

Appendix A: Graphical visualisations

Chapter 3

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1 Introduction

The aim of this appendix is to highlight the importance of an appropriate graphical visualisation for modern ecological experiments such as diversity-functioning studies. Indeed, because of the complexity of their design and of the questions addressed, modern ecological experiments are best visualised with flexible tools that enable us to better understand our data and, as a consequence, to better understand the ecological processes underlying the observed patterns.

This appendix is divided into four sections. After this brief introduction, Section 2 aims to show the power of modern graphical packages. Section 3 introduces an important concept fundamental to the approach presented in this publication. In particular, this section highlights the differences between a marginal and a conditional approach. Finally, Section 4 discusses general aspects of the data visualisation for present ecological experiments.

2 Graphical analysis

This section represents the first step of any statistical analysis: The graphical visualisation of the data. The model that will be fitted to the data is a Linear Mixed Effects Model. We therefore display every potential predictor against the response variable. The examples presented here are based on data sets from two previously published studies. We will use the graphical **R** add-on package *lattice* (Sarkar, 2016).

The "Czech Republic" study

This study was carried out in a experimental forest in the Czech Republic where the species diversity of forest stands was manipulated by assembling trees of different species. In particular, four tree species (*Fagus sylvatica*, *Larix decidua*, *Picea abies* and *Quercus petraea*) were grown together in all possible combinations. There are 15 combinations of these species: Four monocultures, six two-species compositions, four three-species compositions and one full mixture of four species. Each combination was replicated three times, yielding 45 different experimental sites. In each site, six trees of each species were measured for radial growth (557 trees in total). Two cores were taken from each tree to measure annual growth (those were then averaged). For the sake of simplicity we analyse here growth in the period 1991-2000. Further details can be found in Chamagne et al. (2016).

The aim of this analysis is to understand the effects of diversity and species identity on radial growth. The latter was quantified as the width of annual growth rings. In addition, we want to estimate temporal and spatial asynchrony between species to better understand what could modulate the potential effects of diversity (see Appendix B). This experiment was run in semi-natural conditions, where planted trees were left to grow for decades with little human intervention. Therefore, this study can be considered to be half way between experimental and observational (Chamagne et al., 2016). It is thus important to consider possible sources of variation. For that reason, our model will also include stand density, tree age, tree basal area, and other variables. Below, each predictor is visualised against the response variable and discussed.

2.1 Visualising the response variable against the predictors

In this subsection we plot the log-transformed response variable against each potential predictor. This is radial growth which was measured as the yearly ring width. Taking the logarithm of response variables that can take only positive values is standard and recommended practice (Venables and Ripley, 2013; Sarkar, 2008; Limpert and Stahel, 2011). We start with continuous explanatory variables, and then look at categorical predictors¹.

Species diversity

The first explanatory variable presented here is **diversity**. This predictor is a continuous variable measured as the exponential of the Shannon Index. This biodiversity index was measured at site level (there are 45 sites; i.e. three replicates for each of the 15 species compositions). To start with, we use the basic plotting functions available in **R** (R Core Team, 2015). We use a scatterplot to visualise the marginal relationship between the two variables. On top of the scatterplot we add a regression line to better characterise their relationship.

```
plot(log10(ring) ~ diversity, data = d.20)
abline(lm(log10(ring) ~ diversity, data = d.20))
```

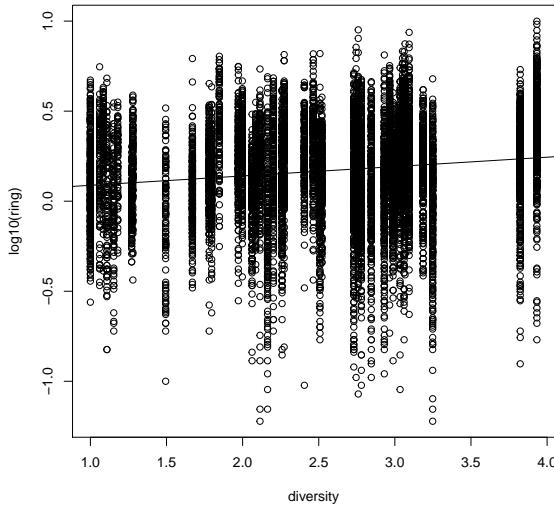


Figure 1: Response variable plotted against stand diversity. Basic R functions are used.

Although somewhat informative, this graph can largely be improved. As an example, we may want check whether different species react differently to the effect of stand diversity or tackle the problem of overplotting (i.e. overlapping observations). Improving this graph is feasible with basic **R** functions, however, this process would be very long and laborious. In the next page we present a similar graph obtained with the `xyplot()` function from *lattice* package.

¹The order in which we present predictors is arbitrary and solely based on the capabilities of *lattice* that we want to present.

As said above, we may want to inspect the relationship between diversity and annual growth independently for each species. This is achieved with the pipe (i.e. `|`) symbol shown at line (a) of the function call below. This notation specifies that a plot must be created for each level of the categorical variable `species` (i.e. the variable that codes species identity). Note that apart from few exceptions, the syntax of the `xyplot()` function is very similar to basic plotting functions. With the argument `type` at code line (b) we specify what has to be drawn. In this case we specify points "p" and a regression line "r".

```
require(lattice)
xyplot(log10(ring) ~ diversity | species, ## (a)
       type = c("p", "r"), ## (b)
       data = d.20)
```

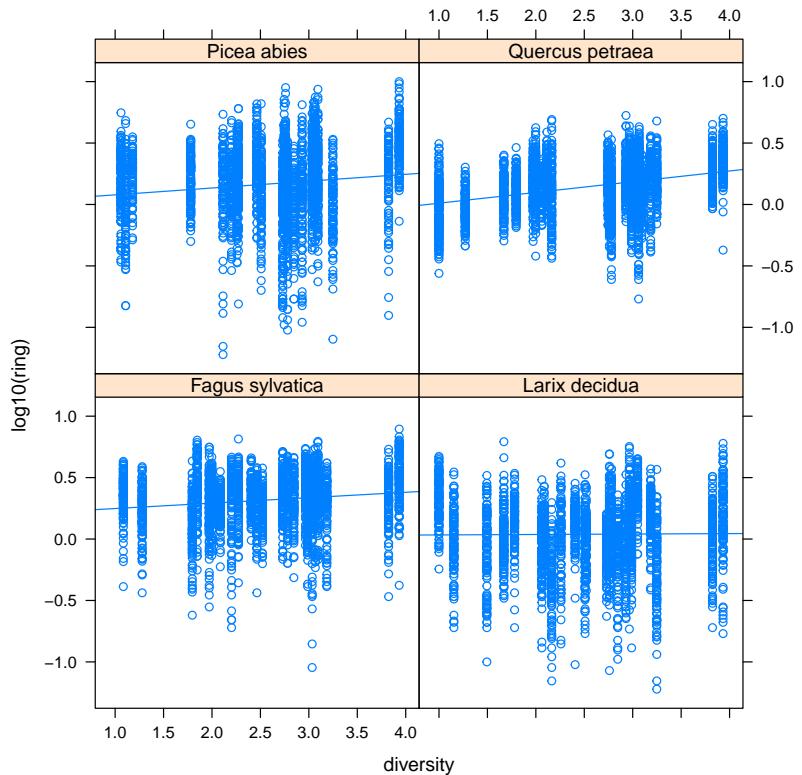


Figure 2: Response variable plotted against species diversity. The function `xyplot()` is used.

The relationship between response variable and predictor is now presented in four different panels. With this visualisation, we can inspect whether species respond differently to stand diversity. It really seems that species do differ in this respect. However, if the aim is to compare regression lines across panels, we make use of additional tools. In particular, in the next plot we will add a grid (`type = "g"`; line (a)) in the background to make comparisons across plots easier. We also change line colour (b) to make them stand out more.

Another important aspect to highlight here is that we are about to fit a Linear Mixed Effects Model. As their names says, Linear Models are linear in their coefficients,

nevertheless they can handle non-linear relationships. As an example, we may assume that the effect of diversity is quadratic and thus we could add a squared term to our model. However, in this first phase we are inspecting data, therefore it is important to avoid making too many assumptions. The obvious choice to characterise the relationship between two variables without making any assumption on its form is to use smoothers. Adding smoothers (a) to the plots instead of regression lines will enable us to evaluate whether the relationship can be considered to be linear or not.

```
xyplot(log10(ring) ~ diversity | species, data = d.20,
       type = c("p", "smooth", "g"), ## (a)
       col.line = "black") ## (b)
```

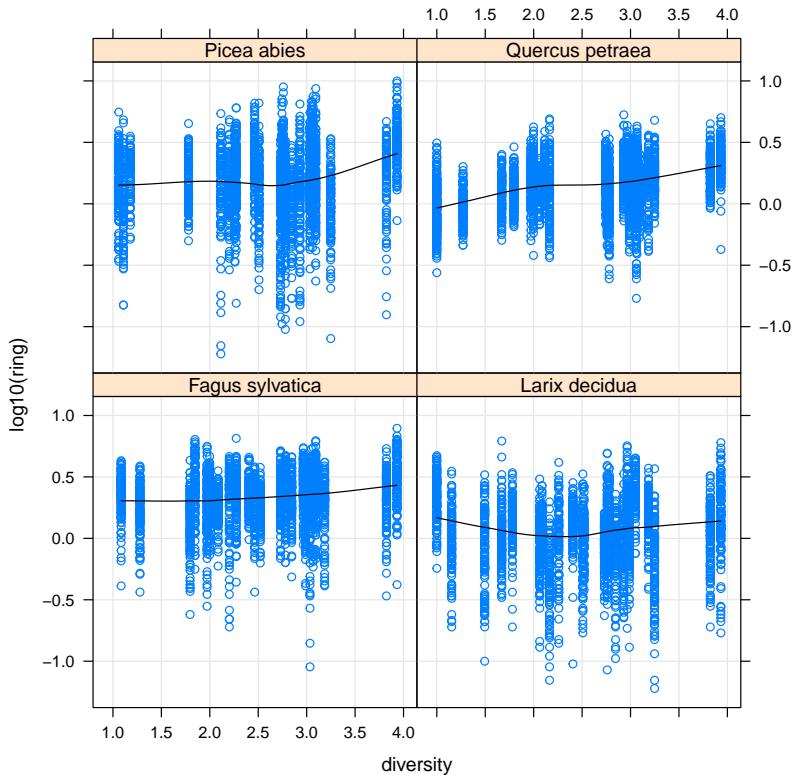


Figure 3: Response variable plotted against species diversity. Non-default arguments of `xyplot()` are used.

The smoothers shown here are not straight lines, suggesting that the effect of diversity may be non-linear. However, it is important to note that these are marginal plots where we control only for species identity. In other words, the apparently non-linear effect of diversity for the European larch (bottom right panel) may be due to the confounding effect of stand density. Ideally, we would like to add the information about all other predictors on this graph. Unfortunately, this is not possible as the graph would become overly complicated and unreadable.

Fitting Linear Models enables us to estimate conditional relationships. In other words, we can estimate the effect of, for example, species diversity while controlling for all the other predictors. In Appendix B we will show how to graphically display the conditional relationship between the response variable and the predictors for Linear

Models. This is done with the so called "partial residual plots" (Faraway, 2014).

Stand density

The next predictor inspected is `density`. This latter quantifies the density of trees within each site (i.e. each site). We first visualise its effects with the same settings used for the previous predictor.

```
xyplot(log10(ring) ~ density | species, data = d.20,
       type = c("p", "smooth", "g"),
       col.line = "black")
```

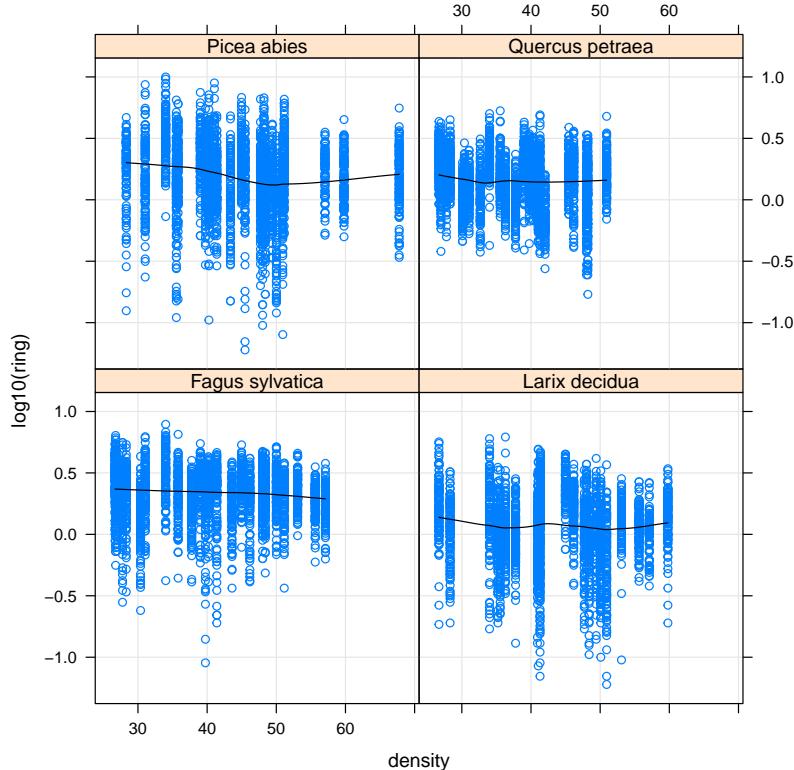


Figure 4: Response variable plotted against stand density.

The range of x-axes shows that the Norway spruce (top left panel) is present in denser areas. To make better use of the space we allow panels to have different x-ranges (a).

```
xyplot(log10(ring) ~ density | species, data = d.20,
       scales = list(x = list(relation = "free")), ## (a)
       type = c("p", "smooth", "g"),
       col.line = "black")
```

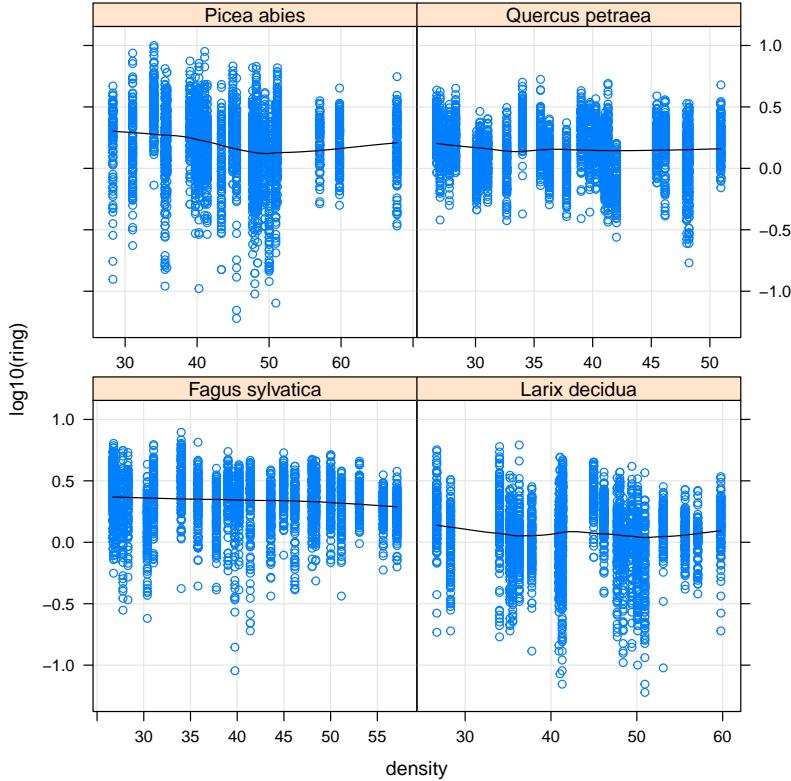


Figure 5: Response variable plotted against stand density. x-axes are allowed to differ among panels.

Not unexpectedly, density seems to have a (weak) negative effect on growth for all four species. Because we modified the x-axes we may also want to improve the appearance of the y-axes. The response variable has been log-transformed here. We may want to use a scale that enable us to understand the actual value of ring width without the need to back-transform values. To do that we can use the package *latticeExtra* (Sarkar and Andrews, 2016). This is achieved providing the untransformed response variable (a) and by specifying the scales need for the y-axes (b).

```
require(latticeExtra)
xyplot(ring ~ density | species, data = d.20,
       scales = list(y = list(log = 10)), ## (a)
       yscale.components = yscale.components.log10ticks, ## (b)
       type = c("p", "g", "smooth"),
       col.line = "black")
```

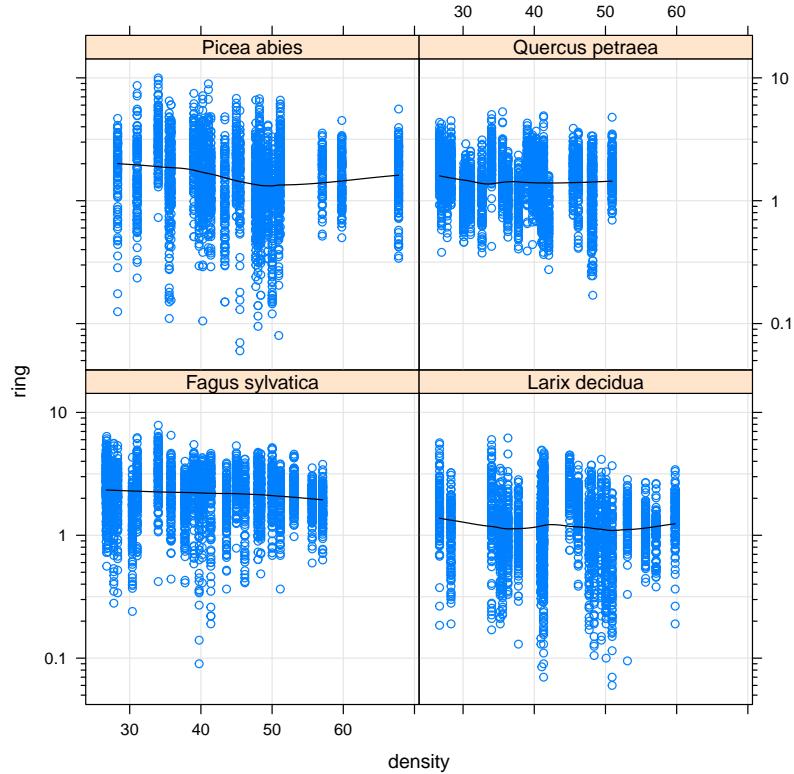


Figure 6: Response variable against stand density. y-axes use logarithmic scales.

From this plot, we can easily grasp the magnitude of ring widths, as the y-axes are in the original scale (i.e. millimetres)².

Basal area

Basal area is measured for each tree and is derived from the diameter measured at breast height. This predictor is expressed in centimetres squared. By looking at examples introduced so far it is clear that producing the best graph is an iterative process, where several options are changed at each step, and where we may even decide to revert back to original settings (as we did for the x-axes when looking at the effect of stand density). We may end up with a seemingly complex call by starting from a simple call where each piece is modified at each step (Sarkar, 2008). Rewriting a long function call can be annoying when we want to make a single small change. To overcome this issue modern graphical packages allow to store a function call into an **R**-object ready to be reused. This procedure is illustrated below with the predictor basal area.

```
xy.basal.area <- xyplot(log10(ring) ~ basal.area | species, data = d.20,
                           type = c("p", "g", "smooth"),
                           col.line = "black")
print(xy.basal.area)
```

²Note that in this plot we reverted back to use the same ranges for all x-axes as the difference in densities is an important pattern that we must keep in mind when interpreting the results of the statistical analysis.

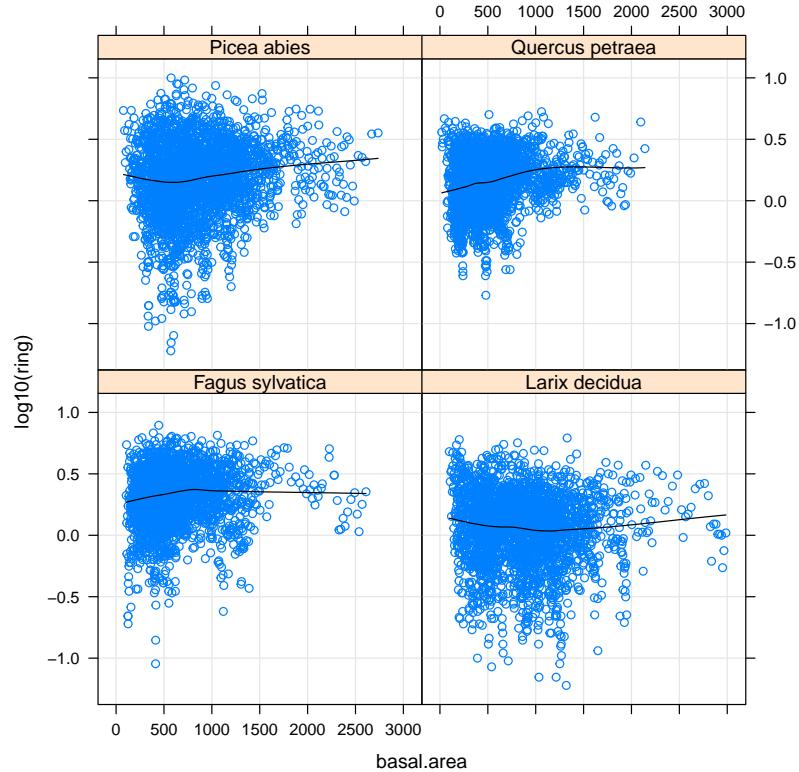


Figure 7: Response variable plotted against basal area.

When the function call is stored in an object the corresponding graph is not produced by default. In order to do that, we use the generic function `print()`. Figure 7 highlights a problem often encountered with large data sets: Overplotting. Many observations overlap making it difficult to draw strong conclusions on the relationship between these two variables. To alleviate this problem we can decrease symbol size. To do that, we can use the function call stored previously and adapt it via the generic function `update()`.

```
update(xy.basal.area, cex = 0.1)
```

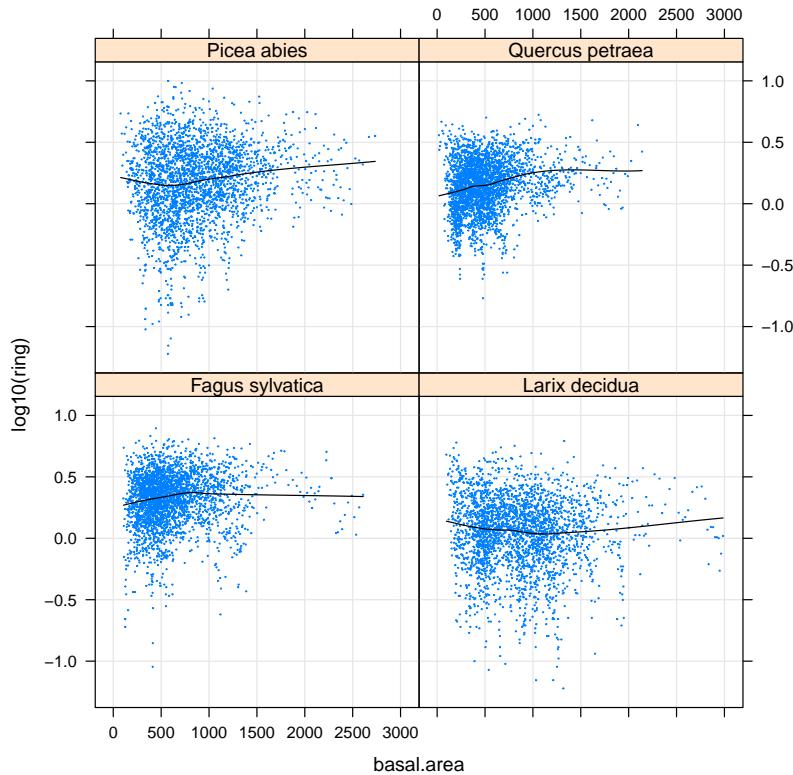


Figure 8: Response variable plotted against basal area. Symbols are drawn as small circles.

The use of `update()` is very handy as we can quickly modify an existing graph. This is another important advantage over basic plotting functions. Although the issue of overplotting is less severe, it is still present. At page 12 we will see how to use transparency to better deal with it.

Trees age

The age of the trees is included in the model as it has been shown to influence radial growth (Chamagne et al., 2016). Older trees are expected to grow slower.

```
xy.age <- xyplot(log10(ring) ~ age | species, data = d.20,
                   type = c("p", "g", "smooth"),
                   col.line = "black",
                   cex = 0.1)
print(xy.age)
```

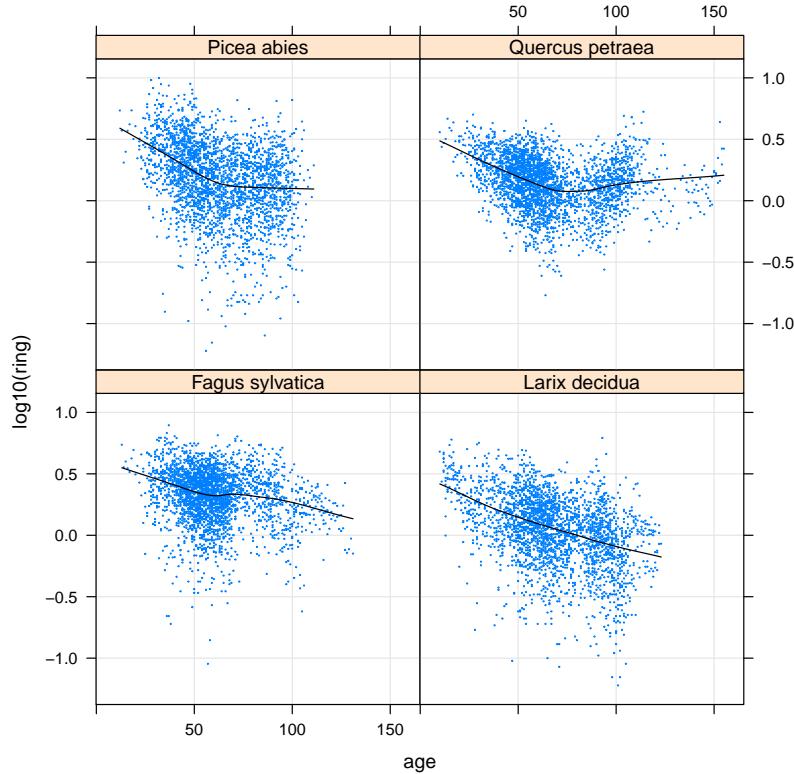


Figure 9: Response variable plotted against tree age.

As expected, there seems to be a negative relationship between radial growth and tree age. However, we observe a unexpected pattern on the panel showing the sessile oak (top right panel). Growth for trees older than 100 years does not seem to decrease, on the contrary growth seems to increase again. To better understand this pattern, we make use of another very powerful graphical technique "superposition" (or grouping). This consists of rendering observations associated with different levels of a grouping variable (e.g. `tree`), with different graphical characteristics. In particular, we connect the observations belonging to the same tree (a) with a coloured line (b). We use the argument `subset` to specify that we want to work only with sessile oak (c).

```
xy.age.2 <- xyplot(log10(ring) ~ age | species, data = d.20,
                     groups = tree, ## (a)
                     type = c("l", "g"), ## (b)
                     subset = species == "Quercus petraea") ## (c)

print(xy.age.2)
```

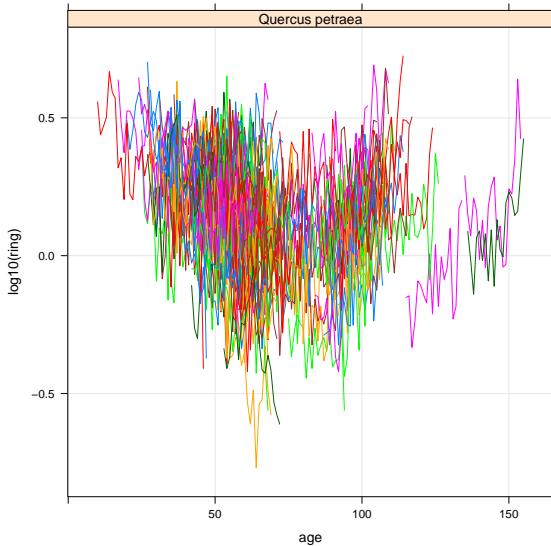


Figure 10: Response variable plotted against tree age for sessile oak. Trees are highlighted with colours.

With this visualisation it is now clearer that the observed pattern is mainly due to a few old trees behaving in an unexpected way. This visualisation is not entirely satisfying yet, as there is a lot of overlapping between lines. The next graph better copes with this issue.

Date (i.e. year of the ring)

The next predictor inspected is `date`. In this context this is a very important predictor as it is used to estimate temporal asynchrony. This latter is a quantity that estimates how species react to time fluctuations. In Figure 10 we used grouping to connect the observations that belong to the same tree. When the number of levels of the categorical variable used to define groups is large as it is the case for trees, using colours may not be fully satisfactory.

This situation is often encountered in the framework of Linear Mixed Effects Models, where we want to highlight random effects (e.g. here trees), but still obtaining a readable graph. A possible solution is to use transparency. Instead of using colours, all groups (i.e. trees) are rendered in black with some transparency. Transparency can be set via the argument `alpha`.

```
xypplot(log10(ring) ~ date | species, data = d.20,
        alpha = 0.2,
        col.line = "black",
        groups = tree, type = c("l", "g"))
```

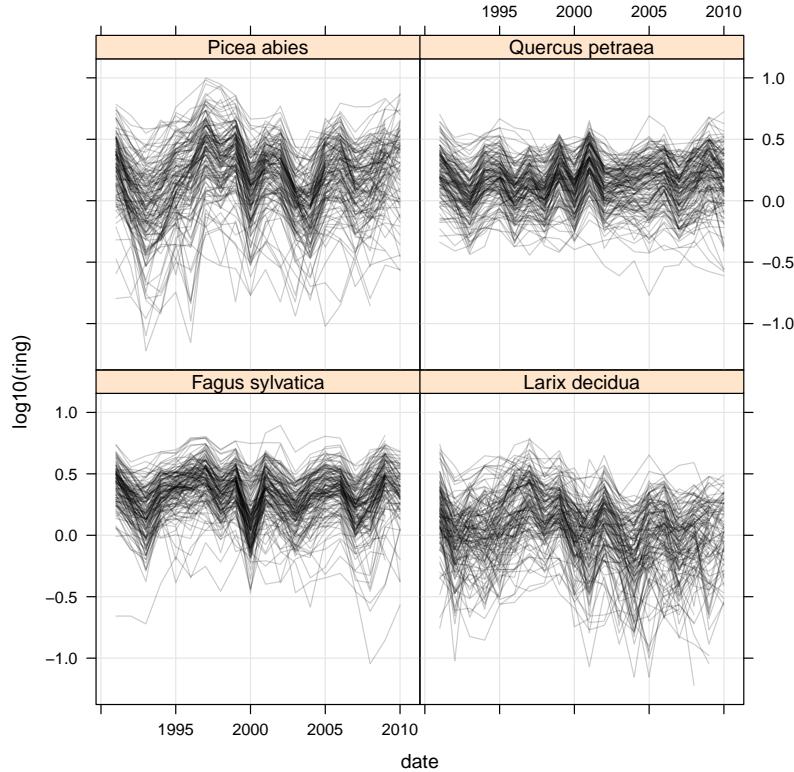


Figure 11: Response variable plotted against date. Trees are highlighted with grouping and transparency is used.

This graph is very helpful, due to the use of transparency, regions with many overlapping lines are rendered darker. This plot shows very clearly that date does not have a linear effect on growth (i.e. it is not just a trend). Indeed, it has a very discontinuous effect. When fitting a model to these data, we will use the maximum of the flexibility by including date as a categorical variable. This step is fundamental to be able to quantify temporal asynchrony. On top of that, we also note that species do not seem to react exactly in the same way to year fluctuations. As an example, year 2000 had lowest radial growth for European beech (bottom left panel), while this was not the case for the European larch (bottom right panel). This implies that an additive effect of years and species may not be enough to properly characterise this data. Very likely, we need to allow species to respond differently to years. Biologically, this is an indication of temporal asynchrony (i.e. species respond differently to annual fluctuations).

This graph can help determine the structure of the random effects of our model. Indeed, we can sense what trees behaviour looks like³. In particular, tree lines seem to run roughly parallel separated by a constant vertical shift. This implies that a model with a random intercept for tree may be adequate to model this data. Similar graphs are invaluable also when analysing grassland biodiversity studies(Tanadini and Hector, in prep.).

Species composition

³tree will be considered to be a random effect as we are not interested in estimating the effect of each tree, but we aim to take this design variable into account and to estimate their variability.

In the previous plots we inspected the effect of the continuous predictors available. We now turn our attention to categorical predictors. For the sake of brevity we only inspect the effect of species composition. This is an important variable in any biodiversity functioning study. We start by displaying this data with a simple boxplot.

```
bwplot(log10(ring) ~ composition, data = d.20)
```

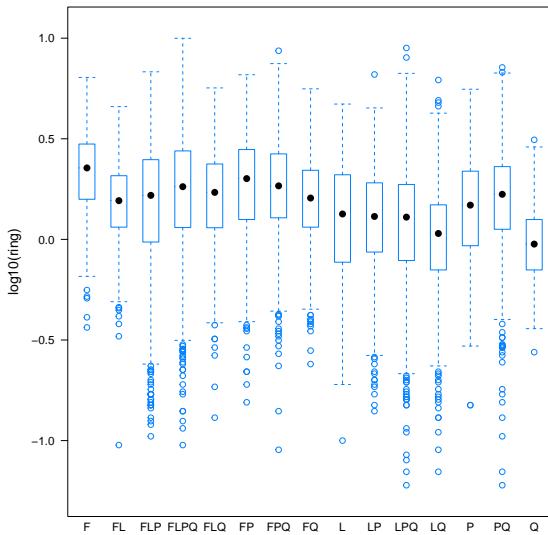


Figure 12: Boxplots of the reponse variable for species compositions.

Although informative this graph does not exploit its full potential. Indeed, the ordering of the groups is alphabetical⁴. However, very often reordering the groups labels is much more informative (Sarkar, 2008). In this context, we may want to order groups by the number of species they contain. This can be easily done with the function `reorder()`. In addition, we may want to separate species richness groups with vertical lines. To achieve that, we introduce here the use of panel functions. We don't discuss them in detail as it would be out of the scope of this publication. We can think of them as functions used to add layers to an existing (empty) graph. Here we first add a grid in the background (a) to better compare compositions, we then add vertical lines separating species richness groups (b) and we finally plot data (c). Sarkar's lattice book devotes an entire chapter to panel functions (Sarkar, 2008).

```
d.20$composition.ord <- reorder(d.20$composition, d.20$sp.rich)
bwplot(log10(ring) ~ composition.ord, data = d.20,
       panel = function(x, y, ...) {
         panel.grid(...) ## (a)
         panel.abline(v = c(4.5, 10.5, 14.5), lty = 2, lwd = 0.5) ## (b)
         panel.bwplot(x, y,...) ## (c)
       })
```

⁴This is the default behaviour of R.

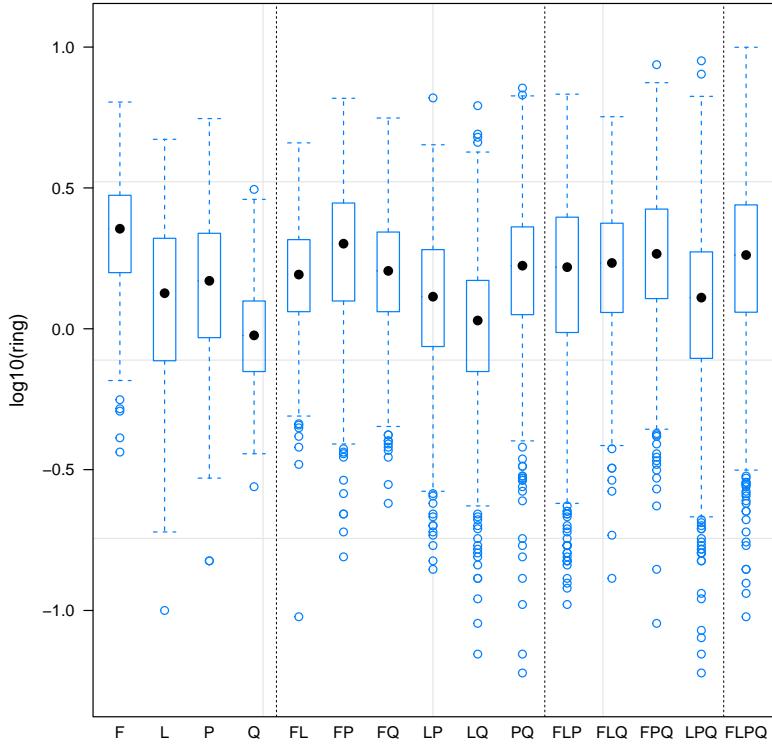


Figure 13: Boxplots of the reponse variable for species compositions. Groups are ordered according to species richness.

This graph conveys substantially more information than the previous one. It indicates that there may be differences between monocultures (boxplots on the left). As an example the sessile oak monoculture ("Q") appears to grow slower than the European beech ("F"). It is not clear whether the differences among non-monoculture compositions can be entirely explained by species identity or not. There seems to be little difference among species richness groups.

This information could hardly be extracted from Figure 12. It is interesting to note that with just a few changes to a graph we have been able to dramatically improve the amount of information that it conveys.

Visualising interactions between continuous predictors (**)

(**) Starred paragraphs, subsections and sections indicate an higher technical content or that these parts of the document are not fundamental to the approach presented here. These parts are presented for the sake of completeness. However, the reader interested in a quick read can skip them.

As stated above, a complete graphical analysis inspects the relationship between the response variable and all predictors. In addition to that, there is some degree of specificity to any analysis, this involves tailored graphs. For example, we may want to test the hypothesis that the effect of species diversity is actually modulated by forest density. We may hypothesise that the effect of diversity is stronger in low-density sites, while this latter is weak or absent in high-density sites. Below we represent one possible

way to inspect this hypothesis in a graphical way. Essentially, we plot the relationship between the response and diversity for different forest densities using panelling. We arbitrarily decided to divide forest density into four groups. To produce this plot we make use of the `equal.count()` function that discretises continuous variables into categorical variables. As the name of the function indicates, the groups obtained are of same size. Note that we specify the layout of the plot to better highlight the effect of increasing density (i.e. all four panels on one row).

```
xyplot(log10(ring) ~ diversity | equal.count(density, 4),
       data = d.20,
       type = c("p", "r"),
       cex = 0.1, col.symbol = "lightgray",
       layout = c(4, 1))
```

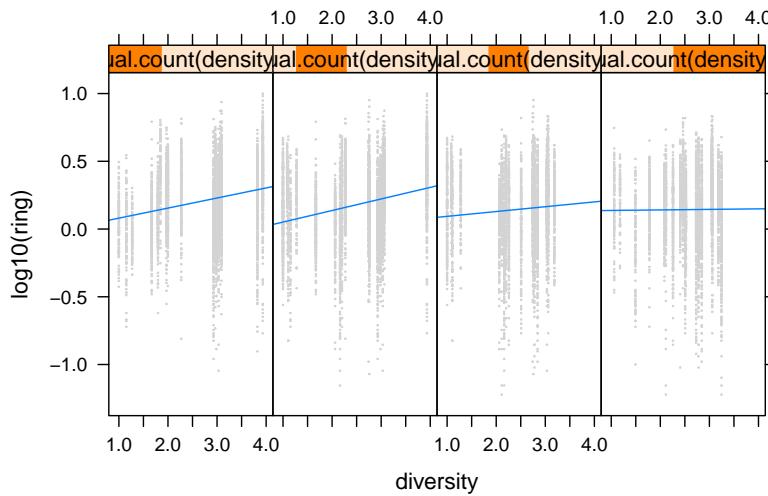


Figure 14: Effect of diversity on tree ring growth for four forest density classes.

Interestingly, it seems that the positive effect of diversity declines at higher densities (left to right). Nevertheless, density was not manipulated experimentally in this study and it is not the main focus here. Therefore, this will not be inspected further. Nevertheless, this graph shows how very specific hypotheses can be easily visualised with modern graphical packages.

2.2 Visualising other aspects of complex ecological experiments

In the previous subsection we have been visualising the marginal effect of each predictor on the response variable. This is fundamental to any analysis, however, there are other aspects of modern experiments that need to be visualised appropriately.

Study design (spatial and temporal structure)

Modern ecological studies often have designs that are not easily described in words.

Powerful graphs can be of great help when trying to understand how a study was actually carried out. A large amount of information can be visualised in a single meaningful graph. To demonstrate that, we introduce a new data set without describing its experimental design with text, but rather with a series of graphs (code not shown).

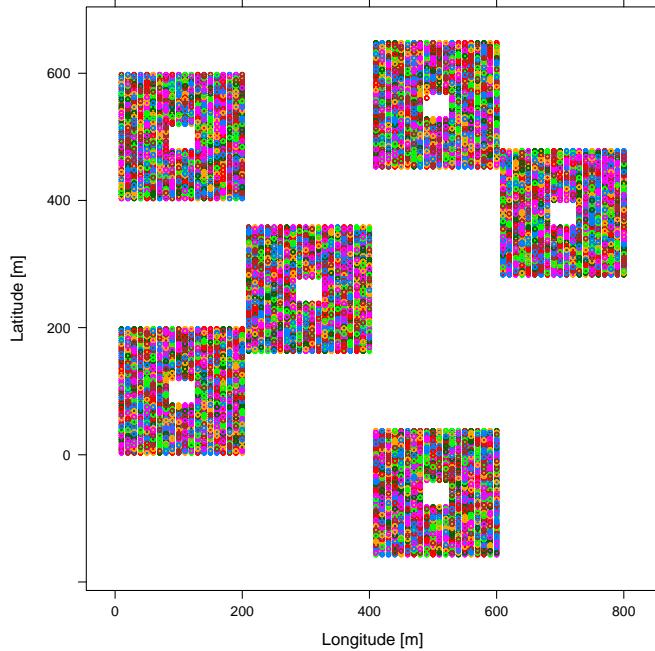


Figure 15: Study site, experimental design.

From Figure 15 we can get a rough idea of how the study was laid out. Based on this Figure is very easy to explain the actual design. This study is a subset of the Sabah Biodiversity Experiment, a large-scale diversity-function experiment run in Malaysia (Hector et al., 2011). In particular, here we look at the subset of plots that were planted with the full-species composition (i.e. 16 species) and that were surveyed more frequently, the so called 'Sabah Intensive Experiment'. As Figure 15 indicates there are six plots (i.e. the six squares). At their centre no seedlings were planted. This data was previously published by other authors (Philipson et al., 2014). We now focus on a single plot to better understand the details of this study.

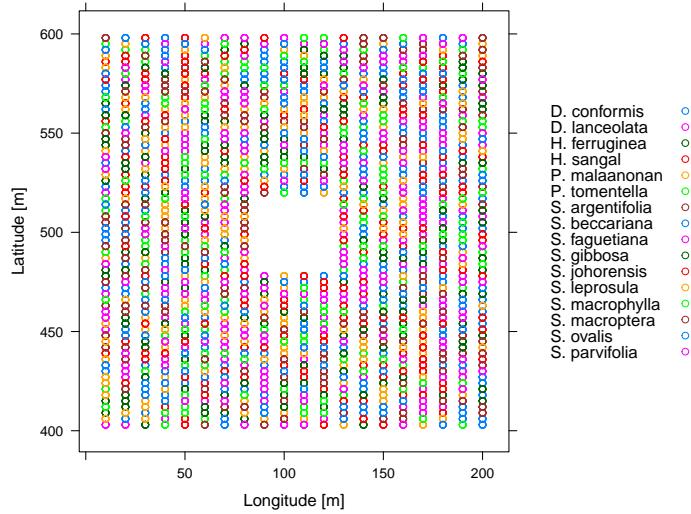


Figure 16: One particular plot of the Sabah Intensive Experiment inspected more closely.

As Figure 16 shows, in each of these plots, 20 (vertical) lines of seedlings were planted. Each line is supposed to contain 66 seedlings (this was not always feasible). So in total each plot contains about 1,200 seedlings. The colours used on Figure 15 represent the sixteen different species (see legend). The two last graphs illustrate the spatial structure of this experiment. It is important to note that these graphs have an isometric aspect ratio (Sarkar, 2008). This latter is the ratio of the physical height and width of a panel. In other words, the x- and y-axes are forced to have the same scales, which is appropriate for situation where both variables have the same units (here metres)⁵. Going back to our study, there is also a time component to it, that we illustrate in the following graph.

⁵When using *lattice* we can use the isometric aspect ratio with `aspect = "iso"`.

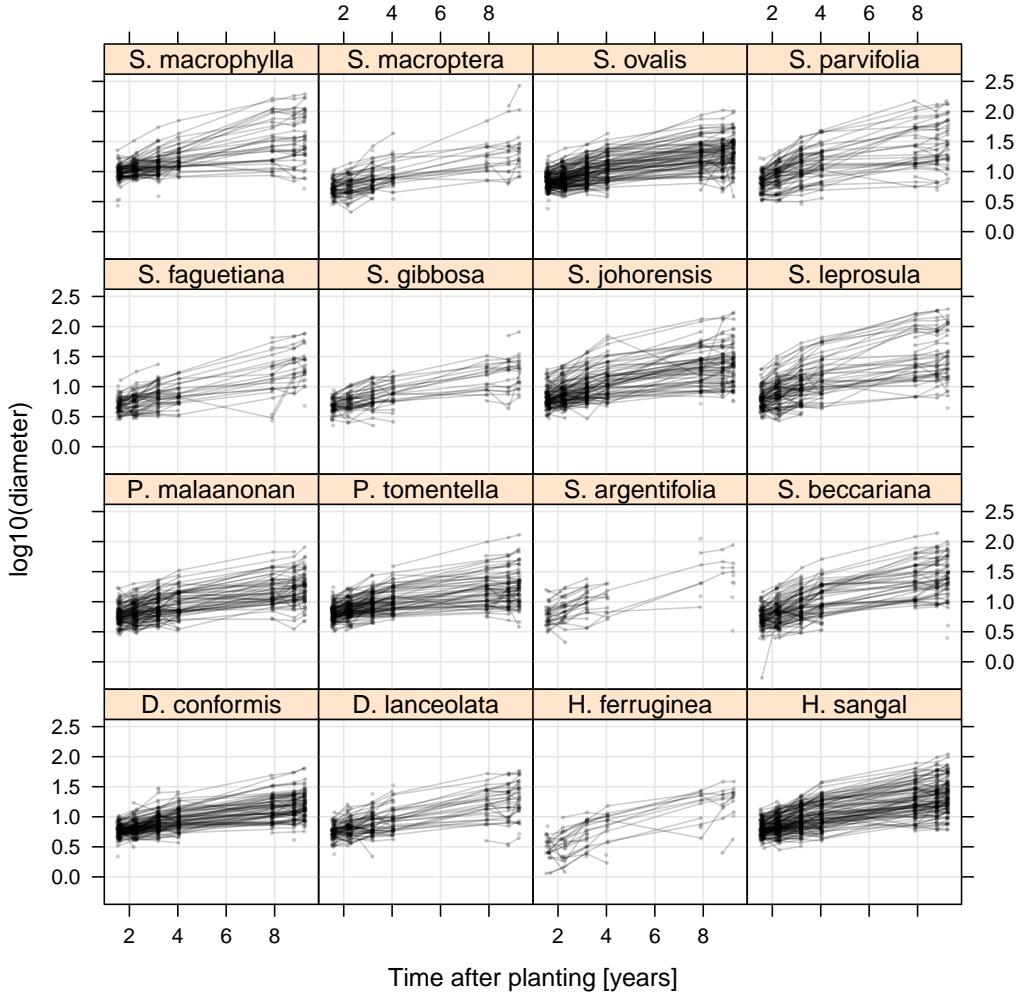


Figure 17: Temporal component of the Sabah Intensive Experiment.

Figure 17 explains the temporal structure of this study. Panels indicate clearly that 16 species were considered. The y-axis indicates that the response variable measured in this study was the diameter (measured at breast height), while the x-axis indicates that seven measurements were taken in a interval of about seven years after planting. In analogy to Figure 11, we used black transparent lines to highlight and group the observations that belong to one particular tree.

These last three graphs are very useful at illustrating a design that is relatively simple, but that would be much more difficult to fully describe in words. On top of the main information (such as six plots), there are a few subtleties that we can grasp from these graphs. As an example, it is trivial to understand that the seven measurements are not equidistant. By looking carefully, we can also understand that the measurements are not carried out at exactly the same seven time points. Indeed, the observations are not perfectly aligned on seven vertical lines, but rather group together into seven pretty compact groups. Given the large number of trees involved in this study, it was indeed impossible to carry out each survey in a single day. This detail is important from the modelling point, especially when looking at temporal asynchrony, as we will see in Appendix B. Finally, it is also clear that some species had more trees inspected

than others (e.g. *S. argentifolia* and *H. sangal*).

Comparing growth patterns

The original publication from this data set focused on comparing the growth rates of the 16 species (Philipson et al., 2014). The analysis was based on the raw measurements. Here, we want to compare the growth rate of the different species and look for evidence of spatial asynchrony. In other words, we are interested in modelling species growth and whether species-specific growth is influenced by environmental variability.

The analysis that we present here uses aggregated data. In particular raw measurements are aggregated at population level. Put simply, for each species we computed the mean (log-transformed) diameter at each time point in each plot. As we were interested in spatial asynchrony we computed these means for the six plots separately. Figure 18 below illustrate the aggregated data.

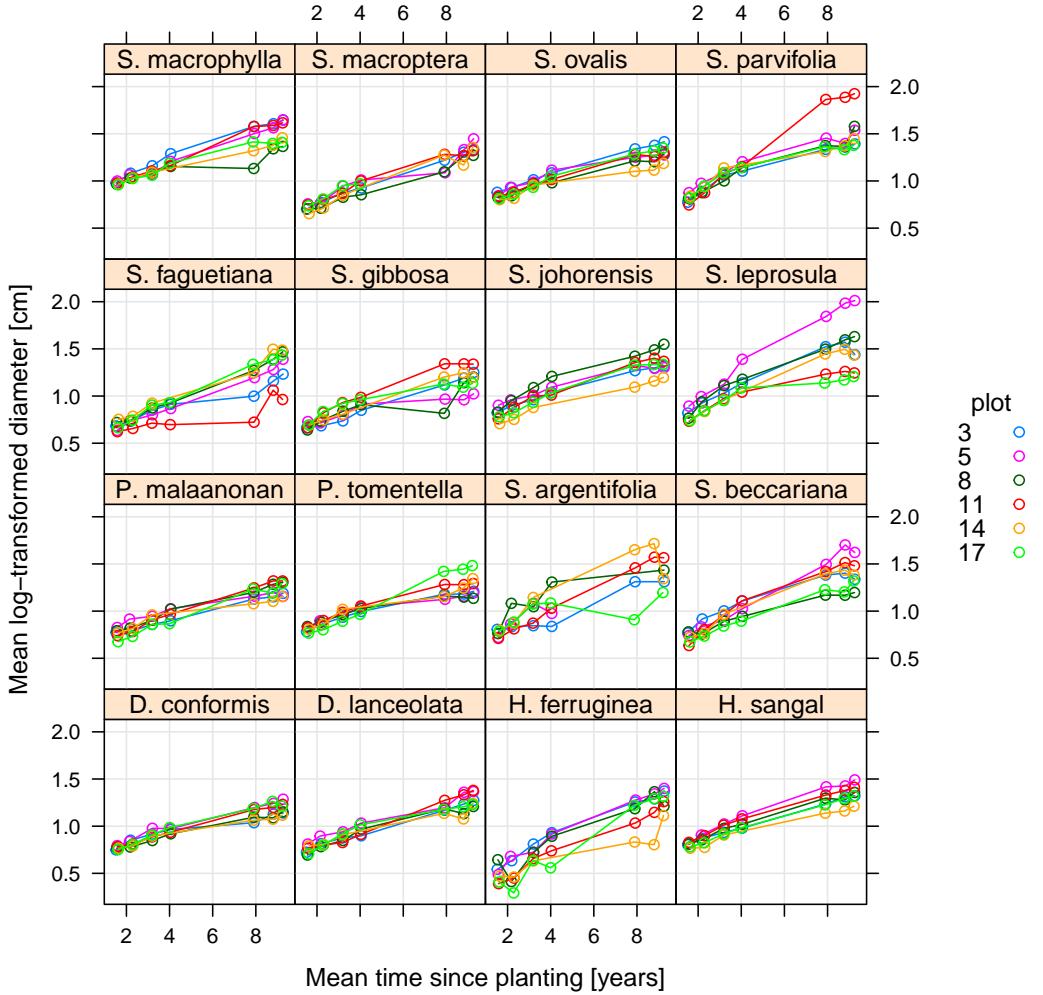


Figure 18: Growth of the 16 species in the Sabah Intensive Experiment. Each panel shows a species, each coloured line refers to a particular plot.

Each coloured line on this graph represents the (log-transformed) averaged diameter in one particular plot, for one particular species at a given time point. To make an example, the top right panel represent the species *S. parvifolia*, the red dots connected through a line in that panel correspond to the plot 11 (see legend). So each of the red dots in this panels is the averaged log-transformed diameters of all trees concerned. This graph is helpful to compare growths, however, it can be drastically improved. Indeed, if we were to put this graph into a publication it would be very difficult to understand the ordering of species in terms of growth. This information could be conveyed in the text, but this would be very inefficient. Here the fastest growing species is *H. ferruginea* (bottom row, third column), the second fastest is *S. leprosula* (last column, second row). So the panel ordering does not help, and in addition, this graph does not highlight differences in growth.

Usually, when graphs are created all the available space is automatically used. This is obviously the best option in a wide variety of situations. However, when comparing slopes (here growth rates) the use of alternative aspect ratios can be very beneficial (Sarkar, 2008). In the next Figure we modify the aspect ratio so that differences

among slopes are better spotted⁶. In addition to that, we order panels by increasing slope, instead of alphabetically.

```
xy.growth.2 <- update(xy.growth.1, aspect = "xy", ## other aspect ratio
                      index.cond = function(x,y) coef(lm(y~x))["x"],
                      ## change order of panels
                      strip = strip.custom(par.strip.text = list(cex = 0.5)))
                      ## to make panel names fit
xy.growth.2
```

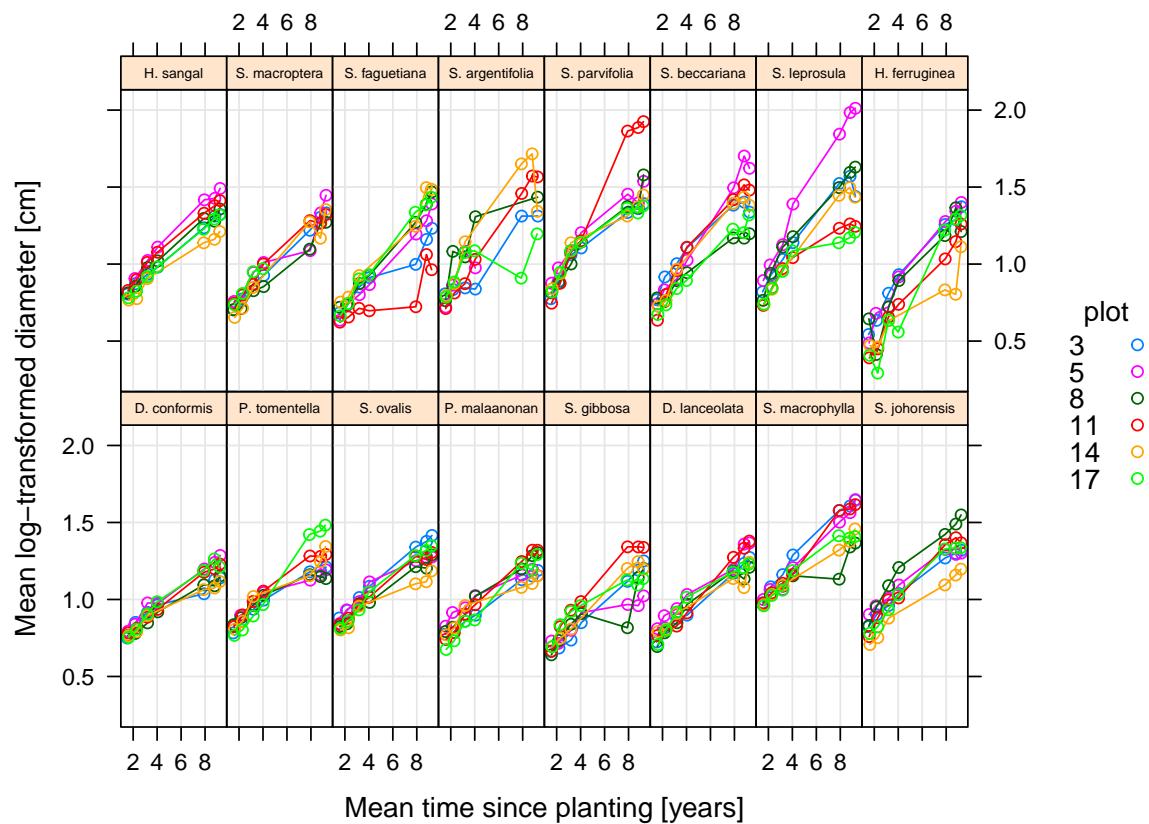


Figure 19: Growth of the 16 species in the Sabah Intensive Experiment. Each panel shows a species, each coloured line refers to a particular plot (see legend). Panels are ordered by increasing slopes (i.e. faster growth rates) from left to right and from bottom to top.

Figure 19 makes it much easier to discuss the differences in growth rates as panels are

⁶In order to do that, we produce a graph that uses the "45 degrees banking rule" (Sarkar, 2008).

ordered and the aspect ratio is adjusted. On top of that, there is new information. The upper right panel (i.e. *H. ferruginea*) has the greatest growth rate, but at the same time has a very small size (i.e. has by far the lowest intercept). As a matter of fact, this species was identified to have an unusual growth and survival pattern by a deeper analysis (Tuck et al., 2016). This pattern was not visible in Figure 18.

The Sabah Intensive Experiment also recorded the survival of each tree at each survey. We can use a similar plot to display mean survival in plots. We ordered panels by mean survival (code not shown).

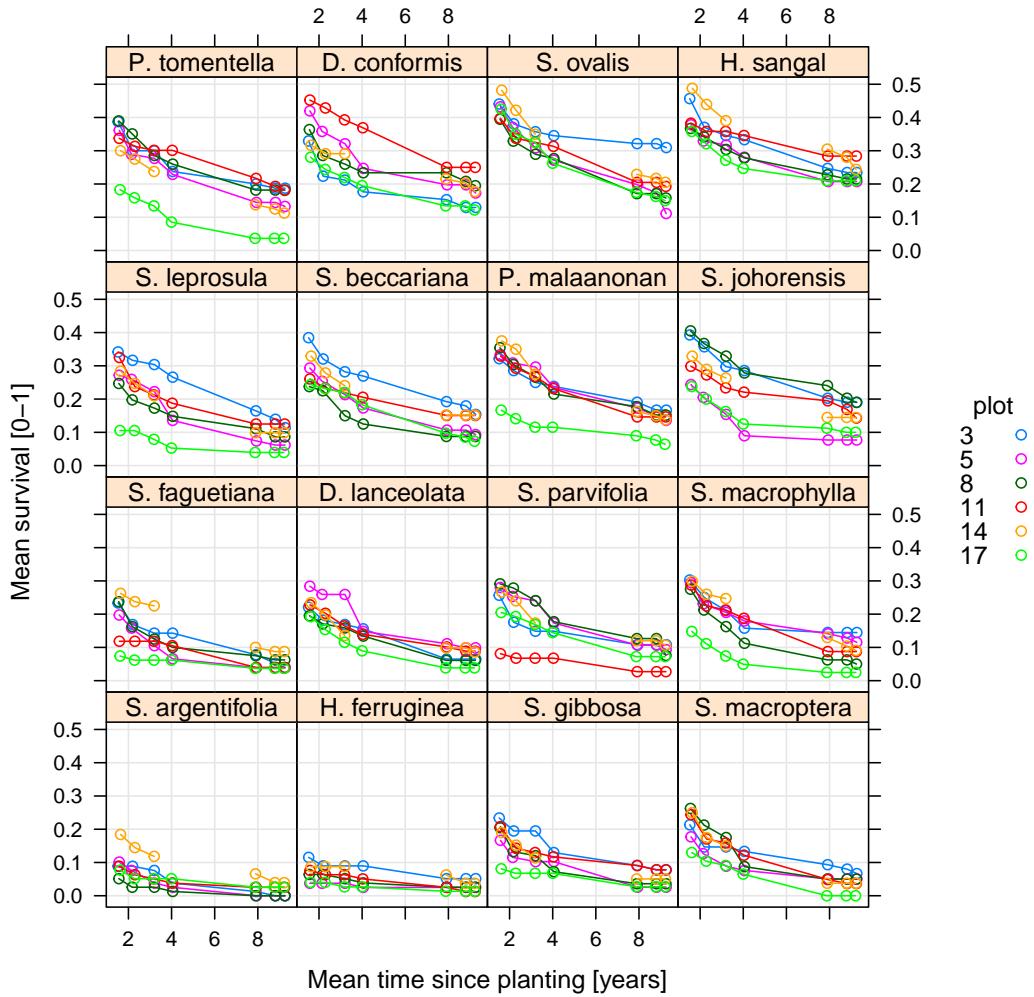


Figure 20: Survival of the 16 species in the Sabah Intensive Experiment. Each panel shows a species, each coloured line refers to a particular plot (see legend).

Figure 20 shows that there are large differences in survival among species and that after about nine years since planting less than 30% of the trees were still alive. There are several other interesting aspects that this graph highlights. As an example, we note that plot 14 (yellow) was not surveyed at all time points (broken line). This information can be relevant when modelling the data. On top of this "technical" detail, this graph is very efficient at putting in evidence important biological information. Indeed, if we look at the effect that plots have on species survival, we note clear differences. Plot

17 seems to have overall the worse condition for survival, however, the magnitude of this effect is varying and not consistent among species. For species *S. johorensis* and *S. parvifolia* this is not the worse plot. This information is biologically very relevant as it indicates that spatial asynchrony is very likely to be present.

Temporal asynchrony and conditional effects

Given that there is a strong indication for spatial asynchrony, we may want to understand whether temporal asynchrony is present. In other words, whether species are affected differently by time (climatic fluctuations). Classical metrics to quantify asynchrony such as that developed by Gross and colleagues (2014), implicitly assumes that "species biomasses are fluctuating around a stable mean". This is obviously untrue here. Indeed, both traits diameter and survival are not constant over time. So by analysing these traits with these classical metrics we would conclude that all species are strongly synchronous. This conclusion would be wrong and misleading. This artefact is simply due to the fact that the trait analysed is not stable over time.

To improve this situation we may want to remove the trend (e.g. growth) before quantifying temporal asynchrony. This way to proceed would remove the biasing effect of growth on temporal asynchrony. Nevertheless, we may also want to remove the obscuring effect of other variables that add noise to the biological process of interest without biasing it. The next section explains this concept in depth with a real example.

3 Estimating conditional effects

As discussed above, we may want to estimate temporal asynchrony when other obscuring or biasing effects are removed from our data. This way to estimate effects is referred as conditional. Indeed, here we would obtain the effect of temporal asynchrony when we control or condition for the effect of growth and other nuisance factors.

To better illustrate this concept we use again the Czech Republic data set inspected in Section 2. In particular we look at tree diameter over time to quantify temporal asynchrony. To start with, we display the diameter of trees against time. Each species is plotted in a separate panel. The observations of trees are connected by a grey line. On top of the raw diameters, we also display the average annual diameter for each species in red. This quantity is important as it is used to quantify temporal asynchrony. In this section the add-on package *ggplot2* is used to produce figures (Wickham and Chang, 2016).

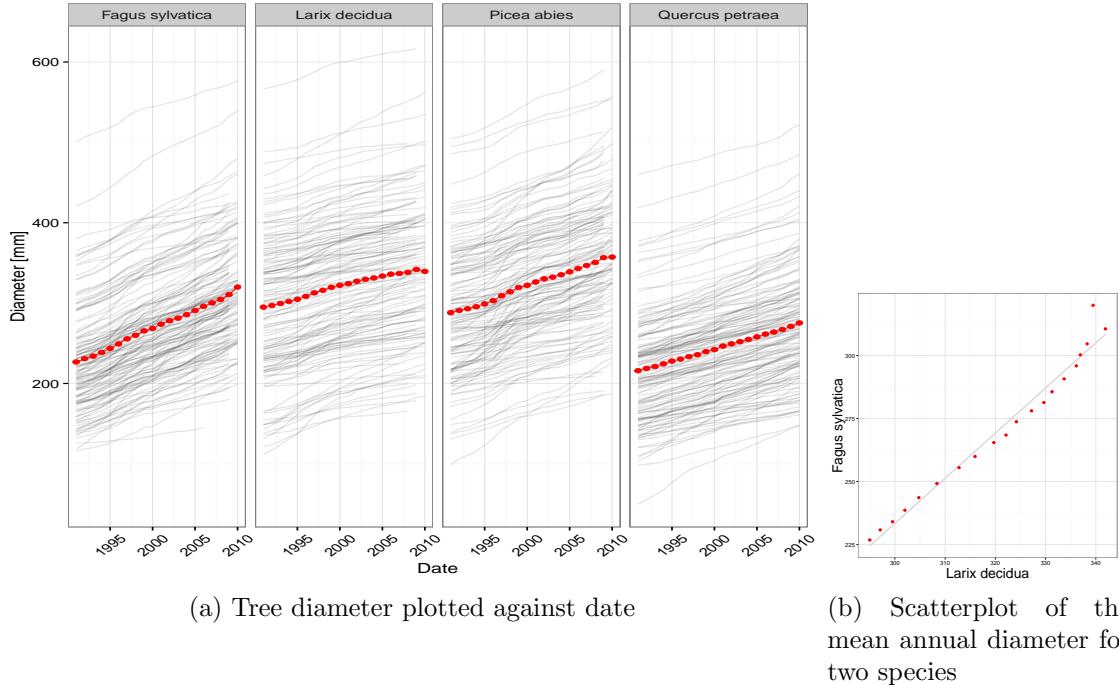


Figure 21: Raw data used to quantify temporal asynchrony.

Many of the currently used temporal asynchrony measures are derived from the temporal correlation of pairs of species. These pairwise correlations are often averaged to obtain a global measure of asynchrony (Gross et al., 2014). In order to keep our reasoning straightforward we start focusing on the relationship of two species (i.e. European beech and European larch which are shown in the two left panels).

If we were to correlate the raw diameters of the two species, we would get a very high correlation. Indeed, the Pearson correlation coefficient estimated is 0.99. However, this correlation does not represent the common response that these two species have towards years (i.e. temporal asynchrony). This highly positive correlation is mainly driven by the fact that trees are growing. In other words, we are not correlating temporal fluctuations, but tree growth. Applying currently used asynchrony measures to raw data like diameter is obviously of little help.

In order to truly correlate year fluctuations we must remove the effect of tree growth. To do that we remove the trend in each species. For the sake of brevity, the exact procedure of these steps are not shown here. Appendix B describes all steps needed to obtain conditional, and thus meaningful, estimates of temporal asynchrony.

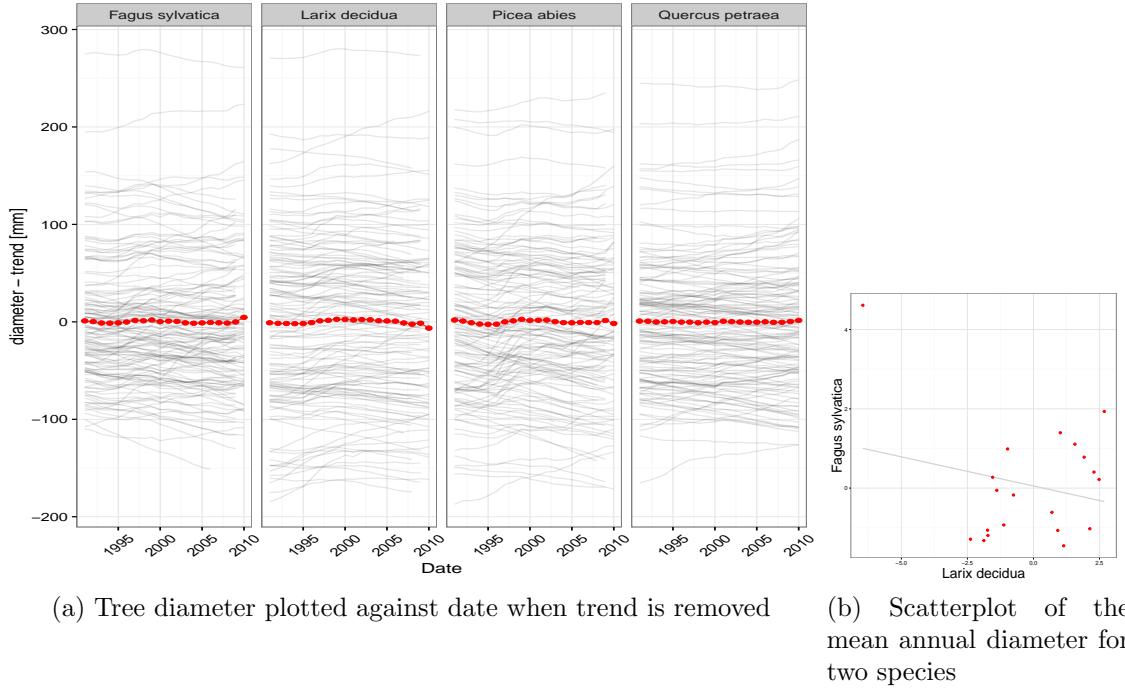
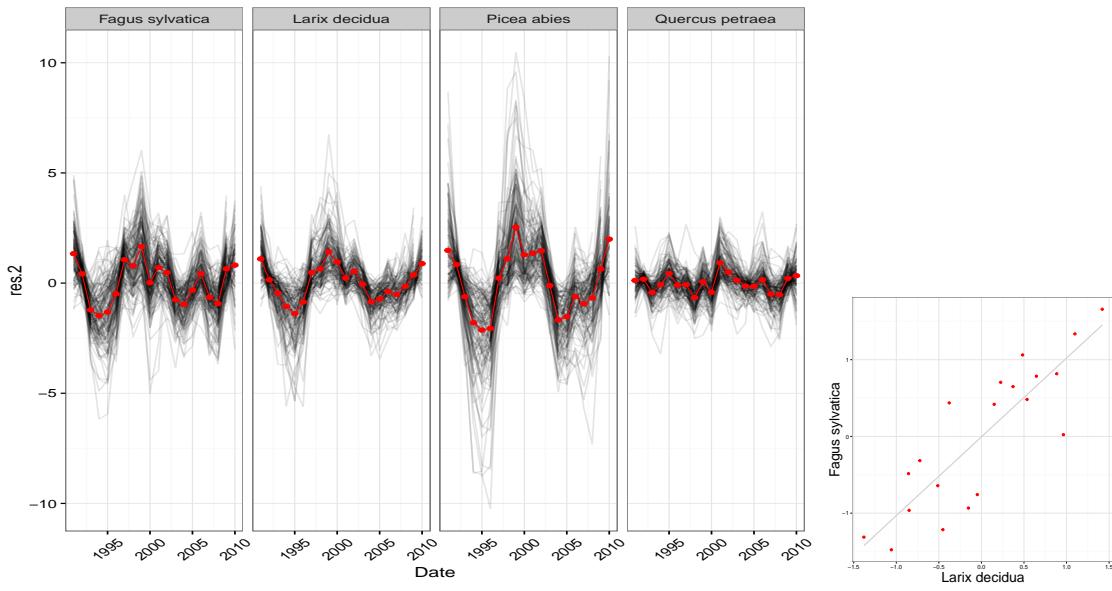


Figure 22: Year effects when trend is removed.

Once that the growth trend has been removed we can truly look at how species react to annual fluctuations. Unfortunately, there is a large scatter due to tree effects that obscures the interesting pattern that we are looking for. The situation depicted here is similar to the one found in medium-long term grassland studies where the biomass is stable over time. Trees can be seen as plots in this context (i.e. they can be rendered with grouping techniques).

The graph on the right (b) shows the correlation of the two species when the growth trend is removed. The estimated Pearson correlation is negative (-0.22). It is important to note that this correlation is strongly affected by a single observation (i.e. year 2010)⁷. To better compare year fluctuations, we may want to remove the confounding effects of trees. Analogously, in a grassland study we may want to remove the obscuring effect of plots, blocks or sites.

⁷It can be argued that a plain Pearson correlation is not a suitable choice in this situation. When the number of species involved is large, it can be difficult to spot this kind of anomalies. In Appendix D we will show how to deal with these situations.



(a) Tree diameter plotted against date when trend and tree effects are removed
(b) Scatterplot of the mean annual diameter for two species

Figure 23: Year effects when trend and tree effects are removed.

Figure 23 shows the year effects once the obscuring effects of growth (i.e. trend) and trees have been removed. The year fluctuations are now very clear. Note that the range of the y-axis has decreased from about 500 mm (see Figure 21) to just 20 mm. In other words, we are now looking at the interesting pattern, temporal fluctuations, while controlling for other nuisance variables.

The correlation between European beech and European larch is strong and positive (0.85). However, when measuring temporal asynchrony we are interested in the fluctuations around a stable mean. It is clear that we cannot consider the mean to be stable here. As an example all species were negatively affected by year 1994. While the year around 2000 seems to be beneficial for all of them. In other words, some years appear to have a positive effect on all species, while others have a negative effect. It is legitimate to be interested in the deviations from the main year to understand how species react to year when the "main year effect" (i.e. the effect shared by all species is removed).

The supporting information dedicated to asynchronies, Appendix B, shows that after the "main year effect" is removed, European beech and European larch are actually strongly asynchronous (i.e. negatively correlated). This does not come unexpected as it is common practice for foresters to grow these two species together as they are thought to exploit different resources. In addition, when these two species are grown together they show the highest stability of all two-species compositions (not shown). This highlights that biological concepts such as asynchrony and stability are tightly interconnected and their analysis must communicate.

On this graph, we note another interesting pattern that will be inspected in Appendix C, differences in variability. The Norway spruce (third panel from left) seems to be more strongly affected by years, while the Sessile Oak (last panel on the right) shows the lowest variability.

The scope of this section was to introduce the concept of conditional estimates. We showed that when quantifying asynchrony, we may want to control for the effects of other nuisance variables that may strongly affect the results. In the above example, we sequentially removed these effects before measuring asynchrony. This way to proceed was used for illustrative purposes only. Our approach uses a model-based framework where all ecological processes (e.g. asynchronies and stabilities) of interest are estimated simultaneously in a single step. This way to proceed gives us conditional estimates.

4 Final remarks

Complexity of modern ecological experiments - the power of modern graphical packages

In this document we highlighted the importance of using appropriate ways to visualising data for present-day ecological experiments. These are often complex with several design structures such as plot, block and sites measured over time. Modern graphical packages such as *lattice* or *ggplot2*⁸ are very well-suited to properly display this kind of data.

Indeed, panelling can be used to display separately the effect of a treatment (e.g. species identity or species richness), while grouping is very powerful to illustrate observations that belong to the same entity (e.g. plot or tree). Other tools of modern graphical packages are very helpful to convey substantially more and better information in a given graph than simple scatterplots. Here we showed the power of ordering panels or changing aspect ratio. This, revealed unseen patterns that are biologically important.

In addition, the approach presented in this publication is fundamentally based on a graphical visualisation of the results obtained from the modelling phase (see Appendices B, C and D).

Conditional effects

In this document we introduced the concept of conditional effects. This concept is fundamental to the approach presented here and will be further discussed in Appendix B.

Notes on reproducibility

This dynamic document, that mixes **R** code, output and figures with plain text, was created using the add-on package *knitr* (Xie, 2016). All the appendices of this publication are created with this method. Each of the appendices is linked to a **R**-script that reproduces exactly the steps used to produce these documents. This is very convenient for those interested in interacting with the code to rerun our analysis or even modify and improve it.

⁸We used these two package for personal preference. However, the approach presented in this publication does not rely on any particular package or software.

Related to that last point (rerunning the analysis), it worth noting that to create this document we used the add-on package *checkpoint* (Corporation, 2016). This package “creates a local library into which it installs a copy of the packages required by your project as they existed on CRAN on the specified snapshot date. Your **R** session is updated to use only these package” (type `?checkpoint()` for further details). This makes sure that rerunning the provided code yields exactly the same results presented here on any computer, regardless of the packages installed by the user⁹.

⁹The R version installed is extremely unlikely to affect the results obtained.

Reproducibility

Checkpoint date was set to 2016-05-01.

```
sessionInfo()

R version 3.3.2 (2016-10-31)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Debian GNU/Linux 8 (jessie)

locale:
[1] LC_CTYPE=en_GB.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_GB.UTF-8       LC_COLLATE=en_GB.UTF-8
[5] LC_MONETARY=en_GB.UTF-8   LC_MESSAGES=en_GB.UTF-8
[7] LC_PAPER=en_GB.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C              LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats      graphics   grDevices utils      datasets  methods   base

other attached packages:
[1] ggplot2_2.1.0      latticeExtra_0.6-28 RColorBrewer_1.1-2
[4] lattice_0.20-34    knitr_1.14

loaded via a namespace (and not attached):
[1] Rcpp_0.12.7        digest_0.6.10    plyr_1.8.4      grid_3.3.2
[5] gtable_0.2.0       formatR_1.4      magrittr_1.5    evaluate_0.10
[9] scales_0.4.0       highr_0.6       stringi_1.1.2   reshape2_1.4.1
[13] labeling_0.3       tools_3.3.2     stringr_1.1.0   munsell_0.4.3
[17] colorspace_1.2-7
```

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