# Semantic annotation in the Alvis project

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Adeline Nazarenko[2], Claire Nédellec[1],
Erick Alphonse[1], Sophie Aubin[2],
Thierry Hamon[2], Alain-Pierre Manine[1]

[1] Laboratoire Mathématique, Informatique et Génome (MIG), INRA

[2] Laboratoire d'Informatique de Paris-Nord (LIPN),
Université Paris-Nord & CNRS

# Alvis project

Developing new technologies for distributed, topic-specific semantic-based search on internet

Query:

*Author*=person:*Crick* and *Author*=person:*Watson* and
*Paper_title*=title:*The structure of DNA* and *Publication_date*=date:*1953*

Search for documents that comment the *famous* paper.

Answer : BBC news in 1953
"*in an article published* ***today*** *in Nature magazine, James D.* ***Watson*** *and Francis* ***Crick*** *describe the structure of a chemical called* ***d****esoxyribo****n****ucleic* ***a****cid,[..].*

# Limitation of the keyword-based search

- Queries and search based on **keywords cooccurrences** do not exploit **semantic roles** (semantic types and relations).
- Although the simple cooccurrence of the four terms (*Crick*, *Watson*, *DNA structure*, *1953*) can be just spurious.

- Variations are not identified (***d**esoxyribo**n**ucleic **a**cid* = *DNA structure* = *structure of DNA*)

- Individual terms may be semantically ambiguous (*Watson*).

# Our framework

- Semantic search in Alvis relies on the **semantic annotation** of fined-grain semantic units and relations in the documents and their indexing.

- In specific domains, non-ambiguous annotation can be achieved by **linguistic analysis** and **domain-dependent resources.**

- Specific resources can be automatically acquired by **corpus-based machine learning methods.**

# Annotation of semantic unit and relation requires linguistic processing

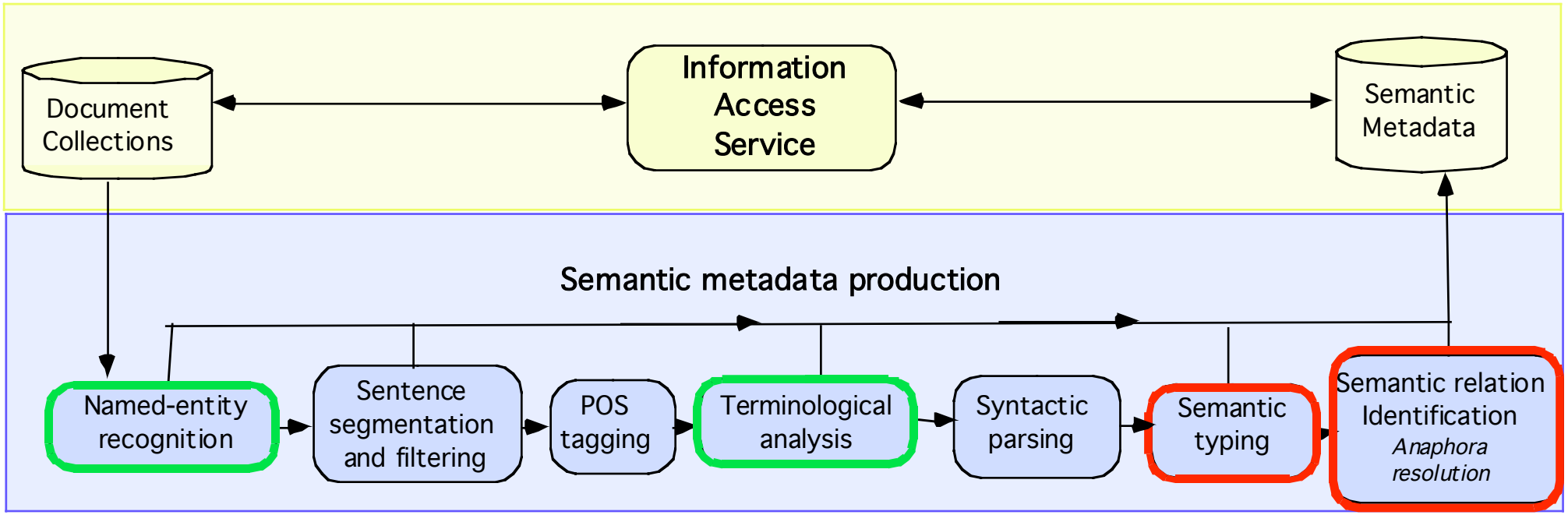
- The semantic units refer to the concepts and objects of the domain.
  - They do not always appear in their canonical form (variation and synonymy issues)
    *Sigma K / sigma(K)*
    *Serum response element / Serum response factor*
  - They may be ambiguous (polysemy issue)
    *Has* (both a gene and a verb)

The linguistic analysis of the semantic unit **morphology** and **contexts** solve these problems.

- Cooccurrence says little about the semantic relations

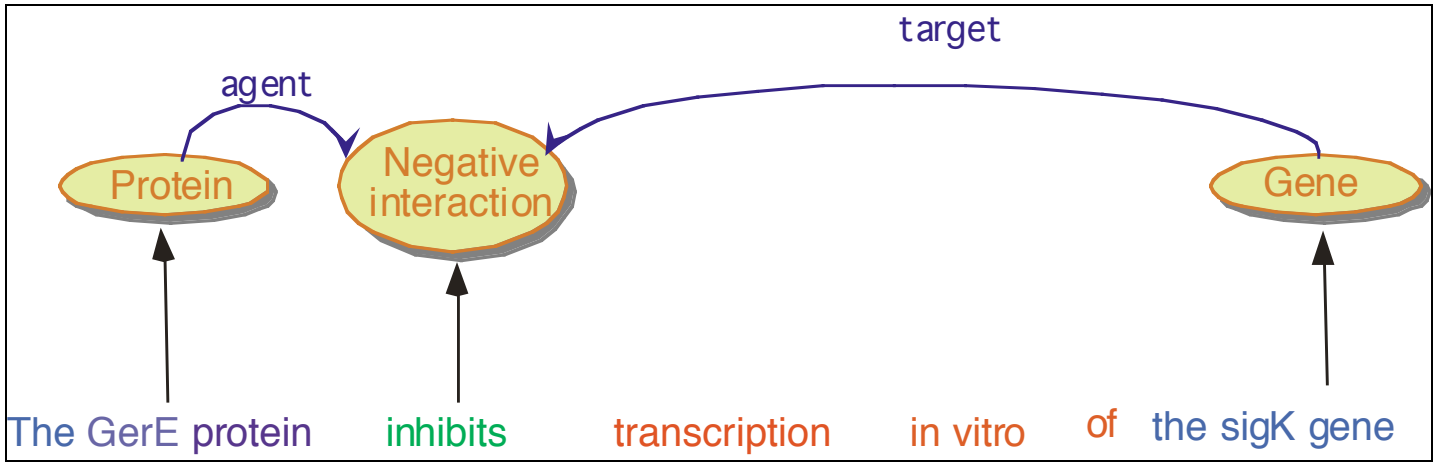
  *GerE stimulates cotD transcription and cotA transcription [...], and, unexpectedly, inhibits [...] transcription of the gene (sigK) [...]*

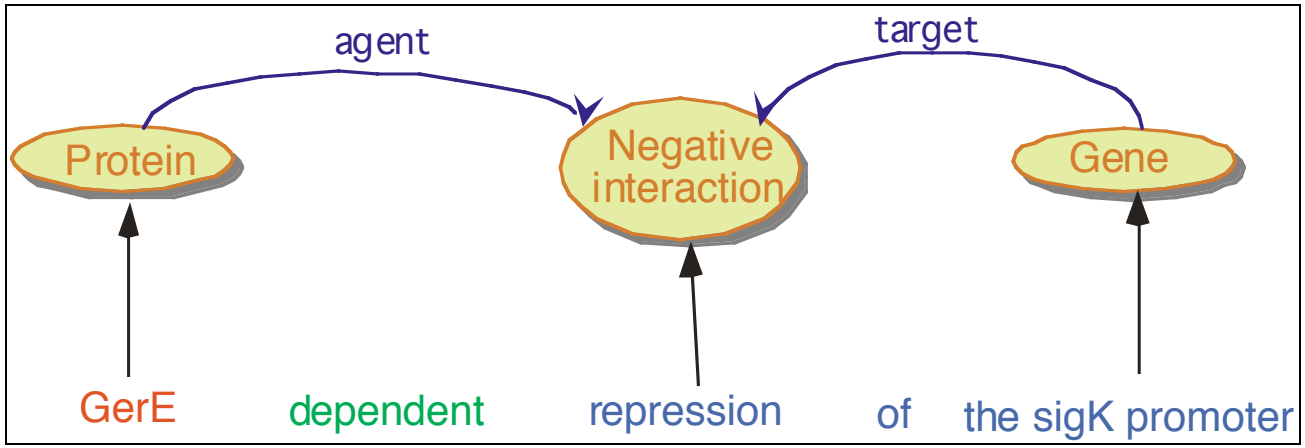
# Semantic annotation with linguistic processing



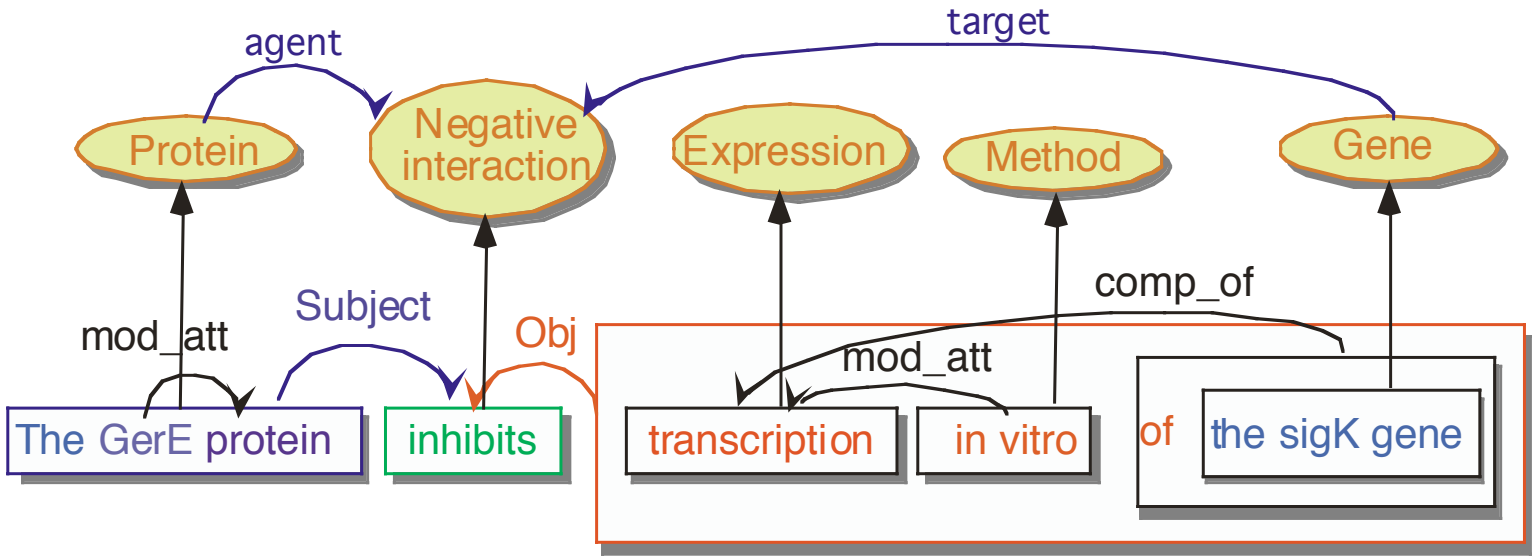
# Semantic abstraction

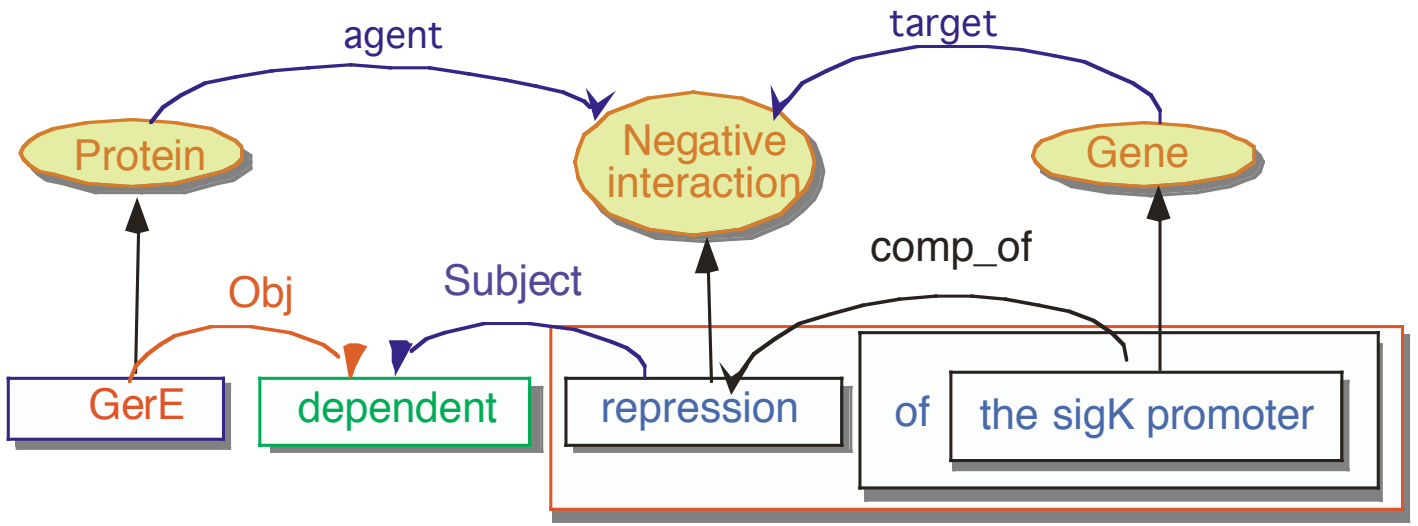
A same semantic representation of different formulations for efficient IR.



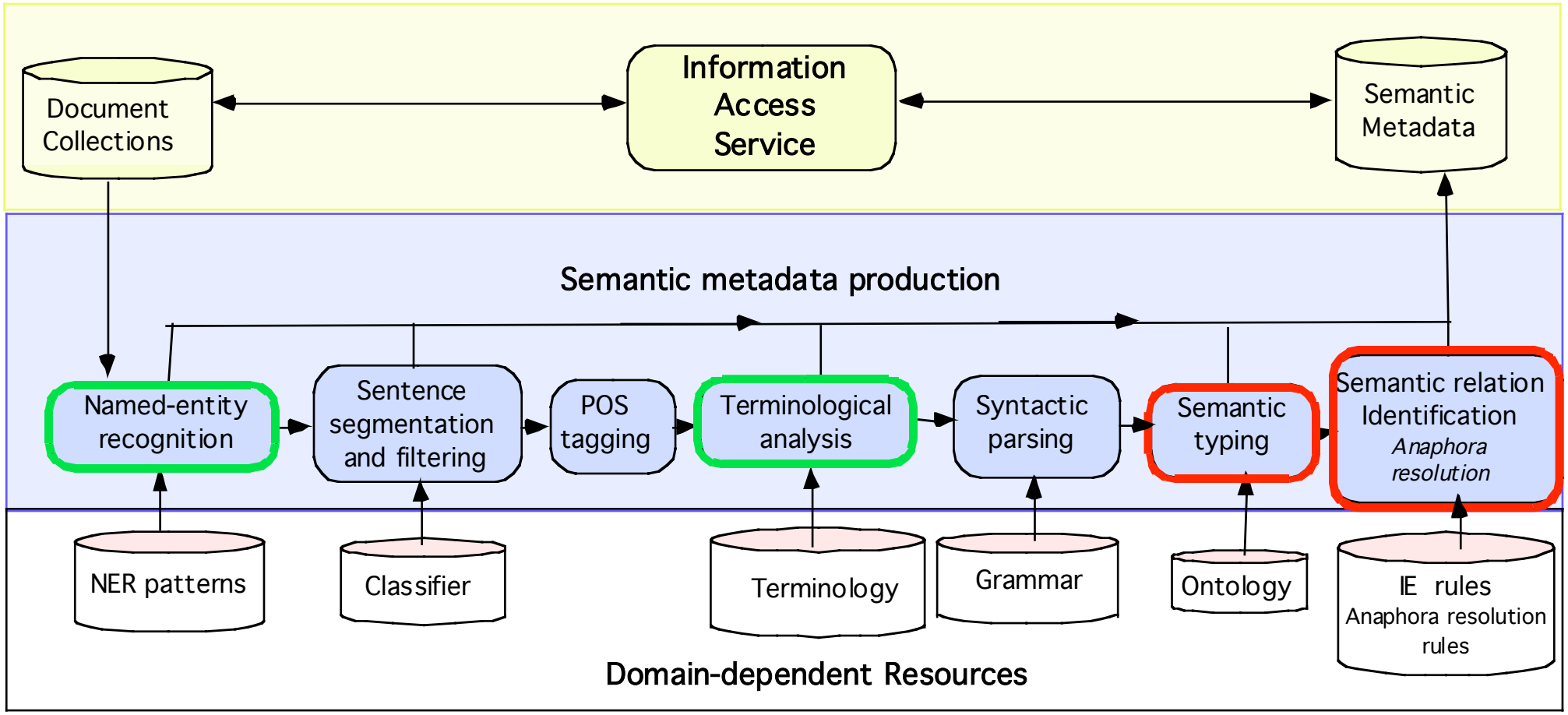



# Linguistic analysis

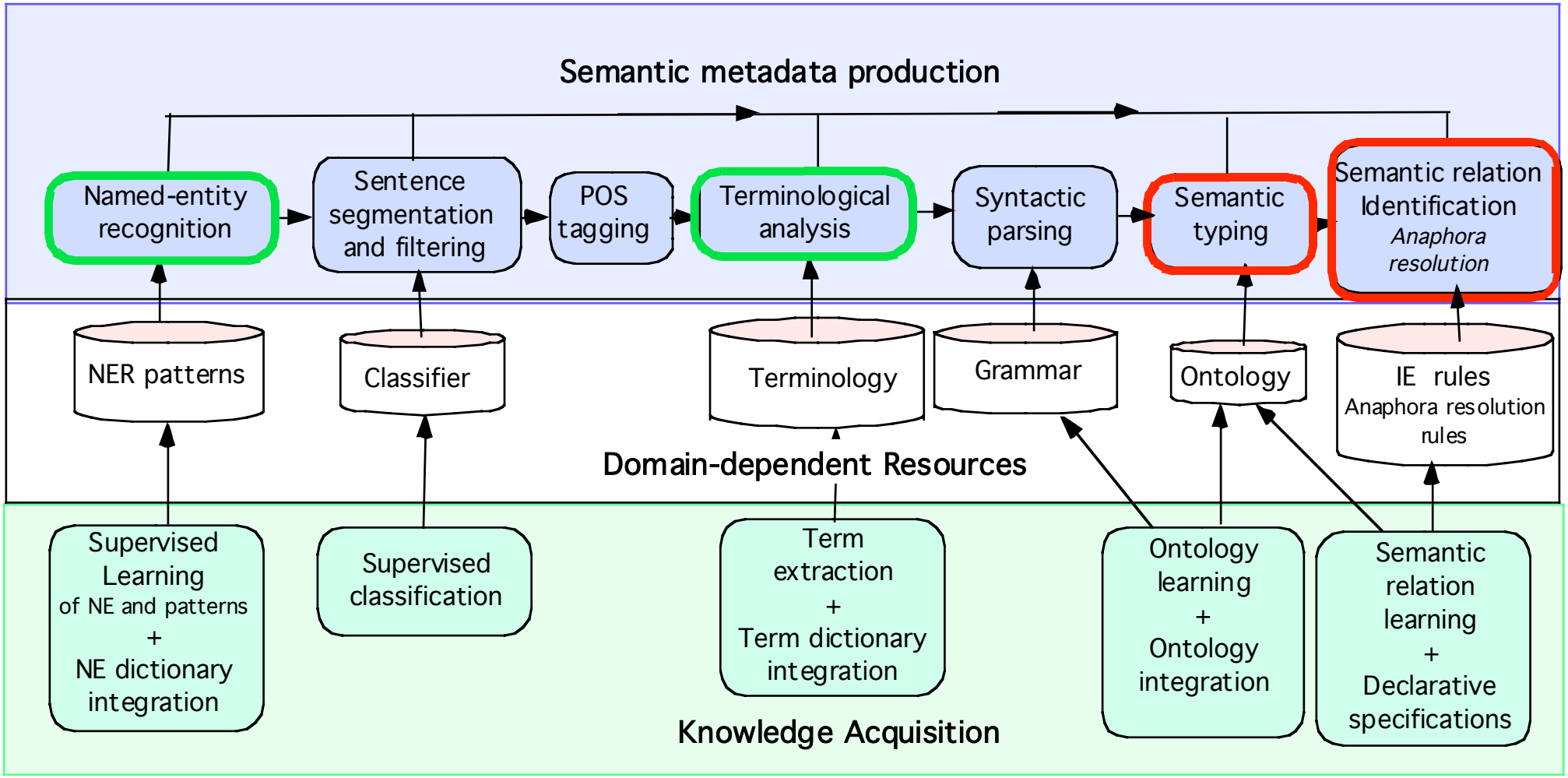


# Specific resources are needed



# Learning the resources



# Named-entity learning

**Supervised learning** for learning NER patterns of gene/protein names

*In eight isolates of M. fermentans examined, malp occurred upstream of an operon encoding the phase-variable P78 ABC transporter;*

**Examples** represented by linguistic features (mainly typographic).

- **First_upper:** the example is capitalized (^[A-Z])
- **Middle_upper:** the example contains a non-initial uppercase letter (^.+[A-Z])
- **Only_upper:** all letters of the example are uppercase? (^[A-Z]*$)
- **Last_digit:** the last character of the example is a digit? ([0-9]$)

...

**Experimental results**

| | Precision | Recall |
|---|---|---|
| C4.5 | 92,5 | 91,6 |
| NB | 88,6 | 73,4 |

Best **NLPBA:** Precision 76% Recall 69,4% **BioCreative:** 83% Recall-Precision

# Terminology acquisition by YaTea

*YaTea* term acquisition tool combines *existing terminology* matching (good precision) and *corpus-based term extraction* (good coverage).

## Input

Training corpus tagged with POS information and existing terminology

*During[ADV] sporulation[NOUN] of[PREP] Bacillus subtilis[P-NOUN], spore[NOUN]*

## Method

1. Corpus chunking based on frontier category detection

   *During / sporulation of Bacillus subtilis /, / spore coat proteins / encoded by /*

2. Recursive parsing of chunks according to
   - Syntactic patterns `NOUN NOUN`
   - Forbidden structures and subcomponents (*of course*)
   - Specific patterns of certified terms (*in vitro)*
   - Generation of term variants using morpho-syntactic rules

     `NOUN1 NOUN2 = NOUN2 of NOUN1`

# Examples of term tagging

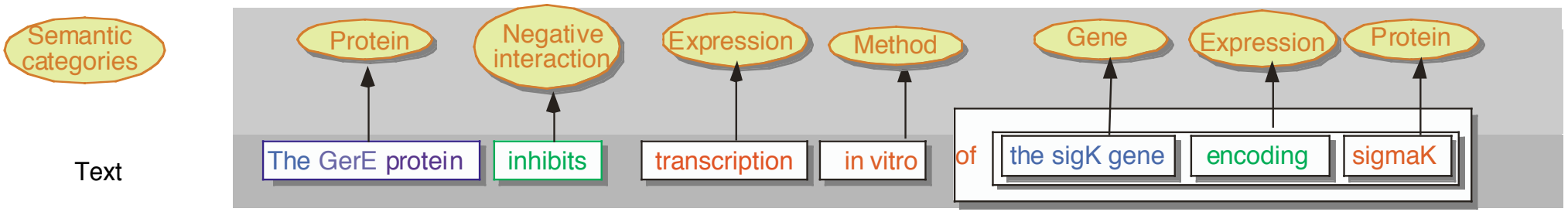
Existing terminology: Gene Ontology terminology mapping (in green)

/**Combined**/ /**action**/ /**of**/ /**two**/ /**transcription**/ /**factors**/ /**regulates**/ /**genes**/ /**encoding**/ /**spore**/ /**coat**/ /**proteins**/ /**of**/ /**Bacillus**/ /**subtilis**/ **.**/During/ /sporulation/ /of/ /Bacillus/ /subtilis/ /,/ /spore/ /coat/ /proteins/ /encoded/ /by/ /cot/ /genes/ /are/ /expressed/ /in/ /the/ /mother/ /cell/ /and/ /deposited/ /on/ /the/ /forespore/ /.//transcription/ /of/ /the/ /cotB/ /,/ /cotC/ /,/ /and/ /cotX/ /genes/ /by/ /final/ /sigma/ /(/ /K/ /)/ /RNA/ /polymerase/ /is/ /activated/ /by/ /a/ /small/ /,/ /DNA/-/binding/ /protein/ /called/ /GerE/ /.//The/ /promoter/ /region/ /of/ /each/ /of/ /these/ /genes/ /has/ /two/ /GerE/ /binding/ /sites/ /.

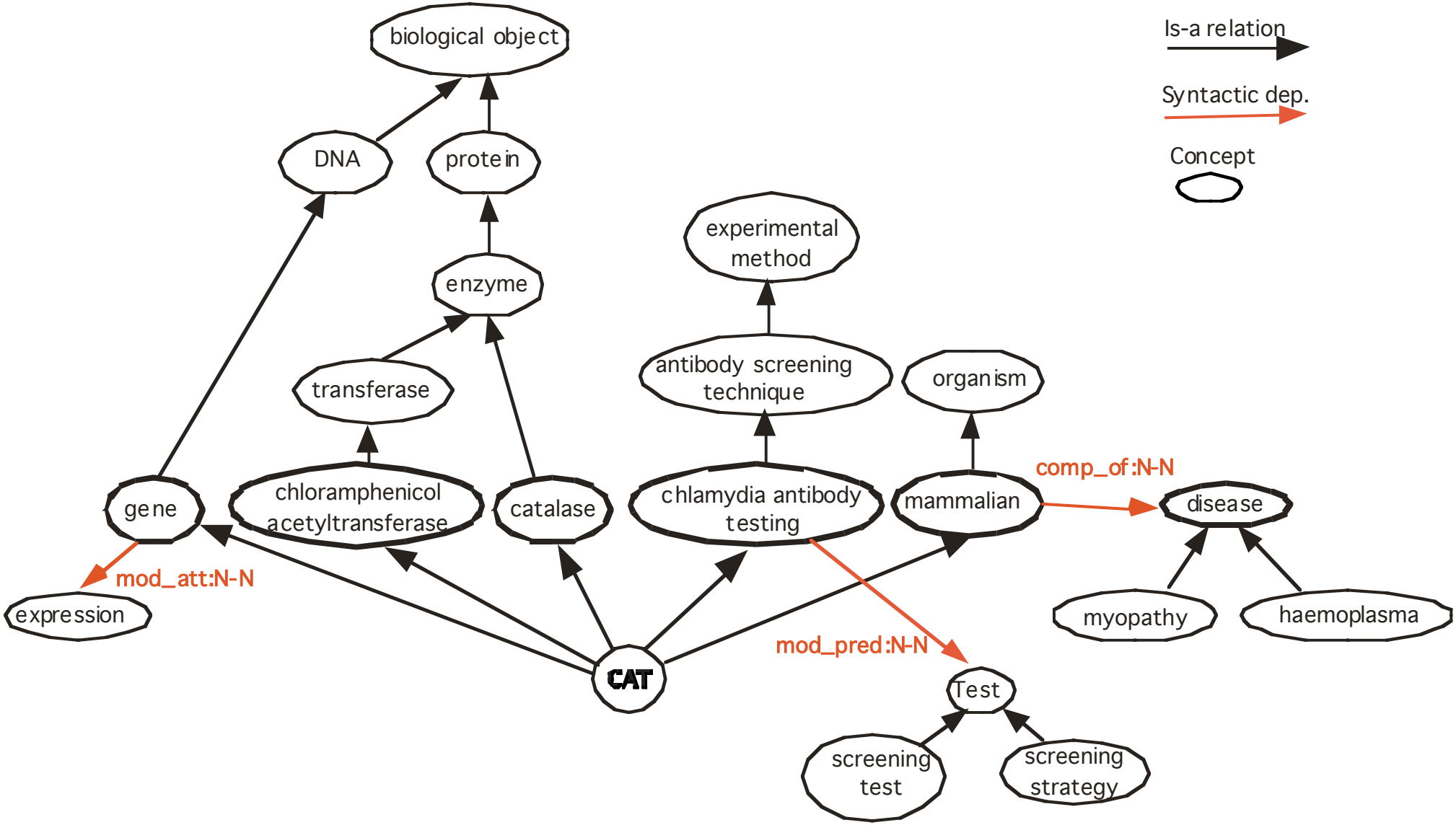
*YaTea* term mapping (in green)

/**Combined**/ /**action**/ /**of**/ /**two**/ /**transcription**/ /**factors**/ /**regulates**/ /**genes**/ /**encoding**/ /**spore**/ /**coat**/ /**proteins**/ /**of**/ /**Bacillus**/ /**subtilis**/ **.**/During/ /sporulation/ /of/ /Bacillus/ /subtilis/ /,/ /spore/ /coat/ /proteins/ /encoded/ /by/ /cot/ /genes/ /are/ /expressed/ /in/ /the/ /mother/ /cell/ /and/ /deposited/ /on/ /the/ /forespore/ /.//Transcription/ /of/ /the/ /cotB/ /,/ /cotC/ /,/ /and/ /cotX/ /genes/ /by/ /final/ /sigma/ /(/ /K/ /)/ /RNA/ /polymerase/ /is/ /activated/ /by/ /a/ /small/ /,/ /DNA/-/binding/ /protein/ /called/ /GerE/ /.//The/ /promoter/ /region/ /of/ /each/ /of/ /these/ /genes/ /has/ /two/ /GerE/ /binding/ /sites/ /.

# Semantic type tagging



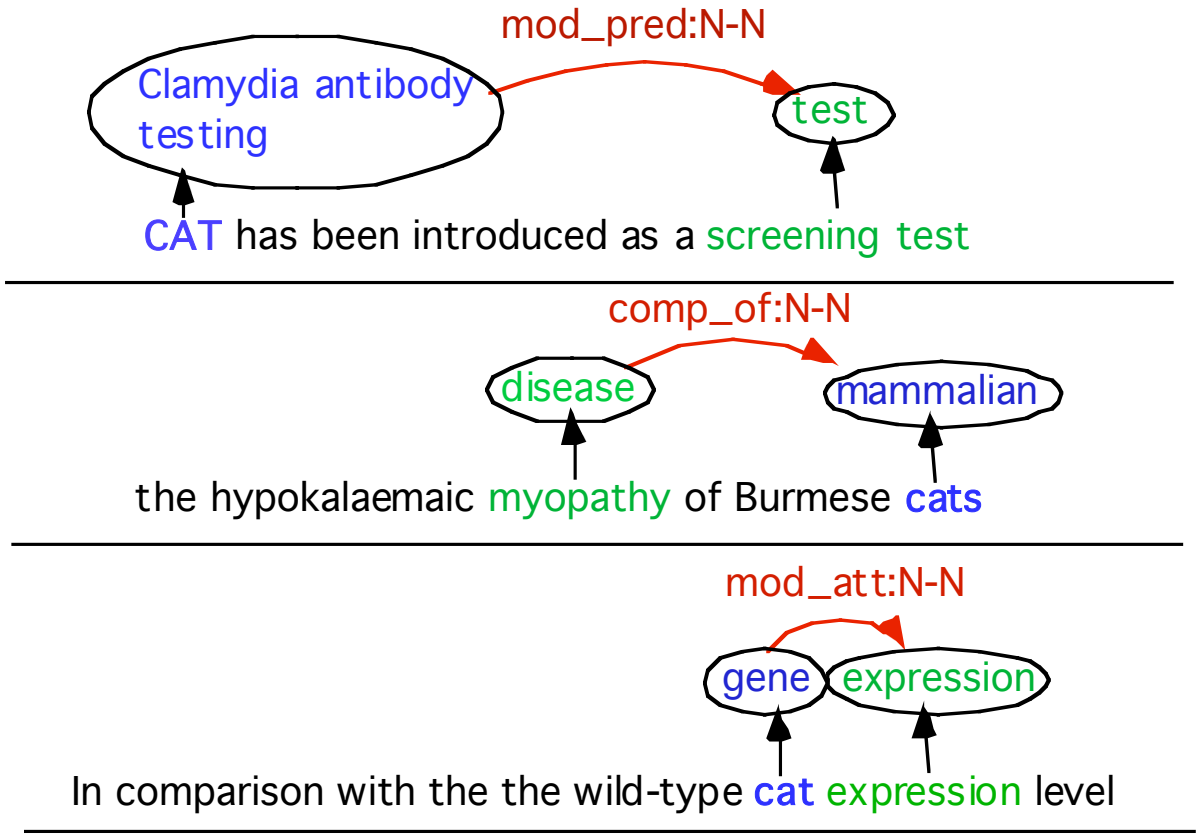
# Semantic type learning by Asium



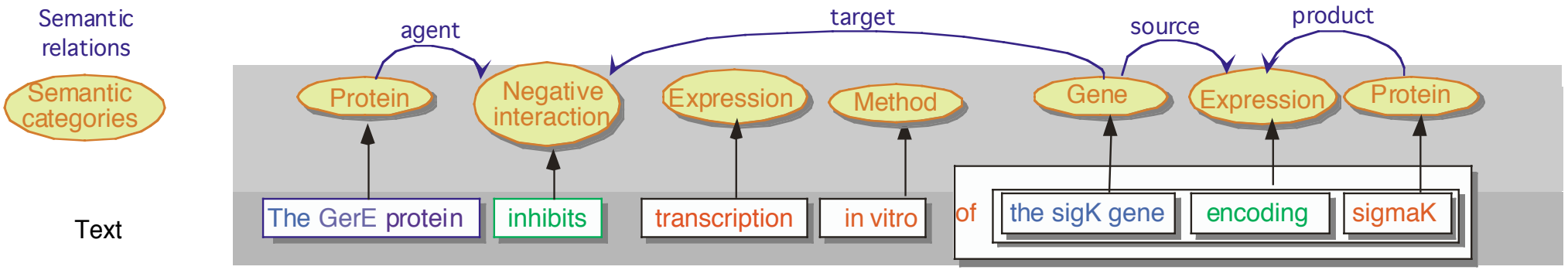
# Semantic disambiguation with syntactic context

Given,

- *Restrictions of selection* associated to the concepts of the ontology
- *Is-A hierarchies*



# Tagging semantic relations



# Rules for semantic relation annotation

*GerE stimulates cotD transcription and cotA transcription [...], and, unexpectedly, inhibits [...] transcription of the gene (sigK) [...]*

## Example of information extraction rule

interaction (X,Z):-

is-a(X,protein), subject(X,Y), cat(Y,verb), is-a(Y,interaction), cat(Z,NP), obj(Z,Y), is-a(Z,gene-expression).

## Interpretation

If the subject X of an interaction verb Y is a protein name, and the object Z is a gene expression,

then, X is the agent and Z is the target of the interaction

# Rule learning with Propal (*ILP-based*)

## Learning method

Supervised relational learning,
Horn clauses
Multi-class learning: top-down ILP method Propal [Alphonse, 2003]

## Training data pre-processing

1. Selection of relevant documents.
2. Segmentation and filtering of relevant sentences.
3. Manual annotation of the relations in the positive training data.
4. Negative example generation (near-miss selection in relevant sentences under closed-word assumption)
5. Training example preprocessing (linguistic processing and saturation by BK).

**Application of the learning method** for acquiring the rules representing the discriminant linguistic attributes.

- "Learning Language in Logic" challenge (*ICML 05 LLL workshop*) see webpage.

# Preliminary results on relation learning

- Training data: gene interactions (agent, target) in *Bacillus subtilis* LLL challenge dataset on "action without coreference"
- Linguistic normalization (lemma and syntactic relations) and abstraction
- Rule learning with **Propal**

| | Recall | Precision | F-measure |
|---|---|---|---|
| [Goadrich et al., 2005], data without linguistics | 80,6 | 42,6 | 58,5 |
| [Riedel and Klein, 2005] data with linguistics | 52,8 | 86,4 | 65,5 |
| [Propal] linguistics + semantic abstraction | 61,8 | 63,6 | 62,7 |

# Conclusion

Semantic annotation of free text in specialized domains is a complex task with high added-value

2 complementary approaches

- Shallow and statistics-based processing

➔ Easy to design
➔ The information retrieved is partially noisy

- Text normalization and Machine Learning

➔ Saves time of adaptation of the resources to the task
➔ Better coverage of the diversity of the linguistic expressions
➔ Complex architecture, difficult to design