Final Report

SwissStandSim:

A climate sensitive single tree stand simulator for Switzerland

Research Programme on
Forests and Climate Change
of FOEN and WSL

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Summary

This is a technical report on the development of a single tree growth simulator for Switzerland (`SwissStandSim`). The simulator can be used for research and education to test the effects of management and silvicultural strategies on stand growth and stand structure. It may possible at a later stage for forest practitioners and forest planners to use it as a decision support system.

The data consists of measurements taken in the long term experimental forest management trials all over Switzerland. For 141 stands a full description of explanatory variables is given which were used in the validation of the simulator. The single statistical models for tree species groups and processes usually rely on more data (depending on the availability of explanatory variables). The 141 stands represent elevations ranging from 385 to 1.800 meters above sea level. The normal plot size is 0.25 ha, but ranges between 0.04 and 20 hectares. Most information is available for spruce, beech, and silver fir. The observation period ranges from 1902 until 2013, usually re-measured every 5 years.

Principally the goal was to reproduce the data generating mechanism inherent in the experimental forest research plots. Hence, the simulator does not use fixed theoretical constructs (e.g. site index), but uses the observed effects (climate, site) as explanatory variables directly in the statistical modeling of the processes (growth, mortality, in-growth). Thus, each single statistical model may become very complex. This also means, that a prediction always needs a (pre-)calculation of time dependent variables, such as temperature, precipitation and nitrogen deposition.

The basic statistical models for growth, mortality and in-growth were estimated for eleven tree species groups separately. Growth in diameter and height was explained with high precision, but the mortality model can only explain about 30% of the variance. The observations also include storm events, which are impossible to predict. However storm vulnerability remained as a predictor in the mortality models.

Statistical modeling of growth and mortality started with the formulations used in BWinPro (Hansen and Nagel, 2014). A re-parameterization of

growth, with the Swiss data, resulted in systematical overestimation of small trees, and slight underestimation of large trees, which was analyzed and found to be an effect of the log-transformation. Several other transformations were tested and square root transformation finally showed good properties. The mortality model, originally published in Dursky (1997), contains some assumptions and an unnecessary correction. In contrast, here, a single tree logistic regression model with a full data set was used. The resulting small expectation and large variance for the probability to die, were maintained in the prediction by stochastic simulation. The processes of growth and mortality were found to be climate sensitive. Like BWinPro, SwissStandSim is independent from the positions of the single trees.

The broad range of possible thinning regimes (except "plenterung") were all reduced to two types: thinning from below and thinning from above. Their broad range of specifications were assumed to be controlled by the beginning, the end, the interval, and the intensity of the thinning. These variables are not random and are specified by the user or are fixed by the research questions for the sample area. However, randomness is inherent in the selection of trees in a stand, hence two statistical models for harvesting types were defined and fitted.

The full program consists of several R-functions, which load data, packages, and statistical models. The prediction of 141 stands over all points in time ($\sim$1200) needs about 1.8 minutes of computing time (8GB RAM, 3.6 GHz, AMD). The output contains predicted diameters, heights, solid volumes, tree species, and the status of the trees, in a stand over time.

Systematic validation showed that mean diameters have good prediction accuracy and low bias, especially for beech stands, while problems occur for longer simulations under spruce stands, due to unpredictable storm events.

Zusammenfassung

Der vorliegende technische Bericht beschreibt die Entwicklung eines Einzelbaumwachstumssimulators für die Schweiz (`SwissStandSim`). Der Simulator kann in der Wissenschaft und Lehre eingesetzt werden, um die Effekte unterschiedlicher waldbaulicher Behandlungsstrategien auf das Bestandeswachstum und die Bestandesstruktur aufzuzeigen. Möglicherweise kann er in einer späteren Entwicklungsphase auch für forstliche Praktiker oder in der Forstplanung als Entscheidungshilfesystem eingesetzt werden.

Die Daten stammen aus den langfristigen ertragskundlichen Versuchsflächen, die überall in der Schweiz angelegt wurden. Für 141 Bestände liegt ein vollständiger Datensatz mit erklärenden Variablen vor und diese wurden verwendet um den Simulator zu validieren. Jedem statistischen Modell, also für alle Baumarten und Prozesse, liegen grössere Datensätze zugrunde (abhängig von den zur Verfügung stehenden erklärenden Variablen). Die 141 Bestände sind über Höhenlagen von 385 bis 1800 m Höhe über dem Meer verteilt. Standardmässig beträgt die Flächengrösse 0.25 Hektar und reicht von 0.04 bis 20 Hektare. Die meisten Informationen sind für die Baumarten Fichte, Buche und Tanne vorhanden. Der Beobachtungszeitraum umfasst die Jahre von 1902 bis 2013, wobei normalerweise alle fünf Jahre gemessen wurde.

Prinzipiell wurde versucht, den Daten generierenden Mechanismus, welcher diesen Beobachtungen innewohnt, mit den Modellen zu reproduzieren. Daher verzichtet der Simulator auf theoretische Grössen (wie z.B. vordefinierte oder modellierte Bonität), verwendet aber stattdessen beobachtbare Effekte (Klima, Standort) als erklärende Variable direkt in der statistischen Modellierung der Prozesse (Wachstum, Mortalität, Einwuchs). Daher können die einzelnen statistischen Modelle sehr gross und komplex werden. Dies bedeutet aber auch, dass für Vorhersagen die zeitabhängigen erklärenden Variablen, in dem Fall Temperatur und Niederschlag sowie die Stickstoffdeposition, vorher berechnet werden müssen.

Die grundlegenden statistischen Modelle für Wachstum, Mortalität und Einwuchs wurden für elf Baumartengruppen separat geschätzt. Wachstum

im Durchmesser und der Höhe konnten mit hoher Präzision modelliert werden, aber die Mortalitätsmodelle erreichen nur etwa 30% erklärte Varianz. Die Beobachtungen enthalten auch Sturmereignisse, welche nicht vorhersagbar sind. Dennoch konnte die Vulnerabilität auf Stürme in den Mortalitätsmodellen abgebildet werden.

Die statistische Modellierung von Wachstum und Mortalität begann mit den Formulierungen, wie sie in BWinPro (Hansen and Nagel, 2014) zu finden sind. Die Reparametrisierung des Grundflächenfzuwachses, mit den Schweizer Daten, resultierte in einer systematischen Überschätzung kleiner Bäume und einer leichten Unterschätzung grosser Bäume. Eine Analyse zeigte, dass dies ein Effekt der Logarithmus-Transformation ist. Einige andere Transformationen wurden getestet und die Quadratwurzeltransformation zeigte gute Eigenschaften. Das ursprüngliche Mortalitätsmodell von Dursky (1997) enthält einige Annahmen und eine unnötige Korrektur. Im Unterschied dazu wurde die logistische Regression auf der Ebene des Einzelbaumes mit dem vollen Datensatz angepasst. Die resultierenden kleinen Erwartungswerte und hohe Varianz für die Wahrscheinlichkeit zu Sterben wurde in der Vorhersage durch stochastische Simulation erhalten. Wie BWinPro ist auch SwissStandSim unabhängig von der Position der Einzelbäume.

Die grosse Bandbreite möglicher waldbaulicher Eingriffe (ohne Plenterung) wurden auf zwei grundsätzliche Typen reduziert: Niederdurchforstung und Hochdurchforstung. Ihre grosse Breite an Ausprägungen wurde über den Beginn, das Ende, das Intervall und die Intensität der Eingriffe versucht zu fassen. Diese Grössen stellen keine Zufallsgrössen dar, da sie vom Benutzer angegeben werden, bzw. über die wissenschaftliche Fragestellung der Versuchsfläche bestimmt sind. Aber der eigentliche Eingriff in das Durchmesserspektrum des Bestandes stellt eine Zufallsgrösse dar, die einer Entnahmewahrscheinlichkeit entspricht. Daher wurden zwei statistische Modelle für die Bewirtschaftung definiert und mit Hilfe der Daten geschätzt.

Das volle Programm enthält etliche `R`-Funktionen, welche die Daten, Pakete und statistische Modelle laden. Um die 141 Bestände über den vollen Satz von ∼1200 Zeitpunkten zu berechnen benötigt man 1,8 Minuten an Rechenzeit (8GB RAM, 3.6 GHz, AMD). Das Ergebnis besteht aus vorhergesagten Durchmessern, Höhen, Derbholzvolumen, Baumarten und dem Status des Einzelbaumes in einem Bestand über der Zeit.

Der Simulator wurde systematisch validiert und es zeigte sich, dass der mittlere Durchmesser gute Übereinstimmung mit den Beobachtungen und eine geringe Verzerrung aufweist, speziell für die Buchenbestände, während die langfristigen Simulationen der Fichtenbestände stark von den Beobachtungen abweichen, was sich auf die Sturmereignisse zurückführen lässt.

Chapter 1

Introduction

The overall aim of this project is the development of a climate sensitive single tree stand simulator for Switzerland. Such a prediction system does not currently exist. Its intended use is for research and education, to test the effects of management and climate change on stand growth and changes in structure. Later versions may be used as a decision support system for practitioners or forest planners.

The aim of the simulator was to describe the processes of growth, mortality, in-growth, and harvesting at the single tree level. Furthermore, it should not use fixed assumptions on the site index, thus better reflecting the effects on processes by directly incorporating climate (and site) properties as explanatory variables. The idea of constant site indexes has a long tradition in forestry, since the fundamental yield tables (e.g. Badoux (1983)) are all represented by some measure of a fixed site index. Statistically this means that we have explanatory variables that change over time and may explain a repeated measured variable (like d, h, which are also measured over time).

The proposed prediction system differs from mechanistic biologically driven models, since it tries to reproduce the data generating mechanism inherent in the long term experimental forest research data on growth and yield, which are heavily influenced by human interventions. As such, it is more oriented towards the data and less to the fundamental laws of biology. Biologically driven models rely on few parameters and many laws. For example, the successional development of a forest may be the focus (so called "gap models" (Bugmann, 2001)). A growth simulator usually relies on considerable amounts of data, hence many parameters and fewer fundamental laws.

Growth simulators can also be used on larger scales, e.g. based on national forest inventories. In this case, usually the knowledge of the current stand is measured with high variance or is unknown, hence simulators aim to

predict on a large scale, normally not using explicit stand information (e.g. MASSIMO in Switzerland (Thürig et al., 2005), PROGNAUS (Hasenauer, 1999) or WEHAM (Bösch, 2012)).

Two simulators, developed in Switzerland, use a functional reformulation of yield tables (Badoux, 1983) in their prediction of growth. One simulator is built to support forest enterprises (Lemm, 1995) and the other one can be used as a decision support system ("WIS.2", Rosset et al. (2014)). Both simulators rely on the concept of a fixed site index and are parametrized based on the printed tables from the yield tables, which makes them unfeasible for prediction under climate change.

In contrast to Switzerland, in Germany two main simulators for forest growth and yield at the stand level exist: BWinPro (Hansen and Nagel, 2014)) and Silva (Pretzsch et al., 2002). Both are based on the measured data from the long term experimental forest research plots. BWinPro has an open source code, which makes it more flexible for research and adaptation. Contrary to BWinPro, Silva uses further distances between trees and has a complex height curve prediction system, which is climate sensitive (Kahn, 1994). Silva makes a fixed arrangement of climate variables in variable groups together with site variables, which shows some plausibility, and may well be altered to other data situations without loss of precision.

However here we focus on a data-driven approach. Model selection was based on physiologically interpretable groups of variables. These include a broad spectrum of different effects: competition, site (including nitrogen deposition), density, thinning, mixture and climate. Each group may be measured by different variables. All of them were sequentially tested to improve the model by a manual forward selection process. This was done separately for each tree species group, which results in different statistical models for each process and tree species group. Especially here, I focus on diameter (and increments in it), which is by far the best observed variable. After that, height is updated by a less complex model, using diameter as explanatory variable (but with a more advanced error structure). Furthermore, complex mortality models were found with the a similar forward selection process.

In chapter 2 an overview of the data and the derived variables can be found. Chapter 3 describes problems and side-paths of the project. Chapters 4 to 8 describe the growth in diameter and height, mortality, in-growth and harvesting as processes. The final chapter 9 describes the functioning of the simulator. The final report serves as a handbook to understand the mechanisms and programming of the simulator, which I call `SwissStandSim`. Further information can be found in a more in-depth analysis of growth and mortality for spruce in my Master's thesis Statistics - (SfS at ETHZ), which can be read in support of this final report.

Chapter 2

Data

2.1 Overview

In this project, the data can be separated into time variant observations (single tree data, climate and nitrogen deposition) and time invariant observations on a stand (site variables). The following table 2.1 reports some important time variant data at the survey (inventory) level. They are reported with their empirical quantiles (5, 25, 50, 75, 95%), including the range of the data. The first row ("n sp.") represents the number of species. Half of the surveys have at least one species, but most stands are not mixed. We also observe that diameters and heights show a wide spectrum of observed values. Normally, the survey (inventory) contains 223 measured trees, but there are some very large sample areas with more than 1,000 measured trees. On a per hectare basis, there are normally 700 stems/ha (ranging from 69 to 5,542 stems/ha). The abbreviation "in. len" stands for interval lengths, which is the time in years for a re-measurement. Climate variables also have (due the large range in height above sea level) a large variation, e.g. mean temperatures range between 0.2 and 10.2 °C. Nitrogen deposition also shows a large variation (5-60 kg/ha/a), which is due to the long time span in the observations (1902-2013).

Quant.	n sp.	dq	h_{dq}	a	t	$ddom$	$hdom$	n obs.	nt	bat	in. len.	$tphy.per$	$nphy.per$	$m.phy$	$ndep$
min	1	7.7	7.1	22	1902	13.5	8.9	14	69	13.9	1	0.2	322	8.2	5.2
5%	1	12.0	14.2	38	1909	21.4	17.8	59	169	22.6	4	3.2	892	14.1	11.2
25%	1	20.2	21.0	58	1927	31.5	24.4	119	399	31.3	5	7.2	1,065	17.9	16.7
50%	2	27.6	26.3	79	1944	39.2	29.2	223	700	39.6	6	8.1	1,169	20.9	21.9
75%	4	35.8	31.0	110	1967	49.4	33.6	437	1,252	49.8	8	8.6	1,303	24.1	30.0
95%	7	52.0	37.3	179	2000	61.0	39.1	967	2,728	64.9	12	9.4	1,601	36.8	40.5
max	9	79.0	44.6	293	2013	88.6	50.1	2,777	5,542	93.6	48	10.2	1,946	51.4	59.9

Table 2.1: Distribution of survey-specific stand variables. Height above sea level (for the time variant climate variables) ranges between 385 and 1.800 m. The overview is based on the data set used for validation, single statistical models may rely on a larger data set and also on single tree data. Definitions and units for the variables can be found in the section 2.2. "n sp." = number of different tree species groups, "in. len." = interval length.

The following site variables (table 2.2) are time independent. Some factor combinations contain only a few observations. Hence, I re-grouped them to three levels only, i.e., a lower, moderate and higher level.

Variable	original level	n	new level
wat.hold.cap	very good	7	good
	good	66	good
	moderate	47	moderate
	low	7	low
	very low	13	low
	extremely low	1	low
wat.perm	high	9	high
	normal	64	normal
	weakly inhibited	61	low
	inhibited	7	low
	strongly inhibited	0	low
nut.ab	very good	0	good
	good	67	good
	moderate	53	moderate
	low	10	low
	very low	11	low
	extremely low	0	low
soil.depth	very deep	6	deep
	deep	66	deep
	normal	48	normal
	flat	7	flat
	very flat	14	flat

Table 2.2: Re-classification of soil attributes. n = number of stands in the final data set for validation.

2.2 Variables

In the following list, the derived variables are presented. The variable name is used throughout the final report and can also be found in the final models in the appendix. Sometimes, scaled versions of the variables are used. They are denoted by $*.s$ and are calculated by $x.s = (x - \bar{x})/sd(x)$.

- d: (single tree-specfic) tree diameter (at 1.3 m height, breast height) in cm

- dq: (survey-specific) root mean square diameter at breast height in cm
- $ddom$: dominant diameter in cm: mean of the 100 thickest trees per hectare
- rd: relative diameter: $(d - min(d))/(max(d - min(d)))$
- h: measured tree height, $\hat{h}$ estimated tree height in m. $r\hat{h}$ is a relative tree height, based on estimated heights: $\hat{h}/max(\hat{h})$
- h_{dq}: estimated height of dq (derived from a stand height curve).
- h_{q90}: 90%-quantile of tree heights in a stand
- $hdom$: estimated height of the dominant diameter (derived from a stand height curve)
- $\bar{h}$: mean height in a stand
- v: solid tree volume in m^3:
  1. $\hat{v}(d)$ estimated tree volume based on measured diameter
  2. $\hat{v}(d, h)$ estimated volume based on d and h (either measured or estimated, depending on context)
- A: total plot area in hectares (10^4 m^2)
- a: tree age in years
- ba: tree basal area (at breast height) in m^2: $\frac{\pi}{40000}d^2$
- bat: total plot basal area in m^2/ha: $\frac{\pi}{4A}\sum_{i=1}^{n} d_i^2$
- t_i: i^{th} year of the measurement
- dt: period length minus 5 years: $(t_i - t_{i-1}) - 5$
- bai_i: basal area increment normalized to 5-year period: $5\frac{\frac{\pi}{4}(d_{t_i}^2 - d_{t_{i-1}}^2)}{t_i - t_{i-1}}$
- $rbai$: relative basal area increment: bai/ba
- cba: cumulative basal area: $cba_j = \frac{1}{bat}\sum_{i=1}^{n}\left(\mathbf{1}_{d_i \leq d_j} ba_i\right)$
- bal: basal area of larger trees: $bal_j = \frac{1}{A}\sum_{i=1}^{n}\left(\mathbf{1}_{d_i > d_j} ba_i\right)$
- $rbal$: relative basal area of larger trees: bal/bat

- *bah*: percentage of basal area previously harvested in relation to *bat*
- *nt*: total number of trees per hectare in a plot
- *nm*: number of trees that died in previous interval (mortality)
- *nh*: percentage of stems harvested since last inventory
- *n.in*: number of ingrowing trees since last inventory
- *nspec*: number of different tree species groups
- *nrem*: number of trees remaining (after cutting)
- *nharv*: number of trees harvested since last inventory
- *csa*: crown surface area in m^2 (definition: 3.2)
- *cb*: crown base (height where the living crown starts), in m
- *cca*: crown cross sectional area in m^2
- *sdi*: stand density index: $nt(dq/25)^{1.605}$
- *cc*: crown competition index (definition: 3.3)
- *ccc*: change in crown competition index (definition: 3.3)
- *t.sp.g*: tree species group, a factor variable containing the eleven tree species of interest (see table 2.3)
- *lead.spec*: leading tree species, that is the tree species group with the holding maximum basal area in a stand
- *year.past*1940: if the observation year is before 1940, it is zero, otherwise the current year of observation - 1940.
- *nphy.*$*$: yearly mean precipitation sum over different period lengths. "*phy*" stands for physiological year, meaning that the sum was taken from October until September, in contrast to calender years (Rohner et al., 2016). Period lengths may take the values "$1, 2, 5, 10, per$" (represented by "*") and stands for previous time spans (in years) and "*per*" stands for "period", i.e. the exact time intervals as given by the re-measurement of the trees in mm
- *tphy.*$*$: mean physiological year temperature, over intervals such as *nphy.*$*$, in °C

- *mphy.∗*: Aridity index (defined by deMartonne (Pretzsch, 2010, p. 520)). $A = \frac{nphy.*}{tphy.*+10}$. Since this index means smaller values have higher aridity, its inverse interpretation is more intuitive. Consequently I labeled it "moisture-index" (*m∗*). In contrast to precipitation and temperature, moisture shows higher explanatory power in the spring months (Rohner et al., 2016); hence only the spring months (March, April, May and June) were used to calculate the moisture index.

The following abbreviations are (geological) site variables. They are widely used in forestry and agriculture (Bodeneignungskarte BEK 200)[1]. These factor variables were re-grouped - the new classification can be found in table 2.2.

- *wat.hold.cap*: water holding capacity
- *wat.perm*: water permeability
- *nut.ab*: nutrient storage ability
- *soil.depth*: soil depth

Within the Research program on Forests and Climate Change, climate variables were calculated and down-scaled for the research plots in Switzerland (Remund et al., 2011). They had a monthly resolution and were used to calculate *tphy.∗*, *nphy.∗* and *mphy.∗*. The data set further contained water holding capacity (*whc*) and the ratio of actual to potential evapotranspiration (*etap*). Hence, for water holding capacity and moisture, two potential explanatory variables were available. *wat.hold.cap* is only a proxy for the true water holding capacity, since it relies on geologically classified substrates, whereas *whc* is a metric variable, which potentially comes closer to the true water holding capacity. *mphy.∗* is based on a simple transformation of precipitation and moisture, whereas a more sophisticated approach was used to model *etap*. In both cases the two variants were used as potential explanatory variables.

In the same project, B. Rihm from meteotest calculated nitrogen deposition for the plots over time (*ndep*). These were yearly approximated and a mean over the period length was used as a potential explanatory variable.

Nonlinear models can not directly use factors. In those cases I renamed the variables by *.low or *.high for lower or upper factor levels to represent their respective contrast. Furthermore, the meta-data from the experimental forest management (EFM) project (Andreas Zingg, WSL) contains

[1] `http://www.blw.admin.ch/dienstleistungen/00334/00337/index.html?lang=de`

exposition, $relief$ and slope (in percentage classes, hence $grad.p$). Exposition was re-grouped to south-oriented, (including: south-east, south, south-west), north-oriented (north-east, north, north-west) and a group containing the rest. The variable $relief$, containing the levels summit, slope, flat, slope toe and depression, was not re-grouped. Slope was set to the middle of the classification bounds (e.g. class 0-5% was set to 2.5%).

t.sp.g	BAGR	Distribution of species	
acer	Ahorn	100% Acer sp.	
olb	aLH	51% Fraxinus sp.	41% Car. be. 5% Ulm. sp. 2% Til. sp. 1% Jug. re.
osb	aLN	40% Sorbus sp.	21% Pru. av. 18% Bet. sp. 13% Aln. sp. 7% Sal. sp. 2% Pop. tr.
beech	Buche	100% Fagus sylvatica	
douglas fir	Douglasie	100% P. menziesii	
oak	Eiche	100% Quercus sp.	
spruce	Fichte	100% Picea abies	
pine	Kiefer	100% Pinus sylvestris	
larch	Lärche	100% Larix decidua	
oc	sNB	50% Pinus strobus	28% Pin. mu. 20% Pin. ce. 1% Pic. si.
silver fir	Tanne	100% Abies alba	

Table 2.3: Classification of tree species in species groups (*t.sp.g*) used throughout the report and within the simulator. Here "olb" means other long-living broadleaved trees, "osb" other short-living broadleaved trees and "oc" other conifers. Distribution is according to single tree observations in the starting data set for the growth model.

Chapter 3

Progress of the full project

Here the problems and side-paths related to the development of the simulator are described. For example stand height curves were necessary to have starting points for heights for each tree and reasonable volume functions were needed to predict volumes of any height-diameter constellation. Both developments were not planned from the beginning and are not part of the proposal. For a direct comparison with the BWinPro diameter growth model, advanced crown models for the trees are needed, which themselves contain many sub-models and hence were time-consuming to construct.

3.1 Data Processing

Initially, it was necessary to read the data while it was being prepared and stored (as db-files *.F) by Andreas Zingg (project: Experimental Forest Management) at WSL. I had access to 629 stands, consisting of all relevant tree species in Switzerland. I did not work with data from provenance experiments with foreign tree species. A larger problem was not merely the technical obstacle to defining convenient data frames for statistical analysis in `R`, but more regarding problems with the data, which was: badly structured, contained zeros were intended to mean that values were not available, and had many inconsistencies.

By structure, I mean that some variables are given at the tree level, but are in truth stand- or survey-specific (e.g. treatment). As a result, it may happen that not all trees in a survey have received the same treatment.

There are also some unclear definitions, which result in extreme distributions. For instance, the basal area increment for trees that died since the last inventory shows many zero values. More than 50% of them have exactly a zero value. This may at times be plausible, since they were really not grow-

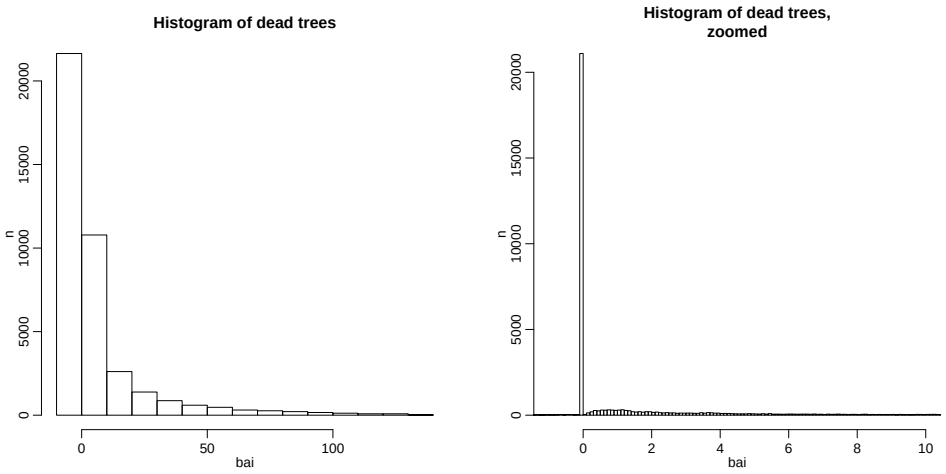

Figure 3.1: Distribution of basal area increment for dead trees

ing or the increment was not detectable. However the histogram in figure 3.1 suggests that some of the diameters were not measured at all, and values were just copied from the last observation.

Furthermore there are tree identifiers which have negative numeric values. Finding tree identifiers over the range of different stands is not straight forward. I write this not to blame those responsible for this, but just to identify some of the problems which needed to be solved. They originate from the long history of the data (which makes it highly valuable) and the different individuals and research questions behind it.

In the appendix A.1, the full code to read in the data can be found together with some preliminary checks for consistency. The resulting data (`dvfl`) is the starting point for all other data sets for each process. They are merged with climate and site variables, nitrogen deposition, and the meta-data from the Experimental Forest Management trials. Some variables needed to be calculated at single tree level (e.g. *bai*, the increment) and at the survey (inventory) level (e.g. *nt*, number of trees per hectare).

3.2 Stand height models

Developing stand height curves was not part of the proposal. However single tree heights are needed to have a full set of heights for each tree at the beginning of the simulation. Here, the development of stand height curves will be described only briefly. As most of the surveys have height measures in a sub-sample of dominant trees, a full set of heights h can be achieved by a

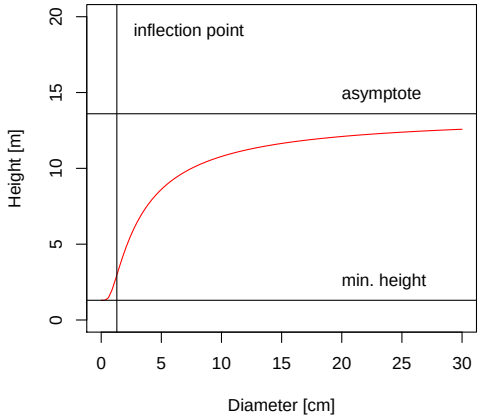

Figure 3.2: Form of the Michajlow-function

model. Because the shapes of these curves change over time and per species, a total of more than 2,200 models were fitted. The estimated heights are only used as a starting point for the simulator and, are not used for fitting the height increment (see chapter 5).

Based on leave-one-out cross validation, I tested nine competing functions to predict h given d. The so-called"Michajlow"-(or "Schumacher")function (Michajlow, 1952) produced stable predictions. It has an interpretable and meaningful form and is able to make useful predictions outside the range of observations. It has the following form:

$$h = 1.3 + \beta_0 \exp(-\beta_1/d) \tag{3.1}$$

where $\beta_0 + 1.3$ is the asymptote of the function. The inflection point of this function is $\beta_1/2$. Figure 3.2 shows an example with $\beta_0 = 12.3$ and $\beta_1 = 2.6$.

In the simplest case, when the survey contains only one tree species or does not have enough observations to fit different curves, the function 3.1 was fitted. In many other situations, we have a leading species and several suppressed tree species, each following different height curves. One could independently estimate the function 3.1 for each species or use a mixed model to incorporate the differences between the tree species as a random variable while using common information (in this case on the slope). The advantage of the mixed model is that using all observations simultaneously makes the predictions much more stable and we have a mean population curve, which is useful for predictions where we do not have any observations (a tree species,

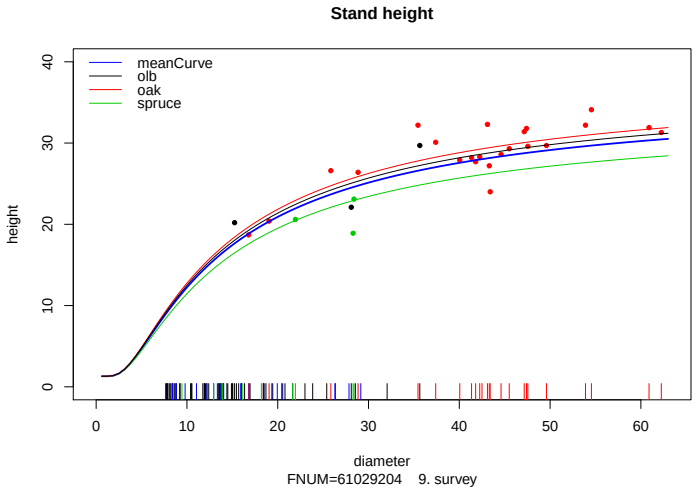

Figure 3.3: Example of a mixed model, as a survey specific stand height curve

without height, but diameter observations).

Such a mixed model has the following structure:

$$\begin{aligned} h_{ij} &= 1.3 + (\beta_0 + b_j)\exp(-\beta_1/d_{ij}) + \epsilon_{ij} \\ b_j &\sim \mathcal{N}(0, \sigma^2_{spec}) \\ \epsilon_{ij} &\sim \mathcal{N}(0, \sigma^2) \end{aligned}$$

Where the sub index j represents the jth tree species group in a survey and i is the ith tree for each species group. Figure 3.3 illustrates the advantages of such a mixed model. On the x-axis there are all observed diameters in the lower part of the plot, where we want to model height. We see that the stand is dominated by the tree species group "oak", for which most observations are available. The mixed model uses the same slope for all tree species. Hence, for the suppressed species "spruce" and "olb" the slope is identical, but the asymptote varies. This allows for the estimation of species-specific curves, although there are only three observations of each. In addition the mean curve allows an estimate of a height even for a species without any height information.

3.3 Estimating volumes

One of the goals of the simulator is the estimate of standing and harvested volume. Because the height and the upper diameter of the trees heavily influence volume, estimates based solely on diameter are imprecise. Some of the stand contain an estimated volume, but the functions are site specific and not transferable to other stands. Some of the local functions contain polynomials, resulting in possibly negative volumes.

Volume functions were fitted based on the data used to construct the volume functions in the Swiss National forest inventory (Brassel and Lischke, 2001), which are based on the largest available data set for Switzerland. I transformed volumes by the natural logarithm and used general additive models (Wood, 2011) for estimation. As explanatory variables, I used d and h, since a second diameter - for example diameter of 7m (d_7) or another measure of the stem form, is rarely given in the data. Here the explanatory variables are not estimated by coefficients, rather by functions. The package `mgcv` in `R` contains a simple cross validation to prevent over-fitting. Due to the transformation, the final estimates are always positive numbers. A deeper analysis of volume estimation is still open and the models, which are automatically loaded at the start of `SwissStandSim` (`m.vol`), should be treated as preliminary results.

3.4 Crown forms

I estimated crown forms in order to refit the growth model as it is given in BWinPro (Hansen and Nagel, 2014), according to the proposal of the project. The resulting crown indexes are potential explanatory variables, which were later used in the selection process for modeling of growth and mortality.

The original form of BWinPro's growth function has some weaknesses. The logarithmic transformation is too strong and shrinks the residuals too much. I also tested various other transformations (for more information see Zell (2016)) and found the square root transformation to be the best.

The growth function of BWinPro explicitly ses crown indexes as explanatory variables. Crowns are not fully measured, but in a sub-sample of the experimental forest management data, the height of the crown base and four radii of the crown width were measured. To estimate crown width ($\hat{r}$) and crown base ($\hat{l}$), two models for were built. Together with some assumptions regarding the crown form (for more technical details, including the `R`-function to calculate crown forms, see Zell (2016)) it is now possible to calculate crown surface area (csa, equation 3.2), the crown competition index (cc, equation

3.3) and the corresponding change in the crown competition index (ccc) after harvesting has taken place. For the crown competition index, we need the crown sectional areas at any height ($cca(h)$).

$$\widehat{csa} = \pi \frac{\hat{r}}{6\hat{l}^2} \left((4\hat{l}^2 + \hat{r}^2)^{3/2} - \hat{r}^3 \right) \tag{3.2}$$

$$cc(h)_j = \frac{1}{A} \sum_{\substack{i=1 \\ i \neq j}}^{n} cca(h)_i \tag{3.3}$$

The BWinPro diameter growth model:

$$\log bai = \beta_0 + \beta_1 \log csa + \beta_2 \log a + \beta_3 cc + \beta_4 ccc + \beta 5 \log dt \tag{3.4}$$

has the form of a multiple linear regression model. After testing other explanatory variables and different forms of the functional relationship, I found that the modeled crown surface area, crown competition index and its change after harvesting all have a physiological interpretation. However, they are usually not better in explaining growth compared to other measures based on observed diameters (see section 4.2). Only the sum of the stand cross sectional area, as a measure of density, is still used to model in-growth (see chapter 7). The crown models may later be used for graphical presentation of growth.

Chapter 4

Diameter growth

4.1 Growth function

The basal area increment (bai_t) was calculated from two consecutively measured diameters. The normalization to 5 years was necessary to make the increment comparable.

$$bai_{t_i} = 5\frac{\frac{\pi}{4}(d_{t_i}^2 - d_{t_{i-1}}^2)}{t_i - t_{i-1}}$$

Given the crown surface area (equation 3.2) and crown competition index (equation 3.3), the starting basal area increment models were of the form proposed in BWinPro (see equation 4.1, Hansen and Nagel (2014)). The logarithmic transformation was too strong, resulting in an overestimation of small trees. The corresponding residuals plots and associated problems can be found in Zell (2016) and were independently discovered from Albrecht et al. (2010) by refitting the BwinPro model for Southwest Germany. I tested several other transformations and found the square root transformation to be adequate for the increment data.

Plotting basal area increment data over diameter shows a clearly nonlinear behavior, implying that a nonlinear function is required. One useful approach is given in Quicke et al. (1994) and was also used in Thürig et al. (2005) in MASSIMO. It has the following form

$$bai = \exp(\beta_0 + \beta_1(1 - \exp(\beta_2 d)) + \dots), \tag{4.1}$$

where the exponent on the right hand side may be expanded by other explanatory variables, represented by the dots. For stable estimates, it is reasonable to (partly) linearize this function by the natural logarithm. However, this is quite a strong transformation. Again, several other transformations

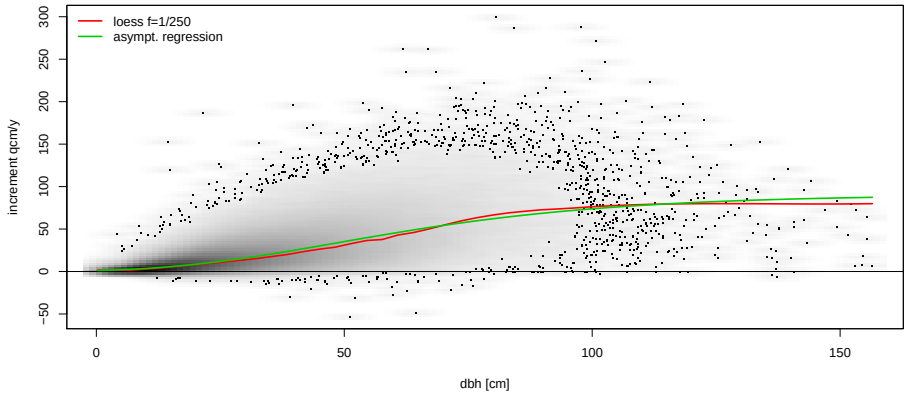

Figure 4.1: Basal area increment over diameter for spruce and modelled by a non-linear regression as given in equation 4.1. Data is illustrated with a 2-dimensional kernel density plot.

were tested. Square root transformation (Zell, 2016) was the best. Since *bai* contains negative values, the sign (function "sign" for signum, in equation 4.2) of *bai* was extracted before applying a square root transformation.

$$\text{sign}(bai)\sqrt{|bai|} = \beta_0 + \beta_1(1 - \exp(\beta_2 d)) + \ldots \tag{4.2}$$

Equation 4.2 is still a non-linear function in the sense of parameter estimation and the data contain outliers. The outliers are due to confounded trees, which can result in negative and extremely positive increments (see figure 4.1). With the data at hand, it seems impossible to automatically detect these outliers. Just ignoring a part of the information through greater trimming will result in lost information not to mention that trimming as such is arbitrary. I therefore used robust methods, which regulate the importance of the residuals by down weighting them with a M-estimation technique, which is implemented in `robustbase` in `R` (Rousseeuw et al., 2015). However, with repeated measures, as presented here, this method may result in over-optimistic p-values or standard errors (see A.2). Nevertheless expectation values of the coefficients are usually not affected.

4.2 Modeling

The number of potential explanatory variables (climate, nitrogen deposition, site, soil, survey-specific variables, and other measures based on diameter)

together with non-linearity requires a procedure to find a best model which does not over-fit. An automatic model selection is not possible for non-linear methods. Consequently, I used a manual forward selection process. This makes sense, since collinearity can also be handled well.

As a result, he potential explanatory variables were separated into seven physiologically interpretable groups. At each step for each of the variables a full model (including previous explanatory variables) was fitted and the models were compared based on their explanatory power. Then the best models at each step were compared to the previous best model using the likelihood ratio test. For each best model, a generalized additive model (package `mgcv`, function `gam` (Wood, 2011)), was also fitted to detect possible non-linear relationships. If non-linearity was present, the models were expanded with quadratic terms (and also tested, if they resulted in significant improvement). The same procedure was applied to each of the eleven tree species groups, hence the procedures are comparable. However the resulting models can be different.

1. **Between-tree competition**: Four variables were used: basal area of larger trees (bal), relative basal area of larger trees ($rbal$), cumulative basal area (cba) and crown competition (cc, equation 3.3).

2. A measure of **deceleration of growth**, which is assumed to be a tree size related effect. Test variables were: a (age), crown surface area (csa, see equation 3.2), $d^2\hat{h}$ and an estimated volume $\hat{v}(d)$.

3. **Site:** Available explanatory variables are: nitrogen deposition ($ndep$), water holding capacity ($wat.hold.cap$), water permeability ($wat.perm$), nutrient storage ability ($nut.ab$), slope ($grad.p$), $exposition$, $relief$, and whc (which is the water holding capacity on a metric scale (see section 2.2)).

4. **Stand density**: was measured by the stand density index sdi (Reineke, 1933), total basal area (bat) and logarithmic number of stems (per hectare) $log10(nt)$.

5. **Thinning effects**: Thinning effects were measured by an indicator variable $treat$, which equals 1, if the stand was ever thinned and 0 if not. Also, percentage of basal area of harvested trees (bah), percentage of number of stems per hectare harvested (nh) and the change of crown competition ccc (see equation 3.3).

6. **Mixture with other species**: An effect measured by sharing of basal area of broadleaved trees ($mixB$). Another variable was used, which contains the information, if the leading species is coniferous ($leadcon$).

7. **Climatic effects**: these are complicated effects, as evidenced by many interactions among them, many of which are non-linear. I used temperature, precipitation, moisture, and *etap* (ratio of actual to potential evapotranspiration) and tested the effects over different previous period lengths. Longer period lengths showed better results ($10, 5$ and the exact last re-measurement periode, per). For comparison between the tree species, I preferred the period length according to the given re-measurement intervals ($*.per$).

8. **Unexplained growth boost**: Residual analysis for spruce showed that after the years around 1940 growth accelerated and the model does not follow this trend (see figure 2.8 in Zell (2016)). At first, I wanted to avoid such an artificial and unexplained effect (year), but it remained for the other tree species as well. As I was unable to explain it with the given data, I introduced a variable $year.past1940$ which is 0 if the year of observation is prior to 1940, otherwise it is the current year - 1940.

4.3 Results and discussion

The variable selection procedure from above resulted in eleven species-specific growth functions. To illustrate, the effects of the resulting beech model are discussed, while comparable results for the other tree species can be obtained based on the outputs in A.2. A discussion of the spruce model can be found in my Master's thesis, including the same data and procedures (Zell, 2016). Based on the models, the expected basal area increment can be calculated as follows:

$$bai = (\beta_0 + \beta_1(1 - e^{\beta_2 d}) + \cdots)^2$$

where the dots represent an additional part. The full formula and parameters can be found in the appendix A.2.4. The interpretation is - due to non-linearity and interactions - not straight forward. Hence I plotted the effects of all explanatory variables in the beech model (see figure 4.2).

The black curve in the middle represents expeceted values based on the mean of the observed explanatory variables. For each explanatory variable, the values were changed to the 10- and 90% quantile of the empirical distribution. This makes the effect sizes comparable. Otherwise a scaling of

the explanatory variables would be necessary (this was avoided in the final model versions).

In the upper row of figure 4.2 the explanatory variables with linear additive terms can be found. The background of the figure contains a two-dimensional density plot of the observed data (due to the large amount of data). Relative basal area of larger trees (*rbal*) predicted best in the first group (between tree competition). A value of 0 represents the largest tree in the stand, with low competition pressure, hence the effect size was negative ("b3" is estimated to be -2.37 see Appendix A.2.4) . It can be observed that *bat* (total basal area of the stand, representing stand density) has a slightly higher effect size, than *rbal*. However, in the same direction, larger total basal area decreases basal area increment. The second figure in the upper row of figure 4.2 shows the small effect of *bah* (basal area harvested), which has an accelerating effect on growth (growth boost after harvesting). Nevertheless, the mixture of broadleaved trees $mixB$ is more important. Mixture with coniferous trees accelerates the growth of beech trees. The blue line in the same figure shows the unexplained growth boost since the 1940's, in this case the year 1971: The dotted line (same figure) represents the years before 1940. The unexplained growth boost might be attributed to industrialization, which lowered the intensity of litter utilization (Gimmi et al., 2013) and at the same time increased atmospheric CO_2 concentrations (or a mixture).

The middle panel of this figure 4.2 shows the effects of the factor (categorical) variables in that model. An untreated and non-north oriented stand growth best, while north exposition has a stronger effect compared to an untreated stand. This seems surprising, since north-oriented forests often grow a bit better, due to water availability. However, in these models, precipitation and moisture are included as explanatory variables.

The generalized additive model revealed the non-linear behavior of age a, which is here included as an additional quadratic term. This means that older trees have accelerated growth again, which may also be an effect caused by treatments. However, this effect is only interpretable with a given diameter. This means that a change in diameter is ignored in that figure. Nitrogen deposition also behaved in a non-linear fashion. The accelerating growth of nitrogen levels over about 25 kg/ha/a seems reasonable, but the increase towards lower deposition is counter-intuitive. This may be better modeled with "Hockey-Stick-Functions", which is when a function with two parameters is estimated with a minimum value and a slope. Below the minimum value, the effect is zero, otherwise it is the given estimated slope. Such a function would intuitively fit that response better, but statistically it was not better. I also had difficulties in parameter estimation due to the non-linearity of the full model and the simultaneous two-parameter approach of the hockey-stick-

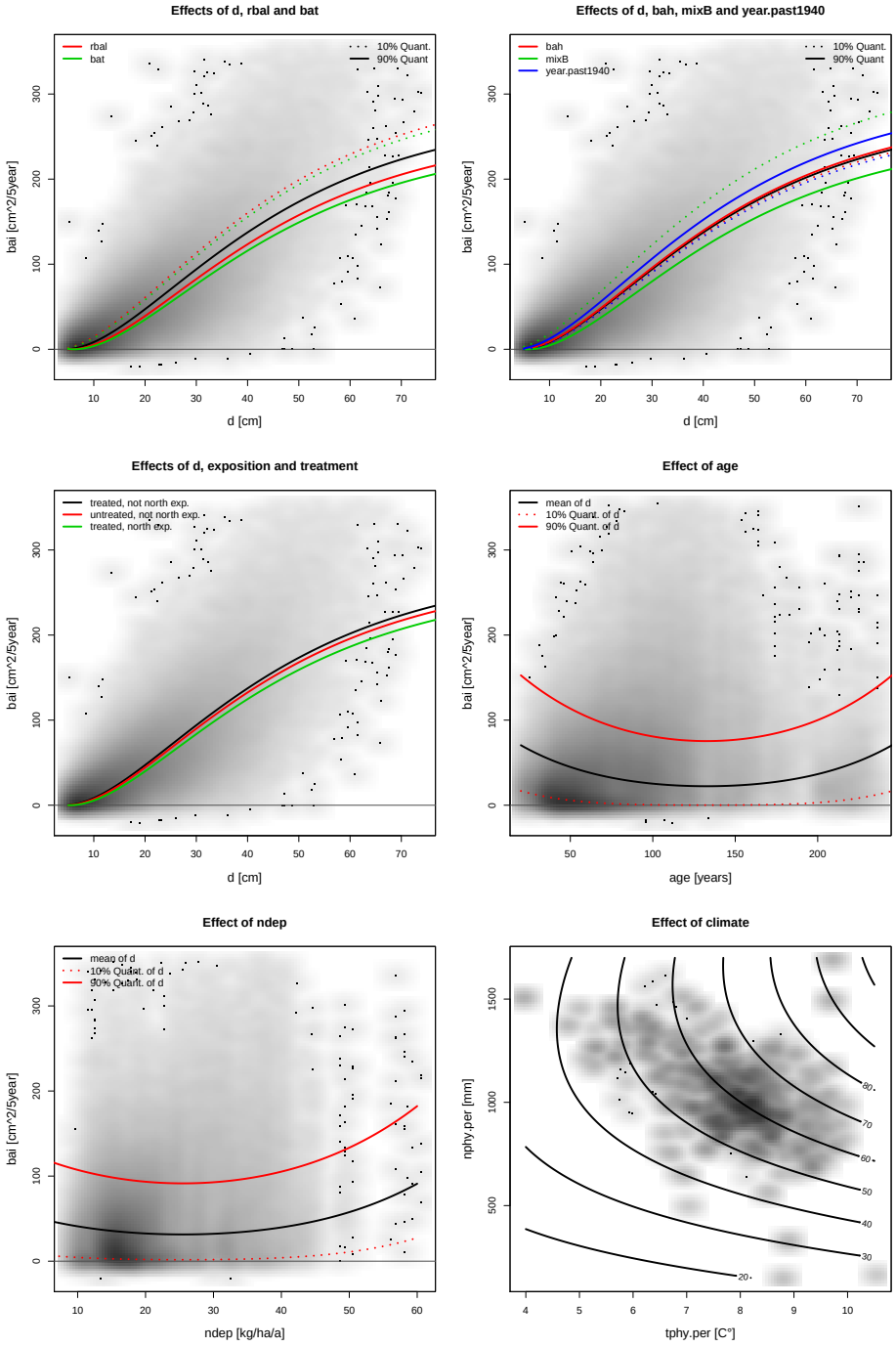

Figure 4.2: Effects on basal area increment for beech (forexplanation see text).

	Acer	Beech	Dou. f.	Larch	Oak	Oc	Olb	Osb	Pine	Sil. f.	Spruce
n [1000]	2.5	149.2	9.8	24.8	45.4	27.1	3.8	0.6	13.4	76.5	190.1
R^2 [%]	68	77	72	58	81	73	61	51	49	70	65

Table 4.1: Summary of the basal area increments models

functions (unstable because many parameter constellations result in equally well fitted models).

The climate variables are the most complicated ones, since they are non-linear and contain interactions. However the contour plot in figure 4.2 in the lower right panel is much easier to understand. The best growing conditions can be found in the upper right corner, with considerable precipitation and high temperatures. The decreasing gradient shows that decreases in precipitation have a larger influence compared to the temperature decrease.

Another graphical example for the spruce basal area increment model can be found in Zell (2016). The effects of the other tree species are only reported in the form of tables and formulas in the appendix A.2. Overall, the basal area increment models reached explained variances ranging 49% for pine, up to 81% for oak - see table 4.1. This is much better than a comparable model based on national forest inventory data in Switzerland. Kaufmann 2001 (Sect. 3.2.2.5, in Brassel and Lischke (2001)) reports R^2 in the range 40-60% for the major tree species.

Chapter 5

Height growth

5.1 Height function and data

Height growth was modeled with the observed heights over tree age, in contrast to the diameter growth model, where the increment was used. This is due to the highly complex re-measure situation. In case of diameters, each tree was revisited, resulting in a full data-set. This is not the case for height observations. Height was usually only measured for a subset of dominant trees, but this varies over time,[1] and a tree height increment estimate is problematic.

The small size of data-sets per tree species enabled the manual detection of outliers (mainly confounded trees). Therefore, all height measures per tree over time in each stand were plotted and manually corrected. Consequently, in the resulting models a normal distribution of the random error is a plausible assumption in contrast to the diameter growth models.

The height growth models used here are directly dependent on diameter. This means that diameter is an explanatory variable, which explains a large part of the variance and the models contain fewer additional explanatory variables. Height can be seen as an update, given a diameter. The complexity of growth should be included in diameter growth models because there is far more information available.

For the interpretation of the growth curve, I used the Chapman-Richards function (Fang and Bailey, 2001) to model the development of height over time. It has the following equation:

[1] Interval length varies greatly between 1 and 48 years. The sub-sample of trees also varies greatly. Sometimes trees are lost over some inventories and but then re-measured after some inventories again. Any combination over time of being in or outside the sample may occur.

$$h(t; a', b', c) = a'(1 - e^{-b't})^c \tag{5.1}$$

where a', b', c are interpretable parameters: a' the asymptote, b' may be "fuzzily" interpreted as slope, and c the form parameter. In this form it usually has a bad convergence, due to the high correlation of parameters. Although Fang and Bailey (2001) suggest a modified version of this function with an *a priori* fixed endpoint this did not improve the convergence for my data constellation. Instead, I re-parameterized the function because I wanted to model the parameters to depend (also non-linear) on diameter. The new parameterization ($a' = e^a$ and $b' = e^b$) should ensure the correct sign of the resulting height growth function. It also had enough stability to be estimated:

$$h(t; a, b, c) = e^a(1 - e^{(-e^b \cdot t)})^c \tag{5.2}$$

5.2 Modeling

As a first step, the random effects in the model were associated with one of the parameters. Stability and ease of interpretation revealed that the parameter a for the asymptote can be used to model the re-measurement of the trees (index j) and a random effect at the stand level (index k).

In the second step, the parameters a, b and c, were all modeled to depend on diameter linearly as well as non-linearly (by quadratic terms). Then, the models were forward expanded like the diameter growth models, by including one variable of groups of explanatory variables, each representing an interpretable effect: tree competition, site effects, treatment, stand density and climate.

In the last step, the auto-correlation of the repeated measures was modeled by auto-regressive models up to fourth order ($AR(1)$- $AR(4)$), a moving average model ($ARMA(1,1)$), and a continuous auto-regressive model, which depends on an explanatory variable ($CAR(1)$) to depend on time (in years) of the repeated measure. For all tree species $CAR(1)$ showed the best results. All model comparisons were based on likelihood ratio tests.

For example, the height growth of beech is calculated with in the following model:

$$h_{ijk}(t) = e^{\beta_0+\beta_1 d+\beta_2 d^2+b_j+b_{jk}}(1 - e^{-e^{\beta_3+\beta_4 ndep+\beta_5 ndep^2+\beta_6 nh+\beta_7 bat} \cdot t})^{\beta_8+\beta_9 d} + \epsilon_{ijk} \tag{5.3}$$

where the parameter a was modeled as a mixed effect, which depends on fixed parameters represented by β, and random variables, represented by b, at different levels. Hence, there are three random variables in the model:

$$\begin{aligned} \epsilon_{ijk} &\sim \mathcal{N}(0, \sigma^2) \\ b_{jk} &\sim \mathcal{N}(0, \sigma^2_{tree.in.stand}) \\ b_k &\sim \mathcal{N}(0, \sigma^2_{stand}) \end{aligned}$$

5.3 Results and discussion

Compared to the complex diameter growth models there are fewer explanatory variables in the height growth models. The main reason for this is the incorporation of diameter (d) as an explanatory variable. In the appendix A.3 the resulting parameters and full model descriptions can be found. Only for other short living broadleaved trees (osb) not enough data was available to fit a model.

The amount of data allowed for outlier detection by hand. Hence, a robust M-estimator like in the diameter growth model was not necessary and made it possible to model a more advanced error structure. The error structure contains mixed effects on the asymptote. Although an attempt was made to explain the random errors by fixed explanatory variables, all tree species contain three levels of randomness: a remaining model error, an error at the tree level in a stand, and an error at the stand level. Since random errors are also estimated, they may be used in the predictions as well. I decided not to use this information, which results in higher prediction errors, but being more general in the prediction (as if we do not know which stand we are in or which tree we want to predict). One of the advantages of the mixed models is the ability to represent the population mean much better than comparable fixed models (Pinheiro et al., 2015). The complicated error structure is the price to be payed for the unrepresentative sample of stands of the EFM-plots in Switzerland. Nevertheless the mixed model structure still enables us to make some conclusions regarding the population.

	Acer	Beech	Dou. f.	Larch	Oak	Oc	Olb	Pine	Sil. f.	Spruce
n	134	13356	1521	4328	6735	190	472	1240	5778	15741
R^2_{pop} [%]	75	77	86	78	48	67	72	61	79	82
R^2_{tree} [%]	98	97	99	98	98	98	93	99	99	96

Table 5.1: Summary of the height increment models

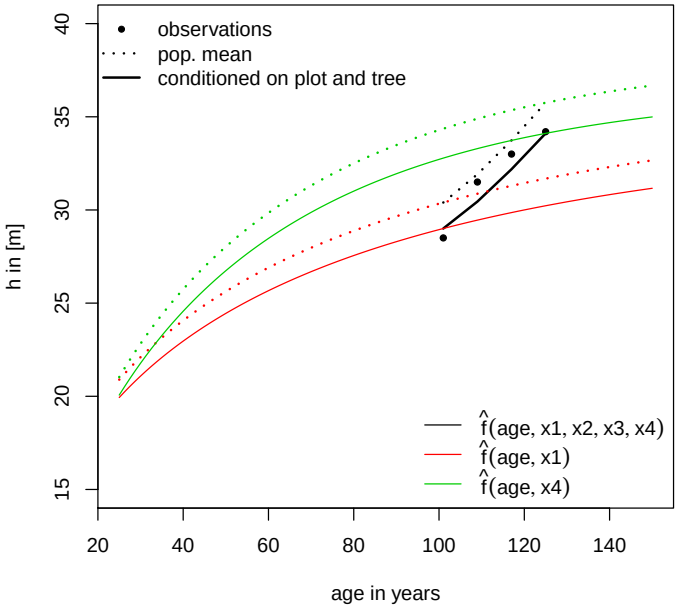

Figure 5.1: Example of height growth for spruce

Figure 5.1 illustrates the effects of such a mixed model. The black dots represent the four observations of spruce over time in a stand. The red and green lines represent predictions based on the full model, for the first and last observations (x1, x4). One notes that the shape of the curve changes over time. This is mainly the effect of the time-dependent explanatory variable diameter. It changes the asymptote, and the shape of the curve. Further the dotted lines represent a population average by ignoring the tree and stand information (on the random error part). The black curve is the resulting predicted height, which fits well with the observations. The prediction accuracy is in line with the resulting fit statistics as reported in table 5.1. Note that for the predictions in the simulator the population level was used.

Chapter 6

Mortality

6.1 Introduction

Although only 3% of all re-measured trees were classified as being recently dead, these trees are significant. Mortality gains importance because forest reserves are being established and, by stopping human intervention, mortality becomes a dominant process in forests. Often the simulators are used to predict growth without treatment, such that mortality is the driving process. In the EFM data (and hence the model) there is no distinguishing the causes of mortality.

At the stand level, the number of trees and their size will reach a limit. One limit is the maximum stand density found by Reineke (1933). On a log-log scale (number of trees per hectare over the quadratic mean diameter) we observe a threshold. Figure 6.1 shows the surveys in Switzerland (divided into tree species groups) together with the assumed maximum stand density. The limit (the black line) was plotted by using a fixed negative slope of -1.605 and fixing the line at the highest observed intercept in the data.

6.2 Material and Methods

In contrast to the growth models, recently dead trees are binary observations. $Y = \{0, 1\}$ is a Bernoulli variable and is equal to 1 if the tree has died and 0 otherwise. One might use the sum of dead trees from each survey (nm) as a realization of a binomially distributed random variable ($nm \sim \mathcal{B}(n, \pi)$).

To model Y, many flexible classification methods may well be used such as linear discriminant analysis (Crow and Hicks, 1990), neuronal networks (Hasenauer et al., 2001), classification trees (Dobbertin and Biging, 1998), Bayesian analysis (Wyckoff and Clark, 2000), or Survival analysis (Woodall

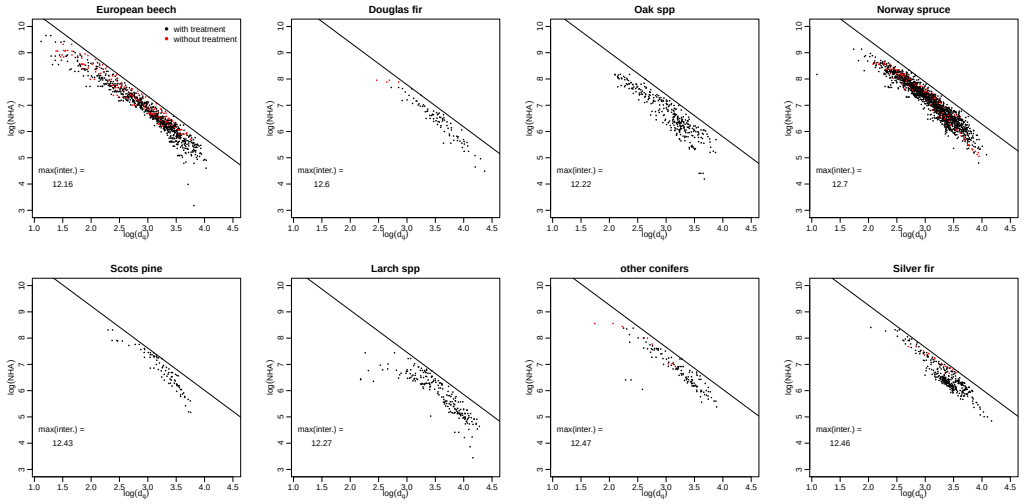

Figure 6.1: Observed realizations of the maximum stand density relationship by tree species. Dots are surveys of plots. The line is the maximum stand density given by a definition in Reineke (1933).

et al., 2005) and (Zell, 2016). Furthermore the linear logistic regression (Bigler and Bugmann, 2003, 2004) can also be extended to a mixed effects logistic regression (e.g. Rohner et al., 2012).

One problem is the different time spans for the observed nm. One might consider normalizing (e.g. to a yearly mortality probability) $\pi = 1 - (N_t/N_0)^{1/t}$ like in Rohner et al. (2012)). This contains the assumption that π is constant over the normalization period.

However, it is also possible to use the Bernoulli observations and to stay at the single tree level. This has the advantage of using most of the information present in the data. This is the approach used in this analysis. To encompass different time spans, I introduced $dt = (t_i - t_{i-1}) - 5$ as the time distance to the 5-year standard period and used it as an explanatory variable in the model.

The probability of being dead, given some osberved explanatory variables (x)

$$\pi(x) = \mathbb{P}\left[Y = 1 | X = x\right] \tag{6.1}$$

can be modeled by the logistic linear regression with the logit transformation $g(.)$:

$$\log\left(\frac{\pi(x)}{1-\pi(x)}\right) = g(x) = X\beta + b_k + b_{jk} + \tag{6.2}$$

The transformed scale (log of odds-ratio) is a linear model and hence all the advantages of linear model building can be used.

The low probability of dying caused a problem for Dursky (1997), since they wanted to separate dead and living trees based on a predicted probability of 50%. For that reason, they took the same number of dead and living trees for the logistic regression model. After that, a correction ("F-function") was applied based on classified (mortality-)data. The procedure is probably based on a false interpretation of logistic regression models. This procedure is still partly used in BWinPro and Silva and is briefly presented in Pretzsch (2001). More details can be found in Dursky (1997).

With low probabilities it may happen that for long runs no trees die. To prevent this application problem, I used simulation. I calculated the expected probability of death and compared it with a random number (uniform distribution [0-1]). If the random number was smaller than the calculated probability, the tree was classified as being dead. This results a number of dead trees, also with a binomial distribution. It has exactly the same expectation (and consequently variance) as the imputed probability of mortality. The statistical properties are preserved, because the uniform random number has the same density as the cumulative distribution of $\hat{\pi}$.

Comparable to the height growth models, two levels of nested random effects (tree within a stand denoted by the subindex jk and stand level denoted by the subindex k) on the intercept were introduced in the models.

$$\begin{aligned} \hat{g}(x) &= X\hat{\beta} + \hat{b}_k + \hat{b}_{jk} + \hat{\epsilon}_{ijk} \\ \epsilon_{ijk} &\sim \mathcal{N}(0, \sigma^2) \\ b_{jk} &\sim \mathcal{N}(0, \sigma^2_{tree.in.stand}) \\ b_k &\sim \mathcal{N}(0, \sigma^2_{stand}) \end{aligned}$$

The mixed model approach prevents again, an automated model selection procedure, which means that a forward selection process, as described in the diameter-growth model (section 4.2), was used, with some minor changes. Again, as a matter of preference [1], only one of several competing variables was introduced stepwise to the model to control for multi-collinearity and enable a better interpretation of the final model:

1. Relative basal area increment *rbai* as a measure of current **vitality** (or stress, or stress memory) of the tree showed excellent classification properties. It was compared to *bai*.

[1] In the case of site variables, some variable combinations are independent, like *ndep* and *wat.hold.cap*. In such cases the combination of two explanatory variables per group of interpretable effects were tested.

2. To measure **size** and **age** related effects d, a, $\hat{v}(d)$ and crown surface area *csa* were used.

3. At the stand level, **density** related effects were estimated by nt, total basal area *bat* and the stand density index *sdi* (Reineke, 1933).

4. As a measure of **between tree competition** *bal*, *rbal*, *cba*, the estimated tree height ($\hat{h}$), the relative height ($r\hat{h}$), and the crown competition index *cc* were tested.

5. **Thinning** effects were measured by percentage of basal area harvested *bah*, percentage of trees being harvested *nh* and the change in crown competition *ccc*. A further a variable *treat*, containing information about whether the stand was ever thinned, was used.

6. **Mixture** with broadleaved trees (measured in shares of basal area) and the leading tree species (*lead.sp*, the species which holds the maximum share of basal area) were tested.

7. **Climate**: like in the growth model, interactions and non-linearity are present. I tested different combinations: a maximal version, maximal without precipitation and maximal without temperature. Maximal means all three main effects plus interactions between precipitation and moisture, between temperature and moisture and non-linearity in temperature and precipitation (by quadratic terms).

8. **Site** related effects are: nitrogen deposition (*ndep*), water holding capacity (*wat.hold.cap*), water permeability (*wat.perm*), nutrient storage ability (*nut.ab*), slope (*grad.p*), *exposition*, *relief* and *whc* (which is the water holding capacity on a metric scale (see section 2.2)).

9. The variable *dt* is a measure of **period length** compared to the standard 5-year period. It was a necessary variable, since different period lengths were used. It was included as a linear and quadratic term.

6.3 Results and Discussion

For all eleven tree species groups, a model was successfully fitted. The resulting full formulas and estimated parameters can be found in the appendix A.4. For ease of interpretation, the beech model is plotted below. Explanatory variables were scaled to make the effect sizes comparable in order to plot them in one figure (except for the influence of climate).

The probability of mortality can be calculated as follows:

$$\hat{\pi} = \frac{1}{1 + e^{-(\hat{\beta}_0 + \dots)}}$$

Figure 6.2 shows the scaled version of the final model for beech. The upper left figure shows positive effects, with $mixB$ as the strongest one. This means that mortality of beech increases, when more broadleaved trees are present. The next important effect is *bat*, which is the stand density measured in terms of total basal area. The third strongest (positive[2]) effect is the length of the period, which makes sense: the longer the observation, the higher the probability of observing dead trees. This size of this effect is of similar importance to nitrogen deposition, which also has a positive influence on mortality. The weakest effect is *bah*, which shows an increase in mortality with harvested basal area, which means that a stand becomes more vulnerable to storm events after harvesting. Notice that the right panel shows negative effects on a different scale in the y-axis. All these effects are stronger than the positive effects. Small diameter shows the strongest negative effect, followed by relative basal area increment (and cumulative basal area (*cba*).

Climate effects are a somewhat counter-intuitive. The upper-left corner of the figure represents the coldest and wettest beech stands. Here the model predicts the highest probability of mortality. This probability decreases towards the middle of the figure (into a standard, normal climate), but increases slightly up to the right lower corner, representing the warmest and driest stands (which is intuitively true again).

An overview of the accuracy of the mortality models may be found in table 6.1. The explained variance is in the range of 10-61%, but for the most important tree species only around 30%.

	Acer	Beech	Dou. f.	Larch	Oak	Oc	Olb	Osb	Pine	Sil. f.	Spruce
n[1000]	2	155	9	23	47	26	4	1	12	82	199
R^2_{pop} [%]	41	43	18	18	51	61	10	29	33	28	29

Table 6.1: Summary statistics of mortality models

[2]Positive and negative is according to the sign of the estimated effect. Positive effects indicate increasing probabilities of death with increases in the explanatory variable.

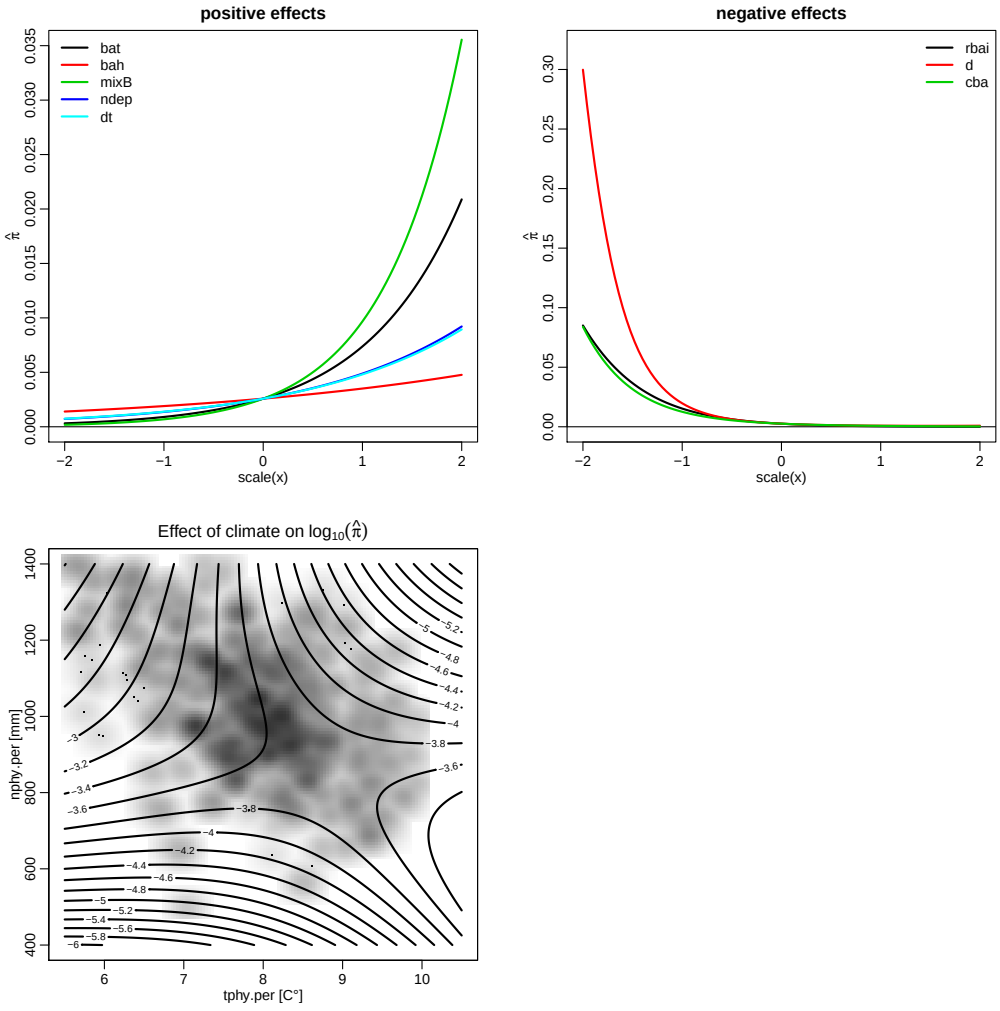

Figure 6.2: All effects of the beech mortality model. For better comparison of simple effects, a model based on scaled explanatory variables is presented (the final model is at the original level). The effects of climate are back-transformed to the original level and are reported on a log_{10} scale for readability.

Chapter 7

In-growth

In-growth refers to those trees which have recently grown over the diameter threshold of 7.5 cm. To reconstruct this process, several sub-models were built. First, the probability that in-growth occurs in a survey was modeled. Secondly, the number of in-grown trees is predicted, also based on a model. In the last step the biometric variables (tree species group, diameter and height) of the in-grown trees are determined.

7.1 Probability of in-growth

The data is survey-specific and a full set of potential explanatory variables resulted from a total of 1,607 surveys. In 13% of these surveys, in-growth occurred. As potential explanatory variables, I used stems per hectare, basal area, basal area harvested, and crown surface areas of several previous surveys. The models showed that variables based on the preceding survey had the best results. An interaction between stems per hectare and total basal area was found and the influence of lead species and thinning regime on the probability of in-growth was tested.

The final logistic regression model depends on the type of the thinning regime, including "Tfa": thinning from above (the standard), "none" (stands that were never thinned), and "Tfb": thinning from below. Thinning from below is associated with a lower probability for in-growth. The preceding number of trees per hectare and the preceding total basal area have a positive influence on the probability of in-growth, but their interaction (both terms together) is negative. Their common influence may best be seen in graphical form, as represented in figure 7.1. The probability of in-growth is high in stands with many stems per hectare and low basal area, a situation typical for young stands that are not very dense. In addition, the probability of

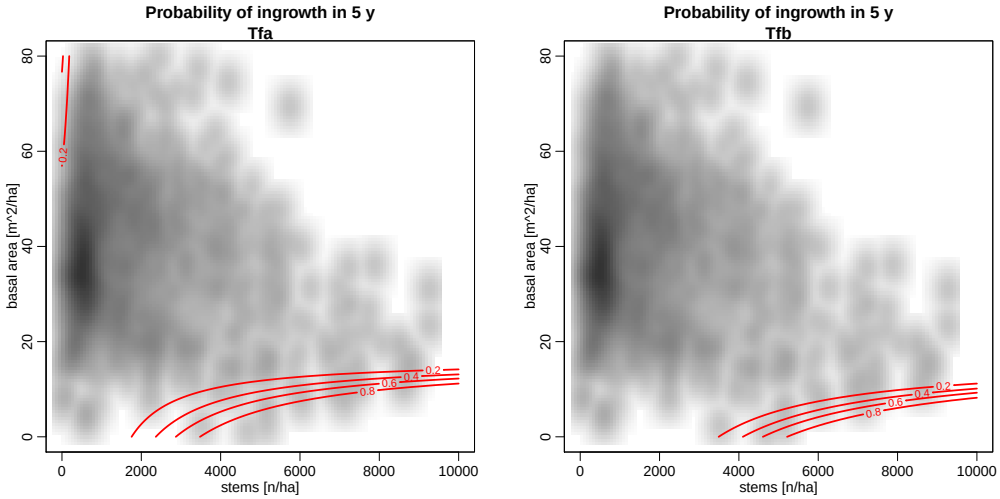

Figure 7.1: Estimated probabilities for ingrowth

in-growth is higher where there is an extremely low number of stems but a high basal area, a distribution which is common for old stands. Under thinning from below, less in-growth occurs.[1]. The population average model for a 5-year probability is:

$$\hat{\pi} = \frac{1}{1 + e^{-(-4.2 - 2.8 \cdot Tfb + 0.0016 \cdot nt + 0.05 \cdot bat - 0.000099 \cdot nt \cdot bat)}} \tag{7.1}$$

where Tfb is equal to 1, if the regime is thinning from below, if not 0. The other variables are defined in section 2.2.

Like in the mortality models, I used the time distance to the 5-year standard interval to normalize for longer or shorter intervals[2]. A further random effect at the stand level was added. The full model description can be found in the appendix A.5

7.2 Number of in-growing trees

The data structure and the basis for calculations is the same as in the previous section on in-growth probability. For comparison, the number of in-growing trees was up-scaled to a hectare and log-transformed to ensure positive predicted values. Furthermore a random effect at the stand levels was intro-

[1] I also tested the basal area harvested which indicates the thinning intensity, but the Regime factor variable was better, both being correlated

[2] In the predictions, I use only 5 years, hence this variable is always 0.

duced. Potential explanatory variables were d_q, age(a), $ddom$, nt, bat, csa, nh, and bat (for definitions see section 2.2).

After analyzing the data with a generalized additive model to find non-linear relationships and after a backwards stepwise comparison of models (tested by likelihood ratio tests), the final model was found to depend on dq, $ddom$, nh, and nt. An interaction between dg and $ddom$ was found.

Figure 7.2 shows the resulting predictions. Low stand densities (low number of stems per hectare, $nt = 100$) are compared to high stand densities (larger number of stems ($nt = 1500$)), on the left and right sides, respectively. This shows a strong influence with clearly more in-growing stems for lower (stem) densities. The upper and lower figures do not show much reaction, hence the number of harvested trees (nh) has a low positive impact. On the left side, the shift of d_q and $ddom$ towards the center of observed values (the black area in the background) increases the amount of in-growth, whilst on the right side a shift to the middle decreases the number of in-growth (no space left for further trees). The full model can be found in the appendix A.6.

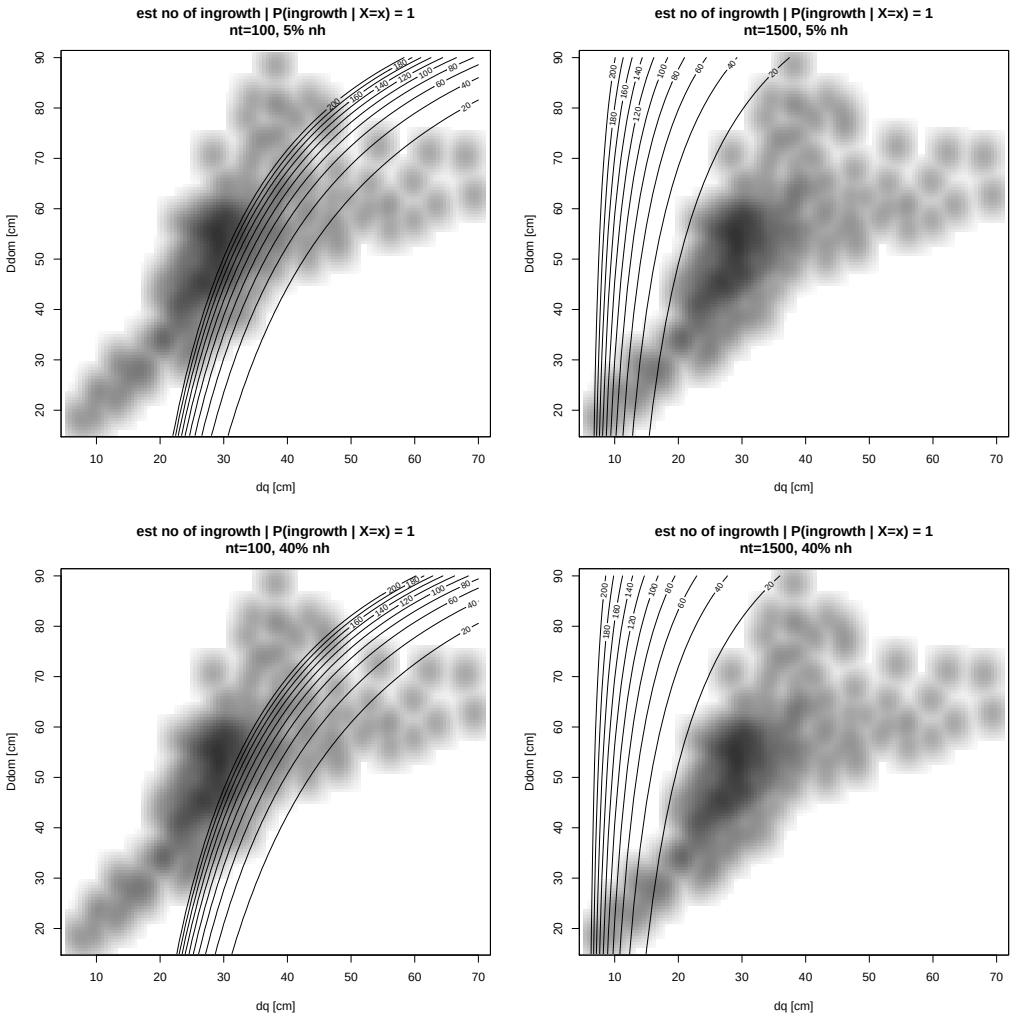

Figure 7.2: Estimated in-growth based on some values of explanatory variables. Amount of in-growth only for those surveys, where in-growth occurred (P(observed ingrowth) = 1). Background shows a two-dimensional density of observations.

7.3 Biometric variables of in-growing trees

7.3.1 Diameter and Height

To describe the density of diameters, the Weibull distribution is a common choice Bailey and Dell (1973). It is a left-truncated distribution and can handle a wide spectrum of stand situations. Here, the distribution was applied to in-growing trees, but applied to each tree species group separately. Since the smallest diameter is 7.5 cm, this offset was an additional fixed parameter. The density function has the following form

$$f(x;\lambda,\kappa) = \frac{\kappa}{\lambda}\left(\frac{x-7.5}{\lambda}\right)^{\kappa-1} e^{-((x-7.5)/\lambda)^{\kappa}}, \tag{7.2}$$

where λ is the scale and κ the shape parameter. They were estimated by maximizing the Likelihood function, given the observations:

$$L(\lambda,\kappa;x_1,\ldots,x_n) = \prod_{i=1}^{n} \frac{\kappa}{\lambda}\left(\frac{x_i-7.5}{\lambda}\right)^{\kappa-1} e^{-((x_i-7.5)/\lambda)^{\kappa}},$$

using the function `fitdistr` in the package `MASS` (Venables and Ripley, 2002). The resulting densities are shown in figure 7.3 per tree species group.

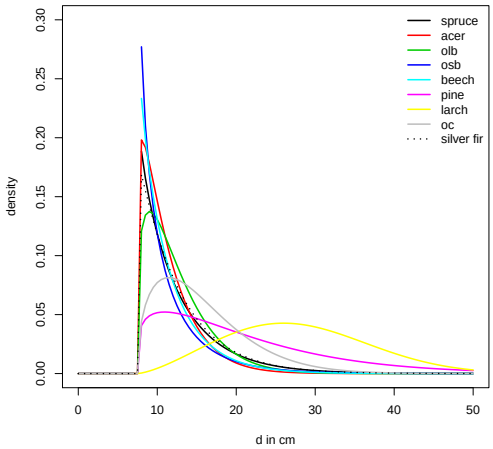

Figure 7.3: Diameter distribution of in-growing trees by tree species groups

A simple model for the heights of in-growing trees was also estimated. Per tree species the observed heights were modeled using equation 3.1.

7.3.2 Tree species group

The tree species group of in-growing trees follows a multinomial distribution, which is a generalization of the binomial distribution, with J levels ($Y \in \{0, 1, \ldots, J-1\}$). This classification problem can either be solved by fitting the multinomial distribution directly, using the function `multinom` in the package `nnet`, which is likelihood based, with restrictions. However, this approach has two weaknesses. Since we have $J = 11$ levels, many parameters for each explanatory variable needs to be estimated, but the data is not equally distributed between the tree species groups. This results in very large standard errors. Moreover, a mixed model approach to account for random errors at the stand level cannot be used. The problem was solved by encoding the multiclass problem with J classes as J binary class problems by using

$$Y_i^{(j)} = \begin{cases} 1 & \text{if} \quad Y_i = j, \\ 0 & \text{otherwise} \end{cases}$$

This means that that each tree species group was considered against all other remaining tree species groups, resulting in eleven logistic regression models. Since number of explanatory variables at the stand level is much smaller (compared to single tree observation based models), the selection of models was based on a "full" model, with backward selection of explanatory variables. Model comparisons were based on likelihood ratio tests. The full model contained the leading tree species group (*lead.spec*), *nph.per*, *tphy.per*, *mphy.per*, *wat.hold.cap*, the sum of cross section crown areas (*cs*, based on the estimated crown width, $\hat{r}$, see equation 3.2), cs^2, $nphy.per^2$ and interactions between *tphy.per* and *mphy.per* as well as between *cs*, and *wat.hold.cap*. The models further contain a random error at the stand level. The models can also be different in terms of explanatory variables. The sum of predicted probabilities for each model ($\hat{\pi}_j$) must not equal 1, therefore a normalization was applied:

$$\widetilde{\pi}_j(x) = \frac{\hat{\pi}_j(x)}{\sum_{j=0}^{J-1} \hat{\pi}_j(x)}$$

The full models are not reported, only an interpretation of the common prediction ($\widetilde{\pi}_j(x)$, see figure 7.4), since in-growth seldom occurs and the eleven models are large. Interested readers can find them in `SwissStandSim` in the object `m.species.in`. For the interpretation, a range of predicted values is given in figure 7.4. For the dependence on climate, a grouping was applied on the variable *mphy.per*, cutting the range of scaled values into three equally sized classes. Then, the mean temperature and mean precipitation within each class was used in the prediction, resulting in wetter,

normal and drier climates. The upper row in figure 7.4 shows the predicted probabilities for stands dominated by spruce and the lower part reports on beech dominated stands. As expected, under spruce stands, spruce also dominates the in-growth, but with increasing stand density (measured by *cs*, the sum of crown cross sectional areas), beech becomes more important. This only holds under better water holding capacity. Under lower water holding capacity silver fir replaces beech.

The lower row in figure 7.4 shows that beech in-growth has higher probabilities of occurrence when water holding capacity is better. For lower water holding capacity silver fir dominates the in-growth.

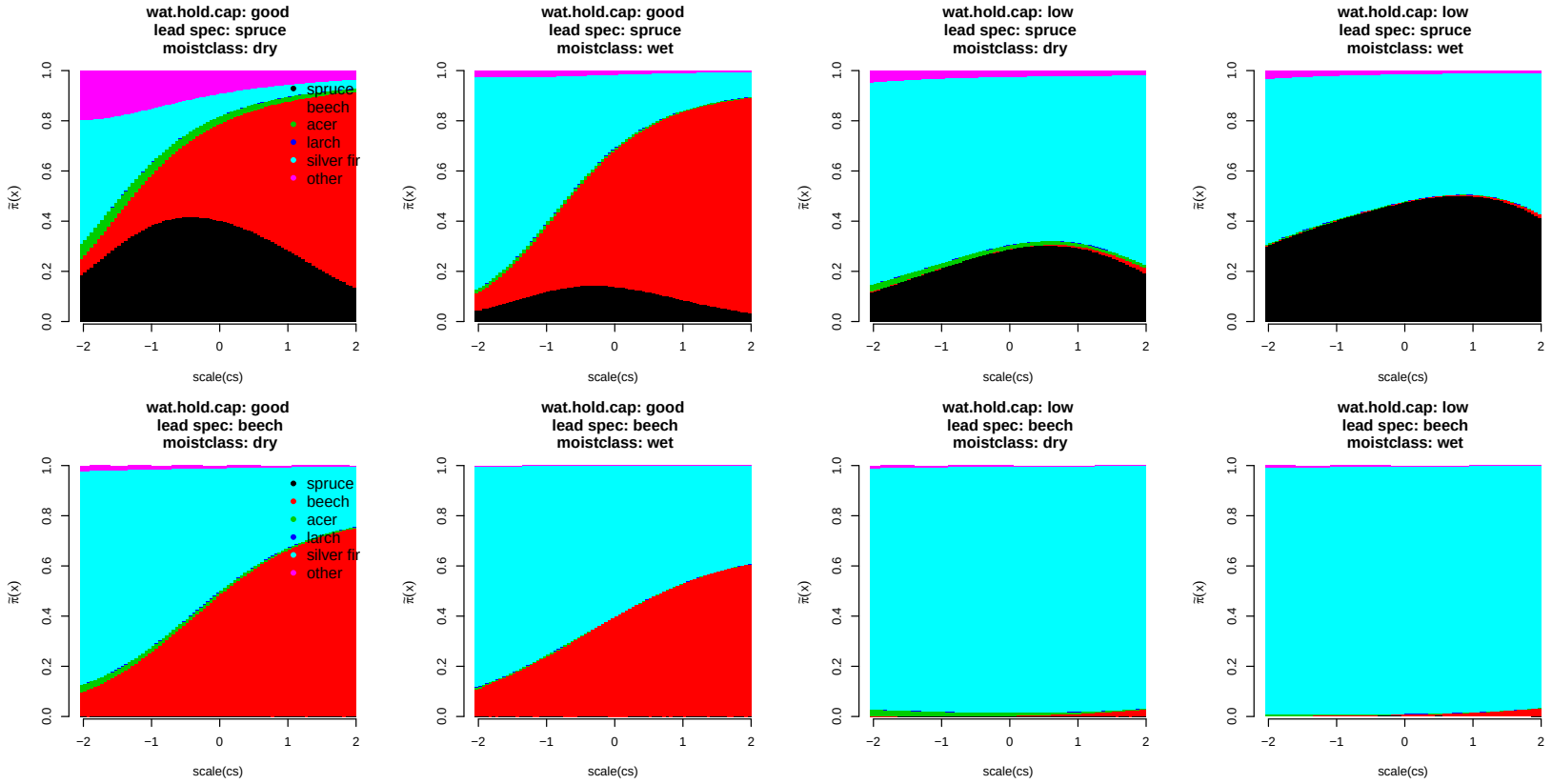

Figure 7.4: Predicted probabilities for tree species in-growth. The range of climate variables was cut by the moisture index (*mphy.per*) into three equally sized classes. Temperature and precipitation are mean values in these classes.

Chapter 8

Harvesting

8.1 Introduction

A full description of the harvesting schedule contains the beginning, the intervals, the end, the intensity, and the type of thinning. All these variables are not random numbers and are also needed for later simulation. Furthermore they need to be fixed by the user of the simulator. The only randomness is the influence on the diameter distribution. Here we need to model the probability of being harvested over the distribution of diameters.

In the original data, three types of thinning from below ("Tfb") are distinguished. I regrouped them to only Tfb because intensity is part of the harvesting schedule. In addition, there is "Tfa" (Thinning from above), which is a thinning whereby dominant trees are supported. "Lichtwuchs" is a special form of Tfa, with a late start and high intensity, so I grouped it with "Tfa". Throughout harvesting, I use thinning intensity as measured by the percentage of basal area harvested (bah). For final felling ("ff"), I regrouped "Abtrieb" (partly clear cut) and "VJ-Hieb" (clear cut to enable natural regeneration). Through the whole analysis, I excluded "Plenterwald", a special form of continuous cover forestry.

8.2 Modeling

For Tfa, Tfb, and ff the probability of a single tree of being harvested needed to be modeled. At the single tree level, being harvested has a Bernoulli distribution, which was modeled by a logistic regression. For each Regime (Tfa, Tfb, ff) I used a different probability model. The simplest one was final felling (ff) since there are only few observations and it was only depending on the thinning intensity (it is independent of diameter). A transformation

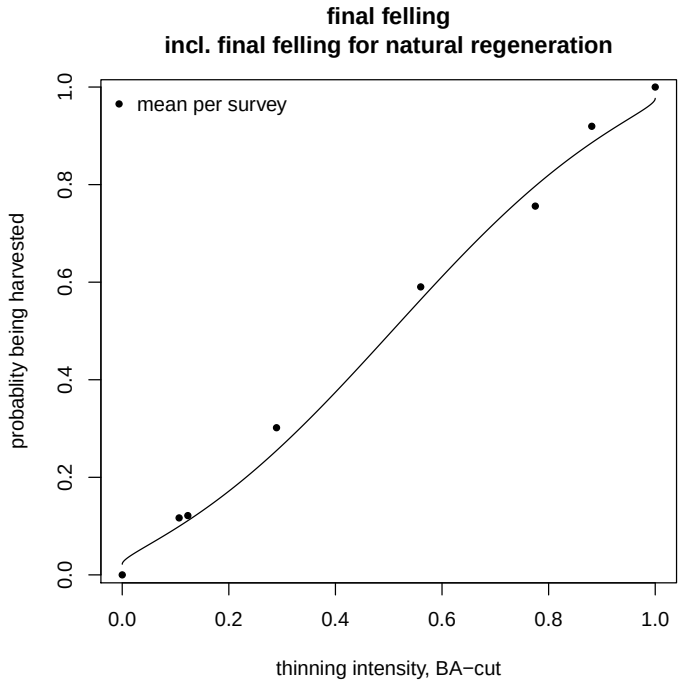

Figure 8.1: Probability of being harvested for final fellings (ff).

of *bah* showed better results (compared to *bah* alone):

$$\pi_{ff} = \frac{1}{1 + e^{-(-3.8+4.8 \cdot \arcsin\sqrt{bah})}} \tag{8.1}$$

For Tfa and Tfb I started with a maximal model with all potential explanatory variables. These were: rd, nt, bah, $lead.spec$ and $t.sp.g$ (see section 2.2 for further explanation). Again, a mixed model approach was used, with a random effect at stand level and, again, only the population mean was used for predictions. Further interactions between nt and rd were found. Model reduction was based on likelihood ratio test.

8.3 Results and Discussion

Thinning from above was found to depend on rd (relative diameter), nt, bah, $lead.sp$, $t.sp.g$, and π_{tfb} on the same variables, but not $lead.sp$.

Thinning from below is an older type of thinning for the purpose of maximizing exploitable harvested volume. In its strongest form, only suppressed trees are cut.

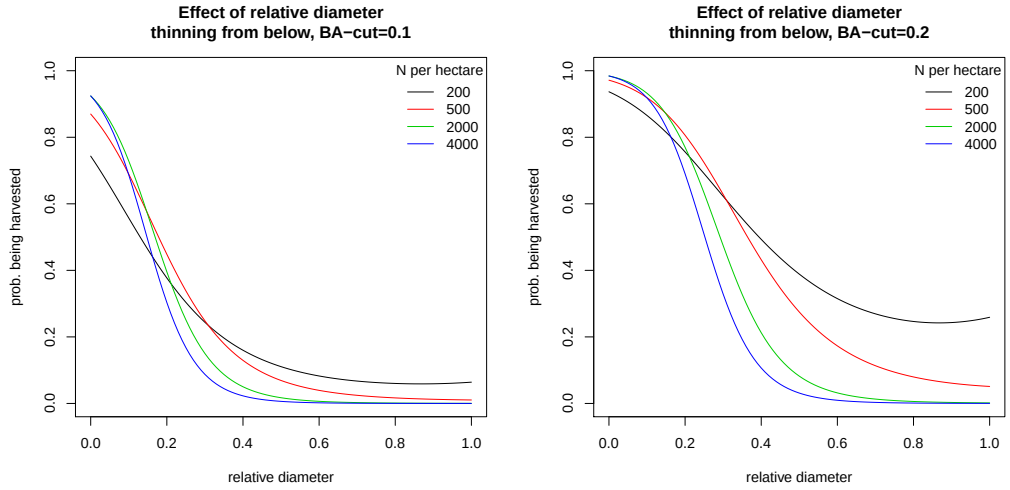

Figure 8.2: Probability of being harvested for Thinning from below (Tfb)

A graphical representation of the Tfb model can be found in figure 8.2. Probability increases sharply at a relative diameter of about 0.3. Stand density (stems per hectare) also increases the steepness of the curves. The right panel shows that the probability is also highly dependent on thinning intensity. The black line, which represents the smallest tree density (200/ha), shows a slightly higher probability for larger trees. This is reasonable, since such stands are older. Here, thinning is aimed at supporting the largest trees in a stand, which means that there is a higher probability of thinning.

This is a transition towards Tfa, which aims to support the dominant trees in a stand (see figure 8.3). Again, we see that the steepness of the curves depend on the density in the stand. Remarkably, the black curve on the right side shows that the probability reaches a maximum at around 0.6 and then decreases. This is due to the nature of Tfa: Cutting pressure is highest on the competitors of the dominant trees, which is represented by the optimum in the curve. The full models can be found in the appendix A.7.

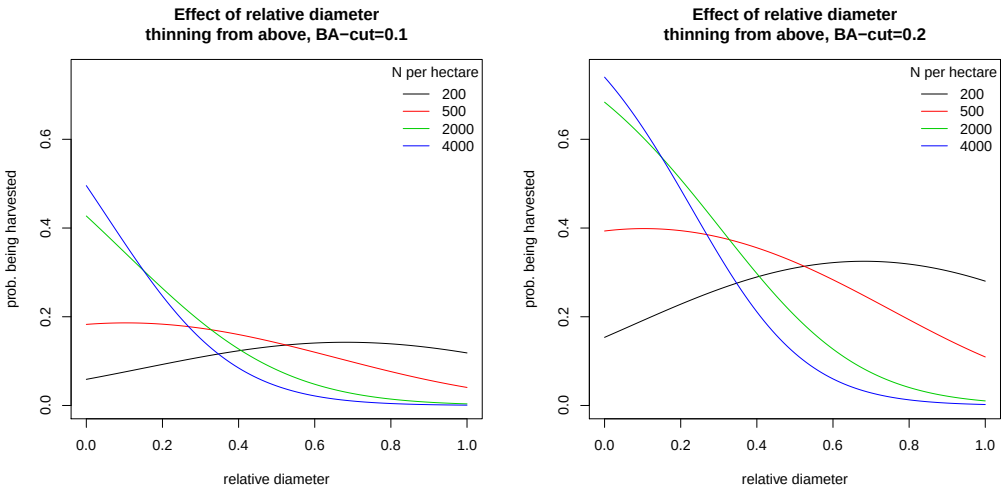

Figure 8.3: Probability of being harvested for thinning from above (Tfa)

Chapter 9

Simulator

9.1 Basics

The simulator (under Windows) can be opened by double clicking on `Swiss-StandSim.bat`. It opens an interactive R program, which is located in the `SwissStandSim` folder, to ensure that the correct version and packages will be loaded. The simulator is stand alone, meaning that there is no need to install `R` on the computer. Loading may require some extra time depending on the computer. Automatically, the function `f.main()` is executed, which has an extremely simple user interface. The function defines whether all stands should be used, or only a subset (by defining the identifiers for stands, FNUM). One can also define how often a stand is repeatedly simulated and a starting random number can be fixed for reproduce-ability. One can specify a new folder for the output as well. Then the simulation starts and reports on the current state of the simulation are reported on the screen and output-files are stored (usually under "results").

9.2 Description and structure of the model

9.2.1 Flow of processes

All relevant processes needed to run the simulator are described in the previous chapters. The simulator is a prediction system, which sequentially predicts new tree and stand states. Very often, it is tree species-specific, but not always. For instance, the harvesting module is not.

Basically, the simulator follows the data recording in the field. This means we first observe a stand with current diameters and tree species. When a thinning operation is planned, foresters mark the trees to be felled. After

the felling, the stats of the stand changes and will be revisited later, when the changes are measured.

This is exactly how the simulator works. In the following code, which is a function that controls the flow of processes, this becomes clearer.

```
1
2  f.run ← function(fnum, g.nsim){
3    # function which steers the simulations: calls many other function and
4    # is the body for harvesting, growth(d,h), mortality and ingrowth
5    if(g.report){
6      cat("-----------------------------------------------\n")
7      cat("Start simulation for ", fnum, "repl. ", g.nsim, "\n")
8      cat("-----------------------------------------------\n")
9    }
10   # redefine seed
11   g.seed <<- g.nsim + g.seed
12
13   f.definePattern(fnum=fnum)
14   years ← g.pattern[g.pattern$FNUM == fnum , "year"]
15
16   # trees in time (t.in.t), a list, later also containg time invariant
         expl. var.
17   t.in.t  ← t.out.t ← vector("list", length(years))
18   names(t.in.t) ← names(t.out.t)  ← as.character(years)
19
20   # define starting data, including time-invariant expl. variables
21   if(g.report) cat("Load starting data\n")
22   start.trees ← subset(d.tree, FNUM == fnum & year == min(years),
23     select=c(FNUM, year, t.ID, t.sp.g, d,h,v,a, status, soil.depth, wat.
           perm,
24     wat.hold.cap, relief, grad.p, exposition) )
25
26   start.trees$appeared ← start.trees$year
27
28   time.invariant.var ← c("FNUM", "soil.depth", "wat.perm", "wat.hold.cap"
         ,
29       "relief","grad.p","exposition")
30
31   re.used ← c("FNUM","year","t.ID","appeared",
32       "t.sp.g","d","h","v","a", "status","exposition", "wat.perm",
33       "wat.hold.cap","soil.depth", "relief", "grad.p")
34
35   var.of.interest ← c("FNUM","year","t.ID","appeared","t.sp.g",
36     "d","h","v","a","status")
37
38   for (i in seq(along=years[-length(years)])){# loop over time steps::
         map state (i) to state (i+1)
39     # define some temp. variables (all scalar)
40     t.year    ←   years[i]
41     t.bah     ← g.pattern$bah[g.pattern$year == t.year] # temp. basal
           area harvested
42     t.regime  ← as.character(g.pattern$Regime[g.pattern$year == t.year ])
           # temp regime
43     if(g.report) cat("Year: ", t.year, " % of BA harvested: ", round(t.
           bah,3)*100, " Regime: ", t.regime,"\n")
44
45     # define current temp-dataset (used for predictions and later to be
           saved)
46     if(i == 1){
47       temp ← start.trees
```

```
48        temp$status ← as.character(temp$status)
49        # start.trees containg the truely cutted trees, here we want to
              estimate harvesting, hence reset status:
50        temp$status ← ifelse(temp$status == "planned","living",temp$status)
51      } else {
52        temp ← t.in.t[[ as.character( t.year ) ]]
53      }
54
55      #-------------------------------------------------------
56      # 1) HARVESTING: expand dataset to calc. harvesting (time variant var
            .)
57      temp$rd     ← f.rd(temp$d)# relative diameter
58      temp$nt     ← nrow(temp) * 1e4/d.meta$HA[d.meta$FNUM == fnum]# stems
            per hectare
59      temp$bah    ← t.bah # basal area harvested
60      # lead.sp.: a character string
61      temp$lead.sp  ← f.lead.sp(t.sp.g=temp$t.sp.g, d=temp$d)
62      temp$lead.con   ← ifelse( temp$lead.sp %in%
63                  c("douglas fir", "spruce", "pine", "larch",
64                  "oc", "silver fir"), 1, 0)
65
66      # predict harvest
67      if ( t.bah > 0 ){
68        # calc harv prob for Tfa, Tfb, ff
69        p.harv ← f.p.harv(Regime=t.regime, data=temp)
70        # determine index of harvested trees
71        idx ← f.do.harv(d=temp$d, p=p.harv, bah=t.bah)
72        if (g.report) cat("Cutted", length(idx), "trees\n")
73        # change status
74        temp$status[idx] ← "planned"
75      }
76
77      # save harvesting with state(t_i)
78      # for internal use
79      t.in.t[[ as.character(  years[i]) ]] ← temp[,re.used]
80      # for external re-use
81      t.out.t[[ as.character( years[i]) ]] ← temp[,var.of.interest]
82
83
84      # calc rel. number of harvested trees
85      temp$nh   ← sum(temp$status == "planned")/nrow(temp)# proportion of
            trees harvested
86      # now take away harvested trees
87      temp ← temp[ !temp$status %in% c("planned","dead"), ]
88
89
90      #-------------------------------------------------------
91      # 2) EXPAND for climate/ndep (time variant):
92      #   that is the (mean) climate for the next 5 year-periode
93      temp ← cbind( temp,
94        d.clim[ d.clim$FNUM == fnum & d.clim$year == t.year,
95          c("tphy.per", "nphy.per", "m.spring", "ndep")  ]
96        )
97      names(temp)[names(temp) == "m.spring"] ← "mphy.per"# renaming
98
99      # here the scaled versions of climate variables:
100     temp$tphy.per.s   ← (temp$tphy.per-7.05)/1.873
101     temp$nphy.per.s   ← (temp$nphy.per-1062.9)/224.14
102     temp$mphy.per.s   ← (temp$mphy.per-25.15)/7.78
103
104
105
```

```
106     #-------------------------------------------------------
107     # 3) D-GROWTH: calc expl. var. to calc bai
108
109     temp$bal  <- f.bal(d=temp$d,fnum=fnum)
110     temp$rbal   <- f.rbal(bal=temp$bal)
111     temp$bat  <- f.bat(d=temp$d, fnum=fnum)
112     temp$mixB   <- f.mixB(d=temp$d, t.sp.g=temp$t.sp.g)
113     temp$cba  <- f.cba(d=temp$d)
114
115     # let it grow: use models to calc bai
116     temp$bai  <- f.bai(data=temp)# used to predict mortality
117     temp$rbai <- f.rbai(bai=temp$bai, d=temp$d)
118     temp$d2   <- f.d2(bai=temp$bai, d=temp$d)
119
120     #-------------------------------------------------------
121     # 4) MORTALITY: expand dataset for mortality, then calc mortality
122     temp$sdi    <- f.sdi(nt=temp$nt, d=temp$d)
123     temp$rh     <- temp$h/mean(temp$h)
124     temp$delta.t5   <- 0
125     # prob. to die
126     p.mort <- f.p.mort(data=temp)
127     # use simulation to determine death (only for trees which are living)
            :
128
129     idx.mort <- f.die(p.mort)
130     if (g.report & (length(idx.mort)>1)) cat(length(idx.mort), "trees
            dying\n")
131     temp$status[idx.mort] <- "dead"
132
133     #-------------------------------------------------------
134     # 5) INGROWTH: calc prob for ingrowth
135
136     p.in <-  f.p.in(nt=temp$nt[1], bat=temp$bat[1], fnum=fnum)
137
138     # does ingrowth occur?
139     set.seed(g.seed)
140     ingrowth <- ifelse(p.in > runif(1), TRUE, FALSE)
141
142
143     #-------------------------------------------------------
144     # 6) calc number of ingrowing trees as data.frame, if ingrowth occurs
145
146     if (ingrowth){
147       n.in <- round(f.n.in(data=temp, fnum=fnum),0)
148       if(g.report) cat(n.in, "ingrowing trees\n")
149       if (n.in >0){
150         p.spec.in     <- f.p.sp.in(data=temp[1,])
151         species.in    <- f.species.in(p=p.spec.in, n=n.in)
152         d.in      <- f.d.in(sp.in=species.in)
153         h.in      <- f.h.in(d.in=d.in)
154
155         data.in <- cbind(
156           data.frame(
157             year = temp$year[1]+5,
158             t.ID = (max(temp$t.ID)+1):(max(temp$t.ID)+n.in),
159             appeared = rep( temp$year[1] + 5, n.in),
160             t.sp.g = species.in,
161             d = d.in,
162             h = h.in,
163             v = f.vol(d=d.in, h=h.in, t.sp.g=species.in),
164             a = temp$a[1] + 5,
165             status="living"
```

```
166             ),
167             temp[1:n.in,time.invariant.var]
168           )
169         }
170       }
171
172       #-------------------------------------------------------
173       # 7) UPDATE old data (overwrite)
174       temp$d    ← temp$d2
175       temp$h    ← f.h.grow(data=temp)
176       temp$a    ← temp$a + 5
177       temp$v    ← f.vol(d=temp$d, h=temp$h, t.sp.g=temp$t.sp.g)
178       temp$year   ← temp$year + 5
179
180
181       #-------------------------------------------------------
182       # 8) data for RE-USE
183
184       # select reused var
185       temp ← temp[,re.used]
186       if (ingrowth){
187         if (n.in>0) temp ← rbind(temp, data.in)
188       }
189
190       #-------------------------------------------------------
191       # 9) SAVE for re-use
192       t.in.t[[ as.character(  years[i+1]) ]] ← temp
193
194       #-------------------------------------------------------
195       # 12) SAVE for external re-use
196       t.out.t[[ as.character( years[i+1]) ]] ← temp[,var.of.interest]
197     }
198
199     if (g.overwrite) {
200       out.path ← paste0("results/",fnum,"_s", g.nsim, ".rds")
201     } else {
202       if (g.nsim == 1 & !dir.exists(paste0(g.path.res,"/"))) dir.create(
              path=paste0(g.path.res,"/"))
203       out.path ← paste0(g.path.res,"/",fnum,"_s", g.nsim, ".rds")
204     }
205     saveRDS(t.out.t, out.path)
206     if(g.report) cat("Output written\n")
207   }
```

In line 22 the stand is observed for the first time. The data, which are loaded here includes the basic biometric information of the single trees at the first observation. Then, a loop in line 38 is opened, which runs over the time points previously defined in the harvesting pattern. The harvesting pattern contains all the information needed for a full description of a harvesting schedule. The first process, harvesting, starts in line 56. Initially, a probability of being harvested for the single tree is calculated (line 69). Based on the calculated probability, the number of trees that were actually harvested is sampled (line 71). In lines 79 and 81, the result of the harvesting operation is stored with the full biometric variables (which have not changed until now) onto the first point in time.

After this, the new diameters are calculated (line 107). The next process

is mortality, which works like harvesting. First, a probability is calculated (line 126) and based on the probability, a realization of dead trees is sampled (line 129). The next few lines describe in-growth. First, the probability of in-growth occurrence is calculated (line 136). Then, actual in-growth, if it occurs, is realized. The code after line 144 is only executed, if in-growth really occurs and it fills a full `dataframe` with all necessary biometric information. It estimates a diameter, height, and a tree species group. Lines 173 ff. update the biometric information and here the growth function for height is applied. New volumes based on the new diameter, the new height, and the tree species group are estimated. Then, only a subset of the data is internally reused (since we have time-dependent explanatory variables, line 182). The external output is defined in lines 195 ff. and contains the most interesting variables like tree species group, diameter, height, volume, and age. The information over the full time-line is stored in `R` as a `list`, which acts as a container for all possible objects. The containers are quickly saved in a binary `R`-specific `*.rds` binary file format.

9.2.2 Harvesting pattern and time-line of the simulation

There is a large discrepancy between the observed (sampled) time-intervals and the regular pattern used in the simulator. In order to reconstruct the observations, it was necessary to build a function that calculates a harvesting pattern, which is as similar as possible to what actually occurs. The following figure 9.1 makes this problem clearer.

Such a harvesting pattern is also necessary for further research questions. The pattern is derived from the following function:

```
1  f.definePattern ← function(fnum){
2    # function to determine global harvesting operation variables
3    # produces g.pattern as global data.frame
4
5    patt    ← subset(d.harvesting, FNUM == fnum)
6    patt$Regime ← as.character(patt$Regime)
7    start.y   ← min(patt$year)
8    end.y     ← max(patt$year)
9
10   # define timeline of 5-yr steps for simulation
11   sim.years ← seq(from=start.y, to=start.y+ceiling((end.y - start.y)/5)*
         5, by=5)
12
13   # at which indeces does harv at neareast take place?
14   idx ← sapply( as.list(patt$year), function(x) which.min(abs(x - sim.
         years)))
15
16   # define regimes
17   Regime ← rep("do nothing", length(sim.years))
18   Regime[idx] ← patt$Regime[rank(idx)]
```

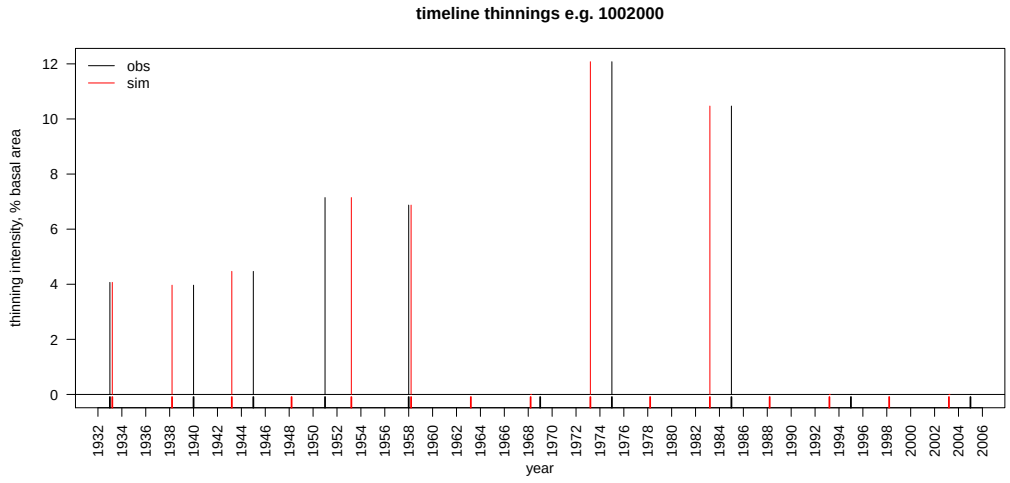

Figure 9.1: Example of harvesting pattern as a time-line

```
19
20    bah ← rep(0, length(sim.years))
21    bah[idx] ← patt$bah[rank(idx)]
22
23    g.pattern ↞ data.frame(  FNUM = rep( patt$FNUM[1], length(sim.years)),
24                year = sim.years,
25                Regime = as.character(Regime),
26                bah = bah)
27    if (nrow(g.pattern)>1 & g.report) cat("Harvesting pattern defined\n")
28  }
```

It produces a `dataframe` in the global workspace called `g.pattern`, which looks like this.

```
      FNUM year     Regime        bah
1  1002000 1933        Tfa 0.04067872
2  1002000 1938        Tfa 0.03965990
3  1002000 1943        Tfa 0.04467326
4  1002000 1948 do nothing 0.00000000
```

Thus, for each stand, the point in time of the simulation is determined by this `dataframe`. The type of thinning (or to do nothing) and the basal area harvested are also defined here.

9.2.3 Workspace

I did not use explicitly different environments in `R` (except for the environments in the functions), so the `workspace` contains many different objects. All `d.*` objects contain pure, given data. This includes the climate data

(`d.clim`), as it was processed especially for the simulation, the starting data (`d.tree`), some information on survey-specific variables (`d.surveys`), and the meta data as given by EFM (`d.meta`).

All functions begin with `f.*`, global variables with `g.*`. The statistical models are loaded at the beginning and named using `m.*`. Unfortunately these are large objects, however, this does not increase the computation dramatically. There is also one plotting function `p.stand`. It is currently the only tool for post-processing. It reads in the binary R-file of a stand and reports on the required variable of interest.

9.3 Validation and Discussion

Validation is over 141 stands, for which all starting values (e.g., climate, nitrogen deposition, ...) were available. The user interface is automatically opened when the `SwissStandSim.bat` file is double clicked and can repeat exactly the full validation by setting the starting seed to 1 (this will be asked by the interface). Since random samples are drawn for in-growth, mortality and harvesting, I repeated each run 20 times. One full run (all 141 stands, all time-points) needs about 1.8 minutes computing time on my PC. This is quite fast compared to Silva or BWinPro.

I started validation using typical stands of beech, spruce, and silver fir, which were observed over a longer time. The comparison is given in figure 9.2. In the upper panel, the development of the beech stand is reported. The lines represent the means of each variable of interest over time (for *dq* with a confidence interval). The only information that is used by the simulator is the starting biometric values of the trees, the stand information, the time-dependent explanatory variables and the harvesting information (intensity, type).

The quadratic mean diameter is in good accordance with the observations for beech and spruce, while silver fir is a bit overestimated. Deviance usually comes from mortality, which has low explanatory power in the probability models. The observed data also contains storm events, which are hard to predict. However, the vulnerability of a stand to storm events is an explanatory variable, measured by *bah*. It is included in the mortality models. A closer look at the right side of the figure shows that the high mortality in spruce is not predicted, but the lower levels in beech and silver fir are predicted and are similar to the pattern in observations.

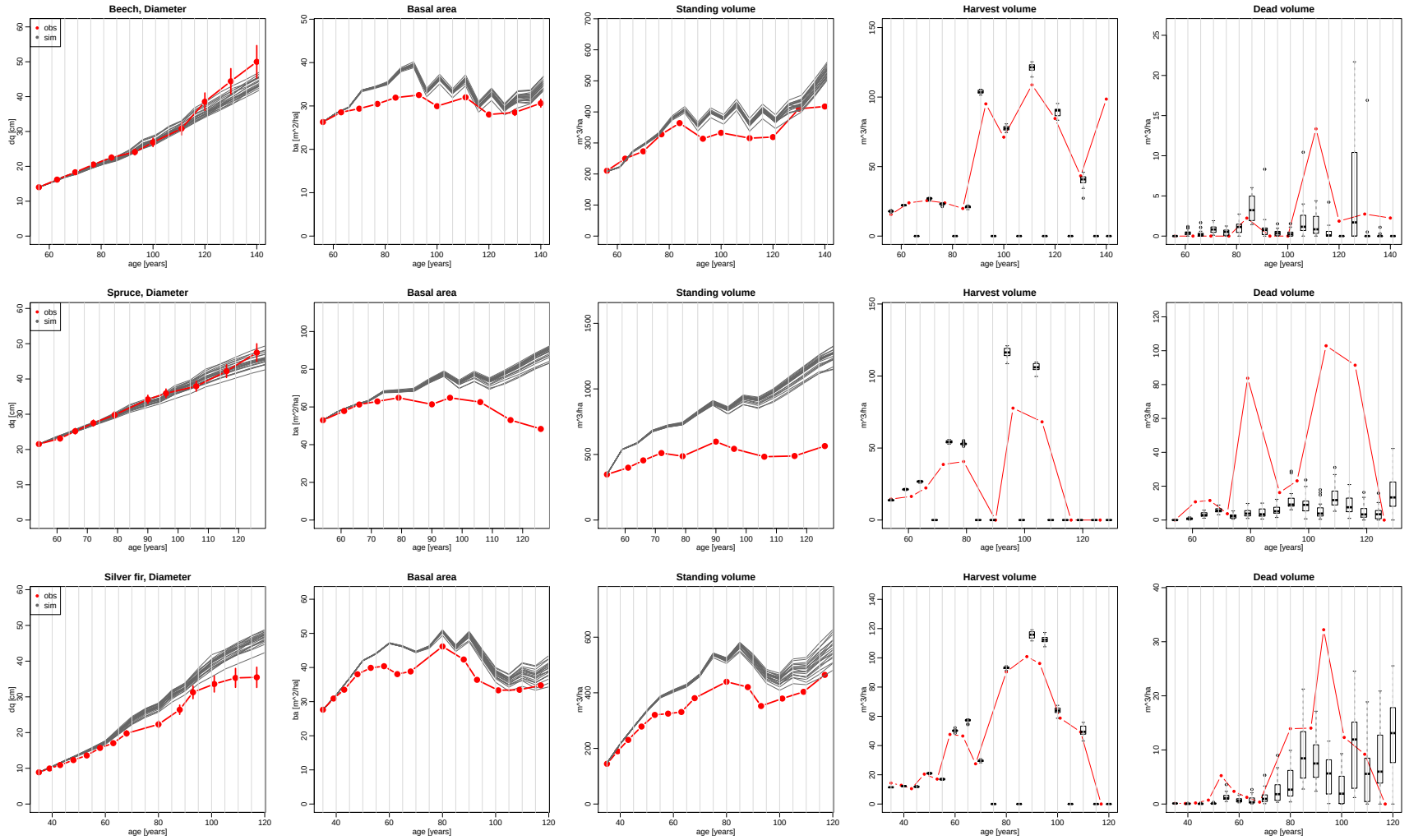

Figure 9.2: Validation over time of three typical stands of beech, spruce and silver fir. The beech stand is located in Baan am Kohlerweg, Zofingen, Aargau, at an altitude of 560m and was measured from 1890 to 2001. The silver fir stand is located in Ob dem Neuhaus, BielBienne, Bern, at an altitude of 670m and was measured from 1921 to 2008. The spruce stand is located at Käppelistein, Hospental, Uri, at an altitude of 1,475m and was measured from 1933 to 2005.

Full systematic validation was carried out over 141 stands. All of them contain a full set of explanatory variables which were re-measured at least 3 times. Harvesting strength was predefined, with the same basal area harvested as given in the observations. Variables of interest were d_q, nt, bat, and v always as a sum or mean value over all trees in a stand at a point in time. After 10, 50, and 90 years, I compared the closest observation (they are never observed exactly at these times) with the predicted values and measured bias, and a relative deviance over the 20 replicates:

$$d = \sum_{i=1}^{20} \frac{|x_{obs} - x_{sim}|}{x_{obs}} / 20 \tag{9.1}$$

where x is the mean or sum of a variable of interest over single trees at a given point in time. Bias was measured by the denominator of that equation, including the sign. The results were aggregated by the leading tree species group at the beginning of simulation. The resulting figures show high accuracy for predicting mean diameters. After ten years, relative deviance is always below 10%, and usually around 3-4%. Only after the simulation gets longer and storms occur more often, does deviance, especially for spruce, show values of 40% (see figure 9.3). Extremely low bias (see figure 9.4) can be found in the beech prediction, even after 50 years, which is in accordance with the high R^2 of the diameter growth model.

The figures 9.5 and 9.6 report the differences in total number of stems over time. The number of stems is predicted with a higher deviance. Note the jump in the y-axis between 10 and 50 years. Over longer times it is clearly less precise. Also bias becomes larger and can deviate enormously from observations (e.g. spruce after 90 years).

The predicted volume is better than the number of stems: see figures 9.7 and 9.8, especially for beech and also over longer time periods. Again, spruce stands cause some problems after longer times due to storm events.

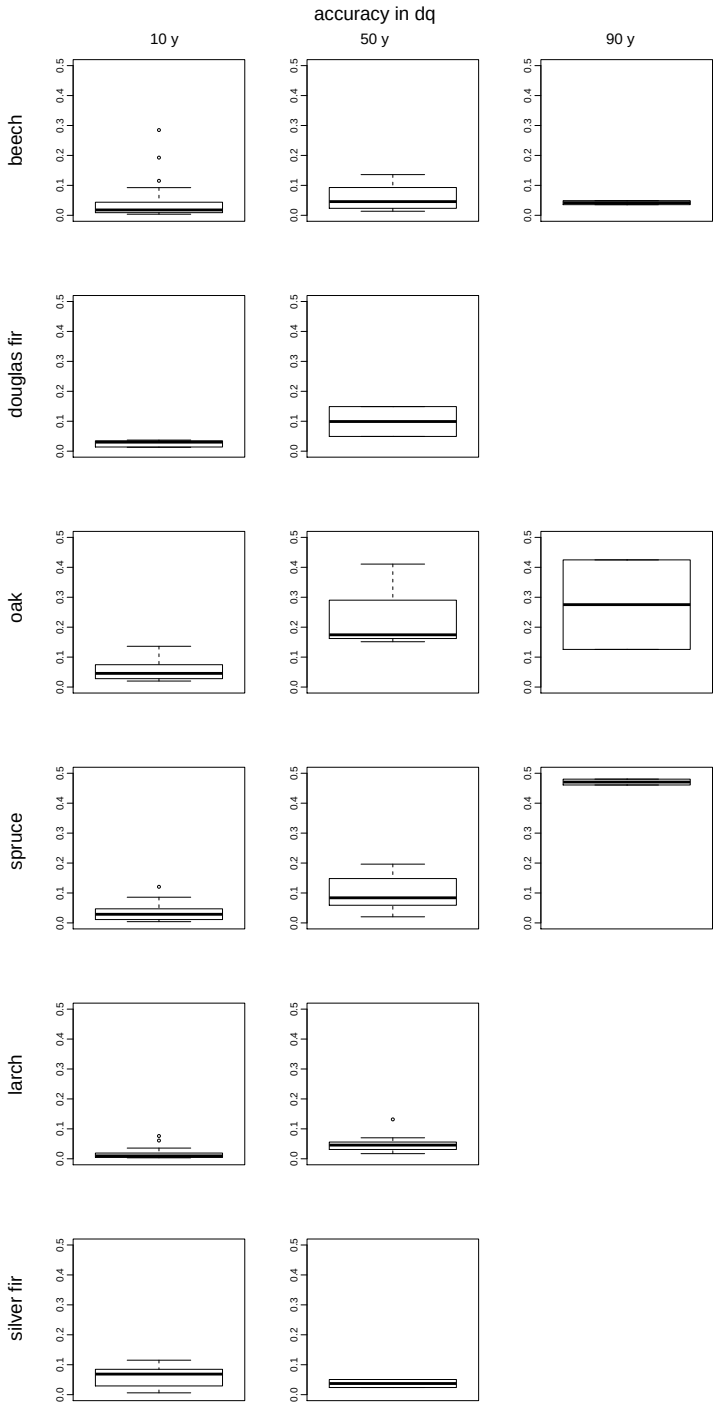

Figure 9.3: Deviance of mean quadratic diameter predictions. The box-plot shows the distribution of deviance over a set of surveys. Each point is a mean over 20 replicates.

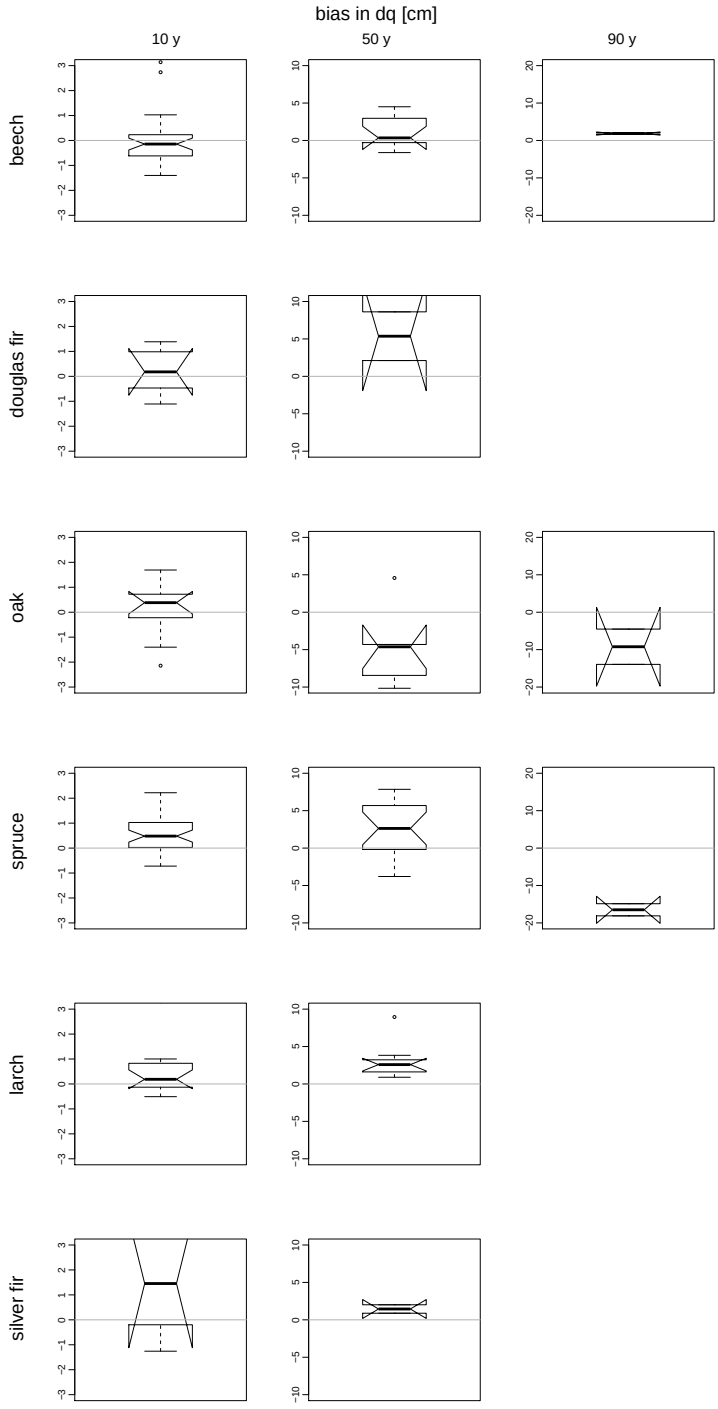

Figure 9.4: Bias of mean quadratic diameter predictions. The box-plot shows the distribution of bias over a set of surveys. Each point is a mean over 20 replicates.

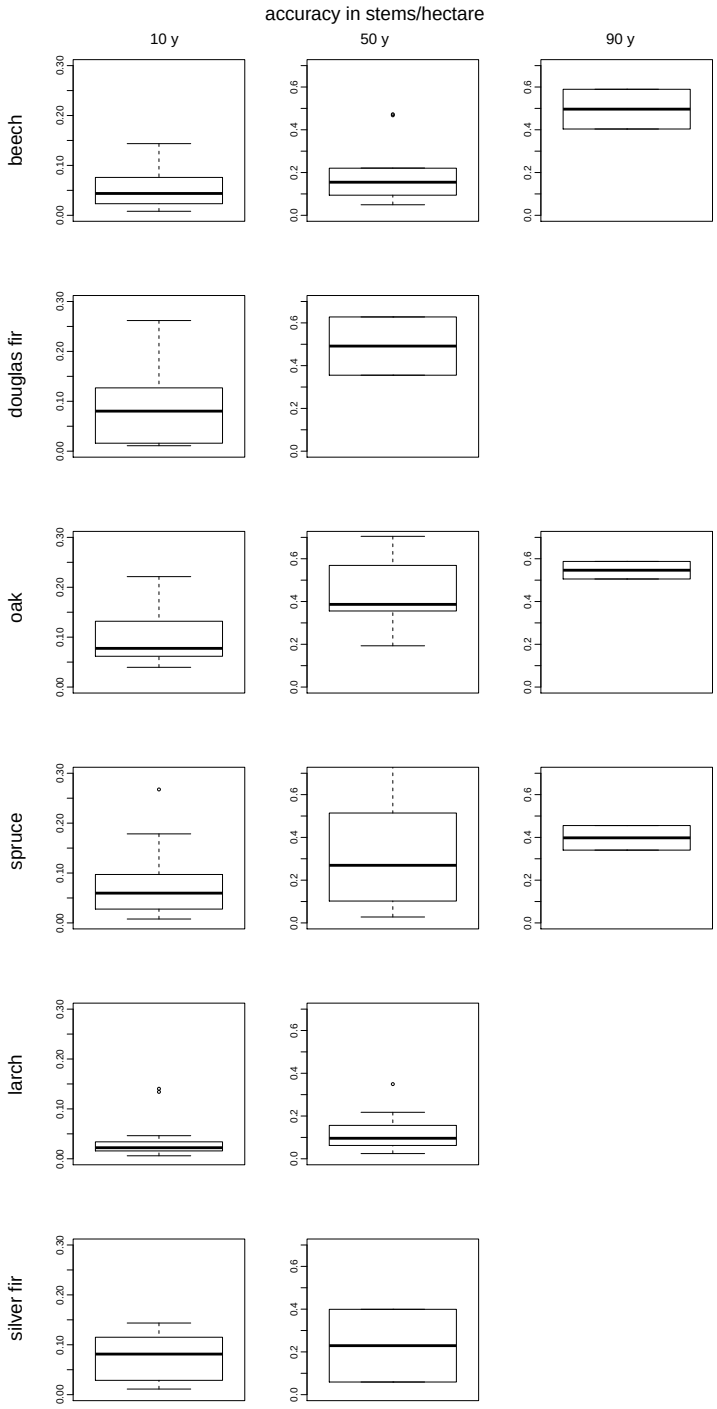

Figure 9.5: Deviance of predicted number of stems per hectare. The box-plot shows the distribution of deviance over a set of surveys. Each point is a mean over 20 replicates.

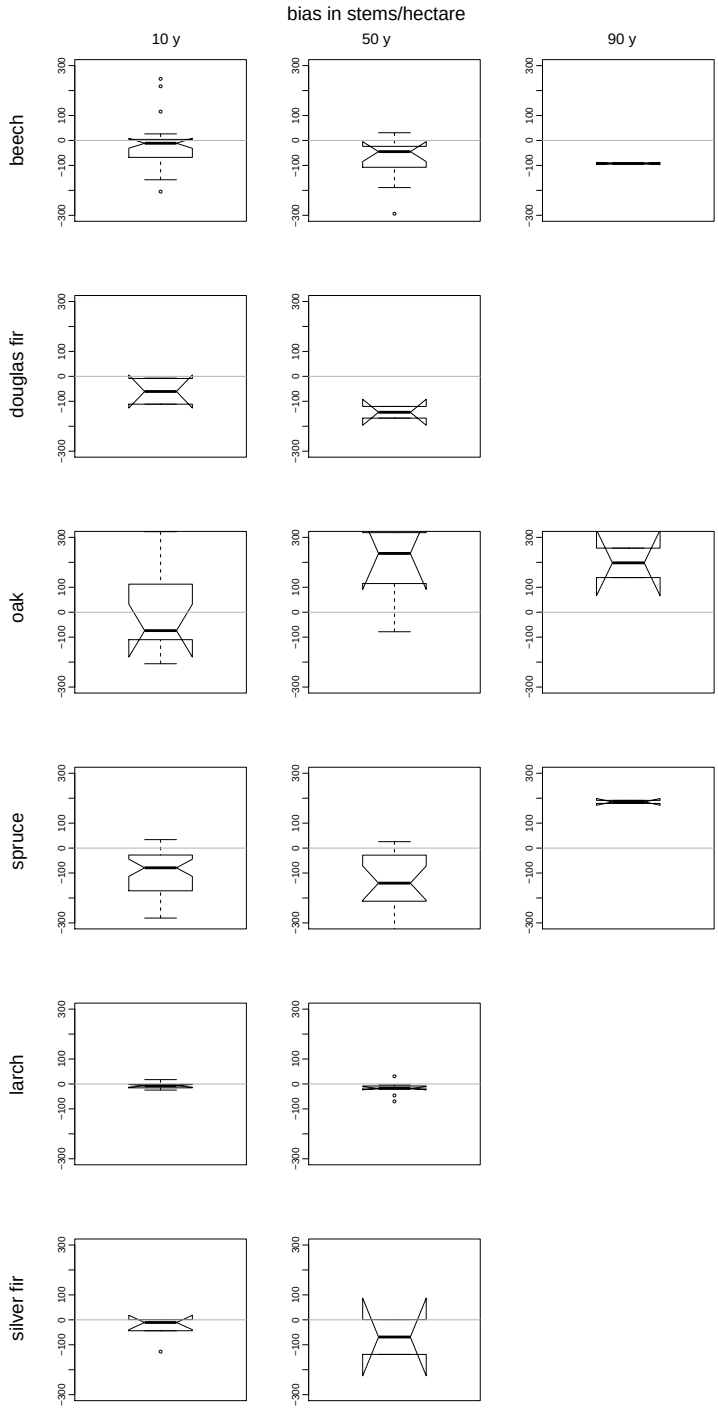

Figure 9.6: Bias of predicted number of stems per hectare. The box-plot shows the distribution of bias over a set of surveys. Each point is a mean over 20 replicates.

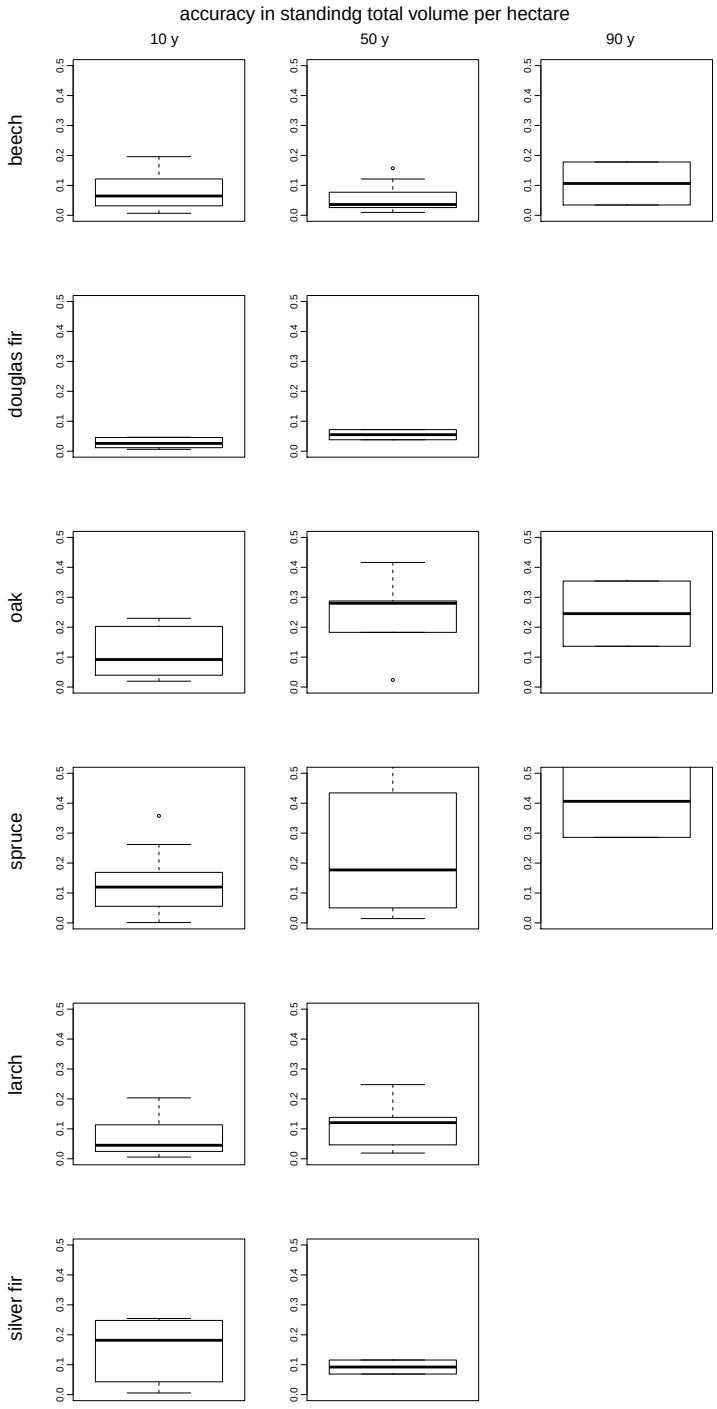

Figure 9.7: Deviance of predicted volume per hectare. The box-plot shows the distribution of deviance over a set of surveys. Each point is a mean over 20 replicates.

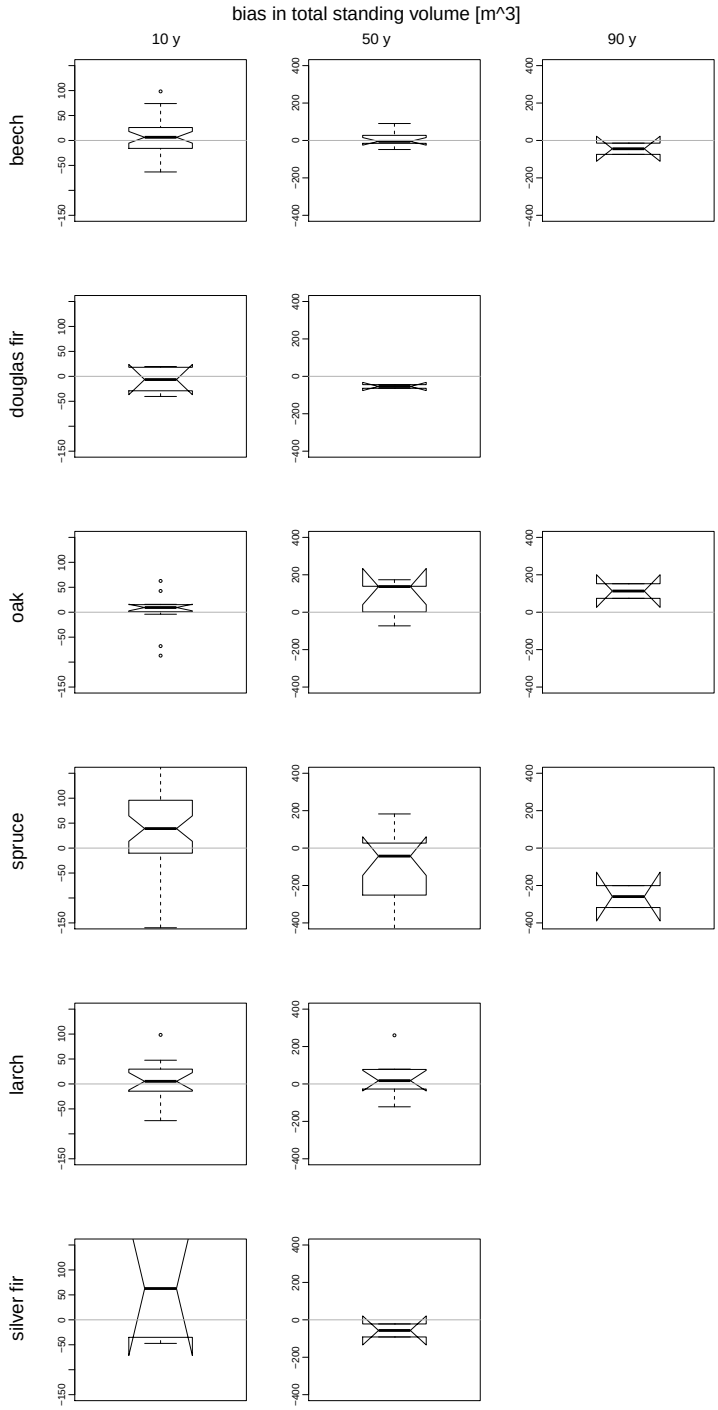

Figure 9.8: Bias of predicted volume per hectare. The box-plot shows the distribution of bias over a set of surveys. Each point is a mean over 20 replicates.

Chapter 10

Outlook

The simulator in its current form invites further improvement with regard to many different aspects. Here is a list of ideas.

- The single statistical models are usually very complex. Perhaps a lighter version would yield similar results. It would be interesting to see the cost of the model complexity in terms of easier pre-calculation of explanatory variables.

- There is a missing link between (sample based) measurements that are usually done in the field and the simulator. At the moment, the goal is to reproduce a given data set of a fully measured area. It would be useful to have a stand generating mechanism that could function as a link between measured samples in the field and the possibility to run the simulator.

- Although I have introduced some stochastic processes by sampling of trees (harvesting, in-growth, mortality), a fully predicted uncertainty is lacking.

- The volume functions are important and need improvement.

- A forest planner or decision maker needs a much simpler version with a graphical user interface.

- From a scientific point of view a graphical representation of growth on a computer screen is perhaps less interesting, but it could improve the dissemination of the simulator enormously. There are already models for crown diameter, crown length, and crown form, which could be used for that technical task.

- Plenterwald and Plenterung are missing, and there is a lot of information to fit the processes.
- In the proposal, we promised to calculate harvesting costs per tree. There is already existing code to be incorporated into the existing simulator, but I had insufficient time to translate the code to be run under the current version (for people with the appropriate background, I would not expect more than one week of work for a very simple version).

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Appendix A

Complementary information

A.1 Reading in the data

```
1
2
3  ##---------------------------------------------------------------------
4  ##  imports *.F files, merges them to a data frame used for analysis,
5  ##  exports dvfl.rds
6  ##---------------------------------------------------------------------
7
8
9  require(foreign)
10 '%nin%' <- function(x,y){
11   x[!x %in% y]
12 }
13
14 # path
15 path <- ""
16
17 # Zugriff Files
18 filenames <- list.files(paste0(path,"dbFiles/"))
19
20 if( length(grep(".F", filenames)) == length(filenames))
21   print("all files correct") else print("check files")
22
23 namescommon <- c(#select the colnames of interest
24   "FNUM", "BNR",  "BA", "AJ", "DFA",
25   "AHC",  "D1", "D2", "DH2",  "V7",
26   "KRO",  "HTOT", "KAG",  "KRA1", "KRA2",
27   "KRA3", "KRA4"
28 )
29
30 datalist <- vector(mode="list", length=length(filenames))
31 names(datalist) <- filenames
32
33 readin <- function(filename){
34   filepath <- paste0(path, "Data/EFM/dbFiles/", filename)
35   datalist[[filename]] <<- subset(read.dbf(filepath),
36   select=namescommon)
37   return()
38 }
39
```

```
cat("Read in...")
if ( is.null(datalist[[1]]) ) {
  # execute
  lapply(filenames, readin)
  #restructure
  dvfl ← do.call(rbind, datalist)
}

dvfl$BAGR ←
    # Def. tree species groups (German)
  with(dvfl,
    ifelse(BA == 21, "Fichte",
    ifelse(BA == 22, "Tanne",
    ifelse(BA == 23, "Kiefer",
    ifelse(BA == 24, "L rche",
    ifelse(BA == 26, "Douglasie",
    ifelse(BA %in% c(25, 27, 28, 29, 30, 36, 40, 60, 61), "sNB",
    ifelse(BA == 41, "Buche",
    ifelse(BA == 42, "Eiche",
    ifelse(BA == 44, "Ahorn",
    ifelse(BA %in% c(43, 48, 50, 51, 55), "aLH",
    ifelse(BA %in% c(45, 47, 49, 52, 53, 54, 56), "aLN",
    ifelse(BA == 46, "Kastanie",
    "sLB")))))))))))) #
)


dvfl$DF ←
    # siehe EK-Anleitung.pdf, thinning regimes:
  with(dvfl,
    ifelse(DFA == 0, NA,
    ifelse(DFA == 1, "keine_DF",
    ifelse(DFA == 2, "schwache_NDF",
    ifelse(DFA == 3, "mittelstarke_NDF",
    ifelse(DFA == 4, "starke_NDF",
    ifelse(DFA == 5, "HDF",
    ifelse(DFA == 6, "Plenter_DF",
    ifelse(DFA == 7, "VJ_Hieb",
    ifelse(DFA == 8, "Lichtwuchs",
    ifelse(DFA == 9, "Abtrieb", NA)
    )))))))))
  )

dvfl$Aushieb ←
    # use  EK-Anleitung.pdf to find more on th background:
  with(dvfl,
    ifelse(AHC == 1, "lebend",
    ifelse(AHC == 2, "geplant",
    ifelse(AHC == 3, "tot neu",
    ifelse(AHC == 4, "nicht gefunden",
    ifelse(AHC == 9, "tot alt",
    # oral Zingg further 5,7:
    ifelse(AHC == 5, "liegend",
    ifelse(AHC == 7, "stehend tot",
    NA)))))))
  )


dvfl$BHD ← (dvfl$D1 + dvfl$D2)/20 # mean of the two diameters in cm.
dvfl$H   ← dvfl$HTOT/10 #measureed tree height in m.

# perform some checks:
```

```
ns ← sapply(datalist, function(df) nrow(df))
names(ns) ← as.numeric(substr(names(ns),1,8))
tab ← table(dvfl$FNUM)
table( ns[names(tab)] == tab )
table( unique(dvfl$FNUM) %in% names(ns))

# check UNIQUENESS bnr %in% AJ %in% flche is unique
table( sapply( datalist, function(df) any(with(df, tapply( BNR, AJ,
    function(bnr) any(duplicated(bnr)))))))
# we find duplicates in 4 plots

# there are some non unique trees (number, year, plot)
rownames( dvfl[dvfl$FNUM == 1027000 & dvfl$BNR == 6285 & dvfl$AJ == 1996
    & dvfl$BHD == 20.45,] )
rownames( dvfl[dvfl$FNUM == 4003000 & dvfl$BNR == 395 & dvfl$AJ == 2002 &
     dvfl$BHD == 21.75,] )
rownames( dvfl[dvfl$FNUM == 42012000 & dvfl$BNR == 1257 & dvfl$AJ == 1996
     & dvfl$BHD == 9.7,])

# many inconsitencies (non uniqueness) in the following plot:
dvfl[dvfl$FNUM == 41015000,]

# filter out the nonunique trees:
dvfl ← subset(dvfl, FNUM != 41015000)
dvfl ← dvfl[!rownames(dvfl) %in%  c("01027000.F.21713", "04003000.F.4691"
    , "42012000.F.8131"), ]

# change some variables to factors
to.factor ← c("Aushieb", "DF", "FNUM")
repNumFac ← function(name){
     dvfl[,name] ↞ factor(dvfl[,name])
     return()
}
invisible(sapply(to.factor, repNumFac ))

# replace some zero values to NA
null.to.NA ← c("DH2", "V7", "KRO", "BHD", "H",
  "KAG", "KRA1", "KRA2", "KRA3", "KRA4")
repNullNA ← function(name){# replaces Null by NA in dvfl for given column
    -name
    vec ← dvfl[,name]
    dvfl[,name] ↞ ifelse(vec == 0, NA, vec)
    return()
}
invisible(sapply(null.to.NA, repNullNA))

# mittlerer Kronenradius im m
dvfl$KRm ← rowMeans( dvfl[,c("KRA1","KRA2","KRA3","KRA4")] )/10
dvfl ← subset(dvfl, select=
      names(dvfl) %nin% c("DFA", "AHC", "D1", "D2", "HTOT","KRO",
      "KRA1","KRA2","KRA3","KRA4")
  )


dvfl ← dvfl[order(dvfl$FNUM, dvfl$AJ, dvfl$BNR),]
rownames(dvfl) ← 1:nrow(dvfl)

# there seems to be an error in the definition of DF, overwrite by the
    most plausible value:
dvfl$DF[dvfl$FNUM== 1042000 ] ← "Plenter_DF"

# add some identifiers:
```

```
dvfl$FID ← as.numeric(factor(dvfl$FNUM))# fl chen ID
# running survey ID
dvfl$lAN ← as.numeric( unlist(tapply( dvfl$AJ, dvfl$FNUM,
  function(x) as.numeric(factor(x)) )))
# area ID and running survey ID
dvfl$FAID ← dvfl$FID*100 + dvfl$lAN

# sort the data frame
dvfl ← dvfl[ order(dvfl$FAID, dvfl$BNR),]
dvfl$FNUM ← factor(as.character(dvfl$FNUM))
dvfl$BAGR ← as.character(dvfl$BAGR)

saveRDS( file=paste0(path, "/dvfl.rds"), dvfl)
cat("dvfl written")
#eof
```

A.2 Diameter Growth models

A.2.1 Acer

```
Call:
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * rbal + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * bah + b8 * treat + b9 * lead.con + b10 * tphy.per +
    b11 * nphy.per + b12 * mphy.per + b13 * nphy.per * mphy.per +
    b14 * nphy.per^2 + b15 * mphy.per^2 + b16 * year.past1940,
    data = acer.sub, start = c(b0 = 0.8, b1 = 26, b2 = -0.012,
        b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0, b8 = 0, b9 = 0,
        b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0, b15 = 0,
        b16 = 0))

Residuals:
       Min         1Q     Median         3Q        Max
-16.074190  -1.100545   0.003985   1.052969  10.421703

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0   1.502e+00  2.071e+00   0.725 0.468512
b1   1.845e+01  5.221e+00   3.534 0.000417 ***
b2  -1.432e-02  5.611e-03  -2.551 0.010795 *
b3  -4.887e+00  2.572e-01 -19.000  < 2e-16 ***
b4  -7.196e-02  8.772e-03  -8.203 3.74e-16 ***
b5   3.011e-04  4.180e-05   7.202 7.85e-13 ***
b6   6.337e-02  1.521e-02   4.165 3.23e-05 ***
b7   6.153e-01  5.557e-01   1.107 0.268311
b8   1.462e+00  1.086e-01  13.460  < 2e-16 ***
b9   1.899e+00  1.594e-01  11.912  < 2e-16 ***
b10 -5.392e-01  9.750e-02  -5.530 3.54e-08 ***
b11  1.431e-02  3.099e-03   4.617 4.09e-06 ***
b12 -1.681e-02  1.210e-01  -0.139 0.889563
b13  4.184e-04  2.295e-04   1.823 0.068364 .
b14 -1.074e-05  3.005e-06  -3.575 0.000357 ***
b15 -1.044e-02  4.483e-03  -2.329 0.019955 *
b16  4.157e-02  6.149e-03   6.760 1.72e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Robust residual standard error: 1.578
Convergence in 14 IRWLS iterations

Robustness weights:
 1920 weights are ~= 1. The remaining 530 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1321  0.5895  0.7407  0.7232  0.8742  0.9961
```

A.2.2 Other long living broadleaves, olb

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * bal + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * exp.north + b8 * exp.south + b9 * bat + b10 * bat^2 +
    b11 * bah + b12 * treat + b13 * mixB + b14 * tphy.per + b15 *
    nphy.per + b16 * mphy.per + b17 * nphy.per * mphy.per + b18 *
    tphy.per * mphy.per + b19 * nphy.per^2 + b20 * year.past1940,
    data = olb.sub, start = c(b0 = 0.8, b1 = 26, b2 = -0.012,
        b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0, b8 = 0, b9 = 0,
        b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0, b15 = 0,
        b16 = 0, b17 = 0, b18 = 0, b19 = 0, b20 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-10.43292  -1.20867   0.03401   1.18858   7.30934

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0   1.296e+00  5.094e+00   0.254 0.799145
b1   1.396e+01  4.956e-01  28.172  < 2e-16 ***
b2  -5.855e-02  4.495e-03 -13.025  < 2e-16 ***
b3  -1.110e-01  9.425e-03 -11.779  < 2e-16 ***
b4  -8.969e-02  1.163e-02  -7.712 1.58e-14 ***
b5   3.462e-04  5.937e-05   5.832 5.95e-09 ***
b6  -1.125e-02  7.996e-03  -1.407 0.159647
b7  -1.198e+00  1.111e-01 -10.781  < 2e-16 ***
b8   5.514e-01  1.567e-01   3.520 0.000437 ***
b9   7.000e-03  2.472e-02   0.283 0.777104
b10  8.477e-04  3.330e-04   2.545 0.010954 *
b11  2.581e+00  5.866e-01   4.399 1.12e-05 ***
b12  2.103e-01  1.703e-01   1.235 0.216907
b13 -1.207e+00  1.752e-01  -6.886 6.69e-12 ***
b14  1.630e-01  4.167e-01   0.391 0.695641
b15  1.517e-03  3.575e-03   0.424 0.671438
b16  5.030e-01  2.251e-01   2.234 0.025510 *
b17 -2.320e-04  1.071e-04  -2.166 0.030387 *
b18 -4.869e-02  1.726e-02  -2.820 0.004822 **
b19  2.955e-06  1.972e-06   1.499 0.133991
b20  2.582e-02  5.100e-03   5.062 4.35e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 1.775
Convergence in 12 IRWLS iterations

Robustness weights:
 3013 weights are ~= 1. The remaining 782 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.2288  0.5964  0.7428  0.7263  0.8790  0.9978
```

A.2.3 Other short living broadleaves, osb

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * bal + b4 * bal^2 + b5 * bat + b6 * bat^2 +
    b7 * mixB + b8 * nphy.per + b9 * mphy.per + b10 * mphy.per^2 +
    b11 * year.past1940, data = osb.sub, start = c(b0 = 0.8,
    b1 = 26, b2 = -0.012, b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0,
    b8 = 0, b9 = 0, b10 = 0, b11 = 0))

Residuals:
     Min       1Q   Median       3Q      Max
-8.52061 -1.37154  0.08342  1.40659  7.11618

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0   6.8000138  1.6816029   4.044 5.97e-05 ***
b1   9.6749888  0.8581367  11.274  < 2e-16 ***
b2  -0.0800591  0.0176454  -4.537 6.93e-06 ***
b3  -0.2228335  0.0372744  -5.978 3.93e-09 ***
b4   0.0033263  0.0008317   4.000 7.16e-05 ***
b5  -0.1303425  0.0735892  -1.771  0.07705 .
b6   0.0003775  0.0012061   0.313  0.75439
b7  -2.2375173  0.3851757  -5.809 1.03e-08 ***
b8   0.0025324  0.0009476   2.673  0.00774 **
b9  -0.2823874  0.0955743  -2.955  0.00326 **
b10  0.0045202  0.0014703   3.074  0.00221 **
b11  0.0301422  0.0067216   4.484 8.81e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 2.083
Convergence in 11 IRWLS iterations

Robustness weights:
 468 weights are ~= 1. The remaining 128 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.3289  0.5999  0.7108  0.7109  0.8454  0.9969
```

A.2.4 Beech

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * rbal + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * ndep^2 + b8 * exp.north + b9 * bat + b10 * bah + b11 *
    treat + b12 * mixB + b13 * tphy.per + b14 * nphy.per + b15 *
    mphy.per + b16 * nphy.per * mphy.per + b17 * tphy.per * mphy.per +
    b18 * mphy.per^2 + b19 * year.past1940, data = bu.sub, start = c(b0 = 0.8,
    b1 = 26, b2 = -0.012, b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0,
    b8 = 0, b9 = 0, b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0,
    b15 = 0, b16 = 0, b17 = 0, b18 = 0, b19 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-15.19638  -0.95506   0.03597   0.95236  11.17032

Parameters:
```

```
      Estimate Std. Error  t value Pr(>|t|)
b0   5.569e+00  5.169e-01   10.772  < 2e-16 ***
b1   1.943e+01  9.290e-02  209.128  < 2e-16 ***
b2  -3.355e-02  2.756e-04 -121.748  < 2e-16 ***
b3  -2.379e+00  3.153e-02  -75.461  < 2e-16 ***
b4  -7.686e-02  9.314e-04  -82.521  < 2e-16 ***
b5   2.900e-04  3.661e-06   79.202  < 2e-16 ***
b6  -1.687e-01  4.891e-03  -34.497  < 2e-16 ***
b7   3.308e-03  9.435e-05   35.062  < 2e-16 ***
b8  -5.540e-01  1.199e-02  -46.225  < 2e-16 ***
b9  -7.709e-02  1.006e-03  -76.668  < 2e-16 ***
b10  1.010e+00  7.114e-02   14.201  < 2e-16 ***
b11  2.098e-01  1.215e-02   17.264  < 2e-16 ***
b12 -2.834e+00  2.567e-02 -110.390  < 2e-16 ***
b13  1.578e-01  4.331e-02    3.643 0.000269 ***
b14  1.344e-03  2.822e-04    4.762 1.92e-06 ***
b15  9.439e-03  2.647e-02    0.357 0.721381
b16 -5.396e-05  1.179e-05   -4.576 4.74e-06 ***
b17  9.058e-03  1.837e-03    4.930 8.24e-07 ***
b18  4.073e-04  3.884e-04    1.049 0.294302
b19  2.664e-02  6.542e-04   40.726  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 1.414
Convergence in 9 IRWLS iterations

Robustness weights:
 118803 weights are ~= 1. The remaining 30405 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1251  0.5706  0.7238  0.7072  0.8615  0.9990
```

A.2.5 Douglas fir

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * bal + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * ndep^2 + b8 * grad.p + b9 * bat + b10 * bat^2 + b11 *
    bah + b12 * treat + b13 * tphy.per + b14 * nphy.per.s + b15 *
    mphy.per + b16 * tphy.per * mphy.per + b17 * year.past1940,
    data = dou.sub, start = c(b0 = 0.8, b1 = 26, b2 = -0.012,
        b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0, b8 = 0, b9 = 0,
        b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0, b15 = 0,
        b16 = 0, b17 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-17.21769  -1.54829   0.05797   1.58574  12.21469

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0  16.3251384  1.9412504   8.410  < 2e-16 ***
b1  35.5490117  1.0669110  33.320  < 2e-16 ***
b2  -0.0230980  0.0009408 -24.551  < 2e-16 ***
b3  -0.0643600  0.0048477 -13.276  < 2e-16 ***
b4  -0.3002053  0.0129193 -23.237  < 2e-16 ***
b5   0.0012397  0.0001042  11.896  < 2e-16 ***
b6  -0.2458873  0.0324604  -7.575 3.92e-14 ***
b7   0.0027211  0.0004543   5.989 2.19e-09 ***
b8  -0.2872704  0.0157512 -18.238  < 2e-16 ***
```

```
b9   0.0138413  0.0318104   0.435  0.66349
b10 -0.0007478  0.0002879  -2.598  0.00940 **
b11 -6.4261485  0.6707446  -9.581  < 2e-16 ***
b12  1.9721542  0.2174087   9.071  < 2e-16 ***
b13 -0.8615735  0.2142322  -4.022 5.82e-05 ***
b14  0.1611238  0.0561397   2.870  0.00411 **
b15 -0.2507674  0.0628235  -3.992 6.61e-05 ***
b16  0.0431246  0.0073117   5.898 3.80e-09 ***
b17  0.1215496  0.0096916  12.542  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 2.322
Convergence in 9 IRWLS iterations

Robustness weights:
 7781 weights are ~= 1. The remaining 1978 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1814  0.5608  0.7266  0.6994  0.8652  0.9985
```

A.2.6 Oak

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * cba + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * ndep^2 + b8 * exp.south + b9 * exp.north + b10 * bat +
    b11 * nh + b12 * treat + b13 * mixB + b14 * tphy.per + b15 *
    nphy.per + b16 * mphy.per + b17 * nphy.per * mphy.per + b18 *
    tphy.per * mphy.per + b19 * tphy.per^2 + b20 * nphy.per^2 +
    b21 * mphy.per^2 + b22 * year.past1940, data = oak.sub, start = c(b0 = 0.8,
    b1 = 26, b2 = -0.012, b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0,
    b8 = 0, b9 = 0, b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0,
    b15 = 0, b16 = 0, b17 = 0, b18 = 0, b19 = 0, b20 = 0, b21 = 0,
    b22 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-13.59783  -0.98733   0.02989   0.97921  13.44332

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0  -1.162e+01  3.787e+00  -3.068  0.00216 **
b1   2.157e+01  2.322e-01  92.879  < 2e-16 ***
b2  -3.309e-02  4.563e-04 -72.515  < 2e-16 ***
b3   3.402e+00  1.009e-01  33.727  < 2e-16 ***
b4  -6.893e-02  1.921e-03 -35.877  < 2e-16 ***
b5   1.632e-04  6.799e-06  24.009  < 2e-16 ***
b6  -1.513e-01  1.080e-02 -14.010  < 2e-16 ***
b7   2.815e-03  1.898e-04  14.829  < 2e-16 ***
b8   3.457e-01  3.452e-02  10.014  < 2e-16 ***
b9  -9.789e-02  3.488e-02  -2.807  0.00501 **
b10 -8.897e-02  2.523e-03 -35.257  < 2e-16 ***
b11 -7.471e-01  8.192e-02  -9.119  < 2e-16 ***
b12 -6.119e-01  7.389e-02  -8.281  < 2e-16 ***
b13 -2.019e+00  7.071e-02 -28.554  < 2e-16 ***
b14  3.648e+00  7.517e-01   4.853 1.22e-06 ***
b15  2.901e-03  6.414e-04   4.523 6.10e-06 ***
b16 -2.160e-01  9.757e-02  -2.214  0.02682 *
b17  7.206e-04  5.389e-05  13.372  < 2e-16 ***
b18 -1.017e-02  8.878e-03  -1.146  0.25187
```

```
b19 -1.826e-01  3.819e-02  -4.781 1.75e-06 ***
b20 -9.105e-06  5.974e-07 -15.241  < 2e-16 ***
b21 -8.280e-03  1.409e-03  -5.878 4.19e-09 ***
b22  4.159e-02  1.449e-03  28.713  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 1.457
Convergence in 13 IRWLS iterations

Robustness weights:
 36461 weights are ~= 1. The remaining 8958 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1442  0.5949  0.7452  0.7235  0.8747  0.9989
```

A.2.7 Spruce

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * bal + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * ndep^2 + b8 * grad.p + b9 * exp.south + b10 * exp.north +
    b11 * bat + b12 * bat^2 + b13 * bah + b14 * treat + b15 *
    mixB + b16 * tphy.per + b17 * nphy.per + b18 * mphy.per +
    b19 * nphy.per * mphy.per + b20 * tphy.per^2 + b21 * nphy.per^2 +
    b22 * mphy.per^2 + b23 * year.past1940, data = fi.sub, start = c(b0 = 0.8,
    b1 = 26, b2 = -0.012, b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0,
    b8 = 0, b9 = 0, b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0,
    b15 = 0, b16 = 0, b17 = 0, b18 = 0, b19 = 0, b20 = 0, b21 = 0,
    b22 = 0, b23 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-14.82567  -1.21384   0.02703   1.21088  12.71579

Parameters:
      Estimate Std. Error  t value Pr(>|t|)
b0   4.559e+00  1.384e-01   32.939  < 2e-16 ***
b1   1.852e+01  1.014e-01  182.723  < 2e-16 ***
b2  -3.366e-02  3.486e-04  -96.575  < 2e-16 ***
b3  -6.760e-02  6.700e-04 -100.899  < 2e-16 ***
b4  -5.218e-02  1.048e-03  -49.802  < 2e-16 ***
b5   1.566e-04  4.438e-06   35.290  < 2e-16 ***
b6  -1.728e-01  3.954e-03  -43.701  < 2e-16 ***
b7   2.726e-03  7.185e-05   37.942  < 2e-16 ***
b8   4.167e-03  4.637e-04    8.985  < 2e-16 ***
b9   2.064e-01  1.878e-02   10.992  < 2e-16 ***
b10 -2.209e-01  1.440e-02  -15.338  < 2e-16 ***
b11 -6.705e-02  3.049e-03  -21.991  < 2e-16 ***
b12  3.902e-04  3.080e-05   12.672  < 2e-16 ***
b13  1.997e-01  8.465e-02    2.359 0.018301 *
b14  3.333e-01  1.683e-02   19.805  < 2e-16 ***
b15 -2.224e+00  4.443e-02  -50.068  < 2e-16 ***
b16  7.195e-02  1.841e-02    3.908 9.31e-05 ***
b17 -5.894e-04  2.406e-04   -2.450 0.014294 *
b18  9.753e-02  5.765e-03   16.918  < 2e-16 ***
b19 -7.508e-05  5.881e-06  -12.765  < 2e-16 ***
b20 -5.686e-03  1.679e-03   -3.387 0.000706 ***
b21  1.425e-06  1.618e-07    8.808  < 2e-16 ***
b22 -3.363e-04  8.779e-05   -3.831 0.000128 ***
b23  3.761e-02  6.065e-04   62.007  < 2e-16 ***
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 1.797
Convergence in 8 IRWLS iterations

Robustness weights:
 151415 weights are ~= 1. The remaining 38632 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1630  0.5828  0.7367  0.7160  0.8700  0.9990
```

A.2.8 Pine

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * cba + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * ndep^2 + b8 * wat.hold.cap.low + b9 * bat + b11 * tphy.per +
    b12 * nphy.per + b13 * mphy.per + b14 * nphy.per * mphy.per +
    b15 * tphy.per * mphy.per + b16 * tphy.per^2 + b17 * nphy.per^2 +
    b18 * mphy.per^2 + b19 * year.past1940, data = ki.sub, start = c(b0 = 0.8,
    b1 = 26, b2 = -0.012, b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0,
    b8 = 0, b9 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0, b15 = 0,
    b16 = 0, b17 = 0, b18 = 0, b19 = 0))

Residuals:
     Min       1Q   Median       3Q      Max
-13.5239  -1.2925   0.1221   1.2749   9.6468

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0  -5.790e+00  3.143e+00  -1.842 0.065503 .
b1   1.824e+01  7.530e-01  24.217  < 2e-16 ***
b2  -2.663e-02  1.939e-03 -13.733  < 2e-16 ***
b3   1.857e+00  2.293e-01   8.098 6.06e-16 ***
b4  -8.253e-02  5.321e-03 -15.508  < 2e-16 ***
b5   2.445e-04  2.647e-05   9.237  < 2e-16 ***
b6  -1.981e-01  2.818e-02  -7.032 2.13e-12 ***
b7   4.386e-03  6.425e-04   6.826 9.14e-12 ***
b8  -3.931e-01  8.130e-02  -4.836 1.34e-06 ***
b9  -5.396e-02  2.513e-03 -21.473  < 2e-16 ***
b11  2.535e+00  4.485e-01   5.652 1.62e-08 ***
b12  4.289e-04  1.397e-03   0.307 0.758828
b13  6.075e-01  1.631e-01   3.725 0.000196 ***
b14 -1.276e-03  1.188e-04 -10.741  < 2e-16 ***
b15 -4.044e-02  1.286e-02  -3.144 0.001668 **
b16 -1.403e-01  1.918e-02  -7.315 2.72e-13 ***
b17  1.348e-05  1.618e-06   8.332  < 2e-16 ***
b18  1.840e-02  2.001e-03   9.194  < 2e-16 ***
b19 -3.681e-02  4.789e-03  -7.686 1.62e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 1.9
Convergence in 9 IRWLS iterations

Robustness weights:
 10830 weights are ~= 1. The remaining 2604 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1889  0.5716  0.7382  0.7118  0.8709  0.9989
```

A.2.9 Larch

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * cba + b4 * a + b5 * a^2 + b6 * ndep +
    b7 * wat.perm.low + b8 * exp.south + b9 * exp.north + b10 *
    I(log10(nt)) + b11 * bah + b12 * lead.con + b13 * tphy.per +
    b14 * nphy.per + b15 * mphy.per + b16 * nphy.per * mphy.per +
    b17 * tphy.per * mphy.per + b18 * tphy.per^2 + b19 * nphy.per^2 +
    b20 * mphy.per^2 + b21 * year.past1940, data = la.sub, start = c(b0 = 0.8,
    b1 = 26, b2 = -0.012, b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0,
    b8 = 0, b9 = 0, b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0,
    b15 = 0, b16 = 0, b17 = 0, b18 = 0, b19 = 0, b20 = 0, b21 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-16.03677  -1.44086   0.07594   1.43089  11.26072

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0   8.415e+00  7.047e-01  11.941  < 2e-16 ***
b1   1.218e+01  3.652e-01  33.367  < 2e-16 ***
b2  -3.911e-02  1.742e-03 -22.446  < 2e-16 ***
b3   4.329e+00  2.113e-01  20.487  < 2e-16 ***
b4  -8.374e-02  2.064e-03 -40.571  < 2e-16 ***
b5   2.030e-04  6.338e-06  32.034  < 2e-16 ***
b6   3.325e-02  4.973e-03   6.687 2.33e-11 ***
b7   1.973e+00  5.453e-02  36.187  < 2e-16 ***
b8  -4.331e-01  5.074e-02  -8.535  < 2e-16 ***
b9   4.464e-01  6.143e-02   7.267 3.79e-13 ***
b10 -3.436e+00  1.041e-01 -33.012  < 2e-16 ***
b11  2.518e+00  2.698e-01   9.333  < 2e-16 ***
b12  1.963e+00  1.527e-01  12.859  < 2e-16 ***
b13  1.170e+00  9.970e-02  11.739  < 2e-16 ***
b14 -7.299e-03  6.888e-04 -10.597  < 2e-16 ***
b15  6.973e-02  2.805e-02   2.486   0.0129 *
b16 -1.234e-04  3.125e-05  -3.949 7.88e-05 ***
b17  1.005e-02  2.456e-03   4.093 4.27e-05 ***
b18 -1.209e-01  5.455e-03 -22.167  < 2e-16 ***
b19  5.181e-06  6.203e-07   8.353  < 2e-16 ***
b20  1.321e-03  6.250e-04   2.114   0.0345 *
b21  3.458e-02  1.620e-03  21.343  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 2.127
Convergence in 9 IRWLS iterations

Robustness weights:
 19634 weights are ~= 1. The remaining 5172 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1784  0.5655  0.7287  0.7072  0.8670  0.9988
```

A.2.10 Other conifers, oc

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * bal + b4 * a + b5 * a^2 + b6 * exp.south +
    b7 * grad.p + b8 * bat + b9 * bat^2 + b10 * nh + b11 * tphy.per +
    b12 * nphy.per + b13 * mphy.per + b14 * nphy.per * mphy.per +
    b15 * tphy.per * mphy.per + b16 * tphy.per^2 + b17 * nphy.per^2,
```

```
    data = oc.sub, start = c(b0 = 0.8, b1 = 26, b2 = -0.012,
        b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0, b8 = 0, b9 = 0,
        b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0, b15 = 0,
        b16 = 0, b17 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-16.67409  -1.21137   0.02116   1.21448  12.06716

Parameters:
      Estimate Std. Error t value Pr(>|t|)
b0   3.954e+00  3.563e-01  11.099  < 2e-16 ***
b1   2.986e+01  1.331e+00  22.432  < 2e-16 ***
b2  -1.191e-02  7.241e-04 -16.453  < 2e-16 ***
b3  -4.433e-02  1.880e-03 -23.583  < 2e-16 ***
b4  -4.413e-02  2.683e-03 -16.449  < 2e-16 ***
b5   1.045e-04  8.962e-06  11.660  < 2e-16 ***
b6   5.548e-01  6.113e-02   9.076  < 2e-16 ***
b7  -1.528e-03  1.158e-03  -1.319 0.187083
b8   3.580e-02  7.109e-03   5.036 4.78e-07 ***
b9  -8.297e-04  8.283e-05 -10.017  < 2e-16 ***
b10  4.632e-01  1.703e-01   2.720 0.006533 **
b11 -1.528e-02  6.709e-02  -0.228 0.819855
b12 -1.297e-03  3.589e-04  -3.614 0.000302 ***
b13 -6.764e-02  1.622e-02  -4.169 3.07e-05 ***
b14  7.565e-05  1.403e-05   5.392 7.02e-08 ***
b15  6.732e-03  1.096e-03   6.144 8.15e-10 ***
b16  8.296e-03  4.826e-03   1.719 0.085637 .
b17 -4.438e-07  2.958e-07  -1.500 0.133602
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 1.798
Convergence in 9 IRWLS iterations

Robustness weights:
 21287 weights are ~= 1. The remaining 5804 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1450  0.5679  0.7238  0.7050  0.8630  0.9990
```

A.2.11 Silver fir

```
nlrob(formula = I(sign(bai) * sqrt(abs(bai))) ~ b0 + b1 * (1 -
    exp(b2 * d)) + b3 * bal + b4 * a + b5 * a^2 + b6 * wat.hold.cap.low +
    b7 * grad.p + b8 * ndep + b9 * ndep^2 + b10 * I(log10(nt)) +
    b11 * treat + b12 * lead.con + b13 * tphy.per + b14 * nphy.per +
    b15 * mphy.per + b16 * nphy.per * mphy.per + b17 * tphy.per *
    mphy.per + b18 * tphy.per^2 + b19 * nphy.per^2 + b20 * mphy.per^2,
    data = ta.sub, start = c(b0 = 0.8, b1 = 26, b2 = -0.012,
        b3 = 0, b4 = 0, b5 = 0, b6 = 0, b7 = 0, b8 = 0, b9 = 0,
        b10 = 0, b11 = 0, b12 = 0, b13 = 0, b14 = 0, b15 = 0,
        b16 = 0, b17 = 0, b18 = 0, b19 = 0, b20 = 0))

Residuals:
      Min        1Q    Median        3Q       Max
-17.13549  -1.20884   0.04007   1.19665  19.21171

Parameters:
      Estimate Std. Error t value Pr(>|t|)
```

```
b0   2.062e+01  1.430e+00  14.427  < 2e-16 ***
b1   1.714e+01  1.828e-01  93.788  < 2e-16 ***
b2  -3.078e-02  5.505e-04 -55.920  < 2e-16 ***
b3  -1.031e-01  1.148e-03 -89.776  < 2e-16 ***
b4  -3.491e-02  1.447e-03 -24.134  < 2e-16 ***
b5   1.784e-04  5.506e-06  32.402  < 2e-16 ***
b6  -9.923e-01  3.159e-02 -31.410  < 2e-16 ***
b7  -1.067e-02  8.100e-04 -13.170  < 2e-16 ***
b8  -2.492e-01  7.436e-03 -33.514  < 2e-16 ***
b9   4.153e-03  1.363e-04  30.462  < 2e-16 ***
b10  1.081e-02  8.215e-02   0.132    0.895
b11  6.611e-01  3.149e-02  20.995  < 2e-16 ***
b12  5.431e-01  3.222e-02  16.857  < 2e-16 ***
b13 -2.151e+00  2.403e-01  -8.954  < 2e-16 ***
b14 -7.426e-03  4.842e-04 -15.337  < 2e-16 ***
b15 -4.134e-01  4.773e-02  -8.662  < 2e-16 ***
b16 -2.726e-05  1.785e-05  -1.527    0.127
b17  6.350e-02  4.023e-03  15.784  < 2e-16 ***
b18  6.260e-02  1.106e-02   5.658 1.54e-08 ***
b19  4.072e-06  2.899e-07  14.047  < 2e-16 ***
b20  8.477e-05  4.829e-04   0.176    0.861
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Robust residual standard error: 1.783
Convergence in 11 IRWLS iterations

Robustness weights:
 60460 weights are ~= 1. The remaining 16019 ones are summarized as
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.1248  0.5560  0.7175  0.6968  0.8583  0.9989
```

A.3 Height Growth models

A.3.1 Acer

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: ahorn.sub
       AIC      BIC    logLik
  464.2302 487.4129 -224.1151

Random effects:
 Formula: a ~ 1 | FNUM
                a
StdDev: 0.1481833

 Formula: a ~ 1 | BNR %in% FNUM
                 a Residual
StdDev: 0.05218124 1.068322

Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
     Phi
0.887504
Fixed effects: list(a ~ 1, b ~ d, c ~ 1)
                  Value Std.Error DF   t-value p-value
a              3.459296 0.0666080 72  51.93516       0
b.(Intercept) -4.915844 0.3242368 72 -15.16128       0
b.d            0.033371 0.0070588 72   4.72756       0
c              0.673918 0.1071161 72   6.29148       0

Standardized Within-Group Residuals:
         Min           Q1          Med           Q3          Max
-2.295180067 -0.452525925  0.007215036  0.475401209  2.458545898

Number of Observations: 134
Number of Groups:
         FNUM BNR %in% FNUM
           12            59
```

A.3.2 Other long living broadleaves, olb

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: olb.sub
       AIC      BIC    logLik
  1777.568 1810.824 -880.7842

Random effects:
 Formula: a ~ 1 | FNUM
                a
StdDev: 0.1211154

 Formula: a ~ 1 | BNR %in% FNUM
                  a Residual
StdDev: 3.110591e-05 1.854167

Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
```

```
 Parameter estimate(s):
      Phi
0.9627483
Fixed effects: list(a ~ 1, b ~ d, c ~ 1)
                  Value  Std.Error  DF   t-value p-value
a              3.612566 0.03981174 249  90.74123       0
b.(Intercept) -5.920181 0.22785558 249 -25.98216       0
b.d            0.038854 0.00482711 249   8.04910       0
c              0.487078 0.04601033 249  10.58627       0

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-3.04221419 -0.58865294  0.06918909  0.58381868  3.43566359

Number of Observations: 472
Number of Groups:
         FNUM BNR %in% FNUM
           32           220
```

A.3.3 Beech

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: buche.sub
       AIC      BIC    logLik
  45069.22 45181.72 -22519.61

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:     0.1450187

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept) Residual
StdDev:    0.03514854 1.621814

Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
      Phi
0.9620861
Fixed effects: list(a ~ d + I(d^2), b ~ d + ndep + I(ndep^2) + nh + bat, c ~   d)
                   Value  Std.Error   DF   t-value p-value
a.(Intercept)  1.6437190 0.02135977 8489  76.95397       0
a.d            0.1102336 0.00218452 8489  50.46114       0
a.I(d^2)      -0.0004721 0.00006336 8489  -7.45093       0
b.(Intercept) -1.4065310 0.07381995 8489 -19.05353       0
b.d           -0.2475628 0.00623136 8489 -39.72855       0
b.ndep         0.0189737 0.00294781 8489   6.43655       0
b.I(ndep^2)   -0.0002702 0.00004565 8489  -5.92026       0
b.nh          -0.0882673 0.01434962 8489  -6.15120       0
b.bat          0.0034602 0.00053654 8489   6.44905       0
c.(Intercept)  0.3694279 0.00942270 8489  39.20617       0
c.d           -0.0015997 0.00029020 8489  -5.51238       0

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-6.2737971 -0.4563746  0.0353387  0.5366222  4.0985229

Number of Observations: 13356
```

```
Number of Groups:
         FNUM BNR %in% FNUM
          141          4857
```

A.3.4 Douglas fir

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: douglas.sub
       AIC      BIC    logLik
  4481.105 4576.993 -2222.552

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:    0.08241124

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept) Residual
StdDev:     0.0328705 1.225499

Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
      Phi
0.9420335
Fixed effects: list(a ~ d + I(d^2),
                    b ~ d + I(d^2) + bal + ndep + I(ndep^2) +  nh +
                              tphy.per.s + I(tphy.per.s^2),
                    c ~ d)
                    Value Std.Error   DF   t-value p-value
a.(Intercept)      3.119084 0.0511491 1103  60.98023  0.0000
a.d                0.013511 0.0014623 1103   9.23948  0.0000
a.I(d^2)          -0.000051 0.0000126 1103  -4.03507  0.0001
b.(Intercept)     -4.540215 0.3775297 1103 -12.02611  0.0000
b.d                0.047970 0.0090951 1103   5.27427  0.0000
b.I(d^2)          -0.000515 0.0000827 1103  -6.22727  0.0000
b.bal              0.008386 0.0015827 1103   5.29834  0.0000
b.ndep            -0.026601 0.0075496 1103  -3.52343  0.0004
b.I(ndep^2)        0.000322 0.0000962 1103   3.34694  0.0008
b.nh               0.118980 0.0546772 1103   2.17604  0.0298
b.tphy.per.s       0.130261 0.0249372 1103   5.22359  0.0000
b.I(tphy.per.s^2) -0.050766 0.0107716 1103  -4.71294  0.0000
c.(Intercept)      0.643915 0.0964430 1103   6.67664  0.0000
c.d               -0.005092 0.0008872 1103  -5.73934  0.0000

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-4.00301827 -0.43523026  0.03660899  0.50427277  3.52872588

Number of Observations: 1521
Number of Groups:
         FNUM BNR %in% FNUM
           14           405
```

A.3.5 Oak

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: eiche.sub
       AIC      BIC    logLik
  22740.68 22836.09 -11356.34

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:     0.1414678

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept) Residual
StdDev:    0.04189941 1.271352

Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
      Phi
0.9269021
Fixed effects: list(a ~ d, b ~ d + bal + tphy.per.s + nphy.per.s + I(tphy.per.s^2),  c ~ d)
                       Value  Std.Error   DF   t-value p-value
a.(Intercept)      1.7049083 0.03091328 3886  55.15133  0.0000
a.d                0.0868750 0.00273505 3886  31.76360  0.0000
b.(Intercept)     -0.8347230 0.08613090 3886  -9.69133  0.0000
b.d               -0.2146287 0.00672616 3886 -31.90953  0.0000
b.bal             -0.0019292 0.00073037 3886  -2.64147  0.0083
b.tphy.per.s       0.0139354 0.03642782 3886   0.38255  0.7021
b.nphy.per.s       0.0334203 0.00553470 3886   6.03832  0.0000
b.I(tphy.per.s^2)  0.0336211 0.02049320 3886   1.64060  0.1010
c.(Intercept)      0.3612143 0.01390140 3886  25.98403  0.0000
c.d                0.0003216 0.00002448 3886  13.14119  0.0000


Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-8.14004967 -0.51726412  0.01796655  0.52914629  3.16699593

Number of Observations: 6735
Number of Groups:
         FNUM BNR %in% FNUM
           53          2840
```

A.3.6 Spruce

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: fichte.sub
       AIC     BIC    logLik
  45760.16 45944.1 -22856.08

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:     0.1583748

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept) Residual
StdDev:  1.241922e-05 1.525715
```

```
Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
      Phi
0.9771033
Fixed effects: list(a ~ d + I(d^2),
                    b ~ d + I(d^2) + bal + ndep + nh + nt +  tphy.per.s +
                        nphy.per.s + mphy.per.s + nphy.per.s:mphy.per.s +
                        tphy.per.s:mphy.per.s + I(tphy.per.s^2) + I(mphy.per.s^2),
                    c ~ d + I(d^2))
                          Value  Std.Error   DF   t-value p-value
a.(Intercept)          3.264572 0.04382699 9280  74.48769  0.0000
a.d                    0.009340 0.00142485 9280   6.55489  0.0000
a.I(d^2)              -0.000043 0.00001261 9280  -3.40663  0.0007
b.(Intercept)         -7.708572 0.26043302 9280 -29.59906  0.0000
b.d                    0.107994 0.00818494 9280  13.19425  0.0000
b.I(d^2)              -0.000700 0.00007235 9280  -9.67158  0.0000
b.bal                  0.010555 0.00077477 9280  13.62294  0.0000
b.ndep                -0.004950 0.00066095 9280  -7.48933  0.0000
b.nh                   0.147253 0.01859721 9280   7.91801  0.0000
b.nt                  -0.000071 0.00001085 9280  -6.54427  0.0000
b.tphy.per.s           0.028314 0.00667623 9280   4.24098  0.0000
b.nphy.per.s           0.000450 0.00289191 9280   0.15576  0.8762
b.mphy.per.s          -0.026522 0.00386476 9280  -6.86241  0.0000
b.I(tphy.per.s^2)     -0.050391 0.00591172 9280  -8.52394  0.0000
b.I(mphy.per.s^2)     -0.007435 0.00272117 9280  -2.73236  0.0063
b.nphy.per.s:mphy.per.s  0.003906 0.00179231 9280   2.17932  0.0293
b.tphy.per.s:mphy.per.s -0.014137 0.00610522 9280  -2.31560  0.0206
c.(Intercept)          0.447315 0.02344445 9280  19.07980  0.0000
c.d                   -0.016911 0.00111622 9280 -15.15032  0.0000
c.I(d^2)               0.000352 0.00002508 9280  14.05131  0.0000


Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-6.37119959 -0.55425996  0.02024992  0.56686576  6.32879991

Number of Observations: 15741
Number of Groups:
         FNUM BNR %in% FNUM
          204          6442
```

A.3.7 Pine

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: kiefer.sub
       AIC      BIC    logLik
  3317.187 3383.784 -1645.593

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:     0.2369875

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept)  Residual
StdDev:    0.03311856 0.8689127

Correlation Structure: Continuous AR(1)
```

```
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
     Phi
0.938551
Fixed effects: list(a ~ d, b ~ d + I(d^2) + bal + bat, c ~ d)
                  Value  Std.Error  DF   t-value p-value
a.(Intercept)  2.910413 0.05519648 637  52.72823  0.0000
a.d            0.011876 0.00095666 637  12.41400  0.0000
b.(Intercept) -4.641210 0.24919340 637 -18.62493  0.0000
b.d            0.056167 0.00886745 637   6.33409  0.0000
b.I(d^2)      -0.001078 0.00012136 637  -8.88381  0.0000
b.bal          0.004052 0.00158049 637   2.56348  0.0106
b.bat          0.003413 0.00126748 637   2.69306  0.0073
c.(Intercept)  1.205198 0.18196934 637   6.62308  0.0000
c.d           -0.013464 0.00224609 637  -5.99437  0.0000

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-2.88200981 -0.44341372 -0.02032317  0.44806192  5.41624942

Number of Observations: 1240
Number of Groups:
         FNUM BNR %in% FNUM
           35           595
```

A.3.8 Larch

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: la.sub
       AIC      BIC    logLik
  13954.75 14050.34 -6962.375

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:     0.1438515

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept) Residual
StdDev:    0.04895258 1.299983

Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
      Phi
0.9613508
Fixed effects: list(a ~ d + I(d^2),
                    b ~ d + I(d^2) + bal + tphy.per.s,
                    c ~ d +      I(d^2))
                   Value  Std.Error   DF   t-value p-value
a.(Intercept)  3.015898 0.04567049 2734  66.03602       0
a.d            0.013180 0.00113840 2734  11.57754       0
a.I(d^2)      -0.000070 0.00000867 2734  -8.09454       0
b.(Intercept) -6.002367 0.30492918 2734 -19.68446       0
b.d            0.057791 0.00835271 2734   6.91878       0
b.I(d^2)      -0.000347 0.00006726 2734  -5.15931       0
b.bal          0.008242 0.00171364 2734   4.80939       0
b.tphy.per.s   0.064213 0.01235746 2734   5.19629       0
c.(Intercept)  0.500081 0.04703697 2734  10.63165       0
```

```
c.d           -0.013647 0.00164398 2734  -8.30120       0
c.I(d^2)       0.000303 0.00004052 2734   7.46726       0

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-4.64175882 -0.44619406  0.02696543  0.50101140  3.87684694

Number of Observations: 4328
Number of Groups:
         FNUM BNR %in% FNUM
           34          1584
```

A.3.9 Other conifers

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: oc.sub
       AIC      BIC    logLik
  4586.643 4697.667 -2273.322

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:     0.2481675

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept) Residual
StdDev:    0.02304989 1.053832

Correlation Structure: Continuous AR(1)
 Formula: ~t_t0 | FNUM/BNR
 Parameter estimate(s):
      Phi
0.9649169
Fixed effects: list(
a ~ d + I(d^2),
b ~ d + I(d^2) + bal + bat + tphy.per.s +
nphy.per.s + mphy.per.s + I(tphy.per.s^2) + I(nphy.per.s^2)
+ I(mphy.per.s^2),
c ~ d)
                      Value Std.Error   DF    t-value p-value
a.(Intercept)      3.235495 0.1286639 1207  25.146872  0.0000
a.d               -0.002820 0.0055916 1207  -0.504401  0.6141
a.I(d^2)           0.000219 0.0000761 1207   2.881000  0.0040
b.(Intercept)     -5.748999 0.3730209 1207 -15.412004  0.0000
b.d                0.093548 0.0152111 1207   6.149974  0.0000
b.I(d^2)          -0.001512 0.0002083 1207  -7.258859  0.0000
b.bal              0.005163 0.0009486 1207   5.442740  0.0000
b.bat              0.001430 0.0005596 1207   2.555282  0.0107
b.tphy.per.s       0.058537 0.0076752 1207   7.626777  0.0000
b.nphy.per.s      -0.000203 0.0031248 1207  -0.065038  0.9482
b.mphy.per.s       0.020175 0.0033251 1207   6.067462  0.0000
b.I(tphy.per.s^2) -0.038721 0.0037018 1207 -10.459814  0.0000
b.I(nphy.per.s^2)  0.004901 0.0013178 1207   3.719082  0.0002
b.I(mphy.per.s^2) -0.005720 0.0016447 1207  -3.477906  0.0005
c.(Intercept)      0.693781 0.0584022 1207  11.879362  0.0000
c.d               -0.005223 0.0007707 1207  -6.776760  0.0000

Standardized Within-Group Residuals:
         Min           Q1          Med           Q3          Max
```

```
-3.201169413 -0.561101430 -0.006923388  0.507678269  3.406831772

Number of Observations: 1903
Number of Groups:
         FNUM BNR %in% FNUM
           29           681
```

A.3.10 Silver fir

```
Nonlinear mixed-effects model fit by maximum likelihood
  Model: h.obs ~ h.fun.3(age, a, b, c)
 Data: tanne.sub
      AIC      BIC    logLik
  20473.1 20566.36 -10222.55

Random effects:
 Formula: a ~ 1 | FNUM
        a.(Intercept)
StdDev:     0.1509562

 Formula: a ~ 1 | BNR %in% FNUM
        a.(Intercept)  Residual
StdDev:    0.08379959 0.8541556

Fixed effects: list(a ~ d, b ~ d + bal + bat + tphy.per.s +
nphy.per.s + I(tphy.per.s^2),      c ~ d)
                       Value  Std.Error   DF   t-value p-value
a.(Intercept)      1.4899127 0.02435357 3236  61.17841  0.0000
a.d                0.0941276 0.00155583 3236  60.49981  0.0000
b.(Intercept)     -0.6297232 0.08757844 3236  -7.19039  0.0000
b.d               -0.2519687 0.00619229 3236 -40.69069  0.0000
b.bal              0.0036338 0.00066862 3236   5.43482  0.0000
b.bat              0.0054947 0.00052110 3236  10.54431  0.0000
b.tphy.per.s      -0.0171535 0.01454687 3236  -1.17919  0.2384
b.nphy.per.s      -0.0170712 0.00440242 3236  -3.87769  0.0001
b.I(tphy.per.s^2) -0.0544949 0.01010422 3236  -5.39328  0.0000
c.(Intercept)      0.3116468 0.01011367 3236  30.81442  0.0000
c.d                0.0003992 0.00001653 3236  24.15238  0.0000

Standardized Within-Group Residuals:
         Min           Q1          Med           Q3          Max
-9.414749938 -0.410701474  0.002288786  0.371932714  4.683491207

Number of Observations: 5778
Number of Groups:
         FNUM BNR %in% FNUM
           77          2532
```

A.4 Mortality models

A.4.1 Acer

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula: tot ~ bai + d + I(d^2) + sdi + cba + I(cba^2) + nh + treat +
    lead.sp + tphy.per + nphy.per + mphy.per + I(tphy.per^2) +
    ndep + delta.t5 + I(delta.t5^2) + (1 | FNUM/BNR) + nphy.per:mphy.per +
    tphy.per:mphy.per
   Data: acer.sub

     AIC      BIC   logLik deviance df.resid
   544.5    696.4   -246.3    492.5     2518

Scaled residuals:
    Min      1Q  Median      3Q     Max
 -4.315  -0.093  -0.023  -0.003 310.592

Random effects:
 Groups   Name        Variance  Std.Dev.
 BNR:FNUM (Intercept) 1.038e-11 3.222e-06
 FNUM     (Intercept) 3.889e-01 6.236e-01
Number of obs: 2544, groups:  BNR:FNUM, 930; FNUM, 59

Fixed effects:
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)          2.615e+02  7.490e+01   3.491 0.000481 ***
bai                 -6.732e-02  1.638e-02  -4.110 3.96e-05 ***
d                   -2.707e-01  1.260e-01  -2.148 0.031696 *
I(d^2)               9.461e-03  2.280e-03   4.149 3.34e-05 ***
sdi                  1.117e-02  2.154e-03   5.189 2.12e-07 ***
cba                 -4.193e+01  9.766e+00  -4.294 1.76e-05 ***
I(cba^2)             4.779e+01  1.236e+01   3.868 0.000110 ***
nh                   6.236e+00  1.967e+00   3.171 0.001519 **
treatyes             6.246e-01  9.079e-01   0.688 0.491470
lead.spdouglas fir -3.056e+01  5.564e+00  -5.492 3.98e-08 ***
lead.spoak           1.671e+00  1.130e+00   1.479 0.139065
lead.spspruce       -1.430e+00  1.241e+00  -1.153 0.248897
lead.splarch        -1.150e+00  1.090e+00  -1.056 0.291163
lead.spoc           -9.657e+00  1.754e+03  -0.006 0.995608
lead.spsilver fir   -2.716e+00  1.983e+00  -1.369 0.170857
tphy.per            -4.564e+01  1.427e+01  -3.197 0.001386 **
nphy.per            -3.167e-02  1.280e-02  -2.473 0.013388 *
mphy.per            -6.597e+00  1.512e+00  -4.363 1.29e-05 ***
I(tphy.per^2)        1.828e+00  6.967e-01   2.624 0.008679 **
ndep                 8.481e-02  4.408e-02   1.924 0.054388 .
delta.t5             1.412e+00  4.427e-01   3.190 0.001422 **
I(delta.t5^2)       -1.599e-01  7.253e-02  -2.205 0.027483 *
nphy.per:mphy.per    1.166e-03  4.914e-04   2.373 0.017654 *
tphy.per:mphy.per    7.214e-01  1.558e-01   4.631 3.64e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.2 Other long living broadleaves, olb

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
```

```
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula: tot ~ bai + tphy.per.s + ndep + (1 | FNUM/BNR) + d
   Data: olb.sub

     AIC      BIC   logLik deviance df.resid
   950.3    994.2   -468.2    936.3     3926

Scaled residuals:
    Min      1Q  Median      3Q     Max
 -1.025  -0.194  -0.098  -0.038 278.396

Random effects:
 Groups   Name        Variance  Std.Dev.
 BNR:FNUM (Intercept) 3.873e-14 1.968e-07
 FNUM     (Intercept) 2.815e-01 5.306e-01
Number of obs: 3933, groups:  BNR:FNUM, 1461; FNUM, 63

Fixed effects:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.658104   0.465111 -10.015  < 2e-16 ***
bai         -0.068267   0.007021  -9.724  < 2e-16 ***
tphy.per.s  -1.184645   0.293646  -4.034 5.48e-05 ***
ndep         0.104478   0.014155   7.381 1.57e-13 ***
d            0.053606   0.017741   3.022  0.00251 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.3 Other short living broadleaves, osb

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula:
tot ~ rbai + cba + nh + I(nh^2) + lead.sp + nphy.per.s + mphy.per.s +
    I(mphy.per.s^2) + delta.t5 + I(delta.t5^2) + (1 | FNUM/BNR)
   Data: osb.sub

     AIC      BIC   logLik deviance df.resid
   272.6    357.5   -117.3    234.6      628

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.8461 -0.2507 -0.0913 -0.0118 10.7938

Random effects:
 Groups   Name        Variance Std.Dev.
 BNR:FNUM (Intercept) 0.00e+00 0.000e+00
 FNUM     (Intercept) 5.04e-15 7.099e-08
Number of obs: 647, groups:  BNR:FNUM, 249; FNUM, 62

Fixed effects:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)        -1.924e+00  4.359e-01  -4.414 1.01e-05 ***
rbai               -1.638e+01  3.000e+00  -5.459 4.80e-08 ***
cba                -3.813e+00  1.490e+00  -2.559 0.010509 *
nh                  2.118e+01  6.685e+00   3.168 0.001533 **
I(nh^2)            -7.842e+01  2.405e+01  -3.260 0.001112 **
lead.spdouglas fir -1.686e+01  6.022e+03  -0.003 0.997766
```

```
lead.spoak           1.087e+00  7.973e-01   1.363 0.172857
lead.spspruce        8.454e-01  4.703e-01   1.798 0.072256 .
lead.sppine         -2.076e+01  1.773e+04  -0.001 0.999066
lead.splarch         3.710e+00  1.003e+00   3.699 0.000216 ***
lead.spoc            2.449e-01  8.937e-01   0.274 0.784081
lead.spsilver fir   -1.879e+01  3.050e+03  -0.006 0.995085
nphy.per.s          -1.466e+00  4.423e-01  -3.314 0.000919 ***
mphy.per.s           2.271e+00  5.331e-01   4.259 2.05e-05 ***
I(mphy.per.s^2)     -5.700e-01  1.766e-01  -3.227 0.001251 **
delta.t5             9.629e-01  2.208e-01   4.361 1.29e-05 ***
I(delta.t5^2)       -8.601e-02  2.572e-02  -3.344 0.000825 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.4 Beech

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula: tot ~ rbai + d + I(d^2) + bat + cba + I(cba^2) + bah + mixB +
    tphy.per + nphy.per + mphy.per + I(nphy.per^2) + I(mphy.per^2) +
    ndep + delta.t5 + I(delta.t5^2) + (1 | FNUM/BNR) + nphy.per:mphy.per
   Data: bu.sub

     AIC      BIC   logLik deviance df.resid
 32823.9  33023.0 -16391.9  32783.9   155606

Scaled residuals:
   Min     1Q Median     3Q    Max
-10.65  -0.14  -0.05  -0.02 317.03

Random effects:
 Groups   Name        Variance Std.Dev.
 BNR:FNUM (Intercept) 0.2549   0.5048
 FNUM     (Intercept) 8.6738   2.9451
Number of obs: 155626, groups:  BNR:FNUM, 41154; FNUM, 194

Fixed effects:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)       -2.345e+00  1.332e+00   -1.76  0.07824 .
rbai              -9.999e+00  2.541e-01  -39.35  < 2e-16 ***
d                 -3.108e-01  1.537e-02  -20.23  < 2e-16 ***
I(d^2)             5.078e-03  2.018e-04   25.16  < 2e-16 ***
bat                1.134e-01  4.940e-03   22.96  < 2e-16 ***
cba               -1.026e+01  1.059e+00   -9.69  < 2e-16 ***
I(cba^2)           6.074e+00  9.108e-01    6.67 2.59e-11 ***
bah                4.287e+00  2.838e-01   15.10  < 2e-16 ***
mixB               4.529e+00  4.327e-01   10.47  < 2e-16 ***
tphy.per          -6.011e-01  6.748e-02   -8.91  < 2e-16 ***
nphy.per           2.261e-02  2.387e-03    9.47  < 2e-16 ***
mphy.per          -1.108e+00  5.041e-02  -21.99  < 2e-16 ***
I(nphy.per^2)     -2.126e-05  1.963e-06  -10.83  < 2e-16 ***
I(mphy.per^2)      5.877e-03  1.857e-03    3.16  0.00155 **
ndep               9.949e-02  5.655e-03   17.59  < 2e-16 ***
delta.t5           3.403e-01  2.410e-02   14.12  < 2e-16 ***
I(delta.t5^2)     -6.329e-03  2.395e-03   -2.64  0.00822 **
nphy.per:mphy.per  8.669e-04  1.102e-04    7.87 3.69e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.5 Douglas fir

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula:
tot ~ rbai + a + h + tphy.per + nphy.per + mphy.per + I(tphy.per^2) +
    I(nphy.per^2) + I(mphy.per^2) + soil.depth + delta.t5 + (1 |
    FNUM/BNR) + nphy.per:mphy.per
   Data: douglas.sub

     AIC      BIC   logLik deviance df.resid
  1656.8   1764.0   -813.4   1626.8     9372

Scaled residuals:
   Min     1Q Median     3Q    Max
-1.785 -0.139 -0.059 -0.018 45.178

Random effects:
 Groups   Name        Variance Std.Dev.
 BNR:FNUM (Intercept) 0.04577  0.2139
 FNUM     (Intercept) 0.09443  0.3073
Number of obs: 9387, groups:  BNR:FNUM, 1671; FNUM, 14

Fixed effects:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)       -2.375e+01  9.589e+00  -2.477  0.01326 *
rbai              -2.676e+01  2.084e+00 -12.840  < 2e-16 ***
a                  2.881e-02  1.032e-02   2.791  0.00526 **
h                 -1.211e-01  2.034e-02  -5.956 2.58e-09 ***
tphy.per           5.180e+00  2.352e+00   2.202  0.02765 *
nphy.per           1.096e-02  6.246e-03   1.755  0.07928 .
mphy.per          -4.385e-01  2.037e-01  -2.153  0.03136 *
I(tphy.per^2)     -2.986e-01  1.422e-01  -2.100  0.03575 *
I(nphy.per^2)     -2.321e-05  4.828e-06  -4.806 1.54e-06 ***
I(mphy.per^2)     -2.174e-02  4.865e-03  -4.467 7.91e-06 ***
soil.depthdeep     1.184e+00  2.857e-01   4.143 3.43e-05 ***
delta.t5           3.994e-01  7.847e-02   5.089 3.60e-07 ***
nphy.per:mphy.per  1.518e-03  2.903e-04   5.229 1.71e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.6 Oak

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula: tot ~ rbai + d + I(d^2) + bah + I(bah^2) + tphy.per + nphy.per +
    mphy.per + I(tphy.per^2) + I(nphy.per^2) + I(mphy.per^2) +
    ndep + delta.t5 + I(delta.t5^2) + (1 | FNUM/BNR) + tphy.per:mphy.per
   Data: ei.sub

     AIC      BIC   logLik deviance df.resid
  5847.2   6004.7  -2905.6   5811.2    46688

Scaled residuals:
    Min      1Q  Median      3Q     Max
  -3.22   -0.09   -0.03   -0.01 1038.98
```

```
Random effects:
 Groups   Name        Variance  Std.Dev.
 BNR:FNUM (Intercept) 4.000e-14 0.0000002
 FNUM     (Intercept) 1.812e+00 1.3459397
Number of obs: 46706, groups:  BNR:FNUM, 14553; FNUM, 121

Fixed effects:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)       -1.687e+02  2.476e+01  -6.813 9.53e-12 ***
rbai              -2.266e+01  9.066e-01 -24.991  < 2e-16 ***
d                 -2.022e-01  1.745e-02 -11.589  < 2e-16 ***
I(d^2)             1.808e-03  2.450e-04   7.379 1.60e-13 ***
bah               -8.265e-01  1.272e+00  -0.650 0.515813
I(bah^2)           1.017e+01  2.715e+00   3.746 0.000180 ***
tphy.per           2.117e+01  4.547e+00   4.656 3.22e-06 ***
nphy.per           4.856e-02  5.406e-03   8.982  < 2e-16 ***
mphy.per           4.891e+00  7.443e-01   6.572 4.97e-11 ***
I(tphy.per^2)     -7.285e-01  2.152e-01  -3.386 0.000709 ***
I(nphy.per^2)     -2.557e-05  2.932e-06  -8.720  < 2e-16 ***
I(mphy.per^2)     -3.431e-02  6.434e-03  -5.334 9.63e-08 ***
ndep               1.253e-01  1.186e-02  10.566  < 2e-16 ***
delta.t5           1.271e-01  4.821e-02   2.636 0.008389 **
I(delta.t5^2)      1.313e-02  3.044e-03   4.314 1.61e-05 ***
tphy.per:mphy.per -3.968e-01  6.428e-02  -6.173 6.69e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.7 Spruce

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula: tot ~ rbai + a + cba + I(cba^2) + bah + tphy.per + mphy.per +
    I(tphy.per^2) + relief + ndep + delta.t5 + I(delta.t5^2) +
    (1 | FNUM/BNR) + tphy.per:mphy.per
   Data: fi.sub

     AIC      BIC   logLik deviance df.resid
 43565.9  43759.7 -21764.0  43527.9   198579

Scaled residuals:
     Min       1Q   Median       3Q      Max
     -26        0        0        0 67108864

Random effects:
 Groups   Name        Variance  Std.Dev.
 BNR:FNUM (Intercept) 4.000e-14 0.0000002
 FNUM     (Intercept) 8.661e-01 0.9306580
Number of obs: 198598, groups:  BNR:FNUM, 68783; FNUM, 266

Fixed effects:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)         7.369831   0.754896    9.76  < 2e-16 ***
rbai              -36.563508   0.454920  -80.37  < 2e-16 ***
a                  -0.010105   0.001322   -7.64 2.13e-14 ***
cba                -3.038824   0.301237  -10.09  < 2e-16 ***
I(cba^2)            3.194567   0.361153    8.85  < 2e-16 ***
bah                 5.681523   0.255663   22.22  < 2e-16 ***
tphy.per           -1.833668   0.180124  -10.18  < 2e-16 ***
mphy.per           -0.164976   0.013909  -11.86  < 2e-16 ***
```

```
I(tphy.per^2)       0.076962   0.010742    7.16 7.82e-13 ***
reliefsummit        0.758233   0.655914    1.16 0.247684
reliefflat          0.089599   0.147430    0.61 0.543360
reliefslope toe    -1.262778   0.462170   -2.73 0.006290 **
reliefdepression   -0.128187   0.909356   -0.14 0.887898
ndep                0.074097   0.004565   16.23  < 2e-16 ***
delta.t5            0.283359   0.014984   18.91  < 2e-16 ***
I(delta.t5^2)      -0.005885   0.001709   -3.44 0.000575 ***
tphy.per:mphy.per   0.018040   0.002177    8.29  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.8 Pine

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula:
tot ~ rbai + d + nt + bah + nphy.per + mphy.per + I(nphy.per^2) +
    delta.t5 + I(delta.t5^2) + (1 | FNUM/BNR)
   Data: pine.sub

     AIC      BIC   logLik deviance df.resid
  2532.0   2620.8  -1254.0   2508.0    12072

Scaled residuals:
   Min     1Q Median     3Q    Max
-2.133 -0.140 -0.067 -0.025 59.863

Random effects:
 Groups   Name        Variance Std.Dev.
 BNR:FNUM (Intercept) 0.2204   0.4695
 FNUM     (Intercept) 3.4008   1.8441
Number of obs: 12084, groups:  BNR:FNUM, 3899; FNUM, 82

Fixed effects:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)   -1.983e+01  4.541e+00  -4.366 1.26e-05 ***
rbai          -2.728e+01  1.576e+00 -17.307  < 2e-16 ***
d             -1.222e-01  1.142e-02 -10.704  < 2e-16 ***
nt            -1.081e-03  3.600e-04  -3.003 0.002669 **
bah           -6.381e+00  1.705e+00  -3.742 0.000183 ***
nphy.per       4.972e-02  9.741e-03   5.105 3.31e-07 ***
mphy.per      -4.734e-01  5.134e-02  -9.221  < 2e-16 ***
I(nphy.per^2) -1.683e-05  4.993e-06  -3.371 0.000750 ***
delta.t5       5.124e-01  8.941e-02   5.730 1.00e-08 ***
I(delta.t5^2) -2.968e-02  7.388e-03  -4.017 5.90e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.9 Larch

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula: tot ~ bai + d + I(d^2) + bah + tphy.per + nphy.per + mphy.per +
    ndep + delta.t5 + I(delta.t5^2) + (1 | FNUM/BNR)
```

```
   Data: larch.sub

     AIC      BIC   logLik deviance df.resid
  2966.5   3071.4  -1470.2   2940.5    23601

Scaled residuals:
    Min      1Q  Median      3Q     Max
  -2.91   -0.10   -0.05   -0.02 1724.69

Random effects:
 Groups   Name        Variance Std.Dev.
 BNR:FNUM (Intercept) 0.0196   0.140
 FNUM     (Intercept) 1.8869   1.374
Number of obs: 23614, groups:  BNR:FNUM, 5511; FNUM, 65

Fixed effects:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)   -2.0578947  0.9278880  -2.218  0.02657 *
bai           -0.0409572  0.0021369 -19.166  < 2e-16 ***
d             -0.0811524  0.0184492  -4.399 1.09e-05 ***
I(d^2)         0.0009371  0.0002031   4.614 3.95e-06 ***
bah            4.4772356  0.8232299   5.439 5.37e-08 ***
tphy.per      -0.3997847  0.1015962  -3.935 8.32e-05 ***
nphy.per      -0.0026541  0.0008505  -3.121  0.00181 **
mphy.per       0.0677571  0.0264270   2.564  0.01035 *
ndep           0.1650991  0.0165450   9.979  < 2e-16 ***
delta.t5       0.3548670  0.0725100   4.894 9.88e-07 ***
I(delta.t5^2) -0.0126823  0.0079210  -1.601  0.10936
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.10 Other conifers

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula: tot ~ rbai + d + I(d^2) + sdi + rh + bah + tphy.per + nphy.per +
    mphy.per + I(tphy.per^2) + I(nphy.per^2) + wat.hold.cap +
    delta.t5 + I(delta.t5^2) + (1 | FNUM/BNR) + nphy.per:mphy.per +
    tphy.per:mphy.per
   Data: oc.sub

     AIC      BIC   logLik deviance df.resid
  9718.5   9881.5  -4839.3   9678.5    25567

Scaled residuals:
     Min       1Q   Median       3Q      Max
      -7        0        0        0 10217310

Random effects:
 Groups   Name        Variance Std.Dev.
 BNR:FNUM (Intercept) 0.000    0.00
 FNUM     (Intercept) 1.989    1.41
Number of obs: 25587, groups:  BNR:FNUM, 7997; FNUM, 51

Fixed effects:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)       9.382e+00  1.713e+00    5.48 4.30e-08 ***
rbai             -2.364e+01  6.695e-01  -35.31  < 2e-16 ***
d                 4.268e-02  1.744e-02    2.45 0.014414 *
```

```
I(d^2)            -4.820e-04  2.368e-04   -2.04 0.041833 *
sdi               -1.268e-03  3.103e-04   -4.09 4.38e-05 ***
rh                -2.395e+00  1.934e-01  -12.38  < 2e-16 ***
bah                3.864e+00  5.367e-01    7.20 6.02e-13 ***
tphy.per          -2.003e+00  3.196e-01   -6.27 3.62e-10 ***
nphy.per           9.601e-03  2.555e-03    3.76 0.000171 ***
mphy.per          -5.010e-01  5.154e-02   -9.72  < 2e-16 ***
I(tphy.per^2)      7.674e-02  2.336e-02    3.28 0.001020 **
I(nphy.per^2)     -9.784e-06  1.641e-06   -5.96 2.50e-09 ***
wat.hold.capgood   1.081e+00  5.852e-01    1.85 0.064628 .
wat.hold.caplow   -2.546e+00  7.543e-01   -3.38 0.000737 ***
delta.t5           3.198e-01  5.554e-02    5.76 8.58e-09 ***
I(delta.t5^2)     -2.321e-02  6.080e-03   -3.82 0.000135 ***
nphy.per:mphy.per  3.348e-04  5.088e-05    6.58 4.69e-11 ***
tphy.per:mphy.per  3.436e-02  3.754e-03    9.15  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.4.11 Silver fir

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula:
tot ~ rbai + a + sdi + bal + tphy.per.s + mphy.per.s + I(tphy.per.s^2) +
    ndep + delta.t5 + (1 | FNUM/BNR) + tphy.per.s:mphy.per.s
   Data: ta.sub

     AIC      BIC   logLik deviance df.resid
 24179.5  24300.6 -12076.8  24153.5    81846

Scaled residuals:
   Min     1Q Median     3Q    Max
    -4      0      0      0 232906

Random effects:
 Groups   Name        Variance  Std.Dev.
 BNR:FNUM (Intercept) 2.747e-07 0.0005241
 FNUM     (Intercept) 8.383e-01 0.9156076
Number of obs: 81859, groups:  BNR:FNUM, 21712; FNUM, 122

Fixed effects:
                       Estimate Std. Error z value Pr(>|z|)
(Intercept)          -2.860e+00  3.200e-01   -8.94  < 2e-16 ***
rbai                 -2.998e+01  5.246e-01  -57.15  < 2e-16 ***
a                     8.547e-03  2.103e-03    4.06 4.81e-05 ***
sdi                  -1.586e-03  2.846e-04   -5.57 2.50e-08 ***
bal                   3.267e-02  2.402e-03   13.60  < 2e-16 ***
tphy.per.s           -6.647e-01  1.459e-01   -4.56 5.22e-06 ***
mphy.per.s           -2.413e-01  5.878e-02   -4.11 4.03e-05 ***
I(tphy.per.s^2)      -4.035e-01  1.186e-01   -3.40 0.000666 ***
ndep                  5.166e-02  5.608e-03    9.21  < 2e-16 ***
delta.t5              1.377e-01  6.873e-03   20.04  < 2e-16 ***
tphy.per.s:mphy.per.s -5.227e-01  9.524e-02   -5.49 4.06e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.5 Probability of in-growth

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula: I ~ Regime + nt + bat + dt + I(dt^2) + (1 | FNUM) +
    nt:bat
   Data: ingrowth.prob

     AIC      BIC   logLik deviance df.resid
   729.7    778.1   -355.8    711.7     1598

Scaled residuals:
   Min     1Q Median     3Q    Max
-5.848 -0.158 -0.048 -0.008 34.340

Random effects:
 Groups Name        Variance Std.Dev.
 FNUM   (Intercept) 5.948    2.439
Number of obs: 1607, groups:  FNUM, 207

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -4.210e+00  8.062e-01  -5.222 1.77e-07 ***
Regimenone   -5.010e-01  1.981e+00  -0.253   0.8003
RegimeTfb    -2.790e+00  6.646e-01  -4.197 2.70e-05 ***
nt            1.608e-03  2.942e-04   5.467 4.58e-08 ***
bat           4.961e-02  2.000e-02   2.481   0.0131 *
dt            5.869e-01  7.160e-02   8.197 2.47e-16 ***
I(dt^2)      -1.187e-02  2.569e-03  -4.621 3.81e-06 ***
nt:bat       -9.861e-05  1.538e-05  -6.411 1.44e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.6 Number of in-growing trees

```
Linear mixed model fit by REML ['lmerMod']
Formula:
I(log(nI)) ~ dq + ddom + nh + dt + (1 | FNUM) + I(log(nt)) +
    I(log(nt_t1)) + dq:ddom
   Data: nIt

REML criterion at convergence: 1210.4

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.1664 -0.4564  0.1425  0.4843  2.8417

Random effects:
 Groups   Name        Variance Std.Dev.
 FNUM     (Intercept) 0.2452   0.4951
 Residual             0.4710   0.6863
Number of obs: 506, groups:  FNUM, 112

Fixed effects:
               Estimate Std. Error t value
(Intercept)  18.2078342  1.9297014   9.436
dq           -0.3022663  0.0331766  -9.111
ddom         -0.0125936  0.0113753  -1.107
nh            4.2769874  0.3944987  10.842
dt            0.0788401  0.0127913   6.164
I(log(nt))    1.4340289  0.2404781   5.963
I(log(nt_t1))-2.9368487  0.1419841 -20.684
dq:ddom       0.0024233  0.0004257   5.692
```

A.7 Harvesting models

A.7.1 Tfa

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
Formula:
harv ~ rd + I(rd^2) + I(log10(nt)) + I(log10(nt)^2) + I(log10(nt) *
    rd) + I(asin(sqrt(bah))) + lead.sp + t.sp.g + (1 | FNUM)
   Data: subset(dvfl.engl, DF == "HDF")

     AIC      BIC   logLik deviance df.resid
  245374   245647  -122662   245324   408211

Scaled residuals:
    Min      1Q  Median      3Q     Max
-12.759  -0.382  -0.246  -0.111  37.119

Random effects:
 Groups Name        Variance Std.Dev.
 FNUM   (Intercept) 0.09767  0.3125
Number of obs: 408236, groups:  FNUM, 129

Fixed effects:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)        -20.10033    0.52871  -38.02  < 2e-16 ***
rd                  16.90044    0.37464   45.11  < 2e-16 ***
I(rd^2)             -2.12302    0.13939  -15.23  < 2e-16 ***
I(log10(nt))         9.18125    0.31864   28.81  < 2e-16 ***
I(log10(nt)^2)      -1.19836    0.04851  -24.70  < 2e-16 ***
I(log10(nt) * rd)   -6.05590    0.10422  -58.11  < 2e-16 ***
I(asin(sqrt(bah)))   7.46344    0.05171  144.33  < 2e-16 ***
lead.spbeech         0.13485    0.05146    2.62  0.00878 **
lead.spdouglas fir  -0.21457    0.16747   -1.28  0.20011
lead.spoak          -0.94421    0.07564  -12.48  < 2e-16 ***
lead.sppine         -1.08057    0.33763   -3.20  0.00137 **
lead.splarch        -0.84416    0.09376   -9.00  < 2e-16 ***
lead.spoc           -9.02449   35.92660   -0.25  0.80167
lead.spsilver fir    0.15155    0.05636    2.69  0.00716 **
t.sp.gacer          -0.51993    0.09736   -5.34 9.28e-08 ***
t.sp.golb           -0.56379    0.06625   -8.51  < 2e-16 ***
t.sp.gosb           -0.12507    0.14793   -0.85  0.39784
t.sp.gbeech         -0.90767    0.02488  -36.48  < 2e-16 ***
t.sp.gdouglas fir    0.21811    0.12534    1.74  0.08182 .
t.sp.goak            0.73424    0.03118   23.55  < 2e-16 ***
t.sp.gpine           0.93935    0.07849   11.97  < 2e-16 ***
t.sp.glarch          0.60580    0.04512   13.43  < 2e-16 ***
t.sp.goc             0.07766    0.05067    1.53  0.12534
t.sp.gsilver fir    -0.64810    0.02721  -23.82  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

A.7.2 Tfb

```
Generalized linear mixed model fit by maximum likelihood (Adaptive
  Gauss-Hermite Quadrature, nAGQ = 0) [glmerMod]
 Family: binomial  ( logit )
```

```
Formula:
harv ~ rd + I(rd^2) + I(log10(nt)) + I(log10(nt)^2) + I(log10(nt) *
    rd) + I(asin(sqrt(bah))) + t.sp.g + (1 | FNUM)
   Data: subset(dvfl.engl, DF == "NDF")

     AIC      BIC   logLik deviance df.resid
113983.3 114171.4 -56973.7 113947.3   254931

Scaled residuals:
   Min     1Q Median     3Q    Max
-26.16  -0.25  -0.09  -0.02 340.30

Random effects:
 Groups Name        Variance Std.Dev.
 FNUM   (Intercept) 0.2567   0.5067
Number of obs: 254949, groups:  FNUM, 81

Fixed effects:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)        -14.35575    0.80178  -17.90  < 2e-16 ***
rd                   6.79797    0.73550    9.24  < 2e-16 ***
I(rd^2)              5.12169    0.34510   14.84  < 2e-16 ***
I(log10(nt))         7.61702    0.47923   15.89  < 2e-16 ***
I(log10(nt)^2)      -1.08553    0.07204  -15.07  < 2e-16 ***
I(log10(nt) * rd)   -6.81381    0.20108  -33.89  < 2e-16 ***
I(asin(sqrt(bah)))  11.48684    0.08821  130.21  < 2e-16 ***
t.sp.gacer          -1.02928    0.12611   -8.16 3.30e-16 ***
t.sp.golb           -1.60404    0.18499   -8.67  < 2e-16 ***
t.sp.gosb           -0.78931    0.29341   -2.69 0.007142 **
t.sp.gbeech         -1.38606    0.05324  -26.03  < 2e-16 ***
t.sp.gdouglas fir    0.18945    0.44260    0.43 0.668628
t.sp.goak           -0.56689    0.07354   -7.71 1.27e-14 ***
t.sp.gpine           0.76602    0.21925    3.49 0.000476 ***
t.sp.glarch         -1.21080    0.82255   -1.47 0.141015
t.sp.goc             2.72691    0.82500    3.31 0.000949 ***
t.sp.gsilver fir    -0.23749    0.06646   -3.57 0.000352 ***
```