In silico dissection of transcriptomes with a tumor immunology focus

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1. Current MSigDB gene sets do not describe all co-regulated groups of genes as found by our independent components based guilt-by-association framework (this thesis).
2. Clustering metabolic transcriptional activity profiles of patient-derived breast cancer samples does not reproduce groups based on receptor status (this thesis).
3. Spliceosome complex subunits are transcriptionally adapted to maintain pair-wise ratios when affected by copy number alterations, thus maintaining complex integrity in cancer cells (this thesis).
4. Visualizing the expected clinical benefit of anti-cancer treatments helps patients, doctors, and stakeholders make more informed decisions (this thesis).
5. Diphencyprone induces transcriptional changes in the skin comparable to changes caused by anti-Programmed Death protein 1 (PD1) and anti-cytotoxic T-lymphocyte-associated protein (CTLA4) therapy (this thesis).
6. Most copy number alterations of oncogenes in cancer cells occur in extrachromosomal DNA.
7. A multiple-regulon small-effect paradigm is replacing the single-gene big-effect paradigm of disease.
8. Double-blind online competitions to benchmark computational methods are a modern actualization of the scientific method.
9. To seize the means of publication and achieve universal open access, researchers should embrace the internet and fully leverage their collective financial, political, and citation power.
10. Modern computational biology sees further by sitting on the shoulders of Google, Twitter, Github, and StackOverflow.