# 1. Finding a flux distribution

**1.1.**  **Setting up the model:**

A) How many reactions does the model have?

B) How many metabolites?

C) How many measured fluxes should be required to compute a solution?

**1.2 Sanity checks and consistency checks:**

A) How many reversible reactions are there in the model? Besides the model.rev field, how else can you see in the model whether a reaction is mathematically defined as reversible in the model? Are there inconsistencies in the two sources of reversibility information for any reactions?

B) Give the names of all the reversible reactions in the model and whether they *should be* reversible according to textbook, databases or literature.

C) Introduce the necessary manual modifications in the model to correct the reversibilities.

**1.3.  Determined problem:**

A) Can you solve the system as if it is determined? Explain why.

B) What is the rank of the matrix, what can be concluded from this? What are the *real* degrees of freedom and what does this signify?

**1.4.  Undetermined problem:**

A) Show all exchange rates in the model as a bar plot (both uptake rates and production rates) and indicate the corresponding units. What can be observed?

B) Comment on how much ATP is being produced/consumed in different pathways, and do the same for NADH and NADPH. Include all figures and describe what you observe.

# 2. Testing objective functions

Show all exchanges fluxes from the different objective functions in a single barplot. Compare the simulation results. In each case, are the results expected? Why?

# 3. Changing growth conditions

Show all exchange fluxes in a single bar plot. Discuss which fluxes are higher in each case and why do you think that is from a biological point of view. And what are the values for the biomass yield [g biomass/g carbon source] in each case?

# 4. *In silico* genetic modifications(bonus question):

List 3 genes that the model shows are essential for growth. Explain why each of these are essential when looking at the metabolic network and explain how you have identified these 3 genes.