Field Day: Phenomic Prediction & Bioinformatic Workflows - AG2PI "Coconut" Grant Outcomes

AG2PI
Agricultural Genome to Phenome Initiative

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

When are models too good to be true? Accurately evaluating Phenomic Prediction as a tool for plant breeding

High-throughput phenotyping (HTP) describes a rapidly developing and expanding toolkit for plant breeders to collect large-scale phenotype data on their candidate varieties. HTP tools can rapidly and cheaply collect dozens to hundreds of data points per plant. These phenomics features can be used by machine learning models to accurately predict other phenotypes of plants such as grain quality or yield, earlier in the season or more cheaply than can be measured directly. In some cases, "Phenomic Prediction" appears competitive with Genomic Prediction in accuracy, and has been proposed as a tool to increase the accuracy and rate of genetic gain in breeding. We'll discuss a key complication with this approach – that directly comparing Phenomic Prediction accuracy and Genomic Prediction accuracy is not an appropriate way to evaluate whether Phenomic Prediction is useful for breeding. We will share ways to appropriately use and evaluate the benefit of Phenomic Prediction in breeding programs.

Presenter:

Daniel Runcie is Associate Professor in Department of Plant Sciences at the University of California Davis. His group studies the genetic basis of plant adaptations to their environments, developing statistical and mechanistic models linking genotype to phenotype in both crop and natural systems.

Developing bioinformatics workflows to support agricultural genomics

Agricultural genotype to phenotype (G2P) applications are hindered by the lack of accessible bioinformatic workflows. Well documented workflows support those new to genomic data analysis, enable G2P integration and allow benchmarking to compare workflows. I will demonstrate how we supported students to develop and provide common genomics workflows as documented, freely available resources for the agricultural research community. I will also provide the initial findings from a discussion of the agricultural community's bioinformatic needs to support genomics analyses.

Presenter:

Fiona McCarthy is a Professor in School of Animal and Comparative Biomedical Sciences at the University of Arizona. She served as a NRSP8Bioinformatics Co-coordinator for 12 years and Co-Chaired the writing committee for the new NRSP8 project.

March 20, 2024

10:30 AM–12:00 PM
(Central Time, UTC–5)

Purpose:

Discussion of outcomes from two AG2PI "coconut" seed grant projects as one addresses the use of phenomic prediction and the other develops new bioinformatic workflows.

Register for this Zoom virtual meeting:

http://tinyurl.com/AG2PI-FD30

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

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

USDA

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