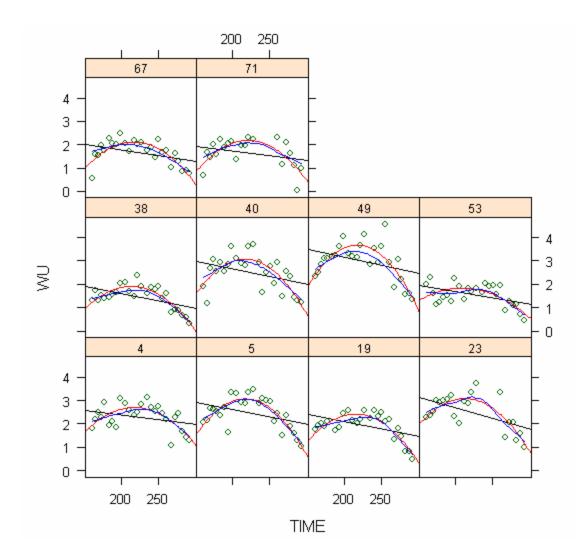
Ecol 145 Assignment 11 Dahl Winters 4/21/06

## **Question 1**

Restrict the data set so that you're only looking at trees of species 2 and in age class 2. For this restricted data set generate a customized lattice plot that resembles the one shown in Fig. 2 of Lecture 43. Each panel should display a different individual tree.

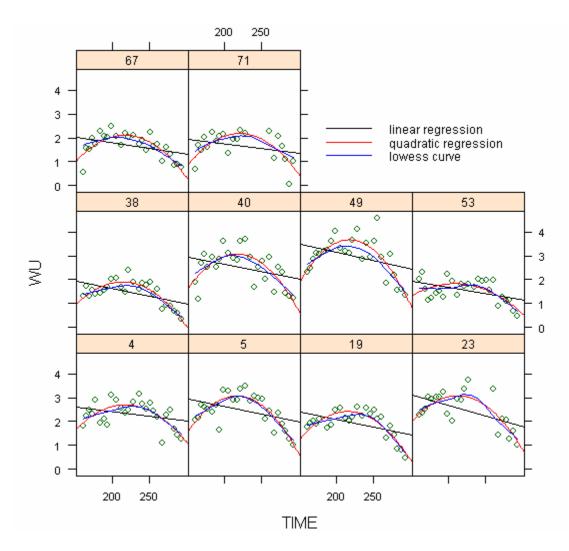
```
waterdata<-
read.table('http://www.unc.edu/courses/2006spring/ecol/145/001/data/lab12/Wat
erUsageData.csv', header=TRUE, sep=',')
water<-waterdata[waterdata$SPECIES==2 & waterdata$AGE==2,</pre>
c("WU","TIME","TREE")]
waterdata$tree.f<-factor(waterdata$TREE)</pre>
water$tree.f<-factor(water$TREE)</pre>
water[1:3,]
      WU TIME TREE tree.f
744 1.80 161 4 4
745 2.04 161
                5
                         5
746 1.78 161 19
                        19
Trying a quadratic model to see what coefficients need to be entered in the xyplot later
quad<-glm(WU~TIME+I(TIME^2), data=water)</pre>
coef(quad)
  (Intercept)
                        TIME
                                  I(TIME<sup>2</sup>)
-1.062155e+01 1.223315e-01 -2.828604e-04
Plotting the graph
library(lattice)
trellis.par.set(col.whitebg())
xyplot(WU~TIME|tree.f, data=water, panel=function(x,y) {
panel.xyplot(x,y)
panel.abline(lm(y~x), col=1)
quad<-glm(y~x+I(x^2), data=water)</pre>
panel.curve(coef(quad)[1]+coef(quad)[2]*x+coef(quad)[3]*x^2, col=2)
panel.loess(x,y, col=4)
},
strip=strip.custom(par.strip.text = list(cex=0.75)))
```



Add a key to the panel display that identifies the color codes and line types you used to indicate the three different regression models. There are ten trees plotted and by default they will be arranged in three rows and four columns. Place the key in the top right corner where two panels are missing.

#### Plotting the graph

```
library(lattice)
trellis.par.set(col.whitebg())
xyplot(WU~TIME|tree.f, data=water, panel=function(x,y) {
panel.xyplot(x,y)
panel.abline(lm(y~x), col=1)
quad<-glm(y~x+I(x^2), data=water)
panel.curve(coef(quad)[1]+coef(quad)[2]*x+coef(quad)[3]*x^2, col=2)
panel.loess(x,y, col=4)
},
strip=strip.custom(par.strip.text = list(cex=0.75)),
par.settings=list(axis.text=list(cex=0.7)),
key=list(lines=list(lty=c(1,1,1),col=c(1,2,4)), text=list(c("linear
regression","quadratic regression","lowess curve"), cex=rep(.75,3)),
border=0, x=0.55, y=0.7, corner=c(0,0))</pre>
```



# **Question 2**

Based on the graphical display of Question 1 a quadratic model looks good. Fit a quadratic level-1 model to the full data set (and not just the ten trees you used to produce the graph). This level-1 model has three parameters which means that there are potentially three level-2 equations that can have random effects. As a start fit three models, one for each parameter, such that in each model you allow a different level-1 parameter to be random, but the remaining parameters are fixed. Decide which of these three models is best.

```
model1<-lme(WU~TIME+I(TIME^2), random=~1|tree.f, data=waterdata, method='ML')
model2<-lme(WU~TIME+I(TIME^2), random=~TIME-1|tree.f, data=waterdata,
method='ML')
model3<-lme(WU~TIME+I(TIME^2), random=~I(TIME^2)-1|tree.f, data=waterdata,
method='ML')
Finding the best model using AIC
sapply(list(model1,model2,model3),AIC)
[1] 1646.792 1568.143 1650.473</pre>
```

The model with the lowest AIC is model2, which has just time as the level 1 parameter that is random.

## **Question 3**

To the model you chose as best in Question 2 try adding the remaining random effects. There are three possible choices here and hence three models that can result. Decide which of these three models is best.

```
Three possible choices: the predictor time affects just the intercept, just
the slope, or both the intercept and slope.
model2a<-lme(WU~TIME+I(TIME^2), random=~TIME-1|tree.f, data=waterdata,
method='ML')
model2a<-lme(WU~TIME+I(TIME^2), random=~TIME|tree.f, data=waterdata,
method='ML')
model2b<-lme(WU~TIME+I(TIME^2), random=~I(TIME^2)|tree.f, data=waterdata,
method='ML')
model2c<-lme(WU~TIME+I(TIME^2), random=~TIME+I(TIME^2)|tree.f,
data=waterdata, method='ML')
```

```
Finding the best model using AIC
sapply(list(model2,model2a,model2b,model2c),AIC)
[1] 1568.143 1422.660 1435.063 1433.934
```

The model with the lowest AIC is model2a, which has random effects for both the time and the intercept (b0 and b1).

## **Question 4**

Since the predictor is time we should check to see whether the default level-1 residual correlation structure is adequate. Try adding a corCAR1 structure and see if the fit is improved. The

```
correlation model specified by corCAR1 is \rho = \phi^s where s is the amount of time that has elapsed between observations.
```

```
model2a<-lme(WU~TIME+I(TIME^2), random=~TIME|tree.f, data=waterdata,
method='ML')
model2acs<-lme(WU~TIME+I(TIME^2), random=~TIME|tree.f, data=waterdata,
method='ML',correlation=corCAR1(form=~TIME|tree.f))
```

```
Finding the best model using AIC
sapply(list(model2,model2acs),AIC)
[1] 1568.143 1384.723
```

The AIC of the model using corCAR1 for the correlation structure is considerably lower than the one without it, so the model's fit must have improved tremendously.

Checking the significance of adding the correlation structure anova (model 2a, model 2acs)

anova (moderna/modernaeb)								
	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
model2a	1	7	1422.660	1456.958	-704.3299			
model2acs	2	8	1384.723	1423.921	-684.3617	1 vs 2	39.93649	<.0001

The p-value is highly significant, which supports the AIC results that adding the correlation structure is important.