

Metabolic network reconstruction of the pathogen *Enterococcus faecalis*

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MOTIVATION:

Enterococcus faecalis is a Gram-positive bacterium that is getting more attention due to its “two-face” behavior. This natural inhabitant of the gastrointestinal mammalian tract is also an opportunist pathogen responsible for urinary tract infections, nosocomial infections, bacteremia and infective endocarditis (1).

BACKGROUND:

Since the metabolic reconstruction of *Haemophilus influenzae* was published in 1999 (2), many other researchers have focused their attention into the possibilities that the new era of genome-scale metabolic models could bring to the scientific scene, both in prokaryotic and eukaryotic organisms.

METHODS:

It is essential to establish a methodology for any metabolic reconstruction. A detailed explanation of the procedure is described on the chapter 29 of reference 3. Figure 1, schematically represents the process of the metabolic reconstruction for *E. faecalis*.

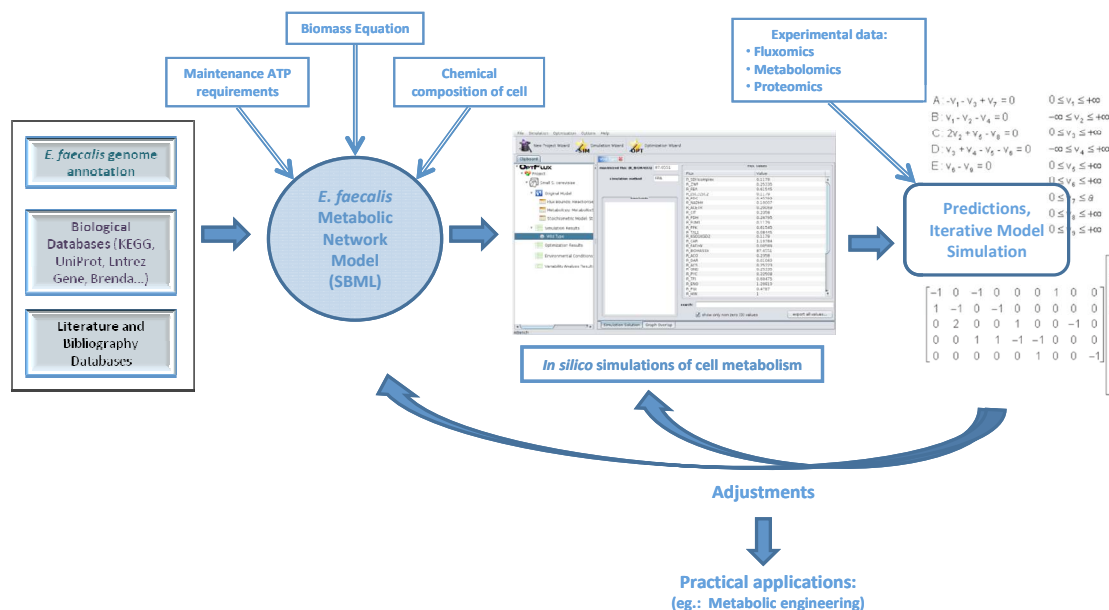


FIG. 1: Metabolic network reconstruction of *Enterococcus faecalis*.

REFERENCES:

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2. Pálsson, Bernhard O., and Edwards, Jeremy S. Systems Properties of the *Haemophilus influenzae* Rd. 18 June 1999.
3. Rocha, I., Förster, J., and Nielsen, J. Design and Application of Genome-Scale Reconstructed: Protocols and Bioinformatics (A.L. Osterman, Gerdes, S., Eds.). In series: Methods in Molecular Biology, Vol. 416, Ch. 29, 409-431, Humana Press 2008 .