The Parkinson's Disease Map: A Framework for Integration, Curation and Exploration of Disease-related Pathways

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Problem statement
- Number of publications on PD grows continuously
- Many molecular pathways are implicated in PD
- Molecular pathology of PD is likely multi-factorial1,2
- Exploration and analysis of molecular pathways require integration of literature and experimental data

Components:
- Gene regulation
- Protein-protein interaction
- Metabolic interactions
- Phenotypic information

Outcomes
- PD map is a rich resource of molecular pathways implicated in PD
- Access to knowledge on PD pathways using tools for browsing, annotation and integration of experimental data
- The map is open for analysis by systems biology approaches, providing insight into its global structure
- Text mining and community curation are invaluable for efficient map enrichment

Components
- GWAS
- Genetic variation
- Perturbation experiments
- Gene and protein expression
- Metabolomics
- Protein-protein interaction data

Focus:
- Mitochondrial dysfunction
- Neuroinflammation
- Protein misfolding
- Synaptic dysfunction
- Failure of protein degradation

Analysis
- New map elements (PathExpand®), hubs, inter-modular links and critical pathways
- Annotation

Curated content:
- 2286 elements
- 989 reactions
- 429 papers
- 223 Reactome reactions
- 31 KEGG reactions
- SBML/SBGN standard

Text mining
- 50 000 full text publications
- PD-related text

Enrichment
- Co-occurrences11
- Contextualized search
- Human in the loop
- Syntax analysis

Outcomes
- 8 datasets of human PD SNpC jointly analysed5 for differentially expressed genes and mapped

References