

## **Spatio-temporal modelling of high-throughput phenotypic data**

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Traditionally, field experiments in plant breeding measure the traits of interest only at the end of the study (or a rather low number of times). This is a consequence of the effort, the cost and especially the use of destructive procedures (e.g., harvesting to measure yield). However, with the arrival of non-destructive high-throughput phenotyping platforms, long time-series of repeated measures come available between seed emergence and final trait. New statistical methods are thus required that can extract the most relevant information from multiple time series data on all aspects of plant growth and development. In particular, the evolution over time of the genetic signal, but also of the environmental factors, need to be adequately addressed, which makes necessary a spatio-temporal perspective for the analysis of field trials.

In this talk, we explore the use of spatio-temporal smoothers jointly with mixed model techniques for the analysis of time-series of phenotypic data. In brief, to correct for spatio-temporal (or environmental) effects use is made of multi-dimensional penalised splines (P-splines), and the evolution over time of genetic effects is modelled using genotype-specific P-spline curves. The proposal is illustrated with data from various experiments with automated phenotyping.

This is joint work with Diana Pérez Valencia, Martin Boer, Emilie Millet and Fred van Eeuwijk.