

UKB-KG: Knowledge Graph for Integrating and Enhancing Biomedical Insights from the UK Biobank

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Content

1. Motivation

2. Methods

3. Results

4. Applications

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4. Applications

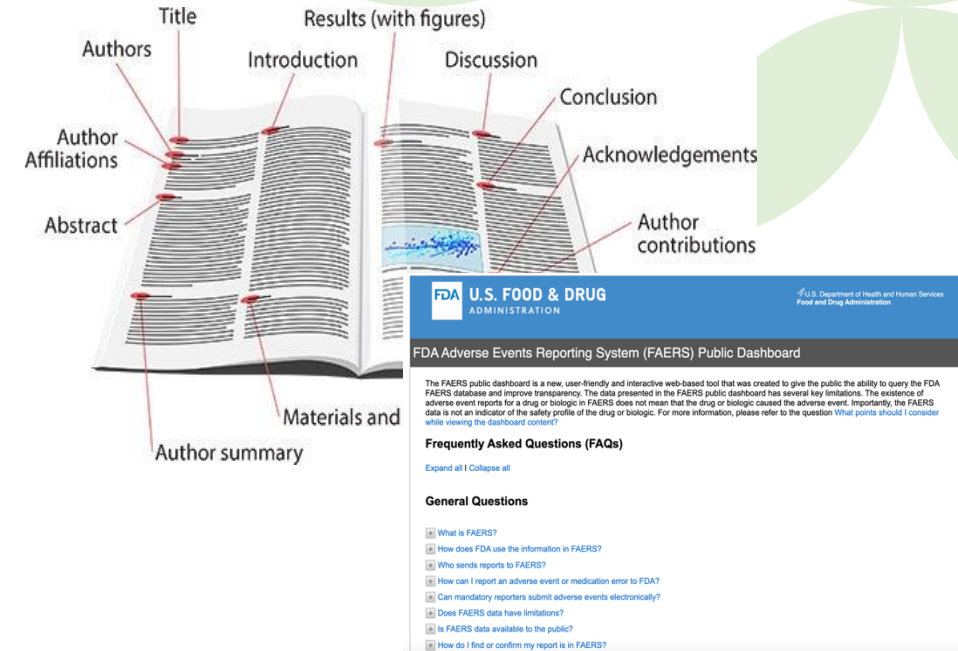
BIOMEDICAL DATA RESOURCES

Literature

- Peer-reviewed articles, preprints, case reports
- Sources: PubMed, bioRxiv, medRxiv

Ontologies

- Standard vocabularies for data harmonization
- Examples: UMLS, SNOMED CT, ICD-10, MeSH

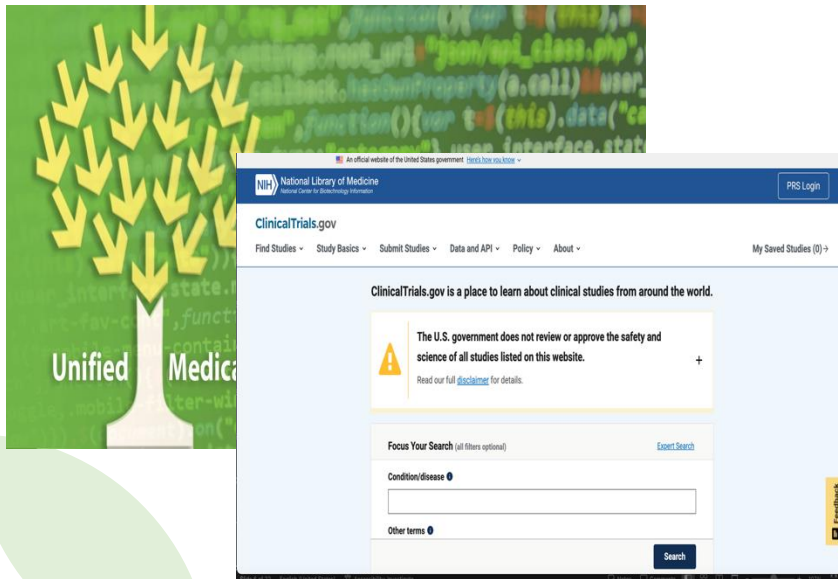


Drug Information

- ❖ Prescription and utilization records
- ❖ Pharmacogenomic annotations (gene–drug interactions)
- ❖ Drug databases and adverse-event reports (e.g., FAERS)

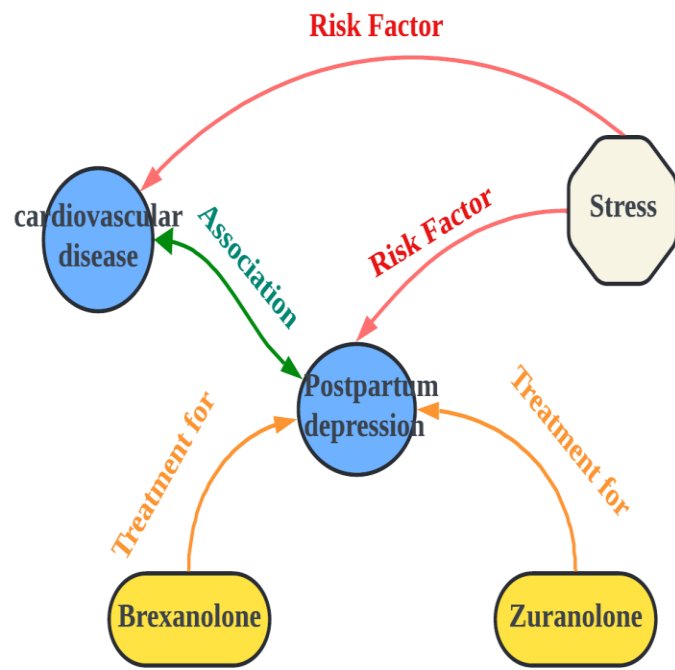
Clinical Trials & Registries

- Interventional protocols and real-world outcomes
- Examples: ClinicalTrials.gov, SEER cancer registry



BIOMEDICAL KNOWLEDGE GRAPH

- A **heterogeneous directed graph** comprising various types of entities (nodes , e.g.,proteins, diseases) connected by relationships (edges , e.g., "causes," "treats").
- Each triple represents a fact in the real world

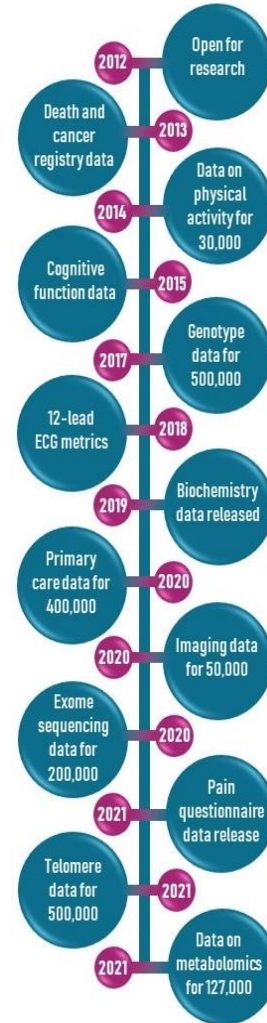
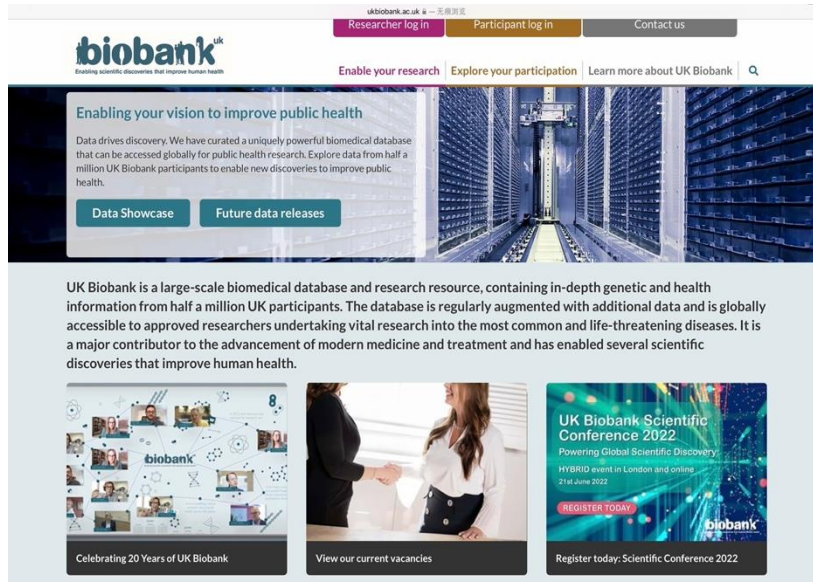


Triples:

(Cardiovascular Disease, Association, Postpartum Depression)
(Stress, Risk Factor, Cardiovascular Disease)
(Stress, Risk Factor, Postpartum Depression)
(Brexanolone, Treatment for, Postpartum Depression)
(Zuranolone, Treatment for, Postpartum Depression)

Any Issues?

THE UK BIOBANK STUDY

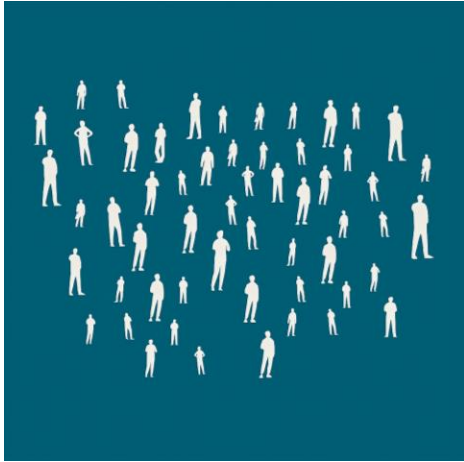


- ❖ Imaging (n = 100 000): Brain, heart & full-body MRI; DEXA; carotid ultrasound
- ❖ Genetics: Genome-wide genotyping, WES & WGS (all participants), Proteomics
- ❖ EHR Linkages: Mortality, cancer registry, hospital admissions & primary-care data
- ❖ Biomarkers: 30+ serum assays at baseline + first repeat
- ❖ Activity: 7-day wrist accelerometry (all) with seasonal follow-up (subset)
- ❖ Surveys: Diet, lifestyle, occupation, pain, cognition & mental/digestive health
- ❖ Samples: Blood & urine (all); saliva (n = 100 000)



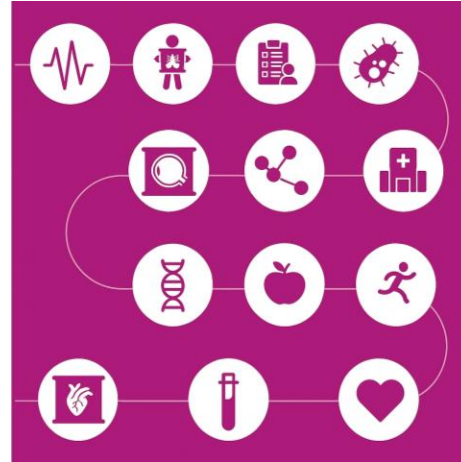
UKB-KG: BACKGROUND

UK Biobank (UKB) - The world's most important health research database



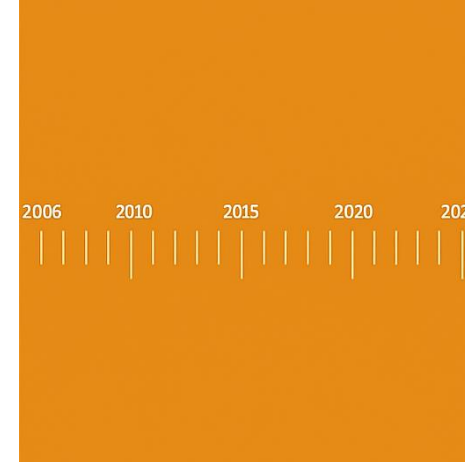
Large

502,467 men and women aged 40-69 with diverse ethnic backgrounds agreed to make all their health-related data available for research.



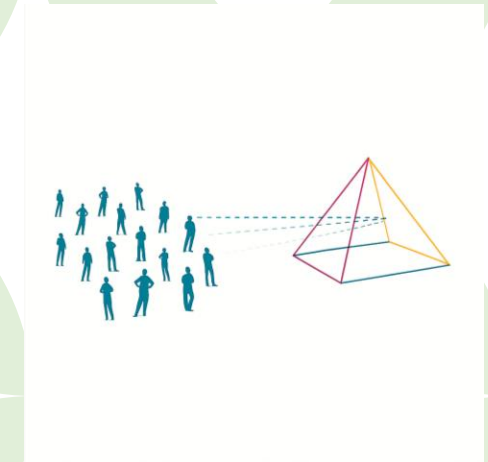
Deep

Extensive dataset includes phenotypic, genomic, lifestyle, environmental and biological factors relevant to subsequent development of different diseases.



Long

Sufficient duration of follow-up for large numbers of many different health outcomes to have occurred since assessment of exposures.



Accessible

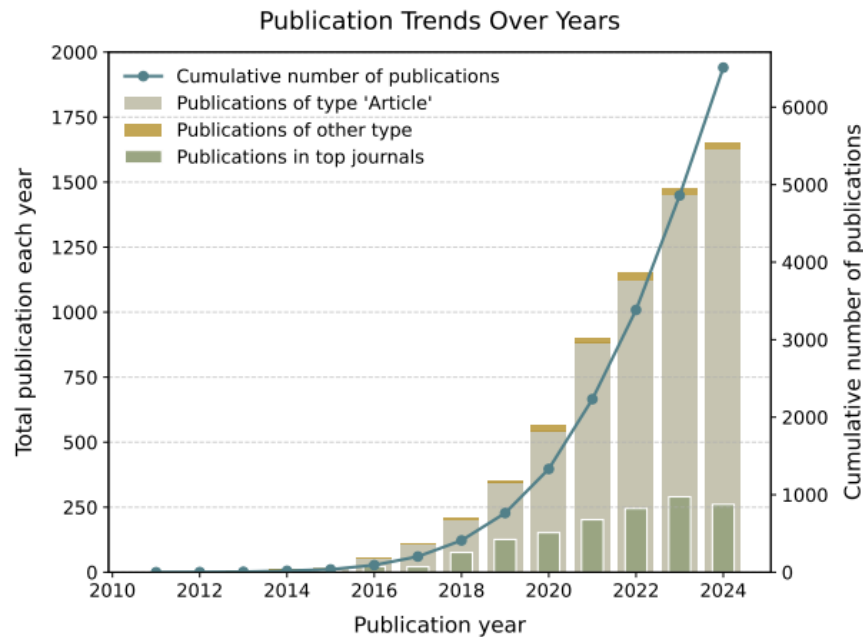
All of the data are readily available for any type of health-related research by academic and commercial researchers worldwide.

UKB has a **significant research impact, supporting numerous high-quality studies** on disease progression, risk factor identification, personalized medicine, disease prediction and prevention, and large-scale genetic research.

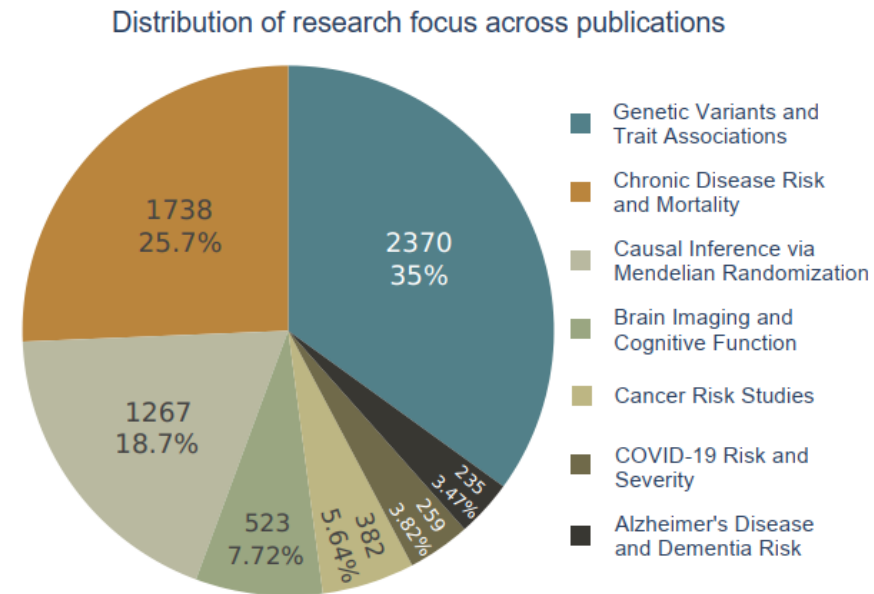
UKB-KG: BACKGROUND

UK Biobank (UKB) - The world's most important health research database

However, the dispersion of UKB-related research across numerous publications poses challenges for efficiently synthesizing and integrating findings.



(a) Publication trends over years

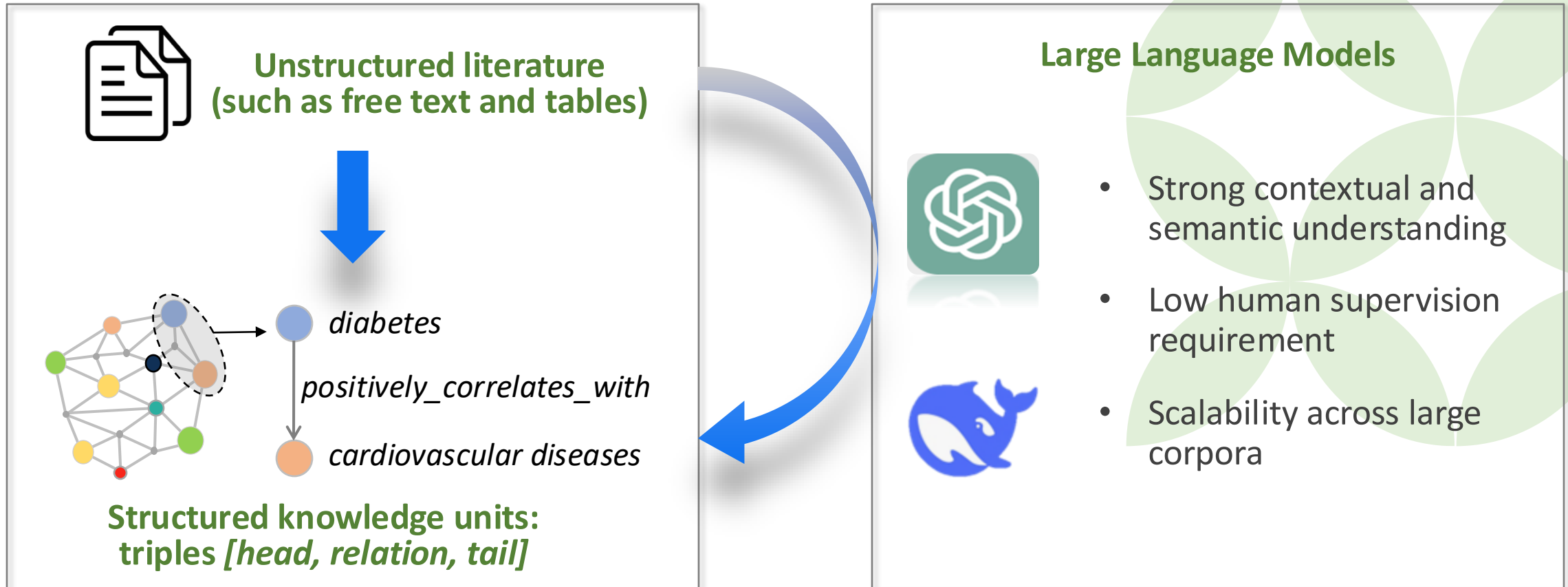


(b) Thematic distribution of publications

A **medical knowledge graph** offers an effective solution to this challenge by structurally organizing and integrating scattered UKB findings, especially with the recent support of **large language models**.

UKB-KG: BACKGROUND

Medical Knowledge Graph - a powerful tool for organizing and utilizing vast, heterogeneous biomedical data



Large language models are revolutionizing MKG construction, significantly enhanced the extraction and organization of medical knowledge from vast literature

UKB-KG: BACKGROUND

Medical Knowledge Graph - a powerful tool for organizing and utilizing vast, heterogeneous biomedical data

Existing MKGs face significant challenges.
A major limitation is the omission of **contextual features**.

❑ Source information

essential for assessing the credibility and relevance of extracted relationships

❑ Baseline characteristics

like gender, age, ethnicity, and lifestyle, influencing disease susceptibility, symptoms, and treatment outcomes.

[severe chest pain, is_a_precursor_to, heart attack]



- May primarily apply to men
- Women often exhibit atypical symptoms like fatigue

UKB-KG, a specialized and reliable MKG designed to support diverse UKB-related biomedical studies, addressing challenges like data reliability and missing contextual features

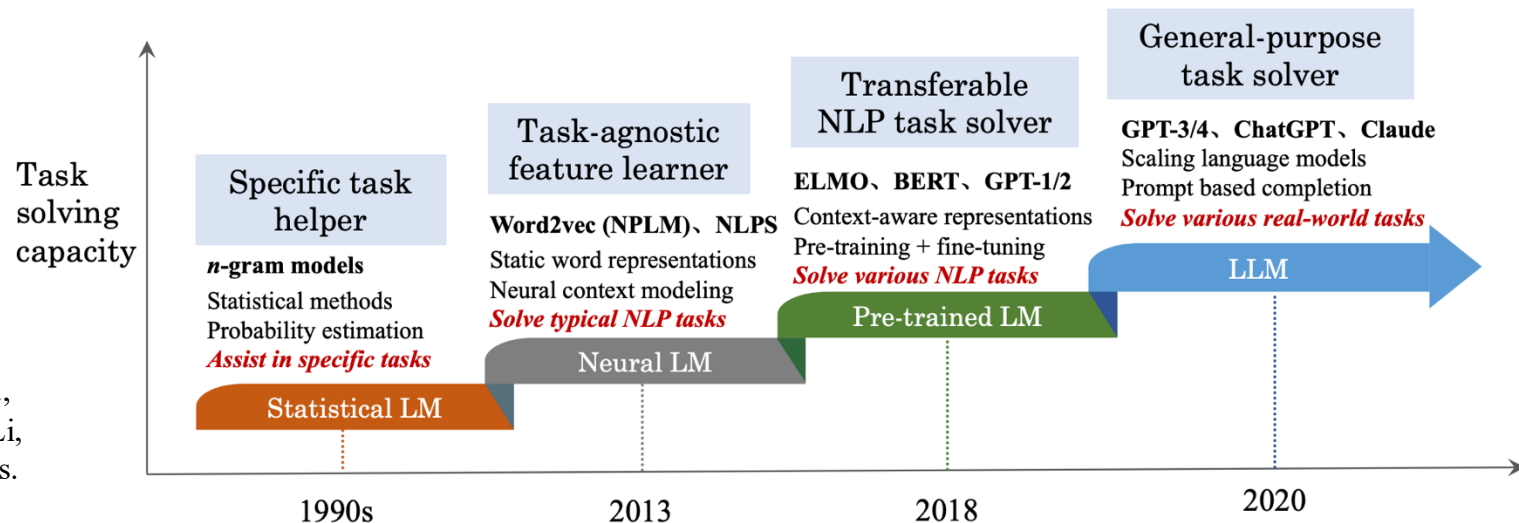
Language Models >> Large LMs (LLMs)

- **Definition:** A language model aims to predict the probability of the occurrence of a token or a sequence of tokens.
- The probability prediction of a language model is closely related to **context** and **corpus** information.
- Language model is **not a new technical** concept specially for LLMs, but has evolved with the advance of artificial intelligence over the decades.
- **Definition:** LLMs have billions of parameters, trained on massive corpora.

The screenshot shows the Hugging Face Inference API interface. On the left, the 'Fill-Mask' example is shown with the input 'I like the Disney films very much. It was [MASK]'. The output shows a list of words: 'fun', 'amazing', 'scary', 'funny', and 'fantastic', each with a probability score. On the right, the 'Mask token: [MASK]' example is shown with the input 'I hate the Disney films very much. It was [MASK]'. The output shows a list of words: 'awful', 'horrible', 'scary', 'disgusting', and 'terrible', each with a probability score. The words 'fun', 'amazing', 'scary', 'funny', 'fantastic', 'awful', 'horrible', 'scary', 'disgusting', and 'terrible' are highlighted with red boxes in the original image.

Word	Probability
fun	0.091
amazing	0.049
scary	0.042
funny	0.037
fantastic	0.036

Word	Probability
awful	0.090
horrible	0.052
scary	0.042
disgusting	0.040
terrible	0.038

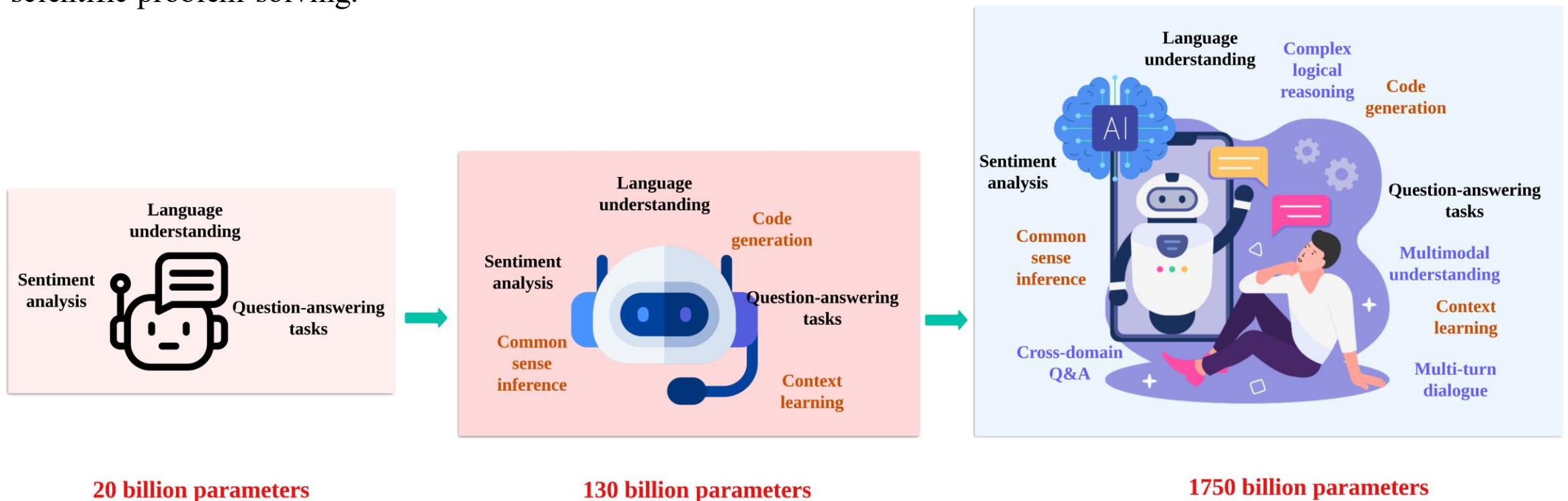


Zhao, W. X., Zhou, K., Li, J., Tang, T., Wang, X., Hou, Y., Min, Y., Zhang, B., Zhang, J., Dong, Z., Du, Y., Yang, C., Chen, Y., Chen, Z., Jiang, J., Ren, R., Li, Y., Tang, X., Liu, Z., . . . Wen, J. (2023). A Survey of Large Language Models. *ArXiv*. <https://arxiv.org/abs/2303.18223>

Evolution brings new abilities

Key Point: With the continuous iteration and updates of LLMs, the range of problems they can solve has become increasingly rich, demonstrating some new abilities.

- ▶ **Growing Complexity:** Each new LLM version shows improvements in reasoning, creativity, and context handling.
- ▶ **Emergent Properties:** Larger, more diverse training corpora lead to surprising capabilities (e.g., zero-shot translation, chain-of-thought prompting).
- ▶ **Broadening Applications:** Beyond text generation, LLMs now assist in code completion, legal drafting, and even scientific problem-solving.



Content

1. Motivation

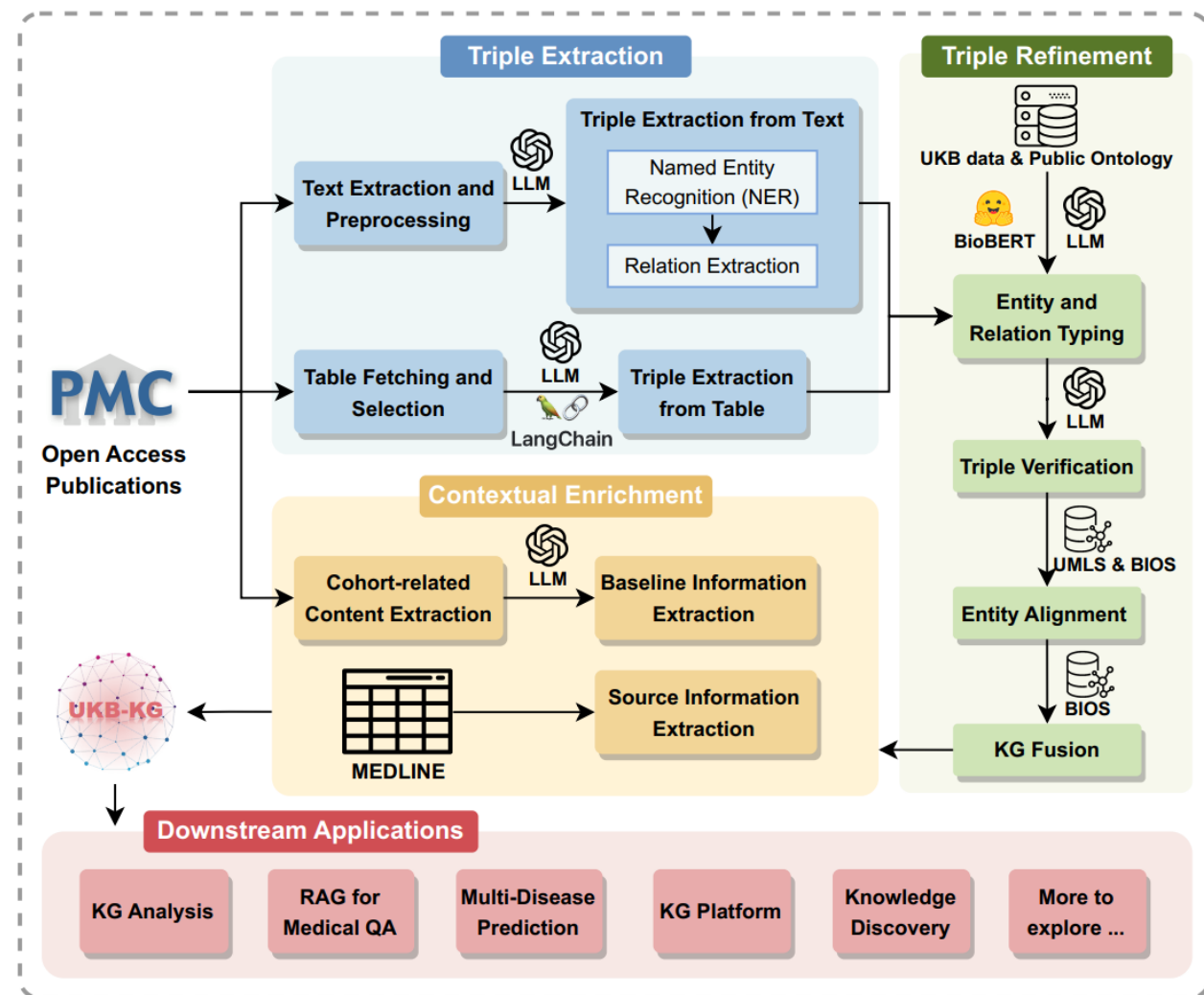
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UKB-KG: METHODS

Pipeline



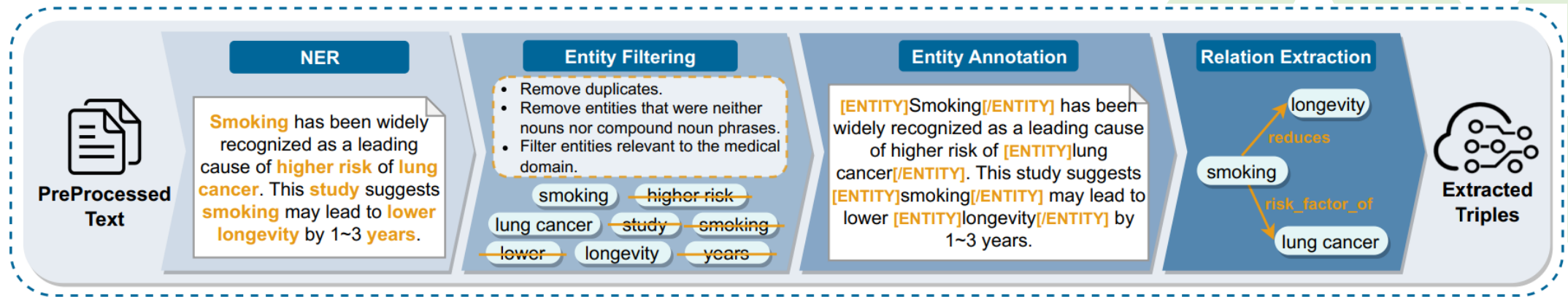
Source: PMC open access publications

- **Module1 – Triple Extraction**
- **Module2 – Triple Refinement**
- **Module3 – Contextual Enrichment**

UKB-KG: can support many downstream applications

UKB-KG: METHODS

Pipeline - Module1: Triple Extraction



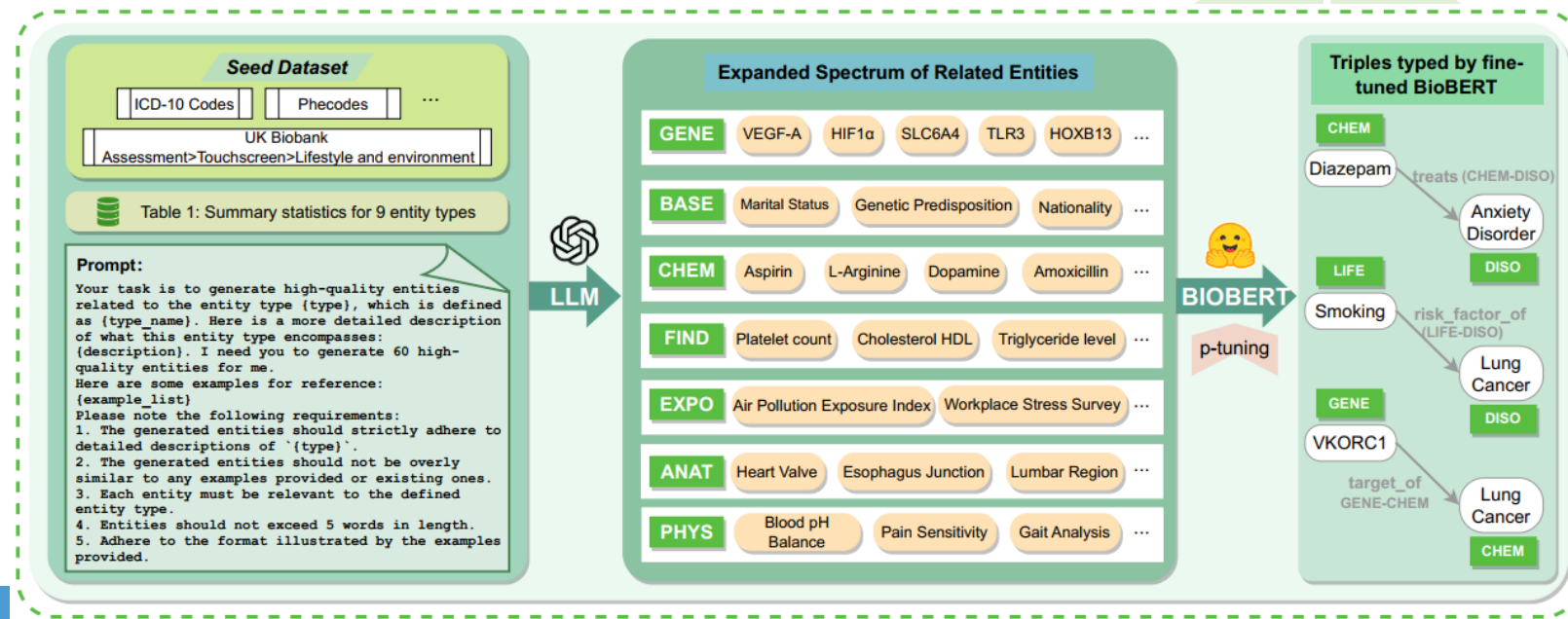
- **Named Entity Recognition (NER)**
Extract meaningful medical entities.
- **Entity Filtering**
Remove duplicates and entities unrelated to medicine.
- **Relation Extraction**
Annotate entities in the corpus using `[ENTITY]` and `[/ENTITY]` tags.
Leverage the In-Context Learning capability of LLM to extract relations.

UKB-KG: METHODS

Pipeline – Module2: Triple Refinement

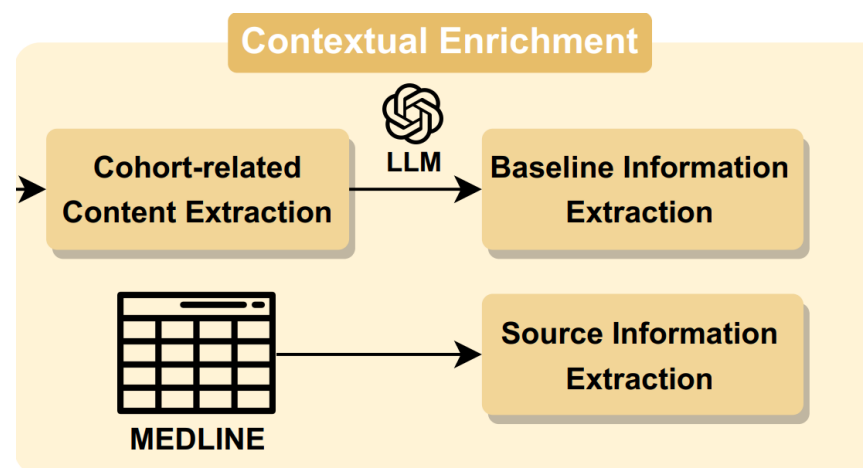
- **Triple Typing:** Classify entities into 10 categories using a BioBERT-based model trained on LLM-generated data.
- **Triple Verifier:** Apply LLM self-verification to reduce hallucinations.
- **Entity Alignment:** Standardize terms by mapping entities to UMLS and BIOS concepts.
- **Graph Fusion:** Improve graph connectivity by integrating relevant relationships by integrating relevant relationships from BIOS

The process of Triple Typing:



UKB-KG: METHODS

Pipeline – Module3: Contextual Enrichment



Add contextual attributes to each triple, including:

- **Source Information** (e.g., author, journal)
Most information was obtained from the MEDLINE Data Element (Field)
- **Baseline Information** (e.g., gender ratio, age distribution, race)
Obtained by parsing baseline tables, or extracted from the description text.



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UKB-KG: RESULTS

UKB-KG - a high quality medical knowledge graph constructed using LLMs

- Constructed from 6,858 UKB-related publications, with key insights extracted from:
 - unstructured texts in abstracts, results, and conclusions
 - structured tables, particularly genetic tables.
- Comprises 64,734 unique nodes and 137,328 relationships.
- Entities are classified into 10 types, like GENE(genes), DISO(diseases) and LIFE(lifestyle).

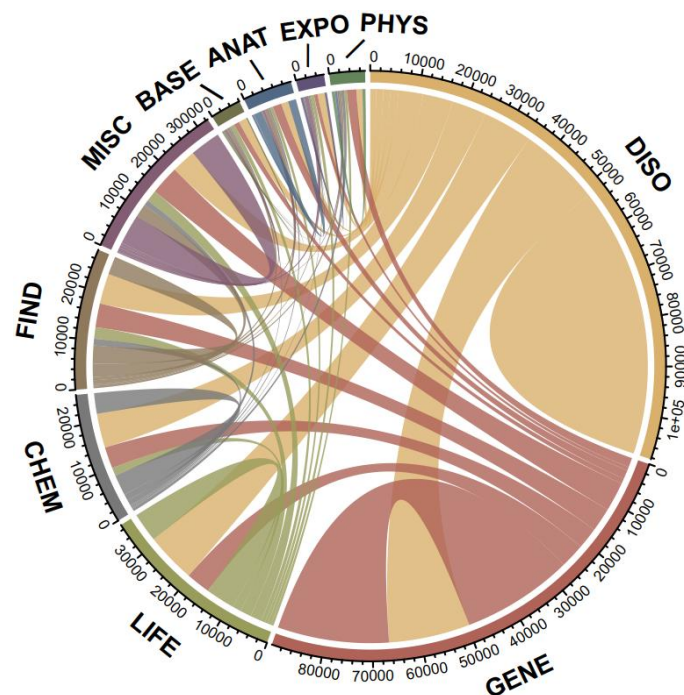
Table 1: Summary statistics for 10 entity types

Abbr	Entity Type	Count	Description
GENE	Genes & Molecular Sequences	18115(28%)	Amino acid sequence, carbohydrate sequence, gene or genome, molecular sequence, nucleotide sequence
DISO	Disorders	12236(19%)	Disease, syndrome, abnormality, injury, dysfunction, pathological function, symptom.
LIFE	Lifestyle	9427(14%)	Activity, alcohol, diet, electronic, mental health, sleep, smoking, other
MISC	Miscellaneous	7443(11%)	Miscellaneous entities that do not fit into any of the above categories
FIND	Findings	6927(11%)	Measurements of blood, eyesight, feeling, hearing, urine; Imaging data of brain MRI, cardiac MRI, abdominal MRI, DXA, carotid ultrasound, OCT
CHEM	Chemicals & Drugs	4833(7%)	A list of chemicals and drugs
EXPO	Exposure	1894(3%)	Types of environmental exposures
PHYS	Physiology	1775(3%)	Physiology-related terms
ANAT	Anatomy	1721(3%)	Various anatomical structures
BASE	Baseline	363(1%)	Baseline demographic information
Total		64734	

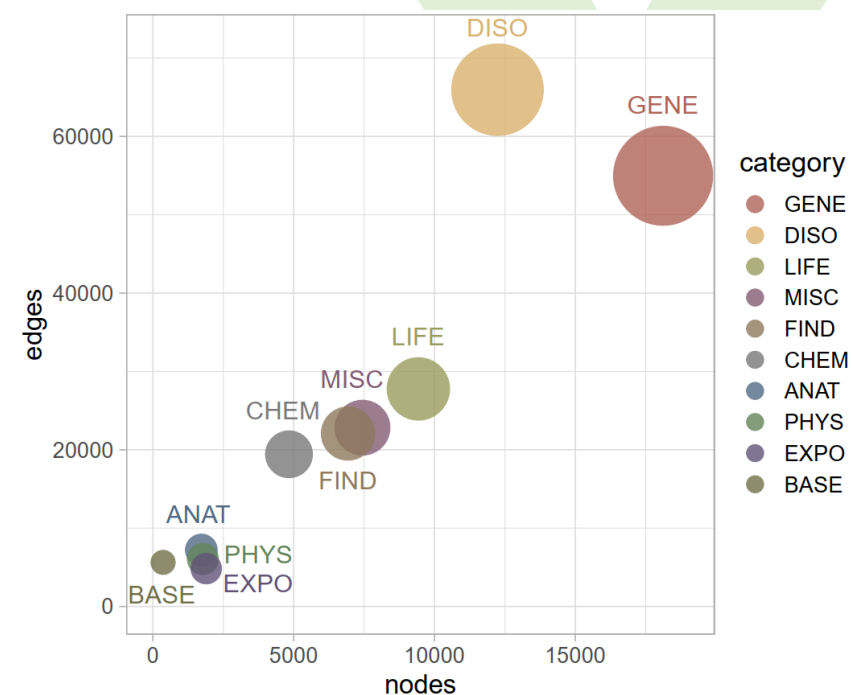
UKB-KG: RESULTS

UKB-KG - a high quality medical knowledge graph constructed using LLMs

- The flow of relationships between different types of nodes:



- The distribution of the number of nodes and edges for each type:



cholesterol
lipoproteins
pharmaceutical preparations
globulin
inhibitors
measurement
25 (oh)d
ciferol
proteins
b
tration
ol
tor i
ound
ides
te
cholesterol
polipoproteins
cholesterol lipoproteins
tration
ol
tor i
ound
ides
te
cholesterol
polipoproteins
cholesterol lipoproteins
tration

UKB-KG - a high quality medical knowledge graph constructed using LLMs

- The Entity Cloud which highlights key nodes in the UKB-KG across DISO, CHEM, LIFE, and FIND categories:



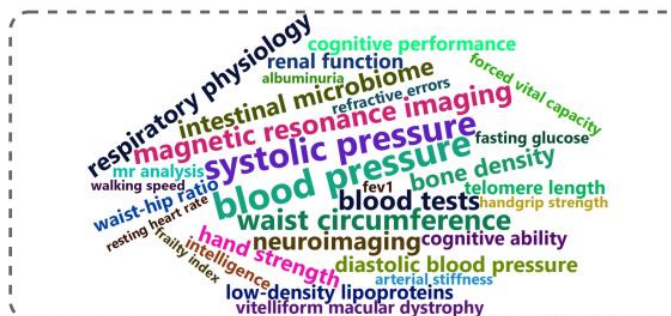
(a) DISO entity cloud



(b) CHEM entity cloud



(c) LIFE entity cloud



(d) FIND entity cloud

UKB-KG: RESULTS

UKB-KG - a high quality medical knowledge graph constructed using LLMs

A distinguishing feature of UKB-KG is the inclusion of extensive contextual information for the triple's relational properties

Source Info	Abstract, Affiliation, Article Identifier, Author, Author Identifier, Full Author, Date of Electronic Publication, Date of Publication, Grant Number, ISSN, Issue, Journal Title Abbreviation, Journal Title, Language, Location Identifier, Publication History Status, Publication Type, PubMed Central Identifier, PubMed Unique Identifier, Source, Title, Volume, Keywords, URL, Journal Impact Factor, Citations, If use UKB data
-------------	---

Baseline Info	Cohort name, Overall sample size, Average age, Age distribution, Gender ratio, Gender distribution, Major race, Racial distribution, Educational attainment, Employment status
---------------	--

```
"relation": {  
  "name": "associated_with",  
  "type": "MISC-DIS0",  
  "PMCID": "PMC10353935",  
  "PMID": "37414900",  
  "Title": "A multi-ancestry polygenic risk score improves risk predict",  
  "Journal": "Nature Medicine",  
  "Publication_Date": "2023",  
  "Keywords": "Risk factors, Myocardial infarction, Genetics research",  
  "URL": "https://doi.org/10.1038/s41591-023-02429-x",  
  "DOI": "10.1038/s41591-023-02429-x",  
  "Confidence_Score": 0.7003599319457624
```

UKB-KG: RESULTS

UKB-KG - a high quality medical knowledge graph constructed using LLMs

➤ Triple Precision Evaluation:

Macro Precision	Micro Precision	Number of Recalls
85.62	85.03	9.37

Evaluation method: A random sample of 150 abstracts is selected, from which triples are extracted using GPT-3.5 and evaluated for accuracy using GPT-4o.

➤ Graph Structure Evaluation:

Node Count	Average Clustering Coefficient	Betweenness Centrality.mean	Betweenness Centrality.max
1423	0.023	3.35	575.00

Evaluation is based on a random sample of 150 abstracts.

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UKB-KG: APPLICATIONS

UKB-KG enables diverse downstream applications across biomedical research, including:

- **Multi-Disease Prediction**
- **Retrieval-Augmented Generation (RAG)**
- **Interactive Platform for UKB-KG**

UKB-KG: APPLICATIONS

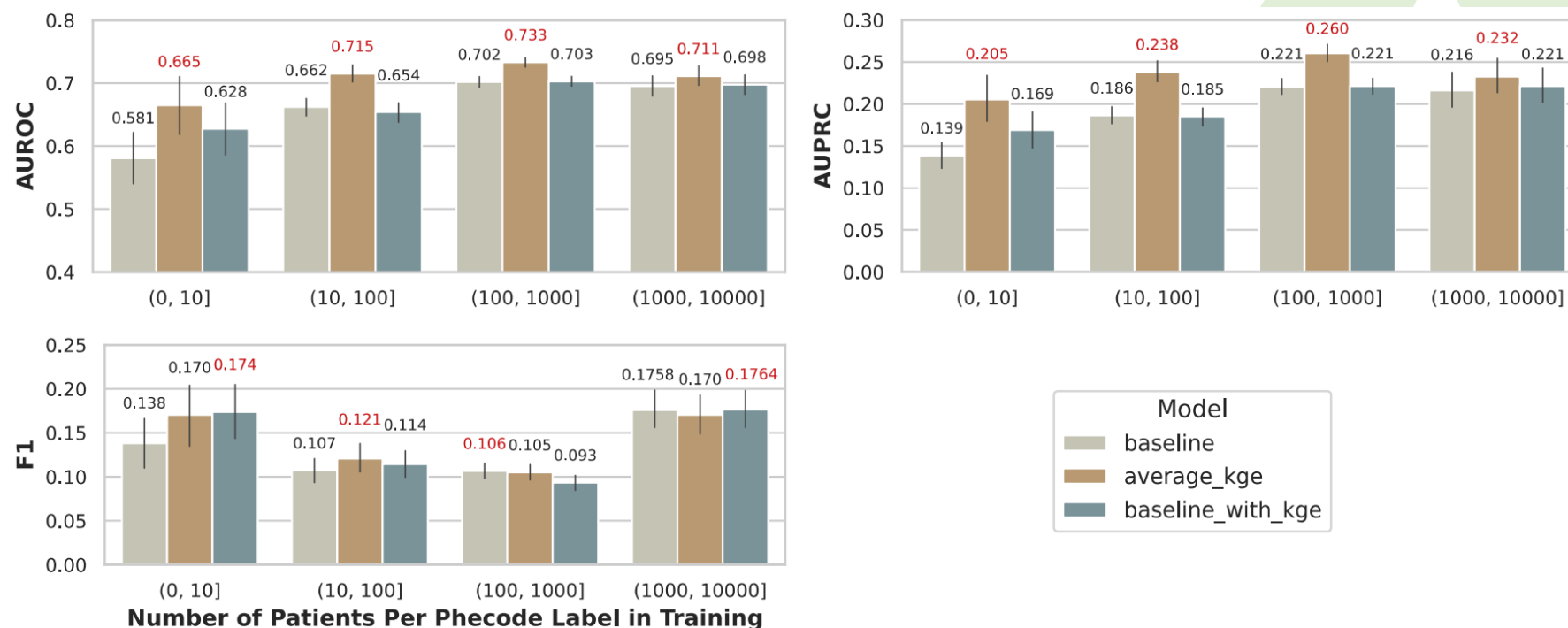
Multi-Disease Prediction

Incorporate domain knowledge through **Knowledge Graph Embeddings (KGE)** of UKB-KG to enhance disease prediction.

- **Task objective:** predict the occurrence of diseases in the next six months, based on prior medical histories.
- **Dataset:** 278,985 instances from UKB
- **Approaches:**
 - **Baseline:** use **binary indicators** (1 for presence, 0 for absence) of medical history variables as input features (1560-d vector)
 - **Average_KGE:** First, each medical history record is mapped to a node in the UKB-KG. Then use the **average KGE** of all mapped nodes as input features (1000-d vector)
 - **Baseline_with_KGE:** the input combines the baseline features with the average KGE features (2560-d vector)

UKB-KG: APPLICATIONS

Multi-Disease Prediction



UKB-KGE significantly enhances multi-disease prediction accuracy, particularly for **rare diseases with limited data**, by mitigating data insufficiency through the integration of prior knowledge.

UKB-KG: APPLICATIONS

Retrieval-Augmented Generation (RAG)

Retrieve relevant knowledge from the UKB-KG to augment medical question answering

- **Task objective:** Answer medical questions with “Yes,” “No,” or “Maybe”
- **Medical QA Dataset:** PubMedQA
- **Approaches:**
 - *LLM itself*
 - *Zero/Few-shot CoT*
 - *UKB-KG based RAG:* A graph-based RAG method tailored to UKB-KG, combining neighbor-based and path-based retrieval strategies while incorporating triple confidence scores derived from contextual features and semantic similarity.

UKB-KG: APPLICATIONS

Retrieval-Augmented Generation (RAG)

	GPT-4o	Zero-shot CoT	One-shot CoT	UKB-KG based RAG
Accuracy	0.508	0.600	0.668	0.720
Macro-F1	0.488	0.544	0.594	0.633
Macro-Precision	0.632	0.612	0.628	0.646

The UKB-KG based RAG leverages the UKB-KG as an **external knowledge source** to retrieve relevant information in real time, thereby enhancing the accuracy and reliability of **medical question answering**

UKB-KG: APPLICATIONS

Interactive Platform for UKB-KG - a user-friendly graph platform for viewing and analyzing UKB-KG data

The platform supports complex graph queries, contextual feature exploration, and a RAG Chatbot, enabling efficient access to essential information and insights, even for users with limited technical expertise.

Customized settings available
for **graph search**:

Advanced Search

Node 1: ☐ Any ☒ Set Node1
Enter Node1 value:

Type 1: ☒ Any ☐ Set Type1

Relation Property: ☐ ☒ Set Relation
Enter Relation property:

Node 2: ☐ Any ☒ Set Node2
Enter Node2 value:


Type 2: ☐ Any ☒ Set Type2

HOP: LIMIT:


☒ Graph ☐ Table


UKB-KG: APPLICATIONS


Interactive Platform for UKB-KG - a user-friendly graph platform for viewing and analyzing UKB-KG data



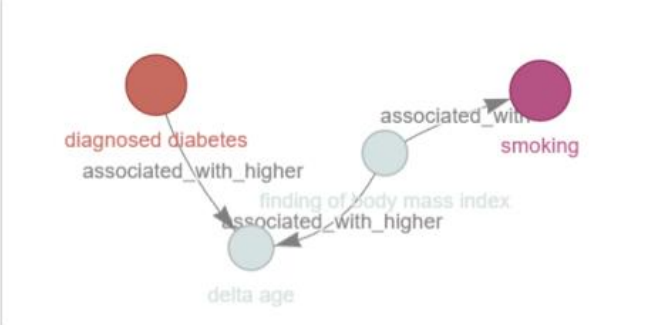
Chatbot

 How can I help you?

 Are diabetes related to smoking?

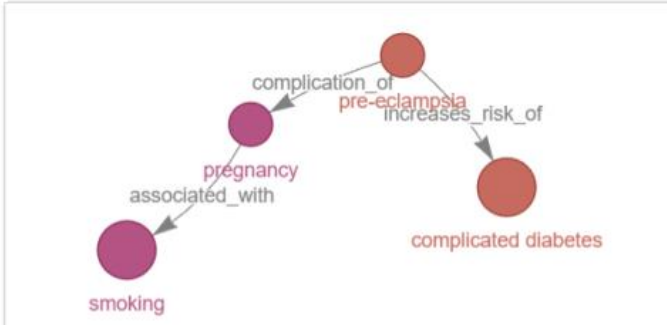
 Yes, smoking is related to an increased risk of developing type 2 diabetes. Smoking initiation has been shown to have widespread risk effects, including on common diseases such as type 2 diabetes. It acts as a risk factor for this condition, adding to the body's stress and potentially contributing to insulin resistance and other metabolic issues related to diabetes.

6. Path from **diagnosed diabetes** to **smoking**



```
graph LR; A((diagnosed diabetes)) -- "associated_with_higher" --> B((delta age)); B -- "associated_with_higher" --> C((finding of body mass index)); C -- "associated_with" --> D((smoking))
```

2. Path from **complicated diabetes** to **smoking**



```
graph LR; A((smoking)) -- "associated_with" --> B((pregnancy)); B -- "complication_of" --> C((pre-eclampsia)); C -- "increases_risk_of" --> D((complicated diabetes))
```

RAG Chatbot example: the answer to “Are diabetes related to smoking?” accompanied by **Path-based Context**, highlighting potential direct or indirect relationships between *diabetes* and *smoking*

UKB-KG: APPLICATIONS

Interactive Platform for UKB-KG - a user-friendly graph platform for viewing and analyzing UKB-KG data

Chatbot

How can I help you?

What diseases are related to COVID-19?

COVID-19 is related to several diseases, particularly through its severity and outcomes. Some key diseases and conditions that are related to COVID-19 include:

- Metabolic Disorders:** These include conditions like diabetes which have been associated with increased severity of COVID-19.
- Cardiovascular Conditions:** Pre-existing heart conditions, hypertension, and other cardiovascular diseases are linked to an increased risk of severe outcomes in COVID-19 patients.
- Obesity:** Obesity is significantly associated with greater severity of COVID-19, increasing the risk of complications and hospitalizations.
- Pre-existing Respiratory Conditions:** Diseases such as asthma have been linked to more severe manifestations of COVID-19.

These conditions can affect the clinical outcomes of COVID-19 and are often used in assessing the risk profiles for those infected with the virus.

See context

See context

Neighbor-based Path-based

Neighbor-based Context

- Triple 1:** [metabolic diseases, related_to, covid-19 severity prs] [PMCID10763941]

Relevant text:

(1)
Abstract: ObjectiveTo overcome the limitations associated with the collection and curation of COVID-19 outcome data in biobanks, this study proposes the use of polygenic risk scores (PRS) as reliable proxies of COVID-19 severity across three large biobanks: the Michigan Genomics

- Triple 2:** [cardiovascular conditions, related_to, covid-19 severity prs] [PMCID10763941]

Relevant text:

(1)
Abstract: ObjectiveTo overcome the limitations associated with the collection and curation of COVID-19 outcome data in biobanks, this study proposes the use of polygenic risk scores (PRS) as reliable proxies of COVID-19 severity across three large biobanks: the Michigan Genomics

- Triple 3:** [obesity, related_to, covid-19 severity prs] [PMCID10763941]

Relevant text:

(1)
Abstract: ObjectiveTo overcome the limitations associated with the collection and curation of COVID-19 outcome data in biobanks, this study proposes the use of polygenic risk scores (PRS) as reliable proxies of COVID-19 severity across three large biobanks: the Michigan Genomics

RAG Chatbot example: response to “What diseases are related to COVID-19?” accompanied by **Neighbor-based Context**, which includes *COVID-19*-related triples, associated PMCIDs, hyperlinks, and source texts.

Thank You!