



BiRC talk– open to all

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Title: Network biology: large-scale data and text mining

Time: Friday 13 December, 2013: 14:15 - 15:00

Venue: Bioinformatics Research Centre, Build. 1110, Aud. 223, C.F. Møllers Allé 8, 8000 Aarhus C

Abstract:

Methodological advances have in recent years given us unprecedented information on the molecular details of living cells. At the same time hospitals are increasingly collecting detailed information on patients in electronic health records. However, it remains an unsolved challenge to bridge the two and systematically link molecular-level data to their phenotypic consequences at the cellular level such as diseases. One reason for this is that biology is facing the limitations of reductionism: most diseases cannot be attributed to a single gene – they can only be understood at the systems level. Networks have proven to be a very useful abstraction for bridging single-gene and systems-level analysis.

In my presentation I will describe the STRING database (<http://string-db.org>), which scores and integrates evidence from a diverse range of curated databases, raw data repositories, text-mining methods, and computational prediction methods to provide the most comprehensive protein association network possible. I will also introduce a suite of three new web-based resources that use similar techniques, including text mining, to associate the proteins in the STRING network with cellular compartments (<http://compartments.jensenlab.org>), tissues (<http://tissues.jensenlab.org>), and diseases (<http://diseases.jensenlab.org>) to enable systems biology studies of diseases, taking into account both interactions and spatial localization of the proteins.

After the talk there will be beer/soda/coffee and chips in the coffee room on the 4th floor.

<http://birc.au.dk/news-events/>



