stav: text annotation visualiser

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Visualisation

- Insights into annotations are relevant for:
- Constructing Natural Language Processing (NLP) systems
- Curating NLP resources
- Visualisations should be:
- Intuitive, at-a-glance
- Accessible, to be discussed with colleagues

First rule: "Look at the data"

(Although the second rule is: "Don't look at the data")

Freely after Eugene Charniak

stav text annotation tool (stav)

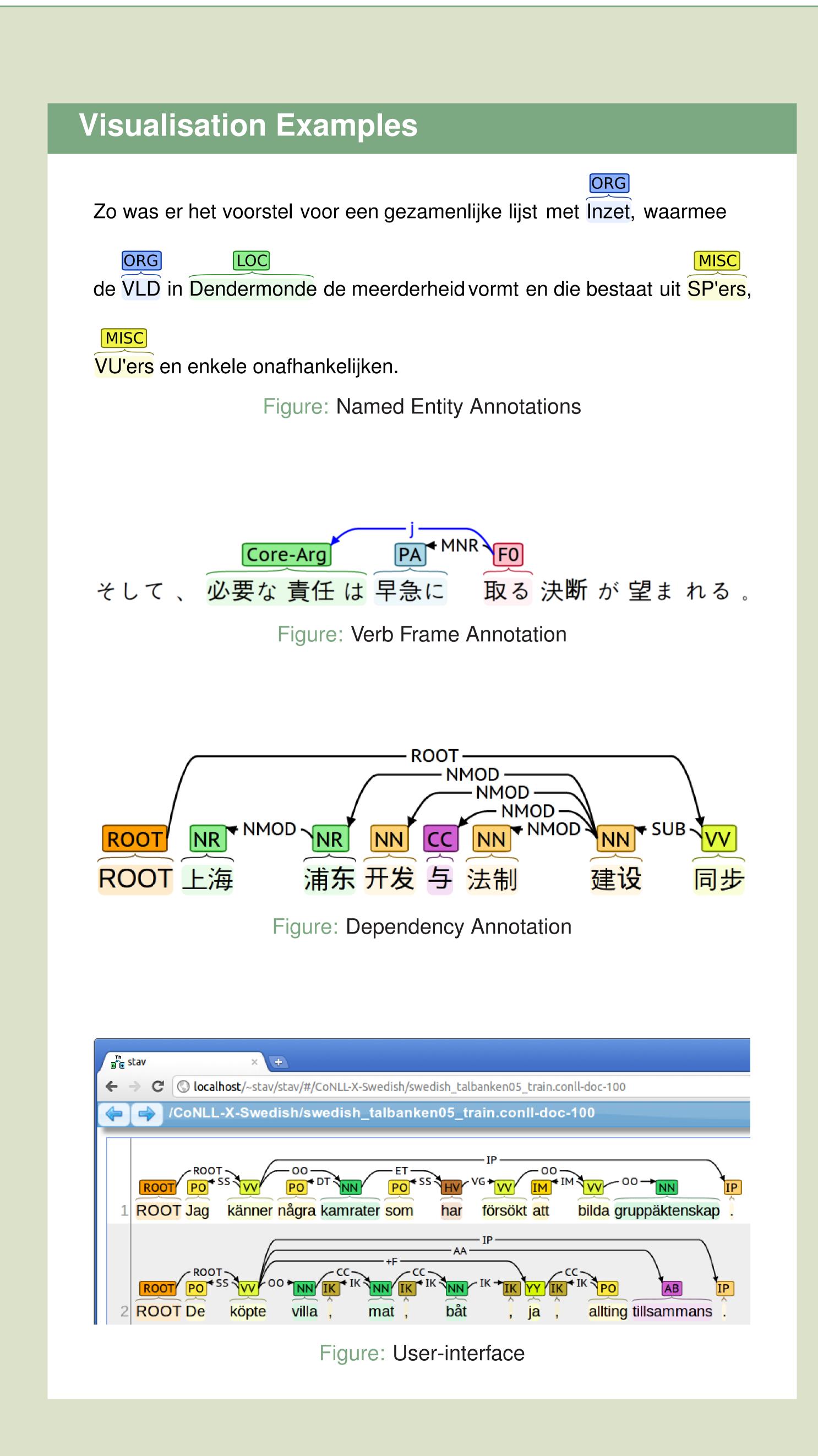
- Initially introduce to visualise biomolecular annotations in the BioNLP 2011 Shared Task (Stenetorp et al. 2011)
- Well-reveived by the shared task participants
- Generalised to support a wide range of annotation tasks:
- Web-based
- Error-analysis capabilities
- End-user facing visualisation
- Format conversion tools
- Full Unicode support
- File-based back-end, GREP/SED-able
- Each annotation reach-able by a URI

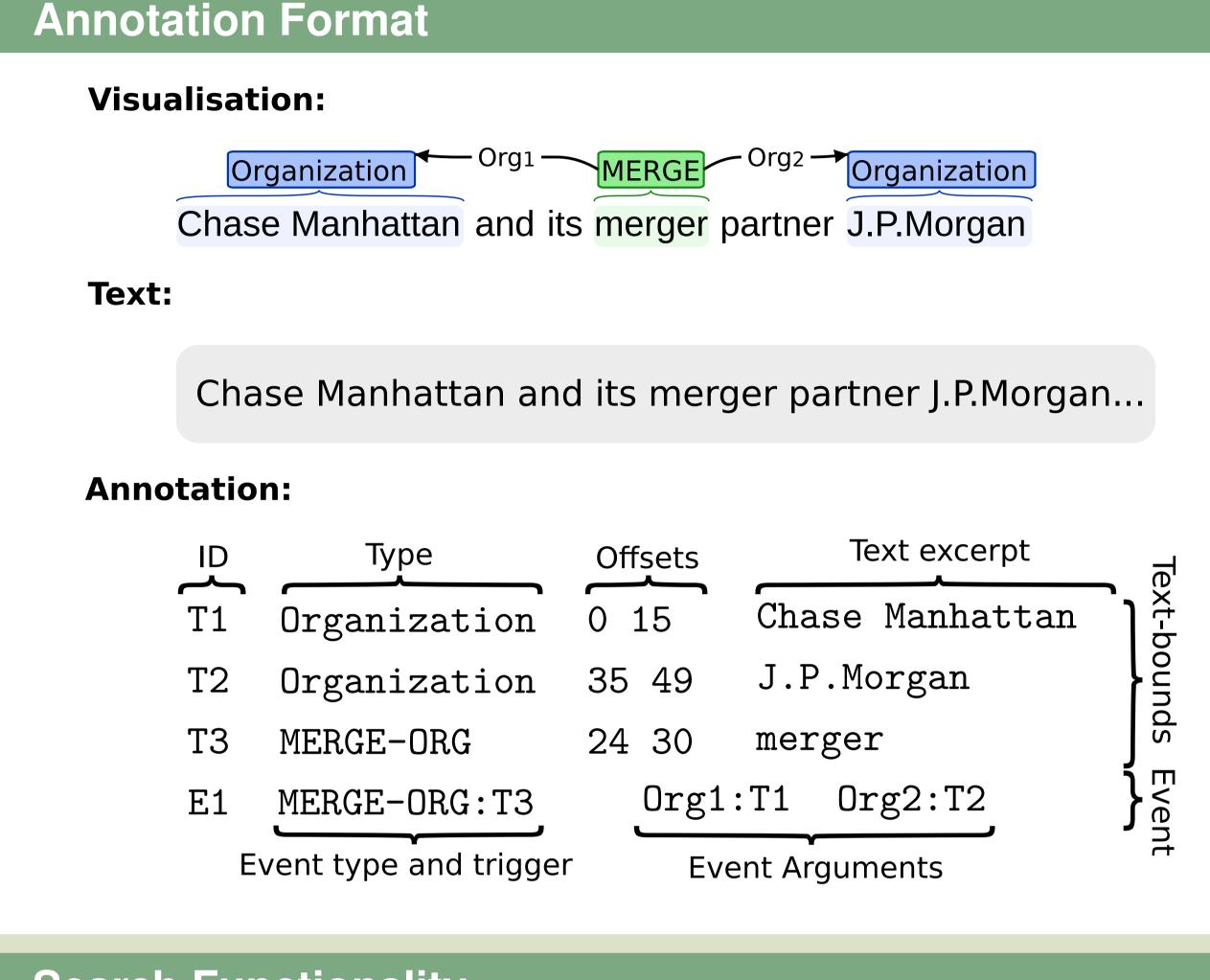
Annotation Primitives

- stav uses the following primitives to represent annotations:
- 1. Typed spans, as applied in e.g. Named Entity Recognition
- 2. Binary relations, as applied in relation extraction
- 3. N-ary associations of annotations, such as event structures
- 4. Binary or multi-valued attributes on any annotation, e.g. NEGATION or CONFIDENCE
- stav is distributed with several conversion tools for popular formats such as CoNLL-X and BIO

Acknowledgements

This work was supported by the Swedish Royal Academy of Sciences and by Grant-in-Aid for Specially Promoted Research (MEXT, Japan). The UK National Centre for Text Mining is funded by the UK Joint Information Systems Committee (JISC).





Search Functionality

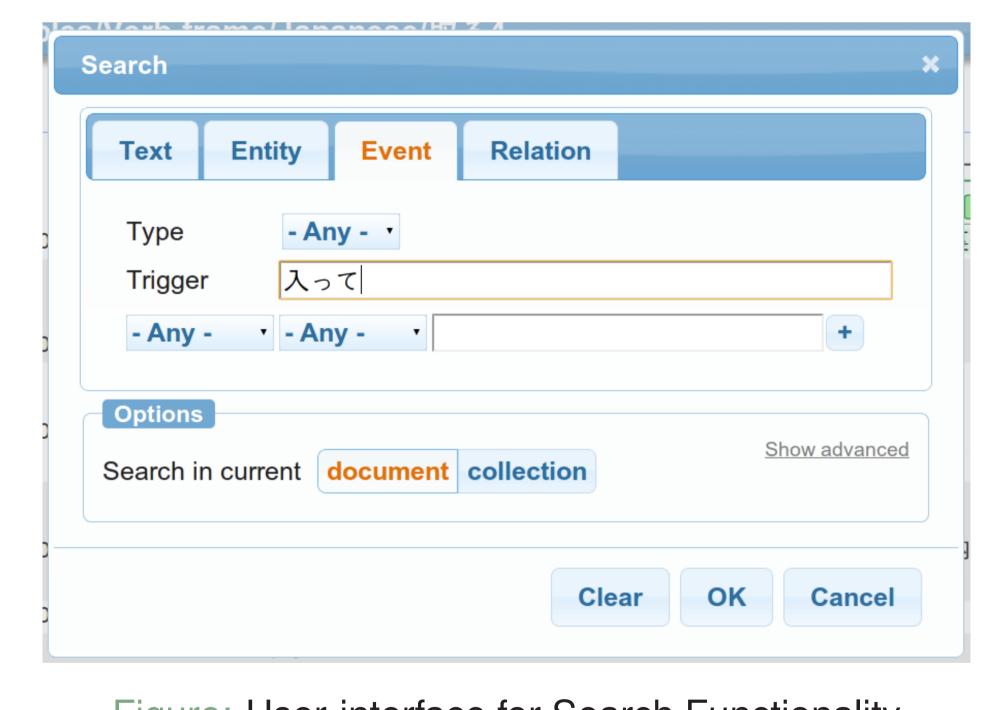


Figure: User-interface for Search Functionality

Availability

Source code, conversion tools and future additions is/will be available at:

http://github.com/nlplab/stav/