

## Interactome Networks

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Despite the considerable success of molecular biology to understand diseases such as cancer, many fundamental questions remain unanswered. Most importantly, since the majority of gene products in the cell mediate their function together with other gene products, biological processes should be considered as complex networks of interconnected components. In other words, for any normal biological process, or any disease mechanism, such as cancer, one might consider a “systems approach” in which the behavior and function of such networks are studied as a whole, in addition to studying some of its components individually. The draft of the human genome sequence is likely to help such a transition from molecular biology to systems biology.

Our laboratory uses a model organism, the nematode *C. elegans*, to study the role of protein networks in development and, doing so, develop the concepts and technologies needed for a transition to systems biology. Our goals are to:

- i) generate protein-protein interaction, or 'interactome', maps for *C. elegans* networks involved in development,
- ii) develop new concepts to integrate such interactome maps with other functional maps such as expression profiles (transcriptome), global phenotypic analysis (phenome), localization of expression projects (localizome), etc.... and
- iii) use such integrated information to discover novel network properties.

