

This work was funded by the Fraunhofer Gesellschaft under the MAVO project: The Human Brain Pharmacome. More information can be found at pharmacome.scai.fraunhofer.de

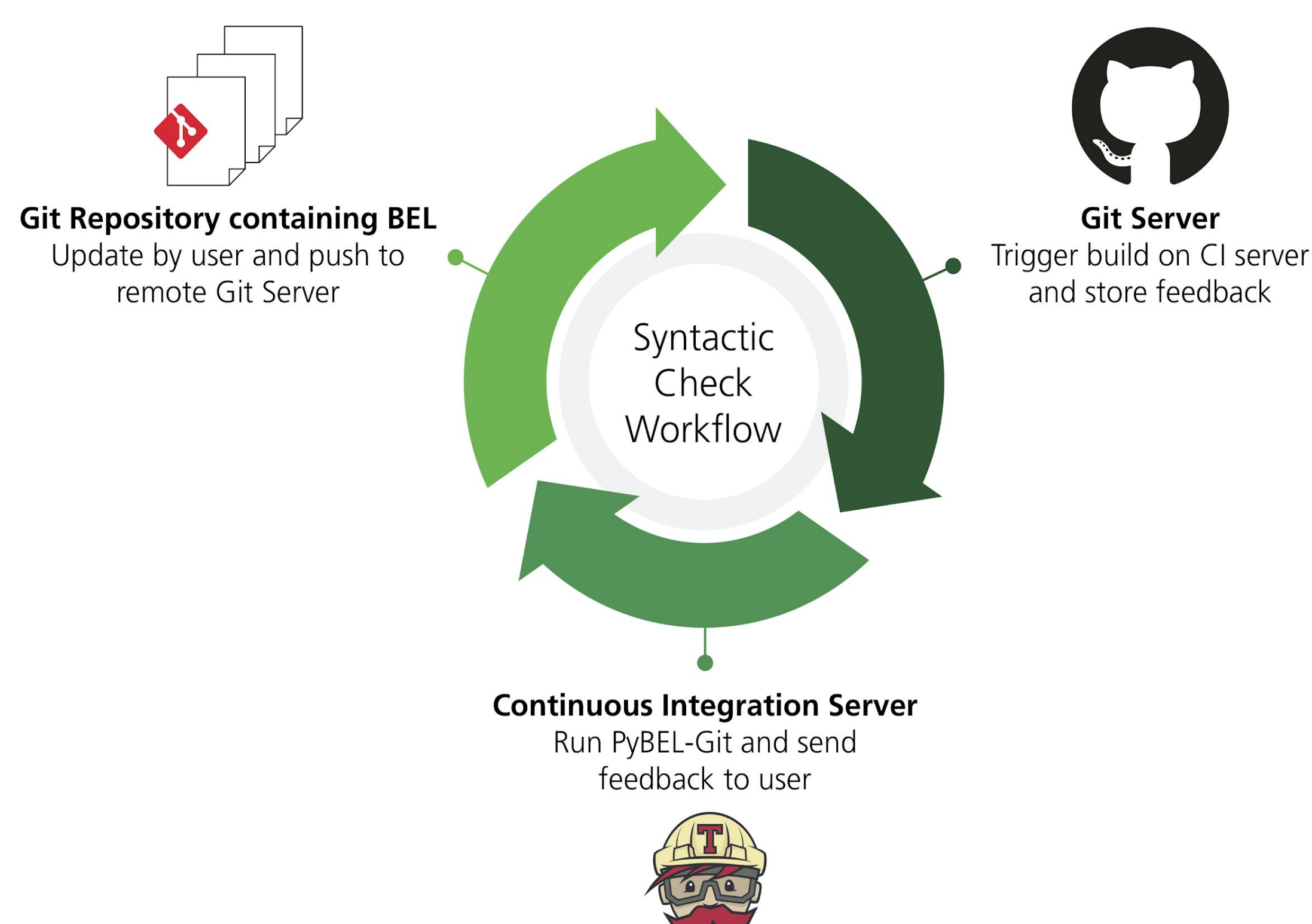
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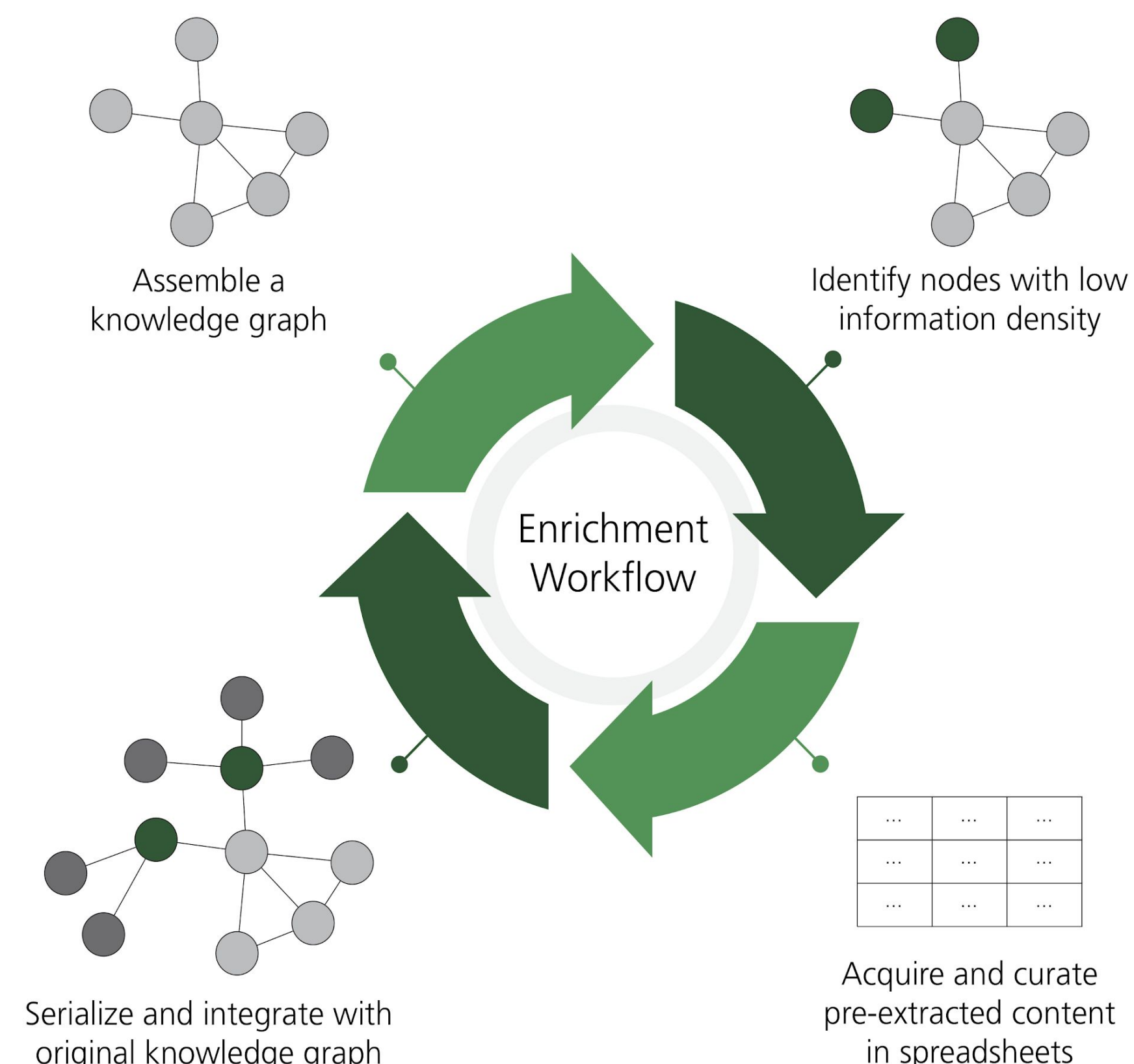
MOTIVATION

While numerous projects have dedicated extensive efforts into generating disease maps, most struggle with maintenance and updating. Moreover, projects' focuses and members' prior knowledge can lead to biases or gaps in coverage of relevant knowledge.

Maintenance Workflow



Rational Enrichment Workflow



Enrichment Tools

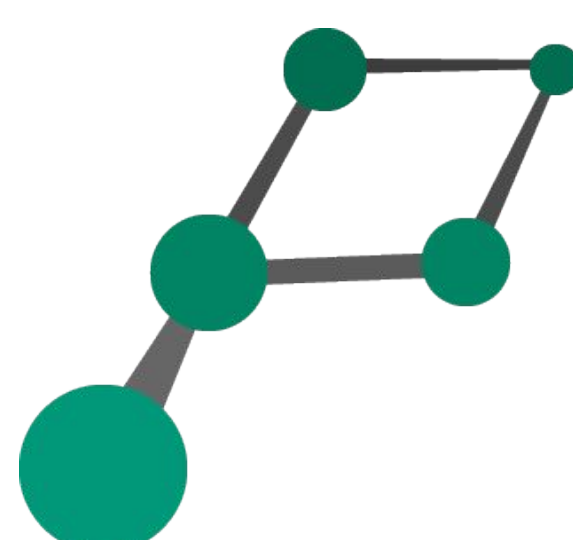
Structured Data Sources



Bio2BEL

github.com/bio2bel

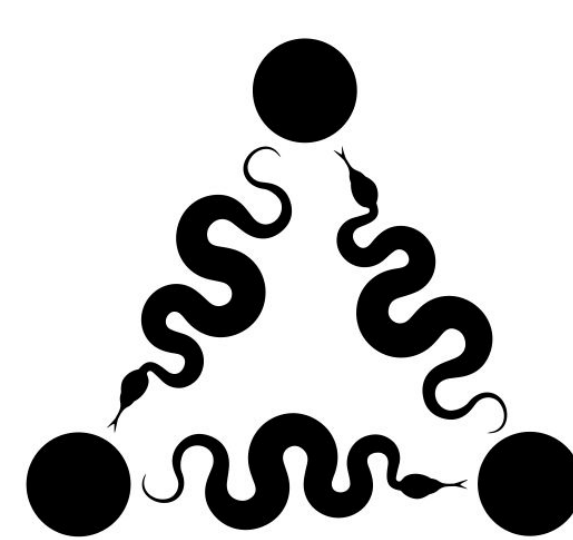
Pathway Databases



PathMe

github.com/pathwaymerger
pathme.scai.fraunhofer.de

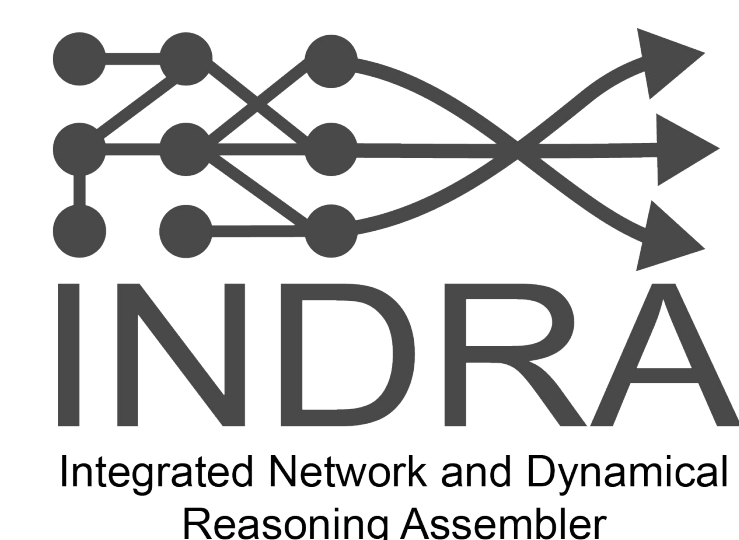
Prediction of Missing Links



PyKEEN

github.com/smartDataAnalytics/pykeen

Text Mining

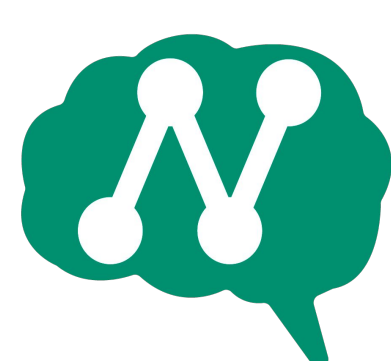


INDRA

github.com/sorgerlab/indra

Disease Maps

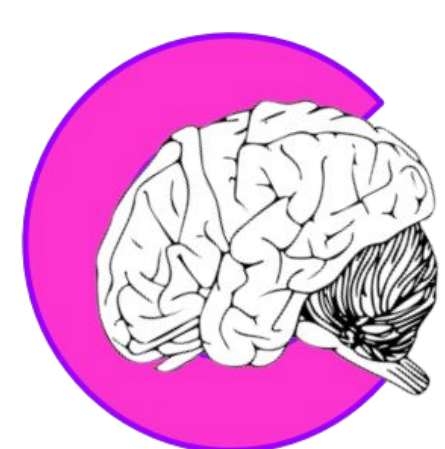
Alzheimer's, Parkinson's,
Epilepsy



NeuroMMSig

neuommsig.scai.fraunhofer.de

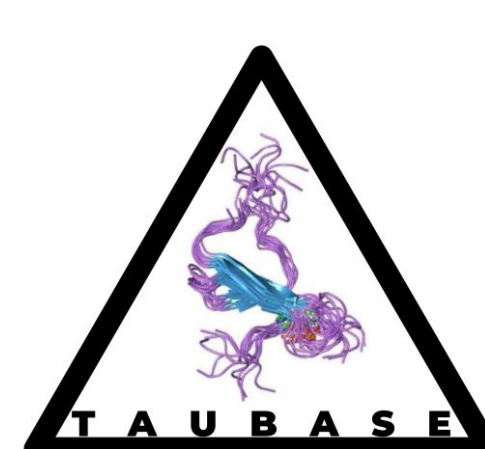
Huntington's, ALS, MS



CONIB

github.com/pharmacome/conib

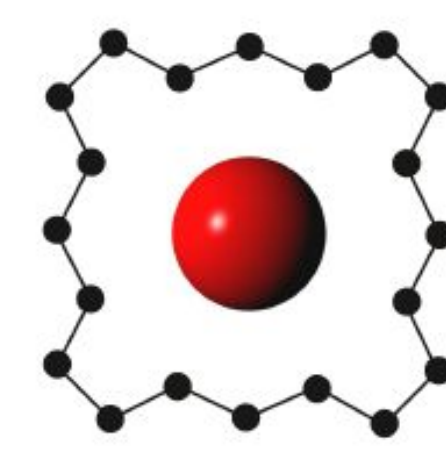
Tauopathies
(AD, PD, PNP)



TauBase

github.com/pharmacome/taubase

Hemolytic Disorders



HemeKG

github.com/hemekg

REFERENCES

1. Hoyt, C. T., et al. (2019). Re-curation and rational enrichment of knowledge graphs in Biological Expression Language. *Database*, baz068.
2. Hoyt, C. T., et al. (2019). Integration of Structured Biological Data Sources using Biological Expression Language. *bioRxiv*, 631812.
3. Domingo-Fernández, D., et al. (2019). PathMe: merging and exploring mechanistic pathway knowledge. *BMC Bioinformatics*, 20:243.
4. Ali, M., et al. (2019). BioKEEN: a library for learning and evaluating biological knowledge graph embeddings. *Bioinformatics*, 35(18):3538–3540.
5. Gyori, B. M., et al. (2017). From word models to executable models of signaling networks using automated assembly. *Molecular Systems Biology*, 13(11):954.
6. Domingo-Fernández, D., et al. (2017). NeuroMMSig: a web server for mechanism enrichment. *Bioinformatics*, 15;33(22):3679-3681.
7. Hoyt, C. T., et al. (2018). A systematic approach for identifying shared mechanisms in epilepsy and its comorbidities. *Database*, bay050.