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Pathway-based analysis of gene expression data: method and applications.

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I will first review a "systems approach"to analysis of high throughput large gene expression datasets. The basic idea, of using existing knowledge (assigning genes to biological pathways) to transform gene level information into "coarse-grained"system-level information, has been implemented in Pathifier [1] –an algorithm that infers pathway deregulation scores for each sample, on the basis of expression data. The algorithm generates a compact and biologically relevant representation of each sample, and as an added benefit, eliminates the "curse of dimensionality"and the need for uncontrolled feature selection, that have plagued standard single-gene based analysis.
Pathifier has been used by us [1,2] and many other groups to study cancer [3] obesity [4] and other biomedical problems. In the second part of my talk I will review a few of these recent applications of the method.
[1] Pathway-based personalized analysis of cancer. Yotam Drier, Michal Sheffer, and Eytan Domany, PNAS 110, 6388 (2013)
[2] Pathway-based personalized analysis of breast cancer data. Anna Livshits et al, Molecular Oncology 9, 1471 (2015).
[3] Personalised pathway analysis reveals association between DNA repair pathway dysregulation and chromosomal instability in sporadic breast cancer. Chao Liu et al Molecular Oncology 10, 179 (2016); Network analysis of EMT and MET micro-RNA regulation in breast cancer. Diana Drago-Garcia et al, Scientific Reports 7, 13534 (2017); Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis. Sijia Huang et al Genome Medicine 8, 34 (2016).
[4] Integrative analysis of pathway deregulation in obesity. Francesc Font-Clos, Stefano Zapperi and Caterina La Porta, Systems Biology and Applications 3, 18 (2017).

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