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

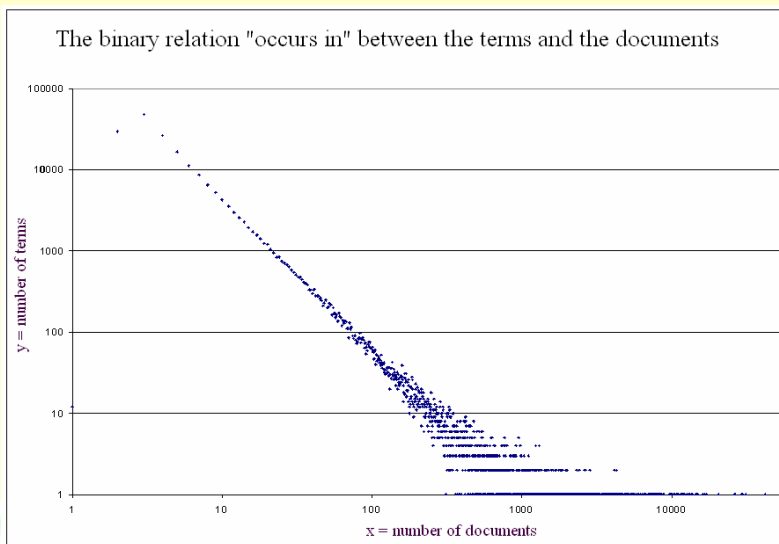
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Words interacting in a text may be compared, to a certain extent, to molecules interacting and building "complexes", i.e. phrases, named entities, or longer-range semantic or syntactic associations. We will call them "k-itemsets", k being their interaction level. We have shown (Cadot 06) that an adequately built subset of these 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](http://www.diatopie.com)). I.e.: *sequence, polymorphism, folded\_structure, chromosome\_4B, greenbug\_resistance\_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).

M1/ Human_genome/ Human_genome_project	M17/ Map/ Linkage_maps/ Polymorphism	M33/ RNA- Virus
M2/ Translocation/ FISH/ leukemia	M18/ Population_genomics	M34/ PCR/ Methods/ applications
M3/ Plant_genomics/ Transgenic_plants	M19/ Repair/ DNA_damage	M35/ C-DNA/ Transcription/ C-DNA_library
M4/ DNA_sequence/ Satellite	M20/ Resistance/ Resistance_genes/ Plant & Fungi_resistance	M36/ Polymorphism
M5/ Strain/ Microbial_genomics	M21/ Hybrid/ Somatic_hybrids/ Fertility	M37/ Cell/ DNA_damage
M6/ Cell_identity & Gene_expression	M22/ Human/ C-DNA/ Gene_annotation	M38/ Genome/ Genome_sizes
M7/ Enzyme/ Escherichia_Coli	M23/ Exon/ Genomic_organization/ Gene_annotation	M39/ DNA/ Arrays/ Genomic_techniques
M8/ Alignment/ Bioinformatics	M24/ System/ Systems_biology/ Bioinformatics	M40/ QTL/ Trait/ Mapping/ Polymorphism
M9/ Genome	M25/ Patient/ Disease_genomics/ Biomarkers/ Pharmacogenomics	M41/ Signaling/ Kinase/ MAPK
M10/ Comparative_genomic_hybridization/ Tumor	M26/ Virus/ Nucleotide_sequence	M42/ Mutation/ Missense_mutation
M11/ SNPs/ Polymorphism	M27/ Evolution/ Evolutionary_genomics	M43/ Mouse/ Murine_genomics
M12/ Network/ Biological_networks/ Model	M28/ Cancer/ Genome & cancer	M44/ Expression/ Cell_identity & Gene_expression
M13/ Transcriptional/ Saccharomyces_cerevisiae/ Transcriptome	M29/ Promoter/ Transcription	M45/ LOD/ Linkage_analysis/ Polymorphism
M14/ Locus/ Microsatellite_locus/ Polymorphism	M30/ Mutant/ Mutagenesis	M46/ Human/ Primate/ Gene_annotation/ Comparative_genomics
M15/ Cell_line/ Tumor/ Genome & Cancer	M31/ LOH/ Tumor_suppressor/ Genome & Cancer	M47/ Species/ Phylogeny/ Evolutionary_genomics
M16/ Spectrometry/ Proteomics	M32/ Marker/ RAPD/ AFLP/ Polymorphism	M48/ C57BL/ Congenic_strains/ Murine_genomics
		M49/ Residue/ Amino_acid_sequence
		M50/ Virus/ Virus_replication/ Virus_recombination

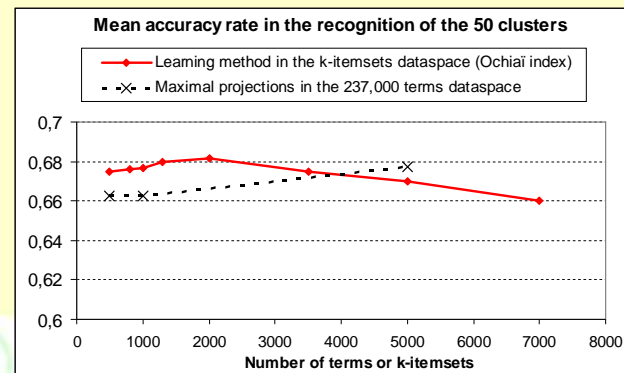
Ex. of the 14 first terms (words and phrases) most typical of the « Human Genome Project » cluster:

No	Phrase	Ochiai			
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

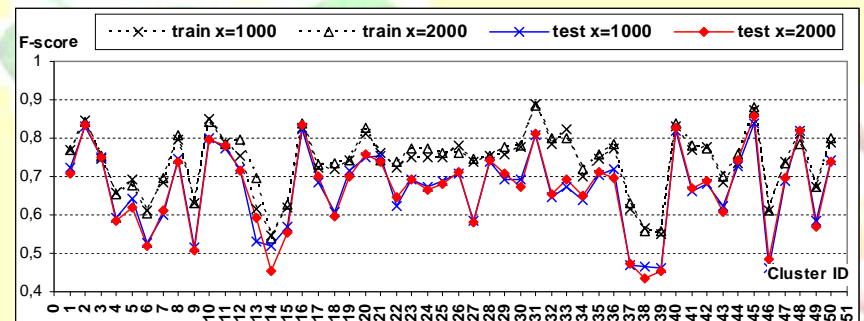
As most of data analysis methods do, this data partition takes into account the only « 2-itemsets » (a k-itemset of support s is an elementary association of k terms present in s documents).

## II - Concise and reproducible representation of the 50 catégories: 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: 1/10<sup>th</sup> of the corpus, test set: 9/10<sup>th</sup>) → 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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