

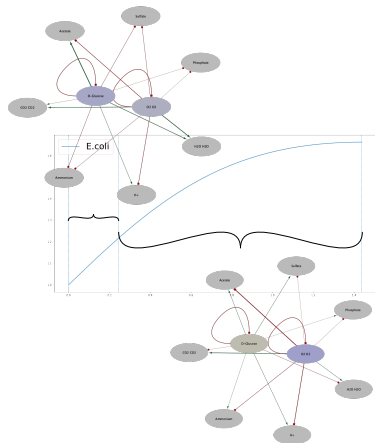


# MetConSIN

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# MetConSIN



During simulated growth of *E. coli*, we observe two distinct networks of interactions between metabolites (as mediated by *E. coli*).

## Idea

Simulating a microbiome (microbes & external metabolites) using genome scale metabolic models provides a dynamically changing network of interactions.

Using GEMs constructed from metagenomic data, MetConSIN will allow us to

- Understand the interactions of microbes & metabolites in a microbiome.
- Predict & manipulate microbial community composition.
- Predict & manipulate microbiome metabolite production.

