R lecture 2023 01 17 (multilevel models)

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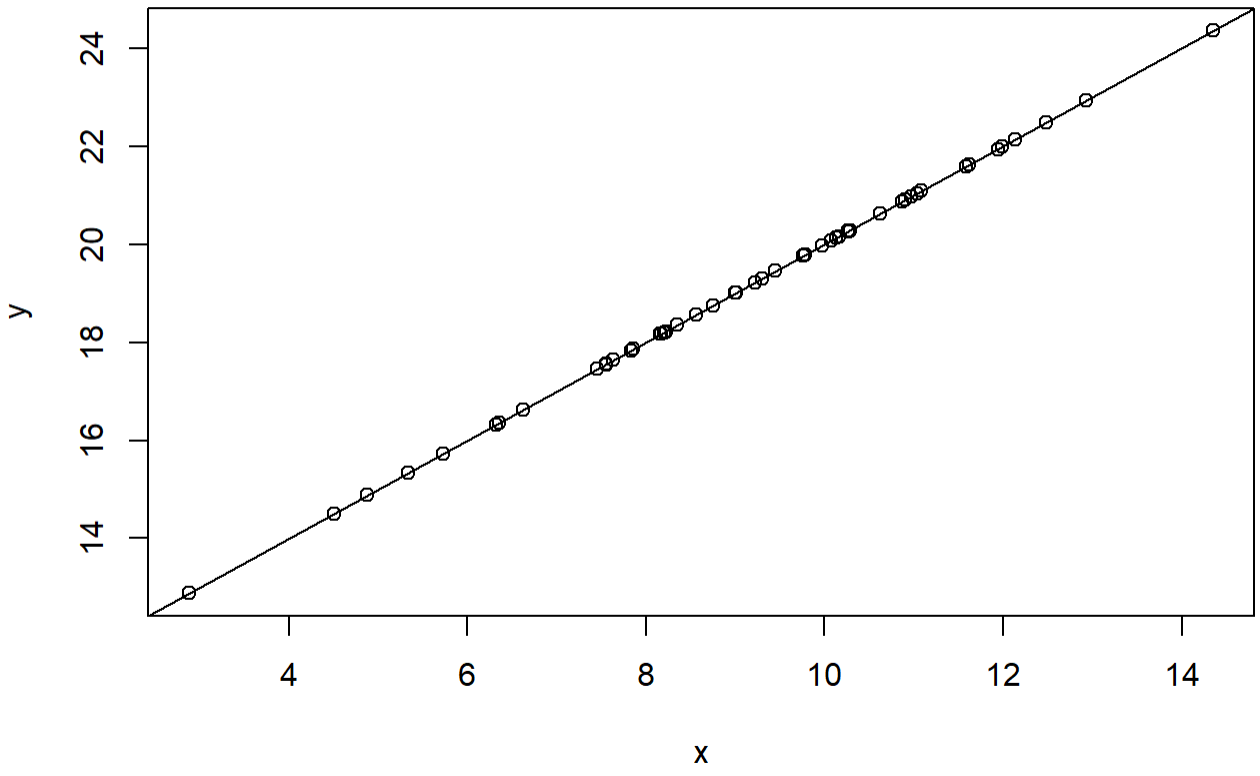
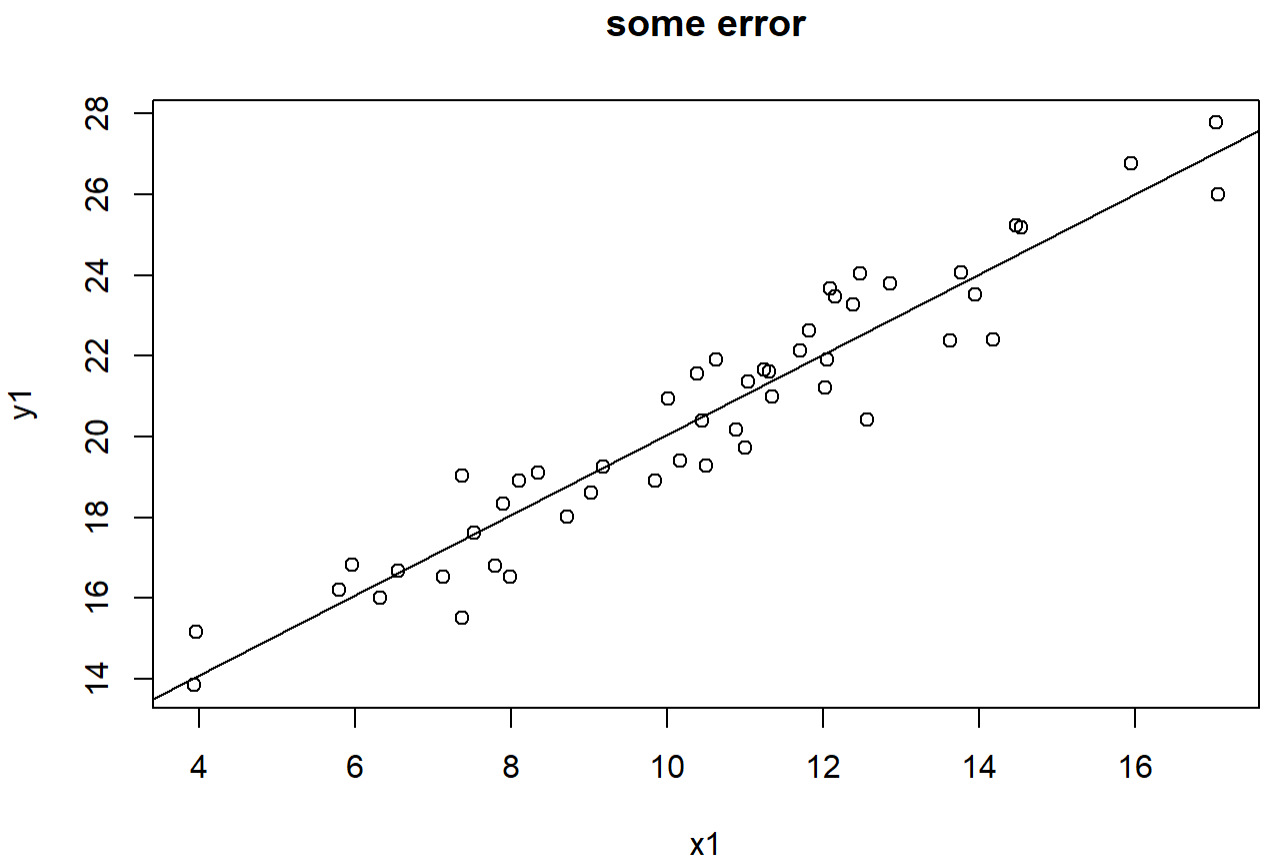
Linear model (perfect prediction)

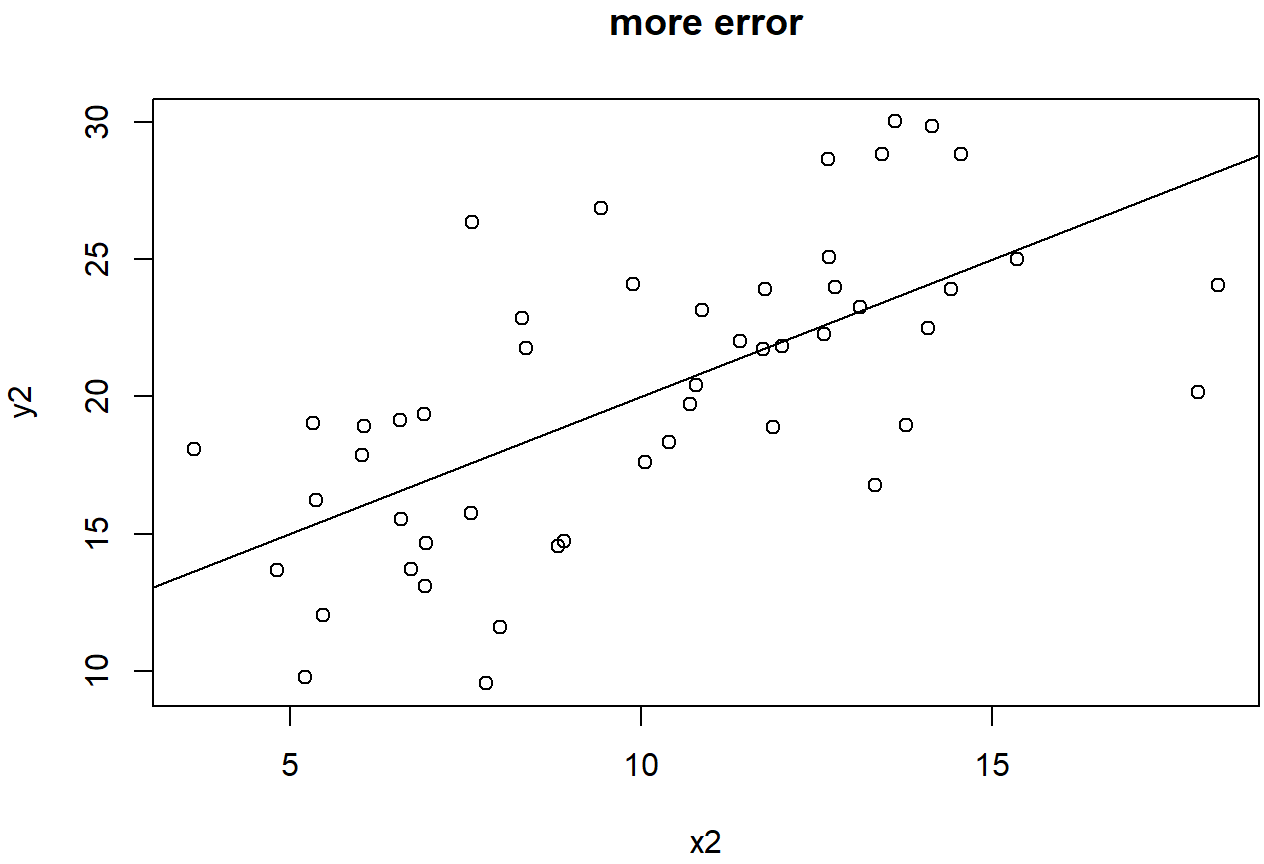
```
x <- rnorm(50, m =10, sd = 3)
a = 10
b = 1
y <- a+b*x
plot(y~x)
abline(coef(lm(y~x)))
```



```
x1 <- rnorm(50, m =10, sd = 3)
a1 = 10
b1 =1
e1 <- rnorm(n=50, m=0, sd=1) #Add an error term
y1 <- a1+b1*x1 +e1
data1 <- data.frame(x1,y1)
plot(y1~x1)
abline(coef(lm(y1~x1)))
title("some error")
```




```
x2 <- rnorm(50, m =10, sd = 3)
a2 = 10
b2 =1
e2 <- rnorm(n=50, m=0, sd=4)
y2 <- a2+b2*x2 +e2
data2 <- data.frame(x2,y2)
data2$group = "large.residuals"
plot(y2~x2)
abline(coef(lm(y~x)))
title("more error")
```




```
ldt <- read.csv("/Users/Adan Tallman/Desktop/levshina.ldt.csv", header=TRUE)

head(ldt)
```

	X <chr>	Length <int>	Freq <int>	Mean_RT <dbl>
1	marveled	8	131	819.19
2	persuaders	10	82	977.63
3	midmost	7	0	908.22
4	crutch	6	592	766.30
5	resuspension	12	2	1125.42
6	efflorescent	12	9	948.33

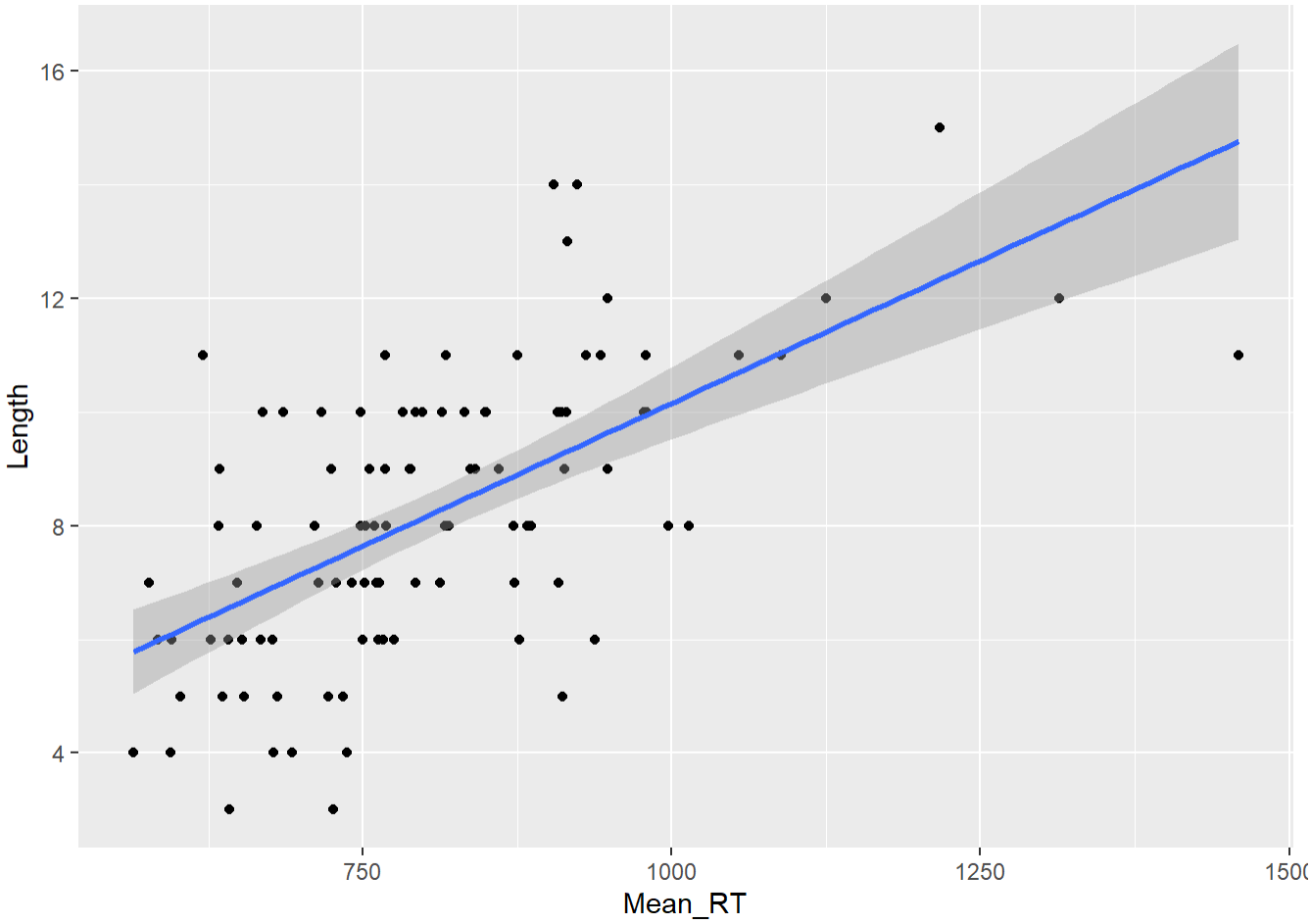
6 rows

```
library(tidyverse)
```

```
## ── Attaching packages ─────────────────────────────────────── tidyverse 1.3.2 ──
## ✓ ggplot2 3.4.0      ✓ purrr   1.0.1
## ✓ tibble  3.1.8      ✓ dplyr   1.0.10
## ✓ tidyr   1.2.1      ✓ stringr 1.5.0
## ✓ readr   2.1.3      ✓ forcats 0.5.2
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
```

```
ggplot(ldt, aes(Mean_RT, Length))+
  geom_point()+
  geom_smooth(method="lm")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



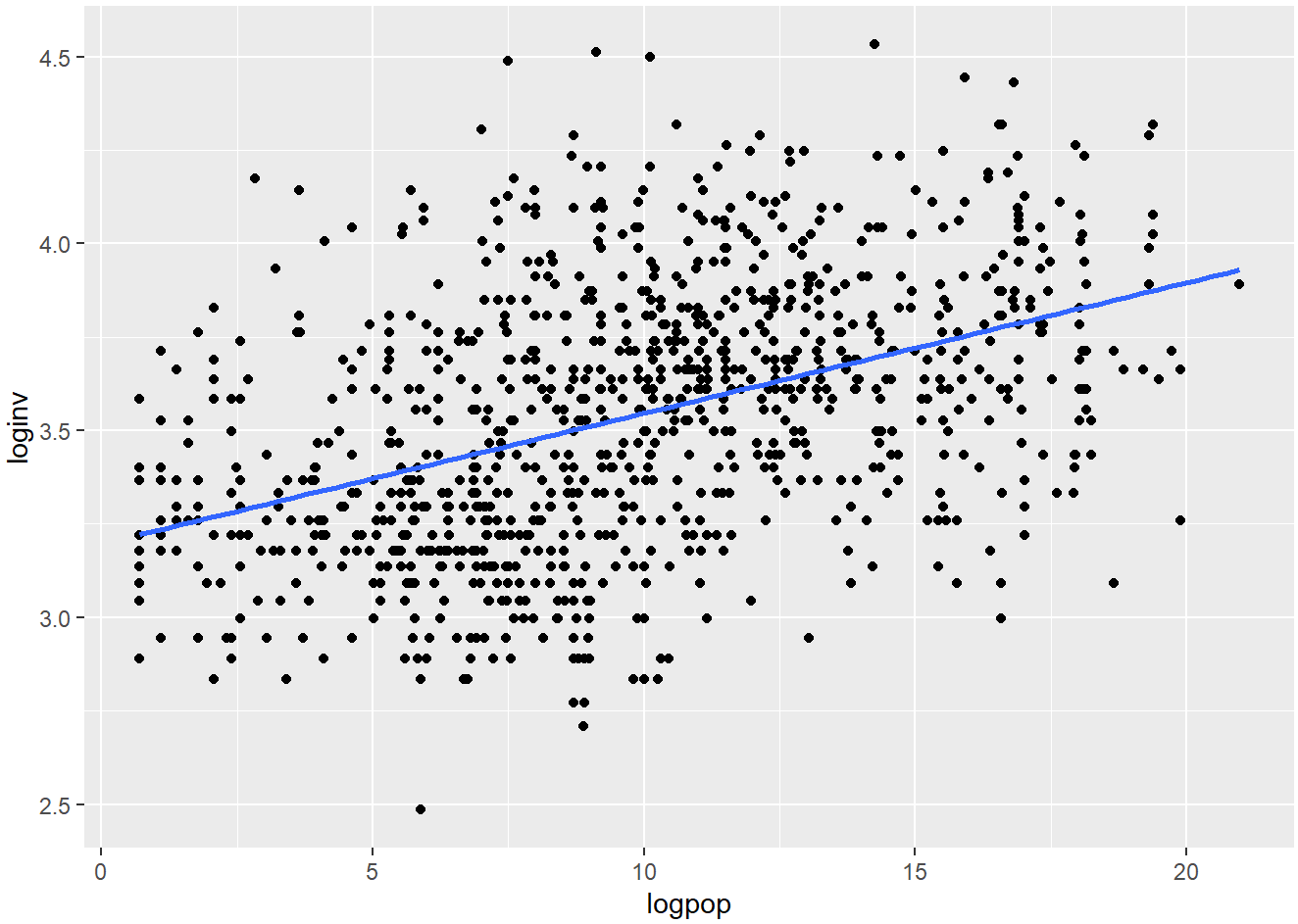
Phoneme inventory

```
df <- read.csv("/Users/Adan Tallman/Desktop/inventories.clean.csv", header=TRUE)
```

It looks like there is a positive correlation between log population and log phoneme inventory. As the population of speakers increases the number of phonemes of their respective language increases.

```
plot.pooleddata <- ggplot(df, aes(x=logpop, y=loginv))+
  geom_point()+
  geom_smooth(method="lm",se=FALSE)
plot.pooleddata
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Let's create a model with log population versus log phoneme inventory.

```
model.ols1<-lm(loginv~logpop, data=df) # ols = ordinary least squares regression
summary(model.ols1)
```

```
##
## Call:
## lm(formula = loginv ~ logpop, data = df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.91777 -0.21683 -0.00495  0.21412  1.02983
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.197035   0.024627  129.82   <2e-16 ***
## logpop      0.034921   0.002296   15.21   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3159 on 1001 degrees of freedom
## Multiple R-squared:  0.1877, Adjusted R-squared:  0.1869
## F-statistic: 231.3 on 1 and 1001 DF,  p-value: < 2.2e-16
```

Subsetting by language

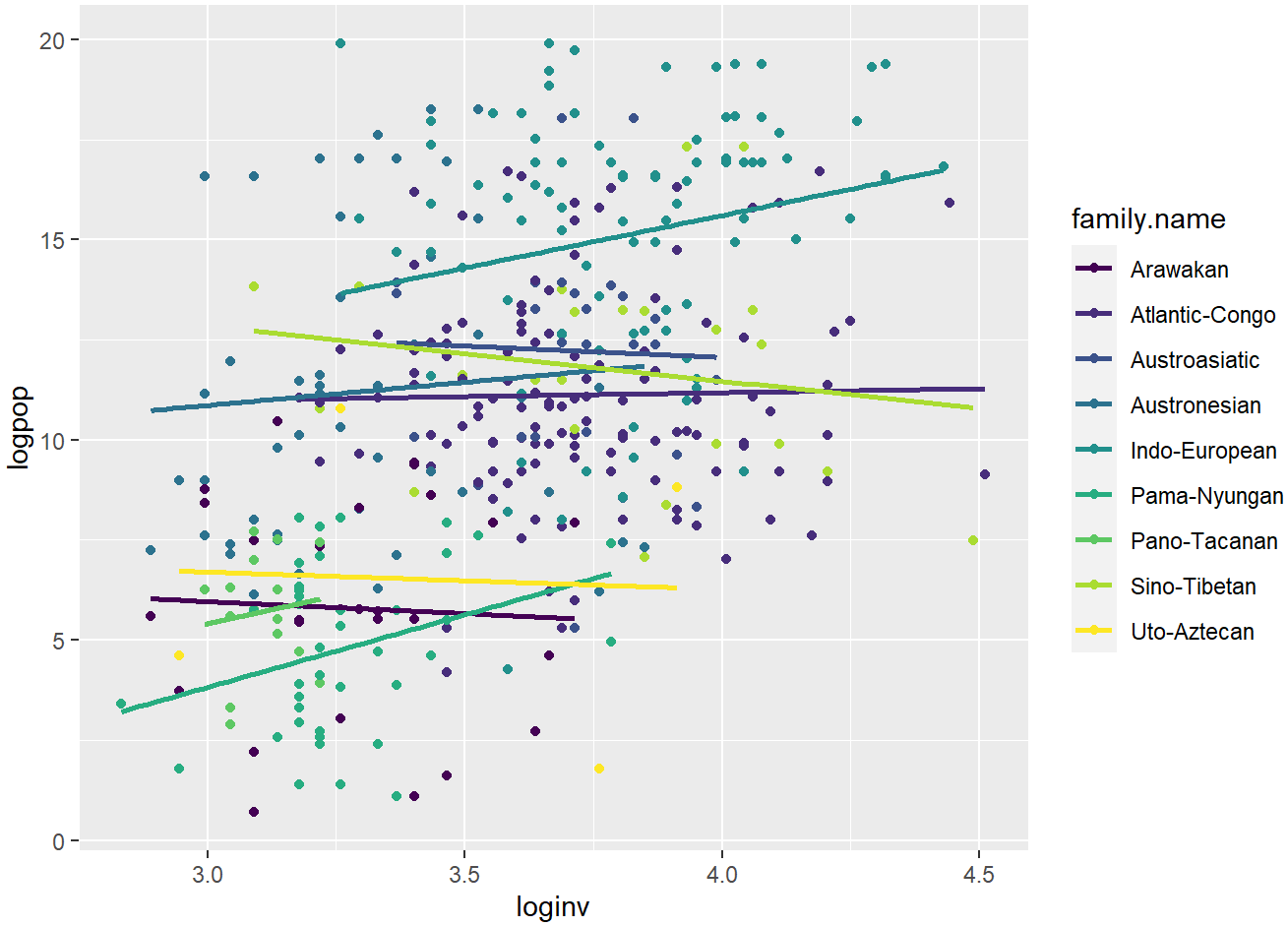
```
df.lgsubset <- subset(df, family.name == "Indo-European"|
                family.name =="Uto-Aztecan"|
                family.name == "Atlantic-Congo"|
                family.name == "Sino-Tibetan"|
                family.name == "Otomanguean"|
                family.name == "Austronesian"|
                family.name == "Pama-Nyungan"|
                family.name == "Austroasiatic"|
                family.name =="Arawakan"|
                family.name == "Pano-Tacanan")
```

```
library(viridis)
```

```
## Loading required package: viridisLite
```

```
library(tidyverse)
df.lgsubset %>%
  ggplot(aes(x=loginv,
             y=logpop,
             color=family.name))+
  geom_point()+
  geom_smooth(method="lm",se = FALSE)+
  scale_colour_viridis_d()
```

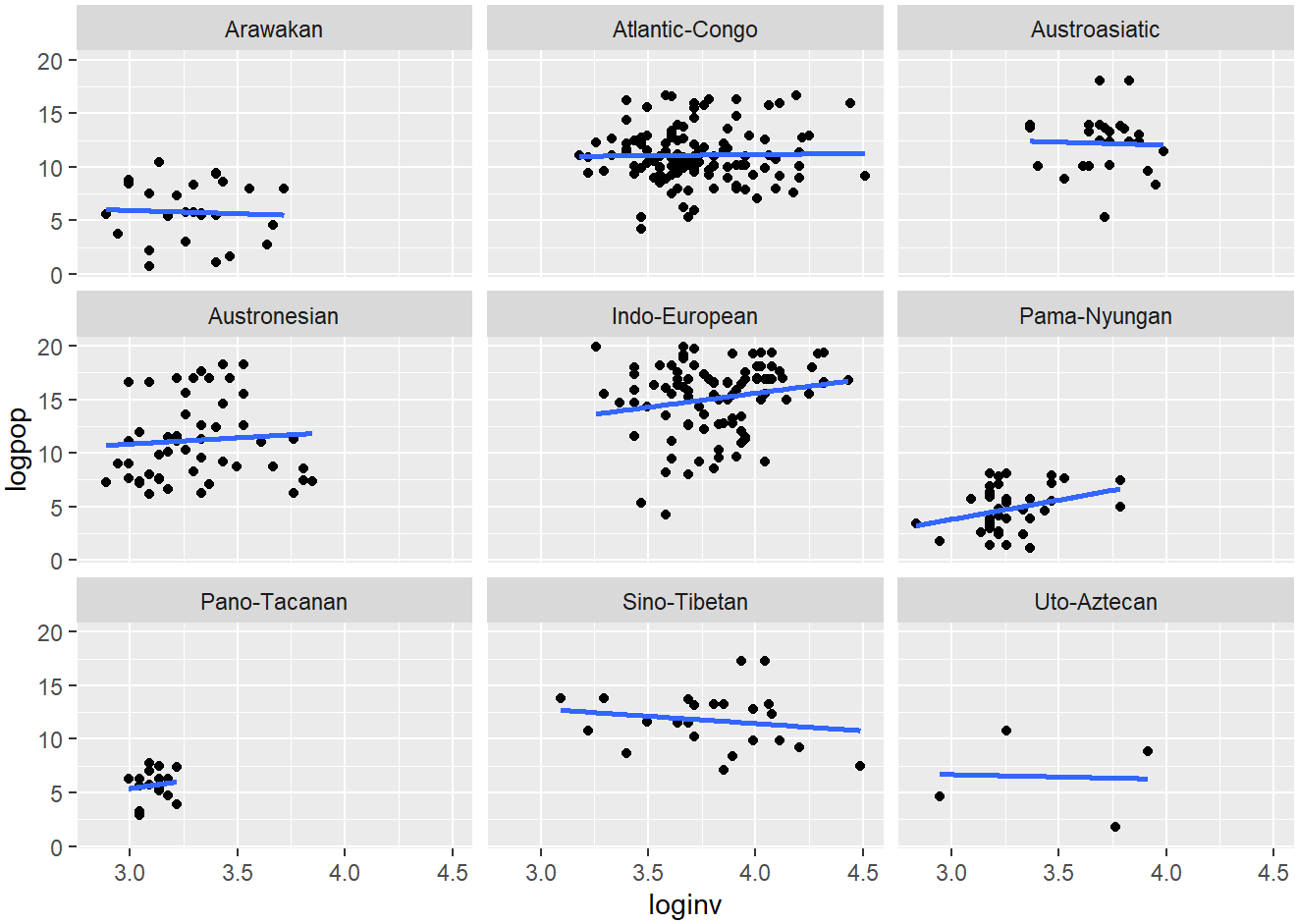
```
## `geom_smooth()` using formula = 'y ~ x'
```



Another way we can see the variation in groups is by looking at regression models for each group.

```
plot <- ggplot(df.lgsubset, aes(x=loginv, y=logpop, group=family.name))+
  geom_point()+
  geom_smooth(method="glm",se = FALSE)
plot +  facet_wrap(~ family.name, ncol=3)
```

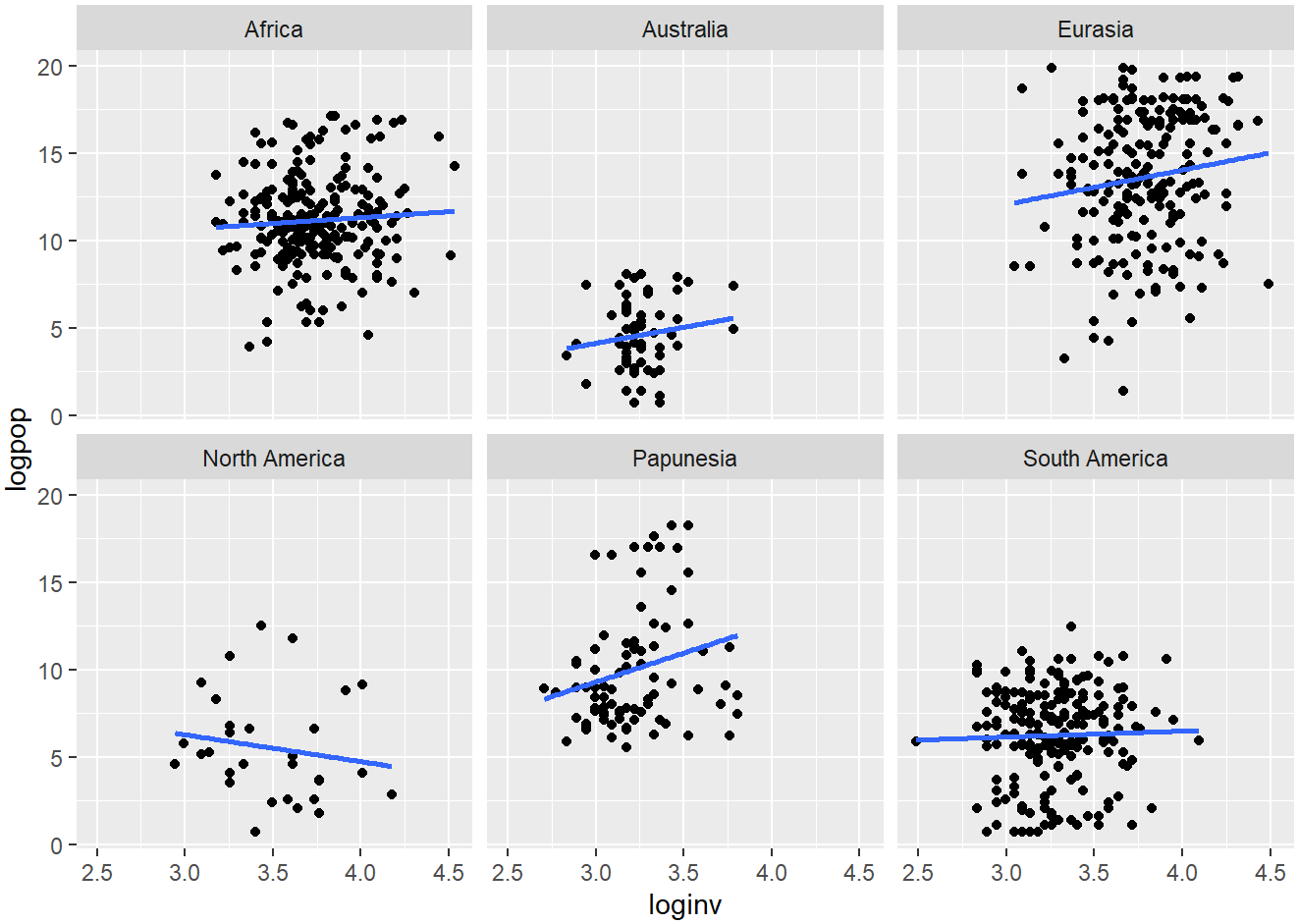
```
## `geom_smooth()` using formula = 'y ~ x'
```



We can also look at differences between areas.

```
df.areasubset <- subset(df, area !="")
plot <- ggplot(df.areasubset, aes(x=loginv, y=logpop, group=area))+
  geom_point()+
  geom_smooth(method="glm",se = FALSE)
plot +  facet_wrap(~ area, ncol=3)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```




```
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'Matrix'
```

```
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```
library(lmerTest)
```

```
##
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':
##
##     lmer
```

```
## The following object is masked from 'package:stats':
##
##     step
```

Multilevel model

One disadvantage of multilevel models is that their complexity makes them hard to interpret.

Its typical to AICs in order to assess multilevel models. These are multilevel models without the predictor variable.

```
mod.lmer.null1 <- lmer(loginv~(1|family.name)+ (1|area), data=df)
mod.lmer.null2 <- lmer(loginv~(1|family.name), data=df)
mod.lmer.null3 <- lmer(loginv~(1|area), data=df)
```

```
anova(mod.lmer.null1,
      mod.lmer.null2,
      mod.lmer.null3)
```

```
## refitting model(s) with ML (instead of REML)
```

	npar <dbl>	AIC <dbl>	BIC <dbl>	logLik <dbl>	deviance <dbl>	Chisq <dbl>	Df <dbl>
mod.lmer.null2	3	156.37384	170.45381	-75.18692	150.37384	*NA*	*NA*
mod.lmer.null3	3	103.49223	117.57220	-48.74612	97.49223	52.88161	0
mod.lmer.null1	4	69.45305	88.22634	-30.72652	61.45305	36.03918	1

3 rows | 1-8 of 9 columns

The first null model is the best because it has the lowest AIC and lowest BIC.

```
mod.lmer.a <- lmer(loginv~logpop+(1|family.name)+(1|area), data=df) #This is the code for a v
arying intercept model


mod.lmer.ab <- lmer(loginv~logpop+(1+logpop|family.name) +(1+logpop|area),data=df) #This is t
he code for a varying intercept and slope model
```

```
## boundary (singular) fit: see help('isSingular')
```

```
summary(mod.lmer.a)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: loginv ~ logpop + (1 | family.name) + (1 | area)
##    Data: df
##
## REML criterion at convergence: 68.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.7071 -0.5947 -0.0535  0.5778  3.4460
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  family.name (Intercept) 0.01817  0.1348
##  area        (Intercept) 0.05347  0.2312
##  Residual                0.05517  0.2349
## Number of obs: 807, groups:  family.name, 104; area, 7
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept) 3.416e+00  9.657e-02 6.766e+00  35.374 6.24e-09 ***
## logpop      6.982e-03  2.986e-03 8.049e+02   2.338   0.0196 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##        (Intr)
## logpop -0.266
```

```
summary(mod.lmer.ab)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: loginv ~ logpop + (1 + logpop | family.name) + (1 + logpop |
##     area)
##    Data: df
##
## REML criterion at convergence: 68.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.7073 -0.5931 -0.0541  0.5811  3.4422
##
## Random effects:
##  Groups      Name        Variance  Std.Dev.  Corr
##  family.name (Intercept) 1.763e-02 0.1327610
##              logpop      9.306e-08 0.0003051 1.00
##  area        (Intercept) 5.621e-02 0.2370947
##              logpop      4.654e-07 0.0006822 -1.00
##  Residual                5.514e-02 0.2348128
## Number of obs: 807, groups:  family.name, 104; area, 7
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept) 3.416e+00  9.874e-02 5.815e+00  34.594 5.88e-08 ***
## logpop      7.132e-03  2.994e-03 2.335e+02   2.382    0.018 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##        (Intr)
## logpop -0.342
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

So the correlation is still weakly statistically significant.

```
anova(mod.lmer.null1, mod.lmer.a, mod.lmer.ab)
```

```
## refitting model(s) with ML (instead of REML)
```

	n… <dbl>	AIC <dbl>	BIC <dbl>	logLik <dbl>	deviance <dbl>	Chisq <dbl>	Df <dbl>	Pr(>Chisq) <dbl>
mod.lmer.null1	4	69.45305	88.22634	-30.72652	61.45305	*NA*	*NA*	*NA*
mod.lmer.a	5	65.92716	89.39378	-27.96358	55.92716	5.52589028	1	0.01873707
mod.lmer.ab	9	73.87447	116.11438	-27.93723	55.87447	0.05269001	4	0.99965901

3 rows

According to the BIC the null model accounts for the variation better than the models with the predictor variables.

Coefficients from a multilevel model

There isn't just a single coefficient for a multilevel model

```
beta1 <- coef(mod.lmer.ab)$family.name
colnames(beta1) <- c("Intercept", "Slope")

beta2 <- coef(mod.lmer.ab)$area
colnames(beta2) <- c("Intercept", "Slope")
```

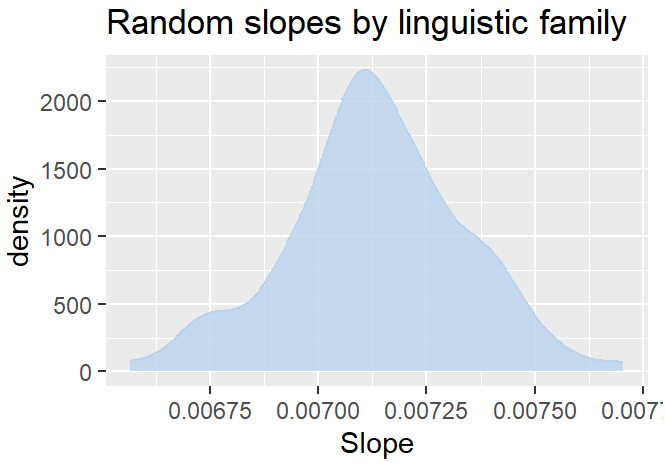
If we plot the coefficients we can see that they follow a normal distribution.

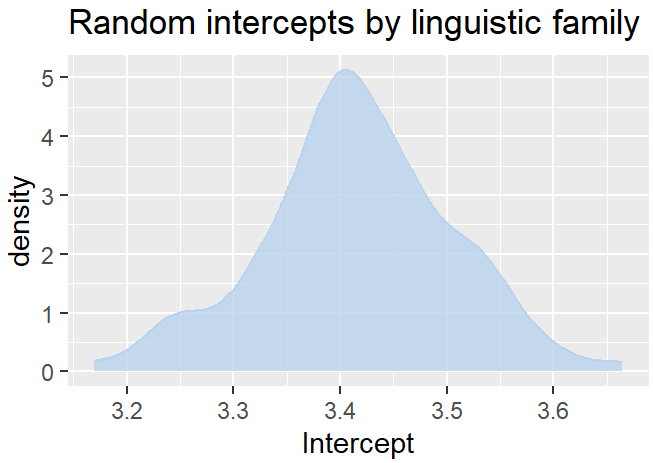
```
library(gridExtra)
```

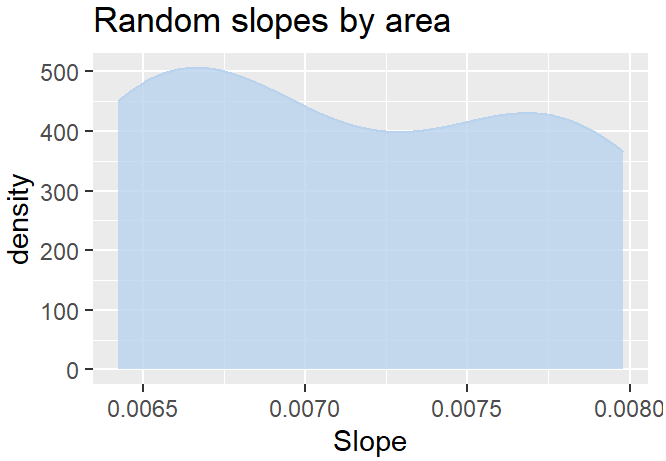
```
##
## Attaching package: 'gridExtra'
```

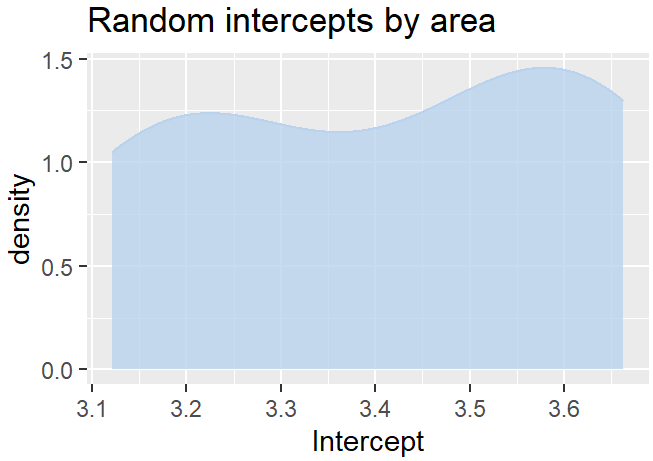
```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
p1 <- ggplot(beta1, aes(Slope))+
  geom_density(fill="slategray2", color="slategray2", alpha=0.8)+
  ggtitle("Random slopes by linguistic family")


p2 <- ggplot(beta1, aes(Intercept))+
  geom_density(fill="slategray2", color="slategray2", alpha=0.8)+
  ggtitle("Random intercepts by linguistic family")

p3 <- ggplot(beta2, aes(Slope))+
  geom_density(fill="slategray2", color="slategray2", alpha=0.8)+
  ggtitle("Random slopes by area")

p4 <- ggplot(beta2, aes(Intercept))+
  geom_density(fill="slategray2", color="slategray2", alpha=0.8)+
  ggtitle("Random intercepts by area")

grid.arrange(p1, p2, p3, p4, ncol=2)
```


Random slopes by linguistic family
density
2000
1500
1000
500
0
0.00675
0.00700
0.00725
0.00750
Slope


Random intercepts by linguistic family
density
5
4
3
2
1
0
3.2
3.3
3.4
3.5
3.6
Intercept


Random slopes by area
density
500
400
300
200
100
0
0.0065
0.0070
0.0075
0.0080
Slope


Random intercepts by area
density
1.5
1.0
0.5
0.0
3.1
3.2
3.3
3.4
3.5
3.6
Intercept