Adding Structural Resolution to Edges in Protein Interaction Networks to Distinguish Driver and Passenger Mutations in Cancers

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AVAILABILITY OF DATA

During the last decade, we have had revolution in cancer research, thousands of tumors have been collected at Hospitals, and their genomes have been sequenced. By comparing the genome of the cancer to the genome of the patient, it is possible to discover differences, which are unique for the cancer cells. There is a possibility that these differences are mutations that have occurred, and are responsible for driving the disease in the tumor.

ANALYSIS

Cancer is a disease where biological networks have been perturbed, due to many mutations. In order to try to understand how biological networks are affected by mutations, we have decided to focus on deleterious single nucleotide variants (dSNVs) causing missense mutations, occurring in protein-protein interacting sites, for protein pairs with existing three dimensional structure.