Network-based approaches to identify disease-relevant mechanisms

In this talk I will give two examples of the kind of projects we work on as part of Computational and Systems Biology at Biogen. Both examples highlight the use of human data to drive target identification and in building therapeutic hypotheses. In the first example, I will describe a method to identify central “dysregulated” genes from transcriptional data. The method can point to potential non-transcriptional events upstream of the observed transcriptional changes. An application of this method to a human ALS dataset reveals mechanisms that might be potential candidates for therapeutic intervention. In the second example, I will describe our efforts to learn a transcriptional network underlying context-specific eQTLs observed in human monocytes. Analysis of these simulated networks helps identify transcriptional connections important for activation of monocytes, which can then be exploited to identify targets upstream of disease-specific signatures. Time permitting, I will briefly touch upon our ongoing efforts in integrating phenotypic, molecular and literature data to construct therapeutic hypotheses for diseases of interest.