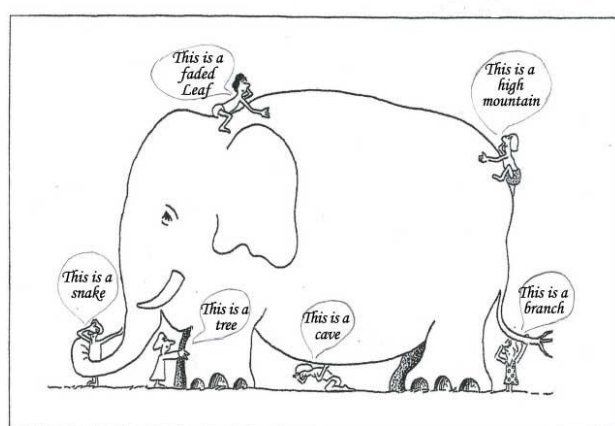


Master thesis project

Systematic evaluation of gap-filling methods in constraint-based metabolic model

Background

The traditional reductionist approach in biology has collected detailed information on individual components of biological systems. Systems biology questions how this detailed information on components relates to the organism as a whole because “the whole is more than the sum of its parts” (Figure).



6 blind men describe an elephant (old indian fable)

Among system biology approaches, Genome-scale metabolic models (GSMM) are powerful tools to study the metabolism of an organism. GSMM are constructed by drafting a model from an automatic tool; followed by a manual curation process. The main purpose of the later step is to eliminate the “gaps”, a so-called gap-filling process. A gap represents a missing metabolic function that is likely to present in the target organism. There are many methods that have been developed to support the gap-filling process. These methods differ in algorithm and parameters and result in different candidate reaction(s). Hence, it is crucial to determine which method eliminates gaps and produces a model in the most suitable biological context.

Goal

The goal of this project is to thoroughly analyze the main methods and algorithm for gap-filling.

Project outline and tasks

- (a)** Literature research to identify available methods for gap-filling
- (b)** Design and perform a small-scale case study (*in-silico* experiment) to apply identified methods to some model organisms
- (c)** Compare and evaluate the performance of these methods

Methodology

In-silico experiments will be carried out using either the COBRAToolbox or COBRAPy _ a MATLAB or Python package for implementing Constraint-based Reconstruction and Analysis methods.

Requirements

The student should be familiar with programming (preferable Matlab or Python) and with solid background in biology.

References

1. Thiele, I. and B.Ø. Palsson, A protocol for generating a high-quality genome-scale metabolic reconstruction. *Nature protocols*, 2010. 5(1): p. 93-121.
2. Hosseini, Zhaleh, and Sayed-Amir Marashi. "Discovering missing reactions of metabolic networks by using gene co-expression data." *Scientific Reports* 7 (2017).

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