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Computational methods for hidden semi-Markov models with mixed effects - applications to plant branching models

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In the framework of plant development modelling, statistical models can be divided into two categories. The first one, referred to as 'genotype x environment', is based on mixed models, which do not account for time dependencies existing in the considered processes. The second category is based on sequence analysis models that are funded on biological models, but currently do not account for genotype or environmental effects.

More specifically, we are here focused on hidden semi-Markov models, introduced about 20 years ago (Guédon et al., 2001) to model dynamical aspects of plant structure development. These models allow modellers to account for different development phases of either plants or their components (branches, roots, etc) through hidden states. The PhD proposal aims at including fixed and random effects within this category of models, the former aiming at characterising the effects of targeted covariates (genotype and environment) ant the latter, to account for constraints related to experimental design. The work to be accomplished, beyond model specification, is to develop inference algorithms suited to the specific complexity of these models .

Beyond plant developement modelling, the methodological advances obtained in the hidden semi-Markov framework will enrich this family of models and offer new possibilities for addressing scientific questions in various domains of application (health, seismology, reliability, ecology, etc).

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