Multi Model Approach for Alternative Taggings

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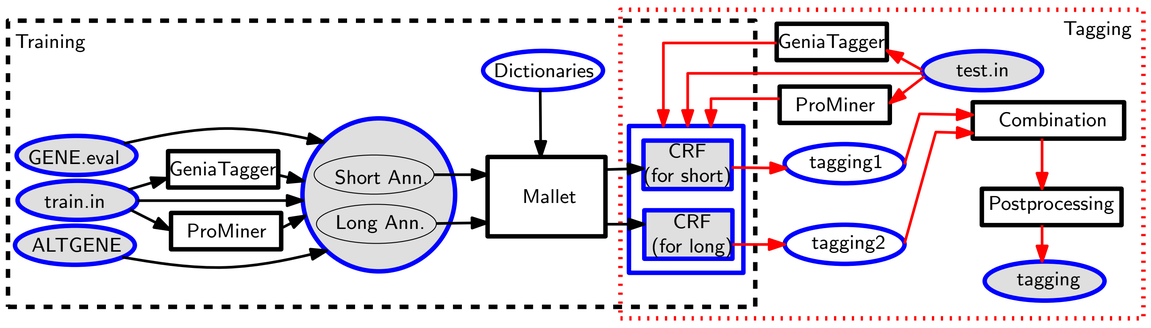
Overview

1. Generate Trainingdata depending on different lengths of annotations
2. Build different Conditional Random Fields
3. Tag testdata and combine it with different strategies
4. Postprocessing
   - Bracket Correction, Acronym Disambiguation using LSA



Problem Description

- Characteristic in BioCreative 2006:
  - Trainingdata provides acceptable alternatives additional to gold standard
- Problem: Ambiguities — Examples:
  - On the other hand factor IX activity is decreased in coumarin treatment with factor IX antigen remaining normal.
  - The arginyl peptide bonds that are cleaved in the conversion of human factor IX to factor IXa by factor XIa were identified as Arg145-Ala146 and Arg180-Val181.

  (Gold Standard Alternative)

Multi Model Approach

How to use the alternative annotations?

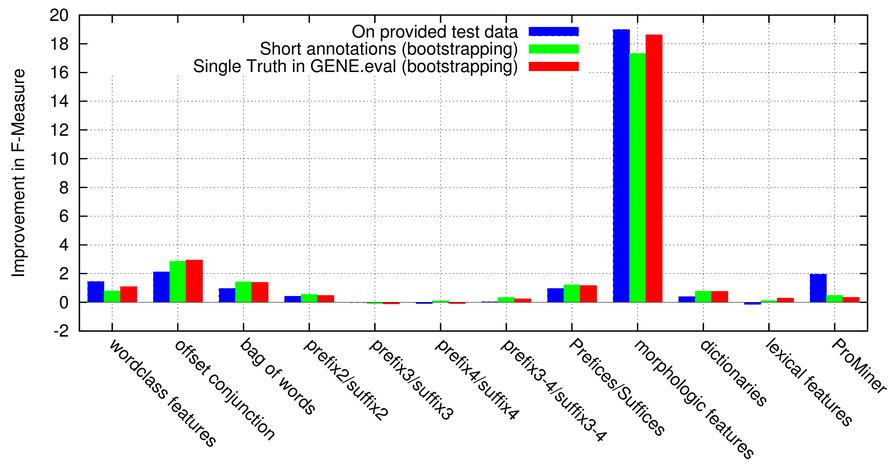
- Two Trainingsets:
  - Shortest possible annotation: Example (see 2nd sentence above): factor IX and factor IXa and factor XIa
  - Longest possible annotation: Example: human factor IX and factor IXa and factor XIa

How to deal with different taggings?

- Assume as example: ...fibrinogen degradation products (FDP)...
  - *Long* Annotator: fibrinogen degradation products
  - *Short* Annotator: fibrinogen ; FDP
- Use long annotation first, then add short annotation (without overlaps): fibrinogen degradation products and FDP
- Use short annotation first, then add long annotation (without overlaps): fibrinogen and FDP
- Greedy: Combine both (with overlaps): fibrinogen and FDP and fibrinogen degradation products

Model Selection

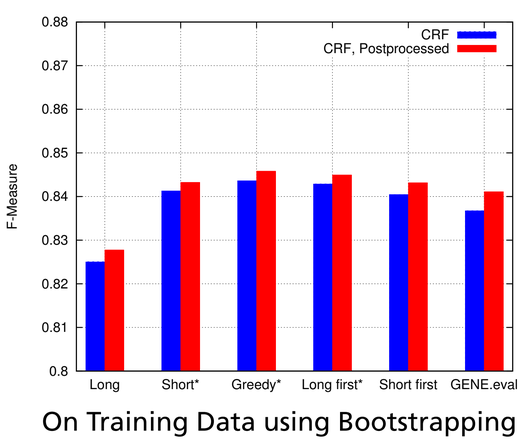
- Bootstrapping with 50 replicates
- Compared different tokenisations, impact is 2.48% on test data
- Rich set of features
  - Morphological, some automatically generated like bag-of-words, prefixes, suffixes, (brief) word class...
  - POS/Shallow Parsing: GeniaTagger
  - Annotations from ProMiner [1] as features
    → Very high precision because of mapping to UniProt and EntrezGene
  - Difficult to analyse optimal combination of features
    Example: prefixes with different length (see figure)



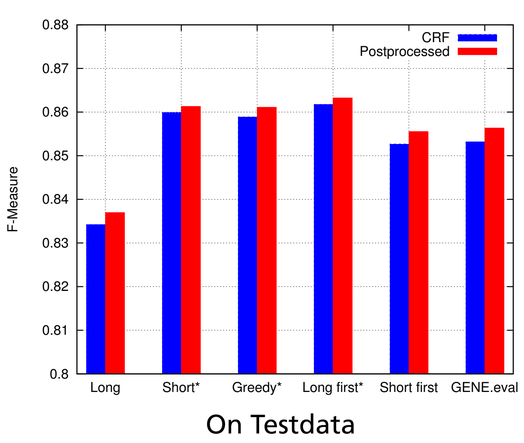
Results and Discussion

Model	Bootstrapping on Trainingset Precision		Recall		F-Score		On Testset Precision	Recall	F-Score
GENE.eval	86.61	(0.0071)	81.76	(0.0123)	84.11	(0.0076)	87.86	83.53	85.64
Long	86.30	(0.0065)	79.53	(0.0094)	82.78	(0.0064)	87.41	80.29	83.70
Short*	86.87	(0.0054)	81.94	(0.0106)	84.33	(0.0069)	88.57	83.83	86.13
Greedy*	80.21	(0.0069)	89.47	(0.0057)	84.58	(0.0047)	82.02	90.63	86.11
Long first*	85.38	(0.0060)	83.63	(0.0079)	84.50	(0.0055)	87.27	85.41	86.33
Short first	83.83	(0.0063)	84.81	(0.0065)	84.32	(0.0048)	85.50	85.61	85.56

(* submitted results)



On Training Data using Bootstrapping



On Testdata

- Short Annotation: best Precision
- Long Annotation: harder to find, but mostly matches author's mind

⇒ Good trade-off: Long first combination

- Greedy Combination: High Recall because of redundant annotation

⇒ good precondition for normalisation tasks

- Remarkable differences between results on test set using bootstrapping and training set are untypical

→ Impact of ProMiner?

References

[1] D. Hanisch, K. Fundel, H. T Mevissen., R. Zimmer, and J. Fluck. ProMiner: Organism-specific protein name detection using approximate string matching. *Proceedings of the BioCreative Challenge Evaluation Workshop 2004*, 2004.

[2] A. K. McCallum. MALLET: A Machine Learning for Language Toolkit. http://mallet.cs.umass.edu, 2002.

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