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iMAT: An Integrative Metabolic Analysis Tool

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ABSTRACT

Summary: iMAT is an Integrative Metabolic Analysis Tool, enabling the integration of transcriptomic and proteomic data with genome-scale metabolic network models to predict enzymes' metabolic flux, based on the method previously described by (Shlomi, Cabili et al. 2008). The prediction of metabolic fluxes based on high-throughput molecular data sources could help advance our understanding of cellular metabolism, since current experimental approaches are limited to measuring fluxes through merely a few dozen enzymes.

Availability and Implementation: http://imat.cs.tau.ac.il/

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Supplementary information: Supplementary data are available at *Bioinformatics* online.

1 INTRODUCTION

Modern genomic sequencing technologies have enabled the rapid reconstruction of metabolic networks, giving rise to more than 50 highly curated metabolic reconstructions published to date (Oberhardt, Palsson et al. 2009), spanning all three domains of life including Eukaryota, Bacteria, and Archaea. Additional computational methods to automatically reconstruct metabolic network models have recently resulted in draft network reconstructions for 160 microbial species (Henry, DeJongh et al. 2010). Such reconstructed metabolic network models have been commonly used for metabolic phenotype prediction, metabolic engineering, studies of network evolution, and biomedical applications (Oberhardt, Palsson et al. 2009). These studies employ various constraint-based modeling (CBM) methods to analyze the network function by solely relying on simple physical-chemical constraints (Price, Reed et al. 2004).

Utilizing gene and protein expression to predict metabolic flux is a challenging task due to the complex mapping between the two. Previous studies have found a strong qualitative correspondence between gene expression and measured (Daran-Lapujade, Jansen et al. 2004) as well as predicted (Famili, Forster et al. 2003) metabolic fluxes in microbes. However, the correlation between expression and metabolic flux is generally moderate and in some cases significant transcriptional changes do not reflect changes in flux, and vice-versa, significant changes in measured flux may not reflect transcriptional changes (Ovacik and Androulakis 2008). These discrepancies may result from post-transcriptional regulatory processes that effect the actual levels of enzymes translated and from metabolic regulation, representing the effect of metabolite concentrations on the actual enzyme activity through allosteric and mass action effects (Rossell, van der Weijden et al. 2006).

Several CBM methods for analyzing and predicting metabolic flux distributions based on gene expression data have been suggested previously. The methods of (Åkesson, Förster et al. 2004; Becker and Palsson 2008) use gene expression data to identify genes that are absent or likely to be absent in certain contexts and search for metabolic states that prevent (or minimize) the flux through the associated metabolic reactions. (Shlomi, Cabili et al. 2008) consider data on both lowly and highly expressed genes in a given context as cues for the likelihood that their associated reactions carry metabolic flux, and employ constraint-based modeling (CBM) to accumulate these cues into a global, consistent prediction of the metabolic state. The latter method was shown to accurately predict human tissue metabolism, based on tissue-specific gene and protein expression data. Its application has demonstrated that in many cases, the activity of genes responsible for metabolic diseases is not directly manifested in enzyme-expression data, though can still be correctly predicted by expression integration with the metabolic network. The implementation of the method based on (Shlomi, Cabili et al. 2008) involves solving multiple, complex Mixed-Integer Linear Programming (MILP) optimization problems, requiring extensive parallel computing resources, and hence has not been readily accessible for the research community since its publication.

Here, we present an integrative metabolic analysis tool (iMAT) that is a web-based implementation based on the method of Shlomi et al. The new tool will serve the community by enabling the prediction of the metabolic state of an organism in a specific condition given pertaining gene and protein expression data. We provide below a high-level description of the iMAT server with an illustrative example of applying it to a toy model.

2 TOOL DESCRIPTION

The usage of iMAT is straightforward. The input is gene and/or protein expression data for a certain organism. The output is a

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visualization map of the organism's metabolic state, showing the most likely predicted metabolic fluxes across its reactions. iMAT supports the integration of functional data with an array of different existing metabolic CBM models, including: (i) a highly curated metabolic network model of human metabolism (accounting for ~1500 genes) by (Duarte, Becker et al. 2007), enabling the prediction of metabolic activity under various tissues and cell-types; (ii) common model organisms such as *E. coli* and *S. cerevisiae* (accounting for ~1300and ~800 genes, respectively); and (iii) an array of automatically reconstructed networks for 160 bacteria (Henry, DeJongh et al. 2010) (for a list of supported organisms, see the iMAT website); (iv) user submitted models in either SBML or matlab format. For any of the organisms in this list, iMAT enables the prediction of metabolic activity under various environmental and genetic conditions.

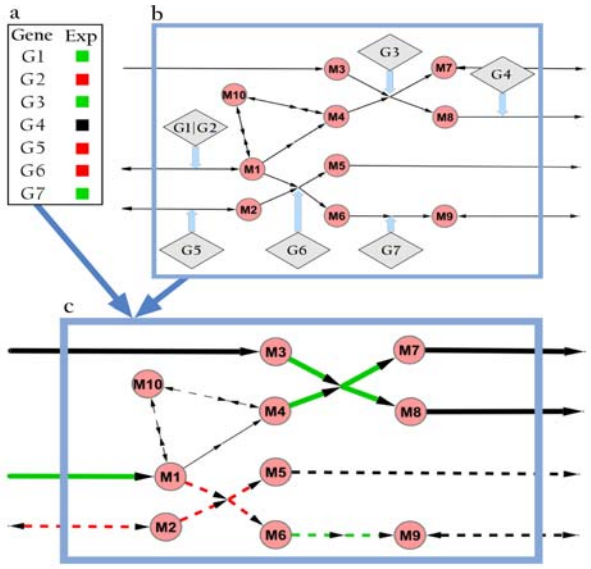
The gene and/or protein expression data submitted to iMAT should be in the form of discrete tri-valued expression states, representing either low, moderate, or high expression in the condition studied. If continuous data is submitted, iMAT will perform discretization automatically. Various parameters can be tuned to control the discretization of the raw input values (see section 2, supplementary information).

Given the target species metabolic model and gene or protein expression data, iMAT predicts a flux activity state for each reaction in the model, reflecting the presence or absence of its associated metabolic flux. For some of the reactions, the flux activity state can be uniquely determined to be active or inactive, with associated confidence estimations. For others, the activity state cannot be uniquely determined because of potential alternative flux distributions with the same overall consistency with the expression data due to isozymes or alternative pathways. In cases where the predicted flux activity of reactions deviates from the given expression state of the corresponding enzyme-coding gene, the corresponding gene is considered to be post-transcriptionally up-or-downregulated.

iMAT provides as output the predicted flux activity state and the corresponding confidence values over all network reactions in both tabular and network visualization forms. The network visualization displays the relevant transcriptomic and proteomic data given as input, as well as the predicted metabolic flux, superimposed on top of the organism's metabolic network, employing the publicly available Cytoscape software (Cline, Smoot et al. 2007). To further facilitate the interpretation of the predicted flux activities, iMAT performs a pathway enrichment analysis, reporting the significant active and inactive pathways comprising the metabolic profile signature of the biological experiment studied. In addition, iMAT reports predicted post-transcriptionally up and down regulated genes.

3 TOY MODEL EXAMPLE

Fig. 1. An illustrative example of applying iMAT to a toy metabolic network (shown in b) given gene expression data (where green (red) denotes high (low) expression and black denoting an intermediate level, as depicted in sub-figure (a)). Circular nodes represent metabolites, edges represent biochemical reactions, and diamond-shaped nodes represent enzyme-coding genes. iMAT's output is an optimal flux distribution (c) that is the most consistent with the input expression data. Reactions associated with highly, lowly or moderately expressed genes are colored in green, red, or black, respectively (c). Solid (dashed) edges represent reactions predicted to be active (inactive). Reactions whose flux activity state is uniquely determined to be active or inactive (across the entire space of alternative optimal flux distributions) are marked with thick edges.



We describe the application of iMAT on a small toy model (Figure 1). The toy model is comprised of 10 metabolites and 13 reactions, including 7 exchange reactions that enable the uptake of substrates and the secretion of metabolic by-products. The predicted flux is consistent with the expression high/low state of 4 of the 5 reactions. One reaction (M6->M9) is predicted to be inactive though its corresponding gene is highly expressed, reflecting the potential effect of post-transcriptional regulation. Of the seven metabolites that can be transported across the membrane boundary in the toy model (M1-3, M5, M7-9), iMAT predicts the uptake of one metabolite (M1) and the secretion of two others (M7 and M8). The reaction M1->M4 is predicted to be active with low confidence, since an alternative flux distribution through M1->M10->M4 in which it is inactivated achieves the same level of consistency with the expression data.

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