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

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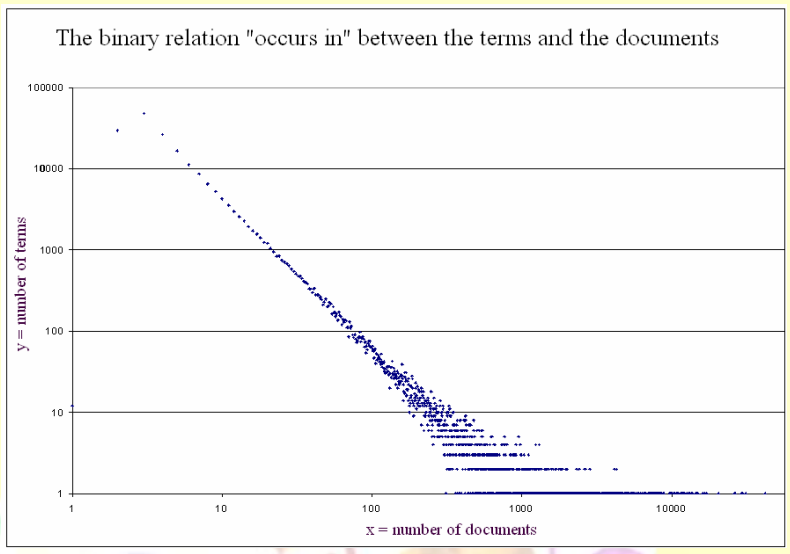
Words interacting in a text may be compared, to a certain extent, to molecules interacting and building "complexes", i.e. phrases, named entities, or longer-range semantic or syntactic associations. We will call them "k-itemsets", k being their interaction level. We have shown (Cadot 06) that an adequately built subset of these k-itemsets 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) → 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).

M 1/Human_genome/Human_genome_project
M 2/Translocation/FISH/leukemia
M 3/Plant_genomics/Transgenic_plants
M 4/DNA_sequence/Satellite
M 5/Strain/Microbial_genomics
M 6/Cell identity & Gene expression
M 7/Enzyme/Escherichia_Coli
M 8/Alignment/Bioinformatics
M 9/Genome/
M10/Comparative_genomic_hybridization_/Tumor
M11/SNPs/Polymorphism
M12/Network/Biological_networks/Model
M13/Transcriptional/Saccharomyces_cerevisiae/Transcriptome
M14/Locus/Microsatellite_locus/Polymorphism
M15/Cell_line/Tumor/Genome_&_Cancer
M16/Spectrometry/Proteomics
M17/Map/Linkage_maps/Polymorphism
M18/Population_genomics
M19/Repair/DNA_damage
M20/Resistance/Resistance_genes/Plant & Trout_resistance
M21/Hybrid/Somatic_hybrids/Ferility
M22/Human/C-DNA/Gene_annotation
M23/Exon/Genomic_organization/Gene_annotation
M24/System/Systems biology/Bioinformatics
M25/Patient/Disease_genomics/Biomarkers/Pharmacogenomics
M26/Virus/Nucleotide_sequence
M27/Evolution/Evolutionary_genomics
M28/Cancer/Genome & cancer
M29/Promoter/Transcription
M30/Mutant/Mutagenesis
M31/LOH/Tumor_suppressor/Genome & Cancer
M32/Marker/RAPD/AFLP/Polymorphism
M33/RNA-/Virus
M34/PCR/Methods/applications
M35/C-DNA/Transcription/C-DNA_library
M36/Polymorphism
M37/Cell/DNA_damage
M38/Genome/Genome_sizes
M39/DNA/Arrays/Genomic techniques
M40/QTL/Trait/Mapping/Polymorphism
M41/Signaling/Kinase/MAPK
M42/Mutation/Missence_mutation
M43/Mouse/Murine_genomics
M44/Expression/Cell_identity&Gene_expression
M45/LOD/Linkage_analysis/Polymorphism
M46/Human/Primate/Gene_annotation/Comparative_genomics
M47/Species/Phylogeny/Evolutionary_genomics
M48/C57BL/Congenic_strains/Murine_genomics
M49/Residue/Amino_acid_sequence
M50/Virus/Virus_replication/Virus_recombin

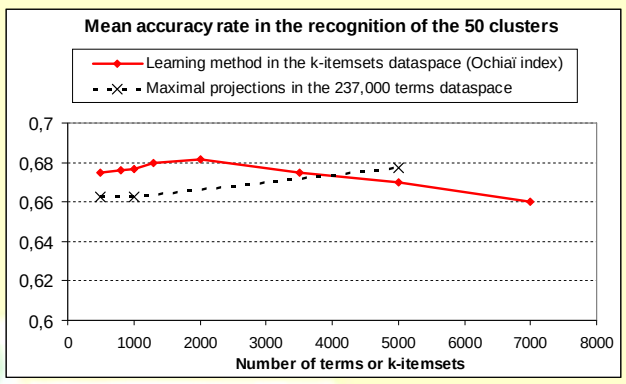
Ex. of the 14 first terms (words and phrases) most typical of the « Human Genome Project » cluster:

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

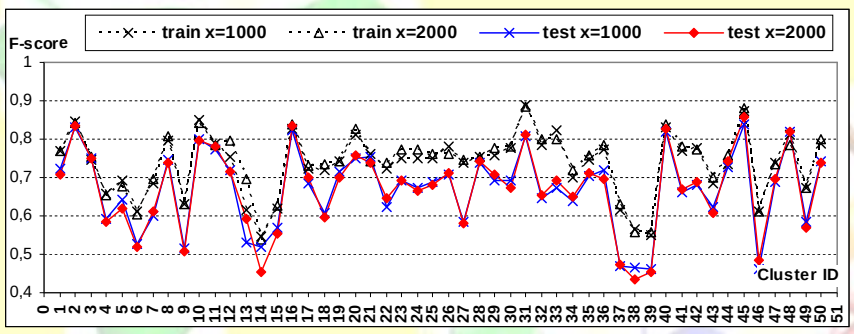
- MIDOVA method (Cadot 2006) for mining ordered lists of informative itemsets specific to each category (train set: 1/10th of the corpus, test set: 9/10 th) → ordered lists of simple Boolean queries for identifying the class of any document out of the corpus, and extending this categorization process 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

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