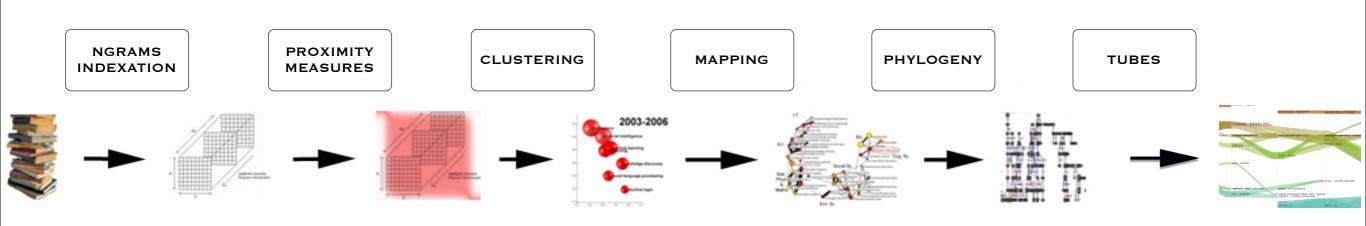
## Predictive Modeling of the Emergence and Development of Scientific Fields

*MIT, 25-26 May 20* 

### From Textual Corpora to Lexical Networks

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## Knowledge dynamics reconstruction



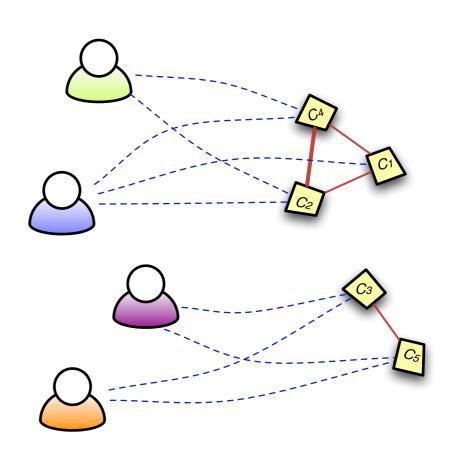
- Lexical networks analysis is a way to investigate knowledge communities
   dynamics based on the structure of the use of terms or concepts,
- Historically, keywords have been privileged as the basic unit of analysis for coword analysis, but...
  - some datasets may not have keywords entries
  - indexer bias can be criticized

## What it is about a text that is interesting?

«Indexing is an intervention between the text and the co-word analysis, and the validity of the map will depend, to a certain extent, on the nature of the indexing. Yet since indexers try to capture what it is about a text that is interesting, they partially reproduce the readings that the texts are given within the field itself'. Thus, despite the fact that indexing is not entirely reliable, validity is never totally absent.»

Callon, M.; Law,,J.; & Rip, A. (Eds.). (1986a). *Mapping the dynamics ofscience and technology: Sociology ok Science in the real world.* London: The Macmillan Press 1,td.

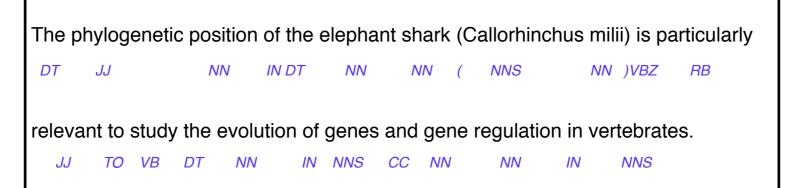
- grammatical criterion, candidate terms are usually limited noun phrases,
- unithood, phrases should represent a proper semantic unit,
- termhood, terms should be domain specific to carry substantial information



The phylogenetic position of the elephant shark (Callorhinchus milii) is particularly

relevant to study the evolution of genes and gene regulation in vertebrates.

i.Part-Of-Speech Tagging



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ii. Tag Chunking - Noun Phrases extraction

ex: Regexp={((Adj|Noun)+|(Adj|Noun)\*NounPrep?)(Adj|Noun)\*)Noun}

The phylogenetic position of the elephant shark (Callorhinchus milii) is particularly

DT JJ NN IN DT NN NN ( NNS NN )VBZ RB

relevant to study the evolution of genes and gene regulation in vertebrates.

JJ TO VB DT NN IN NNS CC NN NN IN NNS

i.Part-Of-Speech Tagging

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ex: Regexp={((Adj|Noun)+|(Adj|Noun)\*NounPrep?)(Adj|Noun)\*)Noun}

iii.Stemming and filtering of empty words

gene regulation in vertebrate -> {gene regul vertebr}
phylogenetic position of the elephant shark : {eleph phylogenet posit shark}
phylogenetic position -> {phylogenet posit}

#### i.Part-Of-Speech Tagging

#### ii. Tag Chunking - Noun Phrases extraction

ex: Regexp={((Adj|Noun)+|(Adj|Noun)\*NounPrep?)(Adj|Noun)\*)Noun}

#### iii.Stemming and filtering of empty words

#### iv.Output: classes of candidate multi-terms:

- cellular isoform prion protein = {isoform of cellular prion protein ; cellular isoform of the prion protein ; cellular prion protein isoform ; isoform of the cellular prion protein ; cellular isoform of prion protein
- conform: {conformers; conformational; conformation; conformer; conformations}
- resist scrapi: {resistance against scrapie ; scrapie resistance ; scrapie resistant ; Scrapie resistance}
- associ genotyp prp = {association of PrP genotype; associations between PrP genotypes; association between PrP genotype; associations of the PrP genotype; associations between PrP genotypes}

## Unithood: extracting semantic units with C-value

- Simple frequency-based approach: «Real» Terms tend to appear more frequently than non-terms
- C-value approach (Frantzi K. & Ananiadou S., 2000):
  - Longer phrases are more likely to be relevant,
  - Nested terms may induce false positive, ex: self organizing maps.

$$C\text{-}value(a) = log_2|a|(f(a) - \frac{1}{P(T_a)} \sum_{b \in T_a} f(b))$$

#### Termhood

- Candidate terms should be thematically specific; terms not specific to a specific thematic subfield have neutral meaning given the whole domain and should be excluded
- On the contrary, terms which distribution is biased toward certain topics are more likely to have interesting meaning.
- Co-occurrences between existing candidate terms are extracted to compute the Khi2 score of specificity of each term compared to other terms (Matsuo Y. & Ishizuka M., 2004).

$$\chi^2(w) = \sum_{g \in G} \frac{(freq(w,g) - n_w p_g)^2}{n_w p_g}$$

## Final output <u>example</u>:

forms

main form

stem

				<u>, , , , , , , , , , , , , , , , , , , </u>	
brassica-campestri	BRASSICA-CAMPESTRIS	BRASSICA-CAMPESTRIS	10,0	686,4	7,0
oilse rape	OILSEED RAPE	OILSEED RAPE	7,0	778,1	9,5
cdna	cDNAs	cDNAsi&icDNAi&iCDNA	16,0	468,3	7,0
brassica rapa	Brassica rapa	Brassica rapa	33,0	1144,8	44,4
alloplasm line	alloplasmic lines	alloplasmic linel&lalloplasmic lines	5,0	404,7	7,9
indian mustard	Indian mustard	Indian mustardl&IINDIAN MUSTARDI&lindian mustard	18,0	2027,6	23,8
crop	crops	cropsl&lCropl&lcrop	58,0	708,8	35,0
hybrid intergener	intergeneric hybrids	INTERGENERIC HYBRIDSI&lintergeneric hybridsl&lintergeneric hybridization	16,0	2208,2	25,4
cm line	CMS line	cms linel&ICMS linel&ICMS lines	13,0	278,5	15,8
anther	anthers	anthersl&IAntherl&IANTHERI&Ianther	62,0	911,5	30,5
high level	high level	high levelsl&lhigh level	5,0	252,5	7,9
express gene	gene expression	expression of genesl&IGENE EXPRESSIONI&Igene expressionl&Igenes in the	22,0	397,1	8,7
gene	genes	genesl&lgene	175,0	296,4	57,4
canola	canola	canolal&ICANOLAl&ICanola	27,0	457,3	23,0
male-steril	male-sterility	MALE-STERILITYI&Imale-sterility	68,0	2606,9	8,3
radish	radish	RADISHI&Iradish	35,0	808,1	20,0
cybrid	cybrids	CYBRIDSI&IcybridI&ICYBRIDI&Icybrids	16,0	463,5	14,0
marker	markers	markerl&lmarkers	60,0	455,2	10,0
genom mitochondri	mitochondrial genome	mitochondrial genomel&Imitochondrial genomes	21,0	423,0	38,0
brassicacea	Brassicaceae	BRASSICACEAEI&IBrassicaceae	20,0	872,5	18,0
flow gene	gene flow	gene flow	15,0	919,6	22,2
fertil restor	fertility restoration	restoration of fertilityl&lrestorer of fertilityl&lfertility restorationl&lfertility restorerl	39,0	440,6	31,7
bud flower	flower buds	flower buds	6,0	311,0	7,9
brassica oleracea	Brassica oleracea	BRASSICA OLERACEAI&IBrassica oleracea	51,0	1399,2	42,8

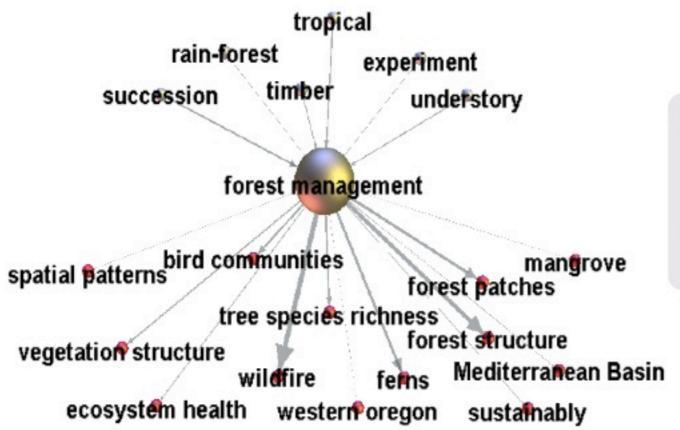
C-value

specificity

occurrences

#### What next?

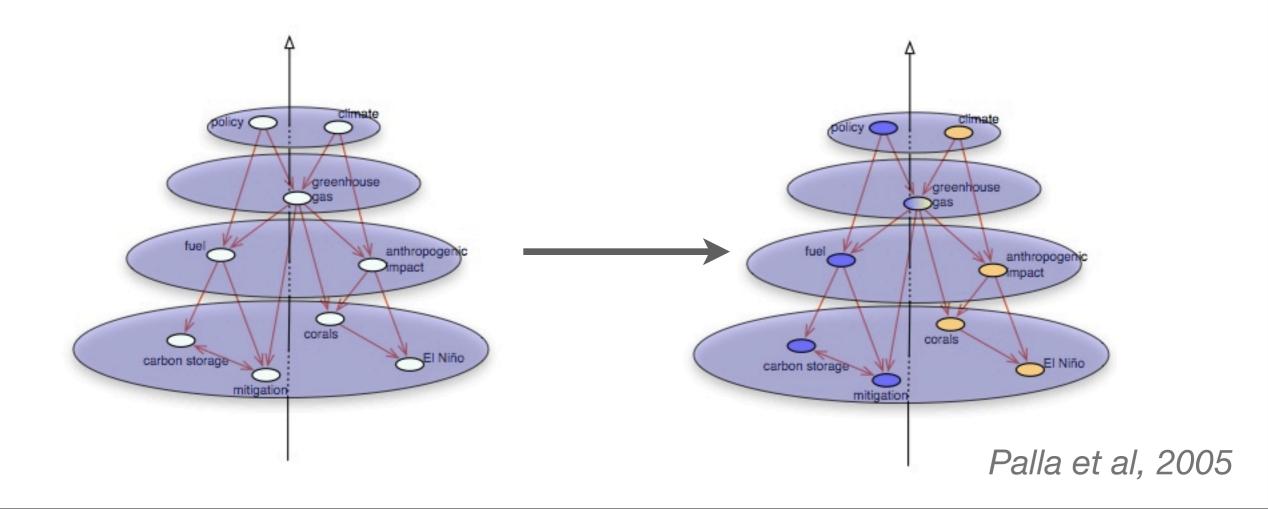
 Reconstruction of the cognitive dynamics in science through the analysis of the lexical network built upon the temporal matrix of co-occurrences within our term list (asymmetric measure of proximity between terms).

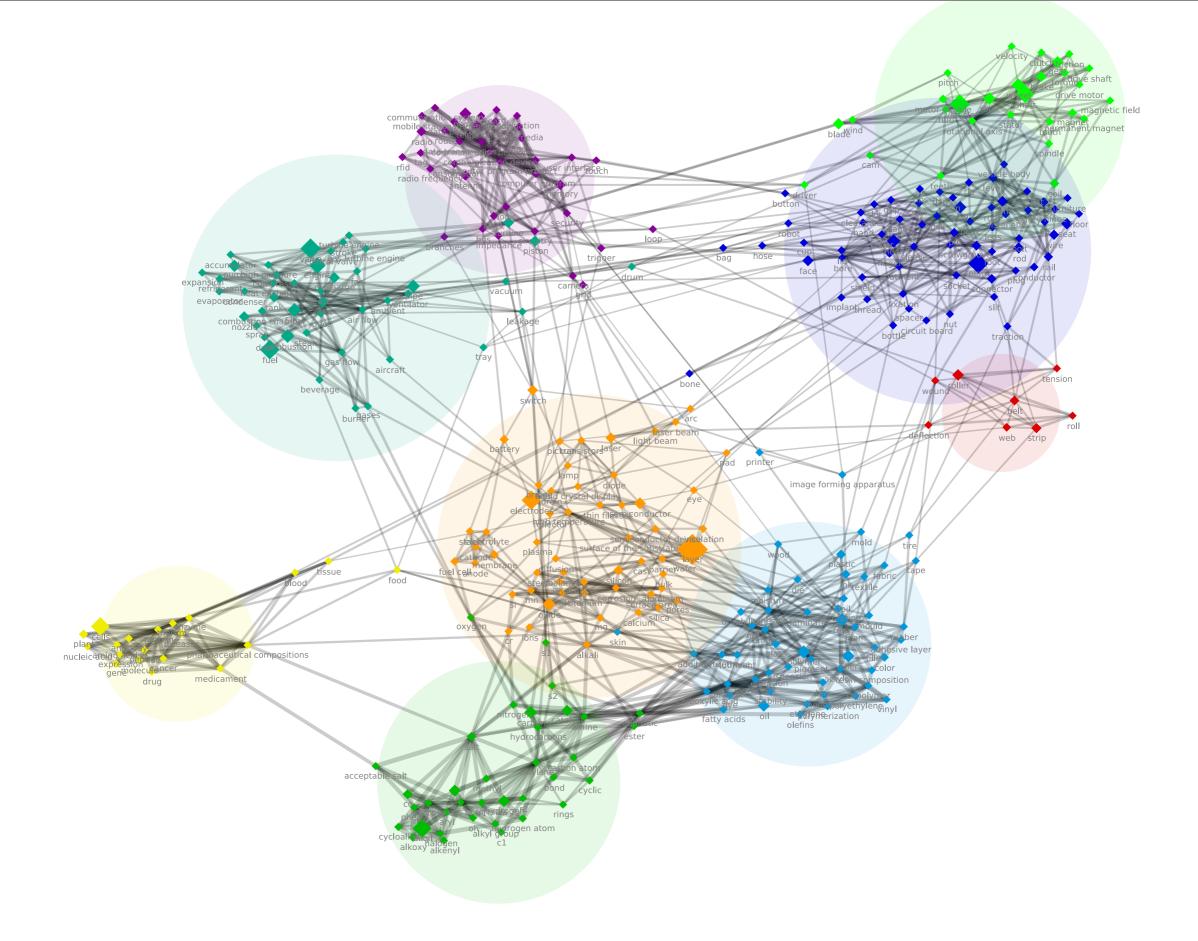


# Distributional approach: $S(w_1, w_2) = \frac{\sum_{\{c, l(c, w_1) > 0, l(c, w_2) > 0\}} I(c, w_1)}{\sum_{\{c, l(c, w_1) > 0\}} I(c, w_1)}$ $I(c, w_1) = \log \frac{p(c, w_1)}{p(c)p(w_1)}$ Weeds & Weir, 2005

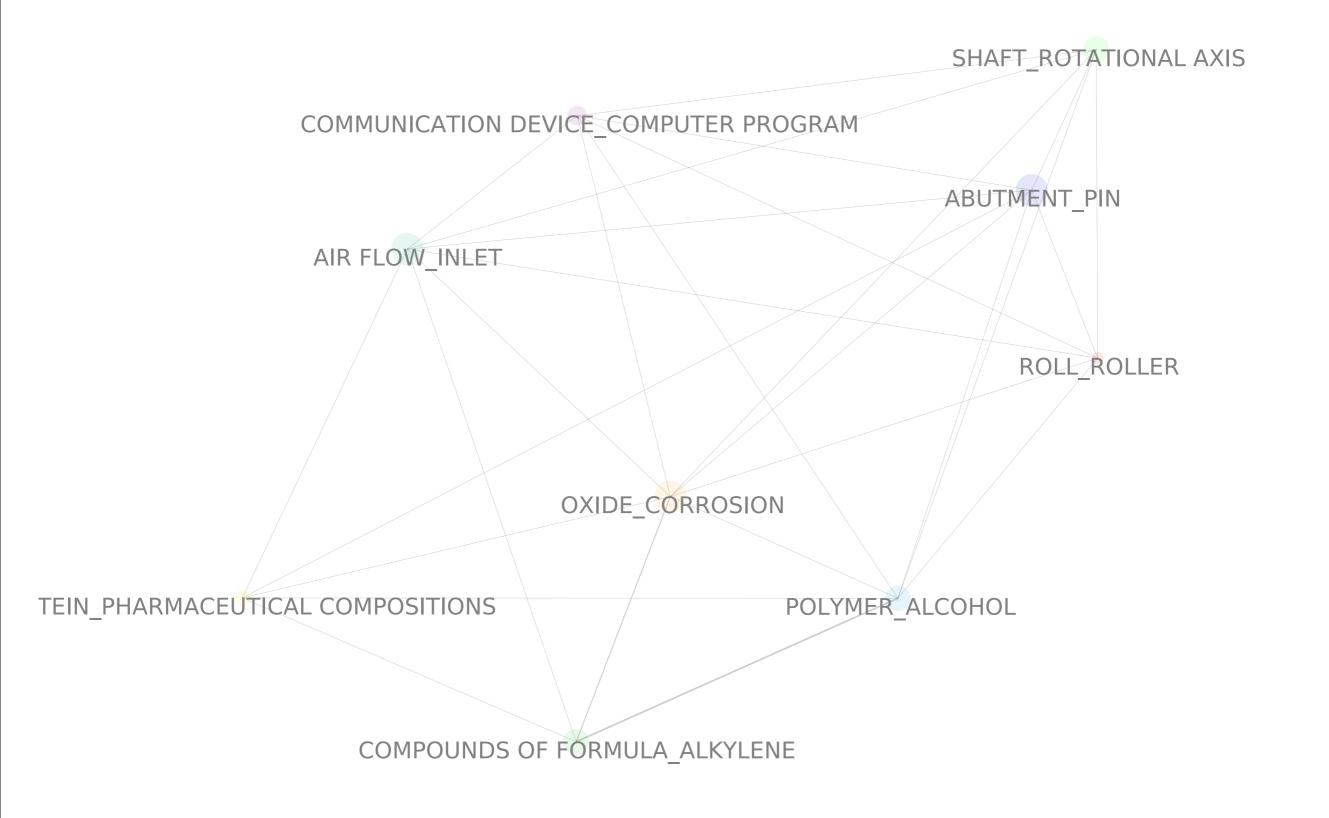
#### What next?

- Reconstruction of the cognitive dynamics in science through the analysis of the **lexical network** built upon the temporal matrix of co-occurrences within our term list (asymmetric measure of proximity between terms).
- Overlapping clusters detection



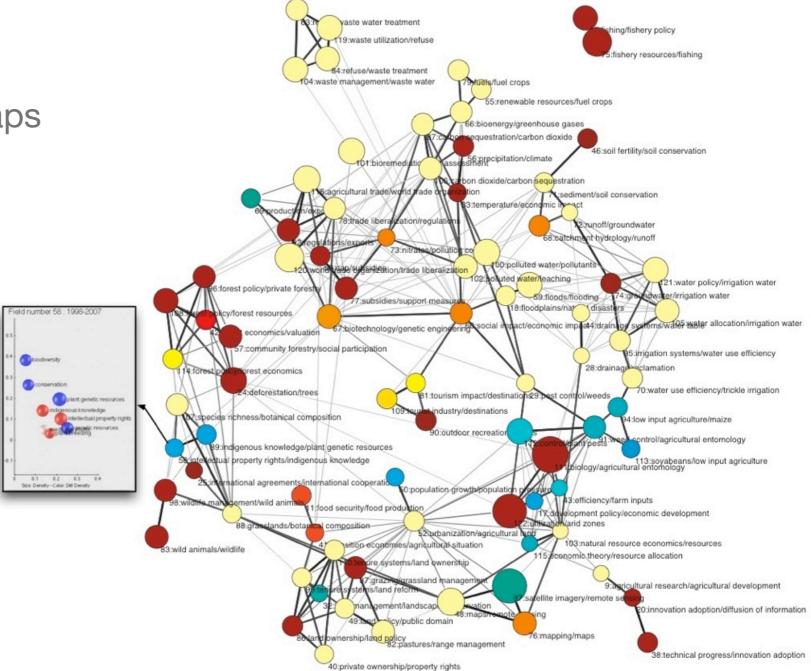


European Patents semantic cartography (Term level)

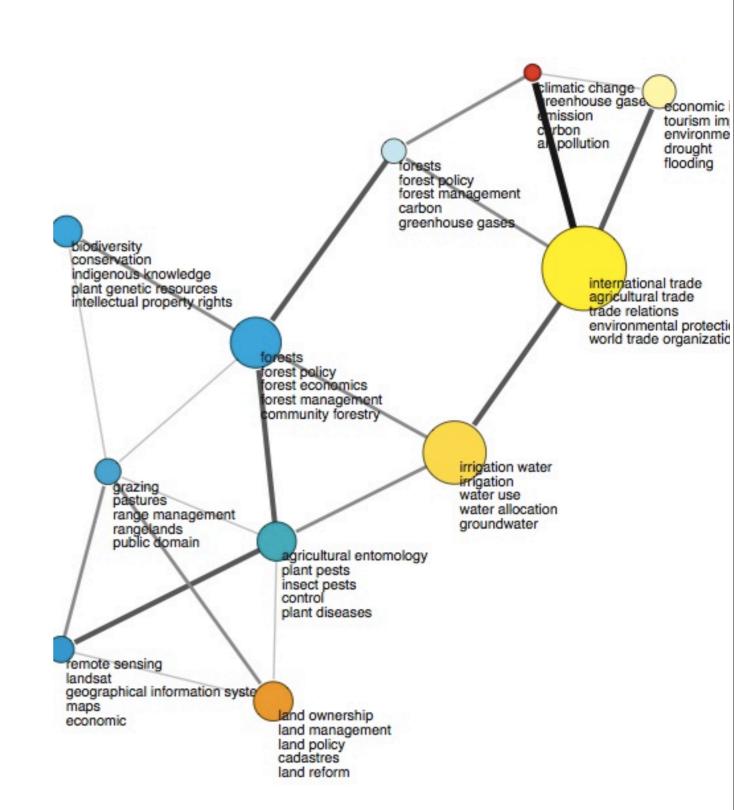


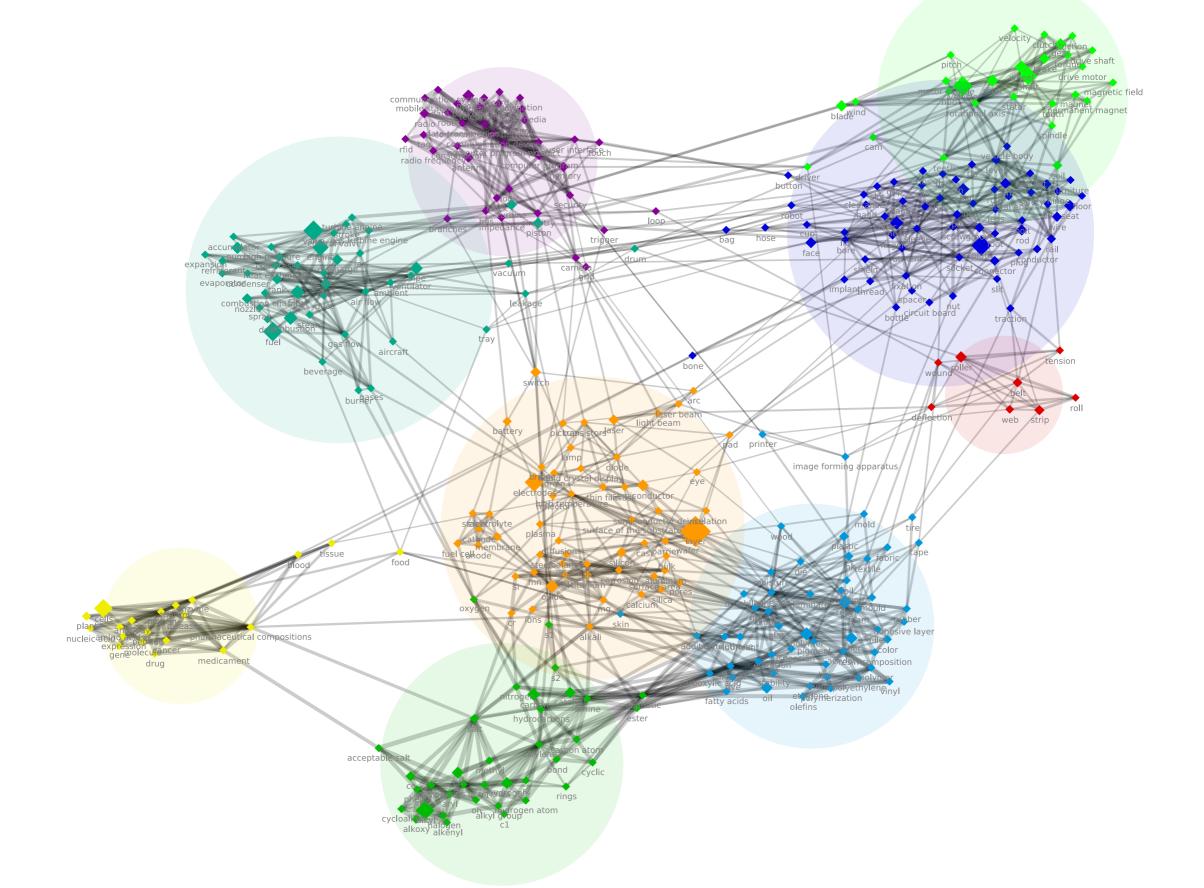
European Patents semantic cartography (High level)

 Semantic distance between clusters build multi-level maps



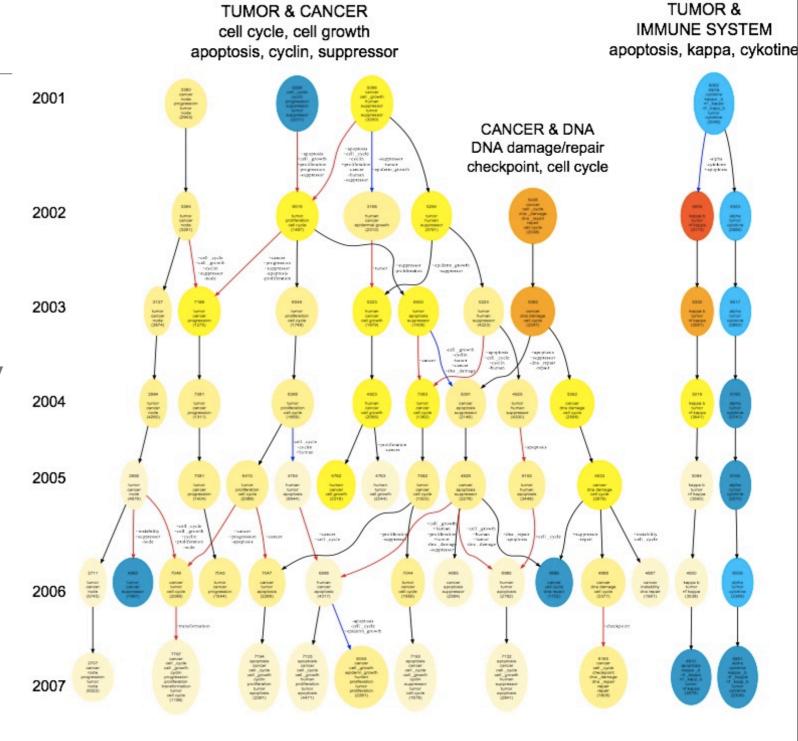
 Semantic distance between clusters build multi-level maps





SHAFT\_ROTATIONAL AXIS COMMUNICATION DEVICE\_COMPUTER PROGRAM ABUTMENT\_PIN AIR FLOW\_INLET ROLL\_ROLLER OXIDE\_CORROSION TEIN\_PHARMACEUTICAL COMPOSITIONS POLYMER\_ALCOHOL COMPOUNDS OF FORMULA\_ALKYLENE

- Semantic distance between clusters build multi-level maps
- A semantic phylogenetic network is built by matching thematic fields inter-temporally



- Semantic distance between clusters build multi-level maps
- A semantic phylogenetic network is built by matching thematic fields inter-temporally
- This structure can be enriched by synchronic proximities to build knowledge <u>tubes</u>

