LINKÖPING UNIVERSITY
Institutionen för datavetenskap
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Tentamen

Advanced Data Models and Databases

2025

Grades:

For a pass grade all questions need to be answered and almost all correctly answered.

Instructions:

- This is an *individual* exam. If you have questions, ask the course leader.
- Send your answers to Patrick Lambrix via internal mail or e-mail.
- You can send answers as soon as you have finished them, i.e., no need to wait until you have answered everything.
- Deadline: February 1, 2026.
- If there are references to papers in the questions, then links to the papers will be on the course home page.

Question 1: Information Retrieval

Assume that we have two documents in our document base. Document 1 contains 'enzyme' 5 times, 'gene' 10 times, 'protein' 0 times and 'signal' 8 times. Document 2 contains 'enzyme' 0 times, 'gene' 0 times, 'protein' 7 times and 'signal' 1 time.

(i) Assume that we use the vector model for information retrieval. Assume that we are only interested in the words 'gene', 'enzyme', 'protein' and 'signal'.
1. Explain tf and idf in the vector model.
2. In which cases is a weight w_{ij} in a document vector equal to 0?
3. Give the document representations for Document 1 and Document 2 according to the tf-idf model.

(ii) Assume that we use the boolean model for information retrieval. Assume that we are only interested in the words 'gene', 'enzyme', 'protein' and 'signal'.
1. Give the document representations for Document 1 and Document 2 according to the Boolean model.
2. Represent the query for all documents containing gene or protein, but not signal. Compute then the completed DNF (disjunctive normal form) of the query.

Question 2: Description Logics

Define the following concepts using description logics:

C1: animals that have at least 4 legs and all foods they eat are wheat plants
C2: animals that have at least 2 legs and all foods they eat are plants

Does C2 subsume C1, i.e. C1 isa C2? Prove your answer using a tableau algorithm. (NOTE: Use the Baader, Nutt chapter in the reading list.)

Question 3: DB vs KB

Describe the difference between open-world assumption and closed-world assumption. Give examples.

Question 4: Ontology Engineering

(i) Give 4 different kinds of matchers for ontology alignment. For each kind of matcher give an example and explain briefly what it does.

(ii) Given the following axioms in an ontology: $A \sqsubseteq B$; $A \sqsubseteq E$; $B \sqsubseteq C$; $B \sqsubseteq D$; $C \sqsubseteq F$; $D \sqsubseteq F$; $F \sqsubseteq G$; $E \sqsubseteq G$; $A \sqsubseteq \neg G$.

Debug the ontology. Compute MIPS and MUPS.

Question 5. Semi-structured data

(i) Below, a (simplified) description of the biological data source PIR-PSD, is given. This data source contains information about protein sequences. Each entry in the data source has information about the entry (identification numbers, dates of creation and update), names of the protein sequence and the parts that it contains, the organism from which the sequence was taken, references to the literature describing the sequence, references to other related databases and the protein sequence. The simplified PIR-PSD schema is given as a DTD. Draw a strong data guide for PIR-PSD. Use the OEM model.

```
<!-- ******************************************************************
PIR-International Protein Sequence Database (PSD)
******************************************************************* -->

<!-- ProteinEntry: the root element. -->
<!ELEMENT ProteinEntry (header,protein,organism,reference*,sequence)>

<!-- header: database information. -->
<!ELEMENT header (uid,accession*,created_date,seq-update_date)>

<!ELEMENT accession (#PCDATA)> <!-- accession number -->
<!ELEMENT created_date (#PCDATA)> <!-- date (DD-MMM-YYYY) -->
<!ELEMENT seq-update_date (#PCDATA)> <!-- date (DD-MMM-YYYY) -->

<!-- protein: the protein-names. -->
<!ELEMENT protein(name,alt-name*,contains*)>

<!ELEMENT name (#PCDATA)> <!-- protein name -->
<!ELEMENT alt-name (#PCDATA)> <!-- alternate protein name -->
<!ELEMENT contains (#PCDATA)> <!-- activity name -->

<!-- organism: identification of the biological source. -->
<!ELEMENT organism (source,common-name?,note*)>

<!ELEMENT source (#PCDATA)> <!-- source name -->
<!ELEMENT common-name (#PCDATA)> <!-- common name -->

<!-- reference -->
<!ELEMENT reference (refinfo,note*)>

<!-- refinfo: identification of the literature source. -->
<!ELEMENT refinfo (authors,citation,title?,xrefs?)>

<!ELEMENT authors (author+)> <!-- list of authors -->
```

```
<!ELEMENT author (#PCDATA)> <!-- author name -->
<!ELEMENT citation (#PCDATA)> <!-- citation name -->
<!ELEMENT title (#PCDATA)> <!-- title text -->

<!ELEMENT xrefs (xref+)> <!-- cross-references -->
<!ELEMENT xref (db,uid)> <!-- a cross-reference -->
<!ELEMENT db (#PCDATA)> <!-- database tag -->

<!-- sequence: the amino acid sequence. -->
<!ELEMENT sequence (#PCDATA)> <!-- amino acid symbols and
 punctuation -->

<!-- General elements. Elements that can be contained in several
 other elements. -->
<!ELEMENT note (#PCDATA)> <!-- note text -->
<!ELEMENT uid (#PCDATA)> <!-- entry identifier -->
```

(ii) In figures 1 and 2 (simplified and slightly modified) data from a SwissProt data source is given. (The dashed nodes in the figures refer to nodes in the other figure. Both figures together make up the data source.) Draw a strong data guide for this data. Use the OEM model.

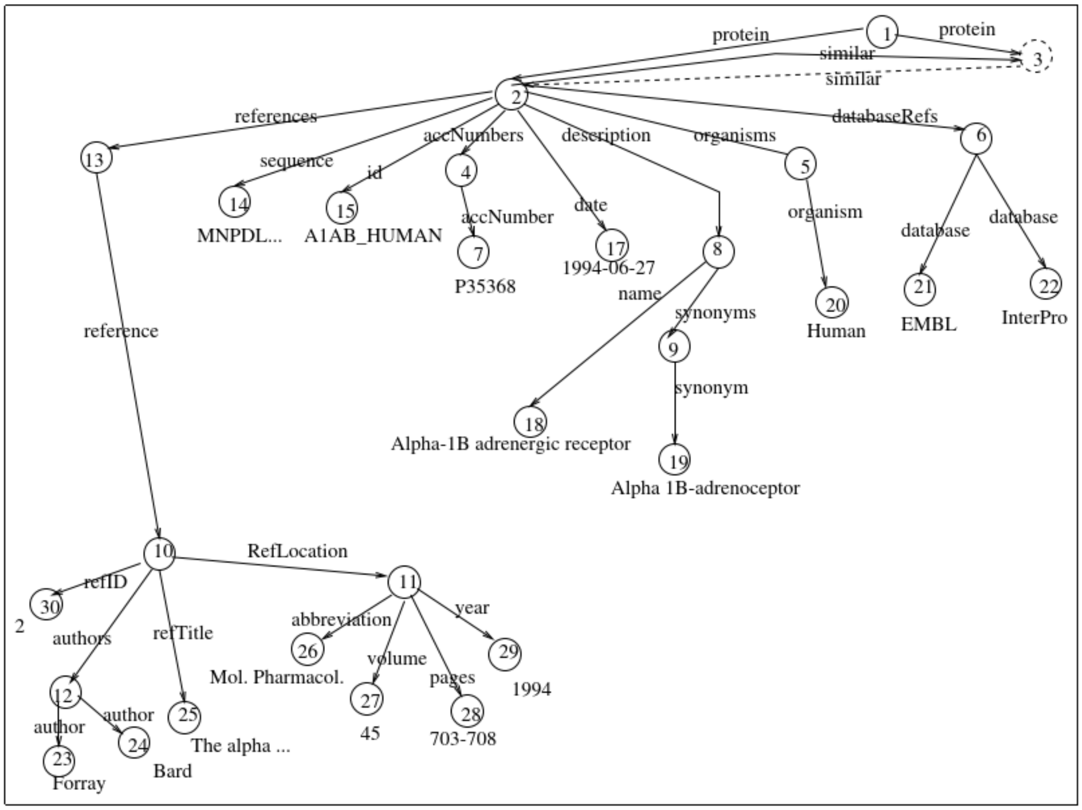

Fig. 1. SwissProt db - 1

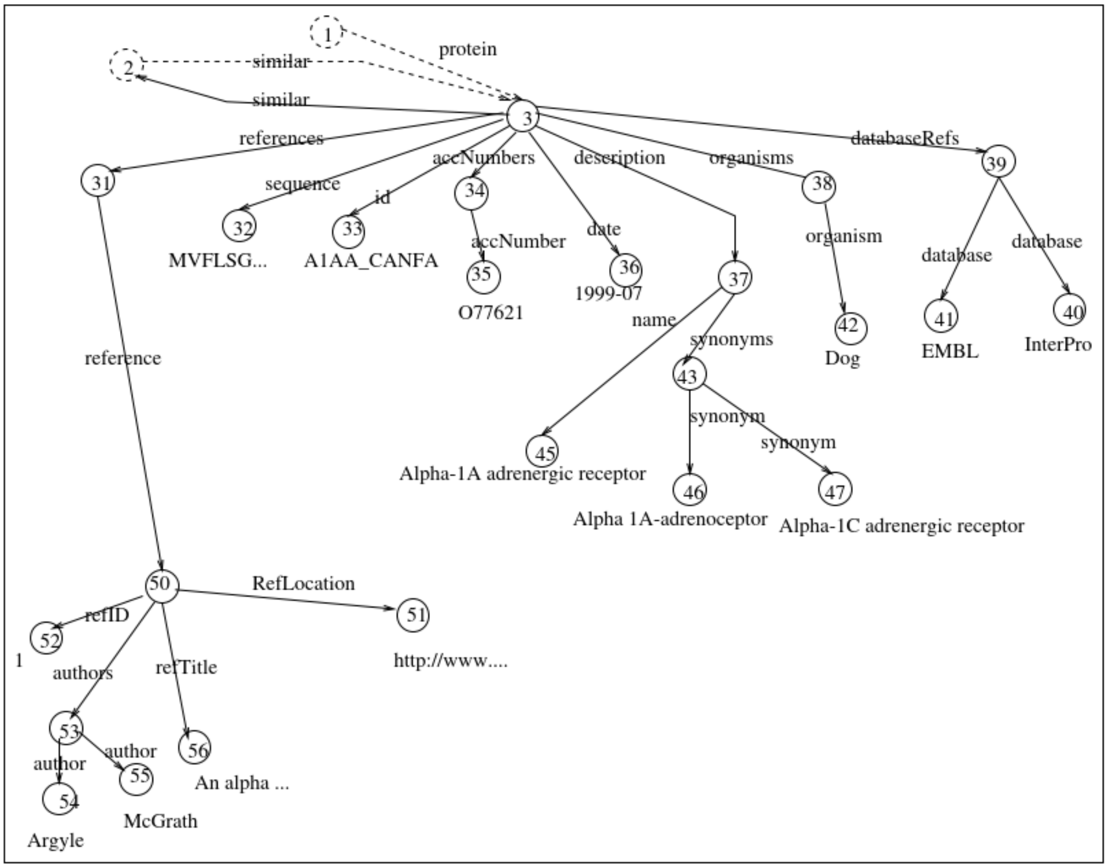

Fig. 2. SwissProt db - 2

More questions to be added later