High throughput phenotyping platforms allow analysis of the genetic variability of traits at several scales of plant organization under contrasting and well-defined environmental scenarios. After that a large number of platforms has been built, the priority now is to design methods for the analysis of heterogeneous datasets involving thousands/millions of data points, contrasting environmental conditions and tens/hundreds of measured traits. This course will firstly discuss criteria for choosing a suitable experimental design for phenotyping experiments. Subsequently we will show options for analysing features extracted from phenotyping platforms with a focus on spatial and longitudinal modelling (in R). We aim at increasing the precision of estimation new phenotypic traits and parameters thereby facilitating the combined analysis of data from multiple scales and platforms.

Organised by
Biometris
Date
Tuesday 7th May 2019 from 13:30 to 17:30
Duration
½ day
Setup
Campus WUR
Venue
Radix, building number 107, Droevendaalsesteeg 1
6708 PB Wageningen
Room
PC0088

Programme
The statistical analysis techniques will be presented in lectures complemented by hands-on computer demonstrations / training.

Tuesday 7th of May
13:30 13:45 Registration and Welcome
13:45 14:15 General introduction to the course
14:15 15:30 Experimental design
15:30 15:50 Coffee
15:50 17:30 Single experiment analysis
17:30 Drinks (Orion building)

Course Leaders
Teachers are Emilie Millet and Fred van Eeuwijk (WUR-Biometris).