ordinal
          FROM #exposure exposure

         UNION ALL
```

```
-- add the end dates with NULL as the row number, padding the end dates by
-- @max_gap to allow a grace period for overlapping ranges.

    SELECT person_id,
           concept_id,
           DATEADD(day, @max_gap, exposure_end_date),
           1 AS event_type,
           NULL
      FROM #exposure exposure
     ) rawdata
  ) events
 WHERE 2 * events.start_ordinal - events.overall_ord = 0
) events
ON exposure.person_id = events.person_id
   AND exposure.concept_id = events.concept_id
   AND events.end_date >= exposure.exposure_end_date
GROUP BY exposure.person_id,
         exposure.concept_id,
         exposure.exposure_start_date
) ends
GROUP BY ends.person_id,
         concept_id,
         ends.era_end_date;"
```

```
renderTranslateExecuteSql(conn,
                           sql,
                           cdm_db_schema = cdmDbSchema,
                           max_gap = 30)
```

This code merges all subsequent exposures, allowing for a gap between exposures as defined by the `max_gap` argument. The resulting drug exposure eras are written to a temp table called `#exposure_era`.

Next, we simply join these ACE inhibitor exposure eras to our original cohort to use the era end dates as our cohort end dates:

```
sql <- "SELECT ee.subject_id,
           CAST(1 AS INT) AS cohort_definition_id,
           ee.cohort_start_date,
           ee.cohort_end_date
      INTO @cohort_db_schema.@cohort_table
     FROM #monotherapy mt
INNER JOIN #exposure_era ee
       ON mt.subject_id = ee.subject_id
      AND mt.cohort_start_date = ee.cohort_start_date;"
```

```
renderTranslateExecuteSql(conn,
                           sql,
```

```
cohort_db_schema = cohortDbSchema,  
cohort_table = cohortTable)
```

Here we store the final cohort in schema and table we defined earlier. We assign it a cohort definition ID of 1, to distinguish it from other cohorts we may wish to store in the same table.

10.8.9 Cleanup

Finally, it is always recommend to clean up any temp tables that were created, and disconnect from the database server:

```
sql <- "TRUNCATE TABLE #first_use;  
DROP TABLE #first_use;  
  
TRUNCATE TABLE #has_prior_obs;  
DROP TABLE #has_prior_obs;  
  
TRUNCATE TABLE #has_ht;  
DROP TABLE #has_ht;  
  
TRUNCATE TABLE #no_prior_ht_drugs;  
DROP TABLE #no_prior_ht_drugs;  
  
TRUNCATE TABLE #monotherapy;  
DROP TABLE #monotherapy;  
  
TRUNCATE TABLE #exposure;  
DROP TABLE #exposure;  
  
TRUNCATE TABLE #exposure_era;  
DROP TABLE #exposure_era;"  
  
renderTranslateExecuteSql(conn, sql)  
  
disconnect(conn)
```

10.9 Summary



- A cohort is set of persons who satisfy one or more inclusion criteria for a duration of time.
- A cohort definition is the description of logic used for identifying a particular cohort.

- Cohorts are used (and re-used) throughout the OHDSI analytics tools to define for example the exposures and outcomes of interest.
- There are two major approaches to building a cohort: rule-based and probabilistic.
- Rule-based cohort definitions can be created in ATLAS, or using SQL

10.10 Exercises

Prerequisites

For the first exercise, access to an ATLAS instance is required. You can use the instance at <http://atlas-demo.ohdsi.org>, or any other instance you have access to.

Exercise 10.1. Use ATLAS to create a cohort definition following these criteria:

- New users of diclofenac
- Ages 16 or older
- With at least 365 days of continuous observation prior to exposure
- Without prior exposure to any NSAID (Non-Steroidal Anti-Inflammatory Drug)
- Without prior diagnosis of cancer
- With cohort exit defined as discontinuation of exposure (allowing for a 30-day gap)

Prerequisites

For the second exercise we assume R, R-Studio and Java have been installed as described in Section 8.4.5. Also required are the SqlRender, DatabaseConnector, and Eunomia packages, which can be installed using:

```
install.packages(c("SqlRender", "DatabaseConnector", "devtools"))
devtools::install_github("ohdsi/Eunomia", ref = "v1.0.0")
```

The Eunomia package provides a simulated dataset in the CDM that will run inside your local R session. The connection details can be obtained using:

```
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
```

The CDM database schema is “main”.

Exercise 10.2. Use SQL and R to create a cohort for acute myocardial infarction (AMI) in the existing COHORT table, following these criteria:

- An occurrence of a myocardial infarction diagnose (concept 4329847 “Myocardial infarction” and all of its descendants, excluding concept 314666 “Old myocardial infarction” and any of its descendants).
- During an inpatient or ER visit (concepts 9201, 9203, and 262 for “Inpatient visit”, “Emergency Room Visit”, and “Emergency Room and Inpatient Visit”, respectively).

Suggested answers can be found in Appendix E.6.

Chapter 11

환자 특성 분석 Characterization

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관찰형 보건의료데이터는 다양한 특성을 바탕으로 인구집단의 변화를 이해할 수 있는 귀중한 자원이다. 기술통계를 통해 인구집단의 특성을 확인하는 것은 건강과 질병에 영향을 주는 요인에 대한 가설 설정을 위한 중요한 첫번째 단계이다. 이번 장에서는 특성 분석 (characterization)을 위한 방법들에 대해 살펴보기로 한다. :

- **데이터베이스 수준의 특성 분석 (Database-level characterization)**: 상위 수준 (top-level)의 요약 통계량을 제공하여 데이터베이스 전체에 대한 이해를 돋는다.
- **코호트의 특성 분석 (Cohort characterization)**: 통합된 의무기록 측면에서 인구집단을 기술한다.
- **치료 경로 (Treatment pathways)**: 특정 기간동안 한 사람에 대하여 행해진 중재 (intervention) 순서를 기술한다.
- **발생 (Incidence)**: 위험 관찰 기간(time at risk, TAR)동안의 outcome의 발생율을 계산한다.

데이터베이스 수준의 특성 분석을 제외하고 이 방법들은 index date라고 하는 시점과 관련된 인구 집단에 대해 설명하는데 목적이 있다. 이와 같은 관심 집단은 코호트라고 정의되며 10 장에 기술되어 있다. 코호트는 관심집단의 개개인에 대한 index date를 정의한다. Index date를 기준으로 index date이전의 시간을 **기저 시간(baseline time)**이라 정의한다. Index date를 포함한 그 이후의 시간들은 **index 후 시간(post-index time)**이라고 부른다.

특성 분석은 질병의 자연 경과, 치료 이용, 진료 질 개선 등과 같은 것에 활용될 수 있다. 이번 장에서는 특성 분석 방법에 대해 기술하며, ATLAS와 R을 이용한 고혈압 환자군에 대한 특성 분석을 해 볼 것이다.

11.1 데이터베이스 수준의 특성 분석 (Database Level Characterization)

관심집단에 대한 특성 분석을 시행하기 전, 사용하고자 하는 데이터베이스의 특성을 이해하는 것이 선행되어야 한다. 데이터베이스 수준의 특성 분석은 전체 데이터베이스에 대한 시간의 흐름에 따른 경향과 분포 측면에서 데이터 번체를 설명하기 위해 사용한다. 데이터베이스의 정량적 분석은 일반적으로 다음과 같은 질문을 포함한다:

- 이 데이터베이스의 총 사람 수는 몇인가?
- 환자들의 연령 분포는 어떠한가?
- 환자들의 관찰 기간은 얼마나 오래되었는가?
- 시간이 지남에 따라 기록/처방된 {치료, 질병, 처치 등}을 받은 사람의 비율은 어떠한가?

데이터베이스 수준의 기술 통계는 연구자로 하여금 어떠한 데이터에서 손실이 있을 수 있는지와 같이 확인할 수 없는 부분을 이해하는데 도움을 주며 15 장 데이터 품질을 설명할 때 자세히 다룬다.

11.2 코호트 특성 분석 (Cohort Characterization)

코호트 특성 분석은 기저 시점과 index 후 코호트 구성원의 특징들을 기술한다. OHDSI는 상태(condition), 약물(drug), 치료재료(device), 시술(procedure), 임상적 관찰(clinical observation) 등 개인의 의무기록에 존재하는 모든 것에 대한 기술 통계량을 바탕으로 특성 분석을 접근한다. 또한, index 시점에서 코호트 구성원에 대한 사회인구학적 내용에 대해 요약해준다. 이와 같은 접근 방식을 통해 관심 코호트에 대한 완벽한 요약을 제공한다. 특히, 이러한 접근을 통해 데이터의 변화에 대한 안목을 가지고 코호트에 대한 전체적인 탐색을 가능하게 하는 한편, 잠재적인 결측 값을 찾을 수 있도록 한다.

코호트 특성 분석 방법은 이미 치료를 받은 사람에서 치료의 적응증 유발율과 금기를 추정하는 개인 수준의 개인 수준의 약물 사용 연구 (person-level drug utilization studies : DUS)에 이용될 수 있다. 코호트 특성 분석의 보급은 역학 관찰연구 보고 강화(Strengthening the Reporting of Observational Studies in Epidemiology, STROBE) 가이드라인에 자세히 제시된 관찰 연구에 권장되는 모범사례이다. (von Elm et al., 2008)

11.3 치료 경로 (Treatment Pathways)

인구 집단의 특성을 분석하는 또 하나의 방법은 index 후(post-index) 시간 동안의 치료 순서를 기술하는 것이다. 예를 들어, 이전 연구(Hripcak et al., 2016)에서 OHDSI의 공통 데이터 표준을 활용해 제 2형 당뇨, 고혈압, 우울증에 대한 치료 경로의 특징을 분석하기 위한 기술 통계를 고안하였다. 이러한 분석 방법을 표준화 함으로써, Hripcak과 그 연구팀은 관심집단의 특성 분석을 OHDSI 네트워크 상에서 동일한 통계방법으로 실행하였다.

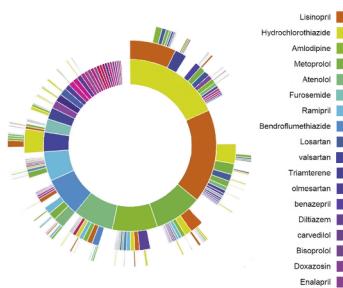


Figure 11.1: 고혈압 환자의 OHDSI 치료 경로 "sunburst" 시각화 사례

치료 경로 분석은 가장 처음 처방/조제된 약물 이후 특정 상태에 있는 환자에 대한 치료 행위(events)를 요약하기 위해 시행한다. 이 연구에서는 제 2형 당뇨, 고혈압, 우울증의 진단 이후의 치료 행위들을 기술했다. 개개인이 받은 치료 행위들(events)은 이후 요약 통계량으로 합쳐지고 각의 질병과 각각의 데이터베이스에서 별로 시각화되었다.

figure 11.1에서 제시된 사례는 고혈압 치료를 시작한 환자집단을 나타낸다. 가운데 위치한 첫번째 고리는 1차 요법(first-line therapy)에 대한 환자의 비율을 나타낸다. 이 사례의 경우 Hydrochlorothiazide는 고혈압 환자군의 1차 요법으로 가장 흔하게 사용되는 약물이라는 것을 알 수 있다. Hydrochlorothiazide에서 파생된 상자들은 해당 코호트 대상자에서 기록된 두번째(2nd), 세번째(3rd) 요법을 의미한다.

치료 경로 분석은 인구집단 내의 치료 이용 현황에 대한 중요한 근거를 제공한다. 이 분석을 통해 우리는 가장 빈번히 사용되는 1차 요법을 기술할 수 있고, 치료가 중단/변경/확대된 사람들의 비율을 알 수 있다. 경로 분석을 통해 metformin이 당뇨에서 가장 일반적으로 처방된 1차 치료제임을 밝혔고, 이를 통해 미국 내분비학회의 당뇨 치료 알고리즘의 일차 요법이 일반적으로 잘 적용되고 있음을 확인했다. 더불어 당뇨 환자의 10%, 고혈압 환자의 24%, 그리고 우울증 환자의 11%는 다른 데이터베이스와 비교했을 때 공유된 적 없는 치료 경로를 따르고 있는 것을 확인했다.

고전적인 약물 사용 연구 (DUS) 개념에서, 치료 경로 분석은 특정 집단에서 하나 이상의 약물 사용율과 같은 집단 수준의 약물 사용 연구 (population-level DUS) 뿐 아니라 치료 방법의 지속률, 서로 다른 치료 간의 전환률과 같은 개인 수준의 약물 사용 연구 (person-level DUS)가 포함된다.

11.4 발생 (Incidence)

발생률과 발생비는 공중 보건에서 위험 관찰 기간(time-at-risk, TAR)동안 인구집단 내 새로운 outcome의 발생의 평가에 사용되는 통계적 지표이다. Figure 11.2 는 한 사람에게서 발생률 계산에 필요한 구성요소를 보여주고 있다:

figure 11.2에서 한 사람은 데이터 내에서 관찰이 시작되고 끝나는 시점이 표시된 기간을 갖는다. 그 다음, 그 사람은 몇몇 연구 기준 (eligibility criteria)에 의해 코호트에 들어가는(enter) 시점과 나오는(exit) 시점을 갖게 된다. 위험을 관찰하는 기간 (time at risk, TAR)은 우리가 outcome의 발생을 보고자 하는 기간을 의미한다. 만

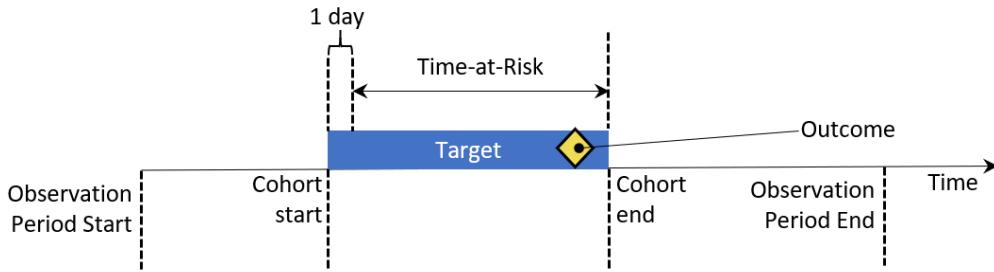


Figure 11.2: 개인 수준에서의 발생률 계산의 구성 성분. 본 예시에서는 위험 관찰 기간은 코호트가 시작하고 하루 이후부터 코호트가 끝나는 시점으로 정의됨.

일 outcome이 위험 관찰 기간(time at risk, TAR) 내에서 발생한다면, outcome이 발생된 것으로 간주한다.

발생을 계산하기 위해서는 두 가지 측정법이 있다:

$$\text{Incidence Rate} = \frac{\# \text{ new outcomes during TAR}}{\# \text{ person-time at risk}}$$

발생 분율은 위험 관찰 기간동안 집단 내 새로운 outcome의 발생을 측정하는 방법이다. 다시 말해, 관심집단에서 정해진 시간의 틀 안에서 발생한 outcome의 비율이다.

$$\text{Incidence Rate} = \frac{\# \text{ new outcomes during TAR}}{\text{person-time at risk}}$$

$$\text{Incidence Rate} = \frac{\# \text{ persons in cohort with new outcome during TAR}}{\text{person-time at risk contributed by persons in cohort}}$$

발생률은 인구집단에서 누적되는 위험 관찰 기간 동안의 새로 발생한 outcome의 횟수를 측정한 것이다. 만일 한 환자가 위험 관찰 기간 (TAR) 내에서 outcome을 경험했을 때, 그 환자가 전체의 인-시(person-time)에 outcome이 발생하기까지의 시간만큼 기여했다고 산정한다. 누적된 위험 관찰 기간은 **인-시(person-time)**라고 하고, 단위는 일, 월, 혹은 연으로 표현된다.

치료 요법에 대하여 계산할 때, 정해진 치료 요법의 사용 비율 혹은 발생률을 계산하는 것은 전형적인 인구 집단 수준의 약물 사용 연구(population-level DUS)라 할 수 있다.

11.5 고혈압 환자의 특성 분석 (Characterizing Hypertensive Persons)

세계보건기구(WHO)의 고혈압에 대한 보고서(Who, 2013)에 따르면, 고혈압의 초기 발견과 적절한 치료 및 양호한 혈압 조절은 건강과 경제적인 면에서 상당한 이득이 있다. WHO의 보고서에는 고혈압의 개요 및 여러 국가들의 질병 부담의 특징들을 보여주고 있다. WHO는 지경과 사회 경제적 계급 및 성별 별 고혈압에 대한 기술통계를 제공하고 있다.

WHO가 수행한 고혈압 환자의 특성 분석과 동일한 분석은 관찰형 데이터 소스를 이용해 할 수 있다. 이 장의 다음 절에서는 고혈압 환자 집단의 구성을 이해하기 위한 데이터베이스의 탐색을 ATLAS와 R을 이용해 시행하는 방법을 살펴볼 것이다. 또한, 동일한 툴을 사용해 고혈압 집단의 자연 경과와 치료 패턴을 알아 설명하려고 한다.

11.6 ATLAS를 활용한 데이터베이스의 특성 분석 (Database Characterization in ATLAS)

여기서는 ATLAS에 탑재된 데이터 소스 모듈을 사용하여 ACHILLES로 생성된 데이터베이스의 특성을 살펴보고, 고혈압 환자와 관련된 데이터베이스 수준의 특성을 찾아내는 방법을 설명하고자 한다. 시작하기 위해 ATLAS의 왼쪽 바에 위치한  Data Sources을 클릭하자. ATLAS의 첫번째 드롭 다운 목록에서 데이터 탐색(database to explore)을 선택한다. 그리고, 데이터베이스 아래의 드롭 다운 목록을 통해 보고서를 탐색을 시작할 수 있다. 고혈압 환자에 대한 데이터베이스 수준의 특성 분석을 위해 두 번째 드롭 다운 목록인 report 드롭 다운 목록에서 Condition Occurrence를 선택하면 해당 데이터베이스의 모든 질병에 대한 treemap 시각화 결과가 표시된다:

특정 관심 질환을 검색하기 위해 Table탭을 클릭하면 환자 수, 유병률, 환자 별 기록들을 포함하는 데이터베이스의 전체 condition 목록이 나타난다. 상단의 filter 상자를 이용해 “hypertension”을 포함하는 concept name만을 걸러낼 수 있다:

하나의 행을 클릭하면 해당 condition에 대한 자세한 드릴다운 보고서를 확인할 수 있다. 이 경우 “essential hypertension”을 선택한 결과이며, 선택된 condition의 시간에 따른 경향과 성별, 월별 유병률, 기록 유형 (주상병 혹은 부상병 등) 그리고 최초 진단 시 나이의 경향을 알 수 있다:

지금까지 고혈압이라는 concept에 대한 데이터의 특징과 시간에 따른 경향을 살펴보았다. 데이터베이스 수준의 특성 분석을 통해 고혈압 환자의 치료에 사용된 약물에 대하여도 확인할 수 있다. 이는 RxNorm Ingredient에 요약된 약물의 특성을 검토를 위해 Drug Era report을 사용한 것 외에는 위와 동일하게 진행된다. 관심있는 항목에 대한 데이터베이스 특성 탐색을 마쳤다면, 이제는 특성화 하고자 하는 고혈압 환자의 특성 분석을 위한 코호트를 설계하는 단계로 나아갈 준비를 마친 것이다.

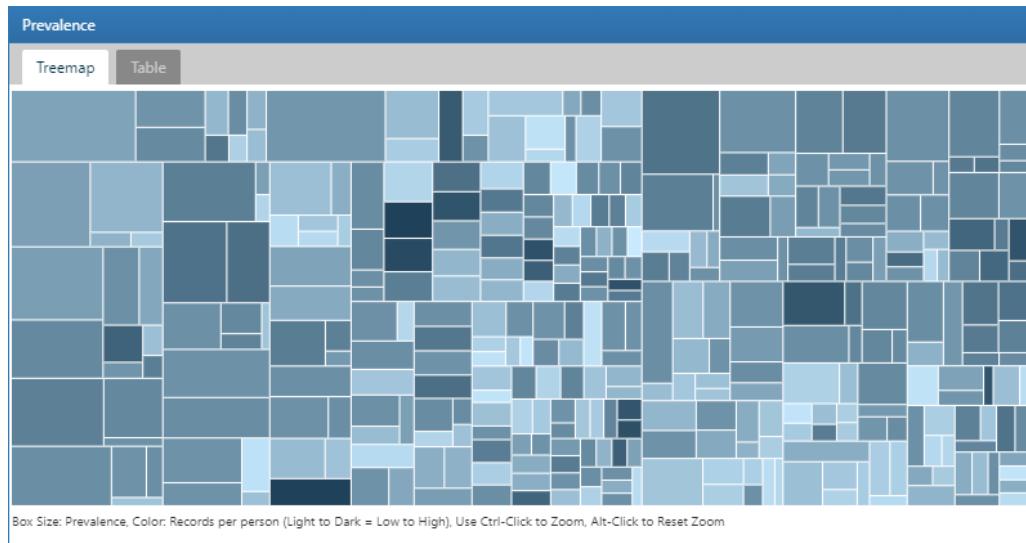


Figure 11.3: Atlas Data Sources: Condition Occurrence Treemap

Prevalence				
Treemap		Table		
		Column visibility	Copy	CSV
		Show 15 ▾ entries		Filter: hypertension
		Showing 1 to 15 of 47 entries (filtered from 15,907 total entries)		Previous 1 2 3 4 Next
Concept	Name	Person Count	Prevalence	Records per person
320128	Essential hypertension	17,814,076	12.30%	5.80
312648	Benign essential hypertension	11,014,877	7.61%	4.35
317898	Malignant essential hypertension	1,021,441	0.70%	2.22
381290	Ocular hypertension	521,264	0.36%	2.40
441922	Transient hypertension of pregnancy	209,317	0.14%	2.45
44782429	Chronic kidney disease due to hypertension	170,534	0.12%	3.60
137940	Transient hypertension of pregnancy - delivered	153,806	0.11%	1.07
321080	Hypertension complicating pregnancy, childbirth and the puerperium	148,728	0.10%	2.15
314423	Benign essential hypertension complicating pregnancy, childbirth and the puerperium - not delivered	132,245	0.09%	3.94
44782690	Chronic kidney disease stage 5 due to hypertension	119,375	0.08%	5.20
44783618	Heritable pulmonary arterial hypertension	104,737	0.07%	3.61
319826	Secondary hypertension	96,356	0.07%	2.14
4167493	Pregnancy-induced hypertension	91,675	0.06%	2.60
321074	Pre-existing hypertension complicating pregnancy, childbirth and puerperium	74,311	0.05%	2.99
192680	Portal hypertension	71,240	0.05%	3.11

Showing 1 to 15 of 47 entries
(filtered from 15,907 total entries)

Previous 1 2 3 4 Next

Figure 11.4: Atlas Data Sources: concept name에서 "hypertension"이라는 단어를 이용해 걸러낸 결과

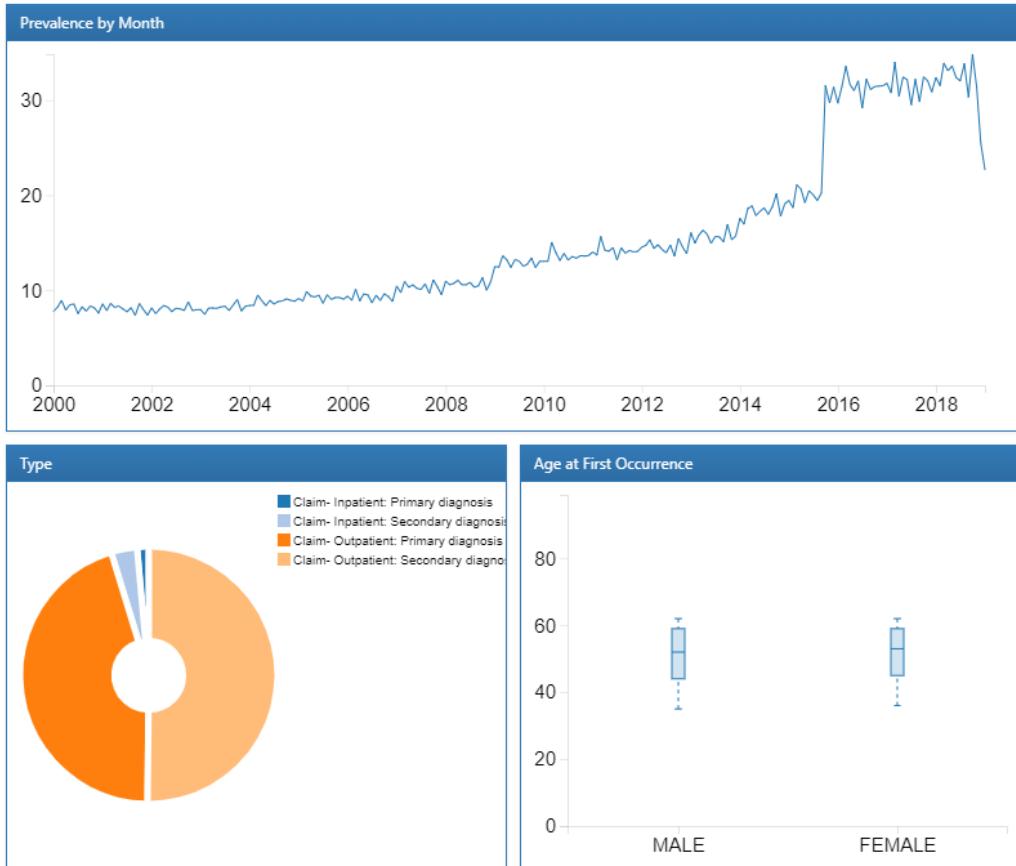


Figure 11.5: Atlas Data Sources: Essential hypertension drill down report

Cohort characterization is defined as the process of generating cohort level descriptive summary statistics from person level covariate data. Summary statistics of these person level covariates may be count, mean, sd, var, min, max, median, range, and quantiles. In addition, covariates during a period may be stratified into temporal units of time for time-series analysis such as fixed intervals of time relative to cohort_start_date (e.g. every 7 days, every 30 days etc.), or in absolute calendar intervals such as calendar-week, calendar-month, calendar-quarter, calendar-year.

Cohort definitions

Import

ID	Name	Edit cohort	Remove
10447	Patients initiating first-line therapy for hypertension with >1 yr follow-up	Edit cohort	Remove
10448	Patients initiating first-line therapy for hypertension with >3 yr follow-up	Edit cohort	Remove

Show 10 entries Search:

Showing 1 to 2 of 2 entries Previous [1](#) Next

Figure 11.6: Characterization design tab - cohort definition selection

11.7 ATLAS를 이용한 코호트 특성 분석 (Cohort Characterization in ATLAS)

이 장에서는 ATLAS를 이용한 대규모의 코호트 특성 분석 방법에 대해 설명할 것이다. ATLAS의 왼쪽 바에 있는 **Characterizations**를 클릭하면, 새로운 특성 분석을 만들 수 있다. 분석을 명명하고 버튼을 눌러 저장한다.

11.7.1 디자인 (Design)

특성 분석은 하나 이상의 코호트와 분석하고자 하는 하나 이상의 속성이 필요하다. 예시의 경우, 두 개의 코호트를 사용할 것이다. 첫번째 코호트는 고혈압 치료를 시작 한 환자로 index date 이전 1년 간 한번이라도 고혈압 진단을 받은 환자로 정의한다고 하자. 또한 이 코호트에 속한 사람들은 고혈압 치료제를 복용하기 시작한 후 최소 1년의 관찰 기간을 갖는다고 하자 (Appendix B.6). 두번째 코호트는 첫 번째 코호트와 모든 조건이 동일하지만 최소 관찰기간을 1년 대신 3년을 갖는다고 하자 (Appendix B.7).

코호트 정의 (Cohort Definitions)

해당 코호트들은 10 장에서 이미 만들어 져 있다고 가정한다. **Import**을 클릭하고 figure 11.6에서 보이는 바와 같이 코호트를 선택한다. 그 다음, 두 코호트 특성 분석을 위해 사용할 속성을 설정한다.

11.7. ATLAS를 이용한 코호트 특성 분석 (Cohort Characterization in ATLAS) 91

Feature analyses

The screenshot shows a table titled "Characterization design tab - feature selection". At the top left is a blue "Import" button. To its right are "Show 25 entries" and a "Search" input field. The table has four columns: "ID", "Name", "Description", and "Actions". The "Actions" column contains "Remove" links for each row. The rows list various features:

ID	Name	Description	Actions
43	Drug Era Short Term	One covariate per drug in the drug_era table overlapping with any part of the short window.	Remove
49	Charlson Index	The Charlson comorbidity index (Romano adaptation) using all conditions prior to the window end.	Remove
67	Condition Occurrence Long Term	One covariate per condition in the condition_occurrence table starting in the long term window.	Remove
71	Demographics Age Group	Age of the subject on the index date (in 5 year age groups)	Remove
72	Demographics Race	Race of the subject.	Remove
73	Demographics Prior Observation Time	Number of continuous days of observation time preceding the index date.	Remove
74	Demographics Gender	Gender of the subject.	Remove
76	Condition Occurrence Medium Term	One covariate per condition in the condition_occurrence table starting in the medium term window.	Remove
77	Demographics Age	Age of the subject on the index date (in years).	Remove
79	Demographics Time In Cohort	Number of days of observation time during cohort period.	Remove
80	Demographics Index Year	Year of the index date.	Remove
81	Demographics Post Observation Time	Number of continuous days of observation time following the index date.	Remove
87	Procedure Occurrence Any Time Prior	One covariate per procedure in the procedure_occurrence table any time prior to index.	Remove
103	Visit Count Long Term	The number of visits observed in the long term window.	Remove

Figure 11.7: Characterization design tab - feature selection.

속성 선택 (Feature Selection)

ATLAS는 OMOP CDM에서 모델링 된 임상 도메인에서 특성 분석을 수행하기 위한 속성들이 100개 이상 사전에 정의되어 있다. 각 사전에 정의된 분석은 선택된 분석 대상 코호트들에 대한 임상 관찰들을 집계하고 요약하는 기능을 수행한다. 이와 같은 계산은 코호트의 기저 그리고 index 후 특징들을 설명하기 위해 수천 가지의 속성을 제공한다. ATLAS는 OHDSI에서 제공하는 FeatureExtraction R package를 이용해 개별 코호트에 대한 특성 분석을 시행하며, 이 FeatureExtraction이라는 R package 을 사용하는 방법에 대하여 다음 절에서 더 자세하게 다룰 것이다.

분석하고자 하는 속성들을 선택하기 위해 **Import** 를 클릭한다. 아래에는 코호트의 특성 분석을 위해 사용할 속성들의 리스트가 있다:

위 그림은 각의 코호트에서 분석할 속성들에 어떤 것들이 있는지를 설명과 함께 목록을 나타낸 것이다. “Demographics”라고 시작하는 속성은 각 환자의 인구 통계학적인 정보를 코호트의 시작 시점에서 계산한다. 도메인 이름으로 시작한 속성들 (예를 들어, Visit, Procedure, Condition, Drug 등)은 해당 도메인에 기록된 모든 관찰 값들의

Subgroup analyses

Figure 11.8: 여성에 대한 하위 그룹 분석을 위한 특성 분석 디자인.

특성을 나타낸 것이다. 각각의 도메인의 특성들은 코호트 시작 지점에 앞서 네 가지의 시간대의 옵션이 있다:

- **Any time prior:** 환자의 관찰 기간 내에서 코호트 시작 지점 이전의 모든 시간대를 사용
- **Long term:** 코호트 시작 지점을 포함하여 365일 이전까지
- **Medium term:** 코호트 시작 지점을 포함하여 180일 이전까지
- **short term:** 코호트 시작 지점을 포함하여 30일 이전까지

하위 집단 분석 (Subgroup Analysis)

만일 성별에 따라 특성이 차이가 있는지가 알고싶다면 어떻게 해야할까? 이때 우리는 “하위 집단 분석 (subgroup analyses)”을 이용할 수 있다. 이는 특성 분석 안에서 새로운 관심 하위 집단에 대한 정의를 할 수 있도록 해준다. 하위 집단을 만들기 위해 하위 그룹에 대한 기준 (criteria)을 클릭해 더하면 된다. 이 단계는 코호트 정의에 사용되는 기준 (criteria)과 유사하다. 이 사례에서 우리는 코호트 내의 여성을 확인할 수 있는 기준 (criteria) 셋을 정의할 것이다:



ATLAS의 하위 그룹 분석은 층화(strata)와 같지 않다. 층화(strata)는 상호배제하는 반면, 하위그룹은 선택된 기준(criteria)에 따라 동일한 사람이 하위그룹에 포함될 수 있다.

11.7.2 실행 (Executions)

특성 분석의 설계가 끝났다면, 우리의 환경 내에서 사용할 수 있는 하나 이상의 데이터베이스에 대하여 설계한 특성 분석을 시행할 수 있다. Execution 탭으로 이동하여 Generate 버튼을 클릭하면 선택된 데이터베이스에서 분석이 시작된다:

11.7. ATLAS를 이용한 코호트 특성 분석 (Cohort Characterization in ATLAS) 93

Design Executions Utilities

Executions

SYNPUF 1K	▶ Generate	View latest result	All executions (3)
SYNPUF 5%	▶ Generate	View latest result	All executions (3)

Figure 11.9: 설계한 특성 분석의 실행 - CDM source 선택.

CONDITION / Condition Occurrence Long Term / stratified by Female												
			Patients initiating first-line therapy for hypertension with >1 yr follow-up				Patients initiating first-line therapy for hypertension with >3 yr follow-up				Std diff ▼	
Covariate	Explore	Concept ID			Female				Female			
			Count	Pct	Count	Pct	Count	Pct	Count	Pct		
Tachycardia	Explore ▾	444070	17,322	1.04%	9,042	1.18%	6,547	0.78%	3,530	0.90%	-0.0193	
Cardiomegaly	Explore ▾	314658	20,958	1.26%	8,007	1.04%	9,016	1.08%	3,465	0.89%	-0.0121	
Cardiac arrhythmia	Explore ▾	44784217	30,474	1.83%	13,221	1.72%	14,540	1.74%	6,318	1.62%	-0.0052	

Showing 1 to 3 of 3 entries (filtered from 206 total entries) Previous [1] Next

Figure 11.10: 특성 분석 결과 - condition occurrence long term.

분석이 완료되면, “All Executions” 버튼을 클릭하고 실행 목록에서 “View Reports”를 선택하면 보고서를 볼 수 있다. 이와 별도로 “view latest result”를 클릭하면 가장 최근에 시행된 분석의 결과를 확인할 수 있다.

11.7.3 결과 (Results)

설계 시 선택된 각 코호트의 다른 속성들은 표의 형식으로 나타난다. 그림 11.10에서 보이는 것처럼 코호트 시작 일로부터 365일 이전에 두 코호트에 존재하는 모든 질환을 요약하여 확인할 수 있다. 각 변수들은 개별 코호트와 우리가 코호트 내에서 정의한 여성 하위그룹에 대한 수 (count)와 백분율 (percentage)를 갖는다.

어떤 심혈관 질환들이 모집단에서 관찰되는지 이해하고자 cardiac arrhythmia 과 거력을 갖는 환자의 비율이 얼마인지를 알아보기 위해 탐색창에서 필터를 사용하였다. cardiac arrhythmia concept 옆의 Explore 링크를 이용하면 그림 11.11에 보여지는 것과 같이 하나의 코호트에 대하여 더 자세한 내용이 들어있는 새로운 창을 띠울 수 있다:

분석하고자 하는 코호트들에 대하여 모든 condition에 대한 컨셉을 분석하고 나면, 탐색 옵션을 통해 선택된 모든 컨셉의 모든 상, 하위 관계에 있는 컨셉을 확인할 수 있다. 본 연구의 경우 cardiac arrhythmia에 대하여 확인했다. 이와 같은 탐색 기능은 컨셉의 계층 구조를 탐색 할 수 있도록 하며, 고혈압 환자들에서 나타날 수 있는 다른

Exploring condition_occurrence during day -365 through 0 days relative to index: Cardiac arrhythmia ✖						
Cohort: Patients initiating first-line therapy for hypertension with >1 yr follow-up						
Relationship type	Distance	Concept name	All stratas		Female	
			Count	Pct	Count	Pct
Explore Ancestor	4	Disorder by body site	32	0.00%	17	0.00%
Explore Ancestor	4	Finding of trunk structure	991	0.06%	605	0.08%
Explore Ancestor	3	Disorder of trunk	23	0.00%	14	0.00%
Explore Ancestor	3	Disorder of thorax	241	0.01%	104	0.01%
Explore Ancestor	3	Disorder of body system	4,135	0.25%	1,992	0.26%
Explore Ancestor	2	Disorder of cardiovascular system	12,979	0.78%	6,073	0.79%
Explore Ancestor	2	Disorder of mediastinum	138	0.01%	62	0.01%
Explore Ancestor	2	Disorder of body cavity	24	0.00%	10	0.00%
Explore Ancestor	1	Heart disease	4,691	0.28%	1,869	0.24%
Explore Selected	0	Cardiac arrhythmia	30,474	1.83%	13,221	1.72%

Showing 1 to 10 of 62 entries

Previous 1 2 3 4 5 6 7 Next

Figure 11.11: 특성 분석 결과 - 하나의 concept에 대하여 자세한 내용이 들어있는 새로운 창.

11.7. ATLAS를 이용한 코호트 특성 분석 (Cohort Characterization in ATLAS)⁹⁵

CONDITION / Condition Occurrence Long Term / stratified by Female												
Export		Export comparison		Show 10 ▾ entries		Search: edema						
Covariate	Explore	Concept ID	Patients initiating first-line therapy for hypertension with > 1 yr follow-up				Patients initiating first-line therapy for hypertension with > 3 yr follow-up				Std diff ▾	
			Count		Pct		Female		Count			
			Count	Pct	Count	Pct	Count	Pct	Count	Pct		
Edema	Explore ▾	433595	32,243	1.94%	20,200	2.63%	15,173	1.81%	9,684	2.48%	-0.0066	

Showing 1 to 1 of 1 entries (filtered from 206 total entries) Previous 1 Next

Figure 11.12: 특성 분석 결과 - 금기되는 상태 이상을 탐색한 결과.

Exploring condition_occurrence during day -365 through 0 days relative to index: Edema											
Cohort: Patients initiating first-line therapy for hypertension with > 1 yr follow-up											
Export		Show 10 ▾ entries		Search: ang							
Relationship type	Distance	Concept name	All stratas				Female				
			Count	Pct	Count	Pct	Count	Pct	Count	Pct	
			Explore Descendant	-2	Angioedema		2,605	0.16%	1,506	0.20%	
Showing 1 to 1 of 1 entries (filtered from 56 total entries) Previous 1 Next											

Figure 11.13: 특성 분석 결과 - 금기되는 상태 이상에 대한 자세한 결과.

심장 질환들을 확인할 수 있도록 한다. 요약된 결과처럼 (갯)수와 백분율로써 화면에 출력된다.

동일한 특성 분석은 혈관 부종과 같은 항 고혈압 제제의 부작용에 의한 상태를 찾는 분석에도 사용할 수 있다. 방법은 위의 분석과 동일하게 그림 11.12에 나온 것처럼 'edema'를 검색하여 진행할 수 있다:

다시 한 번, 고혈압 환자에서 혈관 부종의 발병률을 알아보기 위해 Edema의 특성을 보는 탐색 기능을 사용할 것이다:

항 고혈압 제제를 시작하기 1년 전부터 혈관 부종의 기록이 있었던 사람들의 비율을 확인하 수 있었다.

도메인 변수는 이분법적인 표지자를 사용해 계산되는 반면 (즉, 이전 시간대에 존재했던 코드의 기록), 코호트 시작 시점의 연령과 같은 일부 변수들은 연속적인 값을 갖는다. 위의 예시와 같이 두 코호트에서 연령에 대한 특성 분석 결과는 사람의 총 수, 연령의 평균, 연령의 중앙값 그리고 표준 편차를 통해 확인할 수 있었다.

11.7.4 사용자 정의 속성 (Defining Custom Features)

사전에 정의되어 제공되는 속성들 뿐 아니라 ATLAS에서는 사용자가 필요에 따라 속성들을 커스터마이즈 하고 정의할 수 있는 기능을 지원한다. 윈쪽 메뉴에서

DEMOGRAPHICS / Demographics Age

		Patients initiating first-line therapy for hypertension with >1 yr follow-up				Patients initiating first-line therapy for hypertension with >3 yr follow-up				Std diff ▼
Strata		Count	Avg	Std Dev	Median	Count	Avg	Std Dev	Median	
Female		768,180	49.39	9.78	51.00	390,693	49.01	9.03	51.00	-0.0291
All stratas		1,661,604	48.96	10.00	50.00	837,459	48.64	9.26	50.00	-0.0232

Showing 1 to 2 of 2 entries Previous [1] Next

Figure 11.14: 각 코호트와 하위 집단의 연령 관련 특성 분석 결과.

characterization를 클릭하고, **Feature Analysis**탭을 클릭 한 후, **New Feature Analysis** 버튼을 클릭하면 사용자가 정의한 속성 분석을 할 수 있다. 사용자가 정의하는 속성을 명명하고,  버튼을 통해 저장할 수 있다.

예를 들어, 코호트 시작 이후에 ACE inhibitors의 drug era를 갖는 각각의 코호트에 속하는 사람 수를 알아본다고 하자:

위에서 정의한 기준(criteria)은 코호트 시작 날짜에 적용된다고 가정하자. 이전에 정의한 기준(criteria)을 저장했다면, 이전 절에서 우리가 디자인한 특성 분석에 이를 적용할 수 있다. 이는 위해 characterization을 열고, Feature Analysis로 이동 해 보자.

 버튼을 누르고 메뉴에서 new custom features를 선택하자. 그러면 분석할 속성 목록에 사용자 정의 속성이 올라간 것이 보일 것이다. 앞 절에서 설명한 것과 같이 사용자 정의 속성에 대한 분석을 데이터베이스에 적용하여 시행할 수 있다:

11.8 R을 이용한 코호트 특성 분석 (Cohort Characterization in R)

코호트의 특성 분석은 R을 통해서도 가능하다. R에서 고혈압 코호트에서 기저 속성(변수)을 생성하기 위해 OHDSI의 FeatureExtraction이라고 하는 R package를 사용하는 방법을 알아보기로 한다. FeatureExtraction은 세 가지 방법으로 변수를 구성할 수 있는 기능을 제공한다. 그 방법은 다음과 같다:

- 기본 설정된 변수 셋을 선택
- 사전 지정된 분석 셋 중에서 선택
- 사용자 정의 분석 셋을 생성

FeatureExtraction은 개인 수준 속성 (person-level feature)과 통합된 속성의 두 가지 방법으로 변수를 만든다. 개인 수준의 특성은 기계 학습에 적용할 때 유용하다. 이 절에서는 관심 코호트를 설명하는 기저 변수를 생성할 때 유용한 통합된 속성의 사용 방법을 집중적으로 설명할 것이다. 더불어 사전 지정된 분석과 사용자가 정의하는 분석의 두 가지 변수를 구성 방법에 대해 알아볼 것이다. (기본 설정 세트에 대해서는 독자의 연습을 위해 남겨두도록 하겠다.)

The screenshot shows the ATLAS software's 'Design' tab. At the top, there are two tabs: 'Criteria' (selected) and 'Custom'. Below this is a dropdown menu labeled 'Analysis type' with 'Prevalence' selected. A green button labeled 'Add Criteria feature' is visible. The main area contains a search bar for 'Ace inhibitor exposure after index' and a detailed criteria configuration section. This section includes fields for specifying the number of occurrences ('at least 1 using all'), selecting a drug era ('ACE inhibitors'), setting event start constraints ('event starts between 1 days After and All days After'), and adding additional constraints ('allow events from outside observation period'). A red 'Delete Criteria' button is located on the right side of this section.

Figure 11.15: ATLAS를 이용한 사용자가 정의하는 속성.

DRUG / Ace inhibitor exposure after index / stratified by Female												
Export		Export comparison		Show 10 entries		Search: <input type="text"/>						
Covariate	Explore	Concept ID	Patients initiating first-line therapy for hypertension with > 1 yr follow-up				Patients initiating first-line therapy for hypertension with > 3 yr follow-up				Std diff	
			Count		Pct		Count		Pct			
			Count	Pct	Count	Pct	Count	Pct	Count	Pct		
Ace inhibitor exposure after index	Explore ▾	0	686,034	41.29%	289,215	17.41%	426,280	50.90%	182,219	21.76%	0.1001	

Showing 1 to 1 of 1 entries

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Figure 11.16: 사용자 정의 속성을 적용하여 특성 분석을 진행한 결과 창

11.8.1 Cohort Instantiation

특성 분석을 위해 우선 코호트를 예시를 들어 설명하겠다. 코호트 예시는 10 장에서 실습 했었다. 본 실습에서는 고혈압의 1차 약물 치료를 시작한 사람들 중 1년 간 관찰된 사람들을 사용할 것이다 (Appendix B.6). 부록 B 의 다른 코호트들은 독자의 연습을 위해 남겨두었다. cohort definition ID가 1인 scratch.my_cohorts라는 테이블에 실습에 사용할 코호트가 있다고 가정하자.

11.8.2 데이터 추출 (Data Extraction)

먼저 R이 서버에 접속할 수 있도록 해야한다. FeatureExtraction은 DatabaseConnector package의 `createConnectionDetails` 함수를 이용해 서버와 연결할 수 있다. `?createConnectionDetails`를 입력하면 다양한 데이터베이스 관리 시스템 (DBMS)이 요구하는 설정 값이 어떤것 들이 있는지 확인할 수 있다. 예를 들어, PostgreSQL 데이터베이스와 연결해야 하는 경우 다음과 같이 연결 설정을 해야 한다:

```
library(FeatureExtraction)
connDetails <- createConnectionDetails(dbms = "postgresql",
                                         server = "localhost/ohdsi",
                                         user = "joe",
                                         password = "supersecret")

cdmDbSchema <- "my_cdm_data"
cohortsDbSchema <- "scratch"
cohortsDbTable <- "my_cohorts"
cdmVersion <- "5"
```

마지막 네 줄의 코드는 `cdmDbSchema`, `cohortsDbSchema`, `cohortsDbTable` 변수들을 정의하고 CDM 버전 또한 정의하기 위함이다. 이러한 정의는 나중에 R에게 CDM 형식의 데이터가의 위치, 관심 코호트가 만들어진 위치, 어떤 버전의 CDM이 사용되었는지를 확인할 수 있도록 해준다. Microsoft SQL Server에서 주의할 점은, 데이터베이스 스키마는 데이터베이스와 스키마 정보를 둘 다 필요로 한다는 것이다. 예를 들면 다음과 같다. `cdmDbSchema <- "my_cdm_data.dbo"`.

11.8.3 사전 지정 분석의 사용 (Using Prespecified Analyses)

`createCovariateSettings` 함수는 사전에 미리 정의된 대규모 변수들의 셋을 선택 할 수 있도록 한다. `?createCovariateSettings`를 입력하면 사용 가능한 옵션들을 확인할 수 있다. 예를 들어:

```
settings <- createCovariateSettings(
  useDemographicsGender = TRUE,
  useDemographicsAgeGroup = TRUE,
  useConditionOccurrenceAnyTimePrior = TRUE)
```

다음과 같이 입력하면 성별, 연령 (5년 단위의 연령 그룹), 그리고 코호트 시작 날짜를 포함한 이전의 모든 `condition_occurrence` 테이블에서 관찰된 각각의 컨셉들에

대하여 이분법적인 변수를 생성할 수 있다.

많은 사전 정의 분석은 단기(short term), 중기(medium term), 혹은 장기(long term) 구간(time window)을 지정할 수 있다. 기본적으로 구간들은 다음과 같이 정의 되어 있다:

- **Long term:** 코호트 시작 날짜를 포함한 365일 이전까지의 구간.
- **Medium term:** 코호트 시작 날짜를 포함한 180일 이전까지의 구간.
- **short term:** 코호트 시작 날짜를 포함한 30일 이전까지의 구간.

그러나 아래의 예시와 같이 사용자가 시간 구간을 변경 할 수 있다:

```
settings <- createCovariateSettings(useConditionEraLongTerm = TRUE,
                                      useConditionEraShortTerm = TRUE,
                                      useDrugEraLongTerm = TRUE,
                                      useDrugEraShortTerm = TRUE,
                                      longTermStartDays = -180,
                                      shortTermStartDays = -14,
                                      endDays = -1)
```

이 코드에서 새로 정의된 long-term 구간은 코호트 시작 날짜를 포함하지 않고 180일 이전까지의 구간을 나타내고, short-term 구간은 코호트 시작 날짜를 포함하지 않고 14일 이전까지의 구간을 나타낸다. 또한, 변수 구성에서 필수적으로 들어가야 할 것과 빠져야 할 concept ID를 지정할 수 있다:

```
settings <- createCovariateSettings(useConditionEraLongTerm = TRUE,
                                      useConditionEraShortTerm = TRUE,
                                      useDrugEraLongTerm = TRUE,
                                      useDrugEraShortTerm = TRUE,
                                      longTermStartDays = -180,
                                      shortTermStartDays = -14,
                                      endDays = -1,
                                      excludedCovariateConceptIds = 1124300,
                                      addDescendantsToExclude = TRUE,
                                      aggregated = TRUE)
```



`aggregated = TRUE`로 바꾸면 위에 표시된 모든 사례에 대하여 FeatureExtraction로 하여금 모든 요약 통계치를 표시하도록 한다. 이 지표를 제외하면 코호트 내의 각의 사람에 대한 변수 값이 계산 될 것이다.

11.8.4 통합된 변수의 생성 (Creating Aggregated Covariates)

다음의 코드는 코호트에 대한 통합 변수를 생성하도록 한다:

```

covariateSettings <- createDefaultCovariateSettings()

covariateData2 <-getDbCovariateData(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = cdmDatabaseSchema,
  cohortDatabaseSchema = resultsDatabaseSchema,
  cohortTable = "cohorts_of_interest",
  cohortId = 1,
  covariateSettings = covariateSettings,
  aggregated = TRUE)

summary(covariateData2)

```

그 결과값은 다음과 비슷하게 보일 것이다:

```

## CovariateData Object Summary
##
## Number of Covariates: 41330
## Number of Non-Zero Covariate Values: 41330

```

11.8.5 결과 형식 (Output Format)

통합된 변수 데이터 (covariateData)에서 주요한 두 가지 구성요소는 이분법적인 혹은 연속적 변수에 대한 변수 (covariates)와 변수 량 (covariatesContinuous)이다:

```

covariateData2$covariates
covariateData2$covariatesContinuous

```

11.8.6 사용자 정의 변수 (Custom Covariates)

FeatureExtraction은 또한 변수를 사용자가 정의하고 사용할 수 있도록 사용자 정의 변수 기능을 제공한다. 이는 고급 주제로 다음 링크를 통해 사용자 문서에서 자세히 볼 수 있다. <http://ohdsi.github.io/FeatureExtraction/>.

11.9 ATLAS에서 코호트 경로 (Cohort Pathways in ATLAS)

경로 분석은 하나 이상의 관심 코호트에서 치료 과정의 순서를 이해하기 위해 시행 한다. 분석 방법은 Hripcak의 연구 (Hripcak et al., 2016) 의 디자인을 기반으로 합니다. 이 방법은 ATLAS의 Cohort Pathways기능으로 일반화되고 체계화되었다.

Cohort pathways는 하나 이상의 분석하고자 하는 대상 코호트(target cohort)의 코호트 시작 날짜 이후 발생한 사건들을 요약하는 분석 기능을 제공하는 것을 목표로 한다. 이를 위해 분석 대상 집단에서 관심 임상적 사건들을 식별하기 위한 사건 코호트(event cohort) 세트를 정의하고 생성해야 한다.



Figure 11.17: 한 환자의 경로 분석의 내용.

Design **Executions** **Utilities**

Cohort Pathway is defined as the process of generating an aggregated sequence of transitions between the Event Cohorts among those people in the Target Cohorts.

Target Cohorts

Each of the Target Cohorts will be analyzed for the pathways through the event cohorts.

Import

ID	Name	Edit cohort	Remove
10447	Patients initiating first-line therapy for hypertension with >1 yr follow-up	Edit cohort	Remove
10448	Patients initiating first-line therapy for hypertension with >3 yr follow-up	Edit cohort	Remove

Show 10 entries Search: []

Showing 1 to 2 of 2 entries Previous [] Next

Figure 11.18: 선택된 대상 코호트들을 이용한 경로 분석.

대상 코호트(target cohort)에서 한 환자를 어떻게 찾는지를 보면 다음과 같다:

그림 11.17에서 대상 코호트에 속한 환자의 정의된 시작과 마지막 날짜를 볼 수 있다. 숫자가 매겨진 조각난 선들은 해당 환자에게서 해당 구간 동안 사건 코호트가 식별된 위치를 표현한 것이다. 사건 코호트를 통해 CDM에서 표현되는 관심 있는 모든 임상적 사건을 설명 할 수 있기 때문에 단일 도메인 혹은 컨셉에 대한 경로를 만드는데 제한을 받지 않는다.

경로 분석을 시작하기 위해서는 ATLAS 왼쪽 바에 있는 **Cohort Pathways**를 눌러 새로운 코호트 경로 분석 연구를 생성한다. 분석을 명명하고 저장 버튼을 눌러 저장한다.

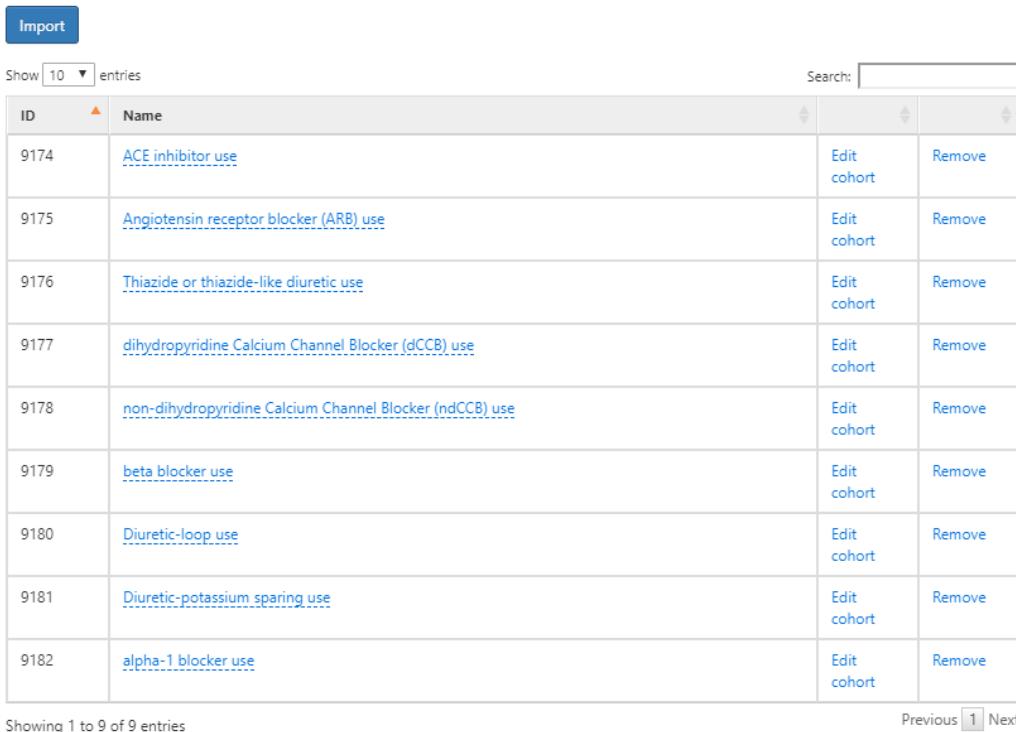
11.9.1 디자인 (Design)

사용할 코호트는 고혈압 1차 치료를 시작하고 환자 1년간 관찰 된 환자 코호트와 3년 간 추적 관찰된 환자 코호트로 이전 분석에서 사용된 코호트를 지속적으로 사용할 것이다 (Appendix B.6, B.7). import 버튼을 사용해 두 개의 코호트를 불러오자.

그 다음, 각각의 분석하고자 하는 일차 고혈압 치료 약제에 대한 코호트를 사건 코호트로 정의한다. 이를 위해 ACE inhibitor 사용에 대한 코호트를 생성하고 코호트

Event Cohorts

Each Event Cohort defines the step in a pathway that may occur for a person in the Target Cohort.



The screenshot shows a table with 9 rows of event cohorts. Each row contains an ID, a name (underlined), an 'Edit cohort' button, and a 'Remove' button. The names correspond to various types of medication use:

ID	Name	Edit cohort	Remove
9174	<u>ACE inhibitor use</u>	Edit cohort	Remove
9175	<u>Angiotensin receptor blocker (ARB) use</u>	Edit cohort	Remove
9176	<u>Thiazide or thiazide-like diuretic use</u>	Edit cohort	Remove
9177	<u>dihydropyridine Calcium Channel Blocker (dCCB) use</u>	Edit cohort	Remove
9178	<u>non-dihydropyridine Calcium Channel Blocker (ndCCB) use</u>	Edit cohort	Remove
9179	<u>beta blocker use</u>	Edit cohort	Remove
9180	<u>Diuretic-loop use</u>	Edit cohort	Remove
9181	<u>Diuretic-potassium sparing use</u>	Edit cohort	Remove
9182	<u>alpha-1 blocker use</u>	Edit cohort	Remove

Showing 1 to 9 of 9 entries

Previous 1 Next

Figure 11.19: 고혈압 일차 치료 시작의 경로 분석을 위한 사건 코호트들.

마지막 날짜를 약물의 마지막 노출이 끝나는 날짜로 정의한다. 여덟개의 다른 고혈압 약제에 대하여 동일한 방식으로 코호트를 생성하고, 코호트 생성에 필요한 여러 정의들은 Appendix B.8-B.16에서 찾아볼 수 있다. 완료한 후 **Import** 버튼을 눌러 경로 분석 디자인의 Event Cohort 부분에 삽입한다:

모든 과정을 완료하고 나면 다음과 같이 된다. 그 이후에 몇 가지 추가 설정을 해야 한다:

- **Combination window:** 이 세팅을 사용하면 사건이 겹쳐질 경우 사건을 조합(combination)으로 간주될 수 있도록 하는 시간의 구간설정할 수 있도록 해주며, 일(days) 단위로 정의할 수 있도록 한다. 예를 들어, 만약 두 개의 약물 노출에 대하여 두 개의 사건 코호트로 표시했을 때 (사건 코호트 1와 사건 코호트 2), 조합 구간 내에서 사건 코호트가 겹치는 경우 경로 알고리즘은 두 사건 코호트를 조합해 “사건 코호트 1 + 사건 코호트 2”로 만든다.
- **Minimum cell count:** 사건 코호트가 이 수보다 작으면 개인정보 보호를 위해 결과에서 제외된다.
- **Max path length:** 분석에 사용되는 최대 연속 사건의 수를 나타낸다.

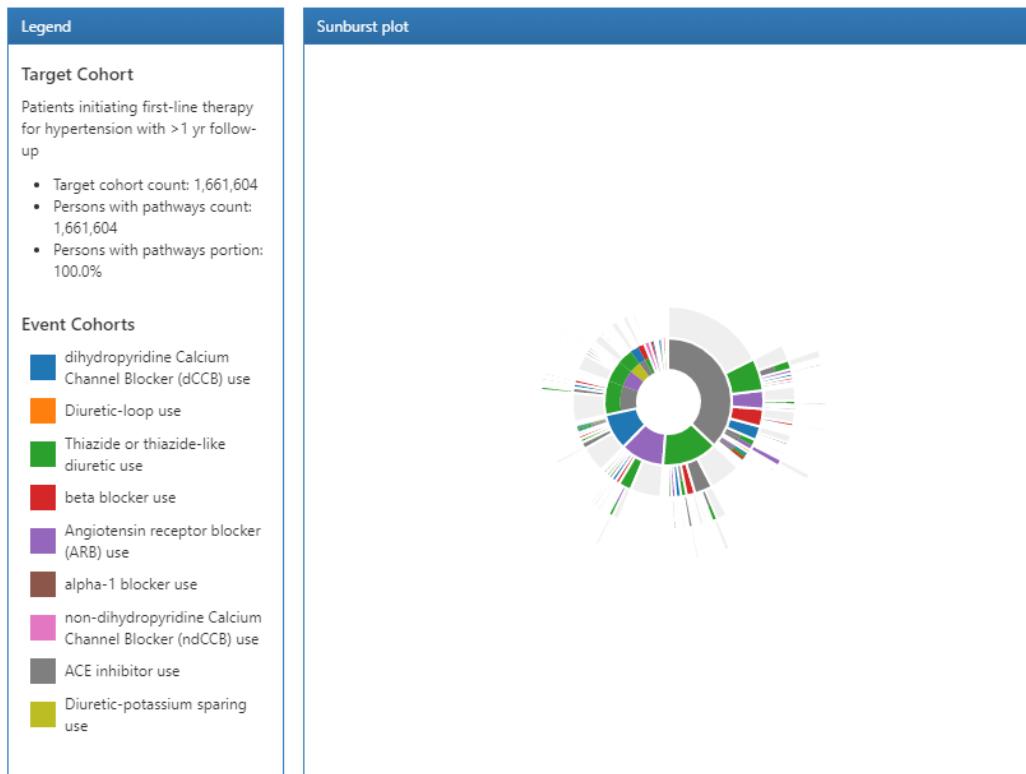


Figure 11.20: 경로 분석 결과의 범례와 sunburst 그래프를 통한 시각화.

11.9.2 실행 (Executions)

경로 분석의 디자인이 완료된 후, 하나 이상의 데이터베이스 내에서 분석 실행할 수 있다. 방법은 ATLAS의 코호트 특성 분석에서 진행한 것과 같은 방식으로 진행된다. 실행이 끝나면 분석 결과를 확인할 수 있다.

11.9.3 결과 확인 (Viewing Results)

경로 분석에 대한 결과는 3개의 부분으로 나누어진다. 범례(legend) 부분은 대상 코호트의 총 환자수를 나타내는데, 이는 하나 이상의 사건이 있는 환자 수를 나타낸다. 아래의 요약은 sunburst plot의 가운데 부분을 각 코호트에 색을 지정해 표현하였다.

sunburst plot은 시간에 따라 한 사람이 겪는 다양한 사건 경로를 시각화한다. 그래프의 가운데 부분은 코호트의 시작부분을 나타내고 첫번째 색으로 구분된 고리는 전체 코호트에서 각 사건 코호트의 환자 비율을 보여준다. 본 예시에서 가장 가운데의 원은 고혈압 환자가 처음으로 시작한 일차 약제를 의미한다. 그리고 sunburst plot의 첫번째 고리는 사건 코호트에서 정의한 것과 같이 시작한 일차 약제의 유형별 비율을 나타낸다 (예를 들어, ACE inhibitor, Angiotensin receptor blocker, 등).

두 번째 고리는 환자들의 두 번째 사건 코호트를 의미한다. 특정 사건의 과정에서, 어떤 환자들은 두 번째 사건 코호트를 가지지 않을 수 있는데, 그럴 경우 그 비중은

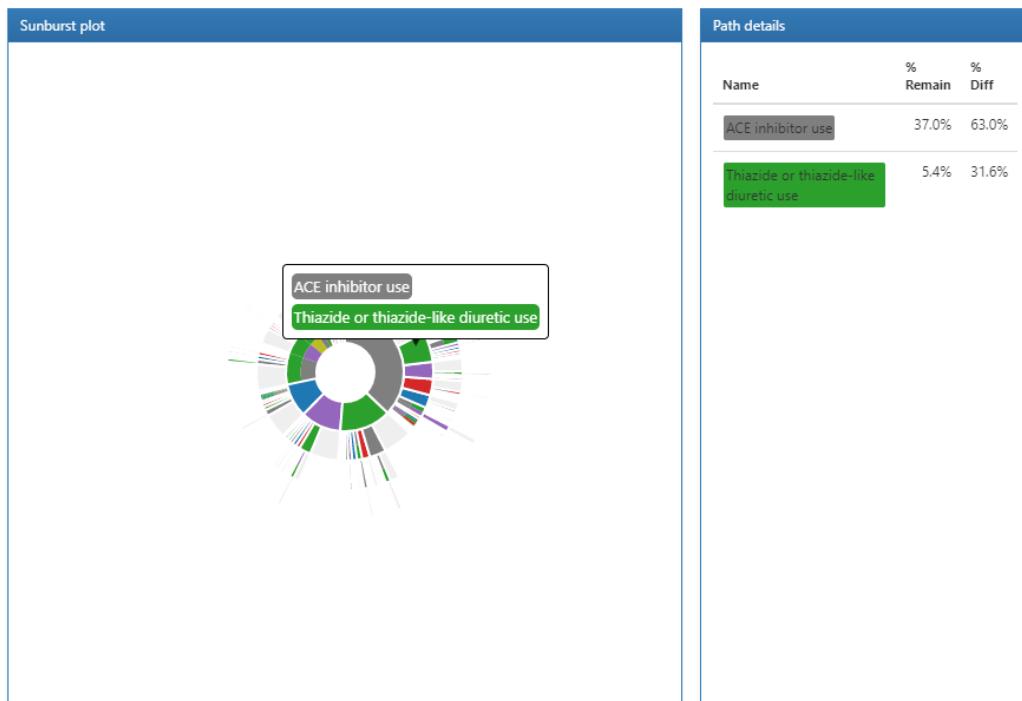


Figure 11.21: 더 자세한 경로 분석의 결과 창.

고리에서 회색으로 표현되어 있다.

sunburst plot의 세션을 클릭하면 오른편에 세부 경로가 나타난다.

이를 통해 대상 코호트에서 가장 많은 비율을 차지하는 환자가 일차 약제로 ACE inhibitor를 시작한 환자임을 알 수 있고, 가장 작은 비율을 차지하는 약제는 thiazide 나 thiazide diuretics임을 알 수 있었다.

11.10 ATLAS를 이용한 발생 분석 (Incidence Analysis in ATLAS)

발생률의 계산 시, 우리는 대상 코호트의 사람들 중 위험 관찰 기간 동안 outcome 코호트를 경험한 환자들에 대하여 설명하기로 했다. 예를 들어, ACE inhibitor (ACEi)를 시작한 사람들과 Thiazides와 tiazide-like diuretics (THZ)를 시작한 사람들 중 혈관 부종과 급성 심근 경색의 outcomes의 발생을 분석하는 발생 분석을 디자인했다고 하자. 이를 위해 약물에 노출된 사람들의 위험 관찰 기간 동안 이들 outcome 을 평가해야 한다. 더불어, Angiotensin receptor blockers (ARBs)에 대한 약물 노출 결과를 추가하기 위해 대상 코호트들(ACEi와 THZ)에 속해 있는 동안 ARBs 약물 사용의 발생을 outcome으로 추가한다. 이 outcome은 대상 코호트에 속해있는 동안 얼마나 ARBs 사용이 발생했는지를 측정 해 줄 수 있다.

발생률 분석을 시작하기 위해서는 ATLAS의 왼쪽 바에서 **⚡ Incidence Rates** 버튼을

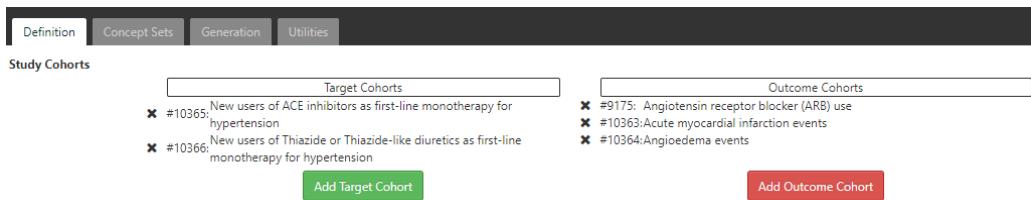


Figure 11.22: 발생률 분석에 사용할 대상 코호트와 outcome 코호트의 정의.

Time At Risk

Time at risk defines the time window relative to the cohort start or end date with an offset to consider the person 'at risk' of the outcome.

- Time at risk starts with plus days.
- Time at risk ends with plus days.

No study window defined.

Figure 11.23: 발생률 분석에 사용할 대상 코호트와 outcome 코호트의 정의.

누른다. 분석의 이름을 적고 버튼을 눌러 저장한다.

11.10.1 디자인 (Design)

이미 이전 10장에서 ATLAS로 예제에 사용할 코호트를 만들었다고 해 보자. 부록에서 예제에 사용할 대상 코호트의 모든 정의를 확인할 수 있다 (Appendix B.2, B.5), and outcomes (Appendix B.4, B.3, B.9).

definition 탭을 클릭해서 *New users of ACE inhibitors* 코호트와 *New users of Thiazide or Thiazide-like diuretics* 코호트를 선택한다. 선택한 코호트들이 분석 디자인에 추가되었는지 확인하기 위해 대화 상자를 닫아야 한다. 그 다음 대화 상자에서 클릭해 outcome 코호트들을 추가한다. *acute myocardial infarction events*, *angioedema events* 와 *Angiotensin receptor blocker (ARB) use* 코호트 등이 outcome 코호트로 선택되어야 한다. 분석 디자인에 outcome 코호트들이 추가되었는지 확인하기 위해 대화 상자를 닫아야 한다.

이후 분석에 필요한 위험 관찰 기간을 정의해야 한다. 위에서 보이는 바와 같이 위험 관찰 기간은 코호트 시작과 마지막 날짜에 기반하여 정해진다. 예제에서는 위험 관찰 기간의 시작일을 대상 코호트의 코호트 시작일보다 1일 후로 정의했다. 위험 관찰 기간의 마지막 날짜는 코호트 마지막 날짜로 정의했다. 이 경우, ACEi와 THZ 코호트의 코호트의 정의에 따라 약물 노출이 끝나면 코호트 또한 종료된다.

ATLAS는 또한 분석의 선택 사항의 일부분으로 대상 코호트의 충화 기능을 제공한다:

분석을 위해서 New Stratify Criteria 버튼을 누르고 11장에서 설명한 것과 같은 단계로 진행한다. 분석 디자인이 완성되면 하나 이상의 데이터베이스를 이용해 실행할 수 있다.

Stratify Criteria: You can provide optional stratification criteria to the analysis that will divide the population into unique groups based on their satisfied criteria.

The screenshot shows a configuration window for stratification criteria. At the top left is a green button labeled 'New stratify criteria'. Below it is a blue button labeled '1. Gender = Female'. The main area contains a text input field with 'Gender = Female' and a 'Copy' and 'Delete' button. Below this is a larger text input field for 'inclusion rule description' with placeholder text 'enter an inclusion rule description'. Underneath is a dropdown menu set to 'all' with the option 'of the following criteria:' and a blue button '+ Add criteria to group...'. A section for 'event criteria' follows, with a blue button '+ Add attribute...' and a red button 'Delete Criteria'. A red checkbox is selected with the label 'with a gender of: FEMALE'. At the bottom right are 'Add' and 'Import' buttons.

Figure 11.24: 여성에 대한 통화를 정의한 발생률.

The screenshot shows a 'Select sources' interface. At the top left are 'Select All' and 'Deselect All' buttons. To the right is a 'Filter' input field. The main area lists data sources under the heading 'Name'. Two entries are shown: 'SYNPUF 1K' with an unchecked checkbox and 'SYNPUF 5%' with a checked checkbox. On the right side, there are navigation buttons 'Previous' and 'Next' with page number '1'. At the bottom right is a large blue 'Generate' button.

Figure 11.25: 발생률 분석의 실행.

11.10.2 실행 (Executions)

Generation 탭을 누르고 버튼을 클릭하면, 분석에 사용할 데이터베이스 목록을 볼 수 있다:

하나 이상의 데이터베이스를 선택하고 Generate 버튼을 누르면 주어진 분석 디자인의 대상과 outcome의 모든 조합에 대하여 발생 분석이 실행된다.

11.10.3 결과 확인 (Viewing Results)

Generation 탭의 상단의 화면은 결과를 확인할 때 대상과 outcome을 선택할 수 있도록 해준다. 바로 아래에는 분석에 사용된 각 데이터베이스에 대한 요약과 발생에 관한 내용이 표시된다.

대상 코호트 중 ACEi 사용자와 outcome 코호트 중에서 Acute Myocardial Infarction (AMI)를 드롭다운 목록에서 선택해 보자. 그리고 버튼을 누르면 발생 분석의 결과가 나온다:

결과를 통해 데이터베이스의 해당 코호트에서 위험 관찰 기간 동안 발생한 모든 case에 해당하는 전체 환자 수를 요약해 보여준다. 발생 비율은 1000명 당 발생 건수로

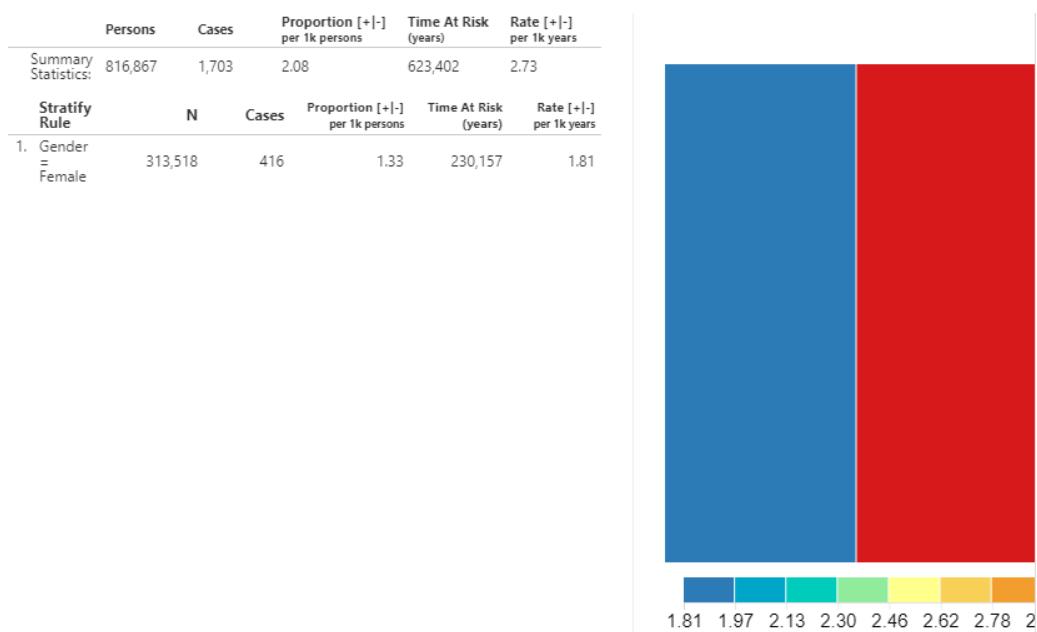


Figure 11.26: ACEi 의 새로운 사용자에서 AMI의 발생률을 분석한 결과.

표시한다. 위험 관찰 기간은 대상 코호트에서 연 단위로 계산된다. 발생률은 1000 인·년 당 발생 건수로 표현된다.

또한 분석 디자인에서 총화를 위해 정의 한 계층에 대한 발생률을 확인할 수 있다. 각 계층에 대해 위에 언급한 바와 동일한 방식으로 계산되었다. 더불어, treemap 시각화 방법을 통해 각 계층의 비율을 상자 공간으로 표현했다. 아래 눈금에 표시된 대로 색상은 발생률을 나타낸다.

ACEi 환자군 내에서 ARBs를 새롭게 사용하기 시작한 신규 환자군의 발생을 확인하기 위한 정보도 얻을 수 있다. 상단의 드롭 다운을 사용하여 ARBs의 사용으로 outcome을 바꾸고, 버튼을 누르면 자세한 내용이 나타난다.

위에 보이는 것처럼, 지금까지 사용한 방법과 동일한 방식으로 계산되었지만, 입력 값이 (ARB 사용)이 건강에 대한 outcome에서 약물 사용에 대한 평가로 바뀌었기 때문에 해석이 달라지게 됩니다.

11.11 요약 (Summary)



- OHDSI는 모든 데이터베이스 혹은 관심 코호트에 대한 특성을 분석하는 툴을 제공합니다.
- 코호트의 특성 분석은 index 날짜 이전 (기저 (baseline))와 이후 (index 후 (post-index)) 시간 동안의 관심 코호트를 설명해 준다.

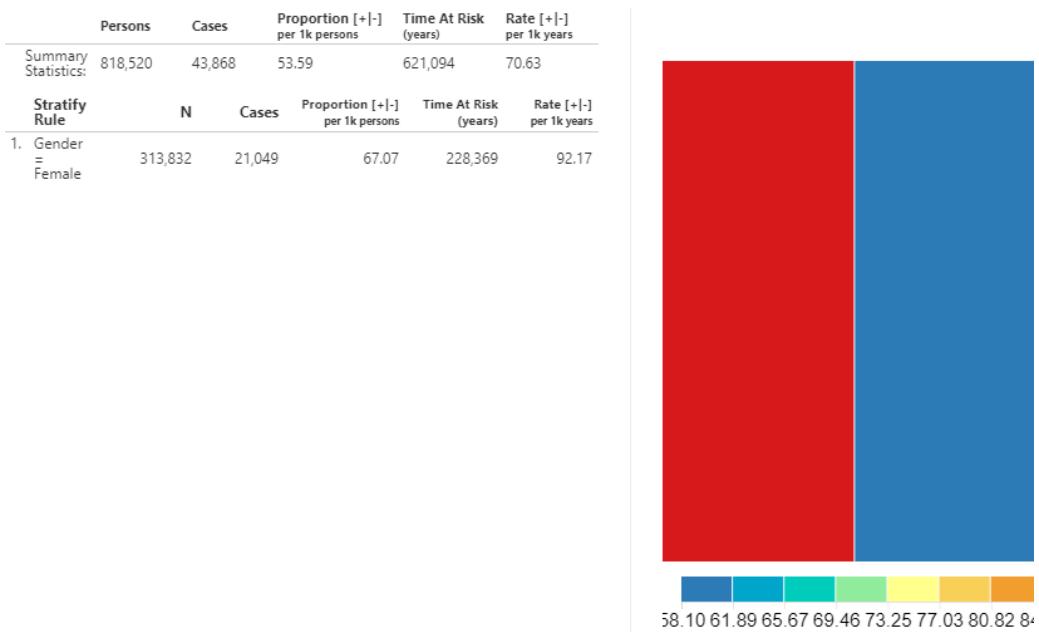


Figure 11.27: 발생률 - ACEi 노출 기간 중 ARBs 치료를 새로 시작한 ACEi 사용 환자군.

- ATLAS의 특성 분석 모듈과 OHDSI Methods Library는 다양한 관찰 기간에 대한 기저 특성에 대해 계산 할 수 있는 기능을 제공한다.
- ATLAS의 경로와 발생률 모듈은 index 후 시간 동안의 기술 통계를 제공 한다.

11.12 실습 (Exercises)

사전 준비사항 (Prerequisites)

본 실습을 위해 ATLAS에 접근할 수 있어야 합니다. 다음의 ATLAS를 사용하시거나 <http://atlas-demo.ohdsi.org>, 혹은 개별적으로 구축하여 접속 가능한 ATLAS가 있다면 사용하셔도 좋습니다.

Exercise 11.1. 실제 임상에서 celecoxib이 얼마나 사용되는지를 알고 싶다. 시작하기에 앞서 데이터베이스에 약물에 대한 데이터베이스의 데이터를 이해해야 합니다. ATLAS의 Data Sources를 이용해 celecoxib에 대한 정보를 찾아보자.

Exercise 11.2. celecoxib 사용자의 질병 자연 경과에 대해 더 알고 싶다. celecoxib의 새로운 사용자들에 대한 간단한 코호트를 만들어라. 이 때, 365일의 washout 기간을 주어라 (어떻게 해야 하는지 자세히 알고 싶다면 10장을 참고하자). 그리고

ATLAS에서 이 코호트의 characterization을 생성하고, 동병상병 질환과 약물 노출을 찾아보자.

Exercise 11.3. celecoxib 치료를 받는 사람들이 이후 기간에 상관없이 gastrointestinal(GI) bleeds가 얼마나 자주 발생하는지를 알고 싶다. 우선 GI bleed의 사건 코호트를 생성해야 한다. 해당 코호트의 정의를 위해 192671 (“Gastrointestinal hemorrhage”)으로 정의된 concept이나 그 하위 concept을 사용하자. 이전 실습에서 정의한 약물 노출 코호트를 이용해, celecoxib을 시작한 이후 GI bleed의 발생률을 계산하자.

답변은 부록 E.7에서 찾을 수 있다.

Chapter 12

Population-Level Estimation

Chapter leads: Martijn Schuemie, David Madigan, Marc Suchard & Patrick Ryan

Observational healthcare data(예: administrative claims, electronic health records)는 환자의 삶을 의미 있게 향상시킬 수 있는 치료효과에 대한 실제 증거를 생성할 수 있는 기회를 제공한다. 이 장에서는 인구 수준 효과 추정(population-level effect estimation), 즉 특정 건강 결과에 대한 노출(예: 약물 노출 또는 시술과 같은 의료 개입)의 평균 인과 관계 효과에 대한 추정에 초점을 맞춘다. 두 가지의 다른 추정 업무를 고려한다.

- **직접 효과 추정(direct effect estimation)**: 노출 위험과 결과의 위험에 대한 노출 효과를 추정.
- **비교 효과 추정(comparative effect estimation)**: 다른 노출(comparator exposure)과 비교하여 노출(target exposure)의 결과 위험에 대한 영향 추정.

In both cases, the patient-level causal effect contrasts a factual outcome, i.e., what happened to the exposed patient, with a counterfactual outcome, i.e., what would have happened had the exposure not occurred (direct) or had a different exposure occurred (comparative). Since any one patient reveals only the factual outcome (the fundamental problem of causal inference), the various effect estimation designs employ different analytic devices to shed light on the counterfactual outcomes.

인구 수준 효과 추정의 사용 사례(use-cases)는 치료선택, 안전 감시(safety surveillance), 비교 효과(comparative effectiveness)를 포함한다. 방법은 특정 가설을 한번에 하나씩 테스트(예: signal evaluation)하거나 다중 가설을 한 번에 탐색(예: signal detection)할 수 있다. 모든 경우에 있어, 목적은 고품질의 인과 관계 추정을 산출하는 것이다.

이 장에서는 우선 OHDSI Methods Library에 R 패키지로 구현되어 있는 다양한 **Population-Level Estimation** study design를 설명한다. 예제 평가 연구의 설계를 자세히 설명한 다음, ATLAS 및 R을 사용하여 설계를 구현하는 방법에 대한 단계별 가이드를 또한 설명한다. 마지막으로 연구 진단 및 효과 크기 추정을 포함하여 연구에서 생성된 다양한 결과를 검토한다.

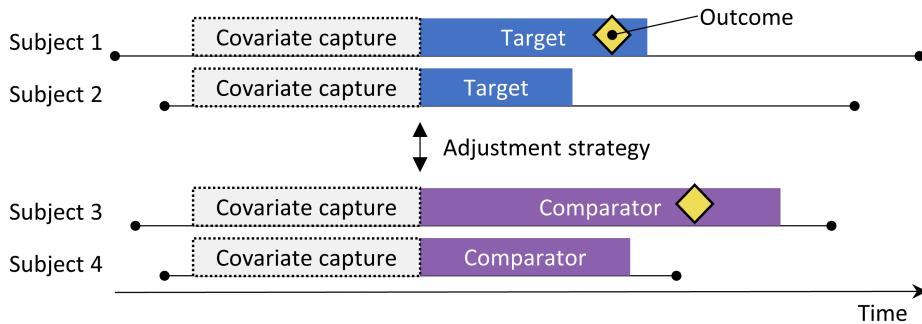


Figure 12.1: 대상 치료(target treatment)를 시작하기 위해 관찰된 대상은 비교 대상 치료(comparator treatment)를 시작한 대상과 비교된다. 두 치료군 간의 차이를 조정하기 위해 층화(stratification), 매칭(matching), 성향 점수에 의한 가중치 부여(weighting), 결과 모델에 기저 특징(baseline characteristics) 보정 추가와 같은 다양한 조정 방법(adjustment strategy)을 사용할 수 있다. 성향 모델 (Propensity model) 또는 결과 모델 (Outcome model)에 포함된 특징은 치료 시작 전에 결정된다.

12.1 The Cohort Method Design

코호트 방법은 무작위 임상 시험을 모방하려고 한다(Hernan and Robins, 2016). 하나의 치료를 시작한 환자(target)는 다른 치료를 시작한 환자(comparator)와 비교되고, 치료를 받은 후 특정 기간 동안(예: 치료를 받는 기간) 추적 관찰된다. 표 12.1에서 강조하는 5가지 사항을 선택함으로써 코호트 연구에서 연구자가 얻기 원하는 답에 대한 질문을 지정할 수 있다.

Table 12.1: Main design choices in a comparative cohort design.

Choice	Description
Target cohort	A cohort representing the target treatment
Comparator cohort	A cohort representing the comparator treatment
Outcome cohort	A cohort representing the outcome of interest
Time-at-risk	At what time (often relative to the target and comparator cohort start and end dates) do we consider the risk of the outcome?
Model	The model used to estimate the effect while adjusting for differences between the target and comparator

모델 선택은 모델 유형을 지정한다. 예를 들어, 결과가 발생했는지 여부를 평가하고 교차비(odds ratio)를 산출하는 로지스틱 회귀분석(logistic regression)을 사용할 수 있다. 로지스틱 회귀분석은 time-at-risk가 target과 comparator 양쪽 모두에서 같거나 무관하다고 가정한다. 대안으로, 포아송 회귀분석(poisson regression)을 선택할

수 있는데, 이는 일정한 발생률(incidence rate)을 가정하고, 발생률 비율(incidence rate ratio)를 추정한다. 콕스 회귀분석(cox regression)을 종종 사용하기도 하는데, 이는 target과 comparator 사이의 비례 위험(proportional hazard)을 가정하며, 위험 비율(hazard ratio)을 추정하려고 time-to-first-outcome을 고려한다.



New-user cohort method는 본질적으로 하나의 치료를 다른 치료에 비교하여 비교 효과를 추정하는 방법이다. 치료 노출 군의 비교 대상인 치료 비노출 군을 정의하기 힘들어 치료와 비치료를 비교하기 위해 이 방법을 사용하기 어렵다. 직접 효과 추정에 이 방법을 사용하려는 경우, 결과에 영향을 미치지 않을, 동일한 적응증이 적용되는 비교 대상을 관심 노출군(exposure of interest)으로 선택하는 방법이 선호된다. 하지만, 이러한 비교 대상을 항상 사용할 수 있는 것은 아니다.

주요 관심사는 치료를 받는 군이 비교 치료를 받는 군과 전체적으로 (systemically) 다를 수 있다는 것이다. 예를 들어, 연구 대상 치료를 받는 실험군 (target cohort)이 평균 60세인 반면, 해당 치료를 받지 않은 대조군 (comparator cohort)이 평균 40세라고 가정하자. 연령과 관련된 건강 결과(예: 뇌졸중)는 양 군간에 상당히 차이가 날 것이다. 이런 정보에 대해 정확히 숙지하지 못한 연구자는 해당 치료가 뇌졸중과 유의미한 인과관계를 보인다고 결론을 내릴 수 있다. 따라서, 해당 치료를 받지 않았다면 실험군의 환자들이 뇌졸중에 걸리지 않을 것이라 생각할 수 있다. 이러한 결과는 전적으로 잘못되었다. 단순히 실험군의 연령이 높기 때문에 뇌졸중을 많이 경험할 수 있기 때문이다. 실험군이 해당 치료를 받지 않았더라도, 뇌졸중의 발생률은 비슷할 수 있다. 여기서 나이는 “교란변수(confounder)”이다. 관찰형 연구에서 교란변수를 통제하는 한 가지 방법은 성향 점수 (propensity score)를 이용하는 것이다.

12.1.1 Propensity Scores

무작위 시험(randomized trial)에서 (가상의) 동전던지기는 환자를 각각의 그룹에 배정한다. 따라서, 설계상 비교 치료 군과 비교하여 환자가 대상치료를 받을 확률은 어떤 식으로든 연령과 같은 환자의 특성과 관련이 없다. 동전에는 환자에 대한 정보가 없으며, 우리는 환자가 대상에 노출될 정확한 확률을 확실하게 알 수 있다. 결과적으로 임상시험에서 환자 수가 증가함에 따라 신뢰도가 증가해 두 환자군은 본질적으로 **어떠한** 환자 특성이라도 **다를 수 없다**. 이 보장된 균형은 무작위 시험이 측정한 특성(예: 연령)과 유전적 특성과 같이 무작위 시험이 측정하지 못한 특성에 적용된다.

주어진 환자의 **성향 점수(Propensity score, PS)**는 환자가 비교 치료군과 비교하여 대상 치료를 받을 확률이다 (Rosenbaum and Rubin, 1983). 균형 잡힌 two-arm 무작위 임상시험에서, 모든 환자의 성향 점수는 0.5이다. 성향 점수 조정된 관찰 연구에서, 우리는 치료개시 시점과 치료개시 전(환자가 실제로 받은 치료와 관계없이)에 관찰할 수 있는 것에 근거해 대상 치료를 받을 환자들의 확률을 추정한다. 이것은 간단한 예측 모델링 응용프로그램이다. 환자가 표적 치료를 받았는지 여부를 예측하는 적합한 모델(예: 로지스틱 회귀분석)을 만들고, 이 모델을 사용하여 각 환자들에 대한 예측 확률을 생성한다. 표준 무작위 임상시험과 달리, 다른 환자는 대상 치료를 받을 확률이 다르다. 성향 점수는 여러 가지 방법으로 사용할 수 있다. 예를 들어, target 피험자를 유사한 PS를 가진 comparator 피험자에게 매칭 (PS matching)

하거나, 성향 점수를 기반으로 연구 집단을 층화 (PS stratification)하거나, 성향 점수에서 파생된 IPTW (Inverse Probability of Treatment Weighting)을 사용하여 피험자에게 가중치를 적용하여 사용할 수 있다. 매칭할 때, 각 대상에 대하여 한 명의 비교 대상을 선택하거나, variable-ratio matching을 활용하여 대상 당 두 명 이상의 비교 대상을 허용할 수 있다. (Rassen et al., 2012)

예를 들어 one-on-one PS 매칭을 사용한다고 가정해보자. Jan이라는 환자가 대상 치료를 받을 선형 확률 (priori probability)이 0.4이고, 실제로 대상 치료 (target treatment)를 받고, Jun이라고 하는 또 다른 환자는 대상 치료를 받을 선형 확률이 0.4이지만, 사실상 대조 치료 (comparator treatment)를 받았다면, 적어도 측정된 교란변수와 대해 Jan과 Jun의 outcome 비교는 작은 무작위 시험과 같다. 이 비교는 Jan과 Jun의 인과적인 대조를 무작위 시험으로 산출한 결과만큼 양호하게 추정할 것이다. 추정은 다음과 같이 진행된다: 대상치료를 받은 모든 환자에 대해, 대조 치료를 받았지만 표적을 받는 선형적 확률이 동일한 하나 이상의 일치하는 환자를 찾는다. 그들의 짹지어진 환자군(matched group) 안에서 대상 환자 (target group)의 결과와 비교 그룹 (comparator group)의 결과를 비교한다.

성향점수 방법은 측정된 교란변수 (measured confounder)를 제어한다. 사실, 측정된 특성 하에서 치료배정(treatment assignment)이 “강하게 무시할 수 있는” 경우라면, 성향 점수는 인과 관계의 비편향적 추정을 산출할 것이다. “강력하게 무시할 수 있는” 조건이란 측정되지 않은 교란변수가 없고, 측정된 교란변수는 적절하게 조정된다는 것을 의미한다. 불행히도, 이것은 검증할만한 가정은 아니다. 챕터 18에서 이에 대한 추가적인 논의를 볼 수 있다.

12.1.2 Variable Selection

이전에 성향 점수는 연구자가 임의로 선택된 특성 (manually selected characteristics)을 기반으로 계산되었다. OHDSI 도구가 그러한 관행을 지원할 수는 있지만, 많은 일반적 특성(즉, 연구의 특정 노출 및 결과에 따라 선택되지 않은 특성)을 포함하는 것을 선호한다. (Tian et al., 2018) 이러한 특성에는 인구학적인 특성뿐만 아니라 치료 개시일 전과 개시일에 관찰된 모든 진단, 약물노출, 측정 및 의료절차가 포함된다. 모델은 전형적으로 10,000 – 100,000가지의 독특한 특성을 포함하며, 이러한 모델은 Cyclops 패키지에서 구현되는 large-scale regularized regression (Suchard et al., 2013)을 사용하여 적합화시킨다. 본질적으로 우리는 치료 배정의 예측을 위하여 어떠한 환자 특성이 알고리즘에 사용되어야 하는지 데이터 스스로 결정하도록 한다.



치료로 이어지는 진단과 같은 많은 관련 데이터 포인트가 해당 날짜에 기록되기 때문에 일반적으로 공변량을 정의할 때 치료 개시일의 변수를 포함한다. 이 날에 연구의 주제가 되는 대상 치료 (target treatment) 과 대조 치료 (comparator treatment) 치료 자체도 기록되는데, 이러한 치료는 우리가 예측하려는 바로 그것이기 때문에 성향 모델에 포함시켜서는 안 된다. 따라서 공변량 집합에서 대상 치료와 대조치료는 반드시 제외해야 한다.

일부 연구자들은 “올바른” 인과 구조를 반영하기 위해 임상적 전문지식에 의존하

지 않는 데이터 기반 접근방식 (data-driven approach) 을 통한 공변량 선택이 소위 도구적 변수 (instrumental variable)와 충돌자 (collider)를 잘못 포함시켜 분산을 증가시키고 잠재적으로 편향을 만들어낼 위험이 있다고 주장해왔다.(Hernan et al., 2002) 하지만 이러한 우려가 실제 시나리오에서 큰 영향을 미칠 가능성은 적다.(Schneeweiss, 2018) 게다가, 의학에서 진정한 인과 관계는 거의 알려지지 않다 시피 하며, 서로 다른 연구자들에게 특정 연구 주제에 대해 ‘올바른’ 공변량을 선택해 달라고 요청한다면, 각 연구자들은 서로 다른 공변량 리스트를 주문할 것이 분명하고, 전체 과정은 재현 불가능해질 것이다. 무엇보다도, 성향 점수 모델의 검사, 모든 공변량의 균형 (balance) 평가, 음성 대조군을 통한 평가 등을 통해 도구적 변수 및 충돌자들에 의해 발생하는 대부분의 문제를 진단할 수 있다.

12.1.3 Caliper

성향 점수가 0에서 1까지의 연속성을 갖기 때문에 정확한 일치는 거의 불가능하다. 그 대신, 매칭 프로세스는 대상 환자의 성향 점수와 일치하는 환자를 “캘리퍼 (caliper)”라고 알려진 내성 범위 내에서 찾는다. 이전 연구 (Austin, 2011)에 따라, 우리는 로짓 척도에서 0.2 표준편차의 기본(default) 캘리퍼를 사용한다.

12.1.4 Overlap: Preference Scores

성향 매칭 방법은 일치하는 환자가 필요하다! 따라서 주요 진단은 두 그룹의 성향 점수 분포를 보여준다. 해석을 용이하게 하기 위해 OHDSI 도구는 “선호 점수(preference score)”라는 성향 점수의 변형을 그린다.(Walker et al., 2013) 선호 점수는 대상 치료와 대조 치료, 두 가지 치료법의 “market share”을 조정하다. 예를 들면, 10%의 환자가 대상 치료를 받고(90%가 비교 치료를 받는 경우), 선호 점수가 0.5인 환자는 대상 치료를 받을 확률이 10%이다. 수학적으로 선호 점수는

$$\ln \left(\frac{F}{1 - F} \right) = \ln \left(\frac{S}{1 - S} \right) - \ln \left(\frac{P}{1 - P} \right)$$

여기서 F 는 선호 점수, S 는 성향 점수, 그리고 P 는 대상치료를 받은 환자의 비율이다.

Walker et al. (2013) 는 “경험적 평형(empirical equipoise)”의 개념을 논의한다. 적어도 노출의 절반이 0.3과 0.7사이의 선호 점수를 갖는 환자에게 노출쌍(exposure pair)이 경험적 평형에서 나오는 것으로 받아 들인다.

12.1.5 Balance

좋은 방침(good practice)은 성향 점수 보정이 균형 잡힌 환자 그룹을 만드는데 성공했는지 항상 확인하는 것이다. 그림 12.19 은 균형을 점검하기 위한 표준 OHDSI 출력물을 보여준다. 각 환자의 특성에 대해 성향 점수 보정 전과 후에 두 노출 그룹 간의 평균 차이를 표준화한다. 일부 지침에서는 조정 후 표준화된 차이의 상한 0.1을 권장한다. (Rubin, 2001)

Table 12.2: Main design choices in a self-controlled cohort design.

Choice	Description
Target cohort	A cohort representing the treatment
Outcome cohort	A cohort representing the outcome of interest
Time-at-risk	At what time (often relative to the target cohort start and end dates) do we consider the risk of the outcome?
Control time	The time period used as the control time

12.2 자가 통제 코호트 연구 설계 (The Self-Controlled Cohort Design)

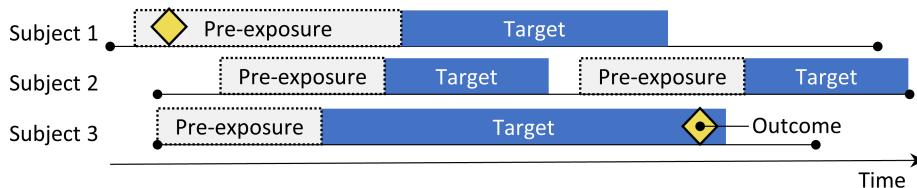


Figure 12.2: The self-controlled cohort design. The rate of outcomes during exposure to the target is compared to the rate of outcomes in the time pre-exposure.

자가 통제 코호트(self-controlled cohort, SCC) 설계(Ryan et al., 2013a)는 노출 직전의 결과 비율을 기준으로 노출 동안의 결과 비율을 비교한다. 표 12.2에 제시된 4가지 선택 사항은 SCC 질문을 정의한다.

노출 그룹을 구성하는 동일한 피험자가 대조 그룹(control group)으로 사용되기 때문에 사람간(between-person)의 차이를 조정할 필요가 없다. 그러나 이 방법은 다른 기간 간의 기준의 위험도 차이 등 다른 차이점에 대해 취약하다.

12.3 환자-대조군 연구 설계 (The Case-Control Design)

환자-대조군 연구(Vandenbroucke and Pearce, 2012)는 “특정 질병 결과가 있는 사람이 질병이 없는 사람보다 특정 치료(agent)에 더 자주 노출되는가?”라는 질문을 고려한다. 따라서, 주요 아이디어는 환자(cases)(i.e., 관심 결과를 경험한 피험자)를 대조군(controls)(i.e., 관심 결과를 경험하지 않은 피험자)에 비교하는 것이다. 표 12.3에 선택 사항은 환자-대조군(case-control) 질문을 정의한다.

종종 우리는 나이와 성별 등 환자군들의 특성을 매칭하여 대조군을 설정한다. 또 달리 많이 사용되는 방법은, 특정 질병이 있는 환자군처럼, 특정 subgroup 환자들 군 안에서 nested analysis를 이용한다.

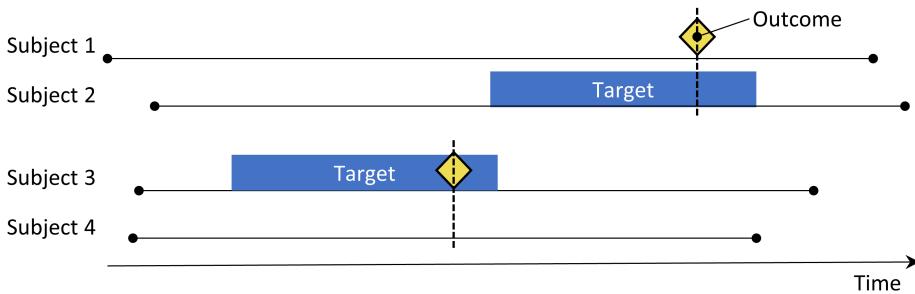


Figure 12.3: The case-control design. Subjects with the outcome ('cases') are compared to subjects without the outcome ('controls') in terms of their exposure status. Often, cases and controls are matched on various characteristics such as age and sex.

Table 12.3: Main design choices in a case-control design.

Choice	Description
Outcome cohort	A cohort representing the cases (the outcome of interest)
Control cohort	A cohort representing the controls. Typically the control cohort is automatically derived from the outcome cohort using some selection logic
Target cohort	A cohort representing the treatment
Nesting cohort	Optionally, a cohort defining the subpopulation from which cases and controls are drawn
Time-at-risk	At what time (often relative to the index date) do we consider exposure status?

12.4 환자-교차 연구 설계 (The Case-Crossover Design)

환자-교차 연구 (case-crossover study (Maclure, 1991)) 설계는 outcome 이전의 정해진 기간 동안 노출율 (rate of exposure)의 차이가 나는지 평가하는 방법이다. 이것은 outcome 발생 시점의 특이한 사항이 있는지 확인하는 방법이다. 표 12.4 는 환자-연구 연구 정의를 위한 선택지를 보여준다.

환자군은 자신들이 대조군으로 사용된다. 자가 통제 코호트 연구 설계처럼, 환자간 차이에 의한 교란변수를 통제할 수 있도록 환자군이 잘 선택되어야 한다. 한 가지 우려는, outcome 일시가 항상 대조군 일시에 비해 뒤에 오기 때문에, 전반적인 노출 빈도가 시간이 갈수록 높아져 양성 편향 (만약 노출빈도가 시간이 갈수록 줄어든다면 음성 편향이)이 일어날 수 있다는 점이다. 이를 통제하기 위하여 환자-교차 연구 연구 설계에 나이, 성별을 이용한 짹짓기를 통한 대조군을 추가하여 노출율을 보정하는 환자-시간-대조군 연구 설계 (case-time-control design (Suissa, 1995))가 개발되었다.

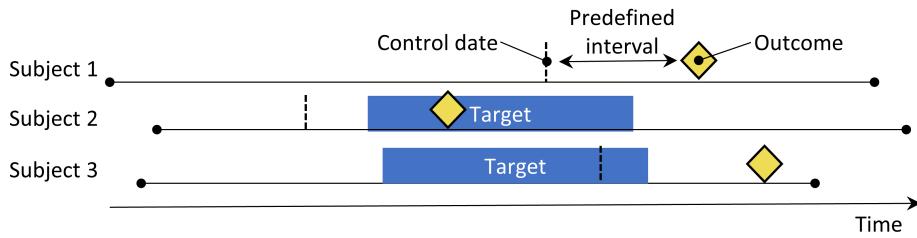


Figure 12.4: The case-crossover design. The time around the outcome is compared to a control date set at a predefined interval prior to the outcome date.

Table 12.4: Main design choices in a case-crossover design.

Choice	Description
Outcome cohort	A cohort representing the cases (the outcome of interest)
Target cohort	A cohort representing the treatment
Time-at-risk	At what time (often relative to the index date) do we consider exposure status?
Control time	The time period used as the control time

12.5 자기 대조군 환자군 연구 설계 (The Self-Controlled Case Series Design)

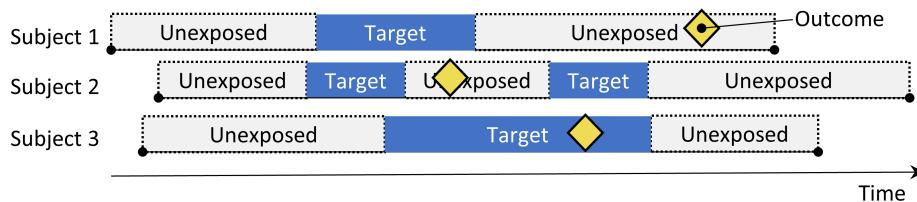


Figure 12.5: The Self-Controlled Case Series design. The rate of outcomes during exposure is compared to the rate of outcomes when not exposed.

자기 대조군 환자군 연구 (Self-Controlled Case Series,SCCS) 설계(Farrington, 1995; Whitaker et al., 2006)는 전체 비노출 기간 (노출 이전, 노출 사이, 노출 후) 과 노출기간 동안의 outcome 발생의 비율 (rate)를 비교한다. 즉 Poisson regression conditioned on the person 이라고 할 수 있다. 따라서, 그것은 “환자에게 outcome이 발생하였을 때, non-exposed time에 비해 exposed time에 발생할 가능성이 더 높은가?”이다. 표 12.5의 선택사항은 SCCS 질문을 정의 한다.

다른 자가 통제 설계 (self-controlled design)와 마찬가지로, SCCS는 사람 간의 교란 변수 (confounding due to between-person difference)는 잘 보정하지만, 시간의 변화에 따른 교란변수 (confounding due to time-varying effect)의 영향에는 취약한다. 이를 위해 몇 가지 보정을 시도할 수 있는데, 예를 들면 나이와 계절을 보정하는 것

Table 12.5: Main design choices in a self-controlled case series design.

Choice	Description
Target cohort	A cohort representing the treatment
Outcome cohort	A cohort representing the outcome of interest
Time-at-risk	At what time (often relative to the target cohort start and end dates) do we consider the risk of the outcome?
Model	The model to estimate the effect, including any adjustments for time-varying confounders

이다. SCCS의 특별한 변형은 관심대상의 노출뿐만 아니라 데이터베이스에 기록된 약물에 대한 다른 모든 노출(Simpson et al., 2013)에 잠재적으로 수천 개의 추가 변수를 모델에 추가하는 것을 포함한다. 정규화 하이퍼파라미터를 선택하기 위해 교차검증(cross-validation)을 사용하는 L1-regularization이 관심 대상 노출을 제외한 모든 노출 계수에 적용된다.

SCCS의 기본 가정 중 하나는 관찰 기간 종료가 결과 날짜 (outcome date)와 독립적이라는 것이다. 몇 가지 outcome의 경우, 예를 들어 뇌졸중과 같은 치명적인(fatal) 질병의 경우, 이러한 가정이 위반될 수 있다. 이러한 종속성을 수정하는 SCCS의 확장이 개발되었다.(Farrington et al., 2011)

12.6 Designing a Hypertension Study

12.6.1 Problem Definition

ACE 억제제(ACEi)는 고혈압이나 허혈성 심장 질환 환자, 특히 울혈성 심부전, 당뇨병 또는 만성 신장 질환과 같은 다른 합병증이 있는 환자에게 널리 사용된다. (Zaman et al., 2002) 일반적으로 입술, 혀, 입, 후두, 인두 또는 눈 주위 부위가 부어 오르는 심각한 중증도의 때로는 생명을 위협하는 부작용은 이러한 약물의 사용과 관련이 있다. (Sabroe and Black, 1997) 그러나 이러한 약물의 사용과 관련된 혈관부종에 대한 절대 및 상대 위험에 대한 정보는 제한적이다. 기존의 증거는 주로 다른 집단에 대한 일반화가 불가능한 특정 코호트(예: 주로 남성 퇴역 군인이나 메디케이드 수혜자)에 대한 조사 또는 불안정한 위험 추정치를 제공하는 경우가 거의 없는 조사를 기반으로 한다. (Powers et al., 2012) 다수의 관찰 연구는 혈관부종의 위험에 대한 ACEi를 베타 차단제와 비교하지만(Magid et al., 2010; Toh et al., 2012), 베타 차단제는 더 이상 고혈압의 1차 치료제로 권장되지 않는다.(Whelton et al., 2018) 사용 가능한 대체 치료제는 thiazide 또는 thiazide-like 이뇨제일 수 있으며, 이는 혈관부종의 위험 증가 없이 급성 심근경색과 같은 고혈압관련 위험을 관리하는데 ACEi만큼 효과적이다.

다음은 다음과 같은 비교 추정 질문을 다루기 위해 인구수준 평가(population-level estimation) 프레임워크를 관찰보건데이터(observational healthcare data)에 적용하는 방법을 보여준다

Thiazide 및 thiazide-like 이뇨제를 새로 사용하는 환자들에 비교해 ACEi

를 새로 사용하는 환자들에서 혈관부종의 위험도는 어떻게 되는가?

Thiazide 및 thiazide-like 이뇨제를 새로 사용하는 환자들에 비교해 ACEi를 새로 사용하는 환자들에서 급성 심근경색의 위험도는 어떻게 되는가?

이들이 비교 효과 추정 (comparative effect estimation) 질문이기 때문에 챕터 12.1에서 설명한대로 Cohort Method 를 적용할 것이다

12.6.2 Target and Comparator

첫 번째 관찰된 고혈압 치료가 ACEi 또는 THZ 계열의 활성 성분을 단독요법으로 사용하는 경우를 new-user로 간주한다. 이 중 치료 시작 후 7일 동안 다른 항고혈압제를 시작하지 않은 경우를 단독요법으로 정의한다. 환자가 첫 번째 노출 전 데이터베이스에서 적어도 1년 동안 지속적으로 관찰되고, 치료시작 전 또는 그 이전에 기록된 고혈압 진단을 받도록 정의했다.

12.6.3 Outcome

입원 또는 응급실 방문 중에 혈관부종이 발생하고, 그 이전 일주일간 혈관부종 발생이 없었던 경우를 혈관부종으로 정의했다. 입원 또는 응급실 방문 중에 심근경색이 발생하고, 그 이전 180일간 심근경색 발생이 없었던 경우를 심근경색으로 정의했다.

12.6.4 Time-At-Risk

30일 까지의 차이 (30-day gap)를 인정하여, 치료 시작 다음날부터 시작하여 연속적인 약물 노출이 중단될 때까지를 “time-at-risk”로 정의했다.

12.6.5 Model

인구학적 특징, 상태, 약물, 절차, 측정, 관찰 결과, 다양한 병존질환을 포함하는 공변량 기본 세트를 사용하여 적합한 성향 점수 모델을 구하는데, 공변량에서 ACEi와 THZ를 제외한다. 여기에서 다비율 짹짓기 (variable-ratio matching)을 수행하고, 성향 점수 짹짓기된 세트에 대해 조건화된 콜스 회귀분석을 실시한다.

12.6.6 Study Summary

Table 12.6: Main design choices for our comparative cohort study.

Choice	Value
Target cohort	New users of ACE inhibitors as first-line monotherapy for hypertension.
Comparator cohort	New users of thiazides or thiazide-like diuretics as first-line monotherapy for hypertension.
Outcome cohort	Angioedema or acute myocardial infarction.

Choice	Value
Time-at-risk	Starting the day after treatment initiation, stopping when exposure stops.
Model	Cox proportional hazards model using variable-ratio matching.

12.6.7 Control Questions

우리 연구 디자인이 실제와 일치하는 추정치를 산출하는지 평가하기 위해 진짜 효과 크기가 알려진 곳에 일련의 통제 질문을 추가로 포함한다. 통제 질문은 위험비(hazard ratio)이 1인 음성 대조군(negative control)과 1보다 큰 위험 비율을 갖는 양성 대조군(positive control)으로 나눌 수 있다. 우리는 몇 가지 이유에서 실제 음성 대조군을 사용하고, 음성 대조군에 근거해 양성 대조군을 만든다. 대조군을 설정하고 사용하는 방법은 챕터 18에서 자세히 다룬다.

12.7 Implementing the Study Using ATLAS

여기서는 ATLAS의 추정 기능(Estimation function)을 사용하여 이 연구를 어떻게 구현하는지 보여준다. ATLAS의 왼쪽 바에서  Estimation 를 클릭하고 새로운 평가 연구를 작성하고, 이 연구에 쉽게 인식할 수 있는 이름을 붙이자. 연구 설계는  를 클릭하여 언제든지 저장할 수 있다.

추정 설계 기능(estimation design function)에는 세 가지 섹션이 있다: 비교(comparisons), 분석 설정(analysis settings), 평가 설정(evaluation settings). 다중 비교 및 다중 분석 설정을 지정할 수 있으며, ATLAS는 이러한 모든 조합을 별도의 분석으로 수행한다. 여기서는 각 섹션에 대해 설명한다:

12.7.1 Comparative Cohort Settings

한 연구에는 하나 이상의 비교대상이 있을 수 있다. “Add Comparison”을 클릭하면 새 대화 상자가 열린다. 대상(target) 및 비교(comparator) 코호트를 선택하려면  을 클릭하면 된다. “Add Outcome”을 클릭하면, 두 개의 결과(outcome) 코호트를 추가할 수 있다. 우리는 챕터 10에서 설명한대로 이미 코호트들이 생성된 것으로 가정한다. 부록에서 대상군 (Appendix B.2), 대조군 (Appendix B.5), outcome (Appendix @ref(Angioedema 과 Appendix B.3) 코호트에 대해 자세히 볼 수 있다. 완료되면 그림 12.6에서와 같은 창이 생성될 것이다.

복수의 대상-비교 쌍(target-comparator pair)에 대해 결과를 선택할 수 있다는 점에 주의하자. 각 결과는 독립적으로 처리되며 별도의 분석이 이루어진다.

Negative Control Outcomes

음성 대조군 outcome (Negative Control Outcome)은 대상군 또는 비교군에 의해 야기된 것으로 생각되지 않는 결과이며, 따라서 실제 위험비는 1과 동일해야 한다.

The screenshot shows the 'Comparison' dialog box. At the top, it says 'Add or update the target, comparator, outcome(s) cohorts and negative control outcomes'. Below this, there are three sections: 'Choose your target cohort:' with 'New users of ACE inhibitors as first-line monotherapy for hypertension', 'Choose your comparator cohort:' with 'New users of Thiazide-like diuretics as first-line monotherapy for hypertension', and 'Choose your outcome cohorts:' with a table.

ID	Name	Edit cohort	Remove
1770712	Angioedema outcome	Edit cohort	Remove
1770713	Acute myocardial infarction outcome	Edit cohort	Remove

At the bottom, it says 'Showing 1 to 2 of 2 entries' and has navigation buttons 'Previous' (page 1), 'Next'.

Figure 12.6: The comparison dialog

이상적으로는 우리는 각 결과 코호트에 대해 적절한 코호트 정의를 가진다고 가정한다. 그러나, 우리는 일반적으로 음성 통제 결과 당 하나의 컨셉 세트(concept set)과 이를 결과 코호트로 변환하는 표준 논리만 가진다. 여기서는 챕터 18에서 설명한대로 컨셉 세트가 이미 생성되었다고 가정하고 간단하게 선택할 수 있다. 음성 통제 컨셉 집합에는 음성 통제 당 하나의 컨셉만을 포함해야 하며, 하위 컨셉들은 포함하지 않아야 한다. 그림 12.7은 본 연구에 사용된 음성 대조군 컨셉 집합을 보여준다.

Concepts to Include

포함 컨셉 (concept to include) 선택시, 우리는 성향점수 모델 등에 어떠한 공변량이 생성되기를 원하는지 선택할 수 있다. 공변량을 지정하면, 모든 다른 공변량(선택하지 않은)은 제외된다. 보통 우리는 환자들의 모든 기저 공변량을 추가하여 regularized regression이 모든 공변량의 균형을 맞출 수 있는 모델을 만들기를 바란다. 만약 특정 공변량만을 선택하기 원한다면, 그것은 연구자들이 직접 공변량을 고른 다른 연구들을 복제해보기 위해서일 것이다. 이러한 공변량 추가들은 비교(comparison) 섹션 또는 분석 (analysis) 섹션에서 정의될 수 있는데, 공변량들이 특정 비교 (비교시 알고 있는 교란변수) 또는 분석 (특정 공변량 선택 전략의 평가)에 연계될 수 있기 때문이다.

Concepts to Exclude

추가하는 컨셉보다는 배제 컨셉을 지정하는 경우가 많다. 배제 컨셉을 지정하면, 배제 컨셉을 제외한 모든 공변량을 사용함을 뜻한다. 기본 공변량 집합 (default set of covoariates) 설정을 이용하면, 치료 시작 시의 모든 약물, 시술을 이용하기 때문에, 우리는 대상 치료 및 비교 치료에 해당되거나 이것들과 직접적으로 관련된 컨셉

Negative controls for ACEi and THZ

Concept Set Expression Included Concepts (75) Included Source Codes Explore Evidence Export Compare

Show 25 entries Search: []

Showing 1 to 25 of 75 entries

Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped
72748	74779009	Strain of rotator cuff capsule	Condition	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
73241	197210001	Anal and rectal polyp	Condition	Standard	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
73560	55260003	Calcanal spur	Condition	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
75911	65358001	Acquired hallux valgus	Condition	Standard	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
76786	63643000	Derangement of knee	Condition	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Figure 12.7: Negative Control concept set.

들을 배제해야 한다. 예를 들어, 만약 대상 치료가 약물 정맥 주입 치료라면, 우리는 약물 뿐 아니라 정맥 주입 시술 역시도 성향 점수 모델에서 제외해야 한다. 이 예제에서 우리는 ACEi와 THZ를 배제했다. 그림 12.8에서 ACEi와 THZ 과 그들의 하위 컨셉을 포함하여 배제 컨셉 집합을 구성함을 볼 수 있다.

음성 대조군과 배제 컨셉을 지정한 후, 비교 섹션의 아래쪽 절반창은 그림 12.9과 같이 보일 것이다.

12.7.2 Effect Estimation Analysis Settings

비교 창을 닫은 후 “Add Analysis Settings” 을 클릭할 수 있다. “Analysis Name”이라는 상자에 추후에 기억하고 분류하기 쉽도록 분석별 고유한 이름을 지정할 수 있다. 예를 들어 “Propensity score matching”을 지어줄 수 있다.

Study Population

분석에 포함시킬 피험자 집단과 같은 연구 집단을 지정하는데 다양한 옵션이 있다. 코호트 정의 (cohort definition) 도구에서 대상 및 대조 코호트를 설계할 때 사용할 수 있는 옵션과 대부분 겹친다. 코호트 정의 대신에 Estimation에서 옵션을 사용하는 한 가지 이유는 재사용성(re-usability)이다. 대상, 대조 및 결과 코호트를 완전히 독립적으로 정의한 후에 나중에 이를 사이의 종속관계를 추가할 수 있다. 예를 들어, 치료 개시 전에 outcome가 있었던 사람들을 제외하기를 원한다면, 대상 및 대조 코호트의 정의에서 그렇게 할 수 있지만, 모든 outcome에 대해 별도의 코호트를 작성해야 한다! 대신에, Estimation 설정에서 이전 결과를 가진 사람들을 제거하도록 선택할 수 있다. 이제 우리는 (음성 대조군 결과뿐만 아니라) 두 가지 관심 결과에 대해 대상 및 대조 코호트를 재사용할 수 있다.

연구 시작 및 종료일 (study start and end dates) 은 분석을 특정 기간으로 제한하는데 사용할 수 있다. 연구 종료일 또한 위험창(risk window)을 제한하기 때문에 연구 종료일 이후의 outcome은 고려되지 않는다. 연구 시작일을 선택하는 한 가지

Concept Set #1798551							
Concepts to exclude for ACEi and THZ					Optimize	Remove	
Concept Set Expression	Included Concepts	38225	Included Source Codes	Explore Evidence	Export	Compare	
Show 25 ▾ entries					Search:		
Showing 1 to 14 of 14 entries					Previous 1	Next	
Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped
1342439	38454	trandolapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
1334456	35296	Ramipril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
1331235	35208	quinapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
1373225	54552	Perindopril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
1310756	30131	moexipril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Figure 12.8: The concept set defining the concepts to exclude.

Negative control concept set:

Negative controls for ACEi and THZ	Save	Remove
Covariate selection		
Concepts to include when constructing the covariates to be used in this study. (Leave blank if you want to include every concept).*	<input type="button" value=""/>	
* Concepts defined here are combined with those defined in the Analysis settings section.		
Concepts to exclude when constructing the covariates to be used in this study.*	<input type="button" value=""/>	
Concepts to exclude for ACEi and THZ	<input type="button" value=""/>	
* Concepts defined here are combined with those defined in the Analysis settings section.		

Figure 12.9: The comparison window showing concept sets for negative controls and concepts to exclude.

이유는 연구 중인 약물 중 하나가 새로운 것이며, 전에는 존재하지 않을 수 있기 때문이다. “**두 노출이 모두 관찰되는 기간으로 분석을 제한하라 (Restrict the analysis to the period when both exposures are present in the data?)**”는 옵션을 “예(yes)”라고 설정하면, 새 약물이 데이터베이스에 존재하는 시점을 자동으로 연구 시작일로 조정할 수 있다. 연구 시작일과 종료일을 조정하는 또 다른 이유는 시기에 따라 (예를 들어 새로운 약물 부작용이 알려지면서) 임상 업무의 변화가 있고, 우리는 보통 특정 방식으로 임상이 이루어질 때만 관심이 있기 때문이다.

“**환자 당 첫 번째 노출만 포함해야 하는가? (Should only the first exposure per subject be included?)**” 옵션을 사용하여 환자 당 첫 번째 노출만으로 코호트를 제한할 수 있다. 이 옵션은 이번 예제에서처럼 코호트 정의에서 이미 수행된 경우가 많다. 유사하게, 코호트 정의에 “**코호트에 포함될 사람이 index date전에 최소 연속적 관측 시기 (The minimum required continuous observation time prior to index date for a person to be included in the cohort)**” 옵션이 설정되어 있는 경우가 많아, 여기에 0으로 남겨둘 수 있다. 이러한 옵션은 index data 이전에 관찰된 시간(OBSERVATION_PERIOD 테이블에서 정의된)을 가짐으로써 성향 점수를 계산할 수 있는 환자에 대한 충분한 정보가 있음을 보장하고, 환자가 이전에 노출된 적 없는, 진정하게 치료의 새로운 사용자 (new user)임을 보장하기 위해 자주 사용된다.

“**만일 피험자가 여러 코호트에 있다면, 겹침(overlap)을 막기 위해 새로운 time-at-risk를 시작할 때 이것이 중도 절단(censor) 되어야 하는가? (If a subject is in multiple cohorts, should time-at-risk be censored when the new time-at-risk starts to prevent overlap?)**” 하는 옵션과 함께 “**대상 및 대조 코호트 모두에 있는 피험자를 제거하는가? (Remove subjects that are in both the target and comparator cohort?)**” 옵션은 피험자가 대상과 대조 코호트 모두에 있을 때 어떻게 할 지 정의한다. “**대상 및 대조 코호트 모두에 있는 피험자를 제거하는가?**” 옵션에 대해서는 세 가지 선택 사항이 있다

- “**Keep All**” 은 양 코호트의 모든 환자들을 보존한다는 뜻이다. 이 옵션은 환자와 outcome의 쌍 갯수를 중복으로 셀 수 있다.
- “**Keep First**” 은 한 환자가 양 코호트에 모두 들어있을 경우, 두 코호트 중 먼저 들어간 코호트에서의 환자만 인정한다는 뜻이다.
- “**Remove All**” 은 양 코호트에 모두 들어간 환자들을 모두 제외하는 것이다.

“Keep all” 또는 “keep first” 옵션이 선택되면, 우리는 연구 대상자가 양쪽 코호트 모두에 속하는 시기를 절단하기를 바랄 수 있다 (그림 12.10). 기본적으로 time-at-risk는 코호트 시작일과 종료일을 기준으로 정의된다. 이번 예에서, time-at-risk는 코호트 시작일 다음날부터 시작되어 코호트 종료일에 끝난다. 절단하지 않는다면, 두 코호트의 time-at-risk가 겹칠 수 있다. 이 겹치는 동안 발생하는 모든 outcome이 (그림과 같이) 두 번 계산되기 때문에 “keep all”을 선택하면 특히 문제가 된다. 만약 절단하기를 선택하면 첫 번째 코호트의 time-at-risk는 두 번째 코호트의 time-at-risk가 시작될 때 종료된다.

최초의 outcome 발생 이후 연속적으로 이후의 outcome이 발생하는 경우가 종종 있어, **risk window**가 시작하기 전 outcome이 발생한 피험자를 제거(remove subjects that have the outcome prior to the risk window start) 할 수

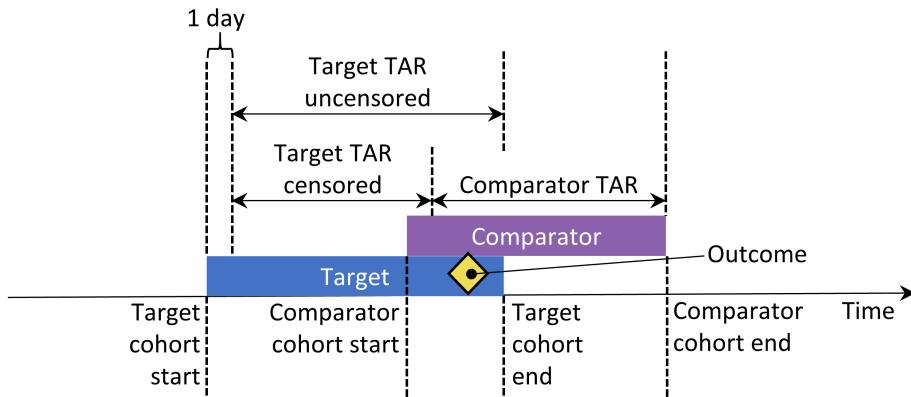


Figure 12.10: Time-at-risk (TAR) for subjects who are in both cohorts, assuming time-at-risk starts the day after treatment initiation, and stops at exposure end.

도 있다. 예를 들어, 누군가에게 심부전과 같은 만성 질병이 최초로 발생한 후, 두 번째 발생이 있을 수 있는데, 이는 심부전이 새로 다시 발생했다기 보다는, 이전의 심부전이 완전히 치료되지 않은 상태를 의미할 가능성이 높다. 한편으로는, 어떠한 outcome들은 일시적일 수도 있다. 예를 들어 상부 호흡기 감염 (upper respiratory infection)과 같은 급성 질병이 한 환자에 여러번 발생한다면, 이는 실제로 독립적인 질병 발생이 시간 간격으로 두고 발생함을 의미할 수도 있다. 이전 outcome을 확인할 때 몇 일전까지 검토해야 할지 (how many days we should look back when identifying prior outcomes)를 선택함으로써, 이전에 outcome이 있는 사람들을 제거하는 방법을 선택할 수 있다.

예제 연구에 대한 우리의 선택은 그림 12.11과 같다. 대상 및 대조 '코호트 정의' 시 이미 첫 번째 노출로 한정하고 치료 개시 전에 관찰시기가 필요하기 때문에 Estimation에서 이러한 기준을 다시 적용하지 않았다.

Covariate Settings

여기서 우리는 사용할 공변량을 지정한다. 이러한 공변량은 일반적으로 성향 점수 모델에서 사용되지만, 결과 모델(이 경우 Cox proportional hazards model)에도 포함될 수 있다. 우리가 공변량 설정의 세부 사항 (click to view details)을 클릭을 하면, 사용할 공변량 세트을 선택할 수 있다. 하지만, 인구학적 정보, 모든 진단명, 약물, 시술, 검사 등에 대한 공변량을 구성하는 기본 집합(default set)을 사용하길 권장한다.

포함하거나 **배제** 할 컨셉을 지정하여 공변량 세트을 수정할 수 있다. 이러한 설정은 비교 설정의 절 12.7.1에 있는 설정과 동일하다. 두 곳에서 이 설정이 가능한 이유는, 비교하는 약물들을 제외하기 위해서이기 하고, 때로는 이 설정이 특정 분석과 관련 있을 수도 있기 때문이다. 특정 분석 설정을 사용하여 특정 비교에 대한 분석을 실행하면 OHDSI 툴이 이러한 세트을 통합한다.

그림 12.12 은 이 연구에 대한 선택을 보여준다. 그림 12.9 의 비교 셋팅에서 배제 컨셉에 하위 컨셉을 포함하도록 설정했다는 점에 주의하자.

Study Population

Study start date - a calendar date specifying the minimum date that a cohort index can appear (leave blank to use all time):

Study end date - a calendar date specifying the maximum date that a cohort index can appear (leave blank to use all time). **Important:** the study end date is also used to truncate risk windows, meaning no outcomes beyond the study end date will be considered.

Restrict the study to the period when both exposures are present in the data? (E.g. when both drugs are on the market)

Should only the first exposure per subject be included?

The minimum required continuous observation time (in days) prior to index date for a person to be included in the cohort.

Remove subjects that are in both the target and comparator cohort?

If a subject is in multiple cohorts, should time-at-risk be censored when the new time-at-risk start to prevent overlap?

Remove subjects that have the outcome prior to the risk window start?

How many days should we look back when identifying prior outcomes?

If either the target or the comparator cohort is larger than this number it will be sampled to this size. (0 for this value indicates no maximum size)

Figure 12.11: Study population settings.

Covariate Settings

Using OHDSI covariates for propensity score model. ([Click to view details](#))

Concepts to **include** when constructing the covariates to be used in this study. (Leave blank if you want to include every concept).*

✖ ✖

* Concepts defined here are combined with those defined in the Comparisons section.

Concepts to **exclude** when constructing the covariates to be used in this study.*

✖ ✖

* Concepts defined here are combined with those defined in the Comparisons section.

Figure 12.12: Covariate settings.

Time At Risk

Define the time-at-risk window start, relative to target/comparator cohort entry:

days from

Define the time-at-risk window end:

days from

The minimum number of days at risk?

Figure 12.13: Time-at-risk settings.

Time At Risk

Time-at-risk는 대상 및 대조 코호트의 시작일과 종료일을 기준으로 정의된다. 이 예제에서는, 치료 시작일을 코호트 시작일로, 약물 노출이 30일 이상 중지되면 코호트 종료일이 되도록 설정하였다. 코호트 시작 후 1일(즉, 치료 시작 후 1일)을 time-at-risk의 시작으로 설정하였다. 치료 시작과 함께 발생한 outcome 이 이론상 치료에 의해 발생한 것이라고 믿기 어려울 때, 코호트 시작 이후에 time-at-risk 가 시작하도록 설정한다.

코호트 종료일을 time-at-risk 종료일로 설정하여, 약물 노출이 중지된 시점으로 설정하였다. 예를 들어, 치료 종료 후에 발생한 event가 노출로 인한 것으로 판단될 경우, time-at-risk의 종료일을 나중으로 설정할 수 있다. 극단적인 경우, time-at-risk 종료를 코호트 종료일 후에 매우 이후 (예: 99999일)로 설정할 수 있다. 이는 관찰 종료까지 피험자를 추적 관찰하는 것을 의미한다. 이러한 연구 설계를 때로는 *intent-to-treat* 설계라고도 한다.

index date이후 절단 또는 outcome 발생 전까지의 관찰 기간 (days at risk) 가 0 일인 환자는 추가적인 정보가 없기 때문에, 최소 관찰 기간 (minimum days at risk) 은 보통 1일로 설정한다. 노출과 outcome 발생에 대한 지연시간(latency)이 알려져 있다면, 이러한 일수를 늘려 더 유익한 비율(more informative proportion)을 얻을 수도 있을 것이다. 이러한 설정은 무작위 임상 시험과 유사한 연구 설계를 위해서도 사용할 수 있다 (예를 들어, 임상시험에 참여한 피험자가 최소한 N 일 동안은 관찰되었다고 할 때).



코호트 연구를 설계할 때, 황금률(golden rule)은 편향(bias)이 개입될 수 있으므로 연구 대상을 정의하기 위해 코호트 시작일 이후의 정보를 절대로 사용하지 않는 것이다. 예를 들어, 모든 피험자들에게 적어도 1년의 time-at-risk가 요구된다면, 우리는 치료를 잘 견디는 피험자들로 분석을 제한했다는 뜻이다. 따라서, 이러한 설정은 세심한 주의를 기울여 사용해야 한다.

Propensity Score Adjustment

극단적이 성향 점수를 갖는 피험자들을 제거하여, 연구 대상을 트리밍 (trimming) 할 수 있다. 상위 또는 하위 비율을 제거하도록 선택하거나, 선호도 점수(preference

score)가 지정된 범위를 벗어나는 피험자를 제거할 수 있다. 코호트 트리밍은 관측치를 제거하여 통계력 (statistical power)을 감소 시키기 때문에 일반적으로 권장되지는 않는다. IPTW를 사용할 때처럼 경우에 따라서는 트리밍을 하는 것이 바람직할 수 있다.

트리밍에 추가하여, 또는 트리밍 대신에, 성향 점수를 이용해 **계층화 (stratification)**하거나 **짝짓기 (matching)**하도록 선택할 수 있다. 계층화할 때, 계층의 수 (**number of strata**)를 지정하고, 대상군, 대조군, 또는 전체 연구 집단을 기준으로 계층을 선택할지 여부를 지정해야 한다. 성향점수 짝짓기 시, 대상군의 각 피험자와 일치시키기 위한 대조군에서의 **최대 피험자 수 비율 (maximum number of people from the comparator group to match to each person in the target group)** 지정하여야 한다. 일반적인 값은 one-on-one matching의 경우 1, variable-ratio matching의 경우 다수 (예: 100)이다. 또한, 매칭을 허용하는 성향 점수 사이의 최대 허용 차이를 뜻하는 **캘리퍼 (caliper)**를 지정해야 한다: 캘리퍼는 다음과 같이 서로 다른 캘리퍼 척도 (caliper scales)로 정의할 수 있다

- **성향 점수 척도 (propensity score scale):** 성향 점수 자체
- **표준화 척도 (standardized scale):** 성향 점수 분포의 표준편차
- **표준화 로짓 척도 (standardized logit scale):** 성향 점수를 보다 정규분포로 만들기 위해 로그 변환 후 성향 점수 분포의 표준편차

의심스러운 경우, 기본값을 사용하거나, 이 주제에 대한 Austin (2011)의 연구를 참고하기를 권장한다.

대규모 성향 점수 모델 (large-scale propensity model)을 적합 (fitting)하는 것은 많은 컴퓨팅 자원을 요구할 수 있어서, 계산 시 샘플링한 자료를 이용하고자 할 수 있다. 디폴트 설정상, 대상 및 비교 코호트의 최대 크기는 250,000으로 설정된다. 대부분의 연구에서 코호트의 전체 피험자 수가 이 한도에 도달하지 못할 것이다. 이보다 많은 데이터를 이용한다고, 더 나은 모델로 이어질 가능성은 희박하다. 비록 샘플링한 데이터를 이용해 성향 점수 모델을 적합하더라도, 전체 집단에 대한 성향 점수가 계산된다는 점에 유의하자.

치료배정과 상관 관계에 대해 각 공변량을 검증하시겠습니까? (Test each covariate for correlation with the target assignment?) 을 'yes'로 설정하면, 만약 어떤 공변량이 치료 배정 (treatment assignment)과 비정상적으로 높은 (양 또는 음의) 상관관계가 있으면 오류를 발생시키고, 프로세스가 중단된다. 이것은 대규모 성향 점수 모델 계산이 완전히 끝날 때까지 기다리는 것을 방지할 수 있다. 매우 높은 단변량 상관 관계를 발견하면, 공변량을 검토하여 치료 배정과 상관 관계가 높은 이유와 이를 제거해야 하는지 여부를 결정할 수 있다.

모델 적합시에 정규화를 사용하시겠습니까? (Use regularization when fitting the model?) 일반적으로 매우 많은 공변량 (일반적으로 만 개 이상)이 성향점수 모델 계산시 사용된다. 이러한 대규모 모델을 적합하기 위해서는 정규화 (regularization)가 필요하다. 만약 수동으로 몇 개의 공변량만 사용된다면, 정규화를 사용하지 않아도 모델을 적합할 수 있다.

그림 12.14은 이 연구에 대한 우리의 선택을 보여준다. 최대 짝짓기 비율을 100으로 설정하여 variable-ratio matching을 선택하였다.

Propensity Score Adjustment

How do you want to trim your cohorts based on the propensity score distribution?

None ▾

Do you want to perform matching or stratification?

Match on propensity score ▾

What is the maximum number of persons in the comparator arm to be matched to each person in the target arm within the defined caliper? (0 = means no maximum - all comparators will be assigned to a target person):

100 ▾

What is the caliper for matching:

0.2

What is the caliper scale:

Standardized Logit ▾

What is the maximum number of people to include in the propensity score model when fitting? Setting this number to 0 means no down-sampling will be applied:

250000 ▾

Test each covariate for correlation with the target assignment? If any covariate has an unusually high correlation (either positive or negative), this will throw an error.

Yes ▾

Use regularization when fitting the propensity model?

Yes ▾

Control Settings ▾ | **Prior** ▾

Figure 12.14: Propensity score adjustment settings.

Outcome Model Settings

먼저, 대상 코호트과 대조 코호트 간 **outcome**의 상대적 위험(relative risk)을 추정하기 위해 사용할 통계 모델을 명시할 필요가 있다. 절 12.1에서 간략히 논의했던 것처럼, Cox, Poisson 및 logistic regression 중에서 선택할 수 있다. 예제에서는 Cox proportional hazards model을 사용하는데, 이 모델은 중도절단을 고려하여 첫 번째 사건까지의 시간(time to first event)을 고려한다. 다음으로, **회귀분석에 충화 조건을 사용해야 할지 (whether the regression should be conditioned on the strata)**를 명시할 필요가 있다. 쉽게 말하자면, 조건화(conditioning)는 별도의 추정치가 각 층(strata)에서 생성된 다음, 층에 걸쳐 추정치가 결합된 것으로 생각할 수 있다. One-to-one PS matching에서는 이러한 과정이 불필요할 것이며, 통계력(statistical power) 감소를 유발할 것이다. 조건화는 충화(stratification) 또는 variable-ratio matching을 위해서 필요하다.

분석을 보정하기 위해 **결과 모델 (outcome model)**에 **공변량을 추가** 할 수도 있다. 이것을 성향 점수 모델 사용에 추가하거나 성향 점수 짹짓기 대신에 수행할 수 있다. 하지만 보통 성향 점수 모델을 적합하기에는 충분한 수의 데이터가 있지만, 결과 모델을 적합하기에는 outcome이 발생한 피험자가 적어 데이터가 모자라는 경우가 많다. 그래서 공변량을 결과 모델에 추가하지 말고, 결과 모델을 가급적 간단하게 유지하기를 권장한다.

성향 점수 이용해 충화하거나 매칭하는 대신에 **역학률 치료가중치 (inverse probability of treatment weighting, IPTW)**를 사용할 수도 있다.

만약 모든 공변량을 결과 모델에 추가한다면, 공변량이 매우 많기 때문에 결과 모델 적합시 정규화를 이용하는 것이 합리적일 것이다. 편향이 없는 추정(unbiased estimation)을 위해서 치료 공변량(treatment variable) 자체에는 정규화가 적용되지 않음에 유의하자.

그림 12.15 이 연구에 대한 선택을 보여준다. Variable-ratio matching을 사용하기 때문에, 회귀분석에 충화 조건화 (condition the regression on the strata (i.e. the matched sets))를 해야함에 주목하자.

12.7.3 Evaluation Settings

장 18에서 기술한 바와 같이, 음성 대조군 및 양성 대조군은 운영 특성 및 empirical calibration을 위하여 추가되어야 한다.

Negative Control Outcome Cohort Definition

절 12.7.1에서 우리는 음성 대조군을 지정하는 컨셉군을 선택했다. 컨셉을 지정하는 것 뿐 아니라, 분석을 위해서는 컨셉을 기반으로 코호트를 생성하는 프로세스가 필요하다. ATLAS는 세 가지 선택 사항을 가진 표준 프로세스를 제공한다. 첫 번째 선택은 **모든 발생**을 사용할지 또는 컨셉의 **첫 번째 발생**만을 사용할지 여부이다. 두 번째 선택은 **하위 컨셉의 발생을 포함할지** 여부를 결정한다. 예를 들어, 하위 컨셉 “내성 발톱(ingrown nail of foot)”의 발생은 상위 컨셉 “내성 손발톱(ingrown nail)”의 발생으로 간주될 수 있다. 세 번째 선택사항은 컨셉을 찾을 때 고려할 도메인(domain)을 지정한다.

Outcome Model Settings

Specify the statistical model used to estimate the risk of outcome between target and comparator cohorts:

Cox proportional hazards ▾

Should the regression be conditioned on the strata defined in the population object (e.g. by matching or stratifying on propensity scores)?

Yes ▾

Should the covariates also be included in the outcome model?

No ▾

Use inverse probability of treatment weighting?

No ▾

Use regularization when fitting the outcome model? *

Yes ▾

* Regularization will not be applied to the exposure of interest, just to the covariates.

Control Settings ▾ **Prior** ▾

Figure 12.15: Outcome model settings.

Negative Control Outcome Cohort Definition

This expression will define the criteria for inclusion and duration of time for cohorts intended for use as negative control outcomes.

The type of occurrence of the event when selecting from the domain.

First occurrence ▾

When true, descendant concepts for the negative control outcome concept IDs will be used to detect the outcome and roll up the occurrence to the concept ID.

Yes ▾

What domains should be considered to detect negative control outcomes? (Hold control to select multiple domains)

Condition
Drug
Device
Measurement
Observation
Procedure
Visit

Figure 12.16: Negative control outcome cohort definition settings.

Positive Control Synthesis

Should we perform positive control synthesis? (to calibrate confidence intervals)

Yes ▾

Model Type:

Survival ▾

Using OHDSI covariates for model. ([Click to view details](#))

Define the time-at-risk window start, relative to target/comparator cohort entry:

1 ▾ days from cohort start date

Define the time-at-risk window end:

0 ▾ days from

The minimum required continuous observation time (in days) prior to exposure:

365 ▾

Should only the first exposure per subject be included?

Yes ▾

Should only the first outcome per person be considered when modeling the outcome?

Yes ▾

Remove people with prior outcomes?

Yes ▾

Advanced Settings start here

Additional Settings ▾

Figure 12.17: Negative control outcome cohort definition settings.

Positive Control Synthesis

음성 대조군 외에도 양성 대조군도 포함할 수 있는데, 이는 알려진 효과 크기 (effect size)와 함께 인과 관계 (causal effect)가 존재하는 것으로 보이는 노출-결과 쌍 (exposure-outcome pair)을 뜻한다. 여러 가지 이유로 실제 양성 대조군 설정은 문제가 있기 때문에, 대신 장 18에서 설명한대로 음성 대조군을 기반으로 합성된 양성 대조군을 사용한다. 우리는 **양성 대조군 합성** 여부를 선택할 수 있다. 만약 “예 (yes)”를 선택하면, 우리는 반드시 모델 타입 (model type)을 선택해야 하는데, 현재는 “Poisson”과 “survival”을 지원하고 있다. 이 예제에서는 생존 (콕스) 분석을 시행하기 때문에, 양성 대조군 합성시에도 “survival”을 선택하도록 하자. 양성 대조군 합성 시 가급적 분석 추정 셋팅에서 사용된 값들을 비슷하게 사용하였다 (**minimum required continuous observation prior to exposure, should only the first exposure be included, should only the first outcome be included, remove people with prior outcomes**). 그림 12.15 을 통해 양성 대조군 합성을 위한 셋팅을 참조할 수 있다.

12.7.4 연구 패키지 실행(Running the study package)

이제 연구를 완전히 정의했으므로, 실행 가능한 R 패키지로 export할 수 있다. 이 패키지는 CDM 데이터가 있는 사이트에서 연구를 실행하는데 필요한 모든 것이 들어 있다. 여기에는 분석을 실행하기 위한 R 코드뿐만 아니라 대상, 대조 및 결과 코호트, 음성 대조군을 정의하기 위한 컨셉 군과 코호트 생성 프로세스가 포함된다. 패키지를 생성하기 전에 연구를 저장한 다음, Utilities 템을 클릭하면, 수행될 일련의 분석을 검토할 수 있다. 앞서 언급했듯이, 개개의 비교와 분석 설정의 조합은 별도의 분석 결과를 생성할 것이다. 이번 예시에서는 성향 점수 매칭을 사용하여 두 가지 분석을 지정하였다: 급성심근경색 위험에 대한 ACEi 대 THZ 비교, 혈관 부종에 대한 ACEi 대 THZ 비교.

“Download”를 클릭하여 zip 파일을 다운로드하기 위해, 패키지의 이름을 입력해야 한다. zip 파일에는 R 패키지의 일반적인 필수 폴더 구조와 함께, R 패키지가 포함되어 있다. (Wickham, 2015) 이 패키지를 사용하려면 R Studio를 사용하는 것이 좋다. R Studio를 로컬로 실행하는 경우 파일의 압축을 푼 다음, .Rproj 파일을 더블 클릭하여 R Studio에서 연다. R Studio 서버에서 R Studio를 실행하는 경우,  Upload 버튼을 클릭하여 파일을 업로드하고 압축을 해제 한 다음, .Rproj 파일을 클릭하여 프로젝트를 연다.

R Studio에서 프로젝트를 열면 README 파일을 열고 파일의 지침을 따라할 수 있다. 모든 파일 경로를 시스템의 기존 경로로 변경하는 것을 잊지 말자.

연구를 진행할 때 나타날 수 있는 흔한 오류 메시지는 “공변량과 치료가 높은 상관 관계를 보임(High correlation between covariate(s) and treatment detected)”이다. 이는 성향 모델을 적용했을 때 일부 공변량이 노출과 높은 상관 관계가 있음을 나타낸다. 오류 메시지에 언급된 공변량을 검토하고 적절한 경우 해당 공변량을 공변량 집합에서 제외하면 된다 (절 12.1.2 참조).

12.8 Implementing the Study Using R

ATLAS를 사용하여 연구를 실행하는 R 코드를 작성하는 대신 R 코드를 직접 작성할 수도 있다. 이는 ATLAS를 이용하는 것보다, 훨씬 큰 유연성 (flexibility)을 제공할 수 있다. 예를 들어 사용자 정의 공변량 또는 선형 결과 모델을 사용하려면 사용자 정의 R 코드를 작성하고 이를 OHDSI R 패키지가 제공하는 기능과 결합해야 한다.

예제 연구에서, 우리는 연구를 수행하기 위해 CohortMethod 패키지를 사용할 것이다. CohortMethod는 CDM 데이터베이스에서 필요한 데이터를 추출하고 성향 점수 모델에 대규모의 공변량 집합을 사용할 수 있다. 다음 예에서는 혈관 부종만을 outcome으로 사용할 것이다. 절 12.8.6 에서는 이것이 어떻게 급성심근경색과 음성 대조군 결과를 포함하도록 확장될 수 있는지 기술한다.

12.8.1 코호트 실체화 (Cohort Instantiation)

먼저 대상 (target) 및 outcome 코호트를 실체화해야 한다. 코호트 실체화 방법은 장 10 에서 자세히 기술되어 있다. 부록에서 대상(부록 B.2), 대조(부록 B.5) 및 outcome(부록 B.4) 코호트들의 정의 전체를 제공한다. ACEi, THZ 및 혈관 부종

코호트가 scratch.my_cohorts 라고 명명된 테이블에서 cohort definition ID 1, 2 및 3을 가지고 함께 실체화되었다고 가정한다.

12.8.2 데이터 추출 (Data Extraction)

먼저 R에 서버에 연결하는 방법을 알려줘야 한다. CohortMethod `createConnectionDetails`라는 함수를 제공하는 DatabaseConnector 패키지를 이용한다. 다양한 데이터베이스 관리 시스템 (database management system, DBMS)에 필요한 설정에 대해 알아보기 위하여 `?createConnectionDetails` 를 입력해보자. 예를 들어, 아래 코드를 사용하여 PostgreSQL 데이터베이스에 연결할 수 있다.

```
library(CohortMethod)
connDetails <- createConnectionDetails(dbms = "postgresql",
                                         server = "localhost/ohdsi",
                                         user = "joe",
                                         password = "supersecret")

cdmDbSchema <- "my_cdm_data"
cohortDbSchema <- "scratch"
cohortTable <- "my_cohorts"
cdmVersion <- "5"
```

마지막 네 줄은 `cdmDbSchema`, `cohortDbSchema` 및 `cohortTable` 변수와 CDM 버전을 정의한다. 이들을 이용하여 이후에 CDM 데이터가 존재하는 위치, 연구용 코호트가 생성된 위치, 그리고 사용된 CDM 버전 정보를 R에 전달한다. Microsoft SQL Server의 경우 데이터베이스 스키마는 데이터베이스와 스키마 (schema)를 모두 지정해야 한다(예: `cdmDbSchema <- "my_cdm_data.dbo"`).

이제 CorhotMethod를 이용해 코호트를 추출하고, 공변량을 구성하며, 분석에 필요한 모든 데이터를 추출할 수 있다.

```
# target and comparator ingredient concepts:
aceI <- c(1335471, 1340128, 1341927, 1363749, 1308216, 1310756, 1373225,
          1331235, 1334456, 1342439)
thz <- c(1395058, 974166, 978555, 907013)

# Define which types of covariates must be constructed:
cs <- createDefaultCovariateSettings(excludedCovariateConceptIds = c(aceI,
                                                                     thz),
                                         addDescendantsToExclude = TRUE)

#Load data:
cmData <- getDbCohortMethodData(connectionDetails = connectionDetails,
                                    cdmDatabaseSchema = cdmDatabaseSchema,
                                    oracleTempSchema = NULL,
                                    targetId = 1,
                                    comparatorId = 2,
```

```

        outcomeIds = 3,
        studyStartDate = "",
        studyEndDate = "",
        exposureDatabaseSchema = cohortDbSchema,
        exposureTable = cohortTable,
        outcomeDatabaseSchema = cohortDbSchema,
        outcomeTable = cohortTable,
        cdmVersion = cdmVersion,
        firstExposureOnly = FALSE,
        removeDuplicateSubjects = FALSE,
        restrictToCommonPeriod = FALSE,
        washoutPeriod = 0,
        covariateSettings = cs)
cmData

## CohortMethodData object
##
## Treatment concept ID: 1
## Comparator concept ID: 2
## Outcome concept ID(s): 3

```

많은 파라미터가 있지만, CohortMethod 매뉴얼에 모두 설명되어 있다. `createDefaultCovariateSettings` 함수는 FeatureExtraction 패키지에 설명되어 있다. 간단이 말해, 코호트를 포함하는 테이블에 함수를 지정하고 해당 테이블의 cohort definition ID가 대상, 대조 및 outcome 코호트를 식별하도록 지정한다. index data 당일 혹은 이전에 발견된 모든 진단명, 약물 노출, 시술기록에 대한 공변량을 포함하여 공변량의 기본 셋을 구성하도록 지시한다. 절 12.1에서 언급했듯이, 공변량 집합에서 대상 및 대조 치료를 배제하여야 하며, 이 예제에서는 두 가지의 약물군에 해당하는 약물 성분(ingredient)을 나열하여 이를 달성한다. 또한, FeatureExtraction에 모든 하위 컨셉을 포함하여 배제하도록 지시하여 나열된 성분을 포함하는 모든 약물 노출을 공변량에서 제외한다.

코호트, 결과 및 공변량에 대한 모든 데이터는 서버에서 추출되어 `cohortMethodData` object에 저장된다. 이러한 object는 ff패키지를 사용하여 절 8.4.2에서 언급한 것처럼 데이터가 크더라도, R이 메모리를 모두 소모하지 않도록 보장한다.

generic `summary()` 함수를 사용하여 추출한 데이터에 대한 추가 정보를 볼 수 있다:

```

summary(cmData)

## CohortMethodData object summary
##
## Treatment concept ID: 1
## Comparator concept ID: 2
## Outcome concept ID(s): 3
##

```

```

## Treated persons: 67166
## Comparator persons: 35333
##
## Outcome counts:
##           Event count Person count
## 3                 980        891
##
## Covariates:
## Number of covariates: 58349
## Number of non-zero covariate values: 24484665

```

`cohortMethodData` 파일을 만들면 상당한 시간이 걸릴 수 있으며 향후 세션을 위해 저장하는 것이 좋다. `cohortMethodData`가 `ff`를 사용하므로 R의 일반 저장 기능을 사용할 수 없다. 대신에, `saveCohortMethodData()` 함수를 사용하도록 한다.

```
saveCohortMethodData(cmData, "AceiVsThzForAngioedema")
```

`loadCohortMethodData()` 함수를 사용하여 향후 세션에서 데이터를 로드할 수 있다.

Defining New Users

일반적으로 **새로운 사용자 (new user)**는 약물(대상 또는 비교)의 최초 사용으로 정의되며, 최초 사용을 보장하는 확률을 높이기 위해 최초 사용 이전의 최소 기간을 뜻하는 휴식기 (washout period)를 사용할 수 있다. `CohortMethod` 패키지를 사용할 때 다음 세 가지 방법으로 새로운 사용자를 정의할 수 있다.

1. 코호트 정의 시 지정
2. `getDbCohortMethodData`함수를 사용하여 코호트를 로딩할 때, `firstExposureOnly`, `removeDuplicateSubjects`, `restrictToCommonPeriod`, `washoutPeriod` 전달인자 (argument)를 사용하여 지정
3. 연구 집단 (study population) 정의시 `createStudyPopulation` 함수를 이용하여 지정

첫번째 방법의 장점은 입력 코호트(input cohort)가 이미 `CohortMethod` 패키지 밖에서 완전히 정의되어 있고, 외부 코호트 특성화 도구(external cohort characterization tool)가 이 분석에 사용된 것과 동일한 코호트에서 사용될 수 있다는 것이다. 두번째, 세번째 방법의 장점은 CDM에서 DRUG_ERA 테이블을 직접 사용할 수 있는 등, 최초 사용자를 정의하는 데 생기는 문제를 줄여준다는 것이다. 최초 사용에 대한 데 이터만 가져올 것이기 때문에 두번째 방법이 세번째 방법보다 더 효율적이다. 세번째 방법이 덜 효율적이긴 하지만, 원래 코호트를 연구 대상 집단 (study population)과 비교할 수 있다.

12.8.3 연구 대상 집단 정의 (Defining the Study Population)

일반적으로, 노출 코호트와 outcome 코호트는 서로 독립적으로 정의된다. 효과 크기 추정치 (effect size estimate)를 생성하려면 노출 전에 결과가 있는 피험자는 제거하고 정의된 risk window에 발생하는 outcome 만을 고려하는 등의 방법을 추가해야 한다. 이를 위하여 `createStudyPopulation` 함수를 사용할 수 있다.

```
studyPop <- createStudyPopulation(cohortMethodData = cmData,
                                    outcomeId = 3,
                                    firstExposureOnly = FALSE,
                                    restrictToCommonPeriod = FALSE,
                                    washoutPeriod = 0,
                                    removeDuplicateSubjects = "remove all",
                                    removeSubjectsWithPriorOutcome = TRUE,
                                    minDaysAtRisk = 1,
                                    riskWindowStart = 1,
                                    startAnchor = "cohort start",
                                    riskWindowEnd = 0,
                                    endAnchor = "cohort end")
```

코호트 정의에 이미 이러한 기준들을 적용했기 때문에 `firstExposureOnly`와 `removeDuplicateSubjects`를 FALSE로, `washoutPeriod`를 0으로 설정하였다. 사용할 outcome ID를 지정하고, risk window 시작일 전에 outcome이 발생한 사람들은 제거할 것이다. Risk window는 코호트 시작일 다음날부터 시작하는 것으로 정의하고(`riskWindowStart = 1` 및 `startAnchor = "cohort start"`), risk window는 코호트 노출이 끝날 때 종료되도록 설정했다(`riskWindowEnd = 0` and `endAnchor = "cohort end"`). 이것은 코호트 정의에서 치료 노출 종료로써 정의되었었다. Risk window는 관찰 종료 또는 연구 종료일에 자동적으로 결단됨에 유의하자. 또한 risk window가 0일인 피험자도 제거했다. 연구 대상자에 남아 있는 사람의 수를 보려면, `getAttritionTable` 함수를 사용하면 된다.

```
getAttritionTable(studyPop)
```

	description	targetPersons	comparatorPersons	...
## 1	Original cohorts	67212	35379	...
## 2	Removed subs in both cohorts	67166	35333	...
## 3	No prior outcome	67061	35238	...
## 4	Have at least 1 days at risk	66780	35086	...

12.8.4 성향 점수 (Propensity Scores)

`getDbcohortMethodData()` 함수로 생성된 공변량을 사용하여 성향 점수 모델을 적합할 수 있으며, 각 피험자별 성향 점수를 계산할 수 있다.

```
ps <- createPs(cohortMethodData = cmData, population = studyPop)
```

`createPs` 함수는 대규모 정규화 로지스틱 회귀분석(large-scale regularized logistic regression)을 적합화하기 위해 Cyclops 패키지를 사용한다. 성향 점수 모델을 적합화하기 위해, Cyclops는 prior의 분산을 지정하는 하이퍼파라미터(hyperparameter) 값을 알아야 한다. 디폴트로, Cyclops는 최적의 하이퍼파라미터를 추정하기 위해 교차 유효성 검사(cross-validation)을 사용할 것이다. 다만, 이 작업은 오랜 시간이 걸릴 수 있음을 알아 두어야 한다. `createPs` 함수의 `prior` 및 `control`의 매개변수(parameter)를 사용하여 병렬 처리를 사용하여 교차 유효성 검사 속도를 높이는 등 Cyclops의 동작을 지정할 수 있다.

예제에서는 성향점수 기반의 variable-ratio matching을 수행했다.

```
matchedPop <- matchOnPs(population = ps, caliper = 0.2,
                         caliperScale = "standardized logit", maxRatio = 100)
```

위와 같은 설정 대신에, `trimByPs`, `trimByPsToEquipoise` 또는 `stratifyByPs` 함수에서 성향 점수를 사용할 수도 있다.

12.8.5 Outcome Models

Outcome 모델은 `outcome`과 어떠한 변수들이 관련이 있는지 설명하는 모델이다. Under strict assumptions, the coefficient for the treatment variable can be interpreted as the causal effect. In this case we fit a Cox proportional hazards model, conditioned (stratified) on the matched sets:

Outcome 모델은 `outcome`과 어떠한 변수들이 관련이 있는지 설명하는 모델이다. 엄격한 가정하에서 치료변수의 계수는 인과 관계 효과(causal effect)로 해석될 수 있다. 이 경우, 짹짓기된 군에 대해 총화 조건화 콕스 비례 위험 모델(Cox proportional hazards model conditioned (stratified) on the matched set)에 적합하였다.

```
outcomeModel <- fitOutcomeModel(population = matchedPop,
                                    modelType = "cox",
                                    stratified = TRUE)
outcomeModel

## Model type: cox
## Stratified: TRUE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Status: OK
##
##           Estimate lower .95 upper .95    logRr seLogRr
## treatment   4.3203    2.4531    8.0771 1.4633    0.304
```

12.8.6 Running Multiple Analyses

음성 대조군을 포함하여 다수의 outcome에 대해 하나 이상의 분석을 수행하기 원할 수 있다. CohortMethod는 이러한 연구를 효율적으로 수행하는 기능을 제공한다. 이것은 다중 분석 실행에 대한 패키지 설명(package vignette on running multiple analyses)에 자세히 설명되어 있다. 간단히 말해서 먼저 필요한 코호트가 모두 생성되어 있다면, 분석하고자 하는 모든 대상-대조-outcome 조합을 지정할 수 있다.

```
# Outcomes of interest:
ois <- c(3, 4) # Angioedema, AMI

# Negative controls:
ncs <- c(434165, 436409, 199192, 4088290, 4092879, 44783954, 75911, 137951, 77965,
       376707, 4103640, 73241, 133655, 73560, 434327, 4213540, 140842, 81378,
       432303, 4201390, 46269889, 134438, 78619, 201606, 76786, 4115402,
       45757370, 433111, 433527, 4170770, 4092896, 259995, 40481632, 4166231,
       433577, 4231770, 440329, 4012570, 4012934, 441788, 4201717, 374375,
       4344500, 139099, 444132, 196168, 432593, 434203, 438329, 195873, 4083487,
       4103703, 4209423, 377572, 40480893, 136368, 140648, 438130, 4091513,
       4202045, 373478, 46286594, 439790, 81634, 380706, 141932, 36713918,
       443172, 81151, 72748, 378427, 437264, 194083, 140641, 440193, 4115367)

tcos <- createTargetComparatorOutcomes(targetId = 1,
                                         comparatorId = 2,
                                         outcomeIds = c(ois, ncs))

tcosList <- list(tcos)
```

다음으로, 하나의 outcome을 분석하는 이번 예제에서 전에 설명한 다양한 함수를 호출하기 위해 어떤 조절인자 (argument)를 사용해야 하는가를 지정한다.

```
aceI <- c(1335471, 1340128, 1341927, 1363749, 1308216, 1310756, 1373225,
          1331235, 1334456, 1342439)
thz <- c(1395058, 974166, 978555, 907013)

cs <- createDefaultCovariateSettings(excludedCovariateConceptIds = c(aceI,
                                                                      thz),
                                         addDescendantsToExclude = TRUE)

cmdArgs <- createGetDbCohortMethodDataArgs(
  studyStartDate = "",
  studyEndDate = "",
  firstExposureOnly = FALSE,
  removeDuplicateSubjects = FALSE,
  restrictToCommonPeriod = FALSE,
  washoutPeriod = 0,
  covariateSettings = cs)
```

```

spArgs <- createCreateStudyPopulationArgs(
  firstExposureOnly = FALSE,
  restrictToCommonPeriod = FALSE,
  washoutPeriod = 0,
  removeDuplicateSubjects = "remove all",
  removeSubjectsWithPriorOutcome = TRUE,
  minDaysAtRisk = 1,
  startAnchor = "cohort start",
  addExposureDaysToStart = FALSE,
  endAnchor = "cohort end",
  addExposureDaysToEnd = TRUE)

psArgs <- createCreatePsArgs()

matchArgs <- createMatchOnPsArgs(
  caliper = 0.2,
  caliperScale = "standardized logit",
  maxRatio = 100)

fomArgs <- createFitOutcomeModelArgs(
  modelType = "cox",
  stratified = TRUE)

```

그럼 다음 이들을 하나의 분석 설정 object로 결합하는데, 이것은 고유 분석 ID(unique analysis ID)와 몇 가지 설명을 제공한다. 하나 이상의 분석 설정 object를 하나의 list로 결합할 수 있다.

```

cmAnalysis <- createCmAnalysis(
  analysisId = 1,
  description = "Propensity score matching",
  getDbCohortMethodDataArgs = cmdArgs,
  createStudyPopArgs = spArgs,
  createPs = TRUE,
  createPsArgs = psArgs,
  matchOnPs = TRUE,
  matchOnPsArgs = matchArgs
  fitOutcomeModel = TRUE,
  fitOutcomeModelArgs = fomArgs)

cmAnalysisList <- list(cmAnalysis)

```

이제 모든 비교 및 분석 설정을 포함하여 연구를 실행할 수 있다.

```

result <- runCmAnalyses(connectionDetails = connectionDetails,
                        cdmDatabaseSchema = cdmDatabaseSchema,
                        exposureDatabaseSchema = cohortDbSchema,
                        exposureTable = cohortTable,

```

```
outcomeDatabaseSchema = cohortDbSchema,
outcomeTable = cohortTable,
cdmVersion = cdmVersion,
outputFolder = outputFolder,
cmAnalysisList = cmAnalysisList,
targetComparatorOutcomesList = tcosList)
```

result object에는 작성된 모든 artifact에 대한 참조가 들어 있다. 예를 들어, 급성 심근경색의 outcome 모델을 추출할 수 있다.

```
omFile <- result$outcomeModelFile[result$targetId == 1 &
                                    result$comparatorId == 2 &
                                    result$outcomeId == 4 &
                                    result$analysisId == 1]
outcomeModel <- readRDS(file.path(outputFolder, omFile))
outcomeModel

## Model type: cox
## Stratified: TRUE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Status: OK
##
##           Estimate lower .95 upper .95   logRr seLogRr
## treatment    1.1338    0.5921    2.1765 0.1256   0.332
```

We can also retrieve the effect size estimates for all outcomes with one command:

```
summ <- summarizeAnalyses(result, outputFolder = outputFolder)
head(summ)
```

	analysisId	targetId	comparatorId	outcomeId	rr	...
## 1	1	1	2	72748	0.9734698	...
## 2	1	1	2	73241	0.7067981	...
## 3	1	1	2	73560	1.0623951	...
## 4	1	1	2	75911	0.9952184	...
## 5	1	1	2	76786	1.0861746	...
## 6	1	1	2	77965	1.1439772	...

12.9 연구 결과 (Study Outputs)

결과로 나오는 추정치는 몇 가지 가정이 충족된 경우에만 유효하다. 유효성을 검증하기 위하여 다양한 진단 기준 (wide set of diagnostics)들을 사용할 것이다. 이것들은 ATLAS로 생성된 R 패키지를 이용한 결과에 자동적으로 포함되어 있으며, 특정 R

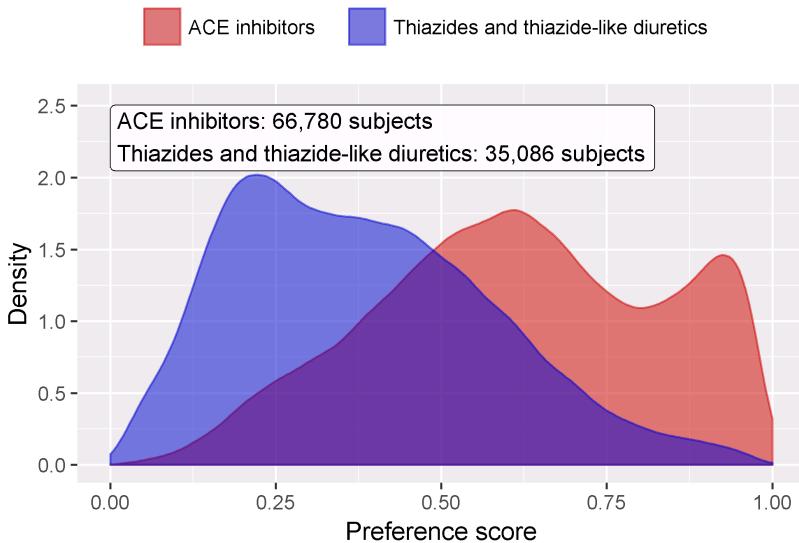


Figure 12.18: Preference score distribution.

함수를 활용하여 즉석에서 생성할 수도 있다.

12.9.1 성향 점수 및 모델 (Propensity Scores and Model)

성향 점수 기반의 짹짓기 이후 먼저 대상 코호트와 비교 코호트가 어느 정도 비슷한지를 평가할 필요가 있다. 이를 위해 성향 점수 모델에 대한 AUC(Area Under the Receiver Operator Curve) 통계값을 계산할 수 있다. AUC 1은 기저 공변량에 근거해 치료배정이 완전히 예측 가능하다는 것을 나타내므로, 두 군은 비교할 수 없다. `computePsAuc` 함수를 사용하여 AUC를 계산할 수 있는데, 우리의 예제에서는 0.79이다. `plotPs` 함수를 사용하여 그림 12.18과 같이 선호 점수 분포(preference score distribution)를 생성할 수도 있다. 많은 피험자들에 대해 그들이 받을 치료가 예측 가능했다는 것을 알 수지만 또한 많은 수의 중첩이 있다. 이는 조정을 통해 비교 가능한 군을 선택할 수 있음을 나타낸다.

일반적으로 성향 점수 모델 자체를 검사하는 것이 좋으며, 특히 모델이 매우 예측 적일 경우에는 그렇다. 그렇게 하면 어떤 변수가 가장 예측적인지를 알 수 있다. 표 12.7은 성향 모델에서 상위 예측 변수를 보여준다. 변수가 너무 예측적일 경우, `CohortMethod` 패키지는 이미 완벽하게 예측된 모델을 적합하려고 시도하기 보단 정보학적 에러를 발생시킬 것이다.

Table 12.7: Top 10 predictors in the propensity model for ACEi and THZ. Positive values mean subjects with the covariate are more likely to receive the target treatment. “(Intercept)” indicates the intercept of this logistic regression model.

Beta	Covariate
-1.42	condition_era group during day -30 through 0 days relative to index: Edema
-1.11	drug_era group during day 0 through 0 days relative to index: Potassium Chloride
0.68	age group: 05-09
0.64	measurement during day -365 through 0 days relative to index: Renin
0.63	condition_era group during day -30 through 0 days relative to index: Urticaria
0.57	condition_era group during day -30 through 0 days relative to index: Proteinuria
0.55	drug_era group during day -365 through 0 days relative to index: INSULINS AND ANALOGUES
-0.54	race = Black or African American
0.52	(Intercept)
0.50	gender = MALE

 만약 어떤 변수가 매우 예측적 ('highly predictive') 이라면, 두 가지 결론을 내릴 수 있다. 하나는 변수가 노출과 매우 밀접한 관계가 있기 때문에 모델 적합 전에 제외해야 한다든가, 또는 대상군과 대조군이 실제로 비교가 불가능하기 때문에 분석을 멈추어야 한다는 것이다.

12.9.2 Covariate Balance

성향점수를 사용하는 목적은 두 군을 비교 가능하게 만드는 (또는 적어도 비교할 수 있는 군을 선택하는) 것이다. 기저 공변량이 조정 후 실제로 균형 (balance)을 이루고 있는지 등을 확인하여 이 목적이 달성되었는지 입증해야 한다. `computeCovariateBalance` 및 `plotCovariateBalanceScatterPlot` 함수를 사용하여 그림12.19을 생성할 수 있다. 한 가지 주요한 원칙은 성향 점수 조정 후 공변량이 0.1보다 큰 표준 차이 값 (absolute standardized difference of means) 을 가져서는 안 된다는 것이다. 여기서는 성향점수 짹짓기 이전에 상당한 불균형이 있었음에도 불구하고, matching 이후에는 이 기준을 충족한다는 것을 알 수 있다.

12.9.3 Follow Up and Power

Outcome 모델을 적합하기 전에, 특정 효과 크기를 감지할 수 있는 충분한 통계력 (power)이 있는지 여부를 파악해보고 싶을 수 있다. 연구 대상 집단이 완전히 정의되면, 다양한 포함/제외 기준(예: 이전 outcome 없음)과 매칭 및/또는 트리밍으로

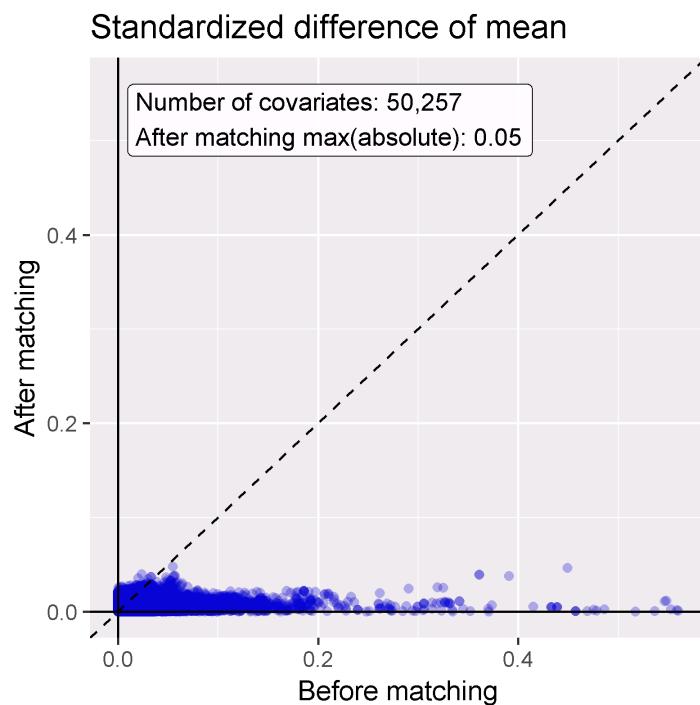


Figure 12.19: Covariate balance, showing the absolute standardized difference of mean before and after propensity score matching. Each dot represents a covariate.

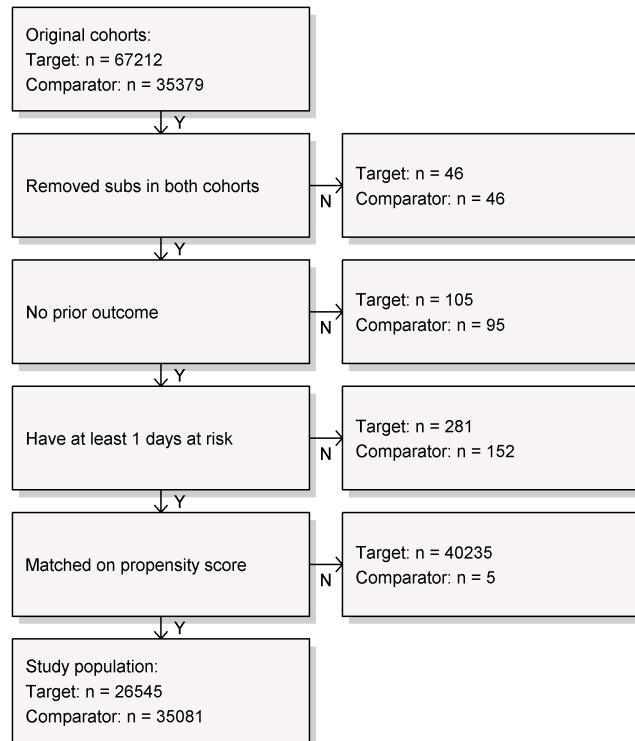


Figure 12.20: Attrition diagram. The counts shown at the top are those that meet our target and comparator cohort definitions. The counts at the bottom are those that enter our outcome model, in this case a Cox regression.

인한 손실을 고려하여 이러한 통계적 계산을 수행하는 것이 좋다. 그림12.20 과 같이 `drawAttritionDiagram` 함수를 사용하여 연구에서 피험자의 소모를 볼 수 있다.

후향적 연구에서 표본 크기가 고정되어 있고(데이터가 이미 수집된 상태이므로), 실제 효과 크기를 알 수 없으므로, 예상 효과 크기에 대한 통계력(power)를 계산하는 것은 의미가 없다. 대신 CohortMethod 패키지는 `computeMdrr` 함수를 제공하여 MDRR(minimum detectable relative risk)을 계산한다. 이 사례에서 MDRR은 1.69이다.

추적기간 (follow-up) 데이터를 더 잘 이해하기 위해서는 추적기간의 분포도 검사할 수 있다. 추적기간을 time at risk로 정의했으므로 outcome 발생으로 인해서는 중도절단되지 않는다. `getFollowUpDistribution` 그림 12.21 과 같은 간단한 개괄을 제공한다. 이는 두 코호트의 follow-up time이 비슷하다는 것을 의미한다.

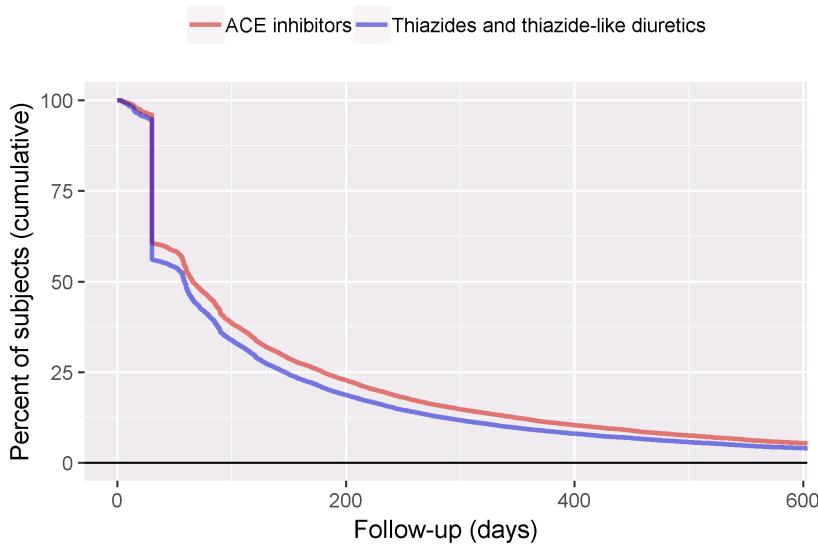


Figure 12.21: Distribution of follow-up time for the target and comparator cohorts.

12.9.4 Kaplan-Meier

마지막으로 한 가지 검사는 두 코호트에서 시간 경과에 따른 생존율을 보여주는 Kaplan-Meier plot을 검토하는 것이다. `plotKaplanMeier` 함수를 사용하여 그림 12.22 을 만들 수 있는데, 여기서 예를 들면 위험 비례 가정이 성립하는지 확인할 수 있다. Kaplan-Meier plot은 성향점수별로 충화 또는 가중치를 자동으로 조정한다. 이 경우, variable-ratio matching을 사용했으므로, 대조군의 생존 곡선이 조정되어 대상군이 대조 약물에 노출되었을 경우 대상 군의 생존 곡선이 어떤 모습인지 모방하여 그려진다.

12.9.5 Effect Size Estimate

혈관 부종에 대한 위험비는 4.32(95% 신뢰 구간: 2.45 - 8.08)이며, 이는 ACEi가 THZ 와 비교하여 혈관 부종의 위험을 증가시키는 것을 의미한다. 마찬가지로, 심근경색에 대한 위험비는 1.13(95% 신뢰 구간: 0.59 - 2.18)이며, 심근경색에 대한 영향은 거의 또는 전혀 없음을 알 수 있다. 앞에서 검토한 것처럼, 우리의 진단(diagnostics)을 통해 본 연구를 검증해보면 이견의 여지가 없다. 그러나 궁극적으로 이러한 근거의 질과 신뢰 여부는 장 14 에서 설명한대로 연구 진단이 커버하지 못하는 많은 요인들에 달려 있다.

12.10 Summary



- Population-level estimation는 관찰형 데이터의 인과 관계를 추론하는 것을 목적으로 한다.

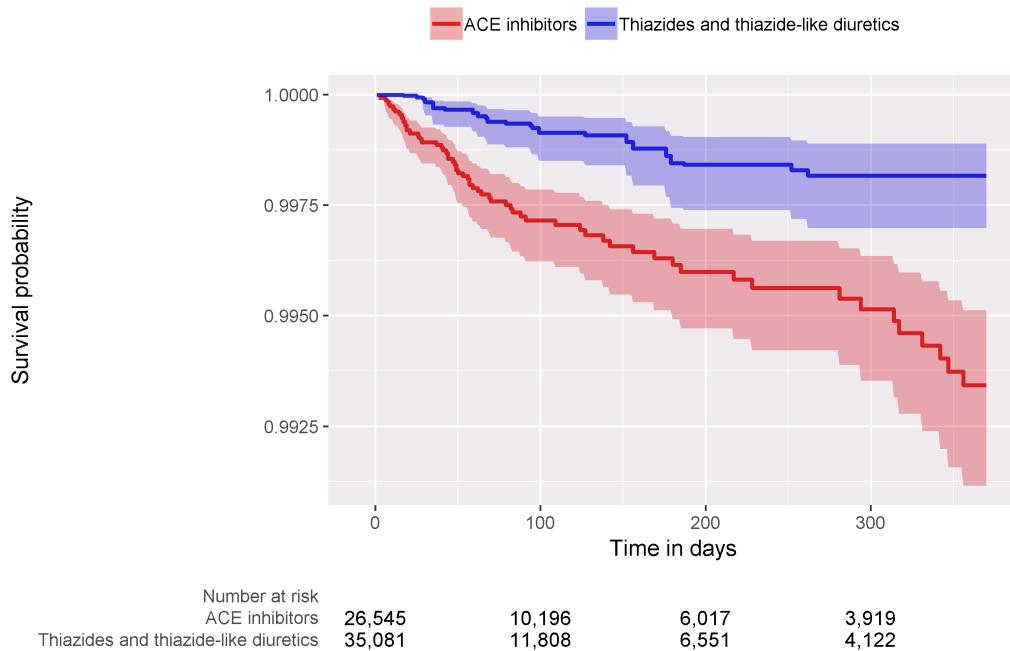


Figure 12.22: Kaplan-Meier plot.

- 상대집합(counterfactual), 즉 피험자가 대체제에 노출되었거나 치료제에 노출되지 않은 경우 일어난 일은 관찰할 수 없다.
- 다른 연구 설계는 다른 방식으로 상대집합(counterfactual)을 구성하는 것을 목적으로 한다.
- OHDSI Methods Library에서 구현되는 다양한 연구설계는 적절한 상대집합(counterfactual)을 작성하기 위한 가정이 충족되었는지 여부를 평가하는 진단(diagnostic)을 제공한다.

12.11 Exercises

Prerequisites

이 연습문제를 위해서는 R, R-studio, Java가 절 8.4.5에서 설명한 바와 같이 설치되어 있어야 한다. 또한 다음과 같이 SqlRender, DatabaseConnector, Eunomia, CohortMethod 패키지를 모두 설치해야 된다.

```
install.packages(c("SqlRender", "DatabaseConnector", "devtools"))
devtools::install_github("ohdsi/Eunomia", ref = "v1.0.0")
devtools::install_github("ohdsi/CohortMethod")
```

Eunomia 패키지는 당신의 로컬 R 세션에서 작동할 수 있도록 CDM 형태의 가상 데이터를 제공한다. 데이터베이스 접속은 다음과 같이 설정하면 된다.

```
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
```

CDM 데이터 스키마는 “main”이다. 이 연습문제는 또한 몇 가지 코호트를 이용한다. Eunomia 패키지의 `createCohorts` 함수를 이용하여 COHORT 테이블에 코호트들을 생성할 수 있다.

```
Eunomia::createCohorts(connectionDetails)
```

Problem Definition

What is the risk of gastrointestinal (GI) bleed in new users of celecoxib compared to new users of diclofenac?

The celecoxib new-user cohort has COHORT_DEFINITION_ID = 1. The diclofenac new-user cohort has COHORT_DEFINITION_ID = 2. The GI bleed cohort has COHORT_DEFINITION_ID = 3. The ingredient concept IDs for celecoxib and diclofenac are 1118084 and 1124300, respectively. Time-at-risk starts on day of treatment initiation, and stops at the end of observation (a so-called intent-to-treat analysis).

Exercise 12.1. Using the CohortMethod R package, use the default set of covariates and extract the CohortMethodData from the CDM. Create the summary of the CohortMethodData.

Exercise 12.2. Create a study population using the `createStudyPopulation` function, requiring a 180-day washout period, excluding people who had a prior outcome, and removing people that appear in both cohorts. Did we lose people?

Exercise 12.3. Fit a Cox proportional hazards model without using any adjustments. What could go wrong if you do this?

Exercise 12.4. Fit a propensity model. Are the two groups comparable?

Exercise 12.5. Perform PS stratification using 5 strata. Is covariate balance achieved?

Exercise 12.6. Fit a Cox proportional hazards model using the PS strata. Why is the result different from the unadjusted model?

Suggested answers can be found in Appendix E.8.

Chapter 13

Patient-Level Prediction

Chapter leads: Peter Rijnbeek & Jenna Reps

Clinical decision making is a complicated task in which the clinician has to infer a diagnosis or treatment pathway based on the available medical history of the patient and the current clinical guidelines. Clinical prediction models have been developed to support this decision-making process and are used in clinical practice in a wide spectrum of specialties. These models predict a diagnostic or prognostic outcome based on a combination of patient characteristics, e.g. demographic information, disease history, and treatment history.

The number of publications describing clinical prediction models has increased strongly over the last 10 years. Most currently-used models are estimated using small datasets and consider only a small set of patient characteristics. This low sample size, and thus low statistical power, forces the data analyst to make strong modelling assumptions. The selection of the limited set of patient characteristics is strongly guided by the expert knowledge at hand. This contrasts sharply with the reality of modern medicine wherein patients generate a rich digital trail, which is well beyond the power of any medical practitioner to fully assimilate. Presently, health care is generating a huge amount of patient-specific information stored in Electronic Health Records (EHRs). This includes structured data in the form of diagnosis, medication, laboratory test results, and unstructured data contained in clinical narratives. It is unknown how much predictive accuracy can be gained by leveraging the large amount of data originating from the complete EHR of a patient.

Advances in machine learning for large dataset analysis have led to increased interest in applying patient-level prediction on this type of data. However, many published efforts in patient-level prediction do not follow the model development guidelines, fail to perform extensive external validation, or provide insufficient model details which limits the ability of independent researchers to reproduce the models and perform external validation. This makes it hard to fairly evaluate the

predictive performance of the models and reduces the likelihood of the model being used appropriately in clinical practice. To improve standards, several papers have been written detailing guidelines for best practices in developing and reporting prediction models. For example, the Transparent Reporting of a multivariable prediction model for Individual Prognosis Or Diagnosis (TRIPOD) statement¹ provides clear recommendations for reporting prediction model development and validation and addresses some of the concerns related to transparency.

Massive-scale, patient-specific predictive modeling has become reality due to OHDSI, where the common data model (CDM) allows for uniform and transparent analysis at an unprecedented scale. The growing network of databases standardized to the CDM enables external validation of models in different healthcare settings on a global scale. We believe this provides immediate opportunity to serve large communities of patients who are in most need of improved quality of care. Such models can inform truly personalized medical care, leading hopefully to sharply improved patient outcomes.

In this chapter we describe OHDSI's standardized framework for patient-level prediction, (Reps et al., 2018) and discuss the PatientLevelPrediction R package that implements established best practices for development and validation. We start with providing the necessary theory behind the development and evaluation of patient-level prediction and provide a high-level overview of the implemented machine learning algorithms. We then discuss an example prediction problem and provide step-by-step guidance on its definition and implementation using ATLAS or custom R code. Finally, we discuss the use of Shiny applications for the dissemination of study results.

13.1 The Prediction Problem

Figure 13.1 illustrates the prediction problem we address. Among a population at risk, we aim to predict which patients at a defined moment in time ($t = 0$) will experience some outcome during a time-at-risk. Prediction is done using only information about the patients in an observation window prior to that moment in time.

As shown in Table 13.1, to define a prediction problem we have to define $t=0$ by a target cohort, the outcome we like to predict by an outcome cohort, and the time-at-risk. We define the standard prediction question as:

Among *[target cohort definition]*, who will go on to have *[outcome cohort definition]* within *[time-at-risk period]*?

Furthermore, we have to make design choices for the model we like to develop, and determine the observational datasets to perform internal and external validation.

¹<https://www.equator-network.org/reporting-guidelines/tripod-statement/>

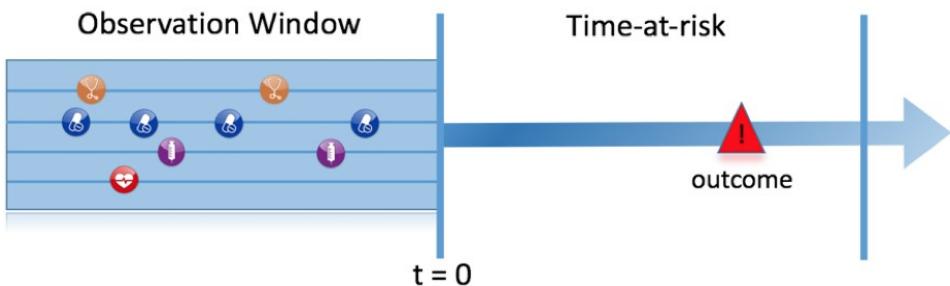


Figure 13.1: The prediction problem.

Table 13.1: Main design choices in a prediction design.

Choice	Description
Target cohort	How do we define the cohort of persons for whom we wish to predict?
Outcome cohort	How do we define the outcome we want to predict?
Time-at-risk	In which time window relative to $t=0$ do we want to make the prediction?
Model	What algorithms do we want to use, and which potential predictor variables do we include?

This conceptual framework works for all types of prediction problems, for example:

- Disease onset and progression
- **Structure:** Among patients who are newly diagnosed with *[a disease]*, who will go on to have *[another disease or complication]* within *[time horizon from diagnosis]*?
- **Example:** Among newly diagnosed atrial fibrillation patients, who will go on to have ischemic stroke in the next three years?
- Treatment choice
- **Structure:** Among patients with *[indicated disease]* who are treated with either *[treatment 1]* or *[treatment 2]*, which patients were treated with *[treatment 1]*?
- **Example:** Among patients with atrial fibrillation who took either warfarin or rivaroxaban, which patients get warfarin? (e.g. for a propensity model)
- Treatment response
- **Structure:** Among new users of *[a treatment]*, who will experience *[some effect]* in *[time window]* ?
- **Example:** Which patients with diabetes who start on metformin stay on metformin for three years?
- Treatment safety

- **Structure:** Among new users of [*a treatment*], who will experience [*adverse event*] in [*time window*]?
- **Example:** Among new users of warfarin, who will have a gastrointestinal bleed in one year?
- Treatment adherence
- **Structure:** Among new users of [*a treatment*], who will achieve [*adherence metric*] at [*time window*]?
- **Example:** Which patients with diabetes who start on metformin achieve >=80% proportion of days covered at one year?

13.2 Data Extraction

When creating a predictive model we use a process known as supervised learning — a form of machine learning — that infers the relationship between the covariates and the outcome status based on a labelled set of examples. Therefore, we need methods to extract the covariates from the CDM for the persons in the target cohort and we need to obtain their outcome labels.

The **covariates** (also referred to as “predictors”, “features” or “independent variables”) describe the characteristics of the patients. Covariates can include age, gender, presence of specific conditions and exposure codes in a patient’s record, etc. Covariates are typically constructed using the FeatureExtraction package, described in more detail in Chapter 11. For prediction we can only use data prior to (and on) the date the person enters the target cohort. This date we will call the index date.

We also need to obtain the **outcome status** (also referred to as the “labels” or “classes”) of all the patients during the time-at-risk. If the outcome occurs within the time-at-risk, the outcome status is defined as “positive.”

13.2.1 Data Extraction Example

Table 13.2 shows an example COHORT table with two cohorts. The cohort with cohort definition ID 1 is the target cohort (e.g. “people recently diagnosed with atrial fibrillation”). Cohort definition ID 2 defines the outcome cohort (e.g. “stroke”).

Table 13.2: Example COHORT table. For simplicity the COHORT_END_DATE has been omitted.

COHORT_DEFINITION_ID	SUBJECT_ID	COHORT_START_DATE
1	1	2000-06-01
1	2	2001-06-01
2	2	2001-07-01

Table 13.3 provides an example CONDITION_OCCURRENCE table. Concept ID 320128 refers to “Essential hypertension.”

Table 13.3: Example CONDITION_OCCURRENCE table.
For simplicity only three columns are shown.

PERSON_ID	CONDITION_CONCEPT_ID	CONDITION_START_DATE
1	320128	2000-10-01
2	320128	2001-05-01

Based on this example data, and assuming the time at risk is the year following the index date (the target cohort start date), we can construct the covariates and the outcome status. A covariate indicating “Essential hypertension in the year prior” will have the value 0 (not present) for person ID 1 (the condition occurred *after* the index date), and the value 1 (present) for person ID 2. Similarly, the outcome status will be 0 for person ID 1 (this person had no entry in the outcome cohort), and 1 for person ID 2 (the outcome occurred within a year following the index date).

13.2.2 Missingness

Observational healthcare data rarely reflects whether data is missing. In the prior example, we simply observed the person with ID 1 had no essential hypertension occurrence prior to the index date. This could be because the condition was not present at that time, or because it was not recorded. It is important to realize that the machine learning algorithm cannot distinguish between the two scenarios and will simply assess the predictive value in the available data.

13.3 Fitting the Model

When fitting a prediction model we are trying to learn the relationship between the covariates and the observed outcome status from labelled examples. Suppose we only have two covariates, systolic and diastolic blood pressure, then we can represent each patient as a point in two dimensional space as shown in Figure 13.2. In this figure the shape of the data point corresponds to the patient’s outcome status (e.g. stroke).

A supervised learning model will try to find a decision boundary that optimally separates the two outcome classes. Different supervised learning techniques lead to different decision boundaries and there are often hyper-parameters that can impact the complexity of the decision boundary.

In Figure 13.2 we can see three different decision boundaries. The boundaries are used to infer the outcome status of any new data point. If a new data point falls

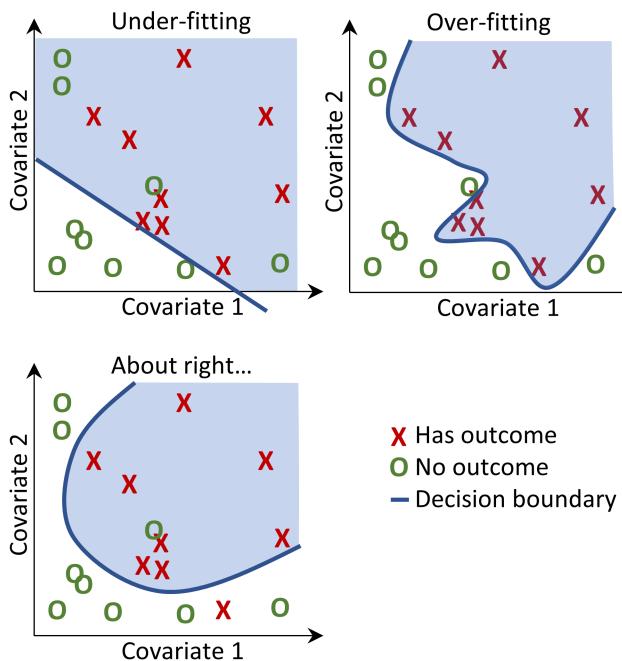


Figure 13.2: Decision boundary.

into the shaded area then the model will predict “has outcome”, otherwise it will predict “no outcome”. Ideally a decision boundary should perfectly partition the two classes. However, there is a risk that too complex models “overfit” to the data. This can negatively impact the generalizability of the model to unseen data. For example, if the data contains noise, with mislabeled or incorrectly positioned data points, we would not want to fit our model to that noise. We therefore may prefer to define a decision boundary that does not perfectly discriminate in our training data but captures the “real” complexity. Techniques such as regularization aim to maximize model performance while minimizing complexity.

Each supervised learning algorithm has a different way to learn the decision boundary and it is not straightforward which algorithm will work best on your data. As the No Free Lunch theorem states not one algorithm is always going to outperform the others on all prediction problems. Therefore, we recommend trying multiple supervised learning algorithms with various hyper-parameter settings when developing patient-level prediction models.

The following algorithms are available in the `PatientLevelPrediction` package:

13.3.1 Regularized Logistic Regression

LASSO (least absolute shrinkage and selection operator) logistic regression belongs to the family of generalized linear models, where a linear combination of the variables is learned and finally a logistic function maps the linear combination

to a value between 0 and 1. The LASSO regularization adds a cost based on model complexity to the objective function when training the model. This cost is the sum of the absolute values of the linear combination of the coefficients. The model automatically performs feature selection by minimizing this cost. We use the Cyclops (Cyclic coordinate descent for logistic, Poisson and survival analysis) package to perform large-scale regularized logistic regression.

Table 13.4: Hyper-parameters for the regularized logistic regression.

Parameter	Description	Typical values
Starting variance	The starting variance of the prior distribution.	0.1

Note that the variance is optimized by maximizing the out-of-sample likelihood in a cross-validation, so the starting variance has little impact on the performance of the resulting model. However, picking a starting variance that is too far from the optimal value may lead to long fitting time.

13.3.2 Gradient Boosting Machines

Gradient boosting machines is a boosting ensemble technique and in our framework it combines multiple decision trees. Boosting works by iteratively adding decision trees but adds more weight to the data-points that are misclassified by prior decision trees in the cost function when training the next tree. We use Extreme Gradient Boosting, which is an efficient implementation of the gradient boosting framework implemented in the xgboost R package available from CRAN.

Table 13.5: Hyper-parameters for gradient boosting machines.

Parameter	Description	Typical values
earlyStopRound	Stopping after rounds without improvement	25
learningRate	The boosting learn rate	0.005,0.01,0.1
maxDepth	Max levels in a tree	4,6,17
minRows	Min data points in a node	2
ntrees	Number of trees	100,1000

13.3.3 Random Forest

Random forest is a bagging ensemble technique that combines multiple decision trees. The idea behind bagging is to reduce the likelihood of overfitting by using weak classifiers and combining them into a strong classifier. Random forest accomplishes this by training multiple decision trees but only using a subset of the variables in each tree and the subset of variables differ between trees. Our package uses the sklearn implementation of Random Forest in Python.

Table 13.6: Hyper-parameters for random forests.

Parameter	Description	Typical values
maxDepth	Max levels in a tree	4,10,17
mtries	Number of features in each tree	-1 = square root of total features,5,20
ntrees	Number of trees	500

13.3.4 K-Nearest Neighbors

K-nearest neighbors (KNN) is an algorithm that uses some distance metric to find the K closest labelled data-points to a new unlabeled data-point. The prediction of the new data-points is then the most prevalent class of the K-nearest labelled data-points. There is a sharing limitation of KNN, as the model requires labelled data to perform the prediction on new data, and it is often not possible to share this data across data sites. We included the BigKnn package developed in OHDSI which is a large scale KNN classifier.

Table 13.7: Hyper-parameters for K-nearest neighbors.

Parameter	Description	Typical values
k	Number of neighbors	1000

13.3.5 Naive Bayes

The Naive Bayes algorithm applies the Bayes theorem with the naive assumption of conditional independence between every pair of features given the value of the class variable. Based on the likelihood the data belongs to a class and the prior distribution of the class, a posterior distribution is obtained. Naive Bayes has no hyper-parameters.

13.3.6 AdaBoost

AdaBoost is a boosting ensemble technique. Boosting works by iteratively adding classifiers but adds more weight to the data-points that are misclassified by prior classifiers in the cost function when training the next classifier. We use the sklearn AdaboostClassifier implementation in Python.

Table 13.8: Hyper-parameters for AdaBoost.

Parameter	Description	Typical values
nEstimators	The maximum number of estimators at which boosting is terminated	4
learningRate	Learning rate shrinks the contribution of each classifier by learning_rate. There is a trade-off between learningRate and nEstimators	1

13.3.7 Decision Tree

A decision tree is a classifier that partitions the variable space using individual tests selected using a greedy approach. It aims to find partitions that have the highest information gain to separate the classes. The decision tree can easily overfit by enabling a large number of partitions (tree depth) and often needs some regularization (e.g., pruning or specifying hyper-parameters that limit the complexity of the model). We use the sklearn DecisionTreeClassifier implementation in Python.

Table: Hyper-parameters for decision trees.

Parameter	Description	Typical values
classWeight	“Balance” or “None”	None
maxDepth	The maximum depth of the tree	10
minImpuritySplit	Threshold for early stopping in tree growth. A node will split if its impurity is above the threshold, otherwise it is a leaf	10^{-7}
minSamplesLeaf	The minimum number of samples per leaf	10
minSamplesSplit	The minimum samples per split	2

13.3.8 Multilayer Perceptron

Multilayer perceptrons are neural networks that contain multiple layers of nodes that weight their inputs using a non-linear function. The first layer is the input layer, the last layer is the output layer, and in between are the hidden layers. Neural networks are generally trained using back-propagation, meaning the training input is propagated forward through the network to produce an output, the error between the output and the outcome status is computed, and this error is propagated backwards through the network to update the linear function weights.

Table 13.9: Hyper-parameters for Multilayer Perceptrons.

Parameter	Description	Typical values
alpha	The l2 regularization	0.00001
size	The number of hidden nodes	4

13.3.9 Deep Learning

Deep learning such as deep nets, convolutional neural networks or recurrent neural networks are similar to Multilayer Perceptrons but have multiple hidden layers that aim to learn latent representations useful for prediction. In a separate vignette in the PatientLevelPrediction package we describe these models and hyper-parameters in more detail.

13.3.10 Other Algorithms

Other algorithms can be added to the patient-level prediction framework. This is out-of-scope for this chapter. Details can be found in the “Adding Custom Patient-Level Prediction Algorithms” vignette in the PatientLevelPrediction package.

13.4 Evaluating Prediction Models

13.4.1 Evaluation Types

We can evaluate a prediction model by measuring the agreement between the model’s prediction and observed outcome status, which means we need data where the outcome status is known.



For evaluation we must use a different dataset than was used to develop the model, or else we run the risk of favoring models that are over-fitted (see Section 13.3) and may not perform well for new patients.

We distinguish between

- **Internal validation:** Using different sets of data extracted from the same database to develop and evaluate the model.
- **External validation:** Developing the model in one database, and evaluating in another database.

There are two ways to perform internal validation:

- A **holdout set** approach splits the labelled data into two independent sets: a train set and a test set (the hold out set). The train set is used to learn the model and the test set is used to evaluate it. We can simply divide our patients randomly into a train and test set, or we may choose to:
 - Split the data based on time (temporal validation), for example training on data before a specific date, and evaluating on data after that date. This may inform us on whether our model generalizes to different time periods.
 - Split the data based on geographic location (spatial validation).
- **Cross validation** is useful when the data are limited. The data is split into n equally-sized sets, where n needs to be prespecified (e.g. $n = 10$). For each of these sets a model is trained on all data except the data in that set and used to generate predictions for the hold-out set. In this way, all data is used once to evaluate the model-building algorithm. In the patient-level prediction framework we use cross validation to pick the optimal hyper-parameters.

External validation aims to assess model performance on data from another database, i.e. outside of the settings it was developed in. This measure of model transportability is important because we want to apply our models not only on the database it was trained on. Different databases may represent different patient populations, different healthcare systems and different data-capture processes. We believe that the external validation of prediction models on a large set of databases is a crucial step in model acceptance and implementation in clinical practice.

13.4.2 Performance Metrics

Threshold Measures

A prediction model assigns a value between 0 and 1 for each patient corresponding to the risk of the patient having the outcome during the time at risk. A value of 0 means 0% risk, a value of 0.5 means 50% risk and a value of 1 means 100% risk. Common metrics such as accuracy, sensitivity, specificity, positive predictive value can be calculated by first specifying a threshold that is used to classify patients as having the outcome or not during the time at risk. For example, given Table 13.10, if we set the threshold as 0.5, patients 1, 3, 7 and 10 have a predicted risk greater than or equal to the threshold of 0.5 so they would be predicted to have the outcome. All other patients had a predicted risk less than 0.5, so they would be predicted to not have the outcome.

Table 13.10: Example of using a threshold on the predicted probability.

Patient ID	Predicted risk	Predicted class at 0.5 threshold	Has outcome during time-at-risk	Type
1	0.8	1	1	TP
2	0.1	0	0	TN
3	0.7	1	0	FP
4	0	0	0	TN
5	0.05	0	0	TN
6	0.1	0	0	TN
7	0.9	1	1	TP
8	0.2	0	1	FN
9	0.3	0	0	TN
10	0.5	1	0	FP

If a patient is predicted to have the outcome and has the outcome (during the time-at-risk) then this is called a true positive (TP). If a patient is predicted to have the outcome but does not have the outcome then this is called a false positive (FP). If a patient is predicted to not have the outcome and does not have the outcome then this is called a true negative (TN). Finally, if a patient is predicted to not have the outcome but does have the outcome then this is called a false negative (FN).

The following threshold-based metrics can be calculated:

- accuracy: $(TP + TN)/(TP + TN + FP + FN)$
- sensitivity: $TP/(TP + FN)$
- specificity: $TN/(TN + FP)$
- positive predictive value: $TP/(TP + FP)$

Note that these values can either decrease or increase if the threshold is lowered. Lowering the threshold of a classifier may increase the denominator by increasing the number of results returned. If the threshold was previously set too high, the new results may all be true positives, which will increase positive predictive value. If the previous threshold was about right or too low, further lowering the threshold will introduce false positives, decreasing positive predictive value. For sensitivity the denominator does not depend on the classifier threshold ($TP + FN$ is a constant). This means that lowering the classifier threshold may increase sensitivity by increasing the number of true positive results. It is also possible that lowering the threshold may leave sensitivity unchanged, while the positive predictive value fluctuates.

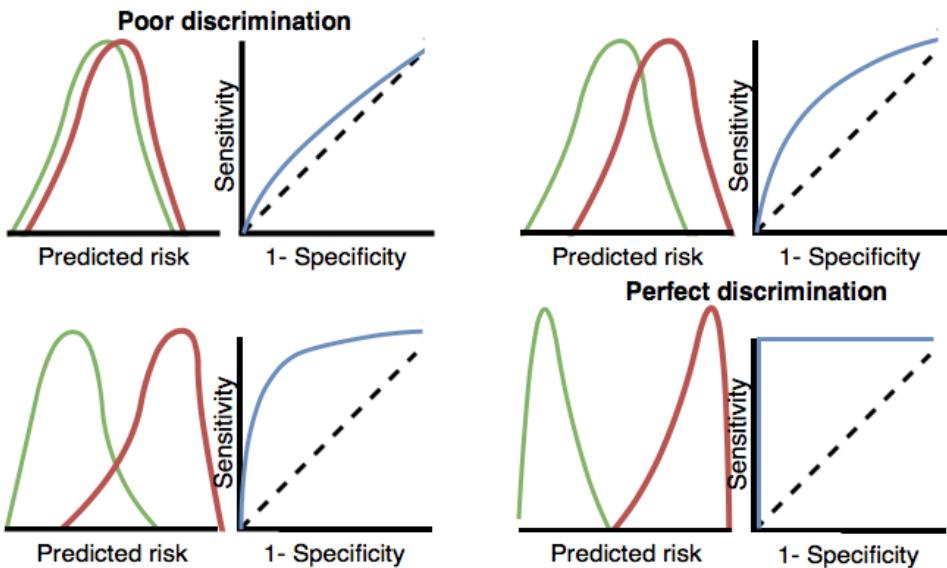


Figure 13.3: How the ROC plots are linked to discrimination. If the two classes have similar distributions of predicted risk, the ROC will be close to the diagonal, with AUC close to 0.5.

Discrimination

Discrimination is the ability to assign a higher risk to patients who will experience the outcome during the time at risk. The Receiver Operating Characteristics (ROC) curve is created by plotting $1 - \text{specificity}$ on the x-axis and sensitivity on the y-axis at all possible thresholds. An example ROC plot is presented later in this chapter in Figure 13.17. The area under the receiver operating characteristic curve (AUC) gives an overall measure of discrimination where a value of 0.5 corresponds to randomly assigning the risk and a value of 1 means perfect discrimination. Most published prediction models obtain AUCs between 0.6-0.8.

The AUC provides a way to determine how different the predicted risk distributions are between the patients who experience the outcome during the time at risk and those who do not. If the AUC is high, then the distributions will be mostly disjointed, whereas when there is a lot of overlap, the AUC will be closer to 0.5, as shown in Figure 13.3.

For rare outcomes even a model with a high AUC may not be practical, because for every positive above a given threshold there could also be many negatives (i.e. the positive predictive value will be low). Depending on the severity of the outcome and cost (health risk and/or monetary) of some intervention, a high false positive rate may be unwanted. When the outcome is rare another measure known as the area under the precision-recall curve (AUPRC) is therefore recommended.

The AUPRC is the area under the line generated by plotting the sensitivity on the x-axis (also known as the recall) and the positive predictive value (also known as the precision) on the y-axis.

Calibration

Calibration is the ability of the model to assign the correct risk. For example, if the model assigned one hundred patients a risk of 10% then ten of the patients should experience the outcome during the time at risk. If the model assigned 100 patients a risk of 80% then eighty of the patients should experience the outcome during the time at risk. The calibration is generally calculated by partitioning the patients into deciles based on the predicted risk and in each group calculating the mean predicted risk and the fraction of the patients who experienced the outcome during the time at risk. We then plot these ten points (predicted risk on the y-axis and observed risk on the x-axis) and see whether they fall on the $x = y$ line, indicating the model is well calibrated. An example calibration plot is presented later in this chapter in Figure 13.18. We also fit a linear model using the points to calculate the intercept (which should be close to zero) and the gradient (which should be close to one). If the gradient is greater than one then the model is assigning a higher risk than the true risk and if the gradient is less than one the model is assigning a lower risk than the true risk. Note that we also implemented Smooth Calibration Curves in our R-package to better capture the non-linear relationship between predicted and observed risk.

13.5 Designing a Patient-Level Prediction Study

In this section we will demonstrate how to design a prediction study. The first step is to clearly define the prediction problem. Interestingly, in many published papers the prediction problem is poorly defined, for example it is unclear how the index date (start of the target cohort) is defined. A poorly defined prediction problem does not allow for external validation by others, let alone implementation in clinical practice. In the patient-level prediction framework we enforce proper specification of the prediction problem by requiring the key choices defined in Table 13.1 to be explicitly defined. Here we will walk through this process using a “treatment safety” type prediction problem as an example.

13.5.1 Problem Definition

Angioedema is a well-known side-effect of ACE inhibitors, and the incidence of angioedema reported in the labeling for ACE inhibitors is in the range of 0.1% to 0.7%. (Byrd et al., 2006) Monitoring patients for this adverse effect is important, because although angioedema is rare, it may be life-threatening, leading to respiratory arrest and death. (Norman et al., 2013) Further, if angioedema is not initially recognized, it may lead to extensive and expensive workups before it is identified as a cause. (Norman et al., 2013; Thompson and Frable, 1993)

Other than the higher risk among African-American patients, there are no known predisposing factors for the development of ACE inhibitor related angioedema. (Byrd et al., 2006) Most reactions occur within the first week or month of initial therapy and often within hours of the initial dose. (Cicardi et al., 2004) However, some cases may occur years after therapy has begun. (O'Mara and O'Mara, 1996) No diagnostic test is available that specifically identifies those at risk. If we could identify those at risk, doctors could act, for example by discontinuing the ACE inhibitor in favor of another hypertension drug.

We will apply the patient-level prediction framework to observational healthcare data to address the following patient-level prediction question:

Among patients who have just started on an ACE inhibitor for the first time, who will experience angioedema in the following year?

13.5.2 Study Population Definition

The final study population in which we will develop our model is often a subset of the target cohort, because we may for example apply criteria that are dependent on the outcome, or we want to perform sensitivity analyses with sub-populations of the target cohort. For this we have to answer the following questions:

- *What is the minimum amount of observation time we require before the start of the target cohort?* This choice could depend on the available patient time in the training data, but also on the time we expect to be available in the data sources we want to apply the model on in the future. The longer the minimum observation time, the more baseline history time is available for each person to use for feature extraction, but the fewer patients will qualify for analysis. Moreover, there could be clinical reasons to choose a short or longer look-back period. For our example, we will use a 365-day prior history as look-back period (washout period).
- *Can patients enter the target cohort multiple times?* In the target cohort definition, a person may qualify for the cohort multiple times during different spans of time, for example if they had different episodes of a disease or separate periods of exposure to a medical product. The cohort definition does not necessarily apply a restriction to only let the patients enter once, but in the context of a particular patient-level prediction problem we may want to restrict the cohort to the first qualifying episode. In our example, a person can only enter the target cohort once since our criteria was based on first use of an ACE inhibitor.
- *Do we allow persons to enter the cohort if they experienced the outcome before?* Do we allow persons to enter the target cohort if they experienced the outcome before qualifying for the target cohort? Depending on the particular patient-level prediction problem, there may be a desire to predict incident first occurrence of an outcome, in which case patients who have previously

experienced the outcome are not at risk for having a first occurrence and therefore should be excluded from the target cohort. In other circumstances, there may be a desire to predict prevalent episodes, whereby patients with prior outcomes can be included in the analysis and the prior outcome itself can be a predictor of future outcomes. For our prediction example, we will choose not to include those with prior angioedema.

- *How do we define the period in which we will predict our outcome relative to the target cohort start?* We have to make two decisions to answer this question. First, does the time-at-risk window start at the date of the start of the target cohort or later? Arguments to make it start later could be that we want to avoid outcomes that were entered late in the record that actually occurred before the start of the target cohort or we want to leave a gap where interventions to prevent the outcome could theoretically be implemented. Second, we need to define the time-at-risk by setting the risk window end, as some specification of days offset relative to the target cohort start or end dates. For our problem we will predict in a time-at-risk window starting 1 day after the start of the target cohort up to 365 days later.
- *Do we require a minimum amount of time-at-risk?* We have to decide if we want to include patients that did not experience the outcome but did leave the database earlier than the end of our time-at-risk period. These patients may experience the outcome when we no longer observe them. For our prediction problem we decide to answer this question with “yes,” requiring a minimum time-at-risk for that reason. Furthermore, we have to decide if this constraint also applies to persons who experienced the outcome or we will include all persons with the outcome irrespective of their total time at risk. For example, if the outcome is death, then persons with the outcome are likely censored before the full time-at-risk period is complete.

13.5.3 Model Development Settings

To develop the prediction model we have to decide which algorithm(s) we like to train. We see the selection of the best algorithm for a certain prediction problem as an empirical question, i.e. we prefer to let the data speak for itself and try different approaches to find the best one. In our framework we have therefore implemented many algorithms as described in Section 13.3, and allow others to be added. In this example, to keep things simple, we select just one algorithm: Gradient Boosting Machines.

Furthermore, we have to decide on the covariates that we will use to train our model. In our example, we like to add gender, age, all conditions, drugs and drug groups, and visit counts. We will look for these clinical events in the year before and any time prior to the index date.

13.5.4 Model Evaluation

Finally, we have to define how we will evaluate our model. For simplicity, we here choose internal validation. We have to decide how we divide our dataset in a training and test dataset and how we assign patients to these two sets. Here we will use a typical 75% - 25% split. Note that for very large datasets we could use more data for training.

13.5.5 Study Summary

We have now completely defined our study as shown in Table 13.11.

Table 13.11: Main design choices for our study.

Choice	Value
Target cohort	Patients who have just started on an ACE inhibitor for the first time. Patients are excluded if they have less than 365 days of prior observation time or have prior angioedema.
Outcome cohort	Angioedema.
Time-at-risk	1 day until 365 days from cohort start. We will require at least 364 days at risk.
Model	Gradient Boosting Machine with hyper-parameters ntree: 5000, max depth: 4 or 7 or 10 and learning rate: 0.001 or 0.01 or 0.1 or 0.9. Covariates will include gender, age, conditions, drugs, drug groups, and visit count. Data split: 75% train - 25% test, randomly assigned by person.

13.6 Implementing the Study in ATLAS

The interface for designing a prediction study can be opened by clicking on the  **Prediction** button in the left hand side ATLAS menu. Create a new prediction study. Make sure to give the study an easy-to-recognize name. The study design can be saved at any time by clicking the  button.

In the Prediction design function, there are four sections: Prediction Problem Settings, Analysis Settings, Execution Settings, and Training Settings. Here we discuss each section:

13.6.1 Prediction Problem Settings

Here we select the target population cohorts and outcome cohorts for the analysis. A prediction model will be developed for all combinations of the target population cohorts and the outcome cohorts. For example, if we specify two target populations and two outcomes, we have specified four prediction problems.

The screenshot shows the 'Prediction Problem Settings' dialog in ATLAS. It has two main sections: 'Target Cohorts' and 'Outcome Cohorts'.
Target Cohorts:
 - Shows 1 entry: "New users of ACE inhibitors as first-line monotherapy for hypertension".
 - Buttons: 'Remove' (with a red X icon), 'Name' (highlighted in blue), and '+ Add Target Cohort'.
 - Other controls: 'Show 10 entries', 'Filter' input field, 'Previous' (page 1), and 'Next' buttons.
Outcome Cohorts:
 - Shows 1 entry: "Angioedema outcome".
 - Buttons: 'Remove' (with a red X icon), 'Name' (highlighted in blue), and '+ Add Outcome Cohort'.
 - Other controls: 'Show 10 entries', 'Filter' input field, 'Previous' (page 1), and 'Next' buttons.

Figure 13.4: Prediction problem settings.

To select a target population cohort we need to have previously defined it in ATLAS. Instantiating cohorts is described in Chapter 10. The Appendix provides the full definitions of the target (Appendix B.1) and outcome (Appendix B.4) cohorts used in this example. To add a target population to the cohort, click on the “Add Target Cohort” button. Adding outcome cohorts similarly works by clicking the “Add Outcome Cohort” button. When done, the dialog should look like Figure 13.4.

13.6.2 Analysis Settings

The analysis settings enable selection of the supervised learning algorithm, the covariates and population settings.

Model Settings

We can pick one or more supervised learning algorithms for model development. To add a supervised learning algorithm click on the “Add Model Settings” button. A dropdown containing all the models currently supported in the ATLAS interface will appear. We can select the supervised learning model we want to include in the study by clicking on the name in the dropdown menu. This will then show a view for that specific model, allowing the selection of the hyper-parameter values. If multiple values are provided, a grid search is performed across all possible combinations of values to select the optimal combination using cross-validation.

For our example we select gradient boosting machines, and set the hyper-parameters as specified in Figure 13.5.

Gradient Boosting Machine Model Settings
Use the options below to edit the model settings

The boosting learn rate (default = 0.01,0.1):

Boosting learn rate	Action
0.001	Remove
0.01	Remove
0.1	Remove
0.9	Remove

Add **Reset to default**

Maximum number of interactions - a large value will lead to slow model training (default = 4,6,17):

Maximum number of interactions	Action
4	Remove
7	Remove
10	Remove

Add **Reset to default**

The minimum number of rows required at each end node of the tree (default = 20):

Minimum number of rows	Action
20	Remove

Add **Using default**

The number of trees to build (default = 10,100):

Trees to build	Action
5000	Remove

Add **Reset to default**

The number of computer threads to use (how many cores do you have?) (default = 20):

20	Using default
----	---------------

Figure 13.5: Gradient boosting machine settings

What concepts do you want to include in baseline covariates in the propensity score model? (Leave blank if you want to include everything)

Should descendant concepts be added to the list of included concepts?

No ▾

What concepts do you want to exclude in baseline covariates in the propensity score model? (Leave blank if you want to include everything)

Should descendant concepts be added to the list of included concepts?

No ▾

A comma delimited list of covariate IDs that should be restricted to:

Figure 13.6: Covariate inclusion and exclusion settings.

Covariate Settings

We have defined a set of standard covariates that can be extracted from the observational data in the CDM format. In the covariate settings view, it is possible to select which of the standard covariates to include. We can define different types of covariate settings, and each model will be created separately with each specified covariate setting.

To add a covariate setting into the study, click on the “Add Covariate Settings”. This will open the covariate setting view.

The first part of the covariate settings view is the exclude/include option. Covariates are generally constructed for any concept. However, we may want to include or exclude specific concepts, for example if a concept is linked to the target cohort definition. To only include certain concepts, create a concept set in ATLAS and then under the **“What concepts do you want to include in baseline covariates in the patient-level prediction model? (Leave blank if you want to include everything)”** select the concept set by clicking on . We can automatically add all descendant concepts to the concepts in the concept set by answering “yes” to the question **“Should descendant concepts be added to the list of included concepts?”** The same process can be repeated for the question **“What concepts do you want to exclude in baseline covariates in the patient-level prediction model? (Leave blank if you want to include everything)”**, allowing covariates corresponding to the selected concepts to be removed. The final option **“A comma delimited list of covariate IDs that should be restricted to”** enables us to add a set of covariate IDs (rather than concept IDs) comma separated that will only be included in the model. This option is for advanced users only. Once done, the inclusion and exclusion settings should look like Figure 13.6.

The next section enables the selection of non-time bound variables.

- Gender: a binary variable indicating male or female gender

Select Covariates

	Gender	Age	Age Groups	Race	Ethnicity	Index Year	Index Month	Prior Observation Time	Post Observation Time	Time In Cohort	Index Year & Month
Demographics	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Figure 13.7: Select covariates.

- Age: a continuous variable corresponding to age in years
- Age group: binary variables for every 5 years of age (0-4, 5-9, 10-14, ..., 95+)
- Race: a binary variable for each race, 1 means the patient has that race recorded, 0 otherwise
- Ethnicity: a binary variable for each ethnicity, 1 means the patient has that ethnicity recorded, 0 otherwise
- Index year: a binary variable for each cohort start date year, 1 means that was the patients cohort start date year, 0 otherwise. **It often does not make sense to include index year, since we would like to apply our model to the future.**
- Index month - a binary variable for each cohort start date month, 1 means that was the patient's cohort start date month, 0 otherwise
- Prior observation time: [Not recommended for prediction] a continuous variable corresponding to how long in days the patient was in the database prior to the cohort start date
- Post observation time: [Not recommended for prediction] a continuous variable corresponding to how long in days the patient was in the database post cohort start date
- Time in cohort: a continuous variable corresponding to how long in days the patient was in the cohort (cohort end date minus cohort start date)
- Index year and month: [Not recommended for prediction] a binary variable for each cohort start date year and month combination, 1 means that was the patients cohort start date year and month, 0 otherwise

Once done, this section should look like Figure 13.7.

The standard covariates enable three flexible time intervals for the covariates:

- end days: when to end the time intervals relative to the cohort start date [default is 0]
- long term [default -365 days to end days prior to cohort start date]
- medium term [default -180 days to end days prior to cohort start date]
- short term [default -30 days to end days prior to cohort start date]

Once done, this section should look like Figure 13.8.

The next option is the covariates extracted from the era tables:

Time bound covariates

Set the time windows for the time bound covariates in days relative to the cohort index

	Any Time Prior	Long Term	Medium Term	Short Term	End Days
Time Windows	All Time	-365	-180	-30	0

Figure 13.8: Time bound covariates.

Set the time bound era covariates

Domain	Any Time Prior				Overlapping	Era Start		
		Long Term (-365 days)	Medium Term (-180 days)	Short Term (-30 days)		Long Term (-365 days)	Medium Term (-180 days)	Short Term (-30 days)
Condition	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Condition Group	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Drug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Drug Group	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Figure 13.9: Time bound era covariates.

- Condition: Construct covariates for each condition concept ID and time interval selected and if a patient has the concept ID with an era (i.e., the condition starts or ends during the time interval or starts before and ends after the time interval) during the specified time interval prior to the cohort start date in the condition era table, the covariate value is 1, otherwise 0.
- Condition group: Construct covariates for each condition concept ID and time interval selected and if a patient has the concept ID **or any descendant concept ID** with an era during the specified time interval prior to the cohort start date in the condition era table, the covariate value is 1, otherwise 0.
- Drug: Construct covariates for each drug concept ID and time interval selected and if a patient has the concept ID with an era during the specified time interval prior to the cohort start date in the drug era table, the covariate value is 1, otherwise 0.
- Drug group: Construct covariates for each drug concept ID and time interval selected and if a patient has the concept ID **or any descendant concept ID** with an era during the specified time interval prior to the cohort start date in the drug era table, the covariate value is 1, otherwise 0.

Overlapping time interval setting means that the drug or condition era should start prior to the cohort start date and end after the cohort start date, so it overlaps with the cohort start date. The **era start** option restricts to finding condition or drug eras that start during the time interval selected.

Once done, this section should look like Figure 13.9.

The next option selects covariates corresponding to concept IDs in each domain for the various time intervals:

- Condition: Construct covariates for each condition concept ID and time interval selected and if a patient has the concept ID recorded during the specified time interval prior to the cohort start date in the condition occurrence table, the covariate value is 1, otherwise 0.
- Condition Primary Inpatient: One binary covariate per condition observed as a primary diagnosis in an inpatient setting in the condition_occurrence table.
- Drug: Construct covariates for each drug concept ID and time interval selected and if a patient has the concept ID recorded during the specified time interval prior to the cohort start date in the drug exposure table, the covariate value is 1, otherwise 0.
- Procedure: Construct covariates for each procedure concept ID and time interval selected and if a patient has the concept ID recorded during the specified time interval prior to the cohort start date in the procedure occurrence table, the covariate value is 1, otherwise 0.
- Measurement: Construct covariates for each measurement concept ID and time interval selected and if a patient has the concept ID recorded during the specified time interval prior to the cohort start date in the measurement table, the covariate value is 1, otherwise 0.
- Measurement Value: Construct covariates for each measurement concept ID with a value and time interval selected and if a patient has the concept ID recorded during the specified time interval prior to the cohort start date in the measurement table, the covariate value is the measurement value, otherwise 0.
- Measurement range group: Binary covariates indicating whether measurements are below, within, or above normal range.
- Observation: Construct covariates for each observation concept ID and time interval selected and if a patient has the concept ID recorded during the specified time interval prior to the cohort start date in the observation table, the covariate value is 1, otherwise 0.
- Device: Construct covariates for each device concept ID and time interval selected and if a patient has the concept ID recorded during the specified time interval prior to the cohort start date in the device table, the covariate value is 1, otherwise 0.
- Visit Count: Construct covariates for each visit and time interval selected and count the number of visits recorded during the time interval as the covariate value.
- Visit Concept Count: Construct covariates for each visit, domain and time interval selected and count the number of records per domain recorded during the visit type and time interval as the covariate value.

The distinct count option counts the number of distinct concept IDs per domain and time interval.

Once done, this section should look like Figure 13.10.

Set the time bound covariates

Domain	Any Time Prior	Long Term (-365 days)	Medium Term (-180 days)	Short Term (-30 days)	Distinct Count		
					Long Term (-365 days)	Medium Term (-180 days)	Short Term (-30 days)
Condition	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Condition - Primary Inpatient	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>			
Drug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Procedure	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Measurement	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Measurement - Value	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>			
Measurement - Range Group	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>			
Observation	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Device	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>			
Visit - Count		<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>			
Visit - Concept Count		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>			

Figure 13.10: Time bound covariates.

Set the index score covariates

Index Score Type	
CHADS ₂	<input type="checkbox"/>
CHA ₂ DS ₂ VASc	<input checked="" type="checkbox"/>
DCSI	<input checked="" type="checkbox"/>
Charlson	<input checked="" type="checkbox"/>

Figure 13.11: Risk score covariate settings.

The final option is whether to include commonly used risk scores as covariates. Once done, the risk score settings should look like Figure 13.11.

Population Settings

The population settings is where addition inclusion criteria can be applied to the target population and is also where the time-at-risk is defined. To add a population setting into the study, click on the “Add Population Settings” button. This will open up the population setting view.

The first set of options enable the user to specify the time-at-risk period. This is the time interval where we look to see whether the outcome of interest occurs. If a patient has the outcome during the time-at-risk period then we will classify them as “Has outcome”, otherwise they are classified as “No outcome”. “**Define the time-at-risk window start, relative to target cohort entry:**” defines the start of the time-at-risk, relative to the target cohort start or end date. Similarly, “**Define the time-at-risk window end:**” defines the end of the time-at-risk.

“**Minimum lookback period applied to target cohort**” specifies the minimum baseline period, the minimum number of days prior to the cohort start date that a

patient is continuously observed. The default is 365 days. Expanding the minimum look-back will give a more complete picture of a patient (as they must have been observed for longer) but will filter patients who do not have the minimum number of days prior observation.

If “**Should subjects without time at risk be removed?**” is set to yes, then a value for “**Minimum time at risk:**” is also required. This allows removing people who are lost to follow-up (i.e. that have left the database during the time-at-risk period). For example, if the time-at-risk period was 1 day from cohort start until 365 days from cohort start, then the full time-at-risk interval is 364 days (365-1). If we only want to include patients who are observed the whole interval, then we set the minimum time at risk to be 364. If we are happy as long as people are in the time-at-risk for the first 100 days, then we select minimum time at risk to be 100. In this case as the time-at-risk start is 1 day from the cohort start, a patient will be included if they remain in the database for at least 101 days from the cohort start date. If we set “Should subjects without time at risk be removed?” to ‘No’, then this will keep all patients, even those who drop out from the database during the time-at-risk.

The option “**Include people with outcomes who are not observed for the whole at risk period?**” is related to the previous option. If set to “yes”, then people who experience the outcome during the time-at-risk are always kept, even if they are not observed for the specified minimum amount of time.

The option “**Should only the first exposure per subject be included?**” is only useful if our target cohort contains patients multiple times with different cohort start dates. In this situation, picking “yes” will result in only keeping the earliest target cohort date per patient in the analysis. Otherwise a patient can be in the dataset multiple times.

Setting “**Remove patients who have observed the outcome prior to cohort entry?**” to “yes” will remove patients who have the outcome prior to the time-at-risk start date, so the model is for patients who have never experienced the outcome before. If “no” is selected, then patients could have had the outcome prior. Often, having the outcome prior is very predictive of having the outcome during the time-at-risk.

Once done, the population settings dialog should look like Figure 13.12.

Now that we are finished with the Analysis Settings, the entire dialog should look like Figure 13.13.

13.6.3 Execution Settings

There are three options:

- “**Perform sampling**”: here we choose whether to perform sampling (default = “no”). If set to “yes”, another option will appear: “**How many patients**

Define the time-at-risk window start, relative to target cohort entry:
 days from

Define the time-at-risk window end:
 days from

Minimum lookback period applied to target cohort:

Should subjects without time at risk be removed?
 Yes Minimum time at risk: days

Include people with outcomes who are not observed for the whole at risk period?
 Yes

Should only the first exposure per subject be included?
 Yes

Remove patients who have observed the outcome prior to cohort entry?
 No

Figure 13.12: Population settings.

to use for a subset?”, where the sample size can be specified. Sampling can be an efficient means to determine if a model for a large population (e.g. 10 million patients) will be predictive by creating and testing the model with a sample of patients. For example, if the AUC is close to 0.5 in the sample, we might abandon the model.

- “**Minimum covariate occurrence: If a covariate occurs in a fraction of the target population less than this value, it will be removed:**”: here we choose the minimum covariate occurrence (default = 0.001). A minimum threshold value for covariate occurrence is necessary to remove rare events that are not representative of the overall population.
- “**Normalize covariate**”: here we choose whether to normalize covariates (default = “yes”). Normalization of the covariates is usually necessary for successful implementation of a LASSO model.

For our example we make the choices shown in Figure 13.14.

13.6.4 Training Settings

There are four options:

- “**Specify how to split the test/train set:**” Select whether to differentiate the train/test data by person (stratified by outcome) or by time (older data to train the model, later data to evaluate the model).
- “**Percentage of the data to be used as the test set (0-100%)**”: Select the percentage of data to be used as test data (default = 25%).
- “**The number of folds used in the cross validation**”: Select the number of folds for cross-validation used to select the optimal hyper-parameter

Analysis Settings

Model Settings

Show 10 entries Filter:

Remove	Model	Options
	GradientBoostingMachineSettings	{"nrtrees":5000,"nthread":20,"maxDepth":4,7,10,"minRows":20,"learnRate": [0.001,0.01,0.1,0.9],"seed":null}

Showing 1 to 1 of 1 entries Previous Next

Covariate Settings

Show 10 entries Filter:

Remove	Options
	DemographicsGender, DemographicsAgeGroup, DemographicsRace, DemographicsEthnicity, DemographicsIndexMonth, ConditionGroupEraLongTerm (+12 more covariate settings)

Showing 1 to 1 of 1 entries Previous Next

Population Settings

Show 10 entries Filter:

Remove	Risk Window Start	Risk Window End	Washout Period	Include All Outcomes	Remove Subjects With Prior Outcome	Minimum Time At Risk
	1d from cohort start date	365d from cohort start date	365d	true	false	364d

Showing 1 to 1 of 1 entries Previous Next

Figure 13.13: Analysis settings.

Execution Settings

Perform sampling:

Yes

How many patients to use for a subset? patients

Minimum covariate occurrence: If a covariate occurs in a fraction of the target population less than this value, it will be removed:

Normalize covariates:

Yes

Figure 13.14: Execution settings.

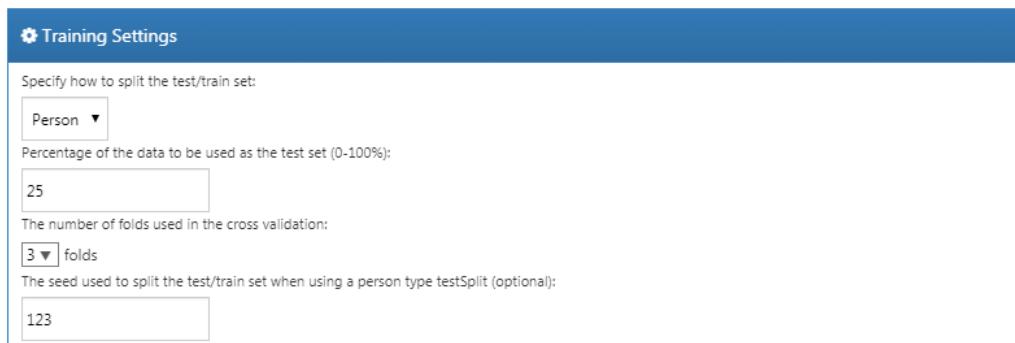


Figure 13.15: Training settings.

(default = 3).

- “**The seed used to split the test/train set when using a person type testSplit (optional):**”: Select the random seed used to split the train/test set when using a person type test split.

For our example we make the choices shown in Figure 13.15.

13.6.5 Importing and Exporting a Study

To export a study, click on the “Export” tab under “Utilities.” ATLAS will produce JSON that can be directly copied and pasted into a file that contains all of the data, such as the study name, cohort definitions, models selected, covariates, settings, needed to run the study.

To import a study, click on the “Import” tab under “Utilities.” Paste the contents of a patient-level prediction study JSON into this window, then click on the Import button below the other tab buttons. Note that this will overwrite all previous settings for that study, so this is typically done using a new, empty study design.

13.6.6 Downloading the Study Package

Click on the “Review & Download” tab under “Utilities.” In the “Download Study Package” section, enter a descriptive name for the R package, noting that any illegal characters in R will automatically be removed from the file name by ATLAS.

Click on **Download** to download the R package to a local folder.

13.6.7 Running the Study

To run the R package requires having R, RStudio, and Java installed as described in Section 8.4.5. Also required is the PatientLevelPrediction package, which can be installed in R using:

```
install.packages("drat")
drat::addRepo("OHDSI")
install.packages("PatientLevelPrediction")
```

Some of the machine learning algorithms require additional software to be installed. For a full description of how to install the PatientLevelPrediction package, see the “Patient-Level Prediction Installation Guide” vignette.

To use the study R package we recommend using R Studio. If you are running R Studio locally, unzip the file generated by ATLAS, and double click the .Rproj file to open it in R Studio. If you are running R Studio on an R studio server, click  **Upload** to upload and unzip the file, then click on the .Rproj file to open the project.

Once you have opened the project in R Studio, you can open the README file, and follow the instructions. Make sure to change all file paths to existing paths on your system.

13.7 Implementing the Study in R

An alternative to implementing our study design using ATLAS is to write the study code ourselves in R. We can make use of the functions provided in the PatientLevelPrediction package. The package enables data extraction, model building, and model evaluation using data from databases that are translated into the OMOP CDM.

13.7.1 Cohort Instantiation

We first need to instantiate the target and outcome cohorts. Instantiating cohorts is described in Chapter 10. The Appendix provides the full definitions of the target (Appendix B.1) and outcome (Appendix B.4) cohorts. In this example we will assume the ACE inhibitors cohort has ID 1, and the angioedema cohort has ID 2.

13.7.2 Data Extraction

We first need to tell R how to connect to the server. `PatientLevelPrediction` uses the `DatabaseConnector` package, which provides a function called `createConnectionDetails`. Type `?createConnectionDetails` for the specific settings required for the various database management systems (DBMS). For example, one might connect to a PostgreSQL database using this code:

```

        user = "joe",
        password = "supersecret")

cdmDbSchema <- "my_cdm_data"
cohortsDbSchema <- "scratch"
cohortsDbTable <- "my_cohorts"
cdmVersion <- "5"

```

The last four lines define the `cdmDbSchema`, `cohortsDbSchema`, and `cohortsDbTable` variables, as well as the CDM version. We will use these later to tell R where the data in CDM format live, where the cohorts of interest have been created, and what version CDM is used. Note that for Microsoft SQL Server, database schemas need to specify both the database and the schema, so for example `cdmDbSchema <- "my_cdm_data.dbo"`.

First it makes sense to verify that the cohort creation has succeeded by counting the number of cohort entries:

```

sql <- paste("SELECT cohort_definition_id, COUNT(*) AS count",
  "FROM @cohortsDbSchema.cohortsDbTable",
  "GROUP BY cohort_definition_id")
conn <- connect(connDetails)
renderTranslateQuerySql(connection = conn,
  sql = sql,
  cohortsDbSchema = cohortsDbSchema,
  cohortsDbTable = cohortsDbTable)

##   cohort_definition_id  count
## 1                      1 527616
## 2                      2    3201

```

Now we can tell `PatientLevelPrediction` to extract all necessary data for our analysis. Covariates are extracted using the `FeatureExtraction` package. For more detailed information on the `FeatureExtraction` package see its vignettes. For our example study we decided to use these settings:

```

covariateSettings <- createCovariateSettings(
useDemographicsGender = TRUE,
  useDemographicsAge = TRUE,
  useConditionGroupEraLongTerm = TRUE,
  useConditionGroupEraAnyTimePrior = TRUE,
  useDrugGroupEraLongTerm = TRUE,
  useDrugGroupEraAnyTimePrior = TRUE,
  useVisitConceptCountLongTerm = TRUE,
  longTermStartDays = -365,
  endDays = -1)

```

The final step for extracting the data is to run the `getPlpData` function and input the connection details, the database schema where the cohorts are stored, the cohort definition IDs for the cohort and outcome, and the washout period which is the minimum number of days prior to cohort index date that the person must have been observed to be included into the data, and finally input the previously constructed covariate settings.

```
plpData <- getPlpData(connectionDetails = connDetails,
                      cdmDatabaseSchema = cdmDbSchema,
                      cohortDatabaseSchema = cohortsDbSchema,
                      cohortTable = cohortsDbSchema,
                      cohortId = 1,
                      covariateSettings = covariateSettings,
                      outcomeDatabaseSchema = cohortsDbSchema,
                      outcomeTable = cohortsDbSchema,
                      outcomeIds = 2,
                      sampleSize = 10000
)
```

There are many additional parameters for the `getPlpData` function which are all documented in the PatientLevelPrediction manual. The resulting `plpData` object uses the package `ff` to store information in a way that ensures R does not run out of memory, even when the data are large.

Creating the `plpData` object can take considerable computing time, and it is probably a good idea to save it for future sessions. Because `plpData` uses `ff`, we cannot use R's regular `save` function. Instead, we'll have to use the `savePlpData` function:

```
savePlpData(plpData, "angio_in_ace_data")
```

We can use the `loadPlpData()` function to load the data in a future session.

13.7.3 Additional Inclusion Criteria

The final study population is obtained by applying additional constraints on the two earlier defined cohorts, e.g., a minimum time at risk can be enforced (`requireTimeAtRisk`, `minTimeAtRisk`) and we can specify if this also applies to patients with the outcome (`includeAllOutcomes`). Here we also specify the start and end of the risk window relative to target cohort start. For example, if we like the risk window to start 30 days after the at-risk cohort start and end a year later we can set `riskWindowStart = 30` and `riskWindowEnd = 365`. In some cases the risk window needs to start at the cohort end date. This can be achieved by setting `addExposureToStart = TRUE` which adds the cohort (exposure) time to the start date.

In the example below all the settings we defined for our study are imposed:

```
population <- createStudyPopulation(plpData = plpData,
                                     outcomeId = 2,
                                     washoutPeriod = 364,
                                     firstExposureOnly = FALSE,
                                     removeSubjectsWithPriorOutcome = TRUE,
                                     priorOutcomeLookback = 9999,
                                     riskWindowStart = 1,
                                     riskWindowEnd = 365,
                                     addExposureDaysToStart = FALSE,
                                     addExposureDaysToEnd = FALSE,
                                     minTimeAtRisk = 364,
                                     requireTimeAtRisk = TRUE,
                                     includeAllOutcomes = TRUE,
                                     verbosity = "DEBUG"
)
```

13.7.4 Model Development

In the set function of an algorithm the user can specify a list of eligible values for each hyper-parameter. All possible combinations of the hyper-parameters are included in a so-called grid search using cross-validation on the training set. If a user does not specify any value then the default value is used instead.

For example, if we use the following settings for the gradient boosting machine: `ntrees = c(100, 200)`, `maxDepth = 4` the grid search will apply the gradient boosting machine algorithm with `ntrees = 100` and `maxDepth = 4` plus the default settings for other hyper-parameters and `ntrees = 200` and `maxDepth = 4` plus the default settings for other hyper-parameters. The hyper-parameters that lead to the best cross-validation performance will then be chosen for the final model. For our problem we choose to build a gradient boosting machine with several hyper-parameter values:

```
gbmModel <- setGradientBoostingMachine(ntrees = 5000,
                                         maxDepth = c(4, 7, 10),
                                         learnRate = c(0.001, 0.01, 0.1, 0.9))
```

The `runPlp` function uses the population, `plpData`, and model settings to train and evaluate the model. We can use the `testSplit` (person/time) and `testFraction` parameters to split the data in a 75%-25% split and run the patient-level prediction pipeline:

```
gbmResults <- runPlp(population = population,
                      plpData = plpData,
```

```
modelSettings = gbmModel,
testSplit = 'person',
testFraction = 0.25,
nfold = 2,
splitSeed = 1234)
```

Under the hood the package will now use the R xgboost package to fit a gradient boosting machine model using 75% of the data and will evaluate the model on the remaining 25%. A results data structure is returned containing information about the model, its performance, etc.

In the `runPlp` function there are several parameters to save the `plpData`, `plpResults`, `plpPlots`, `evaluation`, etc. objects which are all set to TRUE by default.

We can save the model using:

```
savePlpModel(gbmResults$model, dirPath = "model")
```

We can load the model using:

```
plpModel <- loadPlpModel("model")
```

You can also save the full results structure using:

```
savePlpResult(gbmResults, location = "gbmResults")
```

To load the full results structure use:

```
gbmResults <- loadPlpResult("gbmResults")
```

13.7.5 Internal Validation

Once we execute the study, the `runPlp` function returns the trained model and the evaluation of the model on the train/test sets. You can interactively view the results by running: `viewPlp(runPlp = gbmResults)`. This will open a Shiny App in which we can view all performance measures created by the framework, including interactive plots (see Figure 13.16 in the section on the Shiny Application).

To generate and save all the evaluation plots to a folder run the following code:

```
plotPlp(gbmResults, "plots")
```

The plots are described in more detail in Section 13.4.2.

13.7.6 External Validation

We recommend to always perform external validation, i.e. apply the final model on as much new datasets as feasible and evaluate its performance. Here we assume the data extraction has already been performed on a second database and stored in the `newData` folder. We load the model we previously fitted from the `model` folder:

```
# load the trained model
plpModel <- loadPlpModel("model")

#load the new plpData and create the population
plpData <- loadPlpData("newData")

population <- createStudyPopulation(plpData,
                                      outcomeId = 2,
                                      washoutPeriod = 364,
                                      firstExposureOnly = FALSE,
                                      removeSubjectsWithPriorOutcome = TRUE,
                                      priorOutcomeLookback = 9999,
                                      riskWindowStart = 1,
                                      riskWindowEnd = 365,
                                      addExposureDaysToStart = FALSE,
                                      addExposureDaysToEnd = FALSE,
                                      minTimeAtRisk = 364,
                                      requireTimeAtRisk = TRUE,
                                      includeAllOutcomes = TRUE
)

# apply the trained model on the new data
validationResults <- applyModel(population, plpData, plpModel)
```

To make things easier we also provide the `externalValidatePlp` function for performing external validation that also extracts the required data. Assuming we ran `result <- runPlp(...)` then we can extract the data required for the model and evaluate it on new data. Assuming the validation cohorts are in the table `mainschema.dob.cohort` with IDs 1 and 2 and the CDM data is in the schema `cdmschema.dob`:

```
valResult <- externalValidatePlp(
  plpResult = result,
  connectionDetails = connectionDetails,
  validationSchemaTarget = 'mainschema.dob',
  validationSchemaOutcome = 'mainschema.dob',
  validationSchemaCdm = 'cdmschema dbo',
  databaseNames = 'new database',
  validationTableTarget = 'cohort',
```

```

    validationTableOutcome = 'cohort',
    validationIdTarget = 1,
    validationIdOutcome = 2
)

```

If we have multiple databases to validate the model on then we can run:

```

valResults <- externalValidatePlp(
  plpResult = result,
  connectionDetails = connectionDetails,
  validationSchemaTarget = list('mainschema.dob',
                                'difschema.dob',
                                'anotherschema.dob'),
  validationSchemaOutcome = list('mainschema.dob',
                                 'difschema.dob',
                                 'anotherschema.dob'),
  validationSchemaCdm = list('cdms1schema dbo',
                            'cdm2schema dbo',
                            'cdm3schema dbo'),
  databaseNames = list('new database 1',
                       'new database 2',
                       'new database 3'),
  validationTableTarget = list('cohort1',
                               'cohort2',
                               'cohort3'),
  validationTableOutcome = list('cohort1',
                                'cohort2',
                                'cohort3'),
  validationIdTarget = list(1,3,5),
  validationIdOutcome = list(2,4,6)
)

```

13.8 Results Dissemination

13.8.1 Model Performance

Exploring the performance of a prediction model is easiest with the `viewPlp` function. This requires a results object as the input. If developing models in R we can use the result of `runPLp` as the input. If using the ATLAS-generated study package, then we need to load one of the models (in this example we will load `Analysis_1`):

```

plpResult <- loadPlpResult(file.path(outputFolder,
                                      'Analysis_1',
                                      'plpResult'))

```

The screenshot shows a Shiny application window titled "PatientLevelPrediction Explorer". The top navigation bar includes tabs for "Internal Validation" and "External Validation". Below the tabs, a horizontal menu bar contains "Evaluation Summary", "Characterization", "ROC", "Calibration", "Demographics", "Preference", "Box Plot", and "Settings". The "Evaluation Summary" tab is selected, highlighted with a blue border.

The main content area displays a table titled "Evaluation Summary" with 11 rows of data. The columns are "Metric", "test", and "train". The data is as follows:

Metric	test	train
1 AUC	0.72130	0.75348
2 AUC_lb95ci	0.70057	0.74215
3 AUC_ub95ci	0.74203	0.76482
4 AUPRC	0.10971	0.13571
5 BrierScaled	0.03755	0.04902
6 BrierScore	0.03355	0.03304
7 CalibrationIntercept Intercept	-0.00089	-0.00813
8 CalibrationSlope.Gradient	1.02041	1.22457
9 outcomeCount	601.00000	1802.00000
10 populationSize	16685.00000	50054.00000
11 Incidence	3.60204	3.60011

Below the table, a message says "Showing 1 to 11 of 11 entries". To the right, there are buttons for "Previous", "1", and "Next".

Figure 13.16: Summary evaluation statistics in the Shiny app.

Here “Analysis_1” corresponds to the analysis we specified earlier.

We can then launch the Shiny app by running:

```
viewPlp(plpResult)
```

The Shiny app opens with a summary of the performance metrics on the test and train sets (see Figure 13.16). The results show that the AUC on the train set was 0.78 and this dropped to 0.74 on the test set. The test set AUC is the more accurate measure. Overall, the model appears to be able to discriminate those who will develop the outcome in new users of ACE inhibitors but it slightly overfit as the performance on the train set is higher than the test set. The ROC plot is presented in Figure 13.17.

The calibration plot in Figure 13.18 shows that generally the observed risk matches the predicted risk as the dots are around the diagonal line. The demographic calibration plot in Figure 13.19 however shows that the model is not well calibrated for the younger patients, as the curved line (the predicted risk) differs from the red line (the observed risk) for those aged below 40. This may indicate we need

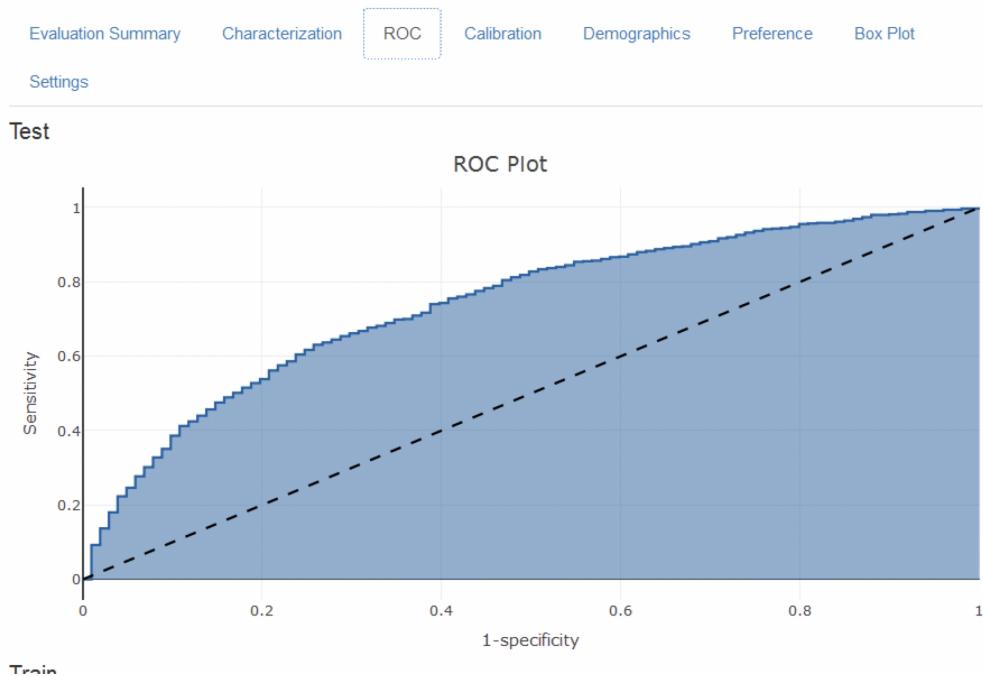


Figure 13.17: The ROC plot.

to remove the under 40s from the target population (as the observed risk for the younger patients is nearly zero).

Finally, the attrition plot shows the loss of patients from the labelled data based on inclusion/exclusion criteria (see Figure 13.20). The plot shows that we lost a large portion of the target population due to them not being observed for the whole time at risk (1 year follow up). Interestingly, not as many patients with the outcome lacked the complete time at risk.

13.8.2 Comparing Models

The study package as generated by ATLAS allows generating and evaluating many different prediction models for different prediction problems. Therefore, specifically for the output generated by the study package an additional Shiny app has been developed for viewing multiple models. To start this app, run `viewMultiplePlp(outputFolder)` where `outputFolder` is the path containing the analysis results as specified when running the `execute` command (and should for example contain a sub-folder named “Analysis_1”).

Viewing the Model Summary and Settings

The interactive Shiny app will start at the summary page as shown in Figure 13.21.

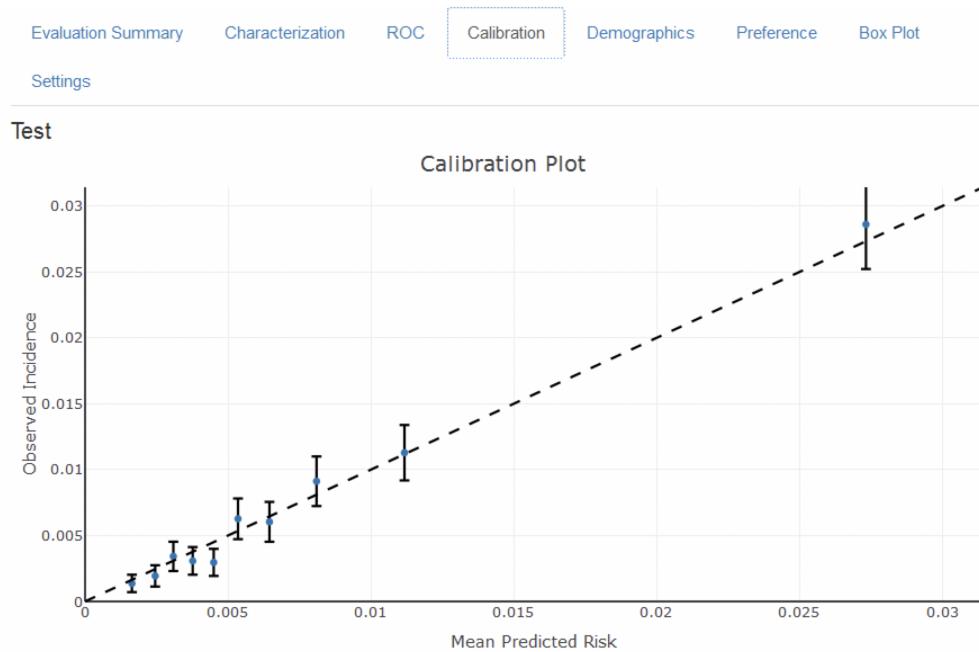


Figure 13.18: The calibration of the model

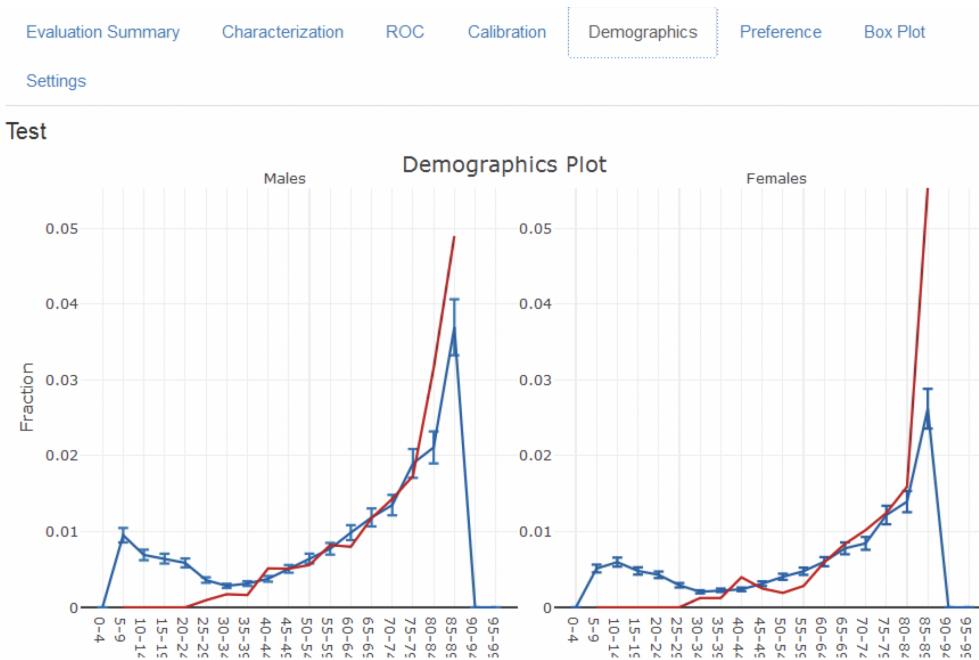


Figure 13.19: The demographic calibration of the model

Evaluation Summary	Characterization	ROC	Calibration	Demographics	Preference	Box Plot
Settings	Options	Attrition				
Attrition						
Show 25 entries	Search:					
description	targetCount	uniquePeople	outcomes			
1 Original cohorts	500000	500000	13746			
2 First exposure only	500000	500000	13746			
3 At least 365 days of observation prior	500000	500000	13746			
4 Have time at risk	351028	351028	12726			
Showing 1 to 4 of 4 entries	Previous	1	Next			

Figure 13.20: The attrition plot for the prediction problem

Filters	Results	Model Settings	Population Settings	Covariate Settings	Search:									
Development Database	Show 10 entries													
All														
Validation Database														
All														
Target Cohort														
New users of ACE inhibitors as first-line monotherapy for hypertension	Analysis_1	Optum claims	Optum claims	New users of ACE inhibitors as first-line monotherapy for hypertension	Acute myocardial infarction events	Lasso Logistic Regression	1	365	0.74486	0.03094	87757	650	0.74068	
	Analysis_3	Optum claims	Optum claims	New users of ACE inhibitors as first-line monotherapy for hypertension	Angioedema events	Lasso Logistic Regression	1	365	0.60523	0.00254	87615	148	0.16892	
	Analysis_5	Optum claims	Optum claims	New users of ACE inhibitors as first-line monotherapy for hypertension	Acute myocardial infarction events	Random forest	1	365	0.71867	0.03102	87757	650	0.74068	
	Analysis_7	Optum claims	Optum claims	New users of ACE inhibitors as first-line monotherapy for hypertension	Angioedema events	Random forest	1	365	0.64163	0.02447	87615	148	0.16892	
Outcome Cohort	Showing 1 to 4 of 4 entries	Previous	1	Next										
All														

Figure 13.21: The shiny summary page containing key hold out set performance metrics for each model trained

The screenshot shows a software interface with a top navigation bar containing tabs: Results, Model Settings, Population Settings, and Covariate Settings. The Model Settings tab is active. Below the tabs, the title "Model Settings: help" is displayed. Underneath the title is a button labeled "Show 10 entries". A table follows, with columns titled "Setting" and "Value". The table contains three rows of data:

Setting	Value
1 Model	lr_lasso
2 variance	0.01
3 seed	50975614

At the bottom left of the table area, it says "Showing 1 to 3 of 3 entries".

Figure 13.22: To view the model settings used when developing the model.

This summary page table contains:

- basic information about the model (e.g., database information, classifier type, time-at-risk settings, target population and outcome names)
- hold out target population count and incidence of outcome
- discrimination metrics: AUC, AUPRC

To the left of the table is the filter option, where we can specify the development/validation databases to focus on, the type of model, the time at risk settings of interest and/or the cohorts of interest. For example, to pick the models corresponding to the target population “New users of ACE inhibitors as first line mono-therapy for hypertension”, select this in the *Target Cohort* option.

To explore a model click on the corresponding row, a selected row will be highlighted. With a row selected, we can now explore the model settings used when developing the model by clicking on the *Model Settings* tab:

Similarly, we can explore the population and covariate settings used to generate the model in the other tabs.

Viewing Model Performance

Once a model row has been selected we can also view the model performance. Click on **Performance** to open the threshold performance summary shown in Figure 13.23.

This summary view shows the selected prediction question in the standard format, a threshold selector and a dashboard containing key threshold-based metrics such as positive predictive value (PPV), negative predictive value (NPV), sensitivity and specificity (see Section 13.4.2). In Figure 13.23 we see that at a threshold of 0.00482 the sensitivity is 83.4% (83.4% of patients with the outcome in the following year have a risk greater than or equal to 0.00482) and the PPV is 1.2%

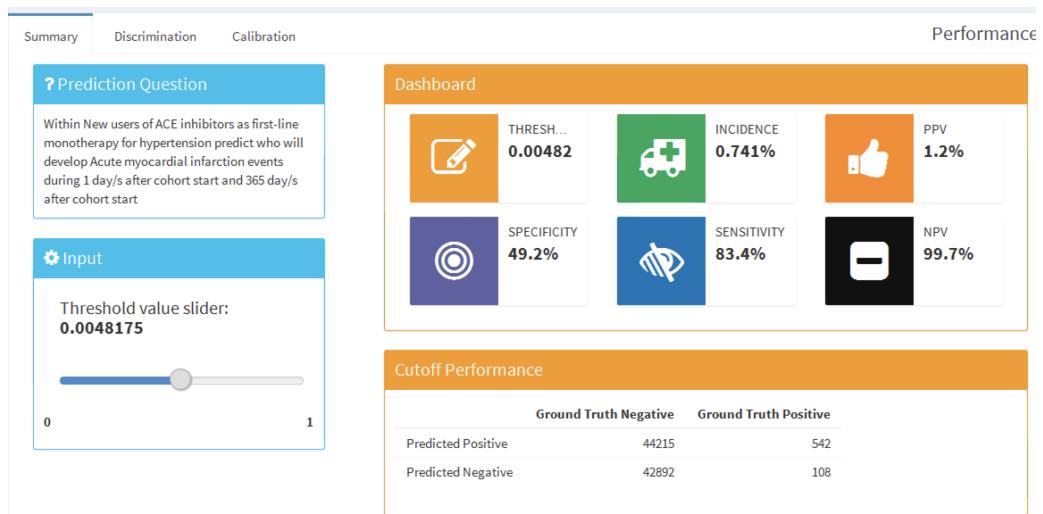


Figure 13.23: The summary performance measures at a set threshold.

(1.2% of patients with a risk greater than or equal to 0.00482 have the outcome in the following year). As the incidence of the outcome within the year is 0.741%, identifying patients with a risk greater than or equal to 0.00482 would find a subgroup of patients that have nearly double the risk of the population average risk. We can adjust the threshold using the slider to view the performance at other values.

To look at the overall discrimination of the model click on the “Discrimination” tab to view the ROC plot, precision-recall plot, and distribution plots. The line on the plots corresponds to the selected threshold point. Figure 13.24 show the ROC and precision-recall plots. The ROC plot shows the model was able to discriminate between those who will have the outcome within the year and those who will not. However, the performance looks less impressive when we see the precision-recall plot, as the low incidence of the outcome means there is a high false positive rate.

Figure 13.25 shows the prediction and preference score distributions.

Finally, we can also inspect the calibration of the model by clicking on the “Calibration” tab. This displays the calibration plot and the demographic calibration shown in Figure 13.26.

We see that the average predicted risk appears to match the observed fraction who experienced the outcome within a year, so the model is well calibrated. Interestingly, the demographic calibration shows that the expected line is higher than the observed line for young patients, so we are predicting a higher risk for young age groups. Conversely, for the patients above 80 the model is predicting a lower risk than the observed risk. This may prompt us to develop separate models for the younger or older patients.

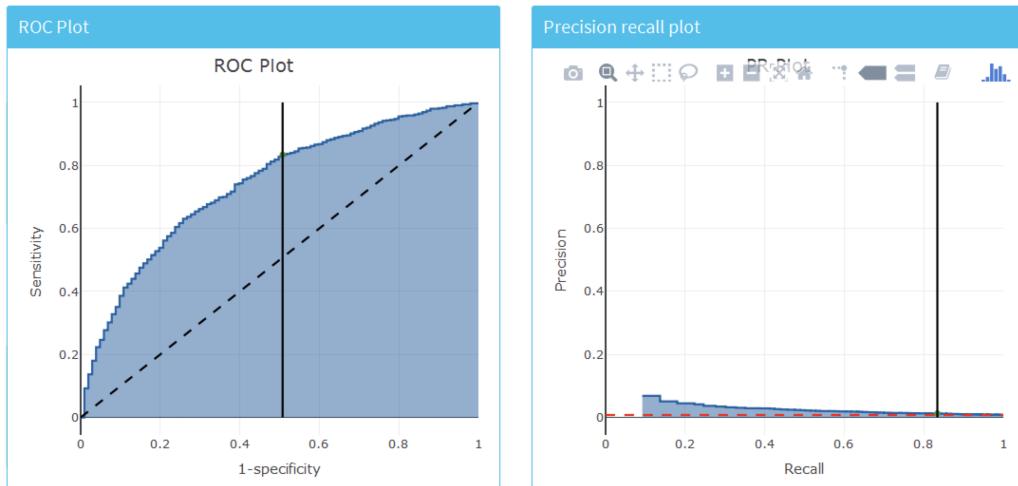


Figure 13.24: The ROC and precision-recall plots used to access the overall discrimination ability of the model.

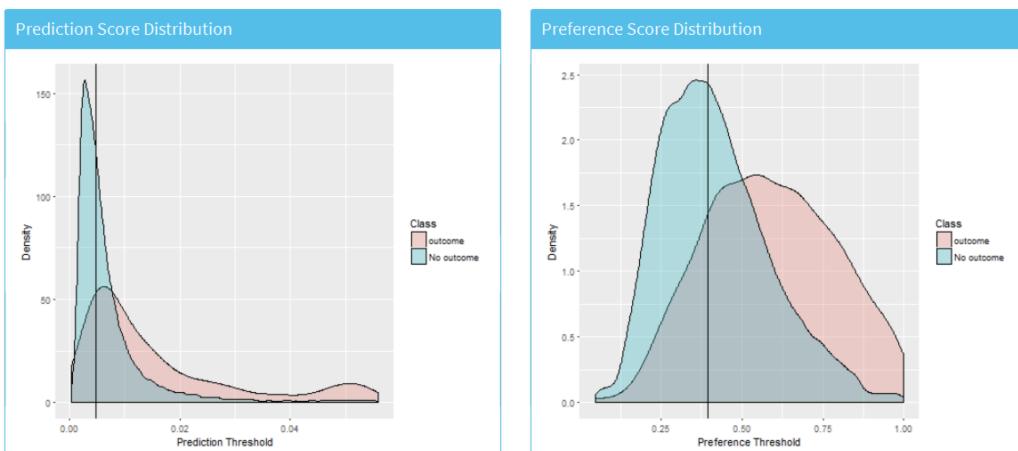


Figure 13.25: The predicted risk distribution for those with and without the outcome. The more these overlap the worse the discrimination

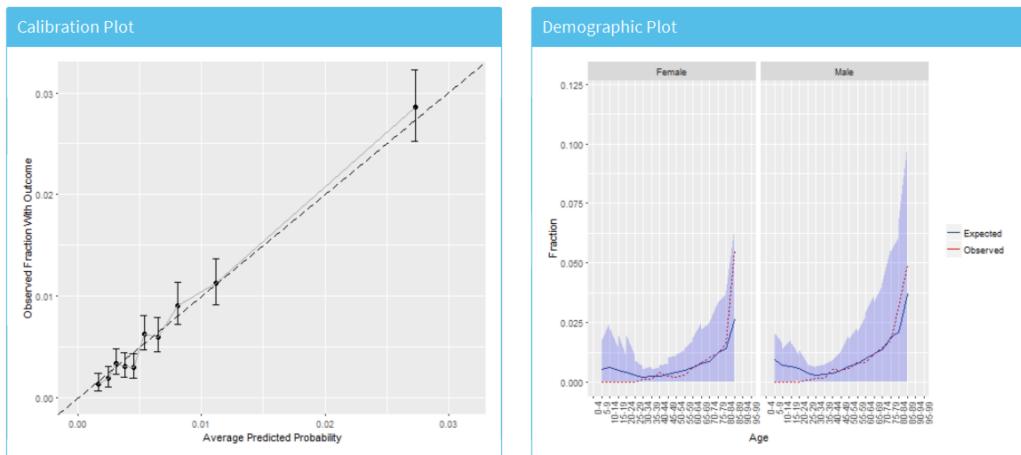


Figure 13.26: The risk stratified calibration and demographic calibration

Viewing the Model

To inspect the final model, select the  **Model** option from the left hand menu. This will open a view containing plots for each variable in the model, shown in Figure 13.27, and a table summarizing all the candidate covariates, shown in Figure 13.28. The variable plots are separated into binary variables and continuous variables. The x-axis is the prevalence/mean in patients without the outcome and the y-axis is the prevalence/mean in patients with the outcome. Therefore, any variable's dot falling above the diagonal is more common in patients with the outcome and any variable's dot falling below the diagonal is less common in patients with the outcome.

The table in Figure 13.28 displays the name, value (coefficient if using a general linear model, or variable importance otherwise) for all the candidate covariates, outcome mean (the mean value for those who have the outcome) and non-outcome mean (the mean value for those who do not have the outcome).



Predictive models are not causal models, and predictors should not be mistaken for causes. There is no guarantee that modifying any of the variables in Figure 13.28 will have an effect on the risk of the outcome.

13.9 Additional Patient-Level Prediction Features

13.9.1 Journal Paper Generation

We have added functionality to automatically generate a word document we can use as start of a journal paper. It contains many of the generated study details and results. If we have performed external validation these results will can be added as

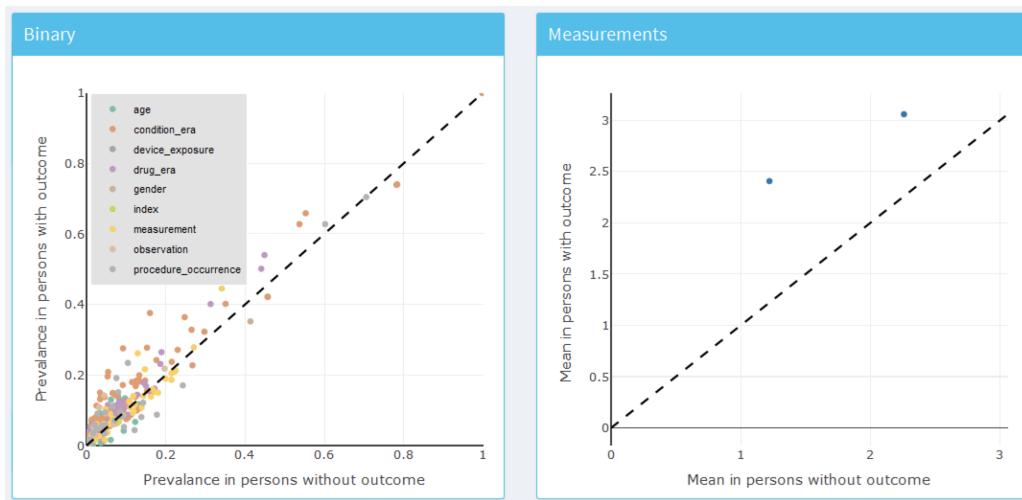


Figure 13.27: Model summary plots. Each dot corresponds to a variable included in the model.

Model Table				
		<input type="button" value="Download Model"/>	Search: <input type="text"/>	
	Covariate Name	Value	Outcome Mean	Non-outcome Mean
1	age group: 00-04	0	0.0004	0.0001
2	age group: 05-09	0	0	0.0003
3	index month: 1	0	0.1307	0.1096
4	observation during day -365 through 0 days relative to index: Domain	0	0.1188	0.0514
5	Charlson index - Romano adaptation	0	2.4783	1.3817
6	Diabetes Comorbidity Severity Index (DCSI)	0.1478	2.4056	1.2207
7	CHADS2VASc	0.9279	3.0573	2.2576
8	visit_occurrence concept count during day -365 through 0 concept_count relative to index	0	19.5263	13.8837
9	age group: 10-14	0	0	0.001
10	index month: 2	0	0.0934	0.0909

Showing 1 to 10 of 67,897 entries Previous 1 2 3 4 5 ... 6790 Next

Figure 13.28: Model details table.

well. Optionally, we can add a “Table 1” that contains data on many covariates for the target population. We can create the draft journal paper by running this function:

```
createPlpJournalDocument(plpResult = <your plp results>,
                         plpValidation = <your validation results>,
                         plpData = <your plp data>,
                         targetName = "<target population>",
                         outcomeName = "<outcome>",
                         table1 = F,
                         connectionDetails = NULL,
                         includeTrain = FALSE,
                         includeTest = TRUE,
                         includePredictionPicture = TRUE,
                         includeAttritionPlot = TRUE,
                         outputLocation = "<your location>")
```

For more details see the help page of the function.

13.10 Summary



- Patient-level prediction aims to develop a model that predicts future events using data from the past.
- The selection of the best machine algorithm for model development is an empirical question, i.e. it should be driven by the problem and data at hand.
- The PatientLevelPrediction Package implements best practices for the development and validation of prediction models using data stored in the OMOP-CDM.
- The dissemination of the model and its performance measures is implemented through interactive dashboards.
- OHDSI’s prediction framework enables large-scale external validation of prediction models which is a pre-requisite for clinical adoption.

13.11 Exercises

Prerequisites

For these exercises we assume R, R-Studio and Java have been installed as described in Section 8.4.5. Also required are the SqlRender, DatabaseConnector, Eunomia and PatientLevelPrediction packages, which can be installed using:

```
install.packages(c("SqlRender", "DatabaseConnector", "devtools"))
devtools::install_github("ohdsi/Eunomia", ref = "v1.0.0")
devtools::install_github("ohdsi/PatientLevelPrediction")
```

The Eunomia package provides a simulated dataset in the CDM that will run inside your local R session. The connection details can be obtained using:

```
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
```

The CDM database schema is “main”. These exercises also make use of several cohorts. The `createCohorts` function in the Eunomia package will create these in the COHORT table:

```
Eunomia::createCohorts(connectionDetails)
```

Problem Definition

In patients that started using NSAIDs for the first time, predict who will develop a gastrointestinal (GI) bleed in the next year.

The NSAID new-user cohort has COHORT_DEFINITION_ID = 4. The GI bleed cohort has COHORT_DEFINITION_ID = 3.

Exercise 13.1. Using the PatientLevelPrediction R package, define the covariates you want to use for the prediction and extract the PLP data from the CDM. Create the summary of the PLP data.

Exercise 13.2. Revisit the design choices you have to make to define the final target population and specify these using the `createStudyPopulation` function. What will the effect of your choices be on the final size of the target population?

Exercise 13.3. Build a prediction model using LASSO and evaluate its performance using the Shiny application. How well is your model performing?

Suggested answers can be found in Appendix E.9.

Part IV

Evidence Quality

Chapter 14

Evidence Quality

Chapter leads: Patrick Ryan & Jon Duke

14.1 Attributes of Reliable Evidence (신뢰성을 위한 근거의 속성)

본격적인 여정 시작에 앞서, 우리가 바라는 이상적인 종착지가 어디인지 상상해보는 것은 도움이 될 것이다. 데이터를 근거로 만들기 위한 우리의 여정을 지원하기 위해서, 우리는 근거의 신뢰도를 높일 수 있는 기반 속성들을 중요시 여긴다.

신뢰할 수 있는 근거는 **반복 가능(repeatable)**해야 한다. 즉, 연구원이 주어진 질문에 대해 동일한 데이터를 이용하여 동일한 분석을 수행할 때 동일한 결과가 나올 것이라 기대할 수 있어야 한다. 근거의 반복 가능성에 대한 최소한의 요구 조건은 근거가 특정 데이터를 입력하고 정의된 절차를 수행하여서 나온 결과라는 점과, 이것은 사후 의사 결정 과정에서의 수동적인 개입으로부터 자유롭다는 점이다. 조금 더 이상적으로는, 신뢰할 수 있는 근거는 **재현 가능(reproducible)** 해야 하는데, 다른 연구자가 주어진 데이터와 분석방법을 가지고 동일한 업무를 수행하였을 때 첫

Desired attribute	Question	Researcher	Data	Analysis	Result
Repeatable	Identical	Identical	Identical	Identical =	Identical
Reproducible	Identical	Different	Identical	Identical =	Identical
Replicable	Identical	Same or different	Similar	Identical =	Similar
Generalizable	Identical	Same or different	Different	Identical =	Similar
Robust	Identical	Same or different	Same or different	Different =	Similar
Calibrated	Similar (controls)	Identical	Identical	Identical =	Statistically consistent

Figure 14.1: Desired attributes of reliable evidence

연구자의 수행 결과와 동일한 결과를 낼 수 있어야 한다. 재현 가능성을 위해서 연구 절차는 일반적인 사람이 읽을 수 있고, 컴퓨터가 실행할 수 있으며 충분히 구체화되어 있어 추가적인 연구자의 결정이 연구 결과에 반영되지 않도록 해야 한다. 반복성과 재현성을 충족시킬 수 있는 가장 효과적인 방법은 사전에 정의한 데이터의 입출력을 이용하여 표준화된 분석 방법을 사용하고, 이러한 절차를 버전관리 데이터베이스에 적용하는 것이다.

또한 우리는 동일한 질문에 대해 비슷한 데이터를 가지고 동일 분석방법을 적용하여 비슷한 결과를 얻을 수 있는, **복제 가능함(replicable)** 것으로 보인다면 우리가 주장하는 근거는 더욱 신뢰할 만하다고 자신할 수 있다. 예를 들어, 한 대규모 보험사의 청구 데이터베이스에 대한 분석에서 생성된 근거는 다른 보험사의 청구 데이터베이스를 이용하여 복제가 가능할 경우 그 근거가 강화될 수 있다. 인구 수준 효과 추정의 관점에서도 이 속성들은 Austin Bradford Hill의 인과적 관점과 잘 일치한다. “다른 사람, 다른 장소, 환경 및 시간에서도 반복적으로 관찰되었습니까? ... (중략) ... 반복적인 상황과 관찰만이 우연으로 설명되는 현상인지 혹은 실재하는 위험인지 답할 수 있다.”(Hill, 1965) 환자 수준 예측의 맥락에서 복제 가능성은 외부 검증(external validation)의 시행에 대한 중요성뿐 아니라, 한 데이터베이스에서 훈련된 모델이 다른 데이터베이스에 적용될 때 결과를 구별할 수 있는 정확도(discriminative accuracy)와 검정능(calibration)을 관찰함으로써 모델의 성능을 평가할 수 있는 능력을 강조한다. 서로 다른 데이터베이스에 대해 동일한 분석을 수행하고, 여전히 유사한 결과를 보이는 상황에서 우리는 우리의 근거가 **일반화될 수 있다(generalizable)**는 확신을 얻는다. 오딧세이 연구 네트워크의 핵심 가치는 다른 인구, 지역, 자료 획득 과정 등으로 대표되는 다양성이다. Madigan et al. (2013b)은 효과 추정치(effect estimates)가 데이터의 선택에 따라 민감하게 변할 수 있음을 보여주었다. 각 데이터 소스가 단일 연구의 신뢰도를 하락시킬 수 있는 고유의 한계점과 비뚤림이 있다는 점을 인식한 상태에서도, 서로 다른 데이터셋을 사용하여 유사한 결과 패턴이 관측된 것은 상당히 강력한 의미를 가지고 있다. 이는 데이터 소스 각각이 가지고 있는 편향의 가능성을 상당 부분 감소시켜, 연구 결과를 설명할 수 있기 때문이다. 네트워크 연구의 인구수준 효과 추정치가 미국, 유럽, 아시아 그리고 다양한 청구데이터, 전자의무기록 데이터상에서 일관된 결과를 보여줄 때 해당 의학적 중재는 의학적 의사 결정과정에서 더 큰 영향을 줄 수 있는 더욱 강력한 근거로서 인식되어야 한다.

신뢰할 만한 근거는 분석 내에서 주관적 선택에 지나치게 민감하지 않는 **완건성(robust)**을 가져야 한다. 주어진 연구에 대해서 잠재적으로 합당하다고 고려되는 대안적인 통계 방법이 있다면, 결과에 따라서 다른 방법을 통해 얻은 동일한 결과로 기존 연구 결과에 대한 확신을 갖거나, 혹은 상충되는 결과를 통해 기존 연구에 대한 경각심을 줄 수 있다. (Madigan et al., 2013a) 인구수준 효과 추정에서 민감도 분석에는 연구 설계 설정 (코호트 비교 연구, 자기 통제 환자군 (self-controlled case series) 연구 등)과 분석적 고려사항의 설정 (코호트 비교에서 혼란변수 조정을 위한 성향점수매칭, 계층화 또는 가중치 유무)과 같은 고급 연구 설계의 문제를 포함할 수 있다.

마지막으로 가장 중요할 수도 있는 부분은 근거는 **검정되어야 한다(calibrated)**는 점이다. 근거 생성 시스템에 대한 성능이 검증되지 않은 상태에서는 해당 시스템이 미지의 연구 질문에 대한 답변을 제공한다 라고 말하기 불충분하다. 폐쇄형 시스템은 잘 알려진 작동 특성을 가져야 하며, 이는 측정 가능하고 시스템이 생성하는 어떠한

결과에 대해서도 그 상황을 잘 전달할 수 있어야 한다. 통계적 표현들은 경험적으로 잘 정립된 특성을 가지고 있음을 보여줄 수 있어야 한다. 예를 들어 95% 신뢰구간이란 95%의 확률 범위를 갖는다는 뜻이고, 10%의 예상 확률이란 인구 집단에서 관측된 사건 발생의 비율이 10%이라는 뜻이다. 관찰 연구에서는 항상 연구 설계, 연구 방법, 연구 데이터에 대한 가정을 검정할 수 있는 방법을 수반해야 한다. 이 검정 방법들은 연구 타당성에 일차적인 위협들에(선택 비뚤림, 교란변수, 측정 오차) 대해 우선적으로 집중하여 평가하여야 한다. 음성 대조군(Negative controls)은 관찰연구에서 발생할 수 있는 계통오차를 확인하고 감소시킬 수 있는 강력한 도구인 것으로 보여졌다. (Schuemie et al., 2016, 2018a,b)

14.2 근거의 질에 대한 이해

하지만 우리의 연구 결과가 충분히 신뢰할만한 수준인지 어떻게 알 수 있을까? 누군가가 우리의 연구에서 설정해놓은 특정 환경들을 신뢰할까? 규제적 의사결정은 어떨까? 향후 연구의 기반이 될 수 있을까? 새로운 연구가 발표되거나 확산되는 과정에서 독자는 연구의 형태(무작위 대조시험, 관찰 연구, 혹은 다른 유형의 분석방법)에 관계없이 이러한 질문들을 염두에 두어야 한다.

흔히 관찰 연구(observational study) 즉, 실제 데이터(real world data)를 활용한 연구를 진행하면서 마주하게 되는 우려는 바로 데이터 품질에 관한 부분이다.(Botsis et al., 2010; Hersh et al., 2013; Sherman et al., 2016) 일반적으로 관찰 연구에 사용된 데이터는 원래 연구 목적으로 수집된 것이 아니므로 고유의 비뚤림(inherent biases)과 같은 불완전하거나 부정확한 데이터의 수집으로 인한 문제를 겪을 수 있다. 이러한 우려로 인해 데이터 품질을 측정하고 특성화하고 이상적으로 데이터 품질을 개선하려는 방법에 대한 연구가 계속해서 증가하고 있다. (Kahn et al., 2012; Liaw et al., 2013; Weiskopf and Weng, 2013) 오딧세이 커뮤니티는 이러한 연구들을 강력히 지지하며, 커뮤니티 회원들은 OMOP 공통데이터모델 및 오딧세이 네트워크의 데이터 품질을 조사하는 많은 연구들을 직접 주도하고 참여하였다.(Huser et al., 2016; Kahn et al., 2015; Callahan et al., 2017; Yoon et al., 2016)

지난 10년간의 결과들을 고려해보면, 데이터 품질이라는 것은 결코 완벽해질 수 없다는 것이 명백해졌다. 이 개념은 의료정보학 분야의 개척자인 Clem McDonald 박사의 인용에도 잘 반영되어 있다. :

사실 데이터 충실도의 감소는 의사의 뇌에서 의료기록으로 데이터가 이동하는 것에서부터 시작된다.

그러므로 우리는 공동체로서 질문을 해야 할 필요가 있다. -불완전한 데이터가 주어지면, 어떻게 우리는 신뢰할만한 근거를 얻을 수 있을까?

이 문제에 대한 대답은 “근거의 품질”에 대한 전반적인 부분을 살펴보는데 있다. 데이터에서부터 근거로의 과정에 대한 검토, 근거 생성 과정의 구성 요소들에 대한 확인, 각 구성 요소의 질에 대한 신뢰 구축 방법의 결정, 그리고 이것을 투명하게 전달하는 방법을 각각 살펴보았다. 근거의 질이란 단순히 관찰 데이터의 품질뿐 아니라 관찰 분석에 사용된 방법, 소프트웨어 및 임상적 정의의 타당성을 고려한다.

뒤이어 나오는 단원에서 우리는 근거의 품질에 해당하는 4가지 구성요소에 대한 부

분을 살펴볼 것이며, 이를 표14.1에 나타내었다.

Table 14.1: 근거의 품질에 해당하는 네가지 구성요소

구성요소	측정 대상
데이터 품질	합의된 구조와 방법을 이용하여 타당한 값을 가진 데이터가 온전히 입력되었는가?
임상적 타당성	수행된 분석이 임상적 의도와 어느 정도 일치하고 있는가?
소프트웨어의 타당성	데이터의 변환과 분석 과정이 우리가 의도한 대로 진행되었다고 신뢰할 수 있는가?
방법론적 타당성	주어진 데이터의 강점과 약점을 인지하고 있는 상태에서, 적절한 연구 방법론을 사용하였는가?

14.3 근거 품질의 전달

근거 품질의 중요한 측면은 데이터에서 근거로의 여정에서 발생하는 불확실성을 표현하는 능력이다. 오딧세이의 활동을 통해 이루고자 하는 거시적인 목표는 오딧세이에서 생성된 근거가 –비록 여러 방면으로 불완전 하더라도– 강점과 약점에 대하여 일관되게 측정되고, 엄격하고 공개적인 방식으로 전달되어 생성되었다는 신뢰감을 의료 전문가들에게 제공해주는 것이다.

14.4 Summary



- 우리가 생성한 근거는 반복 가능성(repeatable), 재현 가능성(reproducible), 복제 가능성(replicable), 일반화 가능성(generalizable), 완건성(robust)을 갖추어야 하며 검정된(calibrated) 결과여야 한다.
- 근거의 품질은 그 근거의 신뢰성 여부를 판단하기 위해 단순히 데이터의 품질만이 아닌 그 이상의 것을 추구한다. :
 - * 데이터 품질
 - * 임상적 타당성
 - * 소프트웨어 타당성
 - * 방법론적 타당성
- 근거를 전달하는 과정에서, 근거의 품질에 대한 다양한 위협으로부터 나타나게 되는 불확실성들 또한 표현해야 한다.

Chapter 15

Data Quality

Chapter leads: Martijn Schuemie, Vojtech Huser & Clair Blacketer

Most of the data used for observational healthcare research were not collected for research purposes. For example, electronic health records (EHRs) aim to capture the information needed to support the care of patients, and administrative claims are collected to provide a grounds for allocating costs to payers. Many have questioned whether it is appropriate to use such data for clinical research, with van der Lei (1991) even stating that “Data shall be used only for the purpose for which they were collected.” The concern is that because the data were not collected for the research that we would like to do, it is not guaranteed to have sufficient quality. If the quality of the data is poor (garbage in), then the quality of the result of research using that data must be poor as well (garbage out). An important aspect of observational healthcare research therefore deals with assessing data quality, aiming to answer the question:

Are the data of sufficient quality for our research purposes?

We can define data quality (DQ) as (Roebuck, 2012):

The state of completeness, validity, consistency, timeliness and accuracy that makes data appropriate for a specific use.

Note that it is unlikely that our data are perfect, but they may be good enough for our purposes.

DQ cannot be observed directly, but methodology has been developed to assess it. Two types of DQ assessments can be distinguished (Weiskopf and Weng, 2013): assessments to evaluate DQ in general, and assessments to evaluate DQ in the context of a specific study.

In this chapter we will first review possible sources of DQ problems, after which we'll discuss the theory of general and study-specific DQ assessments, followed by

a step-by-step description of how these assessments can be performed using the OHDSI tools.

15.1 Sources of Data Quality Problems

There are many threats to the quality of the data, starting as noted in Chapter 14 when the doctor records her or his thoughts. Dasu and Johnson (2003) distinguish the following steps in the life cycle of data, recommending DQ be integrated in each step. They refer to this as the DQ continuum:

1. **Data gathering and integration.** Possible problems include fallible manual entry, biases (e.g. upcoding in claims), erroneous joining of tables in an EHR, and replacing missing values with default ones.
2. **Data storage and knowledge sharing.** Potential problems are lack of documentation of the data model, and lack of meta-data.
3. **Data analysis.** Problems can include incorrect data transformations, incorrect data interpretation, and use of inappropriate methodology.
4. **Data publishing.** When publishing data for downstream use.

Often the data we use has already been collected and integrated, so there is little we can do to improve step 1. We do have ways to check the DQ produced by this step as will be discussed in subsequent sections in this chapter.

Similarly, we often receive the data in a specific form, so we have little influence over part of step 2. However, in OHDSI we convert all our observational data to the Common Data Model (CDM), and we do have ownership over this process. Some have expressed concerns that this specific step can degrade DQ. But because we control this process, we can build stringent safeguards to preserve DQ as discussed later in Section 15.2.2. Several investigations (Defalco et al., 2013; Makadia and Ryan, 2014; Matcho et al., 2014; Voss et al., 2015a,b; Hripcsak et al., 2018) have shown that when properly executed, little to no error is introduced when converting to the CDM. In fact, having a well-documented data model that is shared by a large community facilitates data storage in an unambiguous and clear manner.

Step 3 (data analysis) also falls under our control. In OHDSI, we tend to not use the term DQ for the quality issues during this step, but rather the terms *clinical validity*, *software validity* and *method validity*, which are discussed at length in Chapters 16, 17, and 18, respectively.

15.2 Data Quality in General

We can ask the question whether our data are fit for the general purpose of observational research. Kahn et al. (2016) define such generic DQ as consisting of three components:

1. **Conformance:** Do data values adhere to specified standards and formats?
Three sub-types are identified:
 - **Value:** Are recorded data elements in agreement with the specified formats? For example, are all provider medical specialties valid specialties?
 - **Relational:** Is the recorded data in agreement with specified relational constraints? For example, does the PROVIDER_ID in a DRUG_EXPOSURE data have a corresponding record in the PROVIDER table?
 - **Computation:** Do computations on the data yield the intended results? For example, is BMI computed from height and weight equal to the verbatim BMI recorded in the data?
2. **Completeness:** Refers to whether a particular variable is present (e.g. is weight as measured in the doctor's office recorded?) as well as whether variables contain all recorded values (e.g. do all persons have a known gender?)
3. **Plausibility:** Are data values believable? Three sub-types are defined:
 - **Uniqueness:** For example, does each PERSON_ID occur only once in the PERSON table?
 - **Atemporal:** Do values, distributions, or densities agree with expected values? For example, is the prevalence of diabetes implied by the data in line with the known prevalence?
 - **Temporal:** Are changes in values in line with expectations? For example, are immunization sequences in line with recommendations?

Each component can be evaluated in two ways:

- **Verification** focuses on model and metadata data constraints, system assumptions, and local knowledge. It does not rely on an external reference. The key feature with verification is the ability to determine expected values and distributions using resources within the local environment.
- **Validation** focuses on the alignment of data values with respect to relevant external benchmarks. One possible source of an external benchmark can be to combine results across multiple data sites.

15.2.1 Data Quality Checks

Kahn introduces the term *data quality check* (sometimes referred to as a *data quality rule*) that tests whether data conform to a given requirement (e.g., flagging an implausible age of 141 of a patient, potentially due to incorrect birth year or missing death event). We can implement such checks in software by creating automated DQ tools. One such tool is ACHILLES (Automated Characterization of Health Information at Large-scale Longitudinal Evidence Systems). (Huser et al., 2018) ACHILLES is a software tool that provides characterization and visualization of a database conforming to the CDM. As such, it can be used to evaluate DQ in a network of databases. (Huser et al., 2016) ACHILLES is available as a stand-alone tool, and it is also integrated into ATLAS as the “Data Sources”

function.

ACHILLES pre-computes over 170 data characterization analyses, with each analysis having an analysis ID and a short description of the analysis; two such examples are “715: Distribution of DAYS_SUPPLY by DRUG_CONCEPT_ID” and “506: Distribution of age at death by gender.” The results of these analyses are stored in a database and can be accessed by a web viewer or by ATLAS.

Another tool created by the community to assess DQ is the Data Quality Dashboard (DQD). Where ACHILLES runs characterization analyses to provide an overall visual understanding of a CDM instance, the DQD goes table by table and field by field to quantify the number of records in a CDM that do not conform to the given specifications. In all, over 1,500 checks are performed, each one organized into the Kahn framework. For each check the result is compared to a threshold whereby a FAIL is considered to be any percentage of violating rows falling above that value. Table 15.1 shows some example checks.

Table 15.1: Example data quality rules in the Data Quality Dashboard.

Fraction violated rows	Check description	Threshold	Status
0.34	A yes or no value indicating if the provider_id in the VISIT_OCCURRENCE is the expected data type based on the specification.	0.05	FAIL
0.99	The number and percent of distinct source values in the measurement_source_value field of the MEASUREMENT table mapped to 0.	0.30	FAIL
0.09	The number and percent of records that have a value in the drug_concept_id field in the DRUG_ERA table that do not conform to the ingredient class.	0.10	PASS
0.02	The number and percent of records with a value in the verbatim_end_date field of the DRUG_EXPOSURE that occurs prior to the date in the DRUG_EXPOSURE_START_DATE field of the DRUG_EXPOSURE table.	0.05	PASS

Fraction violated rows	Check description	Threshold	Status
0.00	The number and percent of records that have a duplicate value in the procedure_occurrence_id field of the PROCEDURE_OCCURRENCE.	0.00	PASS

Within the tool the checks are organized in multiple ways, one being into table, field, and concept level checks. Table checks are those done at a high-level within the CDM, for example determining if all required tables are present. The field level checks are carried out in such a way to evaluate every field within every table for conformance to CDM specifications. These include making sure all primary keys are truly unique and all standard concept fields contain concepts ids in the proper domain, among many others. Concept level checks go a little deeper to examine individual concept ids. Many of these fall into the plausibility category of the Kahn framework such as ensuring that gender-specific concepts are not attributed to persons of incorrect gender (i.e. prostate cancer in a female patient).



ACHILLES and DQD are executed against the data in the CDM. DQ issues identified this way may be due to the conversion to the CDM, but may also reflect DQ issues already present in the source data. If the conversion is at fault, it is usually within our control to remedy the problem, but if the underlying data are at fault the only course of action may be to delete the offending records.

15.2.2 ETL Unit Tests

In addition to high level data quality checks, individual level data checks should be performed. The ETL (Extract-Transform-Load) process by which data are converted to the CDM is often quite complex, and with that complexity comes the danger of making mistakes that may go unnoticed. Moreover, as time goes by the source data model may change, or the CDM may be updated, making it necessary to modify the ETL process. Changes to a process as complicated as an ETL can have unintended consequences, requiring all aspects of the ETL to be reconsidered and reviewed.

To make sure the ETL does what it is supposed to do, and continues to do so, it is highly recommended to construct a set of unit tests. A unit test is a small piece of code that automatically checks a single aspect. The Rabbit-in-a-Hat tool described in Chapter 6 can create a unit test framework that makes writing such unit tests easier. This framework is a collection of R functions created specifically for the source database and target CDM version of the ETL. Some of these functions are

for creating fake data entries that adhere to the source data schema, while other functions can be used to specify expectations on the data in the CDM format. Here is an example unit test:

```
source("Framework.R")
declareTest(101, "Person gender mappings")
add_enrollment(member_id = "M000000102", gender_of_member = "male")
add_enrollment(member_id = "M000000103", gender_of_member = "female")
expect_person(PERSON_ID = 102, GENDER_CONCEPT_ID = 8507
expect_person(PERSON_ID = 103, GENDER_CONCEPT_ID = 8532)
```

In this example, the framework generated by Rabbit-in-a-Hat is sourced, loading the functions that are used in the remainder of the code. We then declare we will start testing person gender mappings. The source schema has an ENROLLMENT table, and we use the add_enrollment function created by Rabbit-in-a-Hat to create two entries with different values for the MEMBER_ID and GENDER_OF_MEMBER fields. Finally, we specify the expectation that after the ETL two entries should exist in the PERSON table with various expected values.

Note that the ENROLLMENT table has many other fields, but we do not care much about what values these other fields have in the context of this test. However, leaving those values (e.g. date of birth) empty might cause the ETL to discard the record or throw an error. To overcome this problem while keeping the test code easy to read, the add_enrollment function will assign default values (the most prevalent values as observed in the White Rabbit scan report) to field values that are not explicitly specified by the user.

Similar unit tests can be created for all other logic in an ETL, typically resulting in hundreds of tests. When we are done defining the test, we can use the framework to generate two sets of SQL statements, one to create the fake source data, and one to create the tests on the ETL-ed data:

```
insertSql <- generateInsertSql(databaseSchema = "source_schema")
testSql <- generateTestSql(databaseSchema = "cdm_test_schema")
```

The overall process is depicted in Figure 15.1.

The test SQL returns a table that will look like Table 15.2. In this table we see that we passed the two tests we defined earlier.

Table 15.2: Example ETL unit test results.

ID	Description	Status
101	Person gender mappings	PASS
101	Person gender mappings	PASS

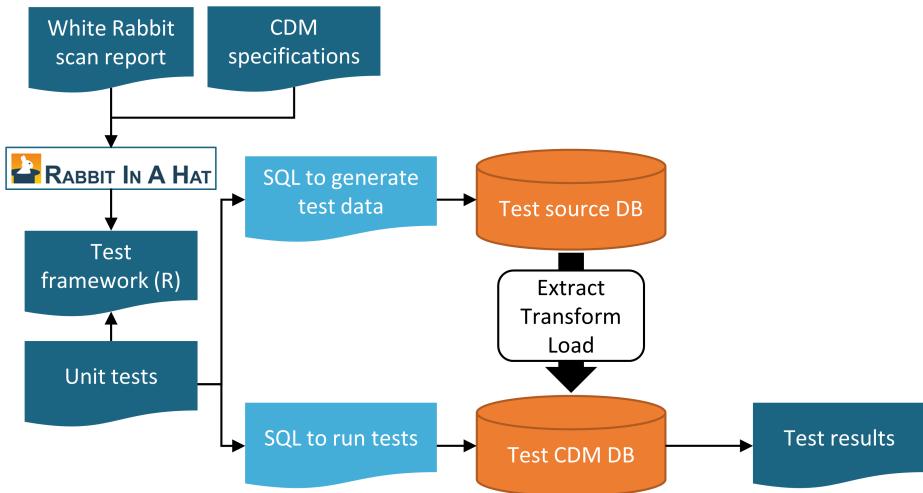


Figure 15.1: Unit testing an ETL (Extract-Transform-Load) process using the Rabbit-in-a-Hat testing framework.

The power of these unit tests is that we can easily rerun them any time the ETL process is changed.

15.3 Study-Specific Checks

The chapter has so far focused on general DQ checks. Such checks should be executed prior to using the data for research. Since these checks are done regardless of the research questions we recommend performing study-specific DQ assessments.

Some of these assessments can take the form of DQ rules that are specifically relevant for the study. For example, we may want to impose a rule that at least 90% of the records for our exposure of interest specify the length of exposure.

A standard assessment is to review the concepts that are most relevant for the study in ACHILLES, for example those specified in the study cohort definitions. Sudden changes over time in the rate with which a code is observed may hint at DQ problems. Some examples will be discussed later in this chapter.

Another assessment is to review the prevalence and changes in prevalence over time of the resulting cohorts generated using the cohort definitions developed for the study, and see whether these agree with expectations based on external clinical knowledge. For example, exposure of a new drug should be absent before introduction to the market, and will likely increase over time after introduction. Similarly, the prevalence of outcomes should be in line with what is known of the prevalence of the condition in the population. If a study is executed across a network of databases, we can compare the prevalence of cohorts across databases. If a cohort is highly prevalent in one database, but is missing in another database,

there might be a DQ issue. Note that such an assessment overlaps with the notion of *clinical validity*, as discussed in Chapter 16; we may find unexpected prevalence in some databases not because of DQ issues, but because our cohort definition is not truly capturing the health states we are interested in, or because these health state rightly vary over databases that capture different patient populations.

15.3.1 Checking Mappings

One possible source of error that firmly falls under our control is the mapping of source codes to Standard Concepts. The mappings in the Vocabulary are meticulously crafted, and errors in the mapping that are noted by members of the community are reported in the Vocabulary issue tracker¹ and fixed in future releases. Nevertheless, it is impossible to completely check all mappings by hand, and errors likely still exist. When performing a study, we therefore recommend reviewing the mappings for those concepts most relevant to the study. Fortunately, this can be achieved quite easily because in the CDM we store not only the Standard Concepts, but also the source codes. We can review both the source codes that map to the concepts used in the study, as well as those that don't.

One way to review the source codes that map is to use the `checkCohortSourceCodes` function in the `MethodEvaluation` R package. This function uses a cohort definition as created by ATLAS as input, and for each concept set used in the cohort definition it checks which source codes map to the concepts in the set. It also computes the prevalence of these codes over time to help identify temporal issues associated with specific source codes. The example output in Figure 15.2 shows a (partial) breakdown of a concept set called “Depressive disorder.” The most prevalent concept in this concept set in the database of interest is concept 440383 (“Depressive disorder”). We see that three source codes in the database map to this concept: ICD-9 code 3.11, and ICD-10 codes F32.8 and F32.89. On the left we see that the concept as a whole first shows a gradual increase over time, but then shows a sharp drop. If we look at the individual codes, we see that this drop can be explained by the fact that the ICD-9 code stops being used at the time of the drop. Even though this is the same time the ICD-10 codes start being used, the combined prevalence of the ICD-10 codes is much smaller than that of the ICD-9 code. This specific example was due to the fact that the ICD-10 code F32.9 (“Major depressive disorder, single episode, unspecified”) should have also mapped to the concept. This problem has since been resolved in the Vocabulary.

Even though the previous example demonstrates a chance finding of a source code that was not mapped, in general identifying missing mappings is more difficult than checking mappings that are present. It requires knowing which source codes should map but don't. A semi-automated way to perform this assessment is to use the `findOrphanSourceCodes` function in the `MethodEvaluation` R package. This function allows one to search the vocabulary for source codes using a simple

¹<https://github.com/OHDSI/Vocabulary-v5.0/issues>

% per month	Max monthly %	Person count	Description
	26.81	92,019,885	Depressive Disorder
	6.64	15,969,198	Depressive disorder 440383
	6.64	15,686,275	311 (ICD9CM) Depressive disorder, not elsewhere classified
	0.46	188,230	F328 (ICD10CM) Other depressive episodes
	0.38	94,693	F3289 (ICD10CM) Other specified depressive episodes
	3.10	12,010,783	Adjustment disorder with mixed emotional features 433454
	3.07	9,839,712	30928 (ICD9CM) Adjustment disorder with mixed anxiety and depressed mood
	3.03	2,049,618	F4323 (ICD10CM) Adjustment disorder with mixed anxiety and depressed mood
	0.04	121,453	3091 (ICD9CM) Prolonged depressive reaction
	3.17	9,237,192	Dysthymia 433440

Figure 15.2: Example output of the checkCohortSourceCodes function.

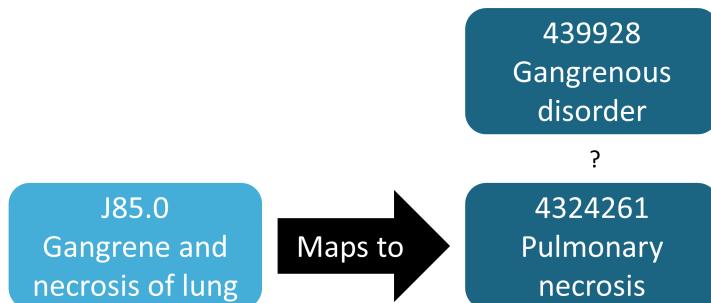


Figure 15.3: Example orphan source code.

text search, and it checks whether these source codes map to a specific concept or to one of the descendants of that concept. The resulting set of source codes is subsequently restricted to only those that appear in the CDM database at hand. For example, in a study the concept “Gangrenous disorder” (439928) and all of its descendants was used to find all occurrences of gangrene. To evaluate whether this truly includes all source codes indicating gangrene, several terms (e.g. “gangrene”) were used to search the descriptions in the CONCEPT and SOURCE_TO_CONCEPT_MAP tables to identify source codes. An automated search is then used to evaluate whether each gangrene source code appearing in the data indeed directly or indirectly (through ancestry) maps to the concept “Gangrenous disorder.” The result of this evaluation is shown in Figure 15.3, revealing that the ICD-10 code J85.0 (“Gangrene and necrosis of lung”) was only mapped to concept 4324261 (“Pulmonary necrosis”), which is not a descendant of “Gangrenous disorder.”

15.4 ACHILLES in Practice

Here we will demonstrate how to run ACHILLES against a database in the CDM format.

We first need to tell R how to connect to the server. ACHILLES uses the DatabaseConnector package, which provides a function called `createConnectionDetails`. Type `?createConnectionDetails` for the specific settings required for the various database management systems (DBMS). For example, one might connect to a PostgreSQL database using this code:

```
library(Achilles)
connDetails <- createConnectionDetails(dbms = "postgresql",
                                         server = "localhost/ohdsi",
                                         user = "joe",
                                         password = "supersecret")

cdmDbSchema <- "my_cdm_data"
cdmVersion <- "5.3.0"
```

The last two lines define the `cdmDbSchema` variable, as well as the CDM version. We will use these later to tell R where the data in the CDM format live, and what version CDM is used. Note that for Microsoft SQL Server, database schemas need to specify both the database and the schema, so for example `cdmDbSchema <- "my_cdm_data.dbo"`.

Next, we run ACHILLES:

```
result <- achilles(connectionDetails,
                     cdmDatabaseSchema = cdmDbSchema,
                     resultsDatabaseSchema = cdmDbSchema,
                     sourceName = "My database",
                     cdmVersion = cdmVersion)
```

This function will create several tables in the `resultsDatabaseSchema`, which we've set here to the same database schema as the CDM data.

We can view the ACHILLES database characterization. This can be done by pointing ATLAS to the ACHILLES results databases, or by exporting the ACHILLES results to a set of JSON files:

```
exportToJson(connectionDetails,
            cdmDatabaseSchema = cdmDatabaseSchema,
            resultsDatabaseSchema = cdmDatabaseSchema,
            outputPath = "achillesOut")
```

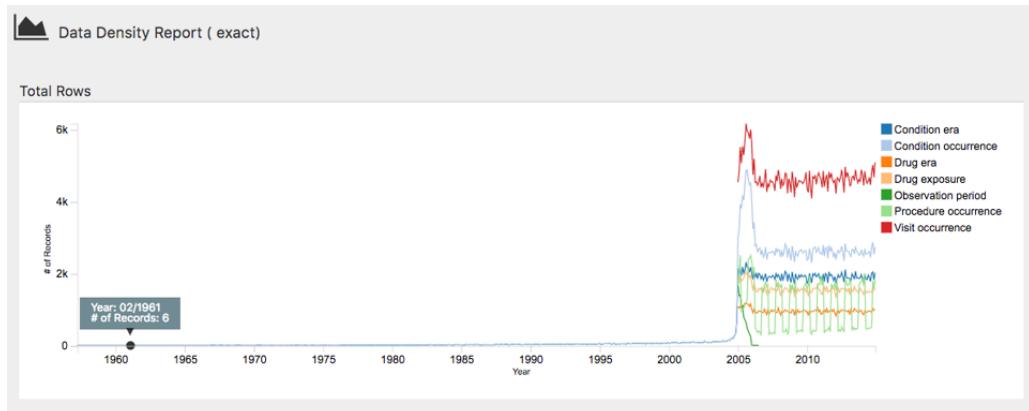


Figure 15.4: The data density plot in the ACHILLES web viewer.

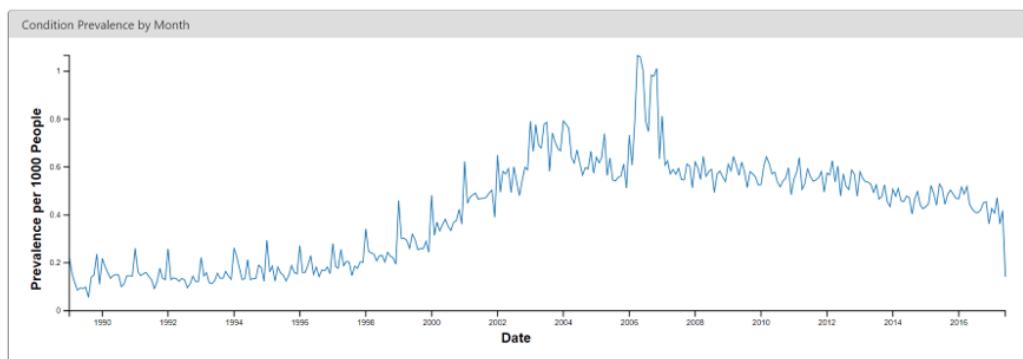


Figure 15.5: Monthly rate of diabetes coded in the ACHILLES web viewer.

The JSON files will be written to the `achillesOut` sub-folder, and can be used together with the `AchillesWeb` web application to explore the results. For example, Figure 15.4 shows the ACHILLES data density plot. This plot shows that the bulk of the data starts in 2005. However, there also appear to be a few records from around 1961, which is likely an error in the data.

Another example is shown in Figure 15.5, revealing a sudden change in the prevalence of a diabetes diagnosis code. This change coincides with changes in the reimbursement rules in this specific country, leading to more diagnoses but probably not a true increase in prevalence in the underlying population.

15.5 Data Quality Dashboard in Practice

Here we will demonstrate how to run the Data Quality Dashboard against a database in the CDM format. We do this by executing a large set of checks against the CDM connection described in Section 15.4. For now the DQD supports only CDM v5.3.1 so before connecting be sure your database is in the correct version.

As with ACHILLES we need to create the variable `cdmDbSchema` to tell R where to look for the data.

```
cdmDbSchema <- "my_cdm_data.dbo"
```

Next, we run the Dashboard...

```
DataQualityDashboard::executeDqChecks(connectionDetails = connectionDetails,
                                       cdmDatabaseSchema = cdmDbSchema,
                                       resultsDatabaseSchema = cdmDbSchema,
                                       cdmSourceName = "My database",
                                       outputFolder = "My output")
```

The above function will execute all available data quality checks on the schema specified. It will then write a table to the `resultsDatabaseSchema` which we have here set to the same schema as the CDM. This table will include all information about each check run including the CDM table, CDM field, check name, check description, Kahn category and subcategory, number of violating rows, the threshold level, and whether the check passes or fails, among others. In addition to a table this function also writes a JSON file to the location specified as the `outputFolder`. Using this JSON file we can launch a web viewer to inspect the results.

```
viewDqDashboard(jsonPath)
```

The variable `jsonPath` should be the path to the JSON file containing the results of the Dashboard, located in the `outputFolder` specified when calling the `executeDqChecks` function above.

When you first open the Dashboard you will be presented with the overview table, as seen in Figure 15.6. This will show you the total number of checks run in each Kahn category broken out by context, the number and percent that pass in each, as well as the overall pass rate.

Clicking on *Results* in the left-hand menu will take you to the drilldown results for each check that was run (Figure 15.7). In this example, the table showing a check run to determine the completeness of individual CDM tables, or, the number and percent of persons in the CDM that have at least one record in the specified table. In this case the five tables listed are all empty which the Dashboard counts as a fail. Clicking on the  icon will open a window that displays the exact query that was run on your data to produce the results listed. This allows for easy identification of the rows that were considered failures by the Dashboard.

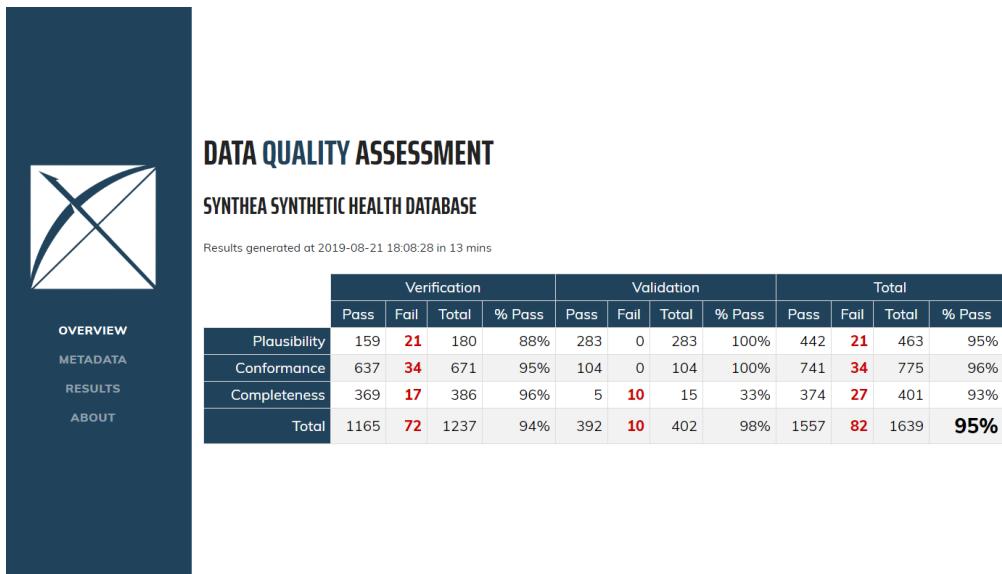


Figure 15.6: Overview of Data Quality Checks in the Data Quality Dashboard.

RESULTS

SYNTHEA SYNTHETIC HEALTH DATABASE

Results generated at 2019-08-22 14:15:06 in 29 mins

Column visibility CSV

Show 5 entries Search:

	STATUS	CONTEXT	CATEGORY	SUBCATEGORY	LEVEL	DESCRIPTION	% RECORDS
[+]	FAIL	Verification	Plausibility	Atemporal	FIELD	The number and percent of records with a value in the gap_days field of the DRUG_ERAS table less than 0. (Threshold=0%).	24.07%
[+]	FAIL	Verification	Completeness	None	FIELD	The number and percent of records with a value of 0 in the standard concept field race_concept_id in the PERSON table. (Threshold=0%).	16.74%
[+]	FAIL	Verification	Conformance	Relational	FIELD	The number and percent of records that have a value in the ethnicity_concept_id field in the PERSON table that does not exist in the CONCEPT table. (Threshold=0%).	16.15%
[+]	PASS	Verification	Completeness	None	FIELD	The number and percent of records with a NULL value in the condition_end_date of the CONDITION_OCCURRENCE. (Threshold=100%).	13.24%
[+]	PASS	Verification	Completeness	None	FIELD	The number and percent of records with a NULL value in the condition_end_datetime of the CONDITION_OCCURRENCE. (Threshold=100%).	13.24%

Showing 71 to 75 of 1,327 entries (filtered from 1,639 total entries)

Previous 1 ... 14 15 16 ... 266 Next

Figure 15.7: Drilldown into Data Quality Checks in the Data Quality Dashboard.

15.6 Study-Specific Checks in Practice

Next, we will execute several checks specifically for the angioedema cohort definition provided in Appendix B.4. We will assume the connection details have been set as described in Section 15.4, and that the cohort definition JSON and SQL of the cohort definition have been saved in the files “cohort.json” and “cohort.sql”, respectively. The JSON and SQL can be obtained from the Export tab in the ATLAS cohort definition function.

```
library(MethodEvaluation)
json <- readChar("cohort.json", file.info("cohort.json")$size)
sql <- readChar("cohort.sql", file.info("cohort.sql")$size)
checkCohortSourceCodes(connectionDetails,
                        cdmDatabaseSchema = cdmDbSchema,
                        cohortJson = json,
                        cohortSql = sql,
                        outputFile = "output.html")
```

We can open the output file in a web browser as shown in Figure 15.8. Here we see that the angioedema cohort definition has two concept sets: “Inpatient or ER visit”, and “Angioedema”. In this example database the visits were found through database-specific source codes “ER” and “IP”, that are not in the Vocabulary, although they were mapped during the ETL to standard concepts. We also see that angioedema is found through one ICD-9 and two ICD-10 codes. We clearly see the point in time of the cut-over between the two coding systems when we look at the spark-lines for the individual codes, but for the concept set as a whole there is no discontinuity at that time.

Next, we can search for orphan source codes, which are source codes that do not map to standard concept codes. Here we look for the Standard Concept “Angioedema,” and then we look for any codes and concepts that have “Angioedema” or any of the synonyms we provide as part of their name:

```
orphans <- findOrphanSourceCodes(connectionDetails,
                                    cdmDatabaseSchema = cdmDbSchema,
                                    conceptName = "Angioedema",
                                    conceptSynonyms = c("Angioneurotic edema",
                                                       "Giant hives",
                                                       "Giant urticaria",
                                                       "Periodic edema"))
View(orphans)
```

code	description	vocabularyId	overallCount
T78.3XXS	Angioneurotic edema, sequela	ICD10CM	508
10002425	Angioedemas	MedDRA	0

code	description	vocabularyId	overallCount
148774	Angioneurotic Edema of Larynx	CIEL	0
402383003	Idiopathic urticaria and/or angioedema	SNOMED	0
232437009	Angioneurotic edema of larynx	SNOMED	0
10002472	Angioneurotic edema, not elsewhere classified	MedDRA	0

The only potential orphan found that is actually used in the data is “Angioneurotic edema, sequela”, which should not be mapped to angioedema. This analysis therefore did not reveal any missing codes.

15.7 Summary



- Most observational healthcare data were not collected for research.
- Data quality checks are an integral part of research. Data quality must be assessed to determine whether the data are of sufficient quality for research purposes.
- We should assess data quality for the purpose of research in general, and critically in the context of a specific study.
- Some aspects of data quality can be assessed automatically through large sets of predefined rules, for example those in the Data Quality Dashboard.
- Other tools exist to evaluate the mapping of codes relevant for a particular study.

15.8 Exercises

Prerequisites

For these exercises we assume R, R-Studio and Java have been installed as described in Section 8.4.5. Also required are the SqlRender, DatabaseConnector, ACHILLES, and Eunomia packages, which can be installed using:

```
install.packages(c("SqlRender", "DatabaseConnector", "devtools"))
devtools::install_github("ohdsi/Achilles")
devtools::install_github("ohdsi/DataQualityDashboard")
devtools::install_github("ohdsi/Eunomia", ref = "v1.0.0")
```

The Eunomia package provides a simulated dataset in the CDM that will run inside your local R session. The connection details can be obtained using:

% per month	Max monthly %	Person count	Description
	60.60	24,189,656	Inpatient or ER visit
	39.50	15,003,249	Emergency Room Visit 9203
	39.50	15,003,249	ER (None) No matching concept
	23.90	9,186,407	Inpatient Visit 9201
	23.90	9,186,407	IP (None) No matching concept
	0.27	76,711	Angioedema
	0.27	76,711	Angioedema 432791
	0.26	64,726	9951 (ICD9CM) Angioneurotic edema, not elsewhere classified
	0.20	8,822	T783XXA (ICD10CM) Angioneurotic edema, initial encounter
	0.09	3,163	T783XXD (ICD10CM) Angioneurotic edema, subsequent encounter

Figure 15.8: Source codes used in the angioedema cohort definition.

```
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
```

The CDM database schema is “main”.

Exercise 15.1. Execute ACHILLES against the Eunomia database.

Exercise 15.2. Execute the DataQualityDashboard against the Eunomia database.

Exercise 15.3. Extract the DQD list of checks.

Suggested answers can be found in Appendix E.10.

Chapter 16

Clinical Validity

Chapter leads: Joel Swerdel, Seng Chan You, Ray Chen & Patrick Ryan

The likelihood of transforming matter into energy is something akin to shooting birds in the dark in a country where there are only a few birds. *Einstein, 1935*

The vision of OHDSI is “A world in which observational research produces a comprehensive understanding of health and disease.” Retrospective designs provide a vehicle for research using existing data but can be riddled with threats to various aspects of validity as discussed in Chapter 14. It is not easy to isolate clinical validity from quality of data and statistical methodology, but here we will focus on three aspects in terms of clinical validity: Characteristics of health care databases, Cohort validation, and Generalizability of the evidence. Let’s go back to the example of population-level estimation (Chapter 12). We tried to answer the question “Do ACE inhibitors cause angioedema compared to thiazide or thiazide-like diuretics?” In that example, we demonstrated that ACE inhibitors caused more angioedema than thiazide or thiazide-like diuretics. This chapter is dedicated to answer the question: “To what extent does the analysis conducted match the clinical intention?”

16.1 Characteristics of Health Care Databases

It is possible that what we found is the relationship between **prescription** of ACE inhibitor and angioedema rather than the relationship between **use** of ACE inhibitor and angioedema. We’ve already discussed data quality in the previous chapter (15). The quality of the converted database into the Common Data Model (CDM) cannot exceed the original database. Here we are addressing the characteristics of most healthcare utilization databases. Many databases used in OHDSI originated from administrative claims or electronic health records (EHR). Claims and EHR have different data capture processes, neither of which has

research as a primary intention. Data elements from claims records are captured for the purpose of reimbursement, financial transactions between clinicians and payers whereby services provided to patients by providers are sufficiently justified to enable agreement on payments by the responsible parties. Data elements in EHR records are captured to support clinical care and administrative operations, and they commonly only reflect the information that providers within a given health system feel are necessary to document the current service and provide necessary context for anticipated follow-up care within their health system. They may not represent a patient's complete medical history and may not integrate data from across health systems.

To generate reliable evidence from observational data, it is useful for a researcher to understand the journey that the data undergoes from the moment that a patient seeks care through the moment that the data reflecting that care are used in an analysis. As an example, "drug exposure" can be inferred from various sources of observational data, including prescriptions written by clinicians, pharmacy dispensing records, hospital procedural administrations, or patient self-reported medication history. The source of data can impact our level of confidence in the inference we draw about which patients did or did not use the drug, as well as when and for how long. The data capture process can result in under-estimation of exposure, such as if free samples or over-the counter drugs are not recorded, or over-estimation of exposure, such as if a patient doesn't fill the prescription written or doesn't adherently consume the prescription dispensed. Understanding the potential biases in exposure and outcome ascertainment, and more ideally quantifying and adjusting for these measurement errors, can improve our confidence in the validity of the evidence we draw from the data we have available.

16.2 Cohort Validation

Hripcak and Albers (2017) described that "a phenotype is a specification of an observable, potentially changing state of an organism, as distinguished from the genotype, which is derived from an organism's genetic makeup. The term phenotype can be applied to patient characteristics inferred from electronic health record (EHR) data. Researchers have been carrying out EHR phenotyping since the beginning of informatics, from both structured data and narrative data. The goal is to draw conclusions about a target concept based on raw EHR data, claims data, or other clinically relevant data. Phenotype algorithms – i.e., algorithms that identify or characterize phenotypes – may be generated by domain experts and knowledge engineers, including recent research in knowledge engineering or through diverse forms of machine learning... to generate novel representations of the data."

This description highlights several attributes useful to reinforce when considering clinical validity: 1) it makes it clear that we are talking about something that is observable (and therefore possible to be captured in our observational data); 2) it

includes the notion of time in the phenotype specification (since a state of a person can change); 3) it draws a distinction between the phenotype as the desired intent vs. the phenotype algorithm, which is the implementation of the desired intent.

OHDSI has adopted the term “cohort” to define the set of persons satisfying one or more inclusion criteria for a duration of time. A “cohort definition” represents the logic necessary to instantiate a cohort against an observational database. In this regard, the cohort definition (or phenotype algorithm) is used to produce a cohort, which is intended to represent the phenotype, being the persons who belong to the observable clinical state of interest.

Most types of observational analyses, including clinical characterization, population-level effect estimation, and patient-level prediction, require one or more cohorts to be established as part of the study process. To evaluate the validity of the evidence produced by these analyses, one must consider this question for each cohort: to what extent do the persons identified in the cohort based on the cohort definition and the available observational data accurately reflect the persons who truly belong to the phenotype?

To return to the population-level estimation example (Chapter 12) “Do ACE inhibitors cause angioedema compared to thiazide or thiazide-like diuretics?”, we must define three cohorts: a target cohort of persons who are new users of ACE inhibitors, a comparator cohort of persons who are new users of thiazide diuretics, and an outcome cohort of persons who develop angioedema. How confident are we that all use of ACE inhibitors or thiazide diuretics is completely captured, such that “new users” can be identified by the first observed exposure, without concern of prior (but unobserved) use? Can we comfortably infer that persons who have a drug exposure record for ACE inhibitors were in fact exposed to the drug, and those without a drug exposure were indeed unexposed? Is there uncertainty in defining the duration of time that a person is classified in the state of “ACE inhibitor use,” either when inferring cohort entry at the time the drug was started or cohort exit when the drug was discontinued? Have persons with a condition occurrence record of “Angioedema” actually experienced rapid swelling beneath the skin, differentiated from other types of dermatologic allergic reactions? What proportion of patients who developed angioedema received medical attention that would give rise to the observational data used to identify these clinical cases based on the cohort definition? How well can the angioedema events which are potentially drug-induced be disambiguated from the events known to be caused by other agents, such as food allergy or viral infection? Is disease onset sufficiently well captured that we have confidence in drawing a temporal association between exposure status and outcome incidence? Answering these types of questions is at the heart of clinical validity.

In this chapter, we will discuss the methods for validating cohort definitions. We first describe the metrics used to measure the validity of a cohort definition. Next, we describe two methods to estimate these metrics: 1) clinical adjudication through

		Gold Standard	
		True	False
Cohort Definition	True	True Positive	False Negative
	False	False Negative	True Negative

Figure 16.1: Confusion matrix.

source record verification, and 2) PheEvaluator, a semi-automated method using diagnostic predictive modeling.

16.2.1 Cohort Evaluation Metrics

Once the cohort definition for the study has been determined, the validity of the definition can be evaluated. A common approach to assess validity is by comparing some or all persons in a defined cohort to a reference ‘gold standard’ and expressing the results in a confusion matrix, a two-by-two contingency table that stratifies persons according to their gold standard classification and qualification within the cohort definition. Figure 16.1 shows the elements of the confusion matrix.

The true and false results from the cohort definition are determined by applying the definition to a group of persons. Those included in the definition are considered positive for the health condition and are labeled “True.” Those persons not included in the cohort definition are considered negative for the health condition and are labeled “False”. While the absolute truth of a person’s health state considered in the cohort definition is very difficult to determine, there are multiple methods to establish a reference gold standard, two of which will be described later in the chapter. Regardless of the method used, the labeling of these persons is the same as described for the cohort definition.

In addition to errors in the binary indication of phenotype designation, the timing of the health condition may also be incorrect. For example, while the cohort definition may correctly label a person as belonging to a phenotype, the definition may incorrectly specify the date and time when a person without the condition became a person with the condition. This error would add bias to studies using survival analysis results, e.g., hazard ratios, as an effect measure.

The next step in the process is to assess the concordance of the gold standard with the cohort definition. Those persons that are labeled by both the gold standard method and the cohort definition as “True” are called “True Positives.” Those persons that are labeled by the gold standard method as “False” and by the cohort definition as “True” are called “False Positives,” i.e., the cohort definition misclassified these persons as having the condition when they do not. Those persons that are labeled by both the gold standard method and the cohort definition as “False” are called “True Negatives.” Those persons that are labeled by the gold standard method as “True” and by the cohort definition as “False” are called

“False Negatives,” i.e., the cohort definition incorrectly classified these persons as not having the condition, when in fact they do belong to the phenotype. Using the counts from the four cells in the confusion matrix, we can quantify the accuracy of the cohort definition in classifying phenotype status in a group of persons. There are standard performance metrics for measuring cohort definition performance:

1. **Sensitivity of the cohort definition** – what proportion of the persons who truly belong to the phenotype in the population were correctly identified to have the health outcome based on the cohort definition? This is determined by the following formula:

$$\text{Sensitivity} = \text{True Positives} / (\text{True Positives} + \text{False Negatives})$$

2. **Specificity of the cohort definition** – what proportion of the persons who do not belong to the phenotype in the population were correctly identified to not have the health outcome based on the cohort definition? This is determined by the following formula:

$$\text{Specificity} = \text{True Negatives} / (\text{True Negatives} + \text{False Positives})$$

3. **Positive predictive value (PPV) of the cohort definition** – what proportion of the persons identified by the cohort definition to have the health condition actually belong to the phenotype? This is determined by the following formula:

$$\text{PPV} = \text{True Positives} / (\text{True Positives} + \text{False Positives})$$

4. **Negative predictive value (NPV) of the cohort definition** – what proportion of the persons identified by the cohort definition to not have the health condition actually did not belong to the phenotype? This is determined by the following formula:

$$\text{NPV} = \text{True Negatives} / (\text{True Negatives} + \text{False Negatives})$$

Perfect scores for these measures are 100%. Due to the nature of observational data, perfect scores are usually far from the norm. Rubbo et al. (2015) reviewed studies validating cohort definitions for myocardial infarction. Of the 33 studies they examined, only one cohort definition in one dataset obtained a perfect score for PPV. Overall, 31 of the 33 studies reported PPVs $\geq 70\%$. They also found, however, that of the 33 studies only 11 reported sensitivity and 5 reported specificity. PPV is a function of sensitivity, specificity, and prevalence. Datasets with different values for prevalence will produce different values for PPV with sensitivity and specificity held constant. Without sensitivity and specificity, correcting for bias due to imperfect cohort definitions is not possible. Additionally, the misclassification of the health condition may be differential, meaning the cohort definition performs differently on one group of persons relative to the comparison group, or non-differentially, when the cohort definition performs similarly on both comparison groups. Prior cohort definition validation studies have not tested for potential

differential misclassification, even though it can lead to strong bias in effect estimates.

Once the performance metrics have been established for the cohort definition, these may be used to adjust the results for studies using these definitions. In theory, adjusting study results for these measurement error estimates has been well established. In practice, though, because of the difficulty in obtaining the performance characteristics, these adjustments are rarely considered. The methods used to determine the gold standard are described in the remainder of this section.

16.3 Source Record Verification

A common method used to validate cohort definitions has been clinical adjudication through source record verification: a thorough examination of a person's records by one or more domain experts with sufficient knowledge to competently classify the clinical condition or characteristic of interest. Chart review generally follows the following steps:

1. Obtain permission from local institutional review board (IRB) and/or persons as needed to conduct study including chart review.
2. Generate cohort using cohort definition to be evaluated. Sample a subset of the persons to manually review if there are insufficient resources to adjudicate the entire cohort.
3. Identify one or more persons with sufficient clinical expertise to review person records.
4. Determine guidelines for adjudicating whether a person is positive or negative for the desired clinical condition or characteristic.
5. Clinical experts review and adjudicate all available data for the persons within the sample to classify each person as to whether they belong to the phenotype or not.
6. Tabulate persons according to the cohort definition classification and clinical adjudication classification into a confusion matrix, and calculate the performance characteristics possible from the data collected.

Results from a chart review are typically limited to the evaluation of one performance characteristic, positive predictive value (PPV). This is because the cohort definition under evaluation only generates persons that are believed to have the desired condition or characteristics. Therefore, each person in the sample of the cohort is classified as either a true positive or false positive based on the clinical adjudication. Without knowledge of all persons in the phenotype in the entire population (including those not identified by the cohort definition), it is not possible to identify the false negatives, and thereby fill in the remainder of the confusion matrix to generate the remaining performance characteristics. Potential methods of identifying all persons in the phenotype across the population include chart review of the entire database, which is generally not feasible unless the overall population is small, or the utilization of comprehensive clinical registries in which all true cases

have already been flagged and adjudicated, such as tumor registries (see example below). Alternatively, one can sample persons who do not qualify for the cohort definition to produce a subset of predicted negatives, and then repeating steps 3-6 of the chart review above to check whether these patients are truly lacking the clinical condition or characteristic of interest can identify true negatives or false negatives. This would allow the estimation of negative predictive value (NPV), and if an appropriate estimate of the phenotype prevalence is available, then sensitivity and specificity can be estimated.

There are a number of limitations to clinical adjudication through source record verification. As alluded to earlier, chart review can be a very time-consuming and resource-intensive process, even just for the evaluation of a single metric such as PPV. This limitation significantly impedes the practicality of evaluating an entire population to fill out a complete confusion matrix. In addition, multiple steps in the above process have the potential to bias the results of the study. For example, if records are not equally accessible in the EHR, if there is no EHR, or if individual patient consent is required, then the subset under evaluation may not be truly random and could introduce sampling or selection bias. In addition, manual adjudication is susceptible to human error or misclassification and thereby may not represent a perfectly accurate metric. There can often be disagreement between clinical adjudicators due to the data in the person's record being vague, subjective, or of low quality. In many studies, the process involves a majority-rules decision for consensus which yields a binary classification for persons that does not reflect the inter-rater discordance.

16.3.1 Example of Source Record Verification

An example of the process to conduct a cohort definition validation using chart review is provided from a study by the Columbia University Irving Medical Center (CUIMC), which validated a cohort definition for multiple cancers as part of a feasibility study for the National Cancer Institute (NCI). The steps used to conduct the validation for the example of one of these cancers—prostate cancer—are as follows:

1. Submitted proposal and obtained IRB consent for OHDSI cancer phenotyping study.
2. Developed a cohort definition for prostate cancer: Using ATHENA and ATLAS to explore the vocabulary, we created a cohort definition to include all patients with a condition occurrence for Malignant Tumor of Prostate (concept ID 4163261), excluding Secondary Neoplasm of Prostate (concept ID 4314337) or Non-Hodgkin's Lymphoma of Prostate (concept ID 4048666).
3. Generated cohort using ATLAS and randomly selected 100 patients for manual review, mapping each PERSON_ID back to patient MRN using mapping tables. 100 patients were selected in order to achieve our desired level of statistical precision for the performance metric of PPV.
4. Manually reviewed records in the various EHRs—both inpatient and

outpatient—in order to determine whether each person in the random subset was a true or false positive.

5. Manual review and clinical adjudication were performed by one physician (although ideally in future more rigorous validation studies would be done by a higher number of reviewers to assess for consensus and inter-rater reliability).
6. Determination of a reference standard was based on clinical documentation, pathology reports, labs, medications and procedures as documented in the entirety of the available electronic patient record.
7. Patients were labeled as 1) prostate cancer 2) no prostate cancer or 3) unable to determine.
8. A conservative estimate of PPV was calculated using the following: prostate cancer/ (no prostate cancer + unable to determine).
9. Then, using the tumor registry as an additional gold standard to identify a reference standard across the entire CUIMC population, we counted the number of persons in the tumor registry which were and were not accurately identified by the cohort definition, which allowed us to estimate sensitivity using these values as true positives and false negatives.
10. Using the estimated sensitivity, PPV, and prevalence, we could then estimate specificity for this cohort definition. As noted previously, this process was time-consuming and labor-intensive, as each cohort definition had to be individually evaluated through manual chart review as well as correlated with the CUIMC tumor registry in order to identify all performance metrics. The IRB approval process itself took weeks despite an expedited review while obtaining access to the tumor registry, and the process of manual chart review itself took a few weeks longer.

A review of validation efforts for myocardial infarction (MI) cohort definitions by Rubbo et al. (2015) found that there was significant heterogeneity in the cohort definitions used in the studies as well as in the validation methods and the results reported. The authors concluded that for acute myocardial infarction there is no gold standard cohort definition available. They noted that the process was both costly and time-consuming. Due to that limitation, most studies had small sample sizes in their validation leading to wide variations in the estimates for the performance characteristics. They also noted that in the 33 studies, while all the studies reported positive predictive value, only 11 studies reported sensitivity and only five studies reported specificity. As mentioned previously, without estimates of sensitivity and specificity, statistical correction for misclassification bias cannot be performed.

16.4 PheValuator

The OHDSI community has developed a different approach to constructing a gold standard by using diagnostic predictive models. (Swerdel et al., 2019) The general idea is to emulate the ascertainment of the health outcome similar to the way

clinicians would in a source record validation, but in an automated way that can be applied at scale. The tool has been developed as an open-source R package called PheEvaluator.¹ PheEvaluator uses functions from the Patient Level Prediction package.

The process is as follows:

1. Create an extremely specific (“xSpec”) cohort: Determine a set of persons with a very high likelihood of having the outcome of interest to be used as noisy positive labels when training a diagnostic predictive model.
2. Create an extremely sensitive (“xSens”) cohort: Determine a set of persons that should include anyone who could possibly have the outcome. This cohort will be used to identify its inverse: the set of people we are confident do not have the outcome, to be used as noisy negative labels when training a diagnostic predictive model.
3. Fit a predictive model using the xSpec and xSens cohort: As described in Chapter 13, we fit a model using a wide array of patient features as predictors, and aim to predict whether a person belongs to the xSpec cohort (those we believe have the outcome) or the inverse of the xSens cohort (those we believe do not have the outcome).
4. Apply the fitted model to estimate the probability of the outcome for a hold-out set of persons who will be used to evaluate cohort definition performance: The set of predictors from the model can be applied to a person’s data to estimate the predicted probability that the person belongs to the phenotype. We use these predictions as a **probabilistic gold standard**.
5. Evaluate the performance characteristics of the cohort definitions: We compare the predicted probability to the binary classification of a cohort definition (the test conditions for the confusion matrix). Using the test conditions and the estimates for the true conditions, we can fully populate the confusion matrix and estimate the entire set of performance characteristics, i.e., sensitivity, specificity, and predictive values.

The primary limitation to using this approach is that the estimation of the probability of a person having the health outcome is limited by the data in the database. Depending on the database, important information, such as clinician notes, may not be available.

In diagnostic predictive modeling we create a model that discriminates between those with the disease and those without the disease. As described in the Patient-Level Prediction chapter (Chapter 13), prediction models are developed using a *target cohort* and an *outcome cohort*. The target cohort includes persons with and without the health outcome; the outcome cohort identifies those persons in the target cohort with the health outcome. For the PheEvaluator process, we use an extremely specific cohort definition, the “xSpec” cohort, to determine the outcome cohort for the prediction model. The xSpec cohort uses a definition to find those

¹<https://github.com/OHDSI/PheEvaluator>

with a very high probability of having the disease of interest. The xSpec cohort may be defined as those persons who have multiple condition occurrence records for the health outcome of interest. For example, for atrial fibrillation, we may have persons who have 10 or more records with the atrial fibrillation diagnosis code. For MI, an acute outcome, we may use 5 occurrences of MI and include the requirement of having at least two occurrences from an inpatient setting. The target cohort for the predictive model is constructed from the union of persons with a low likelihood of having the health outcome of interest and those persons in the xSpec cohort. To determine those persons with a low likelihood of having the health outcome of interest, we sample from the entire database and exclude persons who have some evidence suggestive of belonging to the phenotype, typically by removing persons with any records containing the concepts used to define the xSpec cohort. There are limitations to this method. It is possible that these xSpec cohort persons may have different characteristics than others with the disease. It may also be that these persons had longer observation time after initial diagnosis than the average patient. We use LASSO logistic regression to create the prediction model used to generate the probabilistic gold standard. (Suchard et al., 2013) This algorithm produces a parsimonious model and typically removes many of the collinear covariates which may be present across the dataset. In the current version of the PheEvaluator software, outcome status (yes/no) is evaluated based on all data for a person (all observation time), and does not evaluate the accuracy of the cohort start date.

16.4.1 Example Validation By PheEvaluator

We may use PheEvaluator to assess the complete performance characteristics for a cohort definition to be used in a study where it is necessary to determine those persons who have had an acute myocardial infarction.

The following are the steps for testing cohort definitions for MI using PheEvaluator:

Step 1: Define the xSpec Cohort

Determine those with MI with a high probability. We required a condition occurrence record with a concept for myocardial infarction or any of its descendants, with one or more occurrences of MI recorded from a hospital in-patient visit within 5 days, and 4 or more occurrences of MI in the patient record within 365 days. Figure 16.2 illustrates this cohort definition for MI in ATLAS.

Step 2: Define the xSens Cohort

We then develop an extremely sensitive cohort (xSens). This cohort may be defined for MI as those persons with at least one condition occurrence record containing a myocardial infarction concept at any time in their medical history. Figure 16.3 illustrates the xSens cohort definition for MI in ATLAS.

Cohort #10934

MI xSpec Cohort

Definition Concept Sets Generation Reporting Export

[460] MI xSpec Model

Cohort Entry Events

Events having any of the following criteria:

+ Add Initial Event ▾

a condition occurrence of [460] Myocardial Infarction ▾ + Add attribute... ▾ Delete Criteria

with continuous observation of at least 365 days before and 0 days after event index date

Limit initial events to: earliest event per person.

Restrict initial events to:

having all of the following criteria:

+ Add criteria to group... ▾

with at least 1 using all occurrences of:

+ Add attribute... ▾ Delete Criteria

a condition occurrence of [460] Myocardial Infarction ▾

✖ with a Visit occurrence of: ✖ Inpatient Visit Add Import

where event starts between 0 days Before and 5 days After index start date add additional constraint

restrict to the same visit occurrence

allow events from outside observation period

and with at least 4 using all occurrences of:

+ Add attribute... ▾ Delete Criteria

a condition occurrence of [460] Myocardial Infarction ▾

where event starts between 1 days After and 365 days After index start date add additional constraint

restrict to the same visit occurrence

allow events from outside observation period

Limit initial events to: earliest event per person.

Remove initial event restriction

Figure 16.2: An extremely specific cohort definition (xSpec) for myocardial infarction.

Figure 16.3: An extremely sensitive cohort definition (xSens) for myocardial infarction.

Step 3: Fit the Predictive Model

The function `createPhenoModel` develops the diagnostic predictive model for assessing the probability of having the health outcome of interest in the evaluation cohort. To use this function, we utilize the `xSpec` and `xSens` cohorts developed in Steps 1 and 2. The `xSpec` cohort will be entered as the `xSpecCohort` parameter in the function. The `xSens` cohort will be entered as the `exclCohort` parameter in the function to indicate that those in the `xSens` cohort should be excluded from the target cohort used in the modeling process. Using this exclusion method, we can determine persons with a low likelihood of having the health outcome. We may think of this group as “noisy negative” persons, i.e., a group of persons likely negative for the health outcome but allowing for a small possibility of including some persons positive for the health outcome. We may also use the `xSens` cohort as the `prevCohort` parameter in the function. This parameter is used in the process to determine an approximate prevalence of the health outcome in the population. Normally, a large random sample of persons from a database should produce a population of persons where the persons with the outcome of interest are about in proportion to the prevalence of the outcome in the database. Using the method we described, we no longer have a random sample of persons and need to re-calibrate the predictive model based on resetting the proportion of persons with the outcome to those without the outcome.

All concepts used to define the `xSpec` cohort must be excluded from the modeling process. To do this we set the `excludedConcepts` parameter to the list of concepts used in the `xSpec` definition. For example, for MI we created a concept set in ATLAS using the concept for Myocardial infarction plus all its descendants. For this example, we would set the `excludedConcepts` parameter to 4329847, the concept

ID for Myocardial infarction, and we would also set the `addDescendantsToExclude` parameter to TRUE, indicating that any descendants of the excluded concepts should also be excluded.

There are several parameters that may be used to specify the characteristics of the persons included in the modeling process. We can set the ages of the persons included in the modeling process by setting the `lowerAgeLimit` to the lower bounds of age desired in the model and the `upperAgeLimit` to the upper bounds. We may wish to do this if the cohort definitions for a planned study will be created for a certain age group. For example, if the cohort definition to be used in a study is for Type 1 diabetes mellitus in children, you may want to limit the ages used to develop the diagnostic predictive model to ages 5 to 17 years old for example. In doing so, we will produce a model with features that are likely more closely related to the persons selected by the cohort definitions to be tested. We can also specify which sex is included in the model by setting the `gender` parameter to the concept ID for either male or female. By default, the parameter is set to include both males and females. This feature may be useful in sex-specific health outcomes such as prostate cancer. We can set the time frame for person inclusion based on the first visit in the person's record by setting the `startDate` and `endDate` parameters to the lower and upper bounds of the date range, respectively. Finally, the `mainPopnCohort` parameter may be used to specify a large population cohort from which all persons in the target and outcome cohorts will be selected. In most instances this will be set to 0, indicating no limitation on selecting persons for the target and outcome cohorts. There may be times, however, when this parameter is useful for building a better model, possibly in cases where the prevalence of the health outcome is extremely low, perhaps 0.01% or lower. For example:

```
setwd("c:/temp")
library(PheEvaluator)
connectionDetails <- createConnectionDetails(
  dbms = "postgresql",
  server = "localhost/ohdsi",
  user = "joe",
  password = "supersecret")

phenoTest <- createPhenoModel(
  connectionDetails = connectionDetails,
  xSpecCohort = 10934,
  cdmDatabaseSchema = "my_cdm_data",
  cohortDatabaseSchema = "my_results",
  cohortDatabaseTable = "cohort",
  outDatabaseSchema = "scratch.dbo", #should have write access
  trainOutFile = "5XMI_train",
  exclCohort = 1770120, #the xSens cohort
  prevCohort = 1770119, #the cohort for prevalence determination
  modelAnalysisId = "20181206V1",
```

```

excludedConcepts = c(312327, 314666),
addDescendantsToExclude = TRUE,
cdmShortName = "myCDM",
mainPopnCohort = 0, #use the entire person population
lowerAgeLimit = 18,
upperAgeLimit = 90,
gender = c(8507, 8532),
startDate = "20100101",
endDate = "20171231")

```

In this example, we used the cohorts defined in the “my_results” database, specifying the location of the cohort table (cohortDatabaseSchema, cohortDatabaseTable - “my_results.cohort”) and where the model will find the conditions, drug exposures, etc. to inform the model (cdmDatabaseSchema - “my_cdm_data”). The persons included in the model will be those whose first visit in the CDM is between January 1, 2010 and December 31, 2017. We are also specifically excluding the concept IDs 312327, 314666, and their descendants which were used to create the xSpec cohort. Their ages at the time of first visit will be between 18 and 90. With the parameters above, the name of the predictive model output from this step will be: “c:/temp/lr_results_5XMI_train_myCDM_ePPV0.75_20181206V1.rds”

Step 4: Creating the Evaluation Cohort

The function `createEvalCohort` uses the PatientLevelPrediction package function `applyModel` to produce a large cohort of persons, each with a predicted probability for the health outcome of interest. The function requires specifying the xSpec cohort (by setting the `xSpecCohort` parameter to the xSpec cohort ID). We may also specify the characteristics of the persons included in the evaluation cohort as we did in the previous step. This could include specifying the lower and upper ages limits (by setting, as ages, the `lowerAgeLimit` and `upperAgeLimit` arguments, respectively), the sex (by setting the `gender` parameter to the concept IDs for male and/or female), the starting and ending dates (by setting, as dates, the `startDate` and `endDate` arguments, respectively), and designating a large population from which to select the persons by setting the `mainPopnCohort` to the cohort Id for the population to use.

For example:

```

setwd("c:/temp")
connectionDetails <- createConnectionDetails(
  dbms = "postgresql",
  server = "localhost/ohdsi",
  user = "joe",
  password = "supersecret")

```

```
evalCohort <- createEvalCohort(
  connectionDetails = connectionDetails,
  xSpecCohort = 10934,
  cdmDatabaseSchema = "my_cdm_data",
  cohortDatabaseSchema = "my_results",
  cohortDatabaseTable = "cohort",
  outDatabaseSchema = "scratch.dbo",
  testOutFile = "5XMI_eval",
  trainOutFile = "5XMI_train",
  modelAnalysisId = "20181206V1",
  evalAnalysisId = "20181206V1",
  cdmShortName = "myCDM",
  mainPopnCohort = 0,
  lowerAgeLimit = 18,
  upperAgeLimit = 90,
  gender = c(8507, 8532),
  startDate = "20100101",
  endDate = "20171231")
```

In this example, the parameters specify that the function should use the model file: “c:/temp/lr_results_5XMI_train_myCDM_ePPV0.75_20181206V1.rds” to produce the evaluation cohort file: “c:/temp/lr_results_5XMI_eval_myCDM_ePPV0.75_20181206V1.rds”. The model and the evaluation cohort files created in this step will be used in the evaluation of the cohort definitions provided in the next step.

Step 5: Creating and Testing Cohort Definitions

The next step is to create and test the cohort definitions to be evaluated. The desired performance characteristics may depend on the intended use of the cohort to address the research question of interest. For certain questions, a very sensitive algorithm may be required; others may require a more specific algorithm. The process for determining the performance characteristics for a cohort definition using PheEvaluator is shown in Figure 16.4.

In part A of Figure 16.4, we examined the persons from the cohort definition to be tested and found those persons from the evaluation cohort (created in the previous step) who were included in the cohort definition (Person IDs 016, 019, 022, 023, and 025) and those from the evaluation cohort who were not included (Person IDs 017, 018, 020, 021, and 024). For each of these included/excluded persons, we had previously determined the probability of the health outcome using the predictive model ($p(O)$).

We estimated the values for True Positives, True Negatives, False Positives, and False Negatives as follows (Part B of Figure 16.4):

1. If the cohort definition included a person from the evaluation cohort, i.e., the cohort definition considered the person a “positive.” The predicted

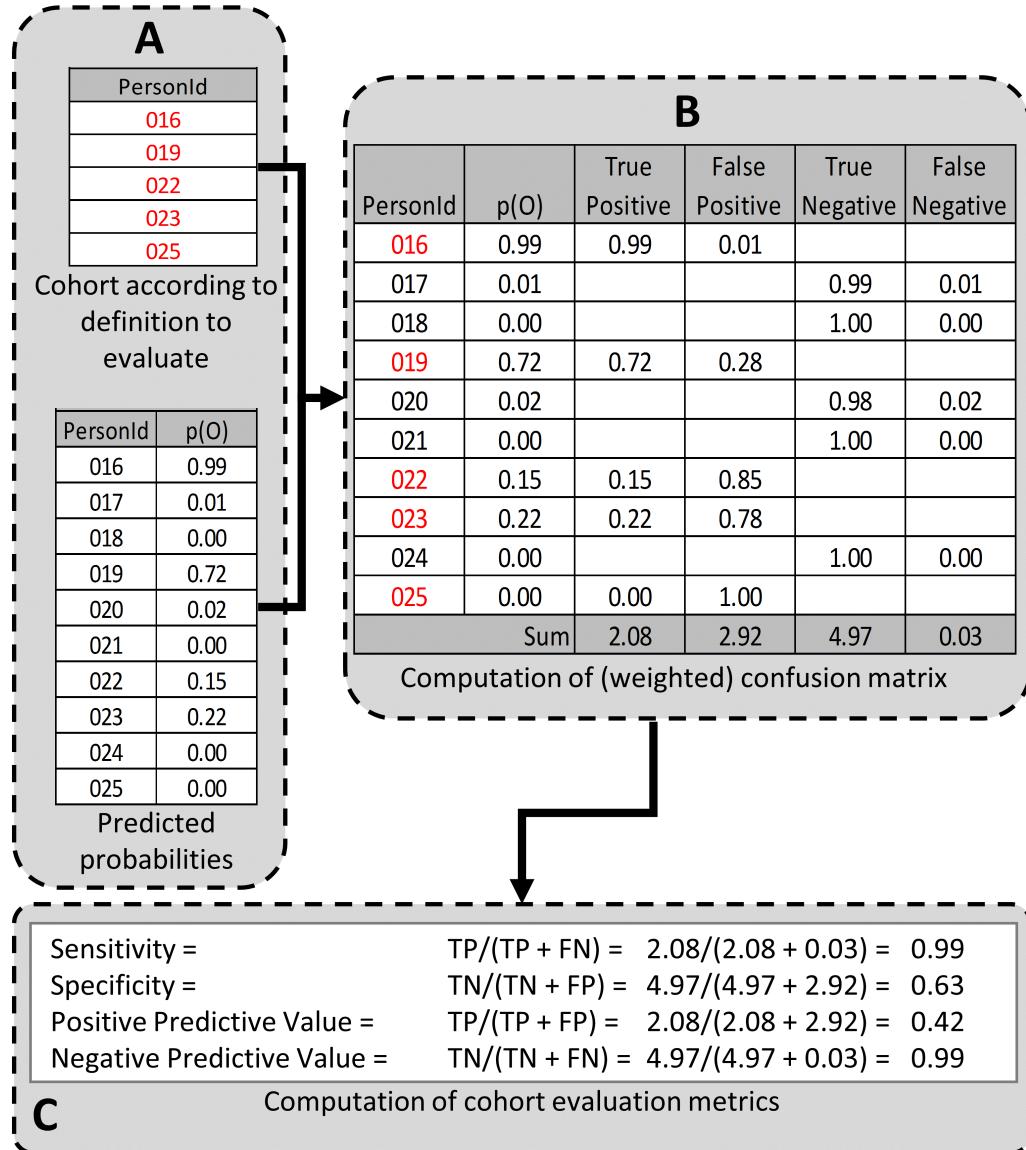


Figure 16.4: Determining the Performance Characteristics of a cohort definition using PheEvaluator. $p(O)$ = Probability of outcome; TP = True Positive; FN = False Negative; TN = True Negative; FP = False Positive.

probability for the health outcome indicated the expected value of the number of counts contributed by that person to the True Positives, and one minus the probability indicated the expected value of the number of counts contributed by that person to the False Positives for that person. We added all the expected values of counts across persons to get the total expected value. For example, PersonId 016 had a predicted probability of 99% for the presence of the health outcome, 0.99 was added to the True Positives (expected value of counts added 0.99) and $1.00 - 0.99 = 0.01$ was added to the False Positives (0.01 expected value). This was repeated for all the persons from the evaluation cohort included in the cohort definition (i.e., PersonIds 019, 022, 023, and 025).

2. Similarly, if the cohort definition did not include a person from the evaluation cohort, i.e. the cohort definition considered the person a “negative,” one minus the predicted probability for the phenotype for that person was the expected value of counts contributed to True Negatives and was added to it, and, in parallel, the predicted probability for the phenotype was the expected value of counts contributed to the False Negatives and was added to it. For example, PersonId 017 had a predicted probability of 1% for the presence of the health outcome (and, correspondingly, 99% for the absence of the health outcome) and $1.00 - 0.01 = 0.99$ was added to the True Negatives and 0.01 was added to the False Negatives. This was repeated for all the persons from the evaluation cohort not included in the cohort definition (i.e., PersonIds 018, 020, 021, and 024).

After adding these values over the full set of persons in the evaluation cohort, we filled the four cells of the confusion matrix with the expected values of counts for each cell, and we were able to create point estimates of the PA performance characteristics like sensitivity, specificity, and positive predictive value (Figure 1C). We emphasize that these expected cell counts cannot be used to assess the variance of the estimates, only the point estimates. In the example, the sensitivity, specificity, PPV, and NPV were 0.99, 0.63, 0.42, and 0.99, respectively.

Determining the performance characteristics of the cohort definition uses the function `testPhenotype`. This function uses the output from the prior two steps where we created the model and evaluation cohorts. We would set the `modelFileName` parameter to the RDS file output from `createPhenoModel` function, in this example, “c:/temp/lr_results_5XMI_train_myCDM_ePPV0.75_20181206V1.rds”. We would set the `resultsFileName` parameter to the RDS file output from `createEvalCohort` function, in this example, “c:/temp/lr_results_5XMI_eval_myCDM_ePPV0.75_20181206V1.rds”. To test the cohort definition we wish to use in our study, we set the `cohortPheno` to the cohort ID for that cohort definition. We can set the `phenText` parameter to some human readable description for the cohort definition, such as “MI Occurrence, Hospital In-Patient Setting”. We will set the `testText` parameter to some human readable description for the `xSpec` definition, such as “5 X MI.” The output from this step is a data frame that contains the performance characteristics

for the cohort definition tested. The settings for the `cutPoints` parameter is a list of values that will be used to develop the performance characteristics results. The performance characteristics are usually calculated using the “expected values” as described in Figure 1. To retrieve the performance characteristics based on the expected values, we include “EV” in the list for the `cutPoints` parameter. We may also want to see the performance characteristics based on specific predicted probabilities, i.e., cut points. For example, if we wanted to see the performance characteristics of all those at or above a predicted probability of 0.5 were considered positive for the health outcome and all those under a predicted probability of 0.5 were considered negative, we would add “0.5” to the `cutPoints` parameter list. For example:

```
setwd("c:/temp")
connectionDetails <- createConnectionDetails(
  dbms = "postgresql",
  server = "localhost/ohdsi",
  user = "joe",
  password = "supersecret")

phenoResult <- testPhenotype(
  connectionDetails = connectionDetails,
  cutPoints = c(0.1, 0.2, 0.3, 0.4, 0.5, "EV", 0.6, 0.7, 0.8, 0.9),
  resultsFileName =
    "c:/temp/lr_results_5XMI_eval_myCDM_ePPV0.75_20181206V1.rds",
  modelFileName =
    "c:/temp/lr_results_5XMI_train_myCDM_ePPV0.75_20181206V1.rds",
  cohortPheno = 1769702,
  phenText = "All MI by Phenotype 1 X In-patient, 1st Position",
  order = 1,
  testText = "MI xSpec Model - 5 X MI",
  cohortDatabaseSchema = "my_results",
  cohortTable = "cohort",
  cdmShortName = "myCDM")
```

In this example, a wide range of prediction thresholds are provided (`cutPoints`) including the expected value (“EV”). Given that parameter setting, the output from this step will provide performance characteristics (i.e, sensitivity, specificity, etc.) at each prediction threshold as well as those using the expected value calculations. The evaluation uses the prediction information for the evaluation cohort developed in the prior step. The data frames produced from this step may be saved to a csv file for detailed examination.

Using this process, Table 16.1 displays the performance characteristics for four cohort definitions for MI across five datasets. For a cohort definition similar to the one evaluated by Cutrona and colleagues, “>=1 X HOI, In-Patient”, we found a mean PPV of 67% (range: 59%-74%).

Table 16.1: Performance characteristics of four cohort definitions using diagnostic condition codes to determine myocardial infarction on multiple datasets using pheEvaluator. Sens – Sensitivity ; PPV – Positive Predictive Value ; Spec – Specificity; NPV – Negative Predictive Value; Dx Code – Diagnosis code for the cohort.

Phenotype Algorithm	Database	Sens	PPV	Spec	NPV
>=1 X HOI	CCAE	0.761	0.598	0.997	0.999
	Optum1862	0.723	0.530	0.995	0.998
	OptumGE66	0.643	0.534	0.973	0.982
	MDCD	0.676	0.468	0.990	0.996
	MDCR	0.665	0.553	0.977	0.985
>= 2 X HOI	CCAE	0.585	0.769	0.999	0.998
	Optum1862	0.495	0.693	0.998	0.996
	OptumGE66	0.382	0.644	0.990	0.971
	MDCD	0.454	0.628	0.996	0.993
	MDCR	0.418	0.674	0.991	0.975
>=1 X HOI, In-Patient	CCAE	0.674	0.737	0.999	0.998
	Optum1862	0.623	0.693	0.998	0.997
	OptumGE66	0.521	0.655	0.987	0.977
	MDCD	0.573	0.593	0.995	0.994
	MDCR	0.544	0.649	0.987	0.980
1 X HOI, In-Patient, 1st Position	CCAE	0.633	0.788	0.999	0.998
	Optum1862	0.581	0.754	0.999	0.997
	OptumGE66	0.445	0.711	0.991	0.974
	MDCD	0.499	0.666	0.997	0.993
	MDCR	0.445	0.711	0.991	0.974

16.5 Generalizability of the Evidence

While a cohort can be well-defined and fully evaluated within the context of a given observational database, the clinical validity is limited by the extent to which the results are considered generalizable to the target population of interest. Multiple observational studies on the same topic can yield different results, which can be caused by not only by their designs and analytic methods, but also by their choice of data source. Madigan et al. (2013b) demonstrated that choice of database affects the result of observational study. They systematically investigated heterogeneity in the results for 53 drug-outcome pairs and two study designs (cohort studies and self-controlled case series) across the 10 observational databases. Even though they held study design constant, substantial heterogeneity in effect estimates was observed.

Across the OHDSI network, observational databases vary considerably in the

populations they represent (e.g. pediatric vs. elderly, privately-insured employees vs. publicly-insured unemployed), the care settings where data are captured (e.g. inpatient vs. outpatient, primary vs. secondary/specialty care), the data capture processes (e.g. administrative claims, EHRs, clinical registries), and the national and regional health system from which care is based. These differences can manifest as heterogeneity observed when studying disease and the effects of medical interventions and can also influence the confidence we have in the quality of each data source that may contribute evidence within a network study. While all databases within the OHDSI network are standardized to the CDM, it is important to reinforce that standardization does not reduce the true inherent heterogeneity that is present across populations, but simply provides a consistent framework to investigate and better understand the heterogeneity across the network. The OHDSI research network provides the environment to apply the same analytic process on various databases across the world, so that researchers can interpret results across multiple data sources while holding other methodological aspects constant. OHDSI's collaborative approach to open science in network research, where researchers across participating data partners work together alongside those with clinical domain knowledge and methodologists with analytical expertise, is one way of reaching a collective level of understanding of the clinical validity of data across a network that should serve as a foundation for building confidence in the evidence generated using these data.

16.6 Summary



- Clinical validity can be established by understanding the characteristics of the underlying data source, evaluating the performance characteristics of the cohorts within an analysis, and assessing the generalizability of the study to the target population of interest.
- A cohort definition can be evaluated on the extent to which persons identified in the cohort based on the cohort definition and the available observational data accurately reflect the persons who truly belong to the phenotype.
- Cohort definition validation requires estimating multiple performance characteristics, including sensitivity, specificity, and positive predictive value, to fully summarize and enable adjustment for measurement error.
- Clinical adjudication through source record verification and PheEvaluator represent two alternative approaches to estimating cohort definition validation.
- OHDSI network studies provide a mechanism to examine data source heterogeneity and expand the generalizability of findings to improve clinical validity of real-world evidence.

Chapter 17

Software Validity

Chapter lead: Martijn Schuemie

번역 : 김청수

이 단원의 주요 질문은 다음과 같다.

소프트웨어가 우리의 예상대로 작동하는가?

소프트웨어의 타당성은 근거 품질의 필수적인 구성 요소이며, 우리의 분석 소프트웨어가 예상 기능을 수행하는 경우에만 신뢰할 수 있는 근거를 생성할 수 있다. 17.1.1 절에 설명한대로, 모든 연구를 소프트웨어 개발 활동으로 보고, 공통데이터모델의 데이터부터 추정치, 그림과 표에 이르는 결과를 생성하는 전체 분석을 실행하는 자동화된 스크립트를 만드는 것이 필수적이며, 이 스크립트와 스크립트 내에 사용된 모든 소프트웨어는 유효성 검증을 반드시 시행해야 한다. 8.1에서 언급하였듯이, 우리는 전체 분석 과정을 사용자의 자신의 코드로 직접 작성하거나, 오딧세이 연구방법 라이브러리(OHDSI Methods Library)에서 적절한 기능들을 사용할 수 있다. 연구방법 라이브러리(Methods Library)를 사용하면 얻을 수 있는 이점은 이미 타당성을 보장하기 위해 여러 노력이 가해진 방법들을 사용함으로써 전체 분석과정의 타당성을 정립하는데 있어 부담을 덜 수 있다는 점이다.

이 단원에서는 먼저 타당한 분석 코드를 작성하기 위한 몇 가지 모범 사례들을 살펴볼 것이고, 그 이후 소프트웨어 개발 과정과 검사를 통해 연구방법 라이브러리(Method Library)의 타당성을 검사하는 방법에 대해 설명할 것이다.

17.1 분석 코드의 타당성

17.1.1 재현성 충족을 위한 자동화

전통적으로 관찰연구는 종종 일련의 과정이라기보다는 여정(journey)에 비유되기도 한다. 데이터베이스 전문가는 데이터베이스에서 데이터셋을 추출하여 이를 데이터 분석가에게 넘겨주고, 데이터 분석가는 스프레드시트 편집기나 다른 편집도구를 사용하여 데이터셋을 열고 분석을 수행한다. 마지막으로 분석 결과가 생성되지만, 어떻

게 이 결과가 도출되었는지는 거의 보존되지 않는다. 여행의 목적지에는 도달했지만, 그 곳에 도달하기 위해 취한 정확한 단계들을 추적할 수는 없다. 이 방법은 재현할 수 없고(not reproducible), 투명성이 부족하기 때문에(lack transparency) 온전히 받아들여지지 않는다.

따라서 근거를 생성하는 모든 분석은 완전히 자동화되어야 한다. 분석의 자동화라는 의미는 단일 스크립트에 CDM 형식의 데이터베이스에서부터 표와 그림을 포함하는 전체 분석 결과를 생성해 내는 과정을 담아내어, 단일 명령으로 모든 과정을 재실행 할 수 있도록 구현하는 것이다. 분석은 단순히 수를 세는 것부터 수백만 건의 연구 문제에 대해 경험적으로 보정된 추정치를 생성하는 것까지 다양한 복잡성을 띠지만, 동일한 원칙이 적용된다. 이 스크립트는 다른 스크립트를 호출하여 하위 분석 절차를 진행하도록 할 수 있다.

분석 스크립트는 모든 컴퓨터 언어를 통해 구현할수 있으나, 오딧세이에서는 R 언어를 선호한다. DatabaseConnector라는 R 패키지 덕분에 R 환경에서 CDM형식의 데이터에 직접 연결하여 사용할 수 있으며, 오딧세이 연구방법론 라이브러리 OHDSI Methods Library 내의 다른 R 패키지들을 통해 고급 분석을 사용할 수 있다.

17.1.2 프로그래밍 모범 사례

관찰연구 분석방법들은 최종 결과를 생성하기 위해 많은 단계를 거치거나 매우 복잡해질 수 있다. 이러한 복잡성으로 인해 분석 코드를 유지 관리하기 더욱 어려워지고, 오류가 발생할 가능성이 높아질 뿐 아니라 오류를 인식하기조차 어려워질 수 있다. 다행히도 많은 컴퓨터 프로그래머들은 수 년 동안 복잡한 코드를 작성하고 다른 데 있어서 이 코드들을 읽고, 재사용하고, 적용하고, 검증하는 과정들이 수월하도록 관리하는 몇 가지 모범 사례들을 개발해놓았다. (Martin 2008) 이 우수 사례들은 상당한 분량을 차지하므로, 여기서는 4가지 중요한 원칙을 강조하도록 하겠다.

- **축약화(Abstraction):** 모든 것을 수행하는 하나의 큰 스크립트(소위 “스파게티 코드”라고 하며 코드 라인간 종속성이 있다. 예를 들면, 10행에서 설정된 값이 1000행에서 사용되는 경우를 들 수 있다.)를 작성하는 대신 코드를 “함수”라고 하는 단위로 구성할 수 있다. 함수는 명확한 목표를 가져야 하며(예를 들면 “무작위 샘플 추출”) 일단 생성하고 나면, 다른 스크립트에서도 직관적으로 사용할 수 있다. 이처럼 우리는 함수를 통해서 이해하기 쉬운 개념으로 코드를 추상화하고, 축약화할 수 있다.
- **캡슐화(Encapsulation):** 축약 작업이 진행되기 위해서, 함수간의 의존성을 명확하게 정의하고 최소화해야 한다. 예로 들었던 무작위 샘플 추출 기능에서는 몇 가지 인수(arguments) (예를 들어, 데이터셋과 추출 집단의 크기)와 하나의 출력값(예를 들어, 추출 집단)이 있어야 한다. 이 함수가 수행하는 기능에 있어서 어떠한 것도 영향을 줄 수 없어야 하며, 함수 외부에서 설정된 소위 “전역 변수(global variables)”는 비록 함수의 인수(arguments)는 아니지만 사용하는 것을 피해야 한다.
- **명확한 명명(Clear naming):** 변수 혹은 함수의 이름은 명확해야하며, 자연어처럼 읽을 수 있도록 하라. 예를 들어, `x <- sp1(y, 100)` 보다는 우리가 읽을 수 있도록 `sampledPatients <- takeSample(patients, sampleSize = 100)`처럼 작성하라. 축약어를 사용하고자 하는 충동에 저항하라. 현대 언어

- 는 변수, 함수의 이름으로 사용하는데 있어 충분히 다양하게 사용할 수 있다.
- 재사용(Reuse):** 명확하고 잘 캡슐화된 기능을 작성하였을 때 얻는 장점 중 하나는 계속해서 재사용할 수 있다는 점이다. 이렇게 하면 시간이 절약될 뿐 아니라 코드가 줄어 복잡성이 줄고, 오류가 발생할 가능성성이 줄어 든다.

17.1.3 코드 검증

소프트웨어 코드의 타당성을 검증하기 위한 여러 가지 방법이 있지만, 관찰연구에서 사용하는 코드와 관련하여 두 가지 방법을 소개하고자 한다.

- 코드 검토(Code review):** 한 사람이 코드를 작성하고, 다른 사람이 코드를 검토한다.
- 이중 코딩(Double coding):** 두 사람이 독립적으로 분석 코드를 작성하고, 이후에 스크립트 실행 결과를 비교한다.

코드 검토는 일반적으로 작업량이 적지만, 검토자가 일부 오류를 놓칠 수 있다는 단점이 있다. 이중 코딩은 다소 노동 집약적이지만 오류를 놓칠 가능성이 적다. 이중 코딩의 다른 단점은 두 개별적인 코드의 구현이 대부분, 아니 언제나 다른 결과를 나타낸다는 점이다. 이는 임의적인 사소한 선택으로 인해 발생한다. (예를 들어 “노출 종료까지”라는 말은 노출 종료일을 포함하는가 포함하지 않는가?) 결과적으로, 독립적인 두 프로그래머는 독립적으로 이중 코딩을 수행해야 함에도, 분석을 상호 조정하기 위해 협력하여야 할 필요가 있다.

단위 검사(unit testing)와 같은 다른 소프트웨어 검증 방법은 관찰 연구 특성상 데이터의 입력(CDM 내의 데이터)과 출력(연구 결과) 사이에 높은 복잡도의 관계를 가진 일회성 과정이므로 다소 유용하지 못하기 때문에 관련성이 적다고 할 수 있다. 이러한 다른 검증방법들은 연구방법론 라이브러리(Method Library) 내에서는 적용되어있다는 점을 주의하라.

17.1.4 연구 방법론 라이브러리의 활용

오딧세이 연구방법론 라이브러리 OHDSI Methods Library 는 수많은 기능(function)을 제공하기 때문에, 대부분의 관찰 연구를 몇 줄의 코드만으로도 구현할 수 있다. 따라서 연구방법론 라이브러리(Method Library)를 사용하면 개인 연구 내에서 타당성을 입증해야 하는 부담이 연구방법론 라이브러리(Method Library)로 옮겨가게 된다. 연구방법론 라이브러리(Method Library)의 타당성은 자체의 소프트웨어 개발 과정과 광범위한 시험들을 통해 보장된다.

17.2 연구 방법론 라이브러리 소프트웨어의 개발 과정

오딧세이 연구방법론 라이브러리(OHDSI Methods Library)는 오딧세이 커뮤니티에서 개발하였으며, 라이브러리에 변경이 제안된 사항들은 GitHub의 issue tracker (예를 들어 CohortMethod issue tracker¹) 와 오딧세이 포럼², 이 두가지 장소에서 논의된다. 두 장소 모두 공개되어 있다. 커뮤니티의 모든 구성원은 소프트웨어 코드를

¹<https://github.com/OHDSI/CohortMethod/issues>

²<http://forums.ohdsi.org/>

라이브러리에 제공할 수 있지만, 기존에 배포된 소프트웨어 버전에 대한 변경사항은 오딧세이 인구수준추정 그룹 리더십(현재 Marc Sucahrd 박사, Martigin Schuemie 박사)과 환자수준예측 그룹 리더십(현재 Peter Rijnbeek 박사, Jenna Reps 박사) 만이 최종 결정할 수 있다.

사용자는 연구방법론 라이브러리(Methods Library)의 GitHub 저장소(master branch)에서 직접 설치할 수 있고, “drat”이라는 시스템을 이용하여서도 최신 버전을 설치할 수 있다. R의 Comprehensive R Archive Network (CRAN)을 통해서 다양한 연구방법론 라이브러리 패키지를 사용할 수 있으며, 이용할 수 있는 패키지의 수는 차차 증가할 것으로 예상된다.

오딧세이 연구방법론 라이브러리의 정확성, 신뢰성 및 일관성을 최대화하기 위해서 합리적인 소프트웨어 개발법 및 시험 방법들을 사용한다. 연구방법론 라이브러리의 모든 소스 코드들은 Apache License V2로 배포됨에 따라, R, C++, SQL, Java 등 어떤 언어로 작성이 되었어도, 오딧세이 커뮤니티의 모든 회원들과 대중들이 동료 평가(peer review)할 수 있다. 따라서, 연구방법론 라이브러리 내부에 구현된 모든 기능은 정확성, 신뢰성 그리고 일관성의 향상을 위해서 지속적인 비판과 이로 인한 개선이 이루어져야 한다.

17.2.1 소스 코드 관리

연구방법론 라이브러리의 모든 소스 코드들은 github을 통해 접근할 수 있는 소스 코드 버전 관리 시스템인 git을 통해 관리되며, 오딧세이 연구방법론 라이브러리 저장소의 접근을 관리하고 있다. 전 세계 누구나 소스 코드를 볼 수 있으며, 오딧세이 커뮤니티의 멤버 누구나 pull request라고 부르는 코드 변경 요청을 제출할 수 있다. 오딧세이 인구수준추정 그룹과 환자수준예측 그룹 리더십들은 이 코드 변경 요청을 승인할 수 있고, master branch을 변경하고 새로운 버전을 배포할 수 있다. 지속적인 코드 변경사항 로그들은 GitHub 저장소에 유지되며, 코드와 문서의 모든 변동 사항들을 반영한다. 이러한 변경사항 로그들이 대중들로부터의 검토를 가능하게 한다.

새로운 버전은 필요 시 두 오딧세이 그룹의 리더십들의 판단 하에 배포 된다. 프로그램 패키지의 DESCRIPTION 파일에 정의된 대로 패키지 버전 번호가 배포 버전의 번호보다 큰 master branch로 변경사항을 push 하여 새 배포가 시작된다. 이는 자동으로 패키지를 테스트하고, 모든 검사를 통과하면 버전관리 시스템에서 새 버전에 자동으로 태그가 지정되고 패키지가 오딧세이 drat 저장소에 자동으로 업로드된다. 새 버전은 3가지 표기 원칙에 따라 번호가 부여된다

- **세부 버전(Micro version)** (4.3.2에서 4.3.3으로 변경하는 경우) 버그를 수 정한 경우에 한 함. 새로운 기능 추가는 없으며, 상위, 하위호환성도 보장됨.
- **부 버전(Minor version)** (4.3.3에서 4.4.0으로 변경하는 경우) 기능적으로 추가가 되었을 때. 하위 호환성이 보장됨.
- **주 버전(Major version)** (4.4.0에서 5.0.0으로 변경하는 경우) 주요 개선사항이 생겼을 때. 호환성을 보장하지 않음.

17.2.2 문서화

연구방법론 라이브러리의 모든 패키지들은 R 내부 문서화 프레임워크를 통해 문서화된다. 각 패키지에는 패키지에서 사용 가능한 기능들을 설명하는 정의서를 가지고 있다. 기능 정의서 및 기능 구현에 관한 사항들을 정리하기 위해서 기능 문서와 소스 코드를 단일 파일로 결합하는 roxygen2 소프트웨어를 사용한다. 패키지 설명서는 R의 명령 입력을 통해 패키지 저장소에 PDF의 형태로 제공된다. 또한 많은 패키지는 패키지의 활용법을 담은 도움글(vignettes)을 가지고 있다. 모든 문서는 연구방법론 라이브러리의 웹사이트에서 확인할 수 있다.³

모든 연구방법론 라이브러리의 소스 코드는 실제 사용자가 사용할 수 있으며, GitHub의 issue 시스템 및 오딧세이 포럼을 사용하여 커뮤니티의 피드백을 받을 수 있다.

17.2.3 현재 및 과거 버전으로의 접근

연구방법론 라이브러리 패키지의 현재 및 과거 버전은 아래 두 위치에서 접근 할 수 있다. 먼저 GitHub 버전관리 시스템은 각 패키지의 전체 개발 과정을 가지고 있으며, 각 단계의 패키지의 상태를 재구성하고 검색할 수 있다. 각각의 출시 버전이 GitHub에 태그 되어있다. 두 번째는 오딧세이 GitHub의 drat 저장소에 R 소스 패키지들이 저장되어 있다.

17.2.4 유지 보수, 지원 및 중단

오딧세이는 각 최신 버전의 연구방법론 라이브러리 내 버그를 보고하고 수정하고 패치하는 것을 적극적으로 지원하고 있다. GitHub 이슈 시스템과 오딧세이 포럼을 활용하여 관련 문제를 제기 및 보고할 수 있다. 각 패키지는 패키지 설명서와 추가적으로 도움글들, 온라인 비디오 튜토리얼 영상이나 자료가 제공된다.

17.2.5 검증된 인력

오딧세이 커뮤니티의 회원들은 통계학의 여러 분야에 해당되는 사람들로 구성되어 있고, 학계, 비영리단체, 산업계 등의 다양한 기반을 가진 전 세계 사람들로 구성되어 있다.

오딧세이의 인구수준추정 그룹과 환자수준예측 그룹의 리더들은 공인된 교육기관의 박사 학위를 보유하며, 동료평가 저널에 다양하게 논문을 게재해오고 있다.

17.2.6 물리적, 논리적 보안체계

오딧세이 연구방법론 라이브러리는 GitHub⁴ 시스템에서 호스팅되고 있다. GitHub의 보안에 관한 부분은 다음 사이트에서 확인할 수 있다. <https://github.com/security> 오딧세이 커뮤니티의 모든 구성원들은 연구 방법론 라이브러리를 변경 요청할 수 있으며, 이 때 사용자아이디와 비밀번호가 요구된다. 변경사항을 승인은 인구수준추정 그룹과 환자수준예측 그룹의 리더들을 통해서 가능하다. 사용자 계정은 표준 보안정책 및 기능 요구사항에 따라 접근이 제한된다.

³<https://ohdsi.github.io/MethodsLibrary/>

⁴<https://github.com/>

17.2.7 복구 체계

오딧세이 연구방법론 라이브러리는 GitHub 시스템에 호스팅되어 있다. GitHub's 사고 복구 체계는 다음 사이트에서 확인할 수 있다. <https://github.com/security>.

17.3 연구방법론 라이브러리 기능 검사

우리는 연구 방법론 라이브러리를 패키지의 단순 기능 검사(단위 검사)와 시뮬레이션을 이용한 고난도 기능검사의 두 가지로 나누어 테스트를 수행하고 있다.

17.3.1 단위 검사

잘 알려진 데이터 및 결과에 대해서는 소스 코드를 자동으로 테스트 할 수 있는 자동 유효성 검사들이 오딧세이에 의해서 운영되고 개선되고 있다. 각 유효성 검사들은 일부 입력데이터를 지정하고, 검사 대상의 패키지 중 하나의 기능을 실행하고 출력이 정상적인지 여부를 평가한다. (예를 들어 소수의 환자군을 가진 임시 데이터를 가지고 성향점수 매칭을 시행함) 보다 복잡한 기능의 경우 R에서 사용할 수 있는 다른 기능들을 조합하여 예상 결과를 생성해볼 수 있다. (예로 대용량 회귀분석 엔진인 Cyclops 는 간단한 문제에 대한 결과를 여러 회귀방법을 통해서 비교하여 테스트 함) 오딧세이에서는 실행 가능한 코드라면 100% 테스트 할 수 있도록 하는 것을 목표로 하고 있다.

이 검사 기능들은 패키지가 수정되었을 때 자동으로 수행되도록 되어 있다. (정확히는 변화된 패키지가 GitHub저장소에 push 되었을 때) 검사 도중 에러 발생 시 자동으로 그룹 리더들에게 이메일이 발송되고, 새로운 패키지 버전 이전에 문제를 반드시 해결하도록 하고 있다. 이 검사들에 대한 코드들과 예상 결과들은 검토 가능할 뿐 아니라 적절한 다른 환경에서도 적용할 수 있으며, 관리자뿐만 아니라 일반 사용자들도 설치 과정의 일부로 실행하여 연구방법론 라이브러리의 정확성, 신뢰성 및 일관성에 대한 객관적 증거를 제공할 수 있다.

17.3.2 모의시행

더 복잡한 기능들은 입력을 주었을 때 어떤 결과를 나타내는지 뚜렷하지 않은 경우들도 있다. 이러한 경우 모의 시행(simulation)을 하기도 하는데, 특정한 통계 모델에서 나온 값을 입력하고 알려진 모델의 결과값을 생성하는지 여부를 확인한다. 예를 들어 SelfControlledCaseSeries 패키지에서 모의 시행은 분석방법이 임시 데이터를 이용해서 시간의 흐름을 적절히 파악해서 모델을 만들었는지 검증하는데 사용한다.

17.4 정리



- 관찰 연구는 재현성과 투명성을 보장하기 위해서 CDM 데이터에서부터 결과에 이르기까지 전체 분석을 실행하는 자동화된 스크립트를 구현해야 한다.

- 연구에 사용하는 분석 코드는 축약화, 캡슐화, 명확한 명명법, 코드 재사용이라는 좋은 프로그래밍 방법을 준수해야 한다.
- 코드 검토 또는 이중 코딩을 사용하여 사용자의 코드를 검증할 수 있다.
- 연구방법론 라이브러리는 관찰 연구에 사용할 수 있는 검증된 기능들을 제공한다.
- 연구 방법론 라이브러리는 검증된 소프트웨어 및 검사법 개발을 목표로 하는 개발 과정들을 통해 검증된다.

Chapter 18

Method Validity

Chapter lead: Martijn Schuemie

When considering method validity we aim to answer the question

Is this method valid for answering this question?

“Method” includes not only the study design, but also the data and the implementation of the design. Method validity is therefore somewhat of a catch-all; it is often not possible to observe good method validity without good data quality, clinical validity, and software validity. Those aspects of evidence quality should have already been addressed separately before we consider method validity.

The core activity when establishing method validity is evaluating whether important assumptions in the analysis have been met. For example, we assume that propensity-score matching makes two populations comparable, but we need to evaluate whether this is the case. Where possible, empirical tests should be performed to verify these assumptions. We can for example generate diagnostics to show that our two populations are indeed comparable on a wide range of characteristics after matching. In OHDSI we have developed many standardized diagnostics that should be generated and evaluated whenever an analysis is performed.

In this chapter we will focus on the validity of methods use in population-level estimation. We will first briefly highlight some study design-specific diagnostics, and will then discuss diagnostics that are applicable to most if not all population-level estimation studies. Following this is a step-by-step description of how to execute these diagnostics using the OHDSI tools. We close this chapter with an advanced topic, reviewing the OHDSI Methods Benchmark and its application to the OHDSI Methods Library.

18.1 Design-Specific Diagnostics

For each study design there are diagnostics specific to such a design. Many of these diagnostics are implemented and readily available in the R packages of the OHDSI Methods Library. For example, Section 12.9 lists a wide range of diagnostics generated by the CohortMethod package, including:

- **Propensity score distribution** to asses initial comparability of cohorts.
- **Propensity model** to identify potential variables that should be excluded from the model.
- **Covariate balance** to evaluate whether propensity score adjustment has made the cohorts comparable (as measured through baseline covariates).
- **Attrition** to observe how many subjects were excluded in the various analysis steps, which may inform on the generalizability of the results to the initial cohorts of interest.
- **Power** to assess whether enough data is available to answer the question.
- **Kaplan Meier curve** to asses typical time to onset, and whether the proportionality assumption underlying Cox models is met.

Other study designs require different diagnostics to test the different assumptions in those designs. For example, for the self-controlled case series (SCCS) design we may check the necessary assumption that the end of observation is independent of the outcome. This assumption is often violated in the case of serious, potentially lethal, events such as myocardial infarction. We can evaluate whether the assumption holds by generating the plot shown in Figure 18.1, which shows histograms of the time to observation period end for those that are censored, and those that are uncensored. In our data we consider those whose observation period ends at the end date of data capture (the date when observation stopped for the entire data base, for example the date of extraction, or the study end date) to be uncensored, and all others to be censored. In Figure 18.1 we see only minor differences between the two distributions, suggesting our assumptions holds.

18.2 Diagnostics for All Estimation

Next to the design-specific diagnostics, there are also several diagnostics that are applicable across all causal effect estimation methods. Many of these rely on the use of control hypotheses, research questions where the answer is already known. Using control hypotheses we can then evaluate whether our design produces results in line with the truth. Controls can be divided into negative controls and positive controls.

18.2.1 Negative Controls

Negative controls are exposure-outcome pairs where one believes no causal effect exists, and it includes negative controls or “falsification endpoints” (Prasad and Jena, 2013) that have been recommended as a means to detect confounding,

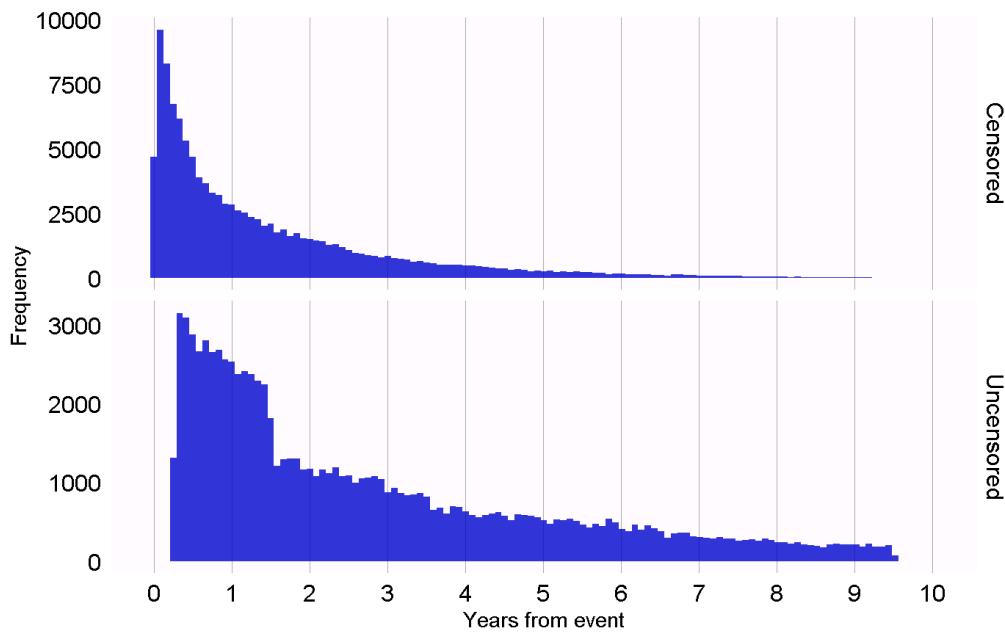


Figure 18.1: Time to observation end for those that are censored, and those that are uncensored.

(Lipsitch et al., 2010) selection bias, and measurement error. (Arnold et al., 2016) For example, in one study (Zaadstra et al., 2008) investigating the relationship between childhood diseases and later multiple sclerosis (MS), the authors include three negative controls that are not believed to cause MS: a broken arm, concussion, and tonsillectomy. Two of these three controls produce statistically significant associations with MS, suggesting that the study may be biased.

We should select negative controls that are comparable to our hypothesis of interest, which means we typically select exposure-outcome pairs that either have the same exposure as the hypothesis of interest (so-called “outcome controls”) or the same outcome (“exposure controls”). Our negative controls should further meet these criteria:

- The exposure **should not cause** the outcome. One way to think of causation is to think of the counterfactual: could the outcome be caused (or prevented) if a patient was not exposed, compared to if the patient had been exposed? Sometimes this is clear, for example ACEi are known to cause angioedema. Other times this is far less obvious. For example, a drug that may cause hypertension can therefore indirectly cause cardiovascular diseases that are a consequence of the hypertension.
- The exposure should also **not prevent or treat** the outcome. This is just another causal relationship that should be absent if we are to believe the true effect size (e.g. the hazard ratio) is 1.
- The negative control should **exist in the data**, ideally with sufficient

numbers. We try to achieve this by prioritizing candidate negative controls based on prevalence.

- Negative controls should ideally be **independent**. For example, we should avoid having negative controls that are either ancestors of each other (e.g. “ingrown nail” and “ingrown nail of foot”) or siblings (e.g. “fracture of left femur” and “fracture of right femur”).
- Negative controls should ideally have **some potential for bias**. For example, the last digit of someone’s social security number is basically a random number, and is unlikely to show confounding. It should therefore not be used as a negative control.

Some argue that negative controls should also have the same confounding structure as the exposure-outcome pair of interest. (Lipsitch et al., 2010) However, we believe this confounding structure is unknowable; the relationships between variables found in reality is often far more complex than people imagine. Also, even if the confounder structure was known, it is unlikely that a negative control exists having that exact same confounding structure, but lacking the direct causal effect. For this reason in OHDSI we rely on a large number of negative controls, assuming that such a set represents many different types of bias, including the ones present in the hypothesis of interest.

The absence of a causal relationship between an exposure and an outcome is rarely documented. Instead, we often make the assumption that a lack of evidence of a relationship implies the lack of a relationship. This assumption is more likely to hold if the exposure and outcome have both been studied extensively, so a relationship could have been detected. For example, the lack of evidence for a completely novel drug likely implies a lack of knowledge, not the lack of a relationship. With this principle in mind we have developed a semi-automated procedure for selecting negative controls. (Voss et al., 2016) In brief, information from literature, product labels, and spontaneous reporting is automatically extracted and synthesized to produce a candidate list of negative controls. This list must then undergo manual review, not only to verify that the automated extraction was accurate, but also to impose additional criteria such as biological plausibility.

18.2.2 Positive Controls

To understand the behavior of a method when the true relative risk is smaller or greater than one requires the use of positive controls where the null is believed to not be true. Unfortunately, real positive controls for observational research tend to be problematic for three reasons. First, in most research contexts, for example when comparing the effect of two treatments, there is a paucity of positive controls relevant for that specific context. Second, even if positive controls are available, the magnitude of the effect size may not be known with great accuracy, and often depends on the population in which one measures it. Third, when treatments are widely known to cause a particular outcome, this shapes the behavior of physicians prescribing the treatment, for example by taking actions to mitigate the risk of

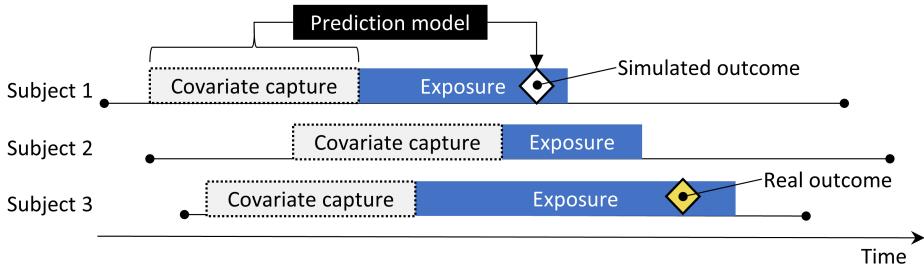


Figure 18.2: Synthesizing positive controls from negative controls.

unwanted outcomes, thereby rendering the positive controls useless as a means for evaluation. (Noren et al., 2014)

In OHDSI we therefore use synthetic positive controls, (Schuemie et al., 2018a) created by modifying a negative control through injection of additional, simulated occurrences of the outcome during the time at risk of the exposure. For example, assume that, during exposure to ACEi, n occurrences of our negative control outcome “ingrowing nail” were observed. If we now add an additional n simulated occurrences during exposure, we have doubled the risk. Since this was a negative control, the relative risk compared to the counterfactual was one, but after injection, it becomes two.

One issue that stands important is the preservation of confounding. The negative controls may show strong confounding, but if we inject additional outcomes randomly, these new outcomes will not be confounded, and we may therefore be optimistic in our evaluation of our capacity to deal with confounding for positive controls. To preserve confounding, we want the new outcomes to show similar associations with baseline subject-specific covariates as the original outcomes. To achieve this, for each outcome we train a model to predict the survival rate with respect to the outcome during exposure using covariates captured prior to exposure. These covariates include demographics, as well as all recorded diagnoses, drug exposures, measurements, and medical procedures. An L1-regularized Poisson regression (Suchard et al., 2013) using 10-fold cross-validation to select the regularization hyperparameter fits the prediction model. We then use the predicted rates to sample simulated outcomes during exposure to increase the true effect size to the desired magnitude. The resulting positive control thus contains both real and simulated outcomes.

Figure 18.2 depicts this process. Note that although this procedure simulates several important sources of bias, it does not capture all. For example, some effects of measurement error are not present. The synthetic positive controls imply constant positive predictive value and sensitivity, which may not be true in reality.

Although we refer to a single true “effect size” for each control, different methods estimate different statistics of the treatment effect. For negative controls, where

we believe no causal effect exists, all such statistics, including the relative risk, hazard ratio, odds ratio, incidence rate ratio, both conditional and marginal, as well as the average treatment effect in the treated (ATT) and the overall average treatment effect (ATE) will be identical to 1. Our process for creating positive controls synthesizes outcomes with a constant incidence rate ratio over time and between patients, using a model conditioned on the patient where this ratio is held constant, up to the point where the marginal effect is achieved. The true effect size is thus guaranteed to hold as the marginal incidence rate ratio in the treated. Under the assumption that our outcome model used during synthesis is correct, this also holds for the conditional effect size and the ATE. Since all outcomes are rare, odds ratios are all but identical to the relative risk.

18.2.3 Empirical Evaluation

Based on the estimates of a particular method for the negative and positive controls, we can then understand the operating characteristics by computing a range of metrics, for example:

- **Area Under the receiver operator Curve (AUC):** the ability to discriminate between positive and negative controls.
- **Coverage:** how often the true effect size is within the 95% confidence interval.
- **Mean precision:** precision is computed as $1/(standard\ error)^2$, higher precision means narrower confidence intervals. We use the geometric mean to account for the skewed distribution of the precision.
- **Mean squared error (MSE):** Mean squared error between the log of the effect size point-estimate and the log of the true effect size.
- **Type 1 error:** For negative controls, how often was the null rejected (at $\alpha = 0.05$). This is equivalent to the false positive rate and $1 - specificity$.
- **Type 2 error:** For positive controls, how often was the null not rejected (at $\alpha = 0.05$). This is equivalent to the false negative rate and $1 - sensitivity$.
- **Non-estimable:** For how many of the controls was the method unable to produce an estimate? There can be various reasons why an estimate cannot be produced, for example because there were no subjects left after propensity score matching, or because no subjects remained having the outcome.

Depending on our use case, we can evaluate whether these operating characteristics are suitable for our goal. For example, if we wish to perform signal detection, we may care about type 1 and type 2 error, or if we are willing to modify our α threshold, we may inspect the AUC instead.

18.2.4 P-Value Calibration

Often the type 1 error (at $\alpha = 0.05$) is larger than 5%. In other words, we are often more likely than 5% to reject the null hypothesis when in fact the null hypothesis is true. The reason is that the p-value only reflects random error, the

error due to having a limited sample size. It does not reflect systematic error, for example the error due to confounding. OHDSI has developed a process for calibrating p-values to restore the type 1 error to nominal. (Schuemie et al., 2014) We derive an empirical null distribution from the actual effect estimates for the negative controls. These negative control estimates give us an indication of what can be expected when the null hypothesis is true, and we use them to estimate an empirical null distribution.

Formally, we fit a Gaussian probability distribution to the estimates, taking into account the sampling error of each estimate. Let $\hat{\theta}_i$ denote the estimated log effect estimate (relative risk, odds or incidence rate ratio) from the i th negative control drug–outcome pair, and let $\hat{\tau}_i$ denote the corresponding estimated standard error, $i = 1, \dots, n$. Let θ_i denote the true log effect size (assumed 0 for negative controls), and let β_i denote the true (but unknown) bias associated with pair i , that is, the difference between the log of the true effect size and the log of the estimate that the study would have returned for control i had it been infinitely large. As in the standard p-value computation, we assume that $\hat{\theta}_i$ is normally distributed with mean $\theta_i + \beta_i$ and standard deviation $\hat{\tau}_i^2$. Note that in traditional p-value calculation, β_i is always assumed to be equal to zero, but that we assume the β_i 's, arise from a normal distribution with mean μ and variance σ^2 . This represents the null (bias) distribution. We estimate μ and σ^2 via maximum likelihood. In summary, we assume the following:

$$\beta_i \sim N(\mu, \sigma^2) \text{ and } \hat{\theta}_i \sim N(\theta_i + \beta_i, \hat{\tau}_i^2)$$

where $N(a, b)$ denotes a Gaussian distribution with mean a and variance b , and estimate μ and σ^2 by maximizing the following likelihood:

$$L(\mu, \sigma | \theta, \tau) \propto \prod_{i=1}^n \int p(\hat{\theta}_i | \beta_i, \theta_i, \hat{\tau}_i) p(\beta_i | \mu, \sigma) d\beta_i$$

yielding maximum likelihood estimates $\hat{\mu}$ and $\hat{\sigma}$. We compute a calibrated p-value that uses the empirical null distribution. Let $\hat{\theta}_{n+1}$ denote the log of the effect estimate from a new drug–outcome pair, and let $\hat{\tau}_{n+1}$ denote the corresponding estimated standard error. From the aforementioned assumptions and assuming β_{n+1} arises from the same null distribution, we have the following:

$$\hat{\theta}_{n+1} \sim N(\hat{\mu}, \hat{\sigma} + \hat{\tau}_{n+1})$$

When $\hat{\theta}_{n+1}$ is smaller than $\hat{\mu}$, the one-sided calibrated p-value for the new pair is then

$$\phi \left(\frac{\theta_{n+1} - \hat{\mu}}{\sqrt{\hat{\sigma}^2 + \hat{\tau}_{n+1}^2}} \right)$$

where $\phi(\cdot)$ denotes the cumulative distribution function of the standard normal distribution. When $\hat{\theta}_{n+1}$ is bigger than $\hat{\mu}$, the one-sided calibrated p-value is then

$$1 - \phi \left(\frac{\theta_{n+1} - \hat{\mu}}{\sqrt{\hat{\sigma}^2 + \hat{\tau}_{n+1}^2}} \right)$$

18.2.5 Confidence Interval Calibration

Similarly, we typically observe that the coverage of the 95% confidence interval is less than 95%: the true effect size is inside the 95% confidence interval less than 95% of the time. For confidence interval calibration (Schuemie et al., 2018a) we extend the framework for p-value calibration by also making use of our positive controls. Typically, but not necessarily, the calibrated confidence interval is wider than the nominal confidence interval, reflecting the problems unaccounted for in the standard procedure (such as unmeasured confounding, selection bias and measurement error) but accounted for in the calibration.

Formally, we assume that β_i , the bias associated with pair i , again comes from a Gaussian distribution, but this time using a mean and standard deviation that are linearly related to θ_i , the true effect size:

$$\beta_i \sim N(\mu(\theta_i), \sigma^2(\theta_i))$$

where

$$\mu(\theta_i) = a + b \times \theta_i \text{ and } \sigma(\theta_i)^2 = c + d \times |\theta_i|$$

We estimate a , b , c and d by maximizing the marginalized likelihood in which we integrate out the unobserved β_i :

$$l(a, b, c, d | \theta, \hat{\theta}, \hat{\tau}) \propto \prod_{i=1}^n \int p(\hat{\theta}_i | \beta_i, \theta_i, \hat{\tau}_i) p(\beta_i | a, b, c, d, \theta_i) d\beta_i,$$

yielding maximum likelihood estimates $(\hat{a}, \hat{b}, \hat{c}, \hat{d})$.

We compute a calibrated CI that uses the systematic error model. Let $\hat{\theta}_{n+1}$ again denote the log of the effect estimate for a new outcome of interest, and let $\hat{\tau}_{n+1}$ denote the corresponding estimated standard error. From the assumptions above, and assuming β_{n+1} arises from the same systematic error model, we have:

$$\hat{\theta}_{n+1} \sim N(\theta_{n+1} + \hat{a} + \hat{b} \times \theta_{n+1}, \hat{c} + \hat{d} \times |\theta_{n+1}|) + \hat{\tau}_{n+1}^2).$$

We find the lower bound of the calibrated 95% CI by solving this equation for θ_{n+1} :

$$\Phi\left(\frac{\theta_{n+1} + \hat{a} + \hat{b} \times \theta_{n+1} - \hat{\theta}_{n+1}}{\sqrt{(\hat{c} + \hat{d} \times |\theta_{n+1}|) + \hat{\tau}_{n+1}^2}}\right) = 0.025,$$

where $\Phi(\cdot)$ denotes the cumulative distribution function of the standard normal distribution. We find the upper bound similarly for probability 0.975. We define the calibrated point estimate by using probability 0.5.

Both p-value calibration and confidence interval calibration are implemented in the `EmpiricalCalibration` package.

18.2.6 Replication Across Sites

Another form of method validation comes from executing the study across several different databases that represent different populations, different health care systems, and/or different data capture processes. Prior research has shown that executing the same study design across different databases can produce vastly different effect size estimates, (Madigan et al., 2013b) suggesting that either the effect differs greatly for different populations, or that the design does not adequately address the different biases found in the different databases. In fact, we observe that accounting for residual bias in a database through empirical calibration of confidence intervals can greatly reduce between-study heterogeneity. (Schuemie et al., 2018a)

One way to express between-database heterogeneity is the I^2 score, describing the percentage of total variation across studies that is due to heterogeneity rather than chance. (Higgins et al., 2003) A naive categorization of values for I^2 would not be appropriate for all circumstances, although one could tentatively assign adjectives of low, moderate, and high to I^2 values of 25%, 50%, and 75%. In a study estimating the effects for many depression treatments using a new-user cohort design with large-scale propensity score adjustment, (Schuemie et al., 2018b) observed only 58% of the estimates to have an I^2 below 25%. After empirical calibration this increased to 83%.



Observing between-database heterogeneity casts doubt on the validity of the estimates. Unfortunately, the inverse is not true. Not observing heterogeneity does not guarantee an unbiased estimate. It is not unlikely that all databases share a similar bias, and that all estimates are therefore consistently wrong.

18.2.7 Sensitivity Analyses

When designing a study there are often design choices that are uncertain. For example, should propensity score matching or stratification be used? If stratification is used, how many strata? What is the appropriate time-at-risk? When faced with such uncertainty, one solution is to evaluate various options, and observe the sensitivity of the results to the design choice. If the estimate remains the same under various options, we can say the study is robust to the uncertainty.

This definition of sensitivity analysis should not be confused with the definitions used by others such as, Rosenbaum (2005) who defines sensitivity analysis to “appraise how the conclusions of a study might be altered by hidden biases of various magnitudes.”

18.3 Method Validation in Practice

Here we build on the example in Chapter 12, where we investigate the effect of ACE inhibitors (ACEi) on the risk of angioedema and acute myocardial infarction (AMI), compared to thiazides and thiazide-like diuretics (THZ). In that chapter we already explore many of the diagnostics specific to the design we used, the cohort method. Here, we apply additional diagnostics that could also have been applied had other designs been used. If the study is implemented using ATLAS as described in Section 12.7 these diagnostics are available in the Shiny app that is included in the study R package generated by ATLAS. If the study is implemented using R instead, as described in Section 12.8, then R functions available in the various packages should be used, as described in the next sections.

18.3.1 Selecting Negative Controls

We must select negative controls, exposure-outcome pairs where no causal effect is believed to exist. For comparative effect estimation such as our example study, we select negative control outcomes that are believed to be neither caused by the target nor the comparator exposure. We want enough negative controls to make sure we have a diverse mix of biases represented in the controls, and also to allow empirical calibration. As a rule-of-thumb we typically aim to have 50-100 such negative controls. We could come up with these controls completely manually, but fortunately ATLAS provides features to aid the selection of negative controls using data from literature, product labels, and spontaneous reports.

To generate a candidate list of negative controls, we first must create a concept set containing all exposures of interest. In this case we select all ingredients in the ACEi and THZ classes, as shown in Figure 18.3.

Next, we go to the “Explore Evidence” tab, and click on the  **Generate** button. Generating the evidence overview will take a few minutes, after which you can

ACEi and THZ combined								
Concept Set Expression		Included Concepts (14)		Included Source Codes		Explore Evidence		
						Export		
Show 25 ▾ entries		Search:						
Showing 1 to 14 of 14 entries								
View Evidence	Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped
	1342439	38454	trandolapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	1334456	35296	Ramipril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	1331235	35208	quinapril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	1373225	54552	Perindopril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
	1310756	30131	moexipril	Drug	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Figure 18.3: A concept set containing the concepts defining the target and comparator exposures.

click on the **View Evidence** button. This will open the list of outcomes as shown in Figure 18.4.

This list shows condition concepts, along with an overview of the evidence linking the condition to any of the exposures we defined. For example, we see the number of publications that link the exposures to the outcomes found in PubMed using various strategies, the number of product labels of our exposures of interest that list the condition as a possible adverse effect, and the number of spontaneous reports. By default the list is sorted to show candidate negative controls first. It is then sorted by the “Sort Order,” which represents the prevalence of the condition in a collection of observational databases. The higher the Sort Order, the higher the prevalence. Although the prevalence in these databases might not correspond with the prevalence in the database we wish to run the study, it is likely a good approximation.

The next step is to manually review the candidate list, typically starting at the top, so with the most prevalent condition, and working our way down until we are satisfied we have enough. One typical way to do this is to export the list to a CSV (comma separated values) file, and have clinicians review these, considering the criteria mentioned in Section 18.2.1.

For our example study we select the 76 negative controls listed in Appendix C.1.

18.3.2 Including Controls

Once we have defined our set of negative controls we must include them in our study. First we must define some logic for turning our negative control condition concepts into outcome cohorts. Section 12.7.3 discusses how ATLAS allows creating such cohorts based on a few choices the user must make. Often we simply choose

Evidence for all conditions for ACEi and THZ combined

Save New Concept Set From Selection Below										View database record counts (RC) and descendant record counts (DRC) for: SYNPUF 5% ▾		
		Column visibility		Copy		CSV		Show 15 ▾ entries			Filter: <input type="text"/>	
Showing 1 to 15 of 13,787 entries										Previous 1 2 3 4 5 ... 920 Next		
Name	Suggested Negative Control	Sort Order	Publication Count (Descendant Concept Match)	Publication Count (Exact Concept Match)	Publication Count (Parent Concept Match)	Product Label Count (Descendant Concept Match)	Product Label (Exact Concept Match)	Product Label (Parent Concept Match)	Product Label (Exact Concept Match)	Product Label (Parent Concept Match)	Product Label (Parent Concept Match)	
Rift valley fever	Y	13,781	0	0	0	0	0	0	0	0	0	
Obstruction due to foreign body accidentally left in operative wound	Y	13,780	0	0	0	0	0	0	0	0	0	
AND/OR body cavity during a procedure												
Infection by Shigella	Y	13,766	0	0	0	0	0	0	0	0	0	

Figure 18.4: Candidate control outcomes with an overview of the evidence found in literature, product labels, and spontaneous reports.

to create a cohort based on any occurrence of a negative control concept or any of its descendants. If the study is implemented in R, then SQL (Structured Query Language) can be used to construct the negative control cohorts. Chapter 9 describes how cohorts can be created using SQL and R. We leave it as an exercise for the reader to write the appropriate SQL and R.

The OHDSI tools also provide functionality for automatically generating and including positive controls derived from the negative controls. This functionality can be found in the Evaluation Settings section in ATLAS described in Section 12.7.3, and it is implemented in the `synthesizePositiveControls` function in the `MethodEvaluation` package. Here we generate three positive controls for each negative control, with true effect sizes of 1.5, 2, and 4, using a survival model:

```
library(MethodEvaluation)
# Create a data frame with all negative control exposure-
# outcome pairs, using only the target exposure (ACEi = 1).
eoPairs <- data.frame(exposureId = 1,
                      outcomeId = ncs)

pcs <- synthesizePositiveControls(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = cdmDbSchema,
  exposureDatabaseSchema = cohortDbSchema,
  exposureTable = cohortTable,
```

```

outcomeDatabaseSchema = cohortDbSchema,
outcomeTable = cohortTable,
outputDatabaseSchema = cohortDbSchema,
outputTable = cohortTable,
createOutputTable = FALSE,
modelType = "survival",
firstExposureOnly = TRUE,
firstOutcomeOnly = TRUE,
removePeopleWithPriorOutcomes = TRUE,
washoutPeriod = 365,
riskWindowStart = 1,
riskWindowEnd = 0,
endAnchor = "cohort end",
exposureOutcomePairs = eoPairs,
effectSizes = c(1.5, 2, 4),
cdmVersion = cdmVersion,
workFolder = file.path(outputFolder, "pcSynthesis"))

```

Note that we must mimic the time-at-risk settings used in our estimation study design. The `synthesizePositiveControls` function will extract information about the exposures and negative control outcomes, fit outcome models per exposure-outcome pair, and synthesize outcomes. The positive control outcome cohorts will be added to the cohort table specified by `cohortDbSchema` and `cohortTable`. The resulting `pcs` data frame contains the information on the synthesized positive controls.

Next we must execute the same study used to estimate the effect of interest to also estimate effects for the negative and positive controls. Setting the set of negative controls in the comparisons dialog in ATLAS instructs ATLAS to compute estimates for these controls. Similarly, specifying that positive controls be generated in the Evaluation Settings includes these in our analysis. In R, the negative and positive controls should be treated as any other outcome. All estimation packages in the OHDSI Methods Library readily allow estimation of many effects in an efficient manner.

18.3.3 Empirical Performance

Figure 18.5 shows the estimated effect sizes for the negative and positive controls included in our example study, stratified by true effect size. This plot is included in the Shiny app that comes with the study R package generated by ATLAS, and can be generated using the `plotControls` function in the `MethodEvaluation` package. Note that the number of controls is often lower than what was defined because there was not enough data to either produce an estimate or to synthesize a positive control.

Based on these estimates we can compute the metrics shown in Table 18.1 using the `computeMetrics` function in the `MethodEvaluation` package.

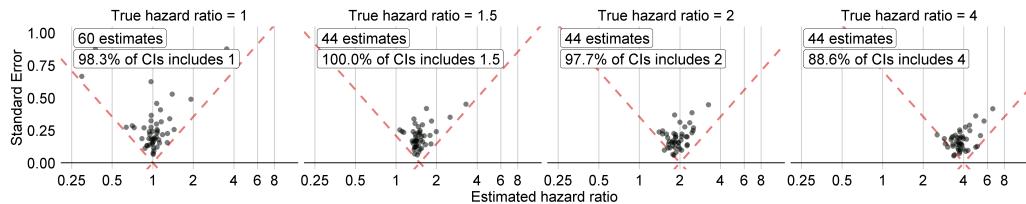


Figure 18.5: Estimates for the negative (true hazard ratio = 1) and positive controls (true hazard ratio > 1). Each dot represents a control. Estimates below the dashed line have a confidence interval that doesn't include the true effect size.

Table 18.1: Method performance metrics derived from the negative and positive control estimates.

Metric	Value
AUC	0.96
Coverage	0.97
Mean Precision	19.33
MSE	2.08
Type 1 error	0.00
Type 2 error	0.18
Non-estimable	0.08

We see that coverage and type 1 error are very close to their nominal values of 95% and 5%, respectively, and that the AUC is very high. This is certainly not always the case.

Note that although in Figure 18.5 not all confidence intervals include one when the true hazard ratio is one, the type 1 error in Table 18.1 is 0%. This is an exceptional situation, caused by the fact that confidence intervals in the Cyclops package are estimated using likelihood profiling, which is more accurate than traditional methods but can result in asymmetric confidence intervals. The p-value instead is computed assuming symmetrical confidence intervals, and this is what was used to compute the type 1 error.

18.3.4 P-Value Calibration

We can use the estimates for our negative controls to calibrate our p-values. This is done automatically in the Shiny app, and can be done manually in R. Assuming we have created the summary object `summ` as described in Section 12.8.6, we can plot the empirical calibration effect plot:

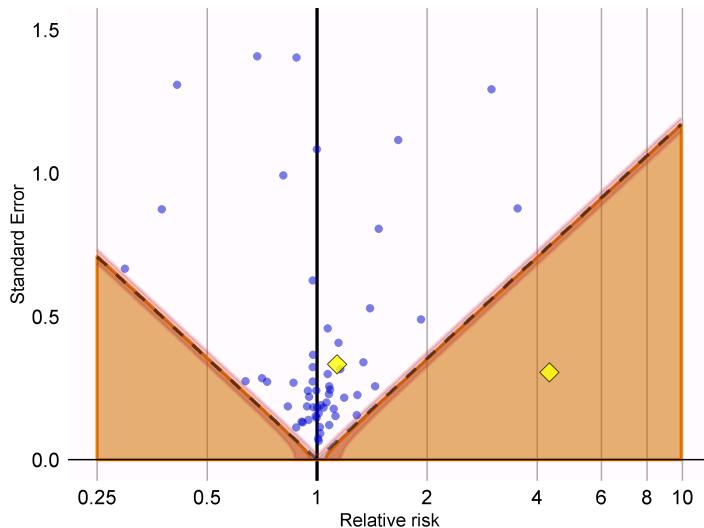


Figure 18.6: P-value calibration: estimates below the dashed line have a conventional $p < 0.05$. Estimates in the shaded area have calibrated $p < 0.05$. The narrow band around the edge of the shaded area denotes the 95% credible interval. Dots indicate negative controls. Diamonds indicate outcomes of interest.

```
# Estimates for negative controls (ncs) and outcomes of interest (ois):
ncEstimates <- summ[summ$outcomeId %in% ncs, ]
oiEstimates <- summ[summ$outcomeId %in% ois, ]

library(EmpiricalCalibration)
plotCalibrationEffect(logRrNegatives = ncEstimates$logRr,
                      seLogRrNegatives = ncEstimates$seLogRr,
                      logRrPositives = oiEstimates$logRr,
                      seLogRrPositives = oiEstimates$seLogRr,
                      showCis = TRUE)
```

In Figure 18.6 we see that the shaded area almost exactly overlaps with the area denoted by the dashed lines, indicating hardly any bias was observed for the negative controls. One of the outcomes of interest (AMI) is above the dashed line and the shaded area, indicating we cannot reject the null according to both the uncalibrated and calibrated p-value. The other outcome (angioedema) clearly stands out from the negative control, and falls well within the area where both uncalibrated and calibrated p-values are smaller than 0.05.

We can compute the calibrated p-values:

```
null <- fitNull(logRr = ncEstimates$logRr,
                  seLogRr = ncEstimates$seLogRr)
```

```
calibrateP(null,
  logRr= oiEstimates$logRr,
  seLogRr = oiEstimates$seLogRr)
```

```
## [1] 1.604351e-06 7.159506e-01
```

And contrast these with the uncalibrated p-values:

```
oiEstimates$p
```

```
## [1] [1] 1.483652e-06 7.052822e-01
```

As expected, because little to no bias was observed, the uncalibrated and calibrated p-values are very similar.

18.3.5 Confidence Interval Calibration

Similarly, we can use the estimates for our negative and positive controls to calibrate the confidence intervals. The Shiny app automatically reports the calibrate confidence intervals. In R we can calibrate intervals using the `fitSystematicModelError` and `calibrateConfidenceInterval` functions in the `EmpiricalCalibration` package, as described in detail in the “Empirical calibration of confidence intervals” vignette.

Before calibration, the estimated hazard ratios (95% confidence interval) are 4.32 (2.45 - 8.08) and 1.13 (0.59 - 2.18), for angioedema and AMI respectively. The calibrated hazard ratios are 4.75 (2.52 - 9.04) and 1.15 (0.58 - 2.30).

18.3.6 Between-Database Heterogeneity

Just as we executed our analysis on one database, in this case the IBM MarketScan Medicaid (MDCD) database, we can also run the same analysis code on other databases that adhere to the Common Data Model (CDM). Figure 18.7 shows the forest plot and meta-analytic estimates (assuming random effects) (DerSimonian and Laird, 1986) across a total of five databases for the outcome of angioedema. This figure was generated using the `plotMetaAnalysisForest` function in the `EvidenceSynthesis` package.

Although all confidence intervals are above one, suggesting agreement on the fact that there is an effect, the I^2 suggests between-database heterogeneity. However, if we compute the I^2 using the calibrated confidence intervals as shown in Figure 18.8, we see that this heterogeneity can be explained by the bias measured in each database through the negative and positive controls. The empirical calibration appears to properly take this bias into account.

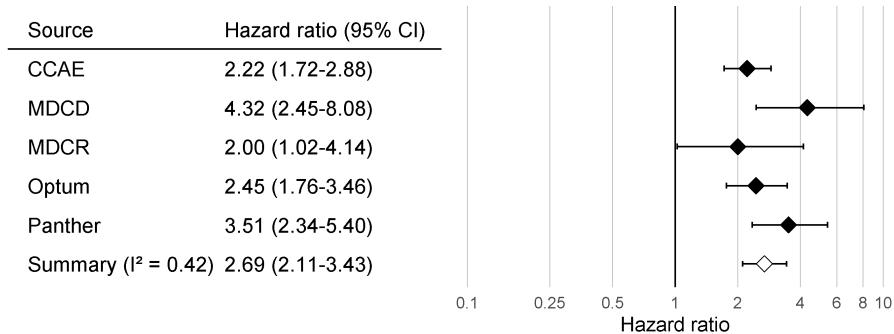


Figure 18.7: Effect size estimates and 95% confidence intervals (CI) from five different databases and a meta-analytic estimate when comparing ACE inhibitors to thiazides and thiazide-like diuretics for the risk of angioedema.

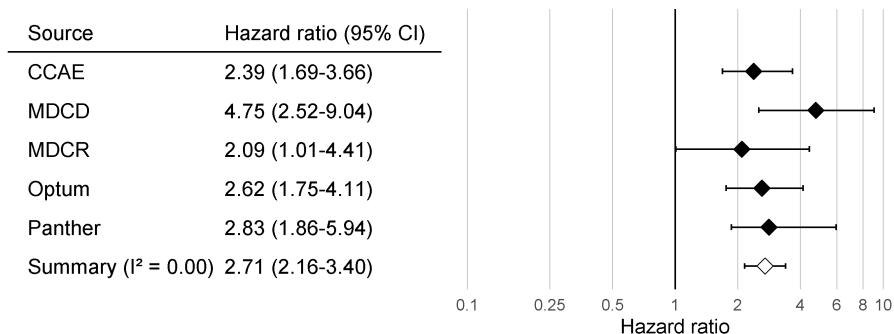


Figure 18.8: Calibrated Effect size estimates and 95% confidence intervals (CI) from five different databases and a meta-analytic estimate for the hazard ratio of angioedema when comparing ACE inhibitors to thiazides and thiazide-like diuretics.

18.3.7 Sensitivity Analyses

One of the design choices in our analysis was to use variable-ratio matching on the propensity score. However, we could have also used stratification on the propensity score. Because we are uncertain about this choice, we may decide to use both. Table 18.2 shows the effect size estimates for AMI and angioedema, both calibrated and uncalibrated, when using variable-ratio matching and stratification (with 10 equally-sized strata).

Table 18.2: Uncalibrated and calibrated hazard ratios (95% confidence interval) for the two analysis variants.

Outcome	Adjustment	Uncalibrated	Calibrated
Angioedema	Matching	4.32 (2.45 - 8.08)	4.75 (2.52 - 9.04)
Angioedema	Stratification	4.57 (3.00 - 7.19)	4.52 (2.85 - 7.19)
Acute myocardial infarction	Matching	1.13 (0.59 - 2.18)	1.15 (0.58 - 2.30)
Acute myocardial infarction	Stratification	1.43 (1.02 - 2.06)	1.45 (1.03 - 2.06)

We see that the estimates from the matched and stratified analysis are in strong agreement, with the confidence intervals for stratification falling completely inside of the confidence intervals for matching. This suggests that our uncertainty around this design choice does not impact the validity of our estimates. Stratification does appear to give us more power (narrower confidence intervals), which is not surprising since matching results in loss of data, whereas stratification does not. The price for this could be an increase in bias, due to within-strata residual confounding, although we see no evidence of increased bias reflected in the calibrated confidence intervals.



Study diagnostics allow us to evaluate design choices even before fully executing a study. It is recommended not to finalize the protocol before generating and reviewing all study diagnostics. To avoid p-hacking (adjusting the design to achieve a desired result), this should be done while blinded to the effect size estimate of interest.

18.4 OHDSI Methods Benchmark

Although the recommended practice is to empirically evaluate a method's performance within the context that it is applied, using negative and positive controls that are in ways similar to the exposures-outcomes pairs of interest (for example

using the same exposure or the same outcome) and on the database used in the study, there is also value in evaluating a method’s performance in general. This is why the OHDSI Methods Evaluation Benchmark was developed. The benchmark evaluates performance using a wide range of control questions, including those with chronic or acute outcomes, and long-term or short-term exposures. The results on this benchmark can help demonstrate the overall usefulness of a method, and can be used to form a prior belief about the performance of a method when a context-specific empirical evaluation is not (yet) available. The benchmark consists of 200 carefully selected negative controls that can be stratified into eight categories, with the controls in each category either sharing the same exposure or the same outcome. From these 200 negative controls, 600 synthetic positive controls are derived as described in Section 18.2.2. To evaluate a method, it must be used to produce effect size estimates for all controls, after which the metrics described in Section 18.2.3 can be computed. The benchmark is publicly available, and can be deployed as described in the Running the OHDSI Methods Benchmark vignette in the MethodEvaluation package.

We have run all the methods in the OHDSI Methods Library through this benchmark, with various analysis choices per method. For example, the cohort method was evaluated using propensity score matching, stratification, and weighting. This experiment was executed on four large observational healthcare databases. The results, viewable in an online Shiny app¹, show that although several methods show high AUC (the ability to distinguish positive controls from negative controls), most methods in most settings demonstrate high type 1 error and low coverage of the 95% confidence interval, as shown in Figure 18.9.

This emphasizes the need for empirical evaluation and calibration: if no empirical evaluation is performed, which is true for almost all published observational studies, we must assume a prior informed by the results in Figure 18.9, and conclude that it is likely that the true effect size is not contained in the 95% confidence interval!

Our evaluation of the designs in the Methods Library also shows that empirical calibration restores type 1 error and coverage to their nominal values, although often at the cost of increasing type 2 error and decreasing precision.

18.5 Summary



- A method’s validity depends on whether the assumptions underlying the method are met.
- Where possible, these assumptions should be empirically tested using study diagnostics.

¹<http://data.ohdsi.org/MethodEvalViewer/>

- Control hypotheses, questions where the answer is known, should be used to evaluate whether a specific study design produces answers in line with the truth.
- Often, p-values and confidence intervals do not demonstrate nominal characteristics as measured using control hypotheses.
- These characteristics can often be restored to nominal using empirical calibration.
- Study diagnostics can be used to guide analytic design choices and adapt the protocol, as long as the researcher remains blinded to the effect of interest to avoid p-hacking.



Figure 18.9: Coverage of the 95% confidence interval for the methods in the Methods Library. Each dot represents the performance of a specific set of analysis choices. The dashed line indicates nominal performance (95% coverage). SCCS = Self-Controlled Case Series, GI = Gastrointestinal, IBD = inflammatory bowel disease.

Part V

OHDSI Studies

Chapter 19

Study steps

Chapter leads: Sara Dempster & Martijn Schuemie

Here we aim to provide a general step-by-step guide to the design and implementation of an observational study with the OHDSI tools. We will break out each stage of the study process and then describe steps generically and in some cases discuss specific aspects of the main study types (1) characterization, (2) population level estimation (PLE), and (3) patient level prediction (PLP) described in earlier chapters of the Book of OHDSI. To do so, we will synthesize many elements discussed in the previous chapters in a way that is accessible for the beginner. At the same time, this chapter can stand alone for a reader who wants practical high-level explanations with options to pursue more in-depth materials in other chapters as needed. Finally, we will illustrate throughout with a few key examples.

In addition, we will summarize guidelines and best practices for observational studies as recommended by the OHDSI community. Some principles that we will discuss are generic and shared with best practice recommendations found in many other guidelines for observational research while other recommended processes are more specific to the OHDSI framework. We will therefore highlight where OHDSI-specific approaches are enabled by the OHDSI tool stack.

Throughout the chapter, we assume that an infrastructure of OHDSI tools, R and SQL are available to the reader and therefore we do not discuss any aspects of setting up this infrastructure in this chapter (see Chapters 8 and 9 for guidance). We also assume our reader is interested in running a study primarily on data at their own site using a database in OMOP CDM (for OMOP ETL, see Chapter 6). However, we emphasize that once a study package is prepared as discussed below, it can in principle be distributed and executed at other sites. Additional considerations specific to running OHDSI network studies, including organizational and technical details, are discussed in detail in Chapter 20.

19.1 General Best Practice Guidelines

19.1.1 Observational Study Definition

An observational study is a study where, by definition, patients are simply observed and no attempt is made to intervene in the treatment of specific patients. Sometimes, observational data are collected for a specific purpose as in a registry study, but in many cases, these data are collected for some purpose other than the specific study question at hand. Common examples of the latter type of data are Electronic Health Records (EHRs) or administrative claims data. Observational studies are often referred to as secondary use of data. A fundamental guiding principle for performing any observational study is to explicitly describe one's research question and fully specify the approach in advance of executing a study. In this regard, an observational study should be no different than a clinical trial, except that in a clinical trial, patients are recruited and followed in time for the primary purpose of answering a specific question, usually about the efficacy and/or safety of a therapeutic intervention. There are many ways in which the analysis methods employed in observational studies are different than those used in clinical trials. Most notably, the lack of randomization in PLE observational studies requires approaches to control confounding if the goal is to draw causal inferences (see Chapters 12 and 18 for detailed discussion of OHDSI-supported study designs and methods for PLE such as methods to remove observed confounding by balancing populations across many characteristics).

19.1.2 Pre-Specification of Study Design

Pre-specification of an observational study design and parameters is critical to avoid introducing further bias by subconsciously or consciously evolving one's approach to achieve a desired result, sometimes referred to as p-hacking. The temptation not to fully specify the study details in advance is greater with secondary use of data than primary use because these data, such as EHR and claims, sometimes give the researcher a sense of infinite possibilities, leading to a meandering line of inquiry. The key then is to still impose the rigorous structure of scientific inquiry despite the apparent easy availability of pre-existing data. The principle of pre-specification is especially important in PLE or PLP to ensure rigorous or reproducible results as these findings may ultimately inform clinical practice or regulatory decisions. Even in the case of a characterization study being conducted purely for exploratory reasons, it is still preferable to have a well-specified plan. Otherwise an evolving study design and analysis process will become unwieldy to document, explain and reproduce.

19.1.3 Protocol

An observational study plan should be documented in the form of a protocol created prior to executing a study. At a minimum, a protocol describes the primary

study question, the approach, and metrics that will be used to answer the question. The study population should be described to a level of detail such that the study population may be fully reproduced by others. In addition, all methods or statistical procedures and the form of expected study results such as metrics, tables and graphs should be described. Often, a protocol will also describe a set of pre-analyses designed to assess the feasibility or statistical power of the study. Furthermore, protocols may contain descriptions of variations on the primary study question referred to as sensitivity analyses. Sensitivity analyses are designed to evaluate the potential impact of study design choices on the overall study findings and should be described in advance whenever possible. Sometimes unanticipated issues arise that may necessitate a protocol amendment after a protocol is completed. If this becomes necessary, it is critical to document the change and the reasons for the change in the protocol itself. Particularly in the case of PLE or PLP, a completed study protocol will ideally be recorded in an independent platform (such as clinicaltrials.gov or OHDSI's studyProtocols sandbox) where its versions and any amendments can be tracked independently with timestamps. It is also often the case that your institution or the owner of the data source will require the opportunity to review and approve your protocol prior to study execution.

19.1.4 Standardized Analyses

A unique advantage of OHDSI is the ways in which the tools support planning, documentation and reporting by recognizing that there are really a few main classes of questions that are asked repeatedly in observational studies (Chapters 2, 7, 11, 12, 13), thereby streamlining the protocol development and study implementation process through automation of aspects that are repeated. Many of the tools are designed to parameterize a few study designs or metrics that address a majority of use cases that will be encountered. For example, the researchers specify their study populations and a few additional parameters and perform numerous comparative studies iterating over different drugs and/or outcomes. If a researcher's questions fit into the general template, there are ways to automate the generation of many of the basic descriptions of study populations and other parameters required for the protocol. Historically, these approaches were motivated out of the OMOP experiments which sought to evaluate how well observational study designs were able to reproduce known causal links between drugs and adverse events by iterating over many different study designs and parameters.

The OHDSI approach supports the inclusion of feasibility and study diagnostics within the protocol by again enabling these steps to be performed relatively simply within a common framework and tools (see section 19.2.4 below).

19.1.5 Study Packages

Another motivation for standardized templates and designs is that even when a researcher thinks a study is described in complete detail in the form of a protocol, there may be elements that are not actually sufficiently specified to generate the

full computer code to execute the study. A related fundamental principle which is enabled by the OHDSI framework is to generate a completely traceable and reproducible process documented in the form of computer code, often referred to as a “study package.” OHDSI best practice is to record such a study package in the git environment. This study package contains all parameters and versioning stamps for the code base. As mentioned previously, observational studies are often asking questions with potential to impact public health decisions and policy. Therefore, before acting on any findings, they should ideally be replicated in multiple settings by different researchers. The only way to achieve such a goal is for every detail required to fully reproduce a study to be mapped out explicitly and not left to guesswork or misinterpretation. To support this best practice, the OHDSI tools are designed to aid in the translation from a protocol in the form of a written document into a computer or machine-readable study package. One tradeoff of this framework is that not every use case or customized analysis can easily be addressed with the existing OHDSI tools. As the community grows and evolves, however, more functionality to address a larger array of use cases is being added. Anyone involved in the community may raise suggestions for new functionality driven by a novel use case.

19.1.6 The Data Underlying the CDM

OHDSI studies are premised on observational databases being translated into the OMOP common data model (CDM). All OHDSI tools and downstream analytics steps make an assumption that the data representation conforms to the specifications of the CDM (see Chapter 4). It is therefore also critical that the ETL process (see Chapter 6) for doing so is well-documented for your specific data sources as this process may introduce artifacts or differences between databases at different sites. The purpose of the OMOP CDM is to move in the direction of reducing site specific data representation, but this is far from a perfect process and still remains a challenging area that the community seeks to improve. It therefore remains critical when executing studies to collaborate with individuals at your site, or at external sites when executing network studies, who are intimately familiar with any source data that has been transformed into the OMOP CDM.

In addition to the CDM, the OMOP standardized vocabulary system (Chapter 5) is also a critical component of working with the OHDSI framework to obtain interoperability across diverse data sources. The standardized vocabulary seeks to define a set of standard concepts within each vocabulary domain to which all other source vocabulary systems are mapped. In this way, two different databases which use a different source vocabulary system for drugs, diagnoses or procedures will be comparable when transformed into the CDM. The OMOP vocabularies also contain hierarchies which are useful in identifying the appropriate codes for a particular cohort definition. Again, it is recommended best practice to implement the vocabulary mappings and use the codes of OMOP standardized vocabularies in downstream queries in order to gain the full benefits of ETLing your database

into the OMOP CDM and using the OMOP vocabulary.

19.2 Study Steps in Detail

19.2.1 Define Question

The first step is to translate your research interest into a precise question that can be addressed with an observational study. Let's say that you are a clinical diabetes researcher and you want to investigate the quality of care being delivered to patients with type 2 diabetes mellitus (T2DM). You can break this bigger objective down into much more specific questions that fall into one of the three types of questions first described in Chapter 7.

In a characterization study, one could ask, "do prescribing practices conform to what is currently recommended for those with mild T2DM versus those with severe T2DM in a given healthcare environment?" This question does not ask a causal question about the effectiveness of any given treatment relative to another; it is simply characterizing prescribing practices in your database relative to a set of existing clinical guidelines.

Maybe you are also skeptical whether or not the prescribing guidelines for T2DM treatment are best for a particular subset of patients such as those with both a diagnosis of T2DM and heart disease. This line of inquiry can be translated into a PLE study. Specifically, you can ask a question about the comparative effectiveness of 2 different T2DM drug classes in preventing cardiovascular events, such as heart failure. You might design a study to examine the relative risks of hospitalization for heart failure in two separate cohorts of patients taking the different drugs, but where both cohorts have a diagnosis of T2DM and heart disease.

Alternatively, you may want to develop a model to predict which patients will progress from mild T2DM to severe T2DM. This can be framed as a PLP question and could serve to flag patients at greater risk of transitioning to severe T2DM for more vigilant care.

From a purely pragmatic point of view, defining a study question also requires assessing whether the approaches required to answer a question conforms to available functionality within the OHDSI tool set (see Chapter 7 for a detailed discussion of question types that can be addressed with current tool). Of course it is always possible to design your own analytic tools or modify those currently available to answer other questions.

19.2.2 Review Data Availability and Quality

Before committing to a particular study question, it is recommended to review the quality of the data (see Chapter 15) and really understand the nature of your particular observational healthcare database in terms of which fields are populated and what care settings the data covers. This can help to quickly identify issues

that may make a study question infeasible in a particular database. Below, we point out some common issues that may arise.

Let's return to the example above of developing a predictive model for progression from mild T2DM to severe T2DM. Ideally severity of T2DM might be assessed by examining glycosylated hemoglobin (HbA1c) levels which is a lab measurement that reflects a patient's blood sugar levels averaged over the prior 3 months. These values may or may not be available for all patients. If unavailable for all or even a portion of patients, you will have to consider whether other clinical criteria for severity of T2DM can be identified and used instead. Alternatively, if the HbA1c values are available for only a subset of patients, you will also need to evaluate whether focusing on this subset of patients only would lead to unwanted bias in the study. See Chapter 7 for additional discussion of the issue of missing data.

Another common issue is the lack of information about a particular care setting. In the PLE example described above, the suggested outcome was hospitalization for heart failure. If a given database does not have any inpatient information, one may need to consider a different outcome to evaluate the comparative effectiveness of different T2DM treatment approaches. In other databases, outpatient diagnosis data may not be available and therefore one would need to consider the design of the cohort.

19.2.3 Study Populations

Defining a study population or populations is a fundamental step of any study. In observational research, a group of individuals that is representative of the study population of interest is often referred to as a cohort. The required patient characteristics for selection into a cohort will be determined by the study population that is relevant for the clinical question at hand. An example of a simple cohort would be patients older than 18 years of age AND with a diagnosis code for T2DM in their medical record. This cohort definition has two criteria connected by AND logic. Often cohort definitions contain many more criteria which are connected by more complex, nested boolean logic and additional temporal criteria such as specific study periods or required lengths of time for a patient's baseline period.

A refined set of cohort definitions requires the review of appropriate scientific literature and advice from clinical and technical experts who understand some of the challenges in interpreting your specific database to identify appropriate groups of patients. It's important to keep in mind when working with observational data that these data do not provide a complete picture of a patient's medical history, but rather a snapshot in time whose fidelity is subject to both human error and bias that may have been introduced in recording of the information. A given patient may only be followed for a finite time referred to as their observation period. For a given database or care setting and disease or treatment under study, a clinical researcher may be able to make suggestions to avoid the most common sources of error. To give a straightforward example, a common issue in identifying

patients with T2DM is that T1DM patients are sometimes mistakenly coded with a diagnosis of T2DM. Because patients with T1DM are fundamentally a different group, the unintentional inclusion of a group of T1DM patients in a study intended to examine T2DM patients could skew the results. In order to have a robust definition of a T2DM cohort, one may want to eliminate patients who have only ever been prescribed insulin as a diabetes treatment to avoid having patients with T1DM erroneously represented. At the same time, however, there may also be situations where one is simply interested in the characteristics of all patients who have a T2DM diagnosis code in their medical record. In this case, it may not be appropriate to apply further qualifying criteria to attempt to remove erroneously coded T1DM patients.

Once the definition of a study population or populations is described, the OHDSI tool ATLAS is a good starting point to create the relevant cohorts. ATLAS and the cohort generation process are described in detail in Chapters 8 and 10. Briefly, ATLAS provides a user interface (UI) to define and generate cohorts with detailed inclusion criteria. Once cohorts are defined in ATLAS, a user can directly export their detailed definitions in a human-readable format for incorporation in a protocol. If for some reason an ATLAS instance is not connected to an observational health database, ATLAS can still be used to create a cohort definition and directly export the underlying SQL code for incorporation into a study package to be run separately on a SQL database server. Directly using ATLAS is recommended when possible because ATLAS provides some advantages above and beyond the creation of SQL code for the cohort definition (see below). Finally, there may be some rare situations where a cohort definition can not be implemented with the ATLAS UI and requires manual custom SQL code.

The ATLAS UI enables defining cohorts based on numerous selection criteria. Criteria for cohort entry and exit as well as baseline criteria can be defined on the basis of any domains of the OMOP CDM such as conditions, drugs, procedures, etc. where standard codes must be specified for each domain. In addition, logical filters on the basis of these domains, as well as time-based filters to define study periods, and baseline timeframes can be defined within ATLAS. ATLAS can be particularly helpful when selecting codes for each criteria. ATLAS incorporates a vocabulary-browsing feature which can be used to build sets of codes required for your cohort definitions. This feature relies solely on the OMOP standard vocabularies and has options to include all descendants in the vocabulary hierarchy (see Chapter 5). Note therefore that this feature requires that all codes have been appropriately mapped to standard codes during the ETL process (see Chapter 6). If the best codesets to use in your inclusion criteria are not clear, this may be a place where some exploratory analysis may be warranted in cohort definitions. Alternatively a more formal sensitivity analysis could be considered to account for different possible definitions of a cohort using different codesets.

Assuming that ATLAS is configured appropriately to connect to a database, SQL queries to generate the defined cohorts can be run directly within ATLAS. ATLAS

will automatically assign each cohort a unique id which can also be used to directly reference the cohort in the backend database for future use. The cohort may be directly used within ATLAS to run an incidence rate study or it may be pointed to directly in the backend database by code in a PLE or PLP study package. For a given cohort, ATLAS saves only the patient ids, index dates and cohort exit dates of the individuals in the cohorts. This information is sufficient to derive all the other attributes or covariates that may be needed for the patients such as patient's baseline covariates for a characterization, PLE or PLP study.

When a cohort is created, summary characteristics of the patient demographics and frequencies of the most frequent drugs and conditions observed can be created and viewed by default directly within ATLAS.

In reality, most studies require specifying multiple cohorts or multiple sets of cohorts which are then compared in various ways to gain new clinical insights. For PLE and PLP, the OHDSI tools provide a structured framework to define these multiple cohorts. For example, in a PLE comparative effectiveness study, you will typically define at least 3 cohorts, a target cohort, a comparator and an outcome cohort (see Chapter 12). In addition, to run a full PLE comparative effectiveness study, you will also need a number of cohorts with negative control outcomes and positive control outcomes. The OHDSI toolset provides ways to help speed and in some cases automate the generation of these negative and positive control cohorts as discussed in detail in Chapter 18.

As a final note, defining cohorts for a study may benefit from ongoing work in the OHDSI community to define a library of robust and validated phenotypes where a phenotype is essentially an exportable cohort definition. If any of these existing cohort definitions are appropriate for your study, the exact definitions can be obtained by import of a json file into your ATLAS instance.

19.2.4 Feasibility and Diagnostics

Once cohorts are defined and generated, a more formal process to examine study feasibility in available data sources can be undertaken and the findings summarized in the finalized protocol. An evaluation of study feasibility can encompass a number of exploratory and sometimes iterative activities. We describe a few common aspects here.

A primary activity at this stage will be to thoroughly review the distributions of characteristics within your cohorts to ensure that the cohort you generated is consistent with the desired clinical characteristics and flag any unexpected characteristics. Returning to our T2DM example above, by characterizing this simple T2DM cohort by reviewing the frequencies of all other diagnoses received, one may be able to flag the issue of also capturing patients with T1DM or other unanticipated issues. It is good practice to build such a step of initially characterizing any new cohort into the study protocol as a quality check of clinical validity of the cohort definition. In terms of implementation, the easiest way to

perform a first pass at this will be to examine the cohort demographics and top drugs and conditions that can be generated by default when a cohort is created in ATLAS. If the option to create the cohorts directly within ATLAS is not available, manual SQL or use of the R feature extraction package can be used to characterize a cohort. In practice, in a larger PLE study or PLP study, these steps can be built into the study package with feature extraction steps.

Another common and important step to assess feasibility for a PLE or PLP is an assessment of cohort sizes and the counts of outcomes in the target and comparator cohorts. The incidence rate feature of ATLAS can be used to find these counts which can be used to perform power calculations as described elsewhere.

Another option which is highly recommended for a PLE study is to complete the propensity score (PS) matching steps and relevant diagnostics to ensure that there is sufficient overlap between the populations in the target and comparator groups. These steps are described in detail in Chapter 12. In addition, using these final matched cohorts, the statistical power can then be calculated.

In some cases, work in the OHDSI community examines the statistical power only after a study is run by reporting a minimal detectable relative risk (MDRR) given the available sample sizes. This approach may be more useful when running high throughput, automated studies across a lot of databases and sites. In this scenario, a study's power in any given database is perhaps better explored after the all analyses have been performed rather than pre-filtering.

19.2.5 Finalize Protocol and Study Package

Once the legwork for all the previous steps has been completed, a final protocol should be assembled that includes detailed cohort definitions and study design information ideally exported from ATLAS. In Appendix D, we provide a sample table of contents for a full protocol for a PLE study. This can also be found on the OHDSI github. We provide this sample as a comprehensive guide and checklist, but note some sections may or may not be relevant for your study.

As shown in Figure 19.1, assembling the final study protocol in human-readable form should be performed in parallel with preparing all the machine-readable study code that is incorporated into the final study package. These latter steps are referred to as study implementation in the diagram below. This will include export of the finalized study package from ATLAS and/or development of any custom code that may be required.

The completed study package can then be used to execute only the preliminary diagnostics steps which in turn can be described in the protocol. For example, in the case of a new user cohort PLE study to examine comparative effectiveness of two treatments, the preliminary execution of study diagnostics steps will require cohort creation, propensity score creation, and matching to confirm that the target and comparator populations have sufficient overlap for the study to be feasible.

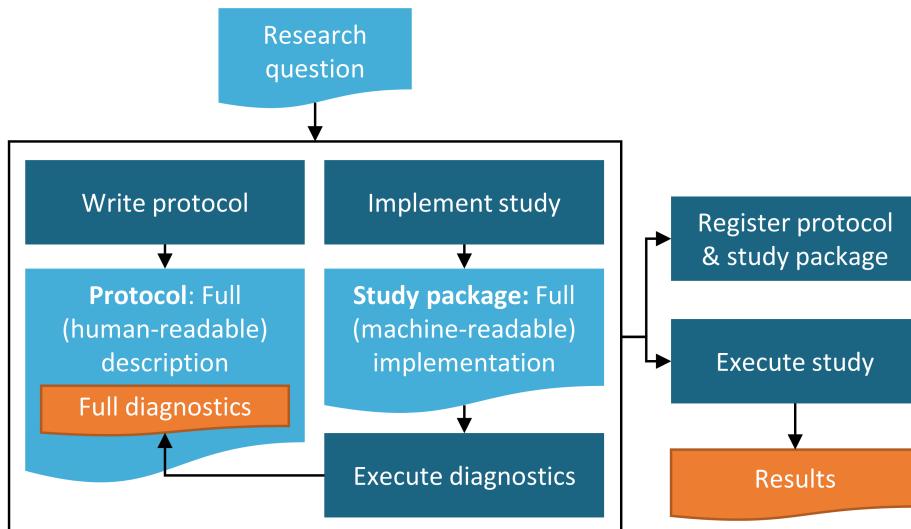


Figure 19.1: Diagram of the study process.

Once this is determined, power calculations can be performed with the matched target and comparator cohorts intersected with the outcome cohort to obtain outcome counts and the results of these calculations can be described in the protocol. On the basis of these diagnostics results, a decision can then be made whether or not to move forward with executing the final outcome model. In the context of a characterization or a PLP study, there may be similar steps that need to be completed at this stage, although we don't attempt to outline all scenarios here.

Importantly, we recommend at this stage to have your finalized protocol reviewed by clinical collaborators and stakeholders.

19.2.6 Execute Study

Once all prior steps have been completed, study execution should ideally be straightforward. Of course, the code or process should be reviewed for fidelity to the methods and parameters outlined in the protocol. It may also be necessary to test and debug a study package to ensure it runs appropriately in your environment.

19.2.7 Interpretation and Write-Up

In a well-defined study where sample sizes are sufficient and data quality is reasonable, the interpretation of results will often be straightforward. Similarly, because most of the work of creating a final report other than writing up the final results is done in the planning and creation of the protocol, the final write-up of a report or manuscript for publication will often be straightforward as well.

There are, however, some common situations where interpretation becomes more

challenging and should be approached with caution.

1. Sample sizes are borderline for significance and confidence intervals become large
2. Specific for PLE: p-value calibration with negative controls may reveal substantial bias
3. Unanticipated data quality issues come to light during the process of running the study

For any given study, it will be up to the discretion of the study authors to report on any concerns above and temper their interpretation of study results accordingly. As with the protocol development process, we also recommend that the study findings and interpretations be reviewed by clinical experts and stakeholders prior to releasing a final report or submitting a manuscript for publication.

19.3 Summary



- Study should examine a well-defined question.
- Perform appropriate checks of data quality, completeness and relevance in advance.
- Recommend to include source database expert in protocol development process if possible.
- Document proposed study in a protocol ahead of time.
- Generate study package code in parallel with written protocol and perform and describe any feasibility and diagnostics prior to executing the final study.
- Study should be registered and approved (if required) ahead of study execution.
- Finalized report or manuscript should be reviewed by clinical experts and other stakeholders.

Chapter 20

OHDSI Network Research

Chapter leads: Kristin Kostka, Greg Klebanov & Sara Dempster

OHDSI의 사명은 관찰 연구를 통해 높은 수준의 증거를 도출하는 것이다. 이것은 공동 연구를 통해 달성할 수 있는데, 이전 장에서 후향성 데이터 베이스 연구를 수행하기 위해, OHDSI 커뮤니티가 OMOP 표준화 어휘, 공통 데이터 모델 (이하 CDM), 분석 방법 패키지, ATLAS 및 연구 단계 (Chapter 19)를 포함하여 높은 수준의 재현 가능한 연구를 용이하게하는 표준과 도구를 어떻게 작성했는지 확인할 수 있었다. OHDSI 네트워크 연구는 공간적으로 분산된 여러 데이터에서 연구를 수행하는 투명하고 일관되며 재현 가능한 최상의 방법을 보여준다. 이 장에서는 OHDSI 네트워크 연구를 구성하는 요소, 네트워크 연구를 실행하는 방법 및 ARACHNE Research Network와 같은 기술에 대해 알아보자 한다.

20.1 연구 네트워크로서의 OHDSI

OHDSI 연구 네트워크는 의료 분야에서 관찰 데이터 연구를 발전시키려는 연구자들의 국제적인 모임이다. 현재 네트워크는 OMOP 공통 데이터 모델로 표준화 된 100 개가 넘는 데이터베이스로 구성되어있고, 총 10 억 건의 환자 기록이 포함되어 있다. OHDSI는 전세계 의료기관들이 데이터를 OMOP 공통 데이터 모델로 변환하고 다기관 네트워크 연구에 참여하도록 유도하고, 누구나 참여할 수 있는 개방형 네트워크로 운영되고 있다. 기관의 데이터 변환이 완료되면 OHDSI 프로그램 관리자(mailto : contact@ohdsi.org)는 데이터 네트워크 인구 조사 현황에 기관의 정보를 게시하도록 알려준다. 각 OHDSI 네트워크 사이트는 자발적으로 참여하고, 어려운 의무는 없다. 각 사이트는 각각의 네트워크 연구를 선택할 수 있고, 각 연구에서 데이터는 기관의 방화벽 안에 위치한다. 또한, 네트워크 사이트에서 환자 수준 데이터 수집되지 않고. 단지, 연구 최종 결과만 공유할 수 있다.



OHDSI 네트워크에 참여하는 기관의 이점

- 무료 도구 이용 : OHDSI는 데이터 특성 분석 및 표준화 된 분석 (예 :

임상 개념 탐색, 코호트 정의 및 특성 분석, 인구 수준 추정 및 환자 수준 예측 연구 실행)을 위한 오픈 소스 도구를 무료로 제공한다.

- **최고의 연구 커뮤니티 참여** : 네트워크 연구를 작성 및 게시하고 다양한 분야 및 관계자 그룹의 리더와 협력할 수 있다.
- **벤치마크 관리 기회** : 네트워크 연구를 통해 데이터 파트너 간에 임상 특성 및 품질 개선 벤치마크를 할 수 있다.

20.2 OHDSI 네트워크 연구

이전 장 (Chapter 19)에서 CDM을 사용하여 연구를 수행하기 위한 일반적인 고려 사항에 대해 알아보았다. 일반적으로 한개의 CDM 또는 여러 CDM에서 연구를 수행 할 수 있고, 단일 기관의 CDM 데이터뿐만 아니라 여러 기관에서도 실행할 수 있다. 이번 장에서는 여러 기관의 분석을 네트워크 연구로 확장하려는 이유를 알아보고자 한다.

20.2.1 OHDSI 네트워크 연구가 필요한 이유

관찰 연구의 전형적인 사용 사례는 “real world”에서 치료의 비교 효과 또는 안전성을 조사하는 것이다. 여러 상황을 구체적으로 이야기하면, 임상 시험에서 얻어지는 일반적 결과에 대한 확인을 위해 약물이 시판된 후 시행되는 임상 시험을 복제해서 동일하게 시행하는 연구를 해야하는 경우, 임상 시험이 이루어지지 않은 상태에서는 약물의 사용시 적응증외 사용(off label)이 되는데, 이러한 상황에서 허용된 약물과의 효과 비교연구를 시행해야 하는 경우, 그리고, 임상 시험에서 관찰하기 어려운 매우 희귀한 부작용에 대한 시판 후 안전성 결과를 연구가 필요할 수 있는 경우가 있다. 만약, 이러한 연구에서 사이트의 하나 또는 두 개의 데이터베이스에서 단일 관측 연구를 시행하면 특정 환자 그룹의 상황에서만 의미있는 결과를 얻기 때문에 정확한 결과를 얻는데 충분하지 않을 수 있다.

관찰 연구의 결과는 순응도, 유전적 다양성 또는 환경적 요인, 전반적인 건강 상태와 같이 데이터 소스의 위치에 따라 달라지는 많은 요인에 의해 영향을 받을 수 있다. 따라서 네트워크에서 관측 연구를 실행하려는 일반적인 이유는 데이터 소스의 다양성을 늘리고 잡재적으로 연구를 통해 일반화된 결과를 얻기 위함으로서, 다시 말해, 연구 결과가 여러 사이트에 걸쳐 같은 결과를 보이는지 아니면 다른지, 만약 다른 경우 그 이유를 설명할 수 있는지이다.

따라서 네트워크 연구를 통해 광범위한 설정과 데이터 소스를 조사하여 관측 연구 결과에 “실제” 요인의 영향을 조사할 수 있다.

20.2.2 OHDSI 네트워크 연구의 정의



어떤 연구를 네트워크 연구라고 할수 있나? OHDSI 연구는 다른 기관의 여러 CDM에서 실행될 때 OHDSI 네트워크 연구라고 할 수 있다.

네트워크 연구에 대한 OHDSI 접근 방식은 OMOP CDM과 표준화된 도구 및 연구 실행을 위해 모든 매개 변수를 지정할 수 있는 연구 패키지를 사용하여 시행된다. OHDSI 표준화 분석은 불필요한 혼란변수를 줄이고 네트워크 연구의 효율성과 확장성을 향상시키도록 설계되었다.

네트워크 연구는 OHDSI 연구 커뮤니티의 중요한 부분이다. 그러나 OHDSI 연구를 전체 OHDSI 네트워크에서 반드시 패키지를 공유할 의무는 없다. 단일 기관 내에서 OMOP CDM 및 OHDSI 분석법 라이브러리를 사용하여 연구를 수행하거나 선택된 기관에서만 시행하도록 제한할 수 있다. 연구가 단일 데이터베이스에서 실행되도록 설계되었는지, 제한된 파트너 집합을 대상으로 연구를 수행하거나, OHDSI 네트워크에 완전히 참여하기 위해 연구를 시작하는지 여부는 각 조사자의 재량에 달려있다. 이 장에서는 OHDSI 커뮤니티가 수행하는 개방형 네트워크 연구에 대해 다루도록 하겠다.

개방형 OHDSI 네트워크 연구 요소 개방형 OHDSI 네트워크 연구를 수행할 때는 완전히 투명한 연구를 수행하는 것이다. OHDSI 연구에서 다음과 같은 특징적인 몇 가지 구성요소가 있다.

- 모든 문서, 연구 코드 및 후속 결과는 OHDSI GitHub에서 공개적으로 제공된다.
- 연구자는 수행 할 분석의 범위와 의도를 자세히 설명하는 공개 학습 프로토콜을 작성하고 게시해야 한다.
- 연구자는 CDM을 준수하는 코드로 연구 패키지 (일반적으로 R 또는 SQL)를 작성해야 한다.
- 연구자는 OHDSI 네트워크 연구를 위해 공동 작업자를 홍보하고 모집하기 위해 OHDSI 커뮤니티 콜에 참석하도록 권장된다.
- 분석이 끝나면 OHDSI GitHub에서 종합 연구 결과를 제공한다.
- 가능하면 연구자들은 연구 R Shiny Applications를 data.ohdsi.org에 게시하도록 권장된다.

다음 장에서는 네트워크 연구를 구현하기 위한 고유한 설계 및 논리적 고려 사항뿐만 아니라 자체 네트워크 연구를 만드는 방법에 대해 설명한다.

20.2.3 OHDSI 네트워크 연구 설계를 위한 고려 사항

OHDSI 네트워크에서 실행할 연구를 설계하려면 연구 코드를 설계하고 조립하는 방법에 대한 패러다임 전환이 필요하다. 일반적으로 목표 데이터 세트를 염두해 두고 연구를 설계하게 되는데, 연구 분석에 이용되는 데이터 중에서 자신의 연구에 유리한 결과가 나오도록 코드를 작성할 가능성이 있다. 예를 들어, 혈관 부종 코호트를 구성하는 경우 CDM에 표시된 혈관 부종에 대한 개념 코드만 선택하게 되는데, 그렇게 하는 경우 연구용 데이터가 특정 간호 설정 (예 : 1 차 간호, 외래 설정) 또는 특정 지역 (예 : 미국 중심)에 있는 경우 문제가 될 수 있다. 결국 이렇게 선택된 연구 코드는 코호트 정의에 있어서 선택 편중(selection bias)가 발생하게 된다.

OHDSI 네트워크 연구에서는 본인의 데이터만을 위한 연구 패키지를 설계 및 구축하지 않고, 전 세계 여러 사이트에서 실행할 연구 패키지를 구축한다. 기관 외부의 참여 사이트에 대한 기본 데이터를 검색하거나 공유하는 것은 불가능하고, 결과 파일만

공유한다. 연구 패키지는 CDM의 도메인에서 사용 가능한 데이터 만 수집할 수 있다. 관찰 의료 연구 데이터가 확인되는 기관은 매우 다양하기 때문에 연구자는 이런 다양한 연구 기관에서 concept set을 적용할 수 있도록 포괄적인 접근법이 필요하다. OHDSI 연구 패키지는 종종 모든 사이트에서 동일한 코호트 정의를 사용해야 한다. 다시 말하면, 적격한 데이터(클래임 데이터 또는 EHR 데이터)의 하부 구조에서만 적용되는 코호트 정의를 함으로서 편중이 발생하지 않도록 주의해야 한다. 따라서, 코호트 정의를 작성할 때는 여러 CDM에서 적용 가능한 코호트 정의를 작성하도록 신경써야 한다. OHDSI 연구 패키지에서는 데이터베이스 연결이나 저장 위치와 같은 일부 부분만 각 사이트에서 변경하고, 연구에 관련된 변수는 모두 같은 메개 변수를 사용하고 있다. 나중에 다양한 데이터셋에서 임상적 소견을 해석하는 데 미치는 영향에 대해 알아보고록 한다.

임상 코딩 변형 외에도 로컬 기술 인프라에서 변형을 예상하여 설계해야 한다. 연구자가 작성한 학습 코드는 단일 기술 환경에서 실행되지 않을 것이다. 각 OHDSI 네트워크 사이트는 데이터베이스를 독립적으로 선택할 수 있다. 이는 연구 패키지를 특정 데이터베이스 용어로만 하드 코딩 할 수 없음을 의미한다. 연구 코드는 해당 데이터베이스의 운영자가 쉽게 수정할 수 있는 SQL 유형으로 매개 변수화되어 있어야 한다. 다행히 OHDSI 커뮤니티에는 ATLAS, DatabaseConnector (<https://ohdsi.github.io/DatabaseConnector/>) 및 SqlRender (<https://ohdsi.github.io/SqlRender/>) 같은 솔루션이 있어, 각자의 데이터베이스 용어로 변환하여 연구자의 연구 패키지를 실행시킬 수 있다. OHDSI 연구자는 여러 환경에서 연구 패키지를 테스트하고 검증 할 수 있도록 다른 네트워크 연구 사이트의 도움을 요청하는 것이 필요하다. 코딩 오류가 발생하면 연구자는 [OHDSI 포럼] (<http://forums.ohdsi.org>) 사용하여 패키지를 다른 연구자들과 논의하고 디버깅 할 수 있다.

20.2.4 OHDSI 네트워크 연구를 위한 논리적 관점

OHDSI는 개방형 연구 커뮤니티이며 OHDSI 중앙 조정 센터는 공동 연구자가 커뮤니티 연구를 이끌고 참여할 수 있도록 커뮤니티 인프라를 제공하는 역할을 한다. 모든 OHDSI 네트워크 연구에는 연구 책임자가 필요하며 OHDSI 커뮤니티의 참여자의 누구라도 될 수 있다. OHDSI 네트워크 연구는 연구 책임자, 공동 연구자 및 참여 네트워크 데이터 파트너 간의 긴밀한 협업이 필요하다. 각 사이트마다 연구 프로토콜이 승인되어 각자의 CDM에서 실행될 수 있도록 자체 승인 절차를 수행해야 한다. 데이터 분석가는 연구를 수행 할 수 있는 적절한 권한을 부여하기 위해 현지 IT 팀의 지원을 받아야 할 수도 있다. 각 사이트에서 연구팀의 규모와 범위는 OMOP CDM과 OHDSI 패키지의 숙련도뿐만 아니라 제안된 네트워크 연구의 크기와 복잡성에 따라 결정되어야 한다. 또한, OHDSI 네트워크 연구를 수행하는 사이트의 숙련도에 따라 필요한 인력이 결정될 수 있다.

각각의 연구에 따라 초기 준비 절차는 다음과 같다.

- 연구에 대해 기관생명윤리위원회에 신청한다
- 기관생명윤리위원회의 승인을 얻은 후 연구를 시행한다.
- 승인된 CDM의 스키마를 읽고 쓸수 있는 권한을 획득한다.
- 연구 패키지를 실행할 수 있도록 RStudio 환경을 조정한다.
- 기술적인 문제가 없는지 연구 패키지 코드를 검토한다.

- 연구 패키지 실행을 위한 연관된 R 패키지를 설치와 실행을 승인받도록 각 기관의 IT team에 업무 협조를 구한다.



데이터 품질 및 네트워크 연구: Chapter 6에서 논의한 것처럼 품질 관리는 ETL 프로세스의 기본적이고 반복적인 부분이다. 이는 네트워크 연구 프로세스와 관계없이 정기적으로 수행해야 한다. 네트워크 연구의 경우, 연구 책임자는 참여 사이트의 데이터 품질 보고서를 검토하거나 사용자 지정 SQL 쿼리를 작성 및 배포하여 데이터 소스간의 차이점을 확인할 수 있습니다. OHDSI 내에서 진행되는 데이터 품질 노력에 대한 자세한 내용은 Chapter 15 을 참조한다.

각 사이트에는 연구 패키지를 실행하는 데이터 분석가가 있을 것이다. 이 인원들은 환자의 민감한 정보가 전송되지 않는지 연구 패키지의 결과를 검토해야 한다. PLE (Population-Level Effect Estimation) 및 PLP (Patient Level Prediction)와 같은 사전 구축 된 OHDSI 패키지를 사용하는 경우 지정된 분석에 대한 최소 셀 수를 정할수 있는 설정이 있다. 데이터 분석가는 이러한 임계 값을 검토하고 각 기관의 정책을 준수하는지 확인해야 한다.

연구 결과를 공유할 때 데이터 분석가는 결과 전송 방법을 포함하여 모든 사항에 대해 각 기관의 정책을 준수해야하며 결과의 외부 반출을 위한 승인 프로세스를 준수해야한다. ** OHDSI 네트워크 연구는 환자 수준 데이터를 공유하지 않는다. 즉, 각 사이트의 환자 수준 데이터는 중앙에 저장되지 않는다. 연구 패키지는 집계 결과(예 : 요약 통계, 포인트 추정치, 진단 플롯 등)로 설계된 결과 파일을 작성하며 환자 수준 정보는 공유되지 않는다. 따라서, 많은 조직에서는 참여 연구 팀 구성원간에 데이터 공유 계약을 실행할 필요가 없다. 그러나 관련 기관 및 데이터 소스에 따라 특정 연구 팀원이 확인하고 보다 공식적인 데이터 공유 계약을 체결해야 할 수도 있다. 네트워크 연구에 관심이 있는 CDM 데이터 소유 연구기관 연구자인 경우 각 기관의 관련팀과 협의하여 OHDSI 커뮤니티 연구에 참여하기 위해 충족해야하는 정책을 확인하는 것이 필요하다.

20.3 OHDSI 네트워크 연구 수행하기

OHDSI 네트워크 연구를 수행하기 위한 세가지 단계는 다음과 같다.

- 연구 설계와 타당성
- 연구 수행
- 결과 배포 및 출판

20.3.1 연구 설계와 타당성

연구 타당성 단계 (또는 사전 학습 단계)는 연구 주제를 정의하고 연구 프로토콜에 따른 주제의 결과를 도출하는 프로세스를 의미한다. 이 단계는 참여 사이트에서 연구 프로토콜을 실행할 수 있는 가능성을 평가하는 데 중점을 둔다.

타당성 단계의 결과는 네트워크 실행 준비가 완료된 최종 프로토콜 및 연구 패키지를 생성하는 것이다. 공식 프로토콜은 지정된 연구 책임자(논문에서는 책임저자) 및

연구 일정에 대한 정보를 포함한 내용으로 연구팀을 자세히 설명한다. 이 프로토콜은 추가로 연구에 참여하는 네트워크 사이트가 CDM 데이터에서 전체 연구 패키지를 검토, 승인 및 실행하는 데 중요한 구성 요소가 되고 있다. 임상 시험 계획서에는 연구 모집단, 사용되는 방법, 결과 저장 및 분석 방법, 완료 후 연구 결과 배포 방법(예: 논문, 프레젠테이션 등)이 포함되어야 한다.

타당성 검증 단계는 정립된 절차는 없다. 이 과정은 연구의 종류에 따라 달라진다. 최소한 연구 책임자는 필요로 하는 약물 노출, 처치 정보, 진단명 또는 환자의 인구학적 정보가 있는 네트워크 사이트를 알아보는데 시간을 할애한다. 가능한 경우, 연구 책임자는 자신의 CDM을 이용하여 연구 대상을 설계해야 한다. 그러나, 연구 책임자는 네트워크 연구를 실행하기 위해 실제 환자 데이터가 있는 OMOP CDM에 접속할 필요는 없다. 책임자는 가상의 데이터 (CMS synthetic Public Use Files, Mitre 또는 Synthea의 syntheticMass)를 사용하여 대상 코호트 정의를 설계하고, OHDSI 네트워크 사이트 공동 연구자들에게 코호트의 타당성을 검증하도록 요청하는 방식으로도 할 수 있다. 타당성 조사 단계는 공동 연구자들에게 ATLAS에서 만들어진 코호트 정의 JSON file을 이용하여 코호트를 생성하도록 요청하거나, 19장 19에서 설명한 것처럼 R 패키지를 실행하여 초기 진단을 실행해 보도록 요청하는 방식으로 할 수 있다. 동시에 연구 책임자는 기관생명윤리위원회와 같은 조직에서 OHDSI 연구를 승인 받기 위한 절차를 진행한다. 타당성 조사 단계에서는 이러한 조직별 절차를 완료하는 작업은 연구 책임자의 역할로 진행되어야 한다.

20.3.2 연구 실행

타당성 연구를 완료한 후에는 실행의 단계로 진행한다. 이 단계는 OHDSI 네트워크 사이트가 분석에 참여하는 시기이다. 이 단계는 우리가 이전에 논의하였던 연구 설계와 논리적 고려 사항이 가장 중요한 시기이다.

연구의 실행은 연구 책임자가 새로운 OHDSI 네트워크 연구에 대해 공식적으로 소개하고 참여 기관을 공식적으로 모집하는 것으로부터 시작한다. 연구 책임자는 연구 프로토콜을 OHDSI GitHub에 공개하고, 매주 열리는 OHDSI 커뮤니티 원격 회의나 OHDSI 포럼에 연구에 대해 소개하고, 참여하는 센터와 공동 연구자를 모집하도록 한다. 연구에 사이트가 참여하려고 하면, 연구 책임자는 각 사이트에 직접 연락하여 연구 프로토콜과 코드뿐만 아니라 연구 패키지를 실행하는 방법 안내서를 저장하고 있는 GitHub 저장소를 알려주도록 한다. 모든 사이트에서 동시에 진행하여 각 사이트의 결과가 동시에 공유되어 다른 사이트의 결과값에 의해 자신의 사이트 결과에 영향을 주지 않도록 하는 것 이상적이다.

각 사이트 연구팀은 각자의 기관에서 패키지를 실행하고 외부로 결과를 공유할 수 있는 절차를 확인해서 진행해야 한다. 어떤 부분에서는 기관생명윤리위원회의 승인을 받거나 동등한 승인을 받는 것과 같은 절차일 것이다. 연구 실행이 승인되면 각자 기관의 연구자나 통계학자가 연구 책임자의 안내서대로 패키지를 실행하고, OHDSI 가이드라인에 따라서 표준화된 형태의 결과를 생성한다. 각자의 기관은 기관생명윤리위원회의 절차에 따라 데이터를 공유하도록 한다. 만약, 기관생명윤리위원회의 승인을 얻지 못한 상태에서는 결과를 공유해서는 안된다.

연구 책임자는 연구 결과를 받을 수 있는 방법 (예를 들면, SFTP 나 Amazon S3 bucket)를 결정해야 하고 결과를 전환하는 시간표를 결정해야 한다. 각 사이트에서는

전송 방법이 내부 규약에 맞지 않는 경우에는 새로운 해결방법을 개발해야 할 수도 있다.

실행 단계에서는 통합된 연구팀(연구 책임자와 참여 사이트 구성원들 포함)은 합당한 조정이 필요한 경우, 실행을 반복해야 할 수 있다. 만약 이러한 과정에서 수정된 연구 프로토콜이 승인된 연구 내용을 벗어난 경우 각 참여 기관에서는 업데이트된 프로토콜을 받아서 각자의 기관생명윤리위원회의 검토 및 재승인 절차를 진행해야 한다.

연구 책임자와 데이터 사이언티스트나 통계학자는 여러 기관에서 공유된 데이터를 모으로, 적절하게 메타분석을 시행하는 최종적인 역할을 한다. OHDSI 커뮤니티에는 단일 결과를 얻기 위해 여러 네트워크 사이트에서 생성된 결과를 모으고 분석하는 검증된 방법들이 있다. EvidenceSynthesis는 여러 사이트에서 생성된 결과로 증거를 통합하고 진단을 실행할 수 있는 공개된 R 패키지이다. 이것은 메타 분석과 포레스트 플롯을 작성할 수 있는 함수를 포함하고 있다.

연구 책임자는 참여 기관의 상황을 모니터하고 정기적으로 확인함으로서 패키지 실행시 문제점을 해결할 수 있도록 도와줘야 한다. 연구 패키지 실행은 각 사이트에 일괄적으로 적용되기 어려울 수 있다. 데이터베이스 측면 (예를 들면 권한 설정 / 스키마 승인)과 연관된 문제점들과 각자의 환경이 달라서 생기는 (예를 들면, 필요한 패키지가 설치되지 않거나, R에서 데이터베이스에 접속이 되지 않는 등) 분석률 실행에 관계된 문제점이 생긴다. 참여 기관은 여러 상황을 직접적으로 처리하게 되고, 결국 연구를 실행시 발생하는 문제점을 해결하는 방법에 대해 의견을 나눌 것이다. 궁극적으로는 각자 CDM에서 발생하는 문제점을 해결하는 적절한 resource를 찾는 절차는 참여하는 사이트에서 고려해야 하는 사항이다.

OHDSI 연구의 실행이 신속하게 진행될 수 있더라도, 모든 참여 기관이 연구를 실행하고, 결과를 배포할 때 적절한 승인을 얻을 수 있는 충분한 시간을 주는 것이 바람직하다. 처음으로 OHDSI 네트워크에 참여하는 기관은 다양한 환경적인 요인, 예를 들어 데이터베이스 권한이나 분석 라이브러리 업데이트 문제와 같은 요인에 의해 처음 시행하는 연구에 참여하는데 많은 시간이 소요된다. OHDSI 커뮤니티를 통해 여러 문제에 대한 지원을 받을 수 있다. OHDSI 포럼에 이슈를 제출할 수 있다.

연구 책임자는 연구 마일스톤을 프로토콜에 정하고 전반적인 연구 일정을 원활하게 하기 예상되는 마감일에 대해 의견을 나눠야 한다. 만약 연구 일정을 준수하지 않을 경우, 연구 책임자는 참여기관에 연구 일정 업데이트를 알려주고 연구 실행의 전반적인 상황을 관리하도록 한다.

20.3.3 결과의 보급와 출판

결과의 보급과 출판 단계에서는 연구 책임자는 보고서 작성과 데이터 시각화와 같은 다양한 업무에 대해 다른 참여자들과 협력한다. 일단 연구가 시행되면, 연구 결과는 중앙에 저장되고 연구 책임자는 추가적인 분석을 할 수 있다. 연구 책임자는 참여 기관의 연구 결과 검토를 위해 전체 연구 결과 (예를 들면 Shiny Application)를 작성하고 배포하도록 한다. 연구 책임자가 OHDSI study skeleton, Atlas에서 생성된 코드 또는 GitHub code를 수동으로 수정해서 사용하고 있으면, Shiny Application이 자동으로 생성된다. 연구 책임자가 custom 코드를 작성하는 경우에는 자신들의

연구 패키지에 대한 shiny application을 생성하는데 문의하거나 도움을 얻을 때는 OHDSI 포럼을 이용할 수 있다.



자신의 OHDSI 네트워크 연구를 어디에 게재할 지 결정하기 어려우면, 초록과 출판물을 검색해서 가장 적절한 저널을 추천해주는 JANE (Journal/Author Name Estimator)를 사용해 보기 바란다.¹

일단 논문이 작성되면, 모든 연구 참여자들이 내용을 검토하고 외부 출판 과정에 이르는 결과를 확인하도록 한다. 최소한 참여한 사이트에서는 출판 책임자를 결정해야 한다. - 이 인원은 논문의 준비와 투고 과정에 내부적인 조정을 담당하게 된다. 어느 저널에 투고할지는 시작 단계에서 연구 참여자들과 논의하는 것이 바람직 하지만 연구자의 재량에 달려있다. OHDSI 연구에서 모든 공저자들은 ICMJE 저자 가이드라인에 충족해야 한다.² 결과의 발표는 OHDSI 심포지움, 다른 학술 심포지움이나 논문 게재 등의 다양한 방법을 사용할 수 있다. 연구자는 OHDSI 네트워크 연구를 매주 열리는 OHDSI 커뮤니티 회의나 국제 OHDSI 심포지움에서 발표하도록 초대한다.

20.4 미래의 모습: 네트워크 연구의 자동화

현재 네트워크 연구 방식은 수동이다. - 연구팀 구성원이 다양한 방법 (wiki, GitHub, email)을 이용하여 연구 디자인, 코드와 결과 공유를 시행하고 있다. 이러한 방법은 일관적이지 못하고 확장성이 낮아, OHDSI 커뮤니티에서는 연구 프로세스를 체계화하기 위해 노력하고 있다.

ARACHNE는 네트워크 연구 과정을 간소화하고 자동화할 수 있도록 고안된 플랫폼이다. ARACHNE는 OHDSI 표준을 사용하여 여러 조직에서 일관되고, 투명하며, 안전하며, 준수하는 관찰 연구 프로세스를 설정한다. ARACHNE는 데이터 접근과 분석 결과 교환을 위한 통신 규약을 표준화 하고 제한된 컨텐츠에 대한 인증 및 권한 부여를 가능하게 한다. 이것은 데이터 제공자, 연구자, 지원업체, 데이터 사이언티스트은 모든 참여 조직을 하나의 협동 연구 조직으로 만들수 있고, 관찰 연구의 모든 단계에서 조정하는 역할을 하게 된다. 이 도구를 사용하면 데이터 관리자가 제어하는 작업을 포함하여 R, Python, SQL 기반 실행 환경을 만들수 있다.

ARACHNE는 ACHILLES 보고서 및 ATLAS 디자인 아티팩트 가져 오기, 자체 포함된 패키지 작성 및 여러 사이트에서 자동으로 실행하는 기능을 포함하여 다른 OHDSI 도구와 완벽하게 통합되도록 설계되었다. 미래 비전은 단일 네트워크 내의 조직뿐만 아니라 여러 네트워크의 조직 간에도 연구를 수행 할 목적으로 여러 네트워크를 서로 연결하는 것이다.

²<http://www.icmje.org/recommendations/browse/roles-and-responsibilities/defining-the-role-of-authors-and-contributors.html>

Network Study Workflow

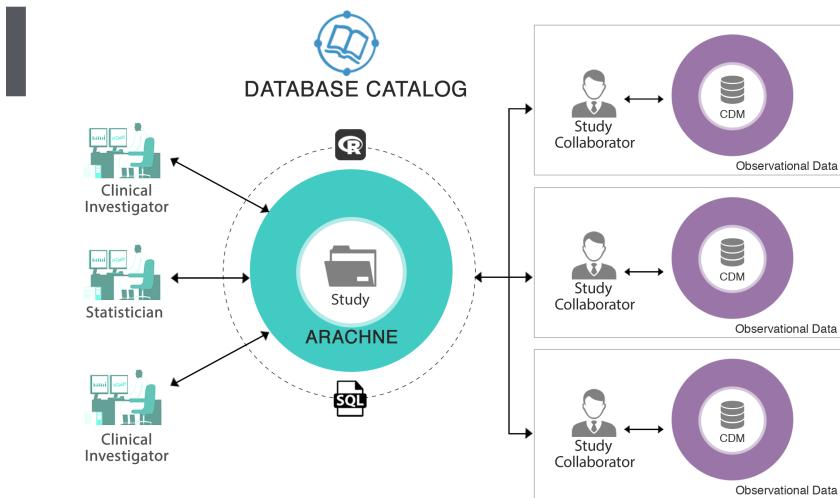


Figure 20.1: The ARACHNE Network Study Process.

20.5 OHDSI 네트워크 연구의 정석

네트워크 연구를 계획하고 있으며, 연구자가 OHDSI 네트워크 연구를 잘 진행할 수 있도록 OHDSI 커뮤니티는 도움을 줄 수 있다.

연구 설계와 타당도 네트워크 연구를 시행할 때, 자신의 연구가 한 형태의 데이터에 편향되어 있지 않는지 확인해야 한다. 모든 사이트에서 동일한 대상을 표현할 수 있는 코호트 정의를 조율하는 과정은 데이터 형태의 이질성의 정도와 연구 사이트에서 데이터를 OMOP CDM으로 변환할 때, 표준규약을 얼마나 잘 따랐는지에 따라 그 난이도가 결정될 것이다. 이 작업이 중요한 이유는 각 네트워크 사이트와 실제 임상적으로 의미있는 데이터 선택, 표현, 변환간의 차이를 조정해야 하기 때문이다. 특히, 효과를 비교하는 연구에서는 각 데이터 사이트간에 일치된 노출 코호트와 결과 코호트 정의가 문제될 수 있다. 예를 들면, 약물 노출 정도는 분류가 잘못되었을 가능성이 존재하는 데이터 소스에서 수집될 수 있다. 약국에서 수집된 건강보험공단 약물 처방전의 경우, 약물에 대한 청구가 있을 때 환자가 처방을 받았을 가능성이 높다는 것을 의미한다. 그러나, EHR에 입력된 처방전은 약물의 실제 소비 여부를 확인하는 데이터와의 연결이 되지 않는다. 또한, 의사가 처방전을 발급한 시간, 약사가 처방전에 따라 약을 조제한 시간, 약국에서 환자가 약을 수령한 시간, 실제로 약의 첫 복용이 일어난 시간 간의 차이가 존재한다. 이러한 측정 오류는 어떠한 연구를 하더라도 bias 가 될 수 있다. 따라서, 연구 계획서를 개발할 때에는 데이터 참여 적절성을 감안하여 타당성 연구를 시행하는 것이 중요하다.

연구 실행 가능하면 연구 책임자가 ATLAS나 OHDSI Method Library, OHDSI Study Skeleton를 이용하여 표준화된 분석 패키지를 사용하여 연구 코드를 작성하는 것을 권장한다. 연구 코드는 OHDSI 패키지를 이용하여 CDM에 호환성을 유지하고, 데이터베이스 레이어 규약에 따라 작성되어야 한다. 모든 기능과 변수는 매개

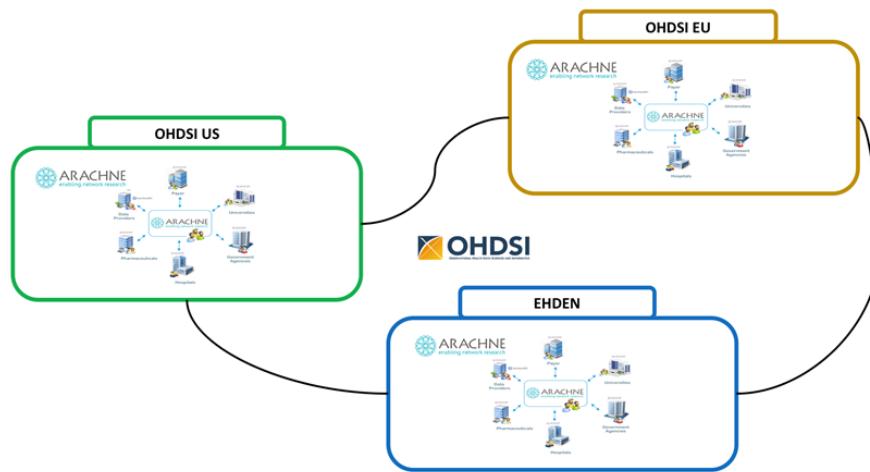


Figure 20.2: The ARACHNE Network of Networks.

변수화해야 한다. (예: 데이터 베이스 연결 정보, 로컬 드라이브 경로, 운영체제를 지정하지 않는다.) 참여 기관을 모집할 때는, 연구 책임자는 각 참여 기관이 CDM 규약에 맞는지, 최신 OMOP 표준 용어집에 따라 업데이트되어 있는지 확인해야 한다. 연구 책임자는 각 네트워크 사이트에서 CDM에 대한 데이터 품질 검사를 수행하고 문서화하도록 하고 이에 대한 점검을 해야한다. (예: ETL 수행이 THEMIS 규약과 규칙에 따라서 올바른 CDM 테이블과 필드로 데이터가 배치되었는지 확인) 각 데이터 분석가는 연구 패키기는 실행하기 전에 R 패키지를 최신 OHDSI 패키지 버전으로 업데이트하도록 한다.

결과와 배포 연구 책임자는 결과를 공유하기 전에 각 사이트가 각 기관의 규칙을 준수하도록 해야한다. 연구가 개방적이고 재현 가능하다는 의미는 설계되고 실행되는 모든 것들이 가능하다는 의미이다. OHDSI 네트워크 연구는 모든 문서와 결과가 OHDSI GitHub 저장소나 data.ohdsi.org R Shiny server에 게시되어 투명하게 관리된다. 논문을 준비할 때는 연구 책임자는 저널에서 OHDSI 네트워크 사이트 간에 데이터가 어떻게 달라질 수 있는지 이해시킬 수 있도록 OMOP CDM과 표준화된 용어 원칙에 대해 언급을 해야한다. 예를 들면, Claim 데이터베이스와 EHR을 이용한 네트워크 연구를 진행할 때에 저널 리뷰어는 다양한 데이터 형태에서 코호트 정의의 일관성을 유지할 수 있는지 설명을 요청할 수 있다. 리뷰어는 OMOP 관찰 기간 (Chapter 4에서 언급된 바와 같이) 자격 파일 (환자가 보험 자격 유지 기간에 있거나 있지 않은 상황에서 claim 데이터베이스에 존재하는 파일)과 비교하는 방법에 대해 궁금해 할 수 있다. 이것은 본질적으로 데이터베이스 자체의 인위적인 요소에 중점을 두고 CDM이 자료를 관찰로 변환하는 방법의 ETL에 중점을 둔다. 이러한 경우 네트워크 연구 책임자는 OMOP CDM OBSERVATION PERIOD 작성 방법을 참조하고 원본 시스템에서 확인되는 상황을 이용하여 관찰기록이 작성되는 방법을 설명하는 것이 도움이 될 수 있다. 논문의 고찰 부분에서는 보험 기간 동안에 모든 청구 내용을 반영하는 claim 데이터와는 달리 EHR 데이터의 경우는 환자가 다른 EHR 기록을 사용하는 병원의 기록은 기록되지 않아서 관찰 기간의 중단이 발생할 수 있는 제한점에 대해 기술해야 한다. 이것은 데이터가 수집된 시스템에서 데이터

가 존재하는 방식의 결과이다. 이것은 임상적으로 의미있는 차이를 보이지는 않지만 OMOP에서 observation period table을 추출하는 방식에 익숙하지 않으면 혼동될 수 있다. 이러한 생소한 분야에 대해서 고찰 부분에서 언급을 하는 것이 필요하다. 비슷하게, 연구 책임자는 OMOP 표준 용어에서 제공되는 용어를 기술하는 것이 유용하며, 수집되는 모든 부분들이 동일할 수 있다. 원본 코드를 표준 concept으로 매핑할 때 항상 결정이 이루어지지만 THEMIS 규칙과 CDM 품질 검사로서 정보 위치와 데이터베이스가 해당 원칙을 얼마나 잘 준수하는지에 대한 정보를 제공하는 것이 도움이 될 수 있다.

20.6 요약



- OHDSI 연구는 서로 다른 기관의 여러 CDM에서 실행될 때 OHDSI 네트워크 연구가 된다.
- OHDSI 네트워크 연구는 개방되어 있다. 누구나 네트워크 연구를 주도할 수 있다. OMOP 호환 데이터베이스를 소유한 사람은 누구나 참여하고 결과를 제공할 수 있다.
- 네트워크 연구를 하는데 도움이 필요하면 연구를 디자인하고 실행하는데 도움을 줄 수 있는 OHDSI 연구 육성 커뮤니티와 상의한다.
- **공유는 조심스럽게 시행한다.** 모든 연구 문서, 코드 및 결과는 OHDSI GitHub 또는 R Shiny 응용프로그램에 게시된다. 연구 책임자는 OHDSI 행사에 자신의 연구를 발표할 수 있도록 한다.

Chapter A

Glossary

ACHILLES A database-level characterization report.

ARACHNE The OHDSI platform that is being developed to allow the orchestration and execution of federated network studies.

ATLAS A web-based application that is installed on participating sites to support the design and execution of observational analyses to generate real world evidence from patient level clinical data.

편향 (Bias) The expected value of the error (the difference between the true value and the estimated value).

Boolean Variable that has only two values (true or false).

Care site A uniquely identified institutional (physical or organizational) unit where healthcare delivery is practiced (office, ward, hospital, clinic, etc.).

환자 대조군 (Case control) A type of retrospective study design for population-level effect estimation. Case-control studies match “cases” with the target outcome to “controls” without the target outcome. Then they look back in time and compare the odds of exposure in the cases and the controls.

인과적 영향 (Causal effect) What population-level estimation concerns itself with. One definition equates a “causal effect” as the average of the “unit-level causal effects” in a target population. The unit-level causal effect is the contrast between the outcome had an individual been exposed and the outcome had that individual not been exposed (or been exposed to A as against B).

Characterization Descriptive study of a cohort or entire database. See Chapter 11.

청구 자료 (Claims data) Data generated for the purpose of billing a health insurance company.

임상 시험 (Clinical trial) Interventional clinical study.

코호트 (Cohort) A set of persons who satisfy one or more inclusion criteria for a duration of time. See Chapter 10.

Concept A term (with a code) defined in a medical terminology (e.g., SNOMED

CT). See Chapter 5.

Concept set A concept set is an expression representing a list of concepts that can be used as a reusable component in various analyses. See Chapter 10.

공통 데이터 모델 (Common Data Model, CDM) A convention for representing healthcare data that allows portability of analysis (the same analysis unmodified can be executed on multiple datasets). See Chapter 4.

비교 효과 Comparative Effectiveness A comparison of the effects of two different exposures on an outcome of interest. See Chapter 12.

Condition A diagnosis, a sign, or a symptom, which is either observed by a provider or reported by the patient.

교란 (Confounding) Confounding is a distortion (inaccuracy) in the estimated measure of association that occurs when the primary exposure of interest is mixed up with some other factor that is associated with the outcome.

변수 (Covariate) Data element (e.g., weight) that is used in a statistical model as independent variable.

데이터 질 (Data quality) The state of completeness, validity, consistency, timeliness and accuracy that makes data appropriate for a specific use.

Device A foreign physical object or instrument which is used for diagnostic or therapeutic purposes through a mechanism beyond chemical action. Devices include implantable objects (e.g. pacemakers, stents, artificial joints), medical equipment and supplies (e.g. bandages, crutches, syringes), other instruments used in medical procedures (e.g. sutures, defibrillators) and material used in clinical care (e.g. adhesives, body material, dental material, surgical material).

Drug A Drug is a biochemical substance formulated in such a way that when administered to a Person it will exert a certain physiological effect. Drugs include prescription and over-the-counter medicines, vaccines, and large-molecule biologic therapies. Radiological devices ingested or applied locally do not count as Drugs.

Domain A Domain defines the set of allowable Concepts for the standardized fields in the CDM tables. For example, the “Condition” Domain contains Concepts that describe a condition of a patient, and these Concepts can only be stored in the condition_concept_id field of the CONDITION_OCCURRENCE and CONDITION_ERA tables.

전자 의무기록 (Electronic Health Record, EHR) Data generated during course of care and recorded in an electronic system.

역학 (Epidemiology) The study of the distribution, patterns and determinants of health and disease conditions in defined populations.

근거 중심 의학 (Evidence-based medicine) The use of empirical and scientific evidence in making decisions about the care of individual patients.

ETL (Extract-Transform-Load) The process of converting data from one format to another, for example from a source format to the CDM. See Chapter 6.

짝짓기 (Matching) Many population-level effect estimation approaches attempt

to identify the causal effects of exposures by comparing outcomes in exposed patients to those same outcomes in unexposed patients (or exposed to A versus B). Since these two patient groups might differ in ways other than exposure, “matching” attempts to create exposed and unexposed patient groups that are as similar as possible at least with respect to measured patient characteristics.

Measurement A structured value (numerical or categorical) obtained through systematic and standardized examination or testing of a person or person’s sample.

측정 오차 (Measurement error) Occurs when a recorded measurement (e.g., blood pressure, patient age, duration of treatment) differs from the corresponding true measurement.

메타데이터 (Metadata) A set of data that describes and gives information about other data and includes descriptive metadata, structural metadata, administrative metadata, reference metadata and statistical metadata.

Methods Library A set of R packages developed by the OHDSI community for performing observational studies.

Model misspecification Many OHDSI methods employ statistical models such as proportional hazards regression or random forests. Insofar as the mechanism that generated the data deviate from the assumed model, the model is “misspecified.”

음성 통제 결과 (Negative control) An exposure-outcome pair where the exposure is believed to not cause or prevent the outcome. Can be used to assess whether effect estimation methods produce results in line with the truth. See Chapter 18.

Observation A clinical fact about a Person obtained in the context of examination, questioning or a procedure.

Observation period The span of time for which a person is at-risk to have clinical events recorded within the source systems, even if no events in fact are recorded (healthy patient with no healthcare interactions).

관찰 연구 (Observational study) A study where the researcher has no control over the intervention.

OHDSI SQL A SQL dialect that can be automatically translated to various other SQL dialects using the SqlRender R package. OHDSI SQL is mostly a subset of SQL Server SQL, but allows for additional parameterization. See Chapter 9.

오픈 사이언스 (Open science) The movement to make scientific research (including publications, data, physical samples, and software) and its dissemination accessible to all levels of an inquiring society, amateur or professional. See Chapter 3.

Outcome An observation that provides a focal point for an analysis. For example, a patient-level predictive model might predict the outcome “stroke.” Or a population-level estimation might estimate the causal effect of a drug on the outcome “headache.”

Patient-level prediction Development and application of predictive models to produce patient-specific probabilities for experiencing some future outcome based on baseline characteristics.

표현형 (Phenotype) A description of physical characteristics. This includes visible characteristics like your weight and hair color, but also your overall health, your disease history, and your behavior.

Population-level estimation A study into causal effects. Estimates an average (population-level) effect size.

양성 통제 결과 (Negative control) An exposure-outcome pair where the exposure is believed to cause or prevent the outcome. Can be used to assess whether effect estimation methods produce results in line with the truth. See Chapter 18.

Procedure Activity or process ordered by, or carried out by, a healthcare provider on the patient to have a diagnostic or therapeutic purpose.

성향 점수 (Propensity score, PS) a single metric used in population-level estimation to balance populations in order to mimic randomization between two treatment groups in an observational study. The PS represents the probability of a patient receiving a treatment of interest as a function of a set of observed baseline covariates. It is most often calculated using a logistic regression model where the binary outcome is set to one for the group receiving the target treatment of interest and to zero for the comparator treatment. See Chapter 12.

프로토콜 (Protocol) A human readable document that fully specifies the design of a study.

Rabbit-in-a-Hat An interactive software tool to help define the ETL from source format to CDM. Uses the database profile generated by White Rabbit as input. See Chapter 7.

선택 편향 (Selection bias) A bias that occurs when the set of patients in your data deviates from the patients in the population in ways that distort statistical analyses.

Self-controlled designs Study designs that compare outcomes during different exposures within the same patient.

민감도 분석 (Sensitivity analysis) A variant of the main analysis used in a study to asses the impact of an analysis choice over which uncertainty exists.

SNOMED A systematically organized computer processable collection of medical terms providing codes, terms, synonyms and definitions used in clinical documentation and reporting.

Study diagnostics Set of analytical steps where the goal is to determine whether a given analytical approach can be used (is valid) for answering a given research question. See Chapter 18.

Study package A computer-executable program that fully executes the study. See Chapter 17.

Source code A code used in a source database. For example an ICD-10 code.

Standard Concept A concept that is designated as valid concept and allowed

to appear in the CDM.

THEMIS OHDSI workgroup that addresses target data format that is of higher granularity and detail with respect to CDM model specifications.

Visit The span of time a person continuously receives medical services from one or more providers at a care site in a given setting within the health care system.

Vocabulary A list of words and often phrases, usually arranged alphabetically and defined or translated. See Chapter 5.

White Rabbit A software tool for profiling a database before defining the ETL to the CDM. See Chapter 6.

Chapter B

Cohort definitions

This Appendix contains cohort definitions used throughout the book.

B.1 ACE Inhibitors

Initial Event Cohort

People having any of the following:

- a drug exposure of *ACE inhibitors* (Table B.1) for the first time in the person's history

with continuous observation of at least 365 days prior and 0 days after event index date, and limit initial events to: all events per person.

Limit qualifying cohort to: all events per person.

End Date Strategy

Custom Drug Era Exit Criteria This strategy creates a drug era from the codes found in the specified concept set. If the index event is found within an era, the cohort end date will use the era's end date. Otherwise, it will use the observation period end date that contains the index event.

Use the era end date of *ACE inhibitors* (Table B.1)

- allowing 30 days between exposures
- adding 0 days after exposure end

Cohort Collapse Strategy

Collapse cohort by era with a gap size of 30 days.

Concept Set Definitions

Table B.1: ACE inhibitors

Concept Id	Concept Name	Excluded	Descendants	Mapped
1308216	Lisinopril	NO	YES	NO
1310756	moexipril	NO	YES	NO
1331235	quinapril	NO	YES	NO
1334456	Ramipril	NO	YES	NO
1335471	benazepril	NO	YES	NO
1340128	Captopril	NO	YES	NO
1341927	Enalapril	NO	YES	NO
1342439	trandolapril	NO	YES	NO
1363749	Fosinopril	NO	YES	NO
1373225	Perindopril	NO	YES	NO

B.2 New Users of ACE Inhibitors Monotherapy

Initial Event Cohort

People having any of the following:

- a drug exposure of *ACE inhibitors* (Table B.2) for the first time in the person's history

with continuous observation of at least 365 days prior and 0 days after event index date, and limit initial events to: earliest event per person.

Inclusion Rules

Inclusion Criteria #1: has hypertension diagnosis in 1 yr prior to treatment

Having all of the following criteria:

- at least 1 occurrences of a condition occurrence of *Hypertensive disorder* (Table B.3) where event starts between 365 days Before and 0 days After index start date

Inclusion Criteria #2: Has no prior antihypertensive drug exposures in medical history

Having all of the following criteria:

- exactly 0 occurrences of a drug exposure of *Hypertension drugs* (Table B.4) where event starts between all days Before and 1 days Before index start date

Inclusion Criteria #3: Is only taking ACE as monotherapy, with no concomitant combination treatments

Having all of the following criteria:

- exactly 1 distinct occurrences of a drug era of *Hypertension drugs* (Table B.4) where event starts between 0 days Before and 7 days After index start date

Limit qualifying cohort to: earliest event per person.

End Date Strategy

Custom Drug Era Exit Criteria. This strategy creates a drug era from the codes found in the specified concept set. If the index event is found within an era, the cohort end date will use the era's end date. Otherwise, it will use the observation period end date that contains the index event.

Use the era end date of *ACE inhibitors* (Table B.2)

- allowing 30 days between exposures
- adding 0 days after exposure end

Cohort Collapse Strategy

Collapse cohort by era with a gap size of 0 days.

Concept Set Definitions

Table B.2: ACE inhibitors

Concept Id	Concept Name	Excluded	Descendants	Mapped
1308216	Lisinopril	NO	YES	NO
1310756	moexipril	NO	YES	NO
1331235	quinapril	NO	YES	NO
1334456	Ramipril	NO	YES	NO
1335471	benazepril	NO	YES	NO
1340128	Captopril	NO	YES	NO
1341927	Enalapril	NO	YES	NO
1342439	trandolapril	NO	YES	NO
1363749	Fosinopril	NO	YES	NO
1373225	Perindopril	NO	YES	NO

Table B.3: Hypertensive disorder

Concept Id	Concept Name	Excluded	Descendants	Mapped
316866	Hypertensive disorder	NO	YES	NO

Table B.4: Hypertension drugs

Concept Id	Concept Name	Excluded	Descendants	Mapped
904542	Triamterene	NO	YES	NO
907013	Metolazone	NO	YES	NO
932745	Bumetanide	NO	YES	NO
942350	torsemide	NO	YES	NO
956874	Furosemide	NO	YES	NO
970250	Spironolactone	NO	YES	NO
974166	Hydrochlorothiazide	NO	YES	NO
978555	Indapamide	NO	YES	NO
991382	Amiloride	NO	YES	NO
1305447	Methyldopa	NO	YES	NO
1307046	Metoprolol	NO	YES	NO
1307863	Verapamil	NO	YES	NO
1308216	Lisinopril	NO	YES	NO
1308842	valsartan	NO	YES	NO
1309068	Minoxidil	NO	YES	NO
1309799	eplerenone	NO	YES	NO
1310756	moexipril	NO	YES	NO
1313200	Nadolol	NO	YES	NO
1314002	Atenolol	NO	YES	NO
1314577	nebivolol	NO	YES	NO
1317640	telmisartan	NO	YES	NO
1317967	aliskiren	NO	YES	NO
1318137	Nicardipine	NO	YES	NO
1318853	Nifedipine	NO	YES	NO
1319880	Nisoldipine	NO	YES	NO
1319998	Acebutolol	NO	YES	NO
1322081	Betaxolol	NO	YES	NO
1326012	Isradipine	NO	YES	NO
1327978	Penbutolol	NO	YES	NO
1328165	Diltiazem	NO	YES	NO
1331235	quinapril	NO	YES	NO
1332418	Amlodipine	NO	YES	NO
1334456	Ramipril	NO	YES	NO
1335471	benazepril	NO	YES	NO
1338005	Bisoprolol	NO	YES	NO

Concept Id	Concept Name	Excluded	Descendants	Mapped
1340128	Captopril	NO	YES	NO
1341238	Terazosin	NO	YES	NO
1341927	Enalapril	NO	YES	NO
1342439	trandolapril	NO	YES	NO
1344965	Guanfacine	NO	YES	NO
1345858	Pindolol	NO	YES	NO
1346686	eprosartan	NO	YES	NO
1346823	carvedilol	NO	YES	NO
1347384	irbesartan	NO	YES	NO
1350489	Prazosin	NO	YES	NO
1351557	candesartan	NO	YES	NO
1353766	Propranolol	NO	YES	NO
1353776	Felodipine	NO	YES	NO
1363053	Doxazosin	NO	YES	NO
1363749	Fosinopril	NO	YES	NO
1367500	Losartan	NO	YES	NO
1373225	Perindopril	NO	YES	NO
1373928	Hydralazine	NO	YES	NO
1386957	Labetalol	NO	YES	NO
1395058	Chlorthalidone	NO	YES	NO
1398937	Clonidine	NO	YES	NO
40226742	olmesartan	NO	YES	NO
40235485	azilsartan	NO	YES	NO

B.3 Acute Myocardial Infarction (AMI)

Initial Event Cohort

People having any of the following:

- a condition occurrence of *Acute myocardial Infarction* (Table B.5)

with continuous observation of at least 0 days prior and 0 days after event index date, and limit initial events to: all events per person.

For people matching the Primary Events, include: Having any of the following criteria:

- at least 1 occurrences of a visit occurrence of *Inpatient or ER visit* (Table B.6) where event starts between all days Before and 0 days After index start date and event ends between 0 days Before and all days After index start date

Limit cohort of initial events to: all events per person.

Limit qualifying cohort to: all events per person.

End Date Strategy

Date Offset Exit Criteria. This cohort definition end date will be the index event's start date plus 7 days

Cohort Collapse Strategy

Collapse cohort by era with a gap size of 180 days.

Concept Set Definitions

Table B.5: Inpatient or ER visit

Concept Id	Concept Name	Excluded	Descendants	Mapped
314666	Old myocardial infarction	YES	YES	NO
4329847	Myocardial infarction	NO	YES	NO

Table B.6: Inpatient or ER visit

Concept Id	Concept Name	Excluded	Descendants	Mapped
262	Emergency Room and Inpatient Visit	NO	YES	NO
9201	Inpatient Visit	NO	YES	NO
9203	Emergency Room Visit	NO	YES	NO

B.4 Angioedema

Initial Event Cohort

People having any of the following:

- a condition occurrence of *Angioedema* (Table B.7)

with continuous observation of at least 0 days prior and 0 days after event index date, and limit initial events to: all events per person.

For people matching the Primary Events, include: Having any of the following criteria:

- at least 1 occurrences of a visit occurrence of *Inpatient or ER visit* (Table B.8) where event starts between all days Before and 0 days After index start date and event ends between 0 days Before and all days After index start date

Limit cohort of initial events to: all events per person.

Limit qualifying cohort to: all events per person.

End Date Strategy

This cohort definition end date will be the index event's start date plus 7 days

Cohort Collapse Strategy

Collapse cohort by era with a gap size of 30 days.

Concept Set Definitions

Table B.7: Angioedema

Concept Id	Concept Name	Excluded	Descendants	Mapped
432791	Angioedema	NO	YES	NO

Table B.8: Inpatient or ER visit

Concept Id	Concept Name	Excluded	Descendants	Mapped
262	Emergency Room and Inpatient Visit	NO	YES	NO
9201	Inpatient Visit	NO	YES	NO
9203	Emergency Room Visit	NO	YES	NO

B.5 New Users of Thiazide-Like Diuretics Monotherapy

Initial Event Cohort

People having any of the following:

- a drug exposure of *Thiazide or thiazide-like diuretic* (Table B.9) for the first time in the person's history

with continuous observation of at least 365 days prior and 0 days after event index date, and limit initial events to: earliest event per person.

Inclusion Rules

Inclusion Criteria #1: has hypertension diagnosis in 1 yr prior to treatment

Having all of the following criteria:

- at least 1 occurrences of a condition occurrence of *Hypertensive disorder* (Table B.10) where event starts between 365 days Before and 0 days After index start date

Inclusion Criteria #2: Has no prior antihypertensive drug exposures in medical history

Having all of the following criteria:

- exactly 0 occurrences of a drug exposure of *Hypertension drugs* (Table B.11) where event starts between all days Before and 1 days Before index start date

Inclusion Criteria #3: Is only taking ACE as monotherapy, with no concomitant combination treatments

Having all of the following criteria:

- exactly 1 distinct occurrences of a drug era of *Hypertension drugs* (Table B.11) where event starts between 0 days Before and 7 days After index start date

Limit qualifying cohort to: earliest event per person.

End Date Strategy

Custom Drug Era Exit Criteria. This strategy creates a drug era from the codes found in the specified concept set. If the index event is found within an era, the cohort end date will use the era's end date. Otherwise, it will use the observation period end date that contains the index event.

Use the era end date of *Thiazide or thiazide-like diuretic* (Table B.9)

- allowing 30 days between exposures
- adding 0 days after exposure end

Cohort Collapse Strategy

Collapse cohort by era with a gap size of 0 days.

Concept Set Definitions

Table B.9: Thiazide or thiazide-like diuretic

Concept Id	Concept Name	Excluded	Descendants	Mapped
907013	Metolazone	NO	YES	NO
974166	Hydrochlorothiazide	NO	YES	NO
978555	Indapamide	NO	YES	NO
1395058	Chlorthalidone	NO	YES	NO

Table B.10: Hypertensive disorder

Concept Id	Concept Name	Excluded	Descendants	Mapped
316866	Hypertensive disorder	NO	YES	NO

Table B.11: Hypertension drugs

Concept Id	Concept Name	Excluded	Descendants	Mapped
904542	Triamterene	NO	YES	NO
907013	Metolazone	NO	YES	NO
932745	Bumetanide	NO	YES	NO
942350	torsemide	NO	YES	NO
956874	Furosemide	NO	YES	NO
970250	Spironolactone	NO	YES	NO
974166	Hydrochlorothiazide	NO	YES	NO
978555	Indapamide	NO	YES	NO
991382	Amiloride	NO	YES	NO
1305447	Methyldopa	NO	YES	NO
1307046	Metoprolol	NO	YES	NO
1307863	Verapamil	NO	YES	NO
1308216	Lisinopril	NO	YES	NO
1308842	valsartan	NO	YES	NO
1309068	Minoxidil	NO	YES	NO
1309799	eplerenone	NO	YES	NO
1310756	moexipril	NO	YES	NO
1313200	Nadolol	NO	YES	NO
1314002	Atenolol	NO	YES	NO
1314577	nebivolol	NO	YES	NO
1317640	telmisartan	NO	YES	NO
1317967	aliskiren	NO	YES	NO
1318137	Nicardipine	NO	YES	NO
1318853	Nifedipine	NO	YES	NO
1319880	Nisoldipine	NO	YES	NO
1319998	Acebutolol	NO	YES	NO
1322081	Betaxolol	NO	YES	NO
1326012	Isradipine	NO	YES	NO
1327978	Penbutolol	NO	YES	NO
1328165	Diltiazem	NO	YES	NO
1331235	quinapril	NO	YES	NO
1332418	Amlodipine	NO	YES	NO
1334456	Ramipril	NO	YES	NO
1335471	benazepril	NO	YES	NO
1338005	Bisoprolol	NO	YES	NO

Concept Id	Concept Name	Excluded	Descendants	Mapped
1340128	Captopril	NO	YES	NO
1341238	Terazosin	NO	YES	NO
1341927	Enalapril	NO	YES	NO
1342439	trandolapril	NO	YES	NO
1344965	Guanfacine	NO	YES	NO
1345858	Pindolol	NO	YES	NO
1346686	eprosartan	NO	YES	NO
1346823	carvedilol	NO	YES	NO
1347384	irbesartan	NO	YES	NO
1350489	Prazosin	NO	YES	NO
1351557	candesartan	NO	YES	NO
1353766	Propranolol	NO	YES	NO
1353776	Felodipine	NO	YES	NO
1363053	Doxazosin	NO	YES	NO
1363749	Fosinopril	NO	YES	NO
1367500	Losartan	NO	YES	NO
1373225	Perindopril	NO	YES	NO
1373928	Hydralazine	NO	YES	NO
1386957	Labetalol	NO	YES	NO
1395058	Chlorthalidone	NO	YES	NO
1398937	Clonidine	NO	YES	NO
40226742	olmesartan	NO	YES	NO
40235485	azilsartan	NO	YES	NO

B.6 Patients Initiating First-Line Therapy for Hypertension

Initial Event Cohort

People having any of the following:

- a drug exposure of *First-line hypertension drugs* (Table B.12) for the first time in the person's history

with continuous observation of at least 365 days prior and 365 days after event index date, and limit initial events to: earliest event per person.

Inclusion Rules

Having all of the following criteria:

- exactly 0 occurrences of a drug exposure of *Hypertension drugs* (Table B.13) where event starts between all days Before and 1 days Before index start date

- and at least 1 occurrences of a condition occurrence of *Hypertensive disorder* (Table B.14) where event starts between 365 days Before and 0 days After index start date

Limit cohort of initial events to: earliest event per person. Limit qualifying cohort to: earliest event per person.

End Date Strategy

No end date strategy selected. By default, the cohort end date will be the end of the observation period that contains the index event.

Cohort Collapse Strategy

Collapse cohort by era with a gap size of 0 days.

Concept Set Definitions

Table B.12: First-line hypertension drugs

Concept Id	Concept Name	Excluded	Descendants	Mapped
907013	Metolazone	NO	YES	NO
974166	Hydrochlorothiazide	NO	YES	NO
978555	Indapamide	NO	YES	NO
1307863	Verapamil	NO	YES	NO
1308216	Lisinopril	NO	YES	NO
1308842	valsartan	NO	YES	NO
1310756	moexipril	NO	YES	NO
1317640	telmisartan	NO	YES	NO
1318137	Nicardipine	NO	YES	NO
1318853	Nifedipine	NO	YES	NO
1319880	Nisoldipine	NO	YES	NO
1326012	Isradipine	NO	YES	NO
1328165	Diltiazem	NO	YES	NO
1331235	quinapril	NO	YES	NO
1332418	Amlodipine	NO	YES	NO
1334456	Ramipril	NO	YES	NO
1335471	benazepril	NO	YES	NO
1340128	Captopril	NO	YES	NO
1341927	Enalapril	NO	YES	NO
1342439	trandolapril	NO	YES	NO
1346686	eprosartan	NO	YES	NO
1347384	irbesartan	NO	YES	NO
1351557	candesartan	NO	YES	NO
1353776	Felodipine	NO	YES	NO

Concept Id	Concept Name	Excluded	Descendants	Mapped
1363749	Fosinopril	NO	YES	NO
1367500	Losartan	NO	YES	NO
1373225	Perindopril	NO	YES	NO
1395058	Chlorthalidone	NO	YES	NO
40226742	olmesartan	NO	YES	NO
40235485	azilsartan	NO	YES	NO

Table B.13: Hypertension drugs

Concept Id	Concept Name	Excluded	Descendants	Mapped
904542	Triamterene	NO	YES	NO
907013	Metolazone	NO	YES	NO
932745	Bumetanide	NO	YES	NO
942350	torsemide	NO	YES	NO
956874	Furosemide	NO	YES	NO
970250	Spironolactone	NO	YES	NO
974166	Hydrochlorothiazide	NO	YES	NO
978555	Indapamide	NO	YES	NO
991382	Amiloride	NO	YES	NO
1305447	Methyldopa	NO	YES	NO
1307046	Metoprolol	NO	YES	NO
1307863	Verapamil	NO	YES	NO
1308216	Lisinopril	NO	YES	NO
1308842	valsartan	NO	YES	NO
1309068	Minoxidil	NO	YES	NO
1309799	eplerenone	NO	YES	NO
1310756	moexipril	NO	YES	NO
1313200	Nadolol	NO	YES	NO
1314002	Atenolol	NO	YES	NO
1314577	nebivolol	NO	YES	NO
1317640	telmisartan	NO	YES	NO
1317967	aliskiren	NO	YES	NO
1318137	Nicardipine	NO	YES	NO
1318853	Nifedipine	NO	YES	NO
1319880	Nisoldipine	NO	YES	NO
1319998	Acebutolol	NO	YES	NO
1322081	Betaxolol	NO	YES	NO
1326012	Isradipine	NO	YES	NO
1327978	Penbutolol	NO	YES	NO
1328165	Diltiazem	NO	YES	NO
1331235	quinapril	NO	YES	NO
1332418	Amlodipine	NO	YES	NO

Concept Id	Concept Name	Excluded	Descendants	Mapped
1334456	Ramipril	NO	YES	NO
1335471	benazepril	NO	YES	NO
1338005	Bisoprolol	NO	YES	NO
1340128	Captopril	NO	YES	NO
1341238	Terazosin	NO	YES	NO
1341927	Enalapril	NO	YES	NO
1342439	trandolapril	NO	YES	NO
1344965	Guanfacine	NO	YES	NO
1345858	Pindolol	NO	YES	NO
1346686	eprosartan	NO	YES	NO
1346823	carvedilol	NO	YES	NO
1347384	irbesartan	NO	YES	NO
1350489	Prazosin	NO	YES	NO
1351557	candesartan	NO	YES	NO
1353766	Propranolol	NO	YES	NO
1353776	Felodipine	NO	YES	NO
1363053	Doxazosin	NO	YES	NO
1363749	Fosinopril	NO	YES	NO
1367500	Losartan	NO	YES	NO
1373225	Perindopril	NO	YES	NO
1373928	Hydralazine	NO	YES	NO
1386957	Labetalol	NO	YES	NO
1395058	Chlorthalidone	NO	YES	NO
1398937	Clonidine	NO	YES	NO
40226742	olmesartan	NO	YES	NO
40235485	azilsartan	NO	YES	NO

Table B.14: Hypertensive disorder

Concept Id	Concept Name	Excluded	Descendants	Mapped
316866	Hypertensive disorder	NO	YES	NO

B.7 Patients Initiating First-Line Therapy for Hypertension With >3 Yr Follow-Up

Same as *cohort definition B.6* but with continuous observation of at least 365 days prior and **1095 days** after event index date

B.8 ACE Inhibitor Use

Initial Event Cohort

People having any of the following:

- a drug exposure of *ACE inhibitors* (Table B.15)

with continuous observation of at least 0 days prior and 0 days after event index date, and limit initial events to: all events per person.

Limit qualifying cohort to: all events per person.

End Date Strategy

This strategy creates a drug era from the codes found in the specified concept set. If the index event is found within an era, the cohort end date will use the era's end date. Otherwise, it will use the observation period end date that contains the index event.

Use the era end date of *ACE inhibitors* (Table B.15)

- allowing 30 days between exposures
- adding 0 days after exposure end

Cohort Collapse Strategy

Collapse cohort by era with a gap size of 30 days.

Concept Set Definitions

Table B.15: ACE inhibitors

Concept Id	Concept Name	Excluded	Descendants	Mapped
1308216	Lisinopril	NO	YES	NO
1310756	moexipril	NO	YES	NO
1331235	quinapril	NO	YES	NO
1334456	Ramipril	NO	YES	NO
1335471	benazepril	NO	YES	NO
1340128	Captopril	NO	YES	NO
1341927	Enalapril	NO	YES	NO
1342439	trandolapril	NO	YES	NO
1363749	Fosinopril	NO	YES	NO
1373225	Perindopril	NO	YES	NO

B.9 Angiotensin Receptor Blocker (ARB) Use

Same as *cohort definition B.8* with *Angiotensin Receptor Blockers (ARBs)* (Table B.16) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.16: Angiotensin Receptor Blockers (ARBs)

Concept Id	Concept Name	Excluded	Descendants	Mapped
1308842	valsartan	NO	YES	NO
1317640	telmisartan	NO	YES	NO
1346686	eprosartan	NO	YES	NO
1347384	irbesartan	NO	YES	NO
1351557	candesartan	NO	YES	NO
1367500	Losartan	NO	YES	NO
40226742	olmesartan	NO	YES	NO
40235485	azilsartan	NO	YES	NO

B.10 Thiazide Or Thiazide-Like Diuretic Use

Same as *cohort definition B.8* with *Thiazide or thiazide-like diuretic* (Table B.17) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.17: Thiazide or thiazide-like diuretic

Concept Id	Concept Name	Excluded	Descendants	Mapped
907013	Metolazone	NO	YES	NO
974166	Hydrochlorothiazide	NO	YES	NO
978555	Indapamide	NO	YES	NO
1395058	Chlorthalidone	NO	YES	NO

B.11 Dihydropyridine Calcium Channel Blocker (dCCB) Use

Same as *cohort definition B.8* with *dihydropyridine Calcium Channel Blocker (dCCB)* (Table B.18) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.18: Dihydropyridine Calcium channel blockers (dCCB)

Concept Id	Concept Name	Excluded	Descendants	Mapped
1318137	Nicardipine	NO	YES	NO
1318853	Nifedipine	NO	YES	NO
1319880	Nisoldipine	NO	YES	NO
1326012	Isradipine	NO	YES	NO
1332418	Amlodipine	NO	YES	NO
1353776	Felodipine	NO	YES	NO

B.12 Non-Dihydropyridine Calcium Channel Blocker (ndCCB) Use

Same as *cohort definition B.8* with *non-dihydropyridine Calcium channel blockers (ndCCB)* (Table B.19) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.19: non-dihydropyridine Calcium channel blockers (ndCCB)

Concept Id	Concept Name	Excluded	Descendants	Mapped
1307863	Verapamil	NO	YES	NO
1328165	Diltiazem	NO	YES	NO

B.13 Beta-Blocker Use

Same as *cohort definition B.8* with *Beta blockers* (Table B.20) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.20: Beta blockers

Concept Id	Concept Name	Excluded	Descendants	Mapped
1307046	Metoprolol	NO	YES	NO
1313200	Nadolol	NO	YES	NO
1314002	Atenolol	NO	YES	NO
1314577	nebivolol	NO	YES	NO
1319998	Acetbutolol	NO	YES	NO

Concept Id	Concept Name	Excluded	Descendants	Mapped
1322081	Betaxolol	NO	YES	NO
1327978	Penbutolol	NO	YES	NO
1338005	Bisoprolol	NO	YES	NO
1345858	Pindolol	NO	YES	NO
1346823	carvedilol	NO	YES	NO
1353766	Propranolol	NO	YES	NO
1386957	Labetalol	NO	YES	NO

B.14 Diuretic-Loop Use

Same as *cohort definition B.8* with *Diuretics - Loop* (Table B.21) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.21: Diuretics - Loop

Concept Id	Concept Name	Excluded	Descendants	Mapped
932745	Bumetanide	NO	YES	NO
942350	torsemide	NO	YES	NO
956874	Furosemide	NO	YES	NO

B.15 Diuretic-Potassium Sparing Use

Same as *cohort definition B.8* with *Diuretics - potassium sparing* (Table B.22) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.22: Diuretics - potassium sparing

Concept Id	Concept Name	Excluded	Descendants	Mapped
904542	Triamterene	NO	YES	NO
991382	Amiloride	NO	YES	NO

B.16 Alpha-1 Blocker Use

Same as *cohort definition B.8* with *Alpha-1 blocker* (Table B.23) in place of *ACE inhibitors* (Table B.15).

Concept Set Definitions

Table B.23: Alpha-1 blocker

Concept Id	Concept Name	Excluded	Descendants	Mapped
1341238	Terazosin	NO	YES	NO
1350489	Prazosin	NO	YES	NO
1363053	Doxazosin	NO	YES	NO

Chapter C

Negative controls

This Appendix contains negative controls used in various chapters of the book.

C.1 ACEi and THZ

Table C.1: Negative control outcomes when comparing ACE inhibitors (ACEi) to thiazides and thiazide-like diuretics (THZ).

Concept ID	Concept Name
434165	Abnormal cervical smear
436409	Abnormal pupil
199192	Abrasion and/or friction burn of trunk without infection
4088290	Absence of breast
4092879	Absent kidney
44783954	Acid reflux
75911	Acquired hallux valgus
137951	Acquired keratoderma
77965	Acquired trigger finger
376707	Acute conjunctivitis
4103640	Amputated foot
73241	Anal and rectal polyp
133655	Burn of forearm
73560	Calcaneal spur
434327	Cannabis abuse
4213540	Cervical somatic dysfunction
140842	Changes in skin texture
81378	Chondromalacia of patella
432303	Cocaine abuse
4201390	Colostomy present

Concept ID	Concept Name
46269889	Complication due to Crohn's disease
134438	Contact dermatitis
78619	Contusion of knee
201606	Crohn's disease
76786	Derangement of knee
4115402	Difficulty sleeping
45757370	Disproportion of reconstructed breast
433111	Effects of hunger
433527	Endometriosis
4170770	Epidermoid cyst
4092896	Feces contents abnormal
259995	Foreign body in orifice
40481632	Ganglion cyst
4166231	Genetic predisposition
433577	Hammer toe
4231770	Hereditary thrombophilia
440329	Herpes zoster without complication
4012570	High risk sexual behavior
4012934	Homocystinuria
441788	Human papilloma virus infection
4201717	Ileostomy present
374375	Impacted cerumen
4344500	Impingement syndrome of shoulder region
139099	Ingrowing nail
444132	Injury of knee
196168	Irregular periods
432593	Kwashiorkor
434203	Late effect of contusion
438329	Late effect of motor vehicle accident
195873	Leukorrhea
4083487	Macular drusen
4103703	Melena
4209423	Nicotine dependence
377572	Noise effects on inner ear
40480893	Nonspecific tuberculin test reaction
136368	Non-toxic multinodular goiter
140648	Onychomycosis due to dermatophyte
438130	Opioid abuse
4091513	Passing flatus
4202045	Postviral fatigue syndrome
373478	Presbyopia
46286594	Problem related to lifestyle
439790	Psychalgia

Concept ID	Concept Name
81634	Ptotic breast
380706	Regular astigmatism
141932	Senile hyperkeratosis
36713918	Somatic dysfunction of lumbar region
443172	Splinter of face, without major open wound
81151	Sprain of ankle
72748	Strain of rotator cuff capsule
378427	Tear film insufficiency
437264	Tobacco dependence syndrome
194083	Vaginitis and vulvovaginitis
140641	Verruca vulgaris
440193	Wristdrop
4115367	Wrist joint pain

Chapter D

Protocol template

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Chapter E

Suggested Answers

This Appendix contains suggested answers for the exercises in the book.

E.1 The Common Data Model

Exercise 4.1

Based on the description in the exercise, John's record should look like Table E.1.

Table E.1: The PERSON table.

Column name	Value	Explanation
PERSON_ID	2	A unique integer.
GENDER_CONCEPT_ID	8507	The concept ID for male gender is 8507.
YEAR_OF_BIRTH	1974	
MONTH_OF_BIRTH	8	
DAY_OF_BIRTH	4	
BIRTH_DATETIME	1974-08-04 00:00:00	When the time is not known midnight is used.
DEATH_DATETIME	NULL	
RACE_CONCEPT_ID	8516	The concept ID for black or African American is 8516. 38003564 refers to "Not hispanic".
ETHNICITY_CONCEPT_ID	38003564	
LOCATION_ID		His address is not known.
PROVIDER_ID		His primary care Provider is not known.
CARE_SITE		His primary Care Site is not known.
PERSON_SOURCE_VALUE	NULL	Not provided.

Column name	Value	Explanation
GENDER_SOURCE_VALUE	Man	The text used in the description.
GENDER_SOURCE_0		
CONCEPT_ID		
RACE_SOURCE_VALUE	African American	The text used in the description.
RACE_SOURCE_0		
CONCEPT_ID		
ETHNICITY_SOURCE_NULL		
ETHNICITY_SOURCE_0		
CONCEPT_ID		

Exercise 4.2

Based on the description in the exercise, John's record should look like Table E.2.

Table E.2: The OBSERVATION_PERIOD table.

Column name	Value	Explanation
OBSERVATION_PERIOD_ID	2	A unique integer.
PERSON_ID	2	This is a foreign key to John's record in the PERSON table.
OBSERVATION_PERIOD	2015-01-01	The date of enrollment.
START_DATE		
OBSERVATION_PERIOD	2019-07-01	No data can be expected after the data extraction date.
END_DATE		
PERIOD_TYPE_ID	44814722	44814724 refers to "Period while enrolled in insurance".
CONCEPT_ID		

Exercise 4.3

Based on the description in the exercise, John's record should look like Table E.3.

Table E.3: The DRUG_EXPOSURE table.

Column name	Value	Explanation
DRUG_EXPOSURE_ID	1001	Some unique integer
PERSON_ID	2	This is a foreign key to John's record in the PERSON table.

Column name	Value	Explanation
DRUG_CONCEPT_ID	19078461	The provided NDC code maps to Standard Concept 19078461.
DRUG_EXPOSURE_START_DATE	2019-05-01	The start date of the exposure to the drug.
DRUG_EXPOSURE_START_DATETIME	2019-05-01 00:00:00	Midnight is used as the time is not known.
DRUG_EXPOSURE_END_DATE	2019-05-31	Based on start date + days supply.
DRUG_EXPOSURE_END_DATETIME	2019-05-31 00:00:00	Midnight is used as time is unknown.
VERBATIM_END_DATE	NULL	Not provided.
DRUG_TYPE	38000177	38000177 indicates “Prescription written”.
CONCEPT_ID		
STOP_REASON	NULL	
REFILLS	NULL	
QUANTITY	NULL	Not provided.
DAYS_SUPPLY	30	As described in the exercise.
SIG	NULL	Not provided.
ROUTE_CONCEPT_ID	4132161	4132161 indicates “Oral”.
LOT_NUMBER	NULL	Not provided.
PROVIDER_ID	NULL	Not provided.
VISIT_OCCURRENCE_ID	NULL	No information on the visit was provided..
VISIT_DETAIL_ID	NULL	
DRUG_SOURCE_VALUE	76168009520	This is provided NDC code.
DRUG_SOURCE_CONCEPT_ID	583945	583945 represents the drug source value (NDC code “76168009520”).
ROUTE_SOURCE_VALUE	NULL	

Exercise 4.4

To find the set of records, we can query the CONDITION_OCCURRENCE table:

```
library(DatabaseConnector)
connection <- connect(connectionDetails)
sql <- "SELECT *
FROM @cdm.condition_occurrence
WHERE condition_concept_id = 192671;"

result <- renderTranslateQuerySql(connection, sql, cdm = "main")
head(result)
```

```
## CONDITION_OCCURRENCE_ID PERSON_ID CONDITION_CONCEPT_ID ...
## 1                      4657      273          192671 ...
## 2                      1021       61          192671 ...
## 3                     5978      351          192671 ...
## 4                     9798      579          192671 ...
## 5                     9301      549          192671 ...
## 6                     1997     116          192671 ...
```

Exercise 4.5

To find the set of records, we can query the CONDITION_OCCURRENCE table using the CONDITION_SOURCE_VALUE field:

```
sql <- "SELECT *
FROM @cdm.condition_occurrence
WHERE condition_source_value = 'K92.2';"

result <- renderTranslateQuerySql(connection, sql, cdm = "main")
head(result)
```

```
## CONDITION_OCCURRENCE_ID PERSON_ID CONDITION_CONCEPT_ID ...
## 1                      4657      273          192671 ...
## 2                      1021       61          192671 ...
## 3                      5978      351          192671 ...
## 4                      9798      579          192671 ...
## 5                      9301      549          192671 ...
## 6                      1997     116          192671 ...
```

Exercise 4.6

This information is stored in the OBSERVATION PERIOD table:

```
library(DatabaseConnector)
connection <- connect(connectionDetails)
sql <- "SELECT *
FROM @cdm.observation_period
WHERE person_id = 61;"

renderTranslateQuerySql(connection, sql, cdm = "main")

##   OBSERVATION_PERIOD_ID PERSON_ID OBSERVATION_PERIOD_START_DATE ...
## 1                      61          61             1968-01-21 ...
```

E.2 Standardized Vocabularies

Exercise 5.1

Concept ID 192671 (“Gastrointestinal hemorrhage”)

Exercise 5.2

ICD-10CM codes:

- K29.91 “Gastroduodenitis, unspecified, with bleeding”
- K92.2 “Gastrointestinal hemorrhage, unspecified”

ICD-9CM codes:

- 578 “Gastrointestinal hemorrhage”
- 578.9 “Hemorrhage of gastrointestinal tract, unspecified”

Exercise 5.3

MedDRA preferred terms:

- “Gastrointestinal haemorrhage” (Concept ID 35707864)
- “Intestinal haemorrhage” (Concept ID 35707858)

E.3 Extract Transform Load

Exercise 6.1

- A) Data experts and CDM experts together design the ETL
- B) People with medical knowledge create the code mappings
- C) A technical person implements the ETL
- D) All are involved in quality control

Exercise 6.2

Column	Value	Answer
PERSON_ID	A123B456	This column has a data type of integer so the source record value needs to be translated to a numeric value.
GENDER_CONCEPTID	532D	

Column	Value	Answer
YEAR_OF_BIRTH	NULL	If we do not know the month or day of birth, we do not guess. A person can exist without a month or day of birth. If a person lacks a birth year that person should be dropped. This person would have to be dropped due to now year of birth.
MONTH_OF_BIRTH	NULL	
DAY_OF_BIRTH	NULL	
RACE_CONCEPT_ID		The race is WHITE which should be mapped to 8527.
ETHNICITY_CONCEPT_ID		No ethnicity was provided, this should be mapped to 0.
PERSON_SOURCE_A123B456		
VALUE		
GENDER_SOURCE_F		
VALUE		
RACE_SOURCE_WHITE		
ETHNICITY_SOURCE_NONE		
VALUE PROVIDED		

Exercise 6.3

Column	Value
VISIT_OCCURRENCE_ID	1
PERSON_ID	11
VISIT_START_DATE	2004-09-26
VISIT_END_DATE	2004-09-30
VISIT_CONCEPT_ID	9201
VISIT_SOURCE_VALUE	inpatient

E.4 Data Analytics Use Cases

Exercise 7.1

1. Characterization

2. Patient-level prediction
3. Population-level estimation

Exercise 7.2

Probably not. Defining a non-exposure cohort that is comparable to your diclofenac exposure cohort is often impossible, since people take diclofenac for a reason. This precludes a between-person comparison. It might be possible to a within-person comparison, so for each patient in the diclofenac cohort identifying time when they are not exposed, but a similar problem occurs here: these times are likely incomparable, because there are reasons when at one time someone is exposed and at other times not.

E.5 SQL and R

Exercise 9.1

To compute the number of people we can simply query the PERSON table:

```
library(DatabaseConnector)
connection <- connect(connectionDetails)
sql <- "SELECT COUNT(*) AS person_count
FROM @cdm.person;

renderTranslateQuerySql(connection, sql, cdm = "main")

##    PERSON_COUNT
## 1      2694
```

Exercise 9.2

To compute the number of people with at least one prescription of celecoxib, we can query the DRUG_EXPOSURE table. To find all drugs containing the ingredient celecoxib, we join to the CONCEPT_ANCESTOR and CONCEPT tables:

```
library(DatabaseConnector)
connection <- connect(connectionDetails)
sql <- "SELECT COUNT(DISTINCT(person_id)) AS person_count
FROM @cdm.drug_exposure
INNER JOIN @cdm.concept_ancestor
  ON drug_concept_id = descendant_concept_id
INNER JOIN @cdm.concept ingredient
  ON ancestor_concept_id = ingredient.concept_id
WHERE LOWER(ingredient.concept_name) = 'celecoxib'
  AND ingredient.concept_class_id = 'Ingredient'
```

```

    AND ingredient.standard_concept = 'S';"

renderTranslateQuerySql(connection, sql, cdm = "main")

```

```

##    PERSON_COUNT
## 1      1844

```

Note that we use `COUNT(DISTINCT(person_id))` to find the number of distinct persons, considering that a person might have more than one prescription. Also note that we use the `LOWER` function to make our search for “celecoxib” case-insensitive.

Alternatively, we can use the `DRUG_ERA` table, which is already rolled up to the ingredient level:

```

library(DatabaseConnector)
connection <- connect(connectionDetails)

sql <- "SELECT COUNT(DISTINCT(person_id)) AS person_count
FROM @cdm.drug_era
INNER JOIN @cdm.concept ingredient
  ON drug_concept_id = ingredient.concept_id
WHERE LOWER(ingredient.concept_name) = 'celecoxib'
  AND ingredient.concept_class_id = 'Ingredient'
  AND ingredient.standard_concept = 'S';"

renderTranslateQuerySql(connection, sql, cdm = "main")

```

```

##    PERSON_COUNT
## 1      1844

```

Exercise 9.3

To compute the number of diagnoses during exposure we extend our previous query by joining to the `CONDITION_OCCURRENCE` table. We join to the `CONCEPT_ANCESTOR` table to find all condition concepts that imply a gastrointestinal haemorrhage:

```

library(DatabaseConnector)
connection <- connect(connectionDetails)
sql <- "SELECT COUNT(*) AS diagnose_count
FROM @cdm.drug_era
INNER JOIN @cdm.concept ingredient
  ON drug_concept_id = ingredient.concept_id
INNER JOIN @cdm.condition_occurrence
  ON condition_start_date >= drug_era_start_date
  AND condition_start_date <= drug_era_end_date

```

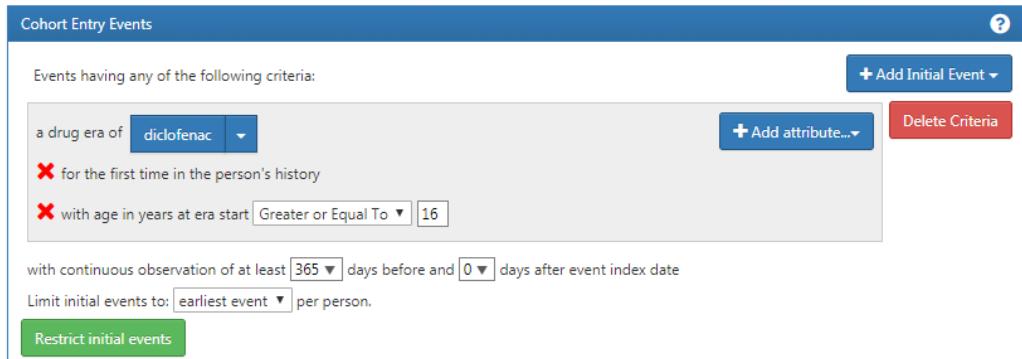


Figure E.1: Cohort entry event settings for new users of diclofenac

```

INNER JOIN @cdm.concept_ancestor
    ON condition_concept_id = descendant_concept_id
WHERE LOWER(ingredient.concept_name) = 'celecoxib'
    AND ingredient.concept_class_id = 'Ingredient'
    AND ingredient.standard_concept = 'S'
    AND ancestor_concept_id = 192671;"

renderTranslateQuerySql(connection, sql, cdm = "main")

##   DIAGNOSE_COUNT
## 1      41

```

Note that in this case it is essential to use the DRUG_ERA table instead of the DRUG_EXPOSURE table, because drug exposures with the same ingredient can overlap, but drug eras can. This could lead to double counting. For example, imagine a person received two drug drugs containing celecoxib at the same time. This would be recorded as two drug exposures, so any diagnoses occurring during the exposure would be counted twice. The two exposures will be merged into a single non-overlapping drug era.

E.6 Defining Cohorts

Exercise 10.1

We create initial event criteria encoding these requirements:

- New users of diclofenac
- Ages 16 or older
- With at least 365 days of continuous observation prior to exposure

When done, the cohort entry event section should look like Figure E.1.

The concept set expression for diclofenac should look like Figure E.2, including the

Concept Set Expression	Included Concepts (11473)	Included Source Codes	Export	Import			
Name:							
diclofenac							
Show 25 ▾ entries	Search: <input type="text"/>	Previous 1 Next					
Showing 1 to 1 of 1 entries							
Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped
1124300	3355	Diclofenac	Drug	Standard	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
					Classification	Non-Standard	Standard

Figure E.2: Concept set expression for diclofenac.

Inclusion Criteria

New inclusion criteria

Without prior exposure to any NSAID Copy Delete

1. Without prior exposure to any NSAID
Excluding subjects with prior exposure to any NSAID

having all of the following criteria: + Add criteria to group...

with exactly 0 using all occurrences of:
a drug exposure of **NSAIDs** + Add attribute...

where **event starts** between All days Before and 1 days Before
index start date [add additional constraint](#)

restrict to the same visit occurrence
 allow events from outside observation period

Delete Criteria

Limit qualifying events to: earliest event per person.

Figure E.3: Requiring no prior exposure to any NSAID.

ingredient ‘Diclofenac’ and all of its descendant, thus including all drugs containing the ingredient diclofenac.

Next, we require no prior exposure to any NSAID, as shown in Figure E.3.

The concept set expression for NSAIDs should look like Figure E.4, including the NSAIDs class and all of its descendant, thus including all drugs containing any NSAID.

Additionally, we require no prior diagnosis of cancer, as shown in Figure E.5.

The concept set expression for “Broad malignancies” should look like Figure E.6, including the high level concept “Malignant neoplastic disease” and all of its descendant.

Finally, we define the cohort exit criteria as discontinuation of exposure (allowing for a 30-day gap), as shown in Figure E.7.

Concept Set Expression Included Concepts 23112 Included Source Codes Export Import

Name: NSAIDs

Show 25 entries Search: _____

Showing 1 to 1 of 1 entries

	Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped
	21603933	M01A	ANTIINFLAMMATORY AND ANTRHEUMATIC PRODUCTS, NON-STEROIDS	Drug	Classification	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Classification Non-Standard Standard

Figure E.4: Concept set expression for NSAIDs

Inclusion Criteria

New inclusion criteria

Without prior diagnose of cancer Copy Delete

1. Without prior exposure to any NSAID
Excluding subjects with prior exposure to any NSAID

2. Without prior diagnose of cancer
Excluding subjects with prior cancer diagnosis

having all of the following criteria:

+ Add criteria to group... Delete Criteria

with exactly 0 using all occurrences of:
a condition occurrence of Broad malignancies + Add attribute...
where event starts between All days Before and 0 days Before
index start date add additional constraint
 restrict to the same visit occurrence
 allow events from outside observation period

Limit qualifying events to: earliest event per person.

Figure E.5: Requiring no prior cancer diagnosis.

Concept Set Expression Included Concepts 4401 Included Source Codes Export Import

Name: Broad malignancies

Show 25 entries Search: _____

Showing 1 to 1 of 1 entries

	Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped
	443392	363346000	Malignant neoplastic disease	Condition	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Classification Non-Standard Standard

Figure E.6: Concept set expression for broad malignancies

Event Persistence:
Event will persist until:

Continuous Exposure Persistence:
Specify a concept set that contains one or more drugs. A drug era will be derived from all drug exposure events for any of the drugs within the concept set, using the specified persistence window as a maximum allowable gap in days between successive exposure events and adding a specified surveillance window to the final exposure event. If no exposure event end date is provided, then an exposure event end date is inferred to be event start date + days supply in cases when days supply is available or event start date + 1 day otherwise. This event persistence assures that the cohort end date will be no greater than the drug era end date.

Concept set containing the drug(s) of interest:

- Persistence window: allow for a maximum of days between exposure records when inferring the era of persistence exposure
- Surveillance window: add days to the end of the era of persistence exposure as an additional period of surveillance prior to cohort exit.

Censoring Events:
Exit Cohort based on the following criteria:

No censoring events selected.

Figure E.7: Setting the cohort exit date.

Exercise 10.2

For readability we here split the SQL into two steps. We first find all condition occurrences of myocardial infarction, and store these in a temp table called “#diagnoses”:

```
library(DatabaseConnector)
connection <- connect(connectionDetails)
sql <- "SELECT person_id AS subject_id,
           condition_start_date AS cohort_start_date
      INTO #diagnoses
     FROM @cdm.condition_occurrence
    WHERE condition_concept_id IN (
        SELECT descendant_concept_id
          FROM @cdm.concept_ancestor
         WHERE ancestor_concept_id = 4329847 -- Myocardial infarction
    )
   AND condition_concept_id NOT IN (
        SELECT descendant_concept_id
          FROM @cdm.concept_ancestor
         WHERE ancestor_concept_id = 314666 -- Old myocardial infarction
    );"

renderTranslateExecuteSql(connection, sql, cdm = "main")
```

We then select only those that occur during an inpatient or ER visit, using some unique COHORT_DEFINITION_ID (we selected ‘1’):

```

sql <- "INSERT INTO @cdm.cohort (
    subject_id,
    cohort_start_date,
    cohort_definition_id
)
SELECT subject_id,
    cohort_start_date,
    CAST (1 AS INT) AS cohort_definition_id
FROM #diagnoses
INNER JOIN @cdm.visit_occurrence
    ON subject_id = person_id
        AND cohort_start_date >= visit_start_date
        AND cohort_start_date <= visit_end_date
WHERE visit_concept_id IN (9201, 9203, 262); -- Inpatient or ER;"

renderTranslateExecuteSql(connection, sql, cdm = "main")

```

Note that an alternative approach would have been to join the conditions to the visits based on the VISIT_OCCURRENCE_ID, instead of requiring the condition date to fall within the visit start and end date. This would likely be more accurate, as it would guarantee that the condition was recorded in relation to the inpatient or ER visit. However, many observational databases do not record the link between visit and diagnose, and we therefore chose to use the dates instead, likely giving us a higher sensitivity but perhaps lower specificity.

Note also that we ignored the cohort end date. Often, when a cohort is used to define an outcome we are only interested in the cohort start date, and there is no point in creating an (ill-defined) cohort end date.

It is recommended to clean up any temp tables when no longer needed:

```

sql <- "TRUNCATE TABLE #diagnoses;
DROP TABLE #diagnoses;

renderTranslateExecuteSql(connection, sql)

```

E.7 Characterization

Exercise 11.1

In ATLAS we click on  **Data Sources** and select the data source we're interested in. We could select the Drug Exposure report, select the “Table” tab, and search for “celecoxib” as shown in Figure E.8. Here we see that this particular database has exposures to various formulations of celecoxib. We could click on any of these drugs to get a more detailed view, for example showing age and gender distributions for

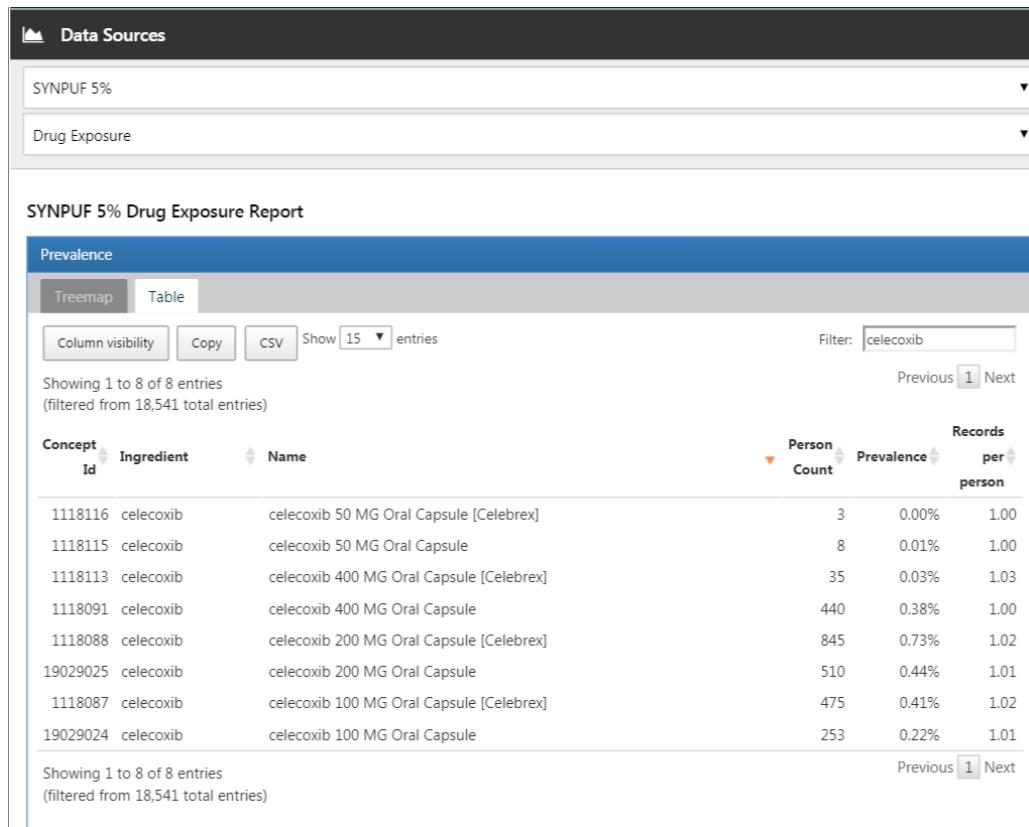


Figure E.8: Data source characterization.

these drugs.

Exercise 11.2

Click on **Cohort Definitions** and then “New cohort” to create a new cohort. Give the cohort a meaningful name (e.g. “Celecoxib new users”) and go to the “Concept Sets” tab. Click on “New Concept Set”, and give your concept set a meaningful names (e.g. “Celecoxib”). Open the **Search** module, search for “celecoxib”, restrict the Class to “Ingredient” and Standard Concept to “Standard”, and click the to add the concept to your concept set as show in Figure E.9.

Click on the left arrow shown at the top left of Figure E.9 to return to your cohort definition. Click on “+Add Initial Event” and then “Add Drug Era”. Select your previously created concept set for the drug era criterion. Click on “Add attribute...” and select “Add First Exposure Criteria.” Set the required continuous observation to at least 365 days before the index date. The result should look like Figure E.10. Leave the Inclusion Criteria, Cohort Exit, and Cohort Eras section as they are. Make sure to save the cohort definition by clicking , and close it by clicking .

← Celecoxib new users → Celecoxib

Q Search

Search Import

celecoxib

Advanced Options

Column visibility Copy CSV Show 15 entries Filter: Previous 1 Next

Vocabulary	Id	Code	Name	Class	RC	DRC	Domain	Vocabulary
RxNorm Extension (1376)	1118084	140587	celecoxib	Ingredient	2,587	5,184	Drug	RxNorm

Showing 1 to 1 of 1 entries Previous 1 Next

Class

- Ingredient (7)
 - Clinical Drug Form (5)
 - Clinical Drug Comp (5)
 - Lab Test (5)

Domain

- Drug (3570)
- Measurement (18)
- Observation (1)
- Meas Value (1)

Standard Concept

- Non-Standard (1831)
- Standard (1292)
- Classification (467)

Figure E.9: Selecting the standard concept for the ingredient "celecoxib".

New Cohort Definition

Celecoxib new users

Definition Concept Sets Generation Reporting Export

enter a cohort definition description here

Cohort Entry Events

Events having any of the following criteria:

a drug era of **Celecoxib**

X for the first time in the person's history

with continuous observation of at least **365** days before and **0** days after event index date

Limit initial events to: **earliest event** per person.

Restrict initial events

Figure E.10: A simple celecoxib new user cohort definition.

The screenshot shows the 'New Characterization' interface. At the top, there's a header bar with a 'New Characterization' icon and a title 'Celecoxib new users characterization'. Below the header are three tabs: 'Design' (selected), 'Executions', and 'Utilities'. A green save button and a blue cancel button are on the right.

Cohort characterization: A detailed description of cohort characterization is provided, mentioning it involves generating cohort level descriptive summary statistics from person level covariate data, with various statistical measures and time-stratification options.

Cohort definitions: A table lists a single cohort entry:

ID	Name	Action
1771701	Celecoxib new users	Edit cohort Remove

Show 10 entries, Search: []

Showing 1 to 1 of 1 entries | Previous [1] Next

Feature analyses: A table lists two feature analysis entries:

ID	Name	Description	Action
15	Drug Group Era Any Time Prior	One covariate per drug rolled up to ATC groups in the drug_era table overlapping with any time prior to index.	Remove
27	Condition Group Era Any Time Prior	One covariate per condition era rolled up to groups in the condition_era table overlapping with any time prior to index.	Remove

Show 10 entries, Search: []

Showing 1 to 2 of 2 entries | Previous [1] Next

Figure E.11: Characterization settings.

Now that we have our cohort defined, we can characterize it. Click on **Characterizations** and then “New Characterization”. Give your characterization a meaningful name (e.g. “Celecoxib new users characterization”). Under Cohort Definitions, click on “Import” and select your recently created cohort definition. Under “Feature Analyses”, click on “Import” and select at least one condition analysis and one drug analysis, for example “Drug Group Era Any Time Prior” and “Condition Group Era Any Time Prior”. Your characterization definition should now look like Figure E.11. Make sure to save the characterization settings by clicking .

Click on the “Executions” tab, and click on “Generate” for one of the data sources. It may take a while for the generation to complete. When done, we can click on “View latest results”. The resulting screen will look something like Figure E.12, showing for example that pain and arthropathy are commonly observed, which should not surprise us as these are indications for celecoxib. Lower on the list we

Covariate	Explore	Concept ID	Count	Pct
Pain	Explore	4329041	1,140	78.62%
Pain finding at anatomical site	Explore	4132926	1,135	78.28%
Inflammation of specific body systems	Explore	4178818	1,135	78.28%
Arthropathy	Explore	73553	1,122	77.38%

Figure E.12: Characterization settings.

may see conditions we were not expecting.

Exercise 11.3

Click on **Cohort Definitions** and then “New cohort” to create a new cohort. Give the cohort a meaningful name (e.g. “GI bleed”) and go to the “Concept Sets” tab. Click on “New Concept Set”, and give your concept set a meaningful names (e.g. “GI bleed”). Open the **Search** module, search for “Gastrointestinal hemorrhage”, and click the **Add** icon next to the top concept to add the concept to your concept set as shown in Figure E.13.

Click on the left arrow shown at the top left of Figure E.13 to return to your cohort definition. Open the “Concept Sets” tab again, and check “Descendants” next to the GI hemorrhage concept, as shown in Figure E.14.

Return to the “Definition” tab, click on “+Add Initial Event” and then “Add Condition Occurrence”. Select your previously created concept set for the condition occurrence criterion. The result should look like Figure E.15. Leave the Inclusion Criteria, Cohort Exit, and Cohort Eras section as they are. Make sure to save the cohort definition by clicking **Save**, and close it by clicking **X**.

The screenshot shows a search interface with a header "GI bleed" and a search bar containing "Gastrointestinal hemorrhage". Below the search bar are buttons for "Search" and "Import". A "Column visibility" button is also present. The results table has columns: Id, Code, Name, Class, RC, DRC, Domain, and Vocabulary. The results are as follows:

	Id	Code	Name	Class	RC	DRC	Domain	Vocabulary
	192671	74474003	Gastrointestinal hemorrhage	Clinical Finding	919	37,144	Condition	SNOMED
	4338544	87763006	Lower gastrointestinal hemorrhage	Clinical Finding	0	15,617	Condition	SNOMED
	4100660	27719009	Acute gastrointestinal hemorrhage	Clinical Finding	0	9,852	Condition	SNOMED

On the left, there are dropdown menus for "Vocabulary" (SNOMED, ICD10CM, ICD9CM, DRG, NDFRT) and "Class" (Clinical Findings). The "Vocabulary" menu is currently expanded.

Figure E.13: Selecting the standard concept for "Gastrointestinal hemorrhage".

The screenshot shows a "Concept Set Expression" interface. The search bar contains "GI bleed". The results table has columns: Concept Id, Concept Code, Concept Name, Domain, Standard Concept Caption, Exclude, Descendants, and Mapped. The results are as follows:

	Concept Id	Concept Code	Concept Name	Domain	Standard Concept Caption	Exclude	Descendants	Mapped
	192671	74474003	Gastrointestinal hemorrhage	Condition	Standard	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

At the bottom, there are color-coded legends: Classification (purple), Non-Standard (red), and Standard (blue).

Figure E.14: Adding all descendants to "Gastrointestinal hemorrhage".

The screenshot shows a "New Cohort Definition" interface. The search bar contains "GI bleed". The tabs at the top are "Definition", "Concept Sets", "Generation", "Reporting", and "Export". The main area is titled "Cohort Entry Events" and contains the following information:

- Events having any of the following criteria: [+ Add Initial Event](#)
- a condition occurrence of [GI bleed](#) [▼](#) [+ Add attribute...](#) [Delete Criteria](#)
- with continuous observation of at least 0 days before and 0 days after event index date
- Limit initial events to: earliest event per person.
- [Restrict initial events](#)

Figure E.15: A simple gastrointestinal bleed cohort definition.

The screenshot shows the 'New Incidence Rate Analysis' interface. At the top, there's a header bar with a 'New Incidence Rate Analysis' icon and tabs for 'Definition', 'Concept Sets', 'Generation', and 'Utilities'. Below the header, there are two input fields: 'Target Cohorts' containing '#1771701:Celecoxib new users' and 'Outcome Cohorts' containing '#1771702:GI bleed'. Buttons for 'Add Target Cohort' and 'Add Outcome Cohort' are present. A section titled 'Time At Risk' describes the time window relative to cohort start or end date. Below this, a note says 'No study window defined.' with a 'Add Study Window' button. A 'Stratify Criteria' section allows for optional stratification criteria, with a 'New stratify criteria' button and a note to 'Please select a qualifying inclusion criteria to edit.'

Figure E.16: A incidence rate analysis.

The screenshot shows the 'Incidence Results' table. It includes columns for 'Source Name', 'Persons', 'Cases', 'Proportion [+/-] per 1k persons', 'Time At Risk (years)', 'Rate [+/-] per 1k years', 'Started', and 'Duration'. A 'C Rerun' button is at the top left. A 'Generate' button and an 'Export Analysis to CSV' button are at the top right. The table data is as follows:

Source Name	Persons	Cases	Proportion [+/-] per 1k persons	Time At Risk (years)	Rate [+/-] per 1k years	Started	Duration
SYNPUF 5%	1,205	95	78.84	1,052	90.30	08/23/2019 1:59 PM 00:00:22	

Figure E.17: Incidence results.

Now that we have our cohort defined, we can compute the incidence rate. Click on **Incidence Rates** and then “New Analysis”. Give your analysis a meaningful name (e.g. “Incidence of GI bleed after celecoxib initiation”). Click “Add Target Cohort” and select our celecoxib new user cohort. Click on “Add Outcome Cohort” and add our new GI bleed cohort. Set the Time At Risk to end 1095 days after the start date. The analysis should now look like Figure E.16. Make sure to save the analysis settings by clicking .

Click on the “Generation” tab, and click on “Generate”. Select one of the data sources and click “Generate”. When done, we can see the computed incidence rate and proportion, as shown in Figure E.17.

E.8 Population-Level Estimation

Exercise 12.1

We specify the default set of covariates, but we must exclude the two drugs we’re comparing, including all their descendants, because else our propensity model will become perfectly predictive:

```

library(CohortMethod)
nsaids <- c(1118084, 1124300) # celecoxib, diclofenac
covSettings <- createDefaultCovariateSettings(
  excludedCovariateConceptIds = nsaids,
  addDescendantsToExclude = TRUE)

# Load data:
cmData <- getDbCohortMethodData(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = "main",
  targetId = 1,
  comparatorId = 2,
  outcomeIds = 3,
  exposureDatabaseSchema = "main",
  exposureTable = "cohort",
  outcomeDatabaseSchema = "main",
  outcomeTable = "cohort",
  covariateSettings = covSettings)
summary(cmData)

```

```

## CohortMethodData object summary
##
## Treatment concept ID: 1
## Comparator concept ID: 2
## Outcome concept ID(s): 3
##
## Treated persons: 1800
## Comparator persons: 830
##
## Outcome counts:
##   Event count Person count
## 3           479          479
##
## Covariates:
## Number of covariates: 389
## Number of non-zero covariate values: 26923

```

Exercise 12.2

We create the study population following the specifications, and output the attrition diagram:

```

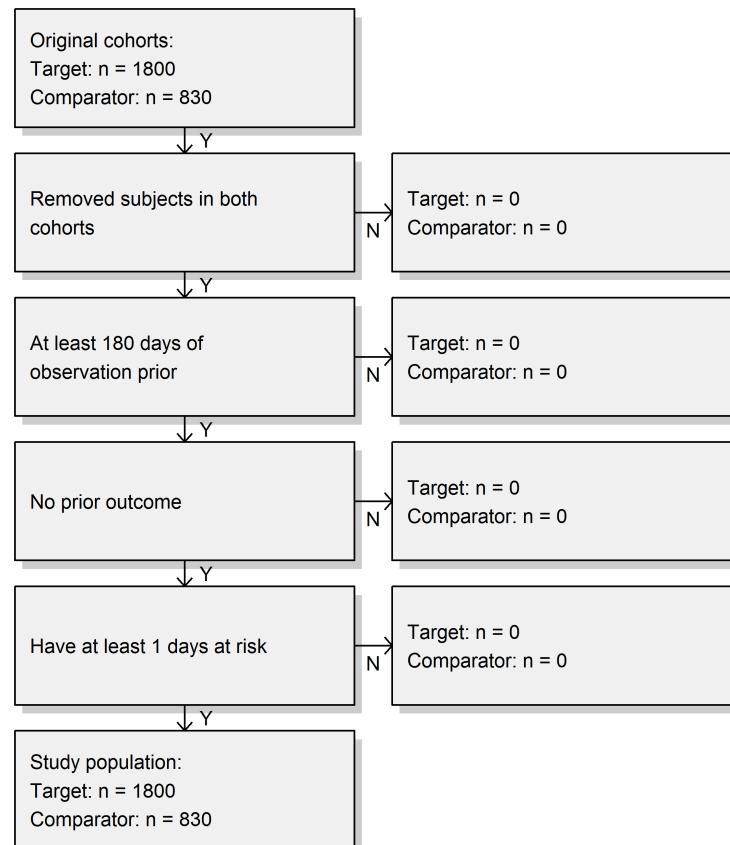
studyPop <- createStudyPopulation(
  cohortMethodData = cmData,
  outcomeId = 3,
  washoutPeriod = 180,

```

```

removeDuplicateSubjects = "remove all",
removeSubjectsWithPriorOutcome = TRUE,
riskWindowStart = 0,
startAnchor = "cohort start",
riskWindowEnd = 99999)
drawAttritionDiagram(studyPop)

```



We see that we did not lose any subjects compared to the original cohorts, probably because the restrictions used here were already applied in the cohort definitions.

Exercise 12.3

We fit a simple outcome model using a Cox regression:

```

model <- fitOutcomeModel(population = studyPop,
                           modelType = "cox")
model

```

```

## Model type: cox
## Stratified: FALSE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Status: OK
##
##           Estimate lower .95 upper .95   logRr seLogRr
## treatment  1.34612   1.10065   1.65741  0.29723  0.1044

```

It is likely that celecoxib users are not exchangeable with diclofenac users, and that these baseline differences already lead to different risks of the outcome. If we do not adjust for these difference, like in this analysis, we are likely producing biased estimates.

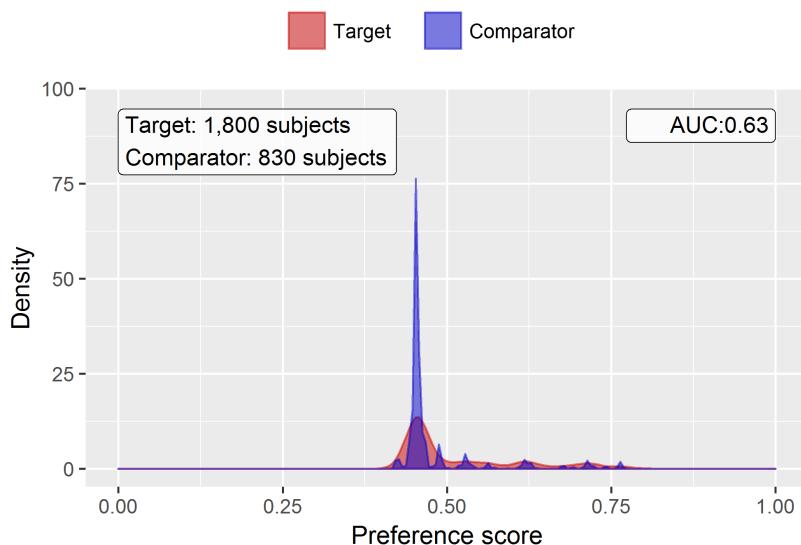
Exercise 12.4

We fit a propensity model on our study population, using all covariates we extracted. We then show the preference score distribution:

```

ps <- createPs(cohortMethodData = cmData,
                population = studyPop)
plotPs(ps, showCountsLabel = TRUE, showAucLabel = TRUE)

```



Note that this distribution looks a bit odd, with several spikes. This is because we are using a very small simulated dataset. Real preference score distributions tend to be much smoother.

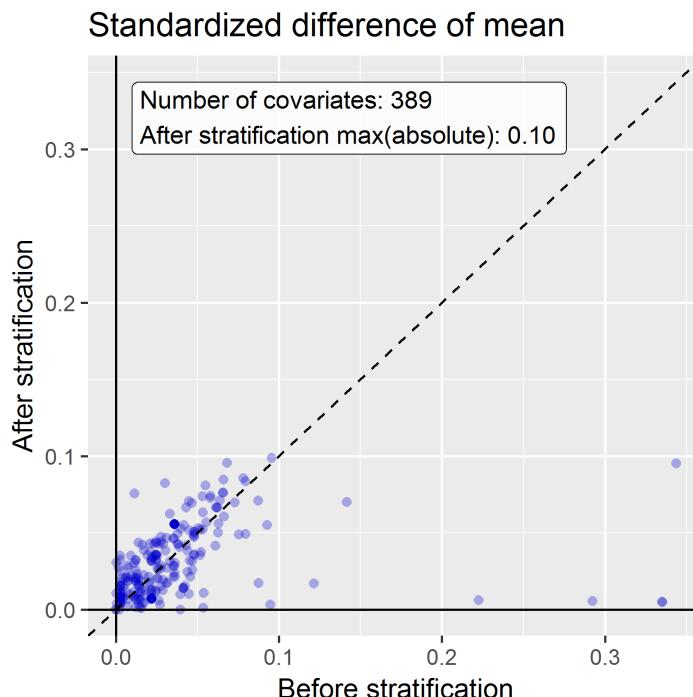
The propensity model achieves an AUC of 0.63, suggesting there are differences between target and comparator cohort. We see quite a lot overlap between the

two groups suggesting PS adjustment can make them more comparable.

Exercise 12.5

We stratify the population based on the propensity scores, and compute the covariate balance before and after stratification:

```
strataPop <- stratifyByPs(ps, number0fStrata = 5)
bal <- computeCovariateBalance(strataPop, cmData)
plotCovariateBalanceScatterPlot(bal,
                                showCovariateCountLabel = TRUE,
                                showMaxLabel = TRUE,
                                beforeLabel = "Before stratification",
                                afterLabel = "After stratification")
```



We see that various baseline covariates showed a large (>0.3) standardized difference of means before stratification (x-axis). After stratification, balance is increased, with the maximum standardized difference ≤ 0.1 .

Exercise 12.6

We fit a outcome model using a Cox regression, but stratify it by the PS strata:

```

adjModel <- fitOutcomeModel(population = strataPop,
                             modelType = "cox",
                             stratified = TRUE)
adjModel

## Model type: cox
## Stratified: TRUE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Status: OK
##
##           Estimate lower .95 upper .95   logRr seLogRr
## treatment  1.13211  0.92132  1.40008 0.12409  0.1068

```

We see the adjusted estimate is lower than the unadjusted estimate, and that the 95% confidence interval now includes 1. This is because we are now adjusting for baseline differences between the two exposure groups, thus reducing bias.

E.9 Patient-Level Prediction

Exercise 13.1

We specify a set of covariate settings, and use the `getPlpData` function to extract the data from the database:

```

library(PatientLevelPrediction)
covSettings <- createCovariateSettings(
  useDemographicsGender = TRUE,
  useDemographicsAge = TRUE,
  useConditionGroupEraLongTerm = TRUE,
  useConditionGroupEraAnyTimePrior = TRUE,
  useDrugGroupEraLongTerm = TRUE,
  useDrugGroupEraAnyTimePrior = TRUE,
  useVisitConceptCountLongTerm = TRUE,
  longTermStartDays = -365,
  endDays = -1)

plpData <- getPlpData(connectionDetails = connectionDetails,
                      cdmDatabaseSchema = "main",
                      cohortDatabaseSchema = "main",
                      cohortTable = "cohort",
                      cohortId = 4,
                      covariateSettings = covSettings,
                      outcomeDatabaseSchema = "main",
                      outcomeTable = "cohort",
                      outcomeIds = 3)

```

```
summary(plpData)

## plpData object summary
##
## At risk cohort concept ID: -1
## Outcome concept ID(s): 3
##
## People: 2630
##
## Outcome counts:
##   Event count Person count
## 3           479           479
##
## Covariates:
## Number of covariates: 245
## Number of non-zero covariate values: 54079
```

Exercise 13.2

We create a study population for the outcome of interest (in this case the only outcome for which we extracted data), removing subjects who experienced the outcome before they started the NSAID, and requiring 364 days of time-at-risk:

```
population <- createStudyPopulation(plpData = plpData,
                                      outcomeId = 3,
                                      washoutPeriod = 364,
                                      firstExposureOnly = FALSE,
                                      removeSubjectsWithPriorOutcome = TRUE,
                                      priorOutcomeLookback = 9999,
                                      riskWindowStart = 1,
                                      riskWindowEnd = 365,
                                      addExposureDaysToStart = FALSE,
                                      addExposureDaysToEnd = FALSE,
                                      minTimeAtRisk = 364,
                                      requireTimeAtRisk = TRUE,
                                      includeAllOutcomes = TRUE)

nrow(population)

## [1] 2578
```

In this case we have lost a few people by removing those that had the outcome prior, and by requiring a time-at-risk of at least 364 days.

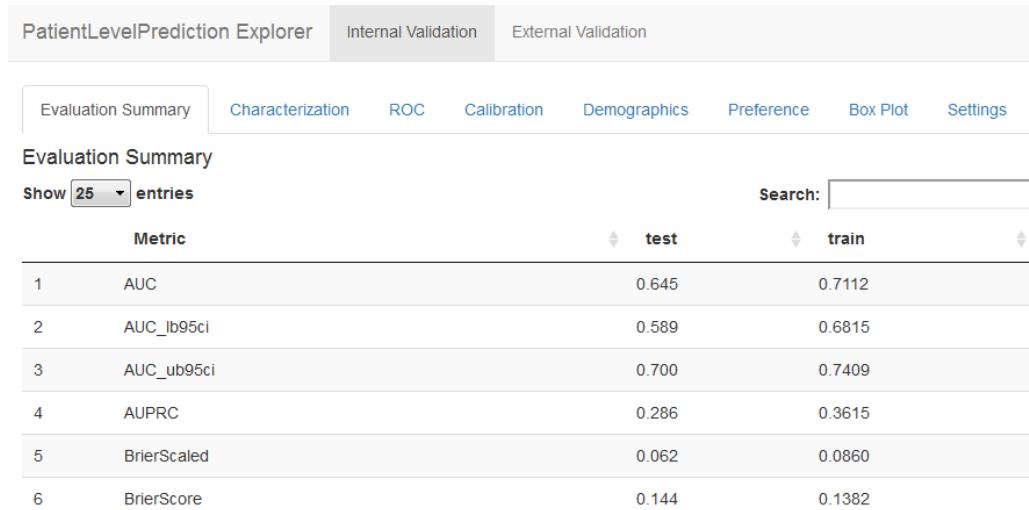


Figure E.18: Patient-level prediction Shiny app.

Exercise 13.3

We run a LASSO model by first creating a model settings object, and then calling the `runPlp` function. In this case we do a person split, training the model on 75% of the data and evaluating on 25% of the data:

```
lassoModel <- setLassoLogisticRegression(seed = 0)

lassoResults <- runPlp(population = population,
                        plpData = plpData,
                        modelSettings = lassoModel,
                        testSplit = 'person',
                        testFraction = 0.25,
                        nfold = 2,
                        splitSeed = 0)
```

Note that for this example set the random seeds both for the LASSO cross-validation and for the train-test split to make sure the results will be the same on multiple runs.

We can now view the results using the Shiny app:

```
viewPlp(lassoResults)
```

This will launch the app as shown in Figure E.18. Here we see an AUC on the test set of 0.645, which is better than random guessing, but maybe not good enough for clinical practice.

E.10 Data Quality

Exercise 15.1

To run ACHILLES:

```
library(ACHILLES)
result <- achilles(connectionDetails,
                     cdmDatabaseSchema = "main",
                     resultsDatabaseSchema = "main",
                     sourceName = "Eunomia",
                     cdmVersion = "5.3.0")
```

Exercise 15.2

To run the Data Quality Dashboard:

```
DataQualityDashboard::executeDqChecks(
  connectionDetails,
  cdmDatabaseSchema = "main",
  resultsDatabaseSchema = "main",
  cdmSourceName = "Eunomia",
  outputFolder = "C:/dataQualityExample")
```

Exercise 15.3

To view the list of data quality checks:

```
DataQualityDashboard::viewDqDashboard(
  "C:/dataQualityExample/Eunomia/results_Eunomia.json")
```


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