

Modelling natural regeneration in SIBYLA tree growth simulator

Ján Merganič, Marek Fabrika

Technical University in Zvolen, Forestry faculty, Department of forest management and geodesy, T.G. Masaryka
24, 960 53 Zvolen, Slovakia, E-mail: merganic@vsld.tuzvo.sk; fabrika@vsld.tuzvo.sk

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Abstract:

Models of natural regeneration represent an important amendment to complex growth models. They allow making prognoses behind one production cycle of a forest, and also simulating the development of natural and virgin forests. This work deals with the modelling of natural regeneration density and of parameters of natural regeneration. The model consists of an empirical part, which simulates regeneration density (number per hectare) at a stand level, and of a process-based part, which simulates seed production and seedling germination at a tree level. The empirical part of the model is based on the data of the National Forest Inventory and Monitoring of the Slovak republic 2005-2006 and climatic rasters with the pixel size of 90×90 m, which capture the spatial distribution of important climatic characteristics. The model simulates regeneration density of individual tree species in relation to quadratic mean diameter of the parent stand and its crown closure. In addition, the model is site-specific. Weibull's function is utilised for the generation of diameter distribution. Tree heights are modelled by Wolf's function. The process-based part of the model is based on seeding functions and fuzzy logic. It is based on the prediction of seed yield of individual trees in relation to such characteristics as seed purity, seed quality, germination capacity, absolute weight of seeds, seed production per adult tree, etc. The production is further modified with the regulators and reduction factors, which describe other conditions necessary for the germination, survival, and the establishment of the next generation. In the next step, empirically derived regeneration density is reduced in relation to the ratio of individual tree species to the total production of all individuals estimated from the process-based model.

Introduction

The expansion of the methods of mathematical modelling and computer techniques bring advancements also in forest modelling. The modelling shifts from the development of the whole stand to the growth of individual trees, or even the growth of individual tree organs. Homogeneous monocultures are replaced by mixed, horizontally and vertically more complex forest stands. The preference of more complex forest stand structures and the tendencies towards sustainable forest management concepts urge professionals to develop models that enable modelling and making prognoses of such complex forest stands. An example of such a model is the tree growth simulator SIBYLA (FABRIKA 2005), which has been developed on Technical University Zvolen.

Since modelling of complex forest stand structures and processes is not simple, a growth simulator usually consists of several sub-modules, which intercommunicate using the pre-defined relationships. The individual tree growth simulator SIBYLA already integrates several sub-modules (increment model, crown model, competition model, mortality model, thinning model). The model of natural regeneration is another important sub-module that is necessary for the simulation and prognosis of complex forest ecosystems particularly due to the following reasons:

- it enables the simulation of the development of forest ecosystems behind one forest production cycle,
- it enables the prognosis of the development of forest stand structures and management forms, that are based on natural regeneration – sustainable forest silviculture (shelterwood forms, selection forests),
- it enables the simulation and the prognosis of the development of natural forests – virgin forests.

The scientists - modellers have recognised the need to simulate the regeneration phase of the forest stand after the final cutting already in 70s of the last century, when the first regeneration models were developed (MONSERUD and EK 1977). During more than 30 years a number of models have been presented starting from the simplest tabular models, which provide us with the information about the distribution of regeneration between tree species and diameter classes (EK *et al.* 1996), up to the complex models simulating partial processes including seed production, germination, mortality and competition of a parent stand (MONSERUD and EK 1977). Considering the beginning of the simulation, several types of models are recognised (MIINA *et al.* 2006):

- regeneration models – simulation starts from seeds (e.g. LEXER and HÖNNINGER 2001),
- regeneration establishment models – simulation starts at the time when seedlings reach higher probability of survival (e.g. SCHWEIGER and STERBA 1997),
- ingrowth models – simulation starts at the time when the trees of young generation reach a specific pre-defined limit, e.g. breast height 1.3 m,
- recruitment models – simulate the number and the size of the new trees that enter the smallest class in the main stand, e.g. trees that reach the diameter at breast height 7 cm (e.g. TRASOBARES *et al.* 2004).

Traditional regeneration models that use the statistical modelling approach are based on very large databases because regeneration data are characterised by large variability (EK *et al.* 1996). Alternative approaches to regression techniques are nonparametric methods (imputation tables according to EK *et al.* 1996, methods kNN, kMSN, i.e. k-nearest neighbours), neuron networks (HASENAUER and MERKL 2001) and decision trees (KINDERMANN *et al.* 2002).

A regeneration model usually consists of partial sub-models, which simulate individual phases (seed production, germination), or individual variables (regeneration probability, number and dimensions of new individuals) in dependence to site (elevation, slope, rock fraction), climate (temperature) and stand (stand density, mean diameter) characteristics. The models differ from each other in the level of detail and the required input depending on the available information and the purpose for which they were developed (HYPPONEN *et al.* 2005).

The goal of the presented paper is to present a proposal of the model of natural regeneration, which will be implemented in the tree growth simulator SIBYLA (FABRIKA 2005).

Data

The construction of the model of natural regeneration is based on the database of the National Forest Inventory and Monitoring of the Slovak republic (NIML SR). NIML SR was performed in 2005 – 2006 as a representative sampling method with complex data gathering in the regular grid of permanent inventory plots (IP) of 4×4 km over the whole area of the Slovak republic (ŠMELKO *et al.* 2006). The total number of IPs was equal to 3,071, while forests occurred on 1,419 IPs.

In this work we primarily used the data about trees, forest regeneration, forest stand and site assessed according to the fieldwork manual for NIML SR (ŠMELKO *et al.* 2006). The data were collected on three types of inventory plots: A - a basic inventory plot in the shape of a circle with radius $r = 12.62$ m and area $p = 500$ m² on which terrain, site, stand, and ecological characteristics were assessed and lying deadwood and stumps were inventoried, B1 and B2 – two concentric circles ($r = 12.62$ m and 3 m, and $p = 500$ m² and 28.26 m²) for measuring tree characteristics of the trees with diameter at breast height $d_{1.3} \geq 12$ cm and $d_{1.3} = 7-12$ cm, respectively, and C – a variable circle for the inventory of regeneration and thin trees with diameter $d_{1.3} < 7$ cm and height equal to or greater than 0.1 m (its radius r and area p is selected with regard to tree density). In the case of great heterogeneity of IP caused e.g. by the border between forest/non-forest, forested/unforested land, or different growth classes within IP, etc., IP was divided into more homogeneous parts – subplots (ŠMELKO *et al.* 2006). For the construction of the regeneration model the data from 1,507 subplots were used, while the trees with the height above 1.3 m and diameter at breast height below 7 cm were classified as “natural regeneration”.

To analyse the relationships between the stand data and site-climatic data, we used the site information of IPs transformed by the fuzzy sets according to FABRIKA (2005) and climatic rasters (ĎURSKÝ *et al.* 2002) with the pixel size of 90×90 m for all necessary climate-site variables (number of days per year with daily average temperature above 10 °C, annual temperature amplitude, average temperature in months from April to September, and average precipitation sum from April to September).

Methodology

The occurrence of natural regeneration depends on several factors. The main factors are climate and site conditions, the condition of the parent stand, and the condition of the close surrounding of the stand. Due to the lack of detailed information, the condition of the close surrounding is not accounted for in the actual version of the model. The model of natural regeneration consists of two branches. The first branch represents the model at a tree level, while the second branch operates at a tree species level. The tree branch is the process-based part of the model that uses seeding functions and fuzzy logic. It is based on the prediction of seed yield of individual trees in relation to such characteristics as seed purity, seed quality, germination capacity, absolute weight of seeds, seed production per adult tree, etc. The production is further modified with the regulators and reduction factors, which describe other conditions necessary for the germination, survival, and the establishment of the next generation. The goal of this branch is to quantify the proportion of tree species in natural regeneration (FABRIKA 2005, FABRIKA *et al.* 2009).

The second branch at a tree species level is aimed at modelling regeneration density, its parameters, and positions. Its algorithm is presented in Figure 1. Density model depends on climate and site conditions and the maturity of the parent stand. Climatic and site conditions are implemented in the model in the form of climate-site strata (MERGANIČ and FABRIKA 2009). The construction of the climate-site strata is based on the two primary ecological factors, namely average air temperature during the vegetation period (from April to September) and average precipitation sum during the vegetation period. Although the stratification was performed using climate data only, MERGANIČ and FABRIKA (2009) documented that these variables also affect site variables, therefore the term climate-site stratum is used.

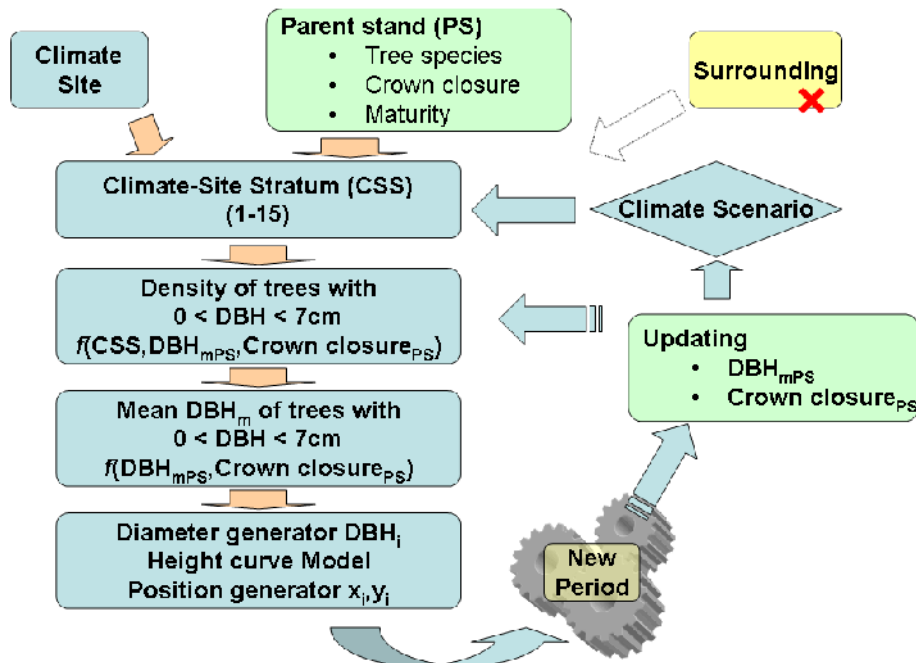


Figure 1: Algorithm of the natural regeneration model

The model of natural regeneration density, i.e. density of trees with diameter at breast height from 0 to 7cm, depends on climate-site strata, mean diameter of the main stand and its crown closure. The model has two sub-models, namely the sub-model of regeneration density at full stocking, which is based on the mathematical relationship defined by REINEKE (1933), and the submodel of the reduction of natural regeneration density for the actual value of the closure of the main stand. In the first submodel, the modification of Reineke's rule was applied in order to determine the density of individuals with diameter from 0 to 7 cm in the stand with a particular mean diameter of the main stand, while the density is quantified for individual climate-site stratum and individual tree species.

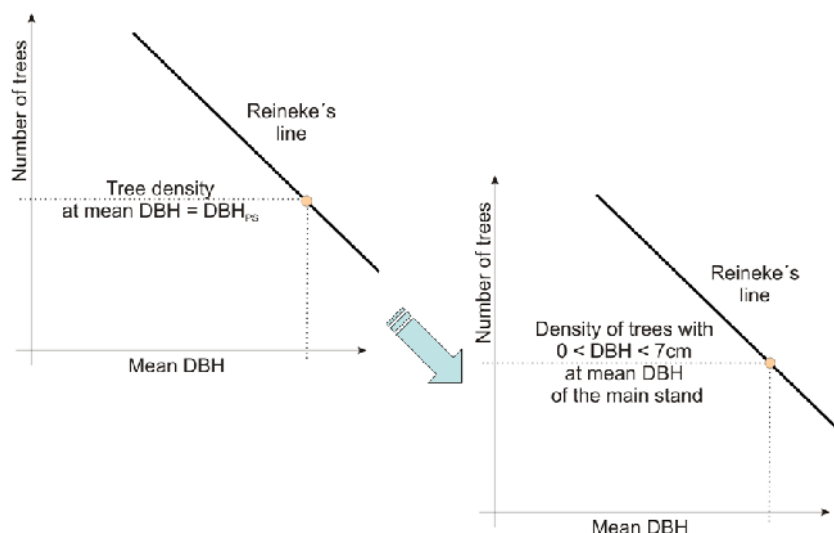


Figure 2: Modification of Reineke's rule for modelling the density of individuals of natural regeneration

In the second step, the sub-model of density reduction reduces the density of trees with diameter from 0 to 7cm with regard to the crown closure of the main stand (FABRIKA et al. 2009).

In addition, the information about the parameters of the regeneration individuals is important for the generation and visualisation of the individuals of natural regeneration. The model of mean diameter of regeneration (Figure 3)

determines the mean diameter of the individuals with diameter 0 to 7 cm on the basis of the mean diameter of the main stand and its crown closure.

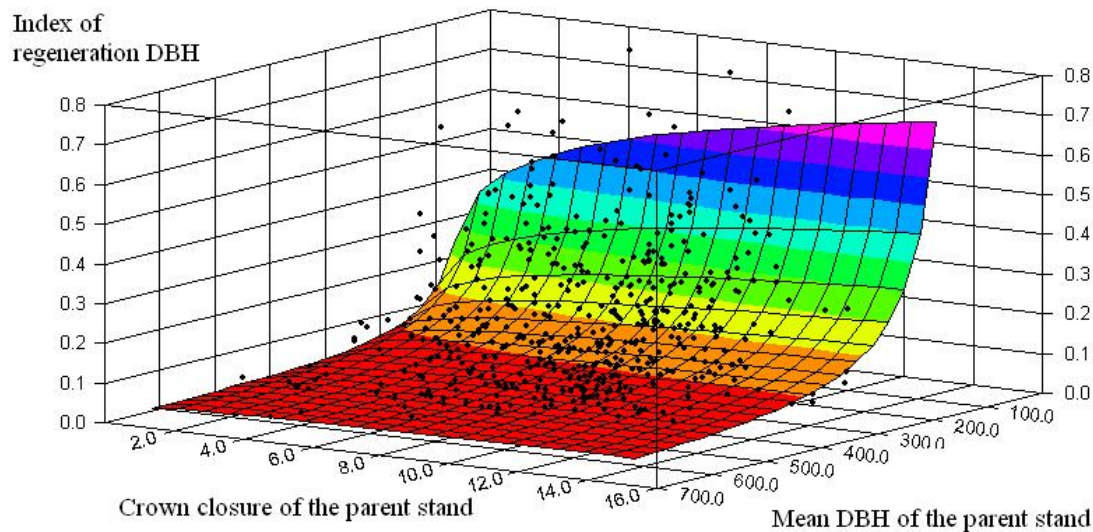


Figure 3: Model of mean diameter of regeneration ($R^2 = 0.49$); mean DBH of regeneration = Index * DBH_{PS}, where Index = $a * DBH_{PS}^b * CrownClosure_{PS}^c$

To generate diameter structure of regeneration individuals, an inverse two-parameter Weibull function was used. The parameters are estimated using the method of moments (MERGANIČ and STERBA 2006). Parameter c depends deterministically on diameter variation, while the value of the variation coefficient was determined from the data of NIML SR 2005-2006. On the base of this empirical material, from which the stands with a typical second layer were selected, the variation coefficient of individuals with diameter below 7 cm obtained values up to 12.6%. Hence, in this case parameter c of Weibull function was set to a constant value $CV\%=15\%$. Parameter b depends deterministically on the mean diameter, which is obtained from the previous model of mean diameter, and on parameter c , which is calculated in the first step.

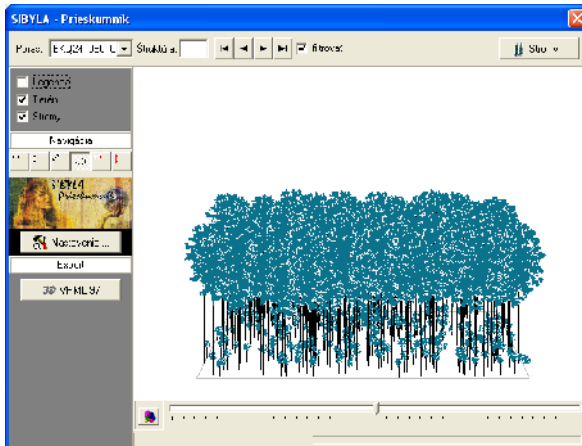
If the diameters of individual trees with diameter below 7cm are known, their heights are calculated using the model of the height curve. From a number of examined height functions (ASSMANN 1943, MICHAJLOV 1952, WOLF 1957, NÄSLUND 1936, PETTERSON 1955, KORSUŃ 1935, KORF 1939), Wolf's function (WOLF 1957) showed the best logical development particularly in the range of young individuals. The function of the height curve model by WOLF (1957) is a two-parameter function, in which parameter a mainly affects the asymptote of the height curve, while parameter b has an influence on its shape. Hence, parameter a is in a close relationship with climate-site conditions. In MERGANIČ *et al.* (2011), its values were determined for each climate-site stratum and 45 tree species.

For generating the positions of regeneration individuals, probability functions are used in order to optimise the position of individuals with regard to light conditions (canopy gaps), the position of parent stands, generalised terrain model, etc. In the presented iterative simulation, the position of individuals was generated using the random probability function.

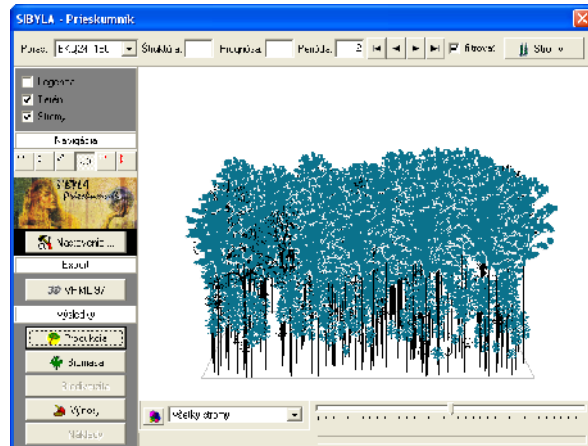
The growth module of the simulator SIBYLA starts after generating the group of individuals and calculating their positions. The growth process results in the changes of tree data (some regeneration individuals pass through the threshold value, some trees from the main stand fell out, e.g. as a result of mortality), and hence in the changes of the parameters of the main stand. Afterwards, the model of regeneration density starts again. The information about the expected, modelled regeneration density is compared with the information about the regeneration density in the forest stand after the growth simulation. If the modelled regeneration density is higher, the difference is amended in the model by applying the above-described models. The cycle is repeated as many growth periods as pre-defined by a user. If the study aims at the evaluation of the climate change, the model of climate-site strata is also applied.

The following set of pictures presents the example of a 400-year simulation of the development of a homogenous beech forest stand after the inclusion of the model of natural regeneration.

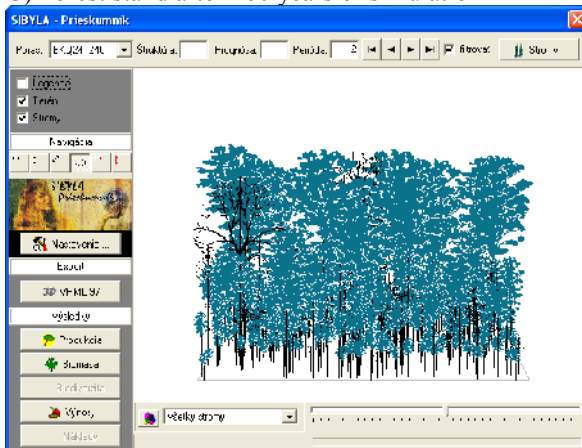
- A) Beginning of simulation, age of main stand – 80 B) Forest stand after 80 years of simulation years



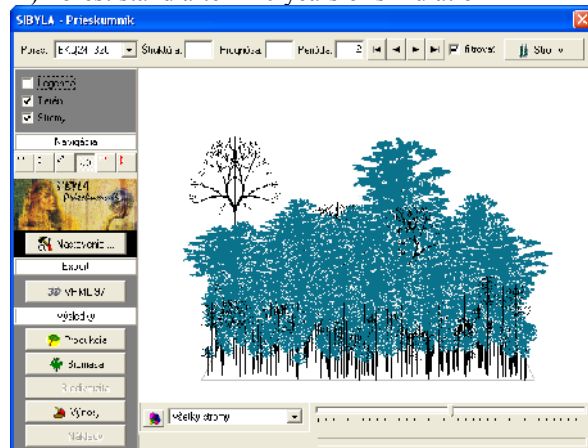
C) Forest stand after 160 years of simulation



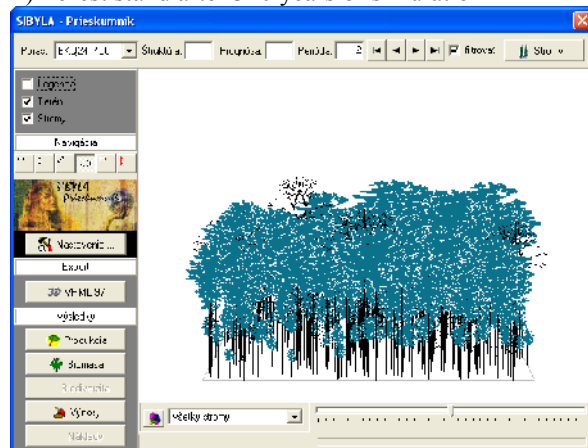
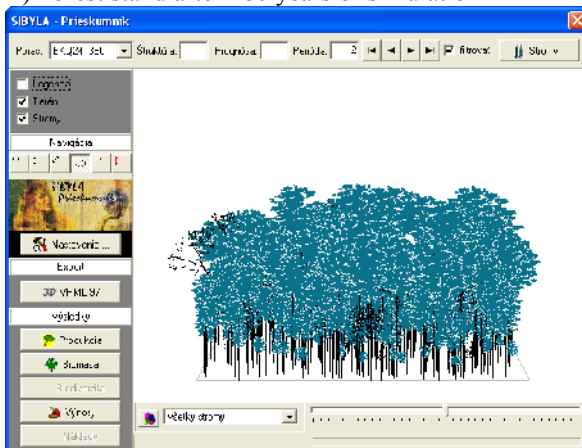
D) Forest stand after 240 years of simulation



E) Forest stand after 280 years of simulation



F) Forest stand after 320 years of simulation



Conclusion

The presented model of natural regeneration enables a user to perform the growth prognoses behind one production cycle, or to simulate the development of forests including natural regeneration (shelterwood management, selection forests, natural forests and virgin forests). The model is based on an extensive database covering the whole Slovakia and all tree species relevant for forest management, which ensures its cross-national validity. The model is sensitive to climatic characteristics and the condition of the parent stand (biometric maturity and density). In addition, it also accounts for the processes of seed production and regeneration in the scope of distributing the individuals between tree species and trees. It comprises the modelling of density and biometric structure of regeneration (diameter and height structure). In future, it will be necessary to add the functionality of the spatial structure, i.e. generating the positions of regeneration individuals in a forest stand. Due to the fact that the actual model of tree crowns of a parent stand does not seem to be suitable for the regeneration individuals, this problem should also be considered in the future research. To conclude we can state that the presented model of natural

regeneration is a significant contribution towards the enrichment and improvement of forest growth simulations that become much more flexible and usable.

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