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Statistical characterization of the root system architecture model CRootBox

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Most 3D root architecture models are stochastic. However, the connection between the parametrization of 3D root architecture models and characteristic measures of the simulated root systems is often not obvious. Model input parameters are for example the lengths of basal and apical zones, the branch spacing, the maximum root length, the initial elongation rate, the root radius or the branching angle. Root system measures computed from the detailed 3D model output are aggregated information such as total surface area of the root system, volume of the convex hull, root length density in the convex hull, the equivalent conductance of the root system of the mean half distance between roots.

We used statistical methods to analyze the simulation outcome of the root architecture model CRootBox and build meta-models that determine the dependency of root system measures on model input parameters. Starting with a reference parameter set, we varied selected input parameters one at a time and used CRootBox to compute 1000 root system realizations as well as the resulting root system measures. The obtained data sets were then statistically analyzed with regard to dependencies between input parameters, as well as distributions and correlations between different root system measures.

While absolute root system measures (e.g. total root length) were approximately normal distributed, distributions of ratios of root system measures (e.g. root tip density) were highly asymmetric and could be approximated with inverse gamma distributions. We derived regression models (meta-models) that link significant model parameters to 18 widely used root system measures, and determined correlations between different root system measures.

Our developed meta-models can be used to determine the effect of parameter variations on the distribution of root system measures without running a full simulation. Our approach also provides a means to compare different models with each other and with experimental data.

Our method also provides a means to quantify the contribution of the dynamic root architecture development to shaping the rhizosphere.