

Thesis Progress Update

Phenotypic Enrichment of Conserved Molecular Pathways - with a Focus on Alternatives for Toxicity Testing

Updates since 5/Oct

1. FDR pvalue corrected multiple testing
2. Slime mould analysis
3. Output with file name
4. Phenotype terms
5. Add new databases needed for phenotype terms (OBO)
6. Overlapping genes

Notes


- For slime mould, there's no phenotype ID, so the enrichment already gives info for phenotype term
- For zebrafish the phenotype is from PATO, while ZF and GO ID only describes the affected structure. I.e. PATO will only explain the variant i.e. 'decreased' while ZF/GO only explains i.e. 'sleep/wake cycle' so to explain the phenotype term correctly needs to combine both.

Database

Pathway	Orthologs	Phenotype (Genotype Association)	Phenotype terms (Onthology)
Reactome	Ensembl	Wormbase ZFIN MGI DlctyBase	OBO



Mapping

	Pathway in Humans	Ortholog	Phenotype	Phenotype term
Input ID	ENSEMBL 	ENSEMBL	-	
Gene set: Worm Zebrafish Mouse		Gene ID Gene name Gene name	Gene ID Gene name Gene name	
Annotated term			Phenotype ID	Phenotype ID
Database	Reactome	Biomart	Wormbase MGI ZFIN	OBO

See the same ID on each database/source for linking information between different entities

Current Shiny

Run the code on the website, or just the output?

Connecting R and Python