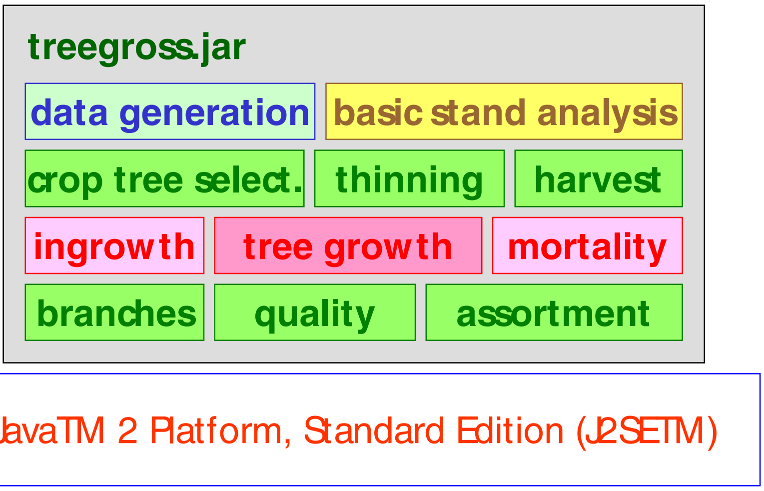
TREEGROSS

TREE GROWTH OPEN SOURCE SOFTWARE

- a tree growth model component -



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Introduction

TreeGrOSS is an Open Source project of the department of growth and yield of the Forest Research Station of Lower Saxony in Germany. About 10 years ago there has been a major shift in Lower Saxony's silvicultural policy. This mainly means an increase in the percentage of hardwoods, natural regeneration instead of clearcutting, more mixed species stands and well structured stands. Consequently the growth and yield department shifted the focus of research from the stand to the tree level and started working on a forest growth model based on single tree information of the experimental plots which a scattered over north west Germany. For practical application the forest growth model was integrated into a computer program to allow forest growth simulation. This program has been updated and extended in the past. Today's version of BWINPro is used by the Forest Service and the public mainly for stand analysis, silvicultural strategy development, education and presentation. A special version KSP is used to analyze and forecast permanent plot inventory.

The interest, the use and the demands of users have reached a point where the small development team of the forest growth simulator BWINPro is tied up by answering questions and making minor changes to optimize the program for special users. In order to get back to further development of additional components the team has decided to start the open source project TreeGrOSS. This should enable users to optimize the program for there needs, verify the code, and -very important- integrate the forest growth model into company software. Since there has been a lot of interest in the growth simulator by foresters and researchers from other countries the programming code is documented in English. This hopefully will allow to use TreeGrOSS as an example or frame for other models to save programming effort.

As a programming language Java was chosen. Java is an easy to learn and object oriented languages. Java programs are platform independent and do run on nearly all modern computer operating systems like, Windows, MacOS, Linux, and Unix. In form of Java applets the programs can be also based on the internet. Another advantage of using the Java language is that the Java 2 Platform, Standard Edition (J2SDK) is provided at no costs by Sun Microsystems and that there is no need for an expensive development environment. In addition to the J2SDK you actually only need a normal text editor. On the internet you can find a lot of free and helpful java programming examples and programming tutorials. So there is even for foresters no excuse, everybody can make use of the TreeGrOSS project.

Software component

TreeGrOSS is no final computer program. Instead it is designed to be a software component which can be utilized to create special software solutions. The treegross.jar includes all necessary Java classes of the tree growth model for north western Germany of the Forest Research Station of Lower Saxony. However, it does not include the routines and components such as a data bank, formatted output, visualization and data interfaces. These you can find in the application example for stand simulation.

The tree growth model component is stored in the treegross.jar. This file contains the programming objects which are called in Java programming language class files. The objects or class files are documented in the following.

The treegross.jar is distributed under the General Public License (GPL). This means that the software component is free and that the source code is available. This assures that every user can check the code and does not have to use the software as a black box. By having the source code checked by other users, the quality of the software will be increased. In addition the user can even alter the source code for his or her needs. He should of course clearly mark those changes, before he distributes the new code to others.

General remarks about the tree growth model

The idea of creating a tree growth model for forest practice was to replace the yield tables by some solution which is more suitable to managing mixed forest and which can give more information to forest management. Yield tables are nearly all set up for pure stands. They assume a fixed treatment like moderate or heavy thinning at specific intervals and they only give stand information such as average diameter, height, total volume and so on. In order to manage our forest today we need more flexibility and more information. To decide about the right time of thinning and the best way of further stand development a modern forest enterprise needs information on a single tree level. From this information it is possible to calculate economical values about actual revenues of thinning and harvest operations by assortment and quality aspects and to derive structural information which is important for the evaluation of ecological values.

The approach which was chosen for modeling is straight forward and oriented on the needs of forest practice and planning. The main variables of interest in this respect are on a tree level the development of tree diameter and height, and the derived assortment. In order to make the tree growth model useable for mixed forest, the size of the tree crowns needed to be included into the model to reflect the different needs of growing space of the different species.

There are different approaches to build tree growth models. A statistical approach can be based on data of long term observations and will therefore give relative precise information on diameter and height growth. In an eco-physiological approach it is possible to model the processes of tree growth, such as light, nutrient uptake and photosynthesis. These models are very useful for the understanding of forest ecosystems. A third approach are tree architectures models, which are mainly based on the botanic knowledge of trees. But the final decision on the model approach is usually also based on the data which is available.

The forest research station of Lower Saxony (NFV) has a net of long-term experiments which range over northwest Germany. The huge data base consists of more than 3500 experimental plots, of which about 2500 are still in observation. To utilize this unique data base a biological but statistical approach seemed to be the best way to build a tree model. However, these growth and yield experiments are for different questions, such as spacing, precommerical and commercial thinning, provenance’s, conversion to mixed forest, ability of species to grow on different sites, mixed forest treatment and plots for monitoring effects of acid rain. Data collection varies between plots with complete data sets of diameter, height, crown base, crown width, tree coordinates and branchiness to classic growth and yield plots where usually diameter is measured on all trees and height is just measured on a sample of about 40 trees.

Statistical tree models are usually divided into distance dependent models, which need spatial information and models that are distance independent and do not need tree coordinates. Since a lot of the long term experiment data was without coordinates the distance independent approach was chosen. The advantage of the distance independent approach is that it can model small plots like from forest inventory data better, because there no edge effects. However, modeling large inhomogeneous stands the distance dependent approach seems more promising. But the distance independent model can be also used for modeling larger inhomogeneous stands, be either dividing the plot in smaller units or calculating the competition of the trees just for a smaller area.

For the actual tree model a simple approach by linear and non linear regression technique used. In order to estimate the growth of a tree the increment of it’s height and diameter needs to be estimated. In addition the crown size is determined by crown width and crown base which are estimated by static crown equations. For pure stands it would be not nescessary to work with crown information, but for modelling mixed forest crown information is important to adjust for species interaction. For the regression analysis of the 4 dependent variables diameter, height, crown base and width, the independent variables crown surface area, the crown competition c66, the change of the crown competition index due to thinnings (c66c) and the tree’s age were chosen (see below). The regression analysis was performed for each species separately. For the parametrisation only the data of those trees was used, where there were at least to following measurements of diameter and height within a time span of 6 years at a maximum.

In order to make the growth model useful for forest simulation additional components like mortality, ingrowth, thinning, harvesting, etc. have been developed (details see below). All these components are combined in the treegross.jar file. To demonstrate to potentiell of the treegross.jar there is the application tgstandsim as an example for forest stand simulation. This application basically provides the graphical user interface (GUI) and specific in- and output routines. However, the treegross.jar can also be used for different applications.

So, how can one integrate the treegross.jar to an own application and use it? If you have some knowledge of Java programming this should be not to hard.

1. You have to “create a stand”, which is done by creating the class **stand**. This virtuell stand needs to have a name, a size and the year your information is gathered. The class stand provides some methods to do so.
2. You have to add the corners of the stand. You will need at least 3 corner coordinates, but you might use several to create a circular stand area. Please note, at this point the stand size is not calculated by the corner point coordinates. You add the coordinates of the corner point by a method of class stand which is called **addcornerpoint**().
3. Now you have to add your trees to the stand. There is a method **addtree()** in class **stand**. Another way would be to create several trees by a diameter distribution using class **gendistribution**.
4. After having created all trees, you have to make sure, that the created trees have all neccessary information, such as height, crown width, crown base, etc. If not all trees have heights, you can use either class **uniformheight** or class **heightcurve** to generate those missing heights. Using the classes **crownbase** and **crownwidth** you can fill in missing crown information.
5. Although the growth model approach is distance independent, you might need coordinates for demonstration output and/or crop tree selection and thinning. The class **generatexy** will provide tree coordinates if they are unknown.
6. At this point you can basically grow your stand by just calling a method of class **stand** which is call **grow()**. All trees will grow, there will be a check for mortality. There is an option to estimate the amount of ingrowth as well. The method **descspecies()** will update general stand information.
7. If you want to perform any treatment to your stand, you can do so by marking the trees as thinned or harvested. This can be your own routine, a given treatment concept like in class **TreatmentbyLoewe**(), or just an interactive graphic, where you can remove trees by mouse.

Of course, some of the classes of the component treegross.jar might be of interest also to other applications than tree growth modelling. You can use most class seperately, i.e. the class **volumebynfv** if you want to calculate the volume by diameter and height of a certain species.

The different species and their specific model coefficients are determined by the species code of the forest service of Lower Saxony (see below). If you want to use your own species code either program a java interface class or change the Java source code.

Working with the example application tgstandsim

The application **tgstandsim** is an example of how to make use of the component treegross.jar for stand simulation. In order work with that application you will have to download the source code or you can download an installation file for either Windows or Linux environments. In case of an Windows environment you can start the application by clicking on the tgstandsim.exe file. If you just have the source code you will need a java virtual machine on your system. If that is installed properly you should give the following statement in a DOS box or on an Linux comment shell:

```
C:\forst\treegross>java –cp .;treegross.jar;chart2d.jar  tgstandsim
```

It is assumed that you start your command from that directory where you placed all your tgstandsim class files (*.class). The program should now start properly. The program should show a box with a browser, giving information about the program.

1. Select from the menu **data** – **open stand**, choose **astand1.txt** and click on **öffnen** (German open). After a short while you stand has been read in.
2. Click on card **stand map**. You will see a map of your stand. Green are living trees, blue are crop trees and red are harvested or thinned trees.
3. Click on card **projection** and you will see a projection of your stand.
4. If you click on the card **Designer**, you can design a new stand or add more tree to your stand. If you hit the bar **create area**, all you existing information will be lost and you start with a new stand.
5. The card **treatment** gives you some information about your stand and some default values i.e. for target diameter. You can change the values and your changes will be considered when you apply a treatment.
6. Click on card **Graphics** and you will get a diameter and height distribution by species.
7. Click on card **projection** again. Then press the **grow** button and you can observe the stand growing.
8. Click on card **stand map** again. The new stand map is displayed. Point at a tree with your mouse and press the left mouse button. You will see that the color of the tree changes to red. It is now thinned. Press **grow** and your stand grows the thinned trees disappear. You can also hit the button **treatment** and a treatment according to the German LöWE- concept is performed.
9. If you hit the button **VRML** you can create a file treegross.wrl which you can view with a VRML-viewer. You can get a viewer from the internet for free like Blaxxun (http://developer.blaxxun.de/download/index.html) or the Cosmo Player (http://www.cai.com/cosmo/).
10. The file will be in the folder \info.
11. Click on **HTML-Reports** in the menu and choose a report. Then click on **report** and you will see your html-report file. The file are stored in folder \info. Every time you create a new report, the old one will be overwritten. You can use the

Class file and what they do

The treegross.jar contains several classes which form a basic and useable tree growth model. In order to simulate the development of a forest stand using the tree model there has to be a complete data set. Since in most cases not all information is collected in the field the treegross.jar contains several classes for missing **data generation** which can be used to create a complete data set.

The complete data set for simulation needs the following information:

Level	Property	Units
Stand	Name	
	size	ha
	start of simulation data	year
Corner points	x and y coordinate (must be positive)	m
Tree	species according to list of NFV (see below)	
	age	years
	diameter (1.3m outside bark)	cm
	height	m
	crown base	m
	crown width	m
	site index (height at age 100)	m
	alive (yes=-1 or no=year when taken out)	
	x- and y- coordinate (must be postive)	m

The next figure shows the order in which trees of one species and of one age group should be checked for complete data.

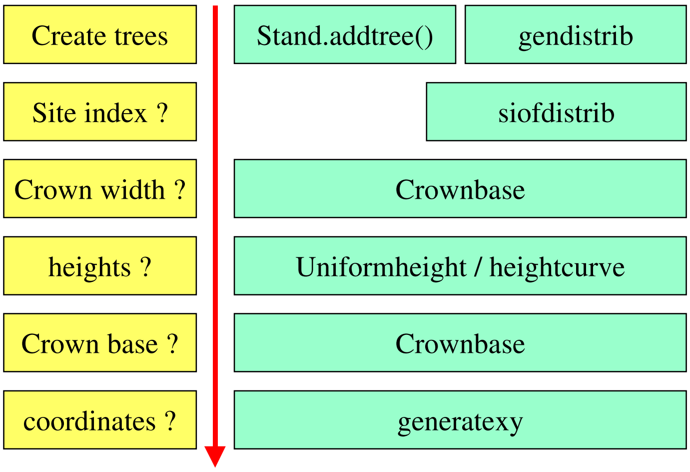


Figure: Process of checking for complete data and treegross.jar classes being used.

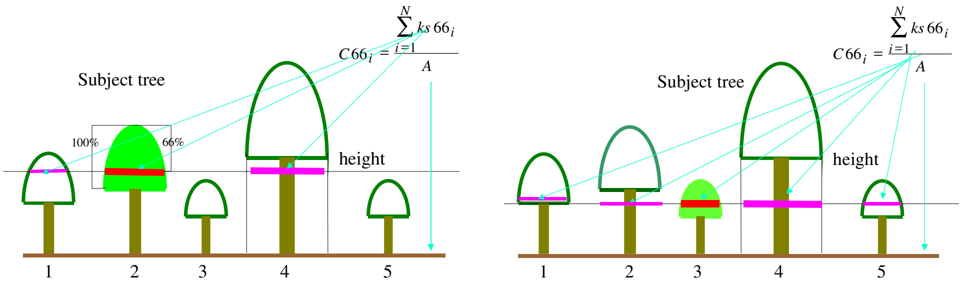
In addition the treegross.jar holds several classes which are used for growth simulation.

In the following describtion the class files are documented in an alphabethtical order and are marked for there purpose; [basic class], [data generation] , [prognosis] , [description]. The [basic class] are needed in any case of tree growth simulation, the [data generation] classes are only needed for data generation, when the tree data is not complete. The [prognosis] class are used to estimate the growth, however, there is in class stand a method grow() which actually performs the growing of the stand. The [description] class marked with are used when the method desc() of class stand is called. But of course if is also possible to call and use all classes by itself.

competition.class

[prognosis]

This class calculates the crown competition index (c66) similar to that of Wensel et al. (1987). It differs in the point that the crown competition index is determined at a height of 66% of the crown length from above.



The figure above shows the calculation of the c66 of two different situation. In the left case the c66 is calculated for tree no. 2, one of the taller trees. At a height of 2/3 (or 66%) of the crown length from above all tree crowns are cut, if they reach that height. If the crown base is above the height then cross sectional area of that tree will be taken. The sum of the cross sectional area is divided by the stand area. The right figure shows the calculation for a smaller understory tree. The height for cutting all crown is this time lower and therefore the sum of cut crown area and the result for the c66 will be greater. So the competition index is low if there is little competition and high when there is more competition. The c66 can be interpreted as the crown closure of the stand at a certain height. However, a value higher than 1.0 is possible if there is overlapping of tree crowns, and/or there is a two story stand. The height 66% of the crown length was chosen, since the border of shade and light crown is assumed in this area. BURGER (1939 a-b) determined for planted spruce the greatest crown width at 2/3 of the crown length. BIGING and DOBBERTIN (1995) showed empirically that they got the best correlation between crown competition index and growth at this height.

There two methods avaliable. One to calculate the c66 distance independent and the other to calculate the c66 for a given zone of influence. The zone of influence is set to a radius of 6m.

corners.class

[basic class]

The object cornes defines the attributes of corner points coordinates of a stand in class stand. This class is created as soon as you create the class stand.

CropTreeSelection.class

[basic class]

sorry needs still to be documented

crownbase.class

[data generation] , [prognosis]
The object crownbase holds the coefficients for different tree species.

The method bwinpro(int code, double d, double h, double h100) returns the trees crown base [m] (cb).

$$cb = h \cdot \left(1 - e^{-abs\left(p_0 + p_1 \cdot \frac{h}{d} + p_2 \cdot d + p_3 \cdot \ln(H100) \right)} \right)$$

cb= crownbase [m]; h= height [m]; d=dbh [cm]; H100 = top height [m]

Species code	P0	P1	P3	P4	R²	Sx	n
110	-0.5268	0.2287	-0.00453	0.4712	0.87	1.9724	12776

113	0.3652	0.3556	-0.00558	0.1373	0.73		2280
211	0.25704	0.11819	-0.0020625	0.13831	0.61	3.2518	23812
221	-0.8466	0.1534	-0.01084	0.6002	0.69		639
311	-0.3708	0.4211	-0.0030	0.3242	0.87		601
321	-0.3191	0.0475	-0.0057	0.4066	0.84		191
420	-0.3298	0.2577	-0.003778	0.6697	0.90		565
511	2.0417	-0.3335	0.00906	-0.9004	0.93	1.8170	19060
523	-3.365	0.0541	-0.01411	1.4014	0.82		1122
611	-1.8796	0.34056	-0.00610	0.8262	0.92		7404
711	1.2085	-0.2392	0.00742	-0.7897	0.97	1.1829	7407
811	0.8225	-0.4688	-0.00317	-0.4282	0.86	1.92	3627
812	-1.041	0.4789	-0.00914	0.6266	0.83		10652

crownwidth.class

[data generation] , [prognosis]

The object crownbase holds the coefficients for different tree species.

The method bwinpro(int code, double d) returns the trees crown width [m] (cw).

$$cw = (p_0 + p_1 \cdot d_{13}) \cdot \left(1 - e^{-\left(\frac{d_{1.3}}{p_3}\right)^{p4}} \right)$$

cw= crownwidth [m]; d=dbh [cm];

Species code	P0	P1	P3	P4	R²	Sx	n
110	2.6618	0.1152	8.3381	1.4083	0.84	1.15	1225
211	2.0837	0.1500	5.7292	1.3341	0.81	1.276	8497
221	3.002	0.1851	0.000001	1.0	0.59	1.67	75
311	17.372	-0.0646	45.371	1.238	0.92		398
321	2.7916	0.1340	2.7198	0.4197	0.81		191
420	0.3234	0.2060	0.000001	1.0			
451	1.792	0.1154	5.3637	0.867	0.82		
511	1.2644	0.1072	0.000001	1.0	0.80	0.7694	959
523	7.1764	-0.0149	23.2663	1.390	0.53		335
611	2.919	0.0939	10.0161	1.362	0.79	0.8593	2126
711	1.2783	0.11388	8.705220	1.33944	.8261	0.6789	636
811	3.6962	0.0762	21.8046	1.530	.6550	1.0160	1201
812	2.3805	0.1073	0.000001	1.0			

DataExchangeFormat.class

[basic class]

sorry needs still to be documented

generatexy.class

[data generation]

The object generatexy can be used to generate missing tree coordinates. The tree coordinates will be choosen randomly, however the methods creates a nearly equal distribution by trying to keep minimum distances. If a location can not be found for a tree then the minimum distance gets reduced until a location is found.

gendistribution.class

[data generation]

The method weibull(stand st, int art, int alter, double dg, double hg, double dmax, double gfl) creates trees in class stand using a weibull diameter distribution.

The diameter distribution is only very rarely measured in the field, although the information is very important for analyzing the value of a stand. In order to generate diameter distributions NAGEL and BIGING (1995) fitted a truncated Weibull distribution to the experiment data of the Forest Research Station of Lower Saxony and estimated the location and the form parameter b and c by linear regression.

The location parameter b is a function of the mean quadratic diameter Dg [cm]:

$$b = p_0 + p_1 \cdot Dg + \varepsilon$$

p_0 and p_1 are coefficients, ε is an error component

Species code	p_0	p_1	r^2	St.Error	n
110	-1,937	1,082	0,98	2,20	601
113	0,267	1,031	0,99	0,39	199
211	-4,282	1,132	0,96	2,43	208
511	-2,492	1,104	0,98	1,52	819
611	-0,621	1,060	0,99	0,69	223
711	-0,047	1,047	0,99	0,47	192

The form parameter c is a function of Dg [cm] and the maximum diameter Dmax [cm]:

$$c = p_0 + p_1 \cdot Dg + p_2 \cdot D\max + \varepsilon$$

Species code	p_0	p_1	p_2	r^2	St.Error	n
110	4,669	0,366	-0,234	0,71	1,14	601
113	6,122	0,374	-0,258	0,60	0,80	199
211	4,518	0,317	-0,200	0,70	1,27	208
511	3,418	0,353	-0,192	0,71	1,02	819
611	4,380	0,236	-0,141	0,58	0,82	223
711	3,640	0,332	-0,180	0,90	0,50	192

p_0 ,p_1 and p_2 are coefficients, ε is an error component

The diameter value are generated by using the estimated parameter values b and c for the inverse transformation of the cumulative distribution function (NAGEL u. BIGING, 1995). The cumulative diameter function is calculated from the integral of the density function with the lower limit (T) and the wanted diameter. The cumulative density function is:

$$F_T(x) = \int_T^x \frac{c}{b} \cdot \left[\frac{x}{b}\right]^{c-1} \cdot e^{\left(\frac{T^c - x^c}{b^c}\right)} \cdot dt \;= \left[1 - e^{\left(\frac{T}{b}\right)^c} \cdot e^{-\left(\frac{x}{b}\right)^c}\right]$$

This formula gives the cumulative percentage of trees of the limit (T) to the desired diameter. A value for $F_T(x)$ can be generated by drawing a random number between 0 and 1. Taking the inverse transformation of the cumulative density function and solving it for diameter (DBH), one will get a diameter value.

$$BHD = b \cdot \left[\left(\frac{T}{b} \right)^{c} - \log_{e}\left(1 - F_{T}(x)\right) \right]^{\frac{1}{c}}$$

In order to create a tree diameter, one has to estimate the parameters b and c first. Then you draw a random number and use the inverse transformation to get a diameter. This is done so often until the desired basal area ([m²/ha]) is reached. All newly created trees are added to class stand.

growth.class

[prognosis]

The class growth calculates the growth of the tree's diameter and height. The crown surface area (km) is calculated by the crown length (kl=h-ka) and the crown radius (kr=kb/2). For all species a quadratic paraboloid is used. It is assumed that the trees have their greatest crown radius at 66% of the crown length.

$$km = \frac{\pi \cdot kr}{6 \cdot kl^2} \cdot \left[\left(4 \cdot kl^2 + kr^2\right)^{\frac{3}{2}} - kr^3 \right]$$

In order to estimate the height increment, the potential relative height increment of a top height tree (iHpotrel) is estimated. This increment value is then corrected by the relation of the tree's height to H_{100} and two coefficients. The potential height is calculated in class siteindex.

$$ihrel = iHpotrel + p_1 \cdot (H100/h)^{p_2} + \varepsilon$$

Baumart	P1	P2	r	Sx	n
Eiche*)	0.01676	1.3349	0.46	0.0493	14062
Roteiche	-0.00102	2.6855	0.45	0.0953	405
Buche	0.00159	1.9086	0.43	0.0827	23006
Hainbuche	0.00330	6.412	0.28	0.0817	830
Esche	0.0	1.0		0.048	306
Ahorn	0.0	1.0		0.069	628
Fichte	0.00271	2.1725	0.89	0.0737	20550
Ktanne	0.0	1.0		0.1060	813
Douglasie	0.00159	2.5255	0.84	0.0687	6387
Kiefer	0.0	1.0	0.88	0.0124	4877
ELärche	0.0	1.0	0.56	0.091	7550
JLärche	0.0188	3.5922	0.65	0.068	20255

The error ε is added randomly by assuming a normal distribution. Adding the error will give a variability to the model.

The basal area growth is estimated similarly to the *Prognosis* model (WYKOFF et al. 1982).

$$\ln(idd) = p_0 + p_1 \cdot \ln(km) + p_2 \cdot \ln(alter) + p_3 \cdot C66 + p_4 \cdot C66c + p_5 \cdot \ln(adiff) + \varepsilon$$

Baumart	P0	P1 lnkm	P2 lnAlt	P3 C66	P4 C66c	P5 Adiff	R²	Sx	n
Eiche	-6.5350	1.3260	-0.8437	-0.9373	0.1239	-0.1263	0.60	0.617	17606
Roteiche	-6.7960	1.4050	-0.8437	-1.0990	0.8281	-0.2111	0.82	0.569	6401
Buche	-7.4146	1.3491	-0.6985	-0.7835	0.7875	-0.2997	0.67	0.764	28998
Hainbuche	-8.7786	1.1773	-0.3176	-0.5691	2.3263	-0.7319	0.35	0.887	1145
Esche	-6.1407	1.1068	-0.5533	-1.2802	2.1916	-0.5044	0.50	0.685	387
Ahorn	-5.9842	1.3801	-0.7104	-0.7518	0.0	-1.0577	0.63	0.563	173

Fichte	-6.2018	1.2984	-0.9366	-1.2835	0.2962	0.2926	0.56	0.638	26256
Ktanne	-1.9337	1.0273	-1.0335	-1.5453	-1.1735	-1.3228	0.73	0.617	1928
Douglasie	-7.9766	1.5135	-1.0009	-0.4481	0.5099	0.3038	0.51	0.725	8088
Kiefer	-5.0479	0.9508	-0.7835	-0.7639	0.7113	-0.1891	0.31	0.649	6866
ELärche	-7.1927	0.8621	-0.5193	-0.7122	0.3619	0.7316	0.60	0.629	11482
JLärche	-8.1122	1.3016	-0.6979	-0.5081	0.4766	0.3520	0.53	0.570	23494

The error component ε is handled as for the height growth.

The height and diameter increment are added to the initial values after the growth is calculated for all trees. The age is increased by the length of the cycle.

$$h_i = h_i + ih_i$$

$$d_i = \sqrt{d_i^2 + idd_i}$$

heightcurve.class

[data generation] , [description]

In forest inventory and experiments it is common to only measure the heights of some trees. The missing values are estimated from the height/diameter relation. In the literature several functions are used to describe this relation. The diameter/height relation is usually evaluated for each species individually. If there are not enough measurements value available for one species the diameter/height relation of a species with similar height growth is taken (NAGEL 1993). The class can be used to estimate missing heights.

The data generating routine provides 6 diameter/height functions which are described by SCHMIDT (1968):

- (1) Parabel $$h = a_0 + a_1 \cdot d + a_2 \cdot d^2$$
- (2) Prodan $$h - 1.3 = \frac{d^2}{a_0 + a_1 \cdot d + a_2 \cdot d^2}$$
- (3) Petterson $$h = 1,3 + (\frac{d}{a_0 + a_1 \cdot d})^{3,0}$$
- (4) Korsun $$h = e^{\left[a_0 + a_1 \cdot \ln(d) + a_2 \cdot \ln^2(d^2)\right]}$$
- (5) logarithm $$h = a_0 + a_1 \cdot \ln(d)$$
- (6) Freese $$h = e^{\left[a_0 + a_1 \cdot \ln(d) + a_2 \cdot d\right]}$$

a_0 ..a_2 are regression coefficients

It is best to choose the function with the best fit to the data. This means that the RMSE should be low, the r² high, and the residual values should be equally scattered. In forest research people set up the assumption that the height has to increase with diameter. For the data generation routine the functions are made linear and fitted by the method of least squares.

ingrowth.class

[prognosis]

The class ingrowth calculates the ingrowth of the trees passing the lower 7 cm diameter limit. The ingrowth model was derived from the experiment plot data of the NFV. A three step approach was mainly chosen in order to make the ingrowth model compatible to the permanent inventory data. In the first step the question whether there is or is no regeneration (tree above 1.3 m) is estimated by a loglinear model. The species coefficients are chosen according to the main species on the plot. This is the species which has the highest basal area. The independent variables are the minimum, the maximum and the mean square diameter (Dmin, Dmax, Dg) of all trees with an diameter greater than 7 cm.

$$F\_\log it = \frac{1}{1+e^{-(p0+p1*D\min+p2*Dg+p3*Dg^2+p4*D\max}}$$

Species	P0	P1	P2	P3	P4	N	% correct
110	14.104	-0.478	-0.795	0.012	-0.013	1012	96,3
211	17.582	-1.602	-0.364	0.004	0.030	1533	90,1
300 (Alh)	13.248	-0.545	-0.757	0.005	0.156	381	93,7
400 (Aln)	10.850	-0.831	-0.248	0.007	-0.091	191	89,9
511	11.078	-0.765	-0.541	0.006	0.103	1729	92,0
611	12.746	-0.752	-0.501	0.005	0.039	2501	92,8
711	11.995	-0.030	-0.994	0.013	0.037	444	92,8
811	35.166	-2.440	-2.216	0.041	0.370	884	98,3
812	23.515	-1.720	-0.971	0.022	-0.011	1157	96,1

If the question is answered that there is regeneration, then the amount of regeneration is measured for each species of the plot weighed by the basal area. The independent variables are the mean square diameter (Dg), the diameter of the top height (D100), the total basal area on the plot (Gha) and the yield class of the species.

$$\ln(nu7) = p0 + p1*\ln(Dg) + p2*\ln(D100) + p3*\ln(Gha) + p4*EKL$$

Species	P0	P1*ln(Dg)	P2*ln(D100)	P3*ln(Gha)	P4*ekl	N	R²
110	14.434	-3.398	0	0	-0.531	64	0.72
211	12.733	-5.975	1.886	0.769	0	745	0.82
300 (Alh)	12.115	-6.494	2.781	0.551	0	250	0.88
511	11.857	-5.733	2.157	0.438	0	349	0.64
611	14.848	-4.569	0	0.656	0	633	0.76
711	18.104	-4.926	0	0	-0.347	53	0.81
811	13.276	-7.195	2.617	0.889	0	245	0.80
812	15.668	-11.563	6.392	0	0	89	0.48

In case of the permanent sample data the information of step one and two are known. In this case it is possible to start with step three, estimating the amount of if ingrowth as a part of the amount of regeneration. The amount of ingrowth is estimated for each species by a non linear regression with the maximum c66 (c66max) of all trees greater equal than 7 cm as an independent variable.

$$neinw = \left(1 - e^{-((p0+p1*c66\max)^2)}\right)$$

Species	P0	P1	N	R²
110	-0.561	0.176	59	0.96
211	-0.607	0.145	433	0.71
300 (Alh)	-0.477	0.015	250	0.54
511	1.1368	-0.472	309	0.75
611	0.594	-0.066	630	0.63

711	-0.893	0.580	51	0.80
811	0.606	-0.163	245	0.76
812	-0.593	0.122	89	0.23

The ingrowth trees are all started at a diameter of 7cm. These trees need to have an age and a tree height. Height and age are estimated by linear regression. If the diameter is set to 7cm than there is for height and age a constant for each species, which is corrected by site class.

$$h = p0 + p1 * d + p2 * EKL$$

Species	P0	P1*d	P2*EKL	N	R²
110	15.694	-0.564	-1.202	20	0.46
211	8.073	0.422	-0.227	283	0.04
300 (Alh)	5.197	0.377	-0.197	1381	0.30
511	5.613	0.331	-0.444	403	0.31
611	7.223	0.398	-1.128	112	0.23
711	14.695	-0.455	-1.231	26	0.42
811	6.772	0.227	-0.276	194	0.28
812	8.446	0.141	-0.287	22	0.05

$$Alter = p0 + p1 * d + p2 * EKL$$

Species	P0	P1*d	P2*EKL	N	R²
110	176.099	-19.221	1.782	20	0.44
211	47.7	-0.633	5.887	283	0.43
300 (Alh)	21.186	-0.568	-1.044	1381	0.20
511	27.154	-1.281	5.740	403	0.52
611	17.674	0.005	1.52	112	0.72
711	36.828	-2.155	-0.545	26	0.62
811	26.968	-1.296	1.356	194	0.69
812	16.293	-0.275	3.123	22	0.47

The ingrowth method should be called before the stand will be “grown” for the next 5 year cycle. However, all ingrowth trees are marked and excluded from the first growing cycle.

missingheights.class

[data generation]

This class can be used to generate missing height values after you have initialized the object stand by starting the method generate(st stand). The class generates missing height values by calculating a height curve for each species if there are more than 5 diameter – height values given. If the number of given height values is greater 0 and less than 5 it uses the uniform height curve. If there is no height observation for one species, than the height information which is available for the whole stand will be used. The class missingheights needs at least one diameter – height observation to be able to generate heights.

There is a special function connected with missing heights. You can add additional diameter – height observations via class DataExchangeFormat(). In this case you have to set the number of trees to zero and the tree number to “nurH”, when you use the method stand.addtree() to the stand. After the missing heights are generated all additional trees will be deleted from stand. This feature is used in some of the NFV experiments, where heights are not individually measured for each plot or when there has been an extraordinary removal of trees.

mortality.class

[prognosis]

Mortality is derived from the growth and yield data of the NFV. If the c66 exceeds a critical value then the tree marked for mortality by the program and the c66 values are renewed for all living trees until none of the trees exceed the critical c66 value. The critical values can be set to different levels. In the following table you find three values, one where 90% of the trees have a lower value, one for 95% and one for 99% than the critical c66. Since shade tolerant species like beech have a higher critical value than shade intolerant species like oak or pine. The shade intolerant species will die first.

Baumart	90%	95%	99%	n
Eiche	1.40	1.55	1.85	64635
Roteiche	1.75	1.88	2.24	49568
Buche	1.78	2.06	2.40	135487
Hainbuche	1.98	2.05	2.11	6020
Esche	1.15	1.24	1.41	685
Ahorn	1.34	1.98	2.27	548
Fichte	1.23	1.39	1.65	166758
Ktanne	1.33	1.41	1.50	9965
Douglasie	1.49	1.61	2.08	35089
Kiefer	0.85	0.90	0.96	32700
ELärche	0.54	0.58	0.75	62093
JLärche	2.28	2.50	2.74	96375

siofdistrib.class

[data generation]

This class calculates the site index of a generated a diameter distribution from stand values. It assigns a site index information for all trees which do not have a site index information when the method si() is called. You have to pass the parameters the stand, species code, age, mean quadratic diameter [cm] and height [m] of dg. The method si() calculates the d100 and uses a uniform height curve to derive the h100. The site index is then defined by species, age and h100. The site index will be attached to each tree of the generated distribution which has no site index. The code for marking no site index information is –9 and created by class gendistribution.

siteindex.class

[prognosis] , [description]

Class siteindex holds the siteindex curves of the model. There are three different type of site index curve functions. The regression approach was used to describe the height development given by some yield tables, which were partly graphically constructed.

a) Regression approach

$$ho = HB0 + HB1 * \ln(Alter) + HB2 * \ln^2(Alter) + HB3 * Hbon + HB4 * Hbon * \ln(Alter)$$

where Hbon Mean or top height (hg bzw. ho) at an age of 50 or 100 years, HB0 to Hb4 are coefficients.

b) Chapman-Richards function

$$H100 = hb_0 \cdot HBon50 \cdot \left(1 - e^{-hb_1 \cdot Alter}\right)^{hb_2}$$

c) Wolf function

$$H100 = hb3 \cdot \left(\frac{H_{abs}}{hb3}\right)^{e^{\frac{-hb2}{(hb1-1)\cdot 100^{(hb1-1)}} + \frac{hb2}{(hb1-1)\cdot Alter^{(a-1)}}}}$$

where H_{abs}= total height at age 100 ; hb_1 ..hb_4 = coeffients

Used table or functon to determine potential height:

No	species	autor	year	Function
1	Eiche	Nagel	1999	Chapman-R.
2	Roteiche	Bauer	1955	Chapman-R.
3	Buche	Schober	1967	Regression
4	Esche	Volquardts	1958	Regression
5	Bergahorn	Nagel	1985	Wolf'sches R.
6	Winterlinde	Böckmann	1990	Wolf'sches R.
7	Kirsche	Röös	1990	Wolf'sches R.
8	Fichte	Wiedemann	1942	Regression
9	Sitkafichte	Schober	1955	Regression
10	Douglasie	Bergel	1985	Regression
11	Kiefer	Wiedemann	1943	Regression
12	Europäische Lärche	Schober	1946	Regression
13	Japanische Lärche	Westphal	1997	Chapman-R.

Nr	Artnr	HB0	HB1	HB2	HB3	HB4
1	110	1,2164	0,0194	1,1344		
2	113	1,3952	0,0321	1,5033		
3	211	-75,659	23,19200	-1,46800	0,00000	0,21520
4	311	-46,046	15,81886	-1,33618	0,00000	0,22808
5	321	0,623880	1,302960	296,042300		
6	342	0,495586	1,101126	96,173358		
7	354	0,800089	1,150926	84,185464		
8	511	-49,87200	7,33090	0,77338	0,52684	0,10542
10	611	-47,09070	11,43220	0,00000	0,00000	0,20063
11	711	-31,67480	11,64500	-1,04989	-0,43221	0,31253
12	811	-0,53515	0,00000	0,00000	-0,78758	0,38982
13	812	1,88062	0,009296	0,6345		

The class siteindex has methods to return siteindex by species, height and age; potential height growth by species, height, age and siteindex; and indexheight by species, age and siteindex.

species.class

[basic class]

The object species defines the attributes of species in class stand. This class is created as soon as you create the class stand and add trees.

stand.class

[basic class]

The class stand defines the basic data structure for modelling with treegross. You have to set the name, the size, and the year of simulation start. In order to do stand simulation you have to add at least three corner points to define the stand area and add at least one tree.

To start a new stand you can overwrite the name, the size and the year of simulation. In addition you will have to set the number of corner points (st.ncpnts) and the number of trees (st.ntrees) to zero.

structure.class

[description]

The class structure is for calculating a couple of structural stand indicies.

The method shannon(st stand) returns the Shannon index of the object stand (SHANNON, 1949).

$$H'(p_1, p_2, \ldots, p_n) = -\sum_{j=1}^{n} p_j \ln(p_j)$$

were p_j: possibility that a tree belongs to a certain species
n: number of species in stand

The method a_index(st stand) returns the A-profile index by Pretzsch of the object stand.
The method neighnormix(st stand) returns the percentage of trees with a nearest neighbor of a different species of the object stand.
The method th(st stand) returns the Th index by Gadow of the object stand. The Th was modified, only pairs of trees are evaluated if the distance is greater than the value of both trees height. If it is further the value 1 is counted, because there might be a gap in the stand.
The method td(st stand) returns the Td index by Gadow of the object stand. The Th was modified, only pairs of trees are evaluated if the distance is greater than the value of both trees height. If it is further the value 1 is counted, because there might be a gap in the stand.

taperbybrink2.class

[basic class]

sorry needs still to be documented

taperbysloboda.class

[description]
needs to be documented

TreatmentbyLoewe.class

[basic class]

sorry needs still to be documented

tree.class

[basic class]

The object tree defines the attributes of trees in class stand. This class is created as soon as you create the class stand.

uniformheight.class

[data generation]

In case there are no height measurements taken, the data generation routine will use a uniform height curve developed by SLOBODA (GAFFREY 1988). In order to use this function one needs to know the height Hg and diameter Dg of the stands quadratic mean diameter

$$h_i = 1,3 + (Hg - 1,3) \cdot e^{-(a_0 \cdot Dg + a_1) \cdot (\frac{1}{d_i} - \frac{1}{Dg})}$$

a_0 and a_1 are coefficients

The uniform height curve was fitted for each species to the experiment data of the NFV.

Species.	a_0	a_1	r^2	RMSE	n
110	0,14657227	3,78686023	0,97	1,60	8968
113	0,26932445	4,32123002	0,95	2,03	7577
211	0,20213328	5,64023296	0,94	3,41	11589
511	0,18290951	5,68789430	0,98	1,80	10678
611	0,19965100	4,63277655	0,97	1,98	11188
711	0,25963741	1,30645374	0,94	2,30	5367
811	0,12931522	4,44234560	0,97	1,06	12779
812	0,53934489	4,16512685	0,98	1,16	10576

volumebynfv.class

[description]

The volume of standing trees is rarely directly measured for standing trees. In general foresters use form and volume functions to estimate the single tree volume. These functions estimate the volume by DBH and height.

FZ	species	function	AUTHOR	year
1	Eiche Derbholz	fd=0.4786-(1.011176/d)+(2.10428/h)-(203.1997/(d*h*h))	BERGEL, D.	1974
2	Buche Derbholz	fd=0.4039+0.0017335*h+1.1267/h-118.188/(d*d*d)+0.0000042*d*d	BERGEL, D.	1973
3	Fichte Schafth.	fs=0.5848+3.34262/(h*h)-1.73375/(h*d)-0.26215*log(d)/log(10.0)+0.18736*log(h)/log(10.0)+11.34436/(d*h*h)	BERGEL, D.	1973
4	Kiefer Schafth.	fs=0.35096+0.93964/d+1.5464/h-2.0482/(d*d)-5.7305/(d*h)+17.444/(h*d*d)	BERGEL, D.	1974
5	Roteiche Derbh.	fs=0.4237+0.039178/d-4.69154/(d*d)+38.5469/(h*d)-335.8731/(h*d*d)	BERGEL, D.	1974
7	Douglasie Schaftholz	fs=0.10798+0.71858/(log(d*10.0)/log(10.0))+0.04065*(h/d)	BERGEL, D.	1971
9	Eur. Lärche Schaftholz	fs=0.583+4.52132/(h*h)-5.59827/(h*d)-0.2101*log(d)/log(10.0)+0.12363*log(h)/log(10.0)+21.92938/(d*h*h)	BERGEL, D.	1974
10	Jap. Lärche Schaftholz	fs=0.5073+7.41736/(h*h)-7.57701/(h*d)-0.32268*log(d)/log(10.0)+0.30583*log(h)/log(10.0)+20.75427/(d*h*h)	BERGEL, D.	1973
12	Douglasie Derbholz	fd=-200.31914/(h*d*d)+0.8734/d-0.0052*log(d*d)+7.3594/(h*d)+0.46155	BERGEL, D.	1974
13	Fichte Derbholz	fd=0.04016-27.56211/(d*d)+1.36195/log(d)+0.057654*h/d	BERGEL, D.	1974
14	Kiefer Derbholz	fd=0.40804-318.3342/(h*d*d)+36.90522/(h*d)-4.05292/(d*d)	BERGEL, D.	1974
15	Europäische Lärche Derbholz	fd=0.69196+38.64556/(h*d*d)-0.01724*log2(d)-20.77608/(d*d)-0.41727/h	BERGEL, D.	1974
16	Gr.Küstentanne Derbholz	vd=exp(1.64134*log(d)+0.84522*log(h-1.3)+0.45253*(1.0-(7.0/d))-8.45379)	NAGEL, J.	1988
17	Gr.Küstentanne Schaftholz	vs=exp(1.86089*log(d)+0.85685*log(h-1.3)-9.31895)	NAGEL, J.	1988

18	Lebensbaum Derbholz	vd=exp(1.35860*log(d)+1.10900*log(h-1.3)+0.50829*log(1.0-(7.0/d))-8.32778)	Nagel, J.	1988
19	Lebensbaum Schaftholz	vs=exp(1.67590*log(d)+1.05313*log(h-1.3)-9.32861)	Nagel, J.	1988
20	Hemlock Derbholz	vd=exp(1.78913*log(d)+1.03195*log(h-1.3)+0.29581*log(1.0-(7.0/d))-9.41554)	Nagel, J.	1988
21	Hemlock Schaftholz	vs=exp(1.83933*log(d)+1.07109*log(h-1.3)-9.78039)	Nagel, J.	1988
22	Scheinzypresse Derbholz	vd=exp(1.69307*log(d)+0.96994*log(h-1.3)+0.39987*log(1.0-(7.0/d))-8.82697)	Nagel, J.	1988
23	Scheinzypresse Schaftholz	vs=exp(1.83305*log(d)+0.96514*log(h-1.3)-9.41531)	Nagel, J.	1988
25	Edeltanne Schaftholz	v=exp(1.85352*log(d)+1.07417*log(h-1.3)-9.76928)	Schübeler, D. et al.	1990

In addition to the form and volume functions there are taper functions which were developed in the seventies. With these it is possible to describe the form of a stem and determine the diameter at different heights. This information can be used to calculate assortments and estimate the value of a trunk (Saborowski 1982, Gaffrey 1991, Riemer et al. 1994).

The form- and volume functions used by the NFV are included.

Species code

The program is setup with the species coding for Lower Saxony. Other species codes are possible.

Species	**code**	**German name**	**Latin name**
Ei	110	Eiche	Quercus
SEi	111	Stieleiche	Quercus robur
TEi	112	Traubeneiche	Quercus petraea
REi	113	Roteiche	Quercus rubra
ZEi	114	Zerreiche	Quercus cerris
SuEi	115	Sumpfeiche	Quercus palustris
Bu	211	Buche	Fagus silvatica
Hbu	221	Hainbuche	Carpinus betulus
Es	311	Esche	Fraxinus excelsior
BAh	321	Bergahorn	Acer pseudoplatanus
SAh	322	Spitzahorn	Acer platanoides
FAh	323	Feldahorn	Acer campestre
Rü	330	Ulme (Rüster)	Ulmus
BRü	331	Bergulme	Ulmus glabra
FlaRü	332	Flatterulme	Ulmus laevis
FRü	333	Feldulme	Ulmus minor
Li	340	Linde	Tilia
SLi	341	Sommerlinde	Tilia platyphyllos
WLi	342	Winterlinde	Tilia cordata
Rob	351	Robinie	Robinia pseudoacacia
Kast	352	Kastanie	Castanea sativa
Nuss	353	Nußbaum	Juglans regia
Kir	354	Kirsche	Prunus avium
Apf	355	Wildapfel	Malus silvestris
Bir	356	Wildbirne	Pyrus pyraster
Els	357	Elsbeere	Sorbus terminalis
Spei	358	Speierling	Sorbus domestica
Mehl	359	Mehlbeere	Sorbus intermedia
Tul	361	Tulpenbaum	Liriodendron tulipifera
Hi	362	Hickory	Carya alba
Pla	363	Platane	Platanus acerifolia
Mispel	364	Mispel	Mespilus germanica
Zwe	365	Wildzwetschge	Prunus spinosa
Bi	410	Birke	Betula
SBi	411	Sandbirke	Betula pendula

MBi	412	Moorbirke	Betula pubescens
JBi	413	Japanische Birke	Betula japonica
Erl	420	Erle	Alnus
RErl	421	Roterle	Alnus glutinosa
WErl	422	Weißerle	Alnus incana
GErl	423	Grünerle	Alnus viridis
Pa	430	Pappel	Populus
As	431	Aspe	Populus tremula
SPa	432	Schwarzpappel	Populus nigra
GPa	433	Graupappel	Populus canescens
BPa	434	Balsampappel	Populus balsamifera
Wei	441	Weide	Salix
RKast	442	Rosskastanie	Aesculus hippocastanum
EbEs	451	Eberesche	Sorbus aucuparia
TKir	452	amerik.Traubenkirsche	Prunus serotina
Fi	511	Fichte	Picea abies
SFi	512	Sitkafichte	Picea sitchensis
OFi	513	Omorikafichte (=serb.)	Picea omorika
SteFi	514	Stechfichte (=Blau-)	Picea pungens
SwFi	515	Schwarzfichte	Picea mariana
SaFi	516	Sachalinfichte	Picea glehni
Ta	520	Tanne	Abies
WTa	521	Weißtanne	Abies alba
NTa	522	Nordmannstanne	Abies nordmanniana
KTa	523	Gr.Küstentanne	Abies grandis
KolTa	524	Koloradotanne	Abies concolor
Eta.	525	Edeltanne	Abies procera
LTa	527	Sierra-Tanne	Abies concolor var.lowian
VTa	528	Veitchs-Tanne	Abies veitchii
PTa	529	Purpurtanne	Abies amabilis
SiTa	531	Sicheltanne	Cryptomeria japonica
RZyp	532	Rauchzypresse	Calocedrus
Ts	541	Hemlockstanne	Tsuga heterophylla
Th	542	Lebensbaum	Thuja plicata
Ch	543	Scheinzypresse	Chamaecyparis
Seqg	551	Mammutbaum	Sequoiadendron giganteum
Metg	552	Urweltmammutbaum	Metasequoia glyptostroboi
Eibe	560	Eibe	Taxus baccata
NikTa	562	Nikko-Tanne	Abies homolepis
SaTa	563	Sachalintanne	Abies sachalinensis
BaTa	564	Balsamtanne	Abies balsamea
MoTa	565	Momi-Tanne	Abies firma
Dgl	611	Douglasie	Pseudotsuga menziesii
Ki	711	Gemeine Kiefer	Pinus silvestris
SKi	712	Schwarzkiefer	Pinus nigra
BKi	713	Bergkiefer	Pinus mugo
BaKi	714	Bankskiefer	Pinus banksiana
PKi	715	Pechkiefer	Pinus rigida
Pcont	716	Drehkiefer	Pinus contorta
Stro	731	Strobe(Weymouthskiefer)	Pinus strobus
RuKi	741	Rumelische Kiefer	Pinus peuce
PP	751	Gelbkiefer	Pinus ponderosa
Lä	810	Lärche	Larix
ELä	811	Europäische Lärche	Larix decidua
JLä	812	Japan Lärche	Larix kaempferi
SuLä	813	Sumpflärche	Larix laricina
HyLä	814	Hybridlärche	Larix eurolepis

Model limits

The model coefficients have been estimated for the main tree species. For this task data from north west Germany was used. Since the model is a statistical one, it is only valid for that area where the data comes from. This does not mean that the model may not be applied to other areas, but it needs to be tested first. The model was revised once on an extended data base (Nagel et al 2002) and has been proven superior to the use of yield tables. However, the user should be always aware that it is a simple growth model made to be useful in forest practise and planning. He should not trust the model blindly. He should always critically discuss the outcome and use it that way for decision making. If the model gets used in this way, it can be helpful in decision making.

Several points you should keep in mind:

1. The growth model is a statistical one. The coefficients are estimated using regression techniques. Such statistical functions are usually precise in estimation if there had been data. They can become complicated in situations of an extrapolation. Therefore, you should be careful simulating stands with very low and high basal area.
2. The potential height growth is determined by the height age relation and not by site information like the model of KAHN (1994).
3. The different production level can only indirectly be integrated into the model by diameter and crown values.
4. Simulation is done under optimum conditions, there no disturbances by storm, ice, beetles and humans.

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Appendix A: Used Abbreviations

A	m^2	Stand Area
C66		Crown competition index
C66c		Change of crown competition
Dg	cm	Mean square diameter
Dgmax	cm	Maximum diameter at Nmax
Dmax	cm	Maximum stand diameter
D100	cm	Diameter of top height tree
G	m^2/ha	Basal area of stand
Gmax	m^2/ha	Maximum basal area
Habs	m	Height at reference age (site index)
Hbon	m	Height at reference age (site index)
Hg	m	Height of tree with mean square diameter
How	m	Weise' sche top height
H100	m	Top height 100
KSGmax		Maximum crown closure
Nmax	St/ha	Maximum number of stems
cr		Crown ratio
d	cm	Diameter of single tree (1.3m)
fd		Form factor (>7cm)
fs		Form factor
h	m	Height of single tree
idd	cm^2	Quadratic diameter increment
ih	m	Height increment
ihpot	m	Potentiell height increment
ihmod		Individual tree height index
ik	m	Change in crown base
ka	m	Crown base
kb	m	Crown width
km	m^2	Crown surface area
kl	m	Crown length
kr	m	Crown radius
ks	m^2	Crown projection area
v	m^3	Single tree volume
vs	m^3	Single tree volume total
vd	m^3	Single tree volume (>7cm)