Expanded genome-scale model of *Haemophilus influenzae*

Background

H. influenzae is a pathogenic bacterium, which colonizes the nasal microbiome of humans (see depiction in Fig. 1). *H. influenzae* can cause multiple diseases and hence has high priority in pathogenic research. It can cause inflammation in a weakened immune system and lead mayor infections of the respiratory tract. Therefore, providing a reliable model of *H. influenzae* can help to understand the mechanisms of the bacterium and designing new antibiotics. Based on the work of Schilling *et al.* in 2000 [2], the most comprehensive model to date includes 546 biochemical reactions and 448 species. This model provides metabolic pathways, but due to new research regarding *H. influenzae*, there are more pathways to add, so that the validity of this model can be maintained, to use it as new research basis for drug and antibiotic design.

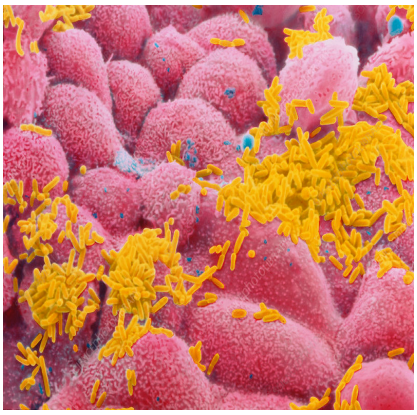

Fig. 1 | *Haemophilus influenzae.* Colored Scanning Electron Micrograph (SEM) of bacterial clusters (yellow) on human nasal lining (pink). Courtesy of Dr. Tony Brain / Science photo library.

Specific Aims

The goal of this thesis is to update the model of *H. influenzae* which is available from [1] to contain more metabolic pathways and hence provide more information. On the updated model, analysis, e.g., FBA or FVA will be performed, in order to collect and verify the information of the newly added metabolites and reactions. Using COBRApy [3], the model will be prepared and expanded to the up to date status of biological research considering *H. influenzae*. Through the different nutrition, it is hoped to collect data about essential amino acids or specific media so that the growth of the models can be minimized. By collecting this information, we can create a model which can be used as a basis in order to discover antibiotics in the future. Considering not every detail of the metabolism might be available for *H. influenzae*, related bacteria will be considered to fill crucial gaps. In the end, a metabolic map of the newly added metabolic pathways using Escher can be created.

Requirements

Python programming and understanding the COBRApy environment, enthusiasm for computational system biology, great sense for detail in comparing the different versions of the *H. influenzae* model [1], drawing networks with Escher or Krayons4SBGN.

References

[1] Schilling CH, Palsson BO. Assessment of the metabolic capabilities of *Haemophilus influenzae* Rd through a genome-scale pathway analysis. J. Theor. Biol. 2000 Apr; 203(3): 249-283 Department of Bioengineering, University of California, San Diego, La Jolla, CA 92093-0412, USA.

[2] Schilling CH, Letscher D, and Palsson BO. Theory for the systemic definition of metabolic pathways and their use in interpreting metabolic function from a pathway-oriented perspective. Journal of Theoretical Biology, 203(3):229 – 248. https://doi.org/10.1006/jtbi.2000.1073.

[3] Ebrahim, A., Lerman, J., Palsson, B. and Hyduke, D. (2013). COBRApy: constraints-Based Reconstruction and Analysis for Python. *BMC Systems Biology*, 7(1),p.74. https://doi.org/10.1186/1752-0509-7-74