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Federal funding, 6 PhD students

Disease-gene prioritization via multiplex heterogeneous networks

Our mission
Developing integrative computational tools utilizing artificial intelligence, machine learning and data mining methods to analyze these high dimensional genomic, genetic and epigenetic datasets to

→ infer context-specific gene regulatory interactions and modules, and

→ predict disease associated genes and patient-specific drug response.

Early prediction of Alzheimer’s Disease using deep learning

Cancer subtype prediction using graph representation learning