The aim of the plant architecture research community is to understand the biological processes involved in the function and growth of plants with explicit representation of their topology and geometry. To understand these systems, which may be quite complex, researchers in botany, ecophysiology, forestry, horticulture, applied mathematics and computer science share experimental data, plant models and software tools. Research in this domain concerns several different scales, such as plant cells, plant organs, entire plants and plant populations. To support this research, we are developing OpenAlea, an open source software platform implemented in Python. OpenAlea is used for the integration and comparison of diverse models and tools provided by the research community. We use Python to glue together components implemented in various languages (e.g. C, C++ and Fortran). Standard wrapping tools, such as Boost.Python, Swig and f2py, are used to support the integration process. Different components can use common data structures such as sequences, tree graphs and multiscale tree graphs. To ease the communication between components, a unique interface has been specified for each data structure. The Zope component framework is used to define interfaces and adapters. Three types of components are integrated into OpenAlea: - analysis of plant architecture (e.g. AMAPmod), - geometric representation and visualization of plants at different scales (e.g. PlantGL), - and simulation models of ecophysiological processes (e.g. RATP, Archimede, PyCaribu, etc.). Users can combine components from OpenAlea and other Python scientific libraries into customised work flows according to their specific needs. Training courses on Python and OpenAlea's modules are given in France and other countries (e.g. Thailand, Brazil, etc.) or through an e-learning platform.
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