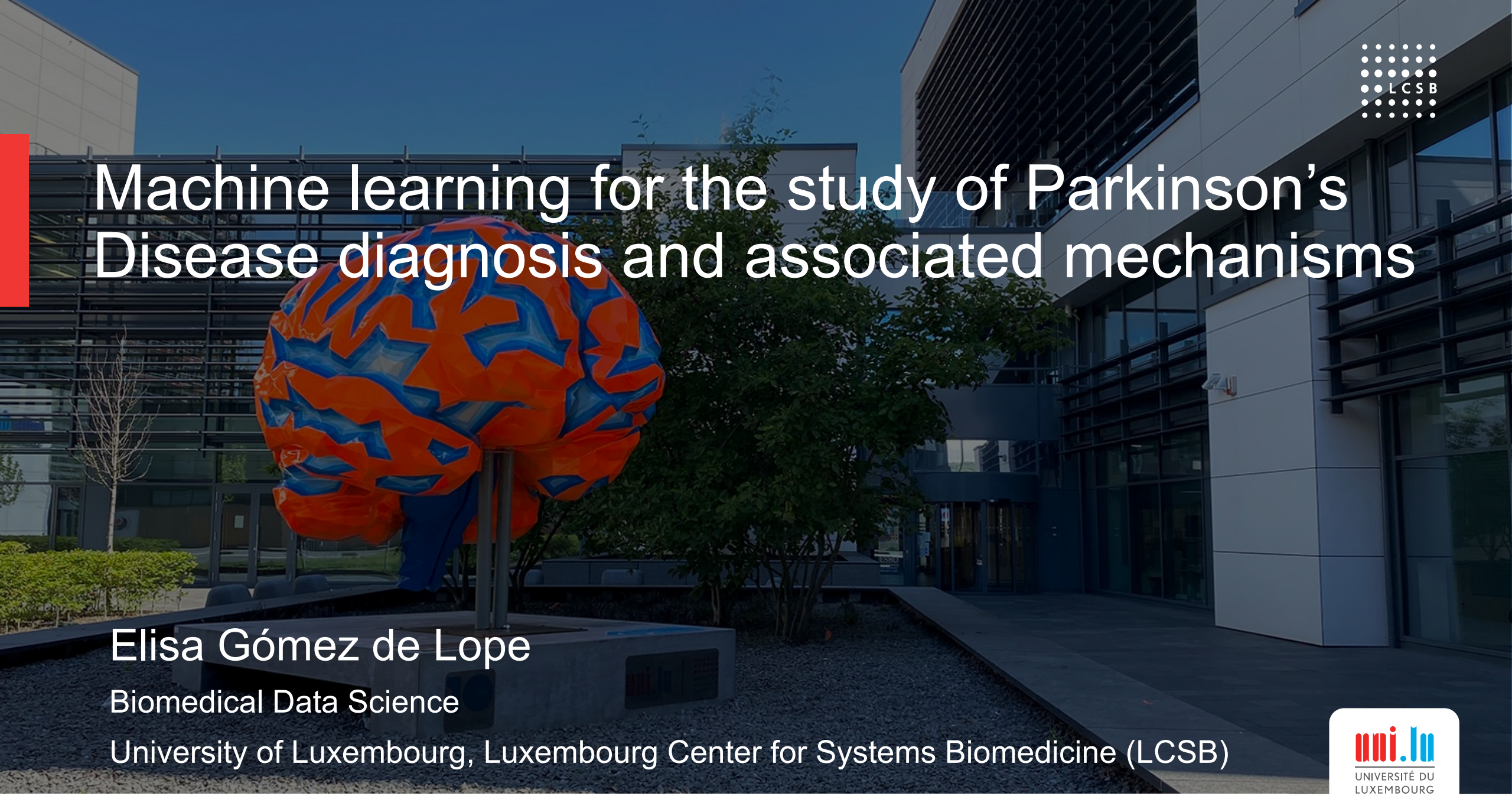

Machine learning for the study of Parkinson's Disease diagnosis and associated mechanisms

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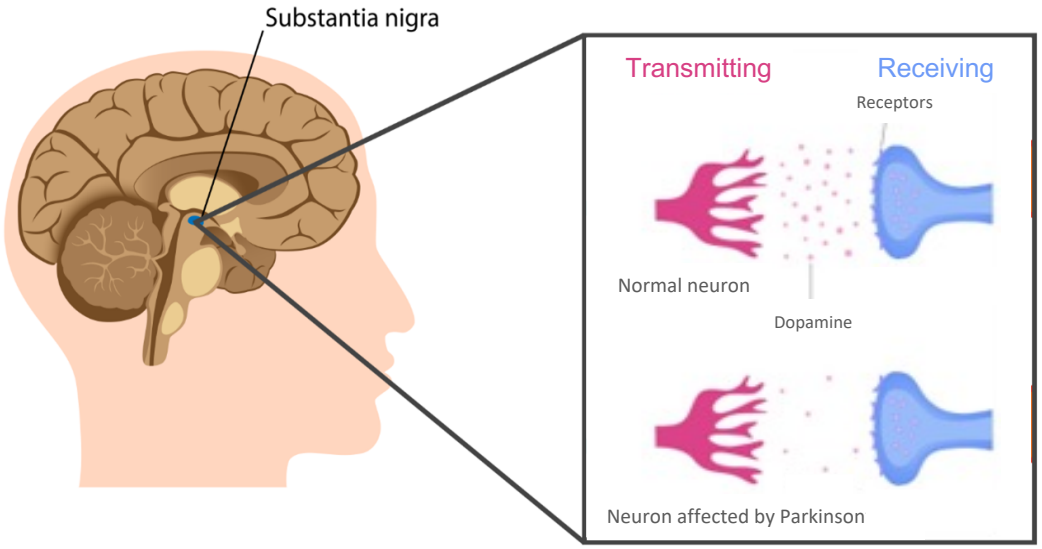
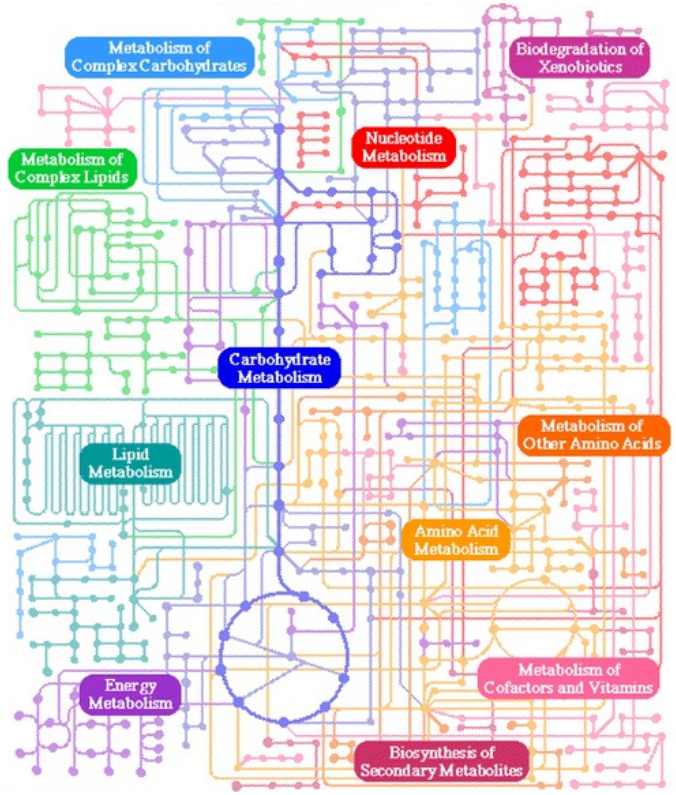
Parkinson's Disease & higher order functional representations



Source: Adapted from shutterstock

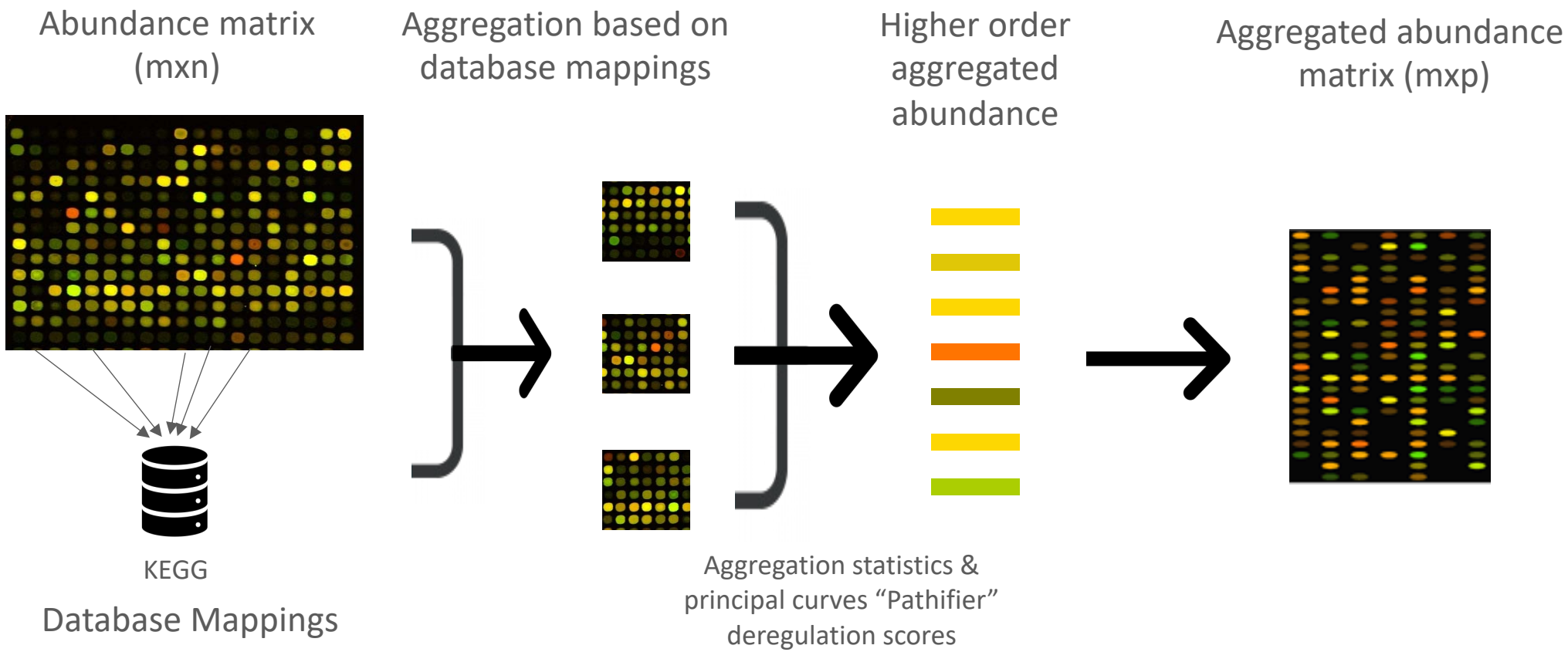
- Single gene mutations?
- Mitochondrial genetics?
- Environmental factors (toxins)?

Diagnosis is clinical & difficult



Schematic representation of metabolic networks
Source: The Origin and Evolution of Metabolic Pathways: Why and How did Primordial Cells Construct Metabolic Routes?

High throughput omics data into higher order functional features

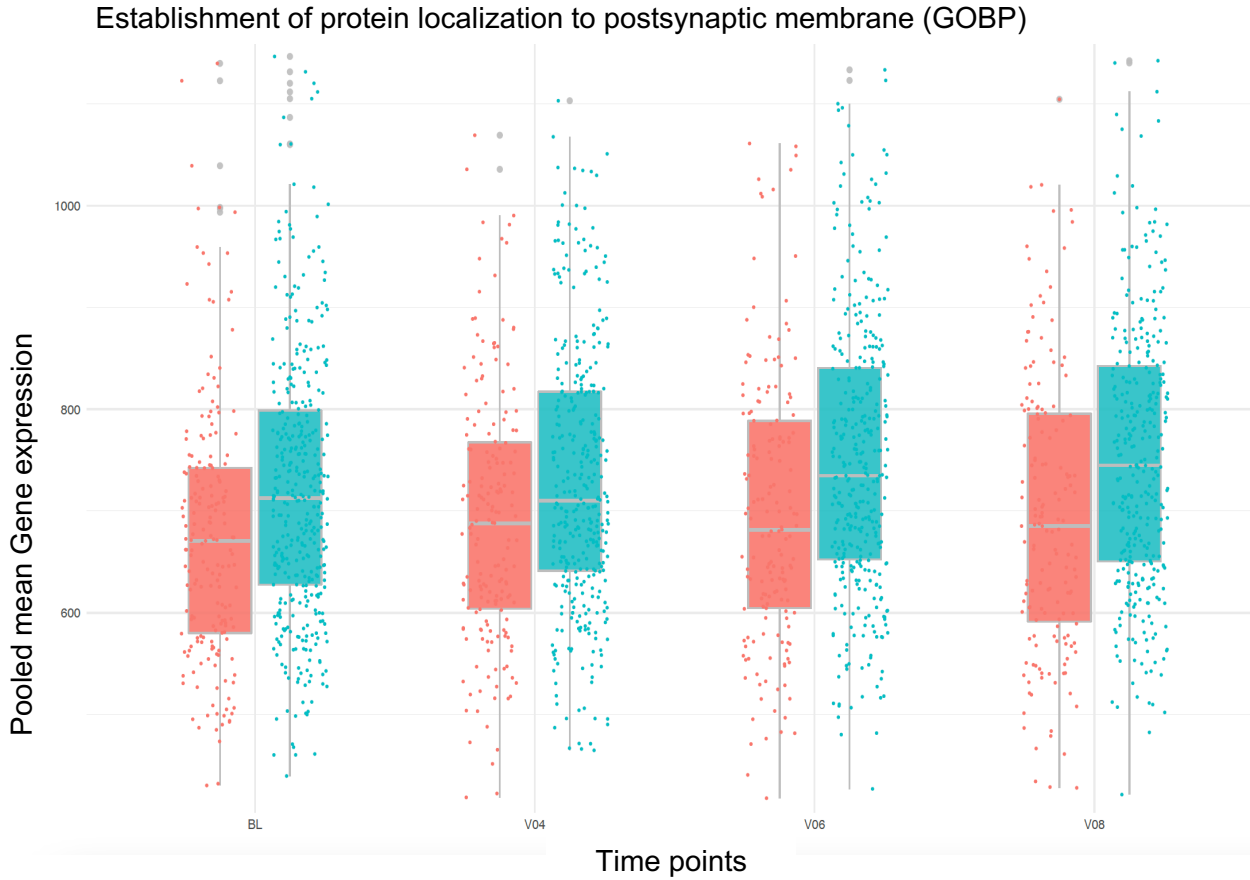


KEGG = Kyoto Encyclopedia of Genes and Genomes
m = number of samples
n = number of single-level features (i.e. genes, metabolites, etc)
p = number of higher order functional aggregates (e.g. number of pathways)

Statistical differential analyses & time course analyses

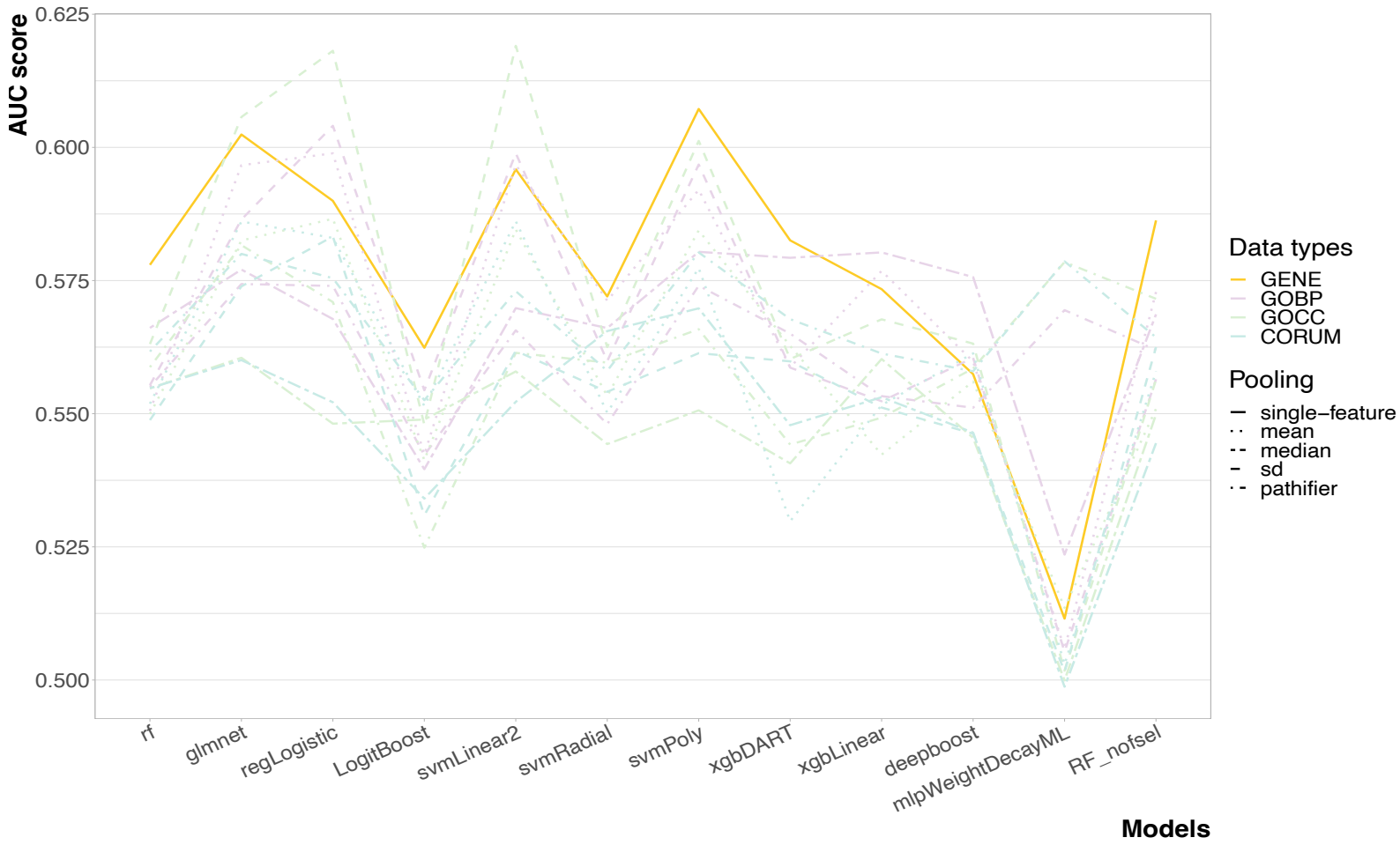
Metabolomics aggregated data on ‘de novo’ patients

Transcriptomics aggregated temporal profiles



Predictive PD diagnosis with ML models on transcriptomics

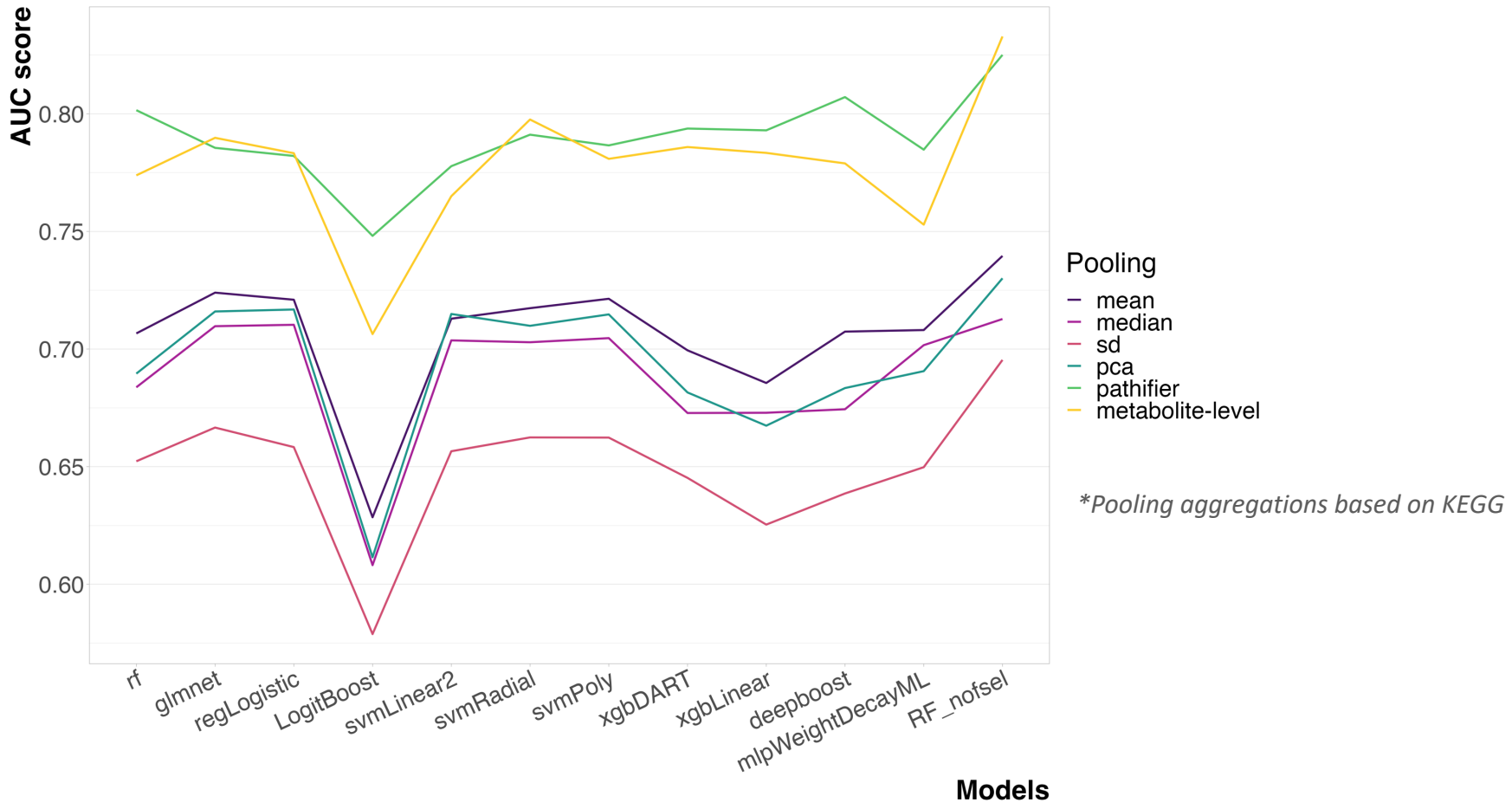
Line chart of crossvalidated AUC scores from models & pooling types on transcriptomics data



External two-level cross-validation was used (including nested feature selection)

Predictive PD diagnosis with ML models on metabolomics

*Line chart of crossvalidated AUC scores from models on metabolomics data**

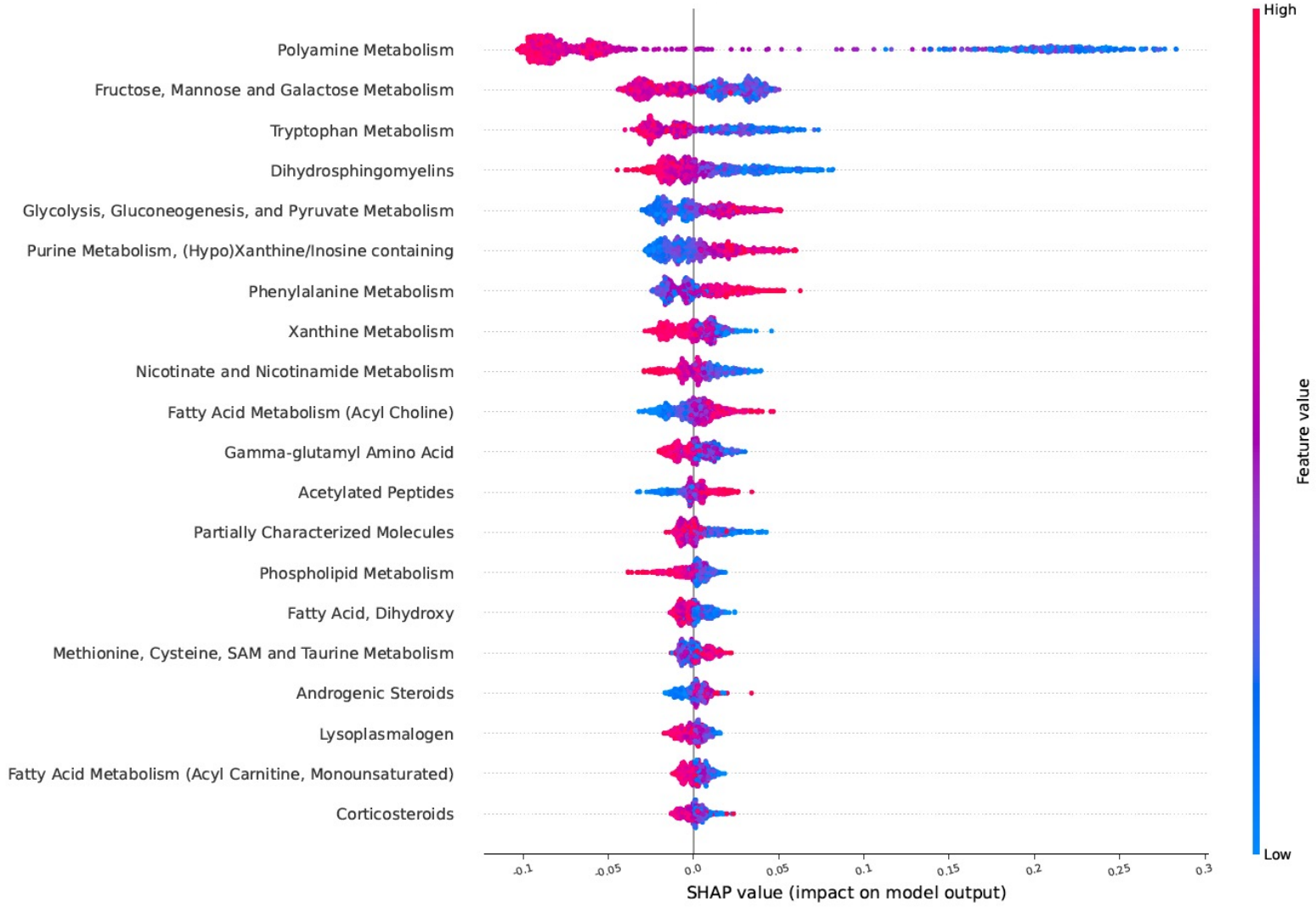


**Pooling aggregations based on KEGG*

External two-level cross-validation was used (including nested feature selection)

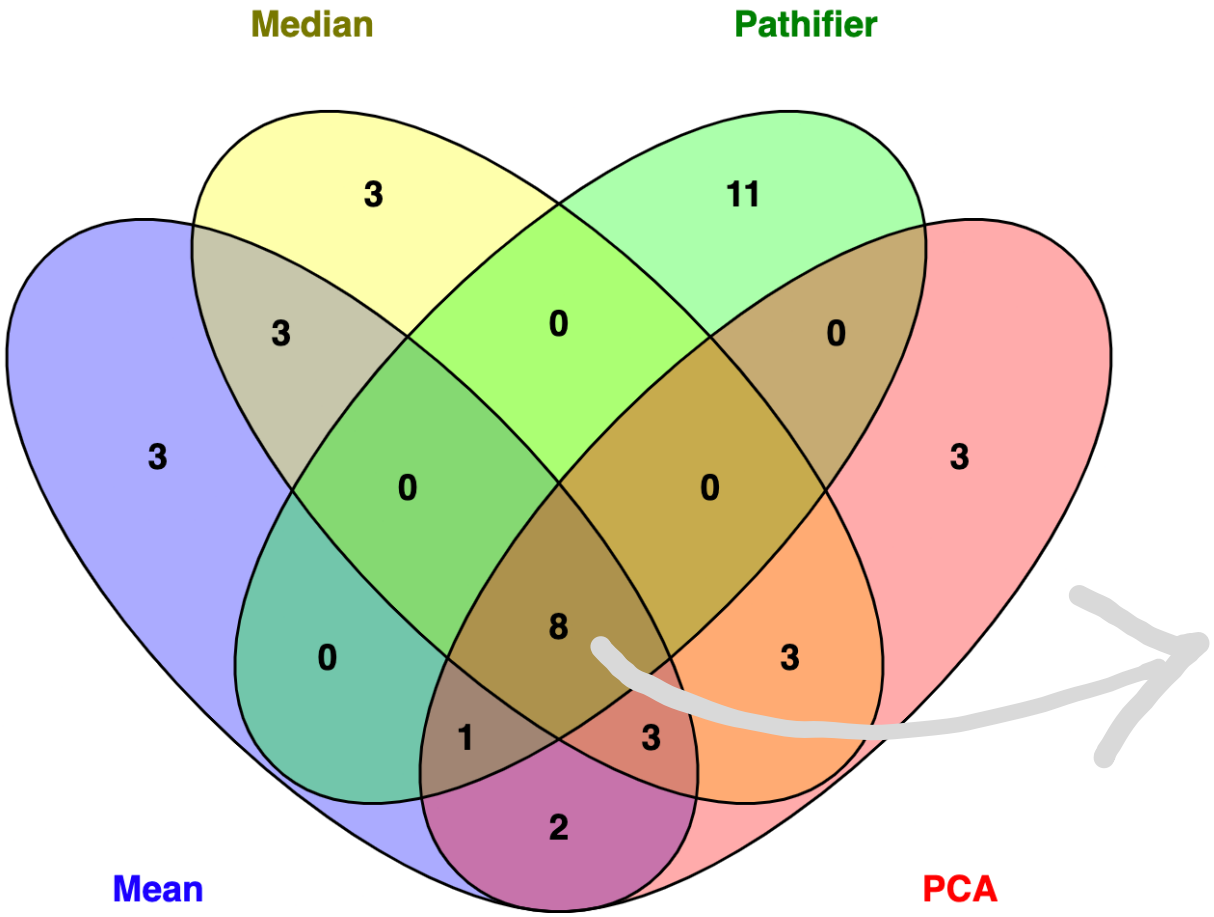
Relevant features from predictive PD diagnosis met/transc

Shap values of (pathifier -aggregated) KEGG metabolic pathways predictors on random forest model



Relevant features from predictive PD diagnosis on metabolomics

Top 20 most relevant features per pooled aggregation based on shapley values

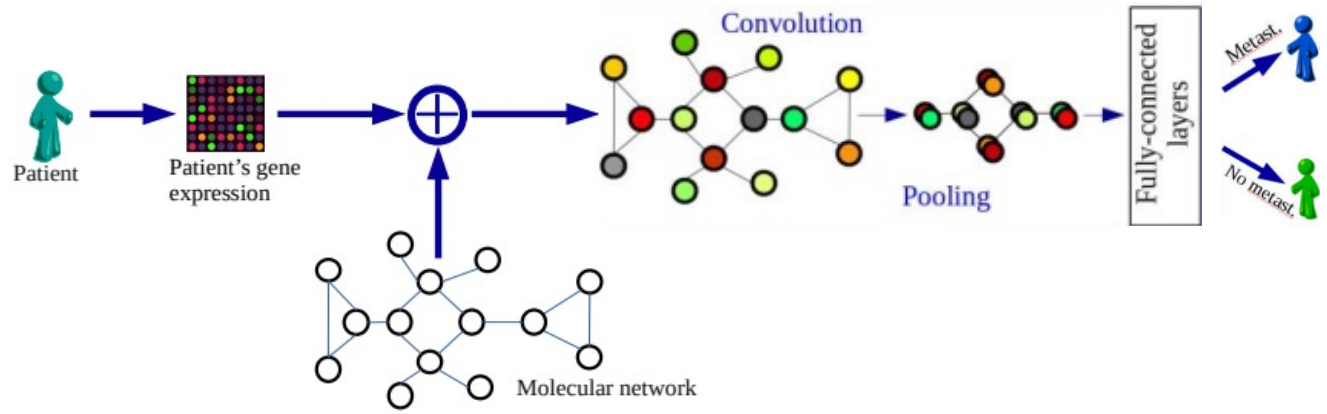


Phenylalanine Metabolism
Gamma-glutamyl Amino Acid
Xanthine Metabolism
Tryptophan Metabolism
Purine Metabolism, (Hypo)Xanthine/Inosine containing
Fatty Acid Metabolism (Acyl Choline)
Partially Characterized Molecules
Phospholipid Metabolism

Limitations & outlook for future analyses

- ✗ Unknown confounders
- ✗ Large variability among PD patients makes identifying common trends dfficult
- ✗ Data represents late stages of the disease

- ➡ Modelling other PD prognostic outcomes (e.g. motor dysfunction scores)
- ➡ Use a graph representation of the data via protein-protein interactions and metabolic networks



Gene expression profile as a graph signal of the molecular network

Source: Chereda, H., 2022. Explaining decisions of graph convolutional neural networks for analyses of molecular subnetworks in cancer [Doctoral thesis, Georg-August-Universität Göttingen]

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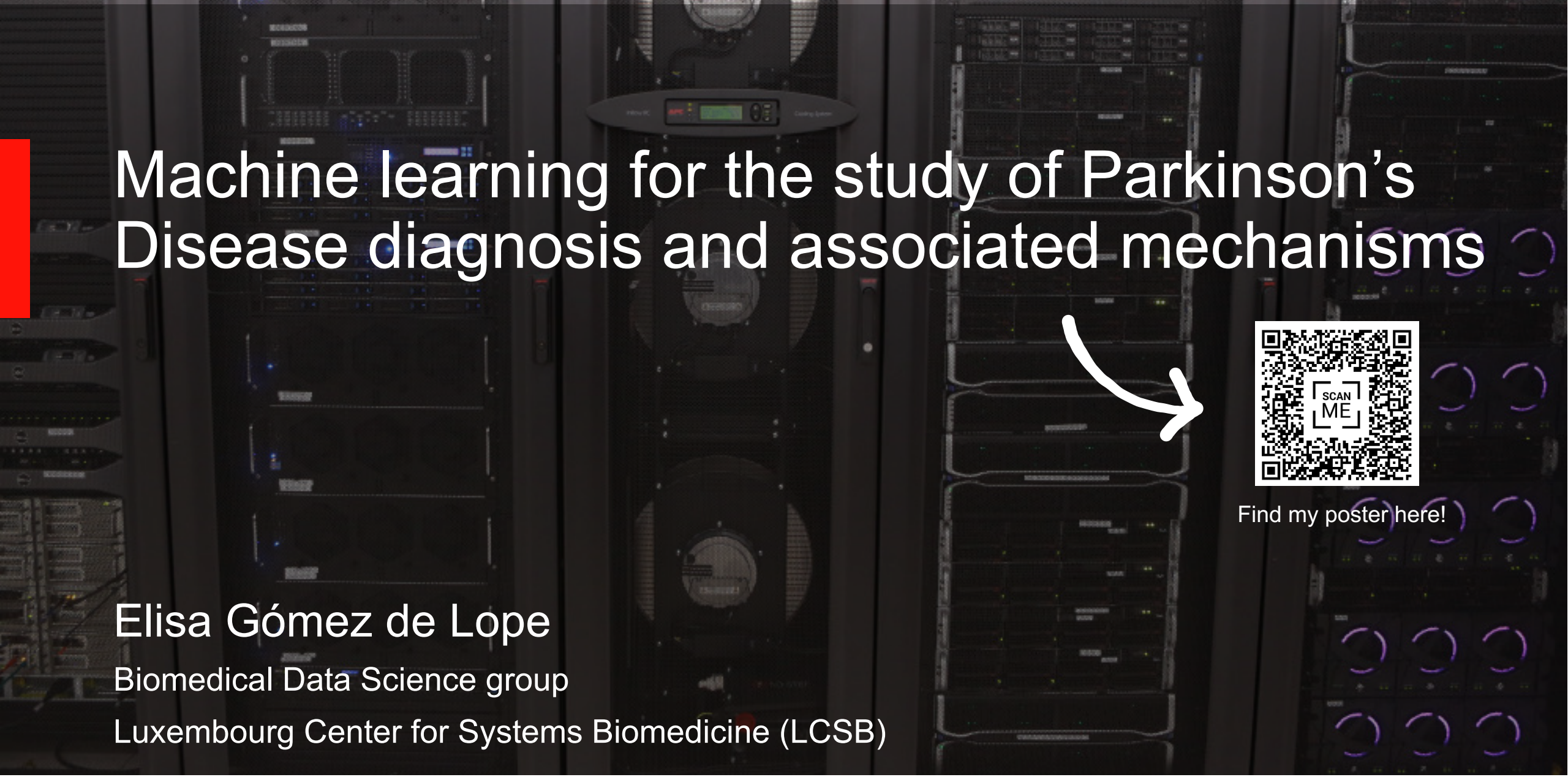

SCAN ME

Find my poster here!

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