AG2PI
Agricultural Genome to
Phenome Initiative

WORKSHOP

Intermediate Omics Data-Enabled Genomic Prediction and Mediation Analysis

Through this two-hour workshop, participants will learn the basic principle of establishing the successive relationship from SNP to intermediate Omics data and then to conventional phenotypes. Participants will then get hands-on experience integrating population-wide Omics data to identify mediator genes and predict breeding values.

Workshop Presenters

Jinliang Yang is an assistant professor at the University of Nebraska-Lincoln. His group focuses on quantitative genetics and statistical genomics of maize and its wild relatives, from historical domestication to future crop improvement.

Hao Cheng is an assistant professor of quantitative genetics in the Deparment of Animal Science at the University of California, Davis. His research interests are broadly involved in the development of statistical and computational methods for the (genetic) improvement of populations through more accurate, efficient, and biologically meaningful analysis. His lab has focused on the use of genomics, phenomics, pedigree, and other sources of big data in various species to better predict desired traits.

July 26, 2022

12:00-2:00 PM

(Central Time, –5 GMT)

Purpose: Learn the basic principles of applying and integrating Omics data to predict genetic loci of agronomic traits.

Register for this Zoom virtual workshop:
https://tinyurl.com/AG2PI-w14

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.

Iowa State University
The University of Arizona
University of Idaho
University of Nebraska Lincoln
USDA

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