HDFS 523: Strategies for Data Analysis in Developmental Research

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# 1 About This Book

This book provides the course notes for HDFS 523. It is currently under development, so any feedback is appreciated (e.g., during class, via email, or the edit link in the header). This first chapter is just about how to use the book – the course content starts in Chapter 2.

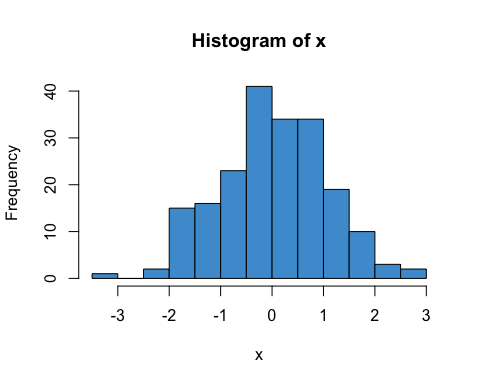
## 1.1 Why this book?

There are a few goals of moving from “textbook + slides + exercises” to an ebook. For now, the main goal is to update and integrate code contents from the course into one consistent format, rather than having multiple files to sort through on Canvas.

## 1.2 Code Folding

The book combines lecture slides and R coding examples. It is often convenient to hide code when introducing new material. This is accomplished using code folding. An example of code folding is given on this page. Below, a histogram integrated into the text. By clicking on the button called “Show Code” on the top of the page, the R code that produced the histogram will also be visible. Notice that you may need to scroll horizontally to see all of the text in the code window. Also notice that when you hover your mouse over the code window, an icon appears in the top right corner – this lets you copy the block of code with one click.

# Here is some R code. You don't have to look at it when reading the book, but it is here when you need it  
x <- rnorm(200)  
hist(x, col = "#4B9CD3")



## 1.3 Acknowledgements

Many people have contributed to the course materials for HDFS 523. Most importantly, the original R markdown files for the course were developed by Nilam Ram and Zita Oravecz.

# 2 Data Cleaning

In Chapter 2 we will work through some basic data cleaning operations useful in longitudinal data analysis. The basic idea is provide a set of scripts to use for exploring new repeated measures data sets.

## 2.1 Example Data

For Chapter 2 we will make use of the longitudinal Wechsler Intelligence Scale for Children (WISC; Wechsler, [1949](#ref-wechsler1949)) dataset described by [Osborne and Suddick](#ref-osborne1972) ([1972](#ref-osborne1972)). These data have been detailed extensively in a number of papers ([McArdle and Epstein 1987](#ref-mcardle1987); [McArdle 1988](#ref-mcardle1988); [Mcardle and Aber 1990](#ref-mcardle1990); [McArdle and Nesselroade 1994](#ref-mcardle1994)) and are used here with with permission.

The WISC data contains repeated measures data from 204 children between the ages of 6 and 11 years old (during grades 6, 7, 9 and 11). Thee repeated measures include component scores for the verbal tests and performance subtests at all four occasions, along with verbal subtest scores for the information, comprehension, similarities, and vocabulary domains at the first and last measurement occasion. The demographics variables mother’s education (continuous in years) and mother graduated high school (dichotomous) are also included.

## 2.2 Reading in Repeated Measures Data

We can read in the WISC data directly from the [QuantDev](https://quantdev.ssri.psu.edu/) website.

filepath <- "https://quantdev.ssri.psu.edu/sites/qdev/files/wisc3raw.csv"  
wisc3raw <- read.csv(file=url(filepath), header=TRUE)

Additional details on importing different data types into R can be found here: <http://www.statmethods.net/input/importingdata.html>.

## 2.3 Familiarize Yourself with the Data

Let’s take an initial look at the structure of our data object using str()

str(wisc3raw)

## 'data.frame': 204 obs. of 20 variables:  
## $ id : int 1 2 3 4 5 6 7 8 9 10 ...  
## $ verb1 : num 24.4 12.4 32.4 22.7 28.2 ...  
## $ verb2 : num 27 14.4 33.5 28.4 37.8 ...  
## $ verb4 : num 39.6 21.9 34.3 42.2 41.1 ...  
## $ verb6 : num 55.6 37.8 50.2 44.7 71 ...  
## $ perfo1 : num 19.8 5.9 27.6 33.2 27.6 ...  
## $ perfo2 : num 23 13.4 45 29.7 44.4 ...  
## $ perfo4 : num 43.9 18.3 47 46 65.5 ...  
## $ perfo6 : num 44.2 40.4 77.7 61.7 64.2 ...  
## $ info1 : num 31.3 13.8 35 24.8 25.3 ...  
## $ comp1 : num 25.6 14.8 34.7 31.4 30.3 ...  
## $ simu1 : num 22.93 7.58 28.05 8.21 15.98 ...  
## $ voca1 : num 22.2 15.4 26.8 20.2 35.4 ...  
## $ info6 : num 69.9 41.9 60.4 52.9 67.4 ...  
## $ comp6 : num 44.4 44.9 50.3 42.7 86.7 ...  
## $ simu6 : num 68 33.9 35.8 45.8 72.4 ...  
## $ voca6 : num 51.2 37.7 55.5 36 60.4 ...  
## $ momed : num 9.5 5.5 14 14 11.5 14 9.5 5.5 9.5 11.5 ...  
## $ grad : int 0 0 1 1 0 1 0 0 0 0 ...  
## $ constant: int 1 1 1 1 1 1 1 1 1 1 ...

From the output, we can also see that the data frame consists of 204 observations (rows) and 20 variables (columns). Each variable’s name and data type is also listed. Methods like the ones above can be an effective way to initially familiarize yourself with the main features of a dataset.

## 2.4 Look for Duplicated IDs

It is always worth looking for non-unique ID numbers when ID labels are included in a dataset. Here we have an id variable indicating the subject number. Since our data is in a long format (more on that later) duplicate IDs may indicate a potential problem with the data source or clues on how the data is structured.

any(duplicated(wisc3raw$id))

## [1] FALSE

## 2.5 Using table() to Spot Irregularities

When a variable takes on a limited range of values it is often useful to screen for irregularities or invalid values. This is common across all variable types and can occur for character strings, numeric, integer and factor types. For example, we would expect the grad variable to only take the values of zero or one. We can use the table() function to quickly confirm this.

By default table() simply omits any values coded as NA. To include a count of the NA values use the useNA argument of table() as follows:

table(wisc3raw$grad, useNA = "always")

##   
## 0 1 <NA>   
## 158 46 0

## 2.6 Missing Data

Dealing with missing data in a consistent manner is one of the most important aspects of data cleaning. When data are imported into R it is common to discover missing values are coded according to a variety of conventions.

Often a first step in handling missing data involves recoding missing values as NA. Writing bespoke code to handle the different types of missing data one might encounter is tedious and unnecessary.

naniar ([Tierney et al. 2021](#ref-naniar)) is a useful package with many convenience functions for managing missing data in R. Here we demonstrate some of this functionality.

### 2.6.1 Generating Example Data

Since the WISC data does not contain missing values it is helpful to generate a synthetic dataset containing some commonly encountered missing data codes.

set.seed(123)  
wisc\_miss <- wisc3raw  
wisc\_miss$verb1[sample(nrow(wisc\_miss),100)] <- -99  
wisc\_miss$comp1[sample(nrow(wisc\_miss),75)] <- "N/A"  
wisc\_miss$info1[sample(nrow(wisc\_miss),50)] <- "NA"

### 2.6.2 Recoding Values with NA

Now that we have a dataset with missing values we can use naniar to recode these values to NA.

na\_strings <- c("NA", "N/A", -99)  
   
wisc\_miss <- naniar::replace\_with\_na\_all(  
 wisc\_miss, condition = ~.x %in% na\_strings  
)

See the [naniar vignette on recoding NA values](https://cran.r-project.org/web/packages/naniar/vignettes/replace-with-na.html) for more detailed information on the package functionality.

### 2.6.3 Missing Data Visualization

Once we have recoded our data in a consistent manner we can use visualizations to explore the missing data. The vis\_miss() function from naniar is a good starting point for visualizing the amount of missing data in our dataset. The plots shows the missing values in black and non-missing values in gray. In addition, percentages of missing data in both the dataset and individual variables are provided.

naniar::vis\_miss(wisc\_miss)



Many missing data visualizations are described in the [naniar vignette on missing data visualization](https://cran.r-project.org/web/packages/naniar/vignettes/naniar-visualisation.html) including plots for exploring missing data mechanisms.

## 2.7 Exporting Data

Depending on work-flow, you may need to export your dataset for use in another statistical software program. The write.csv() function is a convenient method for outputting comma delimited files.

write.csv(wisc3raw, file = "wisc3raw.csv", row.names = FALSE, na = "-99")

Note that by default the write.csv() function will include an extra column of row numbers and will notate missing data with an NA. More information on exporting data is available at <http://www.statmethods.net/input/exportingdata.html>.

## 2.8 Reshaping Repeated Measures Data

Behavioral science tends to use relational data structures - in basic form, spreadsheets. Typically, the data are stored in a data frame (a “fancy” matrix) with multiple rows and columns. Two common schemata used to accommodate repeated measures data are *wide format* and *long format*. Different analysis and plotting functions require different kinds of data input. Thus, it is imperative that one can convert the data back and forth between wide and long formats.

There are lots of ways to do this. We illustrate one way.

*Sidebar*: The dput() function provides a convenient method to get the variable names (or any R object) into a format that can be read back into R. For example, this can be helpful when working with a long vector of strings.

dput(colnames(wisc3raw))

## c("id", "verb1", "verb2", "verb4", "verb6", "perfo1", "perfo2",   
## "perfo4", "perfo6", "info1", "comp1", "simu1", "voca1", "info6",   
## "comp6", "simu6", "voca6", "momed", "grad", "constant")

First, let’s subset our data to only include the variables we need for this analysis.

var\_names\_sub <- c(  
 "id", "verb1", "verb2", "verb4", "verb6",  
 "perfo1", "perfo2", "perfo4", "perfo6",  
 "momed", "grad"  
)  
  
wiscraw <- wisc3raw[,var\_names\_sub]  
head(wiscraw)

## id verb1 verb2 verb4 verb6 perfo1 perfo2 perfo4 perfo6 momed grad  
## 1 1 24.42 26.98 39.61 55.64 19.84 22.97 43.90 44.19 9.5 0  
## 2 2 12.44 14.38 21.92 37.81 5.90 13.44 18.29 40.38 5.5 0  
## 3 3 32.43 33.51 34.30 50.18 27.64 45.02 46.99 77.72 14.0 1  
## 4 4 22.69 28.39 42.16 44.72 33.16 29.68 45.97 61.66 14.0 1  
## 5 5 28.23 37.81 41.06 70.95 27.64 44.42 65.48 64.22 11.5 0  
## 6 6 16.06 20.12 38.02 39.94 8.45 15.78 26.99 39.08 14.0 1

### 2.8.1 Reshape Wide to Long

One way to go *from wide to long* is using the reshape() function from base R.

Notice, the varying argument contains the repeated measures columns we want to stack and the timevar is a new variable containing the grade level information previosuly appended at the end of the colnames listed in varying.

# reshape data from wide to long  
wisclong <- reshape(  
 data = wiscraw,  
 varying = c("verb1", "verb2", "verb4","verb6", "perfo1","perfo2","perfo4","perfo6"),  
 timevar = c("grade"),   
 idvar = c("id"),  
 direction = "long",   
 sep = ""  
)  
  
# reorder by id and day   
wisclong <- wisclong[ order(wisclong$id, wisclong$grade), ]  
  
head(wisclong, 8)

## id momed grad grade verb perfo  
## 1.1 1 9.5 0 1 24.42 19.84  
## 1.2 1 9.5 0 2 26.98 22.97  
## 1.4 1 9.5 0 4 39.61 43.90  
## 1.6 1 9.5 0 6 55.64 44.19  
## 2.1 2 5.5 0 1 12.44 5.90  
## 2.2 2 5.5 0 2 14.38 13.44  
## 2.4 2 5.5 0 4 21.92 18.29  
## 2.6 2 5.5 0 6 37.81 40.38

Again, notice how reshape automatically split verb1, verb2, etc. into a string name and a grade variable.

### 2.8.2 Reshape Long to Wide

Now we go *from long to wide*, again using the reshape() function. The v.names argument specifies the variables to be expanded column wise based on the repeated measure specified in timevar.

#reshaping long to wide  
wiscwide <- reshape(  
 data = wisclong,   
 timevar = c("grade"),   
 idvar = c("id"),  
 v.names = c("verb","perfo"),  
 direction = "wide",   
 sep = ""  
)  
  
# reordering columns   
wiscwide <- wiscwide[, c(  
 "id", "verb1", "verb2", "verb4", "verb6",  
 "perfo1", "perfo2", "perfo4", "perfo6",  
 "momed","grad"   
)]  
  
head(wiscwide)

## id verb1 verb2 verb4 verb6 perfo1 perfo2 perfo4 perfo6 momed grad  
## 1.1 1 24.42 26.98 39.61 55.64 19.84 22.97 43.90 44.19 9.5 0  
## 2.1 2 12.44 14.38 21.92 37.81 5.90 13.44 18.29 40.38 5.5 0  
## 3.1 3 32.43 33.51 34.30 50.18 27.64 45.02 46.99 77.72 14.0 1  
## 4.1 4 22.69 28.39 42.16 44.72 33.16 29.68 45.97 61.66 14.0 1  
## 5.1 5 28.23 37.81 41.06 70.95 27.64 44.42 65.48 64.22 11.5 0  
## 6.1 6 16.06 20.12 38.02 39.94 8.45 15.78 26.99 39.08 14.0 1

Using functions included in base R can be useful in a number of situations. One example is package development where one may wants to limit dependencies.

That said, many people find reshape to be unnecessarily complicated. A similar, and potentially more convenient, set of functions have been developed for reshaping data in the tidyr ([Wickham 2021](#ref-tidyr)) package. For those interested take a look at the pivot\_longer() and pivot\_wider() functions.

For examples using tidyr to reshape data see the [tidyr vignette on pivoting](https://cran.r-project.org/web/packages/tidyr/vignettes/pivot.html).

# 3 Describing Longitudinal Data

In Chapter 3 we will look at some option for describing and visualizing longitudinal data.

## 3.1 Example Data

Again we will make use of the WISC data described in Chapter 2. The following commands recreate the wide and long data we will use throughout this chapter.

filepath <- "https://quantdev.ssri.psu.edu/sites/qdev/files/wisc3raw.csv"  
  
wisc3raw <- read.csv(file=url(filepath),header=TRUE)  
  
var\_names\_sub <- c(  
 "id", "verb1", "verb2", "verb4", "verb6",  
 "perfo1", "perfo2", "perfo4", "perfo6",  
 "momed", "grad"  
)  
  
wiscraw <- wisc3raw[,var\_names\_sub]  
  
# reshaping wide to long  
wisclong <- reshape(  
 data = wiscraw,  
 varying = c("verb1", "verb2", "verb4","verb6", "perfo1","perfo2","perfo4","perfo6"),  
 timevar = c("grade"),   
 idvar = c("id"),  
 direction = "long",   
 sep = ""  
)  
  
# reorder by id and day   
wisclong <- wisclong[ order(wisclong$id, wisclong$grade), ]  
  
#reshaping long to wide  
wiscwide <- reshape(  
 data = wisclong,   
 timevar = c("grade"),   
 idvar = c("id"),  
 v.names = c("verb","perfo"),  
 direction = "wide",   
 sep = ""  
)  
  
# reordering columns   
wiscwide <- wiscwide[, c(  
 "id", "verb1", "verb2", "verb4", "verb6",  
 "perfo1", "perfo2", "perfo4", "perfo6",  
 "momed","grad"   
)]

## 3.2 Describing Means and Variances

Once the wide and long data sets are in place, we can begin describing and plotting the data. Descriptive statistics and visualization are one of the most important aspects of data analysis.

Descriptives and plots will be produced from wide data and long data to show the information that can be gleaned from each construction. Having both in place facilitates learning about the data. Continually keep in mind what portions of the data-box are being described (e.g., persons, variables, occasions).

We can do a quick look at descriptives using the describe() function from the psych ([Revelle 2021](#ref-psych)) package. Note the n in both outputs.

psych::describe(wiscwide)

## vars n mean sd median trimmed mad min max range skew  
## id 1 204 102.50 59.03 102.50 102.50 75.61 1.00 204.00 203.00 0.00  
## verb1 2 204 19.59 5.81 19.34 19.50 5.41 3.33 35.15 31.82 0.13  
## verb2 3 204 25.42 6.11 25.98 25.40 6.57 5.95 39.85 33.90 -0.06  
## verb4 4 204 32.61 7.32 32.82 32.42 7.18 12.60 52.84 40.24 0.23  
## verb6 5 204 43.75 10.67 42.55 43.46 11.30 17.35 72.59 55.24 0.24  
## perfo1 6 204 17.98 8.35 17.66 17.69 8.30 0.00 46.58 46.58 0.35  
## perfo2 7 204 27.69 9.99 26.57 27.34 10.51 7.83 59.58 51.75 0.39  
## perfo4 8 204 39.36 10.27 39.09 39.28 10.04 7.81 75.61 67.80 0.15  
## perfo6 9 204 50.93 12.48 51.76 51.07 13.27 10.26 89.01 78.75 -0.06  
## momed 10 204 10.81 2.70 11.50 11.00 2.97 5.50 18.00 12.50 -0.36  
## grad 11 204 0.23 0.42 0.00 0.16 0.00 0.00 1.00 1.00 1.30  
## kurtosis se  
## id -1.22 4.13  
## verb1 -0.05 0.41  
## verb2 -0.34 0.43  
## verb4 -0.08 0.51  
## verb6 -0.36 0.75  
## perfo1 -0.11 0.58  
## perfo2 -0.21 0.70  
## perfo4 0.59 0.72  
## perfo6 0.18 0.87  
## momed 0.01 0.19  
## grad -0.30 0.03

psych::describe(wisclong)

## vars n mean sd median trimmed mad min max range skew  
## id 1 816 102.50 58.93 102.50 102.50 75.61 1.00 204.00 203.00 0.00  
## momed 2 816 10.81 2.69 11.50 11.00 2.97 5.50 18.00 12.50 -0.36  
## grad 3 816 0.23 0.42 0.00 0.16 0.00 0.00 1.00 1.00 1.31  
## grade 4 816 3.25 1.92 3.00 3.19 2.22 1.00 6.00 5.00 0.28  
## verb 5 816 30.34 11.86 28.46 29.39 11.33 3.33 72.59 69.26 0.71  
## perfo 6 816 33.99 16.14 33.14 33.34 18.14 0.00 89.01 89.01 0.34  
## kurtosis se  
## id -1.20 2.06  
## momed 0.03 0.09  
## grad -0.28 0.01  
## grade -1.43 0.07  
## verb 0.33 0.42  
## perfo -0.43 0.56

### 3.2.1 Verbal Ability (All Persons and Occasions)

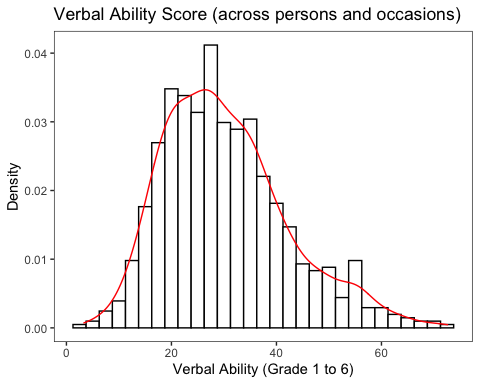
Let’s focus on the repeated measures of verbal ability. This step is useful to get a general view of what verbal ability scores look like across persons and occasions, but note that we are *ignoring Time*. In doing so we are not considering how the repeated measures are nested within individuals.

psych::describe(wisclong$verb)

## vars n mean sd median trimmed mad min max range skew kurtosis  
## X1 1 816 30.34 11.86 28.46 29.39 11.33 3.33 72.59 69.26 0.71 0.33  
## se  
## X1 0.42

In addition to the descriptive statistics we can look at a boxplot of verbal ability scores across persons and occasions. Here we will start to use the ggplot2 ([Wickham 2016](#ref-ggplot2)) package.

library("ggplot2")  
ggplot(data = wisclong, aes(x=verb, y=..density..)) +  
 geom\_histogram(binwidth=2.5, fill = "white", color = "black") +   
 geom\_density(color = "red") +  
 ggtitle("Verbal Ability Score (across persons and occasions)") +  
 xlab("Verbal Ability (Grade 1 to 6)") +  
 ylab("Density") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank()  
 )



### 3.2.2 Verbal Ability (Across Time)

Note that our variable is actually “multivariate” because we have repeated measures. We should really consider the time-dependence when we are looking at descriptive statistics and plots.

Let’s now look at **verbal ability scores across time collapsed across individuals**. This can be done using either the describe() function and the wide data or the describeBy() function and the long data.

Let’s look at descriptives using the wide data.

psych::describe(wiscwide[,c("verb1","verb2","verb4","verb6")])

## vars n mean sd median trimmed mad min max range skew  
## verb1 1 204 19.59 5.81 19.34 19.50 5.41 3.33 35.15 31.82 0.13  
## verb2 2 204 25.42 6.11 25.98 25.40 6.57 5.95 39.85 33.90 -0.06  
## verb4 3 204 32.61 7.32 32.82 32.42 7.18 12.60 52.84 40.24 0.23  
## verb6 4 204 43.75 10.67 42.55 43.46 11.30 17.35 72.59 55.24 0.24  
## kurtosis se  
## verb1 -0.05 0.41  
## verb2 -0.34 0.43  
## verb4 -0.08 0.51  
## verb6 -0.36 0.75

Identical results can be obtained using the long data.

psych::describeBy(wisclong[,c("verb")], group = wisclong$grade)

##   
## Descriptive statistics by group   
## group: 1  
## vars n mean sd median trimmed mad min max range skew kurtosis se  
## X1 1 204 19.59 5.81 19.34 19.5 5.41 3.33 35.15 31.82 0.13 -0.05 0.41  
## ------------------------------------------------------------   
## group: 2  
## vars n mean sd median trimmed mad min max range skew kurtosis se  
## X1 1 204 25.42 6.11 25.98 25.4 6.57 5.95 39.85 33.9 -0.06 -0.34 0.43  
## ------------------------------------------------------------   
## group: 4  
## vars n mean sd median trimmed mad min max range skew kurtosis se  
## X1 1 204 32.61 7.32 32.82 32.42 7.18 12.6 52.84 40.24 0.23 -0.08 0.51  
## ------------------------------------------------------------   
## group: 6  
## vars n mean sd median trimmed mad min max range skew kurtosis  
## X1 1 204 43.75 10.67 42.55 43.46 11.3 17.35 72.59 55.24 0.24 -0.36  
## se  
## X1 0.75

We can visualize the distribution of verbal scores across grades in a number of different ways. Here we have a histogram.

ggplot(data=wisclong, aes(x=verb)) +  
 geom\_histogram(binwidth=5, pad = TRUE, fill="white", color="black") +   
 facet\_grid(grade ~ .) +   
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 xlab("Verbal Ability Score") +  
 ylab("Density") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank()  
 )

## Warning: Duplicated aesthetics after name standardisation: pad

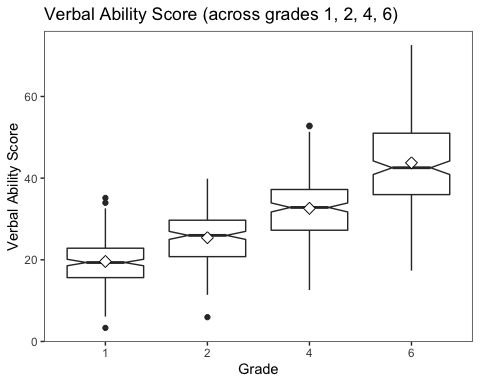


We can also create notched boxplots of the within-grade distributions (across individuals).

From [Wikipedia](https://en.wikipedia.org/wiki/Box_plot): *Notched box plots apply a notch or narrowing of the box around the median. Notches are useful in offering a rough guide of the significance of the difference of medians; if the notches of two boxes do not overlap, this can provide evidence of a statistically significant difference between the medians.*

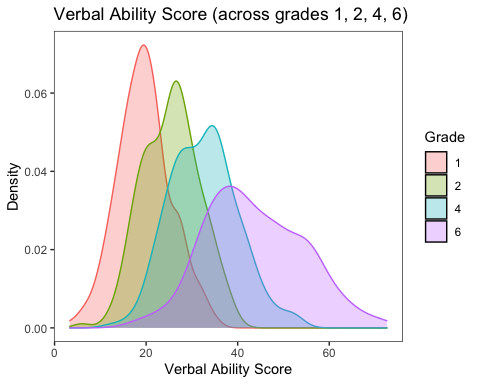
Adding the mean value to the plot gives us additonal information about central tendency and skew of the distribution.

#boxplot by grade  
ggplot(data=wisclong, aes(x=factor(grade), y=verb)) +   
 geom\_boxplot(notch = TRUE) +  
 stat\_summary(fun="mean", geom="point", shape=23, size=3, fill="white") +  
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 ylab("Verbal Ability Score") +  
 xlab("Grade") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank()  
 )



Finally, we can view overlapping densities of the within-grade distributions of verbal ability scores.

ggplot(data=wisclong, aes(x=verb)) +   
 geom\_density(aes(group=factor(grade), colour=factor(grade), fill=factor(grade)), alpha=0.3) +  
 guides(colour="none", fill=guide\_legend(title="Grade")) +  
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 ylab("Density") +  
 xlab("Verbal Ability Score") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank()  
 )



Notice in these plots how much “change” there is at the sample level across grades. Is that expected?

## 3.3 Describing Covariances

In the previous section we looked at the means and variances. Because these are repeated measures, we can also look at covariances and correlations over time. A simple covariance and correlation matrix of the verbal scores across grades can be produced using the cov() and cor() function.

cov(wiscwide[,c("verb1","verb2","verb4","verb6")], use="complete.obs")

## verb1 verb2 verb4 verb6  
## verb1 33.72932 25.46388 30.88886 40.51478  
## verb2 25.46388 37.28784 33.81957 47.40488  
## verb4 30.88886 33.81957 53.58070 62.25489  
## verb6 40.51478 47.40488 62.25489 113.74332

cor(wiscwide[,c("verb1","verb2","verb4","verb6")], use="complete.obs")

## verb1 verb2 verb4 verb6  
## verb1 1.0000000 0.7180209 0.7265974 0.6541040  
## verb2 0.7180209 1.0000000 0.7566242 0.7279080  
## verb4 0.7265974 0.7566242 1.0000000 0.7974552  
## verb6 0.6541040 0.7279080 0.7974552 1.0000000

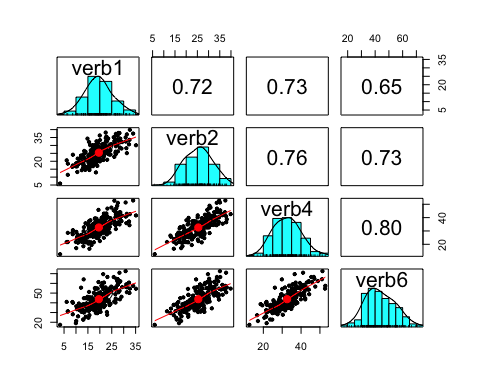
A plot corresponding to the correlation matrix can be obtained in a number of different ways. First, using the pairs() function from base R.

pairs(wiscwide[,c("verb1","verb2","verb4","verb6")])



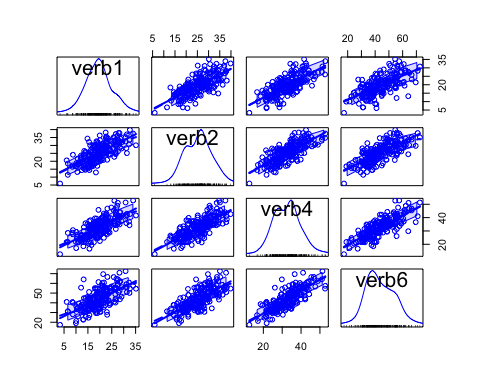
There is also a pairs.panel() function in the psych package. Here we see a LOESS smoothed fit line in red.

psych::pairs.panels(wiscwide[,c("verb1","verb2","verb4","verb6")])



Finally, thescatterplotMatrix() from the car ([Fox and Weisberg 2019](#ref-car)) package can be used to create scatterplot matrices with confidence bands around the line of best fit.

car::scatterplotMatrix(~ verb1 + verb2 + verb4 + verb6, data=wiscwide)



Each of these functions can be customized with additional features. Those interested in specifics should consult the help documentation for each function (e.g. ?car::scatterplotMatrix). It is also worth noting the default behavior of these functions is to provide automatic, data-based ranges for each pair of variables separately.

## 3.4 Individual-Level Descriptives

Note that our interest is often in *individual* development, rather than sample development. We need to consider how each individual is changing over time. Thus, we are interested in verbal ability across Time for each individual person. Visualization is typically our best tool for synthesizing the large amounts of information in individual-level data.

ggplot(data = wisclong, aes(x = grade, y = verb, group = id)) +  
 geom\_point() +   
 geom\_line() +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 ylim(0,80) +  
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 xlab("Grade") +  
 ylab("Verbal Ability Score") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank()  
 )



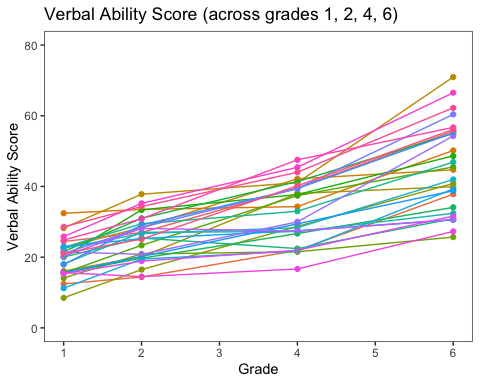
Sometimes the “blob” gets too dense. This can be fixed by selecting a subset of persons to visualize.

ggplot(subset(wisclong, id < 30), aes(x = grade, y = verb, group = id)) +  
 geom\_point() +   
 geom\_line() +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 ylim(0,80) +  
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 xlab("Grade") +  
 ylab("Verbal Ability Score") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank()  
 )



We can add some color to our plot using the color argument and treating id as a factor.

ggplot(subset(wisclong, id < 30), aes(x = grade, y = verb, group = id, color = factor(id))) +  
 geom\_point() +   
 geom\_line() +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 ylim(0,80) +  
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 xlab("Grade") +  
 ylab("Verbal Ability Score") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank(),  
 legend.position = "none"  
 )



We can also get a gradient of colors by treatingid as continuous.

ggplot(subset(wisclong, id < 30), aes(x = grade, y = verb, group = id, color = id)) +  
 geom\_point() +   
 geom\_line() +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 ylim(0,80) +  
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 xlab("Grade") +  
 ylab("Verbal Ability Score") +  
 theme\_bw() +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank(),  
 legend.position = "none"  
 )



It is also sometimes useful to look at the collection of individual-level plots.

ggplot(subset(wisclong, id <= 20), aes(x = grade, y = verb)) +  
 geom\_point() +   
 geom\_line() +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 ylim(0,80) +  
 ggtitle("Verbal Ability Score (across grades 1, 2, 4, 6)") +  
 xlab("Grade") +  
 ylab("Verbal Ability Score") +  
 theme\_bw() +  
 facet\_wrap( ~ id) +  
 theme(  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 strip.background = element\_blank(),  
 legend.position = "none"  
 )



Some other aesthetics to get to the formal APA style.

#ggplot version .. see also http://ggplot.yhathq.com/docs/index.html  
ggplot(subset(wisclong, id <= 20), aes(x = grade, y = verb, group = id)) +  
 geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") +   
 ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 ggtitle("Intraindividual Change in Verbal Ability") +  
 theme\_classic() +   
 #increase font size of axis and point labels  
 theme(axis.title = element\_text(size = rel(1.5)),  
 axis.text = element\_text(size = rel(1.2)),  
 legend.position = "none")



Saving the plot file. See also [outputting plots to a file](http://www.cookbook-r.com/Graphs/Output_to_a_file/).

ggsave(filename = "wiscverbal.png", width = 5, height = 5, dpi=300)

Now we have a good set of strategies to apply when looking at new longitudinal data.

## 3.5 References

# 4 Matrix Algebra

In Chapter 4 we will briefly review some basic algebra results useful for this course. Those needing a reliable reference for basic results in matrix algebra should consult the *The Matrix Cookbook* at <https://www.math.uwaterloo.ca/~hwolkowi/matrixcookbook.pdf>.

## 4.1 Types of matrices

Remember that matrices are defined by rows (the first dimension) and columns (the second dimension):

You can refer to a specific element in matrix using a subscript of the row and column index (e.g. ). For our purposes there are a few *special* matrices worth mentioning,

### 4.1.1 Square

A square matrix has the same number of rows and columns. Covariance and correlation matrices are square.

### 4.1.2 Symmetric

A symmetric matrix is a square matrix that equals its transpose. This means that corresponding entries on either side of the main diagonal are equal.

**Matrix Transpose**

The transpose of a matrix is an operator which flips a matrix over its diagonal. That is, it switches the row and column indices of the matrix by producing another matrix, often denoted by (or ).

**Graphical Depiction of a Matrix Transpose**



<https://leetcode.com/problems/transpose-matrix/>

### 4.1.3 Diagonal

A diagonal matrix is a special case of a square symmetric matrix in which there are values along the diagonal, but zeros elsewhere:

### 4.1.4 Identity

An identity matrix is a special case of a diagonal matrix in which the elements of the diagonal are all 1:

Any matrix multiplied by an identity matrix is unchanged.

## 4.2 Operations on Matrices

### 4.2.1 Matrix Transpose

As stated earlier the transpose of a matrix is an operator which flips a matrix over its diagonal. That is, it switches the row and column indices of the matrix by producing another matrix, often denoted by (or ). Some useful properties of the matrix transpose include:

$$
(\mathbf{A + B})' = \mathbf{A' + B'}\\
(c\mathbf{A'}) = c(\mathbf{A'}) = (\mathbf{A'})c \\
(\mathbf{A'B}) = \mathbf{B'A}\\
(\mathbf{AB})' = \mathbf{B'A'}\\
(\mathbf{A'})' = \mathbf{A}
$$

**Graphical Depiction of a Matrix Transpose**



<https://leetcode.com/problems/transpose-matrix/>

### 4.2.2 Matrix Trace

The *trace* of a square matrix is the sum of elements along the diagonal. The trace is only defined for a square matrix. For an matrix the trace is defined as follows:

**Graphical Depiction of a Matrix Trace**



Some useful properties of the matrix trace include:

$$
tr(\mathbf{A + B}) = tr(\mathbf{A}) + tr(\mathbf{B})\\
tr(c\mathbf{A}) = c(tr(\mathbf{A})) \\
tr(\mathbf{A}) = tr(\mathbf{A'})\\
tr(\mathbf{AB}) = tr(\mathbf{BA})\\
tr(\mathbf{ABC}) = tr(\mathbf{CAB})=tr(\mathbf{BCA})
$$

### 4.2.3 Addition

For addition, matrices must be of the same order. Addition of two matrices is accomplished by adding corresponding elements,

$$
\mathbf{A} = \begin{bmatrix}
10 & 5 \\
9 & 1
\end{bmatrix}
, \enspace
\mathbf{B} = \begin{bmatrix}
2 & 1 \\
20 & 0
\end{bmatrix}, \enspace
\textrm{then }
\mathbf{A}+\mathbf{B}=
\begin{bmatrix}
12 & 6 \\
29 & 1
\end{bmatrix}
$$

Matrix addition is *commutative* (gives the same result whatever the order of the quantities involved),

and *associative* (gives the same result whatever grouping their is, as long as order remains the same),

and

### 4.2.4 Subtraction

Like addition, subtraction requires matrices of the same order. Elements in the difference matrix are given by the algebraic difference between corresponding elements in matrices being subtracted:

$$
\mathbf{A} = \begin{bmatrix}
10 & 5 \\
9 & 1
\end{bmatrix}
, \enspace
\mathbf{B} = \begin{bmatrix}
2 & 1 \\
20 & 0
\end{bmatrix}, \enspace
\textrm{then }
\mathbf{A}-\mathbf{B}=
\begin{bmatrix}
8 & 4 \\
-11 & 1
\end{bmatrix}
$$

### 4.2.5 Matrix Multiplication

Three useful *rules* to keep in mind regarding matrix multiplication:

1. Only matrices of the form are conformable for multiplication. The number of columns in the premultiplier must equal the number of rows in the post multiplier.
2. The product matrix will have the following order: .

**Graphical Depiction of Rules 1 and 2**



1. The element in the product matrix is the result of multiplying row of the premultiplier matrix, and row of the post multiplier matrix (e.g. ()).

**Graphical Depiction of Rule 3**



<https://code.kx.com/q/ref/mmu/>

Matrix multiplication is associative (i.e. rearranging the parentheses in an expression will not change the result). That is,

and is distributive with respect to addition,

$$
\mathbf{A(B+C)} = \mathbf{AB + AC} \\
\mathbf{(B+C)A} = \mathbf{BA + CA} \\
$$

If is a scalar, then

or equivalently,

$$
\mathbf{A} = \begin{bmatrix}
10 & 5 \\
9 & 1
\end{bmatrix}, \enspace
k=2, \enspace
k\mathbf{A} = \begin{bmatrix}
20 & 10 \\
18 & 2
\end{bmatrix}.
$$

In general, matrices that can be multiplied are called ‘compatible’ or ‘comformable.’ Matrices in which the *inner dimensions* (i.e., columns of , rows of ) do not match are called ‘incompatible’ or ‘non-conformable.’ These cannot be multiplied.

### 4.2.6 Matrix Division

Division is not defined for matrix operations, but may be accomplished by multiplication by the inverse matrix. In algebra, the reciprocal of a scalar is, by definition, the scalar raised to the minus one power (e.g. ), and equations may be solved by multiplication by reciprocals.

For example:

$$
5^{-1} = 1/5\\
5x=35\\
5^{-1}(5x)=5^{-1}(35)\\
x = 7
$$

Now consider the following equation where the vector is unknown,

Each element in the column vector is unknown and the solution involves solving a set of simultaneous equations for the unknown element of ,

$$
a\_{11}x\_{1} + a\_{12}x\_{2} + \dots + a\_{1p}x\_{p} = b1 \\
a\_{21}x\_{1} + a\_{22}x\_{2} + \dots + a\_{2p}x\_{p} = b2 \\
\vdots \\
a\_{p1}x\_{1} + a\_{p2}x\_{2} + \dots + a\_{pp}x\_{p} = bp
$$

A solution analogous to the scalar equations above would give the following solution for the elements of the vector :

$$
\mathbf{A}\_{p \times p} \mathbf{x}\_{p \times 1} = \mathbf{b}\_{p \times 1} \\
\mathbf{A}^{-1}\_{p \times p}\mathbf{A}\_{p \times p} \mathbf{x}\_{p \times 1} = \mathbf{A}^{-1}\_{p \times p}\mathbf{b}\_{p \times 1} \\
\mathbf{I}\_{p \times p}\mathbf{x}\_{p \times 1} = \mathbf{A}^{-1}\_{p \times p}\mathbf{b}\_{p \times 1} \\
\mathbf{x}\_{p \times 1} = \mathbf{A}^{-1}\_{p \times p}\mathbf{b}\_{p \times 1}
$$

The inverse of a matrix must satisfy the following properties:

where is the identity matrix with 1’s along the diagonal and 0’s elsewhere.

# 5 Ordinary Least Squares

In Chapter 5 we will briefly review the assumptions and properties of Ordinary Least Squares (OLS) regression, a cornerstone method that supports many of the other methods we will consider. We will present the regression model in both scalar and matrix forms to facilitate the material to follow.

## 5.1 Linear Regression Model

Generally, the regression model is written as

where

* is the value of the outcome variable for individual
* is an *intercept parameter*, the expected value of when the predictor variables are all
* is a regression parameter indicating the relation between and the outcome variable,
* are *errors or disturbances*

## 5.2 Ordinary Least Squares (OLS)

The Ordinary Least Squares (OLS) is one of the most common estimators of the linear regression model. What assumptions do we make with OLS? Why should we care?

How well me meet the assumptions of OLS determines (1) the accuracy of OLS coefficients, and (2) the accuracy of our inferences and substantive hypothesis tests.

## 5.3 Assumptions of OLS

The assumptions of OLS are as follows:

1. for all (homoscedasticity)
2. for all
3. No perfect collinearity among variables
4. for all and

Let’s discuss each assumption in more detail.

### 5.3.1 Assumption 1.

Note that is the expectation operator. The expected value is an “average” of whatever is inside the parentheses. This assumption states that, on average, the error for the observation is zero. Here “for all ” means the same is true for all cases.

### 5.3.2 Assumption 2. Homoscedasticity

In statistics, a vector of random variables is heteroscedastic if the variability of the random disturbance is different across elements of the vector, here our s. The errors or disturbances in our model are homoskedastic if the variance of is a constant (e.g. ), otherwise, they are heteroskedastic.

**Graphical Depiction of Homoskedasticity and Heteroskedasticity**



<https://en.wikipedia.org/wiki/Homoscedasticity>

### 5.3.3 3.

Assumption 3 is sometimes referred to as the *autocorrelation assumption*. This assumption states that the error terms of different observations should not be correlated with each other. For example, when we have time series data and use lagged variables we may want to examine residuals for the possibility of autocorrelation.

**Graphical Depiction of Positive and Negative Autocorrelation**



### 5.3.4 4. No Perfect Collinearity

Perfect collinearity occurs when one variable is a perfect linear function of any other explanatory variable. If perfect collinearity is found among the s then has no inverse and OLS estimation fails. Perfect collinearity is unlikely except for programming mistakes such as dummy coding all the values in a nominal variable.

### 5.3.5 5.

Note that is the covariance operator. Assumption five states that that the error of our equation is uncorrelated with all the s. This is often referred to as an *endogeneity assumption*.

This can be a confusing assumption because by definition the residuals are uncorrelated with the s. Here, however, we are concerned with the true errors . Unfortunately, there are a variety of conditions that lead to in applied contexts.

**Graphical Depiction of Sources of Endogeneity**



Figure 2 from Bollen (2012)

If we meet these assumptions what large sample properties can we expect?

## 5.4 Properties of the OLS Estimator

If assumptions (1) to (5) hold, then the OLS estimator is:

1. A consistent estimator of
2. Asymptotically normally distributed
3. Having a variance of

*Notice that we did not assume normality of $\epsilon\_{i,y\_{i}$ or .*

Let’s discuss each of these properties in a little bit more detail.

### 5.4.1 1. Consistentcy of

is the OLS estimator of . A consistent estimator is one for which, as the sample size () increases, the estimate converges in probability to the value that the estimator is designed to estimate. This is often stated as . Stated differently, as the sample size grows, the OLS coefficients converge to the true coefficients.

### 5.4.2 2. Asymptotic Normality

Asymptotic normality is another property of the OLS estimator when all assumptions are met. “Asymptotic” refers to how an estimator behaves as the sample size tends to infinity. “Normality” refers to the normal distribution, so an estimator that is asymptotically normal will have an approximately normal distribution as the sample size gets larger.

### 5.4.3 Variance of

Having a variance of is another property of the OLS estimator when the previously stated assumptions are met. This means, for example, we can estimate the standard errors from the main diagonal of and perform significance testing based on this variance.

## 5.5 Failure to Meet Assumptions

It is worth thinking about the consequences of not meeting these assumptions.

### 5.5.1 Failure of Assumption 1.

Assumption 1 states . This assumption states that, on average, the error for the observation is zero. If instead, and , and all other assumptions hold, then only the intercept term is biased. Other coefficients OK.

### 5.5.2 Failure of Assumption 2 or 3.

Assumptions 2 and 3 are the *homoskedasticity* and *no autocorrelation* assumption, respectively. If we violate (2) or (3), but all other assumptions hold, (1) variance of is no longer dependable, (2) SEs possibly inaccurate, and (3) significance tests are possibly inaccurate. However, importantly, is still an unbiased and consistent estimator.

### 5.5.3 Failure of Assumption 5.

Assumption (5) states that that the error of our equation is uncorrelated with all the s. If this assumption fails, while others hold, OLS is no longer a consistent estimator.

## 5.6 Regression and Matrix Notation

Now that we have reviewed the assumptions of OLS, let’s return to the linear regression model and translate it into a matrix form.

### 5.6.1 An Intercept-Only Model

First, let’s take a simpler form of the model, an intercept-only model where

Note that we have made the “silent” 1 explicit. This will become important later (e.g., when fitting growth models). It is worthwhile to look at regression model without predictors to understand what it can tell us about the nature of the intercept (or constant).

So here we have no predictors, what is ?

Here, is the mean of the response variable, and we can show this with some algebra,

where (Assumption 1).

### 5.6.2 Intercept-Only Model in Matrix Form

Translating into matrix form, can be written as an x 1 matrix (a column vector). More specifically, for to individuals,

.

(Remember, matrices are often designated as bold capital letters)

Doing the same for all the other parts of the model, we get

Note that we have taken care that each matrix is of an order that will allow for matrix multiplication.

### 5.6.3 Simple Regression in Matrix Form

Now, let’s expand our regression model by adding a predictor . Our model becomes

Written out explicitly in matrix form, the model is

### 5.6.4 Multiple Regression in Matrix Form

Finally, extending the model to the general case with predictor variables, we have

which is written out in matrix form as

Where we have the following elements:

Observe the order of the matrices/vectors. On the right hand side you are matrix multiplying a matrix with a vector. This yields an vector, to which another vector is added, and this is equal to our outcome vector which is also .

When we implement this model in R, it will be important to know the portions of the model that are in our data frame, and , and to have them structured properly. This will become clear in the examples below.

Now that we have the model written out explicitly as matrices, we can easily simplify the notation.

In compact matrix notation, the regression model then can be written as

## 5.7 Solving the Regression Equation

In practice, we would like to know the contents of (i.e., solve for) .

Assuming the model is correct, the expected value of is 0, therefore,

Then we just need to solve for . We can think back about some of the matrix operations we discussed earlier.

### 5.7.1 Matrix Multiplication and Transpose

Our goal is to isolate . One initial idea might be to multiple each side of the equation by in an attempt to remove from the right hand side, and isolate . Why won’t this work?

Instead, let’s pre-multiply each side of the equation by . This would give us

This gets us a quantity, , a square matrix containing information about the relations among the s.

### 5.7.2 Matrix Inverse

Now, since is a square matrix and presumabely has an inverse (e.g. no perfect collinearity), we can premultiply both sides by , to obtain

Remembering our assumptions that a matrix multiplied by its inverse equals the identity matrix, the equation simplifies to

or more succinctly

We’ve now isolated the unknowns, onto one side of the equation and figured out how to use matrix algebra to obtain the regression coefficients. Quite literally, this algebra is what allows for estimation of the parameters when fitting a regression model to data.

We will now work through some practical examples - staying aware that this kind of matrix algebra is being done in the background.

## 5.8 The Linear Probability Model

While we are discussing the assumptions of OLS it is worth pausing to consider a model for dichotomous outcomes: the *linear probability model* (LPM).

In the LPM we don’t do anything fancy with a binary outcome variable. Instead, we simply apply OLS as we would with a continuous out come variable. Since we aren’t considering the normality of our outcome you might be curious how our assumptions would hold.

Remembering the assumptions of OLS:

1. for all (homoscedasticity)
2. for all
3. No perfect collinearity among variables
4. for all and

**Which assumptions are needed for consistency and asymptotic unbiasedness?**

1. No perfect collinearity among variables
2. Errors uncorrelated with all variables.

In regard to (4) having a dependent variable valued at does not cause any problems. In regard to (5), again no, nothing about a dichotomous outcome violates this assumption.

Therefore, in this model is still consistent and asymptotically unbiased.

**What about the remaining assumptions?**

1. Homoscedasticity

Here, *a dichotomous outcome does inherently violate the assumption of homoskedasticity.*

Why is this case? It can be shown that now directly depends on the value of that is taken. If the person has one set of values for the variables, and another individual has another set, the estimates of and will differ. This can be seem by looking at the variacne of a Bernoulli random variable.

This means estimate of variance of is no longer reliable, SEs and significance tests possibly inaccurate. However, this could be addressed using robust standard errors.

It is common to look at plots of predicted values vs residuals to diagnose heteroskedasticity. Generally one would like to see a random blob of points without any discernible pattern. Here is an example of what that plot might look like for an LPM model. Each line represents a different outcome, , or .



### 5.8.1 Advantages of the LPM

1. Simplicity.
2. Regression coefficients give impact of on .
3. Effect same regardless of value of or values of other s.
4. Can extend with traditional methods easily (interactions, quadratic terms).

### 5.8.2 Disadvantages of the LPM

1. Functional form unlikely accurate at extreme lows & highs
2. Binary dependent variable creates heteroscedasticity
3. Some regression diagnostics assume homoscedastic error
4. Predicted probabilities not restricted to 0 to 1 range



# 6 Linear Regression

In Chapter 6 we will demonstrate how to estimate the linear regression model in R with an eye towards the longitudinal modeling to follow.

## 6.1 Example Data

Chapter 6 make use of the same WISC data used in Chapter 3. Here we again read in, subset, and provide descriptives for the WISC data. We will also add a simulated variable childgrad indicating whether the student graduated highschool.

filepath <- "https://quantdev.ssri.psu.edu/sites/qdev/files/wisc3raw.csv"  
  
wisc3raw <- read.csv(file=url(filepath),header=TRUE)  
  
var\_names\_sub <- c(  
 "id", "verb1", "verb2", "verb4", "verb6",  
 "perfo1", "perfo2", "perfo4", "perfo6",  
 "momed", "grad"  
)  
  
wiscsub <- wisc3raw[,var\_names\_sub]  
  
set.seed(1234)  
wiscsub$childgrad <- sample(c(0,1), replace=TRUE, size=nrow(wiscsub))  
  
psych::describe(wiscsub)

## vars n mean sd median trimmed mad min max range skew  
## id 1 204 102.50 59.03 102.50 102.50 75.61 1.00 204.00 203.00 0.00  
## verb1 2 204 19.59 5.81 19.34 19.50 5.41 3.33 35.15 31.82 0.13  
## verb2 3 204 25.42 6.11 25.98 25.40 6.57 5.95 39.85 33.90 -0.06  
## verb4 4 204 32.61 7.32 32.82 32.42 7.18 12.60 52.84 40.24 0.23  
## verb6 5 204 43.75 10.67 42.55 43.46 11.30 17.35 72.59 55.24 0.24  
## perfo1 6 204 17.98 8.35 17.66 17.69 8.30 0.00 46.58 46.58 0.35  
## perfo2 7 204 27.69 9.99 26.57 27.34 10.51 7.83 59.58 51.75 0.39  
## perfo4 8 204 39.36 10.27 39.09 39.28 10.04 7.81 75.61 67.80 0.15  
## perfo6 9 204 50.93 12.48 51.76 51.07 13.27 10.26 89.01 78.75 -0.06  
## momed 10 204 10.81 2.70 11.50 11.00 2.97 5.50 18.00 12.50 -0.36  
## grad 11 204 0.23 0.42 0.00 0.16 0.00 0.00 1.00 1.00 1.30  
## childgrad 12 204 0.55 0.50 1.00 0.56 0.00 0.00 1.00 1.00 -0.20  
## kurtosis se  
## id -1.22 4.13  
## verb1 -0.05 0.41  
## verb2 -0.34 0.43  
## verb4 -0.08 0.51  
## verb6 -0.36 0.75  
## perfo1 -0.11 0.58  
## perfo2 -0.21 0.70  
## perfo4 0.59 0.72  
## perfo6 0.18 0.87  
## momed 0.01 0.19  
## grad -0.30 0.03  
## childgrad -1.97 0.03

## 6.2 Intercept-Only Model

For our first example, we focus on verbal ability at Grade 2 as an outcome (verb2 in the data frame wiscsub). Examining the distribution for ‘verb2.’

library("ggplot2")  
  
psych::describe(wiscsub$verb2)

## vars n mean sd median trimmed mad min max range skew kurtosis se  
## X1 1 204 25.42 6.11 25.98 25.4 6.57 5.95 39.85 33.9 -0.06 -0.34 0.43

ggplot(data=wiscsub, aes(x=verb2)) +   
 geom\_histogram(binwidth=2.5, fill="white", color="black", boundary=0) +  
 xlab("Verbal Ability Grade 2") + ylab("Count") +  
 xlim(0,50) +  
 theme\_classic()



### 6.2.1 Intercept-Only Equation

The simplest model is an intercept only model. In this case, we would fit the model

Written out explicitly with the “silent” 1 in it, we get

This is helpful for explicit translation into the R code, specifically the formula within the lm() function.

### 6.2.2 Intercept-Only Model in R

We fit the model using the following code. Note that the code has the ‘1’ predictor variable stated explicitly.

model1 <- lm(formula = verb2 ~ 1,  
 data = wiscsub,  
 na.action = na.exclude)  
summary(model1)

##   
## Call:  
## lm(formula = verb2 ~ 1, data = wiscsub, na.action = na.exclude)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -19.4653 -4.6403 0.5647 4.2822 14.4347   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 25.4153 0.4275 59.45 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 6.106 on 203 degrees of freedom

Note that we used na.exclude instead of na.omit (default); practically speaking na.omit deletes missing data entries while na.exclude just excludes from the analysis.Therefore with na.exclude, in the residuals and fitted values, NA will show up where there were missing values.

The output indicates that = 25.4153, and its standard error = 0.4275.

The intercept reflects the expected value of the outcome variable when all of the predictor variables (i.e. ) = 0. So, in the absence of any additional information other than the descriptive statistics of , what is our best guess for a person’s score? It is the mean of . The regression above confirms this notion; regressing the outcome on a vector of 1s allows us to ‘recover’ the mean.

### 6.2.3 Intercept as Mean of Outcome

Notice we can confirm this finding using matrix algebra, as well.

From the properties of expectation, we have .

Another property of expectation relates to taking the expectation of a constant, , thus , implying

Remembering Assumption 1, , we have

We can confirm this by looking at Verbal Scores at Wave 2.

mean(wiscsub$verb2)

## [1] 25.41534

### 6.2.4 Intercept-Only Model

Yes - we recovered the *mean*, but we did not attempt to explain any of the *variance*. Let’s take a look at the variance explained for Model 1.

summary(model1)$r.squared

## [1] 0

It thus makes sense that we get 0 as the R-square. From the properties of variance, we know that . There is no variability due to the regression model because there are no predictors, only a constant.

## 6.3 Simple Linear Regression

Let’s build up the model further. For example, we could attempt to explain some of the *between-person variance* in the Grade 2 verbal score from the Grade 1 verbal scores. But, before we do, let’s examine the distribution of the *between-person differences* in the Grade 1 verbal scores.

ggplot(wiscsub, aes(x=verb1)) +   
 geom\_histogram(binwidth=2.5, fill="white", color="black", boundary=0) +  
 xlab("Verbal Ability Grade 1") +   
 ylab("Count") +  
 xlim(0,50) +  
 theme\_classic()

 And the relation between the Grade 2 and Grade 1 verbal ability scores.

ggplot(wiscsub, aes(x=verb1, y = verb2)) +   
 geom\_point() +  
 stat\_ellipse(color="blue", alpha=.7) +  
 xlab("Verbal Ability Grade 1") +   
 ylab("Verbal Ability Grade 2") +  
 ylim(0,45) +   
 xlim(0,45) +  
 theme\_classic()



### 6.3.1 Regression Equation and Model Fitting

Our regression model becomes

model2 <- lm(verb2 ~ 1 + verb1,  
 data = wiscsub,  
 na.action = na.exclude)  
summary(model2)

##   
## Call:  
## lm(formula = verb2 ~ 1 + verb1, data = wiscsub, na.action = na.exclude)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -11.5305 -3.0362 0.2526 2.7147 12.5020   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 10.62965 1.05164 10.11 <2e-16 \*\*\*  
## verb1 0.75495 0.05149 14.66 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 4.261 on 202 degrees of freedom  
## Multiple R-squared: 0.5156, Adjusted R-squared: 0.5132   
## F-statistic: 215 on 1 and 202 DF, p-value: < 2.2e-16

### 6.3.2 Path Diagram

We might also be interested in a graphical depiction of our model. This can be accomplished with the semPaths package.

semPlot::semPaths(model2, what = "paths")



### 6.3.3 Interpreting Model Parameters

How do we interpret the parameters here?

*The intercept, , is the expected value for the outcome variable when all of the predictor variables equal zero.* So, we would expect a child to have a Grade 2 verbal score of 10.62965 *if* they have a Grade 1 verbal score of 0.

*The slope, is the expected difference in the outcome variable for each 1-unit difference in the predictor variable*. So, *across children*, for each 1-point difference in a child’s Grade 1 verbal score, we would expect a 0.75 point difference in the Grade 2 verbal score.

### 6.3.4 Plotting Regression Line

We can plot the relation between ‘verb1’ and ‘verb2,’ and include the predicted line from the analysis.

ggplot(data=wiscsub, aes(x=verb1,y=verb2)) +  
 geom\_point(size = 2, shape=19) +  
 geom\_smooth(method=lm,se=TRUE,fullrange=TRUE,colour="red", size=2) +  
 labs(x= "Verbal Ability Grade 1", y= "Verbal Ability Grade 2") +  
 xlim(0,50) +  
 ylim(0,50) +  
 theme\_bw() +  
 theme(  
 plot.background = element\_blank(),  
 panel.grid.major = element\_blank(),  
 panel.grid.minor = element\_blank(),  
 panel.border = element\_blank()  
 ) +  
 #draws x and y axis line  
 theme(axis.line = element\_line(color = 'black')) +  
 #set size of axis labels and titles  
 theme(axis.text = element\_text(size=12),  
 axis.title = element\_text(size=14))

## `geom\_smooth()` using formula 'y ~ x'



## 6.4 Mean Centering Predictors

In this case, and in many other cases, the intercept does not have a ‘useful’ interpretation for the empirical example. This is because no students had a Grade 1 verbal score equal to 0.

Therefore, if we want to make the intercept more meaningful, we need to make a Grade 1 verbal score with a more meaningful 0 point. Typically we center the *predictor* variables in regression analysis.

For example, we create a centered variable, by subtracting the sample mean, from each observation,

Our model becomes

We can sample-mean center in R as follows

#calculate the mean centered variable  
wiscsub$verb1\_star <- wiscsub$verb1 - mean(wiscsub$verb1, na.rm = TRUE)

Then we can fit a new model using , such that

model3 <- lm(verb2 ~ 1 + verb1\_star,  
 data = wiscsub,  
 na.action = na.exclude)  
summary(model3)

##   
## Call:  
## lm(formula = verb2 ~ 1 + verb1\_star, data = wiscsub, na.action = na.exclude)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -11.5305 -3.0362 0.2526 2.7147 12.5020   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 25.41534 0.29831 85.20 <2e-16 \*\*\*  
## verb1\_star 0.75495 0.05149 14.66 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 4.261 on 202 degrees of freedom  
## Multiple R-squared: 0.5156, Adjusted R-squared: 0.5132   
## F-statistic: 215 on 1 and 202 DF, p-value: < 2.2e-16

**Note**: Mean centering should be used to aid interpretation. Historically, it has been suggested that mean centering will reduce multicollinearity, however this is not the case. See ![Olvera & Kroc (2018)](data:text/html; charset=UTF-8;base64,) for more information.

### 6.4.1 Interpreting Model Parameters

Note that the estimate for the slope stays the same, but the estimate for the intercept is different. This is because the variable ‘verb1\_star’ equals 0 when a child has an average 1st grade verbal score. Therefore the expected value for the 2nd grade verbal score, for *a child with an average 1st grade verbal score*, is 25.41534.

### 6.4.2 Plotting Regression Line

ggplot(data=wiscsub, aes(x=verb1\_star,y=verb2)) +  
 geom\_point(size = 2, shape=19) +  
 geom\_smooth(method=lm,se=TRUE,fullrange=TRUE,colour="red", size=2) +  
 labs(x= "Sample-Centered Verbal Ability Grade 1", y= "Verbal Ability Grade 2") +  
 xlim(-20,20) +  
 ylim(0,50) +  
 #theme with white background  
 theme\_bw() +  
 #eliminate background, gridlines, and chart border  
 theme(  
 plot.background = element\_blank()  
 ,panel.grid.major = element\_blank()  
 ,panel.grid.minor = element\_blank()  
 ,panel.border = element\_blank()  
 ) +  
 #draws x and y axis line  
 theme(axis.line = element\_line(color = 'black')) +  
 #set size of axis labels and titles  
 theme(axis.text = element\_text(size=12),  
 axis.title = element\_text(size=14))

## `geom\_smooth()` using formula 'y ~ x'



Note the change of scale on the x-axis.

## 6.5 Multiple Linear Regression

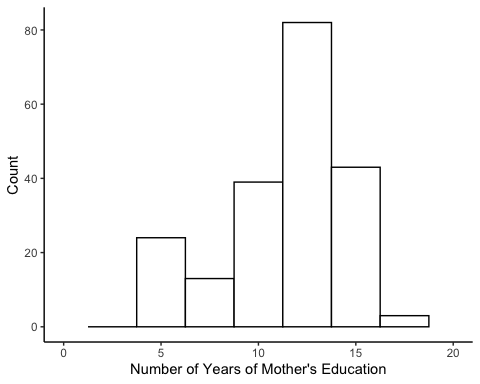
Now, let’s include a second predictor. We have information on the number of years of education for the children’s mothers, variable momed. The values in momed indicate the number of years of education each mother completed. First, let’s take a look at the distribution of this new predictor variable.

psych::describe(wiscsub$momed)

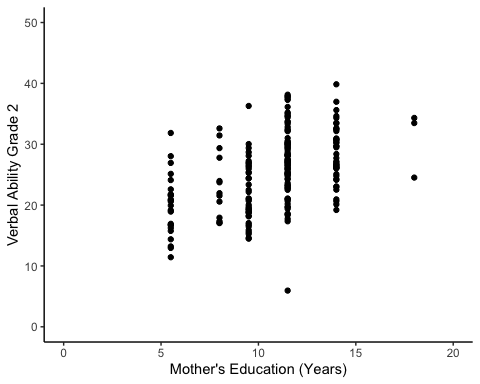
## vars n mean sd median trimmed mad min max range skew kurtosis se  
## X1 1 204 10.81 2.7 11.5 11 2.97 5.5 18 12.5 -0.36 0.01 0.19

ggplot(data=wiscsub, aes(x=momed)) +   
 geom\_histogram(binwidth=2.5, fill="white", color="black") +  
 xlim(0,20) +  
 xlab("Number of Years of Mother's Education") +   
 ylab("Count") +  
 theme\_classic()

## Warning: Removed 2 rows containing missing values (geom\_bar).

 And the relation between Grade 2 verbal scores and momed.

ggplot(data=wiscsub, aes(x=momed, y = verb2)) +   
 geom\_point() +  
 xlim(0,20) +   
 ylim(0,50) +  
 xlab("Mother's Education (Years)") + ylab("Verbal Ability Grade 2") +  
 theme\_classic()



### 6.5.1 Regression Equation

Our model now becomes

where is the sample-centered version of , and is the sample-centered version of .

The slope, is the expected difference in grade 2 verbal score for each 1 year difference in mother’s education.

We can also center the momed variable.

# Calculate mean-centered version of mother's education variable  
wiscsub$momed\_star <- wiscsub$momed - mean(wiscsub$momed)

### 6.5.2 Fit Model in R

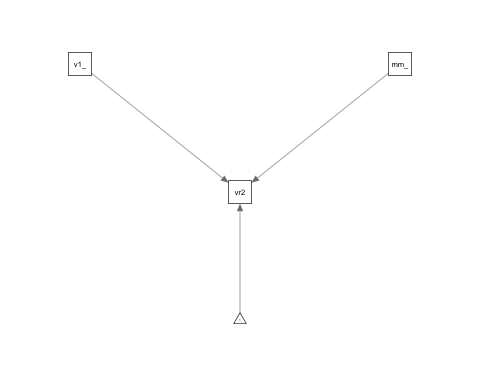
model4 <- lm(verb2 ~ 1 + verb1\_star + momed\_star,  
 data = wiscsub,  
 na.action = na.exclude)  
summary(model4)

##   
## Call:  
## lm(formula = verb2 ~ 1 + verb1\_star + momed\_star, data = wiscsub,   
## na.action = na.exclude)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -9.4354 -2.9189 -0.1542 2.3746 11.1678   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 25.41534 0.29069 87.430 < 2e-16 \*\*\*  
## verb1\_star 0.66786 0.05626 11.872 < 2e-16 \*\*\*  
## momed\_star 0.41454 0.12108 3.424 0.000749 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 4.152 on 201 degrees of freedom  
## Multiple R-squared: 0.5422, Adjusted R-squared: 0.5377   
## F-statistic: 119.1 on 2 and 201 DF, p-value: < 2.2e-16

Now we have an intercept and two slopes.

### 6.5.3 Path Diagram

semPlot::semPaths(model4, what = "paths")



#### 6.5.3.1 Interpreting Model Parameters

is the expected value of the outcome variable when all other variables are 0. Therefore, in this case, is the expected Grade 2 verbal score for a child with an average Grade 1 verbal score (i.e.  = 0) *and* whose mother had an average education (i.e.  = 0, = 10.81 years of education.

is the expected difference in the outcome for a 1-unit difference in . In this example (i.e. ‘model4’), is the expected difference in Grade 2 verbal score (outcome variable, = ) for a 1 point difference in the Grade 1 verbal score ( = ), holding constant the level of mother’s education.

is the expected difference in the outcome for a 1-unit difference in . For this example (i.e. ‘model4’), is the expected difference in Grade 2 verbal score (outcome variable, = ) for each year difference in mother’s education ( = ), holding constant in Grade 1 verbal score.

### 6.5.4 A Note on Interpretation

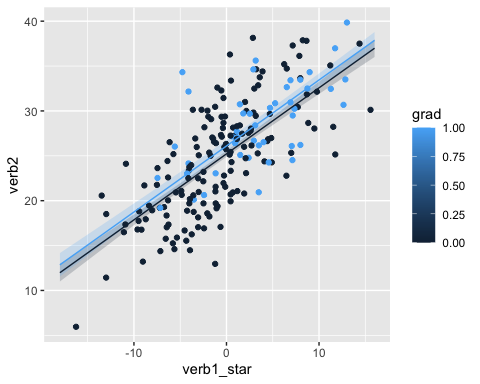
The distinguishing feature for interpretation in linear models without interactions or higher-order terms is that **the effect of a given change in an independent variable is the same regardless of the value of that variable (at the start of its change) and regardless of the level of the other variables in the model.**

Interpretation only needs to specify which variable is changing, by how much, and that other variables are being held constant.

In regard to our last example, years of mother’s education does impact the relationship between Grade 1 and 2 verbal scores. Likewise, the effect of mother’s education on Grade 1 verbal scores does not depend on Grade 1 verbal scores. Said in a different way, no matter what a child’s Grade 1 verbal score was, the effect of mother’s education on Grade 2 verbal scores is the same.

Consider another model with categorical and continuous predictors, grad and verb1\_star, respectively.

library("ggiraphExtra")  
model4b <- lm(verb2 ~ 1 + verb1\_star + grad,  
 data = wiscsub,  
 na.action = na.exclude)  
ggPredict(model4b,se=TRUE,interactive=FALSE)



Notice in the plot, whether a student’s mother graduated HS does not impact the relationship between Grade 1 and 2 verbal scores. Differences in Grade 1 and 2 verbal scores are not dependent on whether or not the mother graduated HS.

**Most importantly, using the coefficients themselves we can easily interpret the model parameters.**

## 6.6 Categorical Variable Interaction

Ok, let’s move on to the topic of an *interaction* which uses the product of two predictor variables as a new predictor.

Working up a slightly different example with the ‘grad’ variable (whether mom graduated high school),

Where is the mean-centered version of , and is a dummy coded variable that equals 0 if the child’s mother *did not* graduate high school, and equals 1 if the child’s mother *did* graduate high school.

We did not sample-mean center in this example because a value of 0 already has substantive meaning for the current example (i.e. when equals 0, the mother *did not* graduate high school).

### 6.6.1 Interaction as Moderation

Often, we describe phenomena in terms of *moderation*; or that the relation between two variables (i.e.  and ) is *moderated* by a third variable (i.e. ). For example, the relation between Grade 1 and Grade 2 verbal scores may be *moderated* by mother’s graduation status. More specifically, the relation between 1st and 2nd grade verbal score may be different for children whose mothers’ did not or did graduate from high school.

The inclusion of product terms (i.e. interactions) allows for a direct investigation of a *moderation* hypothesis.

#### 6.6.1.1 Choosing a Moderator

When we use a product term, we should define one of the variables as the moderator and one of the variables as the predictor of interest. Let’s call the predictor of interest, and the moderator.

### 6.6.2 Moderation by Categorical Variable

When the moderator is a dummy variable then the form of the moderation becomes fairly simple; we will have one equation for , and a second equation for .

#### 6.6.2.1 Rewriting Equation

To illustrate the notion of two equations, let’s rewrite the regression equation

as two separate regression equations, one for mothers who graduated from highschool and one for mothers that did not. We can accomplish this by plugging in and into the regression equation and rearranging some of the terms. Doing so we get

**Equation for Students whose Mother Graduated Highschool**

**Equation for Students whose Mother Did Not Graduate from Highschool**

### 6.6.3 Interpretation

Without an interaction, our linear regression model assumes that the only difference between the regression line for each group (graduate HS vs not) is the intercept. That is, it assumes that the relationship between verbal scores at Grades 1 and 2 is the same for both groups.

*Children Whose Mother’s Did Not Graduate HS*

The expected Grade 2 verbal score for a child whose mother did not graduate high school *and* who had an average Grade 1 verbal score is . Also, for a child whose mother did not graduate high school, is the expected difference in their Grade 2 verbal score for a one-point difference in their Grade 1 verbal score.

*Children Whose Mother’s Did Not Graduate HS*

The parameter estimates and maintain their interpretation from before. But now each of them is *moderated* (i.e. shifted or altered) by or .

Specifically, the expected Grade 2 verbal score for a child whose mother did graduate high school *and* who earned an average Grade 1 verbal score is .

And, for a child whose mother did graduate high school, is the expected difference in their Grade 2 verbal score for a one-point change in their Grade 1 verbal score.

### 6.6.4 Fit Regression Model in R

OK - let’s fit the model! Note that within this model we use the code I(verb1\_star \* grad). This produces the interaction term within the model. The wrapper function I() indicates to R to perform this data computation as-is, otherwise we would need to perform this computation (i.e. the multiplication of verb1\_star by grad) outside of the function lm().

model5 <- lm(verb2 ~ 1 + verb1\_star + grad + I(verb1\_star\*grad),  
 data = wiscsub,  
 na.action = na.exclude)  
summary(model5)

##   
## Call:  
## lm(formula = verb2 ~ 1 + verb1\_star + grad + I(verb1\_star \* grad),   
## data = wiscsub, na.action = na.exclude)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -11.3433 -3.0761 -0.0825 2.5689 10.7289   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 25.2663 0.3416 73.956 <2e-16 \*\*\*  
## verb1\_star 0.7861 0.0604 13.015 <2e-16 \*\*\*  
## grad 1.4632 0.8107 1.805 0.0726 .   
## I(verb1\_star \* grad) -0.2430 0.1324 -1.836 0.0678 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 4.232 on 200 degrees of freedom  
## Multiple R-squared: 0.5268, Adjusted R-squared: 0.5197   
## F-statistic: 74.22 on 3 and 200 DF, p-value: < 2.2e-16

### 6.6.5 Path Diagram

semPlot::semPaths(model5, what = "paths")



The parameter estimates from this model indicate that, for children whose mother did not graduate high school, the expected Grade 2 verbal score for a child that earned an average 1st grade verbal score equals 25.2663 ().

Also, for children whose mother did not graduate high school, a 1-point difference in their Grade 1 verbal score is expected to correspond with a 0.7861 () point difference in the Grade 2 verbal score.

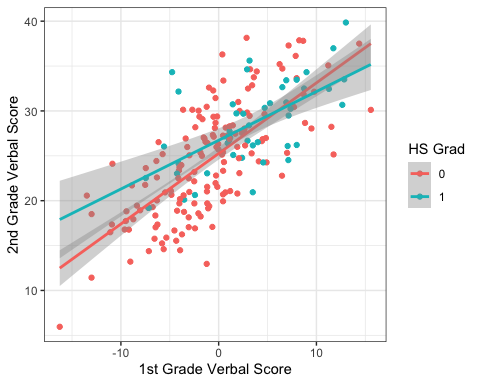
Moreover, the parameter estimates indicate that, for children whose mother did graduate high school, the expected Grade 2 verbal score for a child that earned an average Grade 1 verbal score is 25.2663 + 1.4632 = 26.7295 ().

Also, for children whose mother graduated high school, a 1-point difference in their Grade 1 verbal score is expected to correspond with a () = 0.7861 - 0.2430 = 0.5431 point difference in the Grade 2 verbal score.

Even though the interaction is not significant, we can plot it for illustrating the moderation effect:

#plot of moderation  
ggplot(data=wiscsub,   
 aes(y=verb2,x=verb1\_star, color = factor(grad))) +  
 geom\_jitter() +  
 stat\_smooth(method='lm', se=TRUE, fullrange=TRUE) +  
 xlab("1st Grade Verbal Score") +   
 ylab("2nd Grade Verbal Score") +   
 guides(color=guide\_legend(title="HS Grad")) +  
 theme\_bw()

## `geom\_smooth()` using formula 'y ~ x'



The example from ‘model5’ contained an interaction using a dummy variable (i.e., ). Interactions may also occur between two continuous variables (i.e., and ). We will not cover here, but note that it is still very useful to consider and communicate those interactions as *moderation*. There are many resources on interactions of two (or more) continuous variables.

# 7 Logistic Regression

In Chapter 7 we will introduce the logistic regression model through the lens of generalized linear models (GLMs). The GLM is an essential tool for modeling discretely distributed dependent variables.

## 7.1 Categorical Data in the Social Sciences

Linear regression is a workhorse procedure of modern statistics. Our introduction to regression in this class was framed around the idea of a continuous dependent (outcome) variable. However, categorical data is extremely common in many health, behavioral and social science applications.

### 7.1.1 Examples of Categorical Data

* Binary Variables have two categories and are often used to indicate that an event has occurred or a characteristic is present. Are you sick? Did you vote in the last election? Are you married?
* Ordinal variables have categories that can be ranked. Surveys often ask respondents to indicate their agreement to a statement, how frequently then engage in a behavior, or even educational attainment.
* Nominal variables occur when there are multiple outcomes that cannot be ordered. For example, left or right handedness or occupation.
* Censored variables occur when the value of a variable is unknown over some range of the variable. For example, measuring hourly wages might be restricted on the lower end by minimum wage laws.
* Counts indicate the number of times that some event has occurred. How many drinks last week? How many people living in a house? How many years of education? *Censored and count variables are often lumped in with more traditional categorical variables under the umbrella of limited dependent variables.*

## 7.2 Introduction to GLMs

Earlier we noted linear regression is typically applied to continuous variables. The ubiquity of categorical data leads us to a modeling framework better suited to handling a wide range of categorical outcomes: the Generalized Linear Model (GLM).

In the GLM, the response variable is assumed to follow an exponential distribution with mean , which itself is a nonlinear function of . We can think about as the mean of a conditional response distribution at a given point in the covariate space.

There are three important components to the GLM:

1. *A random component*: The random component of the GLM contains the response variable and its probability distribution (e.g. the binomial distribution of in the binary regression model).
2. *A Linear Predictor*: The linear predictor typically takes the form of where is an matrix of observations and is an column vector.
3. *Link Function*: The link function, typically specified as , is used to relate each component of to the linear predictor, .

### 7.2.1 Linear Regression as GLM

Linear regression can be formulated in the GLM framework as follows:

1. *A random component*: We can make specify .
2. *A Linear Predictor*: are the continuous or discrete explanatory variables. The way we think about the structural component here doesn’t really differ from how we think about it with standard linear models; in fact, that’s one of the nice advantages of the GLM.
3. *Link Function*: For linear regression we use the *identity link* (e.g. ).

### 7.2.2 Logistic Regression as GLM

Let’s also take a look at binary logistic regression formulated as GLM.

1. *A random component*: The distribution of is assumed to be binomial with success probability .
2. *A Linear Predictor*: are the continuous or discrete explanatory variables.
3. *Link Function*: For logistic regression we use the *log-odds (or logit) link* (e.g. ), where is the transformed outcome.

### 7.2.3 Poisson Regression as GLM

Poisson regression can also be formulated as a GLM:

1. *A random component*: The distribution of is assumed to be Poisson with mean .
2. *A Linear Predictor*: are the continuous or discrete explanatory variables.
3. *Link Function*: For Poisson regression the *log link* is used.

### 7.2.4 Additional Remarks

When the outcome data are not normally distributed, we can always do transformation to change its scale. These are typically done via *link functions* denoted as - so we get . If we denote the transformed outcome as , then we can denote it as:

From a conceptual point of view, the link function *transforms* into a normal outcome. Note that we are simplifying notation somewhat: while we are modeling some expectation of , not exactly , we will keep on using . This is to say the link is applied to the parameter governing the response distribution, not the actual response data. We use *link functions* to formalize that the conditional expectation for (conditional because it is the expected value of depending on the level of the predictors and the chosen link).

Each link function also has an inverse, , which allows us to define

The inverse of a link function back-converts the linear combination of predictors into the original outcome.

## 7.3 Binary Logistic Regression

### 7.3.1 Overcoming LPM

To avoid the problems of the LPM we’d like a model where

is forced to be within the range of to . One way to do this is to transform the probability above into the odds metric,

which has a range of to . So, we are halfway there. Indeed, by taking the log of the odds (or logit) we extend the support of to have a range of to . This maps probability ranging between and to log odds ranging from negative infinity to positive infinity.

This is one example of why the logit link is used for logistic regression. Nowe we can seamlessly model the probability of an event occurring, giving the explanatory variables, .

We denote this probability as , or equivalently, .

Often times you will simply see for convenience, but it is important to remember this probability is conditional on the explanatory variables in the model.

### 7.3.2 Model

The binary logistic regression model is expressed as

Where is the odds of an event occurring and is the natural logarithm. Therefore, the parameter estimates from a generalized linear regression using the logistic link function are scaled in *log-odds* or *logit* units.

We can also rewrite the model above, solving for , as

This is also called the inverse function for the logit link function, or the *logistic* link, . In practice, this transformation is what is used for solving the regression equation, and it is called logistic regression:

## 7.4 Example Data

Chapter 7

In Chapter 7 we use data from Dunn, Aknin, and Norton (2007), who examined the relationship between spending habits and happiness using OLS regression. To capture spending habits self-reported monthly spending was categorized as being either personal or prosocial, and then summed to create a category-specific total. Measures of happiness were obtained using a 5-item ordinal scale.

The dependent variable in this analysis (GeneralHappiness) was self-reported general happiness. Participants rated their general happiness by answering the question “Do you feel happy, in general?” by selecting from five possible response options (no, rarely, sometimes, most of the time, and yes), which were then scored from 1-5. Here, higher numbers were indicative of greater happiness. For the purpose of our analysis we will dichotomize GeneralHappiness depending on whether a person was not happy vs happy.

The sample was selected to be a nationally representative sample of 632 Americans (287 males and 345 females). Participants responded as part of a larger, online survey, in return for points that could be redeemed for prizes (Dunn, 2008). No further details on sampling were available.

### 7.4.1 Variables

* **Happy**: Dichotomous variable indicating whether the subject responded “yes” when asked if they felt happy, in general.
* **PersonalSpending**: Self-reported dollars spent per month on (a) bills and expenses, and (b) gifts for themselves.
* **ProsocialSpending**: Self-reported dollars spent per month on (a) gifts for others, and (b) donations to charity.
* **PersonalIncome**: Participants selected their personal income category from 6 options: less than $20,000, $20,000-$35,000, $35001-$50,000, $50,001-$65000, $65,001-$80,000, $80,001+.

library("ggplot2")  
dunn2008 <- read.csv("data/DUNN2008.csv")  
dunn2008$Happy <- ifelse(dunn2008$GeneralHappiness == "yes", 1, 0)  
dunn2008$PersonalSpending <- dunn2008$PersonalSpending/100  
dunn2008$ProsocialSpending <- dunn2008$ProsocialSpending/100  
dunn2008$PersonalSpending\_star <- as.numeric(scale(dunn2008$PersonalSpending, scale = FALSE))  
dunn2008$ProsocialSpending\_star <- as.numeric(scale(dunn2008$ProsocialSpending, scale = FALSE))  
dunn2008$Income <- dplyr::recode(dunn2008$PersonalIncome,   
 "20001-35000" = "20-35K",   
 "35001-50000" = "35-50K",   
 "50001-65000" = "50-65K",   
 "65001-80000" = "65-80K",   
 "80001andup" = "> 80K",   
 "less20000" = "< 20K")  
inc\_lev\_order <- c("< 20K","20-35K", "35-50K","50-65K","65-80K","> 80K")  
dunn2008$Income <- factor(dunn2008$Income, levels=inc\_lev\_order)

## 7.5 Intercept-Only Model

In logistic regression, we are interested in how various predictors are related to the probability of a specific outcome . In this example we are interested in the probability an individual reports being happy, in a general sense.

Making use of the logit link function, the general equation for logistic regression is

Which after back transformation gives us …

### 7.5.1 Intercept-Only Model in R

In our example the variable Happy indicates whether a subject reporting being happy. Let’s start with the simplest model for predicting Happy, the intercept-only model. More specifically, we have $ logit(\_i) = b\_0(1\_i)$where .

We can use the glm() function to fit the model to the data

model9 <- glm(Happy ~ 1,   
 family = "binomial",   
 data = dunn2008,   
 na.action = na.exclude)  
summary(model9)

##   
## Call:  
## glm(formula = Happy ~ 1, family = "binomial", data = dunn2008,   
## na.action = na.exclude)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.9014 -0.9014 -0.9014 1.4812 1.4812   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.69077 0.08435 -8.19 2.62e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 805.02 on 631 degrees of freedom  
## Residual deviance: 805.02 on 631 degrees of freedom  
## AIC: 807.02  
##   
## Number of Fisher Scoring iterations: 4

Without wanting to get to detailed we don’t need to specify the logit link here because it is the canonical link function for the binomial distribution. This essentially means there is a direct correspondence between the predicted mean and the distribution’s canonical location parameter.

### 7.5.2 Interpretation

#### 7.5.2.1 Intercept Parameter

In the intercept-only model, the intercept, , reflects

1. The expected log-odds () of an individual reporting they were happy.
2. The odds of someone reporting being happy .

exp(-0.69077)

## [1] 0.50119

1. The expected probability () of the a subject reported being happy in general.

or, equivalently, in R

exp(-0.69077)/(1 + exp(-0.69077))

## [1] 0.3338618

We can also confirm that the backward transformed parameter from this intercept-only logistic regression matches the expectation we get from the descriptives of the raw data.

mean(dunn2008$Happy)

## [1] 0.3338608

*Note*: If then , indicating a positive relationship between and the probability of the event occurring. If , the opposite relationship holds.

## 7.6 Single Predictor Model

OK, let’s include a predictor in our logistic regression model. Let’s start with PersonalSpending such that

where . Here, is the mean-centered amount of money one spends on themselves in a month (in units of dollars).

Let’s fit the model in R.

model10 <- glm(Happy ~ 1 + PersonalSpending\_star,   
 family = "binomial",   
 data = dunn2008,   
 na.action = na.exclude)  
summary(model10)

##   
## Call:  
## glm(formula = Happy ~ 1 + PersonalSpending\_star, family = "binomial",   
## data = dunn2008, na.action = na.exclude)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.9100 -0.9048 -0.8994 1.4757 1.6242   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.690890 0.084358 -8.190 2.61e-16 \*\*\*  
## PersonalSpending\_star -0.001355 0.004605 -0.294 0.769   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 805.02 on 631 degrees of freedom  
## Residual deviance: 804.93 on 630 degrees of freedom  
## AIC: 808.93  
##   
## Number of Fisher Scoring iterations: 4

### 7.6.1 Overdispersion

A quick digression. In the binary logistic regression model *overdispersion* occurs when the observed variance is larger than what the binomial distribution would predict. For example, if , the mean is $\u\_{i}=n\_{i}\pi\_{i}$ and the variance is . Since both of these moments rely on , it can be overly restrictive, and if overdispersion is present inferences can become distorted. We will talk about this more later.

### 7.6.2 Coefficients

Again, There are essentially three ways to interpret coefficients from a logistic regression model:

1. The log-odds (or logit)
2. The Odds
3. Probabilities

#### 7.6.2.1 Log-Odds

The parameter estimate reflects the expected log-odds () of being happy for an individual with an average amount of personal spending.

The estimate for indicates the expected difference of the log-odds of being happy for a dollar difference in personal spending. Therefore, we expect a difference in the log-odds of being happy for a dollar difference in personal spending.

#### 7.6.2.2 Odds

Parameter estimates from a logistic regression are often reported in terms of *odds* rather than *log-odds*. To obtain parameters in odds units, we simply exponentiate the coefficients. Note that this is just one of the steps of the inverse link function (which would take us all the way to probability units).

exp(cbind(OR = coef(model10), confint(model10)))

## Waiting for profiling to be done...

## OR 2.5 % 97.5 %  
## (Intercept) 0.5011299 0.4240750 0.5903901  
## PersonalSpending\_star 0.9986459 0.9886908 1.0072747

In other words, the odds of being happy when personal spending is at average levels is .

In regard to the slope coefficient, for a dollar difference in monthly personal spending, we expect to see about decrease in the odds of being happy. This decrease does not depend on the value that personal spending is held at. Note this is not significant and we would not report this interpretation in practice. Essentially, if the odds ratio is equal to one, the predictor did not have an impact on the outcome.

#### 7.6.2.3 Probability

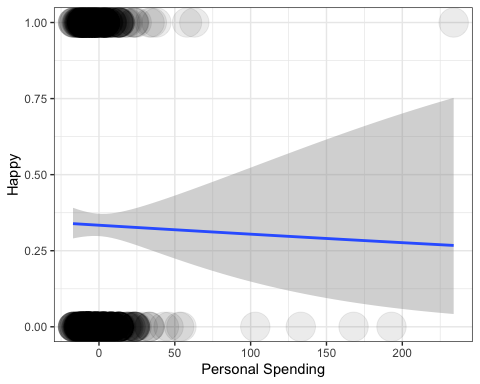
Remember, probabilities range from , whereas log-odds (the output from the raw logistic regression equation) can range from , and odds and odds ratios can range from . Due to the bounded range of probabilities, probabilities are non-linear, but log-odds can be linear.

For example, as personal spending goes up by constant increments, the probability of happiness will increase (decrease) by varying amounts, but the log-odds will increase (decrease) by a constant amount, and the odds will increase (decrease) by a constant multiplicative factor.

For this reason it is not so simple to interpret probabilities in logistic regression from the coefficient directly. Often it is much simpler to plot the probabilities across a range of the predictor variables.

ggplot(data=dunn2008,  
 aes(x=PersonalSpending\_star,y=Happy)) +  
 geom\_point(alpha = .08, size = 10) +  
 xlab("Personal Spending") +  
 ylab("Happy") +  
 theme\_bw() +  
 stat\_smooth(method = 'glm', method.args = list(family = "binomial"), se = TRUE)

## `geom\_smooth()` using formula 'y ~ x'



Notice how the density of the observations is visualized by manipulating the transparency (alpha) level of the data points. The predicted curve based on our model has of course a non-linear shape (however, if we were to plot the relationship between the variables with using the logit link, it would be a straight line).

## 7.7 Marginal Effects

So far we have considered two possibilities for interpreting logistic regression results:

* Interpreting the log-odds directly
* Transforming the log-odds into odds
* A probability metric (for a single explanatory variable)

However, as we include more covariates in our model, interpretation becomes more difficult. We can only think about “holding other variable constant” in the log-odds and odds scale. For nonlinear model **marginal effects** provide us with an intuitive and easy to interpret method for understanding and communicating results.

### 7.7.1 A Definition of Marginal Effects

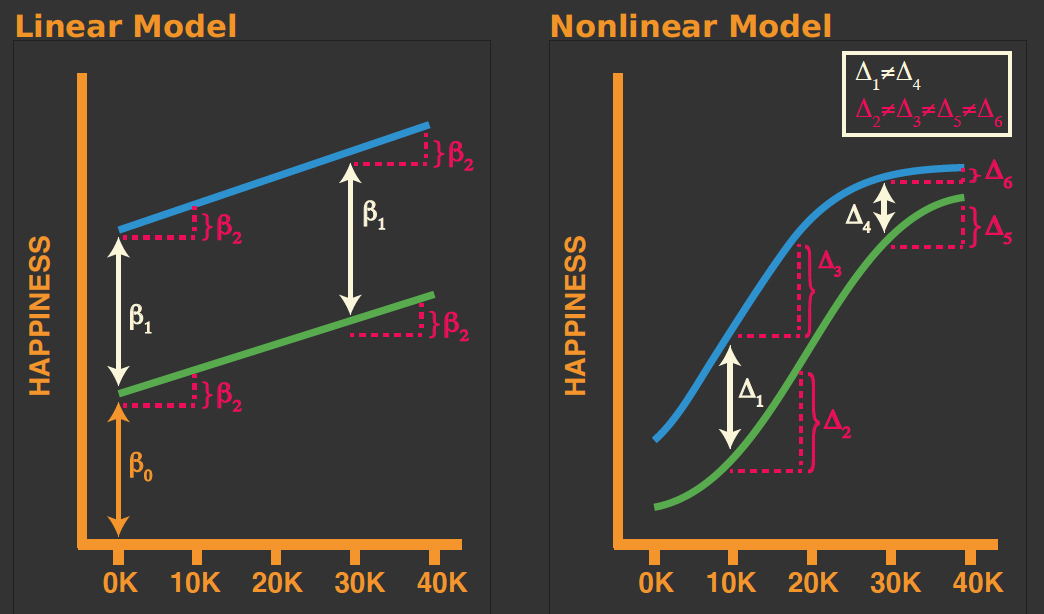
**Marginal effects are partial derivatives of the regression equation with respect to each variable in the model for each unit in the data.**

Put differently, the marginal effect measures the association between a change in an explanatory variable and a change in the response. The marginal effect is the slope of the prediction function, measured at a specific value of the explanatory variable.

In linear models the effect of a given change in an independent variable is the same regardless of (1) the value of that variable at the start of its change, and (2) the level of the other variables in the model.

In nonlinear models the effect of a given change in an independent variable (1) depends on the values of other variables in the model, and (2) is no longer equal to the parameter itself.

Consider a linear and nonlinear model for happiness as a function of personal spending and a dummy variable indicating whether someone is rich.



### 7.7.2 A Few Observations

**For the linear model**: - Whether one is rich or poor does no impact the relationship between happiness and personal spending. - Differences in happiness levels between rich and poor are not dependent on the amount of money one spends.

**From the nonlinear model**: - Whether one is rich or poor does impact the relationship between happiness and personal spending. - Differences in happiness levels between rich and poor are dependent on the amount of money one spends.

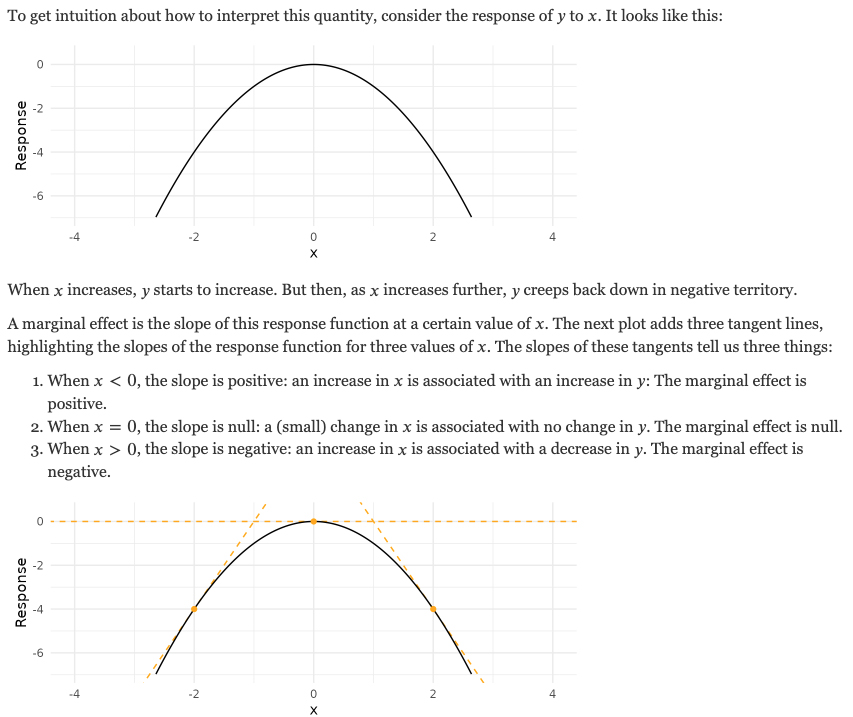
#### 7.7.2.1 Another Nonlinear Example

A helpful example is provided in the [marginaleffects vignette](https://vincentarelbundock.github.io/marginaleffects/articles/mfx.html).

Consider a simple quadratic

$$
y = -x^2 \\
$$

with partial derivative of with respect to



<https://vincentarelbundock.github.io/marginaleffects/articles/mfx.html>

### 7.7.3 Types of Marginal Effects

There are generally three types of *marginal effects* people consider:

* Marginal Effects at the Means (MEM)
* Average Marginal Effects (AME)
* Marginal Effects at Representative Values (MEM)

We will focus on marginal effects at representative values as this is the most powerful option.

### 7.7.4 Example Model

Let’s fit a more complicated model. To look at marginal effects we will use the marginaleffects package.

library("marginaleffects")

## Warning: package 'marginaleffects' was built under R version 4.1.2

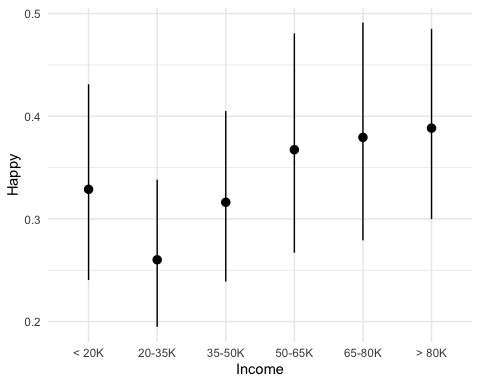
model11 <- glm(Happy ~ 1 + PersonalSpending + ProsocialSpending + Income,   
 family = "binomial",   
 data = dunn2008,   
 na.action = na.exclude)  
summary(model11)

##   
## Call:  
## glm(formula = Happy ~ 1 + PersonalSpending + ProsocialSpending +   
## Income, family = "binomial", data = dunn2008, na.action = na.exclude)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.7348 -0.9121 -0.8107 1.3929 1.7215   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.636366 0.223151 -2.852 0.00435 \*\*  
## PersonalSpending -0.011635 0.006643 -1.752 0.07985 .   
## ProsocialSpending 0.083741 0.032975 2.540 0.01110 \*   
## Income20-35K -0.331327 0.288006 -1.150 0.24997   
## Income35-50K -0.057632 0.297299 -0.194 0.84629   
## Income50-65K 0.170117 0.326317 0.521 0.60214   
## Income65-80K 0.221637 0.323873 0.684 0.49376   
## Income> 80K 0.259641 0.307140 0.845 0.39791   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 805.02 on 631 degrees of freedom  
## Residual deviance: 791.06 on 624 degrees of freedom  
## AIC: 807.06  
##   
## Number of Fisher Scoring iterations: 4

### 7.7.5 Marginal Effects at Representative Values (MER)

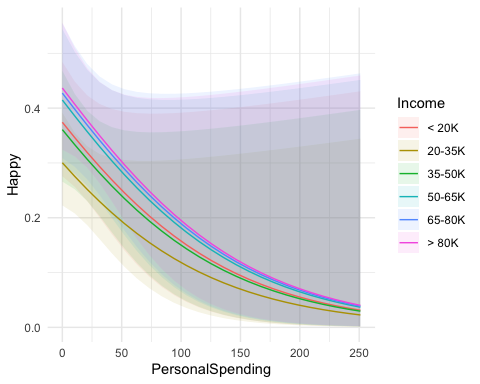
For example, let’s look at the impact of Income on the probability of being happy.

marginaleffects::plot\_cap(model11, condition = c("Income"), conf.int = TRUE)



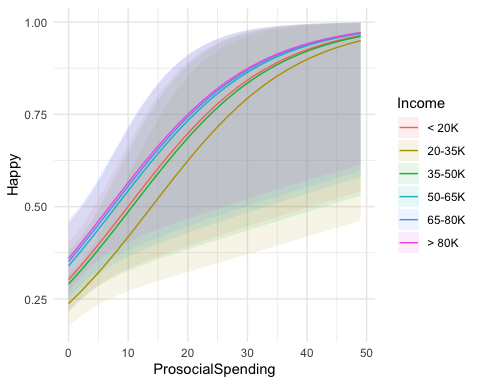
What if we were interested in the relationship between Income and PersonalSpending on the probability of being happy.

marginaleffects::plot\_cap(model11, condition = c("PersonalSpending","Income"))



What if we were interested in the relationship between Income and ProsocialSpending on the probability of being happy.

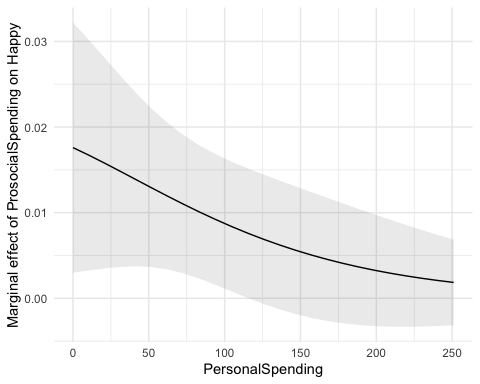
marginaleffects::plot\_cap(model11, condition = c("ProsocialSpending","Income"))



In nonlinear, the marginal effect of one variable is conditional on the value of the other variable. This function draws a plot of the marginal effect of the effect variable for different values of the condition variable.

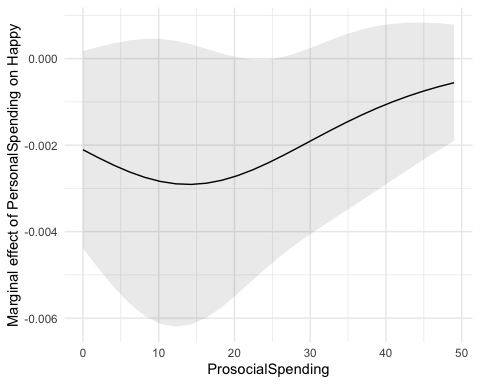
Let’s look at the effect of PersonalSpending on the relationship between ProsocialSpending and Happy.

marginaleffects::plot\_cme(model11, effect = "ProsocialSpending", condition = "PersonalSpending")



In addition, we can look at the effect of PersonalSpending on the relationship between PersonalSpending and Happy.

marginaleffects::plot\_cme(model11, effect = "PersonalSpending", condition = "ProsocialSpending")



# 8 Poisson Regression

In Chapter 8 we will round out our discussion of the GLM with Poisson regression. Poisson regression is a useful modeling approach for handling count dependent variables. One important consideration when fitting Poisson regression models is *overdispersion*. We will look at how one might assess overdispersion in Poisson regression and suggest some alternative procedures. As with logistic regression we will look to marginal effects and visualization as an aid to better understand results from nonlinear models.

## 8.1 Poisson Regression

To review, there are three important components to the GLM:

1. *A random component*: The random component of the GLM contains the response variable and its probability distribution (e.g. the binomial distribution of in the binary regression model).
2. *A Linear Predictor*: The linear predictor typically takes the form of where is an matrix of observations and is an column vector.
3. *Link Function*: The link function, typically specified as , is used to relate each component of to the linear predictor, .

### 8.1.1 Poisson Regression as GLM

Poisson regression can also be formulated as a GLM:

or equivalently,

1. *A random component*: The distribution of is assumed to be Poisson, .
2. *A Linear Predictor*: The systematic component takes the form of .
3. *Link Function*: For Poisson regression the *log link* is used.

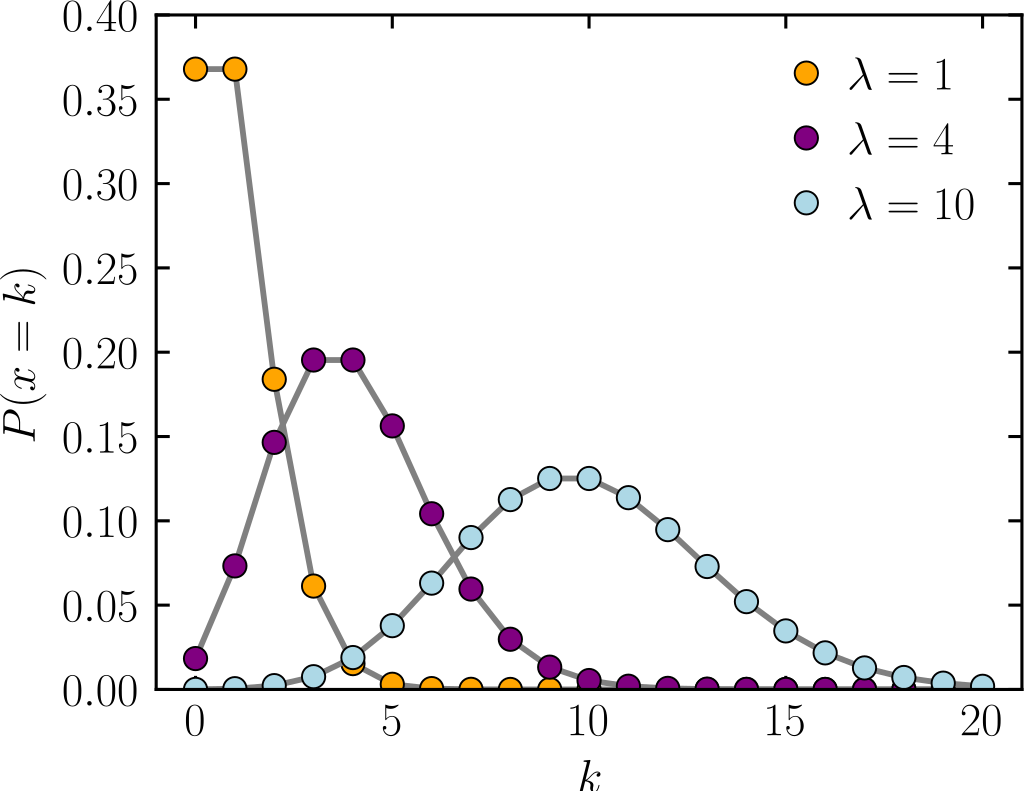
## 8.2 Poisson Distribution

To gain some intuition about the Poisson regression model consider the Poisson distribution

where

* is a random count variable
* is the expected number of times an event ocurrs
* is the factorical operator

The Poisson distribution relies on a single parameter, . Importantly, represents both the mean and the variance of the Poisson distribution (e.g. when is large both the mean and variance are large).



<https://en.wikipedia.org/wiki/Poisson_distribution>

**What Does This Mean In Practice**:

* As grows the center of the distribution shifts to right
* Departure of real count data from predictions from Poisson distribution
  + Variance frequently greater than mean (overdisperion)
  + Frequency of 0 counts exceed number predicted by Poisson

## 8.3 Notes on Interpretation

Consider a one-predictor Poisson regression,

$$
\mathrm{log}(\mu\_{i}) = \beta\_{0} + \beta\_{1}x\_{1i}\\
$$

where

Interpretation of the Poisson regression coefficients is similar to logistic regression. For example,

* is the effect on the mean of when
* is the multiplicative effect on the mean of for each 1-unit difference in

We can also talk about these regression coefficients in terms of percent change as follow,

* If is negative:
  + All else being equal, we might expect to see a percent decrease in the expected count of , with each additional unit increase in , holding constant all other variables in the model.
* If is positive:
  + All else being equal, we might expect to see a percent increase in the expected count of , with each additional unit increase in , holding constant all other variables in the model.

The following relationships are helpful to keep in mind,

* If then and the expected count, , and and are unrelated.
* If then and the expected count, is times larger then when .
* If then and the expected count, is times smaller then when .

**Note** that the parameter estimates will then describe the outcome variable in terms of *log* units. If we prefer to describe the phenomena in terms of the original *count* units we will need to use the inverse link function.

## 8.4 Example Data

Increasingly researchers are taking a life-course perspective to understanding how different life stages shape a variety of later in life outcomes. In this case study, [Ferraro, Schafer, and Wilkinson](#ref-ferraro2016) ([2016](#ref-ferraro2016)) examine the relationship between physical health in adulthood and multiple domains of childhood disadvantage using a count regression model. Data are drawn from the National Survey of Midlife Development in the United States (MIDUS). MIDUS contains a battery of retrospective questions concerning childhood disadvantage, as well as extensive measures of adult risks and resources. Although the authors use data from both waves of MIDUS in the paper, here we focus only on their first model of adult health outcomes, which takes into account both childhood disadvantage and the mediating effects of later life resources and risk behaviors.

### 8.4.1 Dependent variable

The dependent variable for this analysis is health problems at Wave 1 (morbidityw1). Here, adult health problems are measured by the self-reported occurrence of 31 diseases or health conditions. For 29 of these items respondents were asked “In the past 12 month have you experienced or been treated for any of the following?” For the remaining 2, cancer and heart disease, respondents were asked if they had ever been diagnosed with the disease. Finally, morbidityw1 is the sum of these 31 items, where each is coded 1 for yes, and 0 for no.

### 8.4.2 Explanatory Variables

#### 8.4.2.1 Early Life Disadvantage

* *ses*: Childhood SES is a sum score based on standardized measures of (1) the education for the head of household, (2) financial strain and (3) receipt of welfare.
* *family*: Family composition is a sum score based on (1) the presence of a male in the household, (2) parental divorce, and (3) death of parent prior to age 16,
* *abuse\_rare*: Physical or Emotional Child abuse by parents is categorized by frequency of abuse. abuse\_rare indicates respondent rarely experience one or both types of abuse. The reference category is never having experienced emotional or physical abuse.
* *abuse\_frequency1*: abuse\_frequency1 indicates respondents frequently (sometimes or often) experienced one type of abuse during childhood. The reference category is never having experienced emotional or physical abuse.
* *abuse\_frequency2*: abuse\_frequency2 indicates respondents frequently experienced both types of abuse during childhood. The reference category is never having experienced emotional or physical abuse.
* *health*: Adolescent health problems are measured by self-rated physical and mental health at age 16.

#### 8.4.2.2 Adult Characteristics

* *age*: Age at time of Wave 1 interview.
* *nonwhite*: Race (white or nonwhite).
* *female*: Gender (female or male).
* *educate*: Number of years of completed education.
* *catincome*: Household income adjusted by household size and recoded into five percentile categories (< 21st \*percentile, 21st to 40th percentile41st to 60th percentile, 61st to 80th percentile, and > 80th percentile.).
* *a1sj6*: Financial strain during adulthood; responses range from 1 (no difficulty paying monthly bills) to 3 (very difficult to pay monthly bills).
* *smoke\_dose*: Lifetime smoking is calculated from information reported by respondents: age when started smoking, year stopped (for former smokers), and average number of cigarettes smoked daily. Using a yearly metric, lifetime smoking is the product of years smoked and annual number of cigarettes, divided by 10,000 (see Footnote 11, p. 130).
* *heavydr2*: The measurement of heavy drinking is sex differentiated and tapped respondents’ period of greatest lifetime consumption: five or more drinks per day for men and four or more drinks for women.
* *obese*: Obesity, dummy variable coded 1 if body mass index [kg/m2] > 30.
* *fampos*: Family support as measured by four items reflecting the presence of positive relationship characteristics.
* *friendpos*: Friend support as measured by four items reflecting the presence of positive relationship characteristics.
* *famneg*: Family strain as measured by four items reflecting the presence of difficult relationship characteristics.
* *friendneg*: Friend strain as measured by four items reflecting the presence of difficult relationship characteristics.
* *integration*: Social integration as measured by three 7-item Likert–type questions.
* *ever\_divor*: Ever divorced, a dummy variable coded 1 if the respondent reported having been divorced.
* *controlw1*: Average score for a 12-item index of the respondent’s feelings of personal control.

ferraro2016 <- read.csv("data/ferraro2016.csv")  
ferraro2016$income\_star <- as.numeric(scale(ferraro2016$catincome, scale = FALSE))

## 8.5 Single Predictor Model

Let’s fit a single predictor Poisson regression model for morbidity at Wave 1 using income bracket as our predictor. For now let’s treat income bracket as a continuous predictor.

model1 <- glm(  
 formula = morbidityw1 ~ 1 + income\_star,   
 family = poisson(link=log),   
 data = ferraro2016,  
 na.action = na.exclude  
)  
summary(model1)

##   
## Call:  
## glm(formula = morbidityw1 ~ 1 + income\_star, family = poisson(link = log),   
## data = ferraro2016, na.action = na.exclude)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.4131 -1.2984 -0.4633 0.7192 8.8437   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.007472 0.011047 91.195 < 2e-16 \*\*\*  
## income\_star -0.032445 0.007838 -4.139 3.48e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for poisson family taken to be 1)  
##   
## Null deviance: 8166.6 on 2994 degrees of freedom  
## Residual deviance: 8149.5 on 2993 degrees of freedom  
## (27 observations deleted due to missingness)  
## AIC: 14986  
##   
## Number of Fisher Scoring iterations: 5

### 8.5.1 Deviance and Goodness of Fit

We can think about the deviance as a measure of how well the model fits the data. If the model fits well, the observed values will be close to their predicted means , causing the deviance to be small. If this value greatly exceeds one it may be indicative of overdispersion.

The rationale for this heuristic is based on the fact that the residual deviance is distributed with mean equal to the degrees of freedom. Instead of using this rule of thumb it is just as simple to formulate a goodness-of-fit test for our model as follows

1 - pchisq(summary(model1)$deviance, summary(model1)$df.residual )

## [1] 0

The GOF test indicates that the Poisson model fits does not fit the data . This suggests there may be a problem with overdispersion. *Overdispersion indicates there is greater variability in the data than would be expected based on the model.* Overdispersion is often encountered when fitting simple Poisson regression models. The Poisson distribution has one free parameter and does not allow for the variance to be adjusted independently of the mean. If overdispersion is present the resultant model may yield biased parameter estimates and underestimated standard errors, possibly leading to invalid conclusions.

### 8.5.2 Interpretation

#### 8.5.2.1 Intercept

This is the Poisson regression estimate when all variables in the model are evaluated at zero. For our model, we have centered the income variable. This means for an individual with an average income level the log of the expected count for health problems is units.

We can also exponentiate the intercept, indicating that at Wave 1 follow-up, an individual with an average income level is expected to have approximately health problems

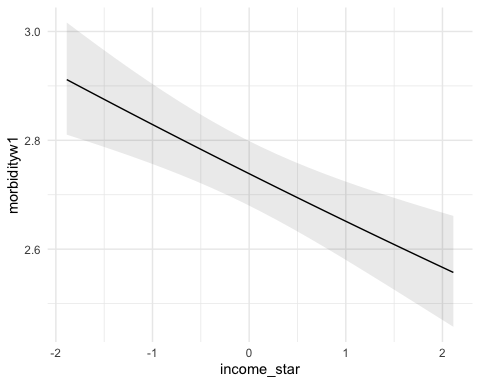
#### 8.5.2.2 Slope

Within our single predictor model, is the difference in *log* number of health problems for a 1-level difference in income bracket. Therefore, we expect a difference in the log-count of health problems for a 1-level difference in income brackets. Or, all else being equal, we might expect to see a percent decrease in the number of health problems with each additional unit-change in income level.

This relation may be difficult to conceptualize because the outcome variable is in terms of logarithm units, so a plot may be a more intuitive display of the results.

Let’s turn to the marginaleffects ([Arel-Bundock 2022](#ref-bundock)) package to look at the marginal effects of income on health.

marginaleffects::plot\_cap(model1, condition = c("income\_star"), conf.int = TRUE)



## 8.6 Multiple Predictor Model

Let’s add another variable into the model. Specifically, the variable abuse\_rare, which equals if the child was rarely abused during early development, and if the child experienced abuse.

ferraro2016$abuse\_rare <- factor(ferraro2016$abuse\_rare)  
model2 <- glm(  
 formula = morbidityw1 ~ 1 + abuse\_rare + income\_star + abuse\_rare:income\_star,   
 family = poisson(link=log),   
 data = ferraro2016,  
 na.action = na.exclude  
)  
summary(model2)

##   
## Call:  
## glm(formula = morbidityw1 ~ 1 + abuse\_rare + income\_star + abuse\_rare:income\_star,   
## family = poisson(link = log), data = ferraro2016, na.action = na.exclude)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.4949 -1.3511 -0.4745 0.6512 8.6487   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.0766511 0.0129647 83.045 < 2e-16 \*\*\*  
## abuse\_rare1 -0.2382614 0.0251265 -9.482 < 2e-16 \*\*\*  
## income\_star -0.0311089 0.0091684 -3.393 0.000691 \*\*\*  
## abuse\_rare1:income\_star -0.0000822 0.0179350 -0.005 0.996343   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for poisson family taken to be 1)  
##   
## Null deviance: 8068.4 on 2966 degrees of freedom  
## Residual deviance: 7956.7 on 2963 degrees of freedom  
## (55 observations deleted due to missingness)  
## AIC: 14737  
##   
## Number of Fisher Scoring iterations: 5

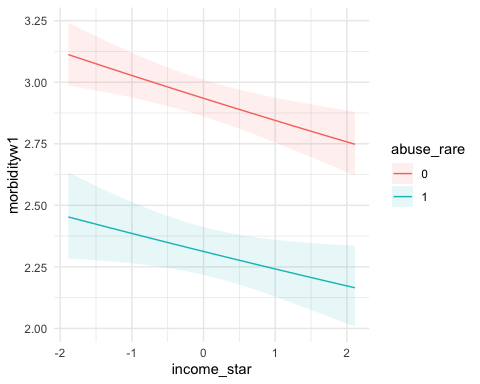
As the model becomes more complicated it can be helpful to write out the equation,

Coefficients and describe the relation between and for those who experienced childhood abuse .

While coefficients and describe the relation for those who rarely experienced childhood abuse . Note that neither is not significantly different from zero, so we would not interpret the interaction between income and abuse directly.

Let’s again turn to the marginaleffects ([Arel-Bundock 2022](#ref-bundock)) package to look at the marginal effects of income and childhood abuse on health.

marginaleffects::plot\_cap(model2, condition = c("income\_star","abuse\_rare"), conf.int = TRUE)



## 8.7 Revisisting Overdispersion

Let’s run our model fit test based on the deviance for model2.

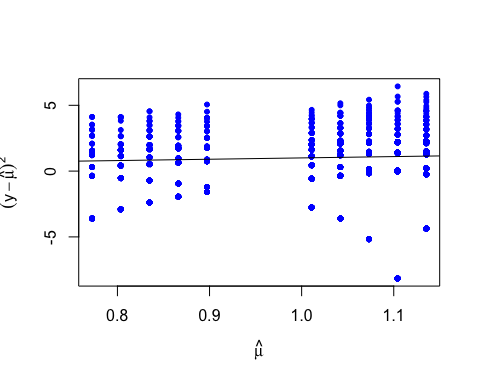
1 - pchisq(summary(model2)$deviance, summary(model2)$df.residual )

## [1] 0

Again, we reject the hypothesis of a close fit between model and data. To gain a little more insight we can plot estimates of the variance against the expected value, alongside a line with an intercept of zero and a slope of 1.

We expect the data points to fall somewhat evenly along that line. Here, it appears our variance is consistently larger than our mean, indicating the possibility of overdispersion.

plot(  
 log(fitted(model2)),  
 log((ferraro2016$morbidityw1-fitted(model2))^2),  
 xlab=expression(hat(mu)),  
 ylab=expression((y-hat(mu))^2),  
 pch=20,col="blue"  
)  
abline(0,1) ## 'varianc = mean' line



Two ways we might handle this overdispersion are **(1)** estimate the overdispersion parameter directly within the model, or **(2)** use a negative binomial model.

### 8.7.1 Quassi-Poisson Family

If we want to test and adjust for overdispersion we can add a scale parameter with the family=quasipoisson option. The estimated scale parameter will be labeled as Overdispersion parameter in the output.

model3 <- glm(  
 formula = morbidityw1 ~ 1 + abuse\_rare + income\_star + abuse\_rare:income\_star,   
 family = quasipoisson(link=log),   
 data = ferraro2016,  
 na.action = na.exclude  
)  
summary(model3)

##   
## Call:  
## glm(formula = morbidityw1 ~ 1 + abuse\_rare + income\_star + abuse\_rare:income\_star,   
## family = quasipoisson(link = log), data = ferraro2016, na.action = na.exclude)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.4949 -1.3511 -0.4745 0.6512 8.6487   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1.0766511 0.0217425 49.518 < 2e-16 \*\*\*  
## abuse\_rare1 -0.2382614 0.0421387 -5.654 1.71e-08 \*\*\*  
## income\_star -0.0311089 0.0153759 -2.023 0.0431 \*   
## abuse\_rare1:income\_star -0.0000822 0.0300781 -0.003 0.9978   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for quasipoisson family taken to be 2.812535)  
##   
## Null deviance: 8068.4 on 2966 degrees of freedom  
## Residual deviance: 7956.7 on 2963 degrees of freedom  
## (55 observations deleted due to missingness)  
## AIC: NA  
##   
## Number of Fisher Scoring iterations: 5

The new standard errors (in comparison to the model without the overdispersion parameter), are larger, Thus, the Wald statistics will be smaller and less likely to be significant.

### 8.7.2 Negative Binomial Regression

We can also fit a negative binomial model, in which allows dispersion or variance in the outcome. The negative binomial distribution has one parameter more than the Poisson regression. This parameters adjusts the variance independently from the mean. In fact, the Poisson distribution is a special case of the negative binomial distribution.

Importantly, the Poisson and Negative Binomial have the same mean structure, so we can interpret coefficients in the same way. However, we will need to use the MASS package ([Venables and Ripley 2002](#ref-venables)) to fit the Negative Binomial regression.

model4 <- MASS::glm.nb(  
 formula = morbidityw1 ~ 1 + abuse\_rare + income\_star + abuse\_rare:income\_star,   
 data = ferraro2016,  
 na.action = na.exclude  
)  
summary(model4)

##   
## Call:  
## MASS::glm.nb(formula = morbidityw1 ~ 1 + abuse\_rare + income\_star +   
## abuse\_rare:income\_star, data = ferraro2016, na.action = na.exclude,   
## init.theta = 1.529056769, link = log)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.8428 -0.8704 -0.2930 0.3709 3.7762   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.0766474 0.0221378 48.634 < 2e-16 \*\*\*  
## abuse\_rare1 -0.2382366 0.0406825 -5.856 4.74e-09 \*\*\*  
## income\_star -0.0311705 0.0156452 -1.992 0.0463 \*   
## abuse\_rare1:income\_star -0.0004478 0.0289957 -0.015 0.9877   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for Negative Binomial(1.5291) family taken to be 1)  
##   
## Null deviance: 3375.4 on 2966 degrees of freedom  
## Residual deviance: 3334.7 on 2963 degrees of freedom  
## (55 observations deleted due to missingness)  
## AIC: 12770  
##   
## Number of Fisher Scoring iterations: 1  
##   
##   
## Theta: 1.5291   
## Std. Err.: 0.0682   
##   
## 2 x log-likelihood: -12760.4610

We notice the smaller dispersion parameter, approximately , providing some support the negative binomial is a better fit for our data.

We can also test the hypothesis of overdispersion formally using a likelihood ratio test. The difference between the two models is captured by estimating a dispersion parameter that is held constant in a Poisson model. Thus, the Poisson model is actually nested in the negative binomial model. We can then use a likelihood ratio test to compare the two and test this model assumption.

pchisq(2 \* (logLik(model4) - logLik(model2)), df = 1, lower.tail = FALSE)

## 'log Lik.' 0 (df=5)

In this example the associated chi-squared value estimated from is with one degree of freedom. This strongly suggests the negative binomial model, estimating the dispersion parameter, is more appropriate than the Poisson model.

# 9 Two-Occassion change

In Chapter 9 we will introduce longitudinal models in their most basic form: repeated measures collected at two occasions. Two-occasions data are a natural starting point for studying change: all longitudinal data collection begins with two occasions. Given any two-occasion repeated measures data, popular analytic approaches include autoregressive and difference score models.

This script works through some basic representations of change, more specifically (1) autoregressive models of change (residualized change), and (2) difference-score models (raw change) of change. These two models consider and answer different kinds of research questions: questions about change in interindividual differences and questions about intraindividual change.

**Importantly, we do not yet consider predictors in our model, which is arguably the most common scenario when these two models are compared: looking at pre- and post-test differences among two groups. However, this will serve as an introduction to the concepts of raw and residualized change.**

## 9.1 Example Data

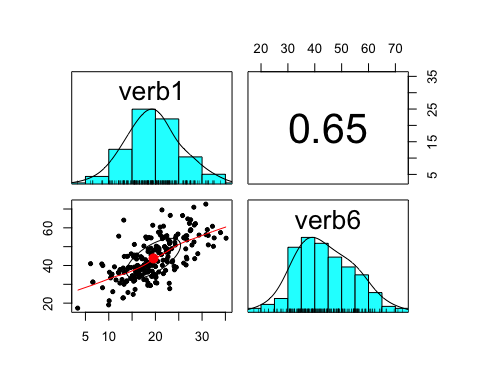
Chapter 6 make use of the same WISC data used in Chapter 3. Here we again read in, subset, and provide descriptives for the WISC data.

filepath <- "https://quantdev.ssri.psu.edu/sites/qdev/files/wisc3raw.csv"  
  
wisc3raw <- read.csv(file=url(filepath),header=TRUE)  
  
var\_names\_sub <- c(  
 "id", "verb1", "verb2", "verb4", "verb6",  
 "perfo1", "perfo2", "perfo4", "perfo6",  
 "momed", "grad"  
)  
  
wiscsub <- wisc3raw[,var\_names\_sub]  
  
psych::describe(wiscsub)

## vars n mean sd median trimmed mad min max range skew  
## id 1 204 102.50 59.03 102.50 102.50 75.61 1.00 204.00 203.00 0.00  
## verb1 2 204 19.59 5.81 19.34 19.50 5.41 3.33 35.15 31.82 0.13  
## verb2 3 204 25.42 6.11 25.98 25.40 6.57 5.95 39.85 33.90 -0.06  
## verb4 4 204 32.61 7.32 32.82 32.42 7.18 12.60 52.84 40.24 0.23  
## verb6 5 204 43.75 10.67 42.55 43.46 11.30 17.35 72.59 55.24 0.24  
## perfo1 6 204 17.98 8.35 17.66 17.69 8.30 0.00 46.58 46.58 0.35  
## perfo2 7 204 27.69 9.99 26.57 27.34 10.51 7.83 59.58 51.75 0.39  
## perfo4 8 204 39.36 10.27 39.09 39.28 10.04 7.81 75.61 67.80 0.15  
## perfo6 9 204 50.93 12.48 51.76 51.07 13.27 10.26 89.01 78.75 -0.06  
## momed 10 204 10.81 2.70 11.50 11.00 2.97 5.50 18.00 12.50 -0.36  
## grad 11 204 0.23 0.42 0.00 0.16 0.00 0.00 1.00 1.00 1.30  
## kurtosis se  
## id -1.22 4.13  
## verb1 -0.05 0.41  
## verb2 -0.34 0.43  
## verb4 -0.08 0.51  
## verb6 -0.36 0.75  
## perfo1 -0.11 0.58  
## perfo2 -0.21 0.70  
## perfo4 0.59 0.72  
## perfo6 0.18 0.87  
## momed 0.01 0.19  
## grad -0.30 0.03

And some bivariate plots of the two-occasion relations.

psych::pairs.panels(wiscsub[,c("verb1","verb6")])



## 9.2 Inroduction

### 9.2.1 A Thought Experiment

Now that we are considering repeated measures data it is helpful to thinking about what repeated measures buy us. Here are a few thoughts:

With cross-sectional data:

* No sense of passage of time
* Cannot control for what happened at earlier timepoints
* Must rely more heavily on theory (e.g. equivalent models ([MacCallum et al. 1993](#ref-maccallum1993)))
* Causality (e.g. cause precedes the effect, cause related to effect, plausible alternatives)
* Depending on true change process, cross-sectional slice may mislead

### 9.2.2 Examples of Equivalent Models

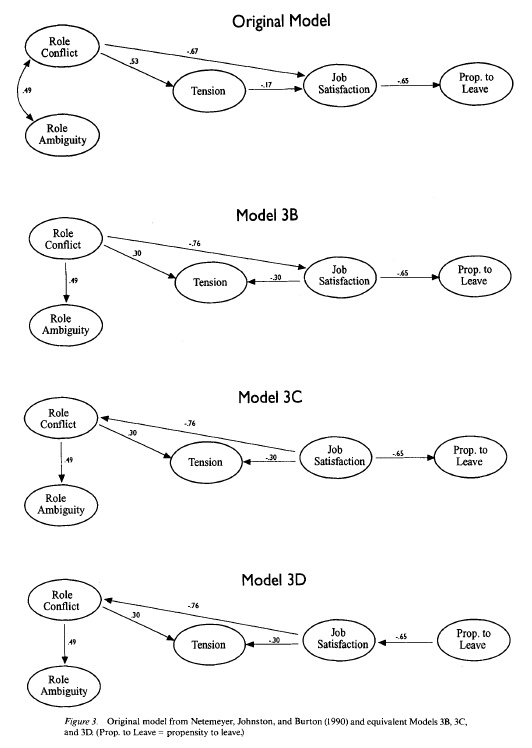


Figure 3 from [MacCallum et al.](#ref-maccallum1993) ([1993](#ref-maccallum1993))

## 9.3 Residualized Change

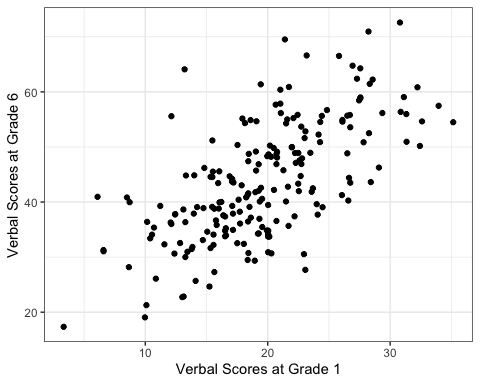
Before introducing the model behind each approach is is helpful to consider the data characteristics underlying each notion of change.

The first approach uses the measure at the second time point as a dependent variable regressed on the the measure at the first time point.

**Importantly, when we look at residualized change, it is not what is the difference between scores at time 1 and time 2, it is where are you at time 2 relative to time 1, based on what we would expect from your time 2 scores.**

In this way it is helpful to view the data as a scatter plot, like we would in a regression model.

library("ggplot2")  
ggplot(data = wiscsub, aes(x = verb1, y = verb6)) +  
 geom\_point() +   
 xlab("Verbal Scores at Grade 1") +   
 ylab("Verbal Scores at Grade 6") +   
 theme\_bw()



## 9.4 Raw Change

The second approach involves computing a change score by subtracting the measure at time 1 from the measure at time 2 (e.g. )

This raw change score is then typically used as the dependent variable in a regression equation.

Here we are speaking in terms of difference scores and raw change. We can plot intraindividual change, by putting time along the x-axis. This requires reshaping the data from wide format to long format.

To recap, our wide data looks like this:

head(round(wiscsub,2))

## id verb1 verb2 verb4 verb6 perfo1 perfo2 perfo4 perfo6 momed grad  
## 1 1 24.42 26.98 39.61 55.64 19.84 22.97 43.90 44.19 9.5 0  
## 2 2 12.44 14.38 21.92 37.81 5.90 13.44 18.29 40.38 5.5 0  
## 3 3 32.43 33.51 34.30 50.18 27.64 45.02 46.99 77.72 14.0 1  
## 4 4 22.69 28.39 42.16 44.72 33.16 29.68 45.97 61.66 14.0 1  
## 5 5 28.23 37.81 41.06 70.95 27.64 44.42 65.48 64.22 11.5 0  
## 6 6 16.06 20.12 38.02 39.94 8.45 15.78 26.99 39.08 14.0 1

We can reshape our data to a long format using the reshape() function as follows

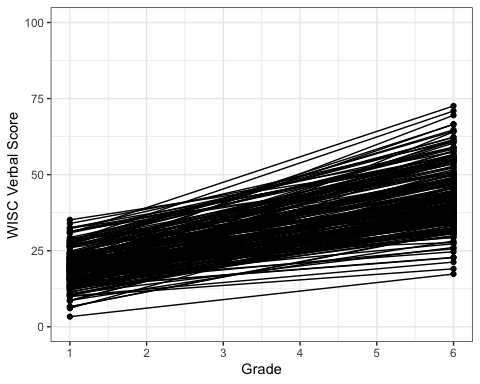
wiscsublong <- reshape(  
 data = wiscsub[c("id","verb1","verb6")],   
 varying = c("verb1","verb6"),   
 timevar = "grade",   
 idvar = "id",   
 direction = "long",   
 sep = ""  
)  
  
wiscsublong <- wiscsublong[order(wiscsublong$id,wiscsublong$grade),]  
  
head(round(wiscsublong,2))

## id grade verb  
## 1.1 1 1 24.42  
## 1.6 1 6 55.64  
## 2.1 2 1 12.44  
## 2.6 2 6 37.81  
## 3.1 3 1 32.43  
## 3.6 3 6 50.18

Now, the long data is structured in a manner amenable to plotting.

**Notice here that each line indicates how an individual’s Grade 6 score differs from their Grade 1 score: intraindividual change.**

library("ggplot2")  
ggplot(data = wiscsublong, aes(x = grade, y = verb, group = id)) +  
 geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +   
 theme\_bw()



## 9.5 Autoregressive Models

When researchers refer to the **autoregressive or residualized change** model for two occasion data they are referring to the following multiple regression model:

where

* is the value of the outcome variable for individual at time
* is the value of the outcome variable for individual at time
* is an intercept parameter, the expected value of when
* is a regression parameter indicating the difference in the predicted score of based on a 1-unit difference in
* is the residual score for individual

Note, the term *residualized change* comes from the fact that the autoregressive effect *residualizes* the outcome. **This leaves only the variability that is unexplained by the previous timepoint, or the variability due to change.**

### 9.5.1 Autoregressive Residuals

With the autoregressive model it is helpful to think more about the residual term. Let’s ignore the scaling constant for now,

If we subtract from both sides of the AR equation we isolate the residuals:

**Here, the residualized change is the function of a weighted combination of your time 1 scores. Instead of talking about raw change we are asking “Where would we predict you to be at time 2 given your standing relative to the mean at time 1?”**

Consider the following scenarios:

* is positive: you changed more in a positive direction than would have been expected.
* is negative: you changed more in a negative direction than would have been expected.

### 9.5.2 Autoregressive Model in R

As we said previously, the autoregressive (AR) model is useful for examining questions about change in interindividual differences. The model for verbal scores at grade 6 can be written as

We note that this is a model of relations among between-person differences. This model is similar to, but is not a single-subject time-series model (which are also called autoregressive models, but are fit to a different kind of data).

Translating the between-person autoregressive model into code and fitting it to the two-occasion WISC data we have

ARfit <- lm(formula= verb6 ~ 1 + verb1,  
 data=wiscsub,  
 na.action=na.exclude)  
summary(ARfit)

##   
## Call:  
## lm(formula = verb6 ~ 1 + verb1, data = wiscsub, na.action = na.exclude)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -20.2459 -5.8651 0.1781 4.9048 27.9976   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 20.22485 1.99608 10.13 <2e-16 \*\*\*  
## verb1 1.20117 0.09773 12.29 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 8.087 on 202 degrees of freedom  
## Multiple R-squared: 0.4279, Adjusted R-squared: 0.425   
## F-statistic: 151.1 on 1 and 202 DF, p-value: < 2.2e-16

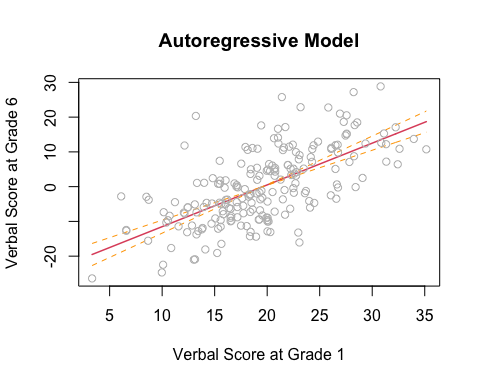
The *intercept* term, = 20.22 is the expected value of Verbal Ability at the 2nd occasion, for an individual with a Verbal Ability score = 0 at the 1st occasion.

The *slope* term, = 1.20 indicates that for every 1-point difference in Verbal Ability at the 1st occasion, we expect a 1.2 point difference at the 2nd occasion.

We can plot the autoregressive model prediction with confidence intervals (CI).

The function termplot takes the fitted lm object. The CI bounds are plotted with the se option and residuals with partial.resid option.

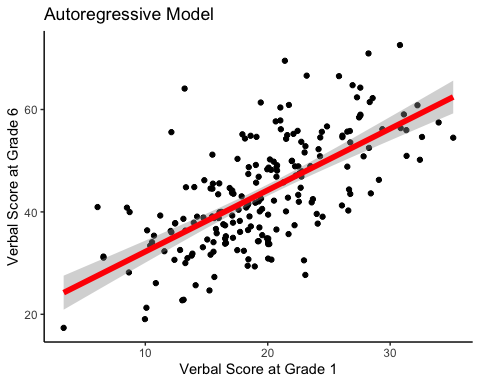
termplot(ARfit,se=TRUE,partial.resid=TRUE,  
 main="Autoregressive Model",  
 xlab="Verbal Score at Grade 1",  
 ylab="Verbal Score at Grade 6")



Note that this code makes use of the lm() model object.

We can also do something similar with the raw data using ggplot.

ggplot(data = wiscsub, aes(x = verb1, y = verb6)) +  
 geom\_point() +   
 geom\_smooth(method="lm", formula= y ~ 1 + x,   
 se=TRUE, fullrange=TRUE, color="red", size=2) +  
 xlab("Verbal Score at Grade 1") +   
 ylab("Verbal Score at Grade 6") +  
 ggtitle("Autoregressive Model") +  
 theme\_classic()



Note that this code embeds an lm() model within the ggplot function.

## 9.6 Difference Score Model

### 9.6.1 Calculating Difference Scores

Using the same repeated measures notation as above we can think about difference scores in the following way

where

* is the value of the outcome variable for individual at time
* is the value of the outcome variable for individual at time
* is the difference score for individual

We can calculate the difference score as

where is a score just like other scores (we can calculate its mean and covariance with other variables, etc.).

### 9.6.2 Comparison to Residualized Change

Remember when we talked about the residualize change model we showed the residual was equal to

**For the autoregressive model, change is the function of a weighted combination of the scores.**

In the difference score approach, we defined the difference scores as

What we see from this relationship is that **raw change is residualized change when .** We can see these concepts are intimately linked.

#### 9.6.2.1 Difference Scores in WISC Data

For our empirical example we can write the difference score, or raw change in verbal ability, between Grades 1 and 6, as

Furthermore, we can calculate the difference score in R as follows

#calculating difference score  
wiscsub$verbD <- wiscsub$verb6-wiscsub$verb1  
  
head(round(wiscsub,2))

## id verb1 verb2 verb4 verb6 perfo1 perfo2 perfo4 perfo6 momed grad verbD  
## 1 1 24.42 26.98 39.61 55.64 19.84 22.97 43.90 44.19 9.5 0 31.22  
## 2 2 12.44 14.38 21.92 37.81 5.90 13.44 18.29 40.38 5.5 0 25.37  
## 3 3 32.43 33.51 34.30 50.18 27.64 45.02 46.99 77.72 14.0 1 17.75  
## 4 4 22.69 28.39 42.16 44.72 33.16 29.68 45.97 61.66 14.0 1 22.03  
## 5 5 28.23 37.81 41.06 70.95 27.64 44.42 65.48 64.22 11.5 0 42.72  
## 6 6 16.06 20.12 38.02 39.94 8.45 15.78 26.99 39.08 14.0 1 23.88

#### 9.6.2.2 Difference Score Descriptives

Look at the descriptives with the difference score.

psych::describe(wiscsub[,c("verb1","verb6","verbD")])

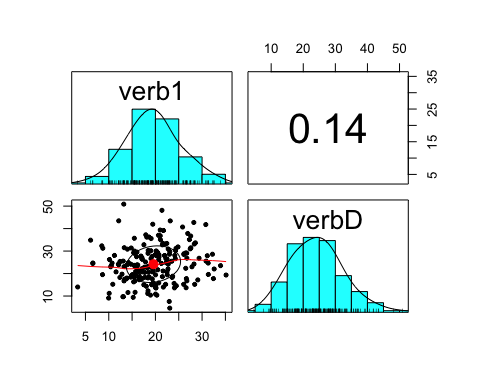
## vars n mean sd median trimmed mad min max range skew kurtosis  
## verb1 1 204 19.59 5.81 19.34 19.50 5.41 3.33 35.15 31.82 0.13 -0.05  
## verb6 2 204 43.75 10.67 42.55 43.46 11.30 17.35 72.59 55.24 0.24 -0.36  
## verbD 3 204 24.16 8.15 23.91 23.85 8.09 4.62 50.88 46.26 0.38 0.14  
## se  
## verb1 0.41  
## verb6 0.75  
## verbD 0.57

psych::corr.test(wiscsub[,c("verb1","verb6","verbD")])

## Call:psych::corr.test(x = wiscsub[, c("verb1", "verb6", "verbD")])  
## Correlation matrix   
## verb1 verb6 verbD  
## verb1 1.00 0.65 0.14  
## verb6 0.65 1.00 0.84  
## verbD 0.14 0.84 1.00  
## Sample Size   
## [1] 204  
## Probability values (Entries above the diagonal are adjusted for multiple tests.)   
## verb1 verb6 verbD  
## verb1 0.00 0 0.04  
## verb6 0.00 0 0.00  
## verbD 0.04 0 0.00  
##   
## To see confidence intervals of the correlations, print with the short=FALSE option

Of particular interest in questions about intraindividual change is the relation between the *pre-test score* and the *amount of intraindividual change*. We can look at the bivariate association.

psych::pairs.panels(wiscsub[,c("verb1","verbD")])



**A note on computing difference scores**: always use raw scores when computing difference scores, Pre-standardizing variables discards important variance information.

### 9.6.3 A Difference Score Regression Model

For the purpose of comparison consider a linear model is expressed for to as

where we are looking at change in verbal test scores while controlling for grade 1 scores,

* is an intercept parameter, the predicted score of when
* is a slope parameter indicating the difference in the predicted score of based on a 1-unit difference in
* is the residual score for individual

#Difference score model  
DIFfit <- lm(formula = verbD ~ 1 + verb1,  
 data=wiscsub,  
 na.action=na.exclude)  
summary(DIFfit)

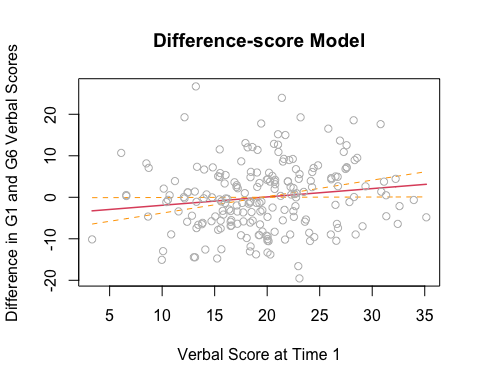
##   
## Call:  
## lm(formula = verbD ~ 1 + verb1, data = wiscsub, na.action = na.exclude)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -20.2459 -5.8651 0.1781 4.9048 27.9976   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 20.22485 1.99608 10.132 <2e-16 \*\*\*  
## verb1 0.20117 0.09773 2.058 0.0408 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 8.087 on 202 degrees of freedom  
## Multiple R-squared: 0.02054, Adjusted R-squared: 0.0157   
## F-statistic: 4.237 on 1 and 202 DF, p-value: 0.04083

The *intercept* term, is the expected value of the difference score (raw change in verbal ability), for an individual with a verbal ability score = 0 at the first occasion.

The *slope* term, indicates that for every 1-point difference in verbal ability at the first occasion, we expect a point difference in the amount of intraindividual change.

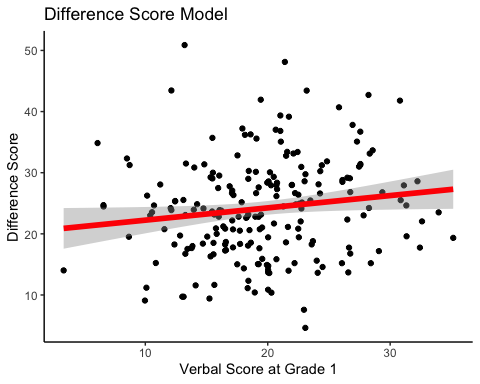
The same methods as above can be used to plot the results of the difference score model.

termplot(DIFfit,se=TRUE,partial.resid=TRUE,  
 main="Difference-score Model",  
 xlab="Verbal Score at Time 1",  
 ylab="Difference in G1 and G6 Verbal Scores")



We can also do something similar using ggplot.

#making interindividual regression plot  
ggplot(data = wiscsub, aes(x = verb1, y = verbD)) +  
 geom\_point() +   
 geom\_smooth(method="lm", formula= y ~ 1 + x,   
 se=TRUE, fullrange=TRUE, color="red", size=2) +  
 xlab("Verbal Score at Grade 1") +   
 ylab("Difference Score") +  
 ggtitle("Difference Score Model") +  
 theme\_classic()



Note that each of these model results plots are regression plots: outcome on the y-axis, predictor on the x-axis.

## 9.7 Critique of Residualized Change

Some interpretational oddities arise from the autoregressive model that are worth considering.

**Consider the following situation**: We are studying a weight loss intervention where we measure weight prior to and after an intervention. The mean weight at time 1 is 250 pounds () and the mean weight at time 2 is 230 pounds (). Now consider two people:

* *Individual 1*: Weight at time 1 was and weight at time 2 is .
  + Relative standing has gone down so there is *positive residualized change*.
* *Individual 2*: Weight at time 1 was and weight at time 2 is .
  + Relative standing is the same so there is *no residualized change*.

## 9.8 Critique of Difference Scores

There have also been some major historical critiques of differences scores (e.g. [Cronbach and Furby](#ref-cronbach1970a) ([1970](#ref-cronbach1970a))).

Much of these critiques are based on reliability and the following rationale. Consider a typical model for a set of repeated measures,

$$
y\_{1i} = y\_{true,i} + e\_{1i} \\
y\_{2i} = y\_{true,i} + e\_{2i}
$$

where

* is the unobserved true score at both occasions
* is the unobserved random error that is independent over each occasion

Note, in this theoretical model the true score remains the same and all changes are based on random noise.

If this model holds then we could write a simple difference score as

$$
D\_{i} = y\_{2i} - y\_{1i} \\
\quad\quad\: \quad\quad\:\quad\quad\:\quad\quad\quad= (y\_{true,i} + e\_{2i}) - (y\_{true,i} + e\_{1i})\\
\quad\quad\: \quad\quad\:\quad\quad\:\quad\quad\quad = (y\_{true,i} - y\_{true,i}) + (e\_{2i} - e\_{1i})\\
\quad\quad = (e\_{2i} - e\_{1i})\\
$$

where

* Variance of the difference score is entirely based on the variance of the differences in random error scores
* the reliability of the difference scores is zero

### 9.8.1 Alternative Interpretation

This has led many to many historical critiques of difference scores. However, other researchers have pointed out this conclusion is based on how one envisions change. If, for example, we have the following theoretical model for change,

$$
y\_{1i} = y\_{true,i} + e\_{1i}\\
y\_{2i} = (y\_{1i} + \Delta y\_{true,i}) + e\_{2i}
$$

where

* is the unobserved true score at both occasions
* is the unobserved true change score between occasions
* is the unobserved random error that is independent over each occasion

If this model holds, as opposed to the alternative model, then the difference scores

$$
D\_{i} = y\_{2i} - y\_{1i} \\
\quad\quad\: \quad\quad\:\quad\quad\:\quad\quad\quad= (y\_{true,i} + e\_{2i}) - (y\_{true,i} + e\_{1i})\\
\quad\quad\: \quad\quad\:\quad\quad\:\quad\quad\quad = (y\_{true,i} - y\_{true,i}) + (e\_{2i} - e\_{1i})\\
\quad\quad \quad\quad\quad= \Delta y\_{1} + (e\_{2i} - e\_{1i})\\
$$

where

* now the variance of the difference score is based on the variance of the differences in the random error scores **and** the gain in the true scores
* the relative size of the true score gain determines variance and reliability of the difference scores
* this implies difference scores may be an entirely appropriate means for measuring change

## 9.9 Comparing Models

To compare the autoregressive (residualized change) and difference score models, it is useful to better understand their equivalence. Let’s start with the autoregressive model and see if we can get to the change score model.

Here we have shown analytically an equivalence relationship between the slope coefficients from the two models, namely,

We can confirm this relationship look at our model output:

coef(ARfit)

## (Intercept) verb1   
## 20.224849 1.201174

coef(DIFfit)

## (Intercept) verb1   
## 20.2248493 0.2011741

## 9.10 Closing Thoughts

* Given any two-occasion repeated measures data, we can do analysis with autoregressive (residualized change) or difference score (raw change) models
* The two-occasion change models presented in this chapter can be transformed into each other, the goodness-of-fit statistics are not good way to distinguish between them
* The models discussed here can be distinguished when t > 2 repeated measures are available.
* Interpretations of change are fundamentally restricted by the choice of model
* When choosing one model it is worth considering what change means in each context (e.g. in a weight loss study is lbs of weight loss the same for people with different baseline weights?)

If you found all of this to be inherently confusing it is worth thinking about the following quote: **“Two waves of data are better than one, but maybe not much better.”** ([Rogosa, Brandt, and Zimowski 1982](#ref-rogosa1982)).

In the next chapter we will extend the notion of raw and residualized change to comparing change among two groups.

# 10 Introduction to Growth

This chapter introduces models for repeated measures data (e.g., RM ANOVA, RM MANOVA) along a *continuum*. The motivation for this introduction is to present how these models are linked together, making the similarities and differences among them easier to identify and understand. We will tie the models together in a multilevel framework, working from repeated measures ANOVA through repeated measures MANOVA to growth models.

## 10.1 Example Data

Loading some new libraries used in this chapter.

library(psych) # for descriptives etc  
library(ggplot2) # for plotting  
library(nlme) # for mixed effects models  
library(lme4) # for mixed effects models  
library(lmerTest) # to get significance tests from lmer

### 10.1.1 Data Preparation and Description

For our examples, we use 3-occasion WISC data that are *equally spaced*.

Load the repeated measures data

filepath <- "https://quantdev.ssri.psu.edu/sites/qdev/files/wisc3raw.csv"  
wisc3raw <- read.csv(file=url(filepath),header=TRUE)

Next, let’s Subset the variables of interest. For this chapter we will include:

* 3-occasion equally spaced repeated measures (verb2, verb4, verb6)
* A person-level grouping variable (grade)
* An ID variable (id)

After subsetting let’s take a look at some basic descriptives.

varnames <- c("id","verb2","verb4","verb6","grad")  
wiscsub <- wisc3raw[ ,varnames]  
describe(wiscsub)

## vars n mean sd median trimmed mad min max range skew  
## id 1 204 102.50 59.03 102.50 102.50 75.61 1.00 204.00 203.00 0.00  
## verb2 2 204 25.42 6.11 25.98 25.40 6.57 5.95 39.85 33.90 -0.06  
## verb4 3 204 32.61 7.32 32.82 32.42 7.18 12.60 52.84 40.24 0.23  
## verb6 4 204 43.75 10.67 42.55 43.46 11.30 17.35 72.59 55.24 0.24  
## grad 5 204 0.23 0.42 0.00 0.16 0.00 0.00 1.00 1.00 1.30  
## kurtosis se  
## id -1.22 4.13  
## verb2 -0.34 0.43  
## verb4 -0.08 0.51  
## verb6 -0.36 0.75  
## grad -0.30 0.03

Multilevel modeling analyses typically require a long data set. So, we also reshape from wide to long in order to have a long data set.

verblong <- reshape(  
 data = wiscsub,   
 varying = c("verb2","verb4","verb6"),   
 timevar = "grade",   
 idvar = "id",   
 direction = "long",   
 sep = ""  
)  
verblong <- verblong[order(verblong$id,verblong$grade), c("id","grade","verb","grad")]  
head(verblong,12)

## id grade verb grad  
## 1.2 1 2 26.98 0  
## 1.4 1 4 39.61 0  
## 1.6 1 6 55.64 0  
## 2.2 2 2 14.38 0  
## 2.4 2 4 21.92 0  
## 2.6 2 6 37.81 0  
## 3.2 3 2 33.51 1  
## 3.4 3 4 34.30 1  
## 3.6 3 6 50.18 1  
## 4.2 4 2 28.39 1  
## 4.4 4 4 42.16 1  
## 4.6 4 6 44.72 1

### 10.1.2 Sample Moments

For clarity, let’s consider the basic information representation of the 3-occasion repeated measures data. In particular, data (even non-repeated measures data) are summarized (at the sample-level) as (1) a vector of means and (2) a variance-covariance matrix.

#mean vector (from wide data)  
meanvector <- sapply(wiscsub[ ,c("verb2","verb4","verb6")], mean, na.rm=TRUE)  
round(meanvector,2)

## verb2 verb4 verb6   
## 25.42 32.61 43.75

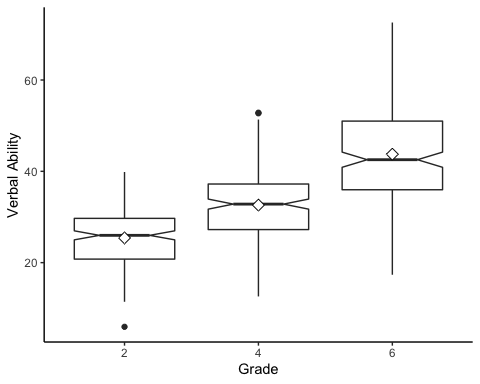
#variance-covariance matrix (from wide data)  
varcovmatrix <- cov(wiscsub[ ,c("verb2","verb4","verb6")], use="pairwise.complete.obs")  
round(varcovmatrix,2)

## verb2 verb4 verb6  
## verb2 37.29 33.82 47.40  
## verb4 33.82 53.58 62.25  
## verb6 47.40 62.25 113.74

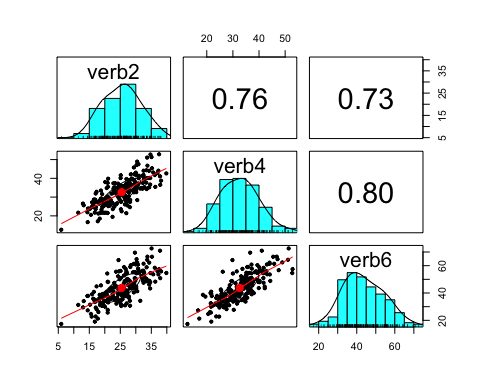
Making visual counterparts can also be extremely useful - especially for facilitating higher-level conversations in a research group. Basic sample-level descriptions in visual form. Note that the time variable has been converted to a factor = categorical

ggplot(data=verblong, aes(x=factor(grade), y=verb)) +   
 geom\_boxplot(notch = TRUE) +  
 stat\_summary(fun.y="mean", geom="point", shape=23, size=3, fill="white") +  
 labs(x = "Grade", y = "Verbal Ability") +  
 theme\_classic()

## Warning: `fun.y` is deprecated. Use `fun` instead.



pairs.panels(wiscsub[,c("verb2","verb4","verb6")])



Reminder, we should always be careful about the scaling of the x- and y-axes in these plots.

One additional recoding for convenience is to center and scale our time variable. This gives us a specific point and an intuitive scale that is useful for our didactic purposes.

unique(verblong$grade)

## [1] 2 4 6

verblong$time0 <- (verblong$grade-2)/2 # from 2,4,6 to 0,1,2  
unique(verblong$time0)

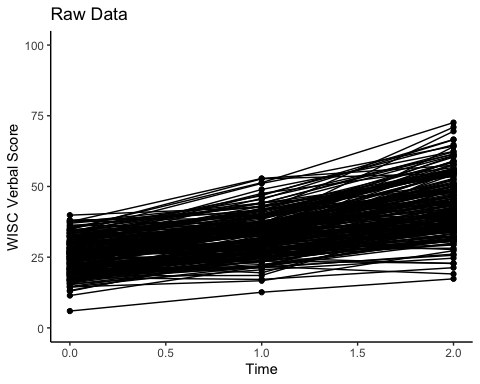
## [1] 0 1 2

head(verblong,12)

## id grade verb grad time0  
## 1.2 1 2 26.98 0 0  
## 1.4 1 4 39.61 0 1  
## 1.6 1 6 55.64 0 2  
## 2.2 2 2 14.38 0 0  
## 2.4 2 4 21.92 0 1  
## 2.6 2 6 37.81 0 2  
## 3.2 3 2 33.51 1 0  
## 3.4 3 4 34.30 1 1  
## 3.6 3 6 50.18 1 2  
## 4.2 4 2 28.39 1 0  
## 4.4 4 4 42.16 1 1  
## 4.6 4 6 44.72 1 2

Plotting the raw data along this new time variable.

#plotting intraindividual change RAW DATA  
ggplot(data = verblong, aes(x = time0, y = verb, group = id)) +  
 ggtitle("Raw Data") +  
 geom\_point() +   
 geom\_line() +  
 xlab("Time") +   
 ylab("WISC Verbal Score") +   
 ylim(0,100) + xlim(0,2) +  
 theme\_classic()



Note that the time variable in this plot has NOT been converted to a factor. It is a continuous variable.

## 10.2 A General Model

The presentation of all of these models here is an attempt to *integrate* traditions that are typically kept separate or set against each other. In reality, they are just a few examples of the many, many possible models that exist. Each model is useful in specific situations.

The objective of all of our analyses is to *deconstruct* the data into meaningful and interpretable pieces. Each *model* does this in a different way, with different assumptions.

We can *judge* the models based on

1. How well they articulate and test our theory, and
2. How well they recover the data (evaluated as misfit to the impled moments).

Recall that the regression model may be compactly written as

We make it into a multilevel regression model by further partitioning the predictor space into between-person and within-person components. Note: this is the very same distinction that is made in traditional presentations of ANOVA when examining between-person factors and within-person factors.

The general model becomes

which is also called the linear mixed model.

## 10.3 Unconditional Means Model

It is often recommended to fit the unconditional means model before moving on to more complicated models. This is primarily because the unconditional means model does well at partitioning variance of the outcome across levels. We can use this model to better understand the amount of outcome variation that exists at the within and between levels of our model. If we fail to find sufficient variation at a given level there may be little reason to proceed with attempts to explain variance at that level of analysis.

### 10.3.1 Leve l

First, let us write out the *level-1* (individual) model

where

* is the repeated measures score for individual at time
* is the random intercept for individual (person-specific mean)
* is the time-specific residual score (within-person deviation)

Note, the level 1 model shows us the true individual-level trajectories are completely flat, sitting at .

### 10.3.2 Level 2

The level-2 (sample) equation for the random intercept can be written as

where

* is the sample mean for the intercept (grand mean)
* is individual ’s deviation from the sample mean (between person deviation)

Note, the looking at the level 1 and level 2 model tells us that while these flat trajectories may differ in elevation, across everyone in the population, their average elevation is .

### 10.3.3 Single Equation

We can write also both models in a single equation as follows

where

* is the repeated measures score for individual at time
* is the sample mean for the intercept (grand mean)
* is individual ’s deviation from the sample mean (between person deviation)
* is the time-specific residual score (within-person deviation)

### 10.3.4 Model Elaboration

#### 10.3.4.1 Within-Person Residual Covariance

For clarity, Let’s write out the full variance covariance matrix of the within-person residuals (spanning across the repeated measures). Remember, we wrote , or in matrix notation,

Note, this is the homoscedasticity of errors assumption.

#### 10.3.4.2 Between-Person Residual Covariance

We can now do the same for the full variance covariance matrix of the between-person residuals,

Note, in the unconditional means model there is no-growth, each individual has an intercept, but no change in scores is predicted because there are no predictors (e.g. time) in the level-1 equation.

### 10.3.5 Estimated Quantities

Importantly, in the unconditional means model we will be interested in estimating three parameters:

* The sample-level mean of the random intercept () or the grand mean across all occasions and individuals.
* The variance of the random intercept ()
  + Provides information about the magnitude of between person differences in scores at each measurement occasion.
* The residual variance ()
  + Provides information about the magnitude of with-person fluctuations in scores over time.

### 10.3.6 More Notation

It is also worth mentioning that through some replacement (e.g., replacing = , the different vectors of 1 with and = 1 we can get to …

which is just the more general notation often used in the statistics literature. The equation we started with, with another multilevel notation …

### 10.3.7 Unconditional Means Model in R

We can write the unconditional means model in R as follows.

um\_fit <- lme(  
 fixed = verb ~ 1,   
 random = ~ 1|id,   
 data = verblong,  
 na.action = na.exclude  
)  
summary(um\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 4682.66 4695.906 -2338.33  
##   
## Random effects:  
## Formula: ~1 | id  
## (Intercept) Residual  
## StdDev: 4.406063 10.277  
##   
## Fixed effects: verb ~ 1   
## Value Std.Error DF t-value p-value  
## (Intercept) 33.92433 0.5174359 408 65.56238 0  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -1.9626206 -0.6924771 -0.1481960 0.5511044 3.1026127   
##   
## Number of Observations: 612  
## Number of Groups: 204

# um\_fit2 <- lmer(  
# verb ~ 1 + (1|id),  
# data=verblong,  
# na.action = na.exclude  
# )  
# summary(um\_fit2)

#### 10.3.7.1 Interpretation

The single fixed effect in our unconditional means model is the grand mean, or . Rejection of the null indicates the average verbal score between Grades 2 and 6 is non-zero.

Next we look at the random effects. The estimated between-person standard deviation is and the estimated within-person standard deviation is .

### 10.3.8 Intra-Class Correlation

The intra-class correlation (ICC) as the ratio of the random intercept variance (between-person) to the total variance, defined as the sum of the random intercept variance and residual variance (between + within). Specifically,

#### 10.3.8.1 Calculating the ICC

The ICC is the ratio of the random intercept variance (between-person var) over the total variance (between + within var):

ICC\_between <- 4.4^2 / (4.4^2 + 10.28^2)  
ICC\_between

## [1] 0.1548324

# Simple function for computing ICC from lme() output  
ICClme <- function(out) {  
 varests <- as.numeric(VarCorr(out)[1:2])  
 return(paste("ICC =", varests[1]/sum(varests)))  
}  
ICClme(um\_fit)

## [1] "ICC = 0.155269768304537"

From the unconditional means model, the ICC was calculated, which indicated that of the total variance in verbal scores, approximately 16%, is attributable to between-person variation whereas 84% is attributable to within-person variation. This means there is a good portion of within-person variance sill to be modeled.

### 10.3.9 Model-Impled Moments

What is the implied representation of the basic information? What are the model-implied moments?

Let’s remember our original equation.

In this *unconditional means* model the and design matrices are simply vectors of s, leaving us with

.

#### 10.3.9.1 Mean Vector

To obtain the model-implied mean vector we want . Remember, from our covariance algebra

which gives us

or after simplifying

#### 10.3.9.2 Mean Vector in R

Let’s make the implied *mean vector* in R.

First, extract the fixed effects from the model using fixef(), specifically the contents of the matrix.

fixef(um\_fit)

## (Intercept)   
## 33.92433

beta <- matrix(fixef(um\_fit)[1], nrow = 1, ncol = 1)  
beta

## [,1]  
## [1,] 33.92433

Create the model design matrix for the fixed effects. In this model this is a matrix of order .

X <- matrix(c(1,1,1), nrow = 3, ncol = 1)  
X

## [,1]  
## [1,] 1  
## [2,] 1  
## [3,] 1

Creating the model implied mean vector through multiplication

meanvector\_um <- X %\*% beta  
meanvector\_um

## [,1]  
## [1,] 33.92433  
## [2,] 33.92433  
## [3,] 33.92433

Note this is the overall (grand) mean.

#### 10.3.9.3 Model-Implied Covariance Matrix

Now, let’s take a look at the model-implied variance-covariance matrix. Before we start let’s review the model again,

where

* is the random effects regressor (design) matrix;
* contains the fixed effects;
* contains the random effects which are distributed normally with mean and covariance matrix and
* are errors which are distributed normally with mean and covariance matrix , and
* our “standard assumption” was that (homogeneity of errors).

We’d like to identify the quantity .

We subtract the “means” from both sides …

So on the left side we now have de-meaned scores and on the right we have a between-portion part and a within-person part. Note that is now mean-centered, and as such, .

This gives us

$$\begin{align}
\mathbf{Y}^{\*} \mathbf{Y}^{\*'} = (\mathbf{Z}\mu\_{0i} + \boldsymbol{\epsilon})(\mathbf{Z}\mu\_{0i} + \boldsymbol{\epsilon})^{'} \\
= (\mathbf{Z}\mu\_{0i} + \boldsymbol{\epsilon})(\mu\_{0i}^{'}\mathbf{Z}^{'} + \boldsymbol{\epsilon}^{'}) & \quad \text{[Distribute transpose]}\\
= \mathbf{Z}\mu\_{0i}\mu\_{0i}^{'}\mathbf{Z}^{'} + \mathbf{Z}\mu\_{0i}\boldsymbol{\epsilon}^{'} + \boldsymbol{\epsilon}\mu\_{0i}^{'}\mathbf{Z}^{'} + \boldsymbol{\epsilon}\boldsymbol{\epsilon}^{'} & \quad \text{[Expand]}\\
= \mathbf{Z}\mu\_{0i}\mu\_{0i}^{'}\mathbf{Z}^{'} + \boldsymbol{\epsilon}\boldsymbol{\epsilon}^{'} & \quad \text{[Orthogonality]}\\
= \mathbf{Z}\boldsymbol{\Psi}\mathbf{Z}^{'} + \boldsymbol{\Lambda} & \quad \text{[De. \: Covariances]}\\
\end{align}$$

Or we can alternatively see this in matrix form, without recalculating all the steps.

Let’s calculate var-cov matrix …

From above we get

#### 10.3.9.4 Covariance Matrix in R

#parsing the model variances & covariances  
VarCorr(um\_fit)

## id = pdLogChol(1)   
## Variance StdDev   
## (Intercept) 19.41339 4.406063  
## Residual 105.61668 10.276997

So, in order to reconstruct the implied variance-covariances, we need to find and to create , and do some multiplication.

1. Parse the between-person variances from the model output.

Psi <- matrix(c(as.numeric(VarCorr(um\_fit)[1])),nrow = 1, ncol = 1)   
Psi

## [,1]  
## [1,] 19.41339

Create the model design matrix, , for the random effects. In this model this is a matrix of order

Z <- matrix(c(1,1,1), nrow=3,ncol=1)  
Z

## [,1]  
## [1,] 1  
## [2,] 1  
## [3,] 1

So, the implied variance-covariance matrix of the between-person random effects for the three occasions is:

Cov1 = Z %\*% Psi %\*% t(Z)  
Cov1

## [,1] [,2] [,3]  
## [1,] 19.41339 19.41339 19.41339  
## [2,] 19.41339 19.41339 19.41339  
## [3,] 19.41339 19.41339 19.41339

Which in correlation units implies

Delta = diag(3)  
Delta[1,1] = 1/sqrt(Cov1[1,1])  
Delta[2,2] = 1/sqrt(Cov1[2,2])  
Delta[3,3] = 1/sqrt(Cov1[3,3])  
Delta %\*% Cov1 %\*% Delta

## [,1] [,2] [,3]  
## [1,] 1 1 1  
## [2,] 1 1 1  
## [3,] 1 1 1

Now, let’s look at the residual error variance-covariance matrix,

sigma2 <- as.numeric(VarCorr(um\_fit)[2])  
Lambda <- sigma2 \* diag(1, nrow = 3, ncol = 3)

Finally, can put the between- and within- pieces together to calculate the model-implied variance-covariance matrix as follows

varcovmatrix\_um <- Z %\*% Psi %\*% t(Z) + (sigma2 \* Lambda)  
varcovmatrix\_um

## [,1] [,2] [,3]  
## [1,] 11174.29648 19.41339 19.41339  
## [2,] 19.41339 11174.29648 19.41339  
## [3,] 19.41339 19.41339 11174.29648

Note, we have a compound symmetry structure in our model-implied covariance matrix.

Together with the implied mean vector, we have the entire picture provided by all the model components.

### 10.3.10 Model Residuals

Recall what the observed mean and var-cov were …

meanvector

## verb2 verb4 verb6   
## 25.41534 32.60775 43.74990

varcovmatrix

## verb2 verb4 verb6  
## verb2 37.28784 33.81957 47.40488  
## verb4 33.81957 53.58070 62.25489  
## verb6 47.40488 62.25489 113.74332

For fun, let’s look at the misfit to the data (observed matrix - model implied matrix)

meanvector - meanvector\_um

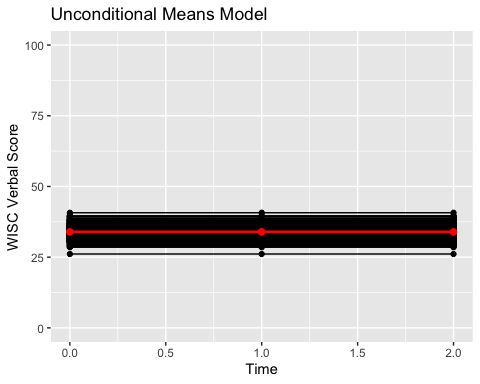
## [,1]  
## [1,] -8.508987  
## [2,] -1.316585  
## [3,] 9.825572

varcovmatrix - varcovmatrix\_um

## verb2 verb4 verb6  
## verb2 -11137.00864 14.40618 27.99149  
## verb4 14.40618 -11120.71578 42.84150  
## verb6 27.99149 42.84150 -11060.55317

Fit is not so good. Let’s visualize the implied model.

#Calculating predicted scores from the models   
verblong$pred\_um <- predict(um\_fit)  
#Making the prototype from the implied means  
proto\_um <- data.frame(cbind(c(1000,1000,1000),c(0,1,2),meanvector\_um))  
names(proto\_um) <- c("id","time0","pred\_um")  
  
#plotting implied individual scores  
ggplot(data = verblong, aes(x = time0, y = pred\_um, group = id)) +  
 ggtitle("Unconditional Means Model") +  
 geom\_point() +   
 geom\_line() +  
 geom\_point(data=proto\_um, color="red", size=2) +  
 geom\_line(data=proto\_um, color="red", size=1) +  
 xlab("Time") +   
 ylab("WISC Verbal Score") +   
 ylim(0,100) + xlim(0,2)



## 10.4 Repeated Measures ANOVA

OK, now let’s move to an repeated measures (RM) ANOVA by adding in effects for categorical time. Recall, we must tell R that time0 is a categorical variable using factor()

verblong$time0 <- factor(verblong$time0, ordered=FALSE)  
str(verblong$time0)

## Factor w/ 3 levels "0","1","2": 1 2 3 1 2 3 1 2 3 1 ...

Here is our RM ANOVA model with time as within-person factor

timecat\_fit <- lme(  
 fixed = verb ~ 1 + time0,   
 random = ~ 1|id,   
 data = verblong,  
 na.action = na.exclude)  
summary(timecat\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 4013.176 4035.235 -2001.588  
##   
## Random effects:  
## Formula: ~1 | id  
## (Intercept) Residual  
## StdDev: 6.915667 4.514145  
##   
## Fixed effects: verb ~ 1 + time0   
## Value Std.Error DF t-value p-value  
## (Intercept) 25.415343 0.5782155 406 43.95480 0  
## time01 7.192402 0.4469670 406 16.09157 0  
## time02 18.334559 0.4469670 406 41.01994 0  
## Correlation:   
## (Intr) time01  
## time01 -0.387   
## time02 -0.387 0.500  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.61263084 -0.54466998 -0.02451831 0.48627468 3.50536334   
##   
## Number of Observations: 612  
## Number of Groups: 204

# timecat\_fit2 <- lmer(verb ~ 1 + time0 + (1|id),   
# data=verblong,  
# na.action = na.exclude)  
# summary(timecat\_fit2)

Remember that interpretation is with respect to *time0*, with the first category set as default intercept which is

str(verblong$time0)

## Factor w/ 3 levels "0","1","2": 1 2 3 1 2 3 1 2 3 1 ...

### 10.4.1 Intra-Class Correlation

The intra-class correlation (ICC) as the ratio of the random intercept variance (between-person) to the total variance, defined as the sum of the random intercept variance and residual variance (between + within). Specifically,

#### 10.4.1.1 Calculating the ICC

The ICC is the ratio of the random intercept variance (between-person var) over the total variance (between + within var):

# Simple function for computing ICC from lme() output  
ICClme <- function(out) {  
 varests <- as.numeric(VarCorr(out)[1:2])  
 return(paste("ICC =", varests[1]/sum(varests)))  
}  
ICClme(timecat\_fit)

## [1] "ICC = 0.701226878908497"

From the current model, the ICC was calculated, which indicated that of the total variance in verbal scores, approximately 70%, is attributable to between-person variation whereas 30% is attributable to within-person variation.

### 10.4.2 Model-Implied Mean Vector

Let’s be explicit with our model

.

Making the implied *mean vector*

fixef(timecat\_fit)

## (Intercept) time01 time02   
## 25.415343 7.192402 18.334559

beta <- matrix(  
 c(  
 fixef(timecat\_fit)[1],   
 fixef(timecat\_fit)[2],   
 fixef(timecat\_fit)[3]  
 ), nrow =3, ncol=1)  
beta

## [,1]  
## [1,] 25.415343  
## [2,] 7.192402  
## [3,] 18.334559

Create the model design matrix for the fixed effects. In this model this is a matrix of order .

X <- matrix(c(1,1,1,0,1,0,0,0,1), nrow=3, ncol=3)  
X

## [,1] [,2] [,3]  
## [1,] 1 0 0  
## [2,] 1 1 0  
## [3,] 1 0 1

Creating the model implied mean vector through multiplication

meanvector\_timecat <- X %\*% beta  
meanvector\_timecat

## [,1]  
## [1,] 25.41534  
## [2,] 32.60775  
## [3,] 43.74990

See the *differences* in the means across levels of time0.

### 10.4.3 Model-Implied Covariance Matrix

Making the implied *variance-covariance matrix*.

VarCorr(timecat\_fit)

## id = pdLogChol(1)   
## Variance StdDev   
## (Intercept) 47.82645 6.915667  
## Residual 20.37751 4.514145

From this, we need to create the model implied variance-covariance.

Parse the between-person variances from the model output.

Psi <- matrix(c(as.numeric(VarCorr(timecat\_fit)[1])), nrow=1,ncol=1)   
Psi

## [,1]  
## [1,] 47.82645

Create the model design matrix for the random effects. In this model this is a matrix of order

Z <- matrix(c(1,1,1), nrow=3,ncol=1)  
Z

## [,1]  
## [1,] 1  
## [2,] 1  
## [3,] 1

So, the implied variance-covariance matrix of the between-person random effects for the three occasions is:

Z %\*% Psi %\*% t(Z)

## [,1] [,2] [,3]  
## [1,] 47.82645 47.82645 47.82645  
## [2,] 47.82645 47.82645 47.82645  
## [3,] 47.82645 47.82645 47.82645

Next, we parse the residual/“error” variance-covariance.

sigma2 <- as.numeric(VarCorr(timecat\_fit)[2])  
Lambda <- sigma2 \* diag(1,nrow=3,ncol=3)

So the residual within-person residual/“error” structure

Lambda

## [,1] [,2] [,3]  
## [1,] 20.37751 0.00000 0.00000  
## [2,] 0.00000 20.37751 0.00000  
## [3,] 0.00000 0.00000 20.37751

As before, we have homogeneity and uncorrelated errors.

Finally, calculate the implied variance-covariances of total model

varcovmatrix\_timecat <- Z %\*% Psi %\*% t(Z) + Lambda  
varcovmatrix\_timecat

## [,1] [,2] [,3]  
## [1,] 68.20396 47.82645 47.82645  
## [2,] 47.82645 68.20396 47.82645  
## [3,] 47.82645 47.82645 68.20396

Again, notice the compound symmetry structure.

For fun, let’s look at the misfit (real matrix - model implied)

#misfit of means  
meanvector - meanvector\_timecat

## [,1]  
## [1,] 2.486900e-14  
## [2,] -2.131628e-14  
## [3,] -5.684342e-14

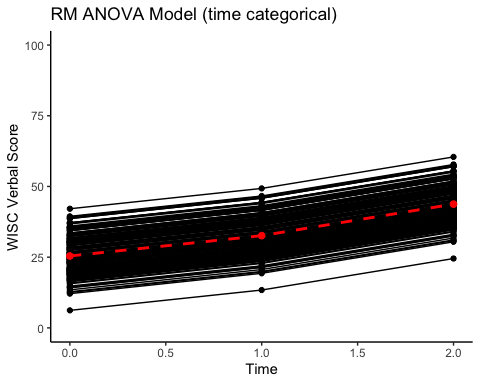
#misfit of var-cov  
varcovmatrix - varcovmatrix\_timecat

## verb2 verb4 verb6  
## verb2 -30.9161173 -14.00688 -0.4215677  
## verb4 -14.0068803 -14.62326 14.4284384  
## verb6 -0.4215677 14.42844 45.5393553

The means are now perfectly reproduced, however, the variances and covariances are not so good, particularly the variances

Let’s make a picture of the implied model.

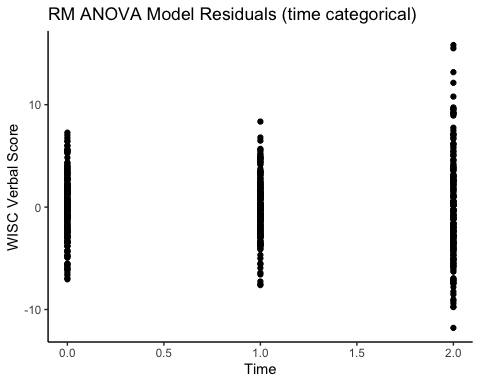
#Calculating predicted scores from the models   
verblong$pred\_timecat <- predict(timecat\_fit)  
#Making the prototype from the implied means  
proto\_timecat <- data.frame(cbind(c(1000,1000,1000),c(0,1,2),meanvector\_timecat))  
names(proto\_timecat) <- c("id","time0","pred\_timecat")  
  
#need to convert time0 back into a continuous variable for plotting as intraindividual change  
verblong$time0 <- as.numeric(unclass(verblong$time0))-1  
#plotting implied individual scores  
ggplot(data = verblong, aes(x = time0, y = pred\_timecat, group = id)) +  
 ggtitle("RM ANOVA Model (time categorical)") +  
 geom\_point() +   
 geom\_line() +  
 geom\_point(data=proto\_timecat, color="red", size=2) +  
 geom\_line(data=proto\_timecat, color="red", size=1, linetype=2) +  
 xlab("Time") +   
 ylab("WISC Verbal Score") +   
 ylim(0,100) + xlim(0,2) +  
 theme\_classic()



Notice that the implied lines are all parallel. This is a model of *mean differences*.

Can also see what the residuals look like.

#Calculating residual scores from the models   
verblong$resid\_timecat <- residuals(timecat\_fit)  
  
#plotting implied individual scores  
ggplot(data = verblong, aes(x = time0, y = resid\_timecat, group = id)) +  
 ggtitle("RM ANOVA Model Residuals (time categorical)") +  
 geom\_point() +   
 xlab("Time") +   
 ylab("WISC Verbal Score") +   
 xlim(0,2) +  
 theme\_classic()



Note, that the points are not connected - this is to highlight the model and the implication that the within-person residuals are from the occasion-specific mean (NOT from a trajectory).Note also the heteroskedasticity of the residuals.

## 10.5 Repeated Measures MANOVA

Now let’s adjust the RM ANOVA error structure to get a RM MANOVA. The *multivariate* part of the MANOVA, has to do with relaxing the assumption on the error structure - this means more flexibility than compound symmetry.

Here is our RM ANOVA model with time as within-person factor. The error structure is *compound symmetry with heterogeneous variances*.

timecathet\_fit <- lme(  
 fixed= verb ~ 1 + time0,   
 random= ~ 1|id,  
 weights=varIdent(form=~1|time0),  
 data=verblong,  
 na.action = na.exclude  
)  
  
summary(timecathet\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 3957.31 3983.79 -1972.655  
##   
## Random effects:  
## Formula: ~1 | id  
## (Intercept) Residual  
## StdDev: 5.971618 2.522185  
##   
## Variance function:  
## Structure: Different standard deviations per stratum  
## Formula: ~1 | time0   
## Parameter estimates:  
## 0 1 2   
## 1.000000 1.617958 2.817727   
## Fixed effects: verb ~ 1 + time0   
## Value Std.Error DF t-value p-value  
## (Intercept) 25.211860 0.4520862 407 55.76781 0  
## time0 8.461235 0.2243887 407 37.70794 0  
## Correlation:   
## (Intr)  
## time0 -0.209  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.53134767 -0.53618240 -0.01851087 0.52803718 3.09584582   
##   
## Number of Observations: 612  
## Number of Groups: 204

### 10.5.1 Model-Implied Mean Vector

So what is the implied representation of the basic information Making the implied *mean vector*.

fixef(timecathet\_fit)

## (Intercept) time0   
## 25.211860 8.461235

beta <- matrix(  
 c(  
 fixef(timecathet\_fit)[1],   
 fixef(timecathet\_fit)[2],   
 fixef(timecathet\_fit)[3]  
 ), nrow=3, ncol=1)  
beta

## [,1]  
## [1,] 25.211860  
## [2,] 8.461235  
## [3,] NA

Create the model design matrix, X, for the fixed effects. In this model this is a matrix of order .

X <- matrix(c(1,1,1,0,1,0,0,0,1), nrow=3,ncol=3)  
X

## [,1] [,2] [,3]  
## [1,] 1 0 0  
## [2,] 1 1 0  
## [3,] 1 0 1

Creating the model implied mean vector through multiplication

meanvector\_timecathet <- X %\*% beta  
meanvector\_timecathet

## [,1]  
## [1,] NA  
## [2,] NA  
## [3,] NA

See the *differences* in the means across levels of time0. This is exactly the same as in the last model

### 10.5.2 Model-Implied Covariance Matrix

#parse the between-person variances  
Psi <- matrix(c(as.numeric(VarCorr(timecathet\_fit)[1])),nrow=1,ncol=1)   
Psi

## [,1]  
## [1,] 35.66023

#create the model design matrix  
Z <- matrix(c(1,1,1), nrow=3,ncol=1)  
Z

## [,1]  
## [1,] 1  
## [2,] 1  
## [3,] 1

So the implied variance covariance of the between-person random effects for the three repeated measures is:

Z %\*% Psi %\*% t(Z)

## [,1] [,2] [,3]  
## [1,] 35.66023 35.66023 35.66023  
## [2,] 35.66023 35.66023 35.66023  
## [3,] 35.66023 35.66023 35.66023

Now for the within-person residual var-cov.

#parse the residual/"error" variance-covariance  
sigma <- as.numeric(VarCorr(timecathet\_fit)[4]) #note this is standard deviation  
sigma

## [1] 2.522185

**Note**: Now we have another step due to the heterogeneous variances. We have to get the heterogeneous weights for the residual standard deviation from the summary(timecathet\_fit).

# Variance function:  
# Structure: Different standard deviations per stratum  
# Formula: ~1 | time0   
# Parameter estimates:  
# 0 1 2   
# 1.000000 1.254186 2.341456

Pulling from the output.

sigmahet <- sigma \* (diag(c(1.000000, 1.254186, 2.341456), nrow=3,ncol=3))  
#Calculate the implied residual error variance-covariance  
Lambda <- sigmahet^2

Finally calculating the model implied between- + within var-cov structure.

varcovmatrix\_timecathet <- Z %\*% Psi %\*% t(Z) + Lambda  
varcovmatrix\_timecathet

## [,1] [,2] [,3]  
## [1,] 42.02164 35.66023 35.66023  
## [2,] 35.66023 45.66663 35.66023  
## [3,] 35.66023 35.66023 70.53616

Note the *heterogeneity* we now have along the diagonal.

Again, Let’s look at the misfit (real matrix - model implied)

meanvector - meanvector\_timecathet

## [,1]  
## [1,] NA  
## [2,] NA  
## [3,] NA

varcovmatrix - varcovmatrix\_timecathet

## verb2 verb4 verb6  
## verb2 -4.733801 -1.840657 11.74466  
## verb4 -1.840657 7.914078 26.59466  
## verb6 11.744655 26.594661 43.20715

Getting better. Note, we can formally compare the models.

anova(timecat\_fit, timecathet\_fit)

## Model df AIC BIC logLik Test L.Ratio p-value  
## timecat\_fit 1 5 4013.176 4035.235 -2001.588   
## timecathet\_fit 2 6 3957.310 3983.790 -1972.655 1 vs 2 57.86679 <.0001

Remember, the null hypothesis of the LRT states that the more constrained model provides as good a fit for the data as the less constrained model. If the null hypothesis is rejected, then the alternative, unconstrained model provides a significant improvement in fit over the smaller model. Thus, allowing for the additional heterogeneity improved our model.

## 10.6 Repeated Measures MANOVA (Unstructed)

Let’s adjust the RM MANOVA error structure to have no constraints. To do this in lme() we can use the correlation argument.

timecatunst\_fit <- lme(  
 fixed= verb ~ 1 + time0,   
 random= ~ 1|id,  
 weights=varIdent(form=~1|time0),  
 correlation=corSymm(form=~1|id),  
 data=verblong,  
 na.action = na.exclude  
)  
summary(timecatunst\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 3906.226 3945.947 -1944.113  
##   
## Random effects:  
## Formula: ~1 | id  
## (Intercept) Residual  
## StdDev: 5.396122 2.989864  
##   
## Correlation Structure: General  
## Formula: ~1 | id   
## Parameter estimate(s):  
## Correlation:   
## 1 2   
## 2 0.282   
## 3 0.710 0.686  
## Variance function:  
## Structure: Different standard deviations per stratum  
## Formula: ~1 | time0   
## Parameter estimates:  
## 0 1 2   
## 1.000000 1.665202 3.140697   
## Fixed effects: verb ~ 1 + time0   
## Value Std.Error DF t-value p-value  
## (Intercept) 24.527488 0.4049598 407 60.56771 0  
## time0 8.657464 0.2504051 407 34.57384 0  
## Correlation:   
## (Intr)  
## time0 0.138   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.15515157 -0.44689483 0.08324398 0.70545373 3.17592136   
##   
## Number of Observations: 612  
## Number of Groups: 204

### 10.6.1 Model-Implied Mean Vector

There will be no differences in the model implied mean vector in this model.

beta <- matrix(fixef(timecatunst\_fit), nrow=3, ncol=1)

## Warning in matrix(fixef(timecatunst\_fit), nrow = 3, ncol = 1): data length [2]  
## is not a sub-multiple or multiple of the number of rows [3]

X <- matrix(c(1,1,1,0,1,0,0,0,1), nrow=3,ncol=3)  
meanvector\_timecatunst <- X %\*% beta  
meanvector\_timecatunst

## [,1]  
## [1,] 24.52749  
## [2,] 33.18495  
## [3,] 49.05498

### 10.6.2 Model-Implied Covariance Matrix

Again, we start with the between-part of our model.

#parsing the model variances & covariances  
VarCorr(timecatunst\_fit)

## id = pdLogChol(1)   
## Variance StdDev   
## (Intercept) 29.118131 5.396122  
## Residual 8.939287 2.989864

Psi <- matrix(c(as.numeric(VarCorr(timecatunst\_fit)[1])),nrow=1,ncol=1)   
Z <- matrix(c(1,1,1), nrow=3,ncol=1)  
Z %\*% Psi %\*% t(Z)

## [,1] [,2] [,3]  
## [1,] 29.11813 29.11813 29.11813  
## [2,] 29.11813 29.11813 29.11813  
## [3,] 29.11813 29.11813 29.11813

Now it gets a bit more complicated, because we have a fully unstructured matrix for the within-person residual variance-covariance.

#parse the residual/"error" variance-covariance  
sigma <- as.numeric(VarCorr(timecatunst\_fit)[4]) #note this is standard deviation  
  
#From the summary(timecatunst\_fit) above  
# Variance function:  
# Structure: Different standard deviations per stratum  
# Formula: ~1 | time0   
# Parameter estimates:  
# 0 1 2   
# 1.000000 1.827573 3.461330   
sigmaunst <- sigma \* (diag(c(1.000000, 1.827573, 3.461330), nrow=3,ncol=3))  
  
#From the summary(timecatunst\_fit) above  
# Correlation Structure: General  
# Formula: ~1 | id   
# Parameter estimate(s):  
# Correlation:   
# 1 2   
# 2 0.275   
# 3 0.709 0.725  
cormatrixunst <- matrix(c(1.000, 0.275, 0.709,  
 0.275, 1.000, 0.725,  
 0.709, 0.725, 1.000),  
 nrow=3,ncol=3)  
  
#Pre and post multiply by SDs to convert Correlation matrix into  
#Covariance matrix  
covresidunst <- sigmaunst %\*% cormatrixunst %\*% t(sigmaunst)  
covresidunst

## [,1] [,2] [,3]  
## [1,] 8.939287 4.49273 21.93775  
## [2,] 4.492730 29.85742 40.99762  
## [3,] 21.937751 40.99762 107.09985

Finally, calculate the implied between- + within-person variance-covariances

varcovmatrix\_timecatunst <- Z %\*% Psi %\*% t(Z) + covresidunst  
varcovmatrix\_timecatunst

## [,1] [,2] [,3]  
## [1,] 38.05742 33.61086 51.05588  
## [2,] 33.61086 58.97555 70.11575  
## [3,] 51.05588 70.11575 136.21799

Let’s look at the misfit (real matrix - model implied).

meanvector - meanvector\_timecatunst

## [,1]  
## [1,] 0.8878550  
## [2,] -0.5772067  
## [3,] -5.3050743

varcovmatrix - varcovmatrix\_timecatunst

## verb2 verb4 verb6  
## verb2 -0.769575 0.208709 -3.65100  
## verb4 0.208709 -5.394852 -7.86086  
## verb6 -3.651000 -7.860860 -22.47467

It appears we have fully reproduced our observed data. We can formally test the improvement of this model using the anove() function.

anova(timecathet\_fit, timecatunst\_fit)

## Model df AIC BIC logLik Test L.Ratio p-value  
## timecathet\_fit 1 6 3957.310 3983.790 -1972.655   
## timecatunst\_fit 2 9 3906.226 3945.947 -1944.113 1 vs 2 57.08328 <.0001

# 11 Growth Curve Modeling

## 11.1 Introduction

In this chapter we work through basics of growth modeling. We describe the data, run some individual level models, and work through no-growth and linear growth modeling examples. We then expand on that model in two ways. We add a predictor - to get the conditional growth model and we change the time-metric - to illustrate how alternative time metrics facilitate different interpretations.

## 11.2 Data Preparation and Description

### 11.2.1 Loading libraries used in this script.

library(psych) #for basic functions  
library(ggplot2) #for plotting  
library(data.table) #for fast data management  
library(nlme) #for mixed effects models  
library(plyr) #for data management  
library(see)

For our examples, we use 4-occasion WISC data. Load the repeated measures data.

filepath <- "https://quantdev.ssri.psu.edu/sites/qdev/files/wisc3raw.csv"  
wisc3raw <- read.csv(file=url(filepath),header=TRUE)

Subsetting to the variables of interest. Specifically, we include the id variable; the repeated measures outcome variables verb1, verb2, verb4, verb6; and the predictors grad and momed variables.

varnames <- c("id","verb1","verb2","verb4","verb6","grad","momed")  
wiscsub <- wisc3raw[ ,varnames]  
describe(wiscsub)

## vars n mean sd median trimmed mad min max range skew  
## id 1 204 102.50 59.03 102.50 102.50 75.61 1.00 204.00 203.00 0.00  
## verb1 2 204 19.59 5.81 19.34 19.50 5.41 3.33 35.15 31.82 0.13  
## verb2 3 204 25.42 6.11 25.98 25.40 6.57 5.95 39.85 33.90 -0.06  
## verb4 4 204 32.61 7.32 32.82 32.42 7.18 12.60 52.84 40.24 0.23  
## verb6 5 204 43.75 10.67 42.55 43.46 11.30 17.35 72.59 55.24 0.24  
## grad 6 204 0.23 0.42 0.00 0.16 0.00 0.00 1.00 1.00 1.30  
## momed 7 204 10.81 2.70 11.50 11.00 2.97 5.50 18.00 12.50 -0.36  
## kurtosis se  
## id -1.22 4.13  
## verb1 -0.05 0.41  
## verb2 -0.34 0.43  
## verb4 -0.08 0.51  
## verb6 -0.36 0.75  
## grad -0.30 0.03  
## momed 0.01 0.19

Multilevel modeling analyses typically require a tall (long) data set. So, we reshape from wide to tall:

verblong <- reshape(  
 data=wiscsub,   
 varying=c("verb1","verb2","verb4","verb6"),   
 timevar="grade",   
 idvar="id",   
 direction="long",   
 sep=""  
)  
verblong <- verblong[order(verblong$id,verblong$grade),c("id","grade","verb","grad","momed")]  
head(verblong,12)

## id grade verb grad momed  
## 1.1 1 1 24.42 0 9.5  
## 1.2 1 2 26.98 0 9.5  
## 1.4 1 4 39.61 0 9.5  
## 1.6 1 6 55.64 0 9.5  
## 2.1 2 1 12.44 0 5.5  
## 2.2 2 2 14.38 0 5.5  
## 2.4 2 4 21.92 0 5.5  
## 2.6 2 6 37.81 0 5.5  
## 3.1 3 1 32.43 1 14.0  
## 3.2 3 2 33.51 1 14.0  
## 3.4 3 4 34.30 1 14.0  
## 3.6 3 6 50.18 1 14.0

## 11.3 Individual Growth Models

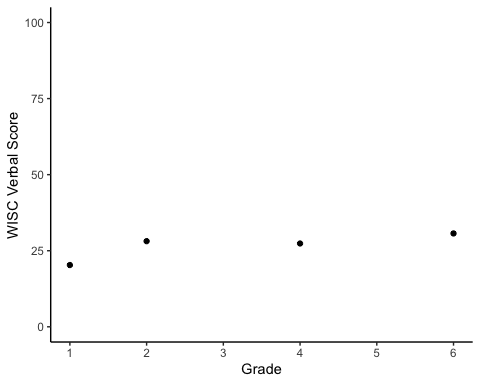
To introduce growth modeling we will begin with data from a single individual. Let’s make a dataset with just 1 person of interest, id = 23,

verb\_id23 <- verblong[which(verblong$id == 23), ]

### 11.3.1 Visualizing Individual Change

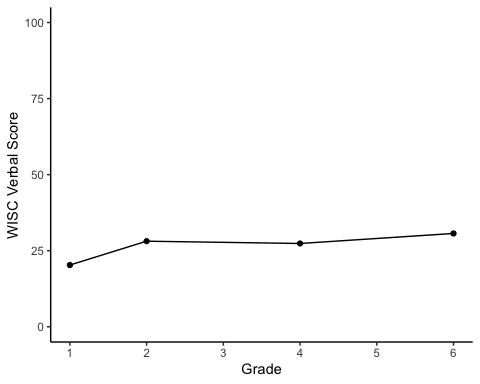
Let’s make a plot of this person’s data,

ggplot(data = verb\_id23, aes(x = grade, y = verb, group = id)) +  
 geom\_point() +   
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()



We could connect the dots to see time-adjacent changes.

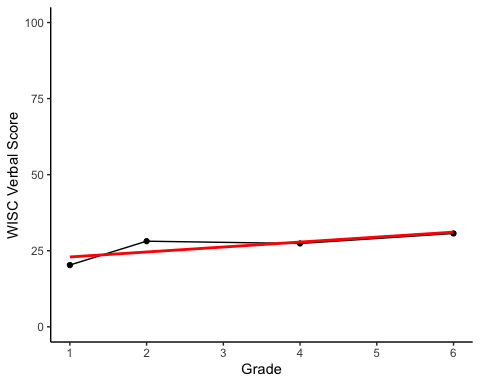
ggplot(data = verb\_id23, aes(x = grade, y = verb, group = id)) +  
 geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()



We could also *smooth* over the repeated measuring using a line of best fit for this individual.

ggplot(data = verb\_id23, aes(x = grade, y = verb, group = id)) +  
 geom\_point() +   
 geom\_line() +  
 geom\_smooth(method=lm, se=FALSE,colour="red", size=1) +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()

## `geom\_smooth()` using formula 'y ~ x'



Notice, we can summarize this line with two pieces of information, (1) an intercept, and (2) a slope, each unique to individual 23.

### 11.3.2 Multiple Individuals

Let’s do an individual regression with time as a predictor. Conceptually, this is a model of intraindividual change corresponding to the plot above.

#regress verb on grade   
linear\_id23 <- lm(formula = verb ~ 1 + grade, data = verb\_id23, na.action=na.exclude)  
#show results  
summary(linear\_id23)

##   
## Call:  
## lm(formula = verb ~ 1 + grade, data = verb\_id23, na.action = na.exclude)  
##   
## Residuals:  
## 23.1 23.2 23.4 23.6   
## -2.6556 3.5536 -0.4681 -0.4298   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 21.3247 3.1147 6.846 0.0207 \*  
## grade 1.6308 0.8251 1.977 0.1867   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 3.169 on 2 degrees of freedom  
## Multiple R-squared: 0.6614, Adjusted R-squared: 0.4921   
## F-statistic: 3.907 on 1 and 2 DF, p-value: 0.1867

Let’s save the 3 parameters into objects and look at them.

id23\_reg\_linear <- as.list(coef(linear\_id23))  
id23\_reg\_linear

## $`(Intercept)`  
## [1] 21.32475  
##   
## $grade  
## [1] 1.630847

**Now let’s do the same thing for all the persons.**

We do this in a speedy way using the data.table package.

#converting to a data.table object  
verblong\_dt <- data.table(verblong)  
  
#collecting regression output by id   
indiv\_reg <- verblong\_dt[,c(  
 reg\_1 = as.list(coef(lm(verb ~ grade)))  
),by=id]

Let’s look at the moments of the parameters

#converting back to data.frame   
names(indiv\_reg)

## [1] "id" "reg\_1.(Intercept)" "reg\_1.grade"

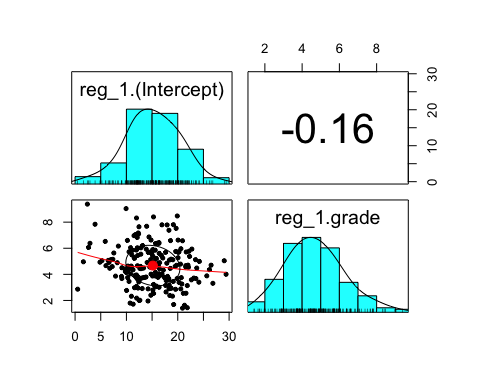
indiv\_reg\_data <- as.data.frame(indiv\_reg)  
  
#descriptives  
describe(indiv\_reg\_data[-1])

## vars n mean sd median trimmed mad min max range  
## reg\_1.(Intercept) 1 204 15.15 5.27 15.14 15.23 5.12 0.50 29.41 28.91  
## reg\_1.grade 2 204 4.67 1.55 4.60 4.61 1.53 1.41 9.38 7.97  
## skew kurtosis se  
## reg\_1.(Intercept) -0.08 0.06 0.37  
## reg\_1.grade 0.38 0.02 0.11

#correlations among parameters  
cor(indiv\_reg\_data[-1], use="complete.obs",method="pearson")

## reg\_1.(Intercept) reg\_1.grade  
## reg\_1.(Intercept) 1.0000000 -0.1551763  
## reg\_1.grade -0.1551763 1.0000000

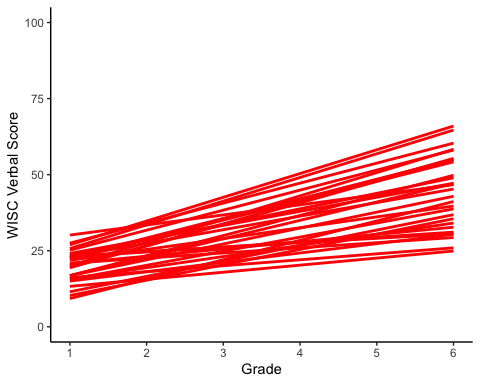
#pairs in the psych library  
pairs.panels(indiv\_reg\_data[-1])



Here, each person has 2 *scores* (intercept + slope) from the individual-level regression models. Now, let’s plot some of the individual regressions

#making intraindividual change plot  
ggplot(data = verblong[which(verblong$id < 30),], aes(x = grade, y = verb, group = id)) +  
 geom\_smooth(method=lm,se=FALSE,colour="red", size=1) +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()

## `geom\_smooth()` using formula 'y ~ x'



The characteristics of the latent trajectories are captured in two ways:

1. **Trajectory Means**:

* The average value of the parameters governing the growth trajectory, pooled over the all individuals in the sample. This is the mean starting point and mean rate of change for the sample. These are often called fixed effects.

1. **Trajectory Variances**:

* The variability of individual cases around the mean trajectory parameters. This is the individual variability in starting point and rate of change over time. Larger variances reflect larger variability in growth. These are often called random effects.

To recap, means captures overall values of parameters that define growth. Variances capture individual variability in those parameters.

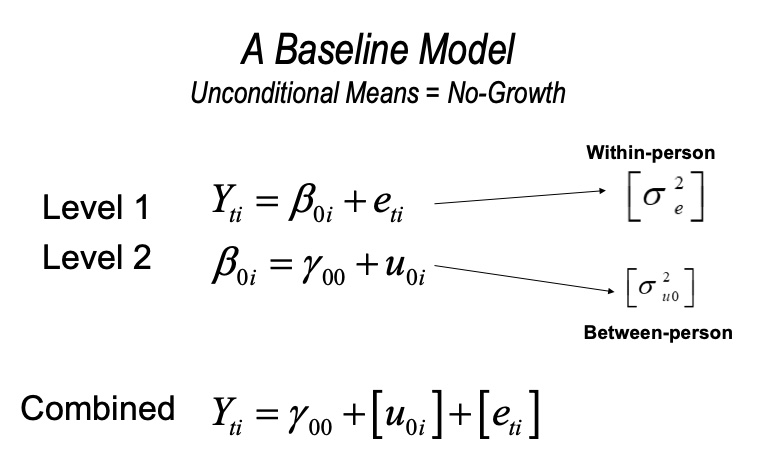
Let’s move to our more familiar framework for handling the analysis of “collections” of regressions.

## 11.4 Unconditional Means Model

We will begin by fitting the unconditional means model, or *no growth* model to the 4-ocasion WISC data.

We use the nlme package for fitting *mixed effects* models, also known as multilevel (MLM) or hierarchical linear models (HLM).

Specifically, we use the lme() function to fits the MLMs: - The ‘fixed’ argument takes the fixed model - The ‘random’ argument takes the random model - The ‘data’ argument specifies the data sources - The ‘na.action’ argument specifies how to handle missing data



Baseline Model

The Unconditional Means model contains a fixed and random intercept only. You can use the constant 1 to designate that only intercepts are being modeled.

um\_fit <- lme(  
 fixed= verb ~ 1,   
 random = ~ 1|id,   
 data = verblong,  
 na.action = na.exclude,  
 method = "ML"  
)  
  
summary(um\_fit)

## Linear mixed-effects model fit by maximum likelihood  
## Data: verblong   
## AIC BIC logLik  
## 6347.936 6362.05 -3170.968  
##   
## Random effects:  
## Formula: ~1 | id  
## (Intercept) Residual  
## StdDev: 3.575939 11.30169  
##   
## Fixed effects: verb ~ 1   
## Value Std.Error DF t-value p-value  
## (Intercept) 30.33951 0.4684887 612 64.76039 0  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -1.9419919 -0.7619298 -0.1621987 0.5568904 3.3055064   
##   
## Number of Observations: 816  
## Number of Groups: 204

Let’s extract the random effects with the VarCorr() function

VarCorr(um\_fit)

## id = pdLogChol(1)   
## Variance StdDev   
## (Intercept) 12.78734 3.575939  
## Residual 127.72821 11.301691

We can compute the intra-class correlation (ICC) as the ratio of the random intercept variance (between-person) to the total variance (between + within), that includes the error.

First let’s store the variance estimates, which will be the first column of the VarCorr object (see above).

RandomEffects <- as.numeric(VarCorr(um\_fit)[,1])  
RandomEffects

## [1] 12.78734 127.72821

Next let’s compute the ICC. It is the ratio of the random intercept variance (between-person var) over the total variance (between + within var).

ICC\_between <- RandomEffects[1]/(RandomEffects[1]+RandomEffects[2])   
ICC\_between

## [1] 0.09100302

From the results we seeM there is lots of within-person variance for us to explain.

* between-person variance =
* within-person variance =

### 11.4.1 Predicted Trajectories

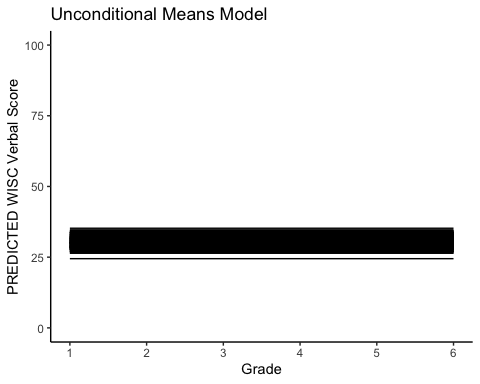
Place individual predictions and residuals from the unconditional means model um\_fit into the dataframe

verblong$pred\_um <- predict(um\_fit)  
verblong$resid\_um <- residuals(um\_fit)  
head(verblong)

## id grade verb grad momed pred\_um resid\_um  
## 1.1 1 1 24.42 0 9.5 32.14754 -7.727545  
## 1.2 1 2 26.98 0 9.5 32.14754 -5.167545  
## 1.4 1 4 39.61 0 9.5 32.14754 7.462455  
## 1.6 1 6 55.64 0 9.5 32.14754 23.492455  
## 2.1 2 1 12.44 0 5.5 27.85120 -15.411203  
## 2.2 2 2 14.38 0 5.5 27.85120 -13.471203

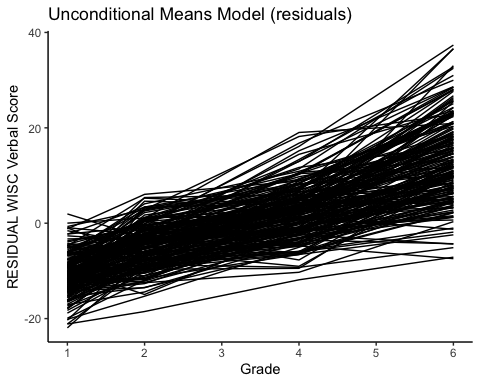
We can make plots of the model outputs. Here we plot the between-person differences in levels ().

ggplot(data = verblong, aes(x = grade, y = pred\_um, group = id)) +  
 ggtitle("Unconditional Means Model") +  
# geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("PREDICTED WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()



Here we plot the between-person differences in levels ().

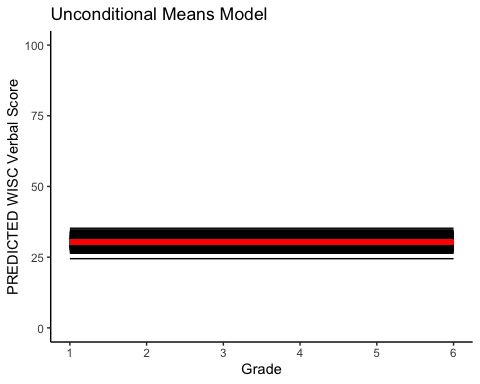
#plotting RESIDUAL intraindividual change  
ggplot(data = verblong, aes(x = grade, y = resid\_um, group = id)) +  
 ggtitle("Unconditional Means Model (residuals)") +  
# geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("RESIDUAL WISC Verbal Score") + #ylim(0,100) + Note the removal of limits on y-axis  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()



We cab also plot the predicted intraindividual change alongside the mean trajectory.

fun\_um <- function(x) { 30.33951 + 0\*x }  
ggplot(data = verblong, aes(x = grade, y = pred\_um, group = id)) +  
 ggtitle("Unconditional Means Model") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("PREDICTED WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 stat\_function(fun=fun\_um, color="red", size = 2) +  
 theme\_classic()

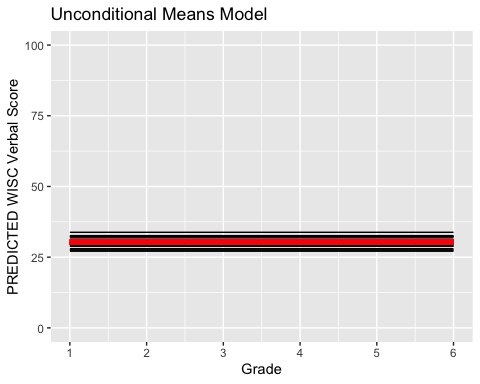
## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct  
## `group`, `colour`, or `fill` aesthetics?



Since it is often too messy to plot all individuals we can also subset the plot.

randomsample <- sample(verblong$id,20)  
ggplot(data = verblong[verblong$id %in% randomsample,], aes(x = grade, y = pred\_um, group = id)) +  
 ggtitle("Unconditional Means Model") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("PREDICTED WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 stat\_function(fun=fun\_um, color="red", size = 2)

## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct  
## `group`, `colour`, or `fill` aesthetics?



## 11.5 Linear Growth Model

Now let’s add in grade as a (time-varying) predictor. We look at the linear relation between the time variable (grade) and the outcome variable (verb).

### 11.5.1 Random Intercept Model

My naming convention for objects here is: fixed linear (fl) and random intercept (ri)

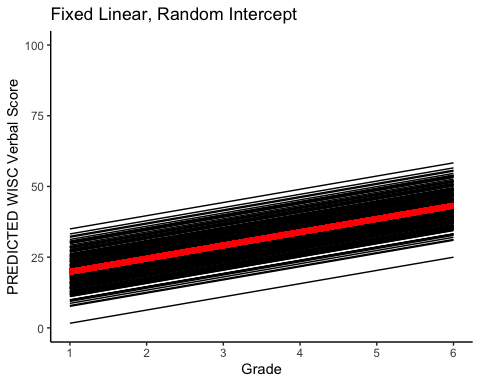
fl\_ri\_fit <- lme(  
 fixed = verb ~ 1 + grade,   
 random = ~ 1|id,   
 data=verblong,  
 na.action = na.exclude,  
 method = "ML"  
)  
summary(fl\_ri\_fit)

## Linear mixed-effects model fit by maximum likelihood  
## Data: verblong   
## AIC BIC logLik  
## 5225.662 5244.48 -2608.831  
##   
## Random effects:  
## Formula: ~1 | id  
## (Intercept) Residual  
## StdDev: 6.295478 4.510587  
##   
## Fixed effects: verb ~ 1 + grade   
## Value Std.Error DF t-value p-value  
## (Intercept) 15.15099 0.5397641 611 28.06966 0  
## grade 4.67339 0.0823294 611 56.76454 0  
## Correlation:   
## (Intr)  
## grade -0.496  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.70731017 -0.54837346 -0.03479899 0.52061645 4.13309807   
##   
## Number of Observations: 816  
## Number of Groups: 204

Let’s look at the predicted trajectories from this model

#Place individual predictions and residuals into the dataframe  
verblong$pred\_fl\_ri <- predict(fl\_ri\_fit)  
verblong$resid\_fl\_ri <- residuals(fl\_ri\_fit)  
#Create a function for the mean trajectory  
fun\_fl\_ri <- function(x) { 15.15099 + 4.67339\*x }  
  
#plotting PREDICTED intraindividual change  
ggplot(data = verblong, aes(x = grade, y = pred\_fl\_ri, group = id)) +  
 ggtitle("Fixed Linear, Random Intercept") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("PREDICTED WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +   
 stat\_function(fun=fun\_fl\_ri, color="red", size = 2) +  
 theme\_classic()

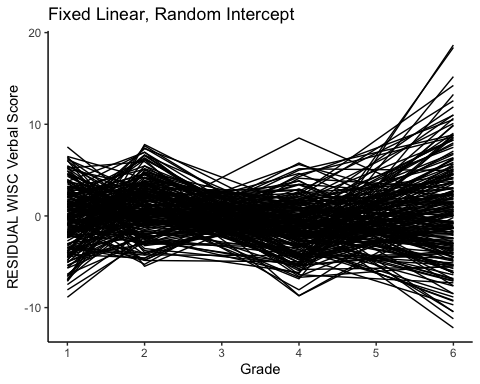
## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct  
## `group`, `colour`, or `fill` aesthetics?



Note how all the lines are parallel. This imples individual variability in starting point *but* a constant rate of change over time.

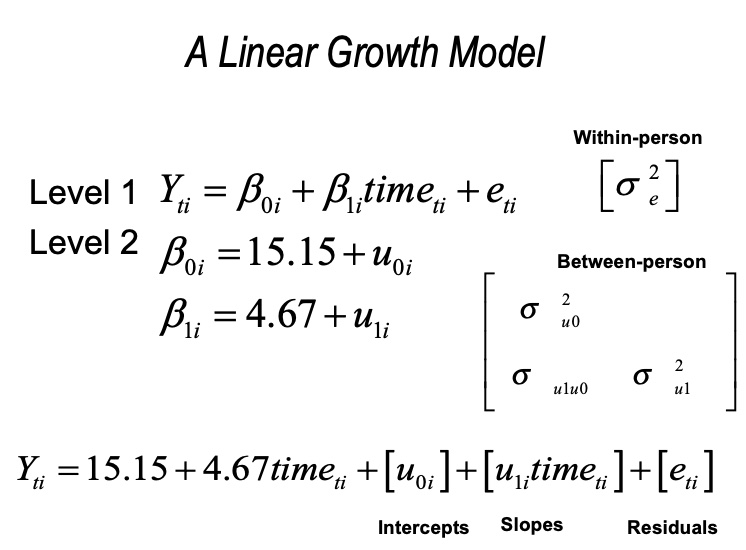
Let’s look at the residuals.

ggplot(data = verblong, aes(x = grade, y = resid\_fl\_ri, group = id)) +  
 ggtitle("Fixed Linear, Random Intercept") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("RESIDUAL WISC Verbal Score") +   
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()



Note the differences in variance.

### 11.5.2 Random Intercept and Slopes Model



Linear Growth Model

fl\_rl\_fit <- lme(  
 fixed = verb ~ 1 + grade,   
 random = ~ 1 + grade|id,   
 data=verblong,  
 na.action = na.exclude,  
 method = "ML"  
)  
summary(fl\_rl\_fit)

## Linear mixed-effects model fit by maximum likelihood  
## Data: verblong   
## AIC BIC logLik  
## 5050.844 5079.071 -2519.422  
##   
## Random effects:  
## Formula: ~1 + grade | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 3.898137 (Intr)  
## grade 1.236530 0.324   
## Residual 3.581590   
##   
## Fixed effects: verb ~ 1 + grade   
## Value Std.Error DF t-value p-value  
## (Intercept) 15.15099 0.3681978 611 41.14906 0  
## grade 4.67339 0.1085687 611 43.04546 0  
## Correlation:   
## (Intr)  
## grade -0.155  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.61515108 -0.54356127 -0.02857269 0.52294867 3.17283579   
##   
## Number of Observations: 816  
## Number of Groups: 204

We can take a look at the ICCs to see if we are doing any better explaining the within-person variance.

RandomEffects <- as.numeric(VarCorr(fl\_rl\_fit)[,1])  
ICC\_between <- sum(RandomEffects[1:2])/sum(RandomEffects)   
ICC\_between

## [1] 0.5659288

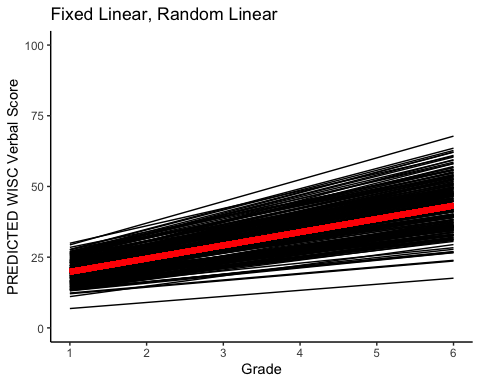
Let’s look at the predicted trajectories from this model. We can start by saving the predicted trajectories and residuals into our dataframe.

verblong$pred\_fl\_rl <- predict(fl\_rl\_fit)  
verblong$resid\_fl\_rl <- residuals(fl\_rl\_fit)

Next, we make a small function to plot the mean trajectory. Now we use the fixedf() function directly rather than type the numbers manually from the output.

#Create a function for the prototype  
#fun\_fl\_rl <- function(x) {  
# 15.15099 + 4.67339\*x  
#}  
  
fun\_fl\_rl <- function(x) {  
 fixef(fl\_rl\_fit)[[1]] + fixef(fl\_rl\_fit)[[2]]\*x  
}  
  
#plotting PREDICTED intraindividual change  
ggplot(data = verblong, aes(x = grade, y = pred\_fl\_rl, group = id)) +  
 ggtitle("Fixed Linear, Random Linear") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("PREDICTED WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +   
 stat\_function(fun=fun\_fl\_rl, color="red", size = 2) +  
 theme\_classic()

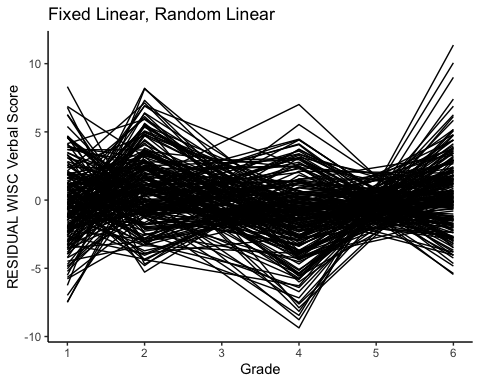
## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct  
## `group`, `colour`, or `fill` aesthetics?



Note how the lines are no longer parallel. We now have a model that implies individual variability in the starting point and rate of change.

We can also plot the residuals.

#plotting RESIDUAL intraindividual change  
ggplot(data = verblong, aes(x = grade, y = resid\_fl\_rl, group = id)) +  
 ggtitle("Fixed Linear, Random Linear") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("RESIDUAL WISC Verbal Score") +   
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()



This model did a bit better on getting the residual variances similar at all grades (in line with assumptions).

### 11.5.3 Model Comparison

Let’s test the significance of having random slopes. We compare models by applying anova() function to examine difference in fit between the two nested models.

anova(fl\_ri\_fit, fl\_rl\_fit)

## Model df AIC BIC logLik Test L.Ratio p-value  
## fl\_ri\_fit 1 4 5225.662 5244.480 -2608.831   
## fl\_rl\_fit 2 6 5050.844 5079.071 -2519.422 1 vs 2 178.8176 <.0001

From the test results we see they are different. This provides a significance test for the variance and covariance (2 degrees of freedom).

### 11.5.4 MLM and Individual Models

Remember, earlier, we ran individual-level regressions.

head(indiv\_reg\_data,12)

## id reg\_1.(Intercept) reg\_1.grade  
## 1 1 15.940169 6.376102  
## 2 2 5.232712 5.047627  
## 3 3 26.838136 3.312881  
## 4 4 19.493729 4.614237  
## 5 5 19.145424 7.805254  
## 6 6 11.554576 5.224746  
## 7 7 2.903559 6.378136  
## 8 8 14.198814 1.957288  
## 9 9 10.816441 6.041864  
## 10 10 18.385763 5.097458  
## 11 11 16.319661 6.437797  
## 12 12 12.089661 3.667797

Let’s also obtain individual-level *estimates* from the MLM model.

FE <- fixef(fl\_rl\_fit) # fixed effects  
FE

## (Intercept) grade   
## 15.15099 4.67339

RE <- ranef(fl\_rl\_fit) # random effects  
head(RE)

## (Intercept) grade  
## 1 2.112944 1.23363572  
## 2 -5.539717 -0.61673174  
## 3 5.640182 0.09800804  
## 4 2.526636 0.34162948  
## 5 5.399309 2.49279596  
## 6 -1.607547 0.06056849

We add the fixed effect and random effect parameters together to get analogues of the individual-level parameters.

#Individual intercepts (MLM model based)  
MLM\_intercept <- FE[1] + RE[,1]  
#Individual slopes (MLM model based)  
MLM\_grade <- FE[2] + RE[,2]

Let’s combine the individual regression intercepts and slopes and the model based intercepts and slopes together in order to compare.

indiv\_parm\_combined <- cbind(MLM\_intercept,MLM\_grade,indiv\_reg\_data[,2:3])  
head(indiv\_parm\_combined)

## MLM\_intercept MLM\_grade reg\_1.(Intercept) reg\_1.grade  
## 1 17.263936 5.907026 15.940169 6.376102  
## 2 9.611275 4.056658 5.232712 5.047627  
## 3 20.791175 4.771398 26.838136 3.312881  
## 4 17.677629 5.015019 19.493729 4.614237  
## 5 20.550302 7.166186 19.145424 7.805254  
## 6 13.543446 4.733958 11.554576 5.224746

Look at the descriptives statistics.

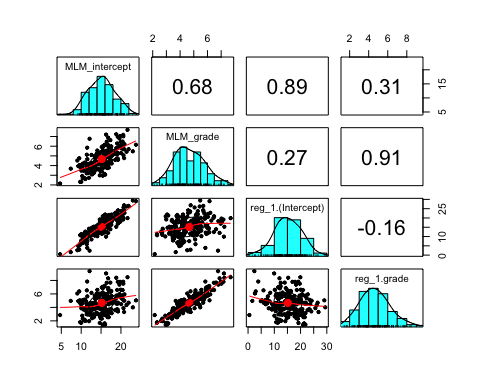
describe(indiv\_parm\_combined)

## vars n mean sd median trimmed mad min max range  
## MLM\_intercept 1 204 15.15 3.26 15.35 15.12 3.25 4.69 23.78 19.09  
## MLM\_grade 2 204 4.67 1.09 4.56 4.64 1.09 2.15 7.69 5.54  
## reg\_1.(Intercept) 3 204 15.15 5.27 15.14 15.23 5.12 0.50 29.41 28.91  
## reg\_1.grade 4 204 4.67 1.55 4.60 4.61 1.53 1.41 9.38 7.97  
## skew kurtosis se  
## MLM\_intercept 0.00 -0.23 0.23  
## MLM\_grade 0.26 -0.31 0.08  
## reg\_1.(Intercept) -0.08 0.06 0.37  
## reg\_1.grade 0.38 0.02 0.11

round(cor(indiv\_parm\_combined),2)

## MLM\_intercept MLM\_grade reg\_1.(Intercept) reg\_1.grade  
## MLM\_intercept 1.00 0.68 0.89 0.31  
## MLM\_grade 0.68 1.00 0.27 0.91  
## reg\_1.(Intercept) 0.89 0.27 1.00 -0.16  
## reg\_1.grade 0.31 0.91 -0.16 1.00

pairs.panels(indiv\_parm\_combined)

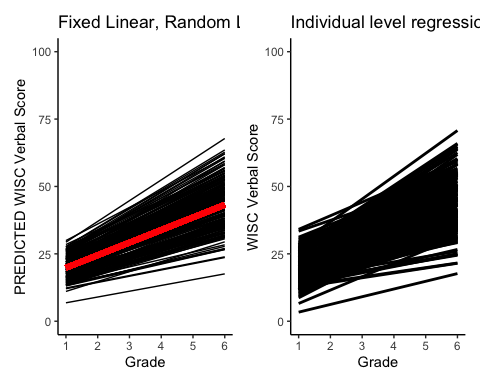


Let’s compare the two predictions. What do you notice?

library(see)  
#plotting PREDICTED intraindividual change  
GCMpred = ggplot(data = verblong, aes(x = grade, y = pred\_fl\_rl, group = id)) +  
 ggtitle("Fixed Linear, Random Linear") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("PREDICTED WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +   
 stat\_function(fun=fun\_fl\_rl, color="red", size = 2) +  
 theme\_classic()  
  
#making intraindividual change plot  
IndPred = ggplot(data = verblong, aes(x = grade, y = verb, group = id)) +  
 ggtitle("Individual level regressions only") +  
 geom\_smooth(method=lm,se=FALSE,colour="black", size=1) +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +  
 theme\_classic()  
  
plots(GCMpred, IndPred)

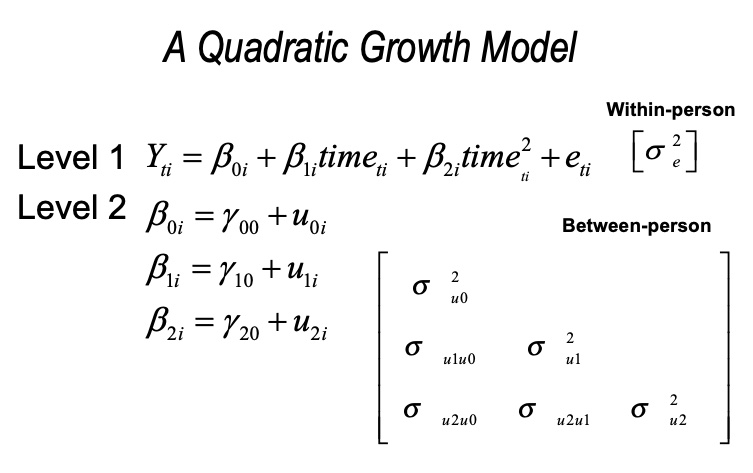
## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct  
## `group`, `colour`, or `fill` aesthetics?

## `geom\_smooth()` using formula 'y ~ x'



## 11.6 Quadratic Growth Model

Quadratic time model (MLM): random intercepts and linear and quadratic slopes.



Quadratic Growth Model

verblong$gradeSquared <- (verblong$grade)^2  
  
fq\_rq\_fit <- lme(  
 fixed = verb ~ 1 + grade + gradeSquared,   
 random = ~ 1 + grade|id + gradeSquared|id,   
 data=verblong,  
 na.action = na.exclude,  
 method = "ML"  
)  
summary(fq\_rq\_fit)

## Linear mixed-effects model fit by maximum likelihood  
## Data: verblong   
## AIC BIC logLik  
## 5226.412 5259.343 -2606.206  
##   
## Random effects:  
## Formula: ~1 + grade | id + gradeSquared | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 5.277258 (Intr)  
## 1 + grade | id + gradeSquaredTRUE 5.277258 -0.288  
## Residual 4.491283   
##   
## Fixed effects: verb ~ 1 + grade + gradeSquared   
## Value Std.Error DF t-value p-value  
## (Intercept) 16.347780 0.7508427 610 21.772576 0.0000  
## grade 3.695700 0.4344000 610 8.507596 0.0000  
## gradeSquared 0.138997 0.0606470 610 2.291899 0.0223  
## Correlation:   
## (Intr) grade   
## grade -0.750   
## gradeSquared 0.695 -0.982  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.79052272 -0.55253516 -0.02974189 0.51054065 4.07582660   
##   
## Number of Observations: 816  
## Number of Groups: 204

Let’s test the significance of having random slopes. We compare models by applying anova() function to examine difference in fit between the two nested models.

anova(fl\_rl\_fit,fq\_rq\_fit)

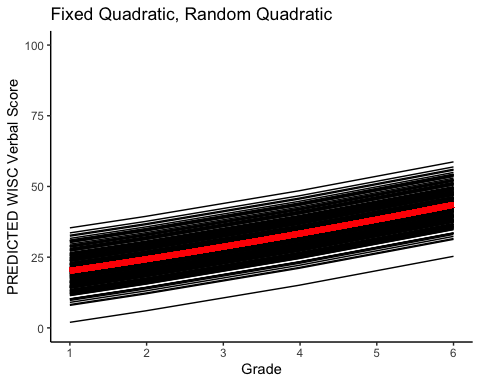
## Model df AIC BIC logLik Test L.Ratio p-value  
## fl\_rl\_fit 1 6 5050.844 5079.071 -2519.422   
## fq\_rq\_fit 2 7 5226.412 5259.343 -2606.206 1 vs 2 173.568 <.0001

From the test results we see they are different.

Let’s look at the predicted trajectories.

verblong$pred\_fq\_rq <- predict(fq\_rq\_fit)  
verblong$resid\_fq\_rq <- residuals(fq\_rq\_fit)  
  
fun\_fq\_rq <- function(x) {  
 fixef(fq\_rq\_fit)[[1]] + fixef(fq\_rq\_fit)[[2]]\*x + fixef(fq\_rq\_fit)[[3]]\*x^2  
}  
  
ggplot(data = verblong, aes(x = grade, y = pred\_fq\_rq, group = id)) +  
 ggtitle("Fixed Quadratic, Random Quadratic") +  
 geom\_line() +  
 xlab("Grade") +   
 ylab("PREDICTED WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +   
 stat\_function(fun=fun\_fq\_rq, color="red", size = 2) +  
 theme\_classic()

## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct  
## `group`, `colour`, or `fill` aesthetics?



## 11.7 Conditional Growth Model

Let’s go back and look at our data. The data include 2 additional time-invariant covariates, momed and grad.

Let’s add a predictor to our model. In this case we will add **Grad as a (categorial) predictor** (which is coded 0,1)

cgm1\_fit <- lme(  
 fixed= verb ~ 1 + grade + grad + grade:grad,   
 random= ~ 1 + grade|id,  
 data=verblong,  
 na.action = na.exclude  
)  
  
summary(cgm1\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5031.753 5069.349 -2507.876  
##   
## Random effects:  
## Formula: ~1 + grade | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 3.761291 (Intr)  
## grade 1.194941 0.255   
## Residual 3.581590   
##   
## Fixed effects: verb ~ 1 + grade + grad + grade:grad   
## Value Std.Error DF t-value p-value  
## (Intercept) 14.533795 0.4098491 610 35.46133 0.0000  
## grade 4.483657 0.1205883 610 37.18152 0.0000  
## grad 2.737137 0.8630981 202 3.17129 0.0018  
## grade:grad 0.841424 0.2539460 610 3.31340 0.0010  
## Correlation:   
## (Intr) grade grad   
## grade -0.215   
## grad -0.475 0.102   
## grade:grad 0.102 -0.475 -0.215  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.57955639 -0.53942830 -0.01662113 0.51067259 3.19891926   
##   
## Number of Observations: 816  
## Number of Groups: 204

Let’s make grad () and non-grad () prototypical trajectories.

#First lets extract the fixed effects  
FE <- fixef(cgm1\_fit)  
FE

## (Intercept) grade grad grade:grad   
## 14.5337953 4.4836569 2.7371369 0.8414241

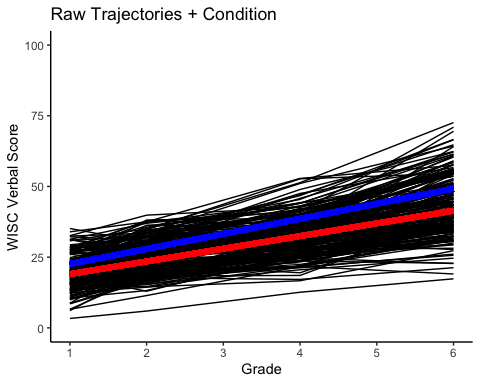
Create a function for the mean trends.

#for grad = 0  
fun\_cgm\_grad0 <- function(x) {  
 grad=0  
 FE[1] + FE[2]\*x + FE[3]\*grad + FE[4]\*x\*grad  
}  
#for grad = 1  
fun\_cgm\_grad1 <- function(x) {  
 grad=1  
 FE[1] + FE[2]\*x + FE[3]\*grad + FE[4]\*x\*grad  
}

Plot with the mean trends for no-grad (red) and grad (blue) trajectories.

#plotting intraindividual change with overlay of group trends   
ggplot(data = verblong, aes(x = grade, y = verb, group = id)) +  
 ggtitle("Raw Trajectories + Condition") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +   
 stat\_function(fun=fun\_cgm\_grad0, color="red", size = 2) +  
 stat\_function(fun=fun\_cgm\_grad1, color="blue", size = 2) +  
 theme\_classic()

## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct `group`, `colour`, or `fill` aesthetics?  
## Multiple drawing groups in `geom\_function()`. Did you use the correct `group`, `colour`, or `fill` aesthetics?



Now, let’s consider momed as a (continuous) predictor. First, we will center momed at sample-level mean. Note this is done using the wide data set.

describe(wiscsub$momed)

## vars n mean sd median trimmed mad min max range skew kurtosis se  
## X1 1 204 10.81 2.7 11.5 11 2.97 5.5 18 12.5 -0.36 0.01 0.19

#Calculating the mean   
momed\_mean <- mean(wiscsub$momed)  
momed\_mean

## [1] 10.81127

#Calculating the sd for later use in plots  
momed\_sd <- sd(wiscsub$momed)  
momed\_sd

## [1] 2.698279

#Computing centered variable in long data  
verblong$momed\_c <- (verblong$momed-momed\_mean)  
describe(verblong$momed\_c)

## vars n mean sd median trimmed mad min max range skew kurtosis se  
## X1 1 816 0 2.69 0.69 0.19 2.97 -5.31 7.19 12.5 -0.36 0.03 0.09

Fitting conditional growth model with momed (centered) as predictor

cgm2\_fit <- lme(  
 fixed= verb ~ 1 + grade + momed\_c + grade:momed\_c,   
 random= ~ 1 + grade|id,  
 data=verblong,  
 na.action = na.exclude  
)  
  
summary(cgm2\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5000.914 5038.51 -2492.457  
##   
## Random effects:  
## Formula: ~1 + grade | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 3.394993 (Intr)  
## grade 1.158314 0.163   
## Residual 3.581594   
##   
## Fixed effects: verb ~ 1 + grade + momed\_c + grade:momed\_c   
## Value Std.Error DF t-value p-value  
## (Intercept) 15.150993 0.3424175 610 44.24713 0  
## grade 4.673390 0.1041157 610 44.88652 0  
## momed\_c 0.734066 0.1272144 202 5.77030 0  
## grade:momed\_c 0.169838 0.0386809 610 4.39075 0  
## Correlation:   
## (Intr) grade momd\_c  
## grade -0.301   
## momed\_c 0.000 0.000   
## grade:momed\_c 0.000 0.000 -0.301  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.56783078 -0.54388373 -0.01862405 0.51810895 3.19394034   
##   
## Number of Observations: 816  
## Number of Groups: 204

We can extraxt the fixed effects for a prototypical trajectory.

#Extract the fixed effects  
FE2 <- fixef(cgm2\_fit)  
FE2

## (Intercept) grade momed\_c grade:momed\_c   
## 15.1509929 4.6733898 0.7340657 0.1698381

Now, let’s consider momed at the mean value, as well as low (-1SD) and high (+1SD) values.

Low value of momed.

fun\_cgm\_momed\_low <- function(x) {  
 momed=0-1\*momed\_sd  
 FE2[1] + FE2[2]\*x + FE2[3]\*momed + FE2[4]\*x\*momed  
}

Average value of momed.

fun\_cgm\_momed\_ave <- function(x) {  
 momed=0  
 FE2[1] + FE2[2]\*x + FE2[3]\*momed + FE2[4]\*x\*momed  
}

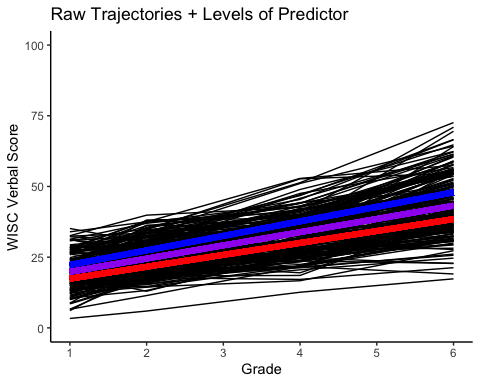
High value of momed.

fun\_cgm\_momed\_high <- function(x) {  
 momed=0+1\*momed\_sd  
 FE2[1] + FE2[2]\*x + FE2[3]\*momed + FE2[4]\*x\*momed  
}

Plot with the prototypical -1SD (red), prototypical 0SD (magenta) and prototypical +1SD (blue) trajectories.

#plotting intraindividual change with overlay  
ggplot(data = verblong, aes(x = grade, y = verb, group = id)) +  
 ggtitle("Raw Trajectories + Levels of Predictor") +  
 # geom\_point() +   
 geom\_line() +  
 xlab("Grade") +   
 ylab("WISC Verbal Score") + ylim(0,100) +  
 scale\_x\_continuous(breaks=seq(1,6,by=1)) +   
 stat\_function(fun=fun\_cgm\_momed\_low, color="red", size = 2) +  
 stat\_function(fun=fun\_cgm\_momed\_ave, color="purple", size = 2) +  
 stat\_function(fun=fun\_cgm\_momed\_high, color="blue", size = 2) +  
 theme\_classic()

## Warning: Multiple drawing groups in `geom\_function()`. Did you use the correct `group`, `colour`, or `fill` aesthetics?  
## Multiple drawing groups in `geom\_function()`. Did you use the correct `group`, `colour`, or `fill` aesthetics?  
## Multiple drawing groups in `geom\_function()`. Did you use the correct `group`, `colour`, or `fill` aesthetics?



## 11.8 Alternative Time Metrics

Let’s go back to the simple *linear growth model*, this time being very explicit about the *scaling and centering* of the time variable. Time metric = original scores, Grade = 1, 2, 4, 6\*\*. Fitting the linear model with grade (as originally coded)

linear\_grade\_fit <- lme(  
 fixed= verb ~ 1 + grade,   
 random= ~ 1 + grade|id,   
 data=verblong,  
 na.action = na.exclude  
)  
  
summary(linear\_grade\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5053.632 5081.844 -2520.816  
##   
## Random effects:  
## Formula: ~1 + grade | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 3.915536 (Intr)  
## grade 1.241299 0.321   
## Residual 3.581590   
##   
## Fixed effects: verb ~ 1 + grade   
## Value Std.Error DF t-value p-value  
## (Intercept) 15.15099 0.3686513 611 41.09844 0  
## grade 4.67339 0.1087023 611 42.99255 0  
## Correlation:   
## (Intr)  
## grade -0.155  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.61615621 -0.54270691 -0.02898115 0.52402090 3.16468334   
##   
## Number of Observations: 816  
## Number of Groups: 204

Creating other time metrics:

where  
- c1 is a centering constant, and  
- c2 is a scaling constant.

**Recentering time metrics**  
time\_cG1 = Grade centered 0-point = grade 1: time\_cG1 = 0, 1, 3, 5 time\_cG6 = Grade centered 0-point = grade 6: time\_cG6 = -5, -4, -2, 0

verblong$time\_cG1 = (verblong$grade - 1)/1  
verblong$time\_cG6 = (verblong$grade - 6)/1

**Rescaling time metric**  
time\_cG6 = Grade centered 0-point = grade 6: time\_cG6rescale = -1.0, -0.8, -0.4, 0.0

verblong$time\_cG6rescale = (verblong$grade - 6)/5

**Remapping time**  
assessment = Number of assessments youth have been exposed to: assessment = 1, 2, 3, 4 Note: the way the mapping is done here only works in this case with no missing data. If have missing data, need to remap in a different way.

#remapping using plyr   
verblong$assessment = mapvalues(verblong$grade,from= c(1,2,4,6),to= c(1,2,3,4))

When ordered …

verblong$counter <- with(verblong, ave(id, id, FUN = seq\_along)) #counts the instances of id, grouped by id

Let’s look at the models with different time-metrics.

Linear Growth Model

A. Time metric = grade

linear\_grade\_fit <- lme(fixed= verb ~ 1 + grade,   
 random= ~ 1 + grade|id,   
 data=verblong,  
 na.action = na.exclude)  
summary(linear\_grade\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5053.632 5081.844 -2520.816  
##   
## Random effects:  
## Formula: ~1 + grade | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 3.915536 (Intr)  
## grade 1.241299 0.321   
## Residual 3.581590   
##   
## Fixed effects: verb ~ 1 + grade   
## Value Std.Error DF t-value p-value  
## (Intercept) 15.15099 0.3686513 611 41.09844 0  
## grade 4.67339 0.1087023 611 42.99255 0  
## Correlation:   
## (Intr)  
## grade -0.155  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.61615621 -0.54270691 -0.02898115 0.52402090 3.16468334   
##   
## Number of Observations: 816  
## Number of Groups: 204

B. Time metric = grade\_cG1

linear\_time\_cG1\_fit <- lme(fixed= verb ~ 1 + time\_cG1,   
 random= ~ 1 + time\_cG1|id,   
 data=verblong,  
 na.action = na.exclude)  
summary(linear\_time\_cG1\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5053.632 5081.844 -2520.816  
##   
## Random effects:  
## Formula: ~1 + time\_cG1 | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 4.470800 (Intr)  
## time\_cG1 1.241299 0.558   
## Residual 3.581590   
##   
## Fixed effects: verb ~ 1 + time\_cG1   
## Value Std.Error DF t-value p-value  
## (Intercept) 19.82438 0.3678085 611 53.89865 0  
## time\_cG1 4.67339 0.1087023 611 42.99256 0  
## Correlation:   
## (Intr)  
## time\_cG1 0.14   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.61615617 -0.54270690 -0.02898114 0.52402093 3.16468320   
##   
## Number of Observations: 816  
## Number of Groups: 204

C. Time metric = grade\_cG6

linear\_time\_cG6\_fit <- lme(fixed= verb ~ 1 + time\_cG6,   
 random= ~ 1 + time\_cG6|id,   
 data=verblong,  
 na.action = na.exclude)  
summary(linear\_time\_cG6\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5053.632 5081.844 -2520.816  
##   
## Random effects:  
## Formula: ~1 + time\_cG6 | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 9.460226 (Intr)  
## time\_cG6 1.241299 0.92   
## Residual 3.581590   
##   
## Fixed effects: verb ~ 1 + time\_cG6   
## Value Std.Error DF t-value p-value  
## (Intercept) 43.19133 0.6976142 611 61.91292 0  
## time\_cG6 4.67339 0.1087023 611 42.99256 0  
## Correlation:   
## (Intr)  
## time\_cG6 0.853   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.61615614 -0.54270686 -0.02898114 0.52402089 3.16468320   
##   
## Number of Observations: 816  
## Number of Groups: 204

D. Time metric = grade\_cG6rescale

linear\_time\_cG6rescale\_fit <- lme(fixed= verb ~ 1 + time\_cG6rescale,   
 random= ~ 1 + time\_cG6rescale|id,   
 data=verblong,  
 na.action = na.exclude)  
summary(linear\_time\_cG6rescale\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5050.413 5078.625 -2519.207  
##   
## Random effects:  
## Formula: ~1 + time\_cG6rescale | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 9.460226 (Intr)  
## time\_cG6rescale 6.206494 0.92   
## Residual 3.581590   
##   
## Fixed effects: verb ~ 1 + time\_cG6rescale   
## Value Std.Error DF t-value p-value  
## (Intercept) 43.19133 0.6976142 611 61.91292 0  
## time\_cG6rescale 23.36695 0.5435115 611 42.99256 0  
## Correlation:   
## (Intr)  
## time\_cG6rescale 0.853   
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.61615617 -0.54270688 -0.02898114 0.52402092 3.16468317   
##   
## Number of Observations: 816  
## Number of Groups: 204

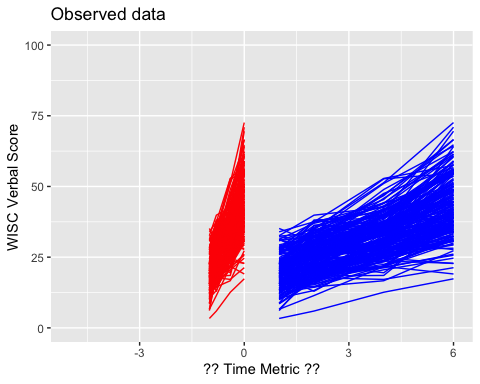
E. Time metric = assessment

linear\_assessment\_fit <- lme(fixed= verb ~ 1 + assessment,   
 random= ~ 1 + assessment|id,   
 data=verblong,  
 na.action = na.exclude)  
summary(linear\_assessment\_fit)

## Linear mixed-effects model fit by REML  
## Data: verblong   
## AIC BIC logLik  
## 5134.792 5163.004 -2561.396  
##   
## Random effects:  
## Formula: ~1 + assessment | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
## StdDev Corr   
## (Intercept) 2.960137 (Intr)  
## assessment 1.892481 0.35   
## Residual 3.997613   
##   
## Fixed effects: verb ~ 1 + assessment   
## Value Std.Error DF t-value p-value  
## (Intercept) 10.417770 0.4005742 611 26.00709 0  
## assessment 7.968696 0.1822741 611 43.71820 0  
## Correlation:   
## (Intr)  
## assessment -0.405  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.41214177 -0.56890699 -0.05446235 0.56436063 3.60513499   
##   
## Number of Observations: 816  
## Number of Groups: 204

Making plots of the raw data

#plotting intraindividual change  
ggplot(data = verblong, aes(x = grade, y = verb, group = id)) +  
 ggtitle("Observed data") +  
# geom\_point() +   
 geom\_line(color="blue") +  
 geom\_line(aes(x = time\_cG6rescale, y = verb, group = id), color="red") +  
 xlab("?? Time Metric ??") +   
 ylab("WISC Verbal Score") +   
 ylim(0,100) + xlim(-5,6)



Always be very careful with interpreting the time metric.

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