

Lab4-Extra.R

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```
source("http://thegrantlab.org/misc/cdc.R")
```

```
head(cdc$height)
```

```
## [1] 70 64 60 66 61 64
```

```
tail(cdc$weight, 20)
```

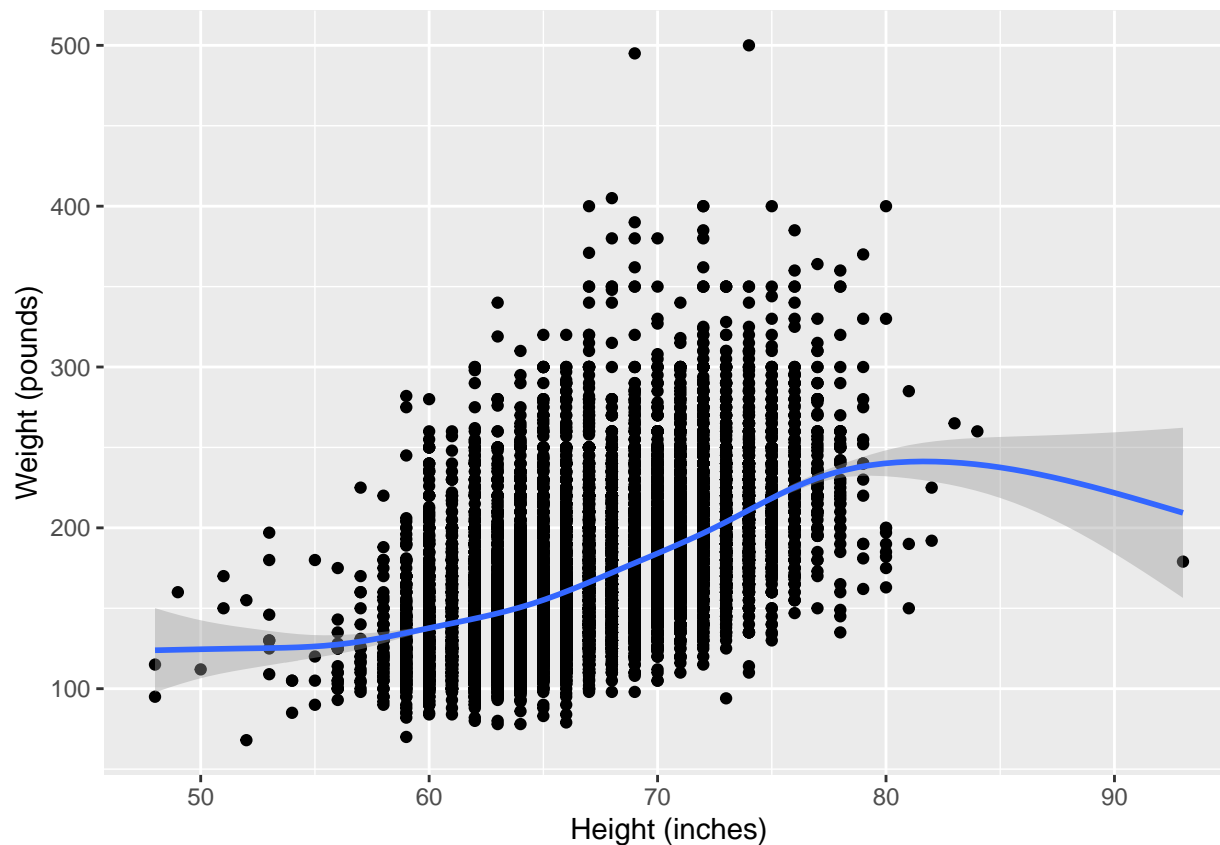
```
## [1] 195 210 171 190 180 120 140 200 230 230 195 210 180 165 224 215 200 216 165  
## [20] 170
```

```
library(ggplot2)  
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --  
## v tibble 3.1.8      v dplyr 1.0.10  
## v tidyr 1.2.1      v stringr 1.4.1  
## v readr 2.1.3      v forcats 0.5.2  
## v purrr 0.3.5  
## -- Conflicts ----- tidyverse_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()
```

```
#Scatter plotting  
ggplot(cdc, aes(x = height, y = weight)) +  
  geom_point() +  
  labs(x = "Height (inches)", y = "Weight (pounds)") +  
  geom_smooth()
```

```
## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```



```
cor.test(cdc$height, cdc$weight)
```

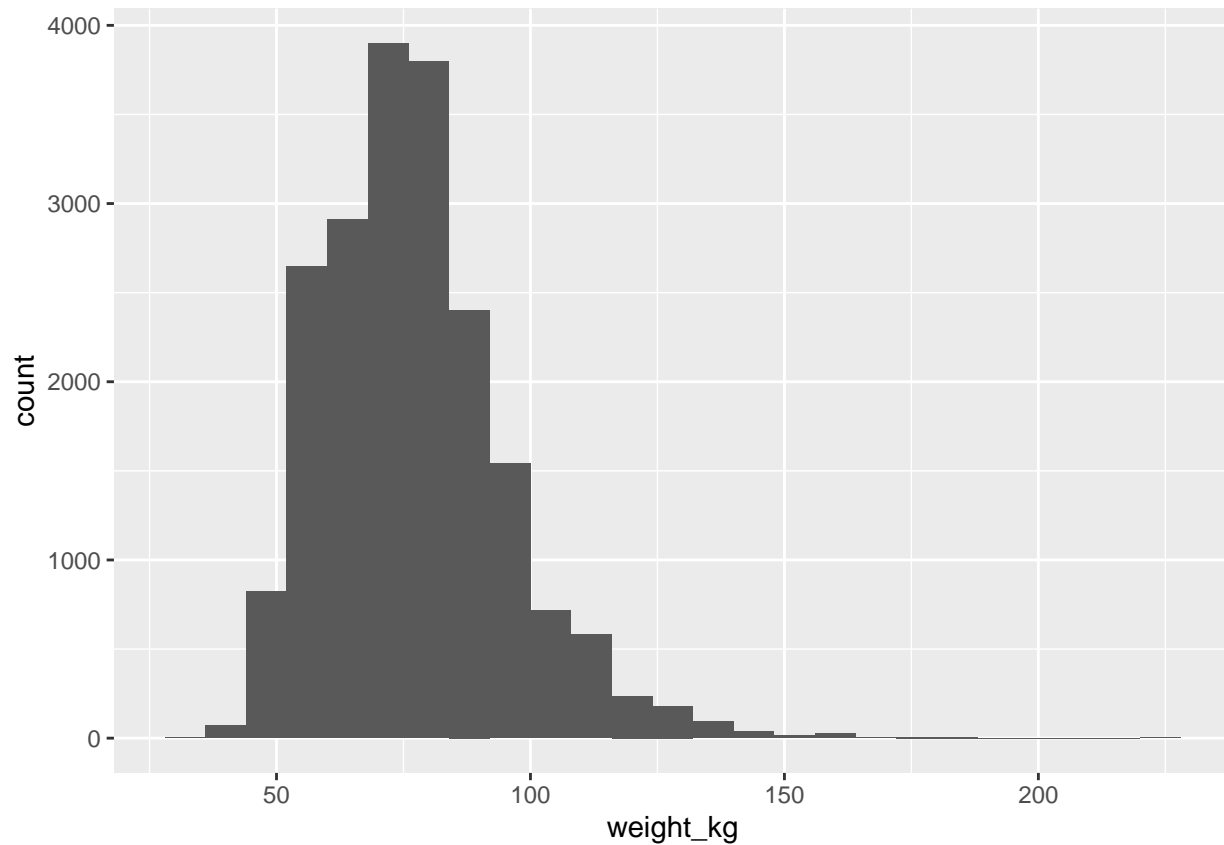
```
##
## Pearson's product-moment correlation
##
## data: cdc$height and cdc$weight
## t = 94.429, df = 19998, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5456626 0.5648342
## sample estimates:
##      cor
## 0.5553222
```

```
#Metrics transformation, histogram, and BMI
```

```
height_m <- cdc$height * 0.0254
```

```
weight_kg <- cdc$weight * 0.454
```

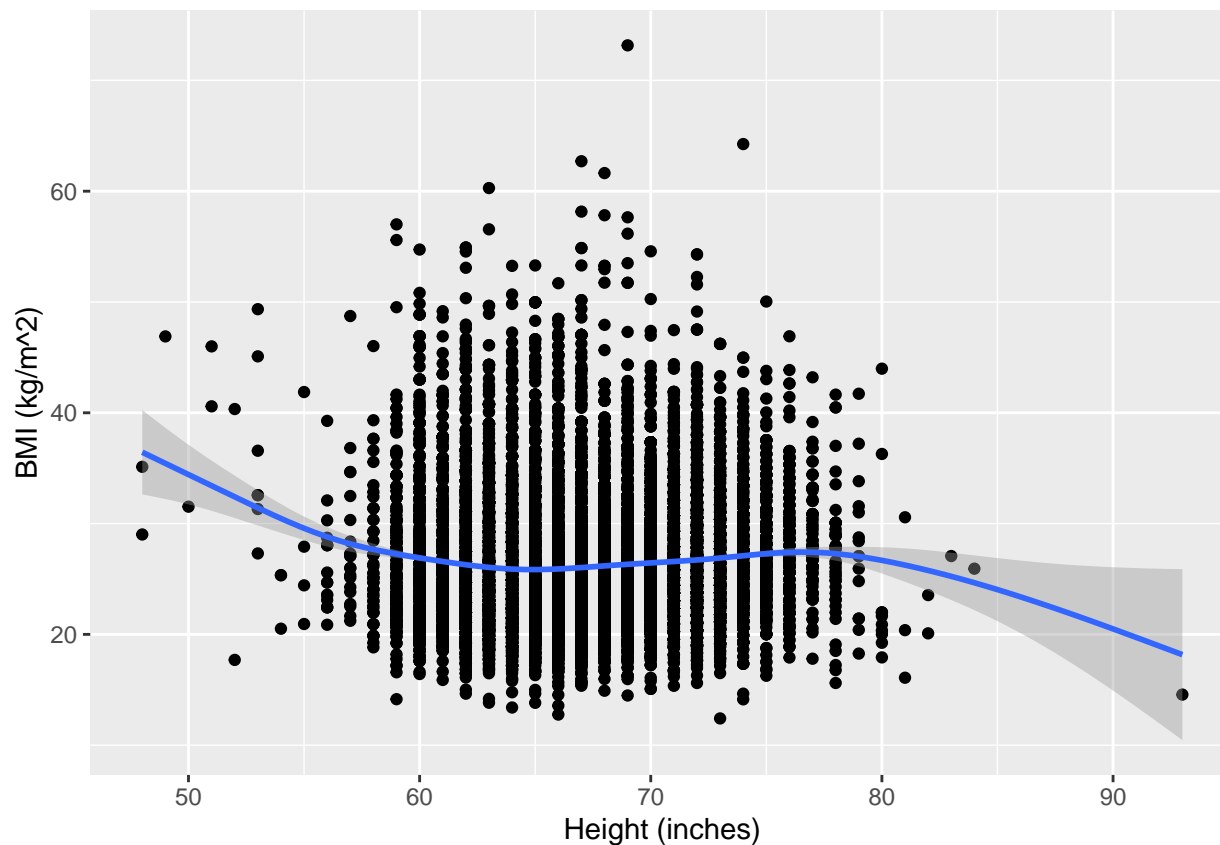
```
ggplot(cdc, aes(x = weight_kg)) +
  geom_histogram(binwidth = 8)
```



```
bmi = weight_kg / (height_m ^ 2)
cdc2 <- cbind(cdc, height_m, weight_kg, bmi)

ggplot(cdc2, aes(x = height, y = bmi)) + geom_point() +
  labs(x = "Height (inches)", y = "BMI (kg/m^2)") +
  geom_smooth()

## 'geom_smooth()' using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```



```
cor.test(cdc2$height, cdc2$bmi)
```

```
##
## Pearson's product-moment correlation
##
## data: cdc2$height and cdc2$bmi
## t = 4.6008, df = 19998, p-value = 4.235e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.01866616 0.04635524
## sample estimates:
## cor
## 0.03251694
```

```
#Logical count and subset
```

```
head(bmi >= 30, 100)
```

```
## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE
## [37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE FALSE
## [49] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE FALSE FALSE
## [61] FALSE FALSE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [73] FALSE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [85] FALSE FALSE FALSE FALSE TRUE FALSE TRUE FALSE FALSE FALSE FALSE
```

```
## [97] TRUE FALSE FALSE FALSE
```

```
round(sum(bmi >= 30) / length(bmi) * 100, 1)
```

```
## [1] 19.5
```

```
cdc[567, 6]
```

```
## [1] 160
```

```
cdc[1:10, 6]
```

```
## [1] 175 125 105 132 150 114 194 170 150 180
```

```
cdc[1:10,]
```

```
##      genhlth exerany hlthplan smoke100 height weight wt Desire age gender
## 1      good      0        1         0    70    175    175  77      m
## 2      good      0        1         1    64    125    115  33      f
## 3      good      1        1         1    60    105    105  49      f
## 4      good      1        1         0    66    132    124  42      f
## 5 very good      0        1         0    61    150    130  55      f
## 6 very good      1        1         0    64    114    114  55      f
## 7 very good      1        1         0    71    194    185  31      m
## 8 very good      0        1         0    67    170    160  45      m
## 9      good      0        1         1    65    150    130  27      f
## 10     good      1        1         0    70    180    170  44      m
```

```
cdc[1:100, c("height", "weight")]
```

```
##      height weight
## 1         70    175
## 2         64    125
## 3         60    105
## 4         66    132
## 5         61    150
## 6         64    114
## 7         71    194
## 8         67    170
## 9         65    150
## 10        70    180
## 11        69    186
## 12        69    168
## 13        66    185
## 14        70    170
## 15        69    170
## 16        73    185
## 17        67    156
## 18        71    185
## 19        75    200
```

## 20	67	125
## 21	69	200
## 22	65	160
## 23	73	160
## 24	67	165
## 25	64	105
## 26	68	190
## 27	67	190
## 28	69	160
## 29	61	115
## 30	74	185
## 31	67	166
## 32	71	180
## 33	71	182
## 34	68	185
## 35	64	220
## 36	63	117
## 37	70	160
## 38	69	190
## 39	65	125
## 40	67	160
## 41	65	124
## 42	66	143
## 43	64	118
## 44	73	210
## 45	64	200
## 46	59	145
## 47	68	175
## 48	68	130
## 49	66	112
## 50	61	141
## 51	65	179
## 52	64	135
## 53	62	140
## 54	72	170
## 55	68	150
## 56	69	172
## 57	64	125
## 58	62	168
## 59	64	120
## 60	65	180
## 61	72	186
## 62	66	144
## 63	73	250
## 64	60	160
## 65	74	164
## 66	68	155
## 67	66	140
## 68	64	125
## 69	63	140
## 70	71	190
## 71	65	140
## 72	66	134
## 73	72	217

```
## 74      71      215
## 75      63      190
## 76      67      215
## 77      64      112
## 78      62      136
## 79      63      142
## 80      74      210
## 81      68      180
## 82      63      120
## 83      74      225
## 84      74      200
## 85      64      148
## 86      66      143
## 87      60      135
## 88      60      115
## 89      66      193
## 90      64      140
## 91      71      265
## 92      67      166
## 93      64      145
## 94      62      138
## 95      67      137
## 96      74      175
## 97      71      230
## 98      65      140
## 99      74      180
## 100     60      100
```

```
sum_gender <- sum(as.integer(cdc[bmi >= 30, "gender"]))
nbmi30 <- sum(bmi >= 30)
nmale <- 2 * nbmi30 - sum_gender
nmale
```

```
## [1] 1961
```