

# WORKSHOP

## **Combined GWAS and TWAS using SVEN**

Genomewide association studies (GWAS) and transcriptomewide association studies (TWAS) help understand the genetic bases of phenotypic variation in species. Although GWAS and TWAS results can be combined using Fisher's Combined Test, the statistical power to detect causal genes could be increased by combining GWAS and TWAS through a single model. This workshop aims to equip you with a tool for combining GWAS and TWAS using a hierarchical Bayesian method called SVEN. In addition to computational scalability, SVEN comes with the theoretical guarantee that both the false negative and the false positive rates converge to zero with increasing sample size.

#### The workshop will cover:

- 1. Fundamental of Bayesian hierarchical models in association studies
- 2. Demonstration of SVEN from R package bravo using data from a maize panel
- 3. Hands-on experience in using SVEN under the R statistical software

By the end of the workshop series, you'll be able to:

- 1. Understand the marginal inclusion probability as an alternative to the p-value
- 2. Use SVEN to analyze your dataset
- 3. Summarize and visualize the output from SVEN

#### **Presenters:**



**Dr. Somak Dutta** is an Associate Professor of Statistics at Iowa State University. He received his Ph.D. in Statistics from the University of Chicago. His research interests include developing theory, methods, and matrix-free computations for high-dimensional problems.

**Dr. Vivekananda Roy** is a faculty member in the Department of Statistics at Iowa State University. His research interests are Markov chain Monte Carlo, importance sampling, high dimensional data analysis and model selection.











**Мау 17, 2024 10:00 ам - 1:00 рм** (Central Time, UTC-5)

### Purpose:

Hands-on training in combined GWAS and TWAS using SVEN from R package bravo.

Register for this <u>Zoom</u> virtual workshop: <u>https://tinyurl.com/</u> <u>AG2PI-w26</u>

Upon registration, you will receive a confirmation email with information about joining the meeting.

A recording will be available at a later date at: www.ag2pi.org.

Registration is not required to view the recording.

Agricultural Genome to Phenome Initiative (AG2PI) is funded by USDA-NIFA awards 2022-70412-38454, 2021-70412-35233 and 2020-70412-32615.