

DARTpaths visualisation

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Background

- <u>Toxicology</u> is the study of toxic substances that can have adverse effects on living organisms.
 - > Developmental And Reproductive Toxicity (DART)
 - > Linking different biological processes to adverse effects.
- DART testing
 - ➤ Required to assess the impact of **new chemicals** on adult fertility and embryonic development
 - > These tests use animals and are very expensive and time consuming

Objectives

- <u>Interest</u>: assessing, predicting and improving the DART testing of the chemicals using computational approaches
 - The chemical component is linked to biochemical pathways and the associated phenotypic changes.
- Goal: Development of an interactive visualization tool to interpret developmental and reproductive toxicity by predicting the potential toxicity of a new chemical

Methods

Data

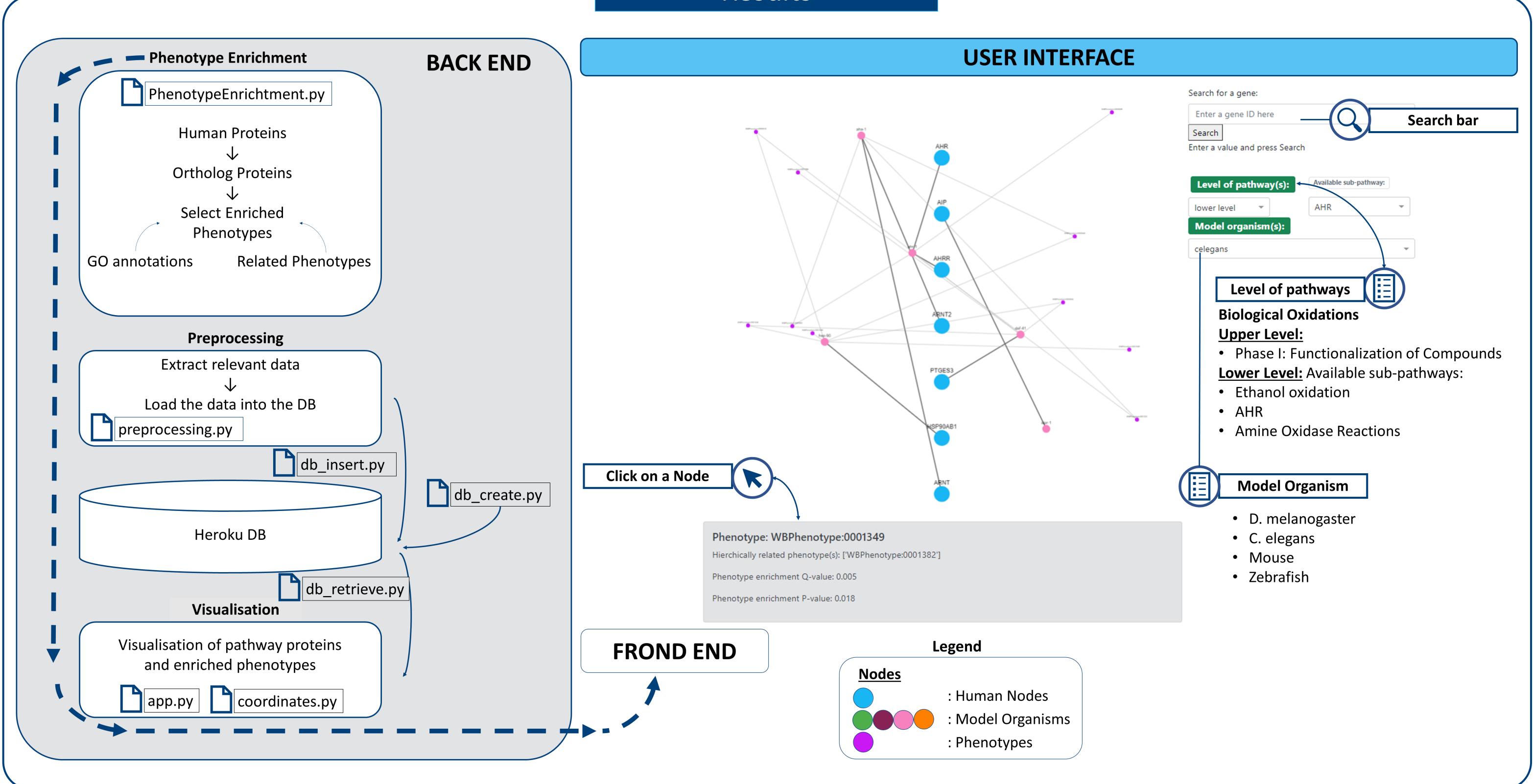
- Databases: Ensemble, Reactome, Wormbase, Zfin, MGI, Ensembl, Flybase
- Pathways: Reactome

Preprocessing

- Extract human protein IDs to ortholog IDs and enriched phenotype IDs
- Link phenotypes with their function (GO annotations) and with other related phenotypes
- Link all IDs to their names

Bar to specify level of pathway hierarchy we are looking at Legend Human gene/protein from tsv input file Mouse ortholog Zebrafish ortholog Drosophila ortholog Phenotype enriched with associated gene

Results



Conclusions

- New tool to visualize phenotypic data related to human metabolic pathways that can be negatively affected by various chemical agents
 - Can make **DART research cheaper and faster**
 - Can ensure that it is properly translated to people from the model organisms
- Limitation of this tool:
- Large pathways have many nodes and are therefore difficult to understand

Future directions

- Upscaling → adding more pathways to our database
- Using graph database instead of a relational one
- Original code refactoring

Acknowledgements

We would like to thank Miss Diksha Bhalla and Professor van Noort for their guidance throughout the project. We would also like to thank Nahdah Sholihah and Miguel Cisneiros for their work on Phenotype enrichment.