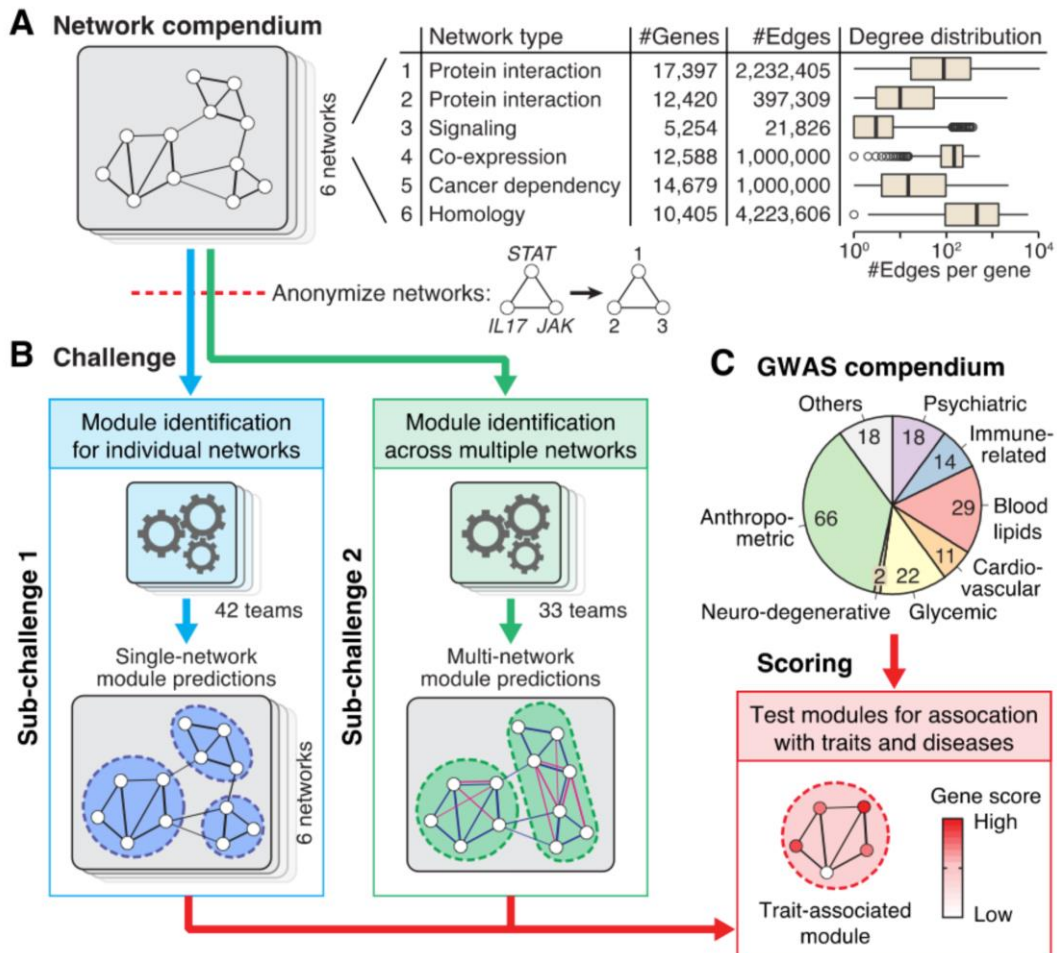# Open Community Challenge Reveals Molecular Network Modules with Key Roles in Diseases

Sven Bergmann[1]

Department of Computational Biology, University of Lausanne & Swiss Institute of Bioinformatics, Switzerland[1]

Identification of modules in molecular networks is at the core of many current analysis methods in biomedical research. However, how well different approaches identify disease-relevant modules in different types of networks remains poorly understood. We launched the "Disease Module Identification DREAM Challenge", an open competition to comprehensively assess module identification methods across diverse gene, protein and signaling networks. Predicted network modules were tested for association with complex traits and diseases using a unique collection of 180 genome-wide association studies (GWAS). While a number of approaches were successful in terms of discovering complementary trait-associated modules, consensus predictions derived from the challenge submissions performed best. We find that most of these modules correspond to core disease-relevant pathways, which often comprise therapeutic targets and correctly prioritize candidate disease genes. This community challenge establishes benchmarks, tools and guidelines for molecular network analysis to study human disease biology.

The full manuscript describing this work is available at: