Step 1: Microarray preprocessing (Bioconductor ecoliLeucine and affy package) Step 2: Statistical analysis [p-value]

Step 3:

<u>(Bioconductor limma package)</u>

Integration of statistical quantities with pathways (KEGGscape REST API and py2cytoscape)

Step 4:

Visualization with Cytoscape

- Omics data acquisition and preprocessing
- Statistical analysis



