New Computational Methods for Characterizing Systems Biology of Low Dose and Adaptive Response

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We present preliminary results on a new computational method for systems biology of adaptive response and low dose effect from transcript and phenotypic data. The underlying concept is that a small subset of genes is triggered for each treatment condition or a phenotypic index. The concept of a small subset of genes translates to the sparsity constraint, which is applied computationally. The main advantage of this technique over traditional statistical methods is (i) direct application of sparsity, (ii) incorporating multi-class and multidimensional phenotypic profiles in one framework, and (iii) hypothesizing interaction networks simultaneously. Our method is versatile in that it can construct an association network with either a treatment groups or a phenotypic index that can potentially be quantified through fluorescence microscopy. We have applied our technology to two data sets: (i) the first data set targets differential analysis of adaptive and challenged response in a cell culture model ; and (ii) the second data set targets differential analysis of dose-, adaptive- , and challenged- response in the mouse model. In both cases, preliminary patterns of preferred network activations are hypothesized.

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