Uncovering the Drug Targets of A Complex Disease of Interest Using Fixed Effect Logistic Regression

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It is presently an open question in the discipline of system biology in connection with identifying drug targets of a complex disease of interest on the basis of hundred of data points for thousands or tens of thousands of genes. To address such a question, we have recently been let to a standard statistical model, namely, fixed effect logistic regression, concordant with all known longitudinal or matched case-control data analysis, and free of arbitrary effects due to time shifts and space variations in gene expression. With this approach, one can measure key genes with a complex disease of interest, check their associated proteins and conserved domains, and uncover the underlying pathophysiological phenomena by mapping key molecules onto acknowledged biochemical pathways representing our current knowledge on metabolisms, genetic information processing, environmental information processing, cellular processes and human diseases. As an example, we have reanalyzed a time course gene expression array in connection with a mice experimental model for a current very little known complex disease- interstitial cystitis (IC), and have given system-level impact for the approaching therapeutic strategies of IC.

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