

Exercise 1

As shown before, there are several human metabolic models. For this work we will be using the redHuman GEM for Recon2. Download the zip file in this link <https://we.tl/t-687118La9g> and add the contents to your home/desktop.

- a) Open the model in Python using the `load_matlab_model` function.
- b) Get information about the biomass, PFK reactions, ATP in cytosol and glucose extracellular.
- c) Run a FBA for the model.
- d) Run a pFBA for the model. What are the main differences between the two optimizations (fluxes, reactions, metabolites)?
- e) Knockout the drain associated with **glucose**. Optimize the model. What happens?
- f) Find the essential reactions for the model after knocking out the previous reaction. What are the differences when compared with the “regular” model?

Exercise 2

We have shown several types of omics data which can be used to reconstruct a tissue specific model. For this exercise, we will use the breast cancer cell lines present in the CCLE panel.

- a) Read the file containing the information with the *pandas* package.
- b) Calculate the mean for 3 different genes.
- c) Select the 'ACH-000019', 'ACH-000028', 'ACH-000349' samples. With them, reconstruct a tissue model for each with the FastCORE algorithm. Perform FBA and pFBA for all the 3 models reconstructed. Highlight the main differences between them.
- d) Try to reproduce the Warburg Effect (if already not present). Hint: Change the uptake of the oxygen drain to a small value.
- e) Select another random sample. Reconstruct 3 models with different thresholds. What are the main differences?