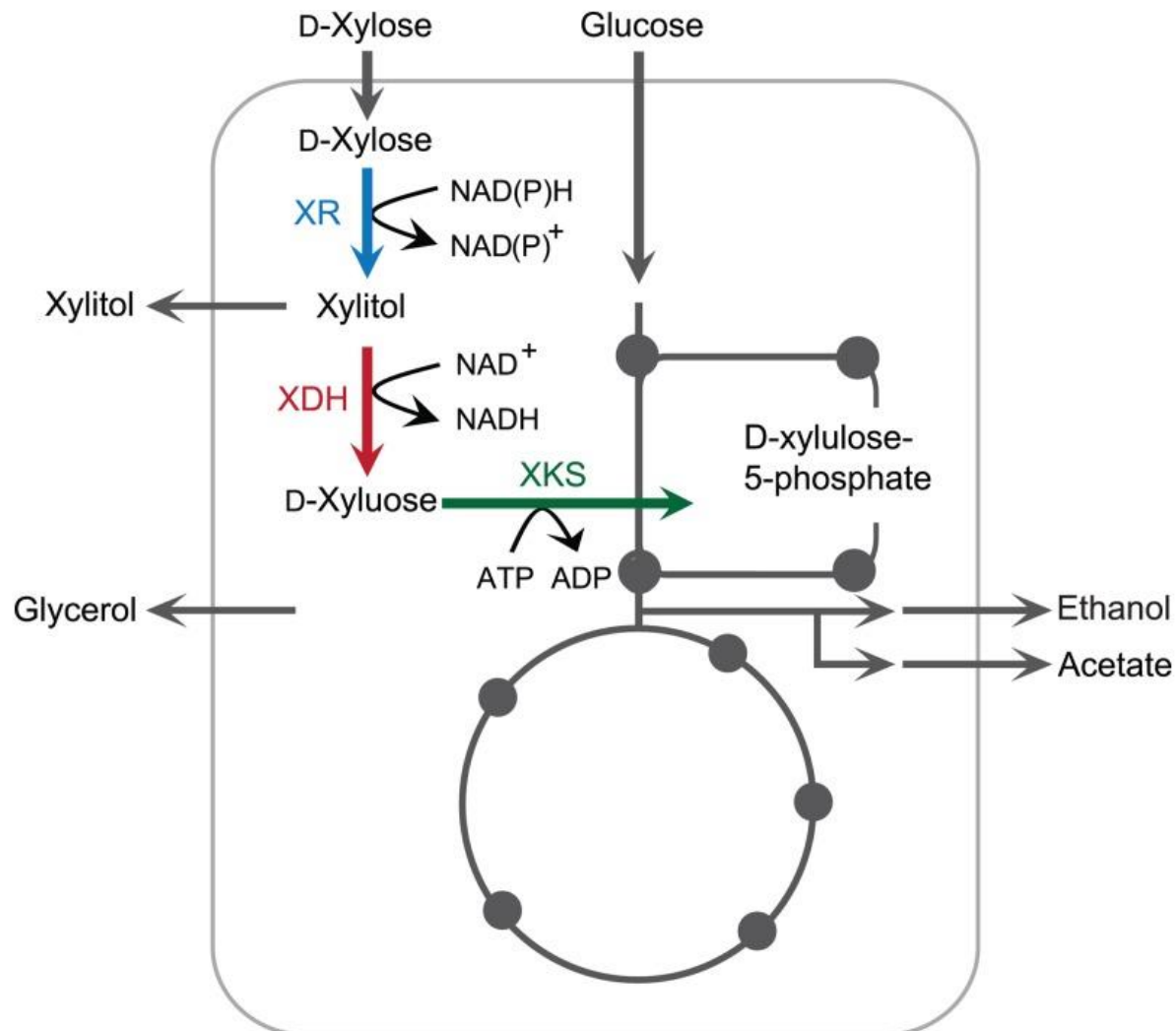


Exercise 1

The yeast *Saccharomyces cerevisiae* grows with glucose as carbon source, which is fermented into ethanol and acetate. Recent studies have tried to produce ethanol using xylose instead of glucose.

The yeast can consume xylose (5C sugar) after a genetic modification: insertion of the XR-XDH pathway. However, xylitol is often accumulated and secreted to the extracellular space, and the pathway is limited by cofactor availability.



1. In this exercise, we will be using the iMM904 *S. cerevisiae* model (Mo et al 2009). Load the model with COBRApy.
<http://bigg.ucsd.edu/models/iMM904>
2. Set the following environmental conditions.
 - a. "EX_glc__D_e": (-10,1000),
 - b. "EX_xyl__D_e": (0,0),
 - c. "EX_epist_e": (-1000,1000),
 - d. "EX_epistest_SC_e": (-1000,1000),

- e. "ERGStt": (-1000,1000),
 - f. "EX_ergstest_SC_e": (-1000,1000),
 - g. "EX_fecost_e": (-1000,1000),
 - h. "EX_lanost_e": (-1000,1000), #sterols
 - i. "EX_lanostest_SC_e": (-1000,1000),
 - j. "EX_zymst_e": (-1000,1000),
 - k. "EX_zymstest_SC_e": (-1000,1000),
 - l. "ERGtETROLter": (-1000,1000),
 - m. "EX_pc_SC_e": (-1000,1000),
 - n. "EX_ptd1ino_SC_e": (-1000,1000),
 - o. "EX_o2_e": (0,0)
3. Perform a simulation with pFBA. What is the flux of the reactions associated with the XR-XDH pathway?
 - a) "XYLR"
 - b) "XYLTD_D"
 - c) "XYLK"
 - d) "RPE"
 - e) "EX_etoh_e"
 4. Block the glucose consumption and enable the xylose uptake ($10 \text{ mmol} \cdot \text{gDW}^{-1} \cdot \text{h}^{-1}$). Run a pFBA simulation and check the flux of the reactions mentioned above. The xylulose is completely catabolized through this pathway?
 5. How many essential genes does the iMM904 model have? What about essential reactions?
 6. Using the *pandas* package, load the gene expression data file (*gene_expression_data.txt*).
 7. For each condition in the dataset, integrate the transcriptomics data into the model, using the GIMME algorithm (check MEWpy git-hub - <https://github.com/BioSystemsUM/mewpy/blob/master/src/mewpy/omics/integration/gimme.py>), and check the flux of the reactions of the XR-XDH pathway. Are they different from the original simulations?