

## Enrichment with MetaboAnalyst

### A. Pros and cons of MetaboAnalyst for enrichment

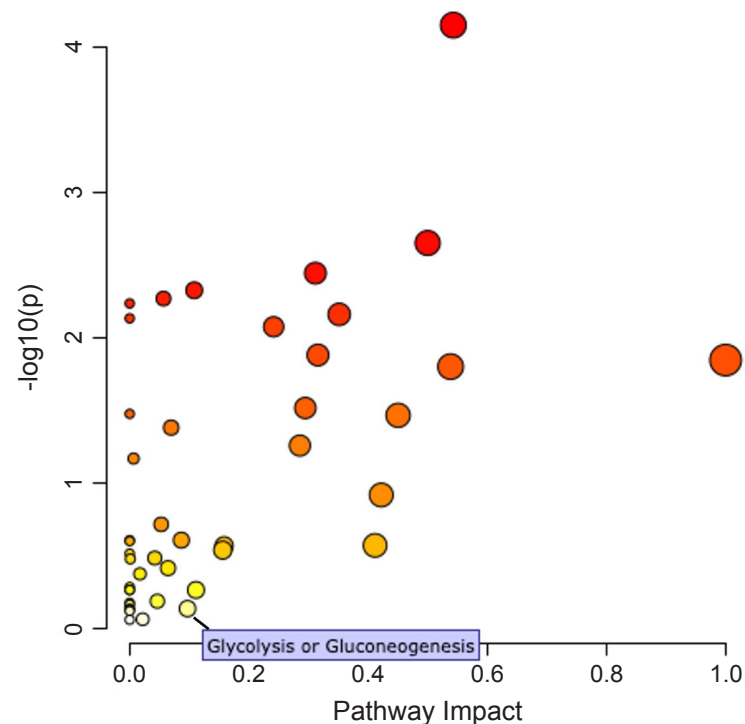
| Pros   | Cons  |
|--|---|
| <ul style="list-style-type: none"> <li>Tools available to analyze data from raw spectra through enrichment and visualization</li> <li>Interactive platform with no coding required</li> <li>Provides the foundation for other analytical packages</li> </ul> | <ul style="list-style-type: none"> <li>Extended capabilities for untargeted data, but better suited for targeted data</li> <li>Issues with shared nomenclature or inability to identify molecules</li> <li>Limited available reference databases</li> </ul> |

### B. Different KEGG databases impact output

| Human Pathway                                | Match Status | FDR   | Impact | <i>C. elegans</i> Pathway                   | Match Status | FDR   | Impact |
|--|--------------|-------|--------|---|--------------|-------|--------|
| Starch and sucrose metabolism                | 6/17         | 0.003 | 0.62   | Starch and sucrose metabolism               | 6/16         | 0.005 | 0.54   |
| Nitrogen metabolism                          | 3/6          | 0.053 | 0      | Phenylalanine metabolism                    | 3/6          | 0.07  | 0.5    |
| Galactose metabolism                         | 4/15         | 0.059 | 0.05   | Amino sugar and nucleotide sugar metabolism | 6/31         | 0.07  | 0.31   |
| Valine, leucine, and isoleucine biosynthesis | 3/8          | 0.059 | 0      | One carbon pool by folate                   | 5/23         | 0.07  | 0.11   |

### C. Nomenclature inconsistencies impact enrichment results

#### Overview of Pathway Analysis



#### Glycolysis or Gluconeogenesis

