# Metaboverse: Metabolic network pattern recognition tools contextualize multi-omic data and reveal disease-relevant signatures

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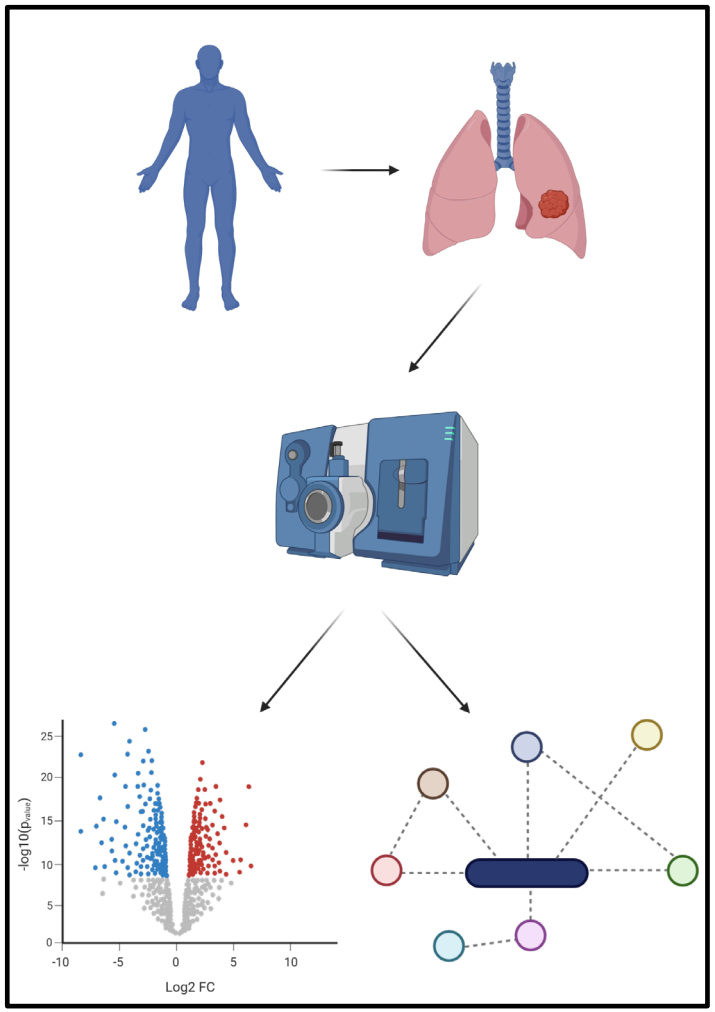
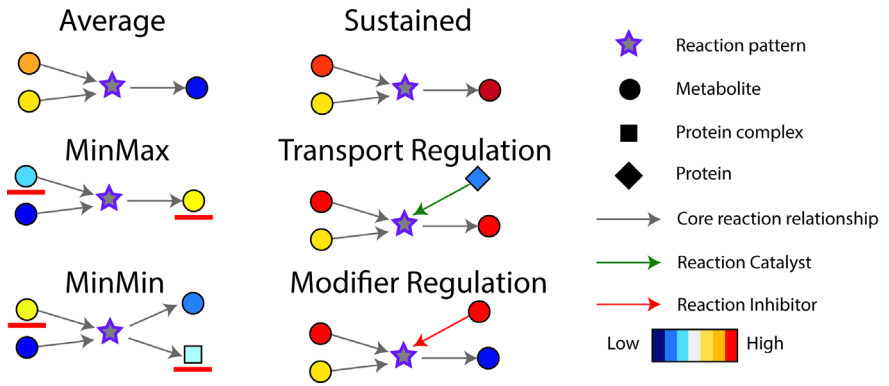
Lung adenocarcinomas and paired healthy lung tissue were obtained in Wikoff, et al. (2015), and assayed for biomarkers.



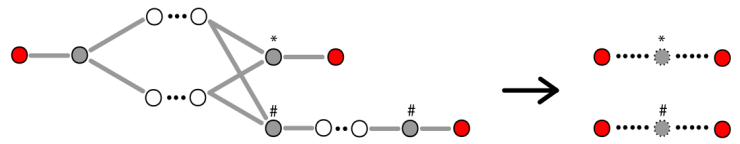

We reprocessed these metabolomics data with our tool, ***Metaboverse***, to identify context-dependent patterns within the data.

Metaboverse offers the ability to perform comprehensive reaction pattern searching across the biological network.

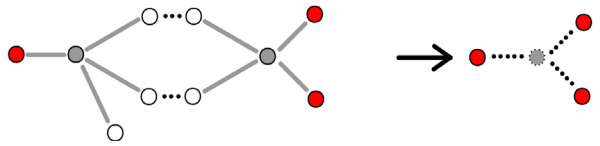



Metaboverse enables the identification of such patterns across multiple reactions where data are missing in intermediate reaction steps.

**Exhaustive collapsing:**

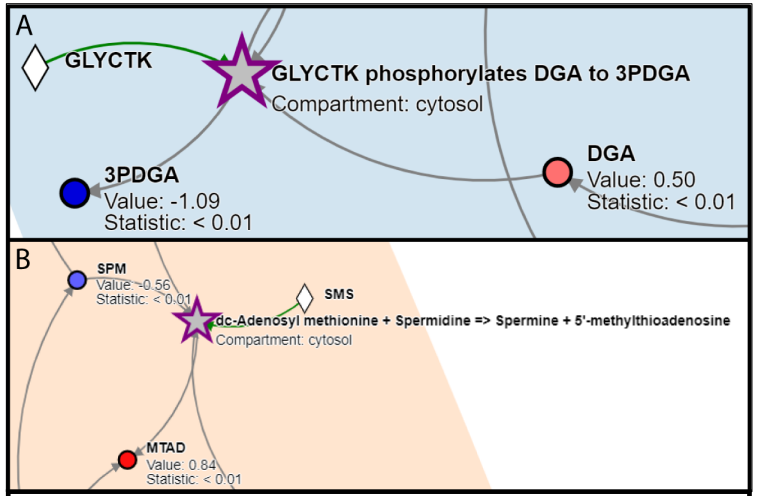


**Partial collapsing:**

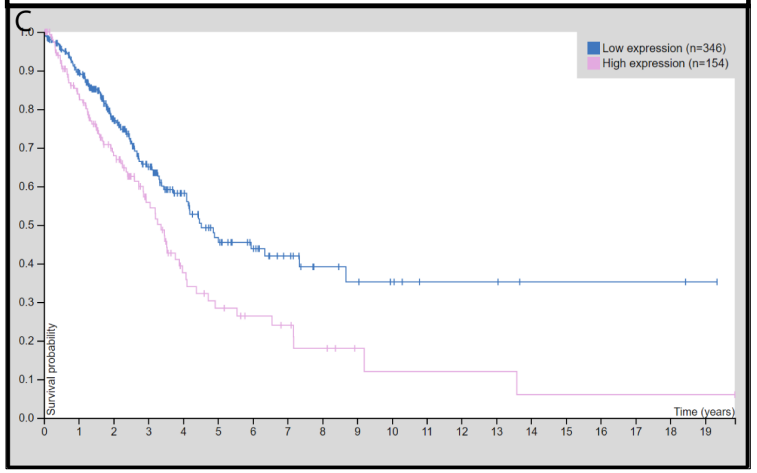


*Download Metaboverse*

We identified novel reaction patterns within the data, one around glycerate kinase (A), and the other around Spermine Synthase (B).




We cross-referenced the SMS pattern with the Human Protein Atlas and discovered SMS expression could be used as a prognostic marker in lung adenocarcinomas (C).




References: Wikoff, 2015, *Cancer Prev Res*; Berg, 2020, *bioRxiv*; Uhlén, 2015, *Science*

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