

Investigating word interactions in texts. Application to text categorization in genomics

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Investigating word interactions in texts. Application to text categorization in genomics.

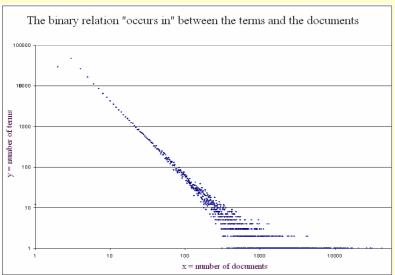
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Words interacting in a text may be compared, to a certain extent, to molecules interacting and building "complexes", i.e. phrases, named entities, or longer-range semantic or syntactic associations. We will call them "k-itemsets", k being their interaction level. We have shown (Cadot 06) that an adequately built subset of these kitemsets is enough for describing the entirety of the relations at work in a corpus represented as a set of "bag-of-words" documents, whatever the level k of these relations.

Our objective is to reconstruct each category into which a corpus of scientific abstracts has been split, using a set of Boolean queries as a best compromise between conciseness and reproducibility of this categorization.

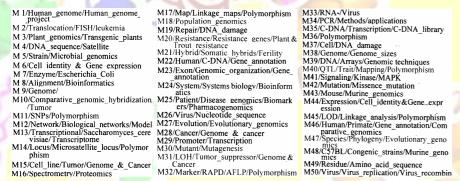
I - The corpus, its 50 catégories.

- Scientific abstracts in genomics, pulled out from the Web of Science (Thomson Scientific ed.).
- This subset has been delineated using a hybrid method, based both on lexical queries and citation expansion/ shrinkage (Zitt et al. 2006) \rightarrow 120,000 abstracts from 1999 to 2005.
- A vocabulary of 237,000 lemmatized words and phrases (>2 occurrences) has been pulled out and filtered (NeuroNav, www.diatopie.com). I.e.: sequence, polymorphism, folded_structure, chromosome_4B, greenbug_resistence_gene,...



This figure reads: e.g. 1047 terms occur each one exactly in 21 documents.

50 categories resulted from a clustering of the abstracts by the Axial K-means method (Bassecoulard et al. 2007).

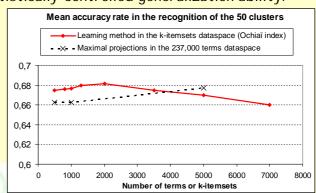


Ex. of the 14 first terms (words and phrases) most typical of the « Human Genome Project » cluster:

No	Phrase	Ochiaï	8	human_genome_sequence	0,122	
1	human_genome	0,467	9	primate	0,107	
2	human	0,336	10	sequence	0,103	
3	genome	0,257	11	chimpanzee	0,099	
4	human_genome_project	0,238	12	completion	0,096	
5	project	0,157	13	disease	0,094	
6	draft	0,138	14	genomics	0,092	
7	human_chromosome	0,125	15	human_gene	0,092	

As most of data analysis methods do, this data partition takes into account the only « 2-itemsets » (a k-itemset of support s is an elementary association of k terms present in s documents).

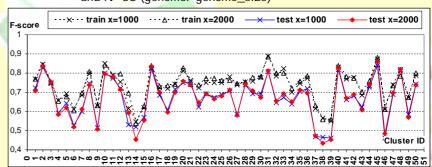
- II Concise and reproducible representation of the 50 categories: using itemsets of order 1, 2, and higher order ones, which express complex interactions between terms in specific contexts.
- MIDOVA method (Cadot 2006) for mining ordered lists of informative itemsets specific to each category (train set: 1/10th of the corpus, test set: $9/10^{th}$) \rightarrow ordered lists of simple Boolean queries for identifying the class of any document out of the corpus, and extending this categorization process to other databases (patents, ...).
- Results
 - At the same time as a 100% intrinsically exact reconstitution rate results from using the whole 237,000 terms, a maximum 68% rate results from using about x = 2000 k-itemsets (and then decreases), with a statistically-controlled generalization ability:



68% is a mean value, embedding many discrepancies:

>80%: clusters N°45 (LOD/ Linkage_analysis/ Polymorphism) and N°16 (Spectrometry/ Proteomics)

<50%: clusters N°14 (Locus/ Microsatellite_Locus/ Polymorphism) and N° 38 (genome/ genome_size)



example of class description: the 6 first k-itemsets of cluster 10:

> comparative_genomic_hybridization, hybridization AND tumor AND genomic, hybridization AND tumor, CGH AND comparative_genomic_hybridization, losses AND genomic, tumor AND genomic.

As may be observed comparative_genomic_hybridization and CGH acronym appear together, integrally or partly, at the top of the list.

References

Bassecoulard E., Lelu A. and Zitt M. (2007). Mapping nanosciences by citation flows: a preliminary analysis, Scientometrics, vol 70, n°3, pp. 859-880.

Cadot M. (2006). Extraire et valider les relations complexes en sciences humaines : statistiques, motifs et règles d'association. Doctoral dissertation, University of Franche-Comté, France.

Laurens P., Zitt M. and Bassecoulard E. (to appear), "Delineation of the genomics field by hybrid citation-lexical methods: interaction with experts and validation process", Scientometrics.

Zitt M., Ramanana-Rahary S. and Bassecoulard E. (2006). Delineating complex scientific fields by a hybrid lexical-citation method: an application to nanosciences, Information Processing and Management Vol. 42-6, pp. 1513-1531.