



Master Thesis in Bioinformatics

Towards a Consensus Genome-scale Reconstruction of *Corynebacterium glutamicum* ATCC 13032

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1 Background and motivation

Corynebacterium glutamicum ATCC 13032 is a Gram-positive, non-pathogenic, facultative anaerobic actinobacterium [9]. It often grows as a V-shaped cell pair [14]. The genus *Corynebacteria* is part of the healthy skin flora and often occurs in moist regions [4]. The species *C. glutamicum* is a soil bacterium [9, 10]. Some other species of *Corynebacterium*, such as *C. accolens* or *C. pseudiphtheriticurn* [11], are part of the nasal microbiome [13].

Within the genus *Corynebacteria*, *C. glutamicum* takes a unique function and position. *C. glutamicum* has been described as an industrial workhorse [16]. This characterization is due to its essential function in the industrial production of L-amino acids (mostly L-glutamate and L-lysine) and other derived products [15]. Since its genome is already successfully sequenced [5], highly specific metabolic engineering, e.g., improved amino acid production [15], is possible. At this point, several genome-scale metabolic models (GEMs) of *C. glutamicum* ATCC 13032 are published (e.g., [7, 12]). In order to enable further work on the metabolism of *C. glutamicum* ATCC 13032, it is highly desirable to possess an upgraded, standardized and extended GEM for this strain.

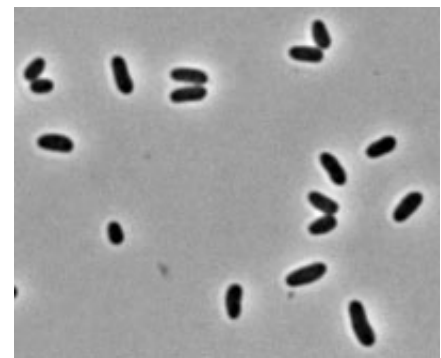


Figure 1 | de.wikipedia.org/wiki/Corynebacterium_glutamicum

2 Aims of the thesis

The focus of this thesis is to extend existing GEMs of *C. glutamicum* ATCC 13032 by incorporating additional information from biological databases such as KEGG [6] or Path2Models [2] to create a standardized GEM of *C. glutamicum* ATCC 13032 using libSBML [1] for Python. Moreover, this thesis aims at finding a consensus model for the strain *C. glutamicum* ATCC 13032. In order to validate the model, established measures of quality, such as the memote score [8], will be applied.

3 Requirements

In order to successfully perform a constraint-based reconstruction and subsequent analysis of *in silico*-models, experience in Python and additional libraries, such as COBRApy [3] or libSBML [1] are necessary. Also, a passion for systems biology with a particular focus on the constraint-based modeling approach is helpful.

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