Learning Metabolic Goals from Omics Data

This project involves developing scalable optimization algorithms to learn the "goals" of microbial and human cells. These goals are studied in the context of metabolism and protein expression, and they are learned from multi-omics data types including fluxomics, transcriptomics, proteomics, and phenotyping across many growth conditions.

This project will produce new computational tools that can improve our ability to model cells operating with complex metabolic objectives. Examples of such cells include drug-resistant microbes, and human tissue that are difficult to model in both healthy and diseased states using conventional modeling approaches.

The project requires expertise in two areas: (1) genome-scale models of cell metabolism, possibly extending to protein-constrained / macromolecular resource-allocation models, and (2) nonlinear optimization and distributed algorithms.

The areas of expertise are described in greater detail below:

(1) Genome-scale models of cell metabolism:

- Expert in flux balance analysis and basic COBRA methods requiring solution of LP, QP, MILP
- Experience using protein-constrained models is a strong plus (i.e., molecular crowding, MOMENT, RBA, ME)
- Experience in analyzing omics data (RNA-Seq, proteomics, fluxomics, growth rates), and integrating omics data with constraint-based models
- Proficiency in programming languages: e.g., Python, Matlab, R

(2) Nonlinear optimization and distributed algorithms:

- Expert in formulating a nonlinear optimization models given an engineering/scientific problem, and solving it using appropriate solvers
- Experience in developing an optimization solver is a plus (e.g., implementing a first- or second-order method)
- Experience in implementing parallel / distributed algorithms using OpenMP, MPI, OpenACC, etc. is a definite plus
- Proficiency in programming languages: e.g., Python, Matlab, R, GAMS/AMPL, Fortran, C/C++