

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

Sarvenaz Choobdar\*, Mehmet E. Ahsen\*, **Jake Crawford\***, Mattia Tomasoni, David Lamparter, Junyuan Lin, Benjamin Hescott, Xiaozhe Hu, Johnathan Mercer, Ted Natoli, Rajiv Narayan, The DREAM Module Identification Challenge Consortium, Aravind Subramanian, Gustavo Stolovitzky, Zoltán Kutalik, Kasper Lage, Donna K. Slonim, Julio Saez-Rodriguez, Lenore J. Cowen, Sven Bergmann, and Daniel Marbach



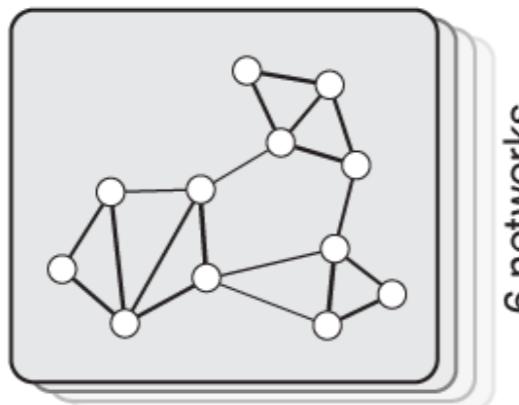
The banner features a background of a network graph with colored nodes and connections, overlaid with a grid of puzzle pieces. The text "Disease Module Identification" and "DREAM Challenge" is prominently displayed in white, with "Discover disease pathways in genomic networks" in a smaller font below. Logos for Unil (Université de Lausanne), SIB (Swiss Institute of Bioinformatics), Joint Research Center for Computational Biomedicine, RWTH Aachen University, IBM, Sage Bionetworks, and Cell are shown at the bottom.

Disease Module Identification  
DREAM Challenge  
Discover disease pathways in genomic networks

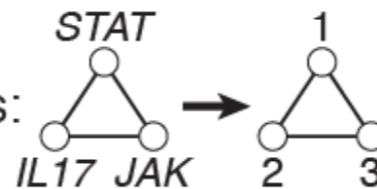
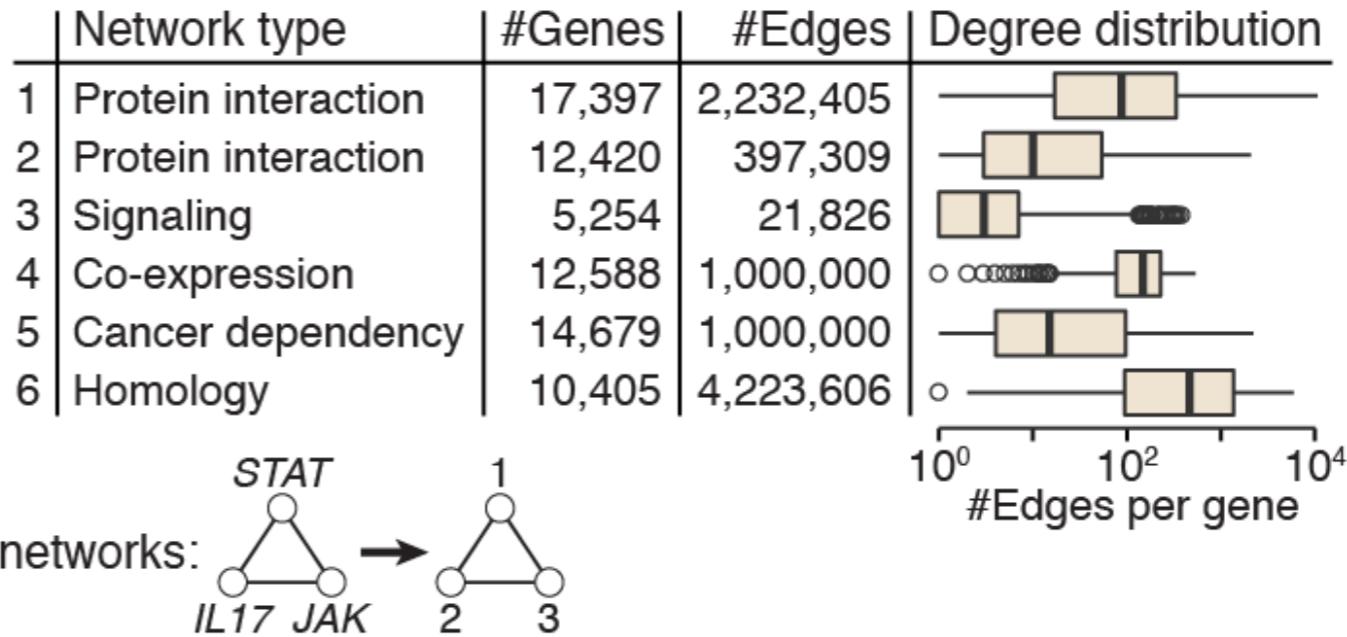
UNIL | Université de Lausanne   SIB Swiss Institute of Bioinformatics   Joint Research Center for Computational Biomedicine   RWTH AACHEN UNIVERSITY   IBM   Sage BIONETWORKS   Cell

DREAM CHALLENGES  
powered by Sage Bionetworks

## A Network compendium



6 networks



Anonymize networks:

## B Challenge

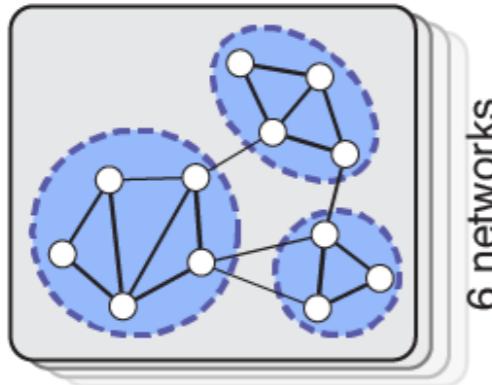
Sub-challenge 1

Module identification  
for individual networks



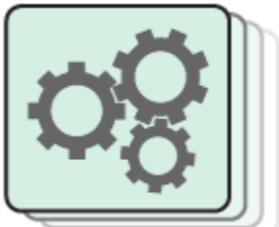
42 teams

Single-network  
module predictions



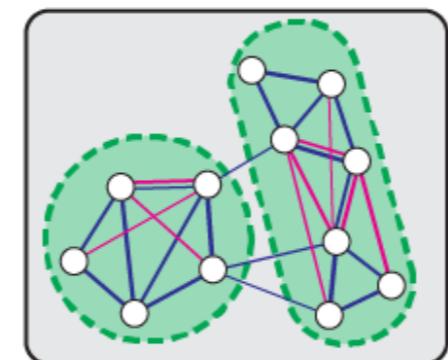
Sub-challenge 2

Module identification  
across multiple networks

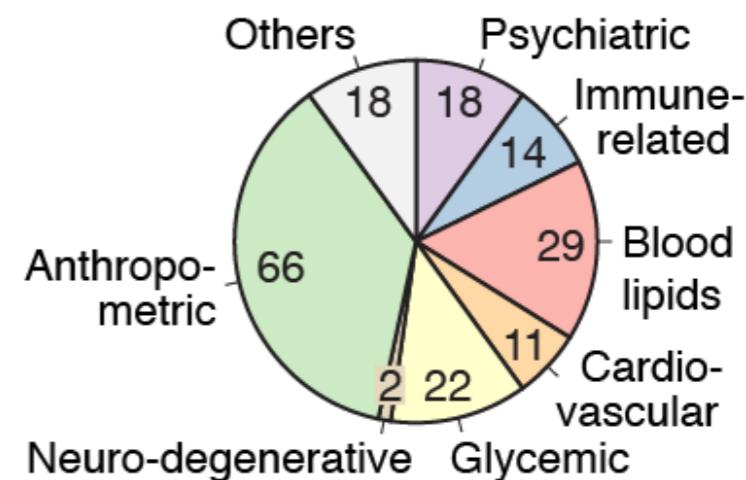


33 teams

Multi-network  
module predictions

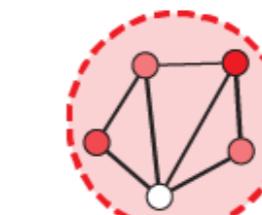


## C GWAS compendium



## Scoring

Test modules for association  
with traits and diseases



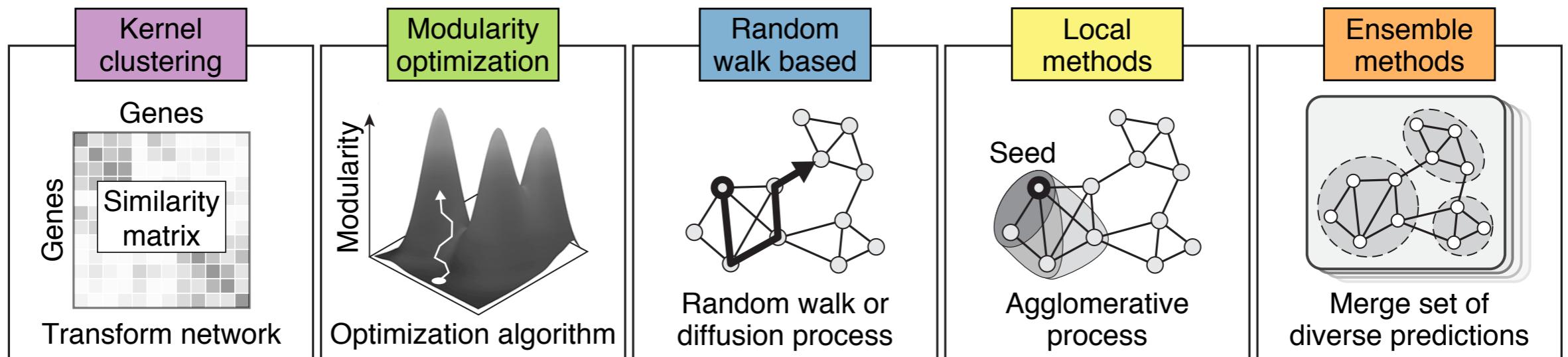
Gene score  
High

Trait-associated  
module

Low

# Results

- 42 teams submitted single-network methods
- Diversity of methods

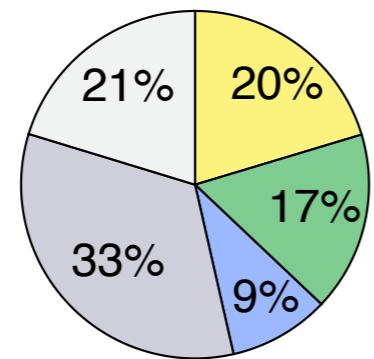


# Results

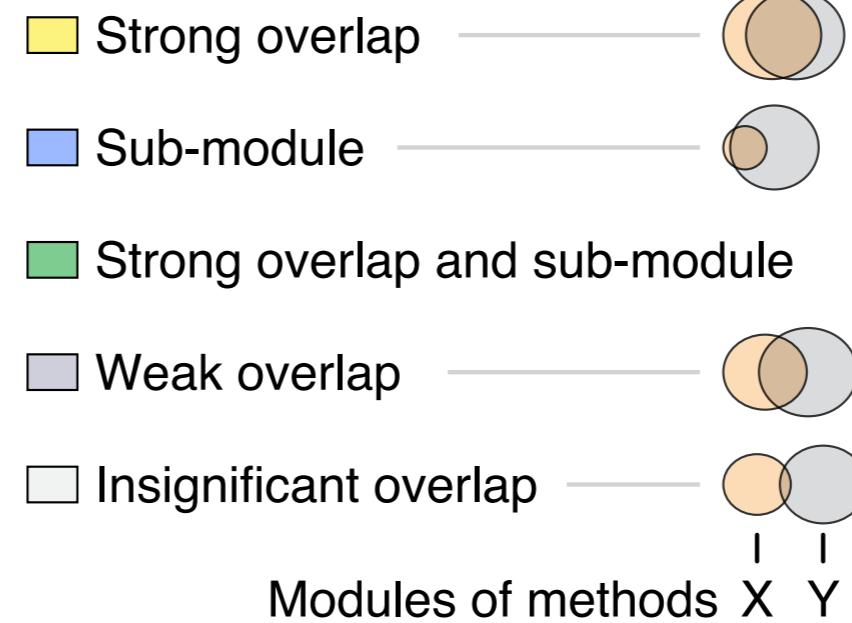
- Methods often find unique trait-associated modules

## Overlap of trait-associated modules between methods

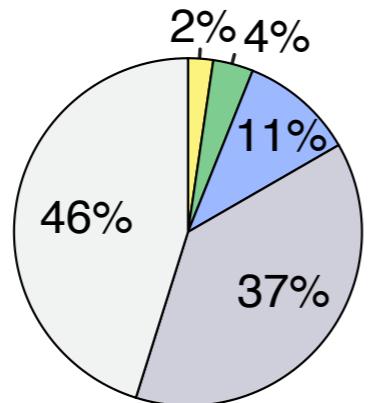
Within networks



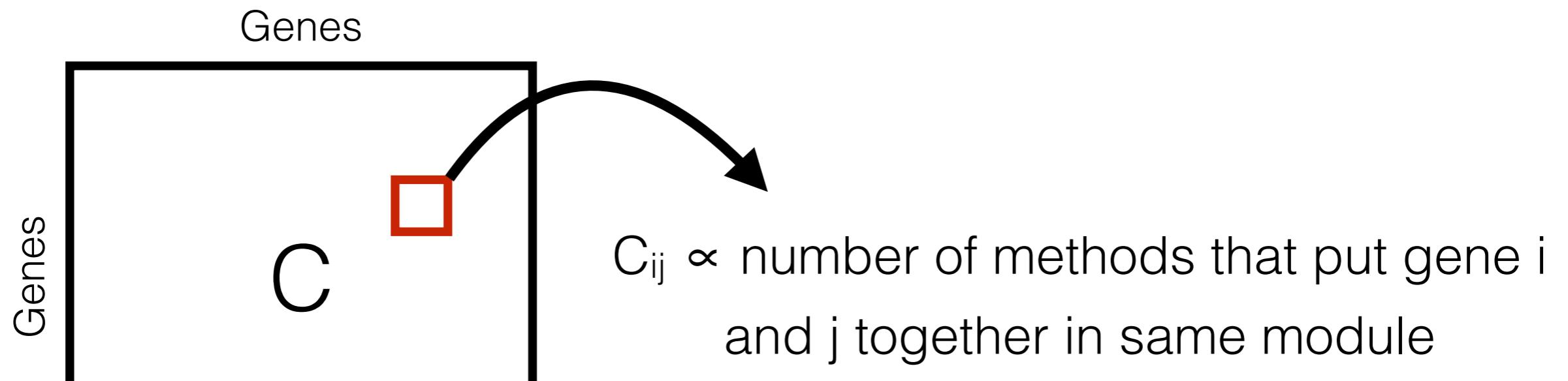
### Type of overlap



Across networks



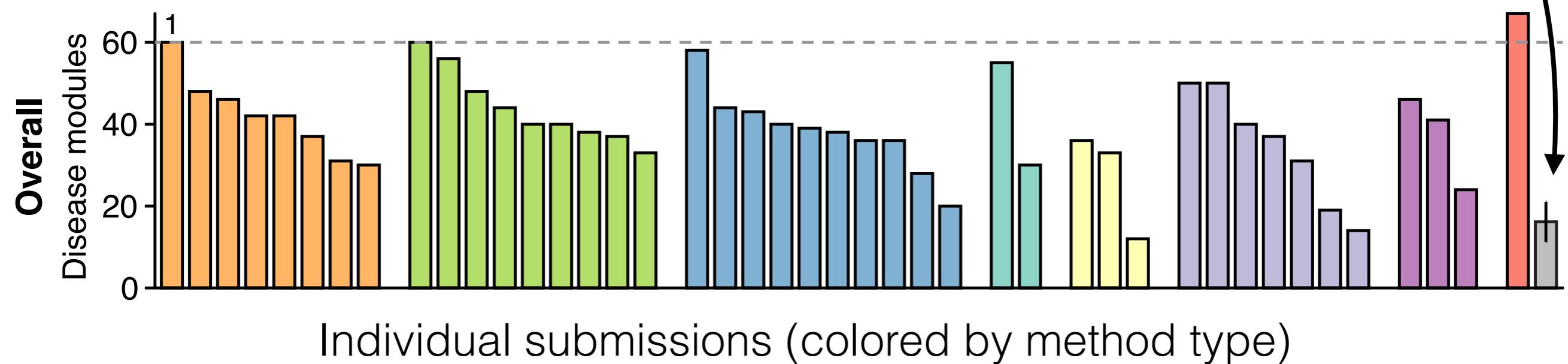
# Consensus predictions



Then, clustered using top-performing method.

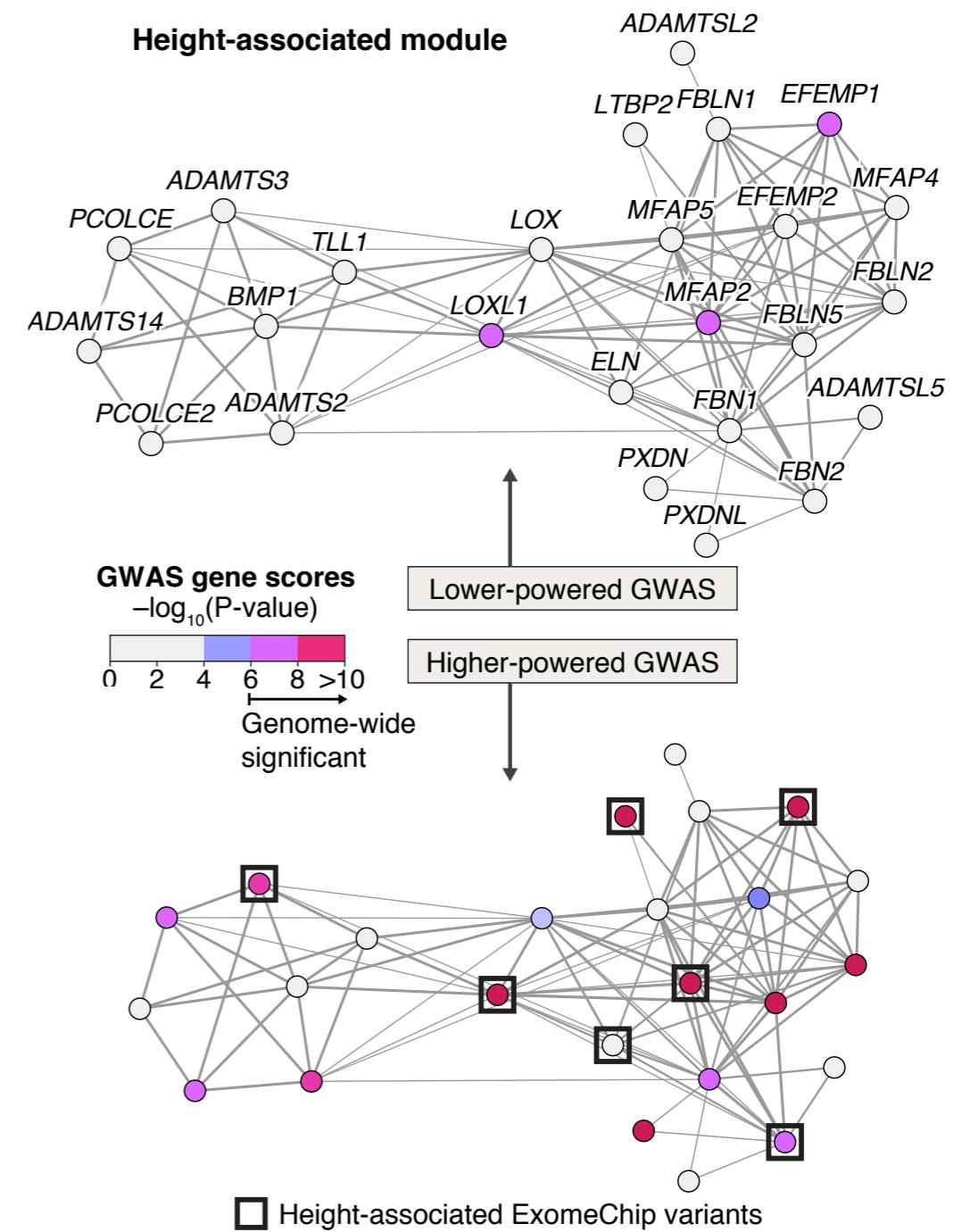
Random predictions

Consensus predictions  
(using top 50% of methods)

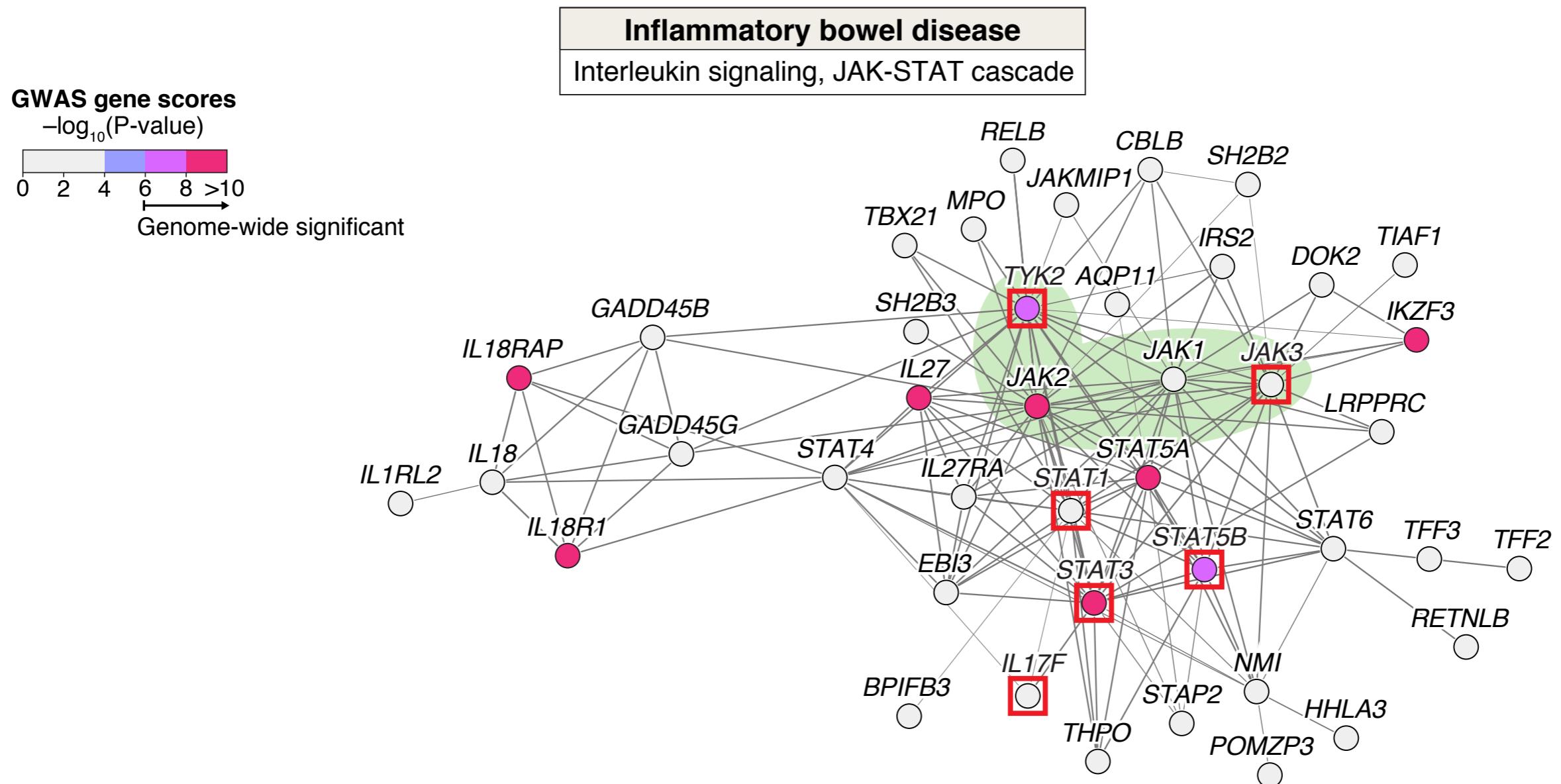


# Validating modules

A height-associated module predicted by a lower-powered GWAS is confirmed by a higher-powered GWAS



# Example interesting module



- JAK-STAT inhibitors are in clinical trials for Crohn's/UC

Link to preprint at [jjc2718.github.io](https://jjc2718.github.io); poster A-200

Most code/data is available at <https://synapse.org/modulechallenge>, more to come

Thanks to all my collaborators!

Sarvenaz Choobdar (UNIL)



Eren Ahsen (Mt. Sinai)



Daniel Marbach (UNIL, Roche)



Sven Bergmann

Julio Saez-Rodriguez

Ted Natoli

“Team Tusk”:

Jake Crawford

Donna Slonim

Ben Hescott

Xiaozhe Hu

Joanne Lin

Lenore Cowen

Gustavo Stolovitzky

Mattia Tomasoni

Rajiv Narayan

David Lamparter

Kasper Lage

Aravind Subramanian

Zoltán Kutalik

Johnathan Mercer



Network providers and challenge participants

