



Channing Network Science Seminar

June 12, 2015, 11am @ 5th floor conference room



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Title: Understanding tissue-specificity through static networks

Abstract: Biological systems are organized as networks of genes and proteins, and understanding the structure of these interactions provide valuable insights into collective behavior of systems in unbiased ways, while complementing limitation of single gene-based hypothesis test methods. However interaction networks currently available in public domain mostly consist of static edges screened from in vitro experiments or limited knowledgebase. Here we propose a novel approach to investigate versatile tissue contexts embedded in co-reaction and physical interaction networks of humans. First, we will discuss inference algorithm of link community model (LCM) that extract mixed membership profiles from relatively large biological networks. Ball and Newman originally proposed the LCM with maximum likelihood estimation algorithm. Second, we will consider a modeling approach that relates network features with gene annotations. We modeled mixed module membership profile of vertices with generalized linear model (GLM), and prevent the GLM from overfitting by posing spike-slab prior on effect sizes. Third, we will demonstrate examples of link communities that show tissue-specific patterns in GTEx expression. We will also briefly describe our principled confounder correction and imputation method. Since this project is actively developing, we welcome feedbacks, concerns, and collaborations.

Bio: Yongjin Park is a postdoctoral researcher in Computational Biology group, CSAIL, MIT. Prior to MIT, he worked on community detection problems of possibly multiple biological networks at the Bader Laboratory, Biomedical Engineering, Johns Hopkins University.

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