Molecular interaction networks controlling neural stem cells

Rupert W. Overall

Institute of Biology, Humboldt University of Berlin, Germany

Gene expression data offer insight into the molecular activity of cells and tissues at an accessible cost. For this reason, large quantities of transcriptomics data have been collected over the last two decades, most of which are available in reusable formats. Whole-transcriptome expression datasets obtained from genetically diverse populations can be used to build correlation networks—and even estimate causal relationships. I will present work from genetic reference populations and transcriptomics experiments, supported by literature mining, and show how interaction networks can be a powerful tool to assist candidate gene discovery and the extension of already-known biological pathways. I will focus on examples from my own work on mouse adult neural stem cells, although the techniques can be applied to many experimental systems. I will also discuss how molecular expression data from additional data sources, including publicly-accessible repositories, can help to strengthen and complete the resulting networks.