Visual Computing Forum

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Untangling intracellular signaling network in cancer

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Room 302O1 (former 3137),

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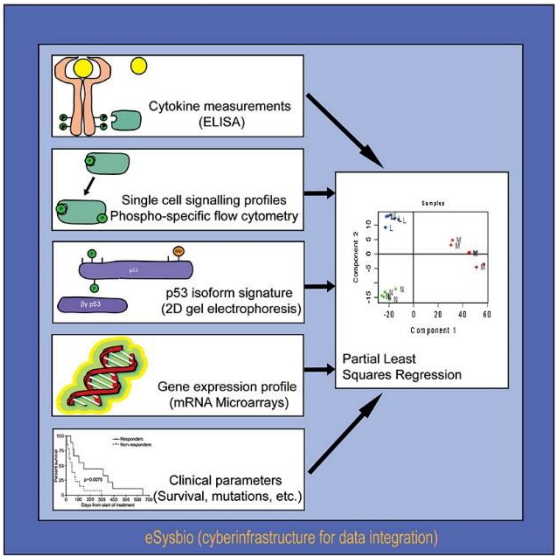
Abstract

Protein and gene networks centered on the regulatory tumor suppressor proteins may be of crucial importance both in carcinogenesis and in the response to chemotherapy. Tumor suppressor protein p53 integrates intracellular data in stress responses, receiving signals and translating these into differential gene expression. Interpretation of the data integrated on p53 may therefore reveal the response to therapy in cancer. Proteomics offers more specific data – closer to "the real action" – than the hitherto more frequently used gene expression profiling.

We are currently working with single cell immune profiles that include information about intracellular signaling systems. Patient cancer cells are sampled before and under therapy to determine response or therapy failure as early as possible, thereby adjusting therapy to the benefit of the patient. Data visualization tools have been imperative for our interpretation of measurements. The question open for discussion is if we need better data visualization tools to easy grasp the dynamics of cancer, and if we have these tools available for visualization with exponentially increasing data density.



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