# IPPS 2022 Conference Book

# 7th International
# Plant Phenotyping Symposium

# 'Plant Phenotyping for a Sustainable Future'

## Wageningen, the Netherlands
## September 26-30, 2022

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The International Plant Phenotyping Network (IPPN) e. V.
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# AN AUTOMATIC PHENOTYPING PIPELINE TO TRACK MAIZE ORGANS OVER TIME

**BENOIT DAVIET**[1]; ROMAIN FERNANDEZ[2]; LLORENÇ CABRERA-BOSQUET[1]; CHRISTOPHE PRADAL[2]; CHRISTIAN FOURNIER[1]

[1] INRAE;
[2] CIRAD

High-throughput phenotyping platforms allow to study the function and form of a large number of genotypes subjected to different growing conditions (GxE). A number of image acquisition and processing pipelines have been developed to automate this process for various plant species. However, complex architecture and developmental shoot traits require extracting both a 3D reconstruction of the plant, and a temporal tracking of each organ, from images. Currently, no such method has been validated for Poaceae with complex experimental conditions (thousands of plants, complete development cycle follow-up). Here we propose a new pipeline to extract a 3D+t reconstruction of maize at organ level from images, which allows studying plant architecture and individual organ development over time during the entire growth cycle. The Phenomenal pipeline [Artzet et al. 2019] is used to segment stem, ligulated leaves, and growing leaves in 3D from RGB images for each date, with an improved stem detection based on deep-learning. Sequence alignment is used as an original way to perform the temporal tracking of ligulated leaves, by exploiting both their consistent shape over time, and unambiguous topology along the stem axis. Growing leaves are tracked afterwards with a distance-based approach. This pipeline was validated on a dataset of 60 maize hybrids imaged daily from emergence to maturity in the PHENOARCH platform. Stem tip was precisely detected (RMSE < 2.1cm) over time. 97.7% and 85.3% of ligulated and growing leaves respectively were assigned to the correct rank after tracking, on 30 plants x 55 dates. The pipeline allowed to extract various development and architecture traits at organ level, with good correlation to manual observations overall, on random subsets of 10 to 355 plants.

These results show the applicability of sequence alignment to the field of phenotyping and temporal tracking, and the usability of this pipeline for large maize GxE analysis.