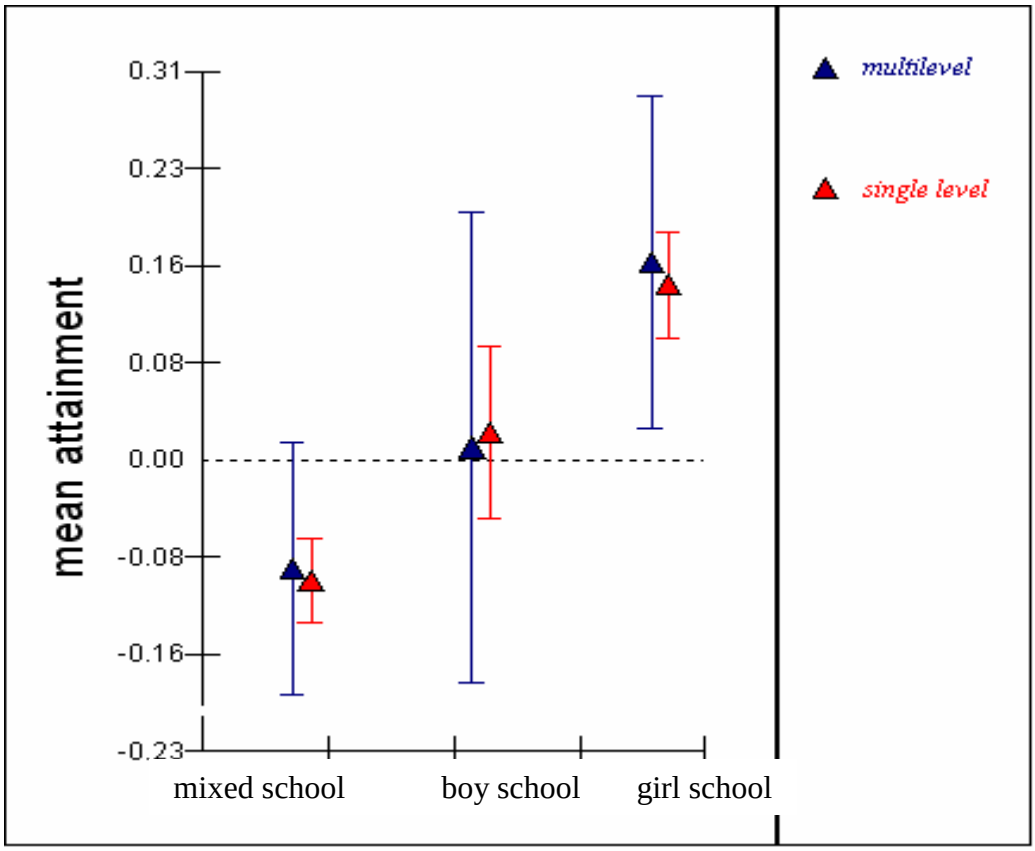
Analyzing Longitudinal Data in R (Formerly HLM in R)

Multi-level Modeling

This Wiki is a basic introduction to analyzing longitudinal data in R. The type of modeling used is sometimes referred to as growth or measurement of change model and is a subset of a broad class of multi-level or hierarchical linear models (Singer & Willett, 2003). The power of these models in social science research is their ability to handle the reality that individuals in society are part of groups and to distinguish between individual-level versus group-level fixed and random effects. In analyzing such datasets, there may be violations of the assumption of independence and homogeneity of variance. For example, there is often dependence in longitudinal data where multiple data points are collected from the same individual over time, and in hierarchical datasets, pupils' scores may be more similar to the their own classroom mean than to an overall school-level mean.

Multilevel-modeling recognizes the hierarchy in a dataset and allows for residual variances at each level in order to properly model more of the variance. Since ordinary least-squares regression (OLS) underestimates the full variance, if you attempt to answer questions about the degree of group-level variance that is due to a given predictor, you are likely to get erroneous results.



For example, in this figure from Day & Rasbash (1996), mean attainment is modeled across three school types, using both traditional regression and multi-level modeling techniques. While there appear to be true between-school effects when traditional regression is applied, the error bars are much wider and there is no effect under multi-level modeling.

Measurement of Change Models

Change will be measured at two levels using a within-person model (Level 1) and a between-person model (Level 2). The goal of this analysis is to model change over time for individuals (i.e. individual growth trajectories) at Level 1, and then consider whether elements of these growth trajectories (i.e., intercept and slope) are related to predictors of interest at Level 2. Individual growth trajectories, which will be demonstrated below in the preliminary analyses section can be specified as follows:

Level-1 (within-person)

$$DV_{ij} = \pi_{0i} + \pi_{1i} (Time)_{ij} + \varepsilon_{ij},$$
$$\varepsilon_{ij} \sim N(0, \sigma_{\varepsilon}^2),$$

where the dependent variable for each person, i at time, j, is a function of π_{0i}, a common baseline score at Time, 0 (initial score); π_{1i} , a common, constant change in scores per unit of Time; and ε_{ij}, a unique residual for each person, i, at time, j.

At Level-2 (between-person), the intercept, π_{0i} and slope, $\pi_{1i,}$ are further defined. In an Unconditional Growth Model, the intercept has an initial mean value specified by the Greek letter, gamma (γ_{00}), and a residual error term specified by zeta (ζ_{0i}). The first number in the subscript for intercepts begins with, 0 and the second indicates the term's relative position among all the factors. This is the same for slope terms, except that the initial subscript is a 1.

Level-2 (between-person) Unconditional Growth Model (UGM)

$$\pi_{0i} = \gamma_{00} + \zeta_{0i}$$
$$\pi_{1i} = \gamma_{10} + \zeta_{1i}$$

Additionally, the covariance structure of the residuals for the intercepts and slopes is specified as follows:

$$\begin{pmatrix} \zeta_{0i} \\ \zeta_{1i} \end{pmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_0^2 & \sigma_{01} \\ \sigma_{10} & \sigma_1^2 \end{bmatrix} \right)$$

Taken together, the Level-1 and Level-2 models indicate that the dependent variable has an initial average value (γ_{00}) with some residual variation (ζ_{0i}) between subjects in that initial value. We also know that scores on the dependent variable change as a function of time (i.e., have a slope) and that this slope has an initial average value (γ_{10}) with some residual variation (ζ_{1i}) between subjects in that initial value.

The model for the between-subject residual intercepts, ζ_{0i} and residual slopes, ζ_{1i} says that these values are each normally distributed with means of 0 and variances specified with covariance

matrix. This matrix also includes a covariance term σ_{10} (= σ_{01}) which can be evaluated to determine the degree to which the error terms for intercepts and slopes are intercorrelated.

This Unconditional Growth Model may actually describe a given dataset or it may be useful as a baseline comparison with other models that introduce new terms at Level-2. We might find, for example, that individuals in one group differ from another group in terms of their intercepts or slopes or both. Such conditional group differences, the Conditional Growth Model might be modeled as follows:

Conditional Growth Model for Treatment (CGM-Treatment)

$\pi_{0i} = \gamma_{00} + \gamma_{01}\ \text{Predictor}_i + \zeta_{0i}$

$\pi_{1i} = \gamma_{10} + \gamma_{11}\ \text{Predictor}_i + \zeta_{1i}$

As in the previous UGM, these Level-1 and Level-2 models specify initial average values and residual variations for the intercept and slope. Additionally, the intercept and slope each varies separately as a function of group membership specified by the predictor variable. For example, if the Predictor is specified by a contrast code (+.5 for Female, -.5 for Male), γ_{01} = -.1, and γ_{11} = .2, then males will have an additional .05 (= -.5 * -.1) units of the DV added to their intercepts and their slopes will change by -.01 (= -.5 * .2) units of the DV per unit of Time.

With these basic models, we can now move forward with a sample dataset to illustrate how to analyze measurement of change models in R.

Smoking Cessation Program

In the following example, a smoking cessation program is tested over the course of two months to determine how successful the intervention is compared with a group of control subjects. We will begin by creating a database of subjects, Subj (S1 to S100), half of whom receive treatment for smoking cessation and the other half who are controls, Treat (T vs N). The dependent variable is NCIG, the number cigarettes smoked daily averaged over a monthly period. Time will be measured at three points, including an initial screening and follow-up at the end of the following two months, Months (0, 1, and 2), and Gender (M vs F) is also recorded as a possible explanatory variable of interest.

Follow along the blue boxes (and especially the explanatory notes) which demonstrate the code in R to generate this data. Green boxes provide output from the R command line, and graphs have been generated from running code below.

```
#Open the nlme library which is used for multi-level modeling and
# the lattice library which is used for the xyplot below
#(You may need to download these first)
library(nlme)
library(lattice)
#Set seed so that any data generated will be the same as this example
set.seed(2345)
```

```
#BUILD PERSON DATASET
#Create unique codes for each individual and other variables
n=500 #total number of subjects
Subj <- paste("s",sample(c(1001:2000),n,replace=FALSE),sep="")
#Assign Treatment to first half; Control to other half
Treat <- c(rep("T",n/2),rep("C",n/2))
#Randomly assign gender with 50/50 distribution
Gender <- sample(c("M","F"),n,replace=TRUE,prob=c(.5,.5))
#Create database from above columns
Smoke <- data.frame(Subj,Treat,Gender)
#Create contrast code for Condition
Smoke$Treat.code=(Smoke$Treat=="T")*1-.5
```

Note that a person-level dataset (in which each person has a single record and multiple dependent variables across measurement times) is a first step which is useful in making certain graphs to see trends in your data by individual. However, in later data analysis, it is necessary to convert this to a person-period dataset (where each person has multiple records for each measurement time and a single dependent variable) which also contains a time-indicating variable in order to make use of the multi-level modeling functions in R.

Using the concept of Level-1 and Level-2 models, we can work backwards to assign the values we want (or discover by playing around) in our dependent variable.

```
#ASSIGN VALUES FOR LEVEL-2 INTERCEPTS AND SLOPES
#Assign the mean value of NCIG at the intercept
G00= 30
#Assign the average slope (unit change in NCIG per month)
G10= -10
#Assign the conditional change in slope for Treatment versus No Treatment
G11= -5
```

```
#COMPUTE INTERCEPT AND SLOPE FOR 1ST ORDER EQUATIONS
#Create an (n X 1) column vector of 1's
ONE_C <- matrix(1,nrow=n,ncol=1)
#Create an (n X 3) matrix of 1's
ONE_R <- matrix(1,nrow=n,ncol=3)
#Create an (n X 3) vector of 2nd-order intercepts
B0 <- G00 * ONE_R
#Create an (n X 1) column vector which includes variance in 2nd-order slopes
B1 <- G10 * ONE_C + G11 * ONE_C * Smoke$Treat.code + rnorm(n,mean=0,sd=.1)
#Create a (1 X 3) matrix representing months
month <- matrix(c(0,1,2),nrow=1,ncol=3)
#Assemble all these elements into a score matrix for number of cigarettes smoked
#including individual variance for all n-subjects over 3 months
NCIG <- B0 + B1 %*% month + rnorm(n*3,mean=0,sd=5)
#Create the individual columns of scores for each month in the data frame
Smoke$NCIG_1 <- round(NCIG[,1],2);Smoke$NCIG_2=round(NCIG[,2],2)
Smoke$NCIG_3=round(NCIG[,3],2)
#Create a lower bound—if any score happens to be negative, make it zero
Smoke[,5:7][Smoke[,5:7]<0] <- 0
```

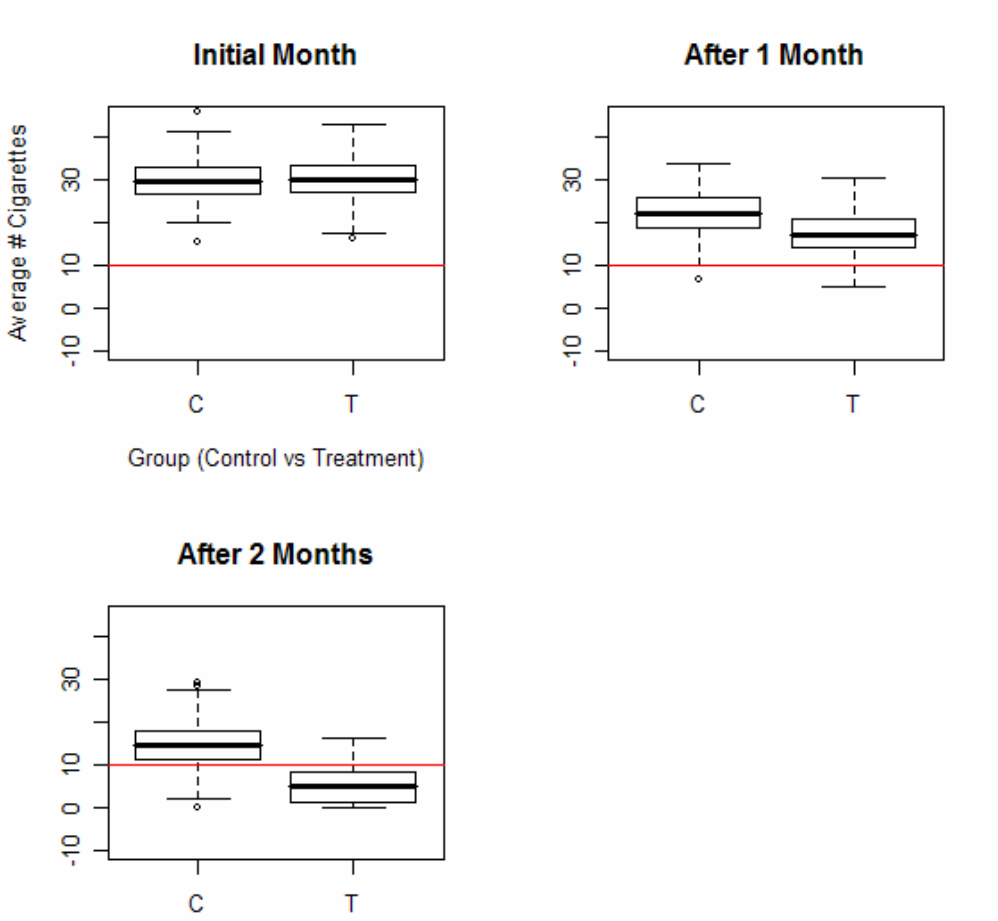
The first few lines of the Smoke dataset will now look like this:

```
> head(Smoke)
  Subj Treat Gender Treat.code NCIG_1 NCIG_2 NCIG_3
1 s1117     T      F         0.5     25.38   12.94   3.93
2 s1195     T      M         0.5     24.99   25.72   5.05
3 s1708     T      M         0.5     37.72   20.31   5.74
4 s1035     T      M         0.5     30.82   19.54   4.42
5 s1474     T      M         0.5     24.00   22.20  13.48
6 s1293     T      M         0.5     24.05   20.24   0.00
```

Peek at the Data

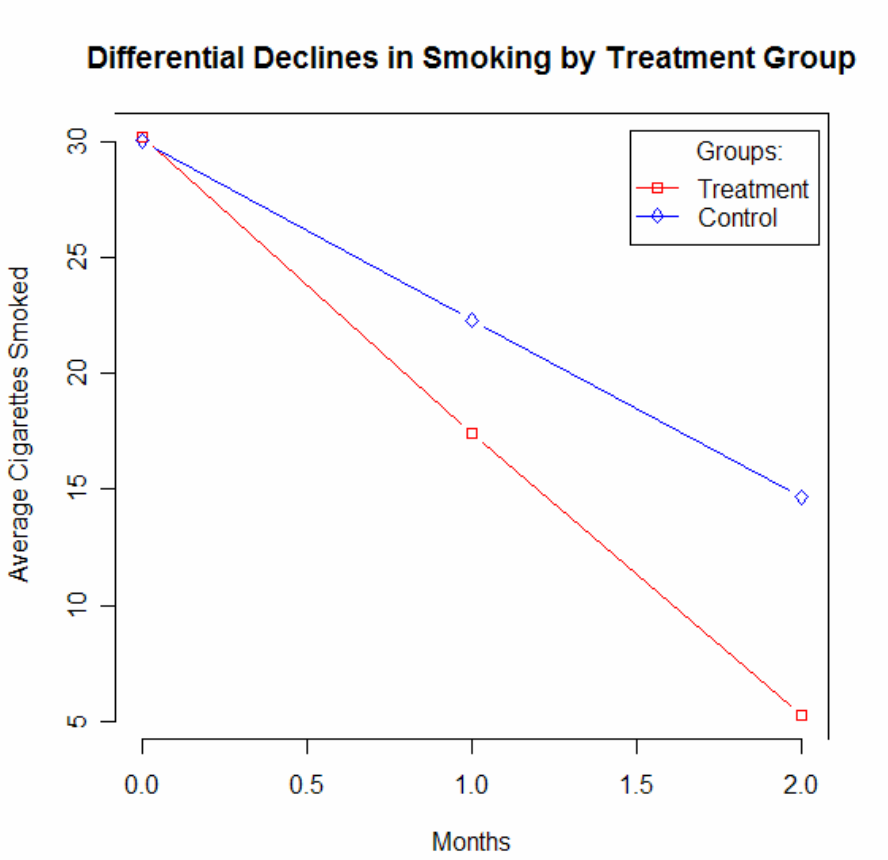
At this point, it may be helpful to take a look at the data to see what trends you have modeled. In this case, we can see that both the control and treatment groups began with similar intercepts (30 cigarettes/ day). After two successive months, both groups declined in their cigarette use (NCIG), but the treatment group declined at a faster rate. While, such a trend is highly improbable, it is still an interesting and useful example of differential slopes, so we won't refine the parameter estimates above.

```
#Show Mean differences between groups
op <- par(mfrow=c(2,2))
boxplot(Smoke$NCIG_1~Smoke$Treat,ylim=c(-10,45),ylab="Average #
Cigarettes", xlab="Group (Control vs Treatment)",main="Initial Month")
abline(h=10,col='red')
boxplot(Smoke$NCIG_2~Smoke$Treat,ylim=c(-10,45),main="After 1 Month")
abline(h=10,col='red')
boxplot(Smoke$NCIG_3~Smoke$Treat,ylim=c(-10,45),main="After 2 Months")
abline(h=10,col='red')
par(op)
```



It is sometimes useful to graph the same trends in different ways in order to see what changes take place over time. Instead of boxplots, you might prefer to see a linear plot of the means.

```
#Alternatively, show different group trends over time using lines
plot(month,colMeans(Smoke[Smoke[,4]==.5,5:7]),type='b',col='red',pch=22,ylab="A
verage Cigarettes Smoked",
xlab="Months",bty='7',main="Differential Declines in Smoking by Treatment
Group",col.main="black")
#plot adjacent line in -.5 is control .5 is treatment
lines(month,colMeans(Smoke[Smoke[,4]== -.5,5:7]),type='b',col='blue',pch=23)
#create a legend for the plot
legend(1.48,30.5, c("Treatment", "Control"), col = c("red","blue"), text.col =
"black", lty = c(1, 1), pch = c(22, 23),merge = TRUE, bg = 'white',title="     Groups:")
```



Person-Period Datset

As noted above, we will also need the data organized into a person-period dataset in which the last three columns showing the dependent variable over the two months (three measurements) of the experiment.

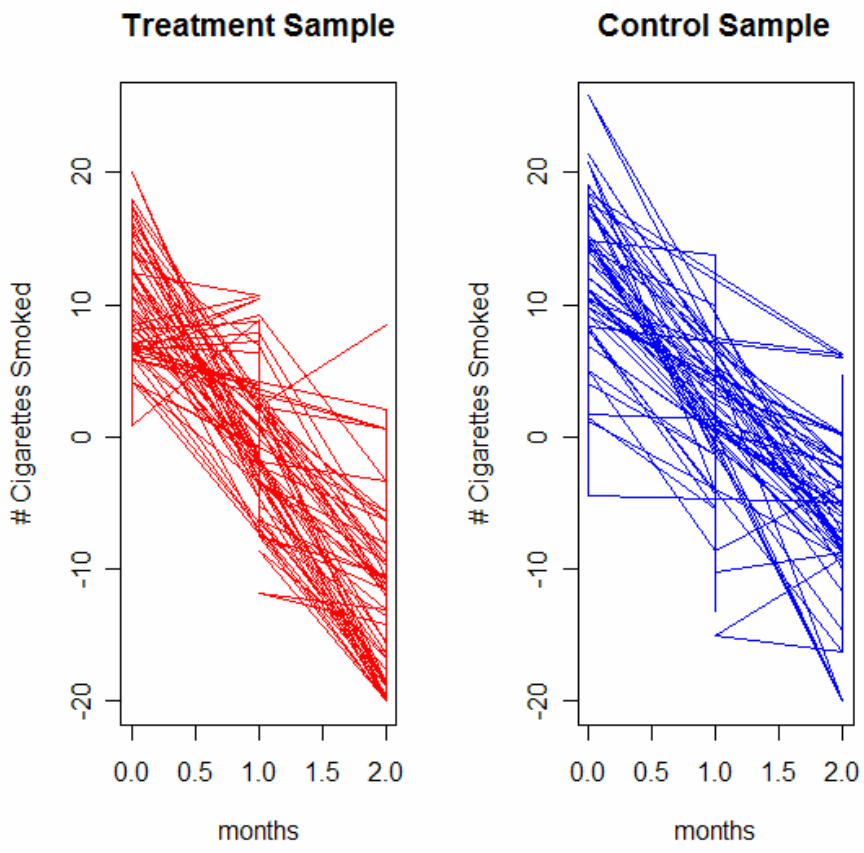
```
#TRANSFORM PERSON DATASET INTO PERSON-PERIOD DATASET
#with 3 measures of NCIG (one per month)

Smoke_long <- reshape(Smoke,direction="long",idvar="Subj",varying=list(5:7),timevar="months")
sort <- order(Smoke_long$Treat,Smoke_long$Gender,Smoke_long$Subj)
Smoke_long$months <- Smoke_long$months-1
Smoke_long <- Smoke_long[sort,]
colnames(Smoke_long) <- c("Subj","Treat","Gender","Treat.code","Months","NCIG")
```

```
> head(Smoke_long)
      Subj Treat Gender Treat.code Months  NCIG
s1002    C      F     -0.5      0  34.64
s1002    C      F     -0.5      1  23.88
s1002    C      F     -0.5      2  25.04
s1011    C      F     -0.5      0  35.59
s1011    C      F     -0.5      1  27.41
s1011    C      F     -0.5      2  23.19
```

With the person-period dataset, we can plot overlapping trajectories for many individuals at once. This may be useful to get a feel for the overall trends and the degree of variability in intercepts and slopes. A random subset of data is chosen because the full dataset of 250 lines per graph would make it difficult to discern very much in terms of variability.

```
#TREATMENT AND CONTROL SAMPLES
#Identify random subset of 40 lines from control and treatment
sampC <- Smoke$Subj %in% sample(Smoke$Subj[1:250],40)
sampT <- Smoke$Subj %in% sample(Smoke$Subj[251:500],40)
op <- par(mfrow=c(1,2))
plot(Smoke_long$NCIG[sampT] ~ Smoke_long$Months[sampT],type='l',col='red',
main="Treatment Sample",xlim=c(0,2),xlab="months",ylim=c(-10,40),ylab="# Cigarettes
Smoked")
plot(Smoke_long$NCIG[sampC] ~ Smoke_long$Months[sampC],type='l',col='blue',
   main="Control Sample",xlim=c(0,2),xlab="months",ylim=c(-10,40),ylab="# Cigarettes
Smoked")
par(op)
```

Notice that these graphs were intentionally plotted to be on the same scale in order to make proper comparisons. This was done by specifying the boundaries (minimum and maximum values) of the y-intercept using the ylim option within the plot command.



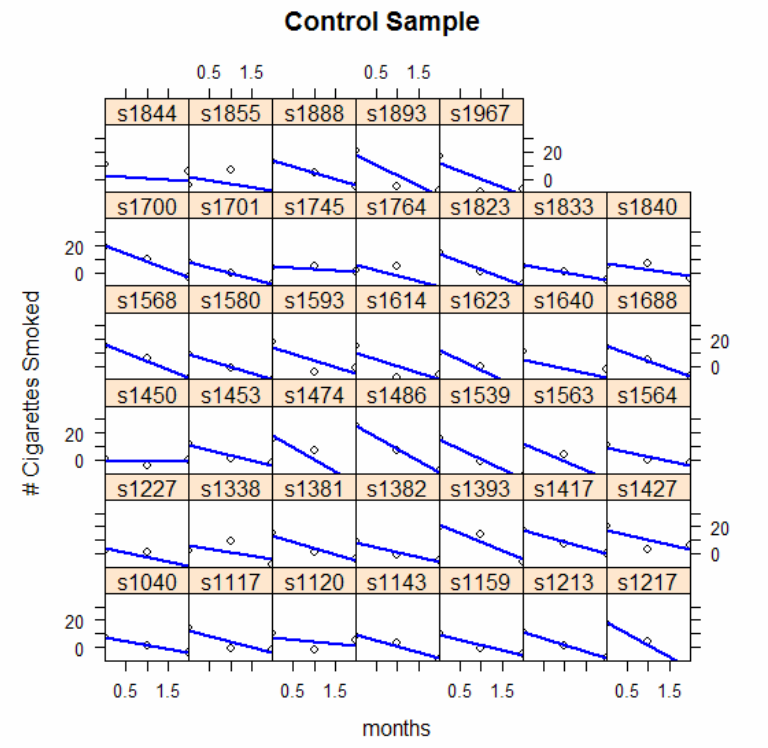
In comparing these subsets of the data, the intercepts (average number of cigarettes smoked per day) appears to be about the same in each group, though there is more within-person variability in the Control sample. It also appears that there is more variability in the individual growth trajectories for the Control versus Treatment group. It is difficult to tell, however, whether the average slopes are the same or slightly steeper in the Treatment group.

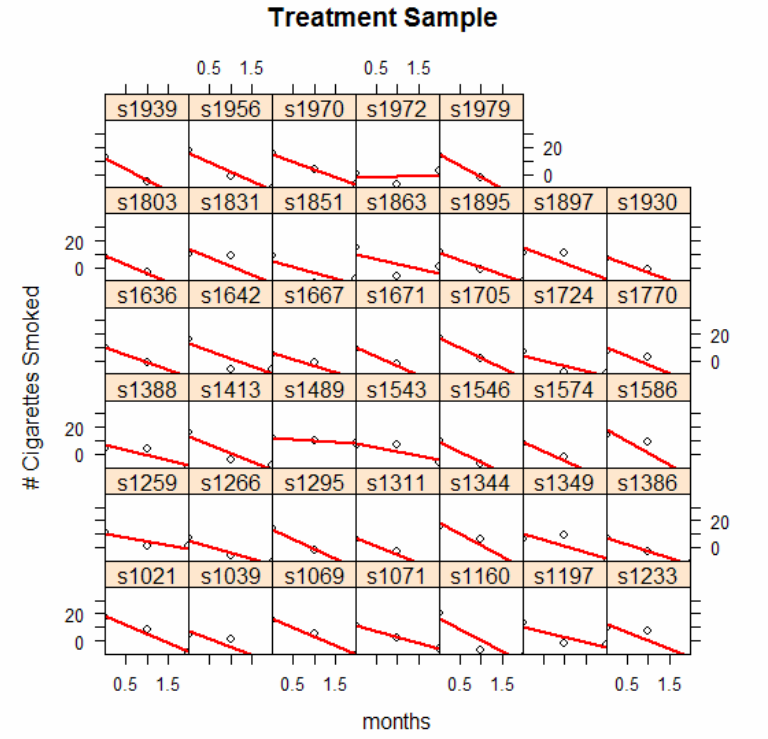
Another way to get a sense of this data is to "break apart" the lines in the above graphs and look at a random sample of individual regression lines. The xyplot function, part of the lattice library you opened above, allows us to do just that.

```
#SAMPLE INDIVIDUAL XYPLOTS WITH REGRESSION LINES
#Control Sample
op <- par(mfrow=c(7,6))
xyplot(Smoke_long$NCIG[sampC] ~ Smoke_long$Months[sampC]|Smoke$Subj[sampC],
main="Control Sample",xlim=c(0,2),xlab="months",ylim=c(-10,40),ylab="# Cigarettes Smoked",
panel=function(x,y){
panel.xyplot(x,y,col='black')
panel.lmline(x,y,col='blue',lwd=2)})

#Treatment sample
xyplot(Smoke_long$NCIG[sampT] ~ Smoke_long$Months[sampT]|Smoke$Subj[sampT],
main="Treatment Sample",xlim=c(0,2),xlab="months",ylim=c(-10,40),
ylab="# Cigarettes Smoked", panel=function(x,y){panel.xyplot(x,y,col='black')
panel.lmline(x,y,col='red',lwd=2)})
par(op)
```

The analysis of these individual regression slopes and intercepts is a subjective classification of these parameters. For example, among the 40 individual data plots for the Control sample, there are about 8 "severely negative" and 19 "moderately negative" slopes compared with about 13 "slightly negative or flat" slopes. This compares with about 22 "severely negative," 8 "moderately negative," and 10 "slightly negative to flat" slopes for the Treatment sample. So while almost all slopes are declining in both groups, the rate of decline is slightly greater (in these random subsets) in the Treatment than the Control sample.

In terms of the mean-centered intercepts, there were about 13 "low" intercepts, 18 "medium" and 9 "high" intercepts. In the Treatment group these frequencies were 14, 21, and 5, and so there doesn't appear to be much difference in the average initial values between the two groups. This is an important finding if we plan to interpret potentially different outcomes in terms of treatment effects.





For a more objective analysis, we could use histograms to summarize and compare the variability in intercepts and slopes among different levels of your grouping variable. We begin by performing a linear regression of NCIG on Months across all subjects. This will generate an "lmList" or list of "lm" objects such as "random.effects," "summary," and "coefficients." The latter are the coefficients of intercept and slope for each individual that we will need to extract

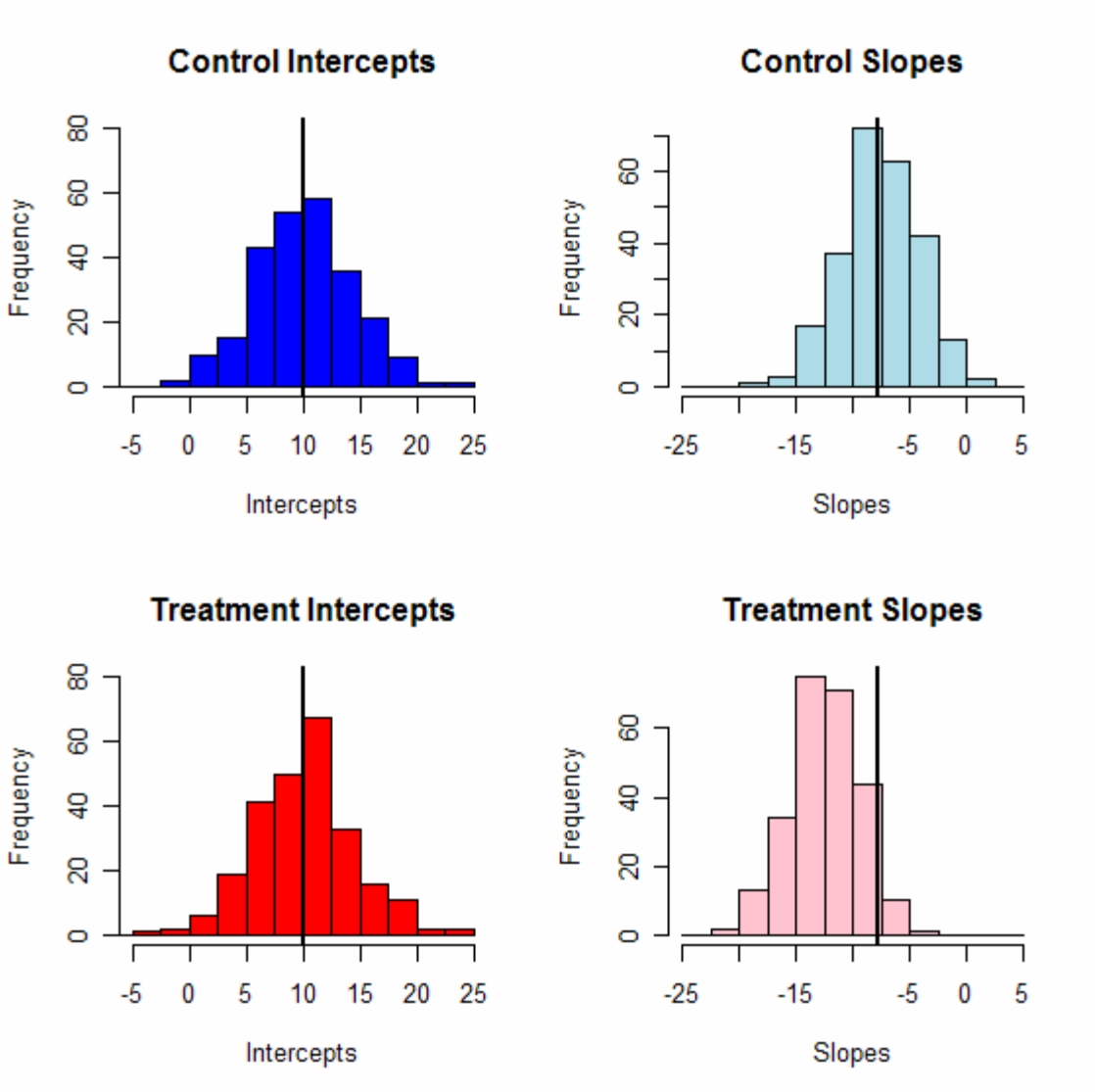
from lm.treat and lm.contr before we can graph them. This is done in the last two lines below by using the coef() command.

```
#Histograms and Bar Graphs comparing slopes and intercepts in sub-samples of Control vs Treatment
#First use linear regression to find intercepts and slopes
lm.treat=lmList(NCIG ~ Months|Subj,subset=Treat=='T',data=Smoke_long)
lm.contr=lmList(NCIG ~ Months|Subj,subset=Treat=='C',data=Smoke_long)
contr.coef <- coef(lm.contr)
treat.coef <- coef(lm.treat)
```

In generating the four histograms below, comparisons are made easier by including all histograms in a single window frame, using similar colors for the slopes and intercepts corresponding to the same group, including the same vertical reference line (one for slopes, one for intercepts) which is centered at the median of the control group, and having common bounds (using xlim and ylim) for the x-axis and y-axis for the treatment and control group. Breaks are also a useful option in the hist() command. This allows you to specify the width (which then also changes the height) of each bar in the histogram.

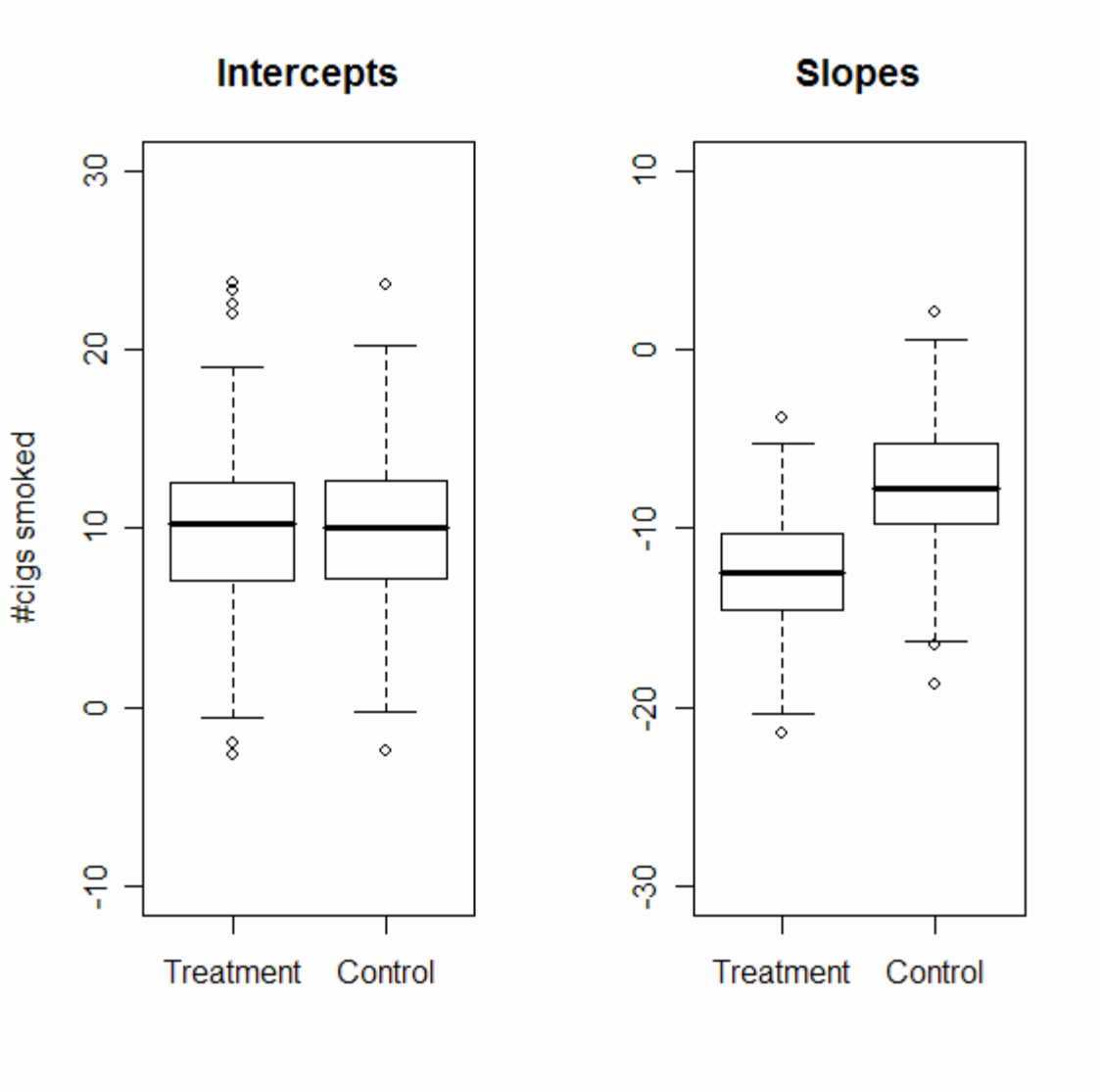
```
#Compare intercepts and slopes using histograms
op <- par(mfrow=c(2,2))
hist(contr.coef[,1],breaks=seq(-10,25,2.5),main='Control
Intercepts',xlab='Intercepts',ylab='Frequency',col='blue',xlim=c(-5,25),ylim=c(0,80))
  abline(v=median(contr.coef[,1]),col='black',lwd=2) #include reference line at median
hist(contr.coef[,2],breaks=seq(-25,5,2.5),main='Control
Slopes',xlab='Slopes',ylab='Frequency',col='lightblue',xlim=c(-25,5))
  abline(v=median(contr.coef[,2]),col='black',lwd=2) #include reference line at median
hist(treat.coef[,1],breaks=seq(-10,25,2.5),main='Treatment
Intercepts',xlab='Intercepts',ylab='Frequency',col='red',xlim=c(-5,25),ylim=c(0,80))
  abline(v=median(contr.coef[,1]),col='black',lwd=2)#same reference line as Control
Intercept
hist(treat.coef[,2],breaks=seq(-25,5,2.5),main='Treatment
Slopes',xlab='Slopes',ylab='Frequency',col='pink',xlim=c(-25,5))
  abline(v=median(contr.coef[,2]),col='black',lwd=2) #same reference line as Control Slope
par(op)
```

Based on these histograms below, it appears that the mean and distribution of intercepts is very similar in the Treatment and Control groups. To compare slopes, it's useful to have the Control group’s median line in both graphs. While these two populations have similar distributions of slopes, there is a mean shift (from about -7 to -12) to the left for almost the entire population of Treatment slopes. So, on average, those in Treatment groups appear to have greater declines than those in the Control group.



Finally, some may prefer to use boxplots, as defined below to arrive at the very same conclusion. Notice that this also makes use of the extracted intercept and slope parameters above in treat.coef and contr.coef.

```
#COMPARE INTERCEPTS AND SLOPES USING BOXPLOTS
op <- par(mfrow=c(1,2))
boxplot(treat.coef[,1],contr.coef[,1],main="Intercepts",
  names=c('Treatment','Control'),ylim=c(10,50),ylab="#cigs smoked")
boxplot(treat.coef[,2],contr.coef[,2],main="Slopes",
  names=c('Treatment','Control'),ylim=c(-30,10))
par(op)
```



Analysis: Return to Modeling

From this preliminary peek at the data, you may have a sense of the type of Level-1 and Level-2 models that might fit the data. In addition to looking across treatment levels, you could also explore Gender as a predictor, and the interaction of Treat X Gender. Unlike graphing, the analyses below may require the creation of contrast codes to address the specific questions of interest (although sometimes categorical variables may be converted automatically). Also, to facilitate meaningful interpretation, it is always helpful to mean-center a given predictor so that, when you refer to a beta weight for the intercept, its value will refer to the average effect of the predictor on the dependent variable. With continuous variables, centering with respect to the grand mean is especially important in models that include an interaction term in order for the algorithms performing maximum likelihood estimation to converge on a solution (Bliese, 2006).

In model building you might begin with an intercept model that is a constant, and then add random variation, or predictors or both. Each addition can be tested against the prior model to see if the added parameter changes the likelihood of the model given the data. Or, if you have a particular model you would like to test based on theory or empirical evidence, you can directly test this model and then determine which components may be dropped. In the present dataset, for example, we might look at the differential declines in the line plot on page 7 and the boxplot on this page and propose the following model with intercepts and slopes that have a constant baseline component, and vary according to Treatment condition, as well as random between-treatment group and individual-level variability.

Level-1 (within-person)

$NCIG_{ij} = \pi_{0i} + \pi_{1i} (Months)_{ij} + \varepsilon_{ij}$,

$\varepsilon_{ij} \sim N(0, \sigma_{\varepsilon}^2)$,

Level-2 (between-person) Unconditional Growth Model (UGM)

$\pi_{0i} = \gamma_{00} + \gamma_{01} (Treat) + \zeta_{0i}$

$\pi_{1i} = \gamma_{10} + \gamma_{11} (Treat) + \zeta_{1i}$

where γ_{00}, is the initial number of daily cigarettes smoked, γ_{01} is the difference in average intercepts between the Treatment and Control groups (since Treat.code =.5 for "T" and -.5 for "C" above), and ζ_{0i} is the residual variability in intercepts between individuals. For the slope model, γ_{10} is a common baseline change in NCIG per month (or per measurement), γ_{01} is the difference in average slopes between the Treatment and Control groups, and ζ_{1i} is the residual variability in slopes between individuals. Finally, ε_{ij} is a unique residual for each person at each time point.

Analysis Using lme()

The code for the above model in R is as follows:

```
# Assign the output of the function lme() to an lmList object, "Treat.lme.1"
Treat.lme.1 <- lme(NCIG ~ Treat.code* I(Months-1),
  random = ~ 1 + I(Months-1)| Treat.code, data=Smoke_long)
summary(Treat.lme.1)
```

There are several parts of this code that require some explanation. Fixed effects are specified first using a tilde between the dependent variable and its predictors. In this case, Months has been mean-centered by subtracting 1 within parentheses and preceded by the capital letter, "I." The use of "I" and the parentheses can be used generally for algebraic manipulation of variables within a model. The random effects are then specified following a tilde. For a random model with both intercepts and slopes, one can use "1 + predictor" or just the predictor; for a random model with intercepts alone, use just the 1; and for a random model with slopes but no intercepts, use "-1 + predictor." The vertical line, "|" is used to indicate that the modeling of the intercept (or slope or both) varies as a function of the predictor on the other side of it. In the above example, the slope and intercept may vary as a function of the treatment code, such that subjects

in the treatment group can have different intercepts and slopes than subjects in the control group. Finally, the long version of the dataset is specified.

The output from lme(), which stands for "linear mixed-effects," is assigned to an lmList object from which you can extract a summary or just parts of the output. For example, Treat.lme.1$tTable will return just the parameter and model estimates for the fixed effects, which includes t-tests and p-values for beta weights testing whether these parameters are different from 0.

Given the above model, we can also test which aspects of the random model are necessary below by using the update function which maintains the fixed effects and allows you to modify just the random component.

```
#Model effects of intercepts alone
Treat.lme.2<-update(Treat.lme.1,random= ~ 1| Treat.code)

#Model effects of slopes alone
Treat.lme.3<-update(Treat.lme.1,random = ~ -1 +  I(Months-1)| Treat.code)

#Compare Treat.lme.1 and Treat.lme.2 to test the importance of keeping slope in the model
anova(Treat.lme.1, Treat.lme.2)

#Compare Models 1 and 3 to test the importance of keeping intercepts in the model
anova(Treat.lme.1,Treat.lme.3)
```

Based on these comparisons, if there is, for example a significant difference in the log-likelihood ratio test when dropping the intercept term but not when dropping the slope, you can conclude that random variation is important in modeling the intercept but not the slope, given these data.

Further Assistance

For help on model building and more advanced features of the lme() function, there are some on-line resources included in the Reference section below.

Reference

Bliese, P. (2006). Multilevel modeling in R (2.2): A brief introduction to R, the multilevel package and the nlme package. Accessed online <cran.r-project.org/doc/contrib/Bliese_Multilevel.pdf>

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Fox, J. (2002). Linear Mixed Models. Appendix to an R and S-Plus Companion to Applied Regression. Accessed 4/15/2008 <cran.r-project.org/doc/contrib/Fox-Companion/appendix-mixed-models.pdf>

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