



COMPUTATIONAL BIOLOGY WEBINAR @ IMSc

REVERSE MODELING METABOLIC NETWORKS

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The growth performance of microbial populations can be studied by an information-theoretic approach relating the mean single-cell growth yield ('fitness') to the entropy of the growth-yield distribution ('information'). Within Mass-Balance models, one finds that, for any value of the information, the achievable fitness is strictly bounded, leading to a theoretical "rate-distortion curve" in the (information,fitness) plane. Next, values of fitness and information for E.coli populations can be inferred from experimental mass spectrometry data probing growth in different conditions. For a large number of experimental datasets, inferred points robustly approach the theoretical bound as the quality of the growth medium improves. Besides giving insight into the interplay between metabolism and gene expression, this approach can yield information that is currently inaccessible by other methods, both in silico and experimental.

GOOGLE MEET LINK:

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