

CM

Dear Students, Quiz 1 will be held on Thursday, 28th August. The syllabus will include all topics covered up to the Tuesday class. The paper will be a combination of subjective and objective questions. Please make sure to carry your ID card.

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- 3. Healthcare Data Standards
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 - FHIR Resource Categories
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 - b> **Administration Resources**
 - c> **Clinical Resources**
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 - Component Types
- 6. ABDM (Ayushman Bharat Digital Mission)
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 - Milestones
 - Key Stakeholders
 - ABHA System
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- Study Tips
- COMPUTING FOR MEDICINE - MOCK QUIZ 2
 - INSTRUCTIONS:
 - MULTIPLE CHOICE QUESTIONS (1 mark each = 17 marks)
 - 1. In the context of EHR phenotype algorithms, what does PPV stand for and why is it crucial for genetic studies?
 - 2. Which NLP task is most critical for extracting clinical concepts from unstructured EMR data?
 - 3. In FHIR terminology, what is the primary purpose of a "Profile"?
 - 4. The relationship between PPV and disease prevalence in EMR algorithms is:
 - 5. Which component of the ABDM framework is responsible for managing patient consent for health data sharing?
 - 6. In SNOMED CT, post-coordinated expressions:
 - 7. The adaptive LASSO penalized logistic regression method is used in EMR phenotype algorithms to:
 - 8. Which database standardizes health terminologies and is essential for NLP concept mapping?
 - 9. In the i2b2 methodology, a "sensitive data mart" is created to:
 - 10. The formula $n(n-1)/2$ in healthcare interoperability represents:
 - 11. Which FHIR resource category would contain a "Coverage" resource for insurance information?
 - 12. Natural Language Processing improves EMR phenotype algorithms most significantly when:
 - 13. In HL7 message structure, segments are:
 - 14. The primary advantage of using probability thresholds in EMR algorithms over Boolean approaches is:
 - 15. ABHA numbers in the ABDM framework:
 - 16. Which type of EMR data typically requires manual medical record review without NLP?
 - 17. In healthcare ontologies, the "is a" relationship represents:
 - SHORT ANSWER QUESTIONS
 - 18. Explain the difference between pre-coordinated and post-coordinated expressions in SNOMED CT with one example each. (3 marks)
 - 19. Describe the validation methodology used in the i2b2 approach for EMR phenotype algorithms. Include the composition of the validation set and the importance of blinding. (5 marks)
 - 20. Compare and contrast the four levels of healthcare data interoperability (Syntactic, Semantic, Process, Human) with specific examples from healthcare systems. (5 marks)
 - ANSWER KEY
 - Multiple Choice Answers:
 - Short Answer Answers:

TAs

Students can reach out to the following TAs during their support hours in Room A316. Please make use of these slots for doubt clarification.

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Computing for Medicine, Lecture 1: Introduction

(For Monsoon 2025, as per C4M-Lecture-1_Introduction.pptx_compressed.pdf)

1. Course Overview

- **Aim:** Learn how computing and data science apply to medicine and healthcare.
- **Key Focus:** Interoperable health data, data science, machine learning (ML), AI, real-world health datasets.
- **Skill Development:**
 - Build systems for safe medical data exchange.
 - Critique and apply modeling for health data.
 - Design solutions for actual healthcare problems.
 - Learn inclusion, safety, and ethics in healthcare AI.

2. Course Structure

- **The Big Picture:** How computing interacts with healthcare systems.
- **Data:**
 - Spotlight on FAIR (Findable, Accessible, Interoperable, Reusable) and Open data.
 - Standards:
 - Syntactic Interoperability: HL7, DICOM, FHIR (for data exchange).
 - Semantic Interoperability: SNOMED, Ontologies (for meaning).
- **Data Science, ML & AI:**
 - Structured data: Statistics, basic ML.
 - Unstructured data: NLP (Natural Language Processing) in healthcare.
 - New Topic: Agentic AI—AI that takes action itself in healthcare.
- **Case Studies:**
 - Exploring/researching open health datasets.
 - Real examples: Antibiotic resistance, ICU predictive modeling.
 - Examining inclusion, safety, ethics.

3. Grading & Assignments

Component	Weight
Assignments	15%
Quizzes	15%
Mid Sem Exam	20%

Component	Weight
End Sem Exam	25%
Project	25%

Quizzes: "n-1 policy" (miss one without penalty).

Projects and activities are central—learn by doing.

4. Academic Integrity

- *What counts as plagiarism:*
 - Copying homework.
 - Using someone else's work/ideas without citation.
 - *Consequences:*
 - First time: Zero marks.
 - Second time: Reported to committee.
 - If in the final report: Grade goes down by one.
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5. Biological Systems Are Unique

- **Features:**
 - Adaptive, self-organizing, constantly changing, oscillatory, far from equilibrium, sensitive, not always optimal.
 - *Physical efficiency* (like perfect networks in lungs) can actually make a system more fragile—not always optimal for health (example: bronchial tree and asthma).
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6. Interdisciplinary Nature

- This field combines computer science, biology, medicine, and social science.
 - Inspired by coursework/programs at Stanford, Harvard, Melbourne, and others.
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7. Uses of Health Data

- **Applications:**
 - Individual care (diagnosis/treatment)
 - Public health planning
 - Policy evaluation
 - Improving safety, cost-effectiveness, outcomes
 - Same data can answer different questions—depends on how/why it is used.
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8. Types of Medical Studies

- **Retrospective:** Look back at old records.
- **Prospective:** Start now, collect data moving forward.

9. Why Data Science Is Important in Health

- Helps:
 - **Identify** risk factors (e.g., cholesterol → heart disease).
 - **Control** for “**confounders**”, **hidden factors** that can mislead results.
 - *Simpson’s Paradox*: Trends in subgroups may be opposite to the whole population. Need care in data interpretation.
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10. Types of Data Analysis Problems

- Must think about *causality*: **What causes what?**
 - *Forks (confounding)*: Multiple factors affect a result.
 - *Colliders*: Sometimes **including too many variables** hides real effects.
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11. AI Failures

- **Common failures**:
 - **Biased** data (e.g., only light skin in melanoma training data).
 - **Human error**.
 - **Regulatory issues**.
 - Over-trusting complex, “**black box**” models.
 - **Disinformation** via AI tools.
 - *Case Study*: **An AI learned that pneumonia patients with asthma had better survival**, but only because they got better care—not because asthma was protective.
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12. Making Data FAIR

Principle	What it means
Findable	Data has a persistent unique identifier, rich metadata
Accessible	Data can be retrieved with standard protocols, metadata always available
Interoperable	Data uses shared vocabularies and formats
Reusable	Data has clear licenses, provenance, and meets community standards

13. Major Example Health Datasets

- **CORD-19**: COVID-19 scholarly articles dataset.
- **MIMIC-III**: ICU patient data (demographics, labs, notes).
- **Johns Hopkins COVID datasets**: For specific clinical research.
- **Vivli**: Clinical trials and antimicrobial resistance data.

*Most are open to global researchers for **free and used for real-world experiments and studies**.*

14. Key Takeaways

- Computing can transform how medicine is practiced, but ethical, safe, and reproducible ways of handling data are critical.
- Interdisciplinary skills are necessary: programming, statistics, domain knowledge.
- Real-world datasets are available to explore and build medical AI and tools.
- Always consider data limitations and risk of bias.
- Plagiarism carries heavy consequences—always cite and do your own work.

Computing for Medicine, Lecture 2: The Big Picture (Continued)

(Based on C4M-Lecture-2_Big_Picture_Contd.pptx_compressed.pdf)

1. Case Study: Simpson's Paradox in Vaccine Data

Efficacy: ability of something like a drug or a medical treatment to bring about the results that are wanted

- **Data Example:** COVID-19/Israeli Data (Aug 2021)
 - **Age Groups:** All ages, Under 50, Over 50
 - **Vaccine Efficacy:**
 - Efficacy appears high in each age group for vaccinated people.
 - But "overall" efficacy looks much lower.
 - **Cause:** Older people (at higher risk) are more vaccinated.
- **Concept:**
 - *Simpson's Paradox* — When trends are present in separate groups but disappear or reverse when groups are combined.
 - **Moral:** Always stratify data and check subgroups before drawing conclusions.

Stratify: to organize something or different parts of something in layers

2. Digitizing Human Health: Challenges

- **Real World:** Health is *continuous* (analogue signals), e.g., heart rate, blood pressure.
- **Computing World:** Works with *digital* (discrete numbers, finite precision).
- **Implication:** Computational models always approximate real health data—never fully capture all details.

3. Types of Medical Studies: Recap

- **Retrospective Study:** Looks back at existing records.
Example: Checking past patient histories to find links between exposure and disease.
- **Prospective Study:** Follows participants forward in time and records events as they happen.
Example: Recruit healthy people, track who develops disease over the years.

4. Conditional Probability and Confounding

- **Conditional Probability:** Probability that one event will occur given that another HAS happened (used to analyze risk factors).
- **Confounding:** A hidden variable affects both the cause and the effect, making it seem like there is a direct link.

- *Example:* Ice cream sales and drowning—both go up in summer, but summer is the confounder.

5. Simpson's Paradox in Depth

- **Description:**
 - Analysis on subgroups/different slices of data can show the opposite trend to analysis on full data.
- **Practical Advice:**
 - Always check data both with and without grouping by possible confounders (e.g., age, risk categories).

6. AI in Healthcare: Potential and Pitfalls

Types of Failures

- **Biased Data:** Training data does not represent all populations (e.g., an AI for skin cancer trained only on light skin fails on dark skin).
- **Epistemic Failure:** Model makes confident predictions on things it was never trained (e.g., confusing Covid for a cat).
- **Regulatory Failure:** No clear rules for safe deployment, leading to risk and uncertainty.
- **Human Error:** Misinterpreting the output, overtrusting or misunderstanding limitations.
- **Disinformation:** AI tools can be misused to produce fake, misleading or harmful medical information at speed.

Case Studies

- *Pneumonia/Asthma Example* (Caruana et al. 2015):
 - A model wrongly concluded asthma patients with pneumonia have lower risk.
 - Why? These patients got much more intensive care, so the data reflected better outcomes, not a lower biological risk.
- *Dedicated AI vs. LLMs for Diagnosis* (2025 study):
 - Dedicated medical expert systems (built for years) still slightly outperform general-purpose LLMs (like ChatGPT, Gemini) for clinical case diagnosis, especially without lab results.
 - When labs are included, differences narrow.

The "Halo Effect":

- People often over-trust complex models just because they are "deep" or "new"—not always justified.
- Transparent, interpretable models are essential in medicine, even if their accuracy is a bit lower.

7. Disinformation and the "Misinfodemic"

- **Infodemia:** Rapid spread of too much info—much of it incorrect/dangerous.
- **Recent Observations:**
 - Researchers made 102 fake medical blog posts with lots of disinfo using an LLM in about an hour.

- Posts targeted specific groups and used fake testimonials and references.
 - Images were fabricated in minutes.
 - **Lesson:**
 - AI speeds up the spread of fake health information (“**weapons of mass disinformation**”).
 - **We need transparency**, human vigilance, regulatory oversight, and **robust “guardrails”** to prevent harm.
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8. Open Discussion: Who Benefits from Health Data?

- **Beneficiaries:**
 - **Patients (better diagnosis/care), policymakers, researchers, tech companies, public health systems.**
 - **Risks:**
 - **Misuse of sensitive** health info, **spread of harmful** fake news, **bias against vulnerable** groups.
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9. Key Takeaways

- **Always consider data context and structure before trusting analytic results.**
- **AI in medicine needs interdisciplinary knowledge, careful design, and oversight.**
- **Transparent, fair, and ethical use of health data benefits everyone—but misuse can be dangerous.**
- **Understanding bias, confounding, and paradoxes like Simpson’s Paradox is crucial for trustworthy medical computing.**

Computing for Medicine, Lecture 3: Data Sources

(Based on C4M-Lecture-3_Data_Sources_compressed.pdf)

1. Who Benefits from Health Data?

- Patients receive better **diagnosis and treatment.**
 - Healthcare providers improve **care quality and coordination.**
 - Researchers **advance medical knowledge.**
 - **Policymakers design** effective health interventions.
 - The public gains from better health systems and **disease control.**
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2. Starting Point: Healthcare Data

- Healthcare data **often starts with patient records** from visits.
- Example of a medical record:
 - Patient **symptoms**: cough, fever, dyspnea.
 - Physical **exam results**: blood pressure, pulse, fever measurement.
 - **Lab data**: blood tests, fecal occult blood.
 - **Imaging**: chest X-rays.
 - **Medications** prescribed and dosage.
 - **Follow-up visits** with changes in symptoms and tests.

- These records have **multiple problems tracked over time**, showing progression and treatment response.

3. **FAIR** Principles for Medical Data

- To **Make Healthcare Data Reproducible and FAIR**:
 - **Findable**: **Assign unique, permanent IDs** and **rich metadata**.
 - **Accessible**: Data must be retrievable with open, standard methods; **even if data is removed, metadata stays available**.
 - **Interoperable**: Use **common languages/vocabularies that all systems can understand** and link to other data.
 - **Reusable**: **Clear licenses, provenance (history of data)**, and community standards ensure data can be safely reused.

4. Why Use Standards?

- Standards allow the **same medical vocabulary to be shared across systems**.
- For example, coding systems like:
 - **ICD-10**: International Classification of Diseases for diagnoses.
 - **SNOMED CT**: Detailed clinical terms.
 - **LOINC**: Laboratory test codes.
 - **RxNorm**: Drug prescriptions.
 - **HL7, FHIR**: Standards for exchanging data electronically.
- With standards, computers can **understand and process** medical records accurately.

5. How Does a Computer Read a Medical Record?

- **Medical records are converted into standardized codes** and data formats.
- Example of **one visit**:
 - **Patient characteristics encoded**: 60 years old, male, obese.
 - **Symptoms and tests coded** with SNOMED CT or LOINC.
 - **Diagnosis coded with ICD-10**.
 - **Medication coded with RxNorm**.
- This enables computers to:
 - Store the data.
 - Exchange it with other systems.
 - Use it for analysis or decision support.

6. Structured vs. Unstructured Data

Type	Description	Example
Structured Data	Organized in clear fields, tables	ICD codes, prescriptions, vitals

Type	Description	Example
Unstructured Data	Free text or reports	Doctor's notes, discharge summaries, radiology reports

- Both types are important; structured data is easier for computers, but unstructured data contains rich clinical details.

7. What is an Electronic Health Record (EHR)?

- ISO Definition: An EHR is a securely stored, computer-processable collection of a patient's health info.
- It supports ongoing healthcare and includes data from past, current, and future care.
- Accessible by authorized providers to improve quality and coordination.
- Contains diverse data: consultations, tests, prescriptions, referrals, hospital stays, and more.

8. Purpose of EHRs Across Countries

- Examples:
 - Australia's HealthConnect: Focus on patient care, quality, and management.
 - Austria's ELGA system: Includes patient care and financial/administrative workflows.
- Common goals:
 - Improve patient care.
 - Help doctors make informed decisions.
 - Facilitate research.
 - Reduce errors and streamline workflows.

9. Interoperability in Healthcare

- Definition (IEEE 1990): Ability of systems to exchange and use information.
- Levels of interoperability:
 - Technical: Ability to send/receive data.
 - Semantic: Recipient understands the data.
 - Process: Data is used effectively in workflows.
 - Human/Clinical: Effective use improves patient care.
- Interoperability enables AI, big data, better medical communication, research, and global cooperation.

10. Examples of Interoperability Standards

- HL7 ADT messages (for patient admissions, transfers, discharges).
- FHIR Standard uses JSON format to exchange medical data in APIs.
- These allow efficient, standardized data exchange across healthcare IT systems.

11. Key Open Health Datasets

- **COVID-19 Open Research Dataset (CORD-19):** Scholarly articles on COVID-19 and coronaviruses.
 - **MIMIC:** Intensive care unit patient data.
 - **Johns Hopkins COVID-19 Collaborative:** Patient records from Epic EHR updated weekly.
 - **National COVID Cohort Collaborative (N3C):** Combined patient-level COVID data from many institutions.
 - Other datasets from [Zenodo](#), [Figshare](#), [GitHub](#), [Harvard Dataverse](#), [ImmPort](#), and [more](#).
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12. Special Mention: Antimicrobial Resistance Data

- Example software: [AMRsteward AI Dashboard for antibiotic stewardship](#).
 - Open-source, [designed to track and optimize antibiotic use in hospitals](#).
 - [Patient data used to monitor infection and resistance trends](#).
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13. Summary

- **Data is the foundation of modern medicine's computing revolution.**
 - Standards and interoperability enable **safe, effective sharing and analysis**.
 - Combining structured and unstructured data gives a complete health picture.
 - FAIR principles ensure data can be reused reliably and ethically.
 - Access to rich, open datasets accelerates research and innovation.
 - Understanding healthcare data sources is key to making impactful AI and computational health tools.
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Thanks for reading!

Computing for Medicine, Lecture 4: Semantic Interoperability

(Based on [C4M-Lecture-4_Semantic_Interoperability_compressed.pdf](#))

1. What is Interoperability?

- **Definition:** The ability of different systems or components to [exchange information and use the exchanged information effectively](#).
- **Levels of Interoperability:**
 - **Technical:** Systems can send/receive data.
 - **Semantic:** Systems understand the meaning of data received.
 - **Process:** Data is used properly in workflows or decisions.
 - **Human (Clinical):** Data improves patient care in meaningful ways.

[Semantic interoperability is key](#) to making digital medicine effective by [ensuring data is not just exchanged but also understood](#).

2. Why Semantic Interoperability Matters

- Many medical data sets today [are isolated in incompatible systems](#).
- Lack of interoperability slows medical progress.

- Technologies like AI, big data analytics, and mobile apps depend on interoperable, meaningful data.
- Broad domains impacted:
 - Artificial intelligence and big data.
 - Medical communication among caregivers.
 - Research that combines data across institutions.
 - International cooperation on diseases and treatments.

3. Sharing Patient Data to Improve Care

- Studies show *electronic health information exchange* among hospitals improves coordination.
- Patients benefit as providers share data quickly, reducing repeated tests and errors.
- Hospitals active in **Health Information Organizations (HIOs)** more often share patient care successfully.

4. Semantic Interoperability with Text

- Medical data often comes as *unstructured text* (e.g., clinical notes).
- To make use of such data:
 - Extract meaningful terms.
 - Turn them into standardized forms computers can analyze.
- Example clinical note about allergies includes symptoms, medication history, and doctor assessments in narrative form.
- Semantic tools help computers interpret this kind of textual, complex data.

5. Terminologies and Ontologies: Tools for Semantic Interoperability

Term	What It Means
Terminology	Standardized set of terms to describe a domain (e.g. medicine).
Thesaurus	Groups similar or related words to help with searching.
Controlled Vocabulary	A list of preferred terms that limits variation for consistency.
Classification	Organizes terms into mutually exclusive groups (e.g., ICD codes).
Ontology	Defines concepts and relationships formally for computers to reason about.

- Ontologies are the most powerful, representing concepts, attributes, and relationships logically to help machines deeply understand data.

6. Common Clinical Ontologies and Terminologies

Use Case	Ontology/Standard	Examples
Diagnoses	SNOMED CT, ICD, Orphanet, NCIT	Breast carcinoma, Rare genetic diseases

Use Case	Ontology/Standard	Examples
Phenotypic abnormalities	Human Phenotype Ontology (HPO)	Specific clinical symptoms
Medications	RxNorm, DrugBank, ChEMBL	Panobinostat (a drug)
Adverse drug reactions	Ontology of Adverse Events (OAE)	Injection-site reaction
Procedures	Medical Dictionary for Regulatory Activities (MedDRA)	Cardiac surgery
Lab tests	LOINC	Serum creatinine measurement
Imaging data	DICOM, RadLex	Bone thinning in X-rays

7. What are Ontologies?

- Ontologies provide both a **shared vocabulary** and the **rules/constraints** for how those terms relate.
- They define:
 - **Concepts** (things like diseases, symptoms).
 - **Attributes** (characteristics like severity, location).
 - **Relationships** (e.g., a disease *affects* a body part).
- Use **description logic** to allow computers to reason about data meaningfully.

8. **SNOMED CT: A Key Clinical Ontology**

- Most **comprehensive clinical healthcare terminology** worldwide.
- Used **in over 80 countries for EHR documentation and reporting**.
- Includes **>300,000 concepts grouped into 10 axes**:
 - **Topography** (body parts)
 - **Morphology** (cell/tissue changes)
 - **Organisms** (bacteria, viruses)
 - **Chemicals and drugs**
 - **Signs and symptoms**
 - **Diagnoses**
 - **Procedures**
 - **Social context and jobs**
 - **Devices and agents**
 - **General qualifiers**
- Concepts have:
 - **Unique machine-readable IDs**.
 - **Human-readable names (Fully Specified Name and synonyms)**.
 - **Relationships to define meaning precisely**.
- Allows **pre-coordinated terms** (single codes) or **post-coordinated expressions** (combining codes for more detail).

9. How Ontologies Help Computer Understand Clinical Data

- Example: Viral pneumonia defined as
 - A type of infective pneumonia.
 - Caused by a virus.
 - Found in the lungs.
 - This logical structure helps in advanced querying, inference, and decision support.
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10. Clinical Data Integration Examples

- Johns Hopkins initiatives use such standards and ontologies to:
 - Combine COVID-19 patient data from many hospitals.
 - Create detailed, computable common data models.
 - Help researchers analyze complex medical questions reliably.
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11. Resources for Health Data and Research

- Repositories & data sources include:
 - 4CE Consortium (COVID-19 clinical data).
 - Figshare, GitHub COVID-19 data.
 - NIH Data Repositories.
 - MIMIC-III (ICU patient data).
 - Vivli (global clinical trial data sharing platform).
 - Open data accelerates medical research, improves AI models, and supports transparent science.
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12. Summary

- Semantic interoperability makes healthcare data **meaningful and shareable** across systems.
 - Controlled vocabularies and ontologies like SNOMED CT allow computers to **understand complex clinical concepts**.
 - This understanding powers:
 - Better clinical decision-making.
 - Advanced AI in healthcare.
 - Collaborative research.
 - Standards adoption is essential as medicine becomes more data-driven and digital.
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Thanks for following along!

Computing for Medicine, Lecture 5: SNOMED CT

Computing for Medicine - Lecture 5

Overview

SNOMED CT (Systematized Nomenclature of Medicine Clinical Terms) is a comprehensive, multilingual clinical healthcare terminology system designed to support the electronic exchange of clinical health

information.

1. Core Architecture: Concepts and Descriptions

Concepts - The Foundation

- **Definition:** Clinical meanings that remain constant and unchanging
- **Characteristics:**
 - SNOMED CT is fundamentally concept-oriented
 - Each concept has a unique machine-readable Concept ID
 - Concepts represent clinical ideas independent of language or presentation

Descriptions - Human Interface

Purpose: Provide human-readable representations of concepts

Types of Descriptions:

1. Fully Specified Name (FSN)

- **Purpose:** Unique and unambiguous identification
- **Target Audience:** NOT for end users (technical/administrative use)
- **Format:** Contains suffix in parentheses indicating primary hierarchy
- **Example:** myocardial infarction (disorder)
- **Importance:** Ensures precise concept identification across systems

2. Display Term

- **Purpose:** User-friendly representation in specific language
- **Format:** Often the FSN without the hierarchical suffix
- **Example:** myocardial infarction (derived from FSN above)
- **Usage:** Primary term shown to clinicians and patients

3. Synonyms

- **Purpose:** Alternative ways to express the same concept
 - **Classification:**
 - **Preferred:** Recommended alternative term
 - **Acceptable:** Valid but not preferred alternative
 - **Benefit:** Accommodates different clinical practices and regional variations
-

2. Relationship Structure

Supertype Relationships (IS-A Hierarchy)

- **Universal Rule:** Every concept (except root) has a supertype
- **Concept ID:** 116680003 for the [is a] relationship itself

- **Function:** Creates taxonomic hierarchy for inheritance and classification
- **Example Hierarchy:**

Clinical Finding → Disorder → Cardiovascular Disorder → Myocardial Infarction

Defining Attributes

- **Purpose:** Specify additional characteristics beyond hierarchy
- **Usage:** Combined with supertype to fully define concepts
- **Examples:**
 - Location attributes (e.g., "finding site")
 - Temporal attributes (e.g., "onset")
 - Severity attributes

3. Concept Definition Completeness

Sufficiently Defined Concepts

- **Criteria:** Defining relationships are adequate to distinguish from:
 - All supertype concepts
 - All sibling concepts (same level in hierarchy)
- **Implication:** Can be automatically classified by reasoning systems
- **Benefit:** Enables precise automated inference

Primitive Concepts

- **Definition:** NOT fully defined by their relationships
- **Limitation:** Lack unique relationships to distinguish from parent/sibling concepts
- **Example:** "Pneumonia" without specific defining characteristics
- **Current State:** Large portions of SNOMED CT remain primitive
- **Impact:** Requires manual classification and limits automated reasoning

Equivalence Principle

- **Rule:** Concepts with identical defining characteristics are either:
 - Equivalent to each other, OR
 - One is a subtype of the other
- **Importance:** Maintains logical consistency in the terminology

4. Clinical Expression Methods

Pre-coordinated Expressions

- **Definition:** Single concept identifier represents complete clinical idea

- **Format:** `ConceptID |Concept Name|`
- **Advantages:**
 - Simple to use
 - Standardized representation
 - Fast lookup
- **Limitations:**
 - May not capture all clinical nuances
 - Limited specificity for complex cases

Post-coordinated Expressions

- **Definition:** Combination of multiple concept identifiers for complex meaning
- **Structure:**

```
Primary Concept : Attribute = Value, Attribute = Value
```

- **Components:**
 - **Primary Concept:** Main clinical idea
 - **Colon (:)** : Indicates refinement
 - **Attributes:** Qualifying characteristics (comma-separated)
 - **Values:** Specific values for each attribute
- **Example Structure:**

```
Fracture : Finding site = Femur, Severity = Complete
```

When to Use Each Method

- **Pre-coordinated:** Standard, common clinical concepts
- **Post-coordinated:** Complex, specific, or unusual clinical situations

5. Description Logic Foundation

Logical Framework

- SNOMED CT is built on formal description logic principles
- Enables:
 - Automated reasoning
 - Consistency checking
 - Logical inference
 - Quality assurance

Benefits of Description Logic

- **Computational:** Machine processing and validation
 - **Clinical:** Supports clinical decision support systems
 - **Interoperability:** Consistent interpretation across systems
 - **Quality:** Identifies inconsistencies and gaps
-

6. SNOMED CT Axes (Historical Context)

Historical Development

- SNOMED CT evolved from earlier SNOMED versions
 - Previous versions used multi-axial structure (3.5 axes mentioned)
 - Current version maintains conceptual organization while improving logical structure
-

7. Practical Applications

Clinical Documentation

- Enables precise coding of:
 - Diagnoses
 - Procedures
 - Findings
 - Symptoms

Healthcare Interoperability

- Facilitates data exchange between:
 - Electronic Health Records (EHRs)
 - Healthcare institutions
 - Different countries/regions

Analytics and Research

- Supports:
 - Population health studies
 - Clinical research
 - Quality measurement
 - Epidemiological analysis
-

8. Implementation Considerations

System Integration

- Requires mapping to local terminologies
- May need customization for specific clinical domains
- Integration with existing workflow systems

User Training

- Clinicians need education on proper concept selection
- Understanding of pre- vs. post-coordination
- Awareness of synonym options

Quality Assurance

- Regular updates and maintenance
 - Consistency checking
 - Gap identification and resolution
-

9. Future Directions

Ongoing Development

- Continuous expansion of sufficiently defined concepts
- Enhanced logical definitions
- Improved multilingual support

Technology Integration

- Natural language processing applications
 - Artificial intelligence systems
 - Clinical decision support enhancement
-

Key Takeaways

1. **Concept Stability:** Clinical concepts remain constant while descriptions provide flexible human interface
 2. **Hierarchical Organization:** IS-A relationships create logical taxonomy
 3. **Expression Flexibility:** Both simple (pre-coordinated) and complex (post-coordinated) expressions supported
 4. **Logical Foundation:** Description logic enables automated reasoning and quality assurance
 5. **Ongoing Evolution:** Continuous improvement toward more complete logical definitions
-

Study Tips

- Focus on understanding the relationship between concepts and descriptions
- Practice identifying when to use pre- vs. post-coordinated expressions
- Understand the importance of the FSN suffix for concept classification
- Remember that many concepts are still "primitive" and require ongoing development

Phenotype Algorithms Using Electronic Health Records and Natural Language Processing

Overview

Source: BMJ 2015;350:h1885 - Liao et al.

Key Concept: Developing algorithms to accurately identify patients with specific diseases/phenotypes using EHR data, incorporating both structured data and natural language processing (NLP) of clinical notes.

Background & Motivation

Why EHR-Based Phenotype Algorithms?

- **Primary Driver:** Increasing use of EMRs creates opportunities for clinical/translational research
- **Applications:** Pharmacovigilance, genetic association studies, pharmacogenetics
- **Advantage:** Can assemble cohorts faster (12-18 months) vs. years for prospective studies
- **Challenge:** Need accurate phenotype identification from EMR data

Data Types in EMRs

1. Structured Data (readily available/searchable):

- ICD-9/10 codes, CPT codes
- Electronic prescriptions
- Laboratory values
- Vital signs

2. Unstructured Data (requires NLP):

- Clinical notes (progress notes, discharge summaries)
 - Radiology reports
 - Pathology reports
 - Family/social history
-

Natural Language Processing (NLP) Fundamentals

What NLP Does

- **Core Function:** Computational method to extract information from text using linguistic rules
- **Process:** Breaks sentences → identifies parts of speech → applies linguistic rules → extracts meaning
- **Key Task:** Identifies "concepts" in clinical text (e.g., "atrial fibrillation" and "auricular fibrillation" = same concept)

Advantages of NLP

1. **Data Availability:** Captures information not in structured data or where structured data accuracy is low
2. **Systematic Linking:** Links multiple terms to single concepts (e.g., "tobacco," "pack-year," "cigarettes" → smoking)
3. **Standardization:** Uses databases like SNOMED CT and RxNorm to standardize terminology

Key Terminology Resources

Resource	Purpose	Example
UMLS	Unified Medical Language System - links standardized biomedical terms	Maps concepts to unique identifiers
SNOMED CT	Systematized Nomenclature of Medicine - organizes health terminologies	Body structure, clinical findings
RxNorm	Normalized clinical drug names	Links simvastatin to Zocor, combination pills

NLP Software Systems (Open Source)

- **cTAKES**: Apache clinical Text Analysis and Knowledge Extraction System
- **HITex**: Health Information Text Extraction system

Methodology: i2b2 Approach

Step 1: Define Research Question

- **Example**: Rheumatoid arthritis genetic risk factors study
- **Goal**: High positive predictive value (PPV >90%) for adequate power
- **Consideration**: Balance between accuracy and sample size

Step 2: Create Sensitive Data Mart

- **Problem**: Low disease prevalence ($\leq 1\%$) in general population limits PPV
- **Solution**: Screen for patients with ANY data suggestive of phenotype
- **Method**: Clinical domain experts determine screening components
- **Example**: Multiple sclerosis screen includes ICD-9 codes for MS, encephalitis, demyelinating diseases

Step 3: Develop Algorithm Variables

1. **Customized Dictionary**: Clinical experts create comprehensive term list
2. **Structured Mapping**: Convert terms to ICD-9, CPT codes, prescriptions, labs
3. **Negative Predictors**: Include phenotypes with similar presentations
4. **NLP Mapping**: Map terms to UMLS concepts and unique identifiers
5. **Data Integration**: Combine structured + narrative data

Step 4: Create Training Set

- **Selection**: Random sampling from data mart
- **Size Determination**: Based on number of variables and phenotype prevalence
- **Gold Standard**: Clinical experts manually review and classify patients
- **Criteria**: Use validated classification criteria when available (e.g., ACR criteria for RA)

Step 5: Develop Classification Algorithm

- **Method**: Adaptive LASSO penalized logistic regression

- **Output:** Probability score (0-1.0) for each patient
- **Formula Example:**

Logit(probability of PA) = intercept - 0.16(sex) + 0.73 log(1 + (NLP PA)) + 0.88 log(1 + (ICD-9 PA)) + 0.63(NLP treatment) + ...

- **Threshold Setting:** Adjustable based on research goals (specificity 90-97%)

Step 6: Validation

- **Validation Set:** All predicted cases + 50% random patients from data mart
- **Blinding:** Reviewers blinded to algorithm results
- **Criteria:** Same classification criteria as training set

Key Performance Metrics

Primary Metrics

- **Positive Predictive Value (PPV):** Accuracy of algorithm
- **Sensitivity:** Proportion of true cases identified
- **Specificity:** Proportion of true non-cases identified

PPV Formula *Prevalence :the fact that something is very common or happens often.

PPV = (sensitivity × prevalence) / [sensitivity × prevalence + (1-specificity) × (1-prevalence)]

Trade-offs

- Lower specificity threshold → more patients classified → potential for better power
- Higher specificity → fewer patients but higher accuracy

NLP Impact: Results from i2b2 Studies

Performance Comparison

Phenotype	Algorithm Type	Sensitivity	PPV	Cohort Size
Crohn's Disease	Structured only	64%	98%	-
	Structured + NLP	72%	98%	-
Ulcerative Colitis	Structured only	60%	97%	4,183
	Structured + NLP	73%	97%	5,522

Phenotype	Algorithm Type	Sensitivity	PPV	Cohort Size
Multiple Sclerosis	Structured only	68%	94%	-
	Structured + NLP	78%	95%	-
Rheumatoid Arthritis	Structured only	51%	88%	3,046
	Structured + NLP	63%	94%	3,585

Key Findings

1. **Universal Improvement:** NLP improved ALL algorithms
2. **Mechanism:** Added independent predictive variables, increased sensitivity
3. **Greatest Impact:** When structured data accuracy is low (e.g., RA ICD-9 PPV = 19%)
4. **Moderate Impact:** When structured data already accurate (e.g., UC ICD-9 PPV = 64%)

Implementation Considerations

Required Team Members

1. **Clinical Investigator:** Domain expertise, phenotype definition
2. **Biostatistician:** Algorithm development, performance evaluation
3. **EMR Informatician:** Data extraction, healthcare system specifics
4. **NLP Expert:** Text processing, concept mapping

Resource Requirements

- **Infrastructure:** Research copy of EMR, secure servers, terabytes of storage
- **Time:** Mapping clinical terms to NLP concepts is rate-limiting
- **Expertise:** Specialized team with multidisciplinary skills

Limitations

1. **Resource Intensive:** Time and expertise for variable identification/extraction
2. **Mapping Complexity:** Clinical terms to NLP concepts requires significant effort
3. **System Specific:** May require adaptation for different EMR systems
4. **Limited Testing:** Method tested on defined diseases, not extensively on outcomes like drug response

Applications and Future Directions

EMR Research Platform Benefits

1. **Speed:** 12-18 months vs. years for prospective cohorts
2. **Rare Diseases:** Particularly valuable for uncommon conditions
3. **Biorepository Integration:** Links clinical + genomic data
4. **Hypothesis Testing:** Traditional clinical/genetic association studies
5. **Hypothesis Generation:** Phenome-wide association studies (PheWAS)

Multi-institutional Applications

- **eMERGE Network**: Electronic Medical Records and Genomics
 - **Portability**: Algorithms can be applied across institutions
 - **Collaborative Studies**: Enable multicenter research
-

Practical FAQs

Institutional Requirements

- **EMR Capabilities**: Advanced EMR with billing codes, e-prescriptions, lab values, narrative notes
- **Technical Infrastructure**: Programmers, relational database expertise, secure research environment
- **Hardware**: Secure servers, terabytes of storage space

Team Assembly

- **Core Team**: Biostatistician, clinical researcher, EMR informatician, NLP expert
 - **Communication**: Regular team meetings essential for multidisciplinary coordination
 - **Common Ground**: Establish shared terminology (e.g., NLP "precision" = PPV, "recall" = sensitivity)
-

Key Takeaways

1. **NLP is Valuable**: Consistently improves algorithm performance across all phenotypes
2. **Team Approach**: Requires multidisciplinary collaboration with regular communication
3. **Context Matters**: NLP impact greatest when structured data accuracy is poor
4. **Flexibility**: Probability-based approach allows threshold adjustment for different research goals
5. **Validation Critical**: Always validate with expert review on independent dataset
6. **Resource Planning**: Significant infrastructure and expertise requirements
7. **Future Potential**: Promising for clinical/translational research, particularly rare diseases

Best Practices

- Start with comprehensive screening to create sensitive data mart
- Include both positive and negative predictors
- Use validated clinical criteria when available
- Plan for iterative refinement of variable mapping
- Consider research goals when setting specificity thresholds
- Always validate with blinded expert review

Computing for Medicine - Quiz 1 Study Notes

1. FAIR Data Principles

FAIR stands for: **F**indable, **A**ccessible, **I**nteroperable, & **R**eusable

- **Findable**: Data should be easy to find by both humans and computers
- **Accessible**: Data should be retrievable by standard protocols
- **Interoperable**: Data should be compatible with other datasets and systems

- **Reusable:** Data should have clear licensing and metadata for reuse
-

2. Interoperability Concepts

Definition

Interoperability: The ability of two or more systems or components to exchange information and use the information that has been exchanged.

Levels of Interoperability (Increasing Complexity)

1. **Syntactic** - Format/structure compatibility
2. **Semantic** - Meaning/content compatibility
3. **Process** - Workflow/business logic compatibility
4. **Human** - User interface/experience compatibility

Network Effect Formula

For **n hospitals** each with different standards:

- **Number of inter-hospital mappings = $n(n-1)/2$**
 - **Example: 12 hospitals = $12(11)/2 = 66$ mappings**
-

3. Healthcare Data Standards

HL7 (Health Level 7)

- **Purpose:** **Standard for exchanging healthcare information**
- **Structure:**
 - Pipe-delimited messages (|)
 - First line always: **Message Header (MSH)**
 - Multiple segments per message allowed
 - Contains numbers, text, symbols within delimiters
- **Use:** Primarily for data exchange between medical equipment

ECG Data Standard

- **Standard Used:** **HL7** (for communicating ECG machine data)
-

4. FHIR (Fast Healthcare Interoperability Resources)

Core Components

- **Base-address:** Identifies a FHIR system service/server
- **Type:** Resource type
- **Id:** Unique identifier
- **URL:** Resource location

Mandatory FHIR Resource Elements

Required:

- Identifier
- Human Readable Summary
- Profile

NOT Mandatory:

- URL link

FHIR Resource Categories

a> Conformance Resources

- **Purpose:** Describe how a system does or should work
- **Examples:** ValueSet, Conformance, StructureDefinition

b> Administration Resources

- **Purpose:** Manage administrative side of healthcare
- **Examples:** Patient, Order, OrderResponse

c> Clinical Resources

- **Purpose:** Clinical summaries, record keeping, and planning
- **Examples:** Observation, Condition, CarePlan, AllergyIntolerance

d> Financial Resources

- **Purpose:** Support financial services in healthcare provision
- **Examples:** Claim, Coverage, ExplanationOfBenefit

Patient Resource

Purpose: Exchange demographic and administrative information of individuals receiving care or healthcare services

Profiles

Definition: Help constrain FHIR resources for specific use cases and specify restrictions

- Used when building FHIR apps for specific contexts (e.g., rural primary healthcare)

5. EHR Meta-Model Components

Functional Component

- **Includes:** Administrative discharge and billing features
- **Purpose:** Operational healthcare functions

Component Types

- **Organizational:** Structure and governance
 - **Information System:** Technical infrastructure
 - **Functional:** Operational features (discharge, billing)
 - **Data Model:** Data structure and relationships
-

6. ABDM (Ayushman Bharat Digital Mission)

Mission

Create a digital platform for evolving the health ecosystem through wide-range of data, information and infrastructure services while ensuring security, confidentiality and privacy.

Milestones

- **M1, M2, M3:** Progressive implementation phases

Key Stakeholders

1. **Patients**
2. **Health Professionals**
3. **Health Facilities**
4. **Digital Solution Companies**

ABHA System

ABHA Address

- **Purpose:** Manage personal health records
- **Format:** `computingformedicine@abdm`
- **Requirement:** Must create account on HIE-CM (Health Information Exchange - Consent Manager)
- **Domain:** `@abdm` indicates which HIE-CM manages the address

ABHA Number

- **Format:** 14-digit unique number
- **Requirement:** Strong KYC verification required
- **Auto-generation:** Automatically available as `<14digitabhano>@abdm`

ABDM FHIR Stack Components

First Component for Patient Sign-up: **Health Information Providers (HIPs)**

Other Components:

- **Health Information Users (HIUs)**
 - **Consent Manager (CMs)**
 - **Gateway**
-

7. Ontologies and Knowledge Representation

Ontology Structure

Representation: Directed Graph with Cycles

- Allows for complex hierarchical and associative relationships
- Can have circular references and multiple inheritance paths

Ontology vs Knowledge Graph

Key Difference:

- **Ontology:** Generalized model explaining relationships between entities based on common properties (not individuals)
- **Knowledge Graph:** Data-specific, establishes links between actual data points
- **Relationship:** Knowledge Graph = Data + Ontology

Terminology Types

Index

Definition: List of relevant terms pulled directly from unstructured or semi-structured text

- Used for document indexing and search

Other Types

- **Ontology:** Formal representation of knowledge
- **Thesaurus:** Controlled vocabulary with synonyms
- **Terminology:** Systematic collection of terms

Biomedical Ontology Applications

Clinical Decision Support Benefits:

- Computational graphs for querying parent/child terms
 - Synonyms, related terms, and preferred terms for biomedical entities
 - Semantic standardization (not syntactic interoperability)
-

8. SNOMED CT Concepts

Key Characteristics

True Statements:

- Concepts are computational meanings that do not change
- Each concept has at least one "is a" relationship
- Relationship types stored as concepts with SNOMED CT IDs

False Statement:

- **Post-coordinated expressions:** Use MULTIPLE concept identifiers (not single) to represent complex clinical ideas
- **Pre-coordinated:** Use single concept identifier

SNOMED CT Structure

- **Concepts:** Stable computational meanings
 - **Relationships:** "Is a" hierarchies and other semantic links
 - **Descriptions:** Human-readable terms for concepts
-

Key Formulas & Numbers to Remember

1. **Interoperability Mappings:** $n(n-1)/2$ for n systems
 2. **ABHA Number:** 14 digits with strong KYC
 3. **FHIR Resource Categories:** 4 main types (Conformance, Administration, Clinical, Financial)
 4. **Interoperability Levels:** 4 levels (Syntactic → Semantic → Process → Human)
 5. **ABDM Milestones:** M1, M2, M3
 6. **ABDM Stakeholders:** 4 main groups
-

Common Exam Traps & Clarifications**FAIR Principles**

- **Not:** Fair, Flexible, Authenticated, Interactive, Responsive
- **Correct:** Findable, Accessible, Interoperable, Reusable

HL7 Messages

- **Can** have multiple segments per message
- **Cannot** only have one segment per message

FHIR Mandatory Elements

- URL link is **NOT** mandatory
- Profile **IS** mandatory

SNOMED CT Post-coordination

- Uses **multiple** concept identifiers, not single

Ontology Representation

- **Directed graph WITH cycles** (not without cycles)
-

Study Tips

1. **Memorize FAIR acronym** - Frequently tested
2. **Understand interoperability complexity order** - Syntactic < Semantic < Process < Human
3. **Know FHIR resource categories** and examples for each
4. **Remember ABDM key numbers** - 14-digit ABHA, @abdm domain
5. **Distinguish ontology vs knowledge graph** - Conceptual model vs data-specific
6. **Know HL7 message structure** - MSH first, pipe-delimited, multiple segments allowed
7. **Understand mapping formula** - $n(n-1)/2$ for interoperability between n systems

COMPUTING FOR MEDICINE - MOCK QUIZ 2

INSTRUCTIONS:

- Fill your credentials carefully
 - Total marks: 30
 - Time: 45 minutes
 - Number of questions: 20
-

MULTIPLE CHOICE QUESTIONS (1 mark each = 17 marks)

1. In the context of EHR phenotype algorithms, what does PPV stand for and why is it crucial for genetic studies?

a> Patient Phenotype Validation - ensures accurate patient classification b> **Positive Predictive Value - determines algorithm accuracy for statistical power** c> Primary Prevention Variable - identifies risk factors for diseases d> Phenotype Processing Validation - confirms data quality standards

2. Which NLP task is most critical for extracting clinical concepts from unstructured EMR data?

a> Part-of-speech tagging of medical terms b> **Named entity recognition and concept mapping** c> Sentiment analysis of clinical notes d> Text summarization of discharge summaries

3. In FHIR terminology, what is the primary purpose of a "Profile"?

a> To authenticate users accessing FHIR resources b> To encrypt sensitive patient information c> **To constrain and customize FHIR resources for specific use cases** d> To monitor system performance and usage

4. The relationship between PPV and disease prevalence in EMR algorithms is:

a> Inversely proportional - lower prevalence leads to higher PPV b> **Directly proportional - higher prevalence leads to higher PPV** c> Independent - prevalence does not affect PPV d> Exponentially related - small prevalence changes cause large PPV changes

5. Which component of the ABDM framework is responsible for managing patient consent for health data sharing?

a> Health Information Providers (HIPs) b> Health Information Users (HIUs) c> Consent Managers (CMs) d> Gateway services

6. In SNOMED CT, post-coordinated expressions:

a> Use a single concept identifier to represent simple clinical ideas b> Use multiple concept identifiers to represent complex clinical ideas c> Are automatically generated by NLP systems d> Replace the need for pre-coordinated concepts

7. The adaptive LASSO penalized logistic regression method is used in EMR phenotype algorithms to:

a> Clean and preprocess unstructured text data b> Identify predictive variables and assign weights c> Validate algorithm performance on test datasets d> Convert clinical notes to structured data formats

8. Which database standardizes health terminologies and is essential for NLP concept mapping?

a> RxNorm only b> SNOMED CT only c> Unified Medical Language System (UMLS) d> ICD-10 classification system

9. In the i2b2 methodology, a "sensitive data mart" is created to:

a> Store patient data securely with encryption b> Include patients with any evidence of the target phenotype c> Remove patients with incomplete medical records d> Validate the accuracy of structured EMR data

10. The formula $n(n-1)/2$ in healthcare interoperability represents:

a> The number of patients needed for algorithm validation b> The computational complexity of NLP processing c> The number of mappings needed between n different systems d> The minimum sample size for phenotype studies

11. Which FHIR resource category would contain a "Coverage" resource for insurance information?

a> Conformance b> Administration c> Clinical d> Financial

12. Natural Language Processing improves EMR phenotype algorithms most significantly when:

a> The EMR contains mostly structured data b> Structured data accuracy for the phenotype is already high c> Structured data accuracy for the phenotype is low d> The patient population is very large

13. In HL7 message structure, segments are:

a> Always limited to one per message transmission b> Separated by comma delimiters c> Multiple segments allowed per message with pipe delimiters d> Encrypted for security purposes

14. The primary advantage of using probability thresholds in EMR algorithms over Boolean approaches is:

a> Faster computation time b> Better data security c> Adjustability based on research objectives d> Simplified implementation process

15. ABHA numbers in the ABDM framework:

a> Are 12-digit identifiers with basic verification b> Are 14-digit unique identifiers requiring strong KYC c> Can be shared among family members d> Are automatically generated without verification

16. Which type of EMR data typically requires manual medical record review without NLP?

a> ICD-9 diagnostic codes b> Electronic prescription data c> Laboratory test results d> Narrative clinical notes

17. In healthcare ontologies, the "is a" relationship represents:

a> Temporal sequences between medical events b> Causal relationships between diseases c> Hierarchical classification structures d> Geographic distribution of health conditions

SHORT ANSWER QUESTIONS

18. Explain the difference between pre-coordinated and post-coordinated expressions in SNOMED CT with one example each. (3 marks)

Answer: *[Space for student answer]*

19. Describe the validation methodology used in the i2b2 approach for EMR phenotype algorithms. Include the composition of the validation set and the importance of blinding. (5 marks)

Answer: *[Space for student answer]*

20. Compare and contrast the four levels of healthcare data interoperability (Syntactic, Semantic, Process, Human) with specific examples from healthcare systems. (5 marks)

Answer: *[Space for student answer]*

ANSWER KEY

Multiple Choice Answers:

1. b> Positive Predictive Value - determines algorithm accuracy for statistical power
2. b> Named entity recognition and concept mapping
3. c> To constrain and customize FHIR resources for specific use cases
4. b> Directly proportional - higher prevalence leads to higher PPV

5. c> Consent Managers (CMs)
6. b> Use multiple concept identifiers to represent complex clinical ideas
7. b> Identify predictive variables and assign weights
8. c> Unified Medical Language System (UMLS)
9. b> Include patients with any evidence of the target phenotype
10. c> The number of mappings needed between n different systems
11. d> Financial
12. c> Structured data accuracy for the phenotype is low
13. c> Multiple segments allowed per message with pipe delimiters
14. c> Adjustability based on research objectives
15. b> Are 14-digit unique identifiers requiring strong KYC
16. d> Narrative clinical notes
17. c> Hierarchical classification structures

Short Answer Answers:

18. SNOMED CT Expressions (3 marks)

- **Pre-coordinated:** Single concept identifier represents a complete clinical idea
 - Example: "Pneumonia" = single SNOMED CT code
- **Post-coordinated:** Multiple concept identifiers combined to represent complex clinical ideas
 - Example: "Pneumonia" + "caused by" + "Streptococcus pneumoniae" = multiple codes combined

19. i2b2 Validation Methodology (5 marks)

- **Validation Set Composition:** All patients classified with the phenotype + additional 50% random patients from data mart
- **Review Process:** Clinical domain experts manually review all patients using same criteria as training set
- **Blinding:** Reviewers are blinded to algorithm classification results to prevent bias
- **Performance Estimation:** Algorithm performance calculated based on validation set results
- **Importance:** Provides unbiased assessment of algorithm accuracy and generalizability

20. Healthcare Data Interoperability Levels (5 marks)

- **Syntactic:** Format and structure compatibility
 - Example: HL7 message format standards, XML vs JSON data formats
- **Semantic:** Meaning and content compatibility
 - Example: SNOMED CT for standardized medical terminology, ICD coding systems
- **Process:** Workflow and business logic compatibility
 - Example: Clinical decision support workflows, care coordination protocols
- **Human:** User interface and experience compatibility
 - Example: Consistent EHR interfaces, standardized clinical workflows for staff

CM2

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 - Distributed Representations of Words and Phrases and their Compositionality
 - Open Source Code: Multiple Implementations
 - Words in Vector Space (Example Embedding)
 - Summary of Embeddings
 - Pretrained Embeddings for Clinical Data and Concepts
 - Available Models
 - Evaluation Tasks for Word Embeddings
 - Sequence Models and Transformers
 - Sequence to Sequence Modeling — Encoder-Decoder Framework
 - Example
 - Structure
 - Steps
 - Attention and Transformer Architecture
 - "Attention Is All You Need" (Vaswani et al., 2017)
 - Transformer Structure (Block Diagram)
 - Input Embeddings (Sample Words)
 - Positional Encoding
 - Attention Mechanism
 - Principle
 - Self Attention
 - Query, Key, and Value Representation
 - Masked Attention
 - Resources
 - End of Lecture
- Computing for Medicine, Lecture 8: Transformer (Continued)
 - Recap: Transformer Architecture
 - Complete Transformer Structure
 - Key Components Flow
 - Scaled Dot Product Attention (Similarity with Context)
 - Mathematical Formula
 - Components Explained
 - Processing Steps
 - Visual Example
 - Mechanics of Attention - Step by Step
 - Step 1: Generate Similarity Score
 - Step 2: Scale and Softmax
 - Step 3: Retrieve the Values (Output Embeddings)
 - Analogies for Understanding Query, Key, Value
 - Library Analogy
 - Practical Example
 - Masked Attention
 - Purpose
 - Look-Ahead Mask
 - Matrix Representation
 - Sequence Processing
 - Multi-Head Attention

- Architecture
- Mathematical Process
- Key Insight
- Benefits
- Positional Encodings
 - Problem Statement
 - Mathematical Formulas
 - Key Properties
 - Visual Pattern
- Feed Forward Layers
 - Mathematical Formula
 - Components
 - Key Characteristics
 - Purpose
- Dropout
 - Application Points
 - Specific Locations
 - Purpose
- Complete Architecture Summary
 - Encoder Stack (Nx layers)
 - Decoder Stack (Nx layers)
 - Input Processing
 - Output Generation
- Key Technical Details
 - Dimensions and Scaling
 - Attention Types
 - Training vs Inference
- References and Additional Resources
- Lecture 9: BERT — Bidirectional Encoder Representations from Transformers
 - Recap: Sequence-to-Sequence Models
 - BERT: Pre-training of Deep Bidirectional Transformers for Language Understanding
 - Key Concepts
 - Input Structure
 - Pre-training Process
 - Fine-tuning Process
 - BERT & the GLUE Benchmark
 - GLUE Tasks Examples
 - BERT Training Steps for GLUE
 - Specialized BERT Models for Biomedical Domain
 - BioBERT
 - BioBERT Workflow
 - Pre-training Corpora
 - Corpus Combinations
 - BioBERT Downstream Tasks
 - Clinical Domain-Specific BERT Models
 - ClinicalBERT & Embeddings
 - Performance Snapshot
 - UMLS BERT — Clinical Domain Knowledge Augmentation
 - PEGASUS — Pre-training for Abstractive Summarization
 - Core Idea
 - Performance
 - Example: BBC News Article
 - Embeddings in Biomedical NLP
 - Concept and Word Embeddings
 - Evaluation Tasks
 - References and Useful Links
 - Summary
- Lecture 10: Shock Modes
 - AI for Multimodal Healthcare Data
 - Why AI in Healthcare?

- Types of Healthcare Data
 - Examples of Data Types
 - Case Study – ShockModes
 - Shock: What is it?
 - Causes of Shock
 - Importance of Early Treatment
 - Shock Index (SI)
 - ShockModes Goal
 - Workflow
 - Dataset - MIMIC-III Clinical Database Details
 - Features from Notes
 - Features from Vitals
 - Model Development and Validation
 - SHAP Analysis for Interpretability
 - Example Feature List with SHAP Impact (selected features):
 - Evaluation Parameters
 - Summary
- Automating the Transformation of Free-Text Clinical Problems into SNOMED CT Expressions
 - Authors
 - Abstract
 - Introduction
 - Background & Related Work
 - Controlled Vocabulary in Clinical Problems
 - Previous Approaches
 - Methods
 - 1. Concept Extraction
 - 2. Focus Concept Selection
 - 3. Relation Identification
 - Deep Learning Approaches
 - Model Architecture
 - Training
 - Evaluation
 - Experiment 1: BiLSTM & CNN vs Naïve Bayes
 - Experiment 2: BiLSTM vs Kate's SVM Model
 - Experiment 3: Real-World Text Corpus
 - Experiment 4: Focus Concept Selection – Dependency Parsing Models
 - Discussion
 - Conclusion
 - Limitations
 - Acknowledgment
 - References
- Language Models as Ontology Encoders
 - Authors & Affiliations
 - Abstract
 - 1. Introduction
 - Two Main Paradigms
 - 1. Geometric Model-Based Methods
 - 2. Language Model-Based Methods
 - Motivation & Solution
 - 2. Related Work
 - Geometric Model-Based Methods
 - Language Model-Based Methods
 - Exclusion
 - 3. Preliminary
 - 3.1 Ontology
 - Example 1
 - Normalization
 - Example 2 (Normalization)
 - Inference
 - 3.2 Hyperbolic Space

- 4. Methodology
 - 4.1 Verbalisation-based Concept Embedding
 - 4.2 Logic-aware Role Embedding
 - 4.3 Training
 - Hierarchy Loss
 - Training & Evaluation
- 5. Evaluation
 - 5.1 Experiment Setting
 - Dataset Statistics (Table: Train/Val/Test axiom counts)
 - Baselines Compared
 - Metrics
 - Protocol
 - 5.2 Prediction Task Results
 - 5.3 Inference Task Results
 - 5.4 Other Results
 - Ablation Study (Language Model Choice)
 - Transfer Learning
 - Case Study (Real Ontology Construction)
- 6. Conclusion & Future Work
- References
- UmlsBERT: Clinical Domain Knowledge Augmentation of Contextual Embeddings
 - Authors
 - Abstract
 - 1. Introduction
 - 2. Related Work
 - 2.1 Contextual Word Embeddings
 - 2.2 Contextual Clinical Embeddings
 - 3. Data
 - 4. Methods
 - 4.1 BERT Model Recap
 - 4.2 Enhancing Contextual Embeddings with Clinical Knowledge
 - Semantic Group Embeddings
 - Updating MLM Loss with CUI Connections
 - 4.3 UmlsBERT Training
 - 5. Results
 - 5.1 Downstream Clinical NLP Tasks
 - 5.2 Qualitative Embedding Comparisons
 - 5.3 Semantic Group Embedding Visualization
 - 6. Conclusion and Future Work
 - References
- BioBERT: Pre-trained Biomedical Language Model for Biomedical Text Mining
 - Abstract
 - Motivation
 - Results
 - Availability
 - Introduction
 - Approach
 - Contributions
 - Materials and Methods
 - BERT: Bidirectional Encoder Representations from Transformers
 - Pre-Training BioBERT
 - Table 1: Text Corpora Used
 - Table 2: Pre-training Combinations
 - Fine-tuning BioBERT
 - Results
 - Datasets
 - Experimental Setups
 - Experimental Results
 - NER Results (Table 6 Highlight)
 - RE Results (Table 7 Highlight)

- QA Results (Table 8 Highlight)
- Discussion
- Conclusion
- Funding
- References
- Attention Is All You Need
 - Abstract
 - 1. Introduction
 - 2. Background
 - 3. Model Architecture
 - Encoder-Decoder Structure
 - Encoder
 - Decoder
 - 3.2 Attention
 - Attention Function
 - 3.2.1 Scaled Dot-Product Attention
 - 3.2.2 Multi-Head Attention
 - 3.2.3 Use in Model
 - 3.3 Position-wise Feed-Forward Networks
 - 3.4 Embeddings and Softmax
 - 3.5 Positional Encoding
 - 4. Why Self-Attention
 - Complexity, Sequential Operations, Max Path Length
 - 5. Training
 - 5.1 Data and Batching
 - 5.2 Hardware and Schedule
 - 5.3 Optimizer
 - 5.4 Regularization
 - 6. Results
 - 6.1 Machine Translation
 - 6.2 Model Variations
 - 6.3 English Constituency Parsing
 - 7. Conclusion
 - Appendix: Attention Visualizations
 - References
 - Key Equations/Blocks
 - Scaled Dot-Product Attention
 - Position-wise Feed Forward
 - Positional Encoding
 - Learning Rate
- LLMonFHIR: A Physician-Validated, LLM-Based Mobile Application for Querying Patient Electronic Health Data
 - Authors and Affiliations
 - Abstract
 - Background
 - Objectives
 - Methods
 - Results
 - Conclusions
 - Keywords
 - Introduction
 - Importance of EHR Access
 - Existing Barriers
 - Need for Innovative Solutions
 - LLMonFHIR Overview
 - Concept and Technology
 - Technical Implementation
 - Handling Large Data and Context Challenges
 - Application User Interface
 - Physician Evaluation Study
 - Study Design

- [Standard Questions Evaluated](#)
- [Scoring Method](#)
- [Results](#)
 - [Scores Summary](#)
 - [Strengths Noted](#)
 - [Limitations Noted](#)
- [Discussion](#)
 - [Interpretation](#)
 - [Challenges](#)
 - [Privacy and Deployment Considerations](#)
 - [Impact on EHR Access](#)
- [Study Limitations](#)
- [Conclusions](#)
- [Data and Software Availability](#)
- [Acknowledgments](#)
- [References](#)
- [Appendices and Figures \(Descriptions\)](#)
 - [Central Illustration](#)
 - [Table 1: Synthetic FHIR Patient Datasets Summary](#)
 - [Table 2: Physician Evaluator Questions](#)
 - [Figure 1: User Interface Samples](#)
 - [Figure 2: Physician Score Distribution](#)
 - [Figure 3: Example LLMonFHIR Responses](#)
- [Competency Statements](#)
 - [Medical Knowledge](#)
 - [Patient Care](#)
 - [Translational Outlook](#)
- [Summary](#)

Quiz 1 Rubric

- [CMQuiz1.pdf](#) Read it

Computing for Medicine, Lecture 6: Word Vectors and Embeddings for Computing in Medicine

Course: Computing for Medicine
Google Classroom Code: dnd5qkt5
Semester: Monsoon 2025
Lecture: 6

International Classification of Diseases (ICD)

The International Classification of Diseases (ICD) is a globally used diagnostic classification system for epidemiology, health management, and clinical purposes.

ICD-10 Chapter Classifications

Code	ICD-10 Chapter	Range
I	Certain infectious and parasitic diseases	A00-B99
II	Neoplasms	C00-D48
III	Diseases of the blood and blood-forming organs and certain disorders involving the immune system	D50-D89
IV	Endocrine, nutritional and metabolic diseases	E00-E90
V	Mental and behavioral disorders	F00-F99
VI	Diseases of the nervous system	G00-G32
VII	Diseases of the eye and adnexia	H00-H59
VIII	Diseases of the ear and mastoid process	H60-H95

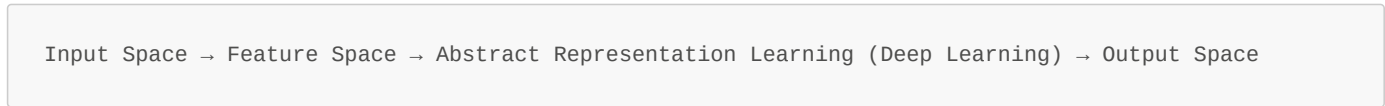
Code	ICD-10 Chapter	Range
IX	Diseases of the circulatory system	I00-I99
X	Diseases of the respiratory system	J00-J99
XI	Diseases of the digestive system	K00-K93
XII	Diseases of the skin and subcutaneous tissue	L00-L99
XIII	Diseases of the musculoskeletal system and connective tissue	M00-M99

ICD Coding for Respiratory System (J00-J99)

Section	Code Range
Acute upper respiratory infections	J00-J06
Influenza and pneumonia	J10-J18
Other acute lower respiratory infections	J20-J22
Other diseases of the upper respiratory tract	J30-J39
Chronic lower respiratory diseases	J40-J47
Lung diseases due to external agents	J60-J70
Other respiratory diseases principally affecting the interstitium	J80-J84
Suppurative and necrotic conditions of the lower respiratory tract	J85-J86
Other diseases of the pleura	J90-J94
Other diseases of the respiratory system	J95-J99

Basic Idea Behind All Modern Representations

Modern representation learning follows a pipeline:



This process transforms raw data into meaningful representations that can be processed by machine learning algorithms.

Word Embeddings

Definition

Word embeddings are mathematical representations of language units that capture semantic meaning and relationships between words.

Types of Word Representations

1. Basic vectorization approaches
2. Distributed representations
3. Universal language representation
4. Handcrafted features

Motivation

The goal is to capture the meaning of language rather than just structure.

Process Steps

1. Break the sentence into lexical units such as lexemes, words, and phrases
2. Derive the meaning for each of the lexical units
3. Understand the syntactic (grammatical) structure of the sentence

4. Understand the context in which the sentence appears

Featurization Methods

One Hot Encoding

One Hot Encoding maps each word to a unique position in a vector where only one element is 1 and all others are 0.

Process

- Map each word $w \rightarrow$ a unique integer wid between 1 and $|V|$
- Each word becomes a V -dimensional binary vector
- Example: Dog = [1 0 0 0 0]
- "Dog Bites Man" = [[1 0 0 0 0] [0 1 0 0 0] [0 0 1 0 0]]

Implementation Example

```
sentences = ["It was the best of times",
             "it was the worst of times",
             "it was the age of wisdom",
             "it was the age of foolishness"]

tokenized_sentences = [[t for t in sentence.split()] for sentence in sentences]
vocabulary = set([w for s in tokenized_sentences for w in s])

import pandas as pd
pd.DataFrame([[w, i] for i, w in enumerate(vocabulary)])
```

```
def onehot_encode(tokenized_sentence):
    return [1 if w in tokenized_sentence else 0 for w in vocabulary]

onehot = [onehot_encode(tokenized_sentence)
          for tokenized_sentence in tokenized_sentences]

for (sentence, oh) in zip(sentences, onehot):
    print("%s: %s" % (oh, sentence))
```

Output Example

```
[0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1]: It was the best of times
[1, 1, 1, 0, 0, 0, 1, 1, 0, 1, 0]: it was the worst of times
[0, 1, 1, 0, 1, 0, 0, 1, 1, 1, 0]: it was the age of wisdom
[0, 1, 1, 1, 1, 0, 0, 1, 0, 1, 0]: it was the age of foolishness
```

Challenges of One Hot Encoding

- Size of a one-hot vector \propto size of the vocabulary $|V|$
- Sparse representations - matrix full of zeroes
- Storage constraints and overfitting due to sparsity
- Does not give fixed length representation
- Assumes independence between words
- Out of Vocabulary (OOV) problem - needs retraining every time a new word is added

Bag of Words (BoW)

Concept

- Assumes that text belonging to a given class in the dataset is characterized by a unique set of words

- Knowing the words present in a text tells about the class (bag)
- Each document is a V-dimensional vector
- Example: "Dog Bites Man" = [1 1 1 0 0 0]

Advantages

- Gives a fixed length representation
- Captures some semantic similarity of documents

Challenges with BoW Representation

- Sparsity
- Same word may mean different things in different contexts
- Out of Vocabulary (OOV) words
- Order information is lost

Bag of N-Grams (BoN)

Purpose

Attempts to preserve context and order information by considering sequences of words.

Example

- Bigrams = {dog bites, bites man, man bites, bites dog, dog eats, eats meat, man eats, eats food}
- "Dog Bites Man" = [1,1,0,0,0,0,0,0]

Types

- Bigram (2 words)
- Trigram (3 words)
- N-gram (n words)

Discriminative vs Generative AI

Discriminative Models

- Learn $p(y|x)$ - probability of output given input
- Focus on decision boundaries

Generative Models

- Learn $p(x,y)$ - joint probability distribution
- Can generate new data samples

Text Generation Models (Large Language Models)

Modern language models can take text input and generate coherent text output, such as summarizing articles.

Probabilistic Autoregressive Models (Traditional Models)

Concept

Traditional language models assign probabilities to word sequences.

Example

For the sentence "John bought a book":

- $p(\text{John, bought, a, book}) = 0.02$
- $p(\text{book, bought, a, John}) = 0.01$
- $p(\text{book, a, John, bought}) = 0.0001$

Sequential Generation

```
John bought a
John bought a book
John bought a book for
John bought a book for coloring
```

Mathematical Formulation

$p(\text{John, bought, a, book}) = p(\text{John}) \times p(\text{bought} \mid \text{John}) \times p(\text{a} \mid \text{John, bought}) \times p(\text{book} \mid \text{John, bought, a})$

Vector Space Paradigm: Distributional Hypothesis

Core Quote

"You shall know a word by the company it keeps!" - Firth (1957)

Distributional Representation

Inducing distributional properties from context to generate a representation. Words that appear in similar contexts tend to have similar meanings.

Core Idea: Vector Space

Key Principles

- Represent words (or tokens) as vectors
- Words with similar meanings have related vector representations
- Associations between words are captured in shared weights
- Vector weights can be trained using neural networks

Word Algebra

Vector representations allow mathematical operations on words:

```
KING - MAN + WOMAN = QUEEN
UNCLE - MAN + WOMAN = AUNT
```

This demonstrates that word vectors capture semantic relationships and analogies.

How Embeddings Capture Context

Word embeddings can distinguish between different meanings of the same word based on context. For example, the word "lie" has multiple meanings:

Different Contexts of "Lie"

Untruth (verb)

- "I will lie for personal benefit"
- "Rob reveals to Tracy that everything was a lie and that he still hated her"

Mathematical Sense (verb)

- "A skew polygon does not lie in a flat plane, but zigzags in three (or more) dimensions"
- "As an open string propagates through spacetime, its endpoints are required to lie on a D-brane"

Lie Down (verb)

- "There Fenrir will lie until Ragnarok"
- "They lie down to sleep deeply"

Geographical (island) - (verb)

- "Some 3,579 islands lie adjacent to the peninsula"
- "The islands lie on the Kerguelen Plateau in the Indian Ocean"

Conceptual Placement (verb)

- "According to Dewey, conversation, debate and dialogue lie at the heart of a democracy"
- "The origins of mathematical thought lie in the concepts of number, magnitude and form"

Geographical (other) - (verb)

- "Very small portions lie within the Pueblo County School District 70"
- "The ruins of the town lie along the river Ziz in the Tafilalt oasis near the town of Rissani"

Word2Vec (Generation 1)

Word2Vec is a popular method for creating word embeddings using neural networks.

Continuous Bag of Words (CBOW)**Concept**

- Predicts the middle word given the context
- Assigns probability to sentences such that "good" sentences are maximized

Example

```
The quick brown fox jumped over the lazy dog
```

Training with CBOW

Source Text: "The quick brown fox jumps over the lazy dog."

Training Samples (context, target):

- ((quick, brown), The)
- ((The, brown, fox), quick)
- ((The, quick, fox, jumps), brown)
- ((quick, brown, jumps, over), fox)

Skip-Gram Variant**Concept**

Predicts the context given the middle word.

Example

```
The quick brown fox jumped over the lazy dog
```

Training with Skip-Gram

Source Text: "The quick brown fox jumps over the lazy dog."

Training Samples (target, context):

- (the, quick)
- (the, brown)
- (quick, the)
- (quick, brown)
- (quick, fox)
- (brown, the)
- (brown, quick)
- (brown, fox)
- (brown, jumps)
- (fox, quick)
- (fox, brown)
- (fox, jumps)
- (fox, over)

Summary

Word vectors represent a fundamental shift from traditional symbolic representations to distributed representations that capture semantic meaning. The evolution from one-hot encoding to sophisticated embedding methods like Word2Vec demonstrates the progression toward more meaningful and efficient representations of language for computational processing.

Key takeaways:

1. Traditional methods like one-hot encoding and bag-of-words have limitations in capturing semantic relationships
2. Distributional hypothesis forms the foundation for modern word embeddings
3. Word2Vec methods (CBOW and Skip-Gram) learn dense vector representations that capture semantic and syntactic relationships
4. Context plays a crucial role in determining word meaning and embeddings capture this through distributional patterns

Computing for Medicine, Lecture 7: Embeddings + Transformers

Google Classroom Code: [dnd5qkt5](#) Monsoon 2025

Word Vectors

Training with CBOW (Continuous Bag of Words)

Source Text:

```
The quick brown fox jumps over the lazy dog.
```

Repeated for multiple training samples.

Training Samples (context, target):

- (quick, brown) → The
- (The, brown, fox) → quick
- (The, quick, fox, jumps) → brown
- (quick, brown, jumps, over) → fox

CBOW Model Architecture

- **Input Layer:** words from context
- **Hidden Layer:** sums up context vectors
- **Output Layer:** predicts the target word
- Dimensionality:
 - N-dim (hidden)
 - V-dim (output)

word2Vec: Skip Gram Variant

- **Skip Gram** predicts the context given the middle word.
- Example text:

The quick brown fox jumped over the lazy dog.

Training Samples (target, context):

- (the, quick)
- (the, brown)
- (quick, the)
- (quick, brown)
- (quick, fox)
- (brown, the)
- (brown, quick)
- (brown, fox)
- (brown, jumps)
- (fox, quick)
- (fox, brown)
- (fox, jumps)
- (fox, over)

Continuous SkipGram Model Architecture

- **Input Layer:** target word
- **Hidden Layer:** context features
- **Output Layer:** context prediction
- Dimensionality:
 - N-dim (hidden)
 - V-dim (output)

Key Papers in Word Embeddings

Efficient Estimation of Word Representations in Vector Space

- **Authors:** Tomas Mikolov, Greg Corrado, Kai Chen, Jeffrey Dean
- **Published by:** Google Inc., Mountain View, CA

Distributed Representations of Words and Phrases and their Compositionality

- **Authors:** Kai Chen, Jeffrey Dean, Tomas Mikolov, Ilya Sutskever, Greg Corrado
- **Published by:** Google Inc.

Open Source Code: Multiple Implementations

- **word2vec project:**
 - Efficient implementation for continuous bag-of-words and skip-gram architectures
 - Used for vector representations of words
- **Quick Start:**
 - Download code via SVN:

```
svn checkout http://word2vec.googlecode.com/svn/trunk
```

- **License:** Apache License 2.0

Words in Vector Space (Example Embedding)

Word	Embedding (example)
------	---------------------

Word	Embedding (example)
pandemic	[0.3, 0.8]
covid	[0.3, 0.7]
hospital	[0.4, 0.5]
football	[0.9, 0.1]

Summary of Embeddings

- **Embeddings capture distributional similarities between words**
- Enable efficient word algebra and analogies
- **Popular Models:**
 - Word2Vec: Pre-trained neural network-based embedding (Unit = Word)
 - GloVe: Pretrained word embedding from Stanford (Unit = Word)
 - FastText: Pretrained embedding from Facebook (Unit = Character)

Pretrained Embeddings for Clinical Data and Concepts

Available Models

Name	Model	Data/Concepts	Terms	Dimension
PubMed-w2v.bin	word2vec	PubMed	2.4M	200
PMC-w2v.bin	word2vec	PubMed Central	25M	200
PubMed-and-PMC-w2v.bin	word2vec	PubMed, PubMed Central	4.1M	200
wikipedia-pubmed-and-PMC-w2v	word2vec	PubMed, PubMed Central, Wikipedia	5.5M	200
drug word embeddings	word2vec	PubMed, DrugBank	553,195	420
AWE-CM [49]	word2vec	UMLS CUI (concepts)	265M	300
claims_codes_hs_300 [55]	word2vec	ICD-9 codes (concepts)	51,327	300
claims_cuis_hs 300 [55]	word2vec	UMLS CUI (concepts)	14,852	300
cui2vec [56]	word2vec/Glove	UMLS CUI (concepts)	108,477	500
concept embeddings [58]	AITextML	MeSH ID (concepts)	26,103	100
word embeddings [58]	AITextML	PubMed	513,196	100
ELMO (PubMed model) [11]	ELMO	PubMed	N/A	1024
BioBERT [15]	BERT	PubMed	N/A	768/1024
ClinicalBERT [16,17]	BERT	MIMIC III	N/A	768

Key Points:

- **ELMO** models use character information
- **BERT** models use sub-word information
- Can represent any concept

Evaluation Tasks for Word Embeddings

- **Evaluation metrics:** relatedness, similarity, cluster quality, conceptual similarity, clinical information extraction, disease prediction, mortality prediction, NER, drug name recognition, high-risk prediction, phenotype classification, term abstraction, etc.
- **Studies:** De Vise et al., Chie et al., Dubois et al., Wang et al., etc.
- **Corpora examples:**
 - PubMed, PMC
 - Mayo Clinic notes, OHSUMED
 - Google News

- MedHelp forum
- Medical claims
- UMLS, MeSH
- MIMIC-III
- Wikipedia

Sequence Models and Transformers

Sequence to Sequence Modeling — Encoder-Decoder Framework

Example

- **INPUT:** Je suis étudiant
- **OUTPUT:** I am a student

Structure

- **Encoder:** Processes input sequence
- **Decoder:** Produces output sequence

Steps

1. Embedding words from input
2. Apply encoder at each time step
3. Use decoder to predict output words step by step

Attention and Transformer Architecture

"Attention Is All You Need" (Vaswani et al., 2017)

- **Main authors:** Ashish Vaswani, Noam Shazeer, Niki Parmar, Llion Jones, Aidan Gomez, Jakob Uszkoreit, Łukasz Kaiser, Illia Polosukhin

Transformer Structure (Block Diagram)

```
Nx layers:  
- Add & Norm  
- Multi-Head Attention  
- Feed Forward  
- Softmax Output  
Input: Embedded sequence + Positional Encoding  
Output: Embedded sequence + Positional Encoding  
Masked Multi-Head Attention in decoder
```

Input Embeddings (Sample Words)

- microwave, refrigerator, bulb, kitchen, light, charger, battery, sink, bathroom, etc.

Positional Encoding

- Adds position information to input embeddings.

Attention Mechanism

Principle

- Context Vector Calculation:
 - For each output token, compute weighted sum over encoder hidden states.
 - Formula:

$$c_i = \sum_j a_{ij} h_j$$

$$a_{ij} = \exp(e_{ij}) / \sum_k \exp(e_{ik})$$

e_{ij} = alignment score for i -th decoder state vs j -th encoder state

Self Attention

- Each word attends to other words in the sequence to capture context.
- Calculation cost: $O(n^2)$ (quadratic in sequence length)

Query, Key, and Value Representation

- For each input, derive three vectors:
 - Query (q)
 - Key (k)
 - Value (v)
- Compute attention scores as dot products of queries and keys:

$$\text{Attention}(Q, K, V) = \text{softmax}(Q \times K^T / \sqrt{d_k}) \times V$$

Masked Attention

- Prevents decoder from attending to future positions
- Look-ahead masking used in generation tasks (next word prediction)

Resources

- Code and downloads:
 - <http://evexdb.org/pmresources/ngrams/PubMed/>
 - <http://evexdb.org/pmresources/ngrams/PMC/>
 - <http://evexdb.org/pmresources/vec-space-models/wikipedia-pubmed-and-PMC-w2v.bin>
 - https://github.com/chop-dbhi/drug_word_embeddings
 - Visual Guides:
 - <https://jalammar.github.io/illustrated-transformer/>
 - <https://becominghuman.ai/attention-is-all-you-need-16bf481d8b5c>
 - <http://peterbloem.nl/blog/transformers>

End of Lecture

Thanks for attending the class!

Computing for Medicine, Lecture 8: Transformer (Continued)

Course: Computing for Medicine

Google Classroom Code: dnd5qkt5

Semester: Monsoon 2025

Lecture: 8 - Transformer (Continued)

Recap: Transformer Architecture

Complete Transformer Structure

The Transformer consists of two main components:

1. **Encoder Stack** (left side)
 - N identical layers ($N \times$)

- Each layer contains:
 - Multi-Head Attention
 - Add & Norm
 - Feed Forward
 - Add & Norm

2. **Decoder Stack** (right side)

- N identical layers (Nx)
- Each layer contains:
 - Masked Multi-Head Attention
 - Add & Norm
 - Multi-Head Attention (encoder-decoder attention)
 - Add & Norm
 - Feed Forward
 - Add & Norm

Key Components Flow

Input → Input Embedding → Positional Encoding → Encoder Stack

Output (shifted right) → Output Embedding → Positional Encoding → Decoder Stack

Decoder Stack → Linear → Softmax → Output Probabilities



Scaled Dot Product Attention (Similarity with Context)

Mathematical Formula

$$\text{Attention}(Q, K, V) = \text{softmax}(QK^T / \sqrt{d_k}) V$$

Components Explained

- **Q (Query):** "What am I asking about?" - the search intent
- **K (Key):** "Where should I look?" - addressing mechanism
- **V (Value):** "What information do I retrieve once I've found the right spots?" - actual content

Processing Steps

1. **Matrix Multiplication:** QK^T
2. **Scaling:** Divide by $\sqrt{d_k}$ (where d_k is dimension of keys)
3. **Softmax:** Convert to probability distribution
4. **Value Retrieval:** Multiply with V matrix

Visual Example

Example sentence: "like this movie very much !"

The attention mechanism processes this through:

- MatMul operation
- Scale by $\sqrt{d_k}$ (where $d=5$ in example)
- Apply SoftMax
- Optional Mask
- Final MatMul with Values



Mechanics of Attention - Step by Step

Step 1: Generate Similarity Score

Like "n judges scoring m keys" - creates similarity matrix between queries and keys.

Step 2: Scale and Softmax

- **Scaling:** Prevents extremely large values that could cause vanishing gradients
- **Softmax:** Turns each row into a probability distribution
- Each row sums to 1.0

Step 3: Retrieve the Values (Output Embeddings)

Use the probability weights to get weighted sum of value vectors.

Analogies for Understanding Query, Key, Value

Library Analogy

Scenario: You're searching for books in a library

- **Key (K):** Book's index card used to locate it
- **Query (Q):** Your search question
- **Value (V):** The actual book content you take home once you've matched the index card

Practical Example

When processing "he bought books":

- "he": 30% attention weight
- "bought": 50% attention weight
- "books": 0.1% attention weight
- "a": 0.1% attention weight
- "boy": 0.1% attention weight

Masked Attention

Purpose

Prevents the decoder from "looking ahead" at future tokens during training.

Look-Ahead Mask

Raw attention weights → Apply mask → Masked attention

Matrix Representation

The mask matrix has:

- 1s for allowed connections
- 0s for blocked connections (future positions)

Example mask pattern:

```
1 0 0 0 0
1 1 0 0 0
1 1 1 0 0
1 1 1 1 0
1 1 1 1 1
```

Sequence Processing

- y1 can only attend to x1
- y2 can attend to x1, x2
- y3 can attend to x1, x2, x3
- And so on...

This ensures that position i can only attend to positions less than i .

Multi-Head Attention

Architecture

Input \rightarrow Linear Transformations (Q, K, V) \rightarrow h parallel attention heads \rightarrow Concat \rightarrow Linear \rightarrow Output

Mathematical Process

1. **Linear Transformations:** Apply separate linear layers to create Q, K, V for each head
2. **Parallel Processing:** Run h attention heads in parallel
3. **Concatenation:** Combine outputs from all heads
4. **Final Linear:** Apply final linear transformation

Key Insight

Mathematical principle: One big linear function, then splitting allows each subspace to compose with the full original vector. Splitting first and then applying linear function restricts the possibilities.

Benefits

- Allows model to attend to information from different representation subspaces
- Each head can learn different types of relationships
- Provides robustness and richer representations

Positional Encodings

Problem Statement

No convolution, no recurrence: Transformer has no inherent sense of position, so we need to add positional information.

Mathematical Formulas

For position pos and dimension i :

```
PE(pos, 2i) = sin(pos / 10000^(2i/d_model))
PE(pos, 2i+1) = cos(pos / 10000^(2i/d_model))
```

Key Properties

- **Even dimensions:** Use sine function
- **Odd dimensions:** Use cosine function
- Creates unique encoding for each position
- Allows model to learn relative positions

Visual Pattern

The positional encoding creates wave-like patterns across dimensions:

- Different frequencies for different dimensions
- Enables the model to distinguish between positions
- Maintains consistent mathematical relationships

Feed Forward Layers

Mathematical Formula

$$\text{FFN}(x) = \max(0, xW_1 + b_1)W_2 + b_2$$

Components

- **First Linear Layer:** $xW_1 + b_1$
- **ReLU Activation:** $\max(0, \dots)$
- **Second Linear Layer:** $\dots W_2 + b_2$

Key Characteristics

- **Fully Connected Dense Layers:** For learning complex patterns
- **Individual Networks:** Each FFN is different for each layer (N_x)
- **Original Paper:** $N_x = 8$ (8 encoder layers, 8 decoder layers)

Purpose

- Processes the attention output
- Adds non-linearity to the model
- Allows for complex feature transformations

Dropout

Application Points

Quote from original paper:

"We apply dropout to the output of each sub-layer before it is added to the sub-layer and normalized. In addition, we apply dropout to the sums of embeddings and positional encodings in both encoder and decoder stacks."

Specific Locations

1. **Sub-layer outputs:** Before Add & Norm operations
2. **Embedding layers:** After combining embeddings with positional encodings
3. **Both stacks:** Applied in encoder and decoder

Purpose

- **Regularization:** Prevents overfitting
- **Robustness:** Makes model less dependent on specific neurons
- **Generalization:** Improves performance on unseen data

Complete Architecture Summary

Encoder Stack (N_x layers)

Each encoder layer contains:

1. Multi-Head Attention
2. Add & Norm
3. Feed Forward Network
4. Add & Norm

Decoder Stack (N_x layers)

Each decoder layer contains:

1. Masked Multi-Head Attention
2. Add & Norm
3. Multi-Head Attention (with encoder)
4. Add & Norm
5. Feed Forward Network
6. Add & Norm

Input Processing

- **Encoder Input:** Input Embedding + Positional Encoding
- **Decoder Input:** Output Embedding (shifted right) + Positional Encoding

Output Generation

- **Final Processing:** Linear layer → Softmax → Output Probabilities
- **Training:** Outputs shifted right for teacher forcing
- **Inference:** Autoregressive generation

Key Technical Details

Dimensions and Scaling

- **dk:** Dimension of key vectors
- **Scaling Factor:** \sqrt{dk} prevents attention weights from becoming too large
- **d_model:** Model dimension used throughout the architecture

Attention Types

1. **Self-Attention (Encoder):** Each position attends to all positions in input
2. **Masked Self-Attention (Decoder):** Each position attends only to earlier positions
3. **Encoder-Decoder Attention:** Decoder attends to encoder representations

Training vs Inference

- **Training:** Uses teacher forcing with shifted outputs
- **Inference:** Generates tokens one by one autoregressively
- **Masking:** Ensures no information leakage from future tokens

References and Additional Resources

- Original reference: <http://nlp.seas.harvard.edu/2018/04/03/attention.html>
- Positional encoding details: <https://timodenk.com/blog/linear-relationships-in-the-transformers-positional-encoding/>
- Transformer visualization: <http://peterbloem.nl/blog/transformers>

Thank you for attending the class!

Lecture 9: BERT — Bidirectional Encoder Representations from Transformers

Recap: Sequence-to-Sequence Models

Transformer architectures enable automated translation and text generation via encoder and decoder components:

- **Transformer Encoder:** Processes input data sequence (e.g., "I love llamas")
- **Transformer Decoder:** Generates output sequence; uses previously generated tokens
- **Self-Attention:** Computes context for each token
- **Feedforward Neural Networks:** Refine representations within both encoder and decoder
- **Masked Self-Attention:** Decoder only attends to known inputs and already generated outputs

BERT: Pre-training of Deep Bidirectional Transformers for Language Understanding

Authors: Jacob Devlin, Ming-Wei Chang, Kenton Lee, Kristina Toutanova (Google AI Language)

Key Concepts

- **Contextualized Word Embeddings:** BERT encoder learns representations from large text corpus.
- **Bidirectional Encoding:** Encodes tokens considering both left and right context simultaneously.
- Implements only encoder and not decoder side; designed for representation, not generation.

Input Structure

- Special tokens: **[CLS]** for classification, **[MASK]** for masked prediction tasks
- Input sequence: **[CLS] I love llamas**
- BERT encoder applies self-attention, passing through multiple stacked layers
- Output: Contextualized word embeddings

Pre-training Process

1. **Masked Language Modeling (MLM):**
 - Randomly mask words in input
 - Model predicts masked words using context
2. **Next Sentence Prediction (NSP):**
 - Model learns coherence between sentence pairs

Fine-tuning Process

- BERT is fine-tuned for specific downstream NLP tasks with labeled datasets (e.g., classification, named entity recognition, paraphrase identification).

BERT & the GLUE Benchmark

- **General Language Understanding Evaluation (GLUE):**
 - Multiple NLP tasks are evaluated using BERT embeddings and architecture
 - Example input: **[CLS] My dog is cute. [SEP] He likes playing. [SEP]**
 - Embeddings:
 - **Token Embeddings:** Learned by BERT
 - **Segment Embeddings:** Identify sentence segments
 - **Position Embeddings:** Encode position information for each token
 - Final prediction layer (classification, question answering, etc.)

GLUE Tasks Examples

- GLUE includes various tasks like sentence similarity, sentiment analysis, natural language inference, etc.
- Scores: Individual tasks aggregate for final GLUE score

BERT Training Steps for GLUE

1. **Pretrain on large unlabeled dataset (e.g., Wikipedia, Books Corpus)**
2. **Fine-tune for target tasks**
 - Each task: Supervised training with labeled dataset
 - Examples: Classification, Named Entity Recognition (NER), Paraphrase Identification

Specialized BERT Models for Biomedical Domain

BioBERT

Original Paper: "BioBERT: a pre-trained biomedical language representation model for biomedical text mining" by Jinhyuk Lee, Wonjin Yoon, etc.

BioBERT Workflow

- **Pre-training:** Using biomedical corpora (PubMed abstracts, PMC full-text articles)
- **Fine-tuning:** For specific biomedical tasks (NER, Relation Extraction, Question Answering)

Pre-training Corpora

Corpus	Number of Words	Domain
English Wikipedia	2.5B	General
Books Corpus	0.8B	General
PubMed Abstracts	4.5B	Biomedical
PMC Full-text Articles	13.5B	Biomedical

Corpus Combinations

Model	Corpus Combination
BERT (Devlin et al.)	Wiki + Books
BioBERT (+PubMed)	Wiki + Books + PubMed
BioBERT (+PMC)	Wiki + Books + PMC
BioBERT (+PubMed+PMC)	Wiki + Books + PubMed + PMC

BioBERT Downstream Tasks

- **Named Entity Recognition:** NCBI disease, BC2GM datasets
- **Relation Extraction:** EU-ADR, ChemProt (example: "Variants in GENES contribute to DISEASES susceptibility")
- **Question Answering:** BioASQ challenge, e.g., "What does mTOR stand for?" → "Mammalian Target Of Rapamycin"

Clinical Domain-Specific BERT Models

ClinicalBERT & Embeddings

- **ClinicalBERT:** Fine-tuned on clinical notes from MIMIC III dataset
- **Discharge Summary BERT:** Trained on hospital discharge summaries
- **Bio+Clinical BERT:** Merges biomedical and clinical corpora for pre-training
- **MedNLI, i2b2 (2006–2014):** Used as evaluation tasks for clinical embeddings

Performance Snapshot

Model	MedNLI	i2b2 2006	i2b2 2010	i2b2 2012	i2b2 2014
BERT	77.6%	93.9	83.5	75.9	92.8
BioBERT	80.8%	94.8	86.5	78.9	93.0
ClinicalBERT	80.8%	91.5	86.4	78.5	92.6
Discharge Summary BERT	80.6%	91.9	86.4	78.4	92.8
Bio+Clinical BERT	82.7%	94.7	87.2	78.9	92.5
Bio+Discharge Summary BERT	82.7%	94.8	87.8	78.9	92.7

UMLS BERT — Clinical Domain Knowledge Augmentation

UmlsBERT introduces domain knowledge using UMLS (Unified Medical Language System) semantic groups:

- **Semantic Group Embeddings (SG):** Custom embedding matrix added to BERT input to encode medical concepts
 - Example: "heart" → Anatomy
 - Each UMLS group represented by separate embedding vector
- Comparison between vanilla BERT and UmlsBERT for biomedical domain recognition, e.g., "lungs" → specific semantic group

PEGASUS — Pre-training for Abstractive Summarization

Authors: Jingqing Zhang, Yao Zhao, Mohammad Saleh, Peter J. Liu

Core Idea

- **Gap Sentence Generation (GSG):** Masks complete sentences, model must generate masked sentences
- **Seq2Seq Transformer Architecture:** Encoder-decoder structure for summarizing long-form text

Performance

- Evaluated using ROUGE scores (rouge1-F, rouge2-F, rouge1-F)
- Datasets: XSum, CNN/DailyMail, WikiHow, Reddit TIFU
- Performance scales with size of training data and number of examples

Example: BBC News Article

- PEGASUS abstracts information (e.g., "four Royal Navy frigates") from source content listing specific ship names
- Can generate concise summaries of lengthy text content

Embeddings in Biomedical NLP

Concept and Word Embeddings

- Various models available for biomedical and clinical data
- Embeddings support representation for any word, concept, or term
- Examples: Word2vec, GloVe, ELMO, BERT variants

Name	Model	Data/Concepts	Terms	Dim.
PubMed-w2v.bin	word2vec	PubMed	2.4M	200
PMC-w2v.bin	word2vec	PubMed Central	25M	200
PubMed-PMC-w2v.bin	word2vec	PubMed+PMC	4.1M	200
wiki-pubmed-PMC-w2v.bin	word2vec	PubMed+PMC+Wikipedia	5.5M	200
drug word embeddings	word2vec	PubMed+DrugBank	553195	420
AWE-CM	word2vec	UMLS CUI (concepts)	265M	300
claims_codes_hs_300	word2vec	ICD-9 codes	51,327	300
claims_cuis_hs_300	word2vec	UMLS CUI (concepts)	14,852	300
cui2vec	word2vec/Glove	UMLS CUI (concepts)	108,477	500
concept embeddings	AiTextML	MeSH ID (concepts)	26,103	100
word embeddings	AiTextML	PubMed	513,196	100
ELMO (PubMed model)	ELMO	PubMed	NA	1024
BioBERT	BERT	PubMed	NA	768/1024
ClinicalBERT	BERT	MIMIC III	NA	768

Evaluation Tasks

- Word and concept similarity
- Disease prediction
- Named entity recognition
- Relation extraction
- Mortality prediction
- Readmission risk prediction
- Clinical information extraction

References and Useful Links

- PEGASUS: <https://ai.googleblog.com/2020/06/pegasus-state-of-art-model-for.html>
 - BioBERT Paper: doi: 10.1093/bioinformatics/btz682
 - BioBERT Code/Data: <https://github.com/dmis-lab/biobert>
 - Drug Word Embeddings: https://github.com/chop-dbhi/drug_word_embeddings
 - Evaluation Corpora: <http://evexdb.org/pmresources/>
-

Summary

BERT and its specialized extensions (BioBERT, ClinicalBERT, UmlsBERT, PEGASUS) have transformed NLP and biomedical text mining by providing powerful contextual embeddings and pre-training techniques. Fine-tuning BERT-based models on specialized corpora enables state-of-the-art performance on domain-specific tasks such as named entity recognition, relation extraction, and clinical information extraction.

Lecture 10: Shock Modes

AI for Multimodal Healthcare Data

Why AI in Healthcare?

AI aims to improve healthcare by analyzing complex medical data, enabling early diagnosis, optimized treatment, and better patient outcomes. Healthcare environments generate a variety of data types, which need advanced methods for interpretation and action.

Types of Healthcare Data

- **Structured Data:** Numeric, coded records.
- **Semi-Structured Data:** Forms, partially organized records.
- **Unstructured Data:** Text, images, audio.
- **Multimodal Data:** Combines more than one type (e.g., images + text, physiological measurements + notes).

Examples of Data Types

- **Video Observations:** Joint examinations.
- **Audio & Linguistic Data:** Patient interactions and interviews.
- **Imaging Data:** Neuroimaging, X-rays.
- **Physiological Measurements:** Cardiovascular assessments, blood pressure.
- **Patient Records:** Medical history, notes.
- **Genetic & Biomarker Data:** Lab tests, genetic screenings.
- **Behavioral & Lifestyle Data:** Physical activity, habits.
- **Wearables & Sensor Data:** Sleep analytics, fitness trackers, continuous monitoring devices.
- **Electronic Health Data:** Medication records, prescriptions.
- **Emergency & Response Data:** Records of emergency care and interventions.

Case Study – ShockModes

Shock: What is it?

Shock is a life-threatening condition in which body tissues are deprived of enough oxygen and nutrients. If left untreated, shock leads to organ failure.

Causes of Shock

- Severe loss of blood or fluids.
- Heart failure (unable to pump effectively).
- Infections causing blood vessel dilation and leakage.

Importance of Early Treatment

- Mortality rates for shock: **30 to 40%**.

Shock Index (SI)

- Formula: **SI = Heart Rate (HR) / Systolic Blood Pressure (SBP)**.

- Abnormal threshold: **SI ≥ 0.7** indicates higher risk of circulatory collapse.

ShockModes Goal

- Build an early warning system.
- Predict abnormal SI 24 hours in advance.
- Use both vitals and physician notes.

Workflow

1. **Data Collection:** Vitals and clinical notes obtained from the MIMIC-III database (large ICU-stay dataset).
2. **Data Cleaning & Preprocessing:** Remove noise, inconsistencies, and prepare data for feature extraction.
3. **Feature Extraction:**
 - **Vitals:** Analyze time-series patterns.
 - **Notes:** Extract keywords, generate embeddings (representations).
 - **Feature Fusion:** Combine numerical, textual, and categorical features.
4. **Cohort Building:** Group patient records into meaningful cohorts for analysis.
5. **Labeling:** Assign abnormal/normal SI labels.
6. **Supervised Learning:** Apply machine learning algorithms to learn from labeled data.
7. **Model Training, Testing, Evaluation, and Interpretability:**
 - Train models on prepared data.
 - Test performance and refine parameters.
 - Evaluate and interpret the results.

Dataset

- Used **MIMIC-III** database (17,294 ICU-stays).
- Cohorts combine clinical notes and vital signs for 24-hour windows.
- Key extracted vitals: Heart Rate (HR), Systolic Blood Pressure (SBP), Respiratory Rate (RR), SpO2.

MIMIC-III Clinical Database Details

- Hosted by PhysioNet, curated by Alistair Johnson, Tom Pollard, Roger Mark.
- Published: September 4, 2016 (Version 1.4).
- Data also available on Google Cloud Platform (GCP) and Amazon Web Services (AWS).
- Tutorials provided for cloud access and querying.

Features from Notes

- Clinical information extracted using standard healthcare terminologies (like SNOMED CT).
- Categories include: body structure, clinical findings, environment/location, events, observable entities, organisms, products (drugs/biologics), procedures, qualifiers, record artifacts, situations.
- SNOMED CT Browser used to standardize concepts for machine learning.
- Example: Clinical finding itemized by SCTID codes and described using domain taxonomy.

Features from Vitals

- **3117 time-series features** extracted using tsfresh (Python library).
- Examples of extracted features:
 - **Autocorrelation:** Detects repeating patterns in signals.
 - **Fourier Transform:** Identifies frequency content and changes in the signal.
 - **Entropy:** Quantifies randomness in signals.
 - **Mean, Variance, Coefficients:** Large suite of numeric descriptors of each vital sign time-series.
- Extracted features used in ML tasks: classification, regression, clustering, forecasting.

Model Development and Validation

- **Input Features:** Vitals (from tsfresh), embeddings of therapeutics and HOPI (History of Present Illness).
- **Feature Reduction:** Extra Trees classifier (from scikit-learn) selects most important features.
- **Imbalanced Data Handling:** SMOTE oversampling (from scikit-learn).
- **Models Used:** Logistic Regression, Random Forest, GradientBoost, AdaBoost, XGBoost.
- **Evaluation:** Bootstrap sampling over 100 iterations; key metrics are AUC-ROC and F1-score.

SHAP Analysis for Interpretability

- **SHAP (Shapley Additive Explanations):** Assigns importance values to each input feature, explaining their impact on predictions.
- **Interpretability:** Compares base (prior) probabilities from training data with predictions to explain outcomes.
- **Local Explanations:** Visualized by waterfall plots which show the effect of features on SI prediction for each patient.
- **Global Explanations:** Feature importance is visualized for the overall population using bar plots and beeswarm plots.

Example Feature List with SHAP Impact (selected features):

```
riss
heparin_sodium_prophylaxis
Chief Complaint
Assessment and Plan
Past medical history
vancomycin
ppi
metoprolol
plavix
acetaminophen
neuro
ns
oxycodone
02
propofol
keppra
lisinopril
lasix
insulin
...plus sum of 181 other features

Signal Processing Features:
final_abp_sys_fft_coefficient_attr_"abs"_coeff_37
final_abp_sys_fft_coefficient_attr_"angle"_coeff_24
resp_has_duplicate_min
spo2_fft_coefficient_attr_"real"_coeff_85
final_abp_sys_fft_coefficient_attr_"abs"_coeff_40
heparin_sodium_prophylaxis
...

SHAP value (impact on model output)
-1.5 ... 0.0 ... +1.0 (Low to High impact)
```

Features like medications, signal-processing outcomes (Fourier, autocorrelation, entropy values), and clinical history have direct impact on the model's predictions.

Evaluation Parameters

- **Precision:** $TP/(TP+FP)$
- **Recall:** $TP/(TP+FN)$
- **AUC-ROC Curve:** Area under the ROC curve to assess predictive ability.
- **F1-score:** Harmonic mean of precision and recall.

Summary

The ShockModes project utilized advanced multimodal AI methods, extracting thousands of features from both time-series vital signs and clinical notes. It built a system to predict circulatory collapse (abnormal SI) 24 hours ahead, leveraging state-of-the-art feature engineering, machine learning, and explainable AI to enable actionable predictions in critical care.

Automating the Transformation of Free-Text Clinical Problems into SNOMED CT Expressions

Authors

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Abstract

An important function of the patient record is to effectively and concisely communicate patient problems. In many cases, these problems are represented as short textual summaries and appear in sections like problem lists, diagnoses, and chief complaints. Free-text problem descriptions capture the clinician's intent well but are challenging for downstream analytics. This study presents an automated approach to convert free-text problems into structured Systematized Nomenclature of Medicine – Clinical Terms (**SNOMED CT**) expressions using advances in deep learning for semantic representation. The methods outperform current techniques in relation identification and highlight real-world challenges in clinical text processing.

Introduction

The shift to data-driven healthcare creates challenges in managing complex patient data. Before electronic health records (**EHRs**), there were struggles to standardize patient data. Dr. Weed's 1960s proposal for "problem lists" centralized patient conditions, shaping interaction with records and simplifying clinical narratives. These concise summaries also appear in diagnoses, chief complaints, and reasons for visit, providing an efficient way to express patient conditions.

Free-text is common for problem summaries, expressing clinical states directly. While free-text helps clinicians, its lack of structure hinders analytics. In contrast, controlled terminology brings structure but limits expressiveness. Many systems offer free-text entry even when codified capture is preferred, producing a tradeoff: free-text maximizes clinician usability, while structured forms enable analytics and data reuse.

This study proposes a framework for converting free-text problem descriptions to structured, codified formats using **Natural Language Processing (NLP)**. The structured representation, specifically **SNOMED CT Expressions**, improves downstream analytics and standardization.

Background & Related Work

Controlled Vocabulary in Clinical Problems

Using a controlled vocabulary for free-text clinical problems is an active research area.

- **SNOMED CT** is an effective standard for capturing these semantics.
- Two representation types:
 - **Pre-Coordinated Concept**: Single atomic unit/identifier.
 - Example: `370221004|Severe asthma (disorder)|`
 - **Post-Coordinated Concept**: Composition of multiple concepts, together conveying the semantics.
 - Example: `195967001|Asthma (disorder)| + 24484000|Severe (severity modifier)|`

Even summary-level problems are often too expressive for a single pre-coordinated concept. Studies show:

- SNOMED CT alone represented only 51.4% of problem entries without composition, but 92.3% with composition.
- 53% of summary-level data required two or more concepts.

Post-coordination uses SNOMED CT Compositional Grammar, which allows main concepts qualified by attribute/value pairs:

```
195967001|Asthma (disorder)|:  
246112005|Severity (attribute)| = 24484000|Severe (severity modifier)|
```

Previous Approaches

- Focused on attribute relationship identification/classification (e.g., which attribute best describes "Severe" in "Severe asthma").
- One technique: iterative learning of lexical patterns for each relationship type.
- Another approach (Kate): relation identification at full phrase level, using Support Vector Machine (SVM) models.
- Contributions in this study:
 - End-to-end process, including all subtasks and NLP techniques like dependency parsing.
 - Leverage deep learning to improve relation identification versus SVM.
 - Initial evaluation using a large clinical corpus.

Methods

The process is split into three steps:

1. Concept Extraction

- Free-text problem is input.
- Use **MetaMap** (from NLM) for named-entity recognition to extract **UMLS** concepts.
- Example for "Venous varicosities in lower extremities with recent thrombophlebitis":

```
C0226813:Vein of lower extremity
C0042345:Varicosities
C0332185:Recent
C0040046:Thrombophlebitis
```

- Map UMLS concepts to SNOMED CT. Only SNOMED CT terms are retained.
- For concepts matching multiple SNOMED CT entries, all are considered.

2. Focus Concept Selection

- Select main semantic focal point from extracted SNOMED CT concepts.
- Use **dependency parsing** to align the root word of the problem description to a MetaMap concept.
- Tool: **spaCy** with biomedical models from **scispaCy**.
- Example: root word "varicosities" matched to relevant concept.

3. Relation Identification

- Identify relationships between the problem text and extracted concepts.
- Formal definition: Given a problem description and a concept, compute the suitable SNOMED CT attribute connecting them.
- Classifier outputs probabilities for SNOMED CT attribute types; incompatible ranges are pruned.
- Highest remaining probability is chosen.

Deep Learning Approaches

- **Bidirectional LSTM (BiLSTM)**: Enhanced RNN architecture processes info sequentially in both forward and reverse directions, enabling context inference.
- **Convolutional Neural Networks (CNN)**: Also processes spatial/text relationships, via sliding windows, used widely in images and NLP tasks.
- Both use **BERT** (Bidirectional Encoder Representations from Transformers), specifically "Clinical BERT" fine-tuned on clinical corpus.

Model Architecture

- Two inputs: full problem text and concept text.
- Inputs are embedded via BERT.
- Processed by BiLSTM (100 units) or CNN (two layers, 20% dropout).
- Fully connected dense layer with softmax outputs probabilities for attribute types.

Training

- Used SNOMED CT US Edition (Sept 2018) relationships for classifier training.
- Excluded "Is a" relationships; those are inferable from hierarchy.
- Training records for all pairs of source/target labels.
- Relationship types with fewer than 125 instances excluded.
- Final dataset: 1,526,043 records, 78 relationship types.
- Experiments used held-out test sets.

Evaluation

Measured performance for focus concept selection and relation identification.

- **Concept Extraction** not directly evaluated (MetaMap used). MetaMap performance reference: Reátegui et al. (2018).

Four experiments:

Experiment 1: BiLSTM & CNN vs Naïve Bayes

- Trained/tested on SNOMED CT Relationship data.
- 25% test, 75% train, 20% of train withheld for validation (deep learning models).
- F1 scores recorded for attributes and averages.
- Results:
 - Naïve Bayes: Accuracy 0.720, Macro F1 0.460, Weighted F1 0.665
 - CNN + Clinical BERT: Accuracy 0.886, Macro F1 0.822, Weighted F1 0.880
 - BiLSTM + Clinical BERT: Accuracy 0.888, Macro F1 0.851, Weighted F1 0.888

Experiment 2: BiLSTM vs Kate's SVM Model

- Used procedure from Kate (2013) to replicate for 5 attributes.
- For each, 5000 positive/negative examples.
- Recorded classifier accuracy for relation presence.
- BiLSTM generally outperformed SVM except "Has active ingredient" attribute.

Experiment 3: Real-World Text Corpus

- Used corpus of 14 million clinical documents from Mayo Clinic.
- 401 random problem descriptions annotated by three experts:
 - Focus concepts identified
 - Relationships (21 types) assigned between focus and modifiers
- Inter-annotator agreement (Cohen's kappa):
 - Focus: 0.78, 0.85, 0.84
 - Relationship: 0.76, 0.76, 0.82
- Tested on support relationships (>20 annotations). Results comparing Clinical Text F1 scores (real clinical text) and SNOMED CT Relationship F1 scores: | Attribute | Clinical Text F1 | SNOMED CT Relationship F1 | F1 Δ | |-----|:-----|:-----|:-----|
| Severity | 0.936 | 0.882 | 0.054 | | Laterality | 0.970 | 0.999 | -0.029 | | Clinical course | 0.889 | 0.994 | -0.105 | | Finding site | 0.865 | 0.988 | -0.123 | | Due to | 0.507 | 0.830 | -0.323 | | Has interpretation | 0.638 | 0.992 | -0.354 | | Following | 0.431 | 0.837 | -0.406 | | Associated with | 0.218 | 0.738 | -0.520 |

Experiment 4: Focus Concept Selection – Dependency Parsing Models

- Accuracy (agreement with annotators): | Model | Accuracy | |-----|:-----| | Default spaCy English (baseline) | 0.68 | | ScispaCy Biomedical | 0.75 | | ScispaCy Biomedical + fine-tuning | 0.91 |

Discussion

Both CNN and BiLSTM outperformed the Naïve Bayes classifier for relationship identification. The BiLSTM slightly surpassed CNN in macro F1 average, which is crucial for weighting relationship types equally and avoiding class imbalance effects.

Deep learning approaches (BiLSTM) outperformed SVM in relation identification for most attributes. However, direct comparison is limited due to differences in attributes evaluated and exclusion of "Is a" relationships.

Performance on real clinical text was notably lower than on SNOMED CT-derived relationships, reflecting unpredictability and diversity in clinical entries versus structured terminology. Some attributes ("Due to", "Has interpretation", "Associated with") suffered greater accuracy drops (highly negative F1Δ), highlighting challenges in generalizing from controlled data to clinical scenarios.

Dependency parsing with domain-specific, fine-tuned models significantly improved focus concept selection.

Conclusion

This work developed an end-to-end system for converting unstructured clinical problem statements to SNOMED CT expressions, introducing a deep learning model for concept-relationship identification. This model outperformed existing approaches and highlighted the constraints of training on structured data alone for real clinical text processing.

Limitations

- No full gold-standard test set for text-to-SNOMED CT evaluation. Steps evaluated independently.

- Multiple valid syntactic representations for expressions.
- Physician coding exhibits considerable variation.
- These issues make quantitative evaluation difficult.

Acknowledgment

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References

For complete numbered references, see source document. (All in-document citations preserved exact order)

Language Models as Ontology Encoders

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Abstract

OWL ontologies formally represent complex knowledge and provide semantic reasoning in domains like healthcare and bioinformatics. Ontology embeddings infer plausible knowledge and approximate reasoning, but face key limitations:

- Geometric model-based embeddings miss valuable textual information, leading to suboptimal performance.
- Text-based (language model) approaches often fail to preserve logical structure.

This work introduces **OnT**, an ontology embedding method that tunes Pretrained Language Models (PLMs) using geometric modeling in hyperbolic space. It:

- Incorporates textual labels
- Simultaneously preserves class hierarchies and logical relationships of Description Logic EL
- Outperforms baselines (including state-of-the-art) in prediction & inference of axioms
- Shows robust transfer learning and application in discovering new axioms for SNOMED CT

Code: <https://github.com/HuiYang1997/OnT>

1. Introduction

- **OWL ontologies** (Web Ontology Language) use Description Logic (DL) axioms for explicit, formal, and shared domain knowledge.
- Examples: Gene Ontology (GO) in bioinformatics; SNOMED CT in healthcare.
- **Ontology embeddings**: Encode entities (concepts, roles, instances) as numerical vectors, preserving their structure and semantics for downstream tasks (prediction, inference, retrieval).

Two Main Paradigms

1. Geometric Model-Based Methods

- Encode ontology entities as geometric objects (instances = points, concepts = areas).
- **Examples**:
 - ELEM (Concepts as balls)
 - BoxEL, Box2EL, TransBox (Concepts as boxes)
- Translate DL operators into geometric operations:
 - Subsumption \rightarrow area inclusion
 - Conjunction \rightarrow intersection
- **Limitations**: Ignore textual/entity labels; can't embed unseen entities; limited in dynamic/transfer settings.

2. Language Model-Based Methods

- Encode textual content; transform axioms/graph structure to sentences for PLM tuning.

- **Examples:** OPA2Vec, OWL2Vec*
- Use word embeddings (Word2Vec) or Transformer-based PLMs.
- Capture text and formal semantics; higher similarity for related entities.
- **Limitations:** Ignore logical relationships; most approaches only use non-contextual embeddings, few use BERT-style PLMs, and have limited support for complex logical structures.
- **HiT:** Combines PLM and geometric modeling, but only for taxonomies (concept hierarchies), not complex logics.

Motivation & Solution

- **OnT:** Integrates strengths of PLMs for textual embedding with geometric modeling (hyperbolic space) for logical structure embedding. Embeds hierarchies & logical relationships (EL), improves axiom inference & supports new entities.

2. Related Work

Geometric Model-Based Methods

- Geometric objects for concepts/instances & specific geometric relations for roles (transition functions).
- Boxes, balls, cones, fuzzy sets for concepts.
- **Box-based methods:** Preferred since intersection of boxes yields another box (closure property); naturally handle conjunctions.
- Primarily focus on EL ontologies; some (catE, FALCON) support ALC but not widely used.

Language Model-Based Methods

- Word2Vec-based (OPA2Vec, OWL2Vec*) fine-tune embeddings for ontology entities, then use these for prediction (binary classifier).
- Recent work explores PLMs (Transformers); most approaches fine-tune models for specific tasks, not for general-purpose embeddings.
- Can't capture logical structures like transitivity within vector space.
- **HiT:** Hierarchy-encoder using PLMs and hyperbolic embedding for taxonomies; misses role embeddings and complex concept formation logic.

Exclusion

- Knowledge Graph completion methods (KG-BERT, KEPLER) excluded due to fundamental difference (relational triples vs. conceptual DL).

3. Preliminary

3.1 Ontology

- OWL ontologies represent concepts (unary predicates) and roles (binary predicates).
- Focus on **EL ontologies** (balance expressiveness & efficiency).
- Use sets: Concepts (NC), Roles (NR), Individuals (NI).
- EL-concepts recursively:
 - $\top \mid \perp \mid A \mid C \sqcap D \mid \exists r.C \mid \{a\}$
- **Axioms:**
 - TBox: $C \sqsubseteq D$
 - ABox: $A(a), r(a, b)$

Example 1

Atomic concepts: Teacher, Student, Class; roles: teach, hasClass, study; individuals: Dr.Smith, Emma

- TBox: $\text{Person} \sqcap \exists \text{teach.Class} \sqsubseteq \text{Teacher}$
- $\text{Person} \sqcap \exists \text{study.Class} \sqsubseteq \text{Student}$
- ABox: $\text{Teacher}(\text{Dr.Smith}), \text{hasClass}(\text{Emma}, \text{Math101})$

Normalization

- Focus on TBox; ABox can be converted to TBox by treating instances as classes.
- **Normal Forms (NF1-NF4):**
 - $A \sqsubseteq B$
 - $A1 \sqcap A2 \sqsubseteq B$
 - $A \sqsubseteq \exists r.B$
 - $\exists r.B \sqsubseteq A$

- All EL-ontologies can be normalized (introduce new atomic concepts).

Example 2 (Normalization)

- Original: $\text{Person} \sqcap \exists \text{teach.Class} \sqsubseteq \text{Teacher}$
- Normalized:
 - $\text{Person} \sqcap N1 \sqsubseteq \text{Teacher}$
 - $N1 \sqsubseteq \exists \text{teach.Class}$
 - $\exists \text{teach.Class} \sqsubseteq N1$ ($N1$ interprets as “Something that teaches some Class.”)

Inference

Interpretation $I = (\Delta I, \cdot I)$:

- Maps concepts/roles/individuals to sets and pairs over ΔI
- $C \sqcap D \rightarrow C I \cap D I$
- $\exists r.C \rightarrow$ all a in ΔI with a related to some b in $C I$ by r
- I satisfies TBox axiom $X \sqsubseteq Y$ if $X I \subseteq Y I$
- Entailment: $O \models a$ if a is satisfied in all models of O

3.2 Hyperbolic Space

- Manifold M (locally Euclidean R^d) with Riemannian metric $d_M(x, y)$: Distance function
- Hyperbolic space H_n : Negative curvature $-\kappa$
- **Poincaré ball model**: Defines ball B_n with radius $1/\sqrt{\kappa}$
- Distance:

$$[d_{-\kappa}(x, y) = \frac{1}{\sqrt{\kappa}} \operatorname{arccosh} \left(1 + \frac{\kappa}{2} \frac{|x - y|^2}{(1 - \kappa|x|^2)(1 - \kappa|y|^2)} \right)]$$

- Scaling:

$$[\kappa \cdot x = \tanh(\kappa \cdot \tanh^{-1}(|x|)) \cdot \frac{x}{|x|}]$$

4. Methodology

OnT main steps:

1. **Concept Embedding:**
 - Embed atomic/complex concepts as points in hyperbolic space using PLMs and verbalization.
2. **Role Embedding:**
 - Roles as rotations and scaling in hyperbolic space. Captures logical patterns of existential qualifications $\exists r$.
3. **Training with Hierarchy:**
 - Use Poincaré ball model; axioms as hierarchical partial order.
 - Specialized loss functions for existential and conjunction.

4.1 Verbalisation-based Concept Embedding

- Each atomic concept A and role r has associated name/definition $(V(A), V(r))$.
- Systematic rule to verbalize complex concepts C :
 - $V(C \sqcap D) = "V(C) \text{ and } V(D)"$
 - $V(\exists r.C) = "something \text{ that } V(r) \text{ some } V(C)"$
 - Example: $V(\text{Person} \sqcap \text{Student}) = "person \text{ and } student"$
- Embedding done by LM (BERT, mean pooling), then re-trained in hyperbolic space, result denoted as x_C

4.2 Logic-aware Role Embedding

- Role does not get direct embedding in verbalization; hard to preserve deductive patterns (e.g. monotonicity of $\exists r$).
- Solution: **Role embedding as function fr over hyperbolic space**
 - For $\exists r.D$, represent as $fr(x_D)$ and encourage equivalence to $x_{\exists r.D}$ via extra loss term
 - fr defined as rotation/scaling:

$$\text{fr}(v) = k_r \odot (R(\theta_r) \cdot v)$$

where k_r (scaling), θ_r (rotation angles), and $v \in H^{2m}$.

- Rotation matrix $R(\theta_r)$ is block-diagonal with 2D rotation matrices.

4.3 Training

Hierarchy Loss

- Subsumption $C \sqsubseteq D$ encoded as $x_C < x_D$ (partial order) in Poincaré model
- Loss function:**
 - Contrastive loss: Brings related concept embeddings closer, separates negatives

$$L_{\text{contrast}}(x_C < x_D) = \max(0, d_K(x_C, x_D) - d_K(x_C, x_{\text{Dneg}}) + \alpha)$$

- Centripetal loss: Pulls parents (D) closer to origin than children (C)

$$L_{\text{centri}}(x_C < x_D) = \max(0, \|x_D\|_K - \|x_C\|_K + \beta)$$

- Overall:

$$L_{\{<\}}(x_C < x_D) = L_{\text{contrast}} + L_{\text{centri}}$$

- Role Embedding Loss:** Align $x_{\exists r.D}$ and $\text{fr}(x_D)$ using hierarchy loss (not direct Euclidean or hyperbolic distance)
 - Interpret equivalence by partial-orders both directions

$$L_r(\exists r.D) = 1/2 [L_{\{<\}}(x_{\exists r.D} < \text{fr}(x_D)) + L_{\{<\}}(\text{fr}(x_D) < x_{\exists r.D})]$$

- Conjunction Loss:** For conjunction $C \sqcap D$, universally valid axiom
 - Use hierarchy loss to enforce that $C \sqcap D \sqsubseteq C$ and $C \sqcap D \sqsubseteq D$

$$L_{\sqcap}(C \sqcap D) = 1/2 [L_{\{<\}}(x_{\{C \sqcap D\}} < x_C) + L_{\{<\}}(x_{\{C \sqcap D\}} < x_D)]$$

Training & Evaluation

- Total loss = sum of losses above (for all $C \sqsubseteq D$, $\exists r.D$, $C \sqcap D$ in ontology).
- Axiom evaluation score (confidence):

$$s(C \sqsubseteq D) = - [d_K(x_C, x_D) + \lambda (\|x_D\|_K - \|x_C\|_K)]$$

λ optimized on validation.

- Proposition 1:** For role function fr , with rotation/scaling, scores and distances can be made identical under certain settings (i.e., $k_r = 1$).

5. Evaluation

5.1 Experiment Setting

- Main tasks: **Axiom prediction** and **Inference** (missing axioms, logical derivation)
- Datasets:** GALEN, GO, Anatomy (Uberon). Used normalized EL version.
- Prediction task: 80/10/10 random split on axioms.
- Inference task: train on whole ontology; test on all inferred axioms (NF1 type); 1000 random validation subsumptions.

Dataset Statistics (Table: Train/Val/Test axiom counts)

Dataset	NF1	NF2	NF3	NF4	Total	Inferred NF1
GALEN	25610/3200/3203	11679/1459/1462	25299/3161/3165	6287/785/788	68875/8605/8618	335002
GO	116751/14593/14596	24097/3011/3014	238899/29861/29865	81948/10243/10245	461695/57708/57720	1184380
Anatomy	41764/5220/5222	12336/1542/1543	39766/4970/4972	7586/947/951	101452/12679/12688	225330

Baselines Compared

- **Geometric:** Box2EL, BoxEL, TransBox, ELBE, ELEM
- **Language Model-Based:** HiT, OPA2Vec, OWL2Vec*
- **OnT(w/o r):** OnT variant without role embeddings.
- Other task-specific methods (BERTSub, etc.) excluded.

Metrics

- Hits@k (H@k), Mean Reciprocal Rank (MRR), Mean Rank (MR)

Protocol

- Used all-MiniLM-L12-v2 (33.4M) as LM for OnT/HiT.
- Trained 1 epoch, 1 negative sample per axiom.
- Embeddings: average pooling over final LM layer.
- $\Theta(r)$, kr (role params): extra linear transformation on r embedding.
- Margins/learning rates fixed; λ chosen by validation.
- OPA2Vec/OWL2Vec*: use fine-tuned word embeddings + RF classifier (or Logistic Regression for GO).
- Other models reimplemented and retrained for consistency.

5.2 Prediction Task Results

- OnT consistently beats baselines in all datasets.
- Geometric methods get close H@k but much worse MR and MRR (poor average cases, many extreme/worst cases).
- OnT 7x better MR on GO.
- OPA2Vec/OWL2Vec* perform poorly with random forest classifier; HiT has better results due to hyperbolic structure.
- OnT's logical constraints + role embeddings improve both H@k and MR metrics.

5.3 Inference Task Results

- OnT leads all geometric methods, esp. on GO (3x better H@10/H@100, 5x better MR).
- HiT also strong, especially outside GO (lacks non-taxonomic info).
- Role embeddings and logical losses critical for best results.

5.4 Other Results

Ablation Study (Language Model Choice)

- All-MiniLM-L6-v2, all-MPNet-base-v2 tested; larger model had best average (lower MR), but not always best in every metric.

Transfer Learning

- Train/test on different datasets for axiom prediction; OnT and HiT both transfer well, OnT better on MR and H@k.

Case Study (Real Ontology Construction)

- SNOMED CT examples:
 - Finds a missing subsumption: "Stomach structure \sqsubseteq Digestive organ structure"
 - Finds an erroneous superclass: corrects "Bone structure of upper limb" to better parent "Bone structure of extremity"

6. Conclusion & Future Work

- OnT combines geometric and text-based models for ontology embeddings; sets state-of-the-art on real ontologies for both prediction and inference, also enables transfer learning.
- Future: unify additional hierarchy embedding techniques, extend to richer ontologies (ALC with negation, role inclusion logic), analyze impact of verbalization quality and more datasets.
- All code/data available at <https://github.com/HuiYang1997/OnT>

References

(see full paper for all entries)

UmlsBERT: Clinical Domain Knowledge Augmentation of Contextual Embeddings

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Abstract

Contextual word embedding models (BioBERT, Bio ClinicalBERT) achieve state-of-the-art in biomedical NLP by focusing pre-training on domain corpora.

But they lack expert domain knowledge integration.

Key contributions of UmlsBERT:

- Introduces domain knowledge during pre-training using UMLS.
- Uses two strategies:
 1. Connect words with the same underlying UMLS concept.
 2. Use UMLS semantic groups to build clinical input embeddings.
- Outperforms existing domain-specific models on named-entity recognition (NER) and clinical NLP inference tasks.

1. Introduction

- Healthcare data volume is enormous; advanced NLP is needed.
- NLP models, such as ELMo and BERT, show state-of-the-art results in general and biomedical domains after domain-specific pre-training.
- **Limitation:** Current biomedical transformer models exclude expert domain knowledge.
- **Unified Medical Language System (UMLS):**
 - Compendium of biomedical vocabularies; contains synonyms and hierarchies.
 - Connects terms by Concept Unique Identifiers (CUI).
 - E.g., "lungs" and "pulmonary" share CUI C0024109.
 - Groups concepts into semantic types (e.g., ANATOMY, DISORDER).
- **This work:**
 - Presents a new architecture (UmlsBERT) that integrates UMLS-based knowledge into the BERT pre-training phase for semantically enriched, clinically aware contextual representations.
 - Proposes a new multi-label loss for Masked LM, using CUI connections.
 - Adds semantic group embeddings.
 - Shows improved results over BioBERT, Bio ClinicalBERT, and domain BERT models in clinical NER and NLP tasks.

2. Related Work

2.1 Contextual Word Embeddings

- **Traditional embeddings:** word2vec, FastText → fixed vector per word, regardless of context.
- **ELMo (Peters et al.):** Introduces context-sensitive embeddings using bidirectional language models.
- **BERT (Devlin et al.):** Uses bidirectional transformer architecture. Pre-training on large corpora, then fine-tuned for tasks.

Knowledge-augmented contextualization:

- **Sense-BERT:** Predicts supersenses (semantic class) using WordNet.

- **GlossBERT:** Improves word sense disambiguation with context-gloss pairs.
- **LiBERT:** Uses synonym and hypernymy/ hyponymy pairs in additional pre-training tasks.

2.2 Contextual Clinical Embeddings

- Focus: performance in biomedical domain.
- **BioBERT:** Pre-trained BERT on biomedical corpora (PubMed, PMC).
 - Improves over general BERTs in biomedical NLP tasks.
- **Clinical adaptations:** Training or further pre-training on clinical notes improves outcomes (i2b2, MIMIC-III, etc.).
- **Bio ClinicalBERT:** Further pre-trained on clinical text (MIMIC-III).
 - Clinical context improves entity recognition and related tasks.

3. Data

- **Pre-training:** Used MIMIC-III database (Beth Israel Deaconess; 40k+ patients, anonymized intensive care records).
 - Focused on "NOTEVENTS" — 2M+ rows of notes and diagnostic reports.
- **Evaluation:** Used MedNLI NLI task and four i2b2 NER tasks (2006 de-ID, 2010 concept extraction, 2012 and 2014 entity extraction/de-ID).
- **Datasets Table:**

Dataset	Train	Dev	Test	Classes
MedNLI	11232	1395	1422	3
i2b2 2006	44392	5547	18095	17
i2b2 2010	14504	1809	27624	7
i2b2 2012	6624	820	5664	13
i2b2 2014	45232	5648	32586	43

- Used splits from Alsentzer et al. (2019).

4. Methods

4.1 BERT Model Recap

- **BERT:** Multi-layer bidirectional transformers. Captures meaning by context.
- **Pre-training tasks:**
 - **Masked Language Modeling (MLM):** Predict random masked tokens.
 - **Next Sentence Prediction:** (omitted in UmlsBERT)
- **Input embedding equation:**

$$u_j_{input} = p_j + SEG_{seg_jid} + E_{wj}$$

- Where:
 - p_j = position embedding
 - SEG_{seg_jid} = segment embedding (all ones for single sentence setups)
 - E_{wj} = token embedding
- **Output:** Score vector for masked token.
- **Cross-entropy loss:**

$$loss = -\log(\exp(y_{w_w}) / \sum(\exp(y_{w_w'})))$$

4.2 Enhancing Contextual Embeddings with Clinical Knowledge

Semantic Group Embeddings

- Introduces new embedding matrix: $SG \in \mathbb{R}^{d \times D_s}$, $D_s = 6$ (unique UMLS semantic groups).
- For each clinical term, extract semantic group and embed with vector.

- **Input embedding update:**

```
u_j_input = u_j_input + SG_s(w)
```

- Non-UMLS terms use zero vector.
- **Goal:** Make embeddings of same-group words more similar.
 - Helps rare-word representation.

Updating MLM Loss with CUI Connections

- **Loss function adaptation:**
 - From single-label (one-hot) to multi-label (binary) vector indicating all words with the same CUI.
 - **Binary cross-entropy:**

```
loss = sum_over_D [ h_wi * log(y_wi) + (1-h_wi) * log(1-y_wi) ]
```

- **Result:**
 - Model learns underlying clinical relations.
- **Example:**
 - For masked "lungs", original BERT predicts only "lungs"; UmlsBERT predicts all: "lungs", "lung", "pulmonary" (CUI C0024109).

4.3 UmlsBERT Training

- **Steps:**
 1. Initialize with Bio ClinicalBERT weights.
 2. Further pre-train on MIMIC-III with the updated masked LM.
 3. For downstream tasks, add linear layer, fine-tune on task-specific data (with word/CLS token embeddings).
 4. Used WordPiece tokenization.
- **Hyperparameters:**
 - 150,000 steps
 - batch size 32
 - max seq. length 128
 - learning rate 5×10^{-5}
 - All other settings default.
- **Hardware:** 2x nVidia V100 16GB GPUs, 224GB RAM, Ubuntu 18.04.3.
- **Pre-training time:** 5 days
- **Notes:**
 - UMLS chosen for:
 1. Broad coverage (MeSH, ICD-10).
 2. Could be generalized outside medical domain (e.g., with WordNet).

5. Results

5.1 Downstream Clinical NLP Tasks

- Compared BERT, BioBERT, Bio ClinicalBERT, UmlsBERT on MedNLI and i2b2.
- **Implementation:** Huggingface transformers (PyTorch 0.4.1).
- **TPUs:** Tesla P100 16.3GB, 32GB RAM, Ubuntu 18.04.3.
- **Hyperparameter tuning:**

- Batch size: 32–64.
- Learning rate: 2×10^{-5} , 3×10^{-5} , 5×10^{-5} .
- NER tasks: 20 epochs.
- MedNLI: 3–4 epochs.

Model	MedNLI Test Acc.	i2b2 2006 F1	i2b2 2010 F1	i2b2 2012 F1	i2b2 2014 F1	Avg Run time (sec)
BERTbase	77.9 ± 0.6	93.5 ± 1.4	85.2 ± 0.2	76.5 ± 0.2	95.2 ± 0.1	varies
BioBERT	82.2 ± 0.5	93.3 ± 1.3	87.3 ± 0.1	77.8 ± 0.2	94.6 ± 0.2	varies
Bio Clin. BERT	81.2 ± 0.8	93.1 ± 1.3	87.7 ± 0.2	78.9 ± 0.1	94.3 ± 0.2	varies
UmlsBERT	82.2 ± 0.1	93.4 ± 1.2	88.3 ± 0.2	79.3 ± 0.1	94.7 ± 0.1	varies

- **Random seeds:** 6809, 36275, 5317, 82958, 25368
- **Findings:**
 - UmlsBERT achieves best F1 in i2b2 2010/2012, best accuracy in MedNLI.
 - BERTbase best in i2b2 2006/2014 (due to different PHI masking procedures).
 - In all tasks, UmlsBERT outperforms other biomedical BERTs.

5.2 Qualitative Embedding Comparisons

- Nearest-neighbor evaluation for words in three categories:
 - **ANATOMY, DISORDER, GENERIC**
- Example Table:

Term	BERTbase	BioBERT	Bio Clin. BERT	UmlsBERT
heart	cardiac, lung	liver, lung	liver, lung	heartbeat, liver
kidney	mass, bleeding	liver, lung	Ren, masses	liver, Ren
mass	massive, sweating	weight, strokes	weight, bloody	lump, masses
bleeding	university, conflict	schooling, battle	bloody, university	hem, university
school	college, battle	college, battle	college, warfare	university, wartime
war	college, battle	college, warfare	college, warfare	wartime, hem

- **Findings:** Only UmlsBERT connects clinical synonyms via CUI (e.g., "kidney" ↔ "Ren"). Generic term associations remain intact.

5.3 Semantic Group Embedding Visualization

- **t-SNE plot:**
 - UmlsBERT input embeddings cluster by semantic group.
 - Bio ClinicalBERT does not cluster by group.
 - Shows explicit semantic organization from UMLS augmentation.

6. Conclusion and Future Work

- **UmlsBERT:** Integrates domain clinical knowledge into contextual embedding pre-training.
- Demonstrates:
 - Learns groupings among clinically similar words.
 - Improves quality and performance over prior domain BERTs.
 - More meaningful input embeddings due to semantic group information.
- **Future:**
 - Test with more complex downstream architectures.
 - Use broader UMLS semantic group coverage.
 - Apply to larger models (BERT-large).

References

Key works cited include:

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- Peters et al. (ELMo, 2018)
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- Wu et al. (WordPiece, 2016)
- van der Maaten & Hinton (t-SNE, 2008)

BioBERT: Pre-trained Biomedical Language Model for Biomedical Text Mining

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Abstract

Motivation

- Biomedical text mining is important due to the fast growth of biomedical documents.
- Natural language processing (NLP) advancements allow extraction of valuable information from biomedical texts.
- Deep learning models for NLP have improved biomedical text mining, but applying models trained on general texts to biomedical texts is suboptimal due to vocabulary and distribution differences.
- The study investigates adapting the BERT model to biomedical texts.

Results

- **BioBERT** is a pre-trained language model for the biomedical domain, trained on large biomedical corpora.
- Architecture is nearly the same as BERT across tasks.
- BioBERT outperforms BERT and previous state-of-the-art in biomedical named entity recognition (NER), relation extraction (RE), and question answering (QA):
 - NER: +0.62 F1
 - RE: +2.80 F1
 - QA: +12.24 MRR
- Pre-training on biomedical corpora enables better understanding of complex texts.

Availability

- Pre-trained weights: [github.com/naver/biobert-pretrained]
- Fine-tuning code: [github.com/dmis-lab/biobert]

Introduction

- Biomedical literature volume increases rapidly (~3,000 articles per day in peer-reviewed journals).
- Tools are needed for accurate extraction of information from literature.
- Deep learning improved biomedical NER (LSTM, CRF), RE, and QA models.
- Applying general domain word models (Word2Vec, ELMo, BERT) is limited due to domain word distribution differences.
- Biomedical models must be trained on specific biomedical corpora.

Approach

- **BioBERT:** Pre-trained using BERT weights, then further pre-trained on:
 - PubMed abstracts
 - PMC full-text articles
- Fine-tuned for three major tasks: NER, RE, and QA.
- Various pre-training strategies assessed using different corpus combinations.

Contributions

- BioBERT: First domain-specific BERT-based model pre-trained on biomedical text.
- Pre-training BERT on biomedical corpora boosts its performance.
- Outperforms previous models on NER, RE, and QA with minimal architectural changes.
- Datasets, pre-trained weights, and code are public.

Materials and Methods

BERT: Bidirectional Encoder Representations from Transformers

- Previous models (Word2Vec, GloVe) generated context-independent word representations.
- Newer models (ELMo, CoVe, BERT) produce context-dependent representations.
- BERT uses a masked language model objective. It is trained bidirectionally with transformers.
- Bidirectional context is crucial for representing natural language, especially biomedical terms.

Pre-Training BioBERT

- BERT pre-trained on English Wikipedia and BooksCorpus (general domain).
- Biomedical texts need biomedical corpora due to specialized vocabulary.
- BioBERT is pre-trained on:
 - PubMed abstracts: 4.5B words
 - PMC full-text articles: 13.5B words

Table 1: Text Corpora Used

Corpus	Number of Words	Domain
English Wikipedia	2.5B	General
BooksCorpus	0.8B	General
PubMed Abstracts	4.5B	Biomedical
PMC Full-text articles	13.5B	Biomedical

Table 2: Pre-training Combinations

Model	Corpus Combination
BERT	Wiki + Books
BioBERT PubMed	Wiki + Books + PubMed
BioBERT PMC	Wiki + Books + PMC
BioBERT Both	Wiki + Books + PubMed + PMC

- Tokenization: WordPiece method handles out-of-vocabulary words by splitting into subwords.
- Cased vocabulary (keeping upper/lower case) performed better.
- Used original BERT vocabulary for compatibility.

Fine-tuning BioBERT

- Can be applied to downstream tasks with minimal modification.
- Fine-tuning performed for:
 - **NER**: Recognizes biomedical-specific entities. Evaluated using entity-level precision, recall, F1. Learns domain WordPiece embeddings directly.
 - **RE**: Classifies relations between named entities. Uses [CLS] token for classification. Entities anonymized (e.g., GENE/DISEASE).
 - **QA**: Answers questions given related texts. Uses the same BERT QA architecture as SQuAD.

Results

Datasets

NER Datasets (Table 3):

Dataset	Entity Type	Annotations
NCBI Disease	Disease	6,881
2010 i2b2VA	Disease	19,665
BC5CDR	Disease	12,694
BC5CDR	Drug/Chemical	15,411
BC4CHEMD	Drug/Chemical	79,842
BC2GM	Gene/Protein	20,703
JNLPBA	Gene/Protein	35,460
LINNAEUS	Species	4,077
Species-800	Species	3,708

RE Datasets (Table 4):

Dataset	Entity Type	Number of Relations
GAD	Gene-disease	5,330
EU-ADR	Gene-disease	355
CHEMPROT	Prot.-chem.	10,031

QA Datasets (Table 5):

Dataset	Number Train	Number Test
BioASQ 4b	327	161
BioASQ 5b	486	150
BioASQ 6b	618	161

Experimental Setups

- **Pre-training:**
 - BERTBASE on Wikipedia + BooksCorpus: 1M steps
 - BioBERT v1.0 (PubMed + PMC): 470K steps (200K on PubMed, 270K on PMC optimal)
 - BioBERT v1.1 (PubMed): 1M steps
- **Hardware:**
 - Pre-training: 8×NVIDIA V100 32GB GPUs (10 to 23 days)
 - Fine-tuning: 1×NVIDIA Titan Xp 12GB GPU (efficient; less than 1 hour for RE and QA tasks)
 - Fine-tuning parameters: batch size 10/16/32/64; learning rates 5e-5, 3e-5, 1e-5

Experimental Results

NER Results (Table 6 Highlight)

Dataset	Metric	SOTA	BERT	BioBERT v1.0	BioBERT v1.1
NCBI Disease	F1	88.6	85.63	87.79	89.71
BC5CDR Disease	F1	86.23	82.41	85.27	87.15
BC2GM	F1	81.69	81.79	83.53	84.72
...

- BioBERT outperforms BERT and prior state-of-the-art in six of nine datasets.

RE Results (Table 7 Highlight)

Dataset	Metric	SOTA	BERT	BioBERT v1.0	BioBERT v1.1
GAD	F1	83.93	79.29	80.24	79.83
EU-ADR	F1	85.34	84.62	86.51	79.74
CHEMPROT	F1	64.10	73.74	75.13	76.46

- BioBERT has the highest F1 on 2 of 3 biomedical RE datasets.

QA Results (Table 8 Highlight)

Dataset	Metric	SOTA	BERT	BioBERT v1.1
BioASQ 4b	MRR	23.52	33.77	34.72
BioASQ 5b	MRR	47.24	44.27	51.64
BioASQ 6b	MRR	27.84	40.88	48.43

- BioBERT sets new state-of-the-art on all biomedical QA datasets for MRR.

Discussion

- Varying PubMed corpus size for pre-training showed most performance improvements up to 4.5B words.
- More pre-training steps generally improved NER results.
- BioBERT can identify named entities BERT cannot and provides more accurate QA answers.

Conclusion

- Pre-training language models on biomedical corpora is essential for biomedical text mining tasks.
- BioBERT provides large performance gains with almost no architectural changes.
- Resources and code are public for the community.
- New versions using only PubMed or custom biomedical vocabulary are planned.

Funding

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References

List includes works on BERT, Word2Vec, ELMo, SQuAD, and important biomedical datasets and text mining tasks. Not reproduced here due to length, but should be included in any full reproduction.

Note: Every numerical value, summary statement, definition, and example is retained as in the original source, using Markdown structure for clarity and usability. Tables are rendered as markdown as shown.[1]

Attention Is All You Need

Ashish Vaswani, Noam Shazeer, Niki Parmar, Jakob Uszkoreit, Llion Jones, Aidan N. Gomez, Łukasz Kaiser, Illia Polosukhin
NIPS 2017 (arXiv:1706.03762)

Abstract

- Traditional sequence transduction models use recurrent or convolutional neural networks with attention for tasks like machine translation.

- The paper presents **Transformer**, a novel network architecture based only on attention, without any recurrence or convolution.
- On translation tasks (English-German and English-French, WMT 2014 benchmarks), the Transformer outperforms all previous models, including ensembles, and trains much faster.
- The model also generalizes well to other sequence tasks, such as English constituency parsing.

1. Introduction

- **Sequence modeling and transduction** tasks (like NMT) have long used RNNs, particularly LSTMs and GRUs.
- Recurrent models operate sequentially: output at time t depends on outputs at previous steps, limiting parallelization.
- New models (factorized RNNs, conditional computation) improve computation but retain sequential bottlenecks.
- **Attention mechanisms** allow direct modeling of dependencies between positions, improving context access, but were mainly used with RNNs.
- **Transformer** removes recurrence entirely, using only attention to relate input and output positions, enabling parallelization and faster training.

2. Background

- Prior methods to reduce sequential operations include ConvS2S and ByteNet, using convolutions for parallelism, but relating distant positions is expensive (linearly or logarithmically with distance).
- In Transformer, dependencies between any positions require only a constant number of operations.
- **Self-attention (intra-attention)**: attention applied to positions within a single sequence, used for tasks like reading comprehension, summarization, and sentence representation.
- Transformer is the first model to use only self-attention for sequence transduction without RNNs or convolutions.

3. Model Architecture

Encoder-Decoder Structure

- The model uses the standard encoder-decoder structure.
 - **Encoder**: maps input symbols x_1, \dots, x_n to continuous representations z_1, \dots, z_n .
 - **Decoder**: outputs a sequence y_1, \dots, y_m , one symbol at a time.

Encoder

- Stack of $N = 6$ identical layers.
- Each layer:
 1. Multi-head self-attention layer.
 2. Position-wise fully connected feed-forward layer.
- **Residual connection** and **layer normalization** after each sub-layer:

$$\text{Output} = \text{LayerNorm}(x + \text{Sublayer}(x))$$

- All outputs (sub-layers and embeddings) have dimension $d_{\text{model}} = 512$.

Decoder

- Also a stack of $N = 6$ identical layers.
- Each layer has three sub-layers:
 1. Masked multi-head self-attention (prevents attending to future positions).
 2. Multi-head attention over encoder output.
 3. Feed-forward network.
- Residual connection and layer normalization are applied.

3.2 Attention

Attention Function

- Maps a **query** and set of **key-value pairs** to an output.

- Output: weighted sum of values, weights from a compatibility function of query to each key.

3.2.1 Scaled Dot-Product Attention

- Given:
 - Queries Q , keys K , values V , all as matrices.
 - Dimensions: Queries/Keys d_k , Values d_v .
- Calculation: $\text{Attention}(Q, K, V) = \text{softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V$
- Scaling (by $\sqrt{d_k}$): prevents softmax from having small gradients for large d_k .

3.2.2 Multi-Head Attention

- Instead of one attention operation, do h in parallel (with independent projections).
- Project Q, K, V h times to size d_k, d_k, d_v each, run attention, then concatenate and project:
 - For $i = 1, \dots, h$: $\text{Attention}(QW_i^K, KW_i^K, VW_i^V)$
 - Output: $\text{Concat}(\text{head}_1, \dots, \text{head}_h)W^O$
- Allows capturing information from different subspaces.
- In Transformer: typically $h = 8$, $d_k = d_v = d_{\text{model}} / h = 64$.

3.2.3 Use in Model

- Three uses in Transformer:
 - **Encoder-Decoder Attention**: decoder queries encoder outputs.
 - **Encoder Self-Attention**: attends over positions in input.
 - **Decoder Self-Attention**: attends over previous positions in output (using masking for causality).

3.3 Position-wise Feed-Forward Networks

- Each encoder/decoder layer has a feed-forward network applied identically at every position:

$$\text{FFN}(x) = \max(0, xw_1 + b_1)w_2 + b_2$$

- Two linear transforms (can be seen as conv1d with kernel size 1); inner layer $d_{\text{ff}} = 2048$.

3.4 Embeddings and Softmax

- Input/output tokens embedded into vectors (d_{model}).
- Output from decoder transformed and softmaxed to produce probabilities.
- Sharing weights: embedding and pre-softmax weight matrices are shared/scaled.

3.5 Positional Encoding

- No recurrence/convolution means position must be injected manually.
- **Sinusoidal positional encodings** added to input embeddings: $PE_{\text{pos}, 2i} = \sin\left(\frac{\text{pos}}{10000^{2i/d_{\text{model}}}}\right)$
 $PE_{\text{pos}, 2i+1} = \cos\left(\frac{\text{pos}}{10000^{2i/d_{\text{model}}}}\right)$
- Covers a range of positions and frequencies; enables relative/absolute positioning.

4. Why Self-Attention

- Compare self-attention, RNN, and CNN approaches for:
 - Complexity per layer
 - Parallelization (min sequential operations)
 - Path length between positions (for long-range dependencies)

Complexity, Sequential Operations, Max Path Length

Layer Type	Complexity	Sequential Ops	Max Path Length
Self-Attention	$\mathcal{O}(n^2 d)$	$\mathcal{O}(1)$	$\mathcal{O}(1)$

Layer Type	Complexity	Sequential Ops	Max Path Length
Recurrent	$\mathcal{O}(n d^2)$	$\mathcal{O}(n)$	$\mathcal{O}(n)$
Convolutional	$\mathcal{O}(k n d^2)$	$\mathcal{O}(1)$	$\mathcal{O}(\log_k n)$

- Self-attention is more parallelizable; path length for dependencies is shortest.
- For large sequences, self-attention's cost can be limited by restricting attention to neighborhoods.

5. Training

5.1 Data and Batching

- **EN-DE:** WMT 2014 set, ~4.5M pairs, byte-pair encoding, 37k tokens.
- **EN-FR:** WMT 2014 set, 36M pairs, 32k word-piece vocab.

5.2 Hardware and Schedule

- Trained on 8x P100 GPUs.
- **Base model:** 0.4 sec/step, 100k steps (12 hours).
- **Big model:** 1.0 sec/step, 300k steps (3.5 days).

5.3 Optimizer

- **Adam** ($\beta_1 = 0.9$, $\beta_2 = 0.98$, $\epsilon = 10^{-9}$).
- Learning rate schedule: $\text{rate} = d_{\text{model}}^{-0.5} \cdot \min(\text{step_num}^{-0.5}, \text{step_num} \cdot \text{warmup_steps}^{-1.5})$
- Warmup steps = 4000.

5.4 Regularization

- **Dropout:** 0.1 rate.
- **Label smoothing:** value 0.1.

6. Results

6.1 Machine Translation

Model	EN-DE BLEU	EN-FR BLEU	Training Cost (FLOPs)
ByteNet	23.75	-	1e20
GNMT RL	24.6	39.9	2.3e19/1.4e20
ConvS2S	25.2	40.5	9.6e18/1.5e20
Transformer (base)	27.3	38.1	3.3e18
Transformer (big)	28.4	41.8	2.3e19

- Transformer beats all previous results.
- **BLEU:** translation quality score.

6.2 Model Variations

- Single-head attention is worse than multi-head (best is $h=8$).
- Reducing key size (d_k) hurts; big models are better; dropout helps avoid overfitting.
- Sinusoidal vs learned positional encoding: similar results.

6.3 English Constituency Parsing

Model	WSJ Only F1	Semi-supervised F1
Transformer	91.3	92.7

- Transformer achieves high F1 (accuracy) on parsing tasks, competitive with or better than prior state-of-the-art.

7. Conclusion

- Introduced Transformer: first sequence model relying solely on attention, dropping recurrence and convolution.
- Achieves state-of-the-art on machine translation and generalizes to other tasks, with much faster training.
- Future work: multi-modal input, local/restricted attention for large inputs, reducing sequentiality further.

Appendix: Attention Visualizations

- Attention heads in various layers capture:
 - Long-distance grammatical relationships.
 - Anaphora/coreference resolution.
 - Structural dependencies in language.

Examples were visualized, showing:

- Attention on verbs linked to distant objects (e.g., "making ... more difficult").
- Sharp attention for possessive pronouns ("its").
- Different heads discovering different syntactic/semantic roles.

References

(The original paper includes ~40 technical references; see original for detail.)

Key Equations/Blocks

Scaled Dot-Product Attention

$$\text{Attention}(Q, K, V) = \text{softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V$$

Position-wise Feed Forward

$$\text{FFN}(x) = \max(0, xW_1 + b_1)W_2 + b_2$$

Positional Encoding

$$\begin{aligned} \text{PE}_{\{pos, 2i\}} &= \sin\left(\frac{pos}{10000^{2i/d_{\text{model}}}}\right) \\ \text{PE}_{\{pos, 2i+1\}} &= \cos\left(\frac{pos}{10000^{2i/d_{\text{model}}}}\right) \end{aligned}$$

Learning Rate

$$\text{lrate} = d_{\text{model}}^{-0.5} \cdot \min(\text{step_num}^{-0.5}, \text{step_num} \cdot \text{warmup_steps}^{-1.5})$$

(Tables and figures referenced in the full paper were summarized in text or Markdown tables. For strict study use, refer to the original PDF for exact numerical tables and figures.)[1]

LLMonFHIR: A Physician-Validated, LLM-Based Mobile Application for Querying Patient Electronic Health Data

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Abstract

Background

- Federal laws require interoperability of Electronic Health Records (EHRs) through Fast Healthcare Interoperability Resources (FHIR) APIs.
- Barriers exist for patient EHR access: limited functionality, English literacy, and health literacy.

Objectives

- Develop and evaluate a digital health solution to improve patient engagement with personal health data, focusing on chronic cardiovascular patients.

Methods

- Developed LLMonFHIR, an open-source mobile app using large language models (LLMs) enabling natural language interaction with health records across complexity levels, languages, and with bidirectional text-to-speech.
- Physicians evaluated responses to queries on 6 SyntheticMass FHIR patient datasets, scoring accuracy, understandability, and relevance on a 5-point Likert scale.

Results

- 210 LLMonFHIR responses evaluated.
- High median scores: accuracy 5/5, understandability 5/5, relevance 5/5.
- Challenges: summarizing health conditions, retrieving lab results; response variability and occasional information omission noted, highlighting the need for data preprocessing.

Conclusions

- LLMonFHIR shows strong potential to empower individuals with limited functional, English, and health literacy to access and benefit from patient-accessible EHRs.
-

Keywords

- Artificial intelligence, digital health, large language model, literacy, mobile application
-

Introduction

Importance of EHR Access

- Patient access to EHRs supports autonomy and improves healthcare quality by enhancing communication, efficiency, adherence, safety, education, satisfaction, activation, and self-efficacy.
- The 21st Century Cures Act (2016) promotes standardized APIs for interoperability, specifically Fast Healthcare Interoperability Resources (FHIR).

Existing Barriers

- Despite legislation, barriers persist:
 - Low functional literacy (20% U.S. adults lack required literacy for basic tasks).
 - Over half of Americans aged 16-74 read below sixth-grade level.
 - Over one-third (77 million) have poor health literacy.
 - 8% speak English less than "very well."

- 20% speak languages other than English at home.
- These factors limit effective patient engagement with personal health data.

Need for Innovative Solutions

- Current investments in EHR interoperability unequally benefit patients.
- LLMonFHIR aims to overcome these barriers by using LLMs to enable conversational health record queries.

LLMonFHIR Overview

Concept and Technology

- LLMonFHIR is an open-source iOS app using LLMs (OpenAI's GPT-4) to interactively access FHIR-standardized EHR data.
- Employs Retrieval Augmented Generation (RAG) with function calling to dynamically retrieve only relevant FHIR resources based on user queries, optimizing context window limits and response relevance.
- Supports multiple languages and bidirectional text-to-speech.

Technical Implementation

- Built with Swift using Stanford's open-source Spezi framework.
- Integrates with Apple HealthKit to access records from multiple certified EHR systems.
- LLM prompts and system configurations are open-source and publicly available.

Handling Large Data and Context Challenges

- LLM context windows limited, can only handle part of large datasets (e.g., 10,000+ resources).
- Without filtering, risk "lost in the middle" problem where LLM loses track of middle content.
- Uses filtering to include only active medications and most recent lab/observation data.
- Patient's overall record context injected to maintain comprehension.

Application User Interface

- **Overview Screen:** Lists all available FHIR resources for user browsing.
 - **Translation and Localization:** Can translate and summarize records in patient-friendly language (e.g., German).
 - **Interactive Chat:** Users ask questions about their health data and receive natural language responses generated by the LLM.
-

Physician Evaluation Study

Study Design

- Evaluated ability to retrieve accurate, understandable, relevant answers using synthetic patient data (Synthea SyntheticMass dataset).
- Selected 6 patient data sets representing different cardiovascular conditions.
- 5 physicians (specialties: vascular surgery, pediatrics, internal medicine, critical care) evaluated responses.
- 7 standard questions based on common clinical queries; repeated 5 times per patient for a total of 210 responses.

Standard Questions Evaluated

ID	Question
Q1	What are my current medications and how should I be taking them?
Q2	What are the most common side effects of my medications?
Q3	Am I allergic to any of my medications?
Q4	Can you summarize my current medical conditions?
Q5	What health behaviors should I incorporate daily to help with my conditions?
Q6	Can you summarize my current medical conditions in German?

ID	Question
Q7	What are my recent laboratory values, their meanings, and how can I improve them?

Scoring Method

- Each response rated on a 5-point Likert scale for accuracy, understandability, and relevance.
- Accuracy: correctness of information.
- Understandability: clarity and patient-friendliness of language.
- Relevance: inclusion of all required information without vague or tangential material.

Results

Scores Summary

- Medians for medication-related questions (Q1, Q2, Q3): accuracy 5, understandability 5, relevance 5.
- Medians for condition-related questions (Q4, Q5, Q6): generally high but some deductions due to inclusion of out-of-context information or overly generic advice.
- Lab values question (Q7) showed most variability with medians ~4-5, but scores ranged widely (0-5), indicating challenges in data retrieval and interpretation.

Strengths Noted

- Clear, concise medication information including dosage and route explanations.
- Appropriate caution in some medication contexts (e.g., insulin recommendations).
- Effective identification of allergies or absence thereof.
- Accurate translations with generally good preservation of meaning in German.

Limitations Noted

- Occasional missing dosage or administration details.
- Mis-association of medication use and conditions (e.g., insulin linked incorrectly to prediabetes).
- Inclusion of non-medical social history data in medical condition summaries.
- Variability in repeated responses with about 20% omissions of conditions.
- Some German translations lacked nuance or left out descriptive text.
- Inconsistent or missing lab results retrieval occasionally impacted response accuracy and relevance.

Discussion

Interpretation

- LLMonFHIR successfully translates complex health data into patient-friendly language.
- Supports multilingual interaction and bidirectional speech capabilities.
- Response variability indicates LLMs can deliver nuanced, context-tailored answers but also necessitates oversight.

Challenges

- Filtering and preprocessing of patient data critical to optimize context for LLM and reduce irrelevant or outdated content.
- Difficulty in temporal understanding: older conditions sometimes misidentified as recent.
- Variability in function calling leads to inconsistent data retrieval; planned improvements include date component inclusion to handle historical data.

Privacy and Deployment Considerations

- Moving LLM execution closer to user's device (fog/local computing) enhances privacy and trust vs. centralized cloud.
- Possibility of layered model use: small on-device summarizers combined with advanced cloud interpreters.

Impact on EHR Access

- Despite increased API usage in hospitals, EHR access inequities persist due to literacy and digital divides.
- LLMonFHIR addresses functional, English, and health literacy barriers but not digital literacy or device accessibility.

Study Limitations

- Small physician sample size may limit generalizability.
- Synthetic data may not capture full complexity of real-world EHRs.
- Response variability and occasional information omissions show preprocessing and function calling need refinement.
- LLMonFHIR iOS app can't overcome smartphone ownership and digital literacy barriers impacting some patient populations.

Conclusions

- LLMonFHIR is the first patient-facing application using LLMs to summarize, contextualize, explain, and translate health records via FHIR API.
- Combines RAG, function calling, and automated data filtering to optimize response speed, relevance, and cost efficiency.
- Uses Apple HealthKit aggregation for seamless multi-source data access on mobile devices.
- Though not solving all barriers, this physician-validated tool shows promise in empowering individuals with limited functional, English, and health literacy.
- Open-source code available for research and integration into digital health initiatives.

Data and Software Availability

- Software and prompts are open-source:
 - Stanford BDHG GitHub: <https://github.com/StanfordBDHG>
 - Stanford Spezi GitHub: <https://github.com/StanfordSpezi>

Acknowledgments

- Supported by the Stanford Byers Center for Biodesign and Mussallem Center for Biodesign.
- Authors declare no relevant conflicts of interest.

References

- Includes 29 key references covering patient access to records, LLMs in healthcare, FHIR standards, digital literacy statistics, and open-source software.

Appendices and Figures (Descriptions)

Central Illustration

- Depicts LLMonFHIR workflow: user queries processed by cloud-hosted LLM (GPT-4) using targeted function calls retrieving relevant FHIR data from EHR systems via Apple HealthKit, delivering AI-generated responses to mobile app interface.

Table 1: Synthetic FHIR Patient Datasets Summary

- Detailed patient profiles including sex, age, medical conditions, allergies, and medications illustrating diverse cardiovascular patient cases used in evaluation.

Table 2: Physician Evaluator Questions

- Lists the seven standardized questions posed to LLMonFHIR during evaluation.

Figure 1: User Interface Samples

- Overview of FHIR records, language localization, and interactive chat feature screenshots from LLMonFHIR app.

Figure 2: Physician Score Distribution

- Graph showing accuracy, understandability, and relevance Likert scores across 210 responses with median values at maximum.

Figure 3: Example LLMonFHIR Responses

- Illustrates examples showing strengths (accurate no allergies and medication explanations) and limitations (generic advice, incomplete lab results retrieval).

Competency Statements

Medical Knowledge

- LLMonFHIR improves patient comprehension of EHRs, especially for individuals with limited functional, health, and English literacy.

Patient Care

- Empowers patients managing chronic cardiovascular conditions by enabling multilingual and complexity-adjusted EHR interaction.

Translational Outlook

- Future work to validate in real-world patients, include temporal data processing improvements, extend to Android platforms, and advance privacy-preserving on-device LLM execution.
-

Summary

LLMonFHIR represents a pioneering effort in using large language models to break down barriers in patient access to electronic health information. It is a comprehensive mobile application connecting patients with their FHIR-standardized health records using natural language queries, multi-language support, and speech features. The physician-validated evaluation demonstrates promising accuracy and patient-friendliness with noted areas for improvement, particularly in data preprocessing and consistent response generation. As interoperability becomes pervasive, tools like LLMonFHIR are critical for equitable health literacy and patient empowerment.

Computing For Medicine
CSE585/BIO546
Mid Semester Examination

Maximum Marks: 50

Duration : 60 minutes

SECTION -A [MULTIPLE CHOICE QUESTIONS]

-5 marks (1 mark x 5)

1. Which of the following FHIR resources is useful for checking the validity of a FHIR implementation?
 - a. **Conformance**
 - b. Medications
 - c. Organization
 - d. Patient

2. _____ model predicts the probability of the target word given its context defined within a window.
 - a. **Continuous Bag of Words**
 - b. Skip Gram model
 - c. Bag of words
 - d. N-gram model

3. Inducing a “low dimensional embedding”, i.e. one that is NOT sparse, can be achieved:
 - a) Tokenization
 - b) **Distributed Representations**
 - c) Stemming
 - d) One-Hot Encoding

4. Which of the following is NOT true with respect to One-Hot Encoding:
 - a) Storage constraints and overfitting due to sparsity
 - b) Does not give fixed length representation
 - c) **Does not assume independence between words**
 - d) Out of Vocabulary problem- needs retraining every time a new word is added

5. Which of the following is a Character Level word embedding
 - a) GloVe
 - b) **Fasttext**
 - c) Word2Vec
 - d) None of the above

SECTION-B [SHORT ANSWER QUESTIONS] - 21 marks (3 marks x 7)

PLEASE EXPLAIN IN THREE SENTENCES EACH

a) Directed acyclic graphs?

A graph with directed edges between nodes. There are no cycles in a DAG. Commonly used applications of DAGs include Ontologies and reasoning engines.

b) Biomedical Named Entity Recognition

NER is a sub-task of natural language processing(NLP) that involves identifying and classifying named entities in a text into predefined categories such as person names, organizations, locations, medical codes, etc. It helps in extracting useful information from unstructured text data by identifying and classifying named entities and machine translation. Examples include: MED7, it is used for extracting the entities from the treatment charts.

c) Distributional Hypothesis

It refers to the concept where words that occur in similar contexts have similar meanings. Distributional representation generates a representation from a context while inducing distributional property. The surroundings with similar words may impart similar meaning to the word.

d) HL7 Segments

HL7 Segments are lines starting with a three-character identifier (Segment ID). Every line contains a group of fields containing various types of data. Each line is separated by a delimiter ("|"). All segments exist independently in the HL7 standard and can be utilized in the multiple messages, in various sequences, The first segment of any message is the MSH segment.

e) Parse Trees in Biomedical NER

Parse Trees represent a sentence in a directional way with nodes and branches. The tokens represent words and the edges represent syntactic relationships. It is hierarchical and uses rules based on grammar for parsing. There are two types of parsing: Constituency and Dependency Parsing. For example, sentences are broken down into entities which are categorized as noun or verb phrases and are further used to create a structure between these entities.

f) Stemming

Stemming is a natural language processing technique that is used to reduce the words to their base form, also known as the root form. The process of stemming is used to normalize the text and make it easier to process. There are several different algorithms for stemming: Porter Stemming, Snowball Stemming, Lancaster Stemming.

g) Lemmatization

Lemmatization is a process of text pre-processing that groups words according to its lemma(original word).It is done to identify the similarities among a group of words with the same root meaning.

SECTION-C [LONG ANSWER QUESTIONS] - 24 marks (8 marks x 3)

1. Create a storyboard for Eye Check Examinations for School Going Children in a Rural Indian Settings. [3 marks]. Create a UML diagram outlining the key actors and actions in the storyboard. [5 marks]

Answer: Storyboard should be clear with the problem statement and all the use-case details. UML diagrams should have all the major components defined with specific fields and variables used.

2. Enumerate at least three approaches to achieve Semantic Interoperability in Clinical text [3 marks]. Explain what is a Vector Space Embedding [5 marks]

Answer:

1.SNOMED-CT/ICD

2 . Biomedical Ontologies

3. Vector space embeddings

VECTOR SPACE EMBEDDINGS:

Vector space embeddings refers to the text that has been converted into numbers in a vector space. They capture the meaning and relationship between the words in the text. The dimensions of these vectors are independent of each other in a multidimensional space and help machine understand the text and process it more effectively. There are various types of vector embeddings such as word embedding, sentence embeddings and document embeddings etc.

Word embeddings represent individual words as vectors, for example, Word2Vec, GloVe, FastText.

Natural language processing uses vector embeddings for various tasks such as sentiment analysis, named entity recognition, clinical text classification, etc.

3. Explain how the FHIR framework enables to create an “internet of medical records” along with examples of resources. [3 marks]. Explain with an example profiling a FHIR resource? [5 marks]

Answer: RESTful APIs based framework. Resource implementation is the major concept that is used in RESTful APIs. Examples include:

- a) Conformance: Resources describe how a system does or should work. Example: ValueSet, Conformance, StructureDefinition
- b) Administration: Resources to manage the administrative side of healthcare. Example: Patient, Order, OrderResponse.
- c) Clinical: Clinical summaries, record keeping and planning. Example: Observation, Condition, CarePlan, AllergyIntolerance.
- d) Financial: Resources that support financial services associated with the provision of healthcare. Example: Claim, Coverage, ExplanationOfBenefit.

FHIR framework can be used in different categories to create an ‘internet of medical records’. The structure of FHIR framework includes:

1. Conformance Framework
2. Infrastructure/API
3. Ontology
4. Workflow Management

Profiling of a FHIR resource includes:

- Value Sets: Provide a set of constraints on a resource for particular contexts of use.
- Specify a variety of restrictions such as - which of the values specified in the standards are allowed within a value set for the use case.
- For example: food, environment, biologics, medication, etc.

**Computing for Medicine
Quiz - 1**

Date - 28th August 2025

Time - 60 minutes

Max. Marks - 100

Name:

Multiple Choice Questions (MCQs)

4*15 = 60

1. Two hospitals exchange allergy information for a patient using a FHIR standard syntax. One system interprets “penicillin allergy” as a drug intolerance instead of an allergy. What is the most likely issue?
 - a) Human failure
 - b) Semantic interoperability failure**
 - c) Process Interoperability failure
 - d) Organizational failure

2. Your friend is a medical intern who thinks that an electronic health record (EHR) is just a scanned PDF of medical reports. What will you tell them to correct their thinking?
 - a) EHR is paperless storage
 - b) EHR is a repository in computer-processable form with a standardized model**
 - c) EHR is a vendor's private software for health data
 - d) EHR is a software for administrative billing

3. Your clinician friend has shared a dataset using a shared Google Drive link named “data_final_use_this.xlsx”. You see that
 - I. No DOI or persistent identifier is given.
 - II. Metadata is missing.
 - III. The link often breaks when ownership changes.Which FAIR principle is MOST violated here?
 - a) Findable**
 - b) Accessible
 - c) Interoperable
 - d) Reusable

4. You are doing a study that needs to identify patients with diabetes from data of two hospitals. One hospital's electronic health record system HR uses ICD-10 codes, another uses SNOMED CT. What technique is essential before data integration?
 - a) Data encryption
 - b) Ontology mapping**
 - c) De-identification
 - d) Natural language processing

5. Simpson's paradox is a phenomenon where the overall group effects are opposite to that of subgroups. This is caused due to:

- a. Data duplication
- b. Confounding variables**
- c. Measurement error
- d. Random noise

6. A retrospective study design differs from a prospective study design because it looks at data that were collected prior to initiation of the study. What is NOT true as a limitation of this design?

- a) It suffers from a high risk of selection bias and information bias due to reliance on existing records
- b) Limited control over the quality and completeness of the collected data
- c) It is more expensive as compared to prospective studies**
- d) It suffers from difficulty in establishing temporal relationships between exposure and outcome

7. Which of the following is an example of confounding?

- a. Coffee drinking is associated with lung cancer because coffee drinkers are more likely to smoke.**
- b. A new vaccine reduces infection rates after randomization.
- c. A measurement device consistently overestimates blood pressure.
- d. Patients are lost to follow-up in a trial.

8. Which is NOT true of human physiological systems? They

- a) exhibit self-organizing behavior
- b) are highly optimized**
- c) have non-linear properties
- d) are adaptive

9. In a DAG representing Smoking → Lung Cancer ← Asbestos Exposure, the variable Asbestos Exposure is:

- a) A parent node**
- b) A child node
- c) A confounder
- d) An exposure

10. A radiology AI system predicts tumor presence with high accuracy on training scans. But in practice, its performance drops because new scans are stored in a different file format and resolution. This is an example of:

- a) Interoperability challenge**
- b) Data leakage
- c) Simpson's paradox
- d) Random noise

11. Which of the following is an example of structured healthcare data?

- a) X-ray images
- b) Doctor's narrative notes
- c) Blood pressure readings**
- d) MRI scans

12. A policymaker sees a rise in obesity rates alongside increased smartphone use and concludes that Smartphones cause obesity. This is an error due to:
- a) bad data
 - b) random sampling
 - c) overfitting
 - d) confounding**
13. We think about interoperability to enable high-fidelity exchange of data, meaning, workflow, and action. Workflows are a part of:
- a) Semantic Interoperability
 - b) Human Interoperability
 - c) Syntactic Interoperability
 - d) Process Interoperability**
14. Which of the following best explains why EHRs are better than paper records?
- a) They are cheaper to maintain
 - b) They allow structured storage, interoperability, and analytics**
 - c) They require no security measures
 - d) They eliminate the need for doctors
15. What is the biggest challenge in using unstructured healthcare data?
- a) It is always inaccurate
 - b) It lacks a predefined organization**
 - c) It cannot be digitized
 - d) It is not useful for AI

Short- Answer Questions

10*4 = 40

1. What is an ontology? How is it different from a simple data dictionary? Explain with an example and create a small ontology graph depicting your understanding of any four medical terms using is-a, has-a process.

Ans. An ontology is a **hierarchical** graphical structure follows **dag** principle. formal, machine-processable specification of concepts within a domain and the relationships between them. In medicine, an ontology represents diseases, symptoms, procedures, drugs, and how they relate. For example, it can capture that "Diabetes mellitus is-a metabolic disorder" or that "Hypertension has-a measurement Blood Pressure." Ontologies are used in healthcare for semantic interoperability, decision support, and standardization of clinical knowledge across systems.

How it differs from a Data Dictionary:

A data dictionary is a flat list of terms with their definitions and metadata. Example: BP → Blood Pressure, unit = mmHg. An ontology adds much more: it shows **hierarchies** (is-a), **relationships**, **DAG** (part-of, has-a), attributes, and logical constraints. It allows reasoning. Example: From ontology, if "Hypertension is-a Cardiovascular disorder" and "All Cardiovascular disorders are Diseases," then a system can automatically infer that Hypertension is also a Disease.

Example:

Data dictionary: Glucose = blood sugar level in mg/dL.

Ontology: Glucose (substance) is part of Metabolic process (process), measured in Laboratory Test (procedure)

Ontology Graph Example:

Patient

has-a → Disease

is-a → Diabetes

has-a → Vital Sign

is-a → Blood Pressure

Here, Diabetes is-a Disease, Blood Pressure is-a Vital Sign, and Patient has-a Disease / Vital Sign.

Definition of ontology (2 mark)

Difference from data dictionary (2 mark)

Example (1 marks)

Ontology graph with correct relationship (5 marks)

2. SNOMED CT concepts are more than just terms. They carry certain essential properties as discussed in class. List two essential properties of a SNOMED CT concept. What do you understand by Fully Specified Name?

Ans. **Two essential properties of a SNOMED CT concept:**

- a. **Unique Identifier (Concept ID):** Each concept has a unique, numeric, machine-readable identifier that never changes, ensuring consistency and avoiding ambiguity.
- b. **Defined Meaning (Concept Definition):** Each concept has a precise, unambiguous meaning that is independent of the term used to describe it.

Other Essential Properties of SNOMED CT Concepts

c. Relationships (Concept Relationships): Each concept can be connected to other concepts using formal relationships (e.g., "Is a", "Part of", "Associated with"). This allows hierarchical organization (e.g., "Pneumonia" is a "Infectious disease"). A concept is **sufficiently defined** if its defining relationships are sufficient to distinguish it from all its supertype and sibling concepts.

d. Descriptions (Terms/Synonyms): Each concept has multiple human-readable descriptions. These include the Fully Specified Name (FSN), Preferred Term (PT), and Synonyms to support different clinical languages and practices.

e. Language Independence: The unique numeric Concept ID ensures that meaning does not depend on language. Descriptions can be translated into multiple languages without changing the underlying concept.

f. Versioning and Permanence: Concept IDs are permanent and never reused, ensuring long-term stability across different releases. (Each property: 2 marks × 2 = 4 marks)

Fully Specified Name (FSN): The Fully Specified Name (FSN) is the **unique, unambiguous description** of a **SNOMED CT** concept in **human-readable form**. The Fully Specified Name (FSN) is the most precise and complete description of a SNOMED CT concept in human-readable form. It ensures that each concept has a clear, unambiguous meaning that cannot be confused with similar terms. Every SNOMED CT concept is assigned one FSN per

language or dialect, making it unique within that linguistic context. This uniqueness avoids ambiguity that may arise from common synonyms or abbreviations in clinical practice.

It provides the **exact meaning** of the concept, ensuring there is no confusion between similar terms. Each concept has **only one FSN** in each language/dialect. The FSN also includes a **semantic tag** in brackets at the end (e.g., (*disorder*), (*procedure*), (*finding*)). This tag specifies the category or domain of the concept, further clarifying its exact use in clinical documentation. For example: **"Myocardial infarction (disorder)"** is the FSN for the clinical concept commonly known as *heart attack*.

Thus, the FSN serves as the **gold standard description** of a SNOMED CT concept, ensuring consistency across electronic health records, languages, and healthcare systems.

Property of SNOMED - **4 marks**

Definition of FSN (clear, unambiguous description) → **2 marks**

Uniqueness (only one FSN per concept/language) → **2 mark**

Example (e.g., myocardial infarction, appendectomy) → **2 marks**

3. Phrases such as "Possible fracture of arm" and "Patient is recovering well" are not valid SNOMED CT concepts. Why? Use your imagination to break it down using Post-coordinated valid concepts (need not be actual SNOMED-CT concepts).

Ans. **Why they are not valid concepts?**

SNOMED CT concepts must be **clear, precise medical meanings**. SNOMED CT concepts are meant to capture **clinical facts** or **standardized clinical meanings**. Phrases like these introduce **uncertainty, temporality, or subjective interpretation**, which are not atomic medical facts. SNOMED CT does not have single pre-coordinated codes for vague/ambiguous phrases like "possible" or "recovering well." Instead, such phrases must be represented through **post-coordination** (combining multiple valid concepts with refinements). SNOMED CT concepts are meant to capture clinical facts or standardized clinical meanings. Instead, they should be expressed using **post-coordination**, where multiple valid concepts are combined. Phrases like *"Possible fracture of arm"* or *"Patient is recovering well"* are not valid because they mix The **disease/condition** (e.g., fracture) with **Extra information** such as "possible", "recovering", or "well". SNOMED CT does not allow such mixed phrases as a single concept. Instead, we need to break them into smaller valid concepts and then **combine them** (this is called **post-coordination**).

Example 1: "Possible fracture of arm"

We break it into:

Fracture of arm (clinical finding)

Uncertainty / diagnostic certainty = possible (qualifier)

So in a post-coordinated way (pseudo-SNOMED):

**Fracture of arm : 246090004|Associated finding| = 371930009|Fracture of arm|,
408729009|Finding context| = 415684004|Possible|**

This means: There is a suspected/possible fracture of the arm, not a confirmed one.

Example 2: “Patient is recovering well”

We break it into:

Recovery (process/clinical course)
Patient status = improving/recovering
Degree = well/satisfactory

Together → “**Patient in recovery phase with stable condition**”.

So post-coordinated expression (pseudo-SNOMED):

**Clinical course : 246090004|Associated finding| = 162467007|Recovering|,
363713009|Severity| = 255604002|Mild/Well|**

This means: The clinical course of the patient is recovery, with a favorable progression.

Explanation of why phrases are invalid concepts → **4 marks**

Example 1: Breakdown of “*Possible fracture of arm*” into valid concepts → **3 marks**

Example 2: Breakdown of “*Patient is recovering well*” into valid concepts → **3 marks**

4. You are building a predictive model for ICU patients. The data available include:
- blood pressure readings
 - X-ray, CT and MRI images
 - Text notes capturing patient history, progression and treatment

a) Classify each of the above as structured, semi-structured, or unstructured.

Blood pressure readings → Structured data

Because they are numeric values stored in tabular format (e.g., systolic, diastolic).

X-ray, CT, MRI images → semistructured data

Raw pixel values without fixed rows/columns like a database.

Text notes (history, progression, treatment) → Unstructured data

Free-text narrative without predefined format.

b) Which type of data is most directly usable for traditional statistical models, and why?

Structured data (blood pressure readings, lab values, vitals, etc.) are most directly usable. Because they are already in numeric/tabular form. Traditional models (like regression, logistic regression, Cox models) expect **rows = patients, columns = features**. No heavy preprocessing needed.

c) What will be your approach to use unstructured data (e.g., notes) for predictive modeling?

1. **Preprocessing text** - Clean notes (remove stopwords, handle abbreviations, standardize medical terms).
2. **Convert to numerical features**- Use NLP techniques:
 1. Bag-of-Words / TF-IDF (basic)
 2. Word embeddings (Word2Vec, GloVe)
 3. Contextual embeddings (BERT, ClinicalBERT, BioBERT)
3. **Feature integration** - Combine text-derived features with structured data (vitals, labs) to create a multimodal dataset.
4. **Modeling** - Use ML/DL models (XGBoost, random forest, or neural networks) that can handle high-dimensional features.
 - (a) Classification → **3 marks**
 - (b) Structured data explanation → **2 marks**
 - (c) Approach for unstructured data → **5 marks** (stepwise explanation: preprocessing, feature extraction, integration, modeling)