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Semantic Annotation in the Alvis Project

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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 *desoxyribonucleic acid*,[..].

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 (*desoxyribonucleic acid = 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**.

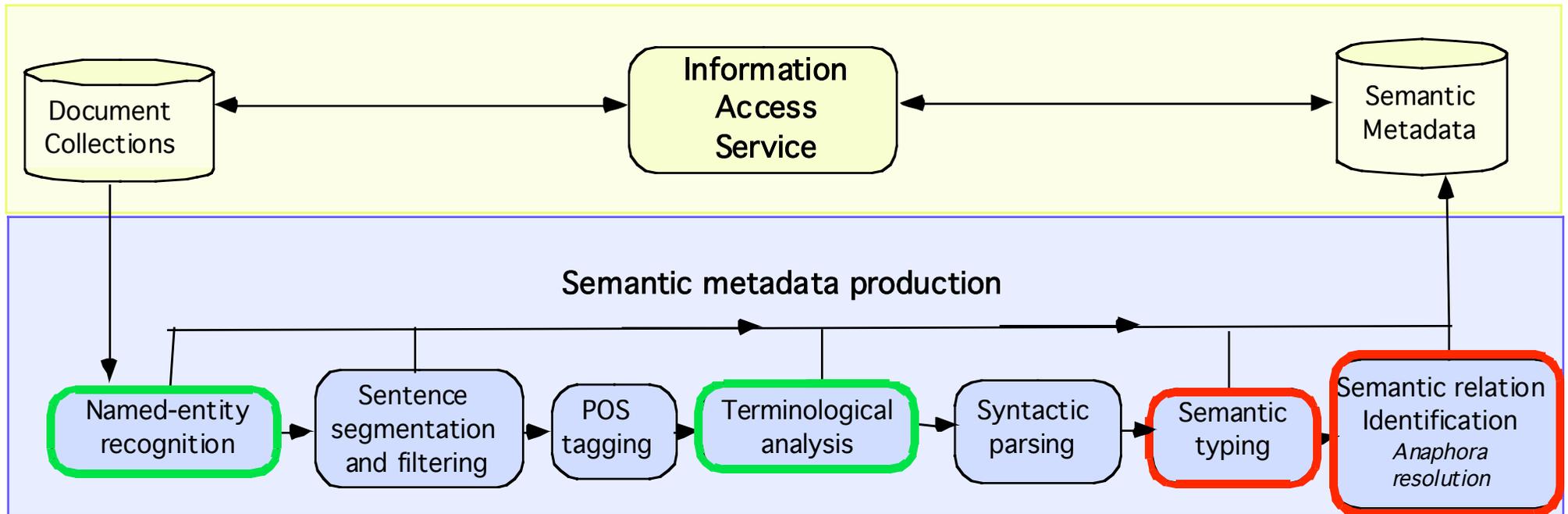
Annotation of semantic unit and relation requires linguistic processing

- 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.

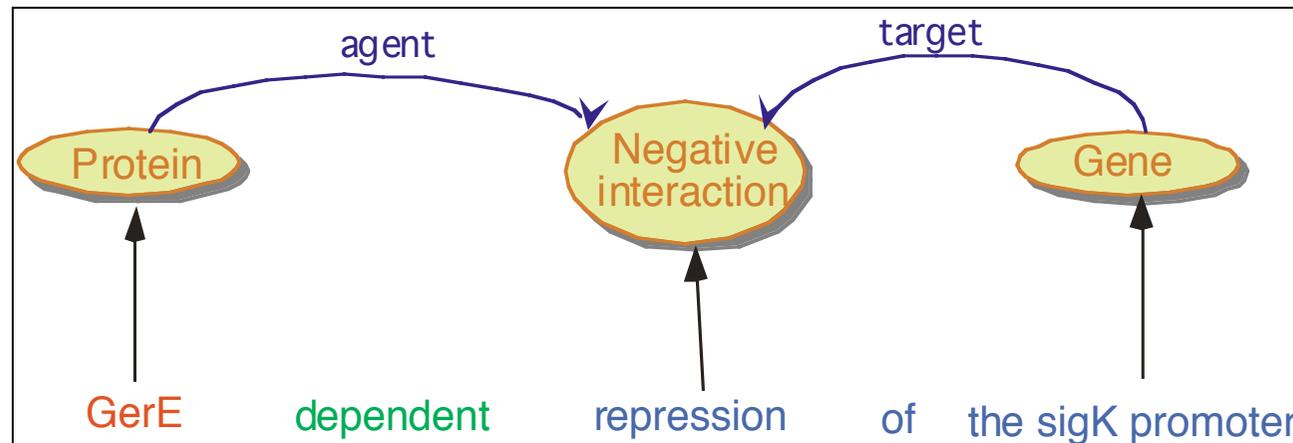
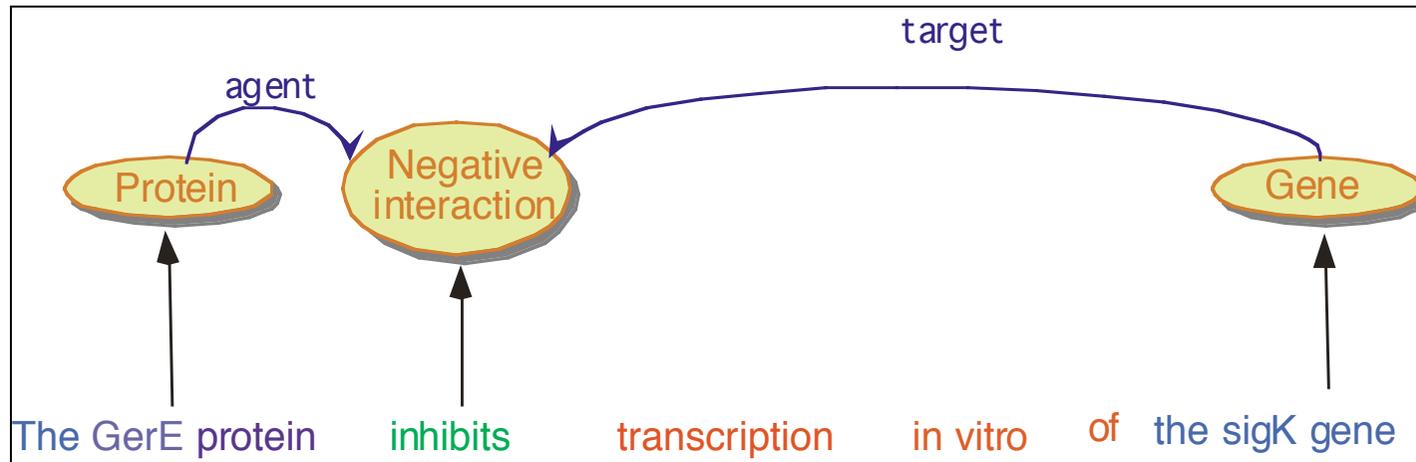
- Cooccurrence says little about the **semantic relations**
 - GerE stimulates cotD transcription and cotA transcription [...], and, unexpectedly, inhibits [...] transcription of the gene (sigK) [...]*

Semantic annotation with linguistic processing

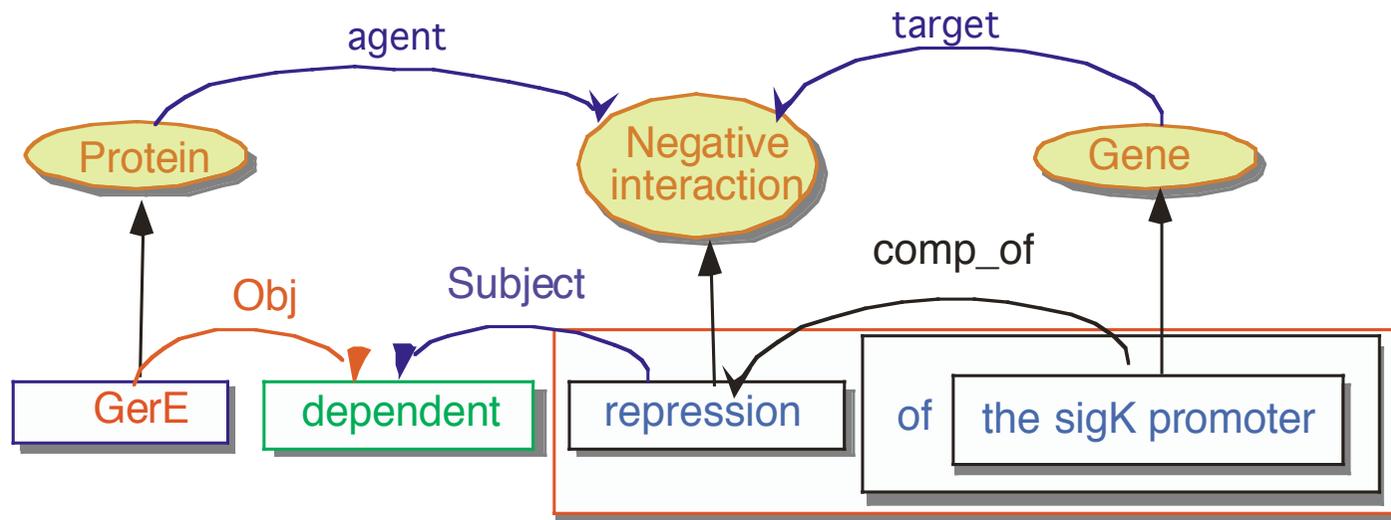
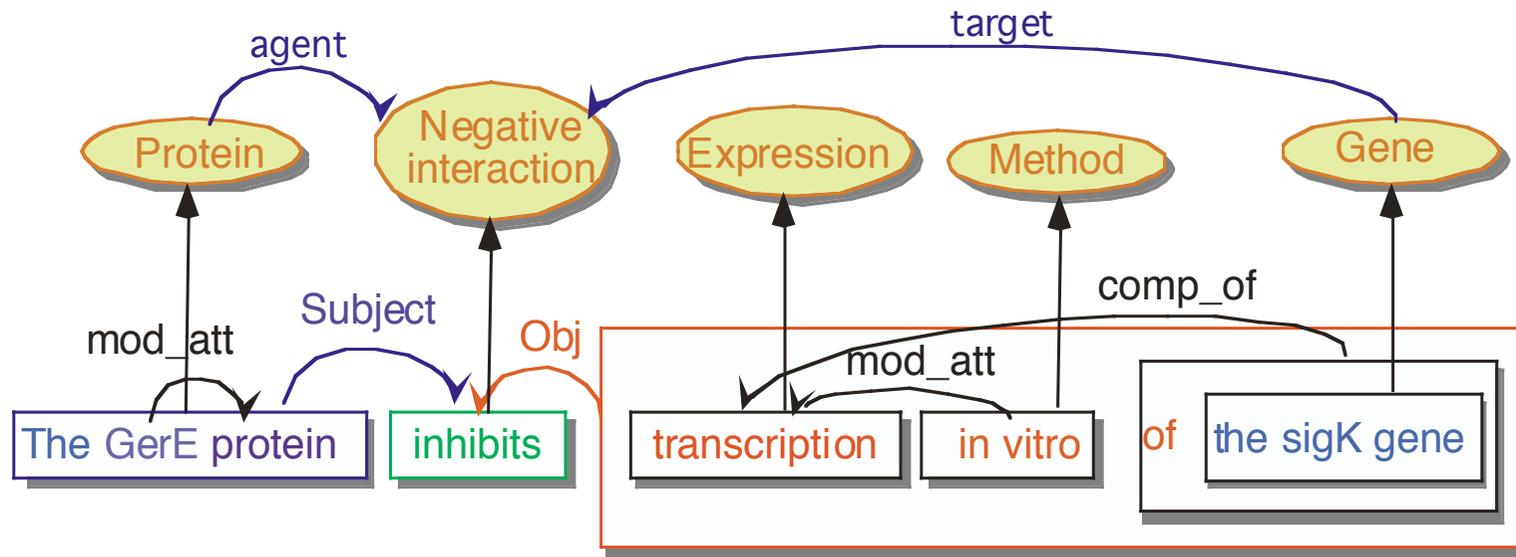


Semantic abstraction

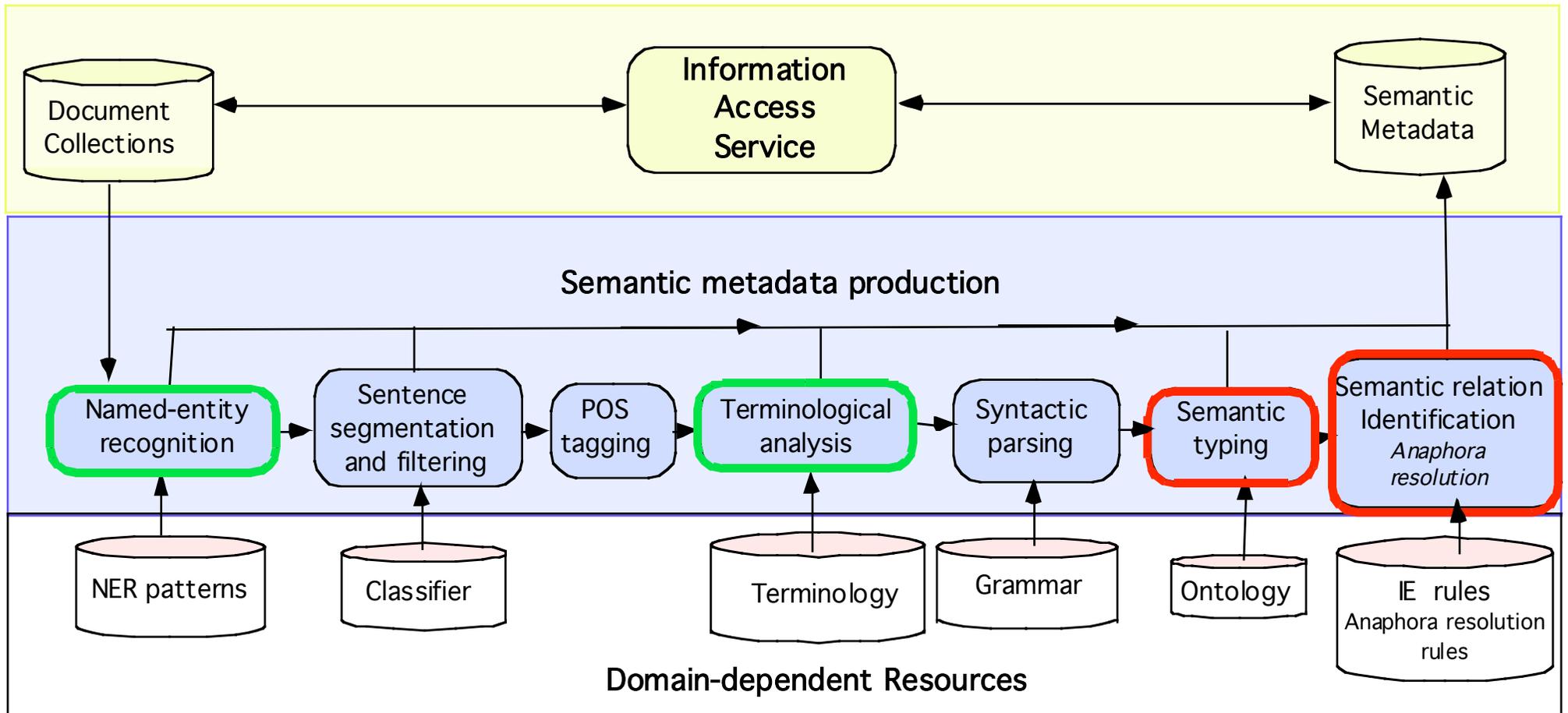
A same semantic representation of different formulations for efficient IR.



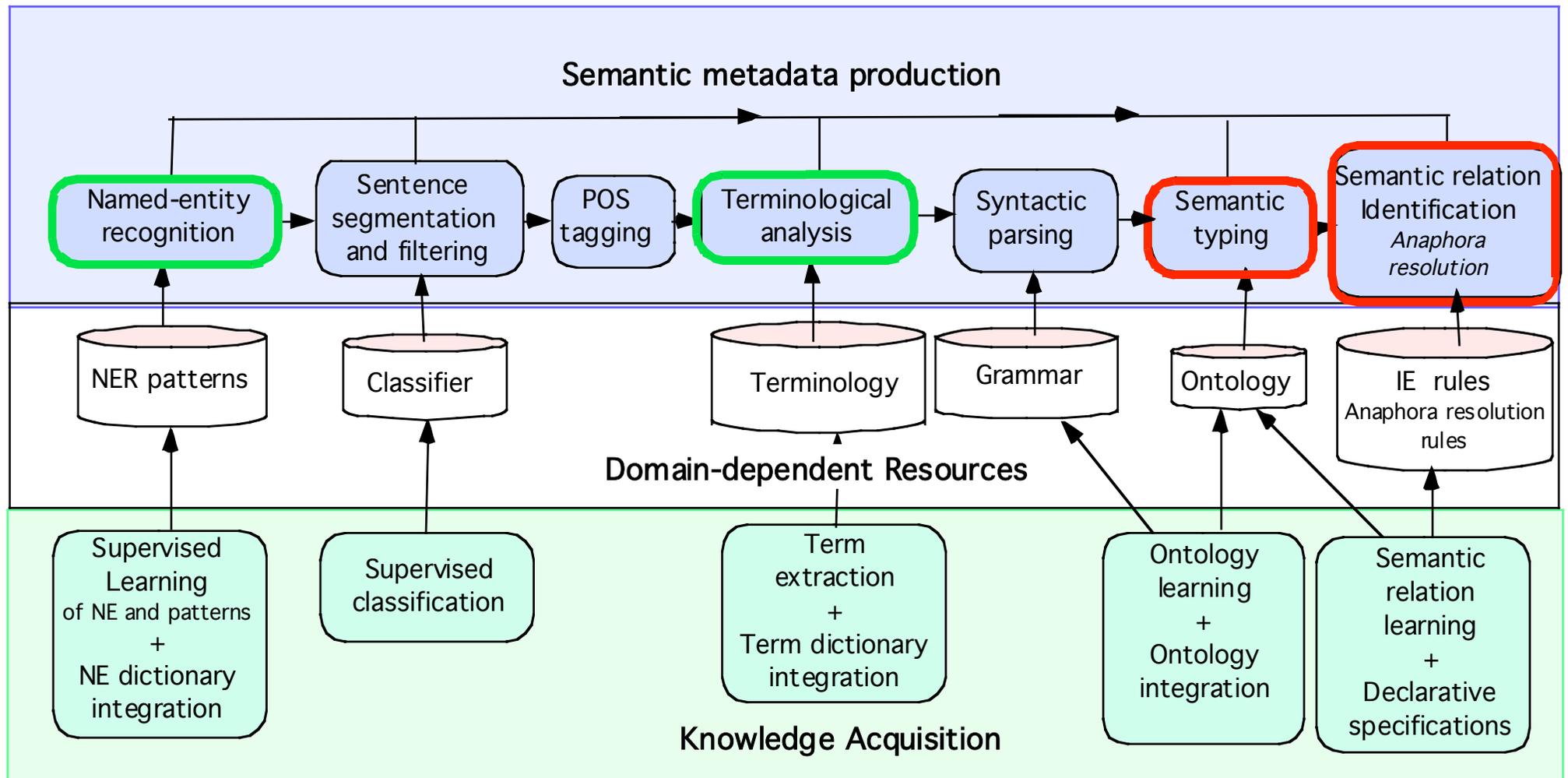
Linguistic analysis



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 ($\wedge[A-Z]$)
- **Middle_upper**: the example contains a non-initial uppercase letter ($\wedge.[A-Z]$)
- **Only_upper**: all letters of the example are uppercase? ($\wedge[A-Z]^*\$$)
- **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

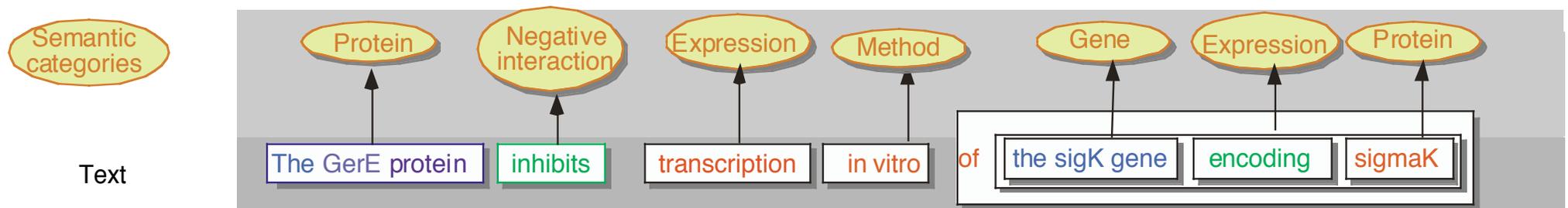
Existing terminology: Gene Ontology terminology mapping (in green)

/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/ ./

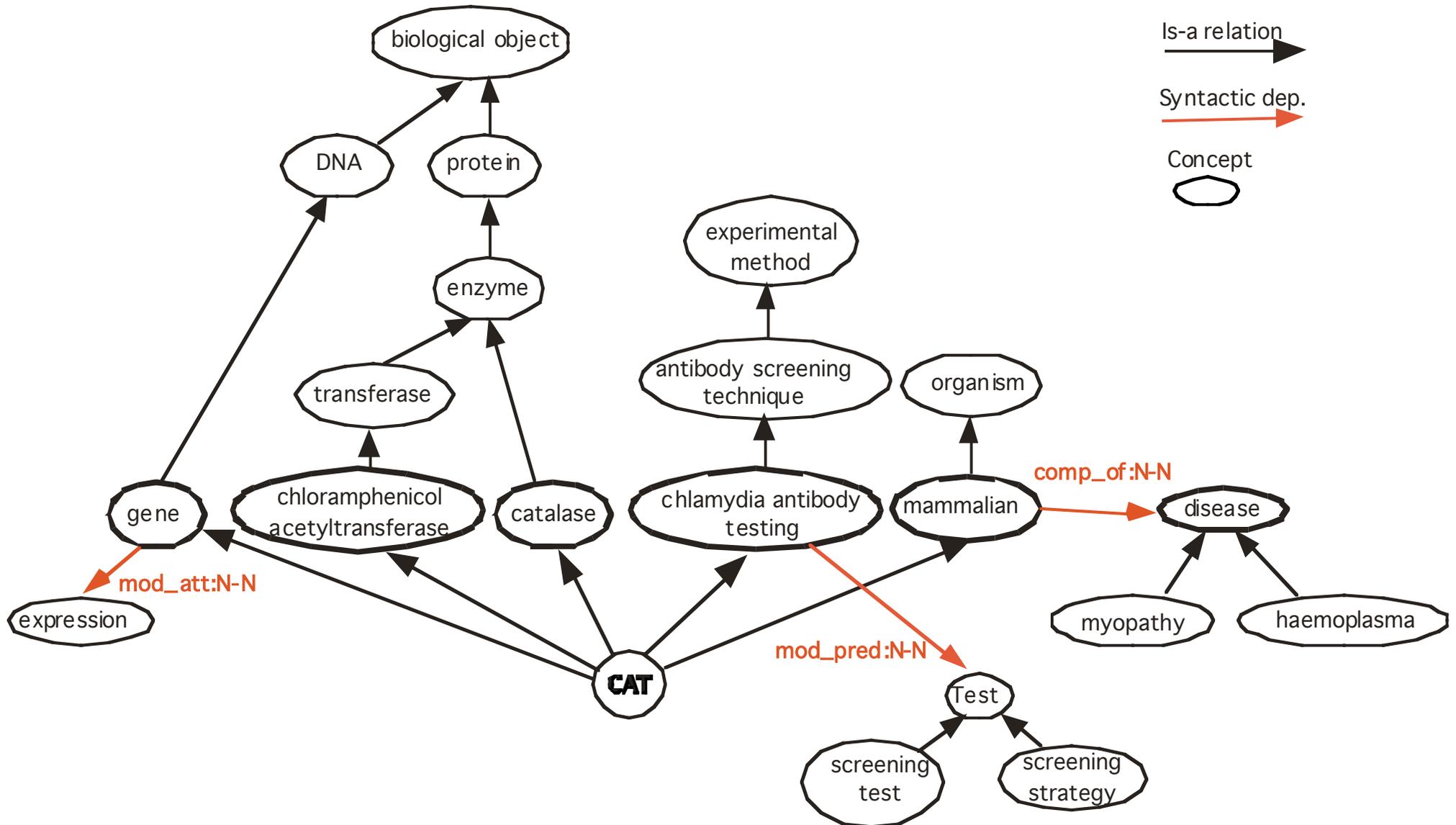
YaTea term mapping (in green)

/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



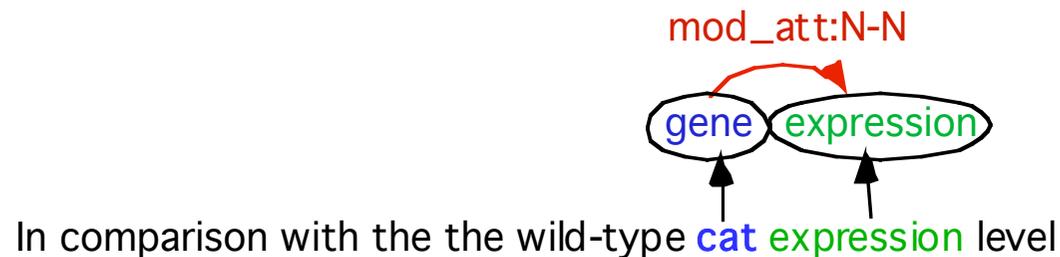
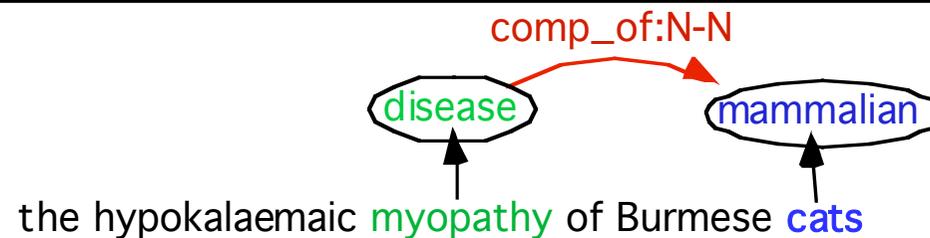
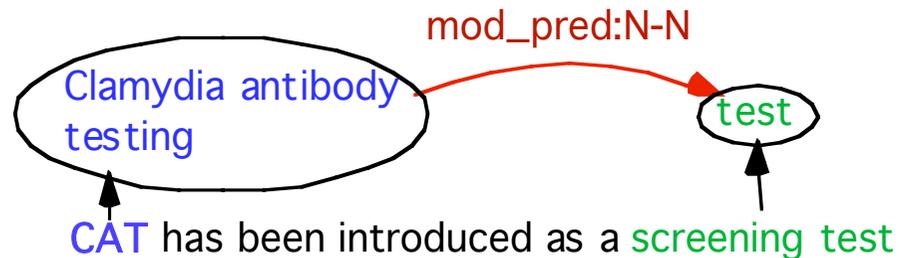
Semantic type learning by Asium



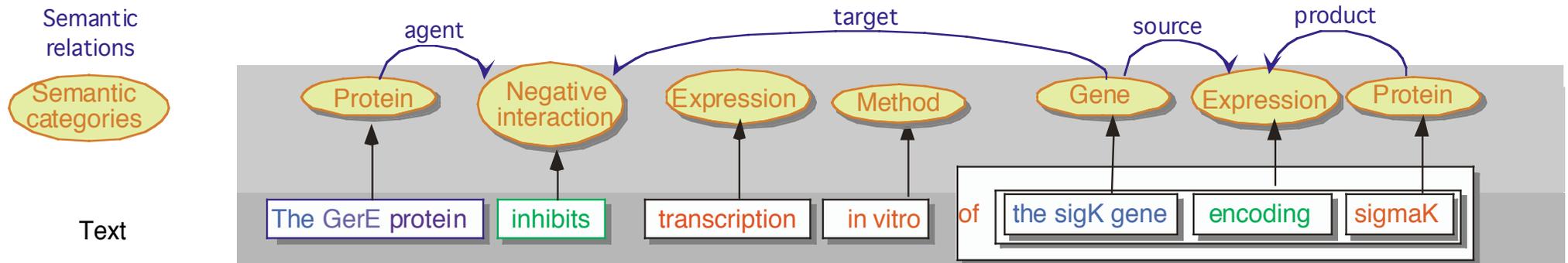
Semantic disambiguation with syntactic context

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