

# Using T-LiDAR scans for high-throughput phenotyping of genotypic variability of apple tree architecture

Benoît Pallas, Emma Carrié, Sébastien Martinez, Evelyne Costes, Frédéric Boudon

UMR AGAP

Univ Montpellier, CIRAD, INRA, Montpellier SupAgro

Montpellier, France

[benoit.pallas@inra.fr](mailto:benoit.pallas@inra.fr)

## ABSTRACT

Despite evidence and previous reports on the genotypic variation of apple tree architecture, phenotyping large populations remains challenging. In this study, we used T-LiDAR scanning for evaluating architectural traits on an apple core collection. After the determination of an adequate protocol considering both data acquisition duration and scan resolution, scans were collected on a large number of individuals (around 1000) corresponding to a French core collection of apple varieties, implanted in Montpellier, France. The analysis relied on different methods and software to segment and extract the point clouds corresponding to each tree. The procedure makes it possible to compute descriptors of the tree shape such as the height, convex volume, alpha hull volume, total leaf area and its vertical distribution, and light interception efficiency estimated through the silhouette to leaf area ratio (*STAR*). Alpha hull volumes were well correlated with in planta measurements such as total leaf area or trunk cross-sectional area emphasizing the relevance of this descriptor. Most descriptors showed high variation and heritability within the population. Highest heritability values were observed for global or integrative traits such as plant volume while lowest heritabilities were observed for more local traits such as leaf area vertical distribution. The estimated variables were then used to define six architectural morphotypes using a clustering method. Differences between groups were first explained by parameters related to the size of the tree and then by differences in *STAR* values within each group of small and big trees. The present results suggest that T-LiDAR scans are relevant for capturing genetic variation of global tree shape within a population with a large diversity and could be extended for phenotyping other architectural traits. In that context, forthcoming works are undergoing for extracting topological traits on the whole population on scans collected in winter conditions.

*Keywords* : tree architecture, morphotype, heritability, clustering, genotypic variability