Personalized metabolic modeling successfully predicts central metabolic traits of individual normal and cancerous human cells (Ramot)

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The emerging field of personalized medicine encompasses the use of marker-assisted diagnosis to improve health care. However, computational models describing human physiology on an individual level have yet to be developed.

Here we present a novel algorithm termed PRIME (Personalized ReconstructIon of MEtabolic models), which generates individualized genome scale metabolic models based on molecular and phenotypic data.

The PRIME-derived models are first shown to successfully predict a range of metabolically-related phenotypes, including proliferation rates, gene essentiality, drug responses and metabolic biomarkers measured across an array of individual normal and cancer cell-lines. Second, PRIME-derived models identify known selective drug treatments in cancer and suggest novel ones. Finally, when applied to clinical samples' data, PRIME-derived models of breast cancer patients enhance the prediction of their prognosis, both independently of classical known predictive factors such as the patients' age, histological grade, tumor size, lymph node status and estrogen receptor status, and vs. the prediction obtained using the metabolic gene expression on its own. Overall, PRIME successfully captures some of the phenotypic effects of transcriptomic differences between human cells, laying a promising foundation for future personalized metabolic modeling applications.

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