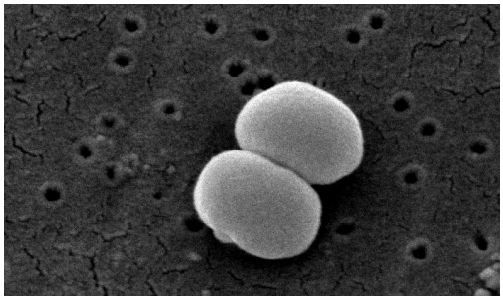
Reconstruction and Analysis of *Staphylococcus epidermidis*

Bachelor Thesis

Background and Motivation



https://de.wikipedia.org/wiki/Staphylococcus_epidermidis#/media/Datei:Staphylococcus_epidermidis_lores.jpg

Staphylococcus epidermidis is a Gram-positive, coagulase-negative (CoNS) bacterium that is carried asymptomatically on the skin and mucous membranes of virtually all human beings. It is a major cause of nosocomial infections and associated with invasive procedures (Méric et al., 2018). Virulent *S. epidermidis* strains contaminate indwelling medical devices, such as catheters or implants (Sabaté Brescó et al., 2017), showing pathogenicity traits, e.g., biofilm formation, cell toxicity, or methicillin resistance (Méric et al., 2018). Apart from that, even the low-virulent, low-biofilm forming strain of *S. epidermidis* ATCC 12228 was shown to form a biofilm under decreased oxygen conditions (Uribe-Alvarez et al., 2015). As a member of the skin and mucosal microbiome, *S. epidermidis* prevents the colonization of *Staphylococcus aureus* (Otto, 2011). Its well-studied metabolism and the ability to grow on known media make *S. epidermidis* a possible reconstruction candidate. During the winter term 2019/20, an initial reconstruction of a genome-scale metabolic model (GEM) of *S. epidermidis* was performed by the group of three students (Alsahan, Jin, Grekova). The model was created using CarveMe (Machado et al., 2018) and the *S. epidermidis* ATCC 12228 strain sequence.

Aim

This thesis focuses on the creation and extension of the comprehensive and extensive GEM of *Staphylococcus epidermidis* by incorporating further information from KEGG (Kanehisa, 2000), BioCyc (Karp et al., 2017), and the Path2Models model (Büchel et al., 2013). QC/QA (quality control/quality assurance) techniques will be applied to validate the model. Since *S. epidermidis* is a part of the nosocomial bacterial community, the ability to grow on the synthetic nasal medium SNM3 (Krismer et al., 2017) is under consideration. Literature and laboratory data (if available) will be studied to obtain statistically meaningful properties of the solution space using the sampling technique. Reported interactions with other bacteria, such as *Staphylococcus aureus*, will be simulated and analyzed numerically.

Requirements

Experience in Python and appropriate libraries, such as COBRApy (Ebrahim et al., 2013) and libSBML (GitHub, 2020) for constraint-based reconstruction and analysis of *in-silico* models. Passion for systems biology, especially the constraint-based modeling approach.

References

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