Centre for Biosystems Science and Engineering

SEMINAR

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MRDG Seminar Hall

Drug discovery by combining genetics, proteomics and model organisms

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Proteins rarely work alone and deciphering the binding partners is the first step towards understanding its function. We have generated protein-protein interaction (PPI) networks from large scale systematic analyses of the Drosophila and Human proteomes. These networks provide functional connections to thousands of proteins and nearly 80% of them are not known in literature. Disease associated genes have also been found to be localized in the human PPI network. Binding partners and differences between normal vs disease-causing variants can aid researchers in drug discovery and uncover useful biomarkers. Until recently, pursuit of new medicines has been based on the reductionist model of targeting a single disease-associated gene/protein. Network medicine is the opposite: it investigates the interdependencies and propagation of disturbance in the system due to disease. This approach will be helpful for complex diseases with diverse genetic and etiological factors such as neurodegeneration. The challenge is in uncovering and targeting critical points in the network to alter the effects of the underlying mutation/disease. Second site genetic modifiers identified in model organisms may point to such critical points in the network. The interactome provides the molecular framework upon which we can layer large-scale genomics, genetics, expression profiles and other disease-relevant datasets with the aim of expertly navigating and identifying unique drug targets for complex diseases.

https://www.biogen.com/en_us/research-pipeline/biogenscience/gururaj_network-medicine.html

www.be.iisc.in/seminars.html