

# ***Book of Abstracts***

## **Editors**

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Thu, 30. March, 9:00-9:40

## K06 Christophe Pradal: Data-intensive scientific workflows for model-assisted high-throughput phenotyping

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**Short Bio:** Christophe is a Senior Researcher at CIRAD, Montpellier and an associate researcher at inria. He co-leads the interdisciplinary group PhenoMen at the crossroads of Data science (modeling & phenotyping), ecophysiology and agro-ecology in the AGAP Institute with Christine Granier. In the last 20 years, he has worked in the FSPM community, leading the OpenAlea platform, and designing models, algorithms and data structures in plant phenotyping and modelling at different scales. He served during 5 years as an associate editor of *Plant Methods*.

**Abstract:** High-throughput phenotyping platforms allow the study of the form and function of a large number of genotypes subjected to different growing conditions (GxE). Automatic computational pipelines for phenotyping are able to characterize the structure and the development of plants at an unprecedented resolution. Scientific workflows are way to schedule these complex pipelines on distributed cloud infrastructure, to manage the huge amount of data and to enhance the reproducibility of such experiments. In this presentation, I will discuss the recent developments in root and shoot phenotyping methods, how it challenges FSPM formalisms and platforms, and how scientific workflows management system can help to improve the connection between phenotyping and modelling communities while reducing the processing and environmental cost of the computation.

**Twitter account:** <https://twitter.com/agapinstitut> #PhenomenTeam

### List of three indicative publication:

G. Heidsieck, D. De Oliveira, E. Pacitti, **C. Pradal**, F. Tardieu, P. Valduriez (2021). Cache-aware scheduling of scientific workflows in a multisite cloud. *Future Generation Computer Systems*, 122, 172-186.

B. Daviet, R. Fernandez, L. Cabrera-Bosquet, **C. Pradal\***, C. Fournier\* (2022). PhenoTrack3D: an automatic high-throughput phenotyping pipeline to track maize organs over time. *bioRxiv*.

H. Takahashi, **C. Pradal** (2021). Root phenotyping: important and minimum information required for root modeling in crop plants. *Breeding Science*, 71(1), 109-116.