Advanced Parser for Biomedical Texts

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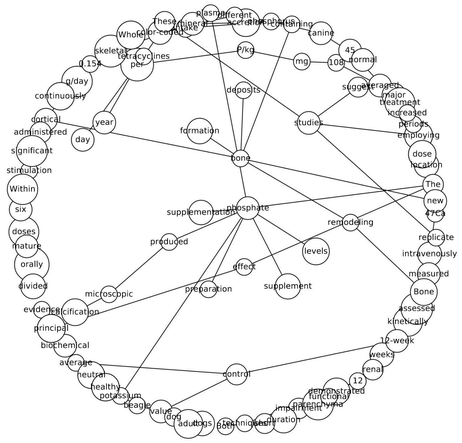
Introduction

Large amounts of biomedical data available to us today from various sources make it at least impractical and in many cases impossible to analyze by hand even if confined within a specific problem. On the other hand most of these data are stored in a natural language form which makes it hard to process automatically. Fortunately a vast experience gained in the field of natural language processing (NLP) can be utilized to automate this process. We developed an advanced parser for biomedical texts that should simplify both data retrieval and analysis.

We considered the following problems:

1. parsing of informative multiword phrases
2. parsing and detection of chemical names written in different notations - trivial notation and IUPAC and SMILES-like
3. assigning word embeddings for parsed words and phrases
4. analyzing complex syntactic dependencies between them



Collocation graph based on the abstract of [Harris et al, Stimulation of bone formation in vivo by phosphate supplementation. Calcif Tissue Res. 1976 Nov 24;22(1): 85-98.]. Stop-words were removed. Arrows skipped for convenience even though the graph is directed. Size of the node is proportional to its PageRank score.

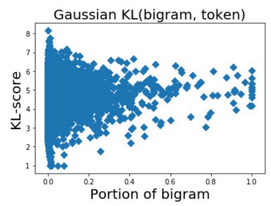
Kullback-Leibler Divergence

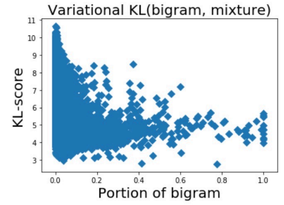
In the context of machine learning, $D_{KL}(P||Q)$ is often called the information gain achieved if P is used instead of Q.

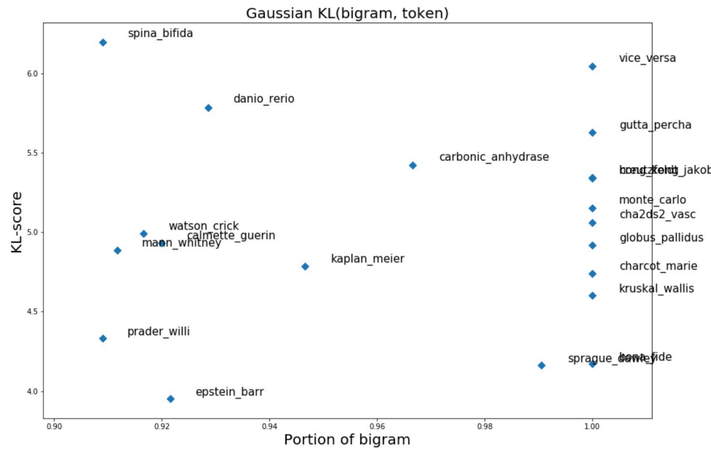
$$D_{\mathrm{KL}}(P\|Q) = \sum_i P(i)\,\log\frac{P(i)}{Q(i)}.$$

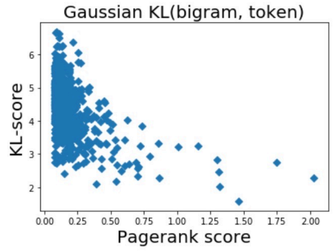
$$D_{\mathrm{variational}}(f\|g) = \sum_a \pi_a \log \frac{\sum_{a'} \pi_{a'} e^{-D(f_a\|f_{a'})}}{\sum_b \omega_b e^{-D(f_a\|g_b)}}$$

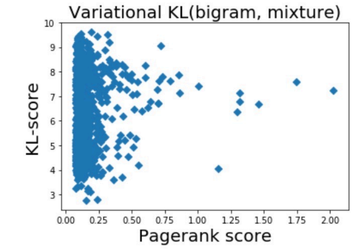
KL-divergence method allows us to determine which sets of words are better to replace with an ngram as we can calculate the informativeness of ngram

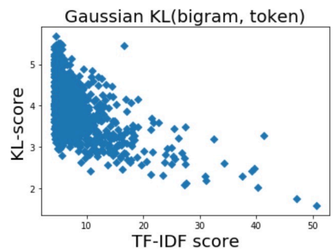


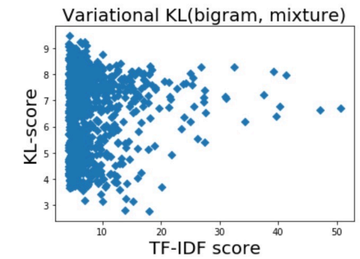












Methods

To improve parsing quality we decided to learn to extract informative n-grams (e.g. instead of [‘amino’, ‘acid’, ...] we want to get [‘amino_acid’, …]) to account for existence of multiword biomedical terms.

To better identify informative n-grams and give a numerical estimate of their validity two main approaches were used.

First one relies on finding the most important edges in word collocation network for analyzed text. Word collocation networks are weighted directed graphs with each vertex corresponding to a word in the text and edge weights equal to the bigram frequency in the document. The most important edges are found by calculating centrality measures of network (degree, closeness, betweenness, etc.) or with the PageRank algorithm [Lahiri et al.]. This process can be applied to analyze documents separately or to generate a custom dictionary of n-grams from a large corpus of texts.

Second approach uses term frequency–inverse document frequency (TF-IDF) statistic. It rewards frequent terms inside a document but punishes words that are frequent in the whole corpus which helps to filter out the words that are just commonly used in a language.

Results

PageRank	Gaussian KL(bigram, token)	Gaussian KL(token, bigram)	Variational KL(bigram, mixture)	Variational KL(mixture, bigram)
breast_cancer	ang_iii	citron_kinase	coli_isolates	early_disease
cancer_cells	citron_kinase	biliary_complications	liver_cancer	hpv_dna
gene_expression	biliary_complications	vte_prophylaxis	hpv_dna	liver_cancer
cell_lines	vte_prophylaxis	serum_calcium	model_group	coli_isolates
tumor_cells	new_drugs	dsrna_binding	molecular_target	viral_rna
stem_cells	status_epilepticus	acute_ethanol	cardiac_fibroblasts	reported_cases
prostate_cancer	tuberculosis_isolates	hand_hygiene	early_disease	molecular_target
gastric_cancer	mrsa_strains	status_epilepticus	reported_cases	model_group
cell_cycle	serum_calcium	ang_iii	genetic_studies	meningococcal_disease
patients_treated	acute_ethanol	synthesized_compounds	meningococcal_disease	molecular_data

TF-IDF	Gaussian KL(bigram, token)	Gaussian KL(token, bigram)	Variational KL(bigram, mixture)	Variational KL(mixture, bigram)
gene_expression	beta_sheet	beneficial_effects	related_protein	related_protein
wild_type	disease_ad	results_mean	combination_therapy	viral_rna
present_study	beneficial_effects	self_renewal	significant_reduction	hiv_positive
cell_lines	self_renewal	remains_unclear	viral_rna	significant_reduction
amino_acid	old_woman	efficacy_safety	study_performed	combination_therapy
results_suggest	insulin_sensitivity	studies_performed	rat_model	tissue_specific
breast_cancer	et_al	beta_sheet	tissue_specific	study_performed
long_term	false_positive	negative_bacteria	terminal_region	methods_total
mg_kg	therapeutic_targets	old_woman	hiv_positive	using_different
growth_factor	negative_bacteria	alpha_helical	gene_transcription	dna_sequence

References

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2. Luke Vilnis and Andrew McCallum, *Word Representations via Gaussian Embedding,* 2014.
3. Moz, *Gaussian Word Embeddings*, https://github.com/seomoz/word2gauss.