

Modeling microbiota-wide metabolism with MICOM

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from the **ISB Microbiome Course 2020**



Let's get the slides first (use your computer, phone, TV, fridge)

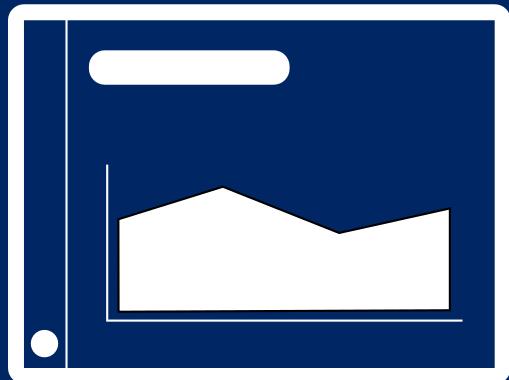
https://gibbons-lab.github.io/isb_course_2020/micom



Quick reminder

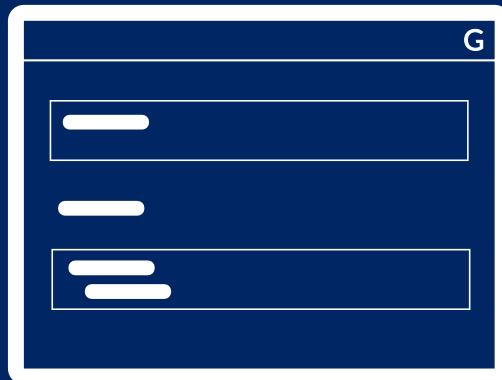


Presentation



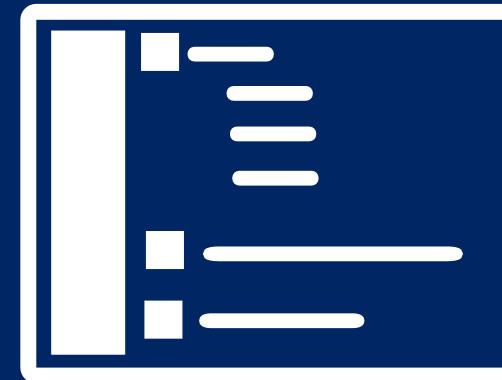
logic
explanations
links

Notebook



technical aspects
materials
visualizations

Chat



support
Q&A

Functional analyses

Tries to predict what the microbiome **does** from sequencing data.

Uses gene abundances (metagenomics, PICRUSt) or metabolomics.

Yields metabolic **capacity** or **potential**.

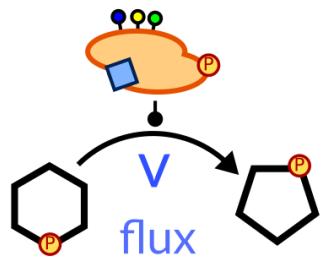


Genes and metabolite abundances are cool but
not what you really care about*

hot take 🔥

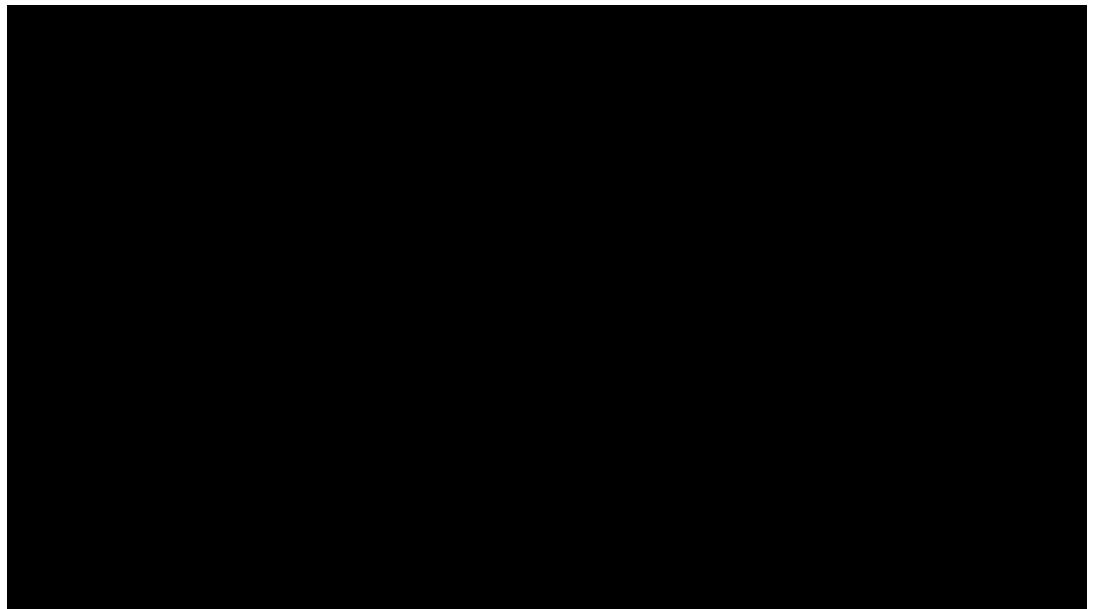


Fluxes



- rate of mass conversion
- unit is mmol/(gDW·h)
- difficult to measure
- targeted temporal ^{13}C or ^{15}N

video courtesy of [S. Nayak](#) and [J. Iwasa](#)



Flux Balance Analysis

Can we infer the most likely fluxes in a biological system?



The flux cone



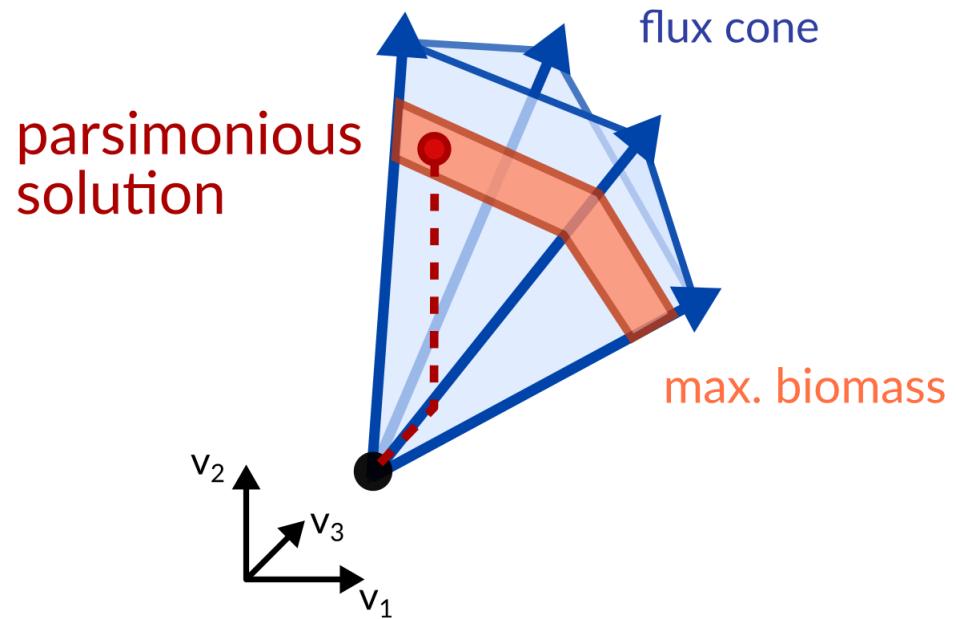
The goal of FBA is to **reduce** the flux space to a **biologically relevant** one.



Genome-scale metabolic modeling



Selecting biological relevant fluxes via parsimony



Reproduces experimental fluxes in *E. coli* very well.



MICOM





Let's continue with our data



Let's switch to the notebook...



Community-wide growth is hard 😢

In a single genome-scale model we only have a single growth rate μ . In a microbial community we have several μ_i and a community growth rate

$$\mu_c = \sum_i a_i \cdot \mu_i$$

What so hard? Can't we just maximize the community growth rate? Well...

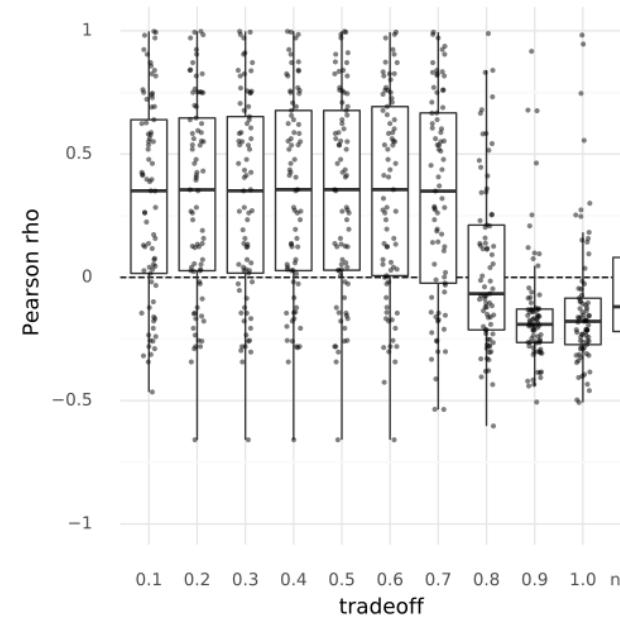
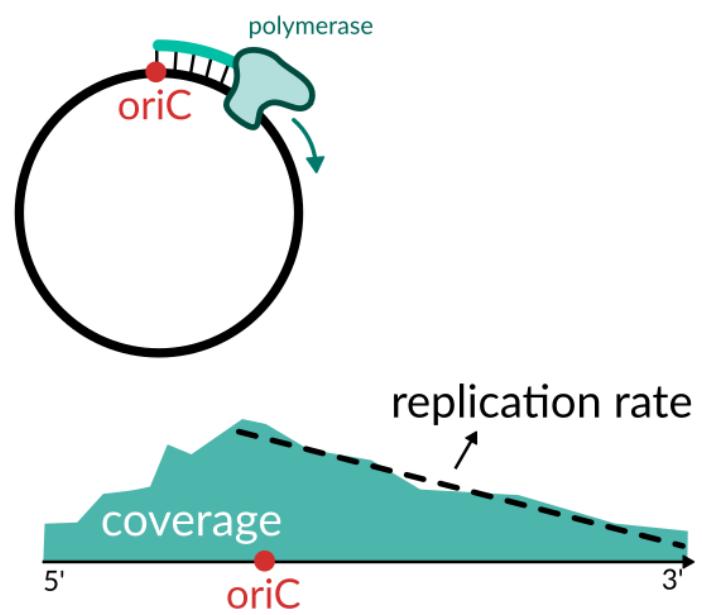
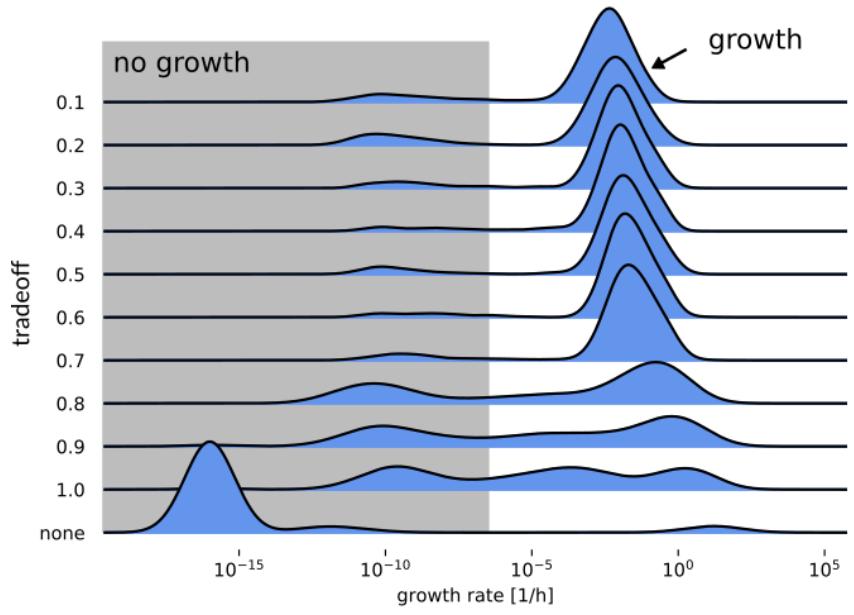
When 2 leads to infinity...



Cooperative Tradeoff FBA allows us to treat metagenome-scale models with the **same** methods as genome-scale metabolic models (pFBA, minimal media, etc).



But does it work?



Easy peasy. What's taking so long then?

Well, metagenome-scale models are slightly larger... 





The niche space



Metabolic connections with disease



We observed that the **overall production flux** $v_p = \sum a_i \cdot v_i^{ex}$ associates the most with the phenotype.

This is the flux the **intestinal cells** can interact with.



Your turn

Check out how to use MICOM for a “n-of-1” analysis.



And we are done 🙌

Thanks!

