Analysis of M1 mouse macrophages compared to M0

Input files

Example data for GAM consists of two files with differential expression (DE) between M0 and M1 states of mouse macrophages:

- DE for genes: https://artyomovlab.wustl.edu/publications/supp_materials/GAM_2015/Ctrl.vs.MandLPSandIFNg.gene.de.tsv
- DE for metabolites: https://artyomovlab.wustl.edu/publications/supp_materials/GAM_2015/Ctrl.vs.MandLPSandIFNg.met.de.tsv

DE data for genes contain information about 16829 transcripts most expressed in at least one of the M0, M1 or M2 states.

DE data for metabolites contain information about 2120 HMDB metabolites (603 different MS signals).

Using differential expression only for metabolites

Figures 1 and 2 show modules found for metabolic data only for flow-centric (default for such data, Fig. 1) and gene-centric (Fig. 2) mapping strategies. Notably, differential regulation of TCA cycle and glycolysis is highlighted even when using only metabolic data while urea cycle and lipid synthesis are not.
Red color corresponds to up-regulation in M1, green corresponds to down-regulation. Size of nodes and edges corresponds to -log(p-value). Circular nodes represent metabolites, square nodes represent reactions. Blue nodes represent instances without p-values, e.g. undetected metabolites. Parameters were set to: metabolite $\log_{10}$ FDR = -2.9, absent metabolite score = -7.1. As a post-processing step, trans-RPAIR connections were added (marked with dashed lines).

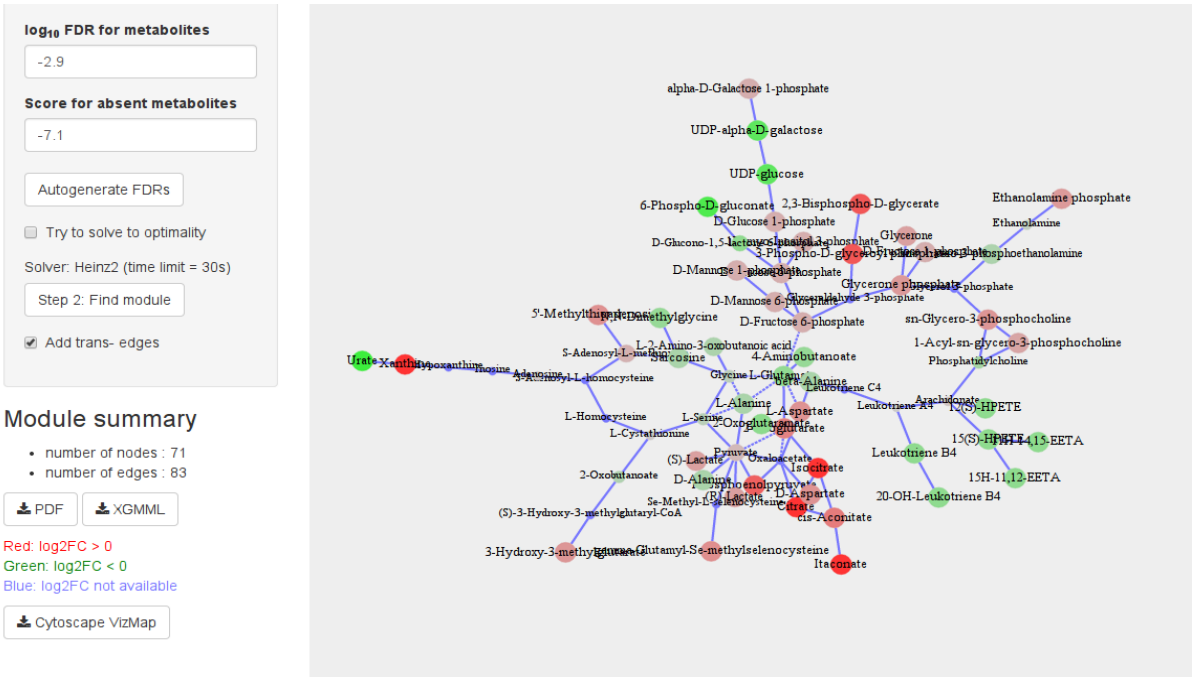

Fig. 1. GAM-module for metabolic data only, with reactions mapped to edges.

Reactions as nodes

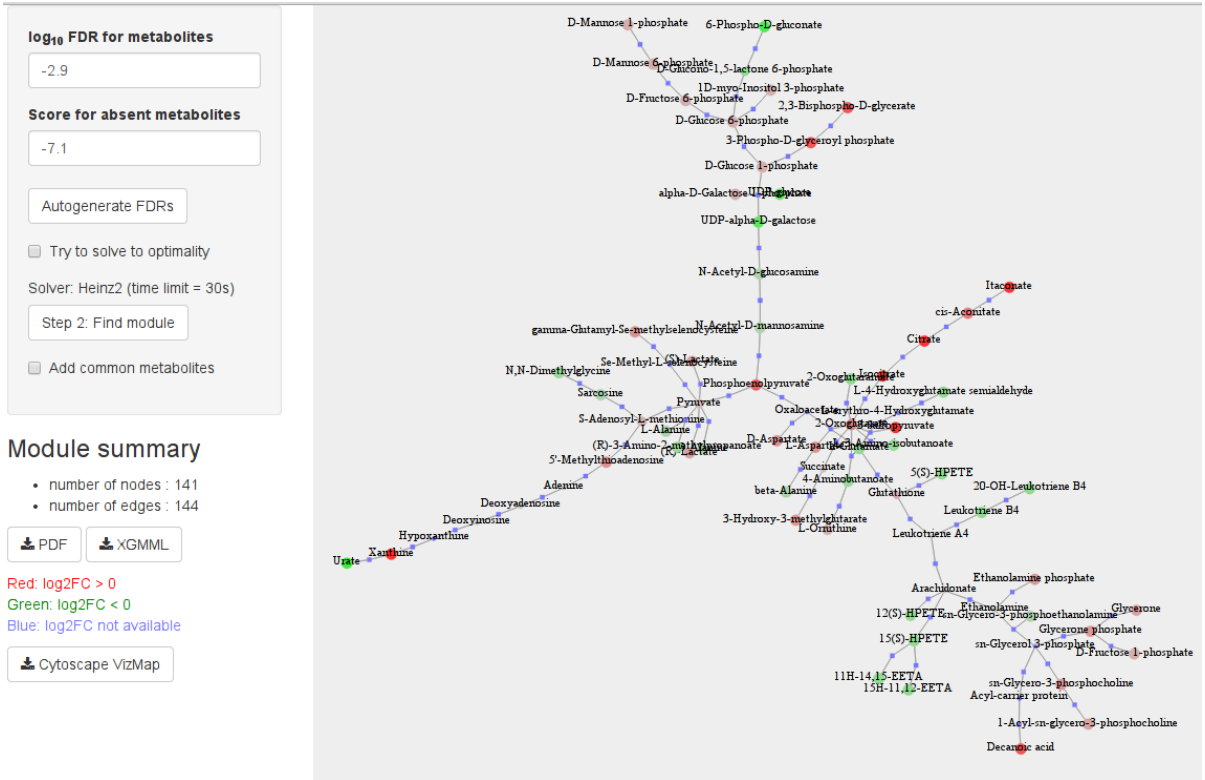

Fig. 2. GAM-module for metabolic data only, with reactions mapped to nodes.

Using differential expression only for genes

Figures 3 and 4 show modules found for transcriptional data only for flow-centric (Fig. 3) and gene-centric (default for such data, Fig. 4) mapping strategies. These modules mainly show differential regulation of urea cycle and lipid synthesis, not of TCA cycle and

glycolysis. However, part of TCA cycle is present on Fig. 4, as a way to reach highly regulated Irg1.

Red color corresponds to up-regulation in M1, green corresponds to down-regulation. Size of nodes and edges corresponds to -log(p-value). Circular nodes represent metabolites, square nodes represent reactions. Blue nodes represent instances without p-values, e.g. undetected metabolites. Parameters were set to: gene $\log_{10}$ FDR = -4.6 for flow-centric approache and $\log_{10}$ FDR = -2.5 for gene-centric approach. As a post-processing step, trans-RPAIR connections were added (marked with dashed lines).

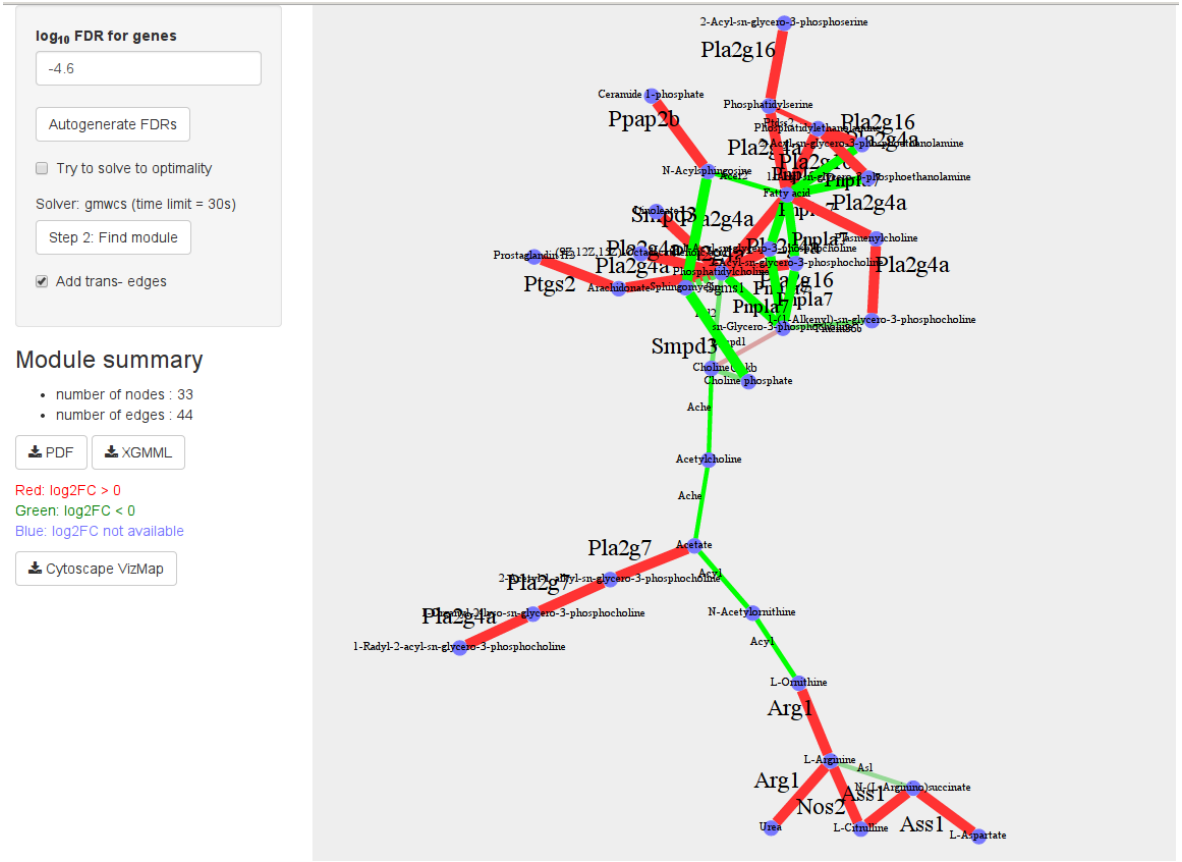

Fig. 3. GAM-module for transcriptional data only, with reactions mapped to edges.

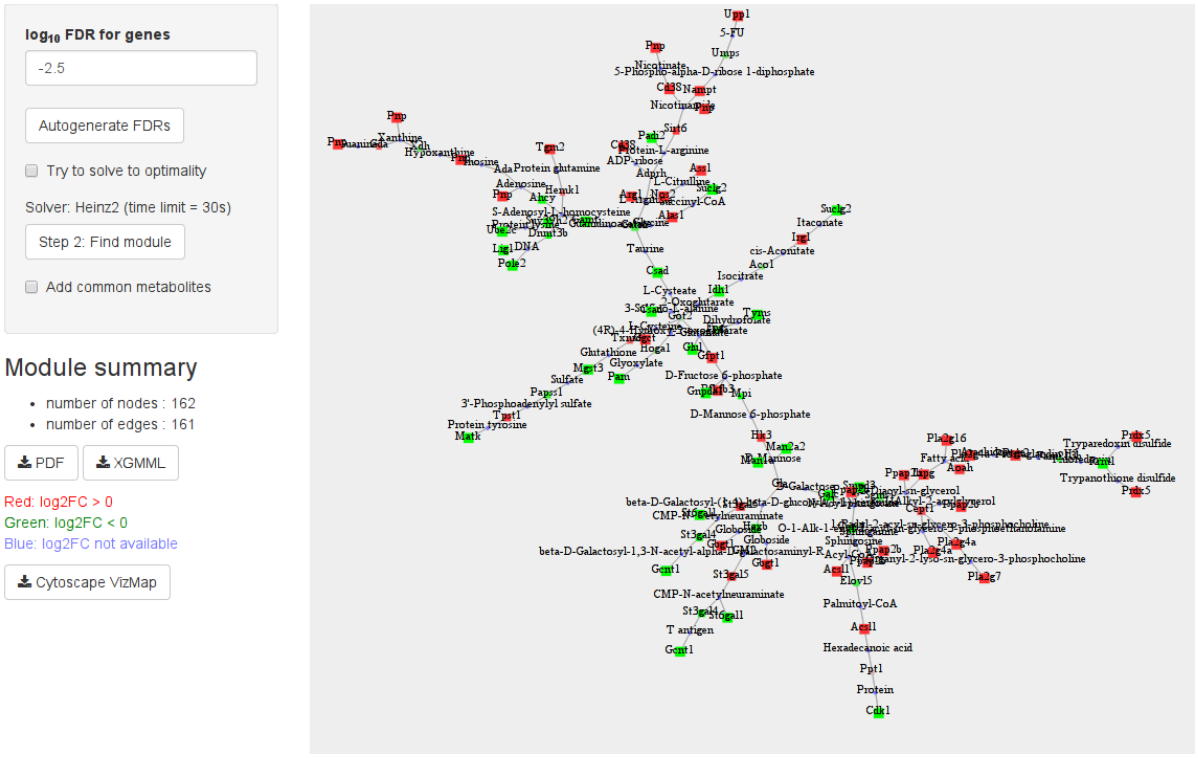

Fig. 4. GAM-module for transcriptional data only, with reactions mapped to nodes.

Using differential expression for both genes and metabolites

Figures 5 and 6 show modules found for both metabolic and transcriptional data for flow-centric (default for such data, Fig. 5) and gene-centric (Fig. 6) mapping strategies. All four pathways: the TCA cycle, glycolysis, urea cycle and lipid synthesis) are present here.
Red color corresponds to up-regulation in M1, green corresponds to down-regulation. Size of nodes and edges corresponds to -log(p-value). Circular nodes represent metabolites, square nodes represent reactions. Blue nodes represent instances without p-values, e.g. undetected metabolites. Parameters were set to: gene $\log_{10}$ FDR = -4.6 for flow-centric approache and $\log_{10}$ FDR = -2.5 for gene-centric approach, metabolite $\log_{10}$ FDR = -2.9, absent metabolite score = -7.1. As a post-processing step, trans-RPAIR connections were added (marked with dashed lines).

Fig. 5. GAM-module for both metabolic and transcriptional data, with reactions mapped to edges.

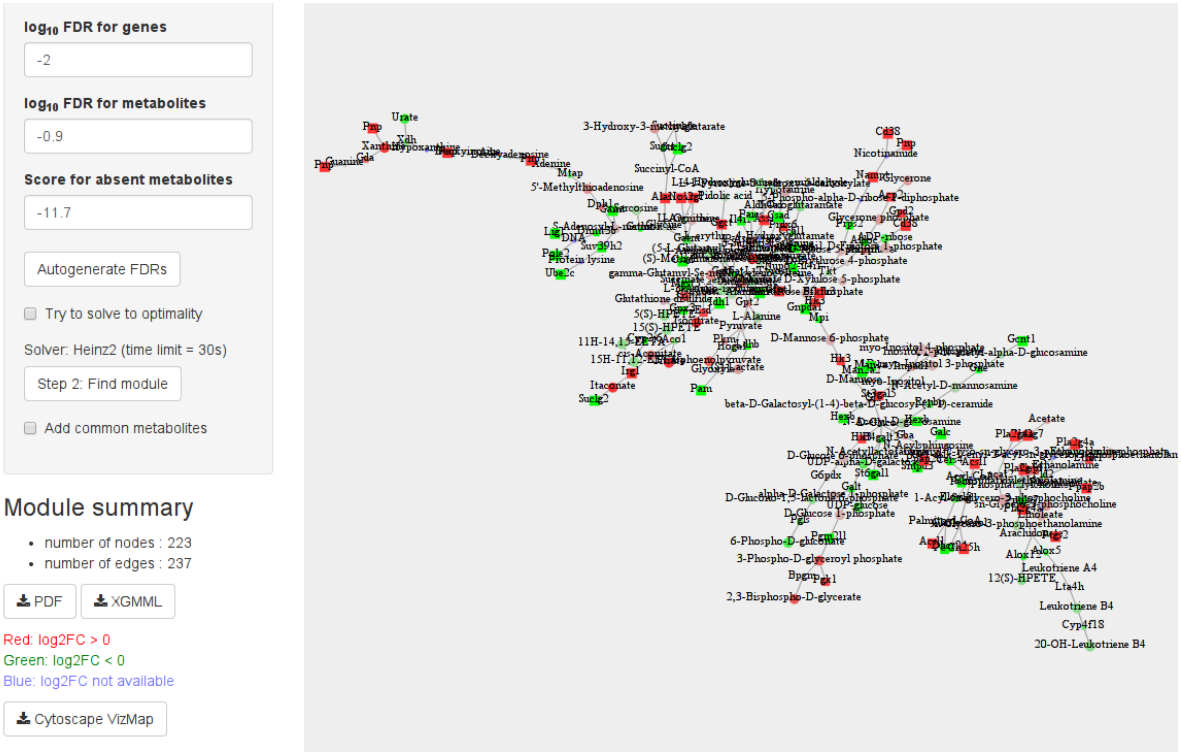

Fig. 6. GAM-module for both metabolic and transcriptional data, with reactions mapped to nodes.