Mixed Effects Models Mini-Series. Part III. Detect and embrace temporal and spatial non-independence

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Contents

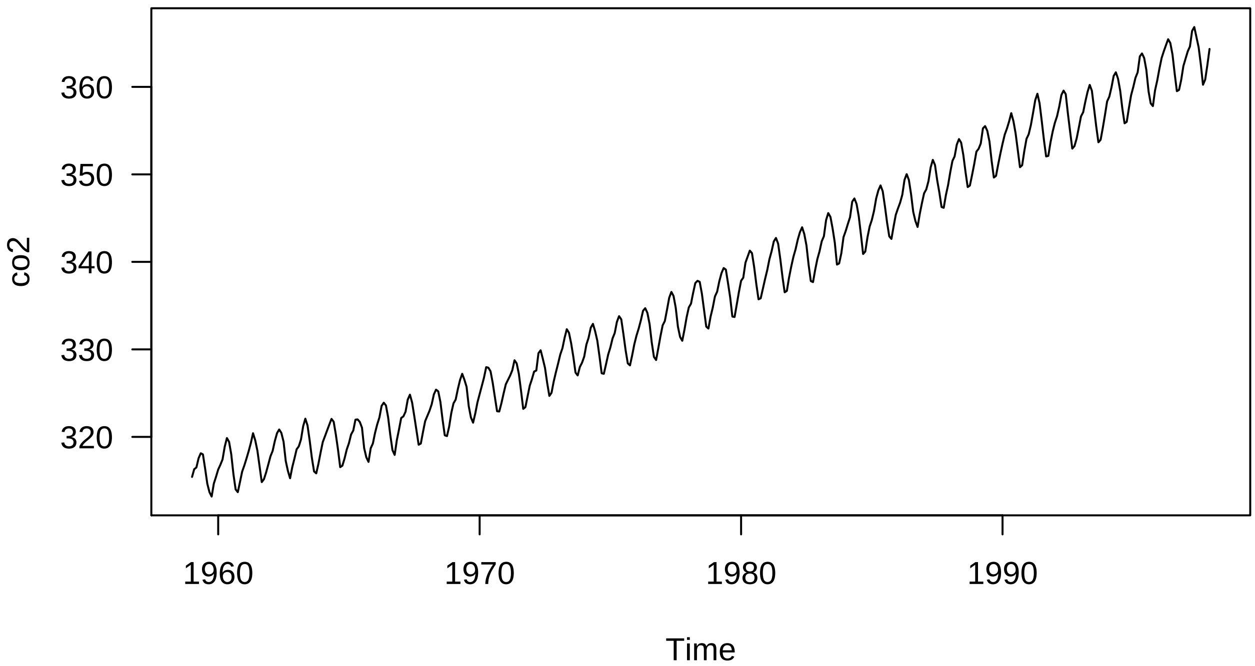
This session will look at a different type of non-independence than the previous one. While there data were non-independent *by design*, in this session they are (or may be not) non-independent due to mechanistic ecological processes (such as dispersal of animals) or statistical artefacts (such as "forgetting" to include an important predictor). Key terms are:

- autocorrelation (temporal and spatial)
- time series

Time series

Imagine a data set consisting of repeated measurements of, say, CO_2 in the atmosphere (plots should ALWAYS be square, except in the case of time series and maps):

```
par(las=1) # globally set las to 1!
plot(co2)
```



We are interested in whether there is a significant trend over time, thus `time` is our fixed effect. Let's start with a simple linear model and see where we go. To do so, we first have to convert this time-series object into two vectors, one with the CO_2 concentrations and one with the date.

```r
TIME <- as.vector(time(co2))
CO2 <- as.vector(co2)
fm1 <- lm(CO2 ~ TIME)
summary(fm1)
```

```
##
## Call:
## lm(formula = CO2 ~ TIME)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.0399 -1.9476 -0.0017  1.9113  6.5149
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.250e+03  2.127e+01  -105.8   <2e-16 ***
## TIME         1.308e+00  1.075e-02   121.6   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.618 on 466 degrees of freedom
## Multiple R-squared:  0.9695, Adjusted R-squared:  0.9694
## F-statistic: 1.479e+04 on 1 and 466 DF,  p-value: < 2.2e-16
```

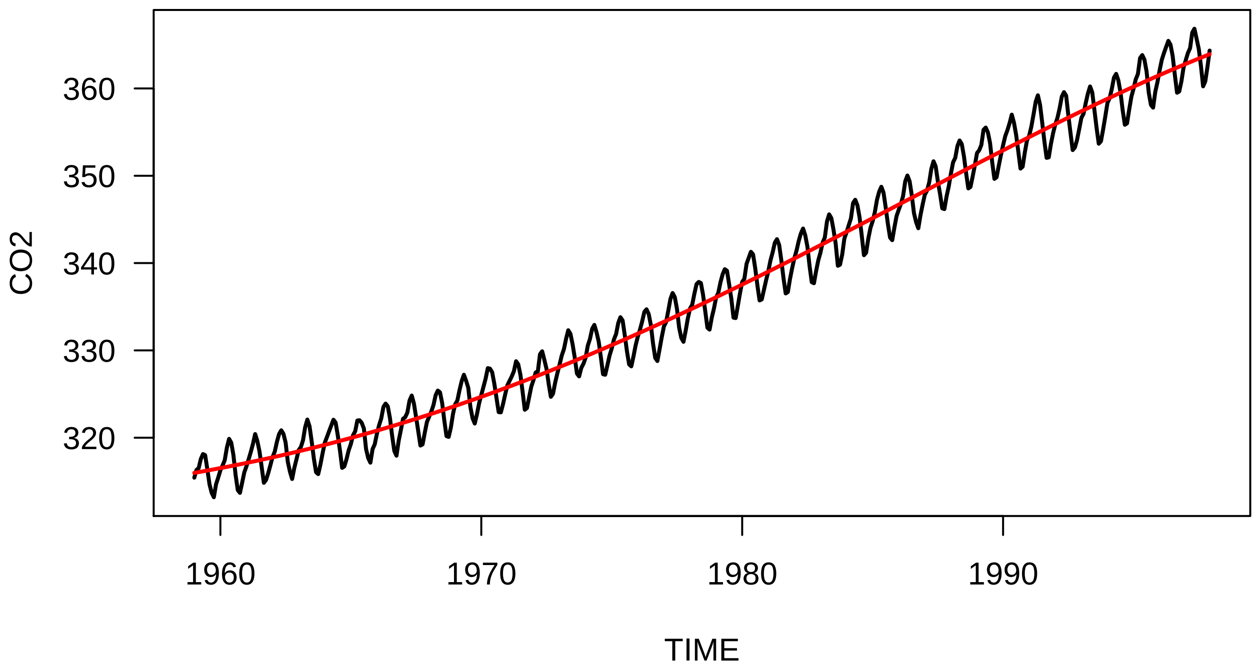
The `TIME` effect is clearly important and highly predictive (with an $R^2 = 0.97$) and we can do even better with a polynomial of `TIME`:

```r
fm2 <- lm(CO2 ~ poly(TIME, 2))
fm3 <- lm(CO2 ~ poly(TIME, 3))
fm4 <- lm(CO2 ~ poly(TIME, 4))
anova(fm1, fm2, fm3, fm4)
```

```
## Analysis of Variance Table
##
## Model 1: CO2 ~ TIME
## Model 2: CO2 ~ poly(TIME, 2)
## Model 3: CO2 ~ poly(TIME, 3)
## Model 4: CO2 ~ poly(TIME, 4)
##   Res.Df    RSS Df Sum of Sq        F  Pr(>F)
## 1    466 3194.1
## 2    465 2214.5  1    979.63 220.0767 < 2e-16 ***
## 3    464 2066.6  1    147.90  33.2253 1.5e-08 ***
## 4    463 2060.9  1      5.61   1.2599  0.2622
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So a cubic function fits best:

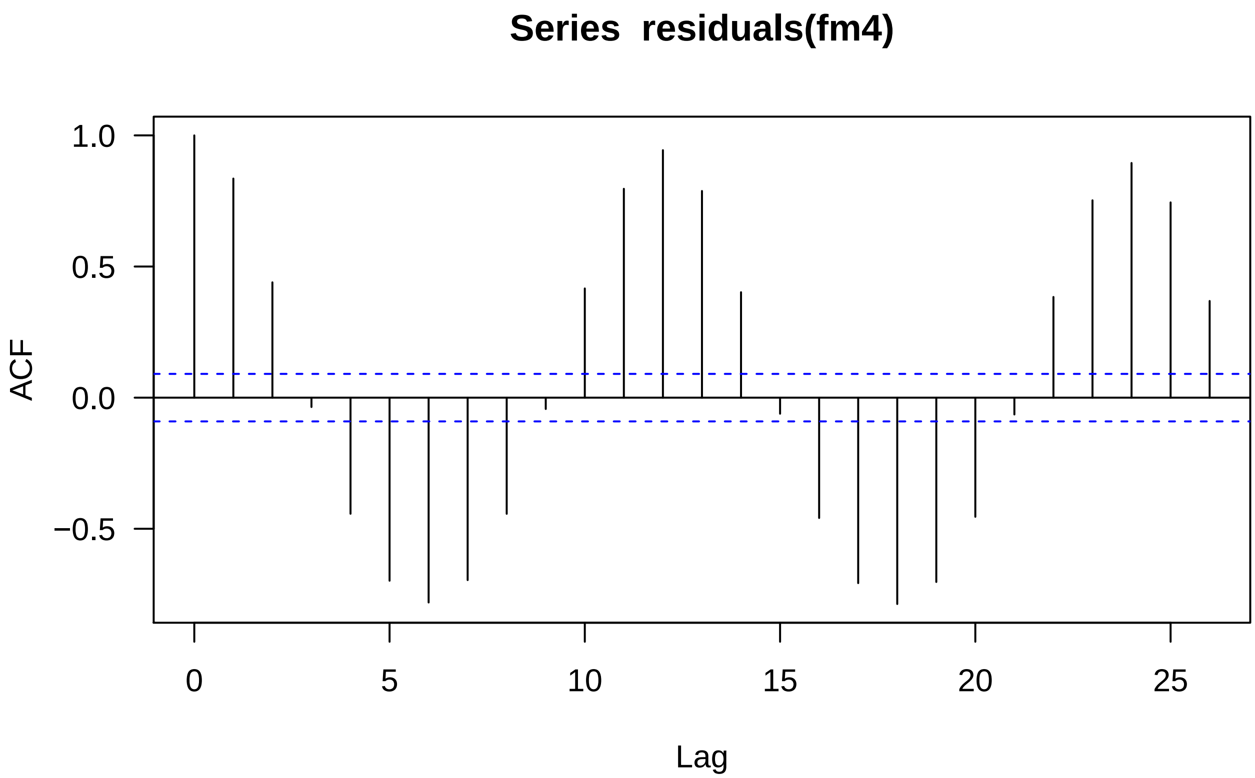
```r
plot(CO2 ~ TIME, type="l", lwd=2)
lines(TIME, predict(fm4), col="red", lwd=2)
```



The autocorrelation function

From the last session, we have the creepy feeling that this regression is some not correct. We *know* that data points are not independent, since they are taken in exactly the same place, month after month. But that is not necessarily a problem! We account for this by using `TIME` as predictor. This may already be enough to accommodate the temporal dependence of data into account. To find out whether indeed our data have a temporal dependence in the response which is **not** accounted for by the model, we use a diagnostic tool called *autocorrelation function*, short ACF. The ACF creates a new data set of `CO2`, which is displaced against the original by 1, 2, 3, ... time units. Then the new vector is correlated with the original and the correlation value is plotted against the displacement (called the *lag*). The result looks like this:

```
acf(residuals(fm4))
```



Thus, as we lag the data set by 1, 2, 3, ... months, the correlation decreases down to a random value (indicated by the stippled blue lines), only then to increase as negative correlation again to a maximum at lag 6. This means that CO_2-concentrations in half a year (and in one year, two years, ...) can be extremely well predicted from the current value, *despite* the fact that our model already accounts for a trend in time!

> The plot shows that we have **temporal autocorrelation** in our model residuals, indicating that they are indeed **not** independent!

We are now left with two possible ways forward:

1. Try to identify the reason for this temporal autocorrelation and use it as fixed effect in our model. Or,
2. try some statistical trick to tell the model that the data are temporally autocorrelated, much in the same way as we did in the last session with design-based non-independence.

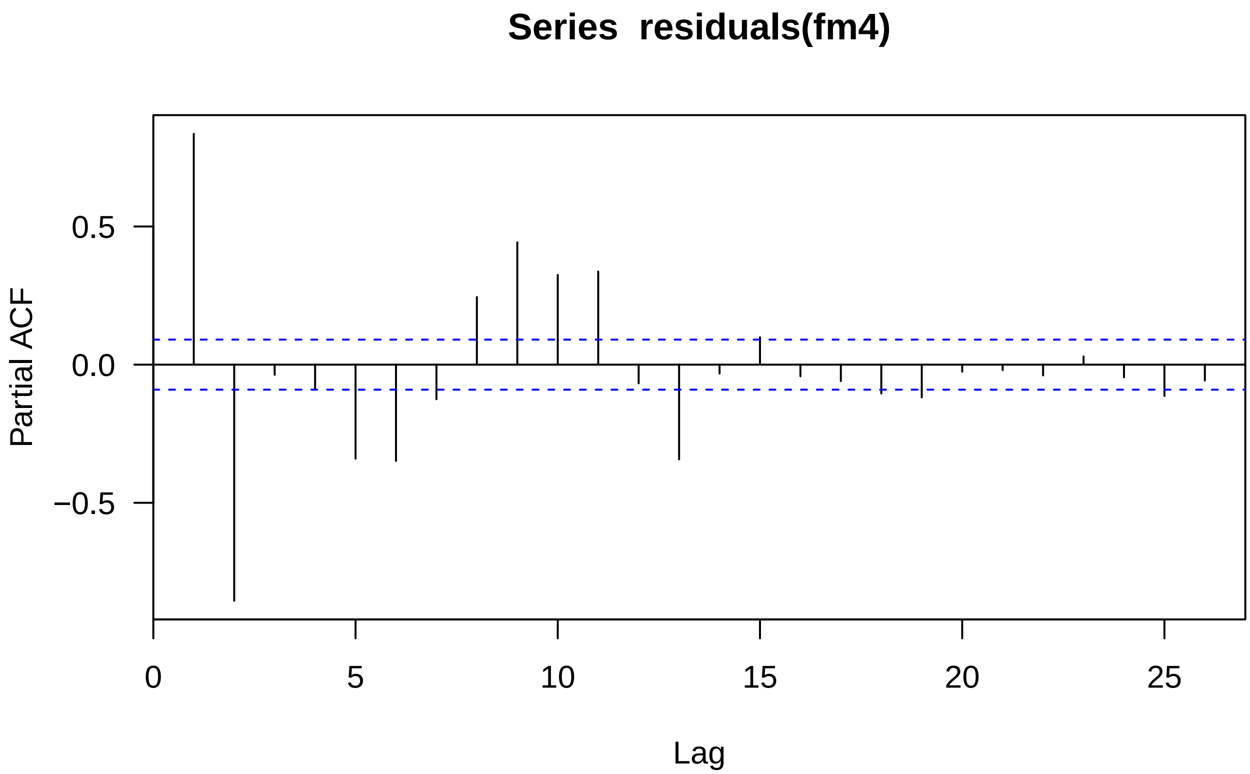
Let's start with the second option, since this is a mixed-effect model series, not a time series analysis workshop.

Accommodating temporal autocorrelation in a linear model: GLS

The key trick we have to do is to tell our model that it should know that data points nearer in time are more correlated than those further apart. Thus, correlation is a function of time-distance. But, you may say, the pattern repeats over and over again, so data points 2 years apart are *more* correlated that those 3 months apart. Well, yes. But they are so closely correlated because the correlation carries over from one lag to the next. So if I know the correlation in lag 12, I also know it (roughly) in lag 24, 36 and so forth. Thus, we don't need to model each lag-distance, because it automatically is predicted by that 12 months earlier.

To visualise this, we use the *partial* autocorrelation function:

```r
pacf(residuals(fm4))
```



> The *partial* autocorrelation function shows us the lag effect *after accounting for what can be predicted from the previous lag effects.*

In this case, it is a bit messy, since the autocorrelation doesn't simply fade away with larger lag, but goes up and down in a damped oscillation. Anyway, this is an example, and we shall now try to modify the `lm` to account for temporal autocorrelation.

The way to do so is called "Generalised Least Squares", short GLS. In addition to the standard linear model, it also models the way that data point expectations covary with each other. In this case, we expect a data point of lag 1 to be highly positively correlated with the data, one of lag 2 highly negatively and so forth. If we imagine that each data point is a random variate drawn from some distribution, then we can think of a variance-covariance matrix of the data: each data point has its own column and row. On the diagonal, we have the variances, and on the off-diagonal, the covariance among data points. In a linear model, the off-diagonal entries are 0, i.e. data points are drawn independently of one another (and the diagonal is constant, i.e. all data points have the same variance). In a GLS, we can make the off-diagonal entries a function of the temporal distance between data! Isn't that cool?

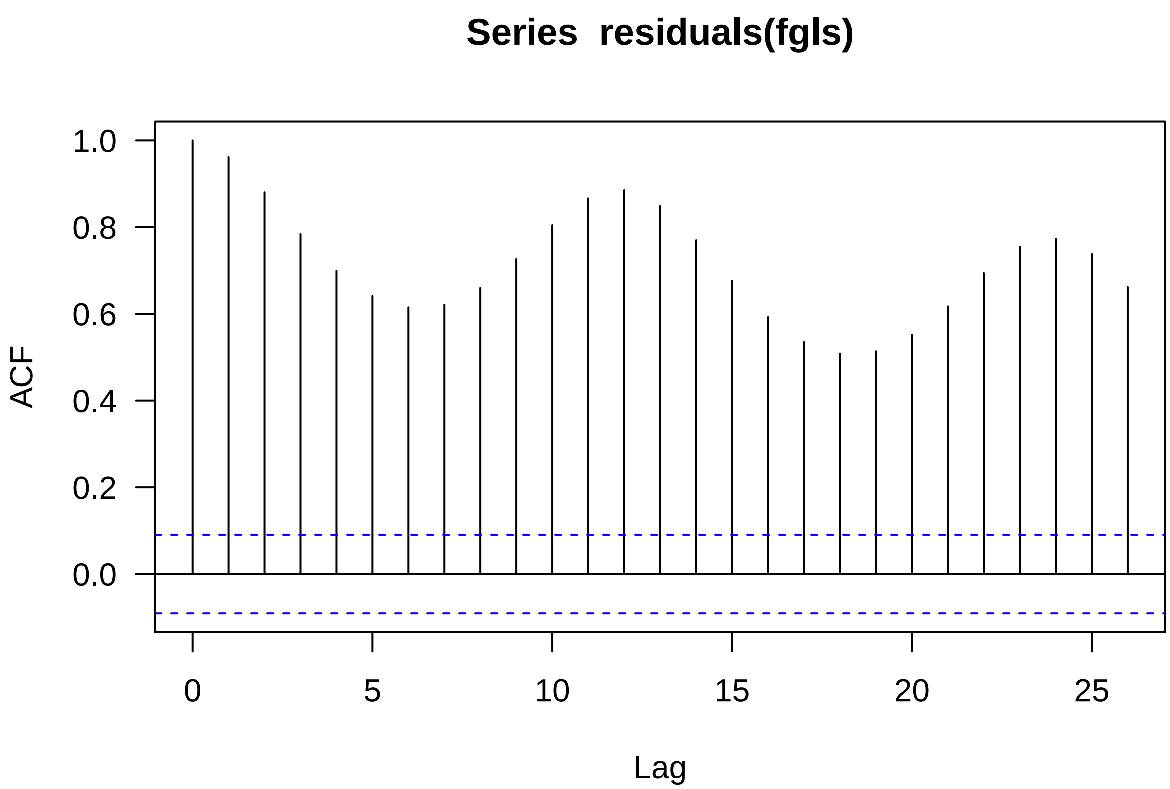
MAYBE A FIGURE WOULDN'T HURT HERE!

In R, we use the `gls`-function from package `nlme`. (Actually, this function is also internally behind the `lme` function.)

```r
library(nlme)
fgls <- gls(CO2 ~ poly(TIME, 3), correlation=corAR1(form=~TIME))
summary(fgls)
```

```
## Generalized least squares fit by REML
##   Model: CO2 ~ poly(TIME, 3)
##   Data: NULL
##       AIC      BIC    logLik
##   1465.39 1490.229 -726.6948
##
## Correlation Structure: ARMA(1,0)
##  Formula: ~TIME
##  Parameter estimate(s):
##      Phi1
## 0.9511127
##
## Coefficients:
##                   Value Std.Error   t-value p-value
## (Intercept)    351.3331   3.51152 100.05155  0.0000
## poly(TIME, 3)1 383.5095  61.85704   6.19993  0.0000
## poly(TIME, 3)2 -36.6866  43.36966  -0.84590  0.3980
## poly(TIME, 3)3  10.5001  35.81249   0.29320  0.7695
##
##  Correlation:
##                (Intr) p(TIME,3)1 p(TIME,3)2
## poly(TIME, 3)1  0.237
## poly(TIME, 3)2 -0.361  0.397
## poly(TIME, 3)3  0.155 -0.520      0.259
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -18.465603 -14.848658 -12.871317 -10.647402   1.372831
##
## Residual standard error: 1.185015
## Degrees of freedom: 468 total; 464 residual
```

```r
acf(residuals(fgls))
```



We see that a correlation of 0.95 was fitted for a lag of 1 ("Parameter estimate Phi1"), so only one lag was accommodated (thus: `corAR1`). With a look at the ACF of the residuals we can see that it is not nearly good enough.

We can construct much more complicated correlation structures using the `corARMA` function, but this is only for illustration:

```
COR3 <- corARMA(form=~TIME, p=3, q=0)
COR3 <- Initialize(COR3, data=data.frame("TIME"=TIME))
flag3 <- gls(CO2 ~ poly(TIME, 3), correlation=COR3) # takes a while
summary(flag3)
```

```
## Generalized least squares fit by REML
##   Model: CO2 ~ poly(TIME, 3)
##   Data: NULL
##        AIC      BIC    logLik
##   1469.31 1502.429 -726.6549
##
## Correlation Structure: ARMA(3,0)
##  Formula: ~TIME
##  Parameter estimate(s):
##       Phi1       Phi2       Phi3
##  1.8094257 -1.3809934  0.5403717
##
## Coefficients:
##                    Value Std.Error  t-value p-value
## (Intercept)     351.5273   3.54070 99.28198  0.0000
## poly(TIME, 3)1 393.1591  59.36127  6.62316  0.0000
## poly(TIME, 3)2 -32.9159  41.34740 -0.79608  0.4264
```

```
## poly(TIME, 3)3   9.0507  34.02375  0.26601  0.7903
##
##  Correlation:
##                 (Intr) p(TIME,3)1 p(TIME,3)2
## poly(TIME, 3)1  0.241
## poly(TIME, 3)2 -0.413  0.368
## poly(TIME, 3)3  0.141 -0.543      0.228
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -18.472352 -15.120912 -13.098248 -10.914279   1.405969
##
## Residual standard error: 1.184642
## Degrees of freedom: 468 total; 464 residual
```

So we need to be smarter about how to embrace multi-lag dependence. Luckily, someone else has thought of an automatic way to fit autoregressive models.

```r
library(forecast)
```

```
## Loading required package: zoo
##
## Attaching package: 'zoo'
##
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
##
## Loading required package: timeDate
## This is forecast 5.6
##
##
## Attaching package: 'forecast'
##
## The following object is masked from 'package:nlme':
##
##     getResponse
```

```r
fautogls <- auto.arima(CO2, xreg=poly(TIME, 3))
```

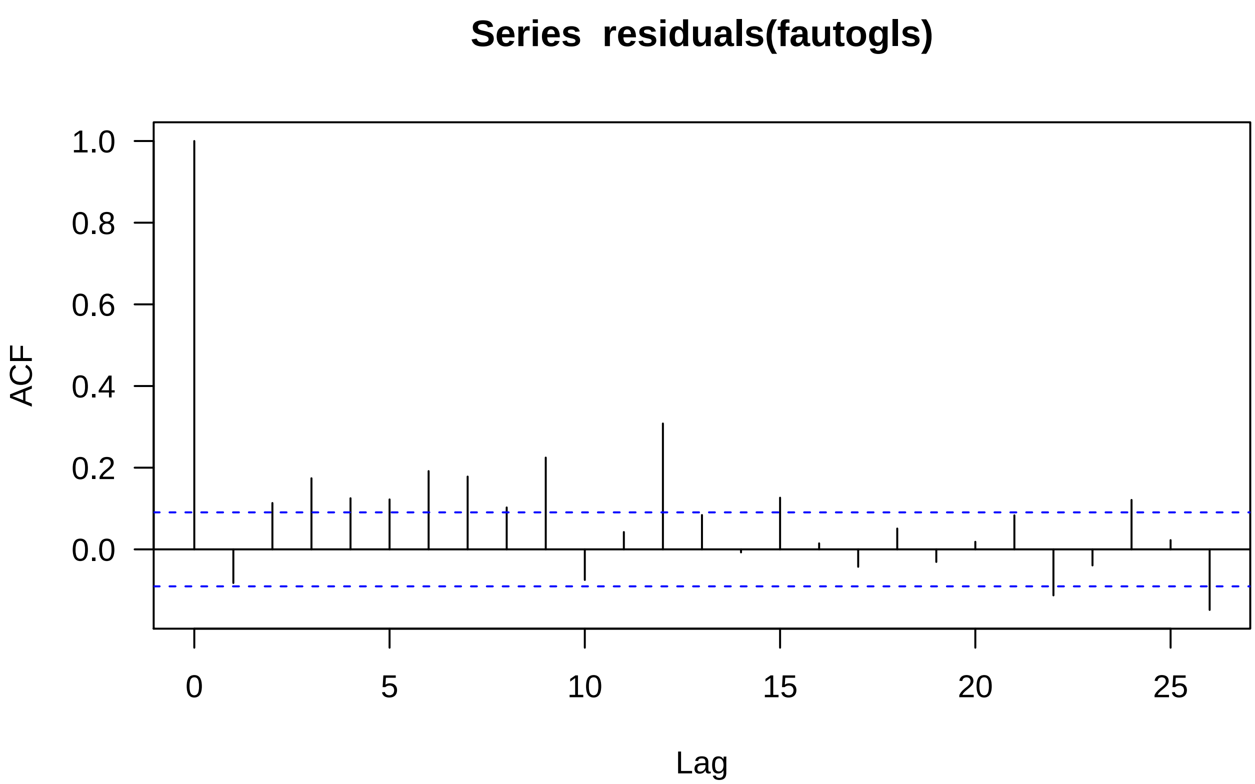
```
## Warning in auto.arima(CO2, xreg = poly(TIME, 3)): Unable to fit final
## model using maximum likelihood. AIC value approximated
```

```r
summary(fautogls)
```

```
## Series: CO2
## ARIMA(4,0,3) with non-zero mean
##
## Coefficients:
##          ar1      ar2     ar3      ar4      ma1     ma2      ma3
##       2.6924  -3.6352  2.6383  -0.9524  -1.4055  1.2651  -0.3368
## s.e.  0.0145   0.0301  0.0302   0.0144   0.0369  0.0455   0.0399
```

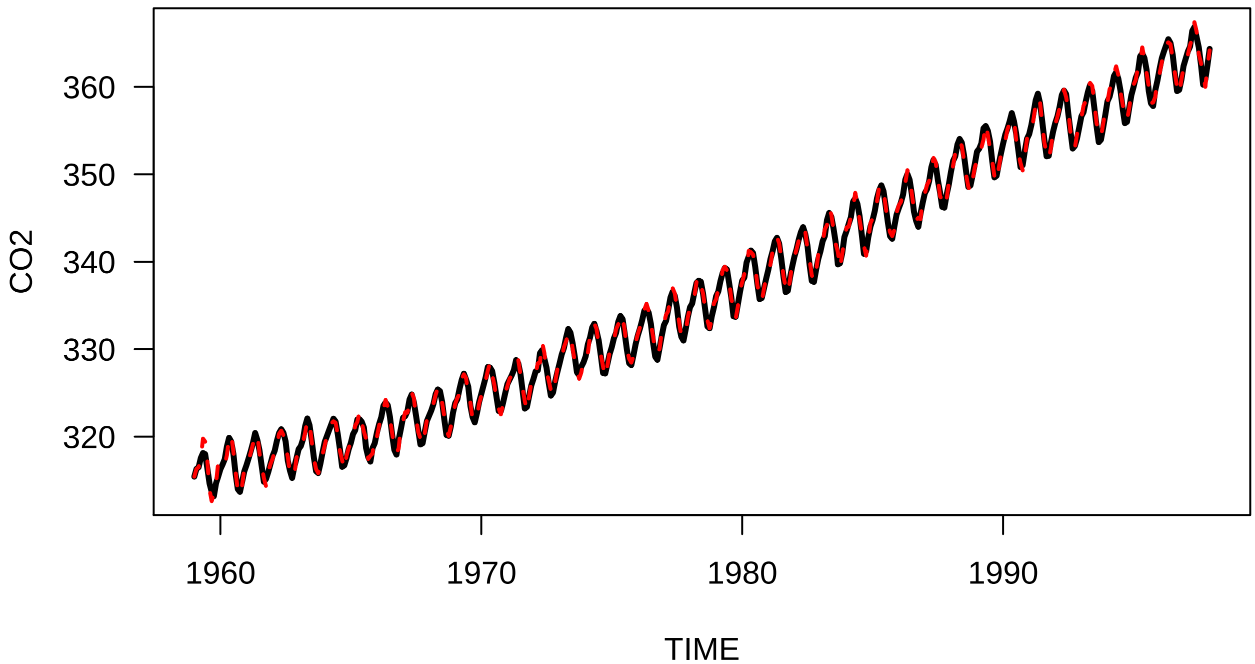
```
##       intercept         1        2         3
##        337.0490  319.4155  31.0893  -10.6938
## s.e.     0.0427    0.9287   0.9322    0.9374
##
## sigma^2 estimated as 0.2073:  log likelihood=-295.79
## AIC=616.78   AICc=617.46   BIC=666.56
##
## Training set error measures:
##                        ME      RMSE       MAE          MPE      MAPE
## Training set 0.0007055813 0.4533035 0.3561352 6.187736e-05 0.1057402
##                   MASE        ACF1
## Training set 0.3308964 -0.08238655
```

```
acf(residuals(fautogls))
```



This is indeed a much better look of the residual autocorrelation. There are occasional peaks here and there, but the overall level is dramatically reduced. Let's plot this model onto the data and see what else can be done.

```
plot(TIME, CO2, type="l", lwd=3)
lines(TIME, fitted.values(fautogls), col="red", lwd=2, lty=2)
```



A marvellous fit! The key thing to notice here is that the *seasonal* pattern of CO_2 is actually fitted using the covariance matrix, **not** using a seasonal predictor. We shouldn't do that, if we can avoid it, because we may want to interpret this seasonality as an actual ecological process, rather than a statistical nuisance.

So, quickly, here is a way to put seasonality into a GLS:

```r
COS <- cos(2*pi*TIME)
SIN <- sin(2*pi*TIME)
fglsseason <- gls(CO2 ~ poly(TIME, 3) + COS + SIN, correlation=COR3)
summary(fglsseason)
```

```
## Generalized least squares fit by REML
##   Model: CO2 ~ poly(TIME, 3) + COS + SIN
##   Data: NULL
##        AIC      BIC    logLik
##   891.9649 933.3205 -435.9824
##
## Correlation Structure: ARMA(3,0)
##  Formula: ~TIME
##  Parameter estimate(s):
##       Phi1       Phi2       Phi3
##  1.6733064 -1.3091694  0.5955463
##
## Coefficients:
##                     Value Std.Error   t-value p-value
## (Intercept)      329.9930  1.905882 173.14448  0.0000
## poly(TIME, 3)1   293.2508 29.689997   9.87709  0.0000
## poly(TIME, 3)2    71.0640 20.830769   3.41149  0.0007
## poly(TIME, 3)3   -14.6249 17.091150  -0.85570  0.3926
## COS               -0.3594  0.079973  -4.49340  0.0000
## SIN                2.8940  0.085547  33.82968  0.0000
##
##  Correlation:
```

```
##                 (Intr) p(TIME,3)1 p(TIME,3)2 p(TIME,3)3 COS
## poly(TIME, 3)1  0.255
## poly(TIME, 3)2 -0.453  0.329
## poly(TIME, 3)3  0.139 -0.550      0.213
## COS            -0.135 -0.033      0.030     -0.015
## SIN            -0.343 -0.103      0.143     -0.042      0.037
##
## Standardized residuals:
##       Min         Q1        Med         Q3        Max
## -2.187965  9.152905 12.387934 13.893225 16.171102
##
## Residual standard error: 0.6299837
## Degrees of freedom: 468 total; 462 residual
```

```
AIC(fgls)
```

```
## [1] 1465.39
```

```
AIC(fglsseason) # much better fit!
```

```
## [1] 891.9649
```

And now the same for the auto.arima (which requires the predictors to be handed over as a matrix):

```
fautoglsseason <- auto.arima(CO2, xreg=cbind(poly(TIME,3), COS, SIN))
summary(fautogls)
```

```
## Series: CO2
## ARIMA(4,0,3) with non-zero mean
##
## Coefficients:
##          ar1      ar2     ar3      ar4      ma1     ma2      ma3
##       2.6924  -3.6352  2.6383  -0.9524  -1.4055  1.2651  -0.3368
## s.e.  0.0145   0.0301  0.0302   0.0144   0.0369  0.0455   0.0399
##       intercept         1        2         3
##        337.0490  319.4155  31.0893  -10.6938
## s.e.     0.0427    0.9287   0.9322    0.9374
##
## sigma^2 estimated as 0.2073:  log likelihood=-295.79
## AIC=616.78   AICc=617.46   BIC=666.56
##
## Training set error measures:
##                        ME      RMSE       MAE          MPE      MAPE
## Training set 0.0007055813 0.4533035 0.3561352 6.187736e-05 0.1057402
##                   MASE        ACF1
## Training set 0.3308964 -0.08238655
```

```
summary(fautoglsseason)
```

```
## Series: CO2
## ARIMA(2,0,2) with non-zero mean
```

```
##
## Coefficients:
##          ar1      ar2     ma1     ma2  intercept         1        2
##       0.8755  -0.7049  0.0733  0.4291   337.0547  319.2127  31.3632
## s.e.  0.0487   0.0466  0.0684  0.0482     0.0367    0.7951   0.7951
##             3      COS     SIN
##      -10.9952  -0.3930  2.7468
## s.e.   0.7956   0.0622  0.0622
##
## sigma^2 estimated as 0.1925:  log likelihood=-279.45
## AIC=580.9   AICc=581.48   BIC=626.53
##
## Training set error measures:
##                         ME      RMSE       MAE           MPE      MAPE
## Training set -0.0002279262 0.4387431 0.3489505 -0.0002288606 0.1033012
##                   MASE      ACF1
## Training set 0.3242209 0.1084915
```

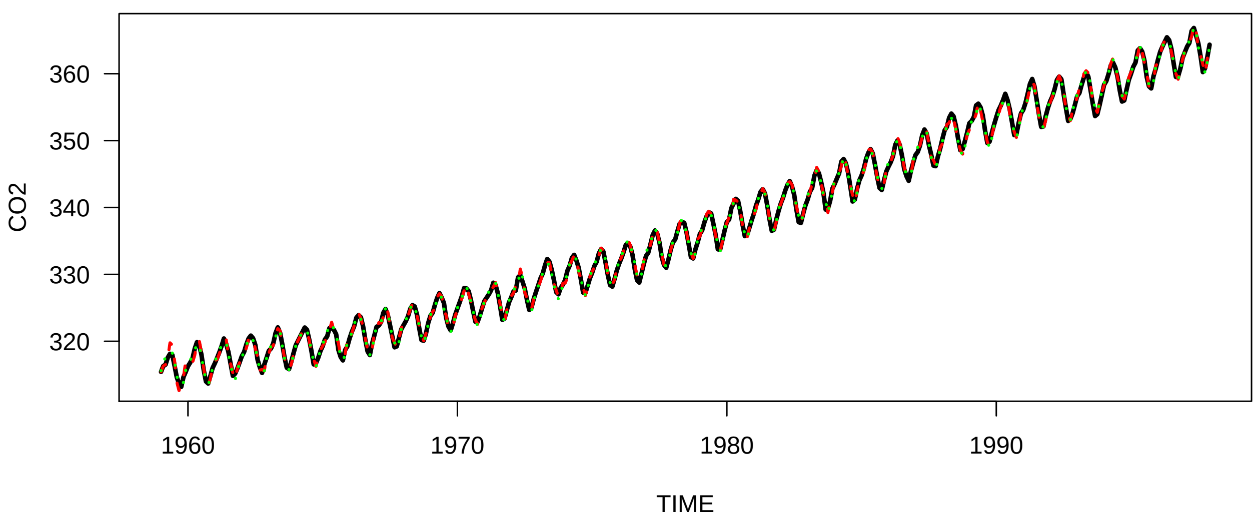
```
AIC(fautogls)
```

```
## [1] 615.5866
```

```
AIC(fautoglsseason)
```

```
## [1] 580.8961
```

```
plot(TIME, CO2, type="l", lwd=3)
lines(TIME, fitted.values(fautogls), col="red", lwd=2, lty=2)
lines(TIME, fitted.values(fautoglsseason), col="green", lwd=2, lty=3)
```



Repeated measurements

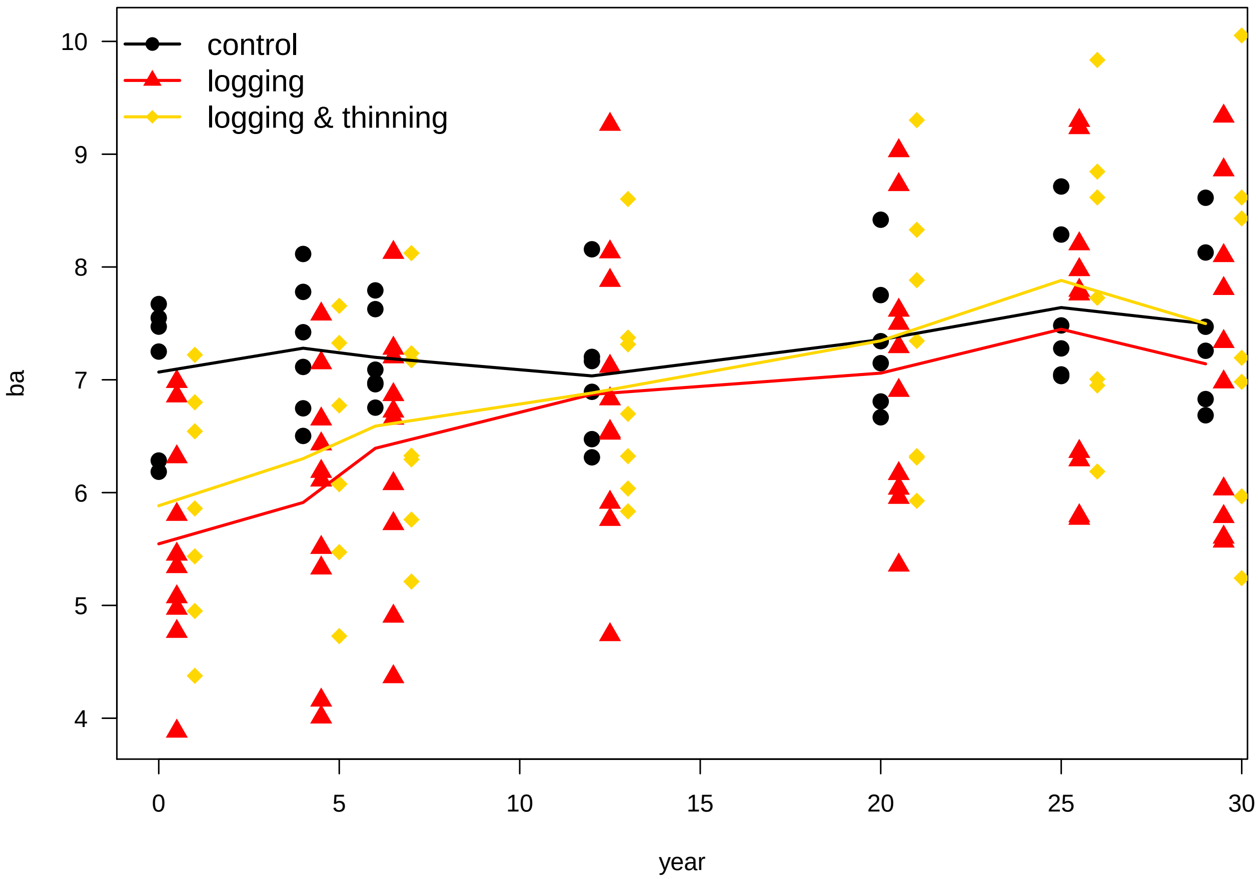
A very common design is to sample units (= subjects, plots) repeatedly, a.k.a. *repeated measurements*. Here we have to tell the model the structure (i.e. samples within plots over time) as well as attempt to represent the temporal dependency itself. Currently, only `lme` and `mgcv::gamm` can handle both a random effect and a correlation structure as in the previous time example.

Let's take a typical example (actually not so typical, but rather exceptional in the long time series these data constitute). In this case, forest plots were treated in three different ways (control, logging, logging and thinning) and monitored repeatedly over decades. Response is basal area (m^2/ha). Additionally, the replicated treatments are arranged in five blocks. First, we make a nice "German" plot of the data.

```
dats <- read.csv("Data_Angela.csv")
summary(dats)
```

```
##      Block       treat    Treat         year           plot
##  Min.   :1.000   T0:42   C   :42   Min.   :1983   Min.   :110.0
##  1st Qu.:2.000   T1:70   L   :70   1st Qu.:1987   1st Qu.:206.0
##  Median :3.000   T2:49   LLTI:49   Median :1995   Median :305.0
##  Mean   :3.174                     Mean   :1997   Mean   :324.3
##  3rd Qu.:5.000                     3rd Qu.:2008   3rd Qu.:504.0
##  Max.   :5.000                     Max.   :2012   Max.   :512.0
##     N.of.Ind           S               H               J
##  Min.   : 77.0   Min.   :40.00   Min.   :3.237   Min.   :0.8281
##  1st Qu.:120.0   1st Qu.:55.00   1st Qu.:3.604   1st Qu.:0.8937
##  Median :126.0   Median :61.00   Median :3.740   Median :0.9137
##  Mean   :127.4   Mean   :59.83   Mean   :3.714   Mean   :0.9092
##  3rd Qu.:136.0   3rd Qu.:65.00   3rd Qu.:3.854   3rd Qu.:0.9250
##  Max.   :158.0   Max.   :76.00   Max.   :4.022   Max.   :0.9521
##       Hstr             ba              vol
##  Min.   :1.532   Min.   : 3.884   Min.   : 36.24
##  1st Qu.:1.778   1st Qu.: 6.078   1st Qu.: 61.72
##  Median :1.869   Median : 6.950   Median : 74.20
##  Mean   :1.848   Mean   : 6.887   Mean   : 73.62
##  3rd Qu.:1.928   3rd Qu.: 7.626   3rd Qu.: 83.02
##  Max.   :2.059   Max.   :10.053   Max.   :115.92
```

```
dats$Block <- as.factor(dats$Block)
dats$plot <- as.factor(dats$plot)
dats$year <- dats$year - 1983 # reset first year to 0
attach(dats)
plot(ba ~ year, las=1, type="n")
points(ba ~ year, data=dats[Treat=="C",], pch=16, cex=1.5)
points(ba ~ I(year+0.5), data=dats[Treat=="L",], pch=17, cex=1.5, col="red")
points(ba ~ I(year+1), data=dats[Treat=="LLTI",], pch=18, cex=1.5, col="gold")
matlines(unique(year), t(tapply(ba, list(Treat, year), mean)), lwd=2, col=c("black", "red", "gold"), lty
legend("topleft", legend=c("control", "logging", "logging & thinning"), col=c("black", "red", "gold"), 
```



Next, we try to fit a model *for the control treatment only*, just as a warm-up exercise. We need to tell the model that `plots` are nested in `Block` and that through the `years` there is a (linear) dependence. For some reason, the grouping structure of the random term and the correlation must be identical. Thus, we fit a correlation for `year` effect per each `plot` in each `Block` (which actually makes sense, too).

```
library(nlme)
flmeC <- lme(ba ~ year, random=~1|Block/plot, correlation=corLin(form=~year|Block/plot), data=dats[Trea
summary(flmeC)
```

```
## Linear mixed-effects model fit by REML
##  Data: dats[Treat == "C", ]
##        AIC      BIC    logLik
##   62.44111 72.57439 -25.22056
##
## Random effects:
##  Formula: ~1 | Block
##         (Intercept)
## StdDev:   0.2018494
##
##  Formula: ~1 | plot %in% Block
##         (Intercept)  Residual
## StdDev:   0.4373343 0.4905449
##
## Correlation Structure: Linear spatial correlation
##  Formula: ~year | Block/plot
##  Parameter estimate(s):
```

```
##    range
## 12.64518
## Fixed effects: ba ~ year
##                 Value Std.Error DF   t-value p-value
## (Intercept) 7.024450 0.3229865 35 21.748429  0.0000
## year        0.015868 0.0096598 35  1.642633  0.1094
##  Correlation:
##      (Intr)
## year -0.425
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.67069908 -0.33653119 -0.01761703  0.74708113  1.90099297
##
## Number of Observations: 42
## Number of Groups:
##           Block plot %in% Block
##               1               6
```

We included **year** as a fixed effect to test, whether over time there was a significant change in basal area (there wasn't, phew, because this is the control and there shouldn't be one).

Now we can ramp up the model and do the same thing across the three treatments:

```
flme <- lme(ba ~ Treat*year, random=~1|Block/plot, correlation=corLin(form=~year|Block/plot), data=dats
anova(flme)
```

```
##             numDF denDF   F-value p-value
## (Intercept)     1   135 315.60604  <.0001
## Treat           2    16   0.29473  0.7487
## year            1   135  52.66428  <.0001
## Treat:year      2   135   3.74813  0.0260
```

```
summary(flme)
```

```
## Linear mixed-effects model fit by REML
##  Data: dats
##        AIC      BIC    logLik
##   292.5515 322.9858 -136.2758
##
## Random effects:
##  Formula: ~1 | Block
##         (Intercept)
## StdDev:   0.7372255
##
##  Formula: ~1 | plot %in% Block
##         (Intercept)  Residual
## StdDev:   0.8154133 0.6011608
##
## Correlation Structure: Linear spatial correlation
##  Formula: ~year | Block/plot
##  Parameter estimate(s):
##   range
```

```
## 12.3611
## Fixed effects: ba ~ Treat * year
##                     Value Std.Error  DF   t-value p-value
## (Intercept)      7.021039 0.8373936 135  8.384396  0.0000
## TreatL          -1.086506 0.9678319  16 -1.122619  0.2782
## TreatLLTI       -1.287857 0.9987940  16 -1.289412  0.2156
## year             0.016007 0.0117984 135  1.356723  0.1771
## TreatL:year      0.036568 0.0149239 135  2.450306  0.0156
## TreatLLTI:year   0.038853 0.0160785 135  2.416486  0.0170
##  Correlation:
##                 (Intr) TreatL TrLLTI year   TrtL:y
## TreatL          -0.865
## TreatLLTI       -0.838  0.858
## year            -0.200  0.173  0.167
## TreatL:year      0.158 -0.219 -0.132 -0.791
## TreatLLTI:year   0.147 -0.127 -0.228 -0.734  0.580
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -2.3961400 -0.3396705  0.0863781  0.6390154  1.8910513
##
## Number of Observations: 161
## Number of Groups:
##          Block plot %in% Block
##              5              23
```

We now see that the three treatments differ in their trajectory over time! They have the same intercept (basal area in year 0 = 1983), as indicated by the non-significant effect of `Treat`. The basal area increases with time (`year` effect), but this time effect is different for the three treatments (`Treat:year` interaction significant). Specifically, for the control there is no trend over time (`year` in the `summary` is not significant), but both treatments exhibit a trend (the interaction effects are significant).

Our model now has various parameters fitted, but how can we "simply" visualise the effect of treatment, across years? To do so, we need to compute the expected value for each level of the random effect(s), for the desired values of the fixed effects. In other words, if we want the value for, say, control in 1990, we need to compute the model prediction *for each `block/plot` combination* and then average those, to get the *population-level* prediction. Let us as an example extract the expected value for one specific plot, treatment and year:

```
newdata <- data.frame("Treat"="C", year=1990, Block="5", plot="504")
predict(flme, newdata=newdata)
```

```
##    5/504
## 39.67845
## attr(,"label")
## [1] "Predicted values"
```

Luckily there is a build-in option in the `predict`-function for `lme` that aggregates across all random effects if we are only interested in the population-level prediction. If we additionally are interested in the confidence interval of this prediction (and I think we should be), then we need to resort to another package and function.

```
newdata <- data.frame("Treat"="C", year=1990)
predict(flme, newdata=newdata, level=0)
```

```
## [1] 38.87518
## attr(,"label")
## [1] "Predicted values"
```

```r
library(AICcmodavg)
predictSE(flme, newdata=newdata, level=0)
```

```
## $fit
## [1] 38.87518
##
## $se.fit
## [1] 23.32589
```

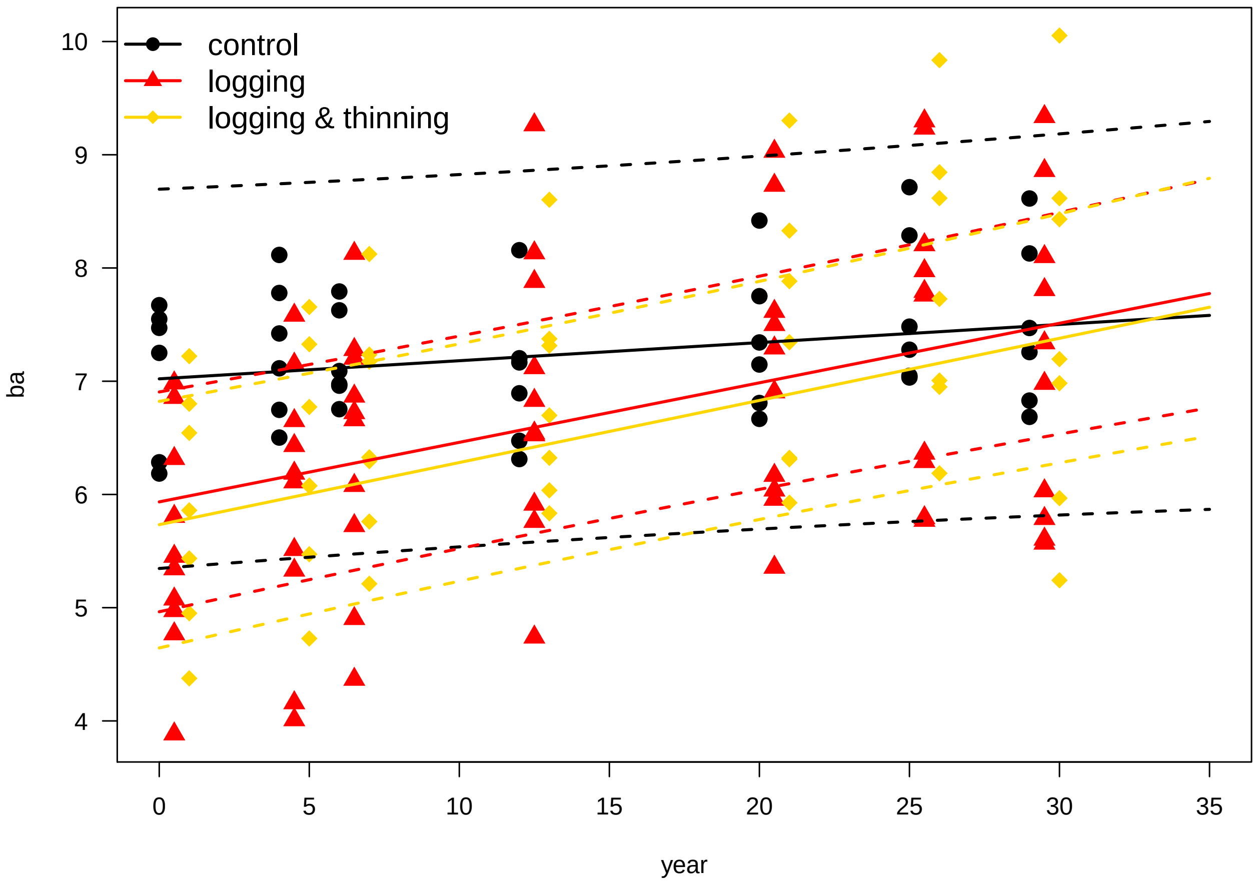
The `level=0` instructs the model to do this averaging over all random effects for us, and only returns the population-level estimate. Note, however, that we cannot just take random values for `Block` and `plot`, but rather use combinations that actually exist!

So now turn this into a nice plot:

```r
attach(dats)
```

```
## The following objects are masked from dats (position 4):
##
##     ba, Block, H, Hstr, J, N.of.Ind, plot, S, treat, Treat, vol,
##     year
```

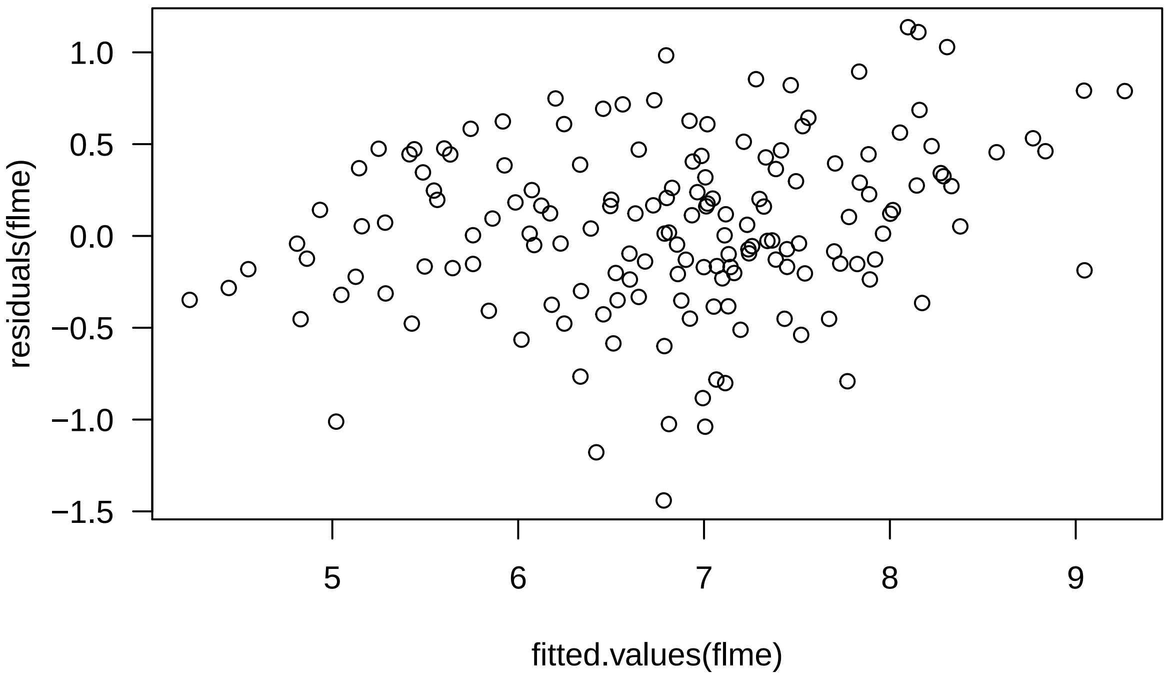
```r
plot(ba ~ year, las=1, type="n", xlim=c(0, 35))
points(ba ~ year, data=dats[Treat=="C",], pch=16, cex=1.5)
points(ba ~ I(year+0.5), data=dats[Treat=="L",], pch=17, cex=1.5, col="red")
points(ba ~ I(year+1), data=dats[Treat=="LLTI",], pch=18, cex=1.5, col="gold")
newC <- data.frame("Treat"="C", year=0:35)
predsC <- predictSE(flme, newdata=newC, level=0)
matlines(0:35, cbind(predsC$fit,predsC$fit + 2*predsC$se.fit, predsC$fit - 2*predsC$se.fit), lwd=2, lty
newL <- data.frame("Treat"="L", year=0:35)
predsL <- predictSE(flme, newdata=newL, level=0)
matlines(0:35, cbind(predsL$fit, predsL$fit + 2*predsL$se.fit, predsL$fit - 2*predsL$se.fit), lwd=2, lt
newLT <- data.frame("Treat"="LLTI", year=0:35)
predsLT <- predictSE(flme, newdata=newLT, level=0)
matlines(0:35, cbind(predsLT$fit, predsLT$fit + 2*predsLT$se.fit, predsLT$fit - 2*predsLT$se.fit), lwd=
legend("topleft", legend=c("control", "logging", "logging & thinning"), col=c("black", "red", "gold"),
```



You may wonder, why the 96%-confidence intervals are so parallel to the expected values. The main reason is that they depict only the effect of the fixed effect. Another that I have not extrapolated much beyond the data. There you should see a substantial increase in spread of the CI.

Finally, we should always do the usual model diagnostics: residual plots, alternative model structure, etc. Here is a plot of residuals over fitted:

```
plot(residuals(flme) ~ fitted.values(flme))
```



Hm. Is it only me who can see some upwards trend in the right half of the plot? Maybe the trend is not linear through time? I add a quadratic term for `year` and its interactions, plus a cubic term for `year` alone (wouldn't converge otherwise).

```
flme2 <- lme(ba ~ Treat*(year+I(year^2)) + I(year^3), random=~1|Block/plot, correlation=corLin(form=~yea
anova(flme2)
```

```
##                   numDF denDF   F-value p-value
## (Intercept)           1   131 315.09821  <.0001
## Treat                 2    16   0.29361  0.7495
## year                  1   131  60.04371  <.0001
## I(year^2)             1   131  17.96329  <.0001
## I(year^3)             1   131   3.25469  0.0735
## Treat:year            2   131   4.30400  0.0155
## Treat:I(year^2)       2   131   2.40724  0.0940
```

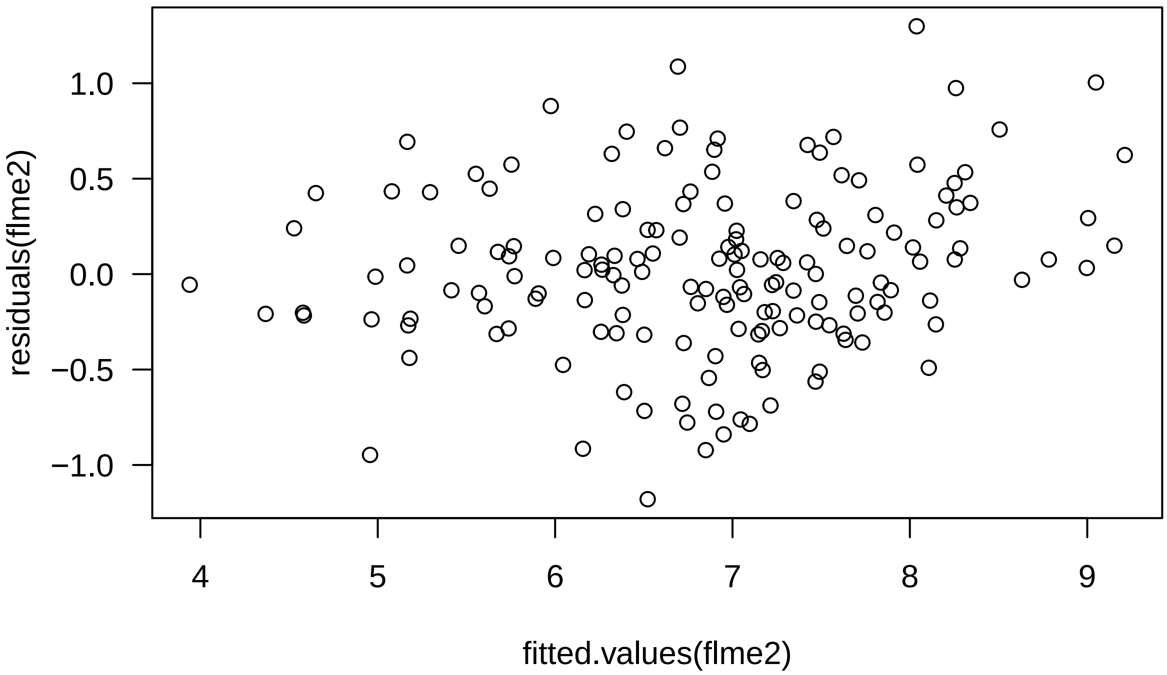
```
summary(flme2)
```

```
## Linear mixed-effects model fit by REML
##  Data: dats
##        AIC      BIC    logLik
##   330.0395 372.2814 -151.0197
##
## Random effects:
##  Formula: ~1 | Block
##         (Intercept)
## StdDev:   0.7383107
##
##  Formula: ~1 | plot %in% Block
##         (Intercept)  Residual
## StdDev:   0.8234325 0.5621305
```

```
##
## Correlation Structure: Linear spatial correlation
##  Formula: ~year | Block/plot
##  Parameter estimate(s):
##    range
## 12.55121
## Fixed effects: ba ~ Treat * (year + I(year^2)) + I(year^3)
##                         Value Std.Error  DF   t-value p-value
## (Intercept)          6.998420 0.8415239 131  8.316365  0.0000
## TreatL              -1.340809 0.9732582  16 -1.377649  0.1873
## TreatLLTI           -1.497400 1.0047462  16 -1.490326  0.1556
## year                -0.017549 0.0409769 131 -0.428261  0.6692
## I(year^2)            0.004059 0.0026633 131  1.523882  0.1299
## I(year^3)           -0.000101 0.0000559 131 -1.804075  0.0735
## TreatL:year          0.121679 0.0421003 131  2.890225  0.0045
## TreatLLTI:year       0.109226 0.0453573 131  2.408127  0.0174
## TreatL:I(year^2)    -0.002923 0.0013674 131 -2.137820  0.0344
## TreatLLTI:I(year^2) -0.002420 0.0014732 131 -1.642706  0.1028
##  Correlation:
##                     (Intr) TreatL TrLLTI year   I(y^2) I(y^3) TrtL:y
## TreatL              -0.865
## TreatLLTI           -0.838  0.856
## year                -0.136  0.117  0.113
## I(year^2)            0.047 -0.039 -0.038 -0.844
## I(year^3)           -0.002  0.000  0.000  0.583 -0.914
## TreatL:year          0.131 -0.182 -0.110 -0.642  0.303  0.000
## TreatLLTI:year       0.122 -0.105 -0.190 -0.596  0.281  0.000  0.580
## TreatL:I(year^2)    -0.087  0.121  0.073  0.606 -0.321  0.000 -0.943
## TreatLLTI:I(year^2) -0.081  0.070  0.126  0.562 -0.298  0.000 -0.547
##                     TrLLTI: TL:I(^
## TreatL
## TreatLLTI
## year
## I(year^2)
## I(year^3)
## TreatL:year
## TreatLLTI:year
## TreatL:I(year^2)    -0.547
## TreatLLTI:I(year^2) -0.943   0.580
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.09762411 -0.41586193  0.03725153  0.50560563  2.30961144
##
## Number of Observations: 161
## Number of Groups:
##           Block plot %in% Block
##               5              23
```

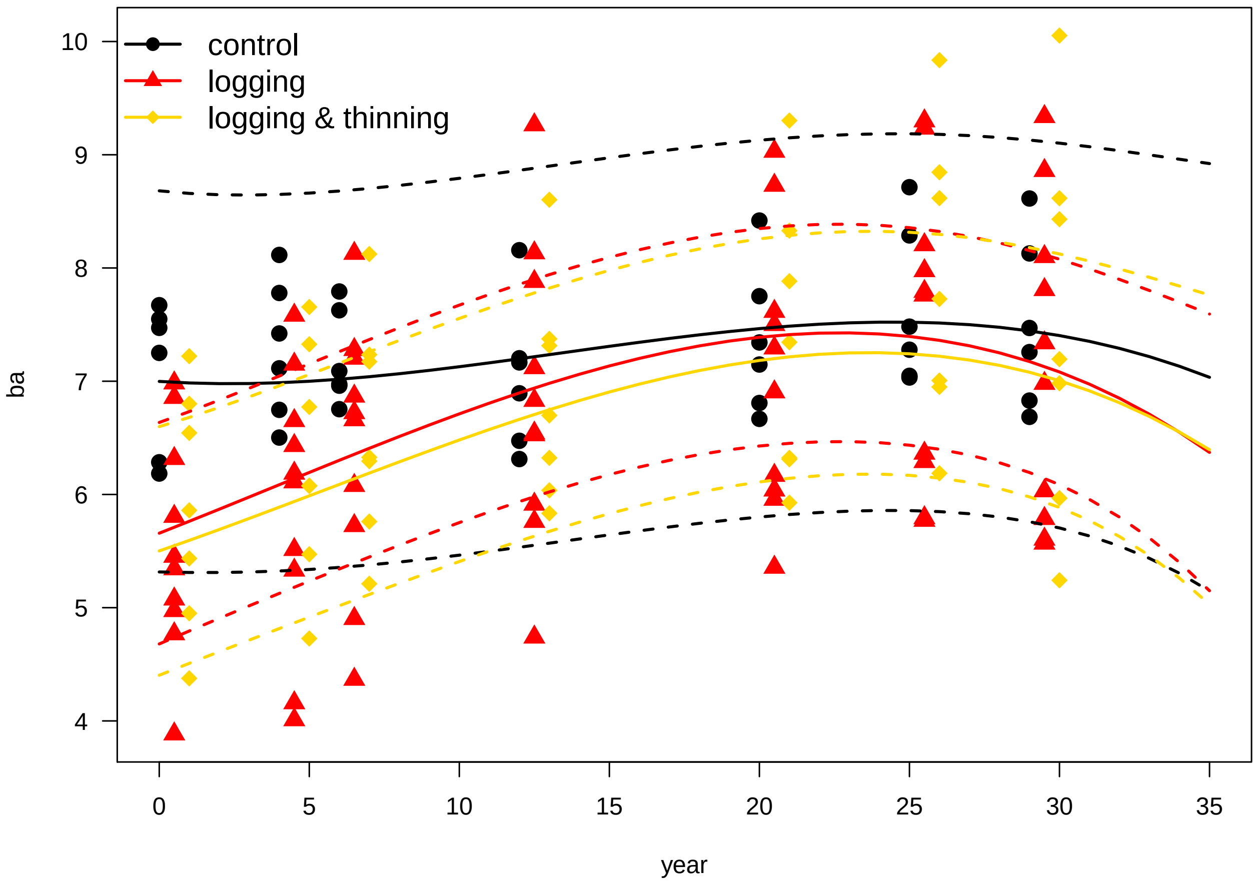
Ah! So there is evidence for a non-linear trend (in the `summary`: `TreatL:poly(year, 2)2` is significant). What do the residuals for this model look like?

```
plot(residuals(flme2)~ fitted.values(flme2))
```



Better! Now we want to see the plot with the new model as well:

```
plot(ba ~ year, las=1, type="n", xlim=c(0, 35))
points(ba ~ year, data=dats[Treat=="C",], pch=16, cex=1.5)
points(ba ~ I(year+0.5), data=dats[Treat=="L",], pch=17, cex=1.5, col="red")
points(ba ~ I(year+1), data=dats[Treat=="LLTI",], pch=18, cex=1.5, col="gold")
newC <- data.frame("Treat"="C", year=0:35)
predsC <- predictSE(flme2, newdata=newC, level=0)
matlines(0:35, cbind(predsC$fit,predsC$fit + 2*predsC$se.fit, predsC$fit - 2*predsC$se.fit), lwd=2, lty
newL <- data.frame("Treat"="L", year=0:35)
predsL <- predictSE(flme2, newdata=newL, level=0)
matlines(0:35, cbind(predsL$fit, predsL$fit + 2*predsL$se.fit, predsL$fit - 2*predsL$se.fit), lwd=2, lt
newLT <- data.frame("Treat"="LLTI", year=0:35)
predsLT <- predictSE(flme2, newdata=newLT, level=0)
matlines(0:35, cbind(predsLT$fit, predsLT$fit + 2*predsLT$se.fit, predsLT$fit - 2*predsLT$se.fit), lwd=
legend("topleft", legend=c("control", "logging", "logging & thinning"), col=c("black", "red", "gold"),
```



We can also fit a spline for each treatment, using `mgcv:gamm`. The arguments in the spline call are necessary to avoid error messages: `k=3` restricts the flexibility of the spline to the equivalent of a cubic polynomial, while `bs="ts"` employs shrinkage to make the splines as straight as possible (this is a very layman's explanation of what shrinkage is):

```
library(mgcv)
```

```
## This is mgcv 1.8-3. For overview type 'help("mgcv-package")'.
```

```
fgamm <- gamm(ba ~ s(year, by=Treat, k=3, bs="ts"), random=list("Block"=~1, "plot"=~1), correlation=corl
summary(fgamm$lme)
```

```
## Linear mixed-effects model fit by maximum likelihood
##  Data: strip.offset(mf)
##        AIC      BIC    logLik
##   266.3589 291.0102 -125.1795
##
## Random effects:
##  Formula: ~Xr - 1 | g
##  Structure: pdIdnot
##                   Xr1          Xr2
## StdDev: 0.0009643875 0.0009643875
##
##  Formula: ~Xr.0 - 1 | g.0 %in% g
##  Structure: pdIdnot
```

```
##            Xr.01    Xr.02
## StdDev: 14.16486 14.16486
##
##  Formula: ~Xr.1 - 1 | g.1 %in% g.0 %in% g
##  Structure: pdIdnot
##            Xr.11    Xr.12
## StdDev: 8.376302 8.376302
##
##  Formula: ~1 | Block %in% g.1 %in% g.0 %in% g
##         (Intercept)
## StdDev:   0.3508668
##
##  Formula: ~1 | plot %in% Block %in% g.1 %in% g.0 %in% g
##         (Intercept) Residual
## StdDev:   0.7353135 0.844924
##
## Correlation Structure: Linear spatial correlation
##  Formula: ~year | g/g.0/g.1/Block/plot
##  Parameter estimate(s):
##   range
## 31.0585
## Fixed effects: y ~ X - 1
##      Value Std.Error  DF  t-value p-value
## X 6.781793 0.2603949 138 26.04426       0
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.47443021 -0.42147990  0.07688521  0.45900763  1.82817432
##
## Number of Observations: 161
## Number of Groups:
##                                       g
##                                       1
##                              g.0 %in% g
##                                       1
##                     g.1 %in% g.0 %in% g
##                                       1
##           Block %in% g.1 %in% g.0 %in% g
##                                       5
## plot %in% Block %in% g.1 %in% g.0 %in% g
##                                      23
```

The interpretation is a bit more awkward, since we now have a GAM-part of the object, and an LME-part. We can use the LME-part of the model to investigate how much variance is attributed to different hierarchical levels. And, citing from the `gamm` help page (see Value: lme), "Note that the model formulae and grouping structures may appear to be rather bizarre, because of the manner in which the GAMM is split up and the calls to lme and gammPQL are constructed." This means that we may not actually be completely sure, whether the coding of the random effects is correct. (You may want to try, e.g. `"Block"=~1|plot` to see that this gives different estimates, especially for the range of spatial autocorrelation! I used this as a guidance that it would *not* be the correct way to communicate the random effect structure to `gamm`.)

First of all, the AIC is (substantially) lower for the GAMM than for the LME. (I actually had `Treat` as an additional fixed effect in the GAMM, but that model was slightly worse and so I deleted it.) Secondly, both range and `Block/plot` random effects are estimated very similarly. And finally, `year:Treat` is also indicating a different slope for the two treatments than for the control.

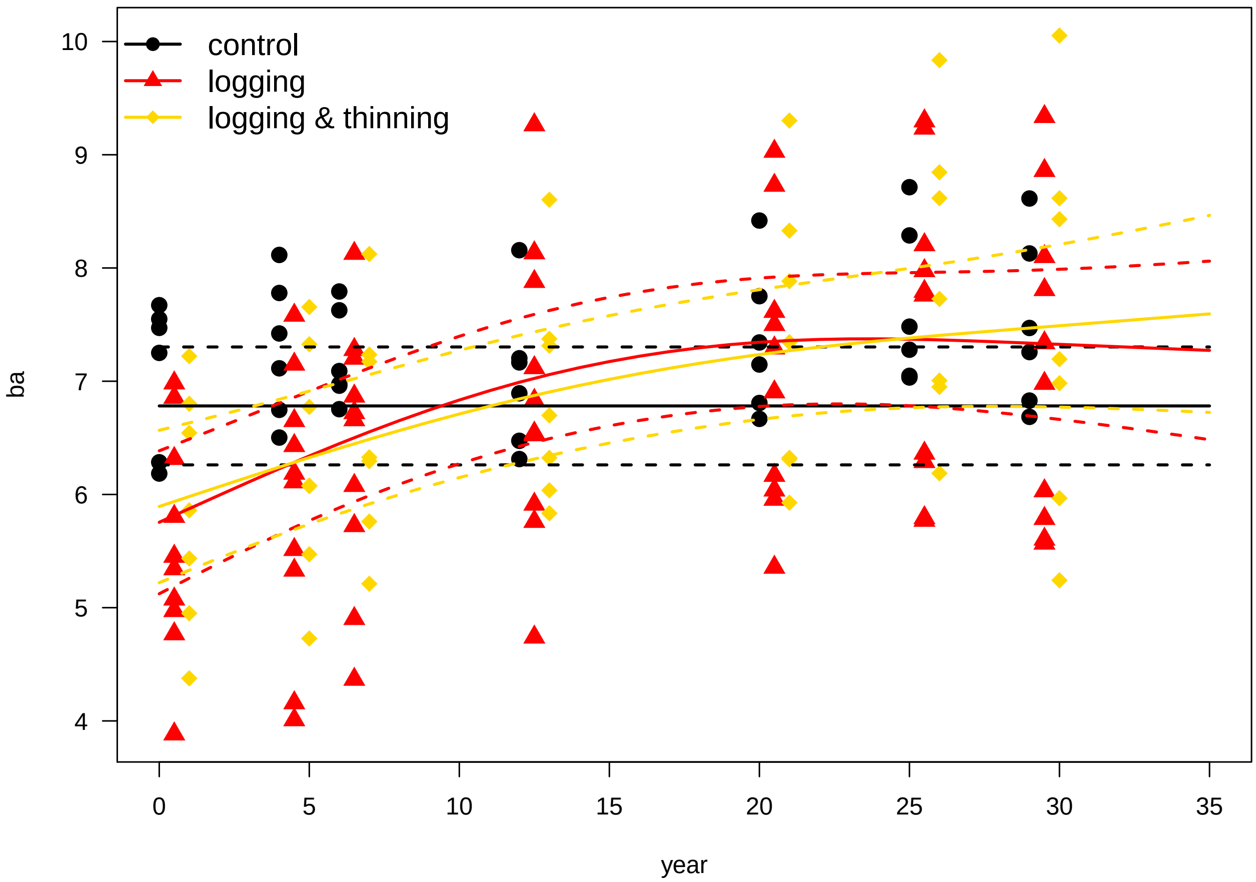
```
summary(fgamm$gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## ba ~ s(year, by = Treat, k = 3, bs = "ts")
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   6.7818     0.2604   26.04   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                         edf Ref.df      F  p-value
## s(year):TreatC    5.207e-07      2  0.000    0.366
## s(year):TreatL    1.877e+00      2 16.904 1.04e-07 ***
## s(year):TreatLLTI 1.626e+00      2  8.537 8.62e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.188
##   Scale est. = 0.7139    n = 161
```

The GAM-part of the model tells us that the "spline" for controls over time is horizontal (has virtually no estimated degree of freedom, edf), while those for the two treatments L and LLTI have a unimodal shape (2 edf). The control-trend is not significant, but those for the two logging treatments are.

Let's plot also this model. Notice that we only use the GAM-part of the model, which has an `se.fit` option. Here the fixed-only structure of the predictions is more explicit than in the previous LMEs.

```
plot(ba ~ year, las=1, type="n", xlim=c(0, 35))
points(ba ~ year, data=dats[Treat=="C",], pch=16, cex=1.5)
points(ba ~ I(year+0.5), data=dats[Treat=="L",], pch=17, cex=1.5, col="red")
points(ba ~ I(year+1), data=dats[Treat=="LLTI",], pch=18, cex=1.5, col="gold")
newC <- data.frame("Treat"="C", year=0:35)
predsC <- predict(fgamm$gam, newdata=newC, se.fit=T)
matlines(0:35, cbind(predsC$fit,predsC$fit + 2*predsC$se.fit, predsC$fit - 2*predsC$se.fit), lwd=2, lty=
newL <- data.frame("Treat"="L", year=0:35)
predsL <- predict(fgamm$gam, newdata=newL, se.fit=T)
matlines(0:35, cbind(predsL$fit, predsL$fit + 2*predsL$se.fit, predsL$fit - 2*predsL$se.fit), lwd=2, lt
newLT <- data.frame("Treat"="LLTI", year=0:35)
predsLT <- predict(fgamm$gam, newdata=newLT, se.fit=T)
matlines(0:35, cbind(predsLT$fit, predsLT$fit + 2*predsLT$se.fit, predsLT$fit - 2*predsLT$se.fit), lwd=
legend("topleft", legend=c("control", "logging", "logging & thinning"), col=c("black", "red", "gold"), 
```




```r
detach(dats)
```