

GAM: a computational pipeline for integrated transcriptional and metabolic network analysis

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Integrated analysis

- Progress of omics profiling technologies
- Metabolic
 - What metabolite concentrations are in cells?
 - Corresponds to a network of biochemical reactions
- Transcriptional
 - How genes are expressed in cells?
 - Corresponds to reactions via enzymes

Numbers

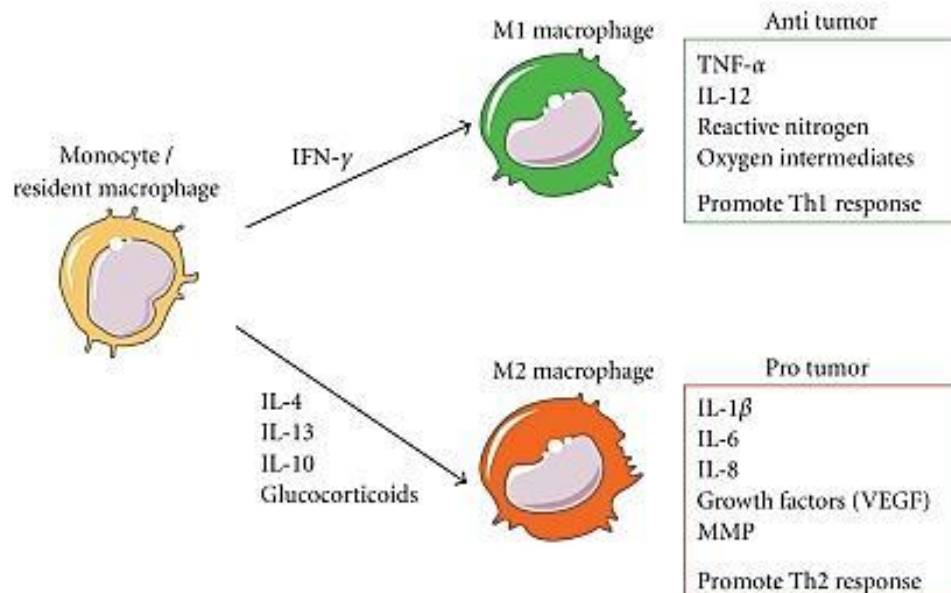
- ~2000 reactions for a species
- Metabolic profiling
 - ~500 metabolites
 - ~50-100 of them look regulated
- Transcriptional profiling
 - ~1000 expressed enzymes
 - ~300-500 of them look regulated

Integrated view

- Find a set of connected reactions that contains most regulated enzymes and metabolites
- Reducing to problem of finding maximum weight connected subgraph (MWCS)
 - It is NP-hard but there are solvers (or not)

Macrophages

- Type of immune cells:
 - Resting M0 macrophages
 - Proinflammatory M1 macrophages
 - Antiinflammatory M2 macrophages



KEGG REACTION database



REACTION: R01786

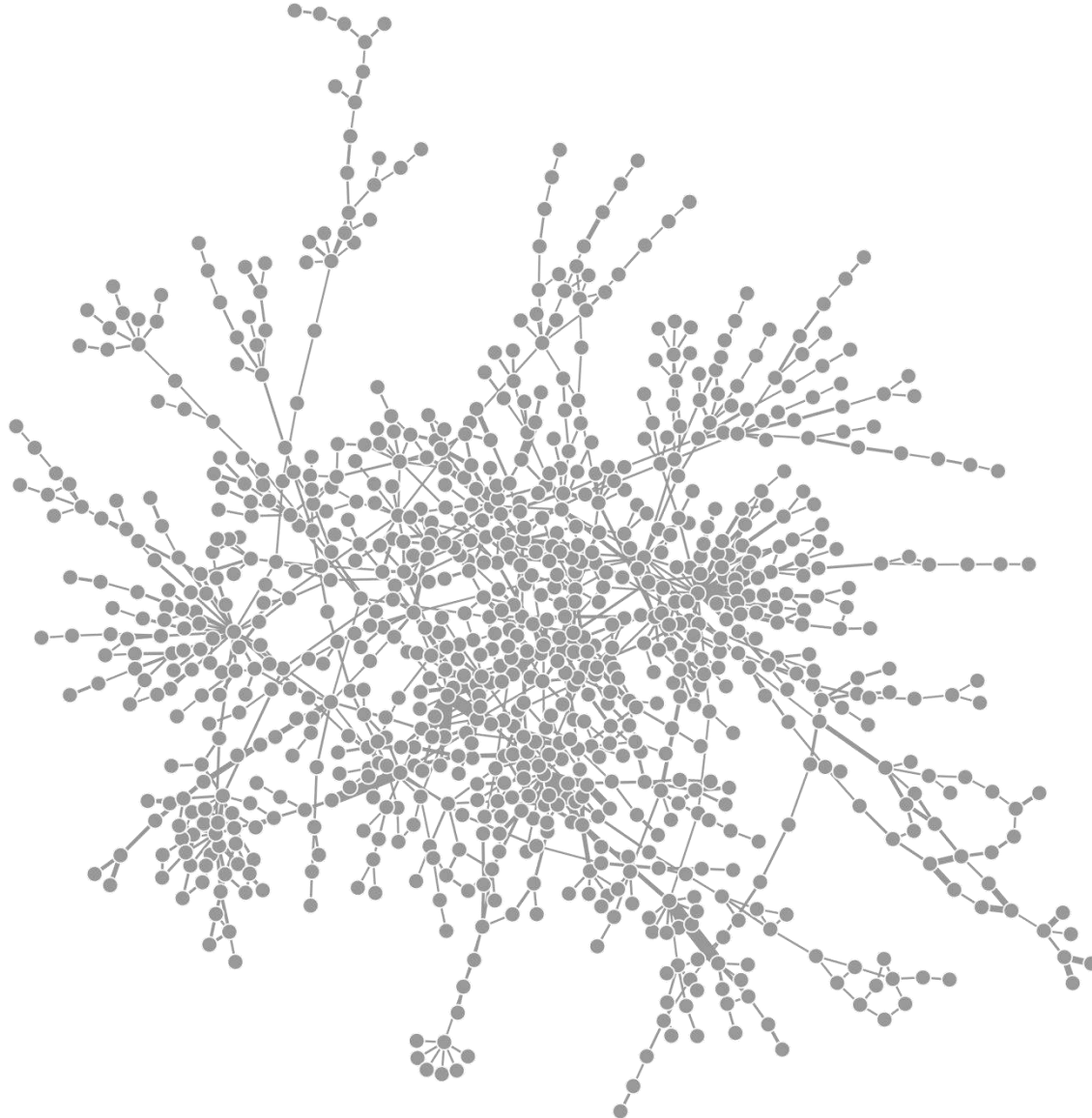
Help

Entry	R01786	Reaction
Name	ATP:alpha-D-glucose 6-phosphotransferase	
Definition	ATP + alpha-D-Glucose <=> ADP + alpha-D-Glucose 6-phosphate	
Equation	C00002 + C00267 <=> C00008 + C00668	
RPair	RP00003	C00002_C00008 main
	RP00216	C00267_C00668 main
	RP06708	C00002_C00668 trans
Enzyme	2.7.1.1	2.7.1.2
Pathway	rn00010 Glycolysis / Gluconeogenesis rn00052 Galactose metabolism rn00500 Starch and sucrose metabolism rn00520 Amino sugar and nucleotide sugar metabolism rn01100 Metabolic pathways rn01110 Biosynthesis of secondary metabolites rn01120 Microbial metabolism in diverse environments rn01200 Carbon metabolism	
Orthology	K00844	hexokinase [EC:2.7.1.1]
	K00845	glucokinase [EC:2.7.1.2]
	K12407	glucokinase [EC:2.7.1.2]

Mapping reaction network to a graph

- MWCS works with simple graphs (without hyperedges)
- Network of reactions is complex
- Bimolecular reactions:
 - Reactions as nodes (+ collapsing connected reactions sharing an enzyme)
 - Reactions as edges (+ RPAIRS)

Raw reaction graph



Scoring graph

- Assigning weights based on p-values from differential expression:
 - Significantly changed metabolites/reactions get positive weight
 - Insignificantly changed metabolites/reactions get negative weight

Weighted graph

Here was a figure

Module

Here was a figure

Major regulatory subnetwork of M1 vs M2

Here was a figure

Major regulatory subnetwork of M1 vs M2

Here was a figure

New modules

Here was a figure

Conclusion

- A pipeline to systematically look at transcriptional and metabolic data together **(and separately)**
- It produces a nice picture of most regulated reactions
- It allows to discover new modules
 - Jha et al. “Network integration of parallel metabolomic-transcriptional data reveals novel metabolic modules regulating divergent macrophage polarization” (to be published)
- However,

Questions

- How to properly handle isomers in metabolic profiling?
- How to properly handle reactions with the same enzyme?
- How to get more (statistically) significant results?
- How to get more meaningful results?
 - Combine with flux balance analysis?

Availability

- A web-service at <https://artyomovlab.wustl.edu/shiny/gam/>
 - Feedback is welcome!
- An R-package to be released
 - Is available now upon a request

References

- Dittrich, M.T. et al. (2008). Identifying functional modules in protein–protein interaction networks: an integrated exact approach. *Bioinformatics*, 24(13), i223-i231.
- Beisser, D., et al. (2012). Integrated pathway modules using time-course metabolic profiles and EST data from *Milnesium tardigradum*. *BMC systems biology*, 6(1), 72.
- Xia, Jianguo, et al (2013). "INVEX—a web-based tool for integrative visualization of expression data." *Bioinformatics* 29(24), 3232-3234.

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