BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

181 Longwood Avenue
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Department of Medicine
Channing Division of Network Medicine

Channing Network Science Seminar
January 18 (Friday), 2019, 11am @ 4th-floor conference room

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Computational Analysis of Gene Regulations in Plants

Abstract: Recent advances in genomic technologies have generated large-scale protein-DNA interaction data for plant species, which constitute complex regulatory networks. However, gene regulations for plant stress response remain poorly understood at system level. Here, we present two computational tools to uncover regulatory information from the networks: 1) CoReg, which aims at identifying co-regulators in large-scale regulatory networks and 2) ConSReg, which combines heterogeneous genomic data and infers condition-specific regulatory interactions. We applied CoReg to a large-scale network of Arabidopsis with more than 2.8 million edges and found that many regulatory modules with common in-coming edges tend to be highly co-expressed, suggesting these modules play key roles in stabilizing stress response in plant species. We constructed stress-response and tissue-specific regulatory maps for Arabidopsis using ConSReg. The result shows that transcription factors can be classified into several distinct groups based on their responses to stress and tissue development.

Reference: Song Q, Grene R, Heath LS, Li S. 2017. Identification of regulatory modules in genome scale transcription regulatory networks. BMC Syst Biol 11

Hosted by Kimbie Glass