

# Impact of drought on the growth of European beech (*Fagus sylvatica* L.): A case study in the canton of Basel-Landschaft, Switzerland



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**Master's Thesis**

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Cover picture: Trees affected by early leaf shedding and discolouration in the study site of Grosszinggibrunn, Basel-Landschaft, Switzerland. October 2019. Personal photograph.

# Summary

The recent very dry and hot summers have induced widespread dieback of European beech (*Fagus sylvatica* L.) in the region around Basel. Although drought frequency, intensity and duration are expected to increase in the near future, the effects of drought events on growth of beech trees are still not completely understood. It is unclear why some beech trees died or have experienced severe vitality decline while other trees have survived the last droughts and remained vital. Here, we took advantage of the unprecedented beech mortality event that is occurring around Basel to investigate the growth response of vital and dying (unvital) beech trees to past and recent extreme droughts.

To do this, different analyses were conducted. First, response and correlation functions were calculated between growth series of individual vital and unvital trees and climate variables such as temperature, precipitation and drought index. Second, a superposed epoch analysis was used to assess the impact of past extreme drought years on growth. Resilience components (resistance, recovery and resilience) were also calculated separately for vital and unvital trees and the differences between the two groups were statistically tested. Finally, linear mixed models were used to assess the influence of tree size, drought and competition on tree growth. We built three models with three time windows in order to assess the impact of the variables previously mentioned over three different time periods of the trees' lifespan. The time windows were 1900-2019, 1970-2019, 2015-2019.

The results showed a divergence in the growth of vital and unvital trees starting from the 1970s, with a strong decrease of the basal area increment for unvital trees in the last five decades. The growth of both vital and unvital trees responded negatively to summer drought. This result was also reflected in the superposed epoch analysis, which showed a strong decrease in growth in the past extreme drought years. Both vital and unvital trees were generally more resistant and had a stronger recovery during past extreme drought years. Tree resilience showed a declining trend, in particular for unvital trees. Finally, the models showed that tree vitality, drought and competition have all had a strong and significant effect on tree growth. The results highlighted a high sensitivity of beech trees to drought and climatic water stress that may impact future growth rate.



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# Chapter 1

## Introduction

The summers of 2018 and 2019 were two of the driest and hottest in Switzerland since the beginning of the instrumental measurements in 1864 (MeteoSvizzera, 2019a; MeteoSvizzera, 2019b). The mean summer temperature of 2019 was 15.5°C, 2°C warmer than the norm 1981-2010. In some regions of Switzerland, the recorded precipitation of 2018 was the most scarce since 1864. Similar climatic conditions were observed during the summer of 2019. Under these circumstances, many forests in Switzerland suffered from heat and drought stress (Bundesamt für Umwelt, 2019a). As a result, many tree species were subject to premature leaf shedding and discolouration. These phenomena were already observed in July and the number of affected trees increased significantly from early to late summer (Rigling et al., 2019). The most affected areas were the regions of Basel, Schaffhausen and Zurich (Bundesamt für Umwelt, 2019b; Wohlgemuth et al., 2018). In the region of Basel, the drought-related damage impacted more than 20% of the forest area (Kanton Basel-Landschaft, 2019). The most affected tree species were European beech (*Fagus sylvatica* L.), silver fir (*Abies alba* Mill.) and oak trees (*Quercus* spp.). Among these species, European beech is one of the most abundant and economically important tree species in Switzerland (Abegg et al., 2014). Although European beech occurs over a wide ecological gradient and dominates the mesic sites at low altitudes (Figure 1.1b) (Leuschner and Ellenberg, 2017; Rudow, 2014), it is rather sensitive to drought (Cavin and Jump, 2017; Kunz et al., 2018).

Considering that dry and hot summers might be more frequent in the future (CH2018, 2018), it remains of central importance for researchers and forest managers to understand the consequences of drought on European beech forests to identify the best strategies to adapt forest ecosystems to a warmer and drier climate (Bosela et al., 2016; DeSoto et al., 2020; Geßler et al., 2007).

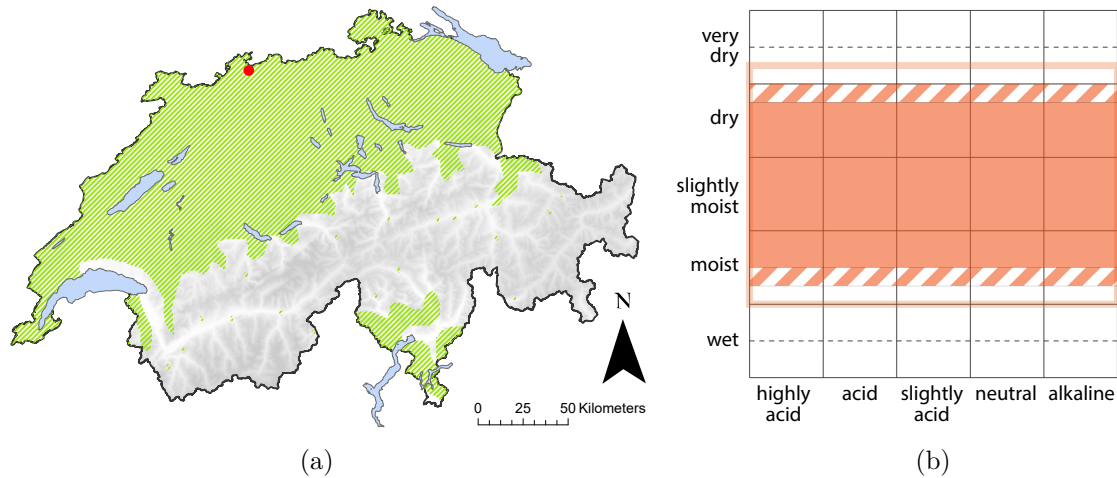


Figure 1.1: Current distribution (green) of European beech (*Fagus sylvatica* L.) in Switzerland (a) and its ecological niche according to a soil moisture and acidity ecogram (b). The study site is marked with the red dot. Map and data adapted from EUFORGEN (2009) and swisstopo. Ecogram adapted from Rudow (2014).

Many studies were conducted on the sensitivity of European beech to drought and assessed the impact of more frequent drought events on tree growth, forest composition and forest management (Cavin and Jump, 2017; Dulamsuren et al., 2017; Geßler et al., 2007; Kunz et al., 2018; Metz et al., 2016; Michelot et al., 2012; Tegel et al., 2014; Weber et al., 2013; Zang et al., 2014). Some of these studies highlighted the negative impact of summer drought and the positive effect of spring and summer precipitation on European beech growth across different regions in Europe (Cavin and Jump, 2017; Dulamsuren et al., 2017; Geßler et al., 2007; Kunz et al., 2018; Michelot et al., 2012; Tegel et al., 2014; Weber et al., 2013). Other studies reported a recent decline in European beech growth patterns due to the increased drought stress (Aertsens et al., 2014; Bontemps et al., 2010; Braun et al., 2017; Gillner et al., 2013; Schwarz and Bauhus, 2019; Zimmermann et al., 2015). Nonetheless, it remains unclear how beech forests in Central Europe and Switzerland will develop under changing climatic conditions. This can be partly attributed to a lack of experience in the management of beech forests (Rigling et al., 2019).

In this framework, our work embraces the opportunity to expand the knowledge on how local forests were impacted by past and recent drought events. We took advantage of the widespread beech dieback that affected the region of Basel in the last years to investigate and compare the growth trends and trajectories of dying (unvital) and vital beech trees. Here, tree-ring data offered the opportunity to assess climate sensitivity over a very long temporal scale at an annual resolution (Fritts, 1976) and to reconstruct the growth resistance, recovery and resilience of beech trees to extreme drought years (Lloret et al., 2011; Vitasse et al., 2019). Thus, a combination of different dendrochronological analyses based



on tree-ring-, stand- and climate data was used in this master's thesis with the aim to assess the following research questions:

- 1) What were the growth trajectories and trends of vital and unvital beech trees over the last hundred years?
- 2) What was the climate sensitivity of vital and unvital beech trees in the region around Basel?
- 3) How did tree growth and growth resistance, recovery, and resilience to past extreme droughts differ between vital and unvital beech trees?
- 4) How did tree size, competition and drought influence the growth of vital and unvital beech trees?

## Chapter 2

# Material and Methods

### 2.1 Study site

Widespread dying beech trees were observed in the canton of Basel-Landschaft (BL) (Kanton Basel-Landschaft, 2019). The surrounding forests of MuttENZ (BL), Pratteln (BL) and Frenkendorf (BL) were thus assessed for the suitability of a fieldwork for this master's thesis. In this thesis, suitable sites are considered beech forests with trees that show clear signs of drought-induced early leaf shedding or discolouration. From this first assessment, three sites were selected as suitable: Grosszinggibrunn, Vogtacher and Dürrenrain (see Appendix A). From each site, possible target trees were selected based on their vitality. Living crown percentage was used as a proxy for tree vitality (Dobbertin, 2005). A vitality filter was applied to the selection of trees so that very unvital ( $\leq 20\%$  of living crown) and very vital ( $\geq 80\%$  of living crown) trees were considered. This was done in order to have two distinct groups (i.e. vital and unvital) for the analysis. All the target trees were marked and assigned a unique number within the stand.

Although initially 139 trees among the three sites were selected, we discarded the site of Dürrenrain because the stand was mixed with different species. Even though vital and unvital trees at both sites Grosszinggibrunn and Vogtacher were initially sampled, one more site had to be discarded because of time constraints. As Grosszinggibrunn had the most homogeneous condition and numerous target trees to be analysed, we decided to keep this site and discard Vogtacher. All the increment cores and tree data of the Vogtacher site are still available for future preparation and analysis.

The site of Grosszinggibrunn (47° 30' 32" N, 7° 40' 11" E, Figure 1.1a) lies in the municipality of MuttENZ, Basel-Landschaft, south-west from the village of MuttENZ. The site is located in the biogeographical region of the High Rhine Valley (German: Hochrheingebiet) of the Swiss Plateau (Gonseth et al., 2001), although sometimes this region has also been reported to belong to the northern end of the eastern Jura Mountain Range (Begert et al.,

2007; Seiz and Foppa, 2007). This region is characterised by Central European humid-continental climate (Beck et al., 2018), with cold temperatures and little precipitation in winter and mid-warm summers with more precipitation. Between 1900 and 2019 the mean annual precipitation sum was 801 mm and the mean annual temperature 9.9°C (Weather station Basel/Binningen, MeteoSwiss) (Figure 2.1).

The site is enclosed in the main distribution range of European beech and presents the typical vegetation of beech communities: an *Aro-Fagetum* forest (Ellenberg-Klötzli 11) and a typical beech forest with *Galium odoratum* (L.) Scop. (Ellenberg-Klötzli 7f and 7j, *Galio odorati-Fagetum*) (Häner and Eichenberger, 2013; Kanton Basel-Landschaft, 2017). The study site encloses approximately six hectares of forest area. The sample stand is not very dense (mean basal area =  $11.4 \pm 3.7$  m<sup>2</sup>/ha) and the last thinning was done in 2015 (M. Eichenberger, personal communication, 28 January 2020). Beech regeneration and ground vegetation composed mainly of *Rubus spp.* are present under the shelter of the remaining mature trees. Tree species include European beech (*Fagus sylvatica* L.), European ash (*Fraxinus excelsior* L.), sycamore maple (*Acer pseudoplatanus* L.), European hornbeam (*Carpinus betulus* L.), common oak (*Quercus robur* L.), sessile oak (*Quercus petraea* (Matt.) Liebl.) and common lime (*Tilia platyphyllos* Scop.).

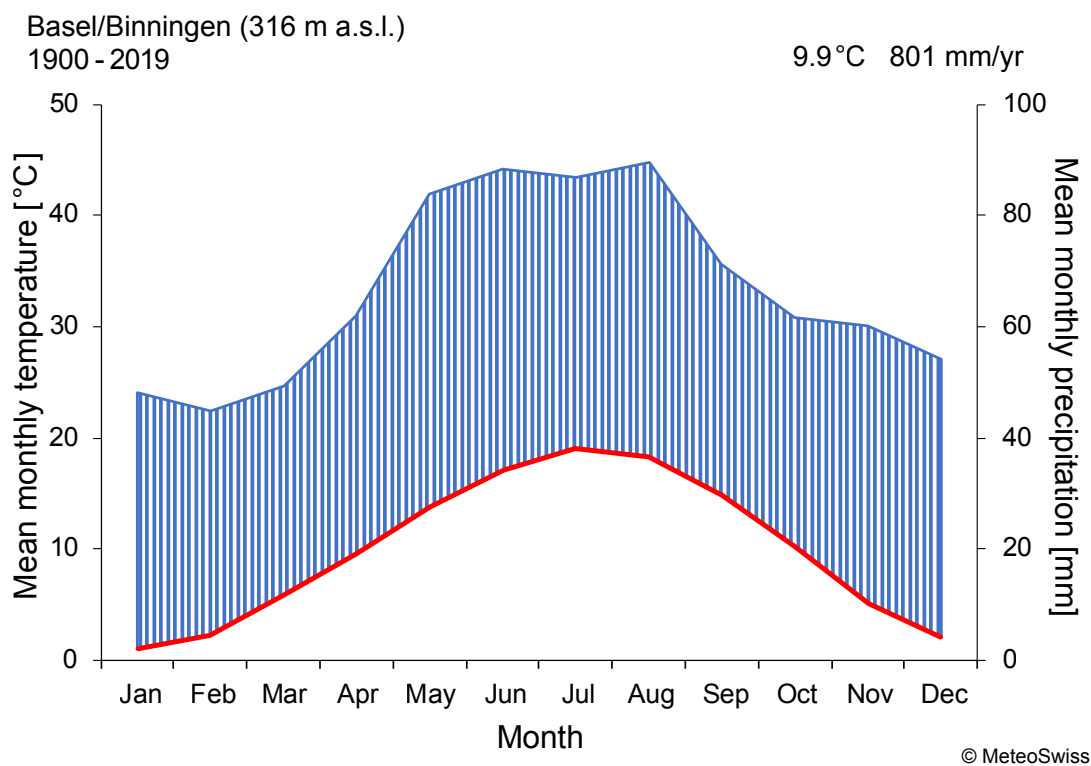


Figure 2.1: Climate diagram of the weather station Basel/Binningen showing monthly mean precipitation and temperature from 1900 to 2019. Diagram produced with Microsoft Excel (Version 16.0, Microsoft Corp., 2019). Source of the data: MeteoSwiss.

## 2.2 Data collection

Tree selection, marking and assessment of the percentage of the living crown were done on the 25<sup>th</sup> and 29<sup>th</sup> October 2019 before the seasonal leaf shedding. Tree coring was carried out between the 12<sup>th</sup> November 2019 and the 6<sup>th</sup> December 2019. For each target tree, two increment cores were taken at DBH (Diameter at Breast Height) height (Cook and Kairiukstis, 1990). The direction of the core extraction was carefully chosen in such a way that the effect of tension wood in the sample is minimized (Cook and Kairiukstis, 1990). Coring was done using a 2-threaded, 5.15 mm diameter and 40 cm length increment borer (Haglöf, Sweden). Once extracted, increment cores were stored in labelled plastic straws and brought to the tree-ring laboratory. For each cored tree, DBH and height were measured and the presence of necrosis was recorded. "Necrosis" was defined as the occurrence of any type of fungal infection or presence of slime on the tree stems. The DBH was measured with a caliper, averaging two measurements taken in perpendicular directions. For trees that were too big to be measured with a caliper, a DBH tape was used. Tree height was measured using a Vertex IV (Haglöf, Sweden). For each tree, three to four height measurements were taken and averaged. Moreover, stand basal area was estimated with the angle count method of Bitterlich (1952). In addition, DBH, distance, azimuth and species of the competitor trees (DBH  $\geq$  12 cm) within a 10 m radius around the target trees were measured and noted (Düggelin and Keller, 2017; Vitali et al., 2018). Competition data were used in a further step to estimate the competition experienced by each target tree by computing a competition index.

Finally, GPS coordinates of target trees were collected using a Topcon HiPer SR GPS tracker (Topcon Corp., Japan) mounted on a two-meter-long pole. Geodata were visualised, manipulated and stored using the Topcon software Magnet Field installed on a Topcon FC-6000 field computer (Topcon Corp., Japan). The GPS coordinates were taken at the base of the trees with an accuracy of  $\leq$  5 cm. Sometimes, due to weak signal caused by the trunks and the crowns of the trees, the pole with the GPS tracker had to be moved up to 0.5 m from the base of the tree. The GPS-coordinates were then exported as a text file and processed with ArcGIS Pro software (Version 2.4.0, ESRI, 2019) (Figure 2.2).

## 2.3 Data preparation and measurement

### 2.3.1 Tree ring width and basal area increment

The tree cores were air-dried and glued on wooden supports using water-resistant glue and were let dry for 2-3 days. Because tree-ring boundaries of beech can be difficult to distinguish, a microtome was used to prepare the surface of the cores (Gärtner and Nievergelt, 2010), instead of using a sanding machine. To increase the contrast of the boundary between tree rings, chalk was applied to the cores before measuring. Tree-ring width mea-



Figure 2.2: Study site Grosszinggibrunn with all the sampled trees. Source of the map: swisstopo (2019).

measurements were performed on a LINTAB 5 support (RINNTECH, Germany), using a Leica MZ6 stereo microscope (Leica, Germany), following a bark to pith direction and with a resolution of 0.01 mm. The software TSAPWin (Version 0.55, RINNTECH, 2005) was employed to record the measurements and visually assess crossdating accuracy. The resulting visually crossdated series were statistically checked with the program COFECHA (Holmes, 1983). The COFECHA crossdating program was run using the default 32-year smoothing spline (Grissino-Mayer, 2001). We decided to use two different combinations of segment length and lag to assess crossdating. The default segment of 50 years lagged by 25 years was used to correct false crossdating that were easy to detect. As near the pith growth can vary strongly among different individuals, a more sensitive approach had to be used. For this reason, a second COFECHA test was run using a segment of 20 years lagged by 10 years. In total, 71 of the 76 measured cores (two cores for each of the 38 trees) were correctly crossdated. Five cores were discarded because we were unable to crossdate them correctly, due to either missing or non-distinguishable rings, false rings or decayed wood. In this case, the other core of the corresponding tree was kept as the main growth series. In all the other cases where both cores were correctly crossdated, the average growth series between the two cores was used. Finally, the growth series of all the 38 trees were exported to a *.rwl* file ready to be used in further analyses.

Tree-ring width raw series may contain some trends that are not related to climate, such as tree's biological age trend (Fritts, 1976). For this reason, raw series were detrended and standardised (Cook and Kairiukstis, 1990) with the R package *dplR* using the function *detrend* (Bunn et al., 2020). We used a cubic smoothing spline with a frequency cutoff of 0.5 applied to two third of the length of the time series. Because first results showed

that the spline was too rigid, which could lead to the loss of some high frequency growth signals, we decided to use a smoothing spline of 16 years. The frequency response was kept at 0.5 by default. The series were then standardised by dividing each series by its growth trend. Basal area increment (BAI) was also calculated from the tree-ring width series. To calculate the BAI there are two possible methods: using the inside-out method (from the pith to the bark, function *bai.in*) or the outside-in method (from the bark to the pith, function *bai.out*). The first method needs an estimation of the missing distance between the last measured tree-ring and the pith. In some cases, the number of missing tree-rings and distance to the pith could be estimated using the Duncan (1989) method. In other cases this was not possible due to the large distance between the last measured tree-ring and the pith. Contrarily, the outside-in method uses the diameter of the tree to estimate the distance of the missing part, assuming circular cross-section (Biondi, 1999). As DBH was measured for all the target trees, the outside-in method was used to extract the BAI. Finally, the past tree diameters were reconstructed at an annual resolution by subtracting the annual diameter increment inferred from the tree-ring width to the DBH measured in the field. This resulted in the DBH time series (DBH<sub>ts</sub>). This operation was performed using Microsoft Excel (Version 16.0, Microsoft Corp., 2019). The summary of the characteristics of selected trees is presented in Table 2.1. It is important to note that the sample trees characteristic differed little between vital and unvital trees, reducing the potential size or age bias.

Table 2.1: Characteristics of the sampled trees at the study site Grosszinggibrunn grouped as "Vital", "Unvital" and "All".

	Vital	Unvital	All
Number of cored trees	21	17	38
DBH [cm] mean	70.90±9.33	64.65±12.53	68.11±11.18
max	89	88	89
min	53	47	47
Height [m]	33.0±5.2	32.9±4.8	32.9±5.0
Basal area [m <sup>2</sup> /ha]	11.2±3.7	11.7±3.7	11.4±3.7
Necrosis	10	15	25
Average tree-ring width [mm]	2.78±0.53	2.49±0.52	2.66±0.54
Average series length [years]	111±15	114±18	112±16
Oldest measured tree-ring [year]	1893	1891	1891

### 2.3.2 Competition index

Competition between trees is one of the major forces that influence the tree growth (Peet and Christensen, 1987). For estimating the competition experienced by each cored tree, we used the distance- and size-dependent competition index (CI) of Hegyi (1974):

$$CI_i = \sum_{j=1}^N \frac{DBH_j}{DBH_i * dist_{ij}}$$

where  $DBH_j$  is the DBH of the competitor tree ( $j$ ),  $DBH_i$  is the DBH of the target tree ( $i$ ) and  $dist_{ij}$  is the distance between the competitor and the target tree. It is important to consider that this computed CI reflects the competition sustained by the target trees at the time of sampling, hence in the year 2019. Unfortunately, we could not reconstruct the CI before the last thinning in 2015 because the DBH and the position of the cut trees were not available. Finally, the significance in the difference among the vital and unvital trees was then tested using a Wilcoxon test.

### 2.3.3 Climate data

Climate data were gathered from the MeteoSwiss web portal IDAWEB<sup>1</sup> for the nearest meteorological station to the study site, i.e. Basel/Binningen (7.4 km from the study site, 316 m a.s.l.). We extracted the mean monthly precipitation sums and monthly mean-, maximum- and minimum air temperatures from January 1900 to December 2019.

Because drought-induced decline and mortality of beech in our study region is of particular concern in recent time and is the main focus of this thesis, the necessity of having a parameter that describes drought severity arose. Of the many existing drought indices, we decided to use the Standardized Precipitation Evapotranspiration Index (SPEI) because it can be easily computed and it is widely used in forest science (Vicente-Serrano et al., 2012). In comparison to the Standardized Precipitation Index (SPI), the SPEI considers evapotranspiration (Vicente-Serrano et al., 2010). Using the R package SPEI (Beguería and Vicente-Serrano, 2017) it is possible to calculate the potential evapotranspiration (PET) with different methods. The Hargreaves method has the advantage of being a simple method, relying only on precipitation and temperature, with the possibility to use latitude to estimate the global radiation (Droogers and Allen, 2002). Thus, the Hargreaves method was used. For this calculation, we used the latitude of the Basel/Binningen weather station (47° 32' N). The next step after calculating the PET is to calculate the climatic water balance (CWB) using the following simplified equation:

$$CWB = precipitation - PET$$

<sup>1</sup><https://gate.meteoswiss.ch/idaweb/login.do>, accessed between 29 January and 2 February 2020.

The climatic water balance is finally used in the *spei* function to calculate the SPEI. The SPEI can be calculated at different time scales (Vicente-Serrano et al., 2010) and considers the influence of past climatic conditions in its computation. In total, 12 different time scales were tested, ranging from one to twelve months lag.

## 2.4 Data analysis

The data analysis subchapter will describe all the different analyses performed in this thesis: the correlation and response function analysis (growth response of vital and unvital trees to climate), the superposed epoch analysis (sensitivity of vital and unvital trees to past extreme droughts) and the building of growth models (influence of tree size, competition and drought on tree growth). All these analyses, together with the data preparation, were done using the R software (Version 3.6.2, R Core Team, 2019).

### 2.4.1 Growth response of vital and unvital trees to climate

To have a first impression of the influence of climate on tree growth, we calculated bootstrapped correlation and response coefficients with the R package *treeclim* using the function *dcc* (Zang and Biondi, 2015). Response functions and correlations were calculated between the standardised tree-ring width or the BAI series of each individual tree and the monthly precipitation sums, the monthly mean minimum and maximum temperatures, as well as the twelve SPEI with the different time windows. To account for a possible time lag, this analysis was done from June prior ring formation to September of the year of ring formation. This analysis was also performed at the seasonal scale (winter: previous December to February; spring: March to May; summer: June to August; autumn: September to November). Based on the results of the correlation and response function analysis, we decided to only consider the current summer SPEI with a time window of three months as a main climate variable (SPEI<sub>3</sub>). We obtained similar results when performing the analysis with the standardised tree-ring width or the BAI series (see Appendix B).

### 2.4.2 Sensitivity of vital and unvital trees to past extreme droughts

The superposed epoch analysis (SEA) in dendrochronology is an analysis where the impact of events such as volcanic eruptions, forest fires or droughts is tested on the growth pattern before, during and after the defined key event years (pointer years) (Lévesque et al., 2014; Lough and Fritts, 1987; Stephens et al., 2003). The SEA was performed using the *sea* function in the R package *dplR* on drought pointer years using standardised tree-ring width as input data. The test was performed separately for vital and unvital trees using a time lag of four years and bootstrapped by 1000 resamples. Pointer years were selected using the most negative SPEI<sub>3</sub> values (Figure 2.3), i.e. 1947 (SPEI<sub>3</sub> = -2.53), 1976 (SPEI<sub>3</sub> = -1.66), 2003 (SPEI<sub>3</sub> = -1.45) and 2011 (SPEI<sub>3</sub> = -1.21).



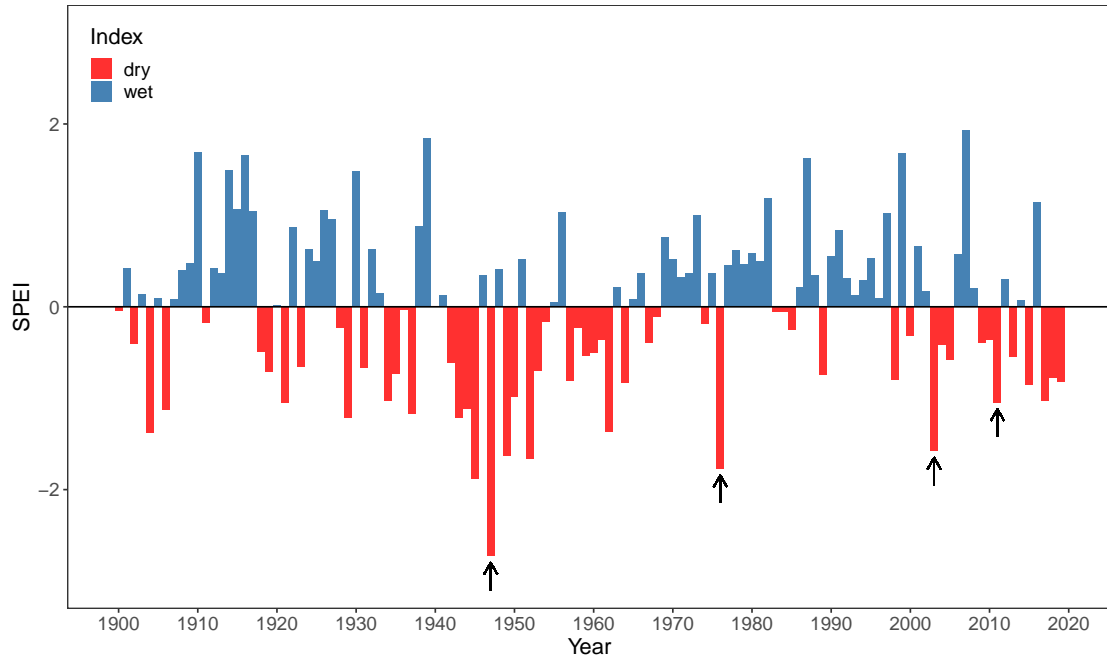


Figure 2.3: Mean summer (June, July, August) SPEI with a time window of three months ( $SPEI_3$ ) between 1900 and 2019 at the weather station of Basel/Binningen. The black arrows indicate the pointer years selected from the extreme negative  $SPEI_3$  values.

The calculation and the analysis of the tree resilience components is another way to assess the effect of extreme dry years on tree growth. Lloret et al. (2011) proposed the following equations for the calculation of the resilience components (i.e., resistance, recovery and resilience):

$$Resistance = \frac{Dr}{PreDr}$$

$$Recovery = \frac{PostDr}{Dr}$$

$$Resilience = \frac{PostDr}{PreDr}$$

where  $Dr$  is the growth during the drought year,  $PreDr$  the mean growth during defined years preceding the drought year and  $PostDr$  is the mean growth during defined years succeeding the drought year. Here, resistance is the ability of the tree to withstand drought events, recovery is the ability of the tree to recover from effects due to drought and resilience is the ability of the tree to restore growth rate to the pre-drought period (Lloret et al., 2011). For the computation of the resilience components, we used the function *res.comp* of the R package *pointRes* (van der Maaten-Theunissen et al., 2015). The components were

calculated separately for vital and unvital trees with the BAI and using the default 4 years of pre- and post-drought period. For this analysis we used the same pointer years as in the SEA. Significance in the difference among the vital and unvital trees was then tested using a Wilcoxon test.

### 2.4.3 Influence of tree size, competition and drought on tree growth

To explore how the growth of target trees was affected by factors such as tree size, competition and drought, linear mixed models were used. We built three models using three different time windows and variables. The first time window covers the period 1900-2019 and investigates most of target trees' lifespan. The second time window covers the period 1970-2019 and investigates the period in which the BAIs between vital and unvital trees have diverged (since 1970, see Figure 3.1 in Chapter 3.1) until today (2019). This was done to investigate if the response changed in more recent times. For these two time windows  $DBH_{ts}$ ,  $SPEI_3$ , presence/absence of necrosis, vitality (vital/unvital) and interaction between  $SPEI_3$  and  $DBH_{ts}$ , and vitality and  $SPEI_3$  were used as explanatory variables, thus as fixed effects (Equation 1). The third time window covers the last five years, from 2015 to 2019 and considers the influence of the last thinning done in 2015 and subsequent competition on growth performance of vital and unvital trees. For this third model, the same explanatory variables as in the first two models were used, but also including CI and the interaction between CI and  $DBH_{ts}$ , and CI and  $SPEI_3$  (Equation 2). The BAI was defined as a response variable for the three models. Multicollinearity between variables was checked with the function *correlogram* in the R package *corrgram* using a Pearson correlation test (Wright, 2018). Non-numeric variables, such as necrosis and vitality, were not included in this test. The results were plotted on a correlation matrix (Appendix C). All the explanatory variables except vitality and necrosis, which are factorial, were scaled by subtracting the mean and dividing by the standard deviation. The BAI was log-transformed to account for non-normality and heteroscedasticity. Tree ID (the identity of the trees) was included into the models as random effect to account for tree-to-tree variability. Temporal autocorrelation was considered by explicitly including a first order autocorrelation structure into the models.

The models were built following Zuur et al. (2009) with the *lme* function in the R package *nlme* (Pinheiro et al., 2019). In a first step, a full model including all the explanatory variables was evaluated using the restricted maximum likelihood (REML). In a next step, the residuals were plotted to check their distribution. Using the *summary* function, it was possible to elicit which variables had the strongest effect and were significant. According to Zuur et al. (2009), the following phase to improve the models is to remove step-by-step the non-significant variables using the maximum likelihood method in an attempt to reduce the complexity of the models. Anovas were iteratively run to test the performance of the updated models to the former model and the model with the lowest Akaike information

criterion (AIC) was selected as final model. At this point, the model was considered adequate and ready to be recalculated again with the REML method. Again, the residuals were plotted to check their distribution (see Appendix D) and the *summary* function was used to extract information from the model. With the function *r.squaredGLMM* in the R package MuMIn (Barton, 2019) was possible to extract the marginal and conditional R-squared coefficients of the model. Finally, the estimates of the model were plotted.

$$\begin{aligned} \log(BAI + 1) = & \text{scale}(DBH_{ts}) + \text{necrosis} + \text{vitality} + \text{scale}(SPEI_3) \\ & + \text{scale}(SPEI_3) * \text{scale}(DBH_{ts}) + \text{vitality} * \text{scale}(SPEI_3) \end{aligned} \quad (1)$$

$$\begin{aligned} \log(BAI + 1) = & \text{scale}(DBH_{ts}) + \text{necrosis} + \text{vitality} + \text{scale}(CI) + \text{scale}(SPEI_3) \\ & + \text{scale}(SPEI_3) * \text{scale}(DBH_{ts}) + \text{scale}(CI) * \text{scale}(DBH_{ts}) \\ & + \text{vitality} * \text{scale}(SPEI_3) + \text{scale}(CI) * \text{scale}(SPEI_3) \end{aligned} \quad (2)$$

## Chapter 3

# Results

### 3.1 Growth trend and competition

From the start of the previous century (year 1900) until the 1970s the BAI had a similar increase between vital and unvital trees (Figure 3.1). Starting from the 1970s the BAI of vital and unvital trees started to diverge, resulting in unvital trees having smaller BAI increase. The BAI of vital trees increased between the 1970s and the mid-1990s, reaching its peak around 1995, then it slowly declined, reaching in 2019 the values of 1970. During the same period, the BAI of unvital trees increased very slowly, reaching its peak around 1985. After that, the BAI started to decline severely, reaching in 2019 its minimum since 1918 (BAI = 8.67 cm<sup>2</sup>). This divergence in the BAI between vital and unvital trees was the reason why we chose 1970 as a reference year for the time window of the second model.

The computed CI of target trees in the last five years (2015-2019) ranged from 0 to 0.99 with a mean of  $0.33 \pm 0.22$ , with a larger variance for unvital trees. Unvital trees were on average subject to higher competition than vital trees, although the difference was not significant ( $p=0.27$ ) (Figure 3.2a). Intraspecific competition accounted for 71% of the total competition experienced by the target trees (Figure 3.2b). The remaining competitor species were hornbeam (25%) and oak, lime and maple (together 4%).

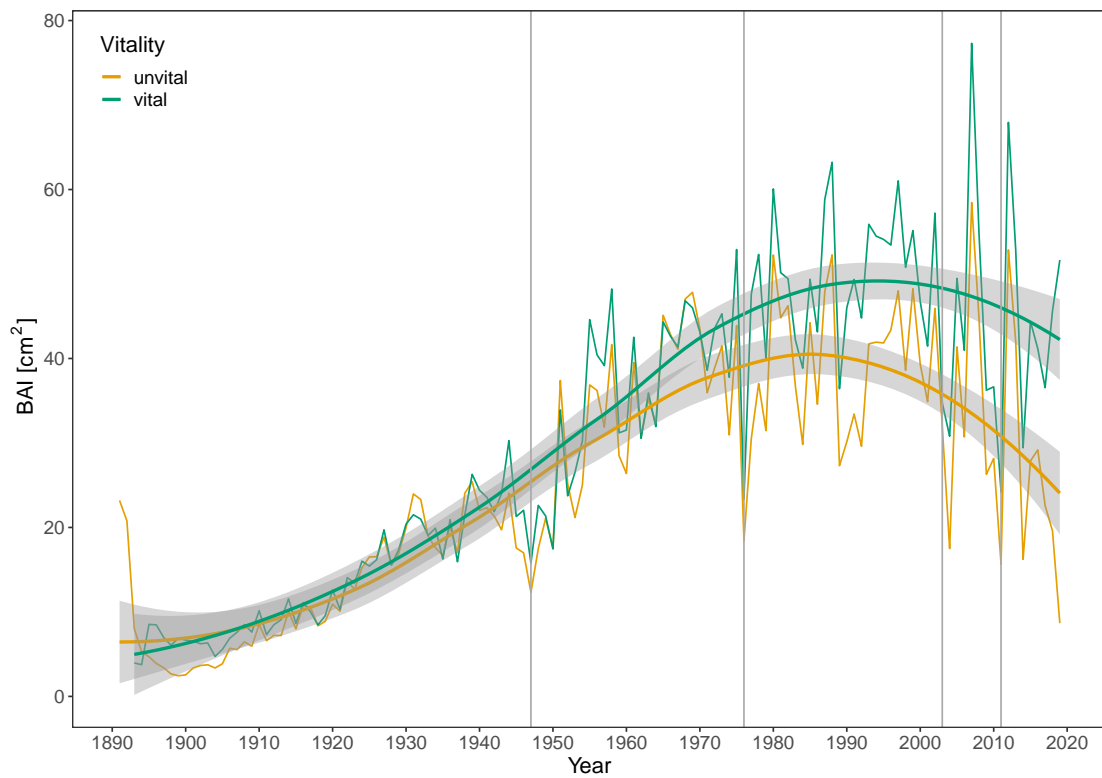


Figure 3.1: Basal area increment (BAI) of vital (green) and unvital (yellow) trees and their respective smoothing splines (bold lines). The shaded area around the bold lines indicates the 95% confidence interval of the smoothing splines. The vertical lines represent the pointer years.

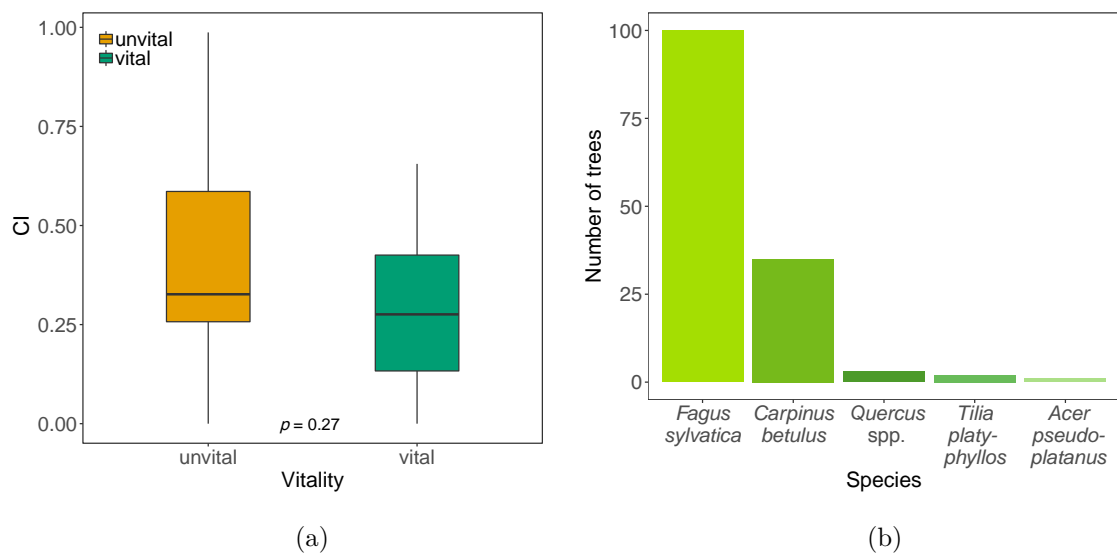


Figure 3.2: Competition index (CI) grouped by vitality (a) and competitor species (b) for target trees. The  $p$ -value at the bottom of the plot (a) is calculated using a Wilcoxon test and gives the significance for the difference between vital and unvital trees.

### 3.2 Growth response of vital and unvital trees to climate

The climate variable SPEI<sub>3</sub> of current summer had the highest and significant positive response on growth (mean =  $0.21 \pm 0.12$ ) (Figure 3.3), which implies a negative effect of drought on growth. In the other seasons, SPEI<sub>3</sub> had a small and non-significant effect. Precipitation had a positive significant effect on growth during previous winter, current spring and current summer. Yet, the effect of precipitation was weaker than SPEI<sub>3</sub> of current summer and in general less significant (mean =  $0.13 \pm 0.06$ ). Precipitation of previous summer and autumn had small effect and were non-significant. Both maximum and minimum temperature had generally non-significant effects or presented a high variance. Climate effects were similar in both vital and unvital groups. The correlation function had generally similar results. The results of the correlation function analysis are shown in Appendix B. Because SPEI<sub>3</sub> of current summer had the strongest and most significant effect on growth, this variable was used in the growth models, instead of precipitation, and maximum- and minimum temperature.

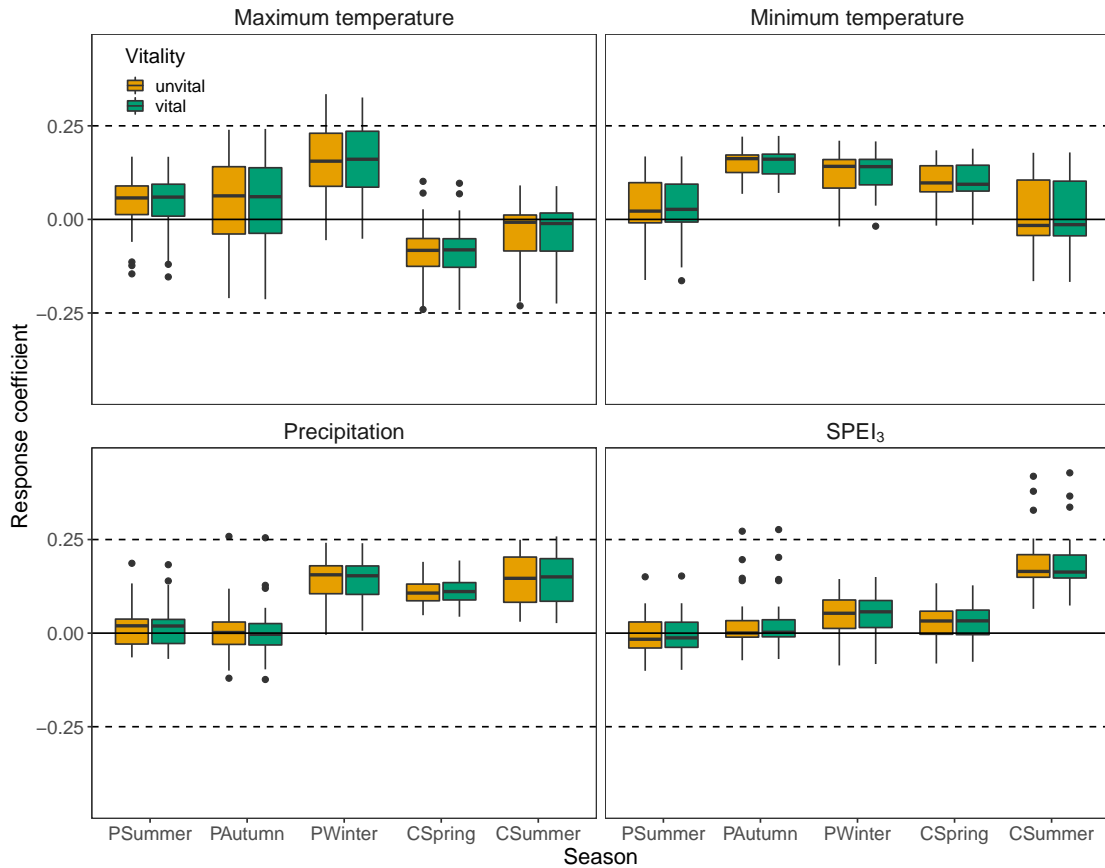


Figure 3.3: Boxplots of response function coefficients calculated between basal area increment (BAI) of each individual vital and unvital tree and different climate variables computed at a seasonal scale from previous summer to current summer. Letter "P" is for "previous", while letter "C" is for "current".

### 3.3 Sensitivity of vital and unvital trees to past extreme droughts

The results of the superposed epoch analysis showed generally different growth response to past extreme droughts (1947, 1976, 2003, 2011) between vital and unvital trees (Figure 3.4). However, in the years of the drought events (year = 0) a drastic and significant reduction of growth affected both vital (departure from mean growth = -1.34) and unvital (departure from mean growth = -1.28) trees in a similar way. In the first two years after the drought events occurred, both vital and unvital trees showed recovery of growth. However, this recovery was stronger for unvital trees than for vital trees and significant only for the unvital trees. The third year after the drought events occurrence, another decline in growth could be observed for both vital and unvital trees. This decline was stronger for unvital trees. Four years after the drought events both vital and unvital trees experienced a similar increase in growth, although this was significant only for the vital trees.

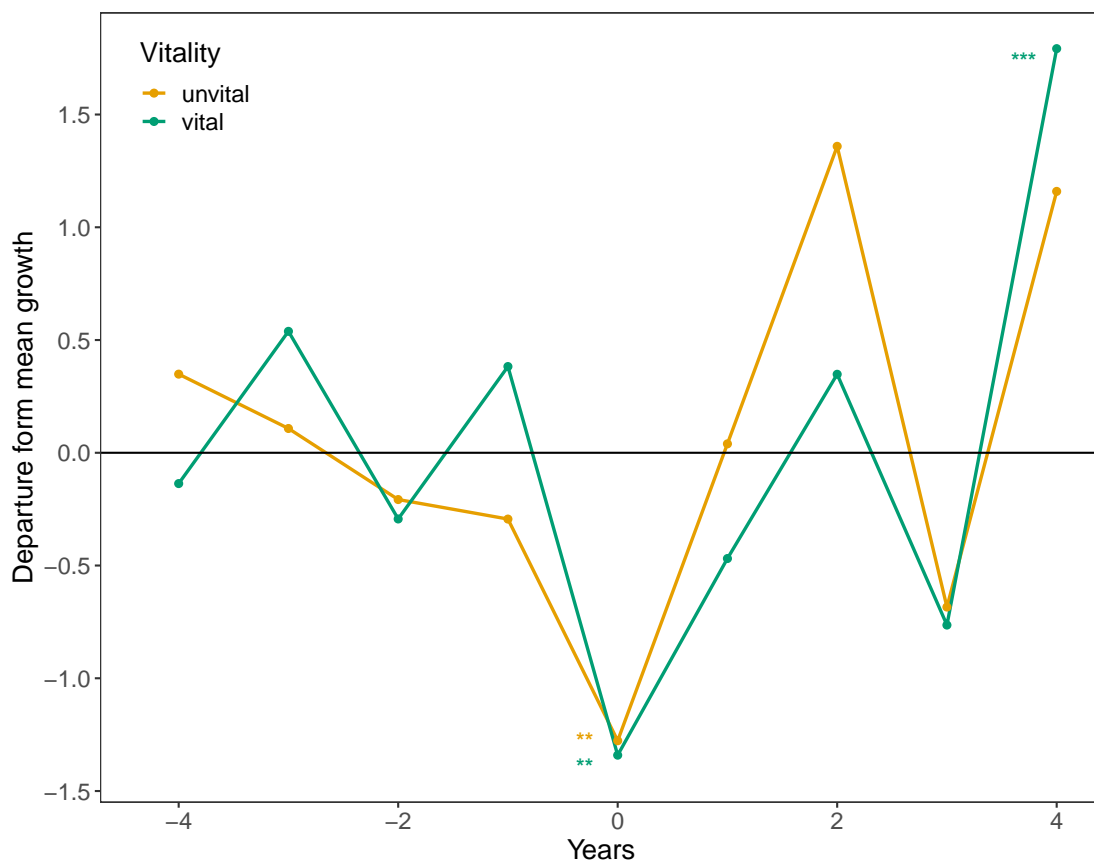


Figure 3.4: Result of the superposed epoch analysis for vital (green) and unvital (yellow) trees showing the departure from the mean growth using a time lag of four years and bootstrapped by 1000 resamples. Year zero is the year when the drought events occurred. The years considered are 1947, 1976, 2003 and 2011. Three asterisks mean a significance of  $p < 0.001$ ; two asterisks mean a significance of  $p < 0.05$ .

The analysis of the resilience components showed different results between resistance, recovery and resilience (Figure 3.5). The resistance index during the extreme drought years was significantly below 1 for all the pointer years except for the year 2003. The mean value for tree resistance was  $0.61 \pm 0.23$ . For the extreme drought years considered, there was no significant difference between vital and unvital trees. The recovery index during the extreme drought years was generally above 1, although this increase in recovery was significant only in 2011. The mean recovery value was  $1.88 \pm 0.73$ . In year 2003 the difference in recovery between vital and unvital trees was significant ( $p=0.017$ ). The resilience index during the extreme drought years showed a decreasing trend for both vital and unvital trees. The mean resilience value was  $1.03 \pm 0.28$ . Except for the year 1947, resilience was not significantly different between vital and unvital trees.

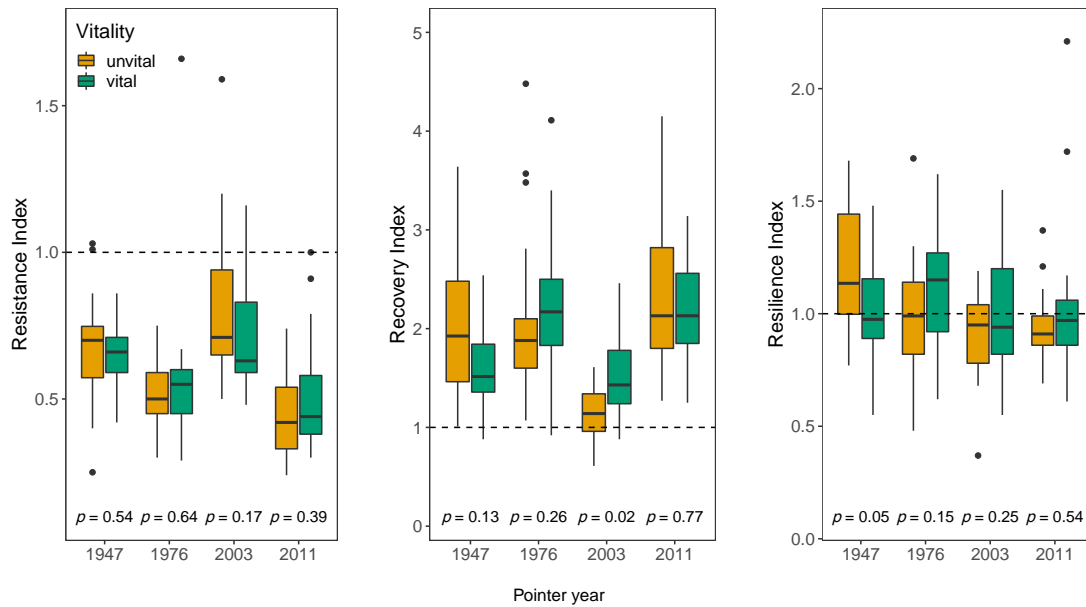


Figure 3.5: Indexes of resistance, recovery and resilience of vital and unvital trees during the extreme drought years 1947, 1976, 2003 and 2011. The dashed line represents the reference index line (value = 1). The points show the outliers. The  $p$ -values at the bottom of the plots are calculated using a Wilcoxon test and give the significance for the difference between vital and unvital trees.

### 3.4 Influence of tree size, competition and drought on tree growth

#### 3.4.1 Growth model for the time window 1900-2019

From the full model for the time window 1900-2019, necrosis and interactions between vitality and  $SPEI_3$  were removed to reduce the complexity of the model, as they were the least significant variables. The variable  $DBH_{ts}$  had the strongest significant effect on



growth ( $0.51 \pm 0.01$ ,  $p < 0.01$ ) (Table 3.1, Figure 3.6). Vitality had the second strongest effect on growth ( $0.17 \pm 0.08$ ) and was significant ( $p < 0.05$ ). All the other variables had less strong effects, but were highly significant ( $p < 0.01$ ). In comparison to the full model (AIC = 6'429.652), the final model performed better having a lower AIC (AIC = 6'420.276). The marginal and conditional  $R^2$  for the final model were 0.49 and 0.56, respectively. The residuals of the final model are shown in Appendix D.

Table 3.1: Summary of the fitted linear mixed model for the time window 1900-2019. The values in brackets are the standard error. Table created using R stargazer package (Hlavac, 2018).

	<i>Dependent variable:</i>	
	log(BAI + 1)	
	Full	Final
DBH <sub>ts</sub>	0.509*** (0.009)	0.509*** (0.009)
Necrosis	0.069 (0.081)	
Vitality	0.172** (0.077)	0.143** (0.070)
SPEI <sub>3</sub>	0.109*** (0.012)	0.092*** (0.008)
DBH <sub>ts</sub> :SPEI <sub>3</sub>	0.069*** (0.008)	0.068*** (0.008)
Vitality:SPEI <sub>3</sub>	-0.030* (0.016)	
Intercept	3.098*** (0.089)	3.160*** (0.052)
Observations	4'197	4'197
Marginal R <sup>2</sup>	0.49	0.49
Conditional R <sup>2</sup>	0.56	0.56
Log Likelihood	-3'204.826	-3'202.138
AIC	6'429.652	6'420.276
BIC	6'493.056	6'471.004

Note: \* $p < 0.1$ ; \*\* $p < 0.05$ ; \*\*\* $p < 0.01$

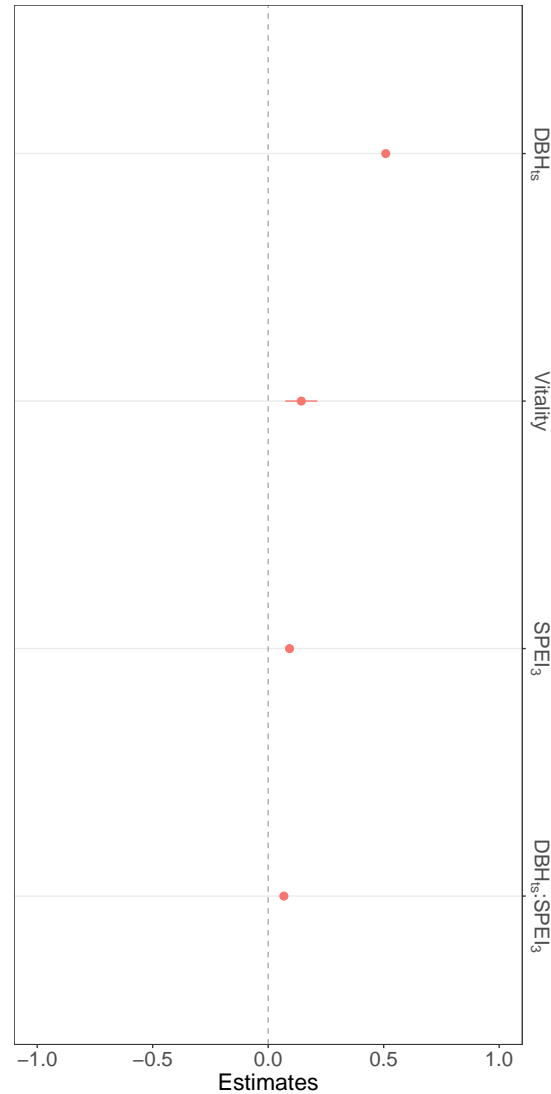


Figure 3.6: Estimates of the final model for the time window 1900-2019.

### 3.4.2 Growth model for the time window 1970-2019

The model performance for the time window 1970-2019, which corresponds to the period with divergent growth trends between vital and unvital trees, did not improve removing the variables. Thus, the full model remained the optimal model structure. In this model, vitality had the strongest significant effect on growth ( $0.40 \pm 0.12$ ,  $p < 0.01$ ) (Table 3.2, Figure 3.7). The variable SPEI<sub>3</sub> had the third strongest effect on growth ( $0.18 \pm 0.01$ ) and was also highly significant ( $p < 0.01$ ). Necrosis had the second strongest effect on growth ( $0.19 \pm 0.13$ ) but was not significant. The interactions between DBH<sub>ts</sub> and SPEI<sub>3</sub> and Vitality and SPEI<sub>3</sub> had less strong effects, but were significant ( $p < 0.05$ ). The variable DBH<sub>ts</sub> had a weak and not significant effect on growth ( $0.021 \pm 0.02$ ). The marginal and conditional R<sup>2</sup> for this model were 0.17 and 0.53, respectively. The residuals of the full model are shown in Appendix D.

Table 3.2: Summary of the fitted linear mixed model for the time window 1970-2019. The values in brackets are the standard error. Table created using R stargazer package (Hlavac, 2018).

	<i>Dependent variable:</i>
	log(BAI + 1)
DBH <sub>ts</sub>	0.021 (0.015)
Necrosis	0.190 (0.125)
Vitality	0.397*** (0.120)
SPEI <sub>3</sub>	0.177*** (0.014)
DBH <sub>ts</sub> :SPEI <sub>3</sub>	0.021** (0.009)
Vitality:SPEI <sub>3</sub>	-0.051*** (0.018)
Intercept	3.300*** (0.137)
Observations	1'895
Marginal R <sup>2</sup>	0.17
Conditional R <sup>2</sup>	0.53
Log Likelihood	-969.895
AIC	1'959.791
BIC	2'015.261

Note: \* $p < 0.1$ ; \*\* $p < 0.05$ ; \*\*\* $p < 0.01$

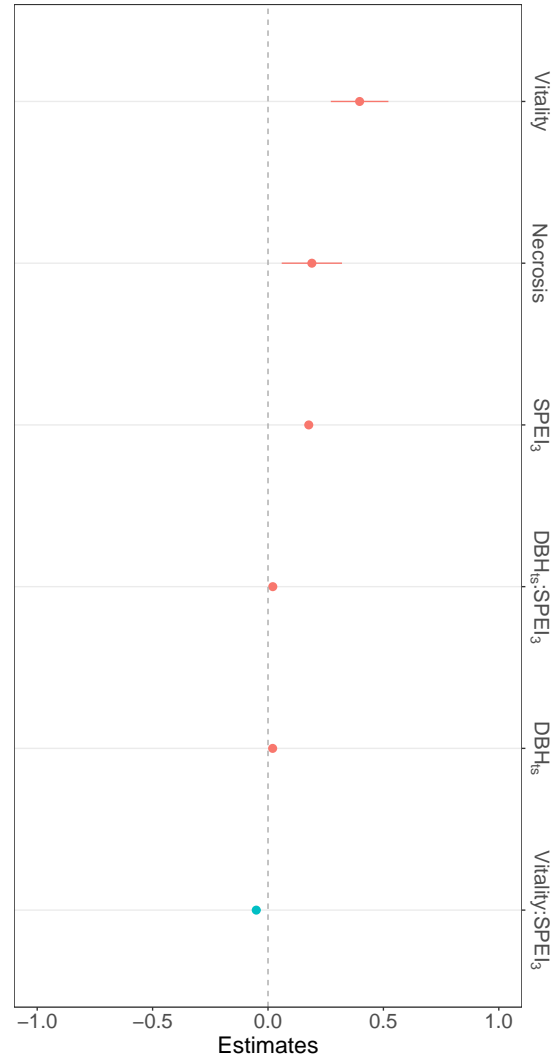


Figure 3.7: Estimates of the full model for the time window 1970-2019.

### 3.4.3 Growth model for the time window 2015-2019

For the time window 2015-2019, which corresponds to the period between the last thinning and the tree sampling, necrosis and interactions between  $DBH_{ts}$  and  $SPEI_3$ ,  $DBH_{ts}$  and CI, and CI and  $SPEI_3$  were removed from the full model to reduce its complexity. Vitality had the strongest significant effect on growth ( $0.62 \pm 0.12$ ,  $p < 0.01$ ) (Table 3.3, Figure 3.8). The variable CI had the second strongest effect on growth ( $-0.16 \pm 0.06$ ) and was very significant ( $p < 0.05$ ). All the other variables had less strong effects and were not significant, except for  $SPEI_3$  ( $p < 0.05$ ). In comparison to the full model (AIC = 312.124), the final model performed better having a lower AIC (AIC = 288.687). The marginal and conditional  $R^2$  for the final model were 0.41 and 0.57, respectively. The residuals of the final model are shown in Appendix D.

Table 3.3: Summary of the fitted linear mixed model for the time window 2015-2019. The values in brackets are the standard error. Table created using R stargazer package (Hlavac, 2018).

	<i>Dependent variable:</i>	
	log(BAI + 1)	
	Full	Final
DBH <sub>ts</sub>	0.094 (0.066)	0.095 (0.064)
Necrosis	0.018 (0.136)	
Vitality	0.619*** (0.138)	0.619*** (0.118)
CI	-0.155** (0.069)	-0.164** (0.063)
SPEI <sub>3</sub>	0.103** (0.048)	0.098** (0.046)
DBH <sub>ts</sub> :SPEI <sub>3</sub>	0.025 (0.035)	
DBH <sub>ts</sub> :CI	0.021 (0.055)	
Vitality:SPEI <sub>3</sub>	-0.109* (0.065)	-0.101 (0.062)
CI:SPEI <sub>3</sub>	0.012 (0.035)	
Intercept	3.082*** (0.159)	3.085*** (0.086)
Observations	185	185
Marginal R <sup>2</sup>	0.41	0.41
Conditional R <sup>2</sup>	0.57	0.57
Log Likelihood	-143.062	-135.344
AIC	312.124	288.687
BIC	353.266	317.374

Note: \* $p < 0.1$ ; \*\* $p < 0.05$ ; \*\*\* $p < 0.01$

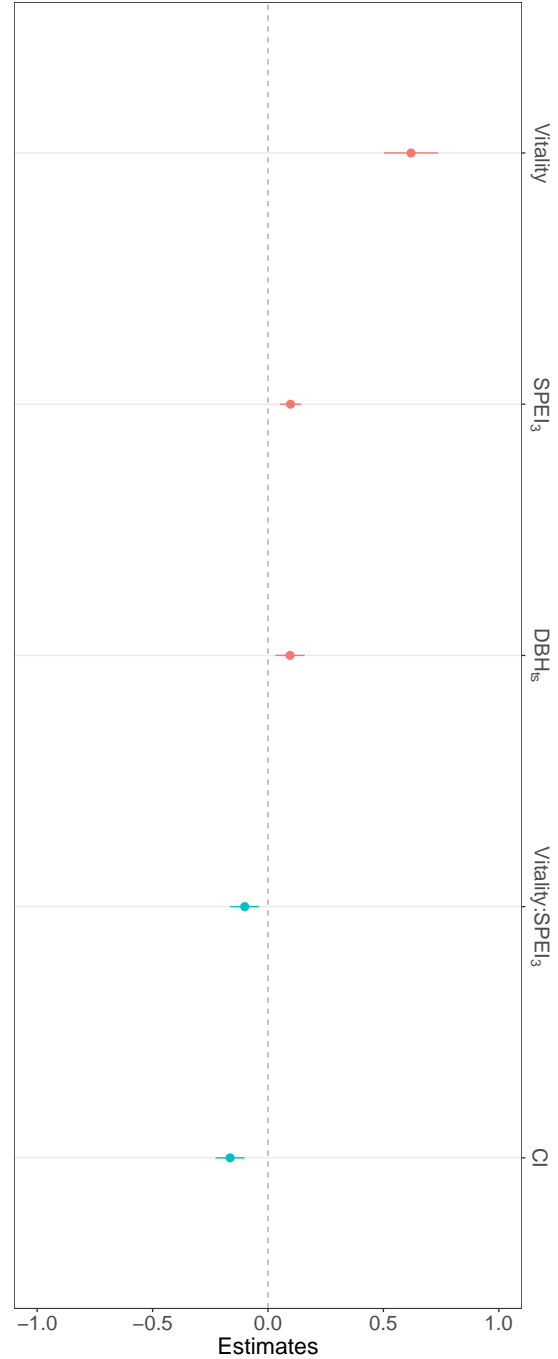


Figure 3.8: Estimates of the final model for the time window 2015-2019.

# Chapter 4

## Discussion

### 4.1 Growth trend and competition

Both vital and unvital trees showed a declining growth trend during the last three decades (Figure 3.1). This decline was clearly more drastic for the unvital trees. Bréda et al. (2006) provided evidence that severe and recurrent droughts can play a major role in the growth decline of a tree. In addition, Wunder et al. (2007) identified higher mortality risk in beech trees with reduced growth. Thus, we underpin that the recent extreme drought events may explain the drastic decline in the BAI experienced by unvital trees from the 1980s onward. Similar BAI decline was also reported for the same period in other studies in Switzerland, Germany and Croatia (Braun et al., 2017; Schwarz and Bauhus, 2019). Moreover, severe drought may cause early leaf shedding (Leuschner and Ellenberg, 2017). In our study site, around 25% of the beech trees showed severe drought-induced defoliation or discolouration. This is in line with the general estimation of the Swiss Federal Institute WSL (Ferretti et al., 2020; Wohlgemuth, 2020) and of the canton Basel-Landschaft (Kanton Basel-Landschaft, 2019).

It is important to note that, based on the field assessment and the public report on the drought event of 2018 in canton Basel-Landschaft (Kanton Basel-Landschaft, 2019), it seems that only older trees were severely affected by the last two drought years. For this reason, we did not include younger beech trees in our study. In their study, Bennett et al. (2015) provided evidence that generally, older and larger trees are more drought sensitive than younger and smaller trees. They attributed this sensitivity to higher vulnerability to hydraulic stress and higher evapotranspiration in the crown of larger trees. According to Bréda et al. (2006) larger trees may be more sensitive to extreme drought due to larger vessels and pores which may facilitate cavitation. Cavitation in the xylem can cause hydraulic failure and lead to the death of trees by desiccation (McDowell et al., 2013). Shortage of water supply in summer may also impact beech growth, in particular at the

lower elevations (Leuschner and Ellenberg, 2017), like at our study site (316 m a.s.l.). The computed values of CI refer to the competition experienced by target trees in the five years after the last thinning occurred. This means that we cannot consider the competition exerted from other trees that were previously around them before the thinning. Therefore, CI was only included in the model for the time window 2015-2019. The CI is an important indicator to assess tree growth potential and stress (Peet and Christensen, 1987; Schwarz and Bauhus, 2019). Unfortunately, we were not able to implement pre-thinning CI in the long-term model because information on the tree size and position of competitors before the last thinning in 2015 were unknown. Thus, future research over drought impact on beech trees in this region may require including the effects of competition.

## 4.2 Growth response of vital and unvital trees to climate

The sensitivity of beech trees to summer (June to August) drought is also confirmed in the response and correlation function analysis, where SPEI<sub>3</sub> had clearly a strong and significant influence on growth (Figure 3.3). A high sensitivity of beech to drought was also reported in other studies. Weber et al. (2013) found that beech trees at their dry distribution limit in Switzerland were sensitive to spring and early-summer (March to June) drought. In contrary, Tegel et al. (2014) found a strong effect of drought on beech growth throughout the year. However, the study of Tegel et al. (2014) took place in a region characterised by a Mediterranean climate, where drought and low precipitation, as well as higher temperature are more pronounced than around Basel. Our results also indicate a significant positive effect of spring and summer precipitation on tree growth. An analogous result was found by Dulamsuren et al. (2017) and Kunz et al. (2018) in beech stands of southern Germany and by Cavin and Jump (2017) in southern Germany and eastern France. In particular, Dulamsuren et al. (2017) highlighted that the decline in the growth that affected beech trees in the region of the High Rhine Valley since the 1970s can be attributed to the decline in precipitation and the rise in temperatures. However, a similar deduction cannot be done with maximum and minimum temperature, because no significant results emerged from the response function analysis.

High sensitivity to summer drought is associated to limited capacity of beech trees to cope with high evapotranspiration rates (Peuke et al., 2002). Competition for water with other trees may also contribute to increase drought stress (Cescatti and Piutti, 1998). As long-term competition data are missing in our study, no conclusion can be drawn on the relationship between competition and climate effect on target trees. It is interesting to note, that no significant differences were found in the climate response between vital and unvital trees, as we would have expected. This means that year-to-year climate variability has affected similarly vital and unvital trees and it does not explain the stronger decline in growth that affected unvital trees. Therefore, we investigated the sensitivity of vital and

unvital trees to the past extreme droughts to probe if differences between the two groups are present.

### 4.3 Sensitivity of vital and unvital trees to past extreme droughts

Growth was impacted most severely on the year that the different extreme drought events occurred (1947, 1976, 2003 and 2011) (Figure 3.4). Our result is also confirmed by the study of Kunz et al. (2018), in which they found a strong significant reduction in beech growth during the drought years 1947, 1976 and 2003. Similar results were reported by Dobbertin (2005) and Schwarz and Bauhus (2019), where they found a decline in growth in year 2003 due to drought stress. In addition, Dobbertin (2005) associated a stronger impact of drought on tree growth at lower elevations. Conversely, Zimmermann et al. (2015) showed a stronger and more significant decrease in growth the year succeeding the drought year, suggesting a short-lagged impact of drought on growth. We could not detect this pattern in our study, as the two years following the drought years showed a strong growth recovery, especially in unvital trees. This result is supported by the study of Burri et al. (2019), where they found that beech trees may partly benefit from hot and dry summers. However, it is still uncertain why the growth recovery was stronger in unvital trees.

A strong increase in growth for both vital and unvital trees was also found four years after the drought events. Similar results were found by Dulamsuren et al. (2017), with a strong increase in beech growth four years after the drought events, in particular at lower elevations (100-300 m a.s.l.). The reason for the increase in growth in the first, the second and the fourth year following the extreme drought years can be explained with the capacity of beech trees to recover from drought events (Burri et al., 2019). Beech trees show evidence of good recovery capacity from drought-induced damage (Burri et al., 2019; Kunz et al., 2018), although sometimes recovery of growth may take many years (Leuschner and Ellenberg, 2017). Hackett-Pain et al. (2018) and Zimmermann et al. (2015) suggested that a decrease in beech growth after a drought year, such as the reduction of growth in our beech trees three years after the drought events, can be associated with higher masting stimulated by high temperatures and radiation (Vacchiano et al., 2017). However, no data on masting years were sampled, thus we cannot affirm that this decline in growth three years after the drought events is caused by an increased fructification or by a delayed effect of drought.

The values for tree resistance to drought and recovery during the selected drought years were in most cases lower, respectively higher than 1. On the contrary, the resilience index was close to 1. Kunz et al. (2018) found similar results analysing beech resistance, recovery and resilience. In their study, beech trees had a mean resilience value larger than one (1.05),



suggesting that beech trees were able to reduce the negative impact of drought on growth. This may also be true for our target trees, as our mean resilience value was  $1.03 \pm 0.28$ . However, resilience of our target trees seemed to decline over the years, in particular for unvital trees. This supports the idea that unvital trees were not able to cope with repeated extreme droughts. High sensitivity of beech to consecutive drought occurrences is also demonstrated by Zimmermann et al. (2015). In addition, factors such as severity and recurrence of drought could play a role in the recent growth decline of beech trees (Bréda et al., 2006). Using the extreme drought years 1947, 1976 and 2003 Zang et al. (2014) found values in a comparable range for resistance, recovery and resilience in beech trees. Regarding the recovery index, it is interesting to note that the values for the selected drought years were generally higher than 1, implying that the trees were able to recover from the drought impact quickly, which is also confirmed by the superposed epoch analysis. This would also partly confirm the great ability of beech trees to recover from drought (Burri et al., 2019; Kunz et al., 2018). In 2003 recovery was generally smaller and there was a significant difference between vital and unvital trees. This suggests a deficit in the recovery capacity of unvital trees. This may be related to the more intensive drought that characterised 2003. A final consideration can be done on the decreasing trend of tree resilience. Although the difference between unvital and vital trees is not significant, it appears that unvital trees may have suffered more in the following years of low resilience capacity. DeSoto et al. (2020) linked low resilience to drought with higher mortality risk. This could explain the dieback that affected the unvital trees of our study, especially after the drought years of 2018 and 2019 that interested the region around Basel and that may have served as an inciting factor (Bigler et al., 2006) for mortality in many weak beech trees.

#### 4.4 Influence of tree size, competition and drought

Generally, the results from the growth model analysis were different depending on the time window considered. The growth model that covered the time window 1900-2019 showed a strong and significant ( $p < 0.01$ ) positive effect of  $DBH_{ts}$  (tree size) on growth (BAI) ( $0.51 \pm 0.01$ ). This can be explained by the strong allometric relationship between diameter and secondary growth of beech, particularly at early age (Bontemps et al., 2010; Podlaski, 2002). More interesting are the less strong but significant effects of vitality ( $0.14 \pm 0.07$ ,  $p < 0.05$ ) and drought ( $SPEI_3$ ) ( $0.09 \pm 0.01$ ,  $p < 0.01$ ). The significant effect of  $SPEI_3$  confirms the impact that drought had on the growth of our target trees, while the significant vitality effect confirms that a difference in the growth between vital and unvital trees was present. Looking at Table 3.2, it emerges that in the second time window (1970-2019) this result is even more emphasised. Here, vitality had a higher effect than in the previous growth model and had the strongest effect ( $0.40 \pm 0.12$ ,  $p < 0.01$ ), highlighting the

divergence in the BAI between vital and unvital trees (Figure 3.1). Similarly, SPEI<sub>3</sub> had a higher effect on the BAI ( $0.18 \pm 0.01$ ,  $p < 0.01$ ), suggesting a stronger impact of drought in the last five decades. As expected, the effect of DBH<sub>ts</sub> was reduced substantially in the time window 1970-2019 ( $0.02 \pm 0.02$ ), confirming the smaller effect of size on growth in mature beech trees (Bontemps et al., 2010; Podlaski, 2002). Finally, in the growth model with the time window 2015-2019 vitality had the strongest effect compared to all the other variables of all three time windows ( $0.62 \pm 0.12$ ,  $p < 0.01$ ), which may reflect the drastic decline in growth which the unvital trees have undergone in the last five years. It is important to note, that in this growth model CI was included and had a notable significant negative impact on the BAI ( $0.16 \pm 0.06$ ,  $p < 0.05$ ). From this result two implications emerged. The first is the influence of competition in a context where water availability is limited. Under high competition regimes, beech trees seem to be more impacted by climatic water stress (Cescatti and Piutti, 1998), in particular in pure beech stands (Metz et al., 2016; Mölder and Leuschner, 2014; Schwarz and Bauhus, 2019). The second implication is that the competition experienced by our target trees reflects only the after-thinning period. The stand density and consequent competition experienced by our sampled trees was thus higher before the 2015 thinning. Thus, future research projects could concentrate on implementing past competition in our growth model to investigate what effect this may had on tree growth.

## 4.5 Limitations

While this study has shown some interesting results on the impact of drought on growth, it is important to note its limitations. As emerged in the discussion, one important limitation was the absence of a reliable long-term competition index. Although the site chosen for the study was suitable for the thesis, a forest site with no recent intervention may have been a better choice, allowing us to account for a long-term competition index. Moreover, a comparison with another stand is missing, although this was initially planned with the forest site of Vogtacher. The time-consuming process of preparing and especially measuring some difficult increment cores precluded the opportunity to measure the increment cores of the Vogtacher site. This impacted the sample size of the study, which was reduced by 36 trees. Furthermore, the inclusion of other species such as common and sessile oak may enable conclusions about the drought responses of other economically important tree species (Abegg et al., 2014; Metz et al., 2016). Finally, soil data could enhance the explanatory power of the constructed growth models. Many other similar studies (Braun et al., 2017; DeSoto et al., 2020; Mölder and Leuschner, 2014) included different soil proprieties in their researched and demonstrated close relationships between soil and physiological aspects of the life of beech trees.

## Chapter 5

# Conclusions

Beech trees in the region around Basel showed a declining growth trend in the last three decades. This decline was more pronounced in the trees that showed clear signs of drought-induced early leaf shedding or discolouration. On the contrary, trees that looked healthy and vital had a higher basal area increment than unvital trees in the last five decades, despite showing a slow decline in the last two decades. This declining growth trend emerged in many stands across Europe (Aertsen et al., 2014; Bontemps et al., 2010; Braun et al., 2017; Gillner et al., 2013; Schwarz and Bauhus, 2019; Zimmermann et al., 2015). Unvital beech trees may have been more sensitive to cavitation due to drought and water shortage and unable to restore their hydraulic system due to reduced carbohydrates production caused by the reduction of photosynthesis capacity following the loss in foliage mass (McDowell et al., 2013). Using a response and correlation function analysis it resulted that both vital and unvital trees responded negatively to summer drought and positive to spring and summer precipitation, confirming that beech trees are sensitive to climatic water deficit. However, no significant difference in the climatic response was found between vital and unvital trees.

The superposed epoch analysis confirmed the strong impact that past drought events had on our target trees. The two years following the drought events showed a strong recovery of growth, in particular for unvital trees, which was unexpected. A decline in growth was observed three years after the drought years. However, it is not clear if this is due to a lagged-impact of drought (Zimmermann et al., 2015) or due to high temperature-induced masting (Vacchiano et al., 2017). In addition, the resilience to past drought of unvital trees showed a declining trend, suggesting an increased mortality risk in unvital trees (DeSoto et al., 2020).

From our growth models it resulted that recent and past drought played an important role in the growth process of the tree and that a significant difference in growth occurred between vital and unvital trees. Competition seemed also to have impacted the tree growth,

although evidence for this is limited in our study. Many other studies suggested a considerable negative effect of competition on tree growth, as well as an important positive admixing effect to reduce the impact of the drought events, in particular with sessile oak and other minor broadleaved tree species (Kunz et al., 2018; Metz et al., 2016; Schwarz and Bauhus, 2019).

We suppose that with more recurrent and intense drought events that may impact Switzerland in the future, beech trees are expected to be affected more frequently by summer droughts (Cavin and Jump, 2017; Geßler et al., 2007; Michelot et al., 2012). Further studies that analyse and compare the impact of drought on other species present in typical beech forest sites (Ellenberg-Klötzli 7\*\*) may help to have a broader perspective on possible future effects of drought on forests in Switzerland and Central Europe. Moreover, genetic studies on the drought effects on beech trees may help us understanding the phenological difference in beech trees that are withstanding drought impact better than others. Our findings, together with the results from previous studies, may help to add a little piece onto the current knowledge on how European beech forests may react to warmer and drier climate.

## Chapter 6

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# Chapter 7

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# Appendix A

## Map of the initial sites

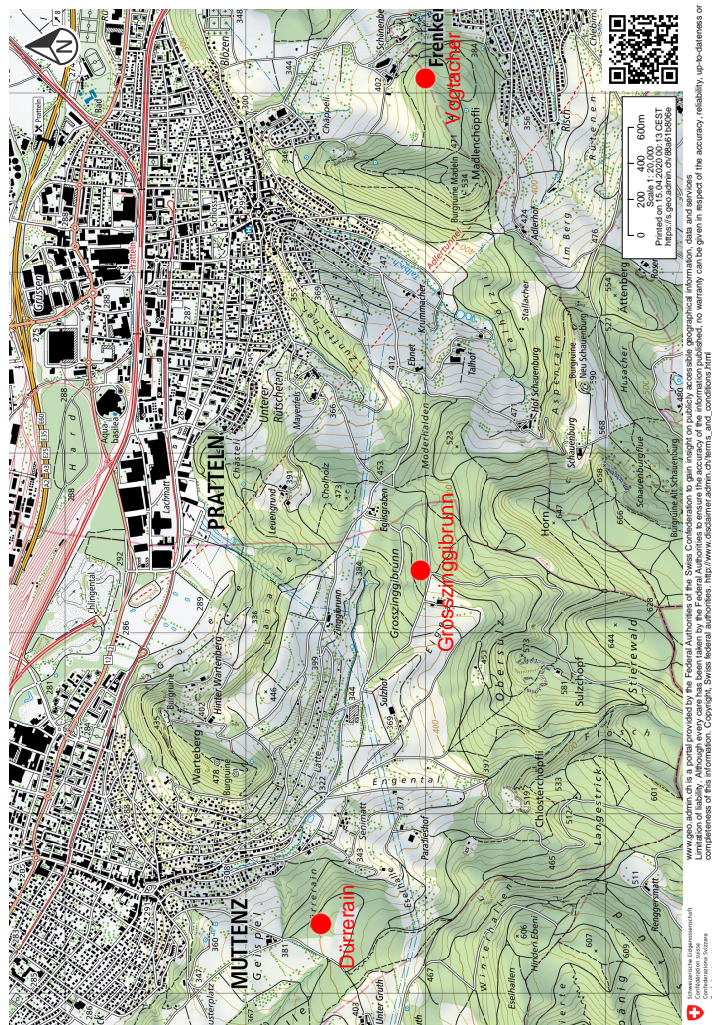


Figure A.1: Sites of Dürerrain, Grosszinggibrunn and Vogtacher were tree were marked.

## Appendix B

# Results of correlation and response function analyses

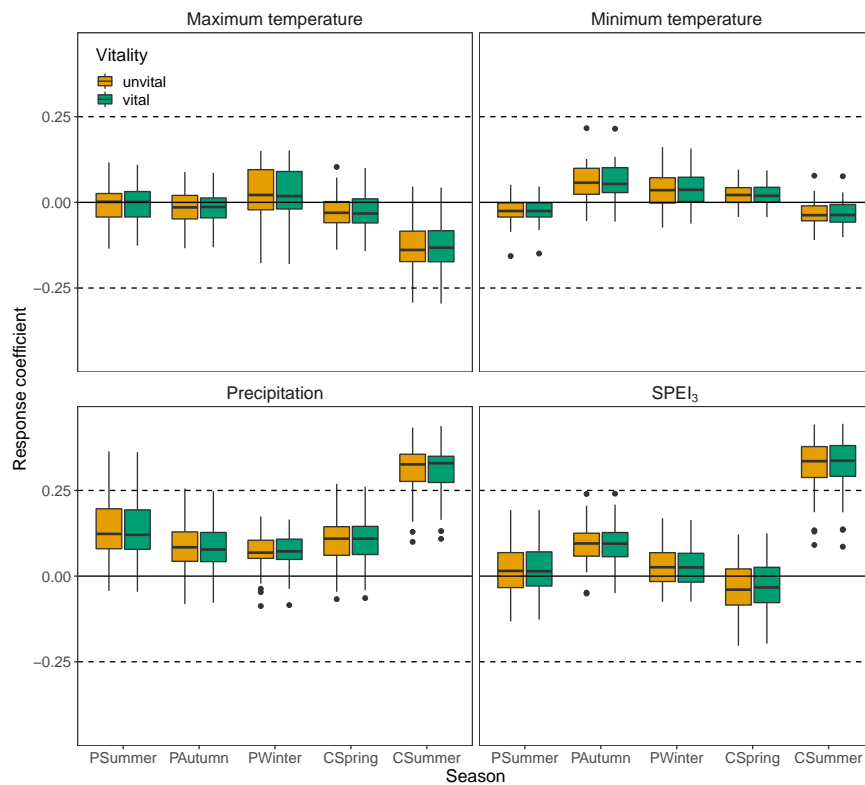


Figure B.1: Boxplots of response function coefficients calculated between tree-ring width of each individual vital and unvital tree and different climate variables computed at a seasonal scale from previous summer to current summer. Letter "P" is for "previous", while letter "C" is for "current".

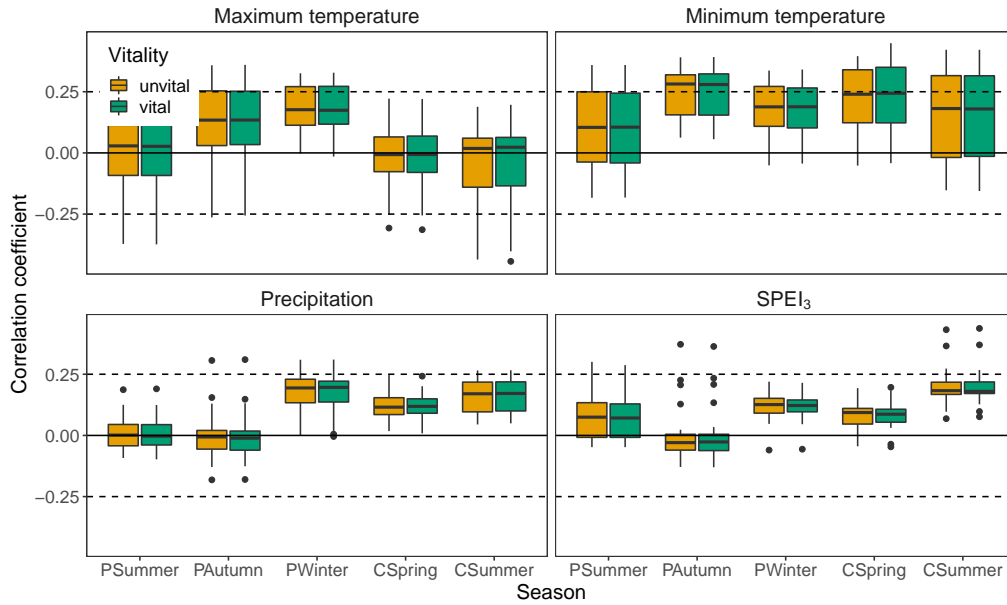


Figure B.2: Boxplots of correlation function coefficients calculated between basal area index (BAI) of each individual vital and unvital tree and different climate variables computed at a seasonal scale from previous summer to current summer. Letter "P" is for "previous", while letter "C" is for "current".

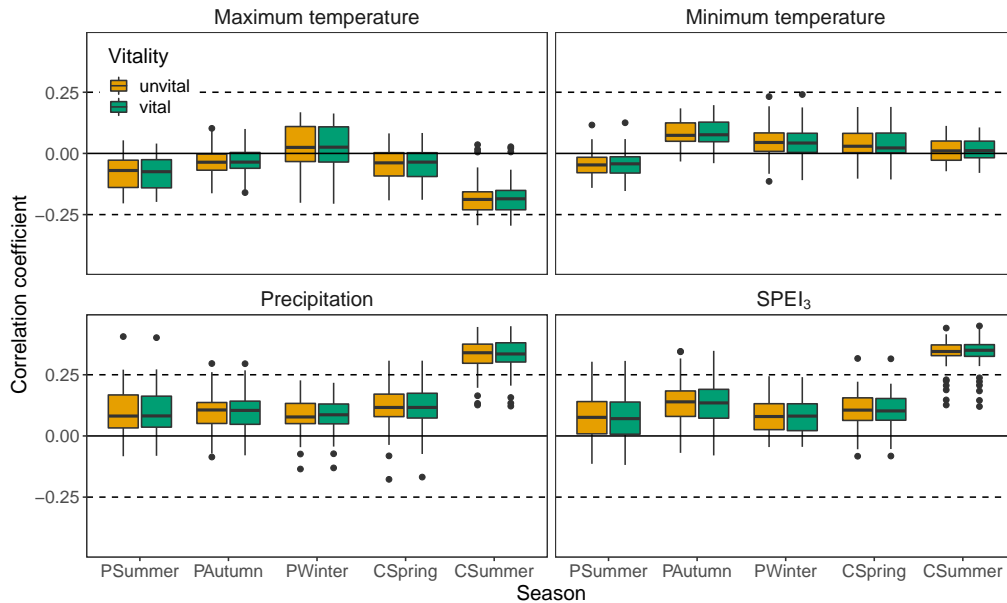


Figure B.3: Boxplots of correlation function coefficients calculated between tree-ring width of each individual vital and unvital tree and different climate variables computed at a seasonal scale from previous summer to current summer. Letter "P" is for "previous", while letter "C" is for "current".



# Appendix C

## Correlation matrices

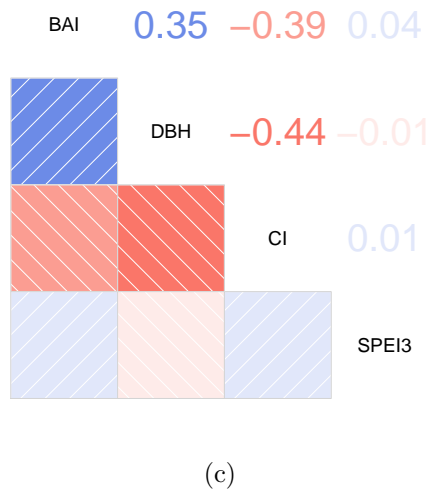
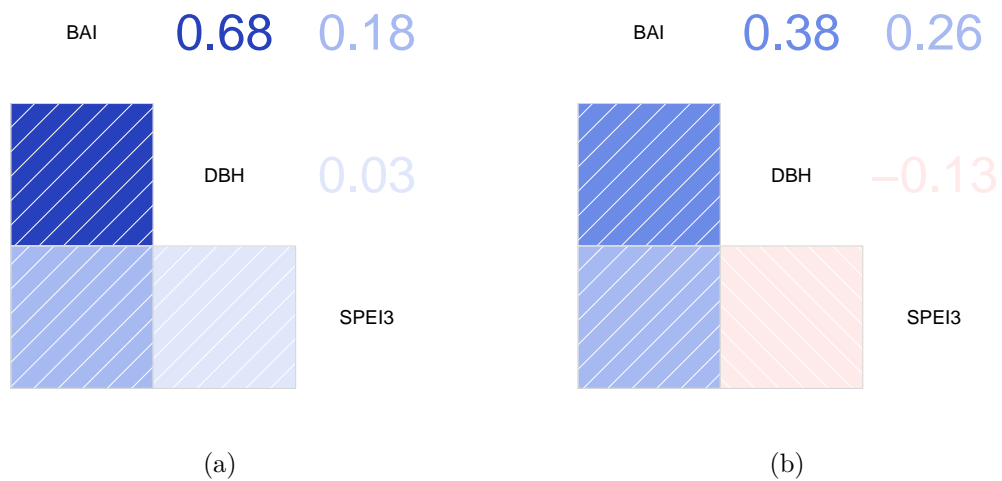
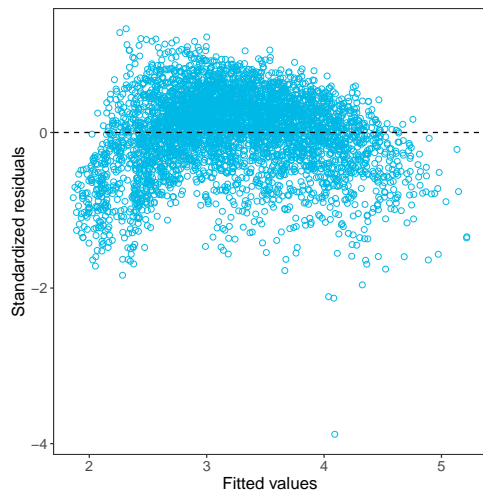


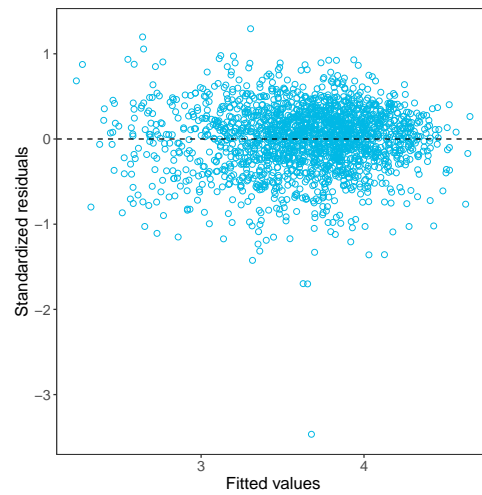
Figure C.1: Correlation matrices of models variables for the time windows (a) 1900-2019, (b) 1970-2019 and (c) 2015-2019. In blue are marked the positive correlations, while in red the negative correlations. Stronger colours suggest a stronger correlation than pale colors.

# Appendix D

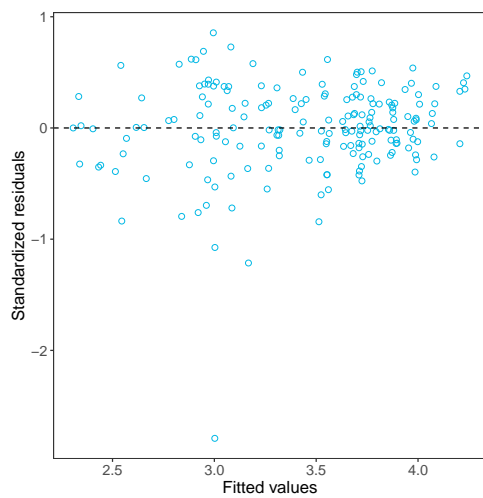
## Models' residuals



(a)



(b)



(c)

Figure D.1: Models' residuals for the time windows (a) 1900-2019, (b) 1970-2019 and (c) 2015-2019.

# Appendix E

## R code

```
#####  
## Michel Scheggia ##  
## Master's Thesis ##  
### 21 April 2020 ###  
#####  
  
# Main script #  
  
# This R script was built to analyse the impact of drought on vital and ↵  
  unvital beech trees in the region around Basel.  
# This script includes part of data preparation and the analysis. All ↵  
  the data necessary for the analysis will be imported at the ↵  
  beginning.  
# Although the data are already prepared, for the illustrative purpose, ↵  
  some of the preparation, such as the detrending of tree-ring width and ↵  
  the calculation of BAI, are presented anyway. The code to produce the ↵  
  plots is reported in another R script.  
  
# Set the working directory  
setwd("Y:/Documents/Master's_Thesis/R/Ranalysis")  
  
# Import libraries  
library(corrgram)  
library(dplR)  
library(dplyr)
```

```
library(ggplot2)
library(ggpubr)
library(graphics)
library(gridExtra)
library(MuMIn)
library(nlme)
library(pointRes)
library(reshape2)
library(SPEI)
library(stargazer)
library(tidyverse)
library(tidyr)
library(treeclim)

# Import all the dataframes
# Note: These data were prepared in previous scripts and formatted so ↵
that they can be used directly
climate_data <- read.table("climate_data.txt", header = TRUE, sep = ";" ↵
) # This combines the climate raw data obtained by MeteoSwiss and the ↵
calculated SPEI
tree_data <- read.table("tree_data.txt", header = TRUE, sep = ";")
tree_values <- read.csv("Tree_Values_GZB.csv", header = TRUE, sep = ";" ↵
)
GZB_series <- read.table("GZB_series.txt", header = TRUE, sep = ";")
  GZB_vital <- read.table("GZB_vital.txt", header = TRUE, sep = ";")
  GZB_unvital <- read.table("GZB_unvital.txt", header = TRUE, sep = ";")
  GZB_series_raw <- read.table("GZB_series_rwl.txt", header = TRUE, sep ↵
= ";")
BAI_series <- read.table("BAI_series.txt", header = TRUE, sep = ";")
  BAI_vital <- read.table("BAI_vital.txt", header = TRUE, sep = ";")
  BAI_unvital <- read.table("BAI_unvital.txt", header = TRUE, sep = ";")
DBH_recon <- read.csv("DBH_data.csv", header = TRUE, sep = ";")
completedf <- read.table("complete.txt", header = TRUE, sep = ";") # ↵
This combines the the tree data, the BAI and the values of resilience ↵
components

#####
```

```
# First part: detrending, calculation of BAI, calculation of CI and ↵
calculation of SPEI

# Import raw tree-ring width data (.rwl)
gzb_rwl <- read.rwl("GZB-series.rwl") # total
gzb_rwl_vital <- read.rwl("GZB-vital.rwl") # vital
gzb_rwl_unvital <- read.rwl("GZB-unvital.rwl") # unvital

# Detrend and standardise the raw tree-ring width
GZB_series <- detrend(rwl = gzb_rwl, method = c("Spline"), nyrs = 16, ↵
make.plot = TRUE) # total
  # Detrend and standardize the vital and unvital trees separately
  GZB_vital <- detrend(rwl = gzb_rwl_vital, method = c("Spline"), nyrs = ↵
  16, make.plot = TRUE) # vital
  GZB_unvital <- detrend(rwl = gzb_rwl_unvital, method = c("Spline"), ↵
  nyrs = 16, make.plot = TRUE) # unvital

# Calculate Basal Area Increment (BAI) with Inside Out method:
diam <- tree_values
diam <- diam %>% select(2, 3)
# Convert DBH from cm in mm and subtracting the bark (approximated to ↵
10 mm)
diam$DBH <- (diam$DBH * 10) - 10

# Group the vital and unvital ones
diam_vital <- diam[c(1:5,7,8,10,11,14,15,19,21,23:27,33,35,36),]
diam_unvital <- diam[c(6,9,12,13,16:18,20,22,28:32,34,37,38),]

# Calculate the BAI
oibai_series <- bai.out(gzb_rwl, diam = diam)
  # Calculate the BAI for vital and unvital trees separately
  oibai_vital <- bai.out(gzb_rwl_vital, diam = diam_vital)
  oibai_unvital <- bai.out(gzb_rwl_unvital, diam = diam_unvital)

# Convert BAI in cm2
oibai_series <- oibai_series/100
oibai_vital <- oibai_vital/100
```

```
oibai_unvital <- oibai_unvital/100

# Calculation of competition index (CI)

# Select the columns useful to calculate the Competition Index (CI) (ID ↵
, Target-Tree-DBH, Competition-Tree-data)
comp.table <- tree_values[, c ↵
(2,3,10,12,14,16,18,20,22,24,26,28,30,32,34,36,38,40,42,44)]

# Create a template for the CI table
comp.index.table <- comp.table
comp.index.table[,2:20] <- NULL

# Calculate the CI between the target tree and each competitor
comp.index.table$first_comp <- comp.table$N_Tree_1_DBH/(comp.table$DBH* ↵
comp.table$N_Tree_1_distance)
comp.index.table$second_comp <- comp.table$N_Tree_2_DBH/(comp.table$DBH ↵
*comp.table$N_Tree_2_distance)
comp.index.table$third_comp <- comp.table$N_Tree_3_DBH/(comp.table$DBH* ↵
comp.table$N_Tree_3_distance)
comp.index.table$fourth_comp <- comp.table$N_Tree_4_DBH/(comp.table$DBH ↵
*comp.table$N_Tree_4_distance)
comp.index.table$fifth_comp <- comp.table$N_Tree_5_DBH/(comp.table$DBH* ↵
comp.table$N_Tree_5_distance)
comp.index.table$sixth_comp <- comp.table$N_Tree_6_DBH/(comp.table$DBH* ↵
comp.table$N_Tree_6_distance)
comp.index.table$seventh_comp <- comp.table$N_Tree_7_DBH/(comp.table$ ↵
DBH*comp.table$N_Tree_7_distance)
comp.index.table$eighth_comp <- comp.table$N_Tree_8_DBH/(comp.table$DBH ↵
*comp.table$N_Tree_8_distance)
comp.index.table$ninth_comp <- comp.table$N_Tree_9_DBH/(comp.table$DBH* ↵
comp.table$N_Tree_9_distance)

# Calculate the CI for the target tree (sum of the CI of single trees)
comp.index.sum <- as.data.frame(rowSums(comp.index.table[2:10], na.rm = ↵
TRUE))
```

```
# Create a data frame with all the target tree data and CI (excluding
the other competitors information)
tree_data <- cbind(tree_values[,2:8], comp.index.sum)
names(tree_data)[8] <- "CI"

# Create a "vitality" variable
tree_data$vitality <- ifelse(tree_data$Vitality_class == "<20", "
unvital", "vital")

# Delete variable not useful variables (age, crown_portion and vitality_
class)
tree_data$Crown_portion <- NULL
tree_data$Vitality_class <- NULL
tree_data$Age <- NULL

# Separated CI for vital and unvital trees
tree_vital_ci <- tree_data[c(1:5,7,8,10,11,14,15,19,21,23:27,33,35,36)
,]
tree_unvital_ci <- tree_data[c(6,9,12,13,16:18,20,22,28:32,34,37,38),]

# Calculate CI mean and standard deviation
mean(tree_vital_ci$CI)
mean(tree_unvital_ci$CI)
sd(tree_vital_ci$CI)
sd(tree_unvital_ci$CI)

# Climate data and calculation of drought index (SPEI)

# Precipitation
prec <- read.table("Precipitation-homogeneous_monthly_total.txt",
header = TRUE, sep = ";")
prec <- select(prec, starts_with("rhs"))

# Adding the year and the month in two separate columns
prec$year <- rep(1900:2019, times=1, each=12)
prec$month <- rep(1:12)

# Reorder the columns
```

```
prec <- prec[, c(2, 3, 1)]
names(prec)[3] <- "precipitation"

# maximum temperature
temp_max <- read.table("Air_temperature_2m-absolute_monthly_maximum.txt",
", header = TRUE, sep = ";")
temp_max <- select(temp_max, starts_with("tre"))

# Adding the year and the month in two separate columns
temp_max$year <- rep(1900:2019, times=1, each=12)
temp_max$month <- rep(1:12)

# Reorder the columns
temp_max <- temp_max[, c(2, 3, 1)]
names(temp_max)[3] <- "tmax"

# Minimum temperature
temp_min <- read.table("Air_temperature_2m-absolute_monthly_minimum.txt",
", header = TRUE, sep = ";")
temp_min <- select(temp_min, starts_with("tre"))

# Adding the year and the month in two separate columns
temp_min$year <- rep(1900:2019, times=1, each=12)
temp_min$month <- rep(1:12)

# Reorder the columns
temp_min <- temp_min[, c(2, 3, 1)]
names(temp_min)[3] <- "tmin"

# Mean temperature
temp_mean <- read.table("Air_temperature_2m-monthly_mean.txt", header =
TRUE, sep = ";")
temp_mean <- select(temp_mean, starts_with("tre"))

# Adding the year and the month in two separate columns
temp_mean$year <- rep(1900:2019, times=1, each=12)
temp_mean$month <- rep(1:12)

# Reorder the columns
```



```
temp_mean <- temp_mean[, c(2, 3, 1)]
names(temp_mean)[3] <- "tmean"

# Calculate Potential Evapotranspiration (PET) with Hargreaves
pet <- hargreaves(temp_min[,3], temp_max[,3], lat = 47.541133434233,
  Pre = prec[,3])

# Calculate climatic water balance
cwb <- prec[,3] - pet

# Calculate the drought index (SPEI withn different time lags)
spei1 <- spei(cwb, 1)
spei1_ts <- spei1$fitted
spei2 <- spei(cwb, 2)
spei2_ts <- spei2$fitted
spei3 <- spei(cwb, 3)
spei3_ts <- spei3$fitted
spei4 <- spei(cwb, 4)
spei4_ts <- spei4$fitted
spei5 <- spei(cwb, 5)
spei5_ts <- spei5$fitted
spei6 <- spei(cwb, 6)
spei6_ts <- spei6$fitted
spei7 <- spei(cwb, 7)
spei7_ts <- spei7$fitted
spei8 <- spei(cwb, 8)
spei8_ts <- spei8$fitted
spei9 <- spei(cwb, 9)
spei9_ts <- spei9$fitted
spei10 <- spei(cwb, 10)
spei10_ts <- spei10$fitted
spei11 <- spei(cwb, 11)
spei11_ts <- spei11$fitted
spei12 <- spei(cwb, 12)
spei12_ts <- spei12$fitted

# Put SPEI as whole table
```

```
spei_all <- cbind(spei1_ts, spei2_ts, spei3_ts, spei4_ts, spei5_ts, ↵
spei6_ts, spei7_ts, spei8_ts, spei9_ts, spei10_ts, spei11_ts, spei12_ts ↵
)
spei_all <- data.frame(spei_all)

# Join all the climat data together
climate_data <- cbind(prec, temp_mean[,3], temp_max[,3], temp_min[,3], ↵
spei_all)
names(climate_data)[4] <- "tmean"
names(climate_data)[5] <- "tmax"
names(climate_data)[6] <- "tmin"

# Select the variables we want to use (precipitation, tmean, tmax, tmin ↵
, spei3)
climate_data <- climate_data[,c(1:6,9)]

# Building one dataframe with summer values (June to August)
summer_month <- climate_data %>% subset(month %in% c(6, 7, 8))
summer_month <- summer_month %>% group_by(year) %>% summarise(SPEI3 = ↵
mean(spei3_ts))

#####

# Second part: correlation and response function
# In order to spare space, we reported only the corr/resp function for ↵
growth
# To do it for BAI just substitute (ctrl+f) the data frame "GZB_xxx" ↵
from the for loop and the dcc parameter with "BAI_xxx"
# Thus, there are two sections for this part, instead of four:
# - correlation function with growth data (trw)
# - response function with growth data (trw)

# Bootstrapped correlations between trw and seasonal climate variables ↵
for UNVITAL trees
cor_list_unvital <- list()

for(j in 1:ncol(GZB_unvital)) {
  for(i in seq(3, ncol(climate_data))) {
```

```

cor_list_unvital[[paste(colnames(GZB_unvital[j]), colnames(climate_
data[i])))] <-
  dcc(GZB_unvital[, j, drop = FALSE], climate_data[-c(1:12), c(1, 2,
i)],
    selection = .mean(-6:-8) + .mean(-9:-11) + .mean(-12:2) + .
mean(3:5) + .mean(6:8),
    method = "correlation", ci = 0.05, boot = "std", var_names =
colnames(climate_data[i]))
}
}

# Create a data frame with correlation coefficients
cor_list_unvital_coef <- lapply(cor_list_unvital, function(x) x[["coef"
]])
cor_unvital_df <- do.call(rbind.data.frame, cor_list_unvital_coef)
cor_unvital_df$treeid <- substring(rownames(cor_unvital_df), first = 1,
last = 3)
cor_unvital_df$vitality <- "unvital"

# Bootstrapped correlations between trw and seasonal climate variables
for VITAL trees
cor_list_vital <- list()

for(j in 1:ncol(GZB_vital)) {
  for(i in seq(3, ncol(climate_data))) {
    cor_list_vital[[paste(colnames(GZB_vital[j]), colnames(climate_data[
i])))] <-
      dcc(GZB_vital[, j, drop = FALSE], climate_data[-c(1:12), c(1, 2, i
)],
        selection = .mean(-6:-8) + .mean(-9:-11) + .mean(-12:2) + .
mean(3:5) + .mean(6:8),
        method = "correlation", ci = 0.05, boot = "std", var_names =
colnames(climate_data[i]))
  }
}

# Create a data frame with correlation coefficients
cor_list_vital_coef <- lapply(cor_list_vital, function(x) x[["coef"]])

```

---

```

cor_vital_df <- do.call(rbind.data.frame, cor_list_vital_coef)
cor_vital_df$treeid <- substring(rownames(cor_vital_df), first = 1, ↵
last = 3)
cor_vital_df$vitality <- "vital"

# bind unvital and vital data frames in one
cor_df_all <- bind_rows(cor_unvital_df, cor_vital_df)
cor_df_all$month <- factor(cor_df_all$month, levels = c("jun...aug", " ↵
sep...nov", "dec...FEB", "MAR...MAY", "JUN...AUG"),
      labels = c("prev.summer", "prev.autumn", "prev. ↵
winter", "current.spring", "current.summer"))
cor_df_all$varname <- factor(cor_df_all$varname,
      levels = c("precipitation.mean", "tmean.mean" ↵
, "tmax.mean", "tmin.mean", "spei3_ts.mean"),
      labels = c("precipitation", "tmean", "tmax", ↵
"tmin", "spei3_ts"))
names(cor_df_all)[3] <- "season"
rownames(cor_df_all) <- 1:nrow(cor_df_all)

# Bootstrapped response function between trw and monthly climate ↵
variables for UNVITAL trees
resfunc_list_unvital <- list()

for(j in 1:ncol(GZB_unvital)) {
  for(i in seq(3, ncol(climate_data))) {
    resfunc_list_unvital[[paste(colnames(GZB_unvital[j]), colnames( ↵
climate_data[i])))] <-
      dcc(GZB_unvital[, j, drop = FALSE], climate_data[-c(1:12), c(1, 2, ↵
i)],
        selection = .mean(-6:-8) + .mean(-9:-11) + .mean(-12:2) + . ↵
mean(3:5) + .mean(6:8),
        method = "response", ci = 0.05, boot = "std", var_names = ↵
colnames(climate_data[i]))
  }
}

# Create a data frame with response coefficients

```

```

respfunc_list_unvital_coef <- lapply(respfunc_list_unvital, function(x) ↵
  x[["coef"]])
respfunc_unvital_df <- do.call(rbind.data.frame, respfunc_list_unvital_ ↵
coef)
respfunc_unvital_df$treeid <- substring(rownames(respfunc_unvital_df), ↵
first = 1, last = 3)
respfunc_unvital_df$vitality <- "unvital"

# Bootstrapped response function between trw and monthly climate ↵
variables for VITAL trees
respfunc_list_vital <- list()

for(j in 1:ncol(GZB_vital)) {
  for(i in seq(3, ncol(climate_data))) {
    respfunc_list_vital[[paste(colnames(GZB_vital[j]), colnames(climate_ ↵
data[i])))] <-
      dcc(GZB_vital[, j, drop = FALSE], climate_data[-c(1:12), c(1, 2, i ↵
)],
        selection = .mean(-6:-8) + .mean(-9:-11) + .mean(-12:2) + . ↵
mean(3:5) + .mean(6:8),
        method = "response", ci = 0.05, boot = "std", var_names = ↵
colnames(climate_data[i]))
  }
}

# Create a data frame with response coefficients
respfunc_list_vital_coef <- lapply(respfunc_list_vital, function(x) x[[ ↵
"coef"]])
respfunc_vital_df <- do.call(rbind.data.frame, respfunc_list_vital_coef ↵
)
respfunc_vital_df$treeid <- substring(rownames(respfunc_vital_df), ↵
first = 1, last = 3)
respfunc_vital_df$vitality <- "vital"

# bind unvital and vital data frames in one
respfunc_df_all <- bind_rows(respfunc_unvital_df, respfunc_vital_df)
respfunc_df_all$month <- factor(respfunc_df_all$month, levels = c("jun ↵
...aug", "sep...nov", "dec...FEB", "MAR...MAY", "JUN...AUG"),

```

```

        labels = c("prev.summer", "prev.autumn", "prev.winter", "current.spring", "current.summer"))
resfunc_df_all$varname <- factor(resfunc_df_all$varname,
        levels = c("precipitation.mean", "tmean.mean", "tmax.mean", "tmin.mean", "spei3_ts.mean"),
        labels = c("precipitation", "tmean", "tmax", "tmin", "spei3_ts"))
names(resfunc_df_all)[3] <- "season"
rownames(resfunc_df_all) <- 1:nrow(resfunc_df_all)

# Calculate summer mean and standard deviation for corr/resp function with SPEI
cor_mitt <- cor_df_all %>% subset(varname == "spei3_ts")
cor_mitt <- cor_mitt %>% subset(season == "current.summer")
summarise(cor_mitt, mean = mean(coef))
summarise(cor_mitt, sd = sd(coef))

resp_mitt <- resfunc_df_all %>% subset(varname == "spei3_ts")
resp_mitt <- resp_mitt %>% subset(season == "current.summer")
summarise(resp_mitt, mean = mean(coef))
summarise(resp_mitt, sd = sd(coef))

#####

# Third part: Superposed Epoch Analysis (SEA) and resilience components

# SEA with pointer years 1947, 1976, 2003, 2011
sea.vital <- sea(GZB_vital, key = c(1947, 1976, 2003, 2011), lag = 4, resample = 1000)
sea.unvital <- sea(GZB_unvital, key = c(1947, 1976, 2003, 2011), lag = 4, resample = 1000)

# Creating vitality factor
sea.vital$vitality <- "vital"
sea.unvital$vitality <- "unvital"

```

```
# Joining the two data frames
sea.both <- bind_rows(sea.vital, sea.unvital)

# Building the significance breakpoints
sea.both$signif <- symnum(sea.both$p, corr = FALSE, na = FALSE,
  cutpoints = c(0, 0.001, 0.01, 1), symbols = c("***", "**", ""))

# Applying resilience component function (on TRW or raw TRW)
res_list <- res.comp(GZB_series)
#res_list <- res.comp(GZB_series_raw)

# Extracting resistance, recovery and resilience
resist <- as.data.frame(res_list$resist)
recov <- as.data.frame(res_list$recov)
resil <- as.data.frame(res_list$resil)

# Extracting the pointer years
re_list <- completedf %>% subset(year == 1947 | year == 1976 | year ==
  2003 | year == 2011)

# Summarise re_list
summarise(re_list, mean = mean(na.omit(recov.val)))
summarise(re_list, sd = sd(na.omit(recov.val)))
summarise(re_list, mean = mean(na.omit(resil.val)))
summarise(re_list, sd = sd(na.omit(resil.val)))
summarise(re_list, mean = mean(na.omit(resist.val)))
summarise(re_list, sd = sd(na.omit(resist.val)))

#####

# Forth part: models

# Creating a data frame with time window 1970-2019
completedf1970 <- completedf %>% subset(year > 1969)

# Creating a data frame with time window 2015-2019
completedf2015 <- completedf %>% subset(year > 2014)
```

```
# Subsetting the needed variables
completedf[, c(3, 4, 5)] <- NULL
completedf1970[, c(3, 4,5)] <- NULL
completedf2015[, c(3, 4, 5)] <- NULL

# To have a smoother analysis delete all the "NA"
completedf <- na.omit(completedf)
completedf1970 <- na.omit(completedf1970)
completedf2015 <- na.omit(completedf2015)

# Correlation matrix (here named PCA, although is not really a PCA...). ↵
This produces also the plots
pca_order <- c("BAI", "DBH", "SPEI3")
pca_order2015 <- c("BAI", "DBH", "CI", "SPEI3")
pca_complete <- corrgram(completedf[pca_order], upper.panel = panel.cor ↵
)
pca_1970 <- corrgram(completedf1970[pca_order], upper.panel = panel.cor ↵
)
pca_2015 <- corrgram(completedf2015[pca_order2015], upper.panel = panel ↵
.cor)

# Summary of the data frames
summarycomplete <- summary(completedf)
str(completedf)
summary1970 <- summary(completedf1970)
str(completedf1970)
summary2015 <- summary(completedf2015)
str(completedf2015)

# Now, let's build the model!

# Fit the model without CI for the first two time windows
form <- formula(log(BAI+1) ~ scale(DBH) + Necrosis + vitality + scale( ↵
SPEI3) + scale(SPEI3) * scale(DBH) + vitality * scale(SPEI3))

## Model for the time window 1900-2019
```



```
mlme_series <- lme(form, random = ~ 1 | Tree_ID, correlation = corAR1() ↵
, method = "REML", data = completedf)
plot(mlme_series)
summary(mlme_series)
r.squaredGLMM(mlme_series)

# To reduce the complexity of the model we exclude the less significant ↵
variables. We apply the maximum likelihood method
mlme.full_series <- lme(form, random = ~ 1 | Tree_ID, correlation = ↵
corAR1(), method = "ML", data = completedf, na.action = na.omit)

# Removing the variables...
mlme.a_series <- update(mlme.full_series, .~. -Necrosis )
summary(mlme.a_series)
anova(mlme.full_series, mlme.a_series)

mlme.b_series <- update(mlme.a_series, .~. -vitality:scale(SPEI3) )
summary(mlme.b_series)
anova(mlme.full_series, mlme.b_series)

# Final model recalculated with REML method
mlme.final_series <- lme(log(BAI+1) ~ scale(DBH) + vitality + scale( ↵
SPEI3) + scale(SPEI3) * scale(DBH),
                      random = ~ 1 | Tree_ID, correlation = corAR1(), ↵
                      method = "REML", data = completedf)
plot(mlme.final_series)
summary(mlme.final_series)
r.squaredGLMM(mlme.final_series)

## Model for the time window 1970-2019
# The removal of variables did not improve model performance. Thus, ↵
this is also the final model
mlme_1970 <- lme(form, random = ~ 1 | Tree_ID, correlation = corAR1(), ↵
method = "REML", data = completedf1970)
plot(mlme_1970)
summary(mlme_1970)
r.squaredGLMM(mlme_1970)
```

```
# This part was actually not used, because the model performance did not improve. Still, for future necessities.
# To reduce the complexity of the model we exclude the less significant variables. We apply the maximum likelihood method
mlme.full_1970 <- lme(form, random = ~ 1 | Tree_ID, correlation = corAR1(), method = "ML", data = completedf1970, na.action = na.omit)

# Removing the variables...
mlme.a_1970 <- update(mlme.full_1970, .~. -scale(DBH):scale(SPEI3) )
summary(mlme.a_1970)
anova(mlme.full_1970, mlme.a_1970)

mlme.b_1970 <- update(mlme.a_1970, .~. -scale(SPEI3):scale(DBH) )
summary(mlme.b_1970)
anova(mlme.full_1970, mlme.b_1970)

mlme.c_1970 <- update(mlme.b_1970, .~. -Necrosis )
summary(mlme.c_1970)
anova(mlme.full_1970, mlme.c_1970)

# Final model recalculated with REML method
mlme.final_1970 <- lme(log(BAI+1) ~ scale(DBH) + Necrosis + vitality + scale(SPEI3) + scale(SPEI3) * scale(DBH),
                      random = ~ 1 | Tree_ID, correlation = corAR1(), method = "REML", data = completedf1970)
plot(mlme.final_1970)
summary(mlme.final_1970)
r.squaredGLMM(mlme.final_1970)

# Fit the model with CI for the time windows 2015-2019
form_2015 <- formula(log(BAI+1) ~ scale(DBH) + Necrosis + vitality + scale(CI) + scale(SPEI3) + scale(SPEI3) * scale(DBH) +
                    scale(CI) * scale(DBH) + vitality * scale(SPEI3) + scale(CI) * scale(SPEI3))

## Model for the time window 2015-2019
```

```
mlme_2015 <- lme(form_2015, random = ~ 1 | Tree_ID, correlation = ↵
corAR1(), method = "REML", data = completedf2015)
plot(mlme_2015)
summary(mlme_2015)
r.squaredGLMM(mlme_2015)

# To reduce the complexity of the model we exclude the less significant ↵
variables. We apply the maximum likelihood method
mlme.full_2015 <- lme(form_2015, random = ~ 1 | Tree_ID, correlation = ↵
corAR1(), method = "ML",
                    data = completedf2015, na.action = na.omit)

# Removing the variables...
# These are different trials!
mlme.a_2015 <- update(mlme.full_2015, .~. -Necrosis )
summary(mlme.a_2015)
anova(mlme.full_2015, mlme.a_2015)

mlme.b_2015 <- update(mlme.a_2015, .~. -scale(CI):scale(SPEI3) )
summary(mlme.b_2015)
anova(mlme.full_2015, mlme.b_2015)

mlme.c_2015 <- update(mlme.b_2015, .~. -scale(DBH):scale(CI) )
summary(mlme.c_2015)
anova(mlme.full_2015, mlme.c_2015)

mlme.d_2015 <- update(mlme.c_2015, .~. -scale(DBH):scale(SPEI3) )
summary(mlme.d_2015)
anova(mlme.full_2015, mlme.d_2015)

mlme.e_2015 <- update(mlme.d_2015, .~. -scale(DBH) )
summary(mlme.e_2015)
anova(mlme.full_2015, mlme.e_2015)

mlme.f_2015 <- update(mlme.e_2015, .~. -vitality:scale(SPEI3) )
summary(mlme.f_2015)
anova(mlme.full_2015, mlme.f_2015)

# Final model recalculated with REML method
```

```
mlme.final_2015 <- lme(log(BAI+1) ~ scale(DBH) + vitality + scale(CI) + ↵  
  scale(SPEI3) + vitality * scale(SPEI3),  
                      random = ~ 1 | Tree_ID, correlation = corAR1(), ↵  
                      method = "REML", data = completedf2015)  
plot(mlme.final_2015)  
summary(mlme.final_2015)  
r.squaredGLMM(mlme.final_2015)
```





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