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Computational Systems Biology
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Assignment 4

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1 Elementary Flux Modes

We want to investigate some properties of growth-related elementary flux modes computed for a metabolic model of the bacterium *Escherichia coli*. The model comprises 115 reactions and 97 metabolites and is capable of describing cellular growth on glucose. The time-consuming task of calculating the elementary flux modes (EFMs) for this setting has already been performed. A MATLAB file (and a json file for Python) is available on the course homepage containing a structure `mnet` with metabolite names, reaction names and formulas, stoichiometric matrix and 53,942 EFMs.

Please analyze the given pathways in the following way:

a) Are all constraints (reversibility/steady state) met by all EFMs?

b) Calculate the number of growth-related elementary flux modes. Note that an (artificial) biomass reaction `mue` is contained in the network, subsuming all necessary components of biomass. The following statement returns the index of the biomass reaction in MATLAB: `find(strcmp(mnet.reactionNames, 'mue'))`

c) Plot the length (cardinality of support) distribution of (i) all EFMs and (ii) the growth-related EFMs into one bar chart (use the 'hold on' command after plotting the first bar chart for this purpose). How do they differ?

d) Compute the reaction participation, i.e. the number of EFMs per reaction divided by the total number of EFMs, only considering biomass relevant modes. Which reactions are essential for biomass production on glucose uptake?

2 Minimal Cut Sets

You have already computed the minimal cut sets (MCSs) of size one in (d) of the previous exercise.

a) Compute all *synthetic lethals*, i.e. all MCSs of size two, only considering pathways enabling biomass production. Does any essential reaction occur in an MCS of size two? Why (not)?

b) Why is it difficult to compute MCSs of size $k \geq 3$?

Submission:

Please address any questions to

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