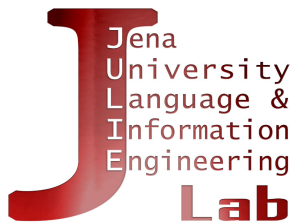


# An UIMA-based Tool Suite for Semantic Text Processing

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# StemNet - Knowledge Management for Immunology



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- in life-sciences: increasing amount of knowledge stored in (unstructured) textual documents
- semantic access to this knowledge necessary
- biomedical subdomain: hematopoietic *stem cell transplantation*
- semantic search engine for advanced document and information retrieval
- example user query:  
“get me relevant documents on **human IL2Ra** and **CTL**”

# StemNet - Knowledge Management for Immunology

- user query: “human IL2Ra” AND “CTL”

[...] on **IL-2Ra**-activated CD34(+) cytotoxic T-cells (**CTLs**). p3hr-1, the Burkitt's lymphoma cell line, was [...]

# StemNet - Knowledge Management for Immunology

- user query: “human IL2Ra” AND “CTL”

[...] on **IL-2Ra**-activated CD34(+)

BLC-stimulated **cytotoxic T-cells** showed [...] ; [...]

[...] a more mature phenotype (low CD69, **CD25**, and CD62L) [...]

# StemNet - Knowledge Management for Immunology

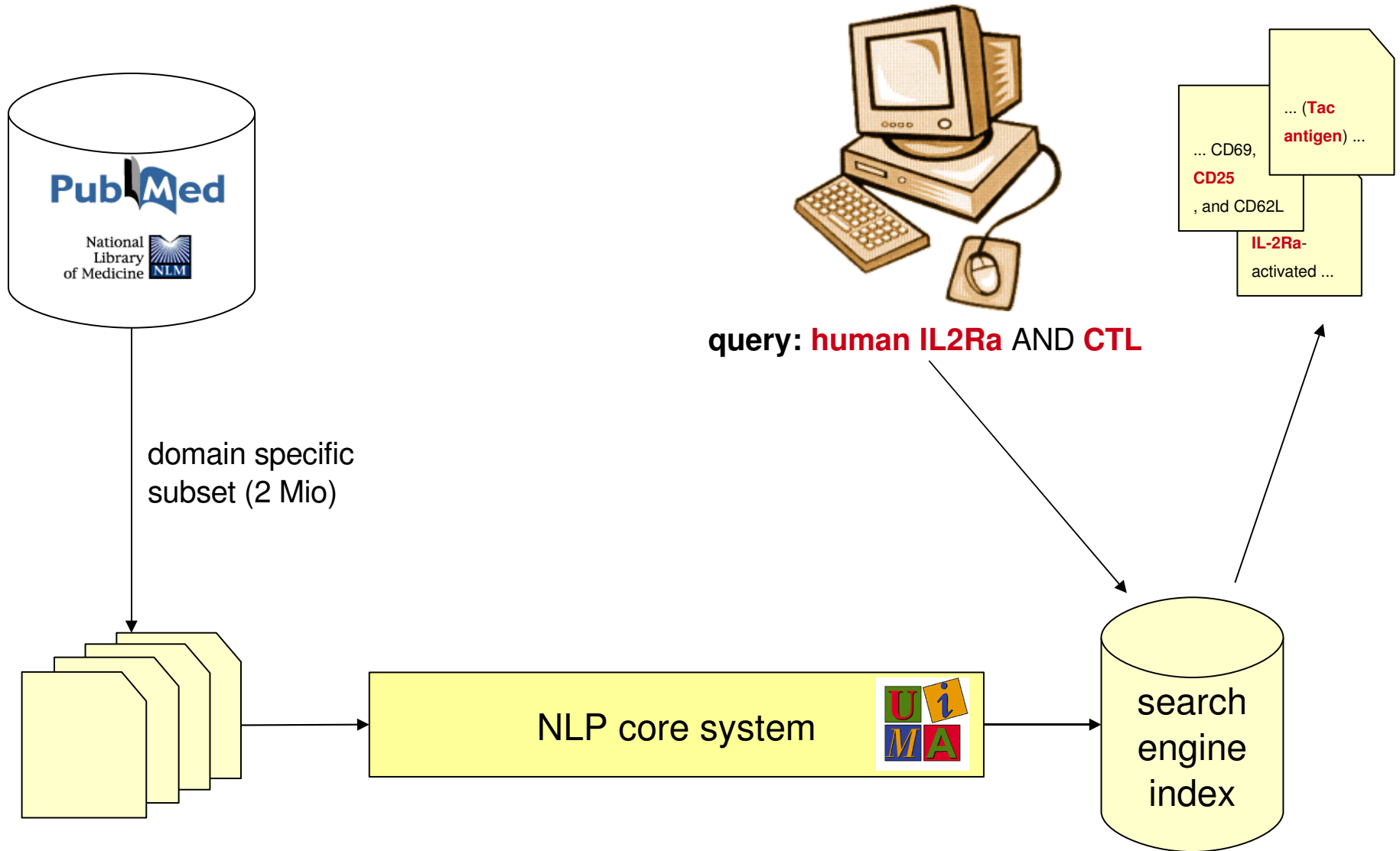
- user query: “human IL2Ra” AND “CTL”

[...] on **IL-2Ra**-activated CD34(+)

BLC-stimulated **cytotoxic T-cells** showed ; [...]

TNF-alpha upregulated the **interleukin 2 receptor alpha chain (Tac antigen)** on the surface of [...] proliferation of tumor specific **CTL** [...]

# UIMA in the StemNet Project



# JULIE NLP Tool Suite based on UIMA (1/2)

## 1) comprehensive UIMA type system

- covers the full NLP pipeline
- five layers:
  - document meta information (bibliographic and content information)
  - document structure and style information (sentences, rhetorical zones, ...)
  - morpho-syntax (tokenisation, POS, acronyms, lemmatisation, ...)
  - syntax (shallow and full parsing information)
  - semantics (named entities, relationships, events...)

# JULIE NLP Tool Suite based on UIMA (2/2)

## 2) collection of NLP components (`Analysis Engines`):

- for morpho-syntactic analysis
- for syntactic analysis
- for named entity recognition and normalisation/mapping

## 3) data import and export (`Collection Reader/CAS Consumer`):

- PubMed Reader
- Search Engine Indexer

- included tools:

- mostly based on machine learning
- external tools for which we have written UIMA wrappers
- JULIE tools; have stand-alone and UIMA mode



# PubMed Reader



- processes PubMed articles (XML)
- reads the following document meta-data:
  - bibliographic information: title, authors, publication date, journal name
  - content information (manually added): keywords (MeSH), list of chemicals
- writes data to CAS
  - our type system contains respective types for this kind of information

# Sentence/Token Splitting, POS Tagging, Chunking

- configurable UIMA wrappers for OpenNLP tools
  - sentence splitter
  - tokeniser
  - POS tagger
  - chunker
- JULIE tools
  - sentence splitter
  - tokeniser
- available models for life-sciences:
  - trained on JULIE corpus (covers special cases and subtleties of bio-medical domain)
  - trained on well-known biomedical corpora (e.g. PennBioIE)

# Parsing

- UIMA wrappers for external parser implementations:
  - OpenNLP Parser (Ratnaparkhi, 1998)
    - constituency parser
  - MST Parser (McDonald, 2006)
    - dependency parser
- different linguistic paradigms supported
- type system supports both constituency and dependency parse information

# Acronym Detection

- detection and resolution of local acronyms
- implementation of M. Hearst's algorithm (Hearst 2003)
- with extension: DB lookup for unresolved acronyms
- Acronym DB generator (CAS Consumer):
  - tuples (acronym, full form), associated with spelling variants, first year of occurrence, keywords (MeSH)

```
[...] on IL-2Ra-activated CD34(+)  
cytotoxic T-cells (CTLs). p3hr-1,  
the Burkitt's lymphoma cell line, was [...]
```

# Named Entity Recognition

- generic named entity recognizer
- ML-based
- flexibly configurable wrt:
  - mapping: predicted labels → UIMA types
  - feature parametrization
    - user defined feature set (turn on/off, configure features)
    - CAS-specified feature information (e.g. POS tags)
- consistency preservation:
  - assures that same entity mentions within one abstract (document zone) are consistently annotated

# Named Entity Mapping (1/2)

- associates identified NEs with DB entries
- in life-sciences: e.g. SwissProt

```
[...] on IL2Ra-activated CD34(+)
cytotoxic T-cells (CTLs). p3hr-1,
the Burkitt's lymphoma cell line, was [...]
```

# Named Entity Mapping (1/2)

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[...] on **IL2Ra**-activate  
cytotoxic T-cells (CTLs  
the Burkitt's lymphoma c

## UniProtKB/Swiss-Prot entry **P01589**

[\[Entry info\]](#) [\[Name and origin\]](#) [\[Re](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information	
Entry name	IL2RA_HUMAN
Primary accession number	P01589
Secondary accession numbers	None
Integrated into Swiss-Prot on	July 21, 1986
Sequence was last modified on	July 21, 1986 (Sequence version 1)
Annotations were last modified on	March 20, 2007 (Entry version 84)
Name and origin of the protein	
Protein name	Interleukin-2 receptor alpha chain [Precursor]
Synonyms	IL-2 receptor alpha subunit IL-2-RA IL2-RA p55 TAC antigen CD25 antigen
Gene name	IL2RA
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
References	
[1]	NUCLEOTIDE SEQUENCE [MRNA]. DOI= <a href="#">10.1038/311631a0</a> ; PubMed=6090949 [NCBI, ExpASY, EBI, Israel, Japan] Nikaido T., Shimizu A., Ishida N., Sabe H., Teshigawara K., Maeda M., Uchiyama T., Yodoi J., "Molecular cloning of cDNA encoding human interleukin-2 receptor."; Nature 311:631-635(1984).
Protein-protein interaction databases	
DIP	<a href="#">DIP:1080N</a> ; -.
Polymorphism databases	
SeattleSNPs	<a href="#">IL2RA</a> .
Organism-specific gene databases	
HGNC	<a href="#">HGNC:6008</a> ; IL2RA.
GeneCards	<a href="#">IL2RA</a> .
GeneLynx	<a href="#">IL2RA</a> ; Homo sapiens.
GenAtlas	<a href="#">IL2RA</a> .
HPA	<a href="#">CAB002419</a> ; -.
MIM	147730; gene. [NCBI / EBI] 606367; phenotype. [NCBI / EBI]
HOVERGEN	[ <a href="#">Family</a> / <a href="#">Alignment</a> / <a href="#">Tree</a> ]
Gene expression databases	
CleanEx	<a href="#">HGNC:6008</a> ; IL2RA.
ArrayExpress	<a href="#">P01589</a> ; -.
GermOnline	<a href="#">ENSG00000134460</a> ; Homo sapiens.
Ontologies	
	<a href="#">GO:0005886</a> ; Cellular component: plasma membrane ( <i>traceable author statement from</i> <a href="#">GO:0004911</a> ; Molecular function: interleukin-2 receptor activity ( <i>traceable author state</i>

# Named Entity Mapping (2/2)

- for gene/protein entity mentions
- principles:
  - normalization rules for bio-medical entities
    - a -> alpha
    - R -> receptor, L -> ligand
    - numbers split away
    - word order ignored
    - "IL2RA" -> "IL 2 receptor alpha"
    - "receptor of IL-4" -> "IL 4 receptor"
  - requires well-curated synonym list



# JULIE Lucene Indexer

- goal: directly build search engine index from processed documents
- Lucene
  - high-performance search engine
  - fielded search and special query types (e.g. range searches)
  - open source, freely available, provides Java API
- Lucene Indexer
  - directly consumes CAS
  - tokenization as in CAS
  - currently indexed fields:
    - document meta-data (as in PubMed)
    - entity mentions + synonyms (with same offset)
- work in progress: flexible configurability
  - external mapping file (UIMA type -> Lucene field)

for further information/download of tools:

<http://www.julielab.de>



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