Text Mining & Bioinformatics

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Overview

- Introduction and objectives
- Metrics
- Words
- Tasks
- Methodologies
- Text Categorization

Objectives

- Introduce how text mining can support bioinformatics tasks
- Explain how text mining operate with biological entities and the « biological » ecosystem
- Stimulate your interest into a satellite - yet very lifeful - bioscience field

Text Data Mining

- Text Mining is like Data Mining but works with textual contents

- … So any statistical analysis can be performed with text mining provided the content is available in text ?

- Answer: **Jein !**

Disciplines

- Natural language processing, Natural language understanding, computational linguistics (+)
- Machine learning / data mining (++)
- **Information retrieval (+++)**

Common application fields

- Information retrieval
- Biocuration support tools
- Biological modelling

User level tasks

- Search – Foundations
- Triage
- Keyword assignment
- (Named-)Entity recognition
- Extract passages or more complex entities (e.g. protein protein interactions)

Metrics

- Precision
- Recall
- Other metrics…

Evaluation

- Like most data mining tasks, information retrieval and text mining tasks are assessed using two dimension metrics

Precision

- Given 5 relevant documents in a collection for a given query, a search engine returns **10** documents, including **3**, which are pertinent

- P = 3/10 = 0.30 or 30%

Recall

- Given **5** relevant documents in a collection for a given query, a search engine returns 10 documents, including **3**, which are pertinent

- Recall = 3/5 = 0.60 or 60%

Precision

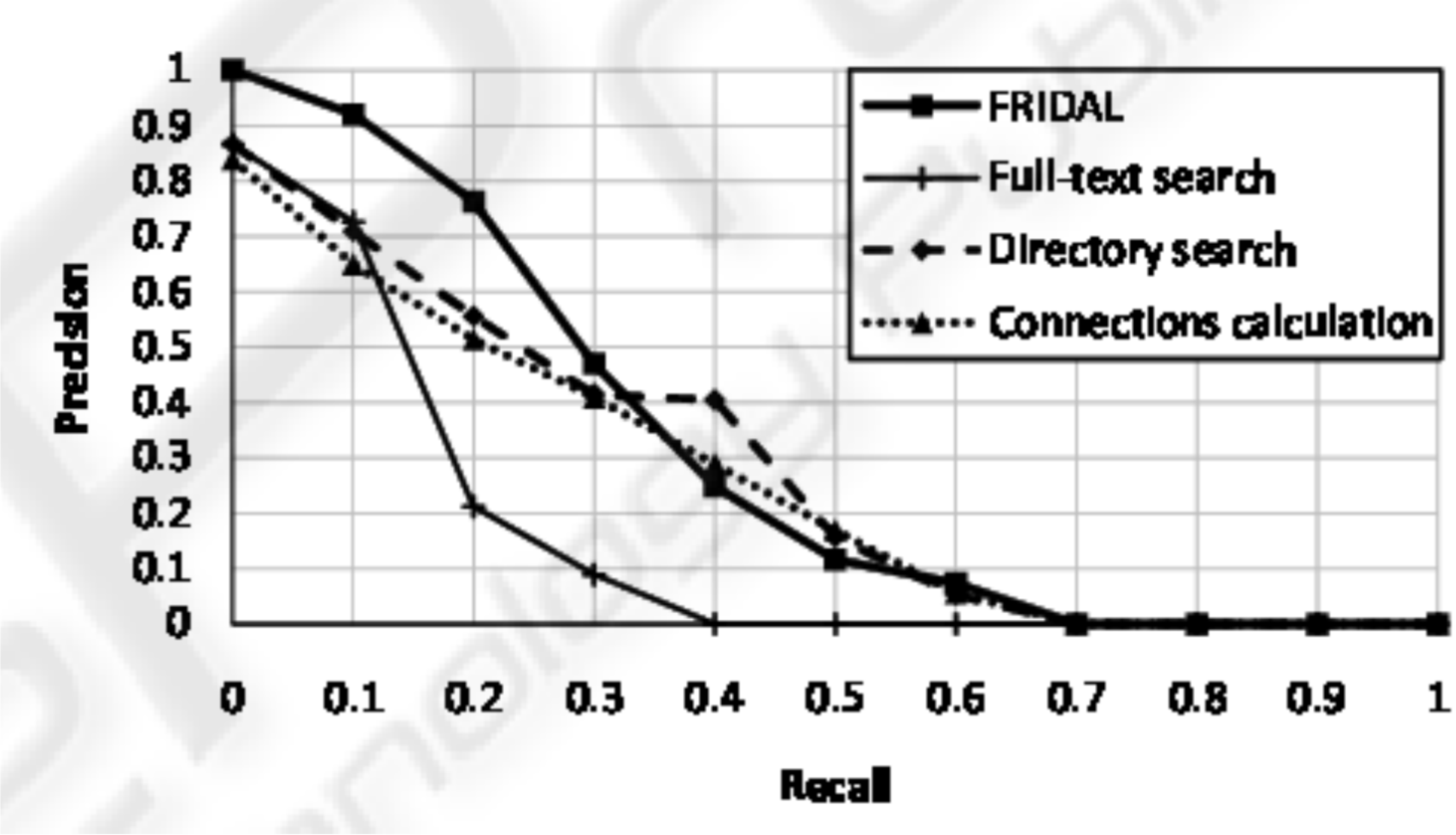
- Given 8 relevant documents in a collection for a given query, a search engine returns **10** documents, including **3**, which are pertinent

- Please compute the precision ?

Synthetic metrics

- Rank
    - R^{th-1} is more important than R^{th}
    - So, we compute average precision at different rank values (10, 20, … 30%, …)
    - Mean average precision
- F1 and related metrics
    - Harmonic or geometric mean
    - Utility metrics
        - E.g. 0.9 x Recall + 0.1 x Precision

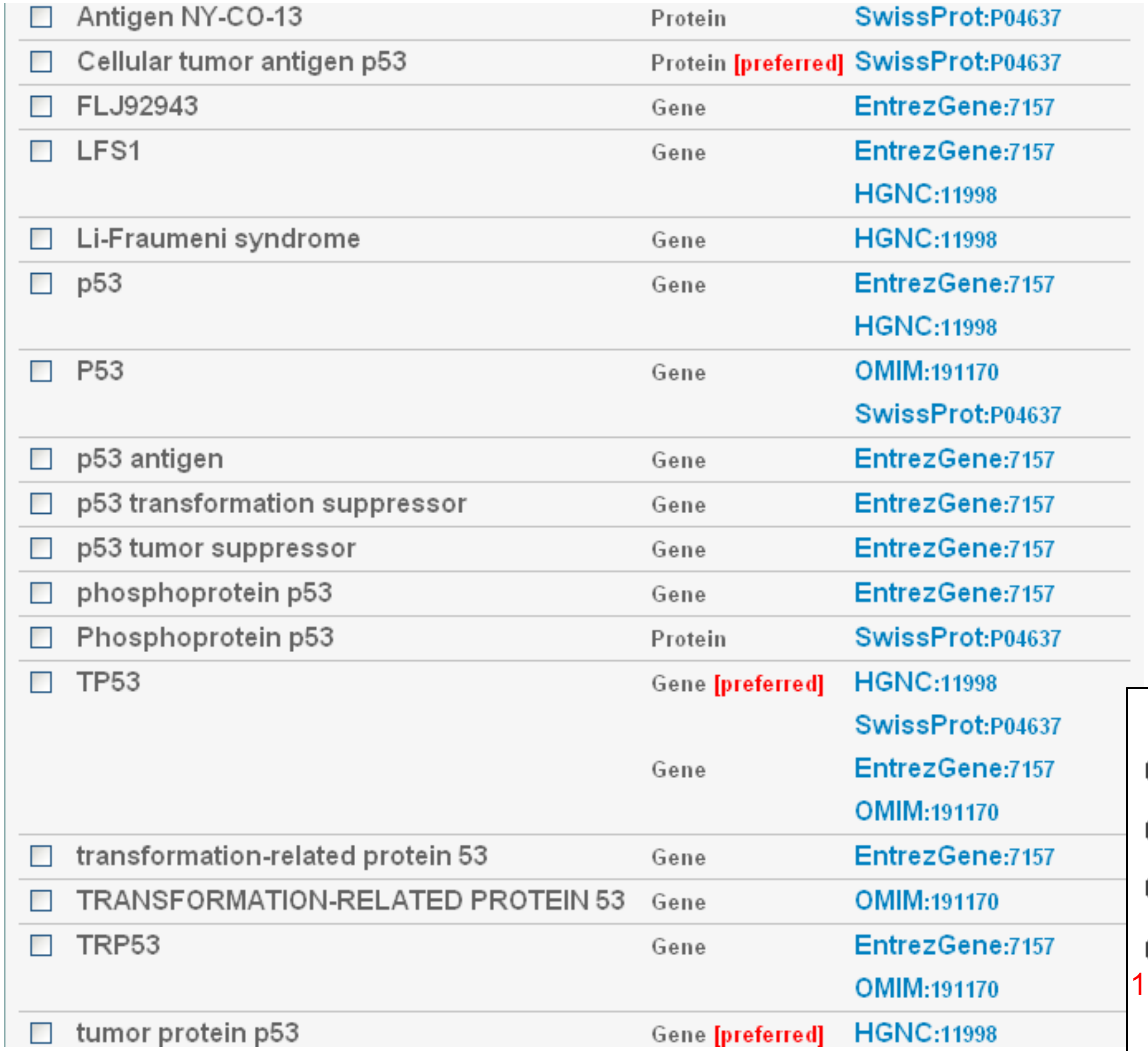
Example


1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Precision
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
Recall
FRIDAL
Full-text search
Directory search
Connections calculation

Feature normalization

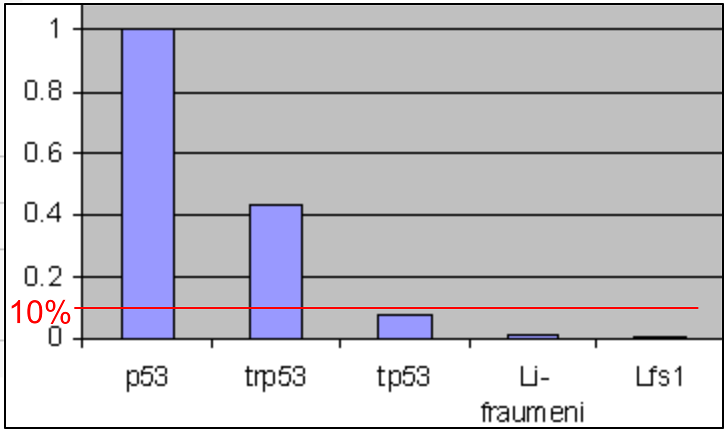
- Words
- Subwords (character N-grams)
- Stems
- Word N-grams
- Syntactic entities (noun phrases, verb phrases, …),
- Semantic entities (gene names, chem. compounds, diseases, …)

Term normalization: database & ontology vs. reality !



□	Antigen NY-CO-13	Protein	SwissProt:P04637
□	Cellular tumor antigen p53	Protein [preferred]	SwissProt:P04637
□	FLJ92943	Gene	EntrezGene:7157
□	LFS1	Gene	EntrezGene:7157 HGNC:11998
□	Li-Fraumeni syndrome	Gene	HGNC:11998
□	p53	Gene	EntrezGene:7157 HGNC:11998
□	P53	Gene	OMIM:191170 SwissProt:P04637
□	p53 antigen	Gene	EntrezGene:7157
□	p53 transformation suppressor	Gene	EntrezGene:7157
□	p53 tumor suppressor	Gene	EntrezGene:7157
□	phosphoprotein p53	Gene	EntrezGene:7157
□	Phosphoprotein p53	Protein	SwissProt:P04637
□	TP53	Gene [preferred] Gene	HGNC:11998 SwissProt:P04637 EntrezGene:7157 OMIM:191170
□	transformation-related protein 53	Gene	EntrezGene:7157
□	TRANSFORMATION-RELATED PROTEIN 53	Gene	OMIM:191170
□	TRP53	Gene	EntrezGene:7157 OMIM:191170
□	tumor protein p53	Gene [preferred]	HGNC:11998

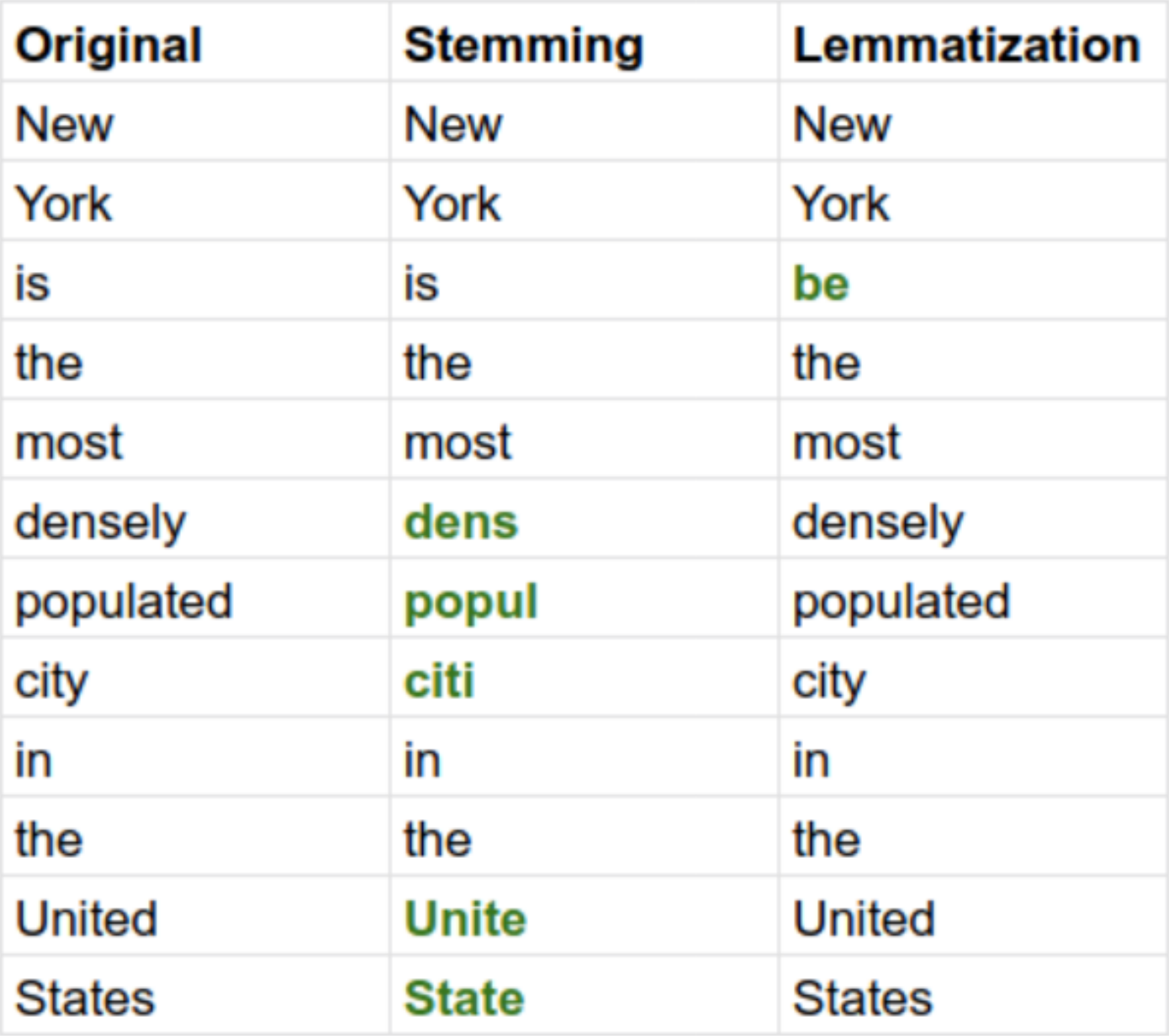
Synonyms	#
p53	53362
trp53	23364
tp53	4156
li-fraumeni	775
lfs1	431



Transformations (ETL, reg. expressions, …)

- i, ii, iii → 1, 2, 3 (e.g. *histone deacetylase iii*)
- Greek letters (e.g *α-tubulin*)
- Hyphenation «-»: {alphatubulin, alpha, tubulin)
- Chemistry
  - Inchi
  - SMILES
  - PubChem, chEBI, DrugBank…

Stemming vs. Lemmatization (needs syntactic analysis)



Original	**Stemming**	**Lemmatization**
New	New	New
York	York	York
is	is	**be**
the	the	the
most	most	most
densely	**dens**	densely
populated	**popul**	populated
city	**citi**	city
in	in	in
the	the	the
United	**Unite**	United
States	**State**	States

Positive impact of normalization and expansion ?

- Recall

- Precision

Normalization and expansion impact

- Recall

Normalization/expansion improves recall

- Precision

Normalization/expansion degrades precision

Contents

- Literature +++
- Electronic Health Records ++
- Grey literature, patents ++
- Social media +
- Other contents (news, archives, …)

- Resources: ontologies, terminologies, dictionaries, large corpora, …

Back end tasks – intelligent stuff that computers can do ☺

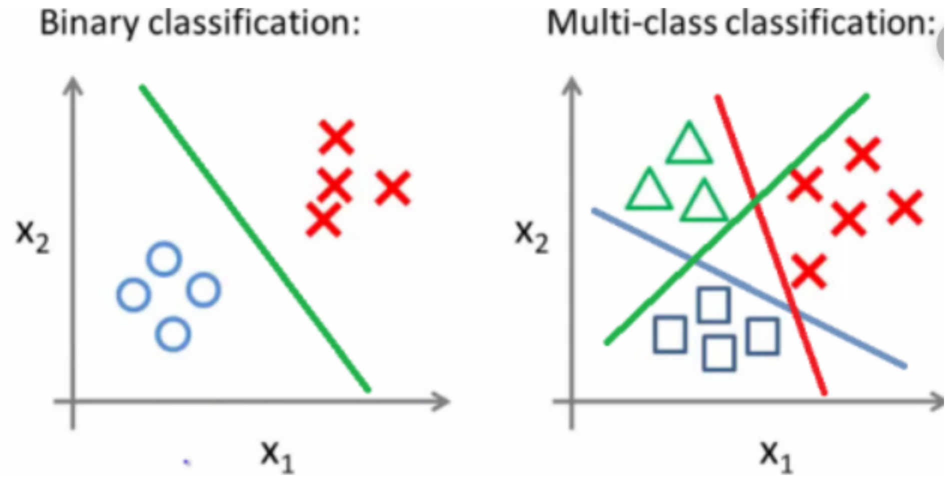
- Ranker
- Classifier
- … and both are the same: a classifier is a ranker with a threshold !
- Regression (ok for structured data)

Ranking and text mining features

- Given an objective function, rank a collection of text !
- Objective function = distance, precision, recall, …

Classification: one-class, binary, N-class

- With N binary classifiers, we can design N-class categorizers



Information retrieval – so called « ad hoc »

- PubMed
  - Boolean & Ante-chronological
  - « Best match »
    - Vector-space
    - Learning to rank
- EuropePMC
  - Vector-space (Lucene)
- SIBiLS
  - Vector-space (Lucene)
  - Combination of weighting schema (Terrier)

Boolean vs. Vector-space systems

- Boolean: would return results satisfying the query using AND, OR, NOT operators

- Vector-space does the same but the ranking is based on the differential weighting of:
  - TF: Term frequency

  The more frequent a term in a document the stronger the association with that document

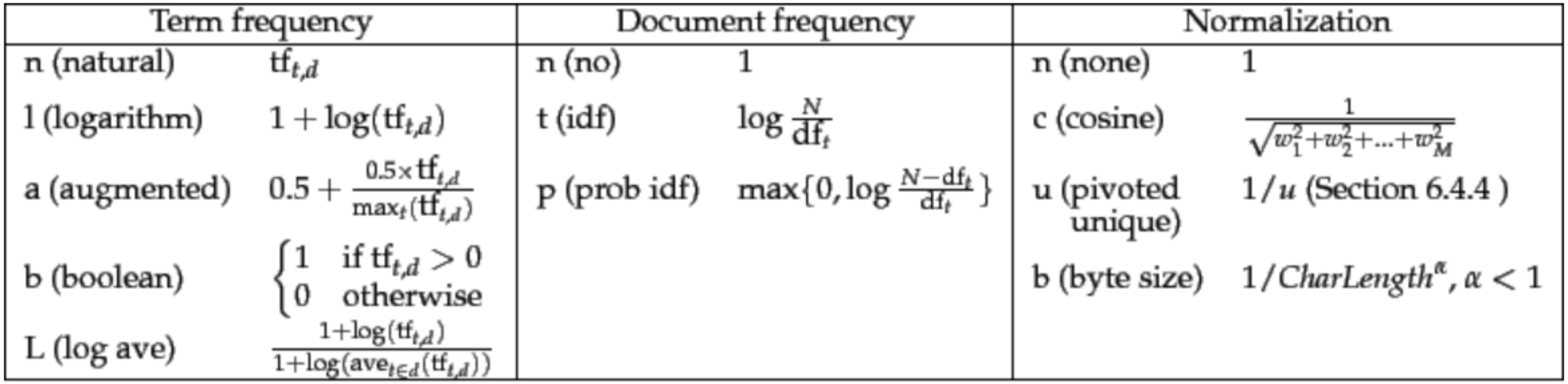
  - IDF: Inverse document frequency

  The more rare a term in a document collection the stronger the association with a document it appears in

  - Document normalization factor

  Longer documents tend to have more words irrespective on the relevance of those words

Weighting schema



Term frequency		Document frequency		Normalization	
n (natural)	$\mathrm{tf}_{t,d}$	n (no)	1	n (none)	1
l (logarithm)	$1+\log(\mathrm{tf}_{t,d})$	t (idf)	$\log \frac{N}{\mathrm{df}_t}$	c (cosine)	$\frac{1}{\sqrt{w_1^2+w_2^2+...+w_M^2}}$
a (augmented)	$0.5+\frac{0.5\times\mathrm{tf}_{t,d}}{\max_t(\mathrm{tf}_{t,d})}$	p (prob idf)	$\max\{0,\log \frac{N-\mathrm{df}_t}{\mathrm{df}_t}\}$	u (pivoted unique)	$1/u$ (Section 6.4.4)
b (boolean)	$\begin{cases} 1 & \text{if } \mathrm{tf}_{t,d} > 0 \\ 0 & \text{otherwise} \end{cases}$			b (byte size)	$1/CharLength^{\alpha}$, $\alpha < 1$
L (log ave)	$\frac{1+\log(\mathrm{tf}_{t,d})}{1+\log(\mathrm{ave}_{t\in d}(\mathrm{tf}_{t,d}))}$				