

431 Class 12

thomaseLove.github.io/431

2021-09-30

Today's Agenda

- ➊ Using data from NHANES
- ➋ A complex data management challenge
- ➌ Using dbp to predict sbp again
- ➍ Considering a transformation of our outcome

Today's Packages

```
library(NHANES) # for access to NHANES data  
library(ggpubr) # to add equation to scatterplot easily  
library(equatiomatic)  
library(glue)  
library(janitor)  
library(knitr)  
library(broom)  
library(magrittr)  
library(patchwork)  
library(tidyverse)  
  
theme_set(theme_bw())
```

Ingesting and Managing Today's Data

Today's Data

The NHANES data file located in the NHANES package is our source.

NHANES stands for National Health and Nutrition Examination surveys. The NHANES target population is “the non-institutionalized civilian resident population of the United States”. Since 1999, approximately 5,000 individuals of all ages are interviewed in their homes every year and complete the health examination component, in a mobile examination centre.

NHANES and NHANESraw each include 75 variables for the 2009-2010 and 2011-2012 sample years, with complex sampling weights included in NHANESraw. NHANES contains 10,000 rows of data resampled from NHANESraw to undo oversampling effects. NHANES can be treated, for educational purposes, as if it were a simple random sample from the American population.

- For today, we'll do the one thing you should never do with NHANES data, which is to ignore the sampling weights.

Today's Data Ingest and Management

- We'll walk through these steps in the next few slides.

```
set.seed(20210930)
nh12 <- NHANES %>%
  filter(SurveyYr == "2011_12") %>%
  select(ID, BPSysAve, BPDiaAve, Age, Smoke100,
         Race1, HealthGen, SurveyYr) %>%
  rename(Subject = ID, SBP = BPSysAve, DBP = BPDiaAve,
         SROH = HealthGen) %>%
  clean_names() %>%
  mutate(across(where(is.character), as_factor)) %>%
  mutate(subject = as.character(subject)) %>%
  filter(age > 20 & age < 80) %>%
  filter(dbp > 39) %>%
  distinct() %>%
  slice_sample(n = 700) %>%
  droplevels()
```

Today's Data Management: Step 1

- Select the eight variables of interest from NHANES.

```
temp1 <- NHANES %>%  
  select(ID, SurveyYr, BPSysAve, BPDiaAve, Age, Smoke100,  
         Race1, HealthGen)  
#   filter(SurveyYr == "2011_12") %>%  
#   rename(Subject = ID, SBP = BPSysAve, DBP = BPDiaAve,  
#         SROH = HealthGen) %>%  
#   clean_names() %>%  
#   mutate(across(where(is.character), as_factor)) %>%  
#   mutate(subject = as.character(subject)) %>%  
#   filter(age > 20 & age < 80) %>%  
#   filter(dbp > 39) %>%  
#   distinct() %>%  
#   slice_sample(n = 700) %>%  
#   droplevels()
```

temp1 is a tibble.

```
temp1
```

```
# A tibble: 10,000 x 8
```

	ID	SurveyYr	BPSysAve	BPDiaAve	Age	Smoke100
	<int>	<fct>	<int>	<int>	<int>	<fct>
1	51624	2009_10	113	85	34	Yes
2	51624	2009_10	113	85	34	Yes
3	51624	2009_10	113	85	34	Yes
4	51625	2009_10	NA	NA	4	<NA>
5	51630	2009_10	112	75	49	Yes
6	51638	2009_10	86	47	9	<NA>
7	51646	2009_10	107	37	8	<NA>
8	51647	2009_10	118	64	45	No
9	51647	2009_10	118	64	45	No
10	51647	2009_10	118	64	45	No

```
# ... with 9,990 more rows, and 2 more variables:
```

```
#   Race1 <fct>, HealthGen <fct>
```


Summarizing temp1

```
> summary(temp1)
```

ID	SurveyYr	BPSysAve	BPDiaAve	Age
Min. :51624	2009_10:5000	Min. : 76.0	Min. : 0.00	Min. : 0.00
1st Qu.:56905	2011_12:5000	1st Qu.:106.0	1st Qu.: 61.00	1st Qu.:17.00
Median :62160		Median :116.0	Median : 69.00	Median :36.00
Mean :61945		Mean :118.2	Mean : 67.48	Mean :36.74
3rd Qu.:67039		3rd Qu.:127.0	3rd Qu.: 76.00	3rd Qu.:54.00
Max. :71915		Max. :226.0	Max. :116.00	Max. :80.00
		NA's :1449	NA's :1449	

Smoke100	Race1	HealthGen
No :4024	Black :1197	Excellent: 878
Yes :3211	Hispanic: 610	Vgood :2508
NA's:2765	Mexican :1015	Good :2956
	White :6372	Fair :1010
	Other : 806	Poor : 187
		NA's :2461

Today's Data: Step 2

- Restrict to 2011-12 data, and rename some variables.

```
temp2 <- NHANES %>%  
  filter(SurveyYr == "2011_12") %>%  
  select(ID, BPSysAve, BPDiaAve, Age,  
         Smoke100, Race1, HealthGen, SurveyYr) %>%  
  rename(Subject = ID, SBP = BPSysAve,  
         DBP = BPDiaAve, SROH = HealthGen)
```

The temp2 tibble

```
temp2
```

```
# A tibble: 5,000 x 8
```

	Subject	SBP	DBP	Age	Smoke100	Race1	SROH
	<int>	<int>	<int>	<int>	<fct>	<fct>	<fct>
1	62163	107	37	14	<NA>	Other	Good
2	62172	103	72	43	Yes	Black	Good
3	62174	97	39	80	No	White	Fair
4	62174	97	39	80	No	White	Fair
5	62175	NA	NA	5	<NA>	White	<NA>
6	62176	107	69	34	No	White	Vgood
7	62178	121	72	80	No	White	Fair
8	62180	107	66	35	No	White	Good
9	62186	108	64	17	<NA>	Black	Vgood
10	62190	113	27	15	<NA>	Mexican	Excellent

```
# ... with 4,990 more rows, and 1 more variable:
```

```
#   SurveyYr <fct>
```

Summary of temp2

```
> summary(temp2)
```

Subject	SBP	DBP	Age	Smoke100
Min. :62163	Min. : 79.0	Min. : 0.0	Min. : 0.00	No :2027
1st Qu.:64544	1st Qu.:107.0	1st Qu.: 62.0	1st Qu.:17.00	Yes :1560
Median :67039	Median :116.0	Median : 69.0	Median :36.00	NA's:1413
Mean :67028	Mean :118.7	Mean : 68.3	Mean :36.71	
3rd Qu.:69509	3rd Qu.:128.0	3rd Qu.: 77.0	3rd Qu.:54.00	
Max. :71915	Max. :221.0	Max. :116.0	Max. :80.00	
	NA's :719	NA's :719		
Race1	SROH	SurveyYr		
Black : 589	Excellent: 486	2009_10: 0		
Hispanic: 350	Vgood :1278	2011_12:5000		
Mexican : 480	Good :1485			
White :3135	Fair : 472			
Other : 446	Poor : 77			
	NA's :1202			

Today's Data: Step 3

- Drop unused level (2009-10) from SurveyYr summary with `droplevels()`.
- Clean up the names to lower case with underscores using `clean_names()`.
- Use only distinct observations with `distinct()`.

```
temp3 <- NHANES %>%  
  filter(SurveyYr == "2011_12") %>%  
  select(ID, BPSysAve, BPDiaAve, Age,  
         Smoke100, Race1, HealthGen, SurveyYr) %>%  
  rename(Subject = ID, SBP = BPSysAve,  
         DBP = BPDiaAve, SROH = HealthGen) %>%  
  clean_names() %>%  
  distinct() %>%  
  droplevels()
```

The temp3 tibble

```
temp3
```

```
# A tibble: 3,211 x 8
```

	subject	sbp	dbp	age	smoke100	race1	sroh
	<int>	<int>	<int>	<int>	<fct>	<fct>	<fct>
1	62163	107	37	14	<NA>	Other	Good
2	62172	103	72	43	Yes	Black	Good
3	62174	97	39	80	No	White	Fair
4	62175	NA	NA	5	<NA>	White	<NA>
5	62176	107	69	34	No	White	Vgood
6	62178	121	72	80	No	White	Fair
7	62180	107	66	35	No	White	Good
8	62186	108	64	17	<NA>	Black	Vgood
9	62190	113	27	15	<NA>	Mexican	Excellent
10	62199	110	65	57	Yes	White	Vgood

```
# ... with 3,201 more rows, and 1 more variable:
```

```
#   survey_yr <fct>
```

Summary of temp3

```
> summary(temp3)
```

subject	sbp	dbp	age	smoke100
Min. :62163	Min. : 79.0	Min. : 0.00	Min. : 0.00	No :1244
1st Qu.:64541	1st Qu.:106.0	1st Qu.: 61.00	1st Qu.:14.00	Yes : 929
Median :67027	Median :116.0	Median : 69.00	Median :33.00	NA's:1038
Mean :67013	Mean :118.5	Mean : 67.35	Mean :35.07	
3rd Qu.:69457	3rd Qu.:128.0	3rd Qu.: 77.00	3rd Qu.:54.00	
Max. :71915	Max. :221.0	Max. :116.00	Max. :80.00	
	NA's :547	NA's :547		
race1	sroh	survey_yr		
Black : 514	Excellent:283	2011_12:3211		
Hispanic: 274	Vgood :732			
Mexican : 390	Good :911			
White :1667	Fair :338			
Other : 366	Poor : 60			
	NA's :887			

Today's Data: Step 4

- Make Race1 and HealthGen into factors, leave ID as character.
- Restrict Age to 21-79, and require DBP \geq 40 mm Hg.

```
temp4 <- NHANES %>%  
  filter(SurveyYr == "2011_12") %>%  
  select(ID, BPSysAve, BPDiaAve, Age, Smoke100,  
         Race1, HealthGen, SurveyYr) %>%  
  rename(Subject = ID, SBP = BPSysAve, DBP = BPDiaAve,  
         SROH = HealthGen) %>%  
  clean_names() %>%  
  mutate(across(where(is.character), as_factor)) %>%  
  mutate(subject = as.character(subject)) %>%  
  filter(age > 20 & age < 80) %>%  
  filter(dbp > 39) %>%  
  distinct() %>%  
  droplevels()
```


The temp4 tibble

```
temp4
```

```
# A tibble: 1,906 x 8
```

	subject	sbp	dbp	age	smoke100	race1	sroh
	<chr>	<int>	<int>	<int>	<fct>	<fct>	<fct>
1	62172	103	72	43	Yes	Black	Good
2	62176	107	69	34	No	White	Vgood
3	62180	107	66	35	No	White	Good
4	62199	110	65	57	Yes	White	Vgood
5	62205	122	87	28	No	White	Good
6	62206	106	50	35	No	White	<NA>
7	62208	105	59	38	No	Hispanic	Good
8	62209	108	57	62	No	Mexican	Fair
9	62220	120	71	31	No	Black	Good
10	62222	104	73	32	No	White	Good

```
# ... with 1,896 more rows, and 1 more variable:  
#   survey_yr <fct>
```

Summarizing the temp4 tibble

```
> summary(temp4)
```

subject	sbp	dbp	age	smoke100
Length:1906	Min. : 81.0	Min. : 41.00	Min. :21.00	No :1082
Class :character	1st Qu.:109.0	1st Qu.: 65.00	1st Qu.:32.00	Yes: 824
Mode :character	Median :119.0	Median : 72.00	Median :45.00	
	Mean :120.9	Mean : 71.88	Mean :45.93	
	3rd Qu.:129.0	3rd Qu.: 79.00	3rd Qu.:58.00	
	Max. :221.0	Max. :116.00	Max. :79.00	

race1	sroh	survey_yr
Black : 306	Excellent:199	2011_12:1906
Hispanic: 153	Vgood :525	
Mexican : 191	Good :684	
White :1038	Fair :272	
Other : 218	Poor : 53	
	NA's :173	

Today's Data: Select random sample of 700

```
set.seed(20210930)
nh12 <- NHANES %>%
  filter(SurveyYr == "2011_12") %>%
  select(ID, BPSysAve, BPDiaAve, Age, Smoke100,
         Race1, HealthGen, SurveyYr) %>%
  rename(Subject = ID, SBP = BPSysAve, DBP = BPDiaAve,
         SROH = HealthGen) %>%
  clean_names() %>%
  mutate(across(where(is.character), as_factor)) %>%
  mutate(subject = as.character(subject)) %>%
  filter(age > 20 & age < 80) %>%
  filter(dbp > 39) %>%
  distinct() %>%
  slice_sample(n = 700) %>%
  droplevels()
```

The nh12 tibble

```
nh12
```

```
# A tibble: 700 x 8
```

	subject	sbp	dbp	age	smoke100	race1	sroh
	<chr>	<int>	<int>	<int>	<fct>	<fct>	<fct>
1	71420	126	69	54	No	Mexican	Good
2	64368	136	74	70	Yes	Black	Vgood
3	62546	150	84	64	Yes	Mexican	Good
4	70531	110	73	49	No	Black	Excelle~
5	62974	98	74	30	No	White	Good
6	66294	143	77	76	Yes	White	Good
7	68762	104	76	34	Yes	White	<NA>
8	70758	125	64	21	Yes	Hispanic	<NA>
9	71315	132	84	44	Yes	White	Good
10	66600	137	72	64	No	Black	Vgood

```
# ... with 690 more rows, and 1 more variable:  
#   survey_yr <fct>
```

Summary of the nh12 tibble

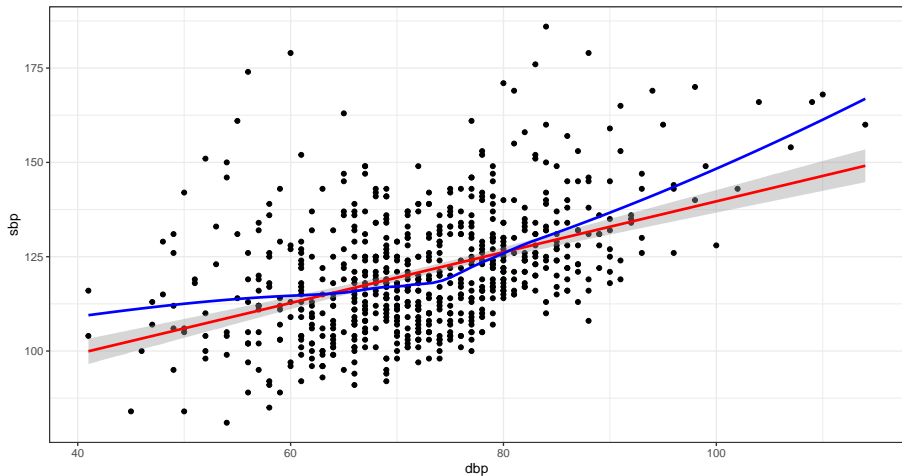
```
> summary(nh12)
  subject      sbp      dbp      age      smoke100
Length:700    Min.   : 81    Min.   : 41.00   Min.   :21.00   No :376
Class :character 1st Qu.:110   1st Qu.: 66.00   1st Qu.:32.00   Yes:324
Mode  :character Median :119   Median : 72.00   Median :45.00
              Mean  :121   Mean  : 72.31   Mean  :45.62
              3rd Qu.:130   3rd Qu.: 79.00   3rd Qu.:58.00
              Max.   :186   Max.   :114.00   Max.   :78.00

  race1      sroh      survey_yr
Black   :115   Excellent: 83   2011_12:700
Hispanic: 61   Vgood    :196
Mexican : 73   Good     :241
White   :367   Fair     : 92
Other   : 84   Poor     : 21
              NA's    : 67
```

- Outcome (quantitative): sbp
- Quantitative predictors: dbp, age
- Binary predictor: smoke100 (Yes/No)
- 5-category predictor: race1 (White, Black, Hispanic, Mexican, Other)
- 5-category predictor with missing data: sroh (E, VG, G, F,)
- Identification code: subject

Building Regression Model m_1 for sbp

Visualizing sbp against dbp



Pearson correlation $r = 0.444$.

Model m1

```
m1 <- lm(sbp ~ dbp, data = nh12)
```

```
tidy(m1, conf.int = TRUE, conf.level = 0.90) %>%  
  select(term, estimate, std.error, conf.low, conf.high) %>%  
  kable(digits = 2)
```

term	estimate	std.error	conf.low	conf.high
(Intercept)	72.33	3.76	66.13	78.52
dbp	0.67	0.05	0.59	0.76

```
glance(m1) %>%  
  select(r.squared, adj.r.squared, sigma, AIC, BIC, nobs) %>%  
  kable(digits = c(3,3,1,1,1,0))
```

r.squared	adj.r.squared	sigma	AIC	BIC	nobs
0.197	0.196	14.3	5717.6	5731.2	700

Model m1

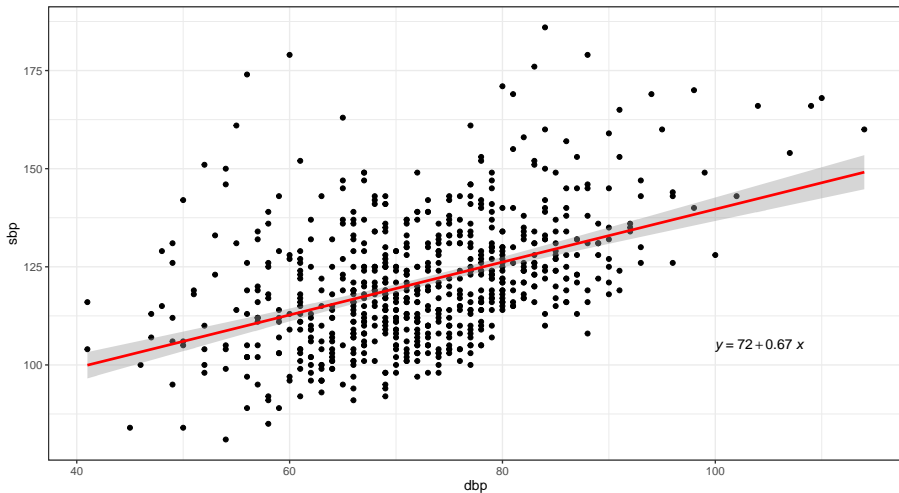
```
extract_eq(m1, use_coefs = TRUE, coef_digits = 3)
```

$$\widehat{\text{sbp}} = 72.326 + 0.673(\text{dbp})$$

To include the equation in the scatterplot, I might use `stat_regline_equation()` from the `ggpubr` package.

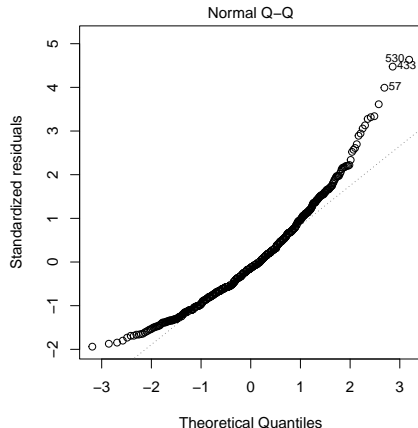
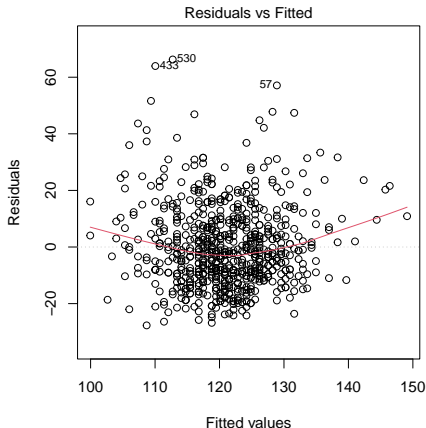
```
ggplot(nh12, aes(x = dbp, y = sbp)) +  
  geom_point() +  
  geom_smooth(method = "lm", col = "red", formula = y ~ x) +  
  stat_regline_equation(label.x = 100, label.y = 105)
```

Including the Equation in the Scatterplot



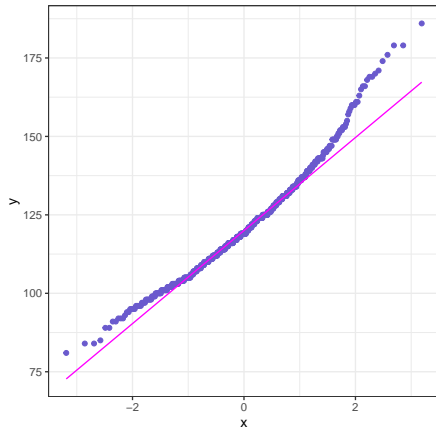
Quick Residual Plots for Model m1

```
par(mfrow = c(1,2))  
plot(m1, which = c(1:2)); par(mfrow = c(1,1))
```

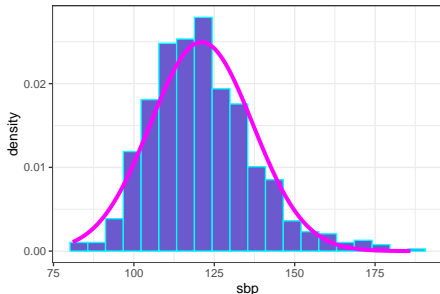


Should we think about transforming sbp here?

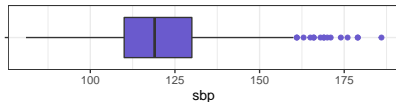
Normal Q-Q plot: nh12 sbp



Density Function: nh12 sbp



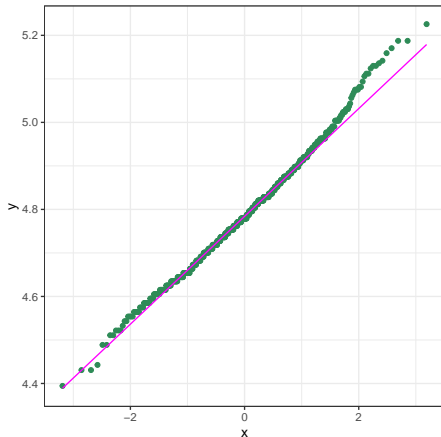
Boxplot: nh12 sbp



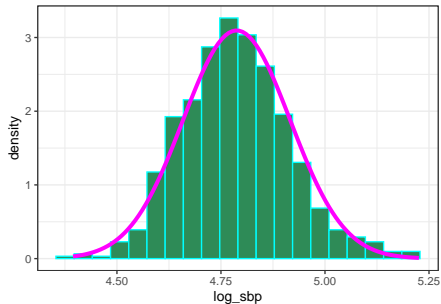
min	Q1	median	Q3	max	mean	sd	n	missing
81	110	119	130	186	121	16	700	0

Logarithm of sbp?

Normal Q-Q plot: log(nh12 sbp)



Density Function: log(nh12 sbp)

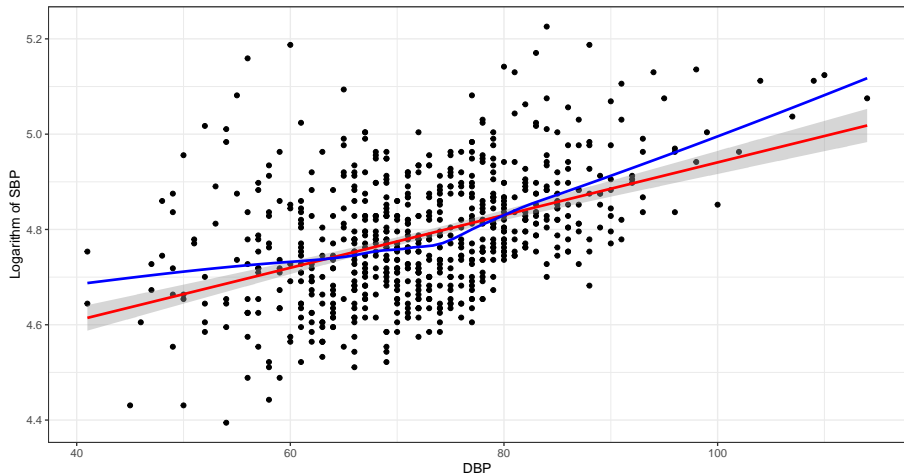


Boxplot: log(nh12 sbp)



min	Q1	median	Q3	max	mean	sd	n	missing
4.4	4.7	4.8	4.9	5.2	4.8	0.1	700	0

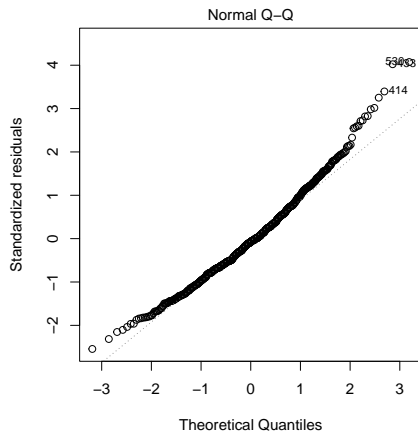
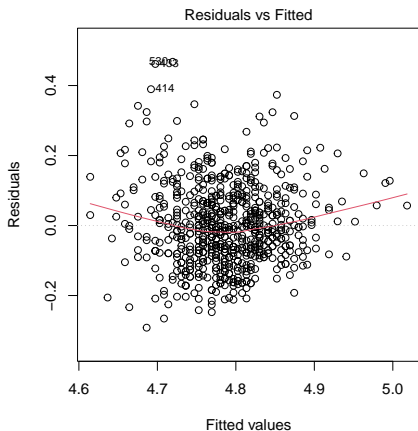
Scatterplot of $\log(\text{sbp})$ vs. dbp



Pearson correlation $r = 0.452$.

Quick Residual Plots for Model m_2

```
m2 <- lm(log(sbp) ~ dbp, data = nh12)
par(mfrow = c(1,2))
plot(m2, which = c(1:2)); par(mfrow = c(1,1))
```



Today's Agenda

- ➊ Using data from NHANES
- ➋ A complex data management challenge
- ➌ Using dbp to predict sbp again
- ➍ Considering a transformation of our outcome