Design and Implementation of a Structural Poplar Model

Entwicklung und Anwendung eines Strukturmodells der Pappel

Master Thesis for attainment of the academic degree of

Master of Science

In Forestry Sciences and Forest Ecology

Submitted to the Department of Ecoinformatics, Biometrics and Forest Growth

Georg-August-Universität Göttingen

09.12.2020

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Abstract

Forest are complex systems that are influenced by many factors. In order to analyze and interpret forest dynamics, there is the possibility to develop models which can describe these systems. The aim is to create a simple representation of the most important factors in order to answer the underlying question which can target different aspects of the forest dynamics. This can include economical or ecological threads but also specific information about individual trees.

A tool for this use is SIBYLA which is a very flexible forest growth simulator in terms of modeling the growth dynamics of any stand type. The growth simulator is able to generate a realistic stand structure under consideration of influence effects of the stand´s density and the competition of trees. While considering a diversity of input information, a large output about individual trees but also about the whole stand, for example the productivity, is given. SIBYLA returns general tree attributes of the individual trees of the modelled stand including age, tree height, diameter at breast height, crown parameters and increments. Since the outputs only include general tree attributes, the aim of this thesis is to use this output information as an input to create an accurate structural model. By fulfilling this task, the model is capable to analyze specific structural threads like the biomass or the carbon allocation of the modelled tree. The existing data foundation is based on a study of the structural growth of the poplar *Populus* spp.; therefore, the model is only applicable to generate the architecture of a poplar. It is a model based on relational growth-grammar implemented within the modeling platform GroIMP. The general tree attributes provided by SIBYLA serve as an input resulting in an explicit structural model of the respective poplar which can be analyzed with the internal functions of GroIMP.

The results based on an exemplary data file with the same structure as the input data of SIBYLA show that the model is reproducing the given general tree attributes in relation to the input data in an accurate way with a mean percentage of deviation of 5.03% – 10.7%. Still, some outliers exist, for example for the crown base height which’s value exceeds the given one by 44.44% at at a tree age of two and three years. The standard deviation of the modelled attributes is relatively low in the modeling range of twenty timesteps. The same is true for the modelled stem biomass and the biomass of the branches. Therefore, the model can be assessed as stable considering the deviation of the outputs. The sensitivity analysis has revealed that the most sensitive parameters are the start angle of the branches of the first order, their amount for each year and the parameters which interfere with the diameter growth of the branches (sensitivity is decreasing with the here presented order).

By comparing the woody branch biomass of the model with data from the literature, it becomes clear that the model does not reproduce the right dimension of output. For example, at a diameter of 8.1 mm a woody branch biomass of around 2.5 kg is expected whereas the model returns a value of 13.6 kg . Also, the relation between the stem volume and the branch volume is not represented well compared to values from the literature. Based on the comparison of the dimensions of the results with the literature, the conclusion can be drawn that the parameterization of the starting diameter as well as the increase in diameter must be changed in order to deliver realistic results in relation to the biomass. The benefit of the

architecture of the model code is that it enables an easy reparameterization of the model. It also provides the opportunity to adjust the model for other tree species in future studies.

Zusammenfassung

Wälder sind komplexe Systeme, die von vielen Faktoren beeinflusst werden. Um die Dynamik von Wäldern zu analysieren und zu interpretieren, können Modelle erstellt werden, die die Waldsysteme beschreiben. Dabei ist das Ziel, die wichtigsten Aspekte in Bezug auf eine zugrundeliegende Frage vereinfacht darzustellen, die sich auf verschiedene Aspekte der Walddynamik beziehen kann. Hier können ökonomische sowie ökologische Eigenschaften, aber auch Informationen über individuelle Einzelbäume in Betracht kommen.

SIBYLA ist ein sehr umfangreicher und anpassungsfähiger Waldwachstumssimulator, der für solche Anwendungen geeignet ist. Es können Wachstumsdynamiken jeglichen Standtyps entwickelt werden. SIBYLA ist befähigt eine realistische Struktur des Bestandes in Anbetracht der Bestandesdichte und Konkurrenz der Bäume zu generieren. Unter Berücksichtigung von einer Vielzahl von Inputs wird ein breites Spektrum an Outputs erzeugt, die sich auf den ganzen Bestand beziehen können, wie die Bestandesproduktivität, aber auch auf individuelle Einzelbäume. Ein Teil der ausgegebenen Informationen sind allgemeine Einzelbaumattribute der jeweiligen Bäume des Bestandes, welche das Alter, die Baumhöhe, der Brusthöhendurchmesser, Kronenparameter und Zuwächse miteinschließen. Da die Outputs nur aus generellen Attributen bestehen und keine Information über die genaue Struktur des inneren Kronenraums liefern, besteht die Aufgabe dieser Arbeit darin, ein akkurates Strukturmodell der Pappel *Populus* spp. auf Einzelbaumbasis in einem *Downscaling*-Prozess zu erstellen. Ein solches Modell ist befähigt spezielle Struktureigenschaften, wie die oberirdische Holzbiomasse, zu bestimmen. Das Modell verwendet relationale Wachstumsgrammatiken und ist in der Software GroIMP implementiert. Hier dienen die generellen Baumattribute als Parameterinput, welche von SIBYLA geliefert werden. Daneben wurden weitere Funktionen aus verschiedenen Arbeiten teilweise übernommen und einige Parameter geschätzt. Als Output entsteht ein explizites Strukturmodell einer Pappel, welches mit den internen Funktionen von GroIMP analysiert werden kann.

Die Ergebnisse, erstellt mit einer exemplarischen Input Datei, welche die gleiche Struktur wie die von SIBYLA gelieferten Daten aufweist, zeigen, dass das Modell die vorgegebenen Baumattribute mit einer durchschnittlichen relativen Abweichung von 5,03 % – 10,7 % gut reproduziert. Es gibt jedoch einige Werte bei denen Ausreißer auftreten, wie zum Beispiel bei der Kronenanasatzhöhe in jungen Jahren (44,44 % im Alter von zwei und drei Jahren). Die reproduzierten Baumattribute, sowie die verschiedenen Outputs zur Biomasse, wie das Astvolumen und das komplette oberirdische Volumen des Holzkörpers, zeigen ausschließlich eine kleine Standardabweichung in allen Jahren. Damit ist das Modell als relativ stabil in Bezug auf die Produktion der Outputs bei verschiedenen Durchläufen zu bewerten. Bei der Untersuchung der Sensitivität der Parameter ergibt sich, dass vor allem der Startwinkel der Äste, die Anzahl der Äste der ersten Ordnung pro Jahr und die Parameter zum Anpassen des Durchmessers der Seitenäste sensitiv auf Änderungen reagieren. Beim Vergleich der Astbiomasse mit Werten aus der Literatur wird deutlich, dass das Modell in der jetzigen Form noch nicht die richtige Dimension an Ergebnissen liefert (Vergleich: ca. 2.5 kg zu 13.6 kg im Modell). Auch das Verhältnis zwischen dem Stammvolumen und dem Volumen der Äste wird nicht korrekt abgebildet.

Aufgrund des Vergleichs der Dimension der Ergebnisse mit der Literatur lässt sich der Schluss ziehen, dass die Parametrisierung des Startdurchmessers sowie des Durchmesserzuwachses verändert werden muss, um realistische Ergebnisse in Bezug auf die Biomasse zu liefern. Die Architektur des Codes erlaubt hier eine einfache Reparameterisierung des Modells und bietet die Möglichkeit der Parametrisierung für weitere Baumarten.

Contents

1. Introduction

1.1. Forest dynamics and management

Forests are complex systems influenced by many different factors. Their dynamics extend over long periods and their key elements change over time. They are intensively influenced by disturbances, which is increasing the complexity even more (Bravo et al., 2019). Looking at managing forest stands, there are several criteria which are involved in the underlying decision-making process. This includes economic, environmental and social issues, like the amount of timber, biodiversity conversation and recreational activities. In addition, the complexity of the decision-making process is increasing due to the interest of different social groups and stakeholders (Diaz-Balteiro & Romero, 2008) and requires considering the mentioned points under the effect of climate change (Lindner et al., 2010). In particular the changing natural conditions in combination with increasing anthropogenic pressure are causing a loss of forest functions, biodiversity and ecosystem services (Zahvoyska & Pelyukh, 2016). This leads to the point that strategies for forest management are partly no longer suitable what urges scientists to overthink the effectiveness and efficiency (Pelyukh et al., 2018).

In order to analyze and interpret the forest dynamics to provide support for the forest decision-making nowadays, there is the possibility to create models which try to describe these complex systems (Sverdrup & Stjernquist, 2002). Here, simulators and numerical optimizations for forest development are globally used since a long period of time (Kangas & Kangas, 2005). The practical use of forest models has been manifested within in the last decade, especially in the "close-to-nature" forestry (Favorskaya & Jain, 2017).

1.2. Plant models

To study, understand and explain different aspects of reality in science, there were always used models to fulfill these tasks (Dejong et al., 2011). Their aim is to create a simple representation of the most important aspects and to answer the main aspects of the underlying scientific question (Vos et al., 2010).

For centuries, plants scientist made efforts to create conceptual models of plant development, including structural growth and functions (Dejong et al., 2011). While in the last decades the common use of such models was mostly scientific because of the lack of accuracy (Kurth & Sloboda, 1997), the today rapidly increasing amount of computation resources provides great chances for the development and analysis of exact and detailed models which can be used in certain fields of application (Lati et al., 2013). A plant model can be either a single tree model, or a model of a specific plant community. While an aim of a single tree model is to maintain the natural look during the rendering, the modeling of plant communities often includes environmental factors like the location and the interaction between the subjects into the model (Favorskaya & Jain, 2017). The modeling range of physiological and environmental factors is still limited due to the available resources, so it is necessary to link several models in order to model complex plant communities (Long et al., 2018).

1.3. Structural models

The so-called Structural growth models can be used to reproduce natural patterns of the structure of plants in a simplified way. This gives the opportunity to simulate and understand processes of plant communities or single plant growth. One frequently used basis for this type of modelling is the work of Aristid Lindenmayer, introducing the L-Systems as a tool for plant modelling. (Lindenmayer, 1968)

The structure of a plant is very complex and can be described in many ways depending on the application of the model, which can be for example the simulation of growth, but also the use in fields like biomechanics (Godin et al., 1999). It needs to be mentioned that the dynamic structure of plants is affected by genetic and by environmental factors. The genetic factors determine the general species-specific shape of an organism which in turn gets modified by the environmental conditions (Fabrika et al., 2019). For example, there are two studies which have shown the large genotypic variability that affects the architectural traits in different plant species (Ben Sadok et al., 2013; Segura et al., 2008). Since plants can be seen as a collection of different components with a special morphology, which are organized at several scales (White, 1979), the representation of the shape of a subject is implemented by an explicit spatial three-dimensional model. The plant is described by several simple units which constitute the architecture. These units can be buds, leaves and branches or metamers just to mention a few. The connection between these units underlies various branching-based rules, which can be determined for example by field surveys or laboratory measurements on plants. Bringing together the units and the branching-rules, results in a structural model of a plant which can be either static or dynamical. The development of the structure of a plant is the primary goal of structural plant models and does not contain functional processes, in particular when looking at growth data statistics-based models (Long, 2019). This type of modeling delivers an explicit geometrical model, which is independent of physiological processes, which could influence the growth and the architecture of a plant (Vos et al., 2010).

The first question that arises while generating a structural model is how the characteristic pattern of the structural development of the modelled species looks like (Vos et al., 2010). For example, the work of Hallé et al. (1978) is often used in this context, which describes 23 different architectural tree models based on architectural analyses. When developing a structural model, the first step is to work out the different types of organs and their interconnections that are essential for the topological body of the plant, while the richness of detail depends on the purpose of the study. After determining that step, the dynamics of the structural development needs to be considered, meaning the rates and durations of the organogenesis and expansion processes which determine the change in the architectural structure of the plant like the leaf expansion and the internode growth. Examples include the position of buds alongside the units where they are formed or different orders of branching. In summary, information about the appearing type of organs, their temporal succession in relation to each other and their characteristics based on the previous organs is needed (Vos et al., 2010). As well, when looking at the development of plant architecture over time it is necessary to look at the relevant development stages and the variable aspects of plants morphology and topology (Barthélémy & Caraglio, 2007). Long (2019) summarizes plant architecture as a compound out of branching structures with different plant modules such as leaves or buds, which are linked with topological interconnections.

This architecture plays a key role when it comes to the collection of light and the related assimilation of carbon which greatly affects the growth of (Valladares et al., 2002). The light itself also influences the architecture, so properties like the leaf area, the dry matter distribution, leaf angles and leaf shape can also adapt to that condition (Vos et al., 2010). Even the microclimatic conditions, for example hygrometry and organ temperature, are affected by the plant architecture which also has an effect on biological and physiological processes within the organs (Niinemets, 2007). However, it needs to be considered that these mentioned interactions are modelled in functional structural models, which are clearly differentiated from straight structural models (Vos et al., 2010).

The use of structural models extends to the application of biophysical models to structural models, like it is done in light interception models, which gives the opportunity to analyze the influence of architectural traits on plant performance. Furthermore, since the structural development of a plant plays a key role in some perennial plant production systems, structural models can be a great tool as a helping feature for the plants’ structure growth manipulation (Vos et al., 2010). Even in phytopathology the architecture plays a role, which is for example presented in two studies (Calonnec et al., 2008; Robert et al., 2008), where the significant impact of the dynamics of plant structure on interactions between plants and pathogens is shown.

1.4. Functional-Structural models

Like mentioned above, it is also possible to combine structural models with functional aspects to create so called functional-structural plant models (FSPMs). From a systems analysis perspective, plants can be represented as a distributed control system of several semi-autonomous organs, which can function fairly independently regarding their development but being dependent on the rest of the plant when it comes to the access of water, nutrients and carbohydrates (Dejong et al., 2011). Taken this into account, these models use the underlying functional processes such as photosynthesis to control the generation of plant structure of the subject (Vos et al., 2010). In addition, they can include environmental influences into the modeling process. Summarizing these aspects, the functional structural plant models can describe several physiological functions and the structural growth of the topological body of the plant in a specific period of time, while there is a interdependence between the functions and the structure (Long et al., 2018). In this context, the development and function of an organ can be modelled quite independently, on the other hand the modelling of plant growth, considering the plant as a complete system, requires an integration of several sub-models (Dejong et al., 2011)

Applications of FSPMs are for example growth dynamics under competition and effects of climate change to tree species (Kurth & Sloboda, 1997), but they can also be used to model interactions within cells or specific organs like a fruit (Saudreau et al., 2011). An example for a specific function modelled within a FSPM is the model by Da Silva et al. (2011) which describes the water flow coupled with the carbon flow in a 3-D branching system. For example, a scientific approach by Merklein et al. (2019) take this work up to develop a plausible model of the coupled flow dynamics in the xylem and phloem, describing the transport of water and sugar in a 1-year old apple tree. Beside the common use described above, even genome-based information can be integrated into a FSPM, like it is presented by Migault et al. (2017). There is also the possibility to analyze hypotheses which are related to interactions between disease development, plant growth and the structure, the environmental conditions and management decisions in a single model (Calonnec et al., 2013; Pangga et al., 2011).

1.5. L-Systems

The Lindenmayer-Systems (L-Systems), which are a programming framework for the research of the development of plant organs, were introduced by Aristid Lindenmayer in the year 1968. Within plant science, both, the structure and the dynamical structure building processes, which proceed within a plant or a plant organ, can be displayed by visualizing geometrical shapes within a software (Lindenmayer, 1968). To describe the structure L-Systems use a number of intuitive rules to describe either the structure or both the static plant structure and the physiological functions dynamically influencing it. This gives the opportunity to describe plants as a set of interconnected modules. Thus, complex structures like plants can be described with a set of rewriting rules, which are applied to a string, that consists of simple symbols. Some of these symbols get graphically interpreted. The modeling approach works with repetitions since the nature of plant structure is also very repetitive. (Vos et al., 2010)

The components of the simplest L-system are an alphabet Σ consisting of different basic symbols for building a string, the initial string that is named "*Axiom*" and several rules that replace a symbol by a string of symbols of the alphabet. In an application step, all symbols in a string get replaced by the corresponding string of symbols (Kurth, 2007). The following example demonstrates the application of a simple L-system:

alphabet Σ = { **A**; **B**; **C**}

Axiom = **ABC**

rules: **A ==> B; B ==> CA; C ==> AB**

application of three steps: **ABC → BCAAB → CAABBBCA → ABBBCACACAABB**

This procedure can be repeated several times, resulting in a sequence of symbols with a continuously increasing length. In this case, there is no graphical presentation of the sequence shown.

When modelling the structure of a plant, it gets represented by simple filaments that get defined by a linear arrangement of cells. As a result, physiological processes like the transport of hormones into a specific organ of the plant can be described as well as the morphological response of the organ or even the response of the total organism. That principle just allows transport processes into one direction. In order to allow transport into different directions, ring structure of organs needs to be included. As the outcome, Aristid Lindenmayer developed a theory where a two-sided input influences the growth of filaments. It is also possible that filaments can develop into additional ramified units.

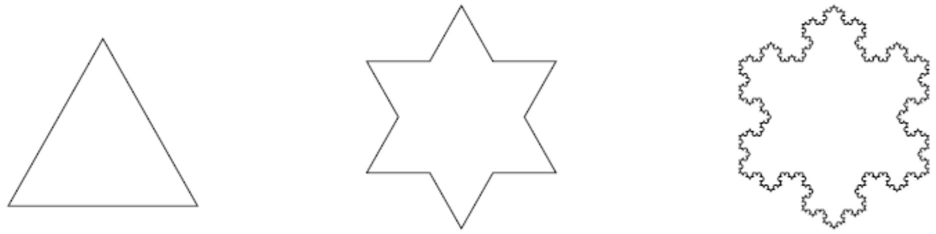
There are several rules which define the L-Systems; specifically, branching rules are of central importance and are specified within the work “Mathematical Models for Cellular Interactions in Development”. (Lindenmayer, 1968)

The graphical representation of these filaments is achieved by turtle programming. Here, a virtual point, the “turtle”, is moving by commands and thereby drawing a graphical object. This gives the possibility to describe angles, different lengths and branching points (Lindenmayer & Prusinkiewicz, 1990). A very simple example of rewriting grammars using the L-systems is the von Koch curve (Koch, 1906) which can be generated using a start word α and a repeated application of a specific rule system which is made up as follows:

$$\propto \rightarrow F + + F + + F$$

$$F \ \rightarrow F - F + + \ F - F$$

The F command communicates the turtle to *move and draw a line*, while + commands a rotation by 60° and – a rotation by – 60° (Kniemeyer, 2004).



α F++F++F F-F++F-F++F-F++F-F++F-F++F-F three steps later

Figure 1: The first steps of the snowflake L-system (Kniemeyer, 2004)

L-Systems are the most commonly used method for rule-based systems within the field of modeling of photorealistic organisms. Here, the modeling of plants is of particular importance. Still, the combination of graph grammar, including L-Systems as a special case, and object-orientated programming may be a better option for the development of three-dimensional plant models, since the morphology and structure building processes can be modelled in a more accurate way. The modelling platform GroIMP offers this opportunity. (Kurth, 2007)

1.6. GroIMP

GroIMP is an open source software which was initially introduced in the year 2007. The modeling platform was developed to give the possibility to model geometric objects including their visualization considering interactions between these objects within a visual interface. It is based on the modeling language XL which is, in its core, the integration of graph grammars into a programming interface. XL is an extension of Java using relational growth grammars. As a result, imperative code can be as well implemented into the model. The XL code is directly integrated into a text editor where it can be easily adjusted and gets automatically compiled, which leads to the point that model changes are directly reflected within the visualization interface. (Kniemeyer et al., 2007)

The current structure of a model is represented as a graph using Java objects as nodes and specific relationships as edges. The application of different rules runs simultaneously. So, it is possible that nodes in the graph can be deleted and created, but also kept when only some parameters of a node are changing while the rest remains unchanged. This is an explicit advantage compared to L-System symbols, where the symbol needs to be deleted and reconstructed. (Hemmerling et al., 2008)

The graphical representation of an object can be achieved by turtle commands. This gives the possibility to describe angles, different lengths and branching points. In addition, there are other three-dimensional geometric classes, describing objects, which are for example primitives like spheres, cones and boxes that can be used for the modeling and visualization of complex objects. To get a rendered image of high quality the free ray-tracer POV-Ray can be applied. (Kniemeyer et al., 2007)

The following part shows a simple example of a L-system graphically presented in GroIMP. The module **A** gets interpreted as a **sphere** which contains the attribute **float length** that is defining the length of the elements produced from **A**. The command **F(x)** draws a cylinder of the respective length **x**, **RU(a)** defines a rotation around the "up" axis by the angle **a**. The design of the growth-grammar is as follows:

```
module A(float length) extends Sphere(0.1);

Axiom ==> A(5);

A(x) ==> F(x/2) [RU(45) A(x*0.5)] [RU(-45) A(x*0.5)] F(x/2) A(x);
```

By applying this deterministic L-system for a total of four steps (1) – (4), the graphical representation in GroIMP looks like presented in the following illustration 2.

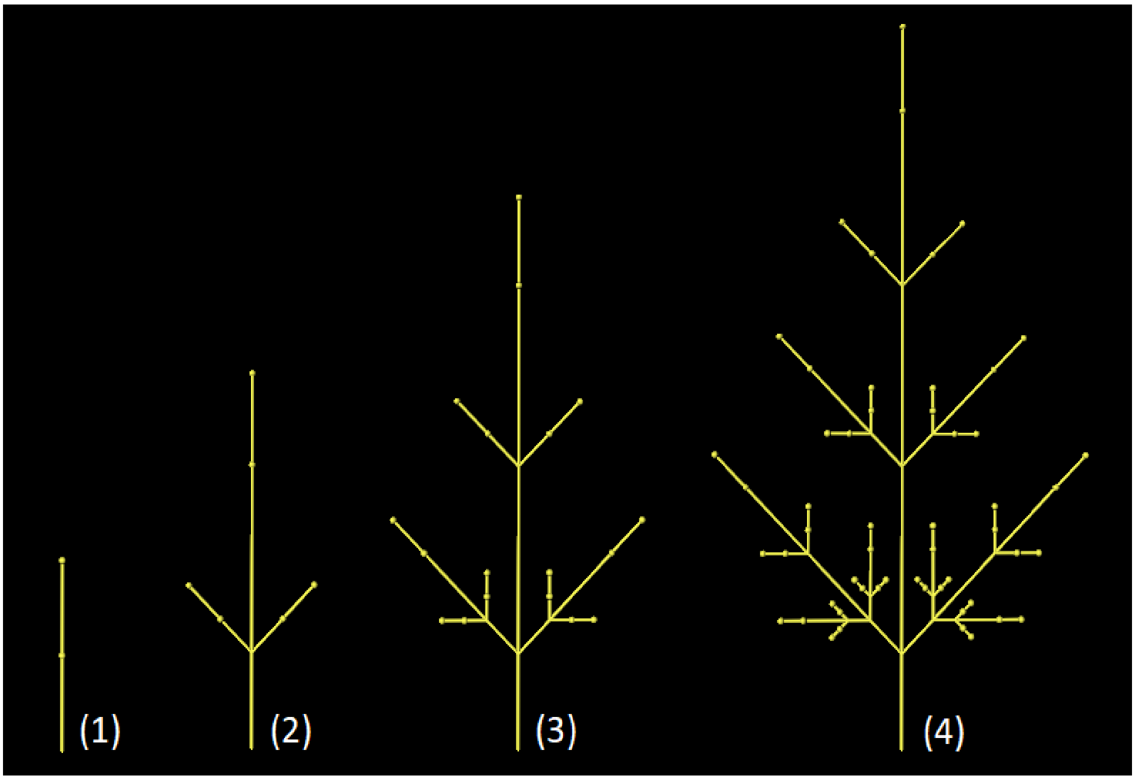


Figure 2: Graphical output of the execution of the first four steps of the above described L-System

A model by GroIMP can interact dynamically and is adjustable by the user. This makes GroIMP suitable and unique in order to develop structural models or combined structural functional models. (Kniemeyer et al., 2007)

These models can be used in different fields of applications for example for the modelling of the forest structure considering competition and plant-herbivore interactions like it was done by (Kurth et al., 2012), for the optimization of the illumination in a greenhouse for example done by de Visser et al. (2014) or for functional-structural plant modelling of beech trees which was done by Hemmerling et al. (2008).

1.7. SIBYLA

SIBYLA is a forest growth simulator which is able to model stand productivity, the stability of a stand and biodiversity, considering the influence of different thinning methods on a specific tree population under a wide range of natural conditions. Its modeling principle is individual-tree distance dependent (Fabrika, 2005). A related model on which SIBYLA is partially based was developed by (Pretzsch et al., 2002) and is called SILVA. The data basis was collected using national forest inventory data from Slovakia and Germany.

There are several features which characterize the model. Shortly summarized they are the generation of realistic stand structure, the influence effects of the stand’s density and intra- and interspecific competition of individual trees. The model considers a set of environmental conditions, tree mortality and any type of forest stand silviculture and harvesting. A large output gives information about individual trees but also about economic and ecologic traits of the whole stand. These points make the model very flexible in terms of modeling the growth of any stand type, whereby the simulation of horizontal and vertical structure of pure or mixed and even or uneven aged stands is possible. (Sedmák et al., 2013)

For the modeling process, the model is reliant on individual tree data which include heights, diameters, coordinates and crown parameters considering the different influencing factors described above. The model consists of several individual units each of them having a specific function and referring to the central SIBYLA database which stores all input data and output generated from the growth prognosis (Fabrika & Ďurský, 2005). The model’s architecture allows it to implement the data into a geographic information system (Fabrika, 2006). The functional principle of the growth simulator SIBYLA is illustrated in Figure 3.

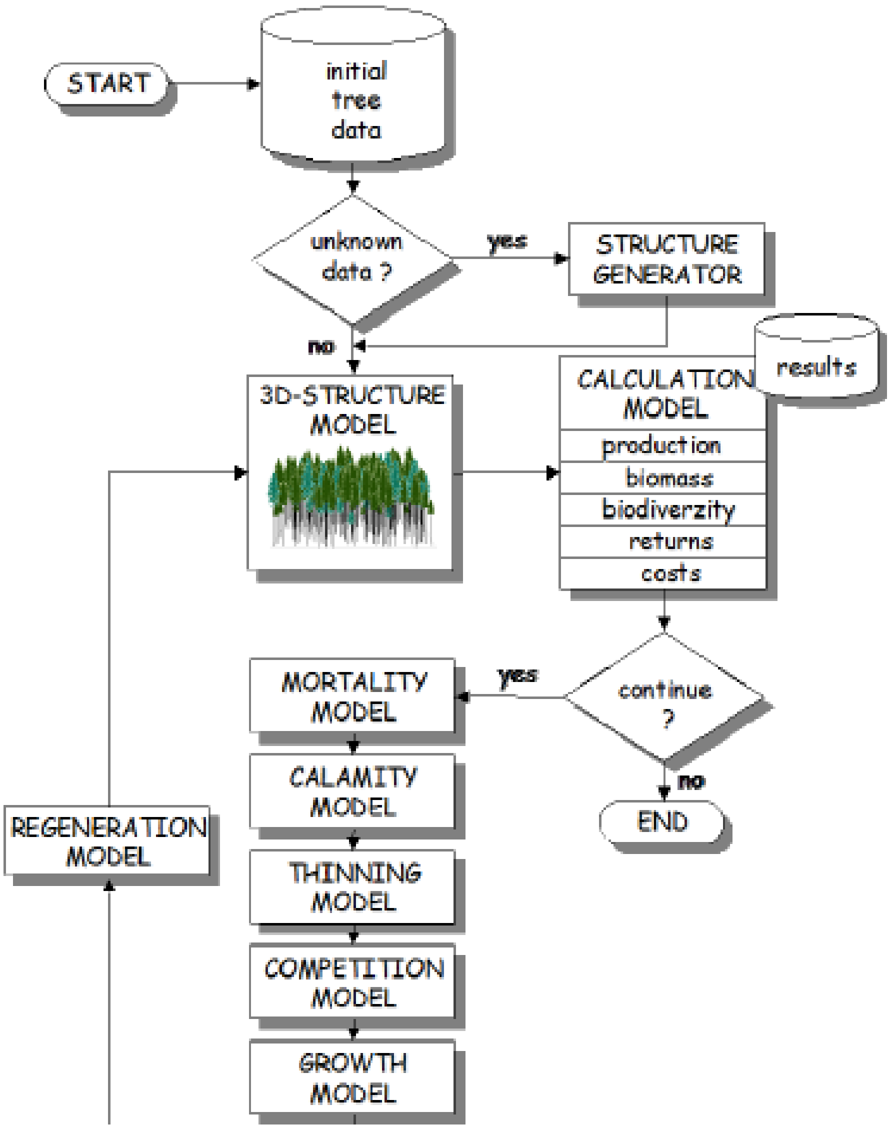


Figure 3: The functional design of the growth simulator SIBYLA (Fabrika, 2005)

The practical use of SIBYLA is shown in the work of Sedmák et al. (2013) where the case study has shown that multi-criteria optimization techniques together with the growth simulator open a possible way to optimize the thinning of forest stands. This process can include a specific functional orientation and can take environmental conditions and a mixture of tree species into account. It was demonstrated that the procedure works in the same way as the common planning procedure but provides a number of advantages. This decision-support-system on the basis of SIBYLA does not have the problem to apply general rules to a specific stand, gives more than only one optimal solution for the treatment, can evaluate the impact of the alternatives and select the optimal management action for a particular stand, is thus way more flexible considering the changes in natural conditions and is more adaptive when it comes to the implementation of new scientific and practical knowledge in the planning process. Therefore, the use of SIBYLA as the base of a decision-support-system can be a great tool to change and improve the forest management planning in Slovakia.

1.8. Topic of the work

The aim of this work is to design a model which is generating the structural development of the poplar (*Populus* ssp.). It is intended to have an interconnection with the forest growth simulator SIBYLA that provides data by simulating specific plots with a structural modeling platform. Therefore, the software GroIMP was chosen since it is providing several features which make it conducive for this type of task (see section GroIMP).

A stand simulation by SIBYLA returns general tree attributes for each year which characterize an individual tree on a specific plot with local environmental conditions. Because the output just includes "simple" tree attributes, like heights, diameters and crown diameters, they are insufficient to analyze features like the production of biomass or the carbon allocation in an accurate way. In this case, the structure-based downscaling of the general tree attributes to an explicit structural model of the tree, in particular of the crown, is needed and thus is the objective of this thesis.

The developed model of this work is parameterized for the poplar and can serve for the described use when simulating a poplar stand (or a mixed stand with poplar). This model should be built up by the outputs from SIBYLA. A short-rotation plantation poplar model extending to a maximum age of three years by Stiehm (2019) as a part of his doctoral thesis "Structural-functional concepts in forest modelling applicable for higher resolution of forest ecosystem simulations" also serves as a basis for the parameterization.

The linkage of GroIMP and SIBYLA for the data flow to GroIMP has already been done by Schön (2014) in his thesis "Structural-functional concepts in forest modelling applicable for higher resolution of forest ecosystem simulations", so this work deals exclusively with the creation of the structural poplar model in GroIMP using the given general tree attributes.

2. Material and Methods

The objective of this part is to describe the structural poplar model including the used data, the modules which represent the architectural units, and the functions on which the model is based. The used modules, functions, parameters and variables are explained in tables in order to make the model more understandable for the reader. Also, the design of the analysis of the model is presented here.

2.1. Further related approaches

A similar work has been done by Martin Schön in the year 2014 who created a structural model of spruce in GroIMP by given tree characteristics from SIBYLA. This work deals as a reference point for the thesis, especially for the interconnection between both software. Additionally, the doctoral thesis by Stiehm (2019) has revealed a large quantity of precise structural information of the crowns of young short-rotational poplar trees which serve as a basis of data for the model. How both of these approaches are used within the modeling process is shown in the following parts.

2.2. Data flow between GroIMP and SIBYLA

The interconnection between both of the software is an essential part of the model to provide the data of the SIBYLA database for the use in GroIMP. This connection has already been implemented by Schön (2014) in the thesis “Structural-functional concepts in forest modelling applicable for higher resolution of forest ecosystem simulations”. The source of data is a database of the MS ACCESS Type which is generated by SIBYLA. The database contains the general tree attributes described in the table below. H2 was chosen as a database tool since it has several benefits that are summed up in the thesis of Martin Schön. The import into GroIMP gets performed via the import of the .jar database file. The data that get transferred consists out of some general tree attribues which describe a poplar under specific conditions in annual steps to a maximum age of 20 years. The name of all attributes that are provided by SIBYLA are shown in the following Table 1, as well as a description and how they are defined in GroIMP.

Table 1: General tree attributes by SIBYLA: designation, description and definition in GroIMP

Designation in SIBYLA database	Description	Definition in GroIMP
age	age of the tree	int age
dbh	diameter at breast height for each year	double dbh
treeHeight	tree height for each year	float treeHeight
incrH	increment of the tree height	double incrH
cd	maximum of the crown diameter	double cd
ch	crown base height	double ch

These attributes give quite general information about the structure; therefore, the poplar gets described at a simple level. Figure 4 shows how the structure of the poplar is theoretically represented on that level of scale.

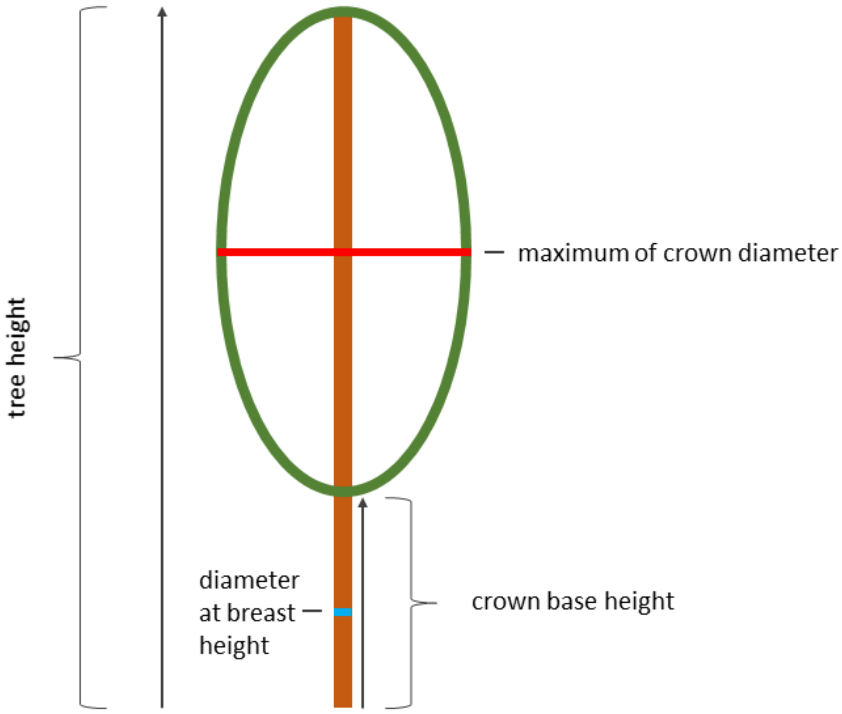


Figure 4: exemplary representation of the tree shape by the given tree attributes

2.3. General description of the poplar model

The generated model of this thesis is based on a structural downscale of the attributes that are described above. Thus, the architecture on a basic level of scale is exactly defined for each annual step. It is a purely structural model and implemented in the modeling platform GroIMP. Within the downscaling process the attributes are used in order to create the architecture of the poplar including above-ground woody biomass and leaves. It gets computed in a total of 20 annual steps. The output of the model is a three-dimensional structural representation of the poplar which is reproducing the attributes from the SIBYLA database but also modelling smaller scales of the structure like the branch distribution within the crown, branch lengths or branching orders. Out if this detailed crown information, the internal functions of GroIMP make it possible to analyze features like the total wood biomass of the model or even the light interception of the poplar if a light model is applied. In order to make the model working, the in Appendix 1 described steps need to be performed.

2.4. Global parameters

Beside the data given by SIBYLA, other global parameters need to be implemented in order to parameterize the functions of the growth grammar that generate the structure of the poplar. Some of these parameters are directly taken from Stiehm (2019) to be used in the functions from the same source. Since the functions are made for a short rotation-plantation poplar with a maximum of three years, they need to be adapted and extended to fulfill the task of modelling a single stem poplar of an age of 20 years. Here, the dimension of the influencing values is of central interest. Therefore, a set of additional global parameters was estimated which are used to scale the existing functions of Stiehm into a fitting range. Besides, other parameters have been introduced to describe the angles between the architectural units of the model. All global parameters are located at the top of the XL code. This gives the opportunity to easily access them and make them adjustable if data is collected in future research in order to make the model more precise. All global parameters are shown in Table 2.

Table 2: list of the global parameters

Designation	Type	Description	Source
year	int	age of the tree	
CLONE	int	clone type	Stiehm (2019)
d_scale	float	increase factor for the start diameter of the branches	estimated
dg_scale	float	deccrease factor for the secondary growth of the branches	estimated
branching_angle_2	int	branching angles of second order branches	estimated
branching_angle_3	int	branching angles of third order branches	estimated
angR	int	rotation angle for phyllotaxis	simplification of Stiehm (2019)
o1_bending	int	bending of a branch of the first order	estimated
o2_iNodeN_scale	int	decrease factor for the number of internodes of the second order	estimated
o3_iNodeN	int	number of internodes of branches of the third order	estimated
scale_ord	float []	factor to scale the length of an occurring branch in relation to the underlying branch length	estimated
startAngle_year	int []	tree age based starting angle of the first order branches	estimated

2.5. Modules and module attributes

The architectural threads of the model consist of different modules which are specific geometric units that form the whole tree and represent the tree organs. It is common practice that the different buds are represented as spheres and that geometric objects like the internodes of higher-order branches and the petiole are modelled as cylinders. A special feature are the leaves which are generated as a pointlist to enable the modeling of the characteristic shape. The *leaf*-module and the related parameterization were taken from Stiehm (2019). Another particularity is that the internodes of the stem are defined as frustums. This gives the opportunity to model the tapering of the stem divided into several trunk parts by defining a bottom and a top diameter at each part. Table 3 presents all used modules with the definition of the type and a description.

Table 3: list of the modules used within the growth grammar

Definition in GroIMP	Type	Description
Bud_GU	sphere	bud of the trunk and all branches except prolongation units
Bud_proLong	sphere	bud for the prolongation units of the branches
Bud_leaf	sphere	bud for the whole leaf including the petiole
Internode_main	frustum	internode of the main axis (trunk)
Internode_minor	cylinder	internode of the side axes (branches)
Leaf	pointlist	leaf with a typal shape
Petiole	cylinder	petiole of a leaf

To describe the current state at a specific point of time, several attributes are assigned to the modules. They can describe the spatial location and expansion as well as other characteristics like the age or the rank of a module. The following Table 4 gives an overview about all attributes that influence the condition of the different modules. The name, the data type, a short description and also the values that they are able to assume are presented.

Table 4: presentation of the module related attributes

Designation	**Data type**	**Description**	**Range**
t	int	age of the module	0 – 20
ord	int	branching order of the module	0 – 3
main	Boolean	affiliation to the main axis	true or false
prolong	Boolean	affiliation to a prolongation unit	true or false
guL	float	length of the growth unit the module is developing from	> 0
relPos	float	relative position alongside the related growth unit	0 – 1
relH	float	relative height of the module according to the height of the tree	0 – 1
baseHeight	float	height of the base of the branch at the trunk	0 – height of the tree
rank	int	rank of the segment	> 0
start_angle	int	start angle of the unit with respect to the horizontal plane	– 360 - 360
r_prev	float	horizontal extension (crown radius) at the specific height of the organ in the previous year	> 0
r_current	float	horizontal extension (crown radius) at the specific height of the organ	> 0
init	boolean	classification as initial unit of a branch	true or false

2.6. Taken over sub-functions of the growth grammar

For the modelling of the crown, some functions have been taken from Stiehm (2019) in order to provide a realistic growth of the related architectural units. Table 5 gives an overview about the functions that have been directly reused. The underlined inputs are the estimated globals which are used to fit the functions to a single stem poplar since they are parameterized for a short rotation-plantation poplar, they are described in previous Table 2.

Table 5: list of the subfunctions of the models including their input, output and description

Function	Inputs	Output variables	Description of the output
getINodeN	int CLONE, int t, int ord, boolean main, boolean proLon, float guL, float relPos, boolean isShrtSh, int o2_iNodeN_scale	int iNodeN	number of internodes per growth unit
budGrowth	int CLONE, int ord, boolean main, int t, float guL, float relPos, boolean proLon	true or false	probability of buds to sprout
isShrtSh	int CLONE, int ord, boolean main, boolean proLon, float guL, float relPos	true or false	determination of a shoot developing a short shoot
getDIncr	int t, int ord, float guL, int CLONE, float d_scale , float dg_scale, without float [] dIncrLOrd	float diameter_GU	start diameter and secondary growth of branches
getBinom	int n, double p	int N	probability based on binominal distribution
getPoisson	double lambda	int N	probability based on poisson distribution
getBladL	int CLONE, float relH, float relPos, int year	float bladL	length of the leaf blade
getPetiL	int CLONE, float bladL	float petiL	length of the petiole
getPetiD	int CLONE, float petiL	float petiD	diameter of the petiole
getPetiBladR	int CLONE, float relH	float petiBladR	angle between leaf and petiole
getLeafShape	int CLONE, float bladL	pointlist []	shape of the leaf

The function for the start diameter and the secondary growth of the trunk part were taken from Schön (2014) using the “method of direct smoothing of a taper curve” by Petráš (1986, 1989, 1990). This method was not parameterized for poplar trees, therefore the function for beech trees is used here. For each trunk part, a top and a bot diameter gets defined. In the following years it gets increased in each annual step. In Table 6 both functions are shown including the inputs they are working with.

Table 6: description of the start diameter defining function for the stem

Designation	Inputs	Output type	Description
base	float dbh, float height, float treeHeight, float incrH	float	defines the base diameter of a trunk element
top	float dbh, float height, float treeHeight	float	defines the top diameter of a trunk element

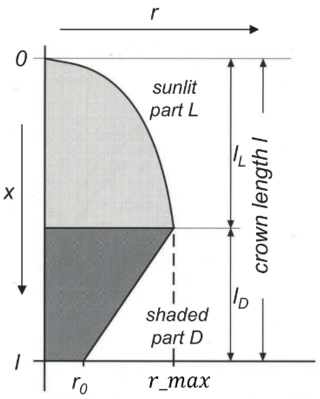
2.7. Self-implemented sub-functions of the growth grammar

For producing an explicit structural model of the crown with the given parameters, the above-mentioned functions were not sufficient. Therefore, additional functions were developed that are needed for the design of the model. This includes two functions which compute the location of each bud (1) (2) and a function to determine the radius at a specific height by a given crown shape (3):

(1) The function ***relH*** computes the relative height of all buds in each annual step in relation to the actual height of the tree. The z-coordinate of the respective bud gets used to calculate this relation.

(2) By the function ***out_of_crown***, the horizontal extension of a module gets analyzed and compared with the current radius at that specific height. If the module extends or will extend the crown radius after the development, the function returns the argument ***true***. This function is used within the growth of the second and third order branches to avoid them growing out of the crown radius.

(3) To produce the typal crown shape of a poplar which gives the current radius at a specific height “the principle of modelling a morphological curve of a crown” by Pretzsch (2001) was implemented as the function ***crown_shape***. It calculates the exact crown radius at a specific height position inside the crown, named in the model as ***r_current***, by using the crown length, the position inside the crown and the maximum of the crown radius provided by SIBYLA. The crown gets divided into a light and a shadow part. How the crown model composes is shown in Figure 5. The parameters ***a***, ***b*** and ***c*** are predetermined based on the modelled tree species; again, the parameterization of the beech serves in this case since it is the closest according to the poplar.



Inputs:

$x = top\ down\ distance\ of\ the\ respective\ bud\ (calculation\ by\ relH)$

$l = crown\ length\ (directly\ calculated\ by\ using\ SIBYLA\ database\ outputs)$

$= maximum\ of\ the\ crown\ radius\ (by\ SIBYLA\ database)$

Calculation of the radius at the specific height:

$$r\_current = \begin{cases} (x \geq 0) \land (x < a \times l) \rightarrow \dfrac{r\_max}{(a \times l)^b} \times x^b \\ (x \geq a \times l) \land (x \leq l) \rightarrow r\_max \times (1 - \dfrac{a \times (c-1)}{1-a} + \dfrac{x \times (c-1)}{l \times (1-a)}) \end{cases}$$

Figure 5: The principle of modelling the contour of a crown; modified version of Pretzsch (2001)

2.8. The growth grammar of the poplar model

The previous parts presented the underlying functions which are producing growth related variables and attributes of the modules. They are used in the relational growth-grammar which generates the structural components and the linkage between them. The relational growth-grammar of the model will be described here. There are a number of variables and parameters that influence the different parts of the growth-grammar. For these parts, only the values that directly influence the formation of the growth units are presented since some of them are influencing other values, like the ***treeHeight*** which is used to determine the current radius (***r_current***) at a specific height.

The model consists of an initiation function ***init*** and the ***growth*** function which determines the order of the application of the functions that form the different parts of the tree structure like the stem, the branches of a specific order or the leaves. The flow chart (Figure 6) shows how all main functions are related to each other and which sub function they use.

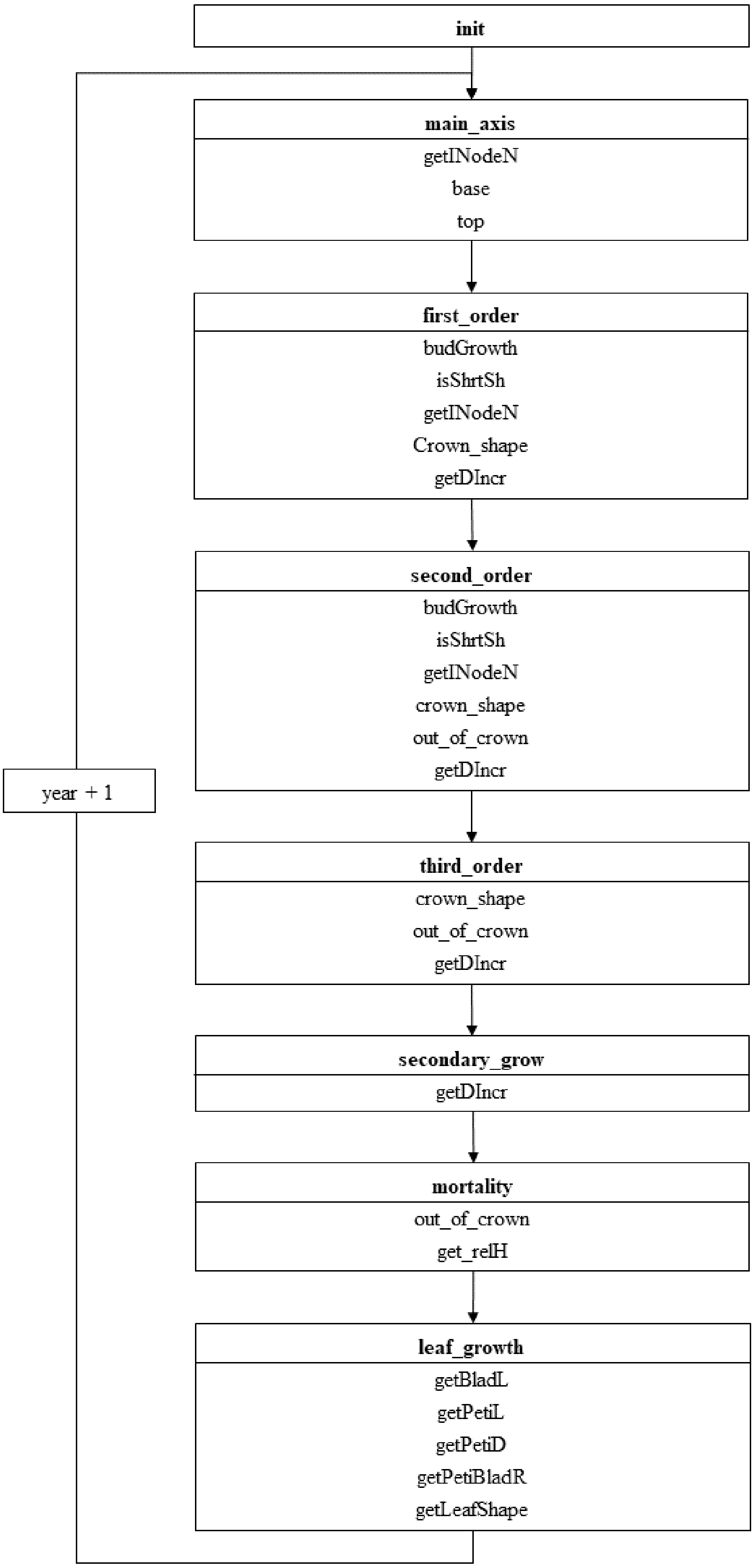


Figure 6: Flowchart of the poplar model Poplar_model.gsz with all main functions and the used subfunctions

2.8.1. The *init* function

The initiation of the model starts with introducing the time variable ***year*** which represents the age of the modelled tree. Also, a bud gets placed that is defined as the module ***Bud_GU***. This bud is the seed of the modelled poplar. The state of the bud is described by several attributes which are summarized in Table 4. Noteworthy is that the boolean ***main*** gets set to ***true*** since the bud is the initiation bud of the main axis.

2.8.2. The *grow* function

Here, the order of the growth functions of the different parts of the poplar is determined. This function gets executed up to a maximum age of 19 years since the data used for the model is extending to that value. In the case that the simulation time is reached, the model is printing out that the maximum age is reached. The order of the application of the functions within ***growth*** is:

i. ***main_axis()***
ii. ***second_order()***
iii. ***third_order()***
iv. ***secondary_growth()***
v. ***mortality()***
vi. ***year()***
vii. ***leaf_growth()***

The purpose of those functions and how they are built up is explained in the upcoming parts.

2.8.3. *main_axis()* – Formation of the main axis

Within this function the development of the main axis, which is equivalent to the stem, gets performed. This function gets executed with each ***Bud_GU*** which has the boolean ***main*** set to ***true*** because that characterizes it as a bud of the stem.

Several variables and parameters influence the growth. Variables which are calculated at this point, for example ***rTreeHeight***, are presented with a short description in the following list:

- ***incrH*** (description in Table 1)
- ***treeHeight*** (description in Table 1)
- ***dbh*** (description in Table 1)
- ***rTreeHeight***: tree height dependent on the rank of the respective trunk part
- ***iNodeN*** (description in Table 5)
- ***iLength***: length of an internode; length of the segment divided by the number of internodes
- ***aziBud***: array for the rotation of the buds around the underlying axis (from Stiehm 2019)
- ***startAngle*** (description in Table 2)

The growth-grammar of the function can be split up into three different parts:

(1) First, the respective part of the trunk gets generated. It consists out of the module ***Internode_main*** which inherits the attributes of the underlying bud. The length is determined of the provided tree height. For computing the diameter of the occurring trunk part, the two functions ***top*** and ***base*** are involved. After the trunk part has been built, a new terminal bud gets placed at the top with a rotation around the head axis of 90 degrees. The rank of the bud gets increased by one in order to make it possible to determine the tree height based on the rank. This is essential for the computation of the diameter function of the trunk parts that are formed in the next timestep.

(2) The buds of the leaves and the first order branches are built after the process of generating the woody part of the main axis and the terminal bud. The starting location of this generation process is at the start of the newly generated trunk part. With a *for*-loop which executes for the range of the number of internodes, the orientation angle around the head axis for the formation of buds gets computed for each internode by ***aziBud*** considering the angle ***AngR***. For further computations, attributes including the relative height compared to the tree height and the actual height are calculated for the end of each internode. In each step of the loop, the command ***M(x)*** moves the turtle to a certain point (***x***) of the newly created trunk part which is the ending position of each related internode. At that location, a bud of a branch (***Bud_GU***) of the first order is created. In addition, by a rotation of 180 degrees, a leaf bud (***Bud_leaf***) gets placed at the same position.

(3) The last part is the implementation of the secondary growth of the main axis. Here, the base and top diameter of all trunk parts is increased by a specific amount with the diameter function for the trunk involving the age-based tree height, the DBH, the ranked-based increment length and tree height as inputs. This implementation has been directly taken from Schön (2014).

The parts concerning the formation of the main axis are done within one step regarding the visualization in the graphical interface of GroIMP. In order to understand how they execute internally within the function; Figure 7 presents the explained parts (1) – (3).

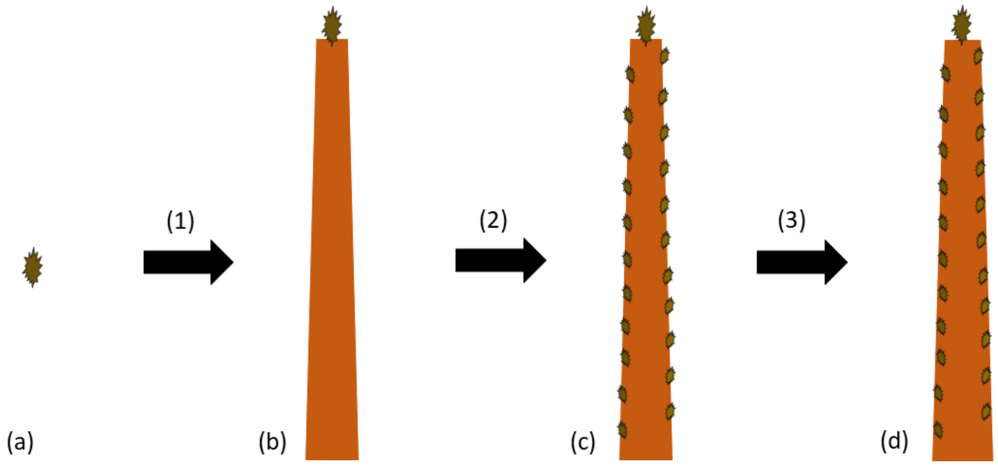


Figure 7: the bud of the main axis (a), the generated trunk with terminal bud (b) after step (1), the trunk with buds of the first order and the leaf buds (c) after step (2) and the secondary growth of the main axis (d) after step 3

2.8.4. *first_order()* – Growth of the branches of the first order

Initial growth

The sprouting of the respective buds into branches of the first order is realized within this function. There is a chance for the buds of the first order to break which is determined by the ***budGrowth*** function. Also, the age of the bud needs to be one as well as the order. Additionally, the height of the treated bud is not allowed to be beneath the crown base height.

For the generation of the branches some variables and parameters are used beside the attributes of the bud. They include data provided by SIBYLA, global parameters and variables which are produced by the subfunctions of the model. They are:

- ***ch*** (description in Table 1)
- ***iNodeN*** (description in Table 5)
- ***r_current*** (description in Table 4)
- ***startAngle*** (description in Table 2)
- ***changeAngle***: here equivalent to ***o1_bending***
- ***endAngle***: sum of ***startAngle*** and ***changeAngle***
- ***partialAngle***: angle between two internodes; ***changeAngle*** divided by the number of internodes minus one
- ***partialXLength***: horizontal extension of a single internode; ***r_current*** divided by the number of internodes

Equally to the main axis, the formation of the branches of the first order is realized by a growth-grammar which can be separated into different parts. They are presented in the following:

(1) A *for*-loop is computing the length of the first internode and the following ones by using a trigonometric calculation. For this purpose, the ***partialXLength*** as the adjacent leg and the angle in relation to the horizontal plane (sum of the partial angles up to the respective internode) as the **α** are taken as components of a triangle. The length of an internode as the hypothenuse gets determined by dividing the value for ***partialXLength*** by the cosine of the angle **α**. The value of **α** gets divided by 57.2958 to convert it from radian measure into degree. The values for each internode are summed up and assigned to the variable ***length_GU,*** which saves the length of the total branch. The calculation of the length of an internode is shown in Figure 8.

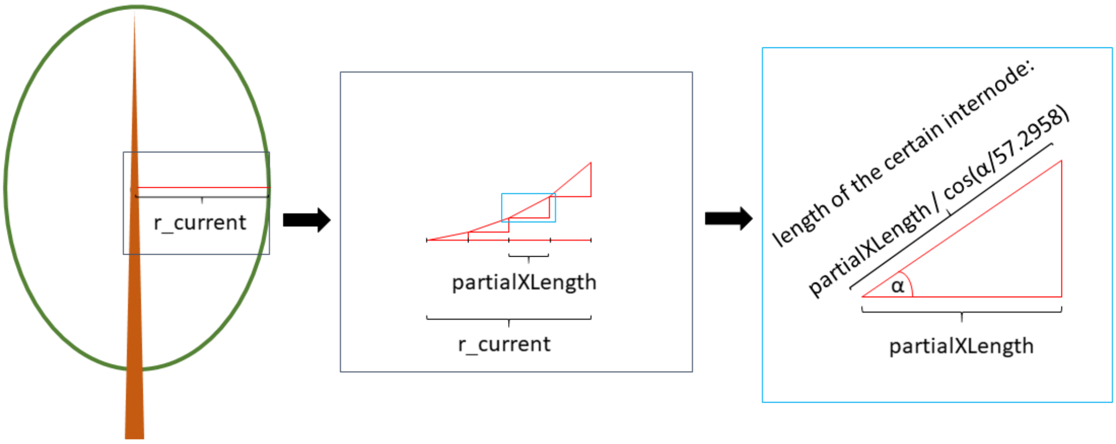


Figure 8: computation of the length of a single internode using the trigonometric function; r_current, partialXLength and the sum of the partialAngle (α) at the respective Internode serve as inputs

(2) The initiation of the axis is the command ***RU(90)*** which adjusts the branch into the horizontal alignment. The phyllotaxis gets determined by ***aziBud*** using the angle ***AngR*** equivalent to the growth of the main axis in order to use it for the formation of buds. In each iteration of another *for*-loop, which computes for the number of internodes, the length of the first internode (***first_length***) and the length of the following ones (***next_length***) are calculated in the same way as done in step (1). The relative position ***relNode*** of each internode gets calculated relating to the number of internodes. In addition, the function ***getDIncr*** determines the diameter (***diameter_GU***) of all internodes on that specific branch. Afterwards, the internodes are formed in consideration of the calculated values and angles. At the end of each occurring internode, a bud for the branches of the second order and a leaf is generated with a specific orientation.

(3) When the branch is fully formed, a bud (***Bud_proLong***) for the longitudinal growth is placed at the top inheriting some attributes including the radius (***r_current***) which is of central interest in the formation of the prolongation.

Longitudinal growth

Here, the prolongation of the branches of the first order that result from the respective buds (***Bud_proLong***) are formed. The bud break is not determined by a probability function which ensures that the prolongation of branches always takes place in the case they are not extending the crown radius. The function only gets applied to buds with an order of one. The values which have an influence on the prolongation are listed below:

- ***r_current*** (description in Table 4)
- ***iNodeN*** (description in Table 5)
- ***startAngle*** (description in Table 2)
- ***r_add***: difference between the previous radius and the current one; horizontal extension of the branch prolongation
- ***partialXLength:*** horizontal extension of a single internode; ***r_current*** divided by the number of internodes
- ***diameter_GU*** (description in Table 5)

Here, the growth-grammar is presented. In the case that the previous radius ***r_prev*** is higher than the current one, the function stops in order to not extend the crown radius. The different parts are shown in order to understand the formation process:

(1) The length of the whole occurring branch part gets determined using the value of ***r_add*** as the horizontal extension, as it was done for the initial growth of the branches of the first order. It also gets assigned to the variable ***length_GU***. How the value for ***r_add*** is determined is illustrated in Figure 9.

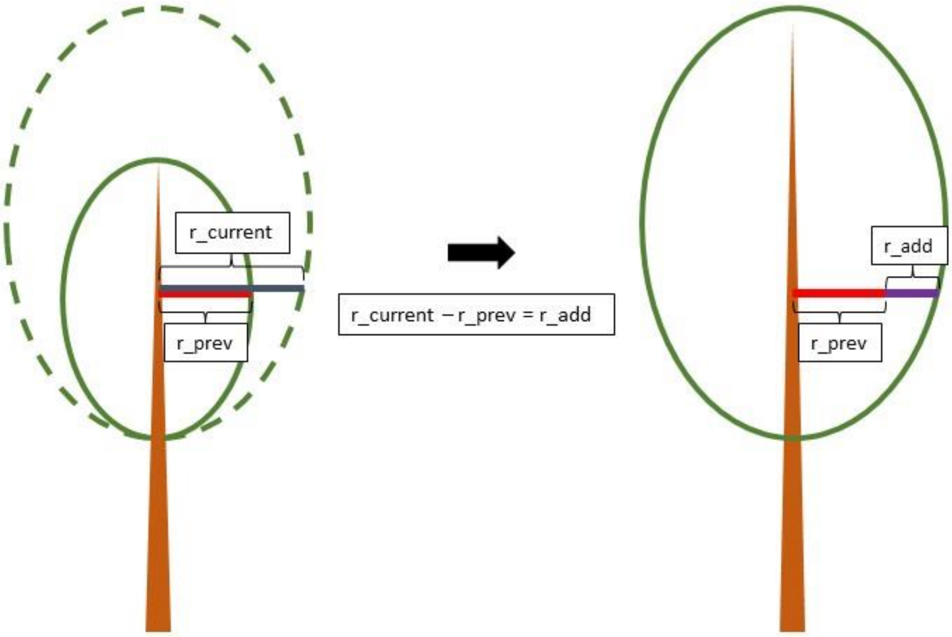


Figure 9: determination of the increase in the horizontal extension of a branch of the second order in a specific height determined by the previous radius (r_prev) and the present one (r_current)

(2) The rotation angle around the axis for the newly occurring buds is, as usual, defined by ***aziBud*** using the angle ***AngR***. Again, the lengths of the internodes are calculated as well as the relative position (***relNode***). Within the process, the single internodes are generated with an additional formation of buds of the second order and leaf buds at the end of each internode. As a start diameter, they use the value that is calculated by the function ***getDIncr***.

(3) At the end of the branch, another bud for the longitudinal growth gets placed with the rank attribute increased by one.

2.8.5. *second_order()* – Growth of the branches of the second order

Initial growth

This function ensures the growth of the branches of the second order. The probability of the break of the buds is determined by the ***budGrowth*** function. The order of the respective bud needs to be two in order to be addressed. The growth-grammar influencing values are the following:

- ***iNodeN*** (description in Table 5)
- ***x_coordinate***: x-coordinate of the respective bud
- ***y_coordinate***: y-coordinate of the respective bud
- ***r_current*** (description in Table 4)
- ***guL_new***: length of the respective branch of the second order; multiplication of the length of the underlying branch of the first order with the global parameter ***scale_ord***
- ***length_new***: length of a single internode; ***guL_new*** divided by the number of internodes
- ***diameter_GU*** (description in Table 5)

The growth of a bud is only executed if the output of the function ***out_of_crown***, using the coordinates for x and y and the length of the newly occurring branch, returns ***false***. This ensures that the branches of the second order do not extend the crown radius. The growth-grammar executes as follows:

First of all, the rotation around the axis for the formation of buds is defined as usual. A *for*-loop is determining the relative position of an occurring internode and then creating all internodes in each iteration. The command **RV(–0 .01)** is simulating the upward bending of the respective branch. Buds of the third order along with buds for the leaves are formed at each end of an internode with the usage of specific angles. At the end of the branch the prolongation bud with the ***rank*** increased by one is placed in order to secure the longitudinal growth of the second order branches.

Longitudinal growth

Like it was done for the branches of the first order, the longitudinal growth of the branches of the second order including all influencing values is presented here. They are:

- ***x_coordinate***: x-coordinate of the respective bud
- ***y_coordinate***: y-coordinate of the respective bud
- ***r_current*** (description in Table 4)
- ***iNodeN*** (description in Table 5)
- ***length_new***: length of a single internode of the prolongation branch; ***guL*** divided by the number of internodes
- ***diameter_GU*** (description in Table 5)

After defining the rotation angle around the axis for newly occurring buds and the relative position of the internode for each iteration, the internodes are generated. This is done with the related lengths and angles and an additional formation of buds for the leaves and the branches of the third order with fixed angles at their endings. A special case in this function is that only at the first and every fifth internode the buds get generated which leads to a decrease of branches of the third order on the prolongation units of the second order. At the end of the branch part, another prolongation bud (***Bud_proLong***) is placed with its ***rank*** increased by one.

2.8.6. *third_order()* – Growth of the branches of the third order

The buds of the third order develop into branches. No buds for a fourth order are placed. Since there are just slight differences between the influential variables and the growth grammar of the second and the third order, no detailed explanation is shown here. Still it needs to be mentioned that the number of internodes of the third order is not determined by the ***getINodeN*** function but is fixed to seven (***o3_iNodeN***).

2.8.7. *secondary_growth()* – diameter increment of the branches of all orders

At the top of this function the age of each minor internode gets increased by one. In the following part, the attribute ***guL*** of the minor internodes of the first order gets actualized. All internodes which have the boolean ***init*** set to ***true*** and ***ord*** to one are targeted, which marks them as the first internode of a first order branch. A query is summing the length of this internode and of all following internodes belonging to the same order. The output value gets assigned to all internodes on the respective branch as the mentioned attribute ***guL***, which represents the length of the branch where the internode is located at. Then the secondary growth of the minor internodes takes place by the function ***getDIncr***, making use of the actualized attribute ***guL*** beside other attributes and parameters which have an influence. Within the function, the order-based influence which is originally included in ***float [] dIncrLOrd*** is not used.

2.8.8. *mortality()* – Aging and mortality of the branches

This function is performed in each timestep after the formation and the diameter increment of the branches of all orders took place. The application of this function removes all branch forming buds which did not break. In addition, the existing leaves of the previous year get removed including their petiole, as well as all minor internodes which are located beneath the crown height value ***ch*** in order to maintain the crown base height. As well internodes which extend the radius at the specific height are removed. There is also a random number generator-based mortality for the minor internodes which is applied to all internodes of the second and third order. It is always done at the branch base where the boolean ***init*** is set to true in order to always remove the whole branch part. Here, the probability is set to 20 percent. The function also includes the computation of the relative height of some elements by applying the function ***get_relH***.

2.8.9. *leaf_growth()* – Growth of the leaves

The growth of the leaves is performed by the sprouting of the leaf buds (***Bud_leaf***). Here, as a parameter input beside the attributes of the buds, the crown base height (***ch***) is used. The function ***bladL*** computes the length of the leaf blade, while ***petiL*** and ***petiD*** calculate the length and the diameter of the petiole. The angle between the leaf and the petiole gets determined by the function ***petiBladR***. Additionally, a probability for developing into a leaf of the buds of the first order is introduced which is is set to four ninth, based on optical estimations.

The development of a leaf starts with the generation of the petiole with the use of the calculation by the functions and the definition of specific angles. The leaf gets placed at the end of the petiole with the use of ***petiBladR*** and additional orientation angles. At the end of the function all buds that did not sprout are removed from the model as well as the leaves that are located beneath the crown base height.

2.9. Analysis of the model

For analyzing the model regarding its accuracy and outputs, several aspects of the model are examined. This includes:

i. Several outputs of GroIMP: shoot surface area, mean of the branching angle, total number of internodes, sum of the shoot length
ii. the reproduction of the general tree parameters in each timestep
iii. the woody above-ground biomass production
iv. the distribution of the woody above-ground biomass among the tree parts (branches and stem)
v. effects of changing global growth parameters on the branch biomass (sensitivity)

How the outputs are obtained that are needed for the analysis is presented in the upcoming part. All analyses were done with R 3.4.2 (R Core Team, 2013) with the package tidyverse (Wickham, 2017).

2.9.1. Design of the parameterization

For the simulation of the poplar growth, the parameterization of the model needs to be specified. The values for the parameters that were used are presented in Table 7. They are based on estimations. The description of them can be found in the Table 2.

Table 7: values of the estimated global parameters

Parameter name	Value
int CLONE	0
float d_scale	10
float dg_scale	0.07
int branching_angle_2	75
int branching_angle_3	45
int angR	135
int o1_bending	10
int o2_iNodeN_scale	4
float [] scale_ord	{1, 1, 0.2, 0.8}
int [] startAngle_year	{45, 45, 45, 45, 50, 50, 50, 50, 55, 55, 55, 55, 60, 60, 60, 60, 65, 65, 65, 65}

In addition, three adjustments to the model have been made:

i. The actualization of the growth unit length ***guL*** within the function ***getDIncr*** is ignored. This is done to decrease the enormous computation time when using it.

ii. The number of internodes (***iNodeN***) of the zeroth order which is decisive for the number of branches of the first order, was set to an estimated value of three. Therefore, in each annual step two branches of the first order will develop. This was done because the model will develop far too much branches of the first order when executed with the probability function ***budGrowth***. The valuation was done by visual assessment.

iii. The growth of the leaves has been left away because it is also extremely slowing down the model and they do not have an influence on the architectural features that will be analyzed.

Another component is the text file **TREE.txt** which provides the general tree attributes as input parameters. It is an exemplary data file which contains the same tree attributes which would be given by the SIBYLA database when using it with the model. The representation of the values for each year of the data file are given in Appendix 2.

2.9.2. Analysis of the reproduced general tree attributes

In order to analyze the correctness of the growth grammar the reproduction of the different general tree attributes by the poplar model should be checked. The data file **TREE.txt** gives the growth parameters that are used within the model in GroIMP in each timestep. The development of the produced tree attributes meaning the **tree height**, the **crown diameter** and the **crown base height** is determined by a total amount of 20 model runs with the model parameterization described in Table 7 and the correspondingly adjusted growth grammar. The reproduction of the general tree attributes of the text file by the poplar model is analyzed and is graphically presented for the simulation period of 20 years. It gets analyzed if the model is producing them in a right way and dimension. The maximum percentage of the deviation of the produced attributes to the given tree attributes is displayed in every case. This is done by calculating the difference between each tree attribute of the data file (**y_{data}**) and the mean of the respective reproduced value for the respective year (**mean(y_{model})**). The difference gets divided by the value from the data file in order to determine the relation of the deviation. The following equation is applied to every annual model output regarding the above-mentioned tree attributes.

$$percentage\ of\ deviation = \frac{|y_{data} - mean(y_{model})|}{y_{data}}$$

The maximum and the mean of these values for each attribute gets determined. It presents the maximal percentage and mean percentage deviation of the reproduced tree attributes to the given ones. These values are showing how well the model is reproducing the tree attributes of the data file. Also, the standard deviation of the produced tree attributes will be illustrated to show the stochasticity of the model. For the analysis the produced tree attributes initially need to be determined. Therefore, the internal functions of GroIMP that can be found under the button “Panels” → “RGG Panels” → “GROGRA Functions” were used most of the time (Kurth, 1994). The following paragraphs present the methods which were specifically applied to access the respective values.

2.9.2.1. Tree height

The stem is modelled as a frustum and therefore cannot be analyzed with the GroIMP internal functions. Therefore, the length of the stem gets computed by the sum of all lengths of the existing trunk parts in the respective year. Also, the height of the highest branch internode in the model is determined by using the GroIMP internal functions which can be found under “GROGRA Functions” → “Analysis” → “elementary” → “max. Z”. The respective value is representing the highest z-coordinate of all growth units within the model and therefore representing the highest point of the tree beside the stem. In the next step, the values for the stem length and the highest point of the branches get compared with each other. The larger value represents the height of the tree in the respective year.

2.9.2.2. Crown diameter

For determining the maximum of the crown diameter, the GroIMP internal function that is located at “GROGRA Functions” → “Analysis” → “elementary” → “max. radius projection xy-plane” was used. The value directly represents the maximum crown radius of the structural poplar model. For comparing it with the tree attribute ***cd***, the value from the text file for each year gets divided by two to convert it into the radius.

2.9.2.3. Crown base height

The crown base height of the poplar model can be taken out of the GroIMP internal functions. This is done by the usage of “GROGRA Functions” → “Analysis” → “elementary” → “min. Z”. The value is representing the height of the lowest growth unit in the model beside the stem since this function does not work with a frustum as well.

2.9.2.4. Method of determining the biomass and distribution

The biomass of the branches is determined analyzed by the GroIMP internal functions (“GROGRA Functions” → “Analysis” → “elementary” → “sum branch volumes”). This was done for total amount of twenty model repetitions. Since the stem gets modelled as a set of frustums the volume cannot be determined by these functions. For the purpose of determining the volume of the stem, the function ***stem_volume_segments()*** was implemented. It outputs a value for each part of the trunk for each annual step that needs to be summed up by hand in order to determine the volume of the whole stem. The function is always ignoring the top segment. Nevertheless, this segment has an extremely small volume compared to the others, so it does not influence the total volume of the stem at all. Since the diameter growth and the longitudinal growth of the stem are strictly deterministic (same value in each model run for each year), the value for the stem only needs to be calculated for one model run. The sum of the volume of the branches and the stem at a certain point of time represents the total woody above-ground biomass of the poplar at that year and also gets computed for 20 times. Beside the mean of the respective variable over the diameter at breast height, the relation between the mean of the branch and stem biomass to the total woody above-ground biomass gets calculated and presented in order to determine the biomass distribution of the woody tree parts.

2.9.3. Design of the analysis of the sensitivity of global parameters

Here, the sensitivity of the global estimated parameters should be examined. With the sensitivity analysis, the change of the output relating to the change of an input of a parameter can be determined (Saltelli et al., 2004). Therefore, the impact of the different parameters within the growth grammar can be analyzed (Grimm & Railsback, 2012). The parameter values which led to the “most similar looking” poplar were used as the standard parameterization (Table 7). For determining the impact of the parameters in the model, the biomass of the branches was chosen as the output variable. All estimated parameters beside the clone type, illustrated in Table 2, are used.

To get an insight of the effect of the estimated parameters the value of each parameter that is used in this analysis is changed by ten percent upwards and downwards while the other parameters stay constant in the model run (Pianosi et al., 2016). There are three parameters which cannot be changed by ten percent since they are defined as integer values. In this case, their value is changed by one upwards and downwards. The respective parameters are ***o2_iNodeN_scale***, ***o3_iNodeN*** and ***iNodeN***. The biomass of the crown is used as the output since it is the important output variable when it comes to the practical use of the model when determining the total biomass. The mean difference of the model output of the changed parameter ($y_{\Delta\ parameter}$) and the standard parameter ($y_{parameter}$) gets determined in percent. The calculation is shown in the following equation.

$$percentage\ change\ in\ output = \frac{|y_{parameter} - y_{\Delta\ parameter}|}{y_{parameter}}$$

The procedure gets repeated just for a total amount of ten times for each parameter (five times downwards, five times upwards) because of the low stochasticity the model is showing (presentation in the results).

3. Results

A structural model of a poplar was created in the platform GroIMP with the use of the data file **TREE.txt**. The internal functions of the platform allow it to present some general attributes of the modelled poplar. Table 8 shows the means of these values determined by 20 model runs. It can be seen that the modelled tree is around 12 m high, of which around 9 m belong to the crown.

Table 8: Presentation of all tree attributes provided by the GroIMP internal functions at the maximum age of 19. The mean of twenty model runs is shown by using the data file ***TREE.txt*** *as input..*

Output variable	Mean value
total number of internodes	45274.65
crown base height [m]	3.01
tree height [m]	12.22
sum of all shoot lengths [m]	484.19
sum of all shoot volumes [m³]	0.04485928
sum of the shoot surface area [m²]	8.8123
crown radius [m]	1.38
branching angle [degree]	51.9
maximal shoot diameter [m]	0.068

Additionally, Figure 10 shows the graphical outputs of the model in five-year steps (4, 9, 14 and 19 years). The architectural structure of the tree can be seen without the leaves.

Figure 10: Graphical output of the model model_poplar.gsz for the ages 4 (a), 9 (b), 14 (c) and the maximum age of 19 years (d)

Figure 11 shows the modelled poplar with leaves at an exemplary simulation period of five to eight years. It should demonstrate how the model looks like when executed with the formation of leaves. Still, this version was not used for any analysis.

Figure 11: Graphical output of the model model_poplar.gsz with the development of leaves at an age of 5 (a), 6 (b), 7 (c) and 8 (d)

3.1. Reproduction of the tree attributes of the data file

In order to analyze the accuracy of the model regarding the given tree attributes, the general tree attributes which are provided by the data file **TREE.txt** are compared with the general variables for each annual step that are produced by the model. A complete presentation of all produced tree attributes with the mean and the standard deviation for each year is shown in Appendix 3. As well, the deviation of the given attributes to the produced means by the model for each timestep in percent is shown in Appendix 4.

Figure 12 shows the graphical output obtained from the used parameterization of the poplar model (1) and also the comparison of the model with the use of the ***budGrowth*** function (2) which was left away since the crown was developing by far too much branches estimated by visual assessment.

Figure 12: Presentation of the graphical output of the poplar model with the used parameterization for the data analysis (1) and with the use of the function budGrowth for the number of internodes of the main axis (2)

3.1.1. Tree height

Figure 13 shows the development of the mean tree height by twenty model repetitions (data points) each with representation of the standard deviation. The progression of the height curve is increasing with age on an approximately linear basis. The values show almost no standard deviation over the whole simulation period of 20 timesteps (0 – 19 years). Comparing the simulated tree height with the one from the data file (line) it should be noted that the values up to a tree age of nine years are almost equal. In the later years the models mean of the tree height is slightly increasing in relation to the ones from the data file but still representing them quite well. The maximum of this trend can be observed at the age of 19, where a deviation of 1.02 m is determined. It is equal to a percentage of deviation of 9.11% between the values. Overall, the total deviation of both data groups is smaller with a mean value of 0.3 m and the respective percentage of 5.03%.

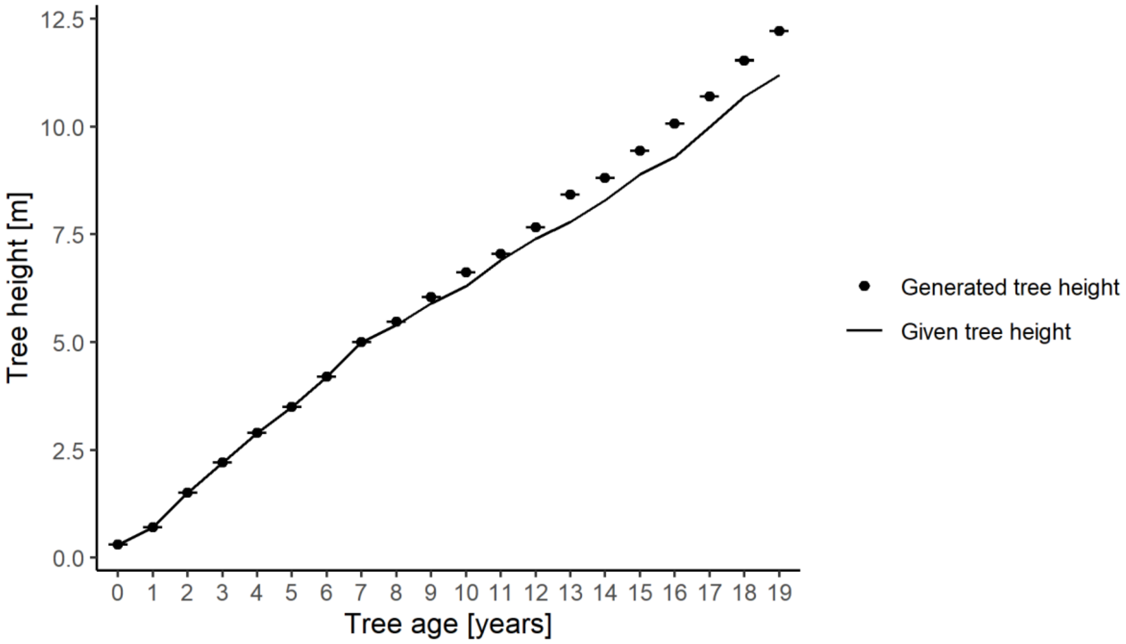


Figure 13: Development of the mean tree height of the model (data points) over the simulation period of 20 years for each year (with standard deviation) and the development of the tree height by the data file (line); Single horizontal lines through the data points denote a standard deviation of zero

3.1.2. Crown base height

The temporal development of the crown base height from the data file (line) and the mean value from the poplar model (points) for each annual step, here also with the standard deviation, is shown in Figure 14. The mean of the crown base height by the model is stable in some growth periods (in years: 2-3; 6-9; 10-14; 15-19) and is always increasing after these periods. The values show no standard deviation in the first fifteen years of the model and a small deviation at the following ages.

The comparison between the simulated data and the provided crown base height shows that the model is always overestimating the given value. Only at the age of one year the values are exactly the same. This can also be seen in the mean deviation of 0.19 m between the expected and generated one which is a relative deviation of 10.7%. The maximum of the relative deviation between the modelled values and the given ones are at the age of two and three with a value of 44.44%.

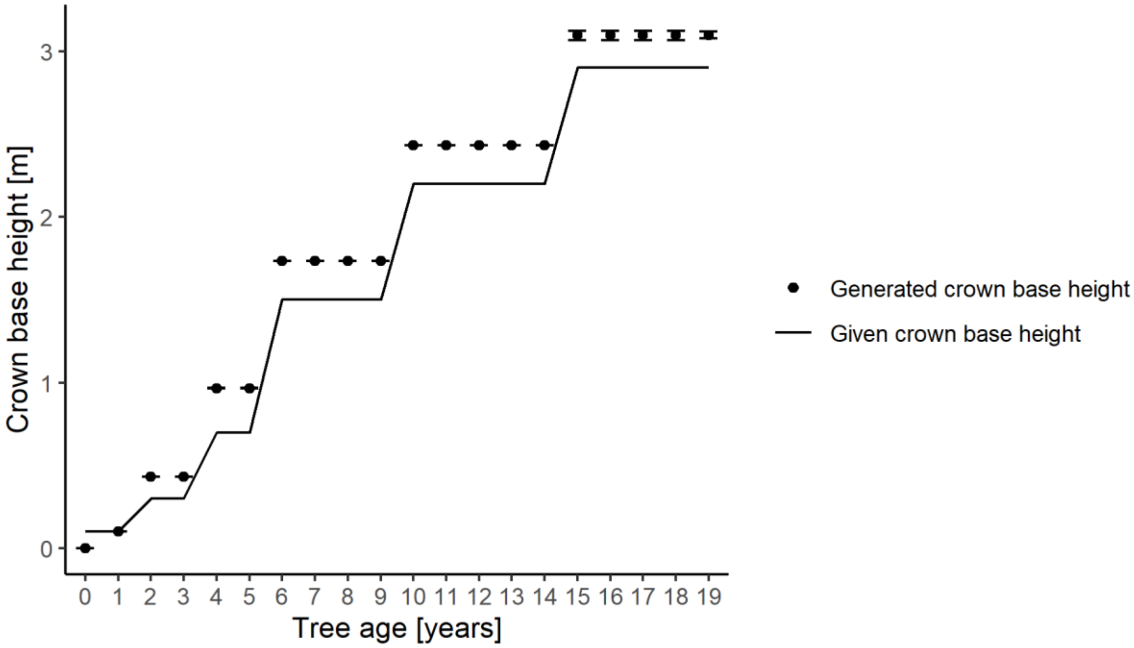


Figure 14: Development of the mean of the crown base height together with the standard deviation of the modelled values (points) and the development of the given crown base height by the data file TREE.txt (line); Single horizontal lines through the data points denote a standard deviation of zero

3.1.3. Crown radius

In Figure 15 the development of the mean crown diameter (points) produced by the model with standard deviation and the given one by the data file (line) is illustrated. The mean of the crown radius is strongly increasing within the first three years and then showing an approximately linear growth. The standard deviation of the mean values is almost zero for the first four years, very small for the years four to eight and slightly bigger for the following years. Still, the coefficient of variation is rather small with a maximum of 4.18% at an age of 15.

The given values of the data file are almost equal to the mean of the generated ones up to a tree age of four. Afterwards the mean of the crown radius by the model is slightly smaller than the one provided by the text file. The deviation between the values does not show an increase with the age of the tree. Still, this deviation is quite small with a mean of -0.08 m, -8.63 expressed in percentage. The maximum of the relative deviation between the data pairs is at the age of six with a percentage of -13.98%.

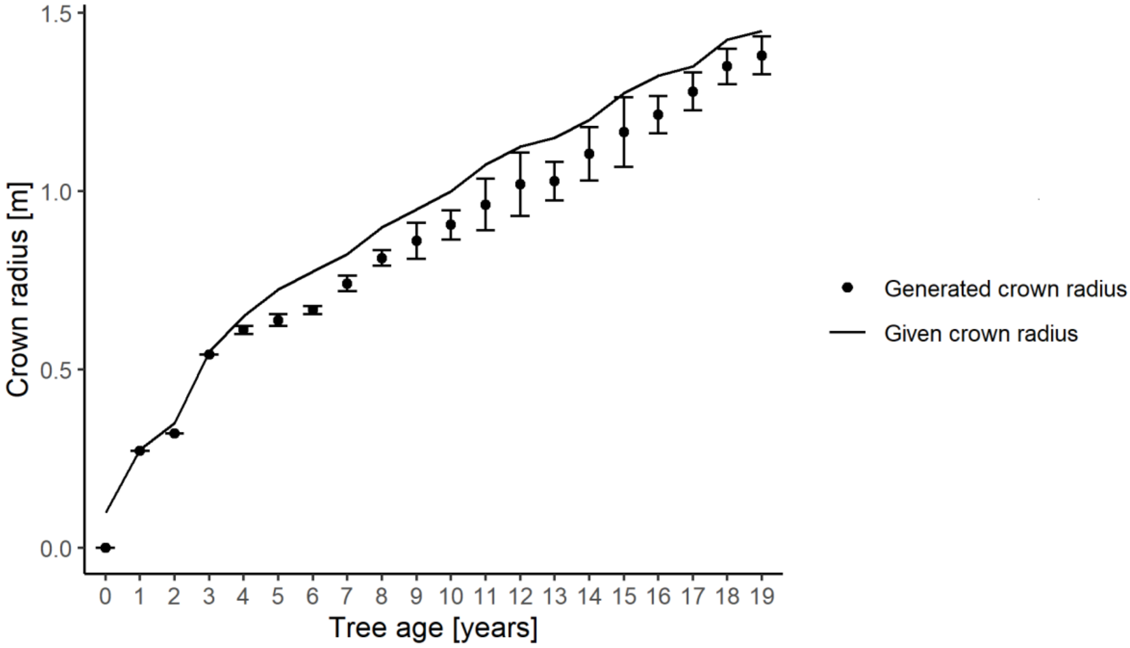


Figure 15: Development of the mean of the crown radius together with the standard deviation of the modelled values (points) and the development of the given crown diameter divided by 2 from the data file TREE.txt (line); Single horizontal lines through the data points denote a standard deviation of zero

3.2.Biomass production and distribution among the tree parts

Here, the production of the woody above-ground biomass by the model is shown. It is the central output variable of the model which is important for several fields of studies. A full presentation of all analyzed values regarding the biomass for each year is shown in Appendix 5.

The development of the respective value in cubic meters for the increase of the diameter at breast height (DBH) is shown in Figure 16, also with the standard deviation. The increase of the woody biomass value for the smaller values for the DBH is quite small but is increasing with increasing diameter. The curve progression is approximately exponential. Each modelled value does not a show a considerable deviation with a maximum coefficient of variation of 0.21% at the age of 19 years.

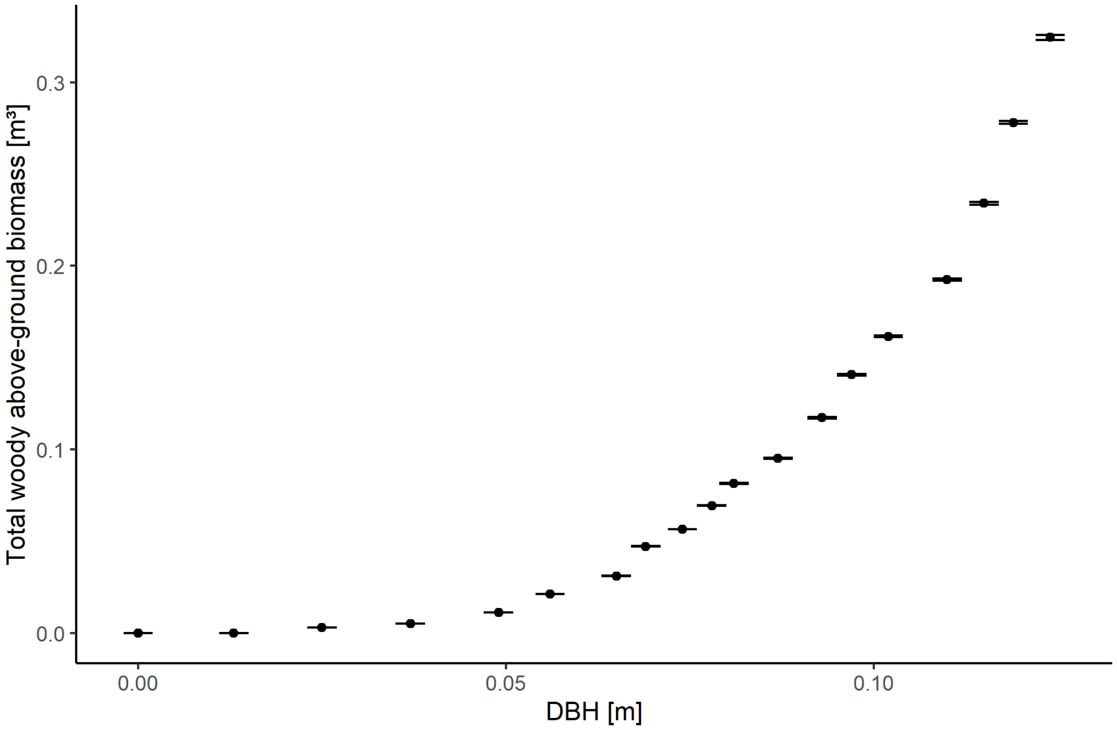


Figure 26: Development of the average aboveground woody biomass (stem + branches) of the poplar model for the simulation period of twenty years in annual steps over the diameter at breast height in meters with standard deviation; Single horizontal lines through the data points denote a standard deviation of zero

Beside the total woody above-ground biomass, the woody biomass of the branches is presented in Figure 17. The DBH range is the same as in the previous graphic for the woody above-ground biomass. The increase of the branch biomass is quite low in the DBH range of zero to five centimeters but shows an exponential increase in the following years. The standard deviation of the modelled value is increasing with the age of the poplar, with a maximum of 0.0007 at the age of 19. The resulting maximal coefficient of variance is quite small with a value of 1.52%.

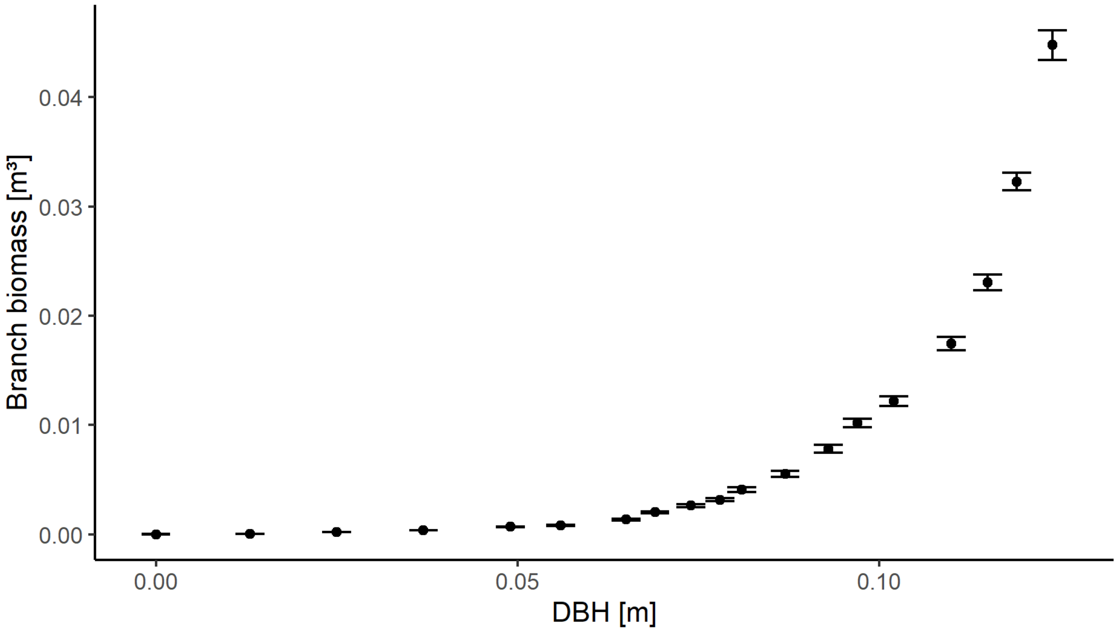


Figure 37: Development of the mean branch biomass of the poplar model for the simulation period of twenty years in annual steps over the diameter at breast height in meters with standard deviation; Single horizontal lines through the data points denote a standard deviation of zero

Since Figures 16 and 17 are just showing the total woody above-ground biomass and the biomass of the branches, the percentage proportion of the stem or rather the branches is not presented. Therefore, Figure 18 shows the mean percentage of both of the tree compartments over the simulation period of 20 years by 20 model runs. It can be seen that the percentage of the stem is much higher than the percentage of the branches in each year except the first year 0. The value for the stem shows a large increase in the DBH range from 0 cm to 4 cm while the value for the branches is decreasing by the same amount. In the past years the values stay quite stable, but the volume of the stem shows a decreasing trend as well as the value for branch volume shows an increasing trend of percentage.

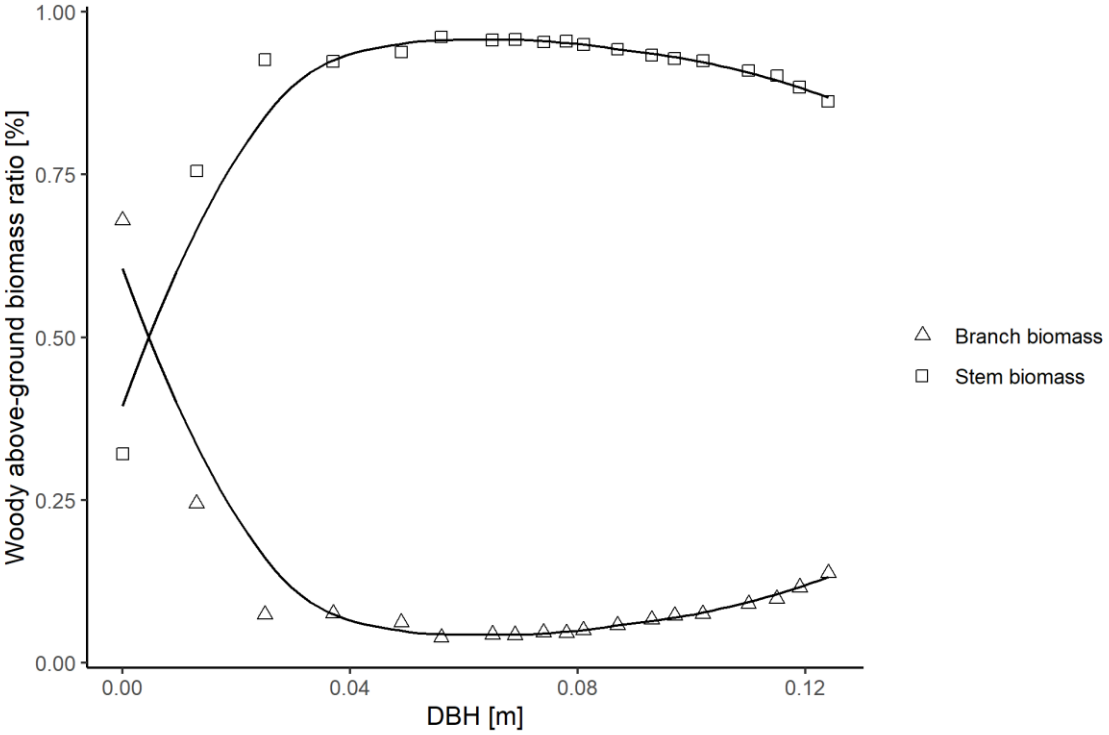


Figure 184: development of the percentage of the stem volume (squares) and the branch volume (triangles) of the poplar model for the simulation of twenty years in annual steps over the diameter at breast height in meters

3.3. Summary of the outputs

Altogether, the deviation of the produced tree attributes is relatively small with regard to the crown radius. Considering the other variables, the model shows almost no deviation between the different model runs. Also, the average biomass output is showing no considerable deviation.

Therefore, the following sensitivity analysis is done with five runs for each parameter. This is done since the results show that it can be expected that the model will not show a high variation in the output by several model runs.

3.4. Sensitivity analysis

Here, the local sensitivity of all estimated global parameters is presented. Figure 19 shows the relative change in the output (woody biomass of the branches) when changing a parameter by ten percent downwards (black) and upwards (grey), or rather by 1 downwards (black) and upwards (grey) in the case of integers. The red lines represent a change in the output of ten percent in relation to the mean value simulated by the twenty models run. When a bar of the relational output change exceeds the red line, it implies, that a relative change in the input of ten percent results in a higher change in the biomass of the branches in relation to the mean value by the model with standard parameterization. The respective changed parameters which are leading to this phenomenon are assumed to be the most sensitive ones with respect to the branch biomass. The parameters which meet this requirement are ***iNodeN***, ***d_scale*** and ***startAngle_year***, since they exceed the "ten-percent-line" when changing their value in both directions. The parameter ***startAngle_year*** is by far the most influencing one. An increase by ten percent leads to an increase of almost 163% of the woody branch biomass. The relative output change caused by the adjustment of ***iNodeN*** also has a great effect with an output change of a value between 50% and 55% in both directions. The increase or rather the decrease of the parameter ***d_scale*** just slightly exceeds the red line with a value of 13.3% by a parameter change of 10% and -12% when decreasing it by 10%. Also, it is noticeable that the value for ***dg_scale*** is quite near to the red line in both directions.

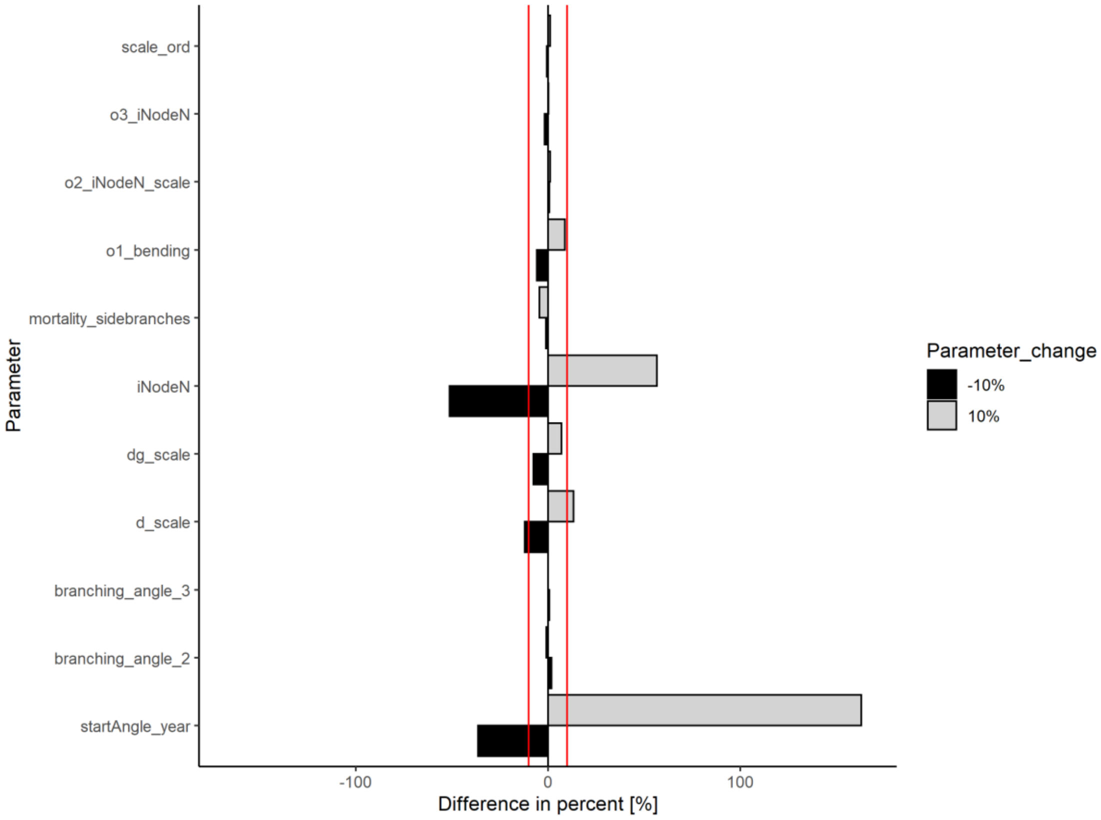


Figure 19: The percentage difference between the mean output of the model with standard parameterization and the output with each parameter increased or decreased by ten percent, or rather by 1; the red line represents the limit of a change in output exceeding the change in the parameter value

4. Discussion

An executable structural poplar model has been successfully implemented. The graphical output of the model at the maximum age of 19 years looks realistic when thinking about the typical shape of a poplar.

Since no complete data basis was used to parameterize the model, several aspects have been estimated and a specific growth-grammar was developed that functions with the estimated inputs. Therefore, the practical use and the quality of the model needs to be validated and discussed in the following part. Of central importance are the reproduction of the general tree attributes that are provided by the text file, as well as the outputs in terms of the woody biomass, its distribution and the sensitivity of the parameters.

4.1. Reproduction of the tree attributes of the data file

This paragraph deals with the analysis of the general tree attributes that are produced by the growth grammar of the model. Also, a discussion about the comparison with the given data by the file **TREE.txt** is presented.

The first attribute that is analyzed is the tree height. Up to a tree age of nine years the values represent the exact values of the data file. This can be explained by the fact that no branches of the first and following orders extended the height of the stem. The stem in turn uses the tree height from the data file which leads to the exact height from the data file. In the following years, some of the branches of the poplar overgrow the stem which results in an oversized tree height of the model. The deviation to the tree height from the database slightly increases with age which is caused by the increasing length of the branches but also by the increasing angle of the branches of the first order. The deviation is still small so it can be assumed that the tree height is well produced by the model. This is revealed by the mean percentage deviation between the model and the given value for the tree height (5%) and the maximum percentage of deviation (9.11%). For a further extension to a higher age, more investigation is necessary to examine if the trend of overproducing the tree height is increasing at higher ages which would be important for the practical use of the model. Still, for a modeling range of 20 years the tree height is represented sufficiently.

Looking at the crown base height, the reproduced tree attribute from the model is, with the exception of the first two years, always slightly higher than the crown base height of the data file. On one hand, this is because the control of the lower crown is done by removing all branch parts and their successors that are located beneath it. On the other hand, the branches do not grow exactly at the height position of the crown base height. Therefore, the lowest branch part which does not fall below the value from the data file defines the crown base height. This causes in an extension of the crown base height in every year. To make the reproduction more accurate the position-placement of the buds of the first order needs to be remodeled since it is not based on the crown base height in its current form. In particular, the relative deviation is relatively high in the younger ages of the poplar with a maximum of 44.44% at the tree age of two and three years. The deviation in meter between the modelled and the given values is quite stable with increasing tree age. Since the values for the crown base height are increasing with each year, the percentage of deviation is decreasing with age. Therefore, it can be assumed that the deviation of the modelled crown base height to the given values is more accurate with rising age. This effect should increase when the modeling time exceeds the current modelled age range.

The crown radius in the model gets reproduced quite well compared to the data file (crown diameter divided by two). In most of the years, it its slightly lower than the one provided by the data file, shown in a mean percentage deviation of -8.63%. The model is producing the crown radius based on the crown shape function that was implemented into the model. This function always computes the radius based on the specific height where the related bud is sprouting. In order to reproduce the exact value from the data file, a bud needs to exist at the exact height position within the crown, where the radius is the maximum based on the shape function. This is quite impossible according to the growth-grammar of the model. In addition, the mortality function cuts all branches which extend the crown radius at the specific height, so the branches can never exceed the crown radius. Therefore, the maximum crown radius of the model is either the same but mostly a little bit lower than the given attribute by the data file.

Summarized it can be said that the model overall reproduces the tree attributes by the data file in an accurate way considering the tree height and the crown diameter, still the functions could be adjusted to make the model even more accurate in terms of reproducing the given tree attributes. Since the maximum relative deviation of the modelled values to the data values strongly varies with 9,11% for the tree height, 44,45% for the crown base height and 13.98% for the crown radius, it should be noted that the model could be more accurate, especially when it comes to the reproduction of the crown base height in earlier years. However, the woody above-ground biomass in the earlier years is decisively influenced by the volume of the stem and not by the branches, as Figure 18 with the distribution of the tree parts shows. So, the high relative deviation of the crown base height in the younger ages compared to the input data does not strongly influence the above-ground woody biomass. With a mean percentage of deviation of 5.03% for the tree height, 10.7% for the crown base height and -8.63% for the crown radius, the model shows a deviation from the input data. The oversized tree height in the respective years has a slight overestimating effect on the woody above-ground biomass, while the undersized crown length based on the crown base height and the undersized crown radius have the opposite effect. Considering this, the overall size of the crown is slightly underrepresented by the model.

4.2. Sensitivity analysis

The results of the sensitivity analysis have revealed the global parameter ***startAngle_year*** as the most sensitive of the model, in particular in the case of an increase. This is explained by the fact that the length of the branches of the first order depends directly on this parameter since the length is computed by the horizontal extension of the crown and the angle (Figure 8). An increase in the start angle can result in a large increase in the branch length. In turn, the branch length highly influences the diameter of the respective branch and thereforealso the branch biomass.

As well, the number of internodes of the main axis plays an important role. This is clear since it determines the number of the branches of the first order whichs amount is decisive for the total volume. Like expected, an adjustment in both direction (one branch more or less) has nearly the same impact on the mean of the branch biomass.

Beside the already mentioned parameters, ***d_scale*** also is assumed to be sensitive. This is explained due to its direct influence on the start diameter of all branches which in turn strongly influences the branch volume. The parameter ***dg_scale*** which is decisive for the increment diameter growth of the branches is slightly beneath the limit of being indicated as sensitive but its effect is assumed to increase when the tree age range of the model is extended since its impact is increasing when the function ***DIncr*** is applied multiply times to a specific branch part. The model was simulated for only 20 timessteps, so a higher modeling range should reveal an increased sensitivity of this parameter.

4.3. Biomass and biomass distribution

The values of the woody biomass of the branches show an increasing standard deviation with increasing age. This is based on the random sprouting probability of the buds of the second and third order as well as on the random mortality of the branches of the respective orders. For the practical use of modeling older stands, the model should be analyzed if the increasing trend is continuously growing in order to determine its stability.

Both woody biomass curves (whole above-ground woody biomass and biomass of the branches) show an exponential development. This is consistent with the analyzed relationships between the aboveground biomass and tree components of the poplar, sampled in the work of Zhang et al. (2016), the allometric relationships between the DBH, stem biomass, branch and the aboveground woody biomass of hybrid poplars by Fortier et al. (2017) and the biomass model for leafless above ground biomass, considering the different tree compartments (Morhart et al., 2013). Still, it should be noted that the mentioned studies analyzed the biomass in weight units while the model in this work returns the volume. To make both comparable, the following graphic (Figure 20) shows on the right (b) the output of the model in a comparable range with a conversion of the volume into a weight unit (branch dry biomass in gram). This was based on the work of (Pliura et al., 2007) which estimated the mean density of poplar wood to 340 kilograms per cubic meter. On the left (a) the branch biomass development over the DBH in millimeter from the work of Morhart et al. (2013) is shown for comparison. It can be seen that the value of the literature for the branch biomass is already showing a visual increasement at a DBH of 20 mm while a visible effect for the modelled values is being observed at a DBH of around 70 mm. After that point, the modelled data is quickly exceeding the values of the literature data. For example, this is shown at a DBH of 8.1 mm where the branch dry biomass of the model with a value of 13.6 kg is much higher than the one by Morhart et al. (2013) where the values is between 2 and 3 kg at the respective diameter. Thus, it becomes clear, that the model is underproducing the branch dry biomass up to a DBH of 70 mm compared to the referred data and afterwards is increasing it by an oversized amount.

The fact, that no visible increase of the branch volume is seen in the DBH class up to 70 mm indicates that the start diameter of the branches needs to be increased. The high gradient at the end could be initiated by the increment growth of the branch diameter that might be too high. Another explanation could be the data itself. The relation between the DBH and the values for the crown base height and crown diameter are not necessarily specific for a poplar. If this is the case, a relation between the DBH and the branch biomass will not be in a right dimension. Still, a difference of more than 500% percent cannot be only explained by that, a combination of both assumptions is likely.

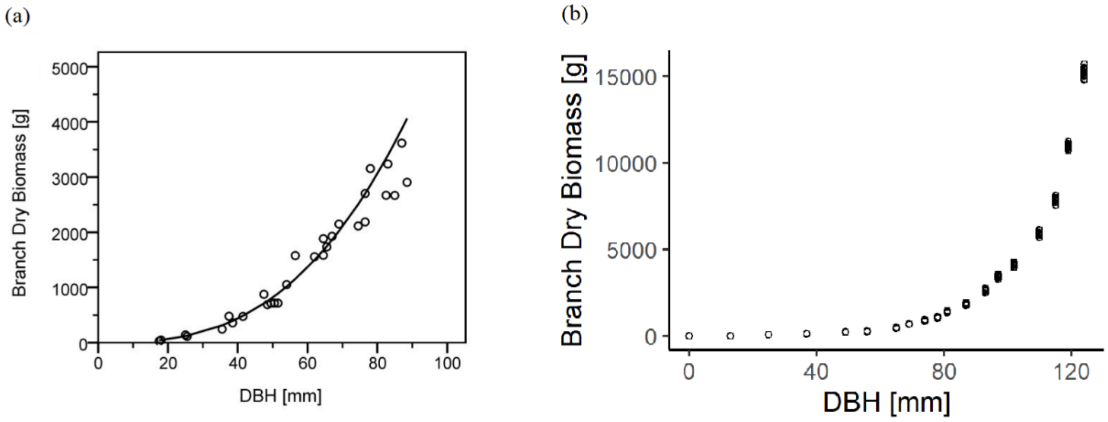


Figure 205: (a) Biomass model for leafless branch biomass in g over the DBH in mm from Morhart et al. (2013); (b) total branch volume development in cubic meters over the DBH generated by the poplar model in twenty runs

Not only the woody biomass of the crown, but also the ratio between the stem and the crown biomass plays a role. To analyze the correctness of the biomass distribution, Figure 18 of the results part is compared with a similar graphic from the literature. The distribution of the biomass among the branches, the stem and the leaves of a trembling aspen calculated by allometric equations (Johnson et al., 2009) is shown in the following Figure 21. By comparing it with the model, a clear difference becomes visible. In the literature data, the percentage of the stem biomass is continuously increasing while the percentage of the branch biomass is decreasing. On the other side, the model only shows this trend for the DBH of 1.3 cm – 3.7 cm. Past this DBH range, the percentage of the branch biomass is increasing while the stem biomass decreases.

A reason could be the parameterization of the model considering the increment growth of the branch diameter. A decrease of it would lead to a decrease of the branch volume and the typical relation as seen in Figure 21 could be reproduced. Another explanation could also lie in the underlying data provided by the text file **TREE.txt**. If the data for the stem and the crown does not fit to a poplar, the relation between the crown woody biomass and the total above-ground biomass would be incorrect. This is the case when either the diameter value or the crown length of the text file or even both of them are significantly larger than in reality while the stem volume stays in the same range.

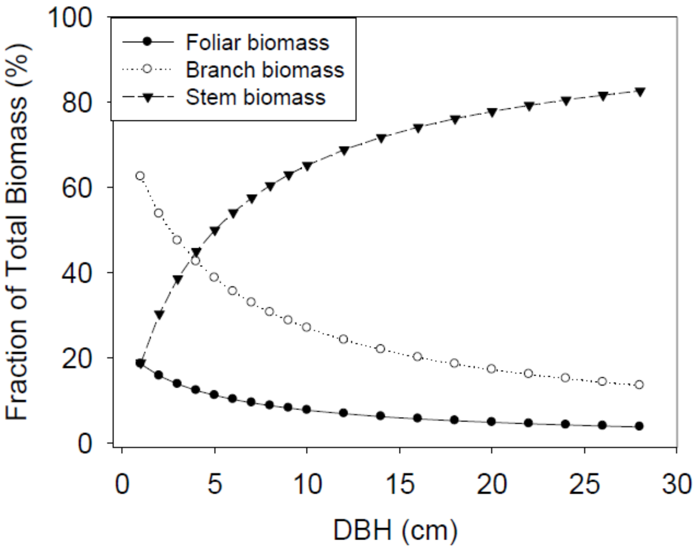


Figure 6: Biomass distribution among the branches, stem and leaves of Populus tremuloides by allometric equations in the ALMANAC$_{BF}$ *model on the basis of allometric equations from Ter-Mikaelian & Korzukhin (1997)*

4.4. Conclusion

The results have shown that the model reproduces the general tree attributes mostly in a good way, also the optical assessment of the graphical output supports this assumption. Still, some inconsistencies considering the production of the woody above-ground biomass maintain. When evaluating the model, it needs to be considered, that no data for a single stem poplar was used for creating the model since there was no specific data available which could be used. Therefore, the results were compared to data from the literature.

The comparison shows that the model is underrepresenting the amount of the branch biomass in the lower DBH range (0 – 70 mm), while the gradient of the curve is extremely high for the larger diameters and the value easily extend the ones from the literature. The relation between the woody biomass of the crown and the above-ground woody biomass also shows that the branch volume is oversized in relation to the stem volume starting from a DBH of 70 mm. Combining both of these facts, the difference between the model and the literature data could result from the diameter growth of the branches addressing both, the start diameter and the increment of the diameter. A possible solution would be to increase the scale parameter ***d_scale*** for the start diameter of the branches. On the other side, the diameter increment, defined by ***dg_scale***, needs to be decreased in that case. The problem could also or additionally be in the underlying data **TREE.txt**. Here, specific data for a poplar should be obtained and used to analyze the model. If the mentioned discrepancies maintain with input data for a poplar, the parameters should be adjusted. If, after adjusting the parameters, the results are still in an unrealistic dimension, then more data should be collected. On the one hand general tree attributes like in the text file, but on the other hand also branch numbers, angles lengths and diameters of the respective branches. The new parameters could be used to adjust the model since all global parameters are located at the top of the code and are therefore easily changeable.

In its current form, the model can be used to describe the explicit structure of a poplar based on the output of SIBYLA. A validation and reparameterization of certain parameters could resolve uncertainties regarding the modeling of the branch biomass. Due to the architecture of the growth-grammar of the model, it is possible to adjust the model by newly sampled data. The model uses general tree attributes as the input that can be provided by SIBYLA and is modelling the specific crown shape based on the work of Pretzsch (2001) which is parameterized for several tree species. Since all other growth related parameters are either directly set, like the start angle of the branches of the first order, or are calculated out of the mentioned inputs and the crown shape, like the length of the branches of the first order, it should be possible to reparametrize the model even for other tree species in further studies to make it applicable for a greater range of use by using it with the outputs from SIBYLA.

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6. Appendix

Appendix 1: General information for the execution of the model Poplar_mode.gsz

In order to execute the model, the folder “umontreal-simul-ssj-6005840” needs to be placed into the plugin folder of GroIMP. As well, the folder “Poplar_model_data” which contains the text document TREE.txt and the H2 database tool should be put into drive D:\ .

Appendix 2: the values of TREE.txt for each year which serve as exemplary data for the model

age	dbh [cm]	incrDbh [cm]	treeHeight [m]	incrH [m]	cd [m]	ch [m]
0	0.0	0.0	0.3	0.3	0.20	0.1
1	0.0	0.0	0.7	0.4	0.55	0.1
2	1.3	1.3	1.5	0.8	0.70	0.3
3	2.5	1.2	2.2	0.7	1.10	0.3
4	3.7	1.2	2.9	0.7	1.30	0.7
5	4.9	1.2	3.5	0.6	1.45	0.7
6	5.6	0.7	4.2	0.7	1.55	1.5
7	6.5	0.9	5.0	0.8	1.65	1.5
8	6.9	0.4	5.4	0.4	1.80	1.5
9	7.4	0.5	5.9	0.5	1.90	1.5
10	7.8	0.4	6.3	0.4	2.00	2.2
11	8.1	0.3	6.9	0.6	2.15	2.2
12	8.7	0.6	7.4	0.5	2.25	2.2
13	9.3	0.6	7.8	0.4	2.30	2.2
14	9.7	0.4	8.3	0.5	2.40	2.2
15	10.2	0.5	8.9	0.6	2.55	2.9
16	11.0	0.5	9.3	0.6	2.65	2.9
17	11.5	0.5	10.0	0.7	2.70	2.9
18	11.9	0.4	10.7	0.7	2.85	2.9
19	12.4	0.5	11.2	0.5	2.90	2.9

Appendix 3: mean values with standard deviation of the analyzed tree attributes by the model Poplar_model.gsz

Tree age	**Tree height [m]**	**Crown base height [m]**	**Crown radius [m]**
0	0.30 ± 0.0000	0.00 ± 0.0000	0.00 ± 0.0000
1	0.70 ± 0.0000	0.10 ± 0.0000	0.27 ± 0.0000
2	1.50 ± 0.0000	0.43 ± 0.0000	0.32 ± 0.0000
3	2.20 ± 0.0000	0.43 ± 0.0000	0.54 ± 0.0000
4	2.90 ± 0.0000	0.97 ± 0.0012	0.61 ± 0.0056
5	3.50 ± 0.0000	0.97 ± 0.0006	0.64 ± 0.0081
6	4.20 ± 0.0000	1.73 ± 0.0000	0.67 ± 0.0060
7	5.00 ± 0.0000	1.73 ± 0.0000	0.74 ± 0.0107
8	5.47 ± 0.0001	1.73 ± 0.0000	0.81 ± 0.0108
9	6.05 ± 0.0001	1.73 ± 0.0000	0.86 ± 0.0252
10	6.62 ± 0.0001	2.43 ± 0.0000	0.91 ± 0.0204
11	7.05 ± 0.0001	2.43 ± 0.0000	0.96 ± 0.0357
12	7.66 ± 0.0001	2.43 ± 0.0000	1.02 ± 0.0445
13	8.42 ± 0.0002	2.43 ± 0.0000	1.03 ± 0.0273
14	8.81 ± 0.0002	2.43 ± 0.0000	1.11 ± 0.0373
15	9.44 ± 0.0003	3.10 ± 0.0140	1.17 ± 0.0488
16	10.08 ± 0.0003	3.10 ± 0.0140	1.12 ± 0.0263
17	10.71 ± 0.0004	3.10 ± 0.0140	1.28 ± 0.0262
18	11.54 ± 0.0004	3.10 ± 0.0140	1.35 ± 0.0246
19	12.22 ± 0.0003	3.10 ± 0.0100	1.38 ± 0.0269

Appendix 4: relative deviation of the given tree attribute by the data file TREE.txt to the reproduced means by the model

age	**deviation to tree height [%]**	**deviation to crown base height [%]**	**deviation to crown radius [%]**
0	0.00	-	-
1	0.00	0.00	-0.93
2	0.00	44.44	-8.51
3	0.00	44.44	-1.31
4	0.00	38.04	-5.98
5	0.00	38.08	-11.90
6	0.00	15.56	-13.98
7	0.00	15.56	-10.12
8	1.32	15.56	-9.67
9	2.49	15.56	-9.30
10	5.06	10.61	-9.42
11	2.10	10.61	-10.43
12	3.57	10.61	-9.34
13	7.91	10.61	-10.58
14	6.13	10.61	-7.96
15	6.05	6.74	-8.51
16	8.35	6.74	-8.35
17	7.07	6.74	-5.19
18	7.85	6.74	-5.28
19	9.11	6.82	-4.77

Appendix 5: mean value of the woody above-ground biomass, the stem and the branches

DBH [m]	**total above-ground woody biomass [m³]**	**stem biomass [m³]**	**branch biomass [m³]**
0.000	-	-	-
0.000	0.00003	0.000009	0.00002
0.013	0.0020	0.0001	0.00004
0.025	0.0030	0.0027	0.0002
0.037	0.0051	0.0047	0.0004
0.049	0.0114	0.0107	0.0007
0.056	0.0213	0.0204	0.0008
0.065	0.0312	0.0298	0.0014
0.069	0.0473	0.0453	0.0020
0.074	0.0566	0.0540	0.0026
0.078	0.0695	0.0663	0.0032
0.081	0.0816	0.0775	0.0041
0.087	0.0953	0.0897	0.0055
0.093	0.1173	0.1095	0.0078
0.097	0.1407	0.1305	0.0102
0.102	0.1616	0.1494	0.0122
0.110	0.1925	0.1750	0.0175
0.115	0.2341	0.2111	0.0230
0.119	0.2781	0.2459	0.0323
0.124	0.3244	0.2797	0.0447

Eidesstaatliche Erklärung

Hiermit versichere ich gemäß §7 Abs. 5 der Master-Prüfungsordnung vom 23.09.2012, dass ich die vorliegende Arbeit selbständig verfasst und keine anderen als die angegeben Quellen und Hilfsmittel benutzt habe. Ich versichere, dass schriftliche und digitale Version der Arbeit übereinstimmen.

Marius Heidenreich

06.12.2020, Göttingen