Exercise set # 4 for the course
"Networked Dynamical Systems"

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1. **Flux Balance Analysis**

   The file `MetabolicNetwork.mat` contains a Matlab structure (called `network`) with the metabolic network of central metabolism of the bacterium *E.coli*. The stoichiometric matrix is the field `network.S`: columns correspond to reactions and rows to metabolites. The fields `network.lower_bound` and `network.upper_bound` contain lower and upper bounds on the reaction fluxes. The structure also has a "biomass" reaction, indexed by `network.index_biomass`. This reaction will be used as cost function to be used for the optimization of growth.

   - What is the maximal biomass achievable by this model (i.e. what is the value of the cost function in the flux vector that solves the LP problem)?

   - How many reactions are active at the optimum you found?

   - Is the optimal flux vector unique? Can you write an algorithm that checks the existence of degenerate optimal solutions?

   - FACULTATIVE: Can you even estimate how many?

   - A "knock-out" can be represented in this model as imposing 0 flux on a certain reaction. This can be obtained by putting lower and upper bound equal to 0 for that reaction. In some cases, when a reaction is missing the organism cannot grow (that reaction is hence called "essential" for the growth). How many essential reactions are there in the E.coli central metabolism?