



ΠΑΝΕΠΙΣΤΗΜΙΟ ΠΕΙΡΑΙΩΣ
ΣΧΟΛΗ ΧΡΗΜΑΤΟΟΙΚΟΝΟΜΙΚΗΣ ΚΑΙ ΣΤΑΤΙΣΤΙΚΗΣ
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ΠΡΟΣΚΛΗΣΗ

Σας προσκαλούμε στη **διαδικτυακή ομιλία** του

Υπ. Διδάκτορα κ. Γ. Μπάρτζη
«Wageningen University and Research, Biometris,
Department of plant sciences»

η οποία θα διεξαχθεί

την Παρασκευή 09 Απριλίου και ώρα 16:00-17:00,

μέσω της εφαρμογής Webex, με θέμα:

«psBLUP: proximity smoothed Best Linear Unbiased Predictor»

Georgios Bartzis, Fred van Eeuwijk Biometris, Wageningen UR, the Netherlands

In systems biology, where an organism is viewed as as a web of interacting molecules, new methods that combine biology with mathematical modeling have been developed for gaining knowledge that is otherwise not evident. Over the past decades rapid advances in sequencing technologies enabled the generation of massive datasets, and therefore statistical methods utilizing all available information are increasingly popular. For example, in plant sciences, genomic selection is used for improving quantitative traits by building a prediction model describing a marker-trait relationship. Typically, in such cases, the number of variables far exceeds the number of samples (high-dimensionality) and therefore, regularized regression models are commonly used. The most common approach is by using the genomic best linear unbiased predictor (GBLUP) method, where a mixed model is fitted to the data. GBLUP has also been alternatively parameterized as a ridge regression (RRBLUP). GBLUP/RRBLUP is based on the assumption of independence between predictor variables. Nonetheless, it is expected that variables will be correlated due to their physical proximity. Here, we propose a regularized linear model (namely proximity smoothed BLUP; psBLUP) explicitly modeling the dependence between predictor effects. Since it is anticipated that correlated predictors influence the response similarly, by penalizing the differences between adjacent effects, we encourage smoothness on neighboring coefficients. Using plant data coming from the Seed Lab of Wageningen University and Research, we show that psBLUP yields higher accuracy compared to the standard methods (GBLUP/RRBLUP)

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