

## Seminar articles

1. D. Hanisch, A. Zien, R. Zimmer, T. Lengauer, Co-clustering of biological networks and gene expression data. *Bioinformatics* **18 Suppl 1**, S145 (2002).
2. T. Ideker, O. Ozier, B. Schwikowski, A. F. Siegel, Discovering regulatory and signalling circuits in molecular interaction networks. *Bioinformatics* **18 Suppl 1**, 233 (2002).
3. I. Ulitsky, R. Shamir, Identification of functional modules using network topology and high-throughput data. *BMC Syst Biol* **1**, 8 (2007).
4. M. Narayanan, A. Vetta, E. E. Schadt, J. Zhu, Simultaneous Clustering of Multiple Gene Expression and Physical Interaction Datasets. *Plos Computational Biology* **6**, (2010).
5. C. J. Vaske *et al.*, Inference of patient-specific pathway activities from multi-dimensional cancer genomics data using PARADIGM. *Bioinformatics* **26**, i237 (2010).
6. I. Ulitsky, A. Krishnamurthy, R. M. Karp, R. Shamir, DEGAS: de novo discovery of dysregulated pathways in human diseases. *PLoS One* **5**, (2010).
7. Y. Prat, M. Fromer, N. Linial, M. Linial, Recovering key biological constituents through sparse representation of gene expression. *Bioinformatics* **27**, 655 (2011).
8. E. Yeger-Lotem *et al.*, Bridging high-throughput genetic and transcriptional data reveals cellular responses to alpha-synuclein toxicity. *Nat Genet* **41**, 316 (2009).
9. S. S. Huang *et al.*, Linking Proteomic and Transcriptional Data through the Interactome and Epigenome Reveals a Map of Oncogene-induced Signaling. *PLoS Comput Biol* **9**, e1002887 (2013).
10. O. Tzfadia, D. Amar, L. M. Bradbury, E. T. Wurtzel, R. Shamir, The MORPH algorithm: ranking candidate genes for membership in Arabidopsis and tomato pathways. *The Plant cell* **24**, 4389 (2012).
11. H. Y. Huang, C. C. Liu, X. J. Zhou, Bayesian approach to transforming public gene expression repositories into disease diagnosis databases. *P Natl Acad Sci USA* **107**, 6823 (2010).
12. P. R. Schmid, N. P. Palmer, I. S. Kohane, B. Berger, Making sense out of massive data by going beyond differential expression. *Proc Natl Acad Sci U S A* **109**, 5594 (2012).