Ontology-based text mining for microbiology research

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DataIA-JIST International Symposium on Data Science and AI – 10 juillet 2018

How can we make sense of textual data

Over 60 million articles, 2.5 per year
160 million scientific documents indexed

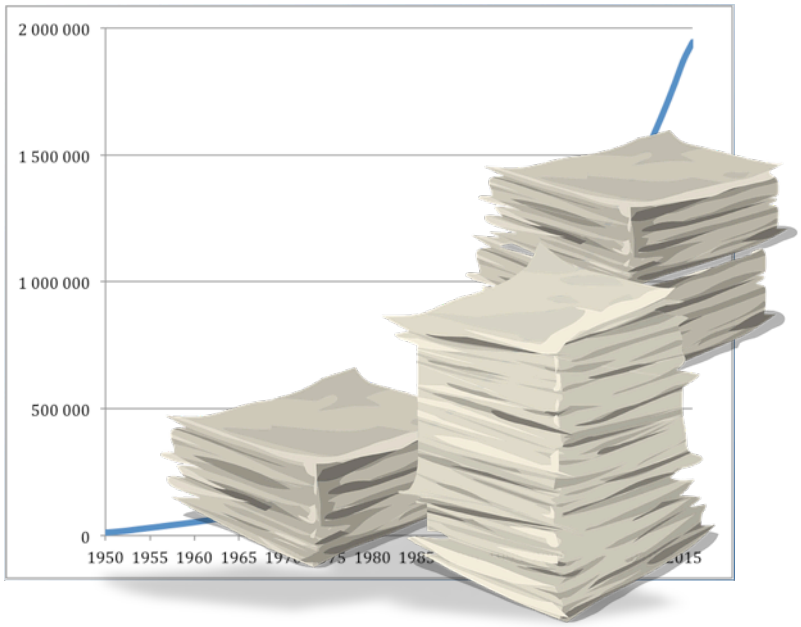
The STM report, 2015

Orduña-Malea et al. , 2014

50% of the papers are not read
90% of the papers are not cited
80% of the cited papers are not read
...

Lokman I. Meho, the rise and rise of citation analysis, 2007.

Simkin & Roychowdhury. Read before you cite!

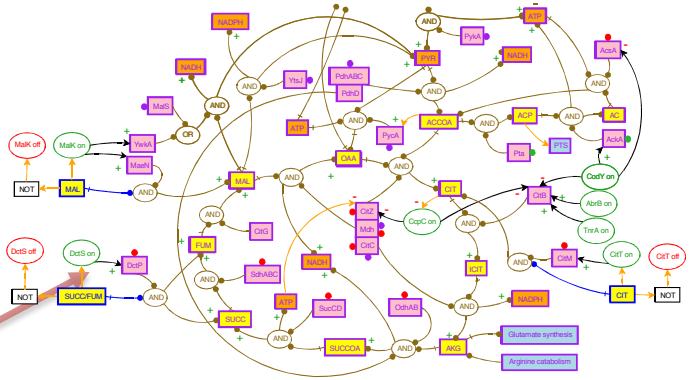


Text-mining (TDM)
Make sense of textual data
Transform unstructured data into structured, machine-readable data

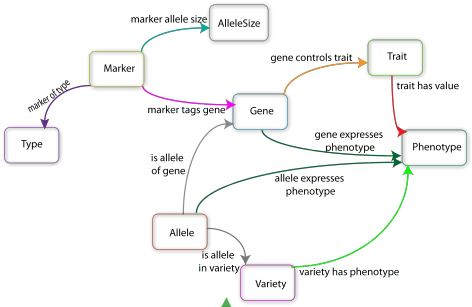
at the heart of the activity of non specialist researchers

Research needs data integration, management, reasoning provided by *formal representation*

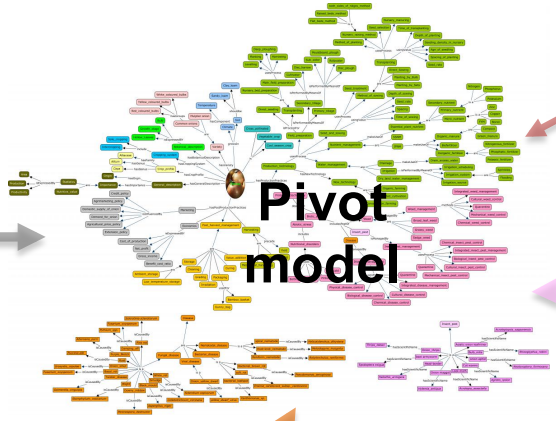
Dynamic model



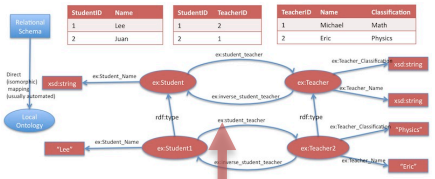
Knowledge model of the text



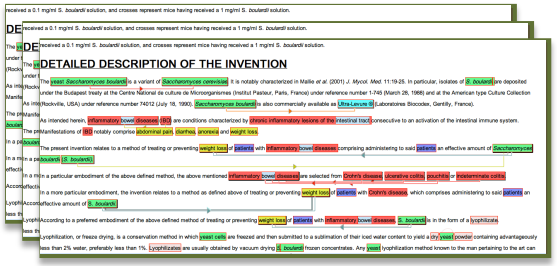
Pivot model



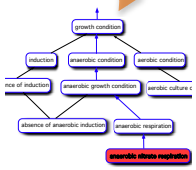
Data model



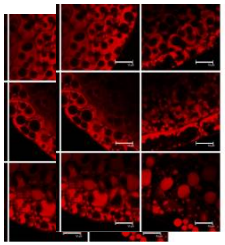
Text



DETAILED DESCRIPTION OF THE INVENTION



Image



Data

Country	Unique Audience (000)	Time per Person (hh:mm:ss)
United States	142,052	6:09:13
Japan	46,558	2:50:21
Brazil	31,345	4:33:10
United Kingdom	29,129	6:07:54
Germany	28,057	4:11:45
France	26,786	4:04:39
Spain	19,456	5:30:55
Italy	18,256	6:00:07
Australia	9,895	6:52:28
Switzerland	2,451	3:54:34

Source: The Nielsen Company

Text: a source of information that requires specific treatments

Massive, diverse and under-exploited scientific information
Raising specific questions of access, analysis and interpretation

Handled at INRA by automatic *text-mining* methods
deployed on the new European infrastructure **OpenMinTeD**

An example

- microbial biodiversity

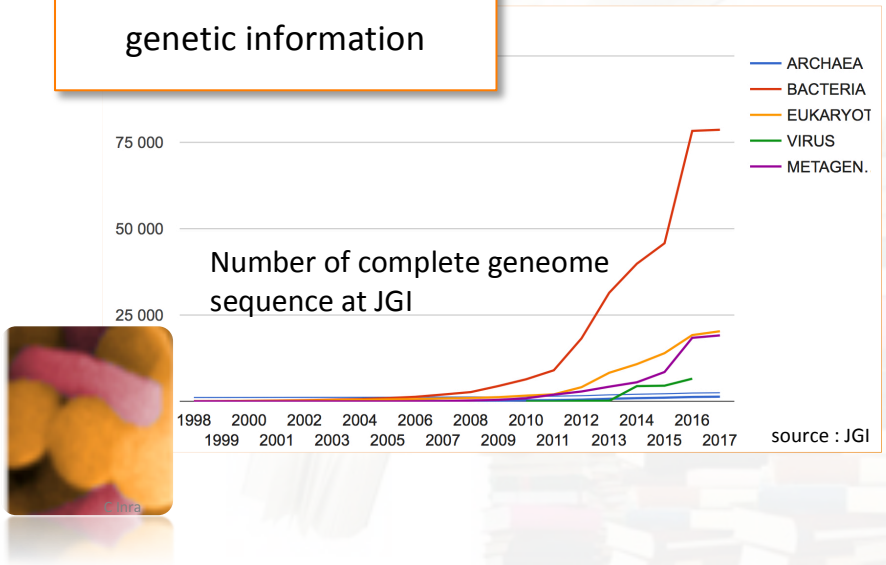
Microorganisms, food and scientific litterature

Billions of microorganisms everywhere, mostly unknown.

Play a critical role in food quality and transformation and its effect on health.

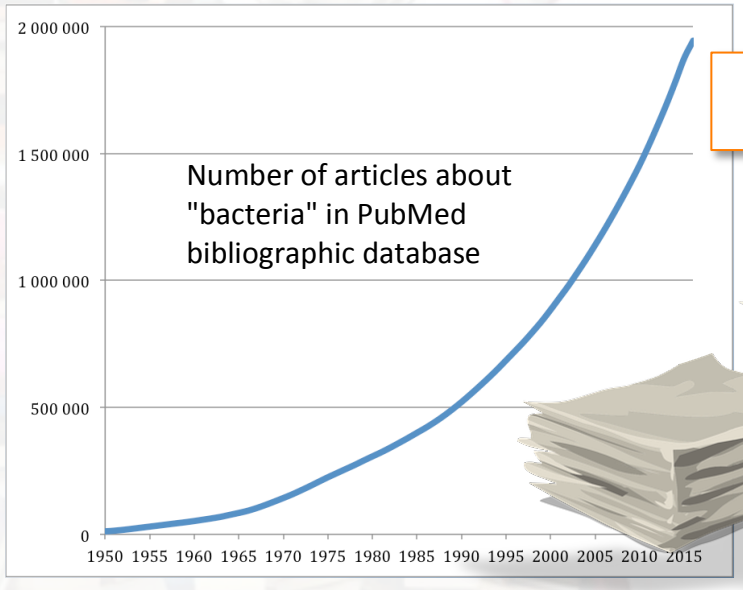
Microbiology research study their ecosystem and genetics for a better understanding, control and use.

Exponential growth of genetic information

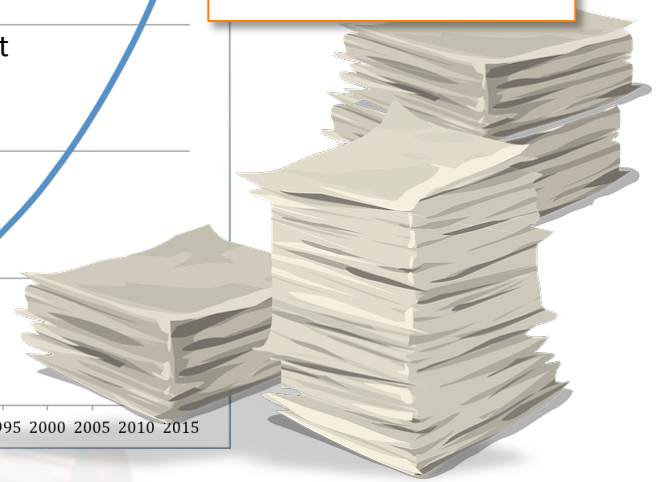


©Inra

Ecosystems, habitats, properties in millions of documents



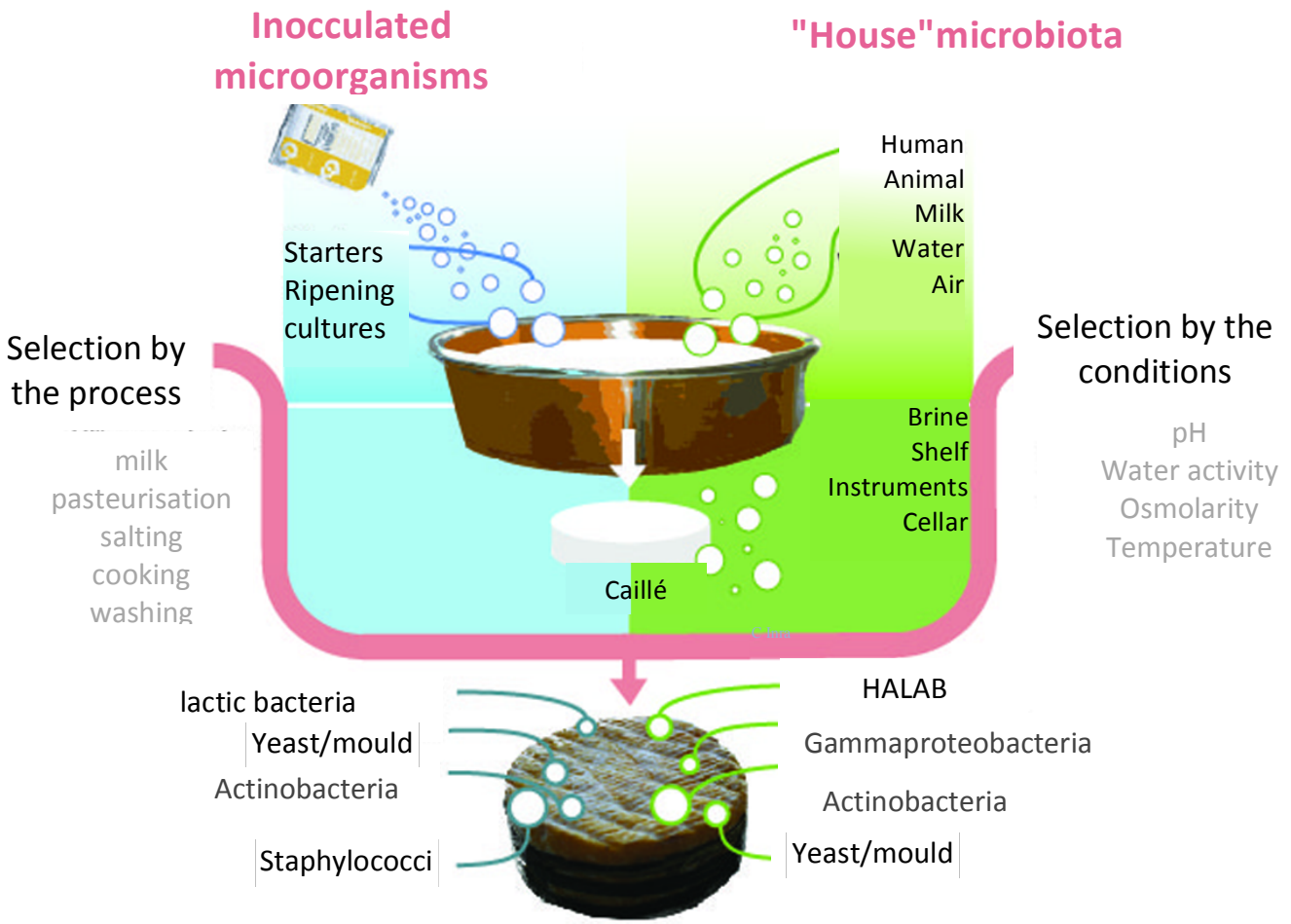
... and publications



Pixabay

http://cm1douzant.blogspot.fr/2014/11/conte-des-droits-des-enfants-2.html

What microbes in my cheese?



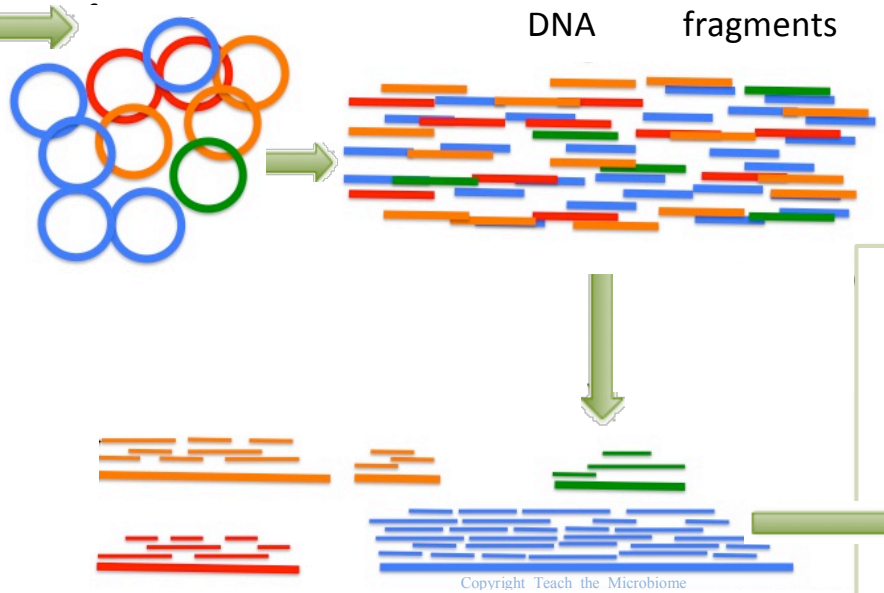
Irlinger et al., FEMS Microbiol Lett (2015) 362 (2).

Identification of microorganisms by their DNA

Genetics

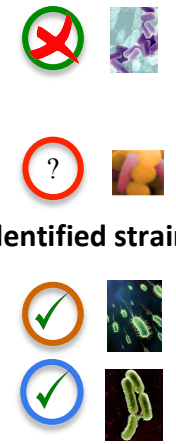
DNA sequence of cheese sample microorganisms

DNA fragments



Alignment with known reference genomes

identified strains



Text mining

Confirm
Interpret
Explain

2.3 millions scientific papers

Habitat classes from ontology

Extracts of scientific articles

two L. monocytogenes cheese dairy isolates

L. monocytogenes persisting in a cold-smoked fish processing plant.

Listeria monocytogenes contamination in Chinese beef processing plants.

Listeria monocytogenes isolated from artisanal Portuguese cheses-making dairy.

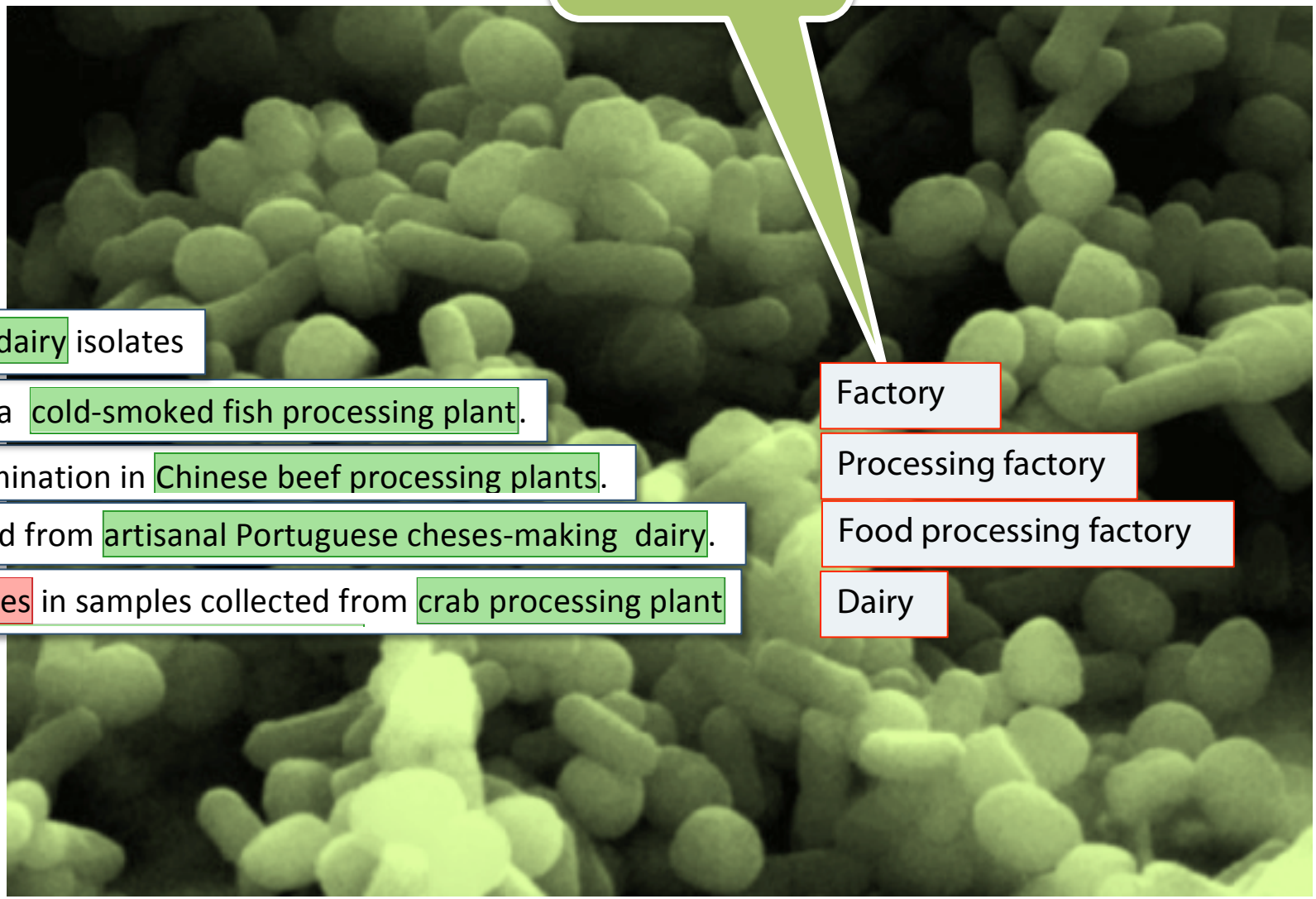
the presence of L. monocytogenes in samples collected from crab processing plant

Factory

Processing factory

Food processing factory

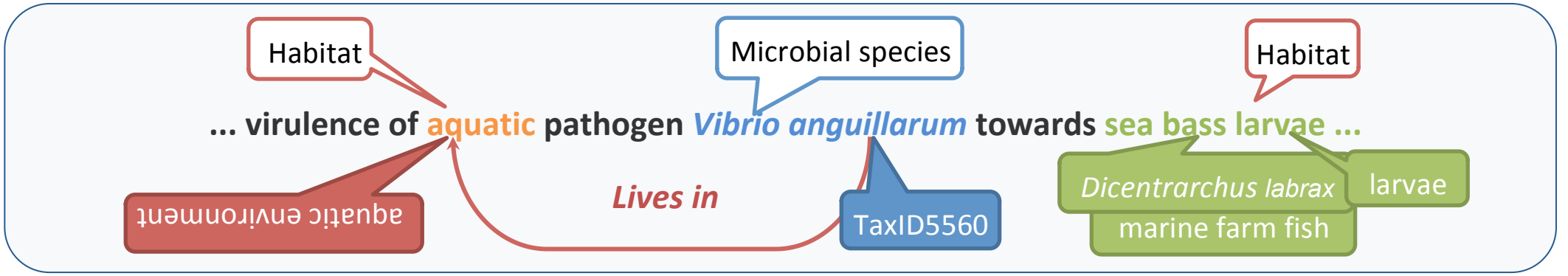
Dairy



TDM challenge:
transform millions of text extracts into formal information despite the high variability

10,000 habitats of *Listeria monocytogenes* described in PubMed

Information extraction



1. Entity recognition = detection (text boundaries) and broad type assignment

2. Entity normalization = assignment to a category from a large set, >2,500 in OntoBiotope ontology

3. Relationship prediction = links entities together over sentences, microorganism to their properties

Artificial Intelligence methods

Natural language processing for semantics analysis

Machine learning for generalization from examples

Knowledge-intensive approach to deal with sparse small data

http://agroportal.lirmm.fr/ontologies/ONTOBIOTOPE

Ratkovic et al., *BMC Bioinformatics*, 2012

Nédellec et al., *Microbial diversity*, *EGC* 2018

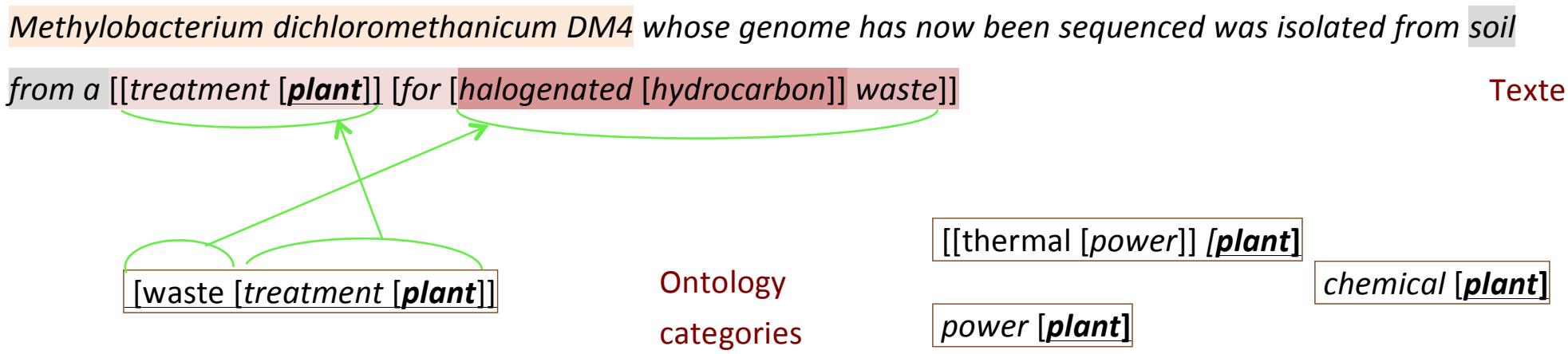
Entity recognition and normalisation

Entity recognition by term extraction by BioYateA

Entity normalization

by *Honor*, a 2-steps method to map the text terms to the labels of the ontology categories

Step 1. *ToMap* computes term similarity using syntactic structures (syntactic heads and subterms) and word similarities

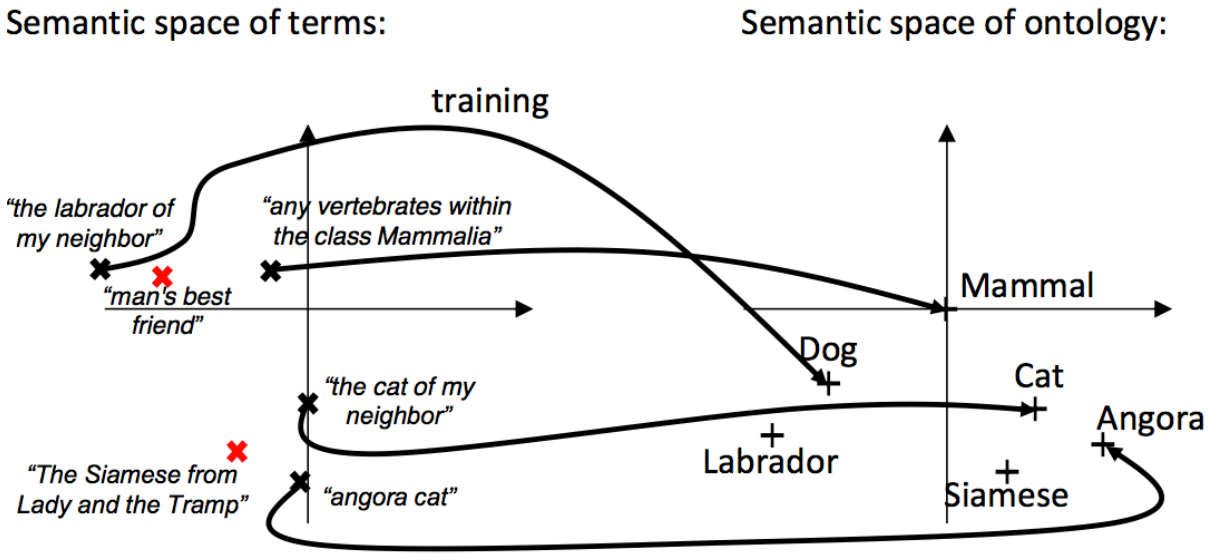


Ratkovic et al., BMC Bioinformatics, 2012

Golik et al., CiCLING, 2013

Entity recognition and normalisation

Step 2. *Contes* learns the projection of the term vector space to the ontology category vector space
by linear regression
from training examples
using the ontology structure



System	Score
HONOR with domain specific heuristics	**0.73**
Distant supervised HONOR	**0.72**
ToMap with domain specific heuristics	0,66
Turku (2017)	0.63
BOUN (2016)	0.62
ToMap	0,61
CONTES	0.61

Honor system over performs other state of the art systems, as measured on Bacteria Biotope BioNLP-Shared Task 2016

Deléger et al., *BioNLP*, 2016

Ferré et al., *BioNLP* 2017 ; Ferré et al., *LREC* 2018

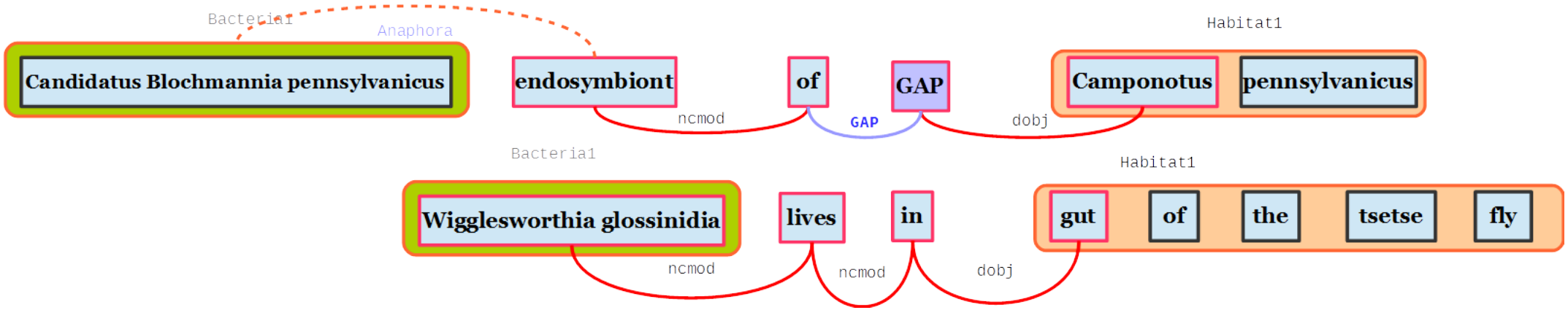
Automatic extraction of binary relationships, AlvisRE

System	PRE	REC	F-M
AlvisRE	0.51	**0.70**	**0.59**
Boun revised	0.52	0.53	0.53
LIMSI revised	0.42	0.60	0.49
TEES-2.1-2	**0.82**	0.28	0.42
IRISA-TexMex	0.46	0.36	0.40
Boun	0.38	0.21	0.27
LIMSI	0.19	0.04	0.06

BioNLP ’13: Bacteria Biotopes - Task 2

Machine learning method based on *shortest dependency path kernel*

- Dependency path computed by CCG and abstracted by Alvis Grammar.
- Anaphora resolution
- Word distance based on word embeddings
- Global alignments computed between dependency pathes (edit distance allowing gaps + Needleman-Wunsch dynamic programming algorithm)
- Empirical Kernel Map transformation



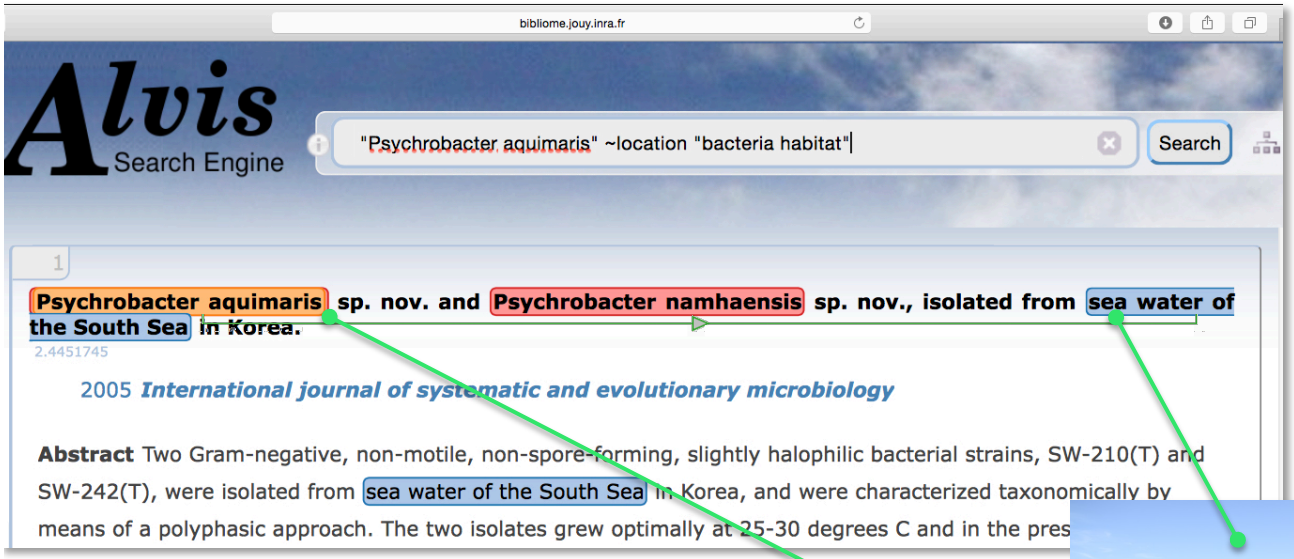
Bossy et al., BMC Bioinformatics, 2015
Ratkovic, PhD thesis, 2014
Valsamou, PhD thesis, 2017

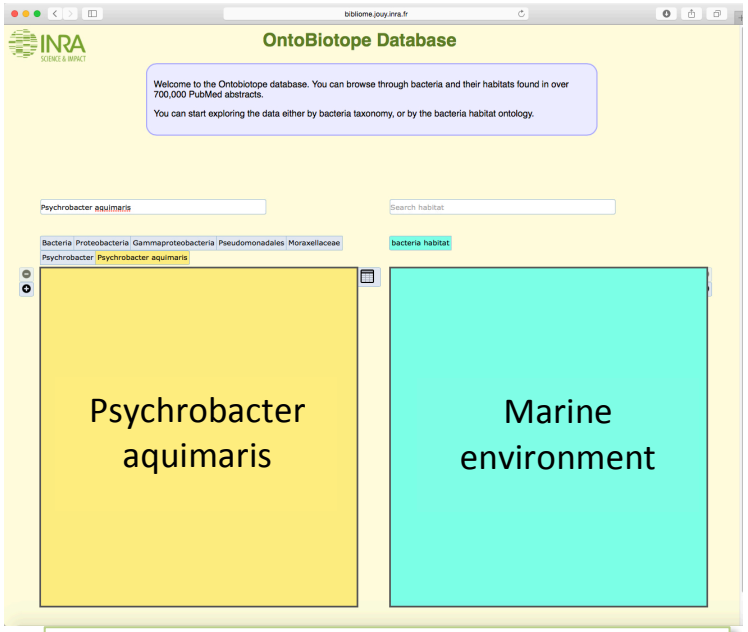
Implementation and use

- All methods implemented in interoperable tools,
- combined into TDM workflows on **OpenMinTeD platform**
- Services on microbiology available at **IFP Migale Bioinformatics** plaform
  - Semantic search engine **AlvisIR**
  - **Florilege** database
- *OntoBiotope* ontology available on **AgroPortal**

openMINTED

Back to microbiology: text-mining explains *Psychrobacter aquimaris* presence in cheese samples





Querying and parsing PubMed yields

- 2,3 millions documents
- 8,3 microorganisms
- 18,5 millions habitats and phenotypes assigned to more than 2500 hierarchical classes
- 7,4 millions relationships

The researcher understands : added salt brings *P. aquimaris* to cheese

http://bibliome.jouy.inra.fr/demo/ontobiotope/alvisir2/webapi/search
http://genome.jouy.inra.fr/Florilege
Chaix et al., *Food Microbiology*, 2018

Using Florilege database for food research and innovation

what bacteria for a new salted cheese?

Welcome | Taxon lives in Habitat | Habitat is inhabited by Taxon | Taxon exhibits Phenotype | **Phenotype is exhibited by Taxon**

http://genome.jouy.inra.fr/Florilege/

Search relations by phenotype: halotolerant — TSV Download | Filter Selection

9 relations for the phenotype "halotolerant"

Source: OpenMinTeD, GenBank, CIRM, DSMZ — Taxon: — QPS only — Apply

SOURCE TEXT	PHENOTYPE	RELATION TYPE	TAXON	SOURCE
9327565	halotolerant	is exhibited by	Saccharomyces cerevisiae	OpenMinTeD
25039289	halotolerant	is exhibited by	Lactobacillus plantarum	OpenMinTeD
17897213, 25542205	halotolerant	is exhibited by	Bacillus pumilus	OpenMinTeD

what known habitat for *Lactobacillus plantarum*

FJ915735, FJ915814, FJ915815	Lactobacillus pl		camel milk	GenBank
FJ538531, FJ538504, FJ538512	Lactobacillus plantarum	Lives in	cattle	GenBank
HM462426, HM462423, AB326301	Lactobacillus plantarum	Lives in	cheese	GenBank
HM218104, HM218301, FJ607272	Lactobacillus plantarum	Lives in	dairy industry	GenBank
FJ227310, FJ227315	Lactobacillus plantarum	Lives in	drink	GenBank

1-20 of 622