

Linear models 3

Models behaving badly

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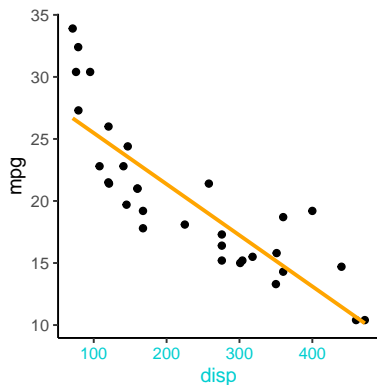
October 23, 2020

Motivation

- ① Are my model results reliable?
 - Residual checks
 - Transformations
 - Collinearity
- ② How do I tell if terms are important or not?
 - Drop-1 ANOVA
 - Wald t-tests
 - How much stuff should I put into my model?

Are my model results reliable?

Assumptions of linear regression



There are 3 main assumptions to this model:

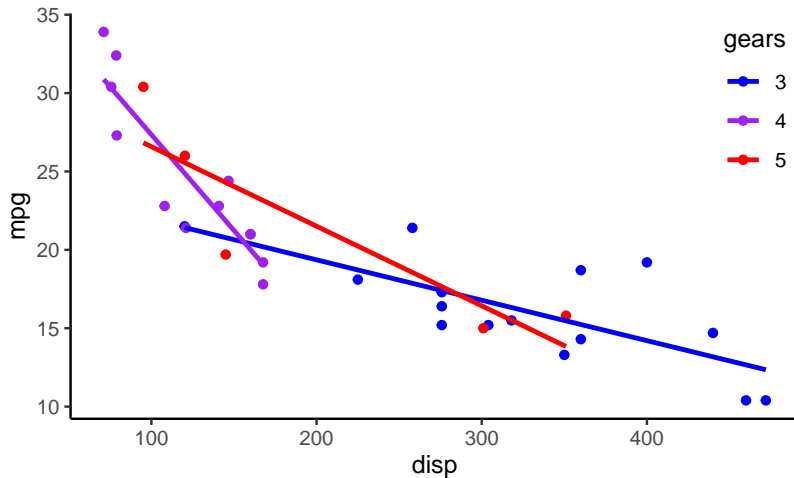
- 1 The relationship between *disp* and *mpg* is linear
- 2 *mpg* (the data) is Normally distributed around *m^{hat}pg* (the line)
- 3 σ is the same everywhere

This is pretty easy to see if you only have 1 variable, but...

$$\hat{mpg} = b_0 + b_1 disp$$

$$mpg \sim Normal(\hat{mpg}, \sigma)$$

What if I have many variables?

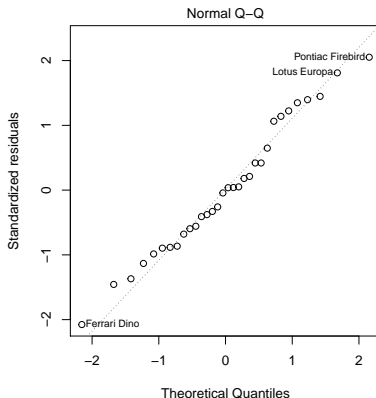
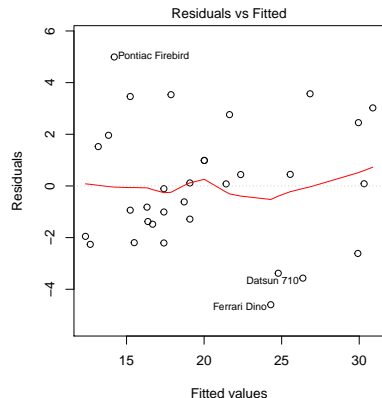


Difficult to see if the assumptions are met

Solution: residual checks

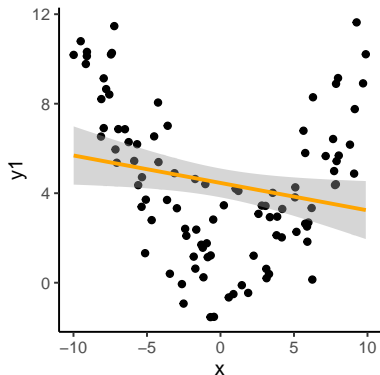
Some common ways of checking the assumptions: **residual plots**

```
mod1 <- lm(mpg~disp*factor(gear),data=mtcars)
par(mfrow=c(1,2),mar=c(3,3,1,1)+1)
plot(mod1, which=c(1,2))
```



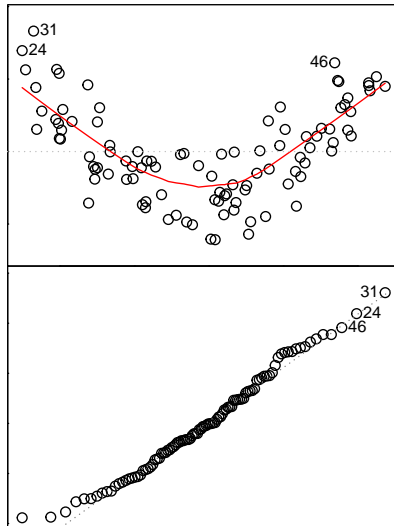
- 1 Points in Plot 1 should show *no pattern* (shotgun blast)
- 2 Points in Plot 2 should be *roughly* on top of the 1:1 line

Problem 1: Non-linear relationship

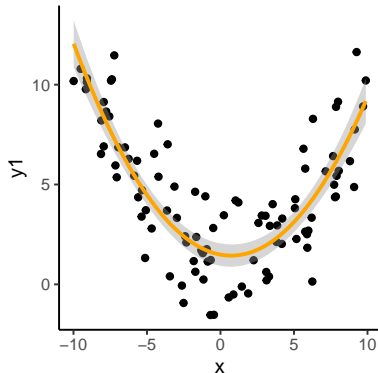


```
lm(y1~x,data=d1)
```

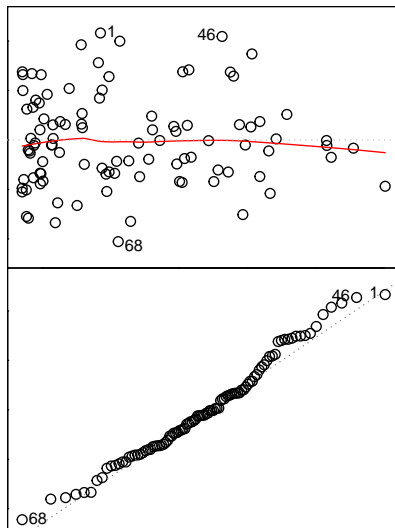
y_1 clearly follows a
hump-shaped relationship



Solution: transform predictors

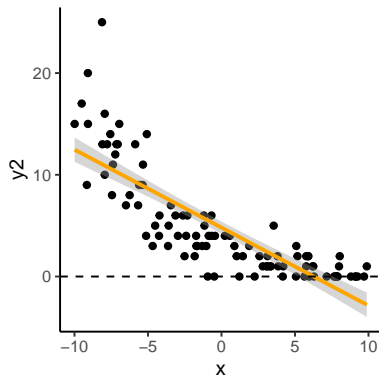


```
lm(y1~poly(x,2),data=d1)
```



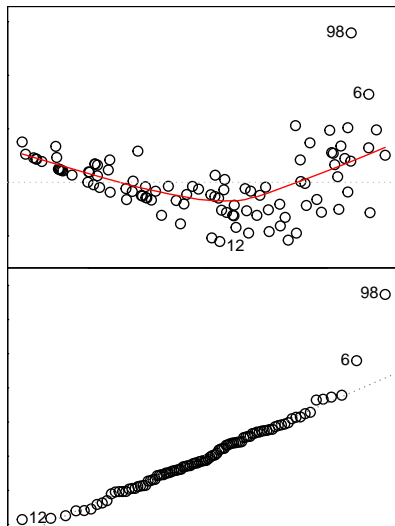
Warning: Polynomials can do weird things, especially at the edges of the distribution. Consider whether this is biologically reasonable!

Problem 2a: Non-normal response

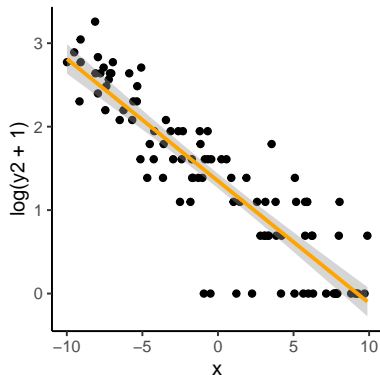


```
lm(y2~x,data=d1)
```

y_2 is count data (integers ≥ 0).
Very common in ecological data.

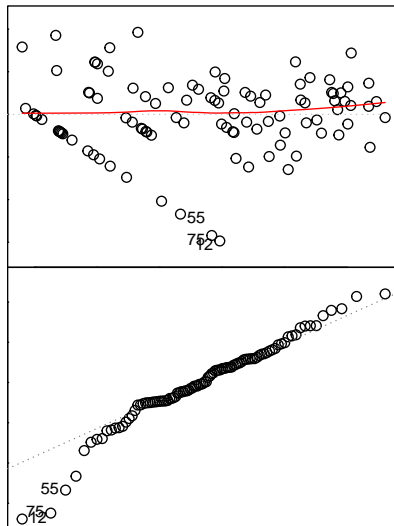


Solution: transform data to meet assumptions

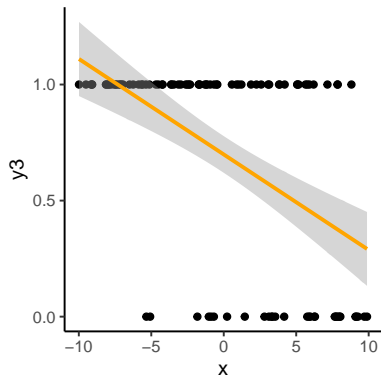


```
lm(log(y2+1)~x,data=d1)
```

Square-root transformations are also common

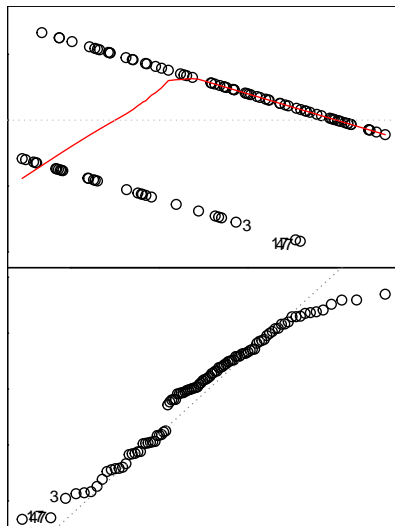


Problem 2b: Non-normal response

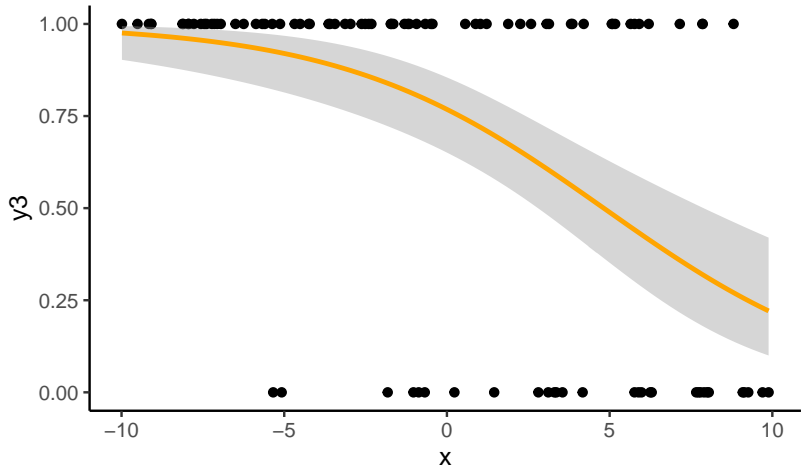


```
lm(y3~x,data=d1)
```

y_3 is binomial data
(success/failure, 0 or 1). Very
common in ecological data.

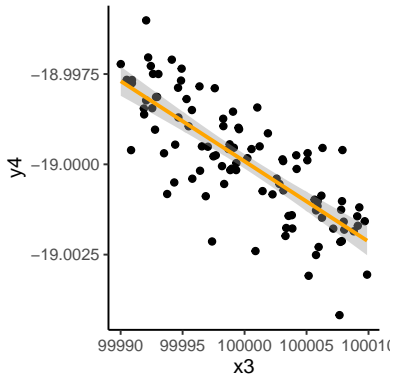


Solution: use a Generalized Linear Model (GLM)



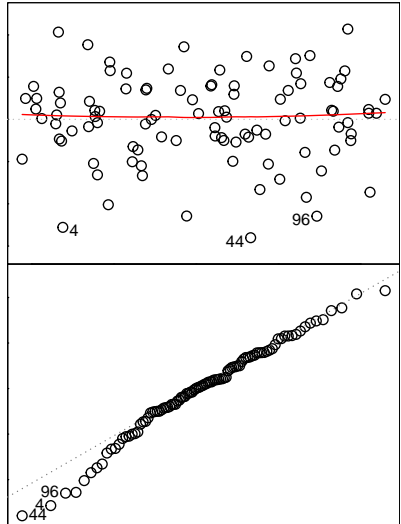
This is a topic for another lecture. Hold tight!

Problem: variables are on different scales

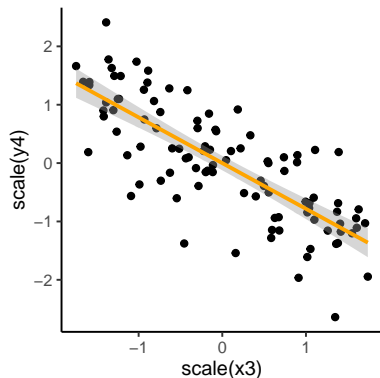


```
lm(y4~x3,data=d1)
```

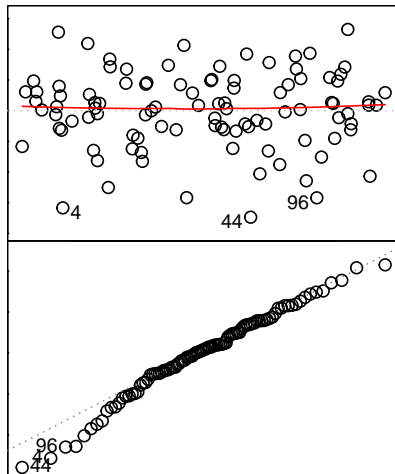
- y_4 is tiny, while x_3 is huge
- This is fine for now, but can cause problems when fitting more complicated models



Solution: scale data/predictors before fitting



```
#Subtracts mean, divides by SD  
d1$s.y4 <- scale(y4)  
d1$s.x3 <- scale(x3)  
lm(s.y4~s.x3,data=d1) #Refit
```



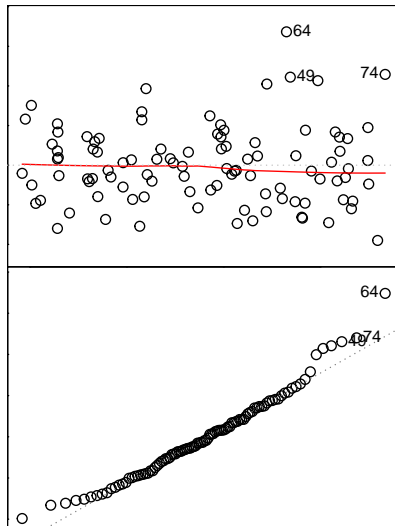
- Residuals are the same as before
- Coefficients are now related to *scaled* data and predictor

But wait... there's more (assumptions)!

- Additional assumption for models with many predictors:
- ④ If you have 2+ predictors in your model, the predictors are not related to each other
- Say we have 2 predictors, x and x_2 :

```
lm(y0~x+x2,data=d1)
```

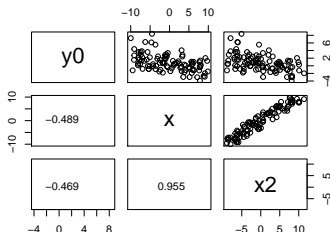
- Model fits, and residuals look OK, but there's trouble ahead!



Here comes trouble!

```
#Function to print correlation (r) value
corText <- function(x,y){
  text(0.5,0.5,round(cor(x,y),3))
}

#Pairplot of y0, x, and x2
pairs(d1[,c('y0','x','x2')],lower.panel=corText)
```



- x and x2 mean basically the same thing!
- Also revealed using variance-inflation factors (VIFs):

```
library(car)
```

```
#VIF scores:
```

```
# 1 = no problem
```

```
# 1-5 = some problems
```

```
# 5+ = big problems!
```

```
vif(m2)
```

```
##           x           x2
```

```
## 11.31812 11.31812
```


Is this problem really that bad?

#Correct model

```
m1 <- lm(y0~x,data=d1)
```

	Estimate	Std. Error	Pr(> t)
(Intercept)	0.7851936	0.1943002	0.0001059
x	-0.1900346	0.0342596	0.0000002

#Incorrect model

```
m2 <- lm(y0~x+x2,data=d1)
```

	Estimate	Std. Error	Pr(> t)
(Intercept)	0.7860300	0.1955770	0.0001155
x	-0.1812556	0.1158464	0.1209288
x2	-0.0094931	0.1196074	0.9369028

- Increases SE of each term, so model may “miss” important terms
- Gets worse with increasing correlation, or if many terms are correlated!

How do we fix this? Depends on your goals:

- ① I care about predicting things
 - Use dimensional reduction (e.g. PCA) and re-run model
- ② I care about what's causing things
 - Design experiment to separate cause and effect
 - Think about what is causing what. *Graphical models* are helpful for this

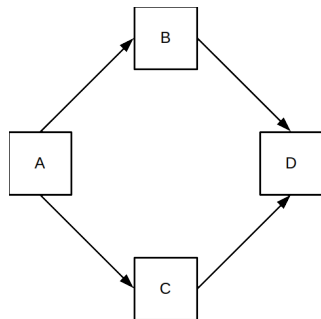


Figure 1: A simple graphical model

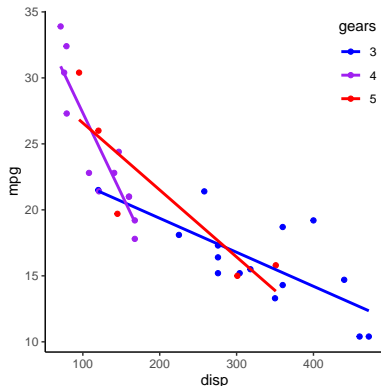
How do I tell if terms are important or not?

The mpg model, once again:

```
m2 <- lm(mpg~disp*factor(gear)  
         data=mtcars)
```

	Estimate	Std. Error	Pr(> t)
(Intercept)	24.5156	2.4624	0.0000
disp	-0.0258	0.0073	0.0015
factor(gear)4	15.0520	3.5580	0.0003
factor(gear)5	7.1454	3.5359	0.0537
disp:factor(gear)4	-0.0964	0.0213	0.0001
disp:factor(gear)5	-0.0250	0.0133	0.0717

- This tells us about individual coefficients (slopes and intercepts), but...
- What if we're interested in entire factors?



- e.g. “Is *gears* important as a group for predicting *mpg*?”

Relative strength of terms:

How do I check if the things that I put in my model are useful for predicting the thing that I'm interested in?

① drop-1 (Type III) ANOVA for *entire factors*

- e.g. “Does adding *gear* matter for predicting *mpg*?”
- Tests for changes in sum of squares with factor

② Wald t-scores for *levels of factors*

- e.g. “Is the coefficient for *gear3* different from *gear4*?”
- Tests whether a coefficient = 0, given the estimated value (mean) and the variability (SE) of the coefficient

p-values are only meaningful if the model assumptions are valid!

drop-1 ANOVA

```
#mpg depends on gears
mod1 <- lm(mpg ~ factor(gear), data = mtcars)
drop1(mod1,test='F') #Effect of gears is very strong
```

```
## Single term deletions
##
## Model:
## mpg ~ factor(gear)
##           Df Sum of Sq    RSS    AIC F value    Pr(>F)
## <none>                642.8 102.00
## factor(gear)  2      483.24 1126.0 115.94   10.901 0.0002948 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#mpg depends on disp
mod2 <- lm(mpg ~ disp, data = mtcars)
drop1(mod2,test='F') #Effect of disp is also very strong
```

```
## Single term deletions
##
## Model:
## mpg ~ disp
##           Df Sum of Sq    RSS    AIC F value    Pr(>F)
## <none>                317.16  77.397
## disp      1      808.89 1126.05 115.943  76.513 9.38e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

drop-1 ANOVA

```
#mpg depends on disp and gear
mod3 <- lm(mpg ~ disp + factor(gear), data = mtcars)
drop1(mod3,test='F') #Effect of disp is very strong, and erases the effect of gear
```

```
## Single term deletions
##
## Model:
## mpg ~ disp + factor(gear)
##
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			317.01	81.383		
disp	1	325.79	642.80	102.003	28.7755	1.025e-05 ***
factor(gear)	2	0.15	317.16	77.397	0.0065	0.9935

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#mpg depends on disp interacted with gear
mod4 <- lm(mpg ~ disp*factor(gear), data = mtcars)
drop1(mod4,test='F') #Interaction effect is strong. Why are disp and gear not shown?
```

```
## Single term deletions
##
## Model:
## mpg ~ disp * factor(gear)
##
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			172.87	65.978		
disp:factor(gear)	2	144.14	317.01	81.383	10.839	0.0003771 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Wald t-scores

- Wald t-scores are shown in model summary
- $t\text{-score} = \text{mean} \div \text{SD}$
- p-value comes from Student's t-distribution (similar to Normal, but has longer tails depending on sample size)

```
summary(mod1)
```

```
##
## Call:
## lm(formula = mpg ~ factor(gear), data = mtcars)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.7333 -3.2333 -0.9067  2.8483  9.3667
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    16.107      1.216   13.250 7.87e-14 ***
## factor(gear)4     8.427      1.823    4.621 7.26e-05 ***
## factor(gear)5     5.273      2.431    2.169  0.0384 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.708 on 29 degrees of freedom
## Multiple R-squared:  0.4292, Adjusted R-squared:  0.3898
## F-statistic: 10.9 on 2 and 29 DF, p-value: 0.0002948
```


Comparing between intercepts

- If you've found that *gear* is important, are the levels different from each other?
- If number of levels = 3+, then you need to account for *multiple comparisons*
- One common method: Bonferroni correction

```
library(multcomp) #Loads the multcomp package (needs to be installed first)
mod1Comp <- glht(mod1, linfct = mcp('factor(gear)'='Tukey')) #Fits multcomp object using gear
summary(mod1Comp, test=adjusted('bonferroni')) #gear4 different from gear3 only
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = mpg ~ factor(gear), data = mtcars)
##
## Linear Hypotheses:
##      Estimate Std. Error t value Pr(>|t|)
## 4 - 3 == 0      8.427      1.823   4.621 0.000218 ***
## 5 - 3 == 0      5.273      2.431   2.169 0.115267
## 5 - 4 == 0     -3.153      2.506  -1.258 0.654971
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- bonferroni method)
```