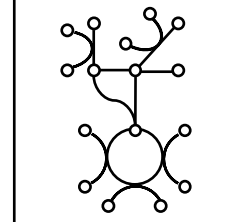


Tutorial 3.1: Tissue-Specific FBA



(i) Load GSMM and associated variables

*Load fbamodel, genes,
pos_genes_in_react_expr,
reaction_expression, ixs_genes_by_length*

(ii) Load gene expression data
and define its dimensions

*Read table (gene_expression_data)
with p genes and n patients*

(iii) Create output vectors

*Define variables to store outputs of flux balance
analysis (biomass and fluxes) and gene
expression values (GeneExpressionArray)*

(iv) Run model

*Perform regularized flux balance analysis using
evaluate_objective with optimal gamma*

(v) Obtain flux values for use as
features in future analyses

Save table (fluxes)