A systems biology method to predict oncogenes and perturbation targets on a cellular level

Technology #2339

There exists a need for a computational approach to predict oncogenes and key oncogenic relationships responsible for tumor phenotypes on a cellular network level. This technology is a systems biology method for predicting oncogenes and the specific interactions that underlie multiple types of non-Hodgkin B cell lymphomas. The technology analyzes oncogenic interactions from a comprehensive cellular network, such as the B Cell Interactome (BCI), and statistically ranks the genes whose interactions are affected by a phenotype (e.g., disease, tumor and cancer) or perturbation (e.g., drug target). Rankings are based on correlation changes between the expression profiles of gene pairs upon being affected by a phenotype or perturbation.

Cellular network-based strategy predicts molecular interactions implicated in oncogenic pathways

Existing computational methods to identify oncogenes and oncogenic pathways rely on high-throughput technologies to reveal differences between cancer cells and normal cells. These methods focus only on perturbations at the level of genes or gene products. This technology predicts which molecular interactions, as opposed to which genes, are dysregulated in a particular tumor phenotype. The technology’s performance was benchmarked using three well-characterized non-Hodgkin B cell lymphomas (FL, BL, and MCL) having a known causal gene, and also using a biochemical perturbation assay in cell lines stimulated with CD40 ligand or antibody. Experiments demonstrated that this technology consistently outperformed differential expression analysis in identifying key oncogenes, as well as secondary effector genes.

Lead Inventor:

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Applications:

- Prediction of diagnostic markers and/or therapeutic targets for various cancers and other diseases
- Development of personalized diagnostic and therapeutic cancer solutions
- Research tool to generate hypotheses about network interactions in any cellular context
- Generating interactome databases for various cell types

Advantages:

- Considers multiple levels of cellular relationships dysregulated during cancer progression
- Predicts which molecular interactions, as opposed to which genes, are dysregulated in a particular tumor phenotype
- Consistently outperformed existing methods such as differential expression analysis in identifying key oncogenes and secondary effector genes.

Patent Information:


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Related Publications:


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