Patients with neurodegenerative diseases have insufficient treatments to manage the debilitating and prolonged symptoms of their diseases, therefore, there are no curative options. Here we used our PPI model, PathFX, to assess the connections between approved drugs and neurodegenerative disease pathways to better understand potential treatment strategies. We identified 8 neurodegenerative phenotypes in the PathFX database and found network associations with 5 of them among approved drugs in DrugBank. Our analysis revealed 2,142 drug-phenotype relationships involving 1,113 unique drugs. Supporting literature validated pathways identified by PathFX, including a genetic association between Bridging Integrator 1 (BIN1) and Alzheimer’s disease. Our results indicate robust connectivity between druggable targets and neurodegenerative disease pathways, showing potential for treatment strategies. Furthermore, our analysis demonstrated high gene similarity across neurodegenerative diseases.

PathFX

A Protein-Protein Interaction Network Method for Predicting Drug Downstream Effects

Figure 1. A schematic of PathFX –
(1) input a drug
(2) PathFX identifies the primary drug targets
(3) and predicts phenotypes

Figure 2. The bar graph illustrates the top genes associated with drug-phenotype predictions from PathFX: Alzheimer’s Disease “AD” (1010 drugs), Parkinson’s Disease “PD” (422 drugs), Dementia “DEM” (256 drugs), Familial Alzheimer’s Disease “FAD” (452 drugs).

Figure 3. The heat map shows each drug (rows) and the top genes (columns) to which they are associated. This data is generated from 2142 total drug-phenotype relationships discovered from PathFX.

References


Acknowledgements

Special thanks to Dr. Jennifer Wilson, the Lab for Understanding Network Effects @ UCLA, the UCLA Department of Bioengineering and the Bruins - In - Genomics (B.I.G.) Summer Program.