

MOFA: Microbial Optimization without Forced Altruism

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This tutorial demonstrates the use of the MOFA algorithm to compute the maximum community growth rate in a microbial community. (MOFA.py)

Requirements

To run this tutorial, the COBRA Toolbox and Pyomo must be installed in the Python environment.

- `pip install cobra` (or `python -m pip install cobra`)
- `pip install pyomo` (or `python -m pip install pyomo`)
- `pip install numpy`
- `pip install pandas`

Prepare Input data and models

In this tutorial, MOFA is used. Please define the path to the directory containing the species' metabolic network files and specify the biomass reaction name of each species.

- `SAVEDIR = Path("D:\\ models")`
- `models_name = ["model1.xml", "model2.xml"]`
- `biomass_id=['biomass536_species1','biomass525_species2']`

After calling the `add_model_to_community()` function, the species models are merged to build the community model. You can then set the diet as demonstrated in `MOFA_GutMicrobiome.py`. Finally, run `MOFA.py` to compute the maximum community growth rate.