

Otras herramientas para el análisis de datos OMOP

Berta Raventós
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Meet (some) of the developers



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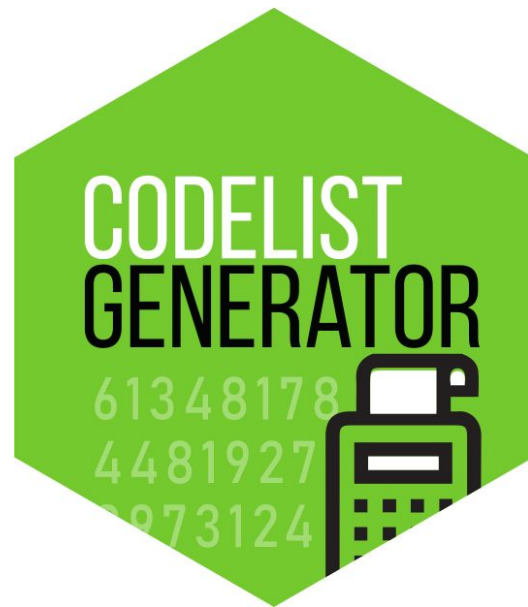


Núria Mercadé

..and many more!

Contents


1. **CodelistGenerator**
2. DrugUtilisation
3. TreatmentPatterns
4. CohortSymetry



¿Qué permite hacer?:

1. Generar listas de códigos basadas en el vocabulario
2. Búsqueda sistemática de códigos

CodelistGenerator

ATHENA

SEARCHDOWNLOADLOGIN?

← Dementia

DETAILS	
Domain ID	Condition
Concept Class ID	Disorder
Vocabulary ID	SNOMED ?
Concept ID	4182210
Concept code	52448006
Validity	Valid
Concept	Standard
Synonyms	Organic dementia Dementia (disorder)
Valid start	31-Jan-2002
Valid end	31-Dec-2099

TERM CONNECTIONS (39)

HIERARCHY

RELATED CONCEPTS

LEVEL OF DETAILS MINIMUM

+

-

25 Ancestor vocabs

Dementia

37 Descendant vocabs

¿BÚSQUEDA COMPLETA?

```
dementiaCodes1 <- getCandidateCodes(  
  cdm = cdm,  
  keywords = "dementia",  
  domains = "Condition",  
  includeDescendants = TRUE  
)
```

```
dementiaCodes1%>%  
  glimpse()  
#> Rows: 187  
#> Columns: 6  
#> $ concept_id      <int> 374326, 374888, 375791, 376085, 376094, 376095, 37694...  
#> $ found_from      <chr> "From initial search", "From initial search", "From i...  
#> $ concept_name     <chr> "Arteriosclerotic dementia with depression", "Dementi...  
#> $ domain_id       <chr> "Condition", "Condition", "Condition", "Condition", "...  
#> $ vocabulary_id   <chr> "SNOMED", "SNOMED", "SNOMED", "SNOMED", "SNOMED", "SN...  
#> $ standard_concept <chr> "standard", "standard", "standard", "standard", "stan...
```

CodelistGenerator

```
codeComparison <- compareCodelists(  
  codesFromDescendants, ← Descendientes código "4182210" Dementia  
  dementiaCodes1 ← Códigos búsqueda CodelistGenerator  
)
```

```
codeComparison %>%  
  group_by(codelist) %>%  
  tally()  
#> # A tibble: 2 × 2  
#>   codelist      n  
#>   <chr>      <int>  
#> 1 Both      151  
#> 2 Only codelist 2 36
```

```
codeComparison <- compareCodelists(  
  codesFromDescendants,  
  dementiaCodes1  
)
```

Descendientes código "4182210" Dementia

Códigos búsqueda CodelistGenerator

```
codeComparison %>%  
  group_by(codelist) %>%  
  tally()  
#> # A tibble: 2 x 2  
#>   codelist      n  
#>   <chr>      <int>  
#> 1 Both      151  
#> 2 Only codelist 2 36
```



NO DESCENDIENTES DE "4182210":

- Wandering due to dementia (37312577)
- Anxiety due to dementia (37312031)
-

CodelistGenerator

[SEARCH](#)[DOWNLOAD](#)[LOGIN](#)[Dementia](#)

DETAILS

Domain ID	Condition
Concept Class ID	Disorder
Vocabulary ID	SNOMED
Concept ID	4182210
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Concept	Standard
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TERM CONNECTIONS (39)

[HIERARCHY](#)[RELATED CONCEPTS](#)

LEVEL OF DETAILS

MINIMUM



```
oaCodes3 <- getCandidateCodes(  
  cdm = cdm,  
  keywords = "osteoarthritis",  
  domains = c("Condition", "Observation"),  
  searchInSynonyms = FALSE,  
  searchNonStandard = FALSE,  
  exclude = c(  
    "post-infection",  
    "post-traumatic"  
  ),  
  includeDescendants = FALSE,  
  includeAncestor = FALSE  
)
```

Buscar palabras clave

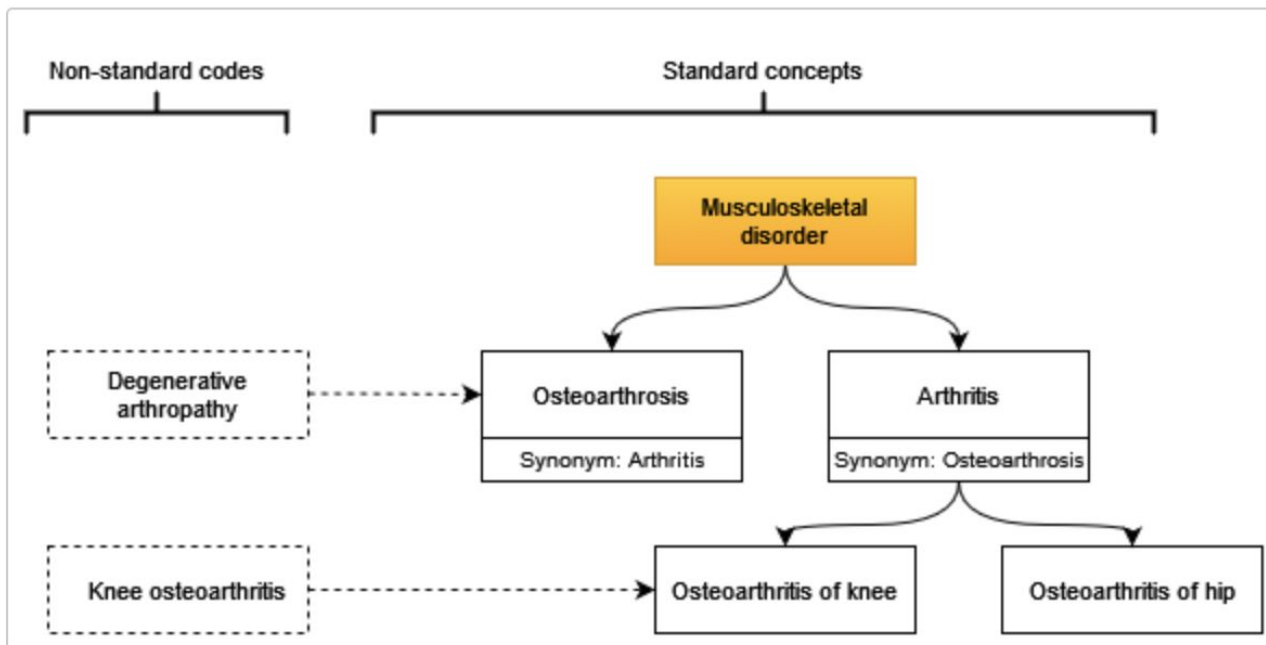
Buscar en diferentes dominios

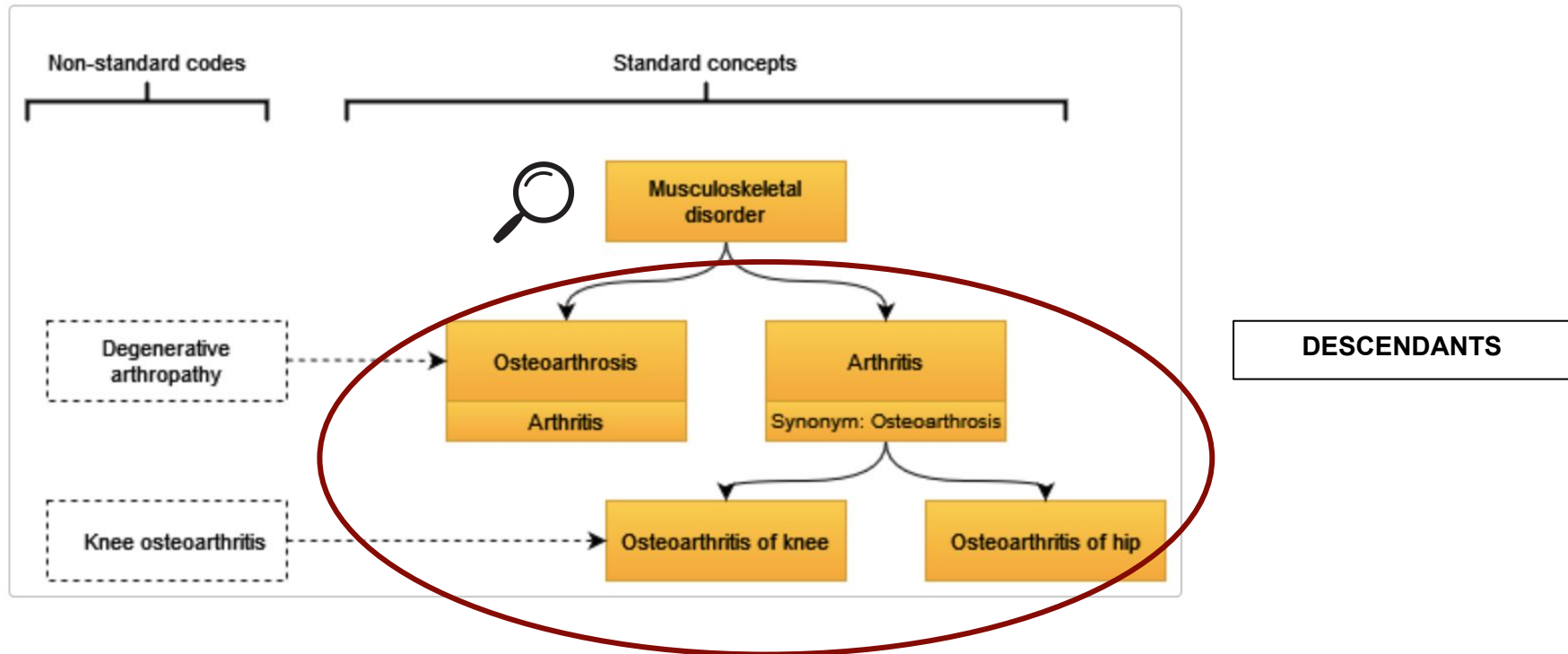
Buscar sinónimos

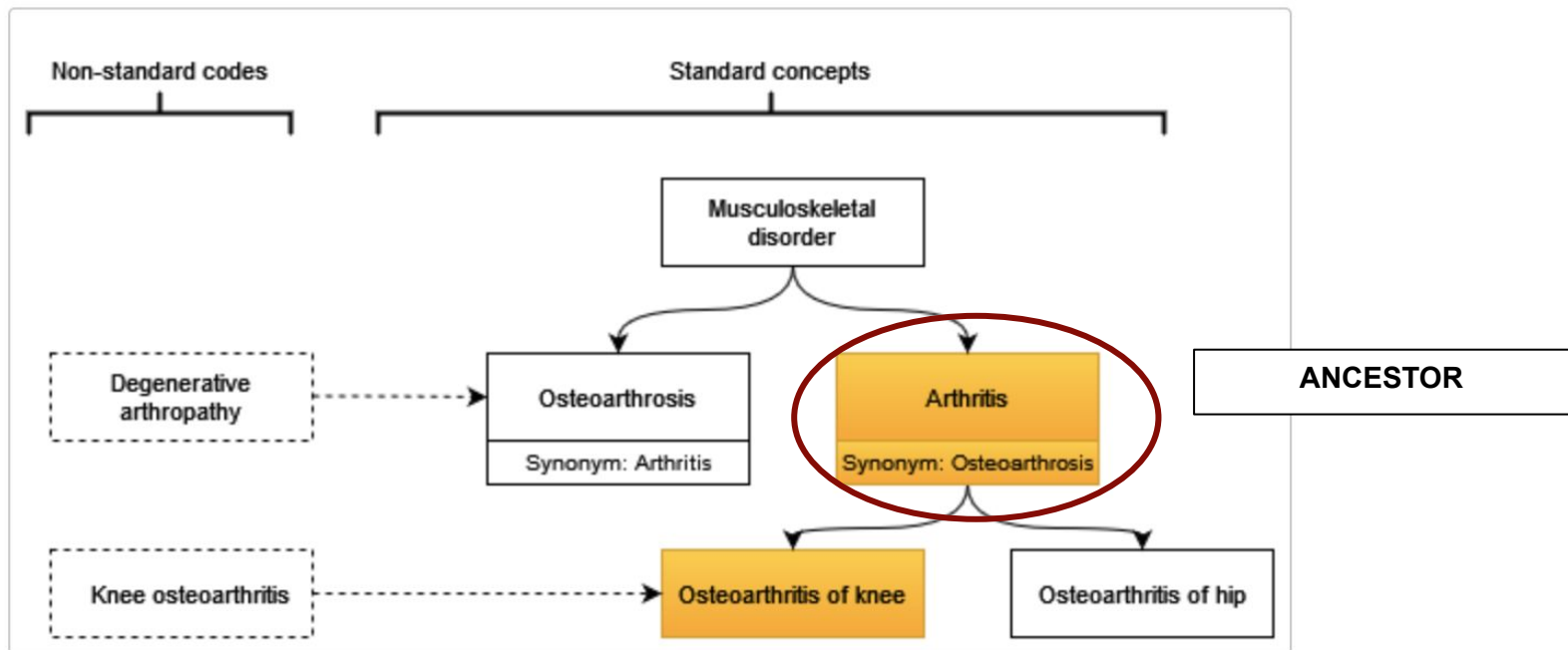
Buscar códigos no standard

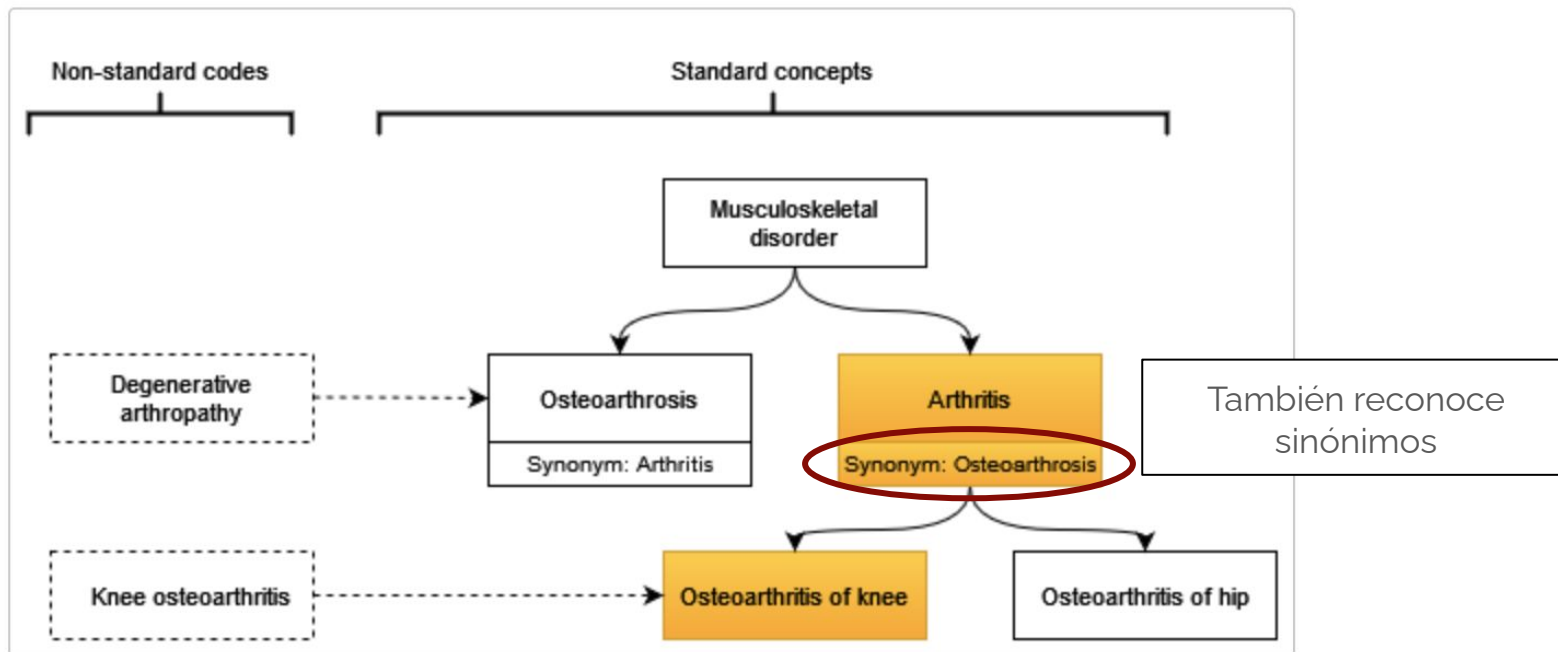
Excluir ciertas palabras

Incluir descendientes y/o
ascendentes









No es necesario usar "términos exactos"
"KNEE OSTEOARTHRITIS"

```
icdMappings <- getMappings(  
  cdm = cdm,  
  candidateCodeList = dementiaCodes1,  
  nonStandardVocabularies = "ICD10CM"  
)
```

Permite revisar mapeos
de vocabularios no
standard

(ICD-10CM, READ)

```
icdMappings %>%  
  glimpse()  
#> Rows: 191  
#> Columns: 7  
#> $ standard_concept_id      <int> 372610, 374341, 374888, 374888, 374888, 374...  
#> $ standard_concept_name    <chr> "Postconcussion syndrome", "Huntington's ch...  
#> $ standard_vocabulary_id   <chr> "SNOMED", "SNOMED", "SNOMED", "SNOMED", "SN...  
#> $ non_standard_concept_id   <int> 45571706, 35207314, 1568088, 1568089, 37402...  
#> $ non_standard_concept_name <chr> "Postconcussional syndrome", "Huntington's ...  
#> $ non_standard_concept_code <chr> "F07.81", "G10", "F02", "F02.8", "F02.811",...  
#> $ non_standard_vocabulary_id <chr> "ICD10CM", "ICD10CM", "ICD10CM", "ICD10CM",...
```

Ventajas respecto búsqueda manual:

1. Punto de partida para revisores clínicos
2. Acotar la lista inicial
3. Documentación del proceso de búsqueda
4. **BÚSQUEDA SISTEMÁTICA**

¿Existe una estrategia perfecta?:

No es tan fácil cómo parece....

¿Existe una estrategia perfecta?:

No es tan fácil cómo parece....

1. Proceso **iterativo**
2. Probar y comparar búsquedas
3. Revisión por parte de clínicos (>1!) - Consenso
4. Ejecutar CohortDiagnostics

Y con la ayuda de otros paquetes..:



```
asthma_code_use <- summariseCodeUse(asthma_cs,  
  byYear = TRUE,  
  bySex = TRUE,  
  ageGroup = list(c(0,17),  
                  c(18,65),  
                  c(66, 150)),  
  cdm=cdm,  
  minCellCount = 0)  
  
asthma_code_use %>%  
  filter(strata_name == "Overall") %>%  
  select(group_name, group_level, variable_name, estimate) %>%  
  pivot_wider(names_from = variable_name, values_from = estimate)
```

**Descriptiva de
cómo/cuándo se utiliza
un código**

```
# A tibble: 3 × 4  
  group_name group_level `Record count` `Person count`  
  <chr>      <chr>      <int>      <int>  
1 Codelist Overall      101      101  
2 By concept Standard concept: Childhood asthma (... 96      96  
3 By concept Standard concept: Asthma (317009) So... 5      5
```

CodelistGenerator: Identify Relevant Clinical Codes and Evaluate Their Use

Generate a candidate code list for the Observational Medical Outcomes Partnership (OMOP) common data model based on string matching. For a given search strategy, a candidate code list will be returned.

Version: 2.2.3
Depends: R (≥ 3.5.0)
Imports: [CDMConnector](#) (≥ 1.3.0), [checkmate](#) (≥ 2.0.0), [DBI](#) (≥ 1.1.0), [duckdb](#), [dplyr](#) (≥ 1.1.0), [magrittr](#) (≥ 2.0.0), [omopgenerics](#) (≥ 0.0.2), [rlang](#) (≥ 1.0.0), [glue](#) (≥ 1.5.0), [stringr](#) (≥ 1.4.0), [tidyselect](#) (≥ 1.2.0), [tidyr](#) (≥ 1.2.0), [cli](#) (≥ 3.1.0), [purrr](#), [lubridate](#), [PatientProfiles](#) (≥ 0.3.0), [RJSONIO](#), [vctrs](#)
Suggests: [covr](#), [knitr](#), [rmarkdown](#), [testthat](#) (≥ 3.0.0), [RPostgres](#), [odbc](#), [spelling](#), [tibble](#)
Published: 2024-03-08
Author: Edward Burn  [aut, cre], Marti Catala  [ctb]
Maintainer: Edward Burn <edward.burn at ndorms.ox.ac.uk>
License: [Apache License \(≥ 2\)](#)
URL: <https://darwin-eu.github.io/CodelistGenerator/>
NeedsCompilation: no
Language: en-US
Materials: [README NEWS](#)
CRAN checks: [CodelistGenerator results](#)

Documentation:

Reference manual: [CodelistGenerator.pdf](#)
Vignettes: [01 Introduction to CodelistGenerator](#)
[a02 Candidate codes OA](#)
[03 Options for CodelistGenerator](#)
[a04 codelists for medications](#)

iDisponible en CRAN!

<https://cran.r-project.org/web/packages/CodelistGenerator/index.html>
<https://darwin-eu.github.io/CodelistGenerator/>

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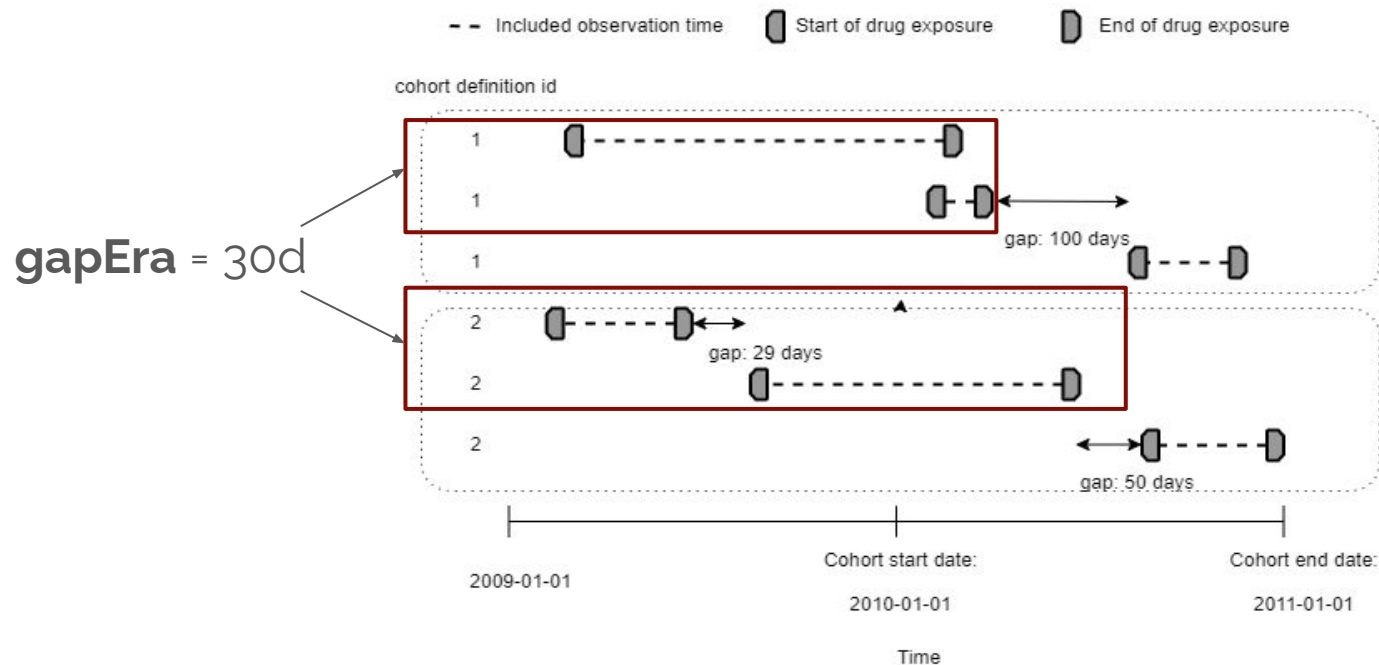
¿Qué permite hacer?:

1. Crear cohorte de “drug users”
2. Calcular dosis diaria
3. Identificar indicaciones potenciales
4. “Resumir” el uso de fármacos
5. Identificar tratamientos alternativos

1. Crear una cohorte de “drug users”

- Cohorte de fármacos - misma estructura y atributos
- A partir de:
 - Concept set
 - Ingredientes
 - Códigos ATC
- Criterios similares + gapEra

1. Crear una cohorte de “drug users”



2. Calcular dosis diaria

Añadir información a la cohorte “drug users” sobre:

- Dosis diaria y unidades

3. Identificar indicaciones potenciales



3. Identificar indicaciones potenciales

Añadir información a la cohorte “drug users” sobre:

- Dx de indicaciones potenciales en ventanas de tiempo concretas


5. Identificar tratamientos alternativos

Añadir información a la cohorte “drug users” sobre:

- Uso de otros tratamientos en ventanas de tiempo concretas

DrugUtilisation: Summarise Patient-Level Drug Utilisation in Data Mapped to the OMOP Common Data Model

Summarise patient-level drug utilisation cohorts using data mapped to the Observational Medical Outcomes Partnership (OMOP) common data model. New users and prevalent users cohorts can be generated and their characteristics, indication and drug use summarised.

Version: 0.5.3
Depends: R (≥ 2.10)
Imports: [CDMConnector](#) (≥ 1.3.0), [checkmate](#), [DBI](#), [dbplyr](#), [dplyr](#), [glue](#), [lubridate](#), [tidyr](#), [rlang](#), [RJSONIO](#), [cli](#), [PatientProfiles](#) (≥ 0.7.0), [magrittr](#), [purrr](#), [tictoc](#), [omopgenerics](#) (≥ 0.0.2), [visOmopResults](#), [lifecycle](#)
Suggests: [covr](#), [testthat](#) (≥ 3.1.5), [odbc](#), [here](#), [RPostgres](#), [duckdb](#), [CodelistGenerator](#), [knitr](#), [PaRe](#), [rmarkdown](#), [DT](#), [magick](#), [DiagrammeRsvg](#), [ggplot2](#), [cowplot](#), [plotly](#), [tibble](#)
Published: 2024-04-02
Author: Marti Catala  [aut, cre], Mike Du  [aut], Yuchen Guo  [aut], Kim Lopez-Guell  [aut], Edward Burn  [ctb], Xintong Li  [ctb], Marta Alcalde-Herraiz  [ctb]
Maintainer: Marti Catala <marti.catalasabate@ndorms.ox.ac.uk>
License: [Apache License \(≥ 2\)](#)
URL: <https://darwin-eu-dev.github.io/DrugUtilisation/>
NeedsCompilation: no
Materials: [README](#)
CRAN checks: [DrugUtilisation results](#)

Documentation:

Reference manual: [DrugUtilisation.pdf](#)

iDisponible en CRAN!

<https://cran.r-project.org/web/packages/DrugUtilisation/index.html>
<https://darwin-eu-dev.github.io/DrugUtilisation/>

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4. CohortSymetry

¿Qué permite hacer?:

1. Describir secuencias de tratamientos
2. Analizar uso de fármacos más allá de la dosis



Potencial para estudiar adherencia a guías terapéuticas

Parámetros a tener en cuenta:

1. *Lookback period treatments*
2. *Minimum duration treatment*
3. *Maximum time interval between treatments*
4. *Minimum overlap of different treatments to be considered as combination of treatments*
5. *Minimum duration of post combination treatment*
6. *Select which treatments should be included in the pathway*

TreatmentPatterns

Computer Methods and Programs in Biomedicine 225 (2022) 107081



Contents lists available at ScienceDirect

Computer Methods and Programs in Biomedicine

journal homepage: www.elsevier.com/locate/cmpb



TreatmentPatterns: An R package to facilitate the standardized development and analysis of treatment patterns across disease domains



Aniek F. Markus^{a,*}, Katia M.C. Verhamme^{a,b}, Jan A. Kors^a, Peter R. Rijnbeek^a

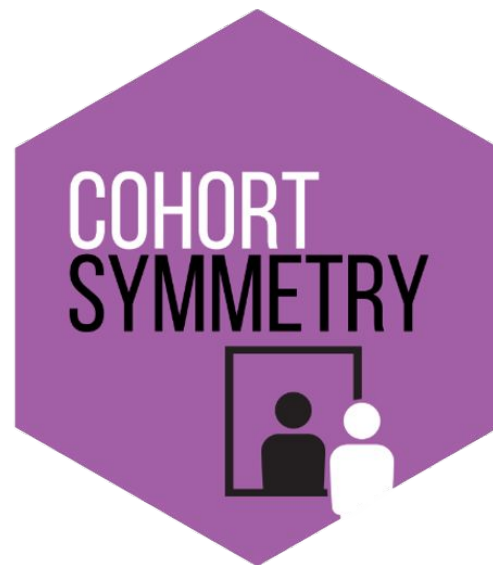
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<https://mi-erasmusmc.shinyapps.io/TreatmentPatterns/>
<https://github.com/mi-erasmusmc/TreatmentPatterns>

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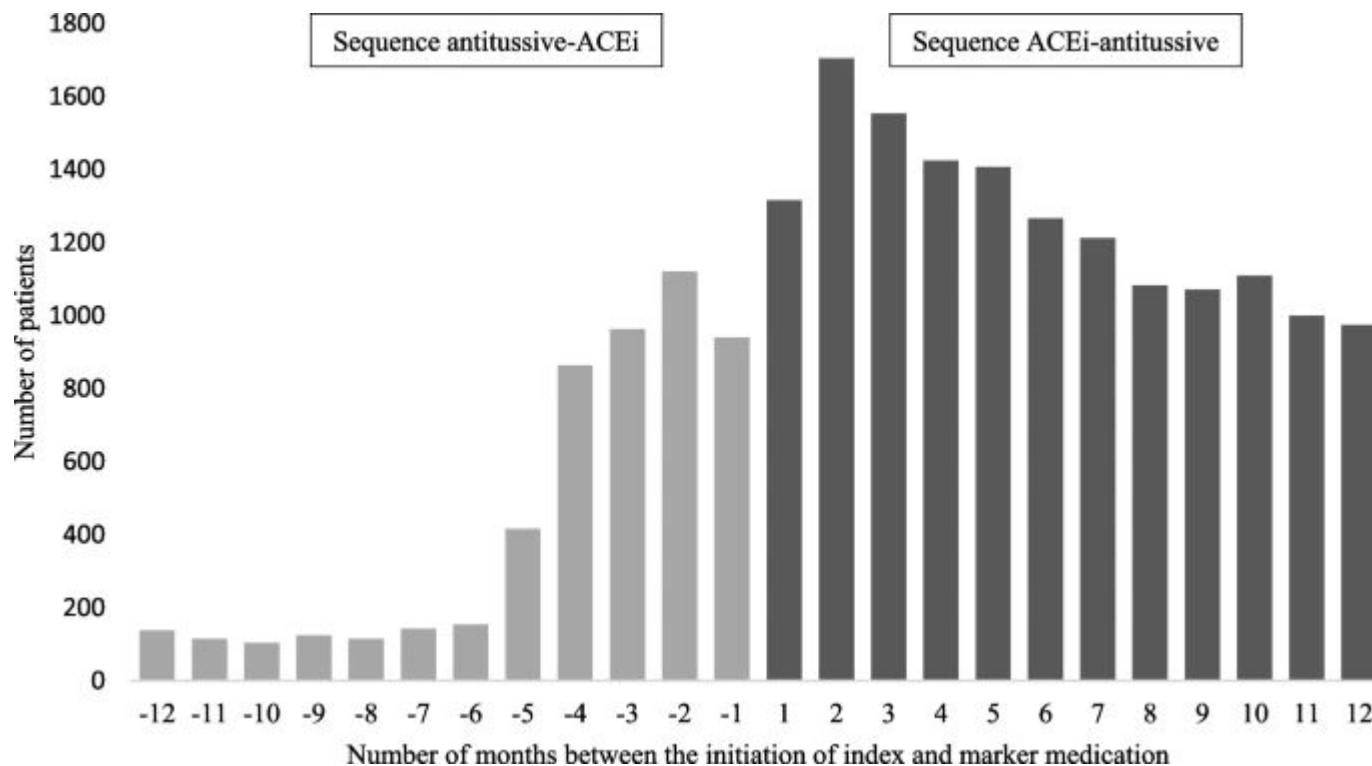
¿Qué permite hacer?:

- Prescription Sequence Symmetry Analysis (PSSA):
 - Detección de eventos adversos (AEs)
 - Asociación entre:
 - Index drug (medicación inicial)
 - Marker drug (medicación tto. AE)

N patients with index → marker

N patients with marker → index





Source: Hendrix MRS, Yasar M, Mohammad AK, et al. Prescription Sequence Symmetry Analysis (PSSA) to assess prescribing cascades: a step-by-step guide. *BMC Med Res Methodol.* 2024;24(1):8. Published 2024 Jan 11. doi:10.1186/s12874-023-02108-y



iPronto en CRAN!

<https://github.com/oxford-pharmacoepi/CohortSymmetry>

Generar herramientas que sean:

- Estandarizadas
- Accesibles
- Transparentes
- Fáciles de utilizar e interpretar
- Pensadas para la epidemiología

¿Y OHDSI?



<https://ohdsi.github.io/Hades/packages.html>

¡Muchas más herramientas a utilizar!

Generar herramientas que sean:

- Estandarizadas
- Accesibles
- Transparentes
- Fáciles de utilizar e interpretar
- Pensadas para la epidemiología