Analysing the extent of cell type information present in Wikidata

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Abstract

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Keywords: wikidata, knowledge graph, cell type, ontology.

Introduction

Wikidata

<u>Wikidata</u> is an open, freely editable, knowledge graph database within the <u>semantic web</u> that stores knowledge across a multitude of domains, such as arts, history, chemistry and biology, using an itemproperty-value linked data model (Figure 1). It is easy to use and edit, by both humans and machines, with a rich web user interface and wrapper packages available in common programming languages such as R and Python. All the data within Wikidata is linked and inherently public domain, thus, it presents a great opportunity to make scientific data more FAIR (Findable, accessible, interoperable and reusable), as well as provides the necessary tools to curate and develop ontologies.

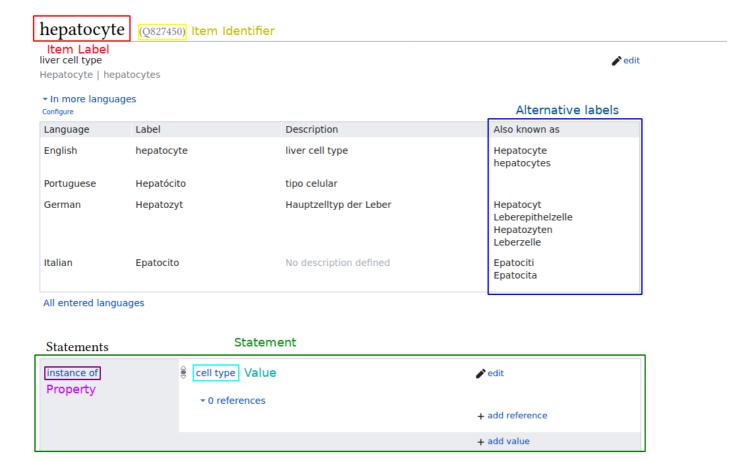


Figure 1: Wikidata item example, showing item hepatocyte (Q827450), the labels change according to the user's language, but each item has a universal identifier, called QID.

Several advances towards biological data integration and biological data analysis in Wikidata have been made before, yielding positive results [1] [2] and showcasing it's potential for bioinformatics-related analyses, such as drug repurposing and ID conversion [2]. Wikidata has been proposed as a unified base to gather and distribute biomedical knowledge, with more than 50 000 human gene items indexed and hundreds of biomedical-related properties [3]. However, as of August 2020, cell type information is still very scarse, with only 264 items being categorized as instances of cell types (Q189118), of those, only nine have a "Cell Ontology ID"[4] (P7963) associated, and most have a varying amount of statements (Table 1).

Table 1: As of August 2020, Wikidata items regarding cell types have a varying amount of information, with most having very few statements.

Cell type Item	Number of statements
red blood cell (Q37187)	48
myocyte (Q428914) 18	
mesenchymal cell (Q66568500)	2

PanglaoDB

<u>PanglaoDB</u> [5] is a public database that contains data and metadata on hundreds of single-cell RNA sequencing experiments, providing extensive information on cell types, genes and tissues, as well as manually and community curated cell type markers (Table 2). It also provides a rich web user interface for easy data acquisition, including database dumps for bulk downloads.

Table 2: Database statistics for each species in PanglaoDB, as of 31st August 2020.

	Mus musculus	Homo sapiens
Samples	1063	305
Tissues	184	74
Cells	4,459,768	1,126,580
Cell Clusters	8,651	1,748

Objectives

In this study, we aim to answer questions regarding the integration of biological data from PanglaoDB in Wikidata, analysing items such as cell types, genes and tissues. Some of the questions we gathered so far are:

- How many cell types in PanglaoDB are also present in Wikidata? How many of those items are exact matches?
- Of those that are exact matches, how many statements do they have associated? Are these items well annotated?
- How does the coverage of biological items differ within Wikidata? Are the items for tissues and genes better annotated? How so?
 - Do items with alternative identifiers, such as genes, have their alternative identifiers indexed within Wikidata?

In the end, we'll have gathered and analysed enough data to formulate a report on the integration of this knowledge. We also intend to migrate the missing data, enriching Wikidata with more biological information.

Methodology

Data acquisition

Data from Wikidata will be acquired using the <u>Wikidata Query Service</u> and associated wrapper packages in Python, such as <u>WikidataIntegrator</u> and <u>wikidata2df</u>.

Data from PanglaoDB will be acquired through their <u>web interface</u> and <u>metadata database dump repository</u>.

All data used will be handled with commonly used Python data science packages, such as Pandas[6], Seaborn[7] and Jupyter[8].

Reconciliation

The data from PanglaoDB will be matched to Wikidata items using the <u>reconciler</u> Python package, which is itself a wrapper around the well known <u>OpenRefine</u> reconciliation service, as well as manual intersections of both data sources. Data from the reconciliation service will be considered a match if the service returns a value of "match" equals to "True" or if the actual labels are semantically similar, which can be assessed either manually or using automated sequence similarity approaches, such as Levenshtein distance and word2vec.

Item quality assessment

Wikidata items will be assessed for their quality by their number of statements, which can be acquired via both the <u>MediaWiki API</u> and Wikidata's own query service. And also by the presence of external identifiers, such as Ensembl Gene[9] and Entrez Gene[10] IDs for genes, Cell Ontology[4] IDs for cell types and Uberon[11] IDs for organs and tissues.

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