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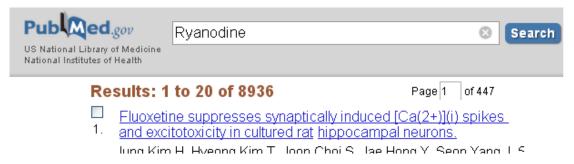
# Answering Gene Ontology terms to proteomics questions by supervised macro reading in MEDLINE

#### Data deluge...

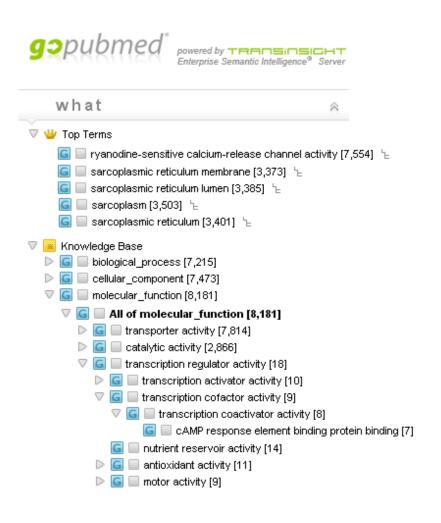
" What is the subcellular location of protein MEN1?"

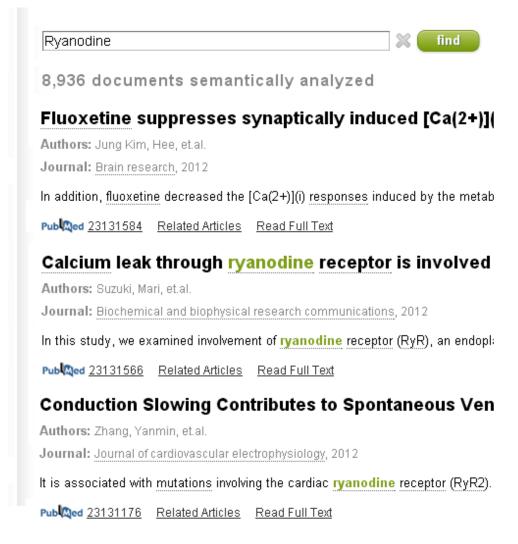


"What molecular functions are affected by Ryanodine?"

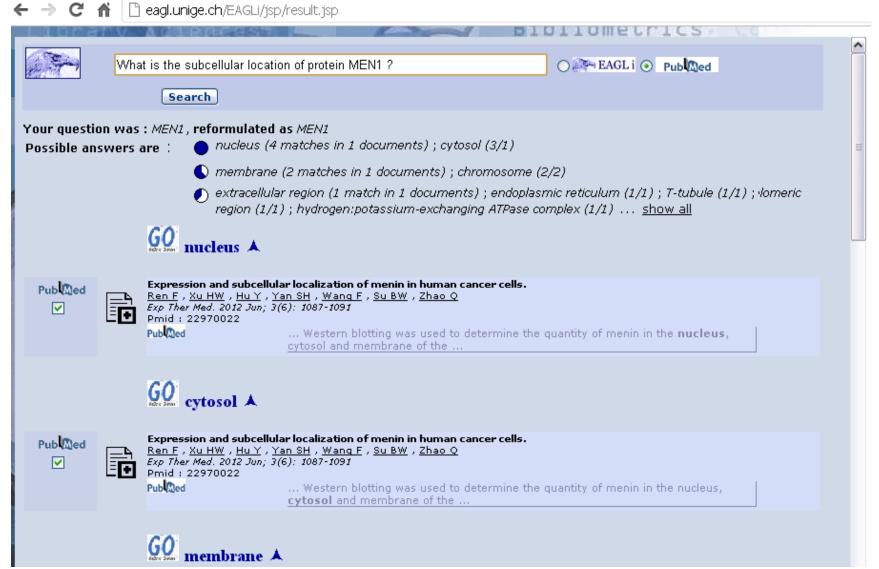


#### **Ontology-based search engines**





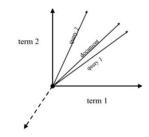
#### **Question Answering (EAGLi system)**



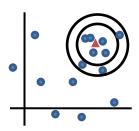
Redundancy hypothesis: The number of associated/co-occurring answers dominate other dimensions

# Best way for extracting GO terms from a set of abstracts? (1/3)

- Comparison based in two categorizers :
  - Thesaurus-Based (EAGL)
    - Competitive with MetaMap (Trieschnigg et al., 2009)
    - Compute lex. similarity between text and GO terms



- Machine Learning (GOCat)
  - k-NN
  - · Similarity between input text and already curated abstracts
  - KB derived from GOA: ~90'000 instances



# Best way for extracting GO terms from a set of abstracts? (2/3)

- Two tasks :
  - Classical categorization (micro reading ~ biocuration)



Redundancy-based QA (macro reading)



# Best way for extracting GO terms from a set of abstracts? (3/3)

- One benchmark for micro reading evaluation
  - 1'000 abstracts and GO descriptors from GOA

- Two benchmarks for macro reading evaluation
  - 50 questions derived from a set of biological databases:

What molecular functions are affected by [chemical]?



What cellular component is the location of [protein]?

#### **Results**

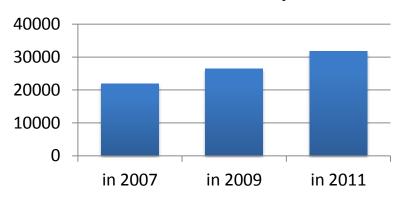
	micro reading task		macro reading task			
Benchmark	1'000 abstracts		CTD		UniProt	
Metrics	PO	R10	P0	R100	P0	R10
EAGL (Thesaurus Based)	.23	.16	.34	.15	.33	.45
GOCat (k-NN)	.43 (+86%)	.47 (+193%)	.69 (+102%)	.33 (+120%)	.58 (+75%)	.73 (+62%)

+ **75/120%** for k-NN (sup. learning)

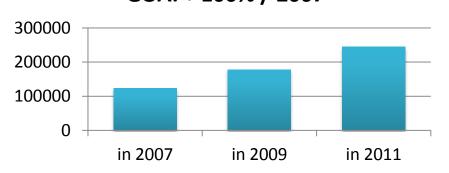
→ Redundancy hypothesis insufficient
Why/Where is the power? Size does or does not matter?

### Deluge is self-compensated ©

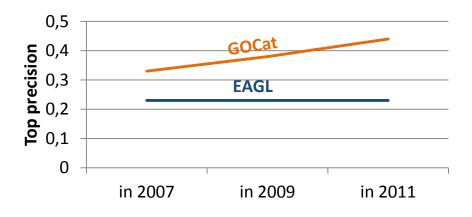
# terms in GO: +150% / 2003



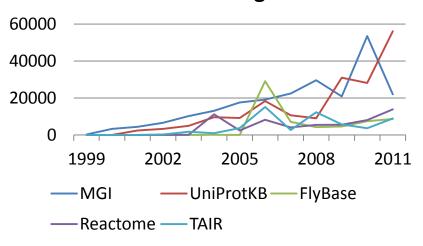
# annotations with a PMID in GOA: + 100% / 2007



Performances of both categorizers across the time

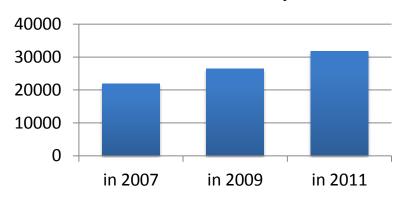


## Annotations in GOA for the top 5 most contributing source

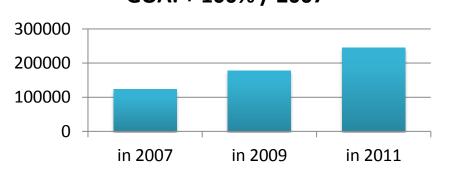


### Deluge is self-compensated ©

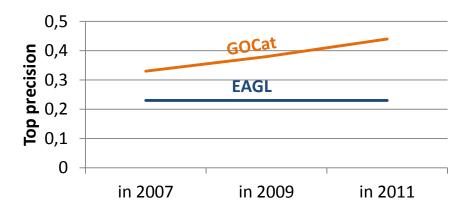
# terms in GO: +150% / 2003



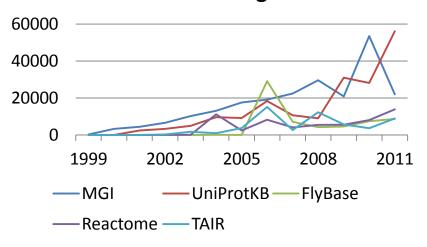
# annotations with a PMID in GOA: + 100% / 2007



Categorization effectiveness moves faster than data



### Annotations in GOA for the top 5 most contributing source



#### Magic!

The automatic categorization based on a PMID<sub>2007</sub> performed in 2011 is of higher quality than a categorization on the same PMID<sub>2007</sub> performed in 2007

No concept drift at all and even some improvement!

#### Example in toxicogenomics: CTD vs. GOCat

"What molecular functions are affected by Ryanodine?"



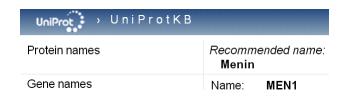
**GOCat** 

GO Level	GO Term	
9	GO0005219 : ryanodine-sensitive calcium- release channel activity	✓
7	GO0015279 : calcium-release channel activity	<b>√</b>
7	GO0005262 : calcium channel activity	1
6	GO0022834 : ligand-gated channel activity	
6	GO0015276 : ligand-gated ion channel activity	
3	GO0005516 : calmodulin binding	1

Rank	GO Term
1.	GO0005515 : protein binding
<b>√</b> 2.	GO0005219 : ryanodine-sensitive calcium- release channel activity
3.	GO0005245 : voltage-gated calcium channel activity
4.	GO0005509 : calcium ion binding
<b>√</b> 5.	GO 0005262 : calcium channel activity
6.	GO0005102 : receptor binding
<b>√</b> 7.	GO0005516 : calmodulin binding
8.	GO0005388 calcium-transporting ATPase activity
<b>√</b> 9.	GO0015279 : calcium-release channel activity
10.	GO0005528 : FK506 binding

#### **Example in UniProt**

"What is the subcellular location of protein MEN1?"

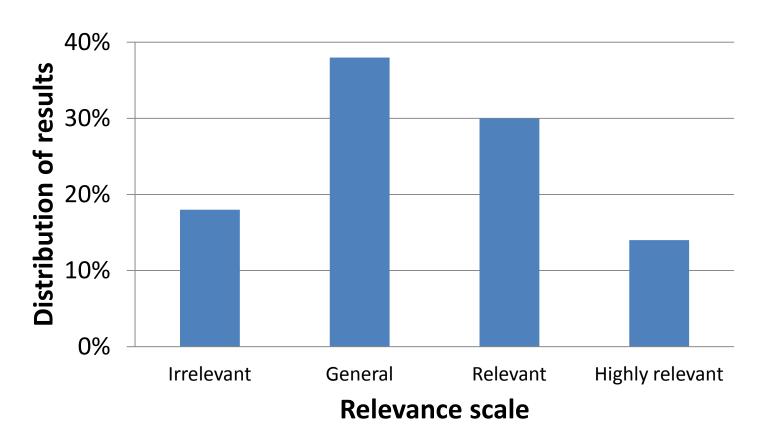


GO Level	GO Term	
6	GO0035097 : histone methyltransferase complex	<b>√</b>
5	GO0000785 : chromatin	1
5	GO0016363 : nuclear matrix	1
4	GO0005829 : cytosol	1
3	GO0032154 : cleavage furrow	

**GOCat** 

R	ank	GO Term
	1.	GO0005634 : nucleus
	2.	GO0005737 : cytoplasm
	3.	GO0005886 : plasma membrane
	4.	GO0005615 : extracellular space
	5.	GO0005887: integral to plasma membrane
	6.	GO0005739 : mitochondrion
<b>√</b>	7.	GO0005829 : cytosol
	8.	GO0005576: extracellular region
1	9.	GO0035097 : histone methyltransferase
_		complex
1	10.	GO0000785 : chromatin
1	15.	GO0016363 : nuclear matrix

#### **Qualitative evaluation**



Relevant vs irrelevant: 82% - 18%

#### **Conclusion and future work**

- Automatic assignment of GO categories ~ 43%
   [Camon et al 2003: GO kappa ~ 40%]
- Classification model improves faster than drift
   [→ Consistency of annotation guidelines ☺]

 Next: Effective integration into the EAGLi' question-answering platform

#### **Collaborations**

 Automatic Functional Annotation of PubChem BioAssays

Generates semantic similarity clusters

Automatically populating large protein datasets

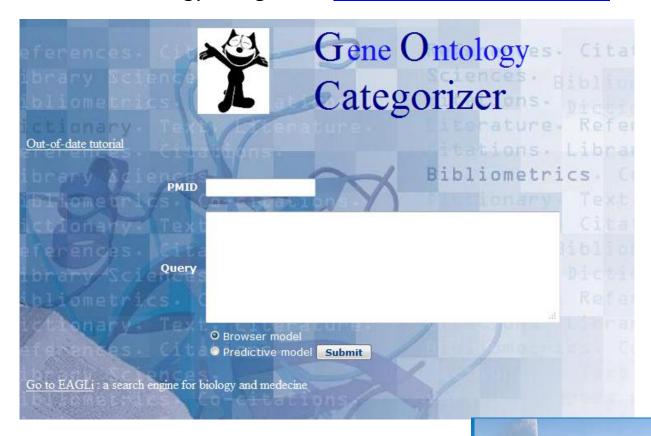
All genes in COMBREX (3302393 genes)

COMputational BRidges to Experiments

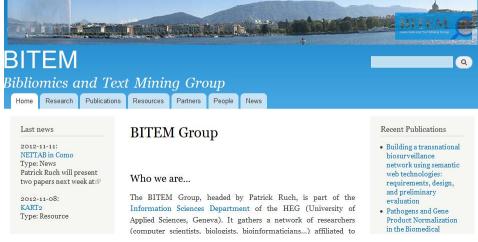
#### Please visit EAGLi, the Bio-medical question answering engine <a href="http://eagl.unige.ch/EAGLi/">http://eagl.unige.ch/EAGLi/</a>!



The Gene Ontology Categorizer: <a href="http://eagl.unige.ch/GOCat/">http://eagl.unige.ch/GOCat/</a>



Other resources... TWINC (patent retrieval...) <a href="http://bitem.hesge.ch">http://bitem.hesge.ch</a>



#### **Acknowledgments**

- Swiss-prot group (SIB): Anne-Lise Veuthey, Yoannis Yenarios
- U. Indiana/SCRIPPS:
   Rajarshi Guha / Stephan Schurer
- The COMBREX project: Martin Steffen
- NextProt: Pascale Gaudet

- SNF Grant: EAGL # 120758
- EU FP7: <u>www.KHRESMOI.eu</u> # 257528