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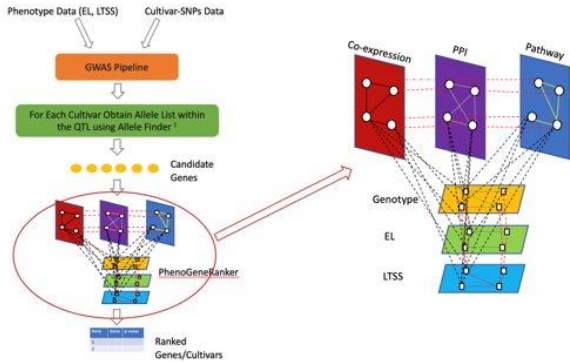
Bioinformatics, Computational Biology, Machine Learning, Network Biology, Graph representation learning, Cancer genomics

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Federal funding, 6 PhD students



Disease-gene prioritization via multiplex heterogeneous networks



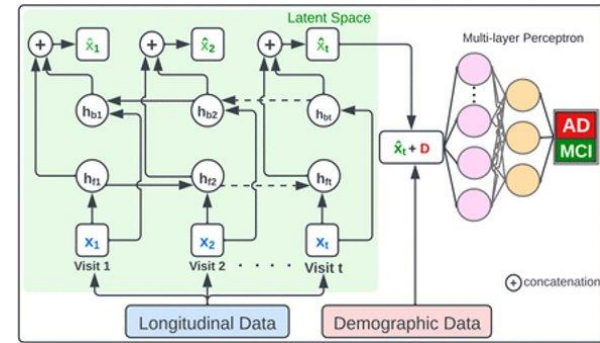
Our mission

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

