Growth and yield models in the Heureka system

The Heureka system contains a set of software for different users and problem areas. Three of the software (StandWise, PlanWise, and RegWise) handles forest dynamics. These software are built around a common core of models projecting tree and stand development. The core contains a large number of interlinked models. In many cases there are optional models (users choice), e.g., optional growth models.

Information on the Heureka system is found on <u>www.slu.se/heureka</u> and in Wikström et al. (2011). Help documentation is available on <u>www.heurekaslu.org/help/en/</u>, technical documentation and download pages (the software are available for free) on the Heureka wiki <u>http://heurekaslu.org/wiki/</u>. Below we shortly describe central models in the core of the Heureka system for growth, mortality, biomass, etc. That is, it does not claim to be a complete description of the core.

The growth models concern two stand growth key stages: the stand establishment period and the development of the established stand, the transition between these stages being at 6-7 m stand height. Basal area growth of established forest is modelled by individual tree models of Söderberg (1986) or of Elfving (2011b). Optionally the individual tree models are used in combination with a stand level basal area growth model of Elfving (2011a). When used, the stand level model projects the total growth and the individual tree model then distributes growth to individual trees. The models mentioned are based on data from the Swedish National Forest Inventory (NFI) and have been evaluated by Fahlvik et al. (2014) on NFI data and on data from long-term thinning experiments with a wide variation of thinning programs. For a multi-layered forest stand Drössler et al. (2015) show that the models underestimates basal area and volume growth (eight years stand growth).

The effects on growth due to climate change can be included by adjusting the empirical growth functions based on results from an analyses (50x50 km grid over all Sweden) with the BIOMASS process-based model (McMurtrie et al. 1990). Three climate scenarios are available, ECHAM5_A1B, MPI 4.5 and MPI 8.5 (Freeman 2009). The climate change model does not take into account increased risks that are expected to follow climate change, such as more storm-fellings and more insect infestations.

For stand establishment on initially bare land or after clear felling, height and species distributions in the new stand are either imported from a large database containing data from field measured plots (Elfving 1982) or estimated with functions based on data from this data-base. Growth of seedlings/plants are calculated with height growth functions (Elfving 1982, the model "Funktioner för huvudstammarnas höjdutveckling"). Damages on young trees (2-6 m) by browsing, snow, frost and some other factors are simulated according to Näslund (1986), and lead to mortality and reduced height growth.

Height development in established stands is modelled by functions of Elfving and Kiviste (1997) for Scots pine and of Liziniewicz et al. (2016) for lodgepole pine and there are also functions for Norway spruce, birch, aspen, beech, oak and larch. Ingrowth of trees (diameter at breast height \geq 4 cm) in established stand is calculated according to Wikberg (2004). For tree mortality either models of Fridman and Ståhl (2001) or more recent ones of Elfving (2014) are used. Mortality of retention trees after clear felling is based on empirical data from Sweden (Jönsson et al. 2007), Finland (Hautala and Vanha-Majamaa 2006), and Estonia (Rosenvald et al. 2008).

Above stump tree biomass is estimated either by models of Petersson (1999) or by Marklund (1999) and stump and root by Petersson and Ståhl (2006). For young stands above ground tree biomass is

estimated by models of Claesson et al. (2001). Decay of coarse woody debris is modelled based on Kruys et al. (2002), Harmon et al. (2000) and Sandström et al. (2007).

The occurrence and decomposition of soil carbon and soil nitrogen is depicted with a mechanistic model, which is based on the so called Q model by Ågren and Bosatta (1998). Input to the Q model is provided by a litter production model and by harvest residues.

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