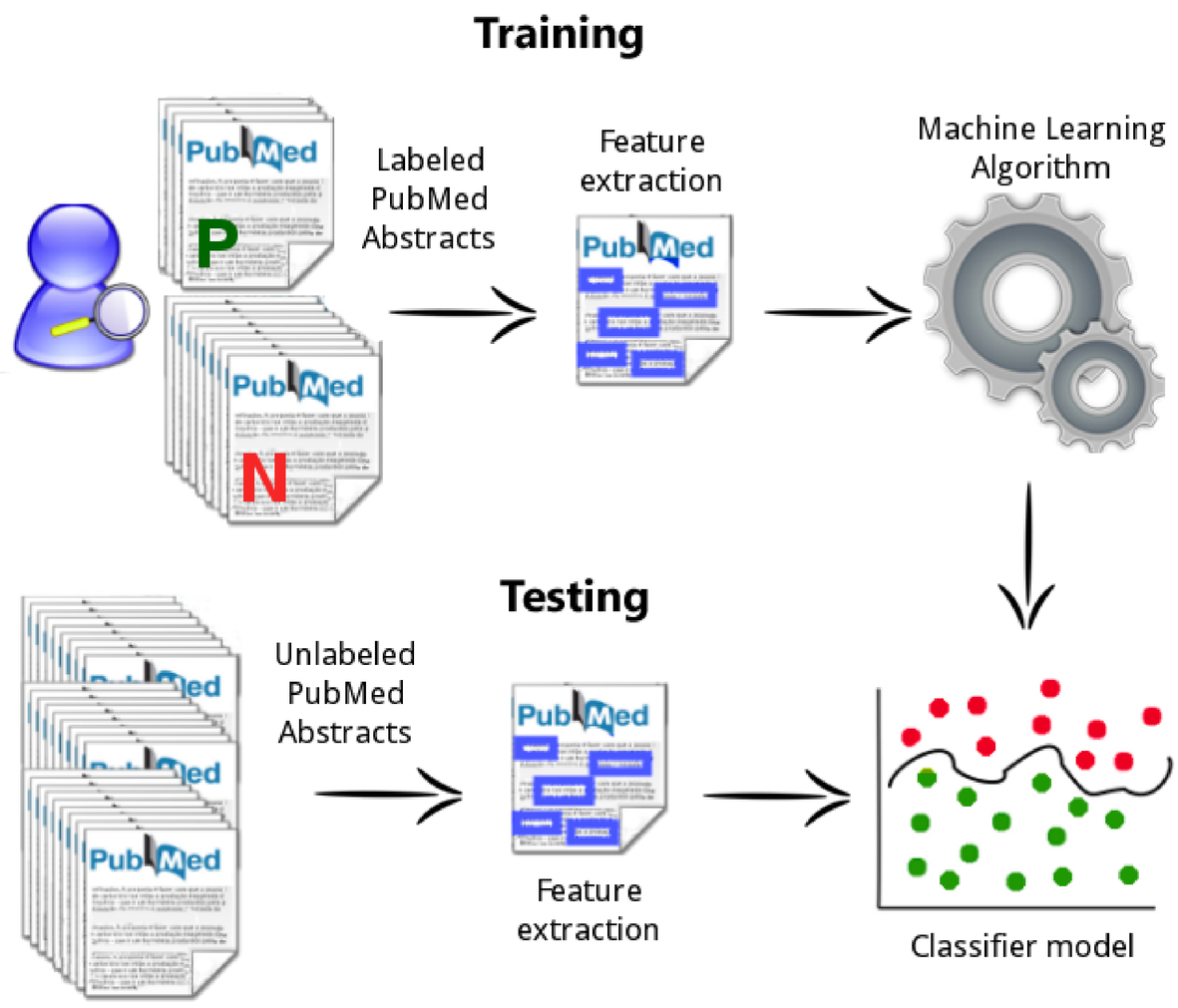
Biomedical Literature Triage

Hayda Almeida[1], **Marie-Jean Meurs**[2], **Leila Kosseim**[1],
1 *Department of Computer Science and Software Engineering*, Concordia University

The mycoSORT System

mycoSORT utilizes supervised machine learning to perform **automatic text classification** of PubMed abstracts.
The system goal is to support the **triage of candidate articles** for the mycoCLAP database [1].
Over 100 classification models were evaluated to identify the best performance under different settings.
The purpose is to be able to handle the triage task under an **imbalanced class distribution**.

mycoSORT Pipeline



Training phase

1. Input curated abstracts
2. Extraction of relevant features
3. Classification model building

Testing phase

1. Input unlabeled abstracts
2. Extraction of relevant features
3. Classification model application
4. Evaluation of system predictions

Feature Extraction

- Pre-processing: stop-words, ASCII characters, markup tags
- Content: abstract, paper title and Enzyme Comission (EC) numbers
- mycoMINE [2] annotations: 22 bioentities
- Annotation spans: entity and sentence
- Filtering criteria: length > 3 and occurrence > 2

*<SubstrateSpecificity>*The substrate specificity of three *<Enzyme>*ligninase*</Enzyme>* isozymes from the white-rot fungus *<Fungus>*Trametes versicolor*</Fungus>* has been investigated(...).*</SubstrateSpecificity>*(...) *<RegistryNumber>*EC 1.14.99.*</RegistryNumber>*

Bioentities of the entity span

[ligninase, Enzyme], [Trametes versicolor, fungus]

Bioentities of the sentence span

[substrate, substratespecificity], [specificity, substratespecificity], [three, substratespecificity], [ligninase, substratespecificity], [isozymes, substratespecificity], [whiterot, substratespecificity], [fungus, substratespecificity], [trametes versicolor, substratespecificity], [investigated, substratespecificity]

Feature Vector

substrate	*specificity*	*three*	*enzyme*	*ligninase*	*isozymes*	*whiterot*	*fungus*	*Trametes versicolor*	*investigated*	*11499*	...
1	1	1	1	2	1	1	2	2	1	1	...

Feature Representation

Set of Features

- F1: Bioentities
- F2: Content of entity spans
- F3: Content of sentence spans (bag-of-words)
- F4: EC Numbers
- F5: Bag-of-words of abstract and title

Dataset

- Over 7,580 manually curated PubMed abstracts
- 749 relevant (POS) and 6,834 not relevant (NEG)
- Evaluation of several class distributions
- Training: random undersampling of majority class
- Testing: real class distribution (10%POS, 90%NEG)

using Supervised Learning

Greg Butler[1,2], **Adrian Tsang**[2]
2 *Centre of Structural and Functional Genomics*, Concordia University

Experimental Settings

Classification algorithms

- Naive Bayes (NB)
- Support Vector Machine (SVM)
- Logistic Model Trees (LMT)

Feature Settings

#1: F1

#2: F1 + F4

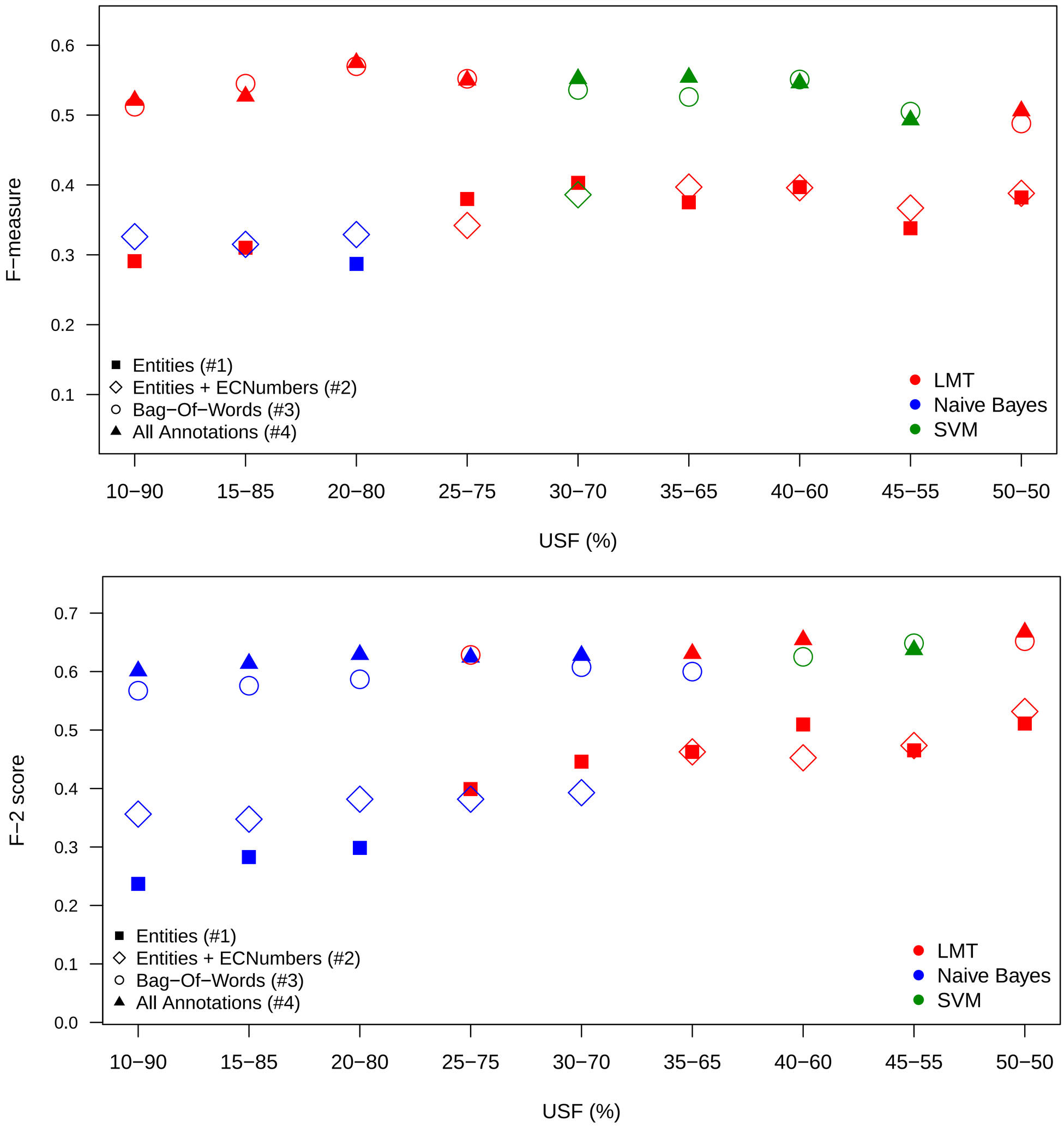
#3: F5

#4: F1 + F2 + F3 + F4

Undersampling Factors

- 0% USF: 90%NEG, 10%POS
- USFs gradually increased by 5%
- 40% USF: 50%NEG, 50%POS

mycoSORT results



Discussion

- Baseline: #3 (bag-of-words)
- #3 feature space: from 7,622 to 20,729
- #4 feature space: from 3,338 to 8,931
- #4 outperforms #3 by using domain annotations

Future Work

- Study the statistical relevance of features
- Use feature selection to refine existing models
- Evaluate system on different biomedical datasets

References

[1] Murphy C. et al., **Curation of characterized glycoside hydrolases of fungal origin**, Database, 2011.
[2] Meurs et al., **Semantic text mining support for lignocellulose research**, BMC MIDM, 2012