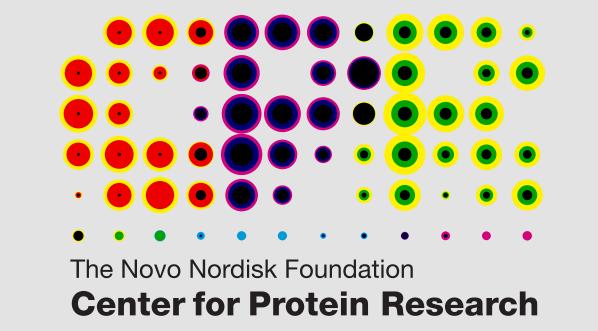
The DISEASES database: improved scoring of disease-gene associations mined from the literature

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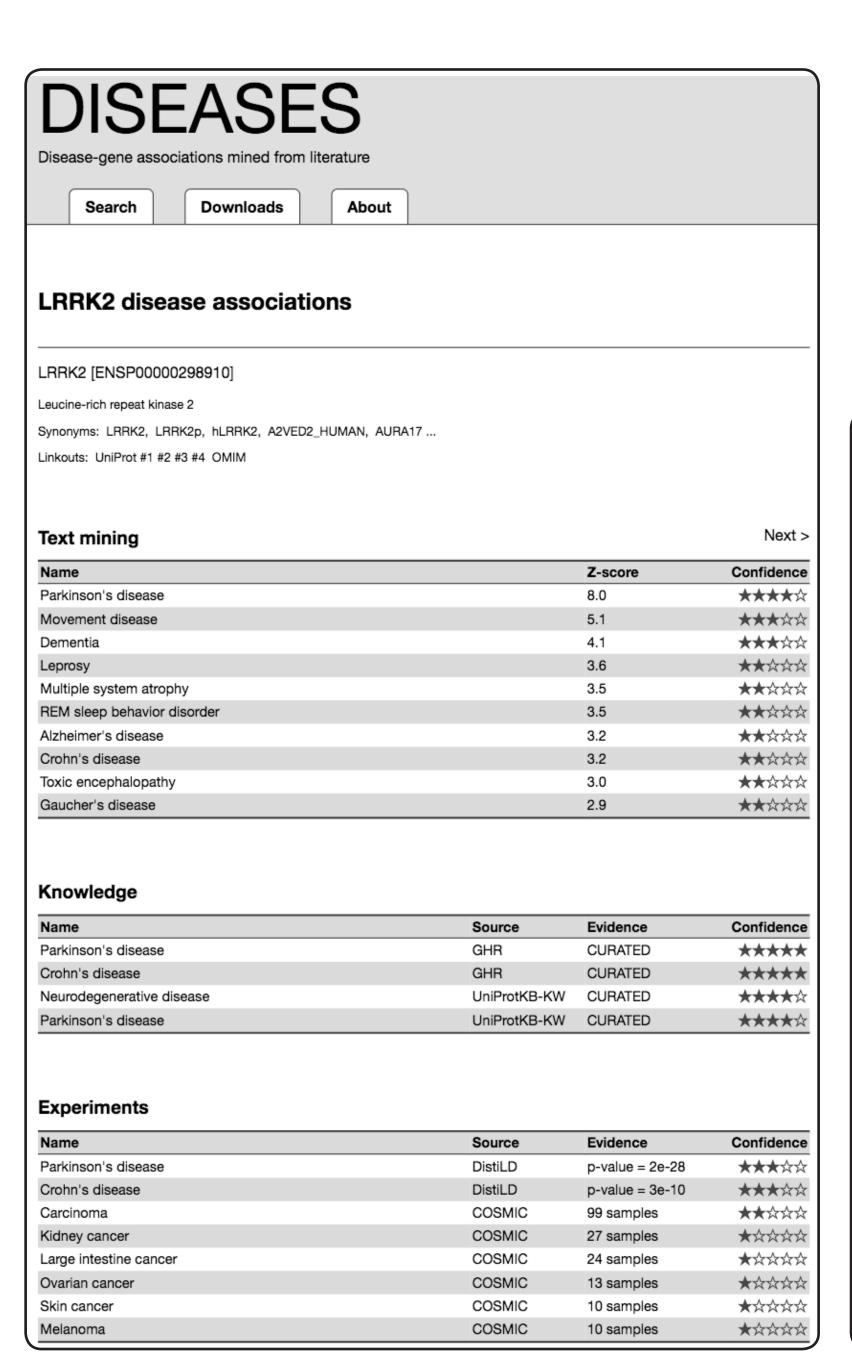
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Relevance

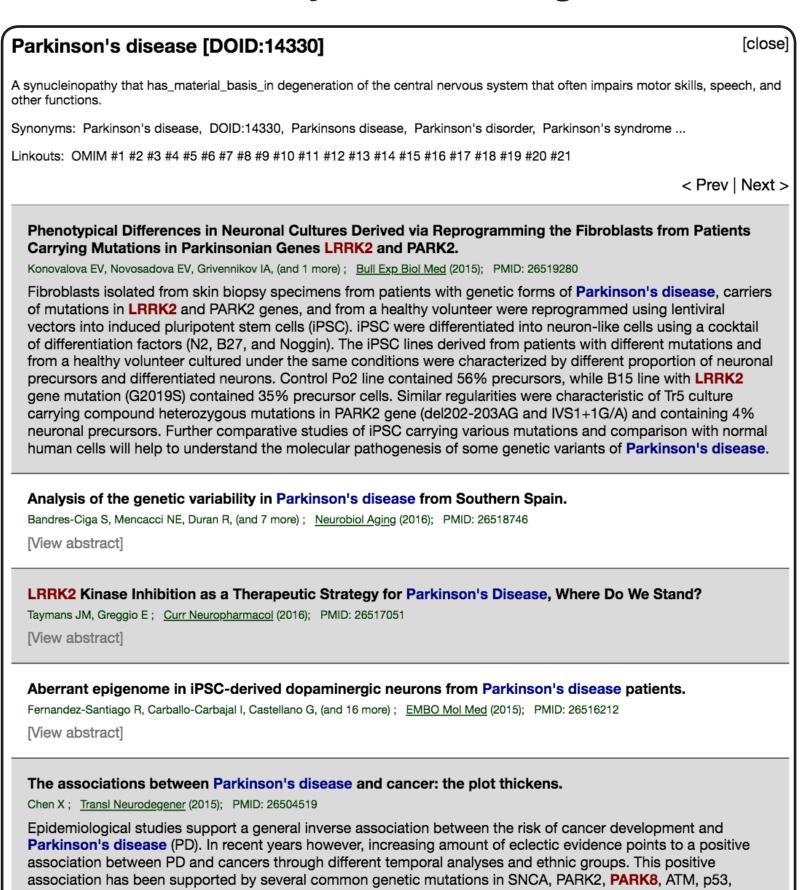
Text mining is an established approach to identify associations between biomedical entities. The DISEASES database integrates disease-gene associations found by text mining with expert-curated evidence, cancer mutation data, and genome-wide association studies. Our improved context-aware scoring scheme CoCoScore [3] further improves the text mining pipeline.

DISEASES URL: https://diseases.jensenlab.org/



The DISEASES search interface allows to query genes or diseases.

Detailed evidence viewer for associations found by text mining.



All disease—gene associations, the tagger software, and dictionaries used for text mining are available under open licenses [2]. The tissue ex- Coverage by evidence channel. pression database TISSUES (https:// tissues.jensenlab.org) uses the same text mining approach.

Evidence	Genes	Diseases	Associations
Text mining	15631	4598	478407
Knowledge	2001	735	15231
Experiments	10711	423	89073

Improved text mining via CoCoScore

The DISEASES text mining scheme ignores context when scoring disease-gene pairs. CoCoScore [3] uses textual context to score whether an association is described.

The co-occurrence count C(G,D) of gene G and disease D is defined as:

$$C(G,D) = \sum_{k=1}^n \omega_k(G,D) + w_a \delta_{ak}(G,D)$$
 Best score of sentences co-mentioning D and G Constant score if D and G appear in the same abstract
$$\omega_k(G,D) = \max_{i \in T(k,G,D)} r(i)$$

T(k,G,D) are all sentences in abstract k that co-mention G and D. r(i) is the sentence-level score returned by a fastText-based model [4] (see Figure).

The co-occurrence score S(G,D) is:

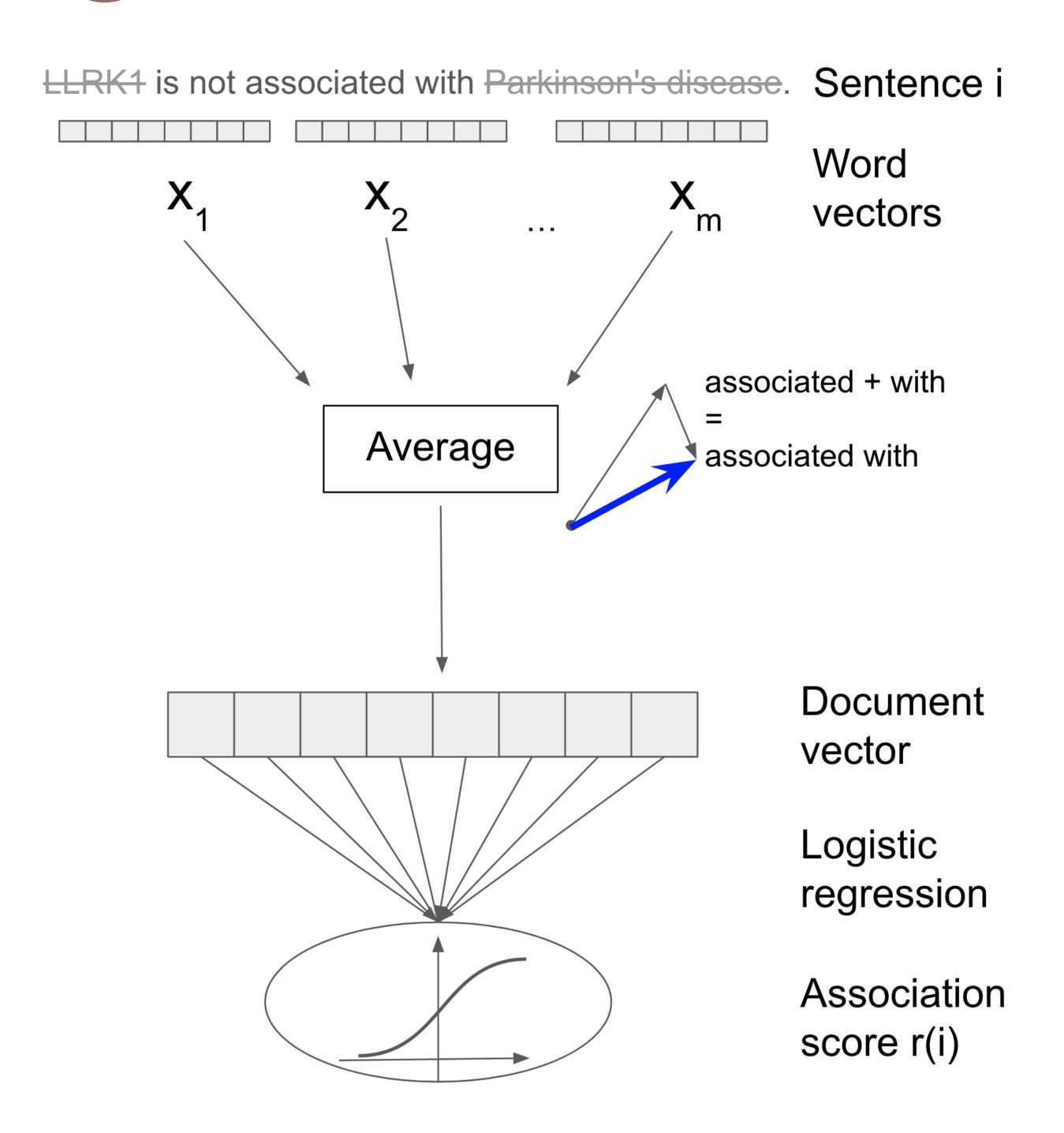
$$S(G,D) = C(G,D)^{\alpha} \left(\frac{C(G,D) \ C(\cdot,\cdot)}{C(G,\cdot) \ C(\cdot,D)} \right)^{1-\alpha}$$
 Observed-over-expected ratio

data-Performance test curated associderived from distant supervision. using

	AUROC	AP
CoCoScore	0.97	0.77
DISEASES score	0.96	0.72

AUROC: Area under the ROC curve AP: Average Precision





Key features

- DISEASES integrates scored disease—gene associations from text mining, curated knowledge, and experiments
- weekly text mining updates and data downloads
- CoCoScore, our novel context-aware scoring scheme, improves the text mining performance

Funding: Novo Nordisk Foundation, NIH Common Fund

Want to know more? [1] Pletscher-Frankild et al., Methods (2015)

[2] tagger on Bitbucket: https://goo.gl/hefLqj

[3] CoCoScore on GitHub: https://goo.gl/xCxdjt

[4] Joulin, Grave et al., arXiv (2016)

Visit https://diseases.jensenlab.org/