5_Scatter_Plots

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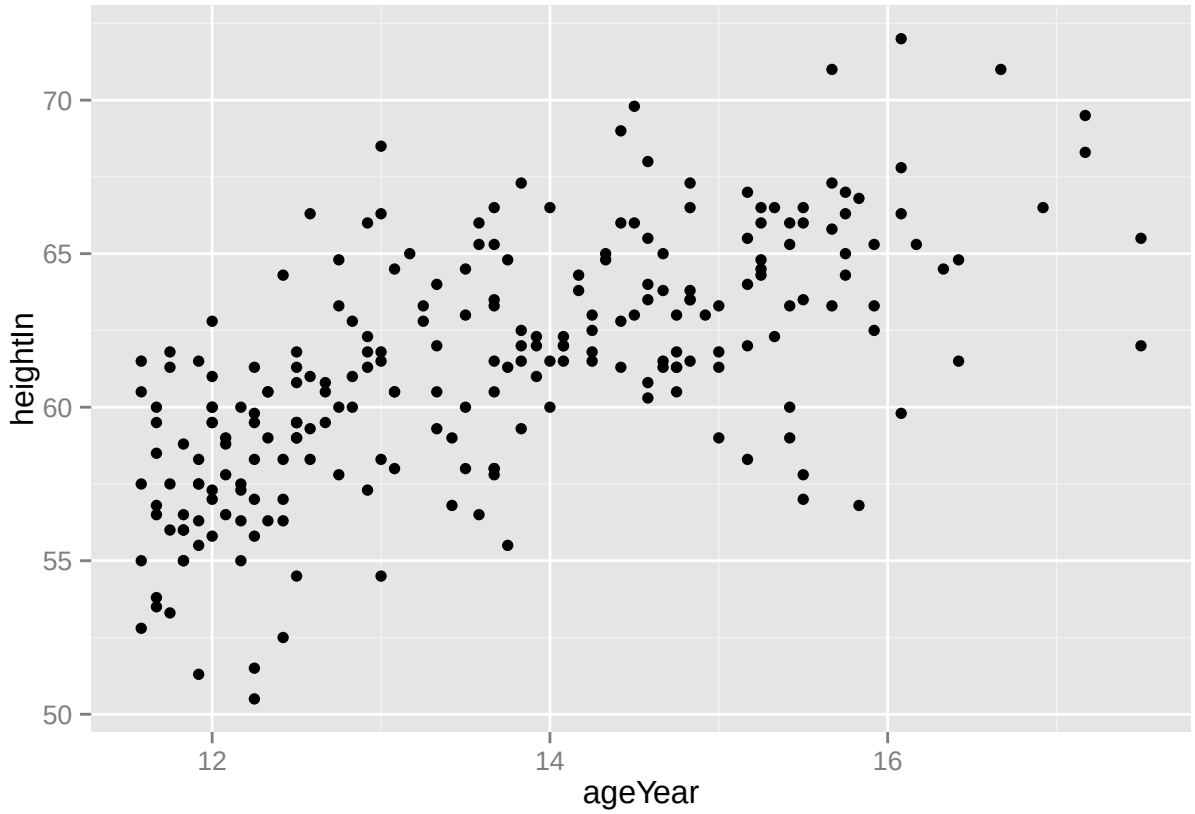
1. Making a Basic Scatter Plot

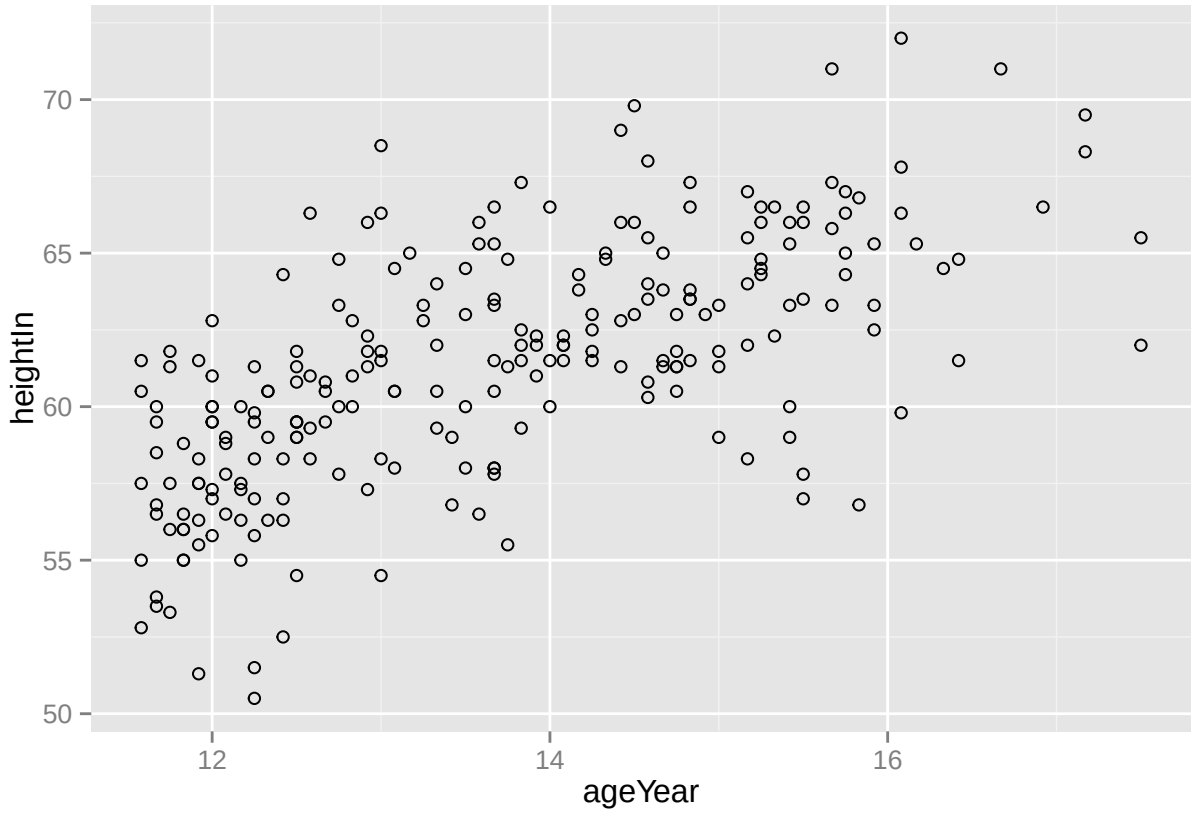
```
library(ggplot2)
library(gcookbook) # For the data set

library(plyr) ##

# List the two columns we'll use
head(heightweight[, c("ageYear", "heightIn")])
```

```
##   ageYear heightIn
## 1   11.92     56.3
## 2   12.92     62.3
## 3   12.75     63.3
## 4   13.42     59.0
## 5   15.92     62.5
## 6   14.25     62.5
```

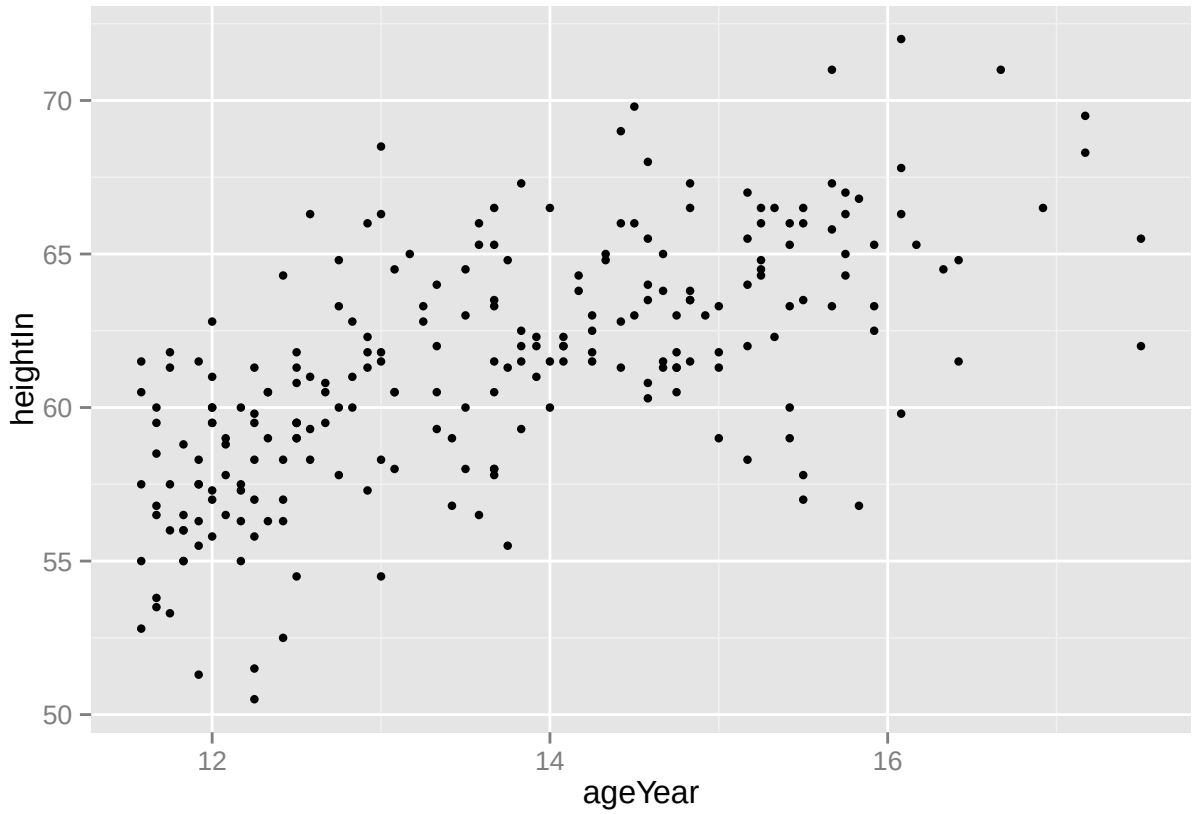
```
ggplot( heightweight, aes( x = ageYear, y = heightIn)) +
  geom_point()
```



```
## To use different shapes in a scatter plot, set shape.
ggplot( heightweight, aes( x = ageYear, y = heightIn)) + geom_point( shape = 21)
```




```
## The size of the points can be controlled with size.
ggplot( heightweight, aes( x = ageYear, y = heightIn)) + geom_point( size = 1.5)
```

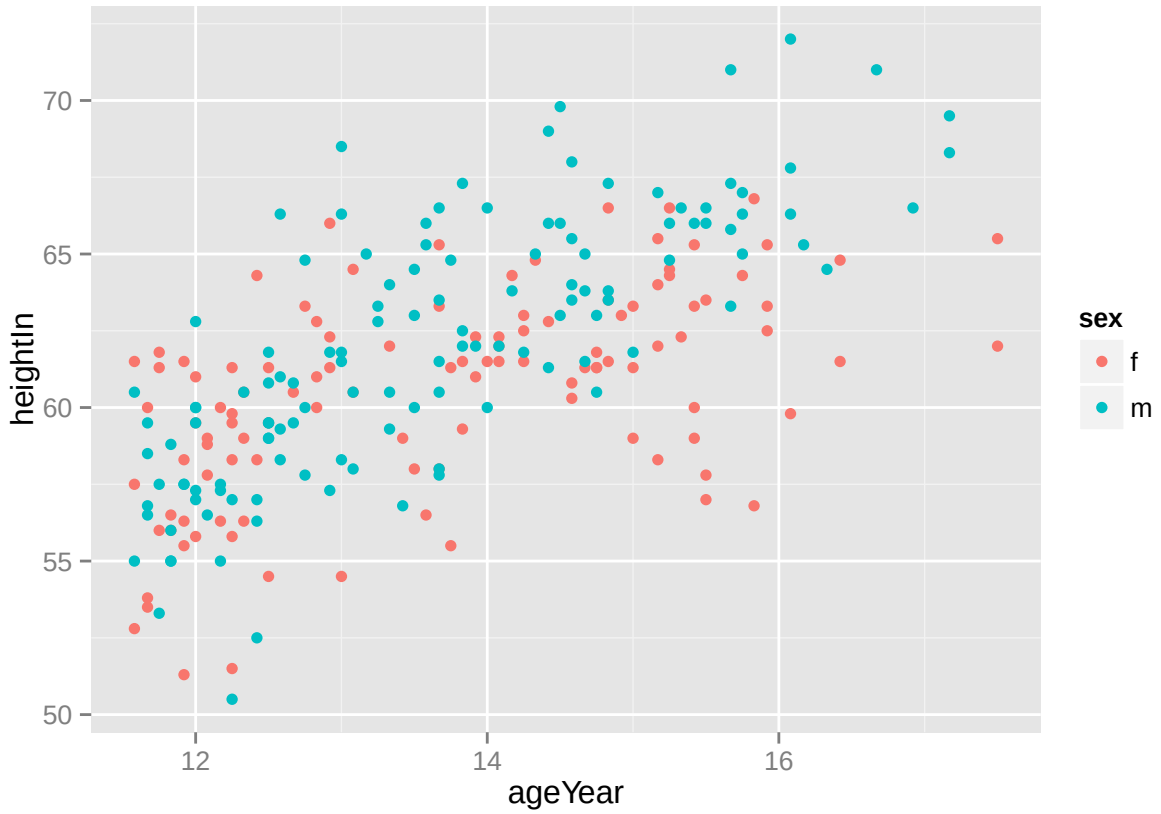


2. Grouping Data Points by a Variable Using Shape or Color

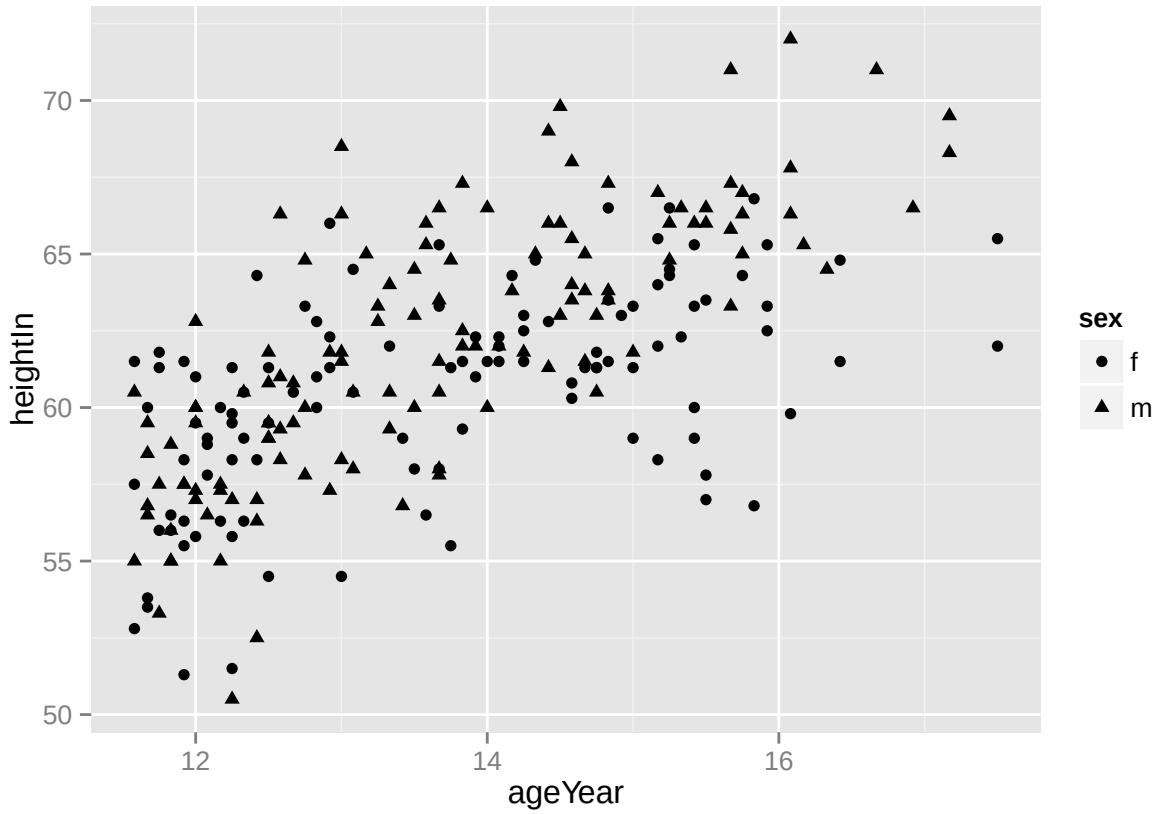
```
# Show the three columns we'll use
head(heightweight[, c("sex", "ageYear", "heightIn")])
```

```
##   sex ageYear heightIn
## 1   f   11.92     56.3
## 2   f   12.92     62.3
## 3   f   12.75     63.3
## 4   f   13.42     59.0
## 5   f   15.92     62.5
## 6   f   14.25     62.5
```

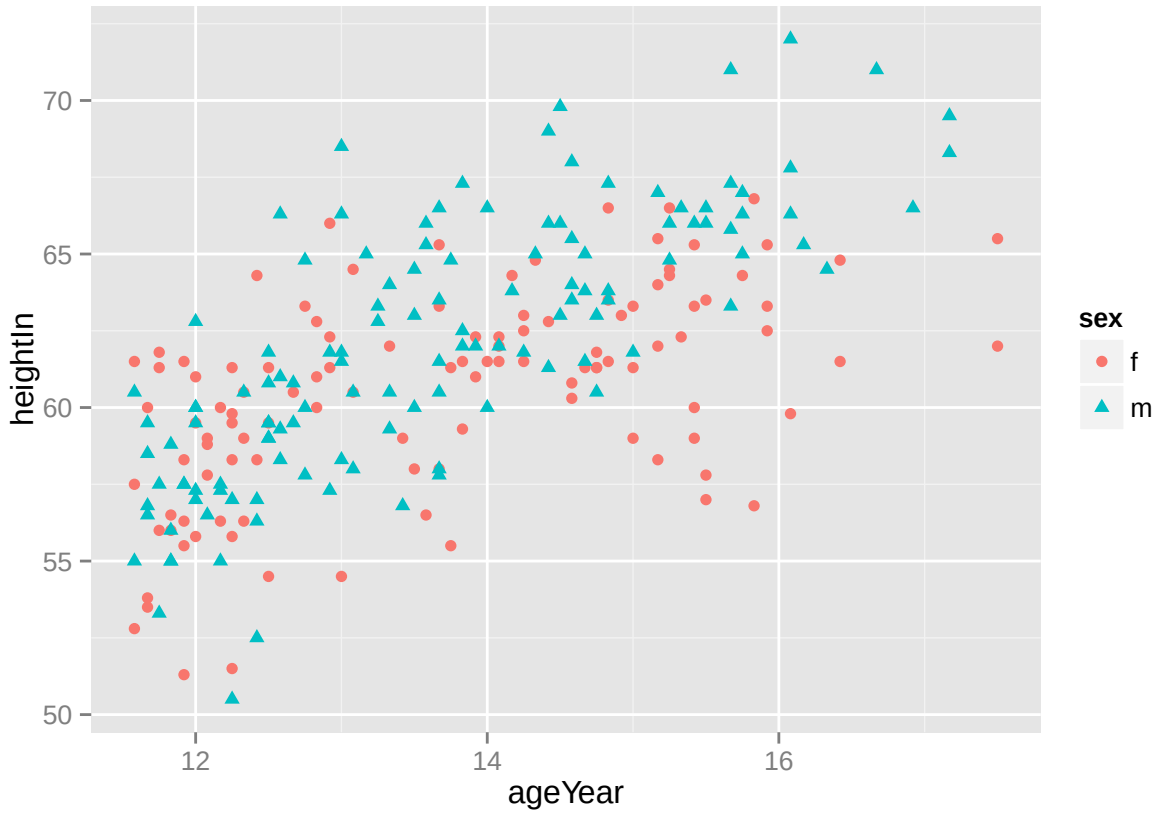
```
ggplot( heightweight, aes( x = ageYear, y = heightIn, colour = sex)) +
  geom_point()
```



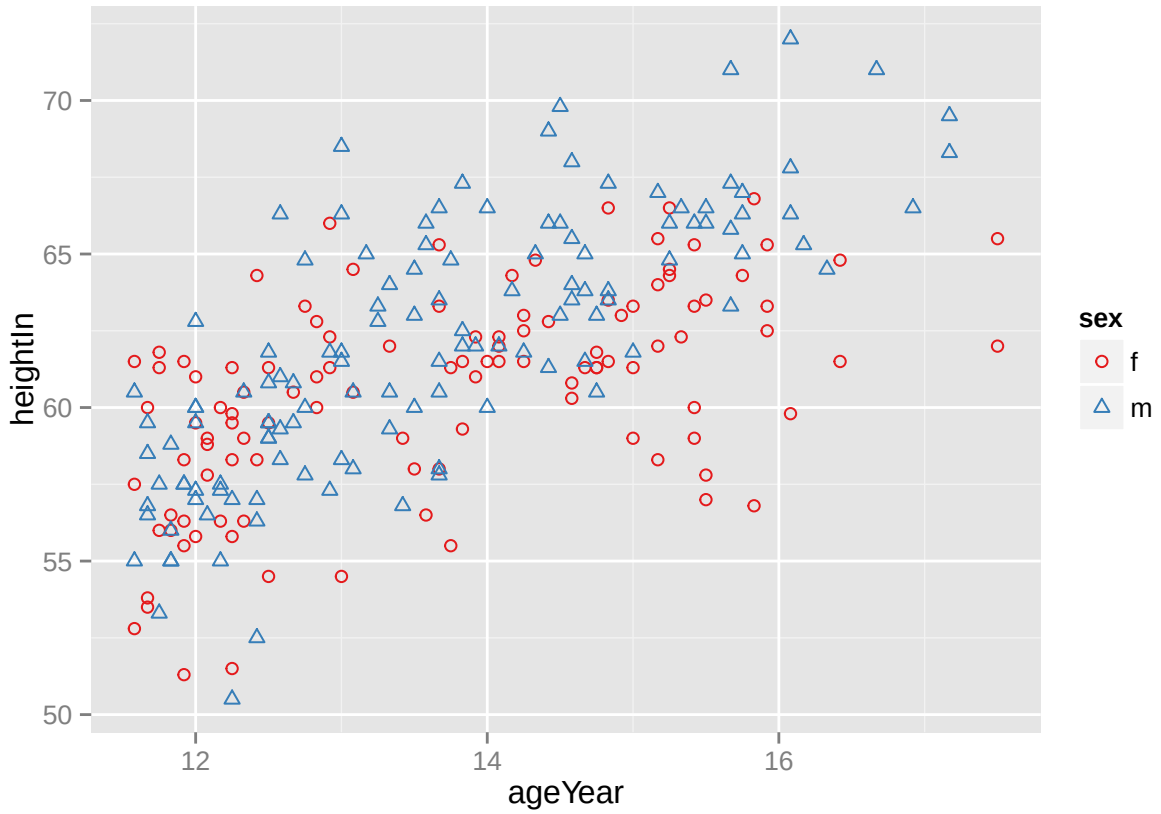

```
ggplot( heightweight, aes( x = ageYear, y = heightIn, shape = sex)) +
  geom_point()
```




```
## It is possible to map a variable to both shape and colour,
ggplot( heightweight, aes( x = ageYear, y = heightIn, shape = sex, colour = sex)) + geom_point()
```

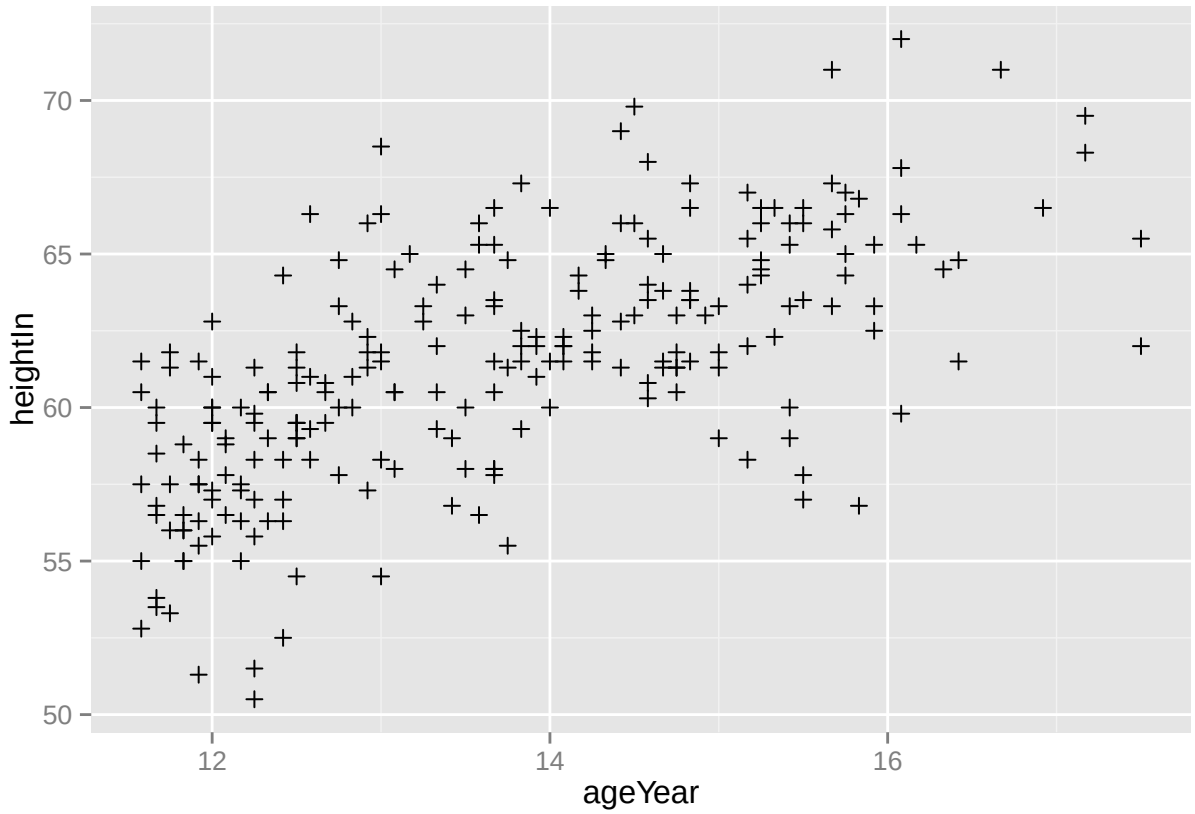



```
## set different shapes and colors for the grouping variables
ggplot( heightweight, aes( x = ageYear, y = heightIn, shape = sex, colour = sex)) +
  geom_point() +
  scale_shape_manual( values = c(1,2)) +
  scale_colour_brewer( palette ="Set1")
```

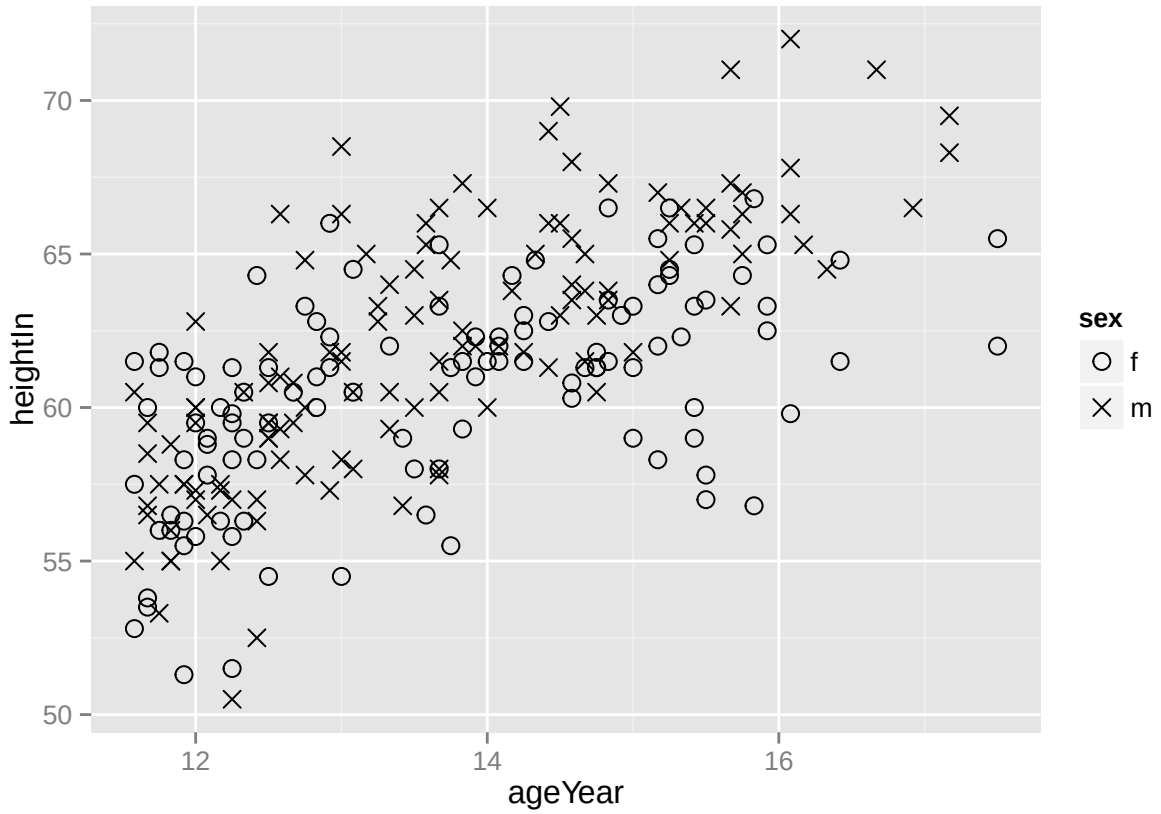


3. Using Different Point Shapes

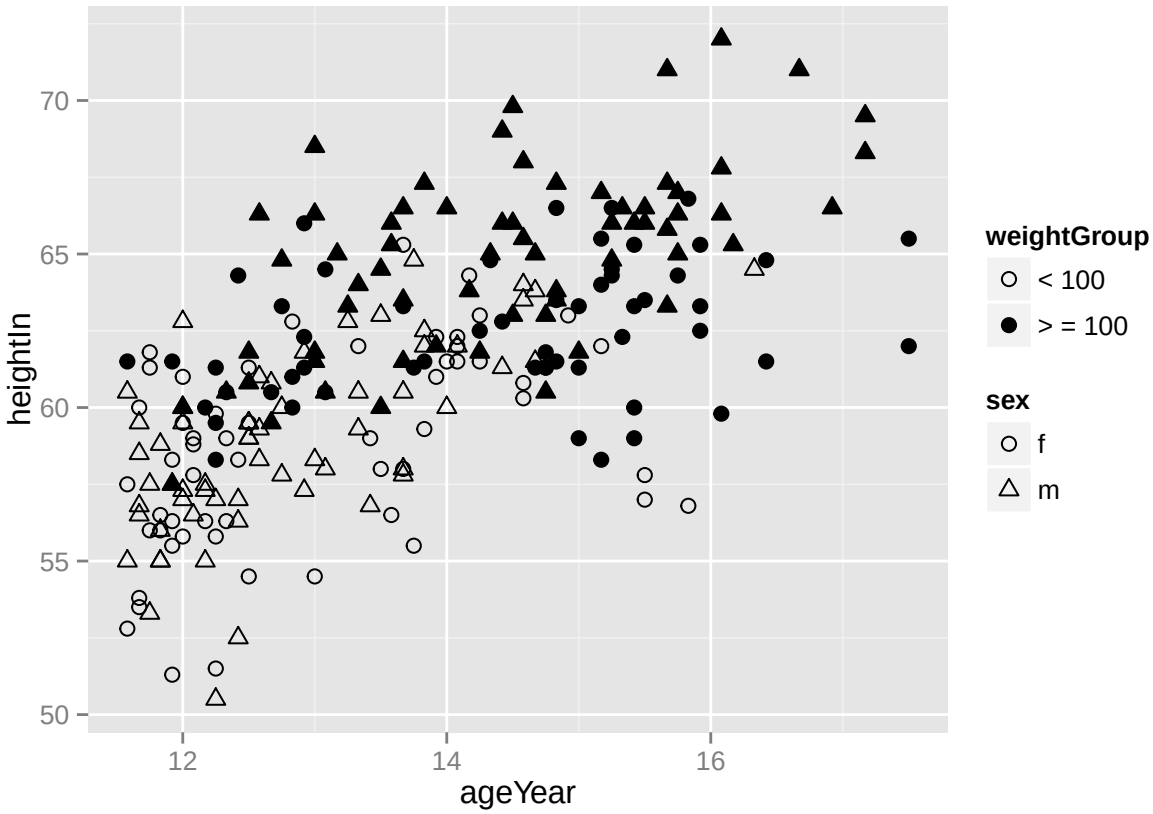
```
ggplot( heightweight, aes( x = ageYear, y = heightIn)) +
  geom_point( shape = 3)
```




```
# Use slightly larger points and use a shape scale with custom values
ggplot( heightweight, aes( x = ageYear, y = heightIn, shape = sex)) +
  geom_point( size = 3) +
  scale_shape_manual( values = c( 1, 4))
```




```
## It's possible to have the shape represent one variable and the fill (empty or solid) represent anothe
# Make a copy of the data
hw <- heightweight

# Categorize into < 100 and > = 100 groups
hw$weightGroup <- cut( hw$weightLb, breaks = c(-Inf, 100, Inf),
                       labels = c("< 100", "> = 100"))

# Use shapes with fill and color, and use colors that are empty (NA) and # filled
ggplot( hw, aes( x = ageYear, y = heightIn, shape = sex, fill = weightGroup)) +
  geom_point( size = 2.5) + scale_shape_manual( values = c( 21, 24)) +
  scale_fill_manual( values = c( NA, "black"), guide = guide_legend( override.aes = list( shape = 21)))
```

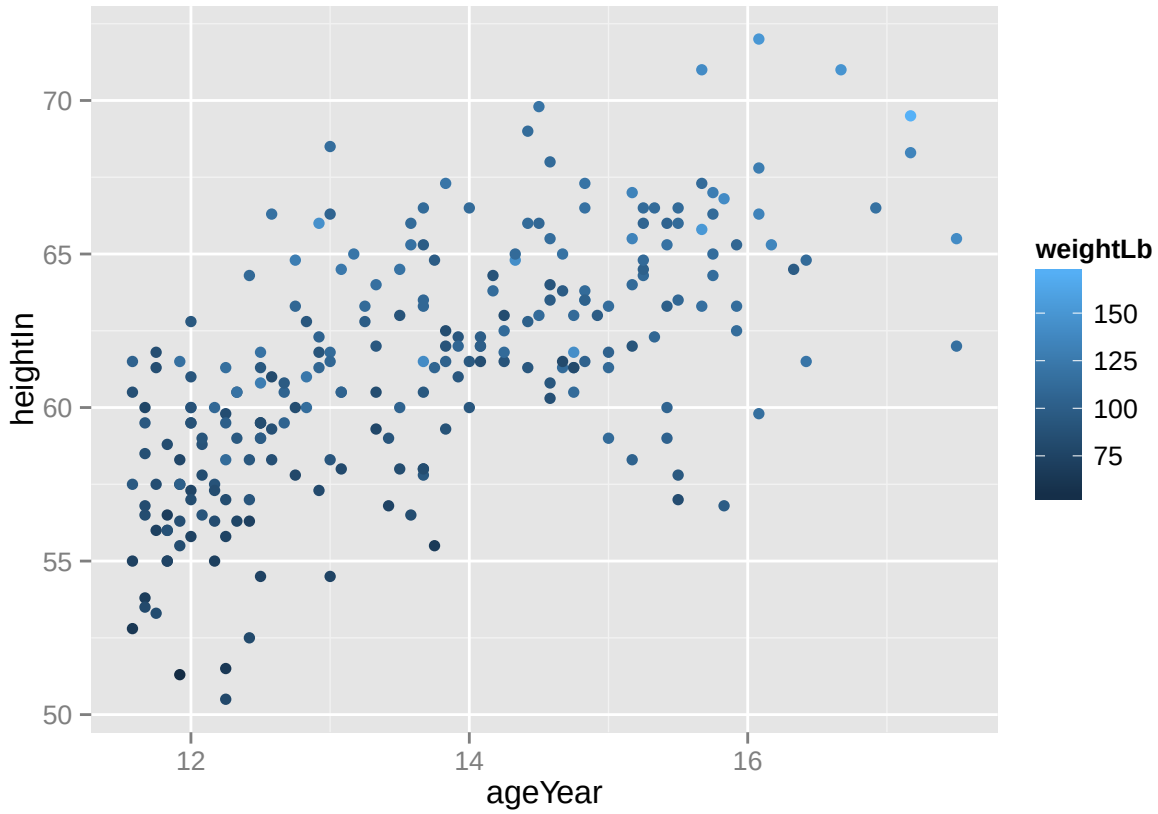


4. Mapping a Continuous Variable to Color or Size

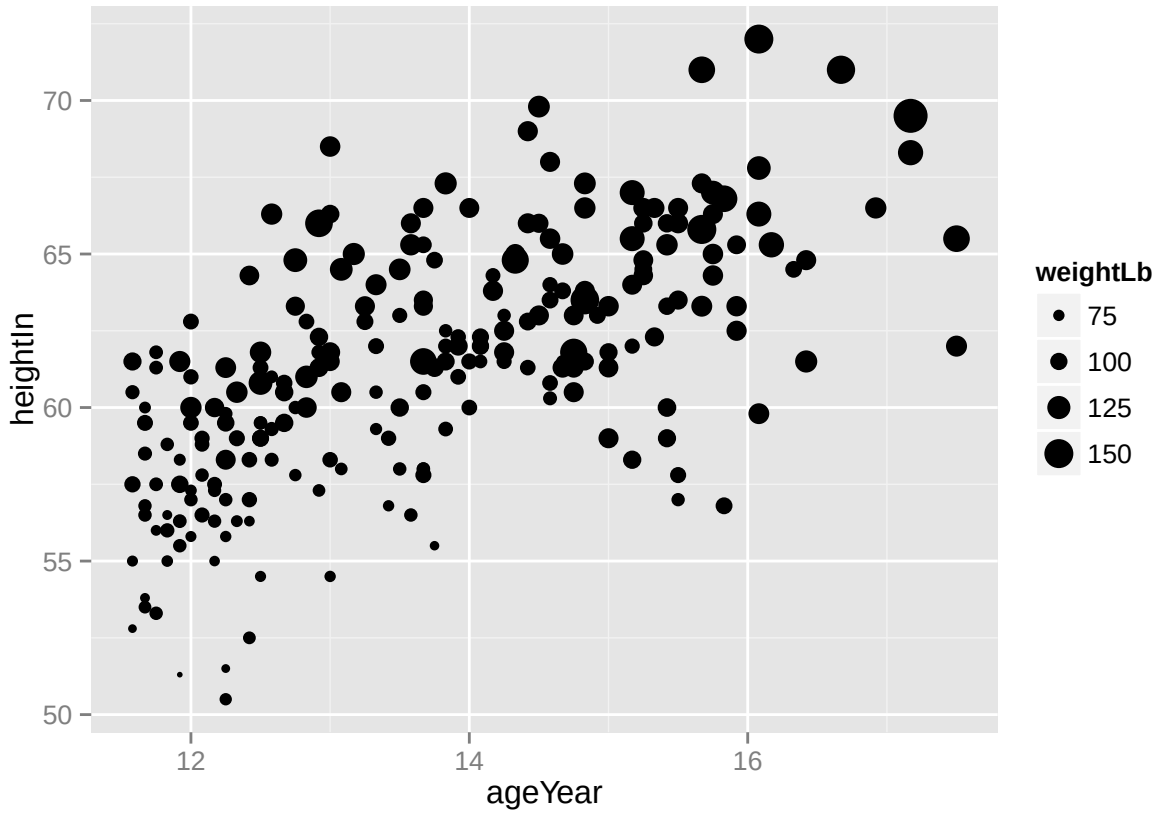
```
# List the four columns we'll use
head(heightweight[, c("sex", "ageYear", "heightIn", "weightLb")])
```

```
##   sex ageYear heightIn weightLb
## 1   f   11.92     56.3     85.0
## 2   f   12.92     62.3    105.0
## 3   f   12.75     63.3    108.0
## 4   f   13.42     59.0     92.0
## 5   f   15.92     62.5    112.5
## 6   f   14.25     62.5    112.0
```

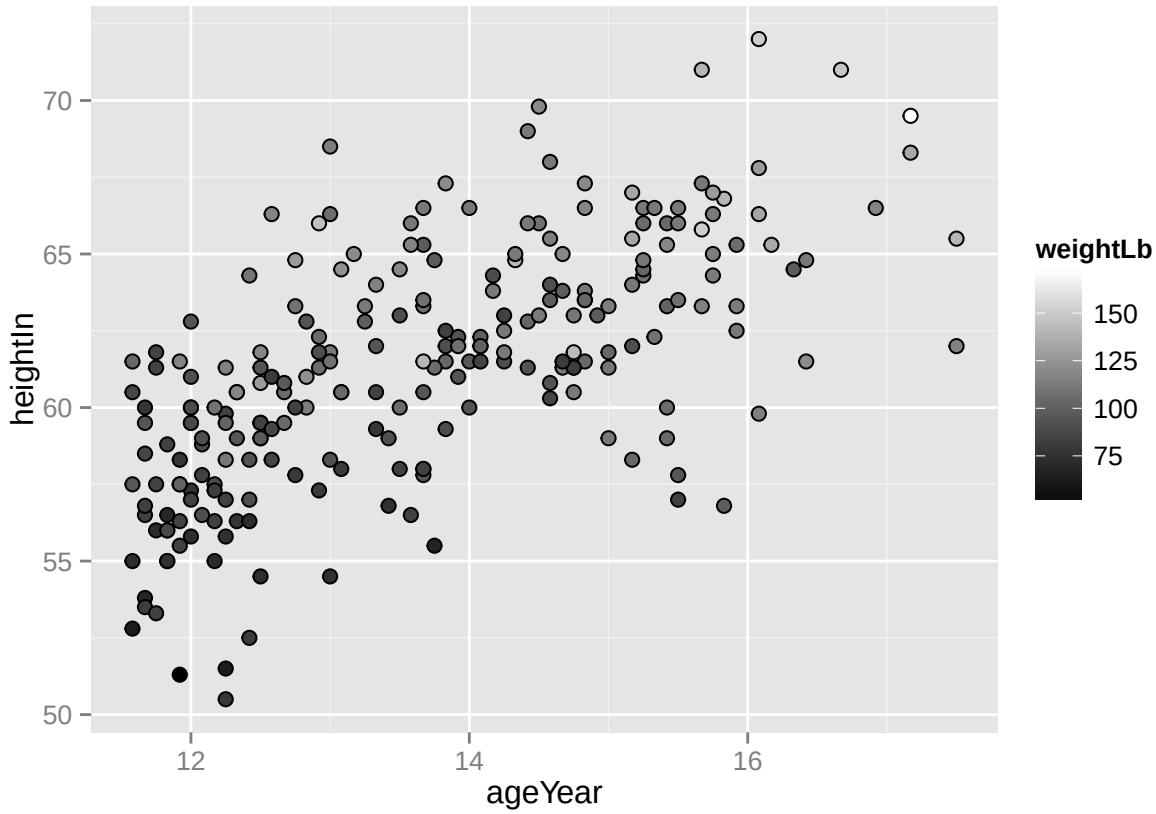
```
ggplot( heightweight, aes( x = ageYear, y = heightIn, colour = weightLb)) +
  geom_point()
```



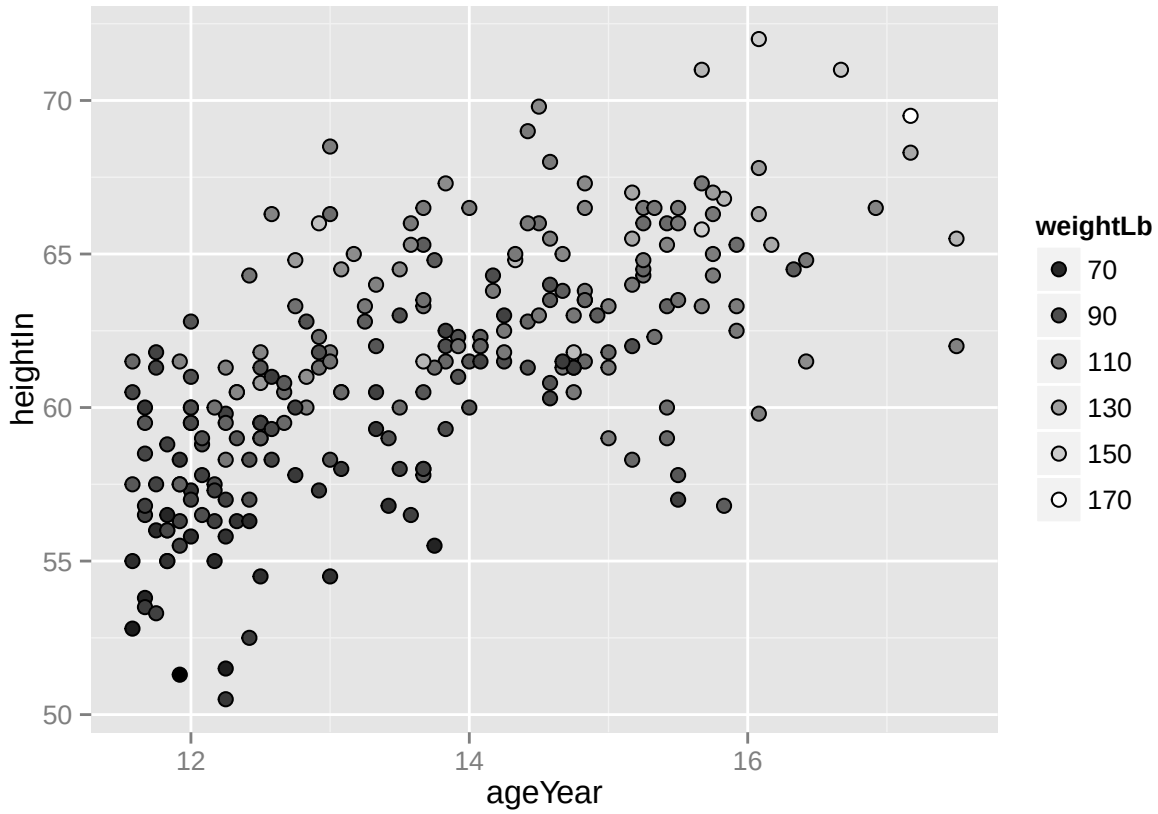

```
ggplot( heightweight, aes( x = ageYear, y = heightIn, size = weightLb )) +
  geom_point()
```



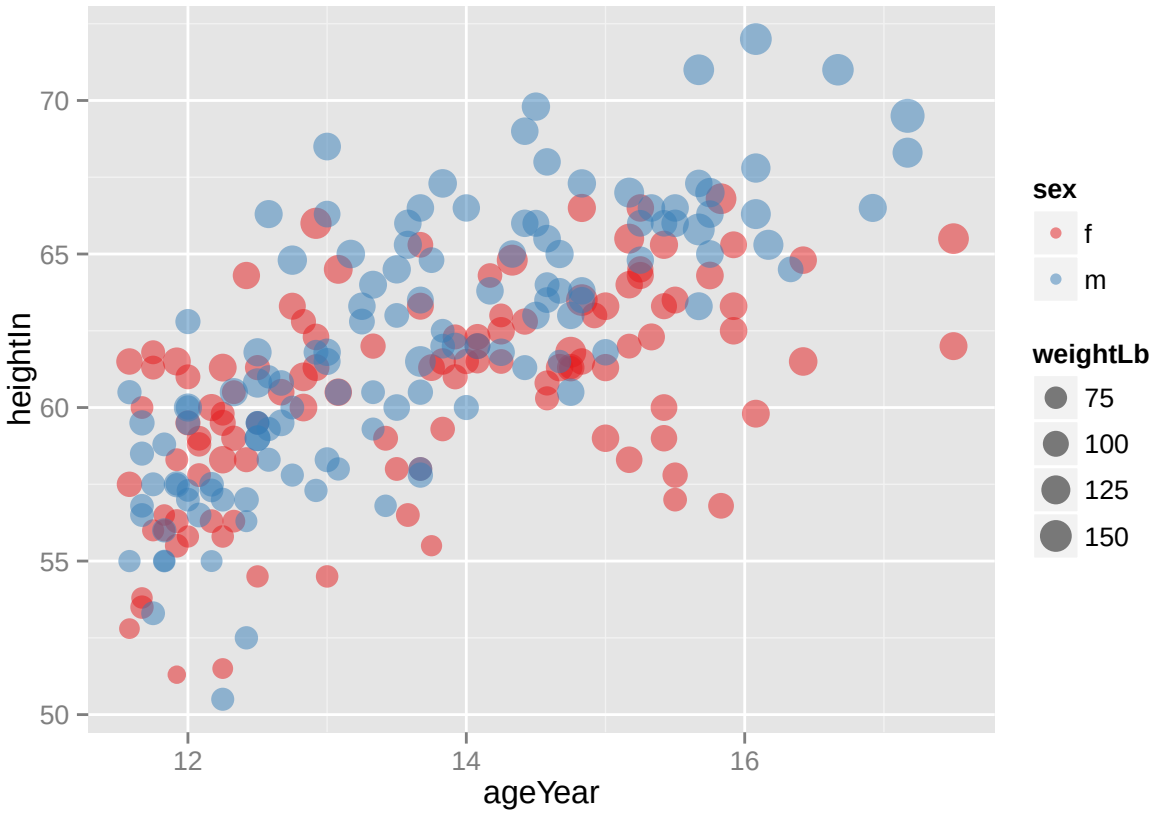

```
## set the fill gradient to go from black to white and make the points larger
ggplot( heightweight, aes( x = ageYear, y = heightIn, fill = weightLb)) +
  geom_point( shape = 21, size = 2.5) +
  scale_fill_gradient( low ="black", high ="white")
```




```
# Using guide_legend() will result in a discrete legend instead of a colorbar
ggplot( heightweight, aes( x = ageYear, y = heightIn, fill = weightLb)) +
  geom_point( shape = 21, size = 2.5) +
  scale_fill_gradient( low ="black", high ="white", breaks = seq( 70, 170, by = 20), guide = guide_lege
```



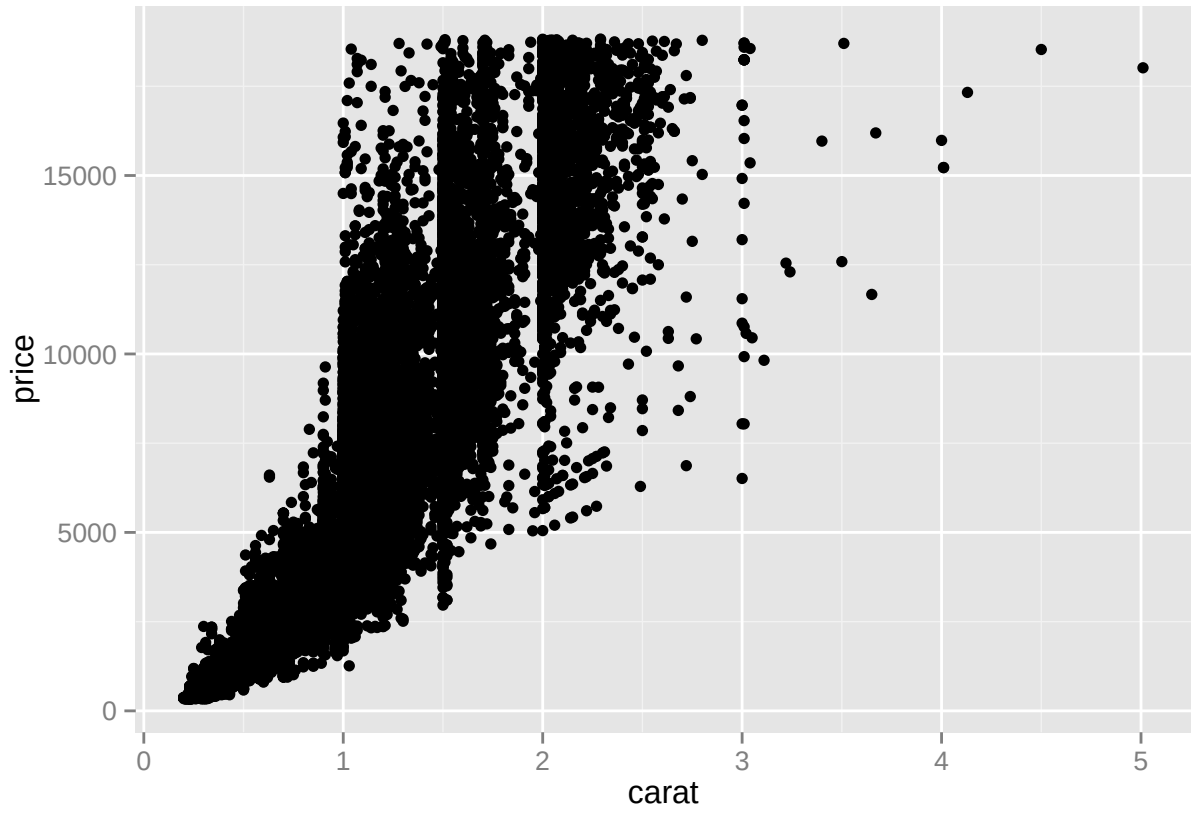

```
## best
ggplot( heightweight, aes( x = ageYear, y = heightIn, size = weightLb, colour = sex)) +
  geom_point( alpha =.5) +
  scale_size_area() + # Make area proportional to numeric value
  scale_colour_brewer( palette ="Set1")
```



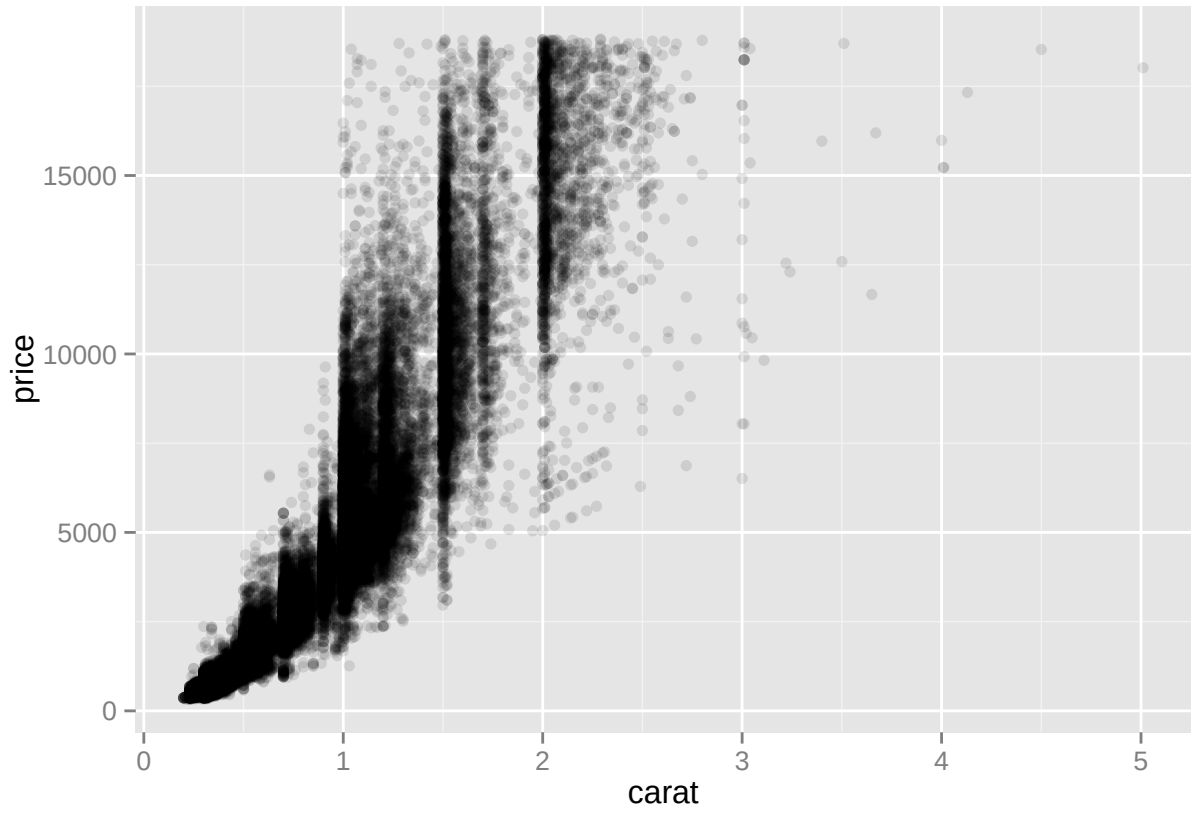
5. Dealing with Overplotting

You have many points and they obscure each other.

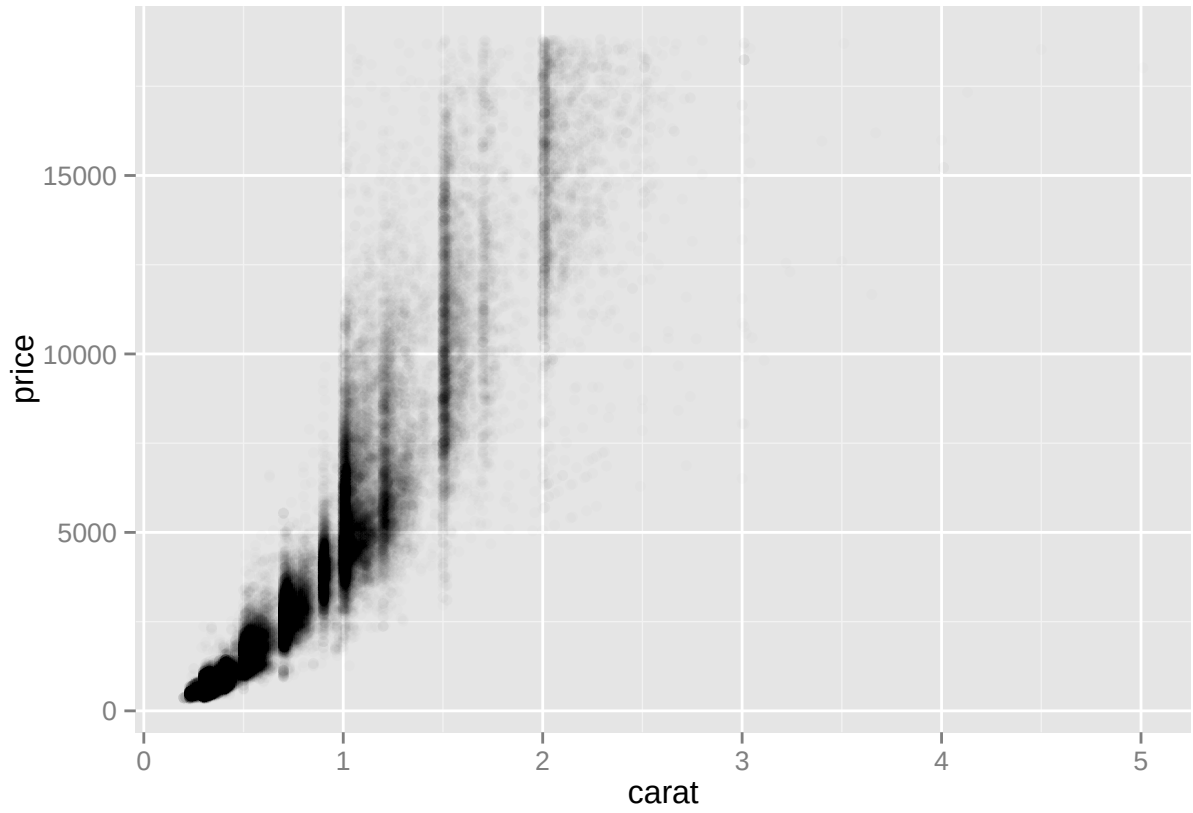
```
sp <- ggplot( diamonds, aes( x = carat, y = price))
sp +
  geom_point()
```



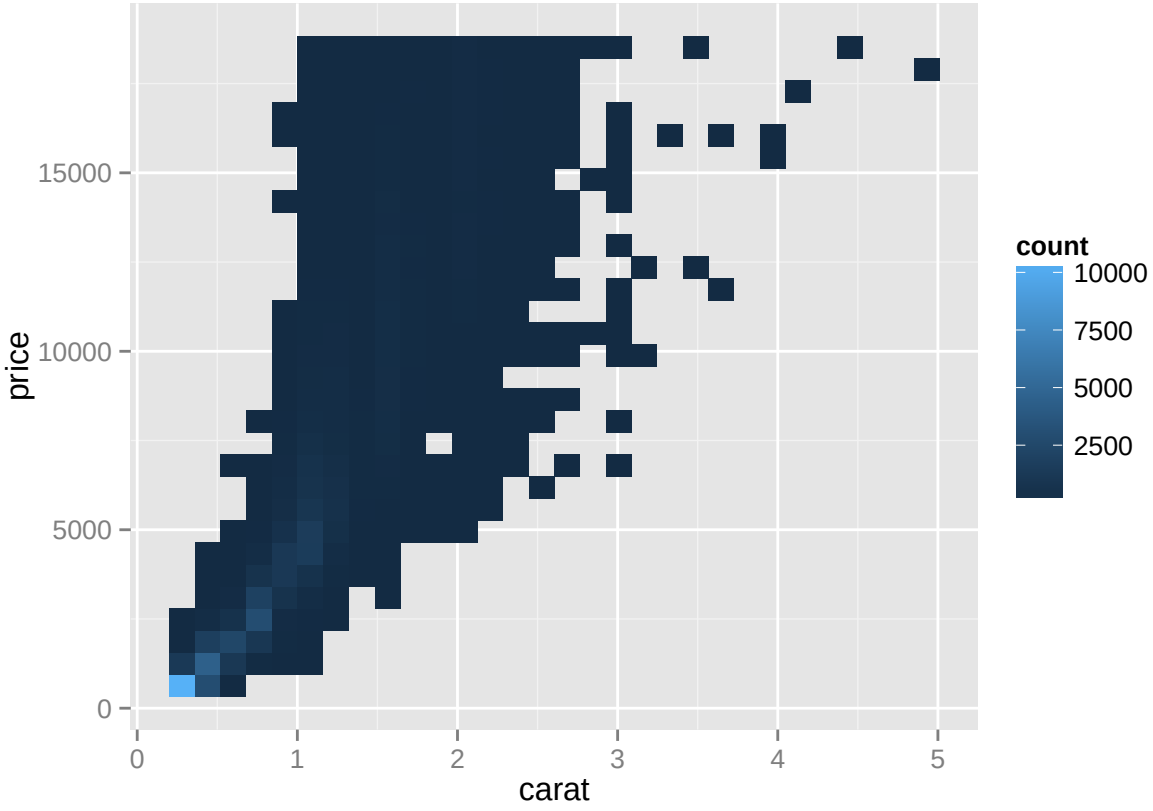

```
## We can make the points semitransparent using alpha,
sp +
  geom_point( alpha =.1)
```



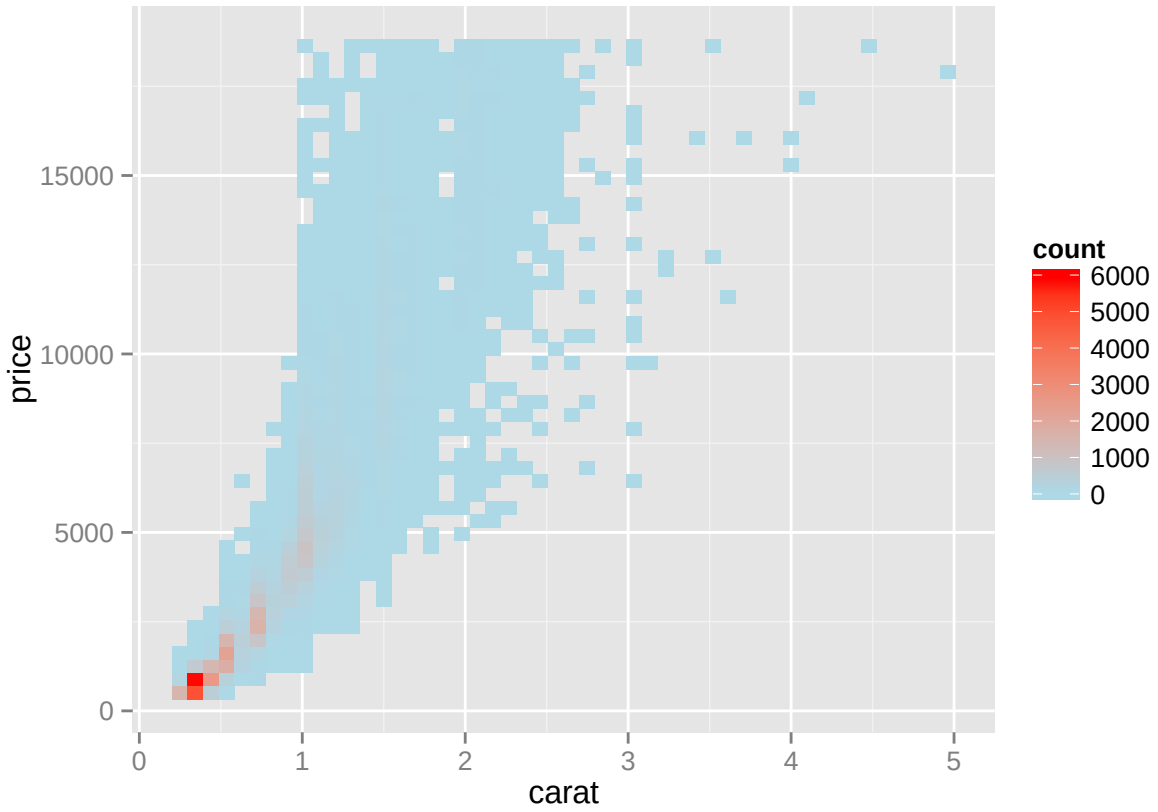

```
sp +
  geom_point( alpha =.01)
```



```
## Another solution is to bin the points into rectangles and map the density of the points to the fill
sp +
  stat_bin2d()
```

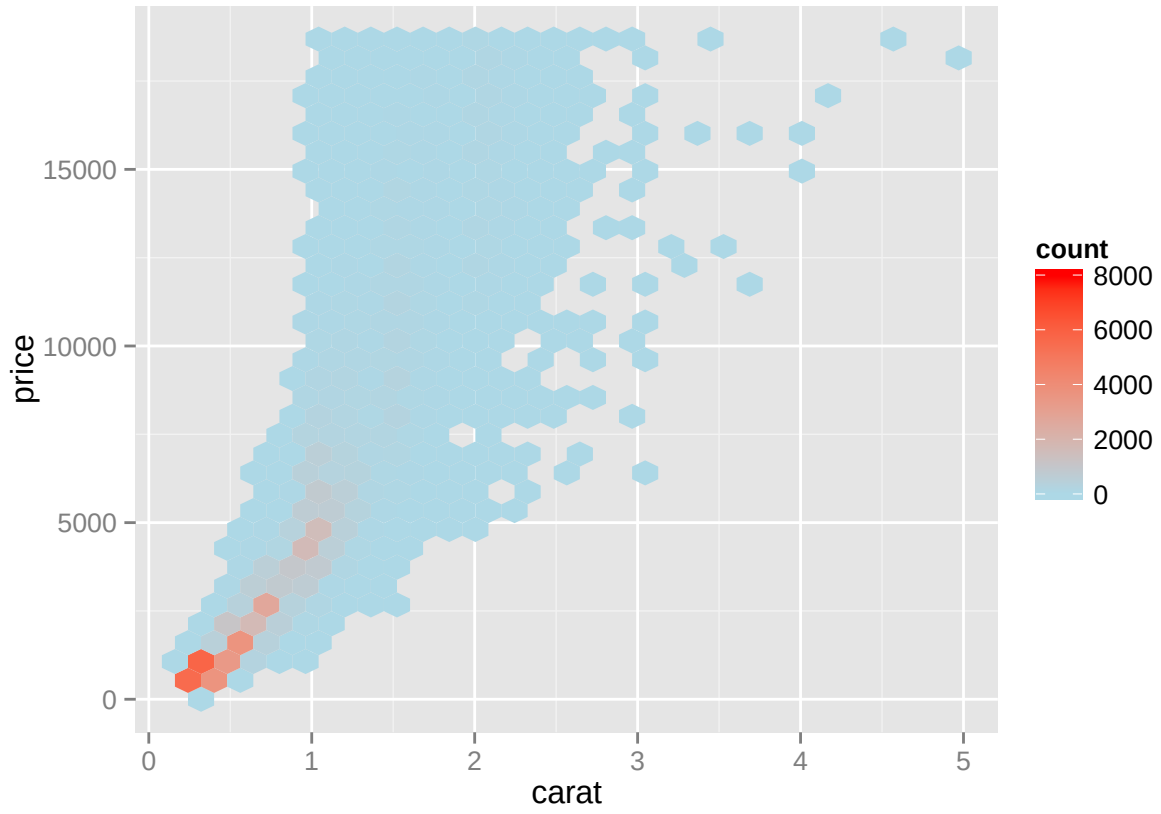



```
sp +
  stat_bin2d( bins = 50) +
  scale_fill_gradient( low ="lightblue", high ="red", limits = c( 0, 6000))
```

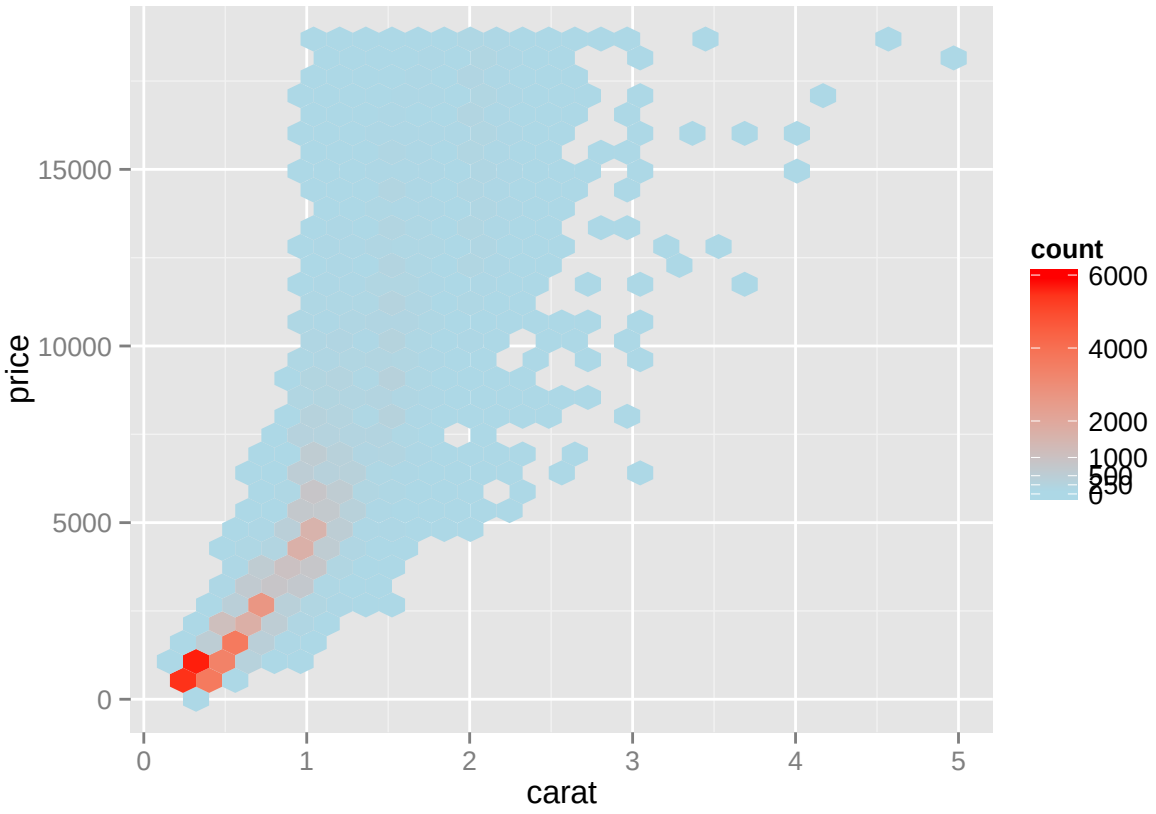


Another alternative is to bin the data into hexagons instead of rectangles, with stat_binhex. It works just like stat_bin2d().

```
library( hexbin)
sp +
  stat_binhex() +
  scale_fill_gradient( low ="lightblue", high ="red", limits = c( 0, 8000))
```

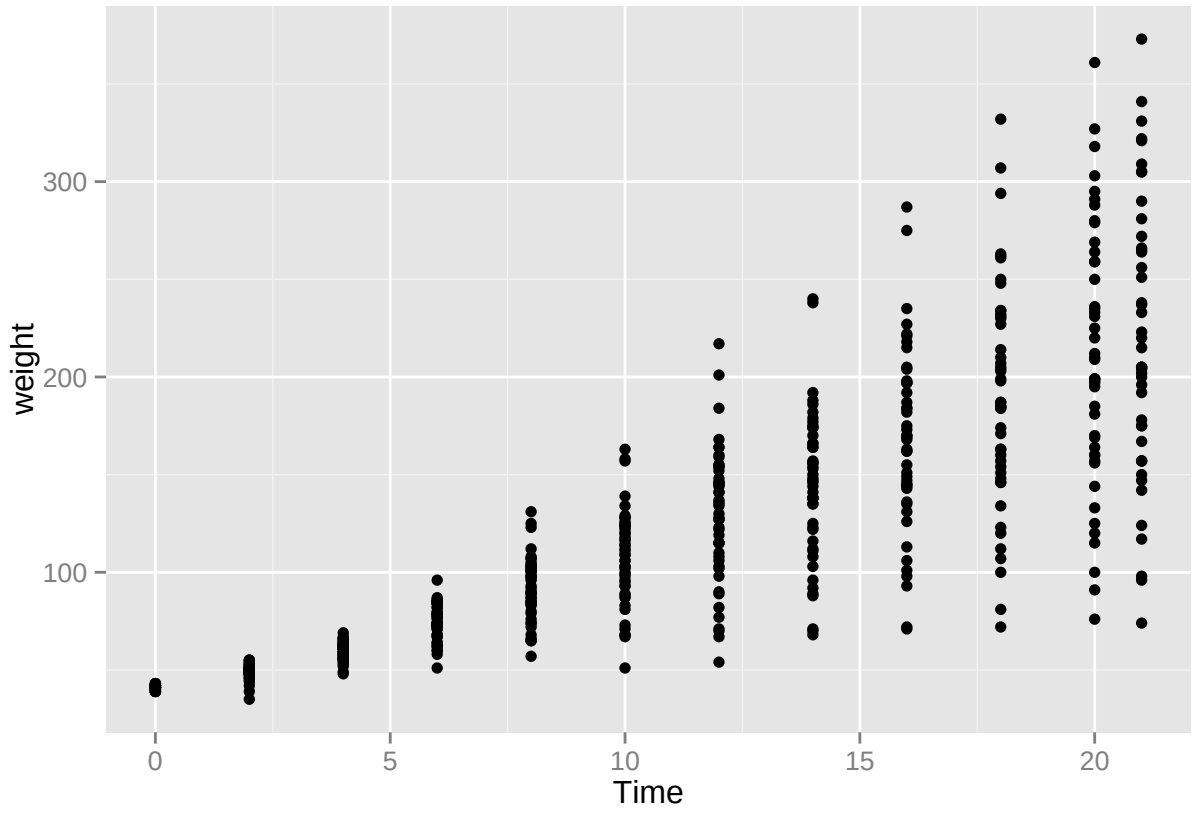



```
sp +
  stat_binhex() +
  scale_fill_gradient( low ="lightblue", high ="red", breaks = c( 0, 250, 500, 1000, 2000, 4000, 6000),
                       limits = c( 0, 6000))
```

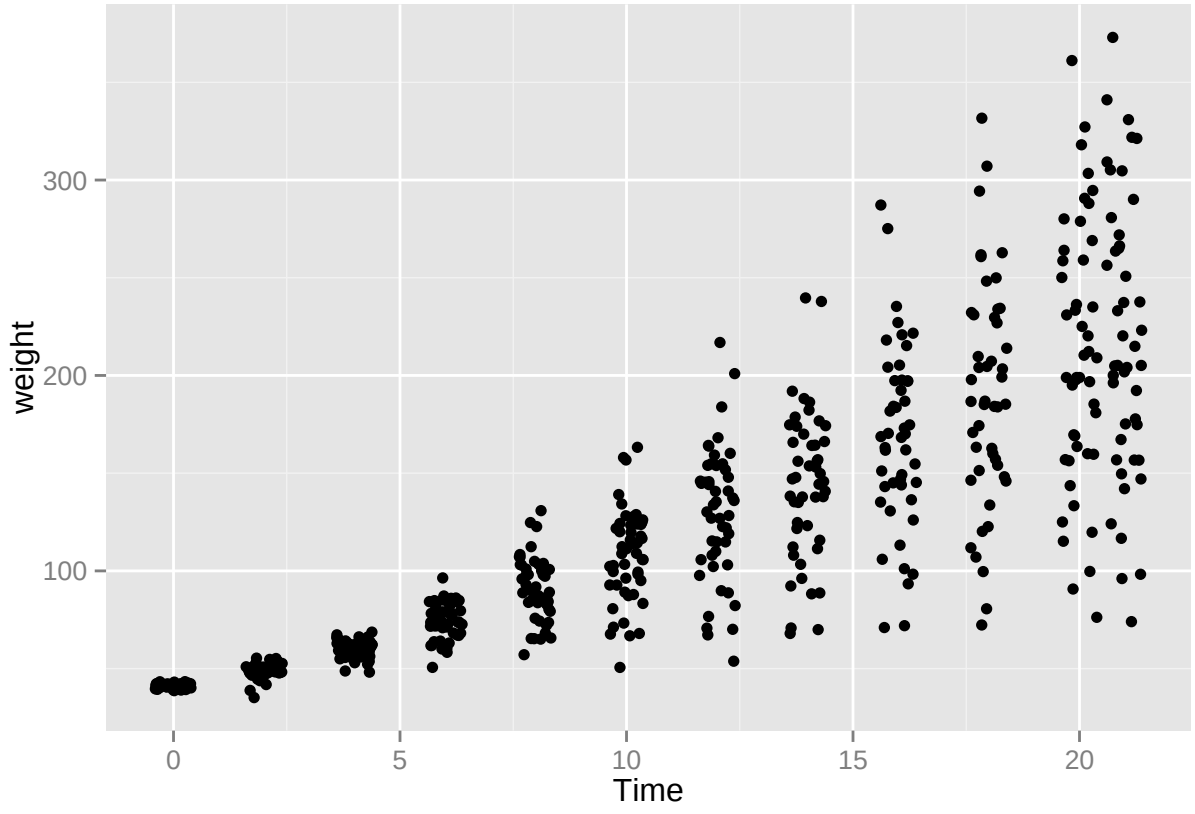


Overplotting can also occur when the data is discrete on one or both axes. In these cases, you can randomly jitter the points with position_jitter().

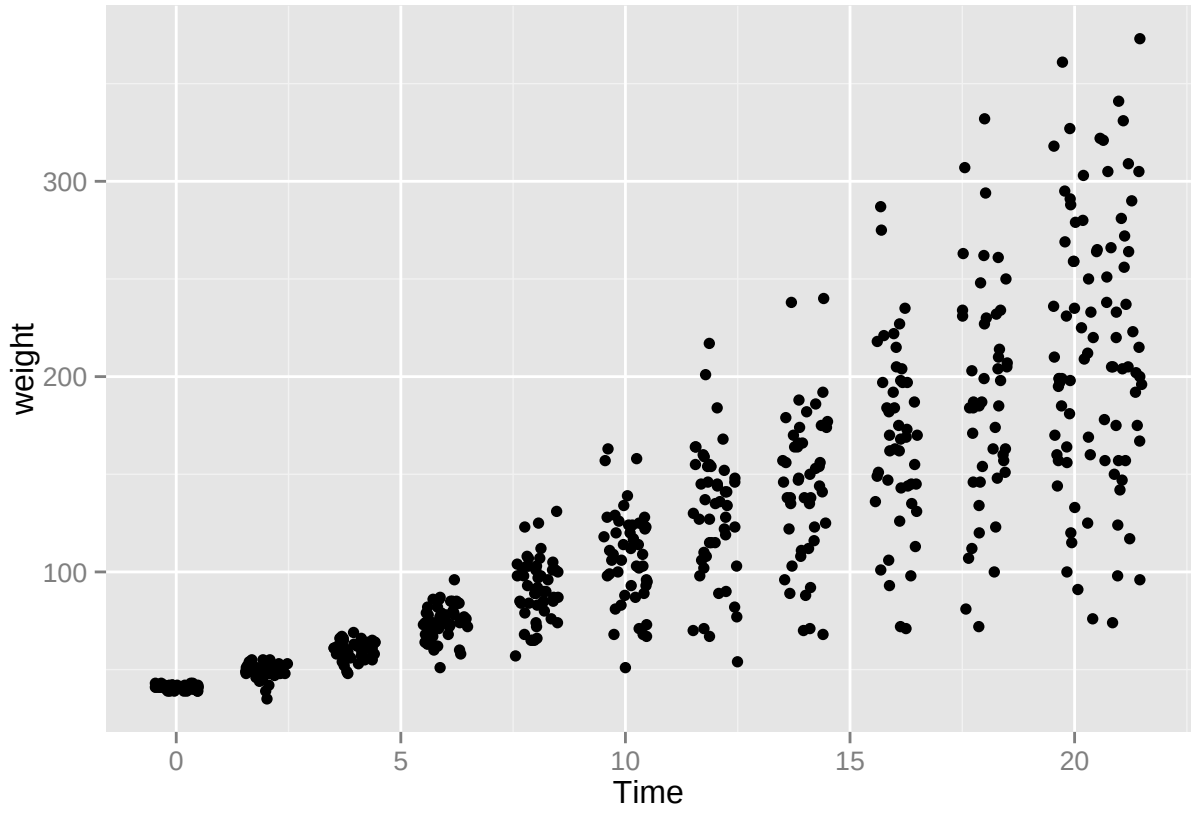
```
sp1 <- ggplot( ChickWeight, aes( x = Time, y = weight))

sp1 + geom_point()
```



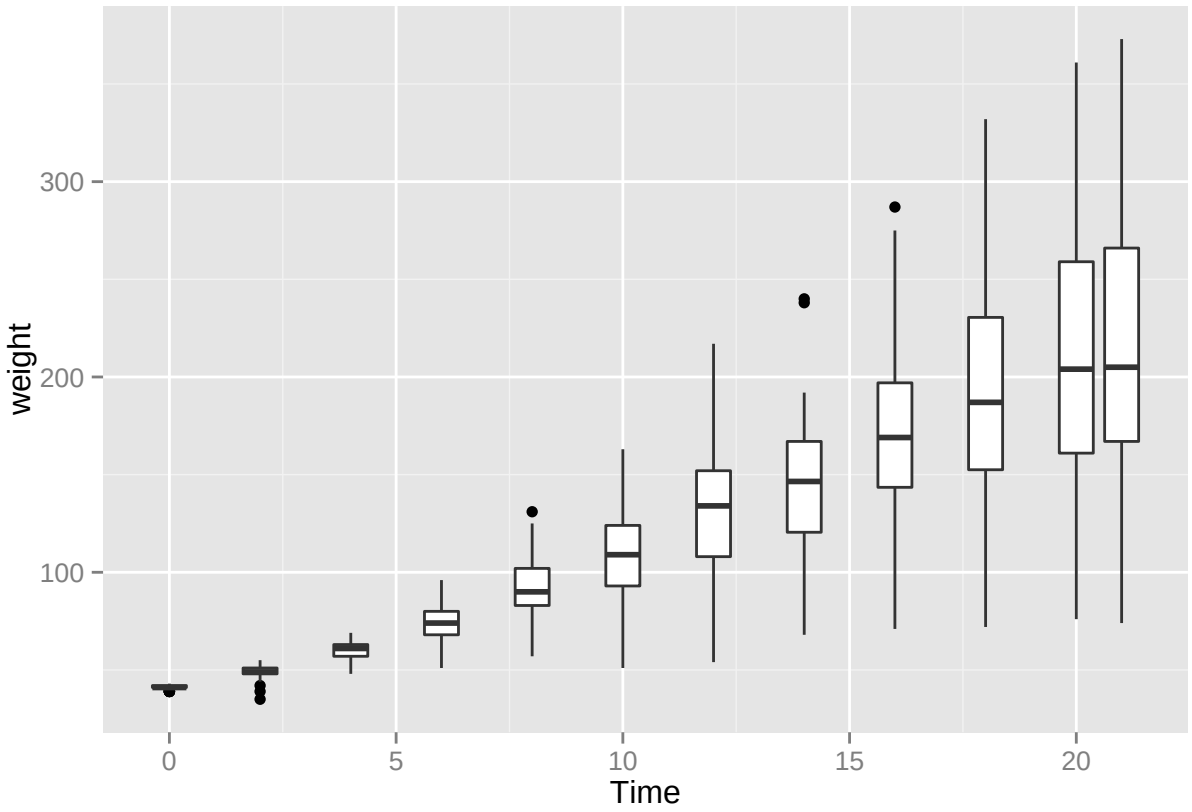

```
sp1 + geom_point( position ="jitter")
```



```
# Could also use geom_jitter(), which is equivalent
sp1 + geom_point( position = position_jitter( width =.5, height = 0))
```

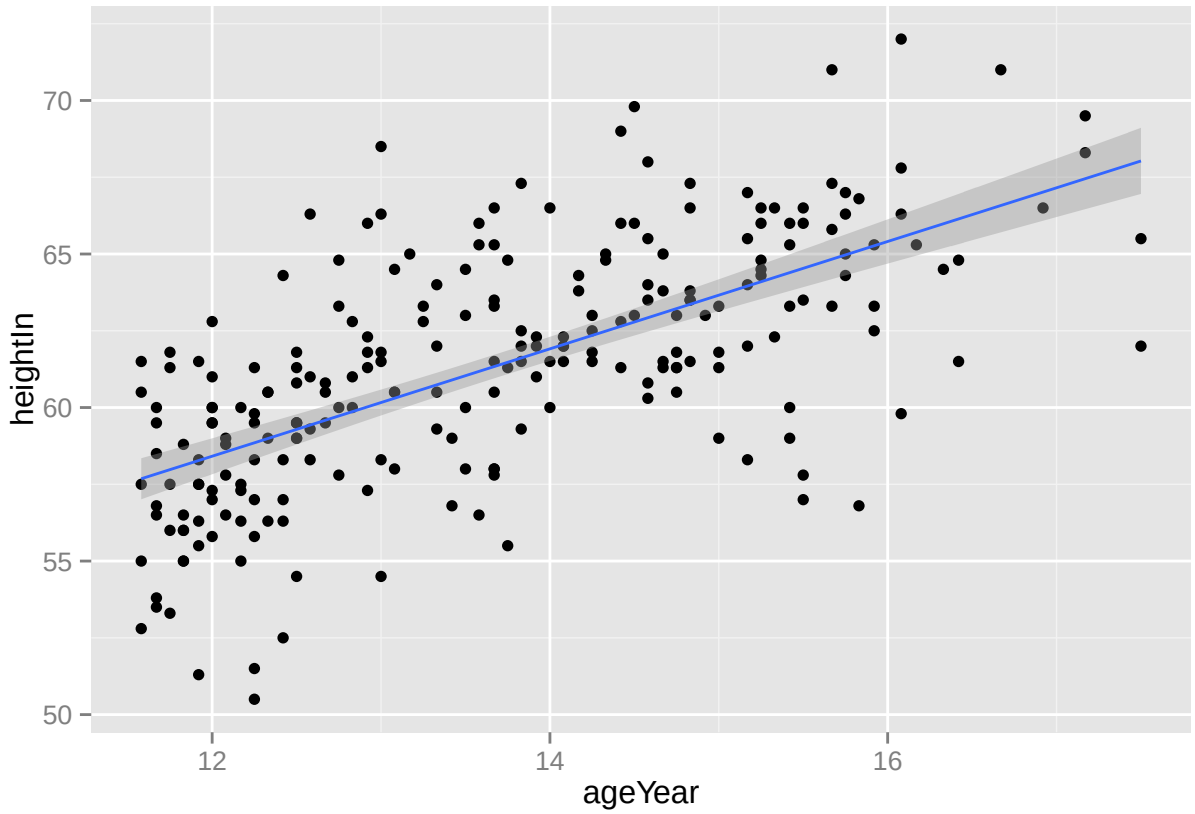



```
##
sp1 + geom_boxplot( aes( group = Time))
```

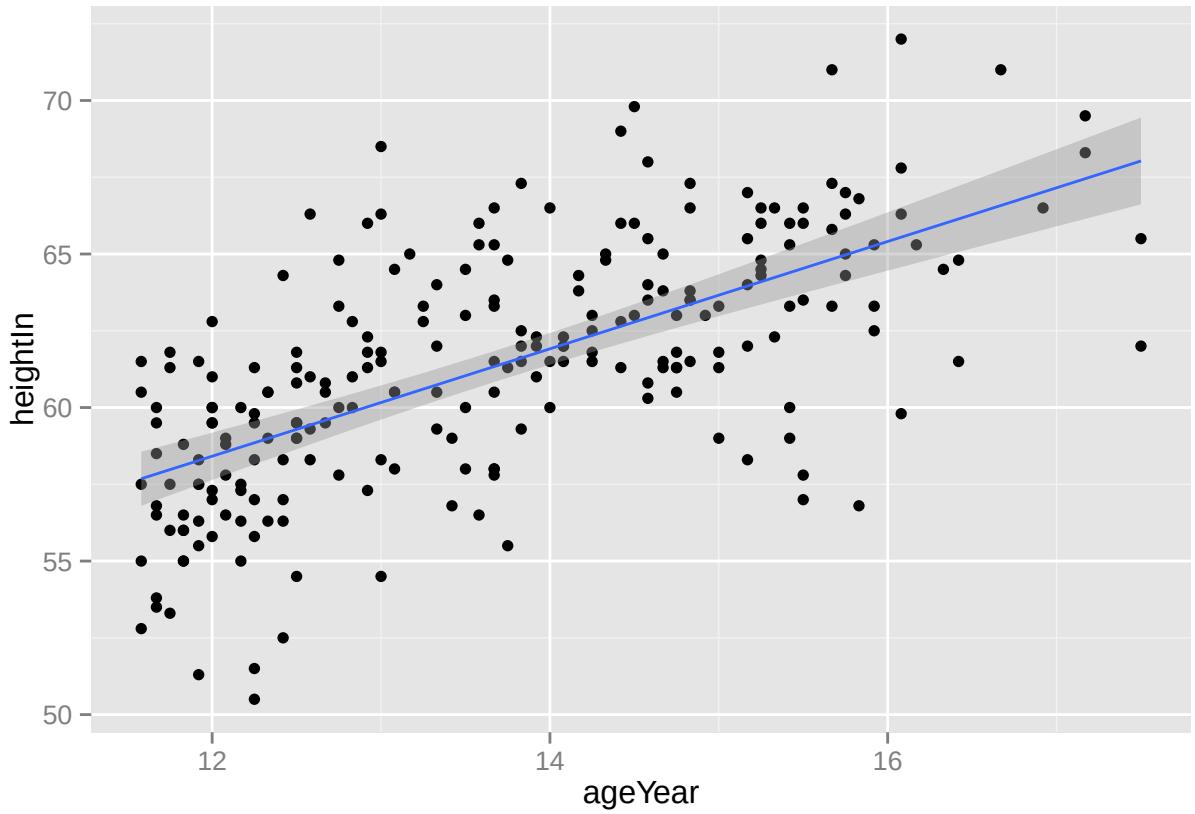


6. Adding Fitted Regression Model Lines

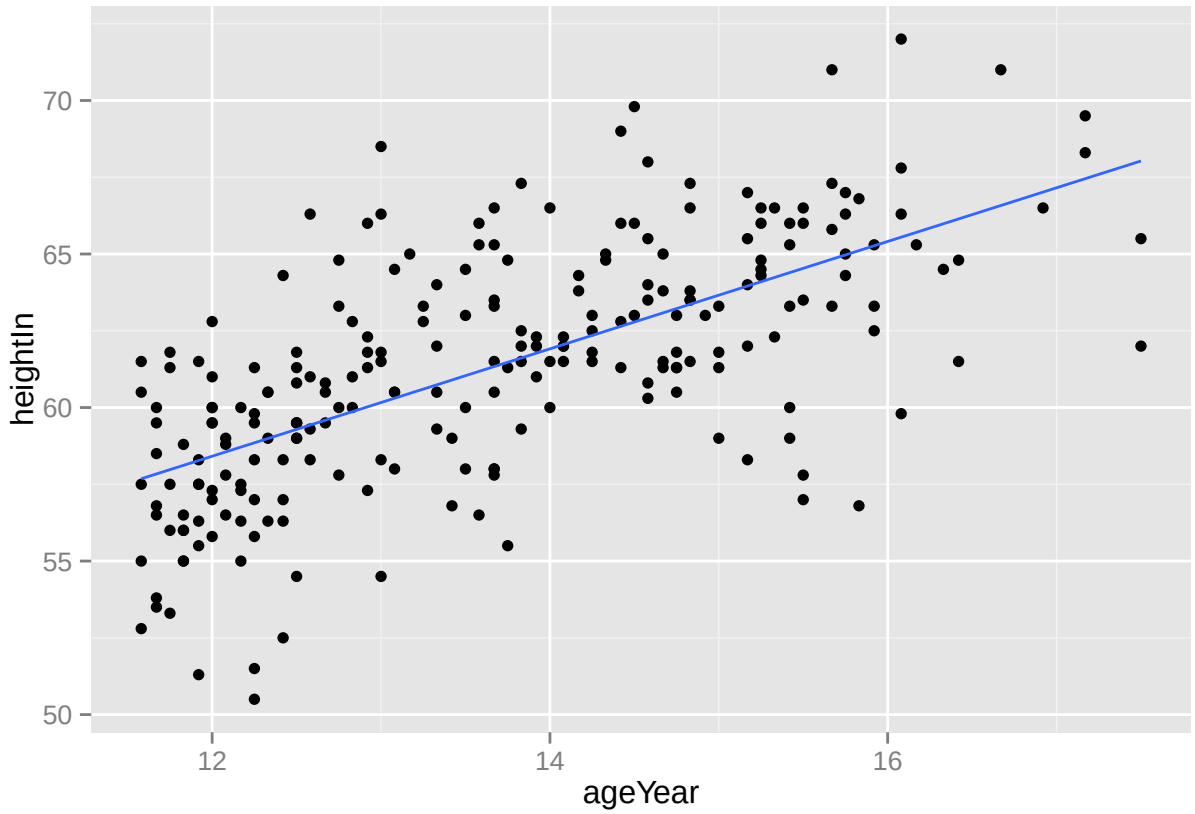
```
# The base plot
sp <- ggplot( heightweight, aes( x = ageYear, y = heightIn))

# By default, stat_smooth() also adds a 95% confidence region for the regression fit
sp +
  geom_point() +
  stat_smooth( method = lm)
```



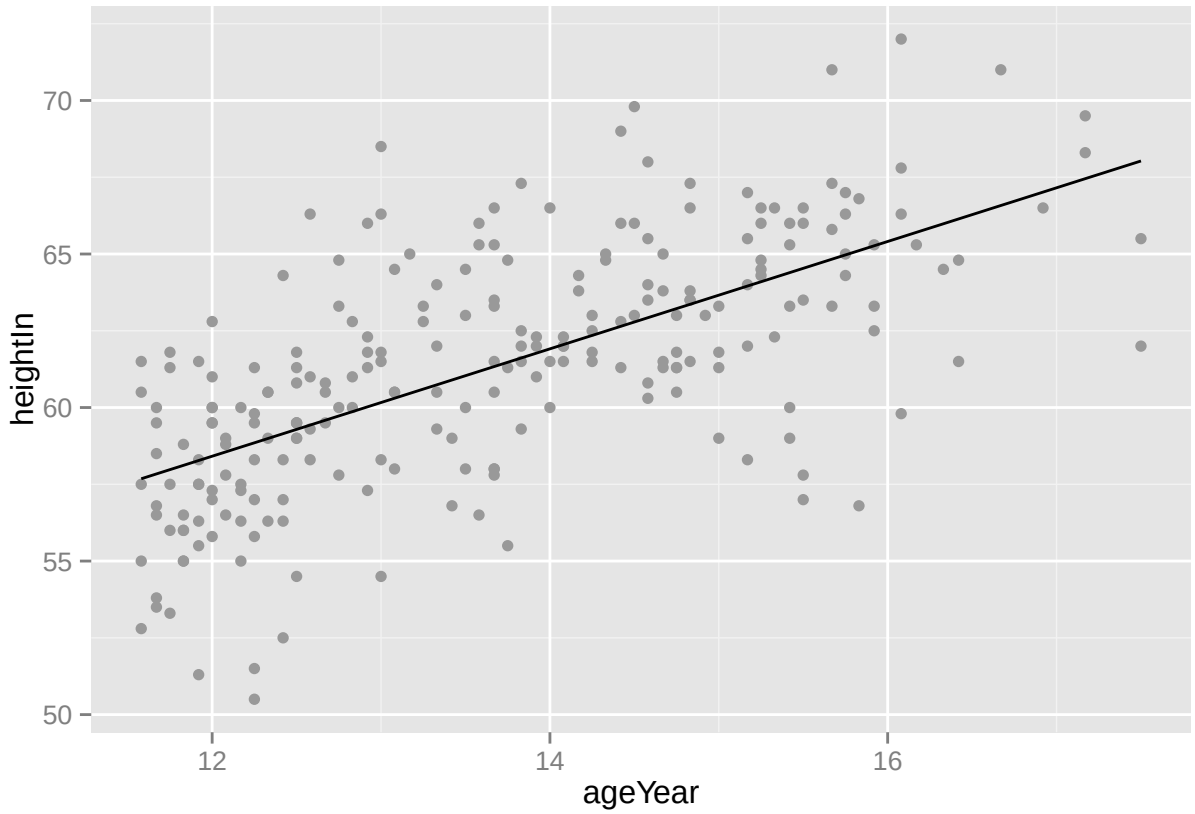

```
# 99% confidence region
sp +
  geom_point() +
  stat_smooth( method = lm, level = 0.99)
```




```
# No confidence region
sp +
  geom_point() +
  stat_smooth( method = lm, se = FALSE)
```

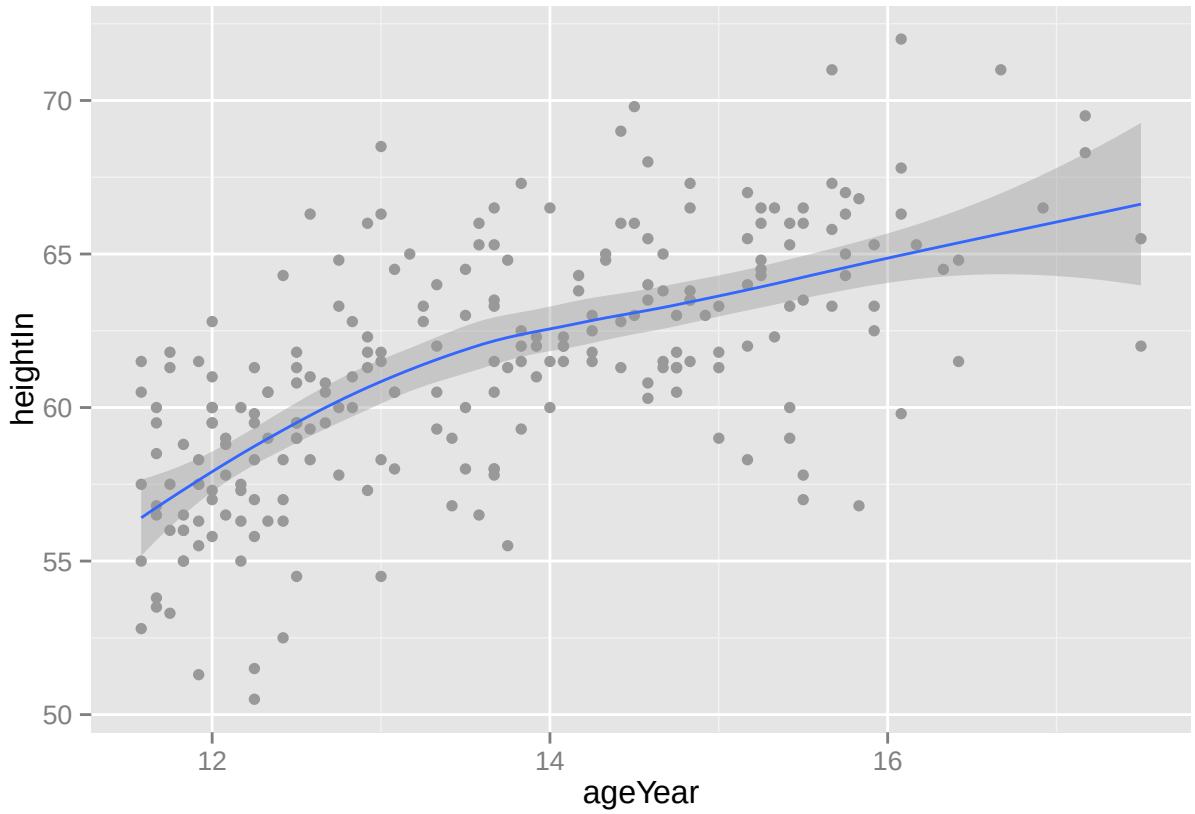



```
# The default color of the fit line is blue. This can be change by setting colour.
sp +
  geom_point( colour ="grey60") +
  stat_smooth( method = lm, se = FALSE, colour ="black")
```

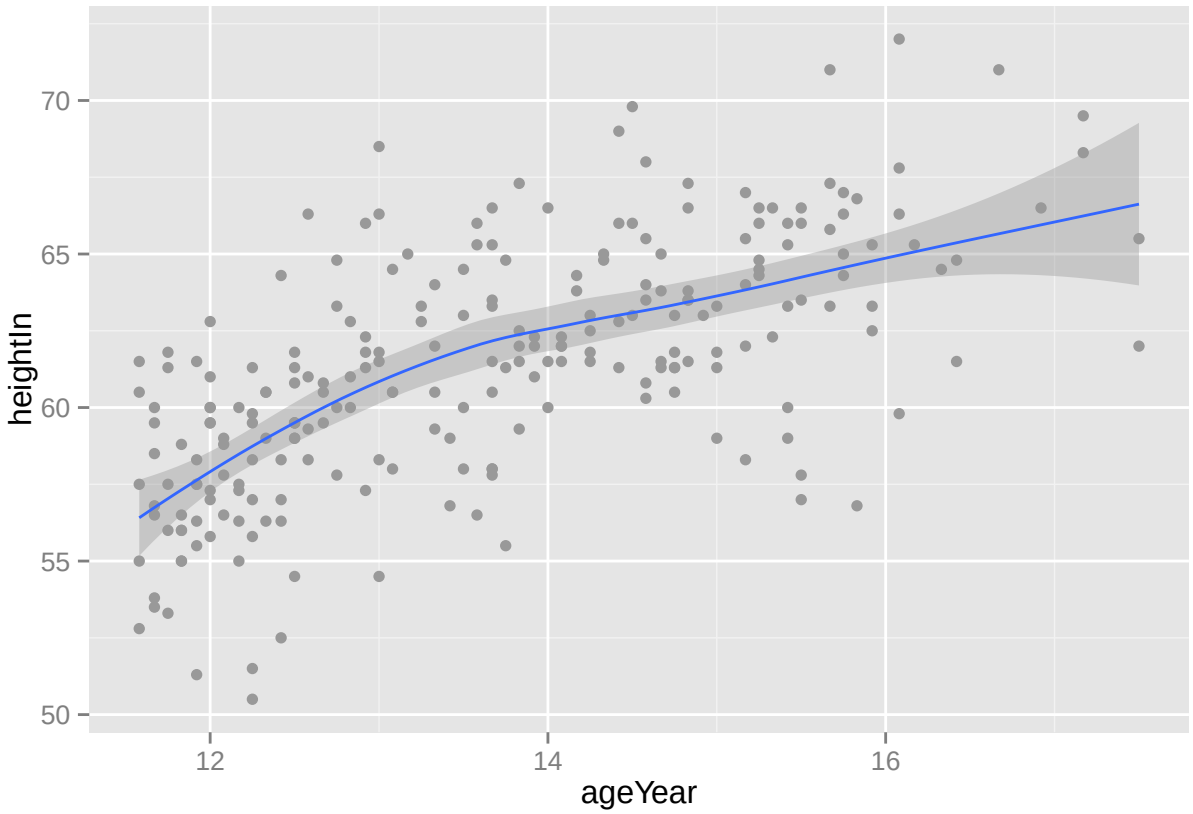



```
# If you add stat_smooth() without specifying the method, it will use a loess (locally weighted polynom
sp +
  geom_point( colour ="grey60") +
  stat_smooth()
```

```
## geom_smooth: method="auto" and size of largest group is <1000, so using loess. Use 'method = x' to cl
```




```
sp +
  geom_point( colour ="grey60") +
  stat_smooth( method = loess)
```

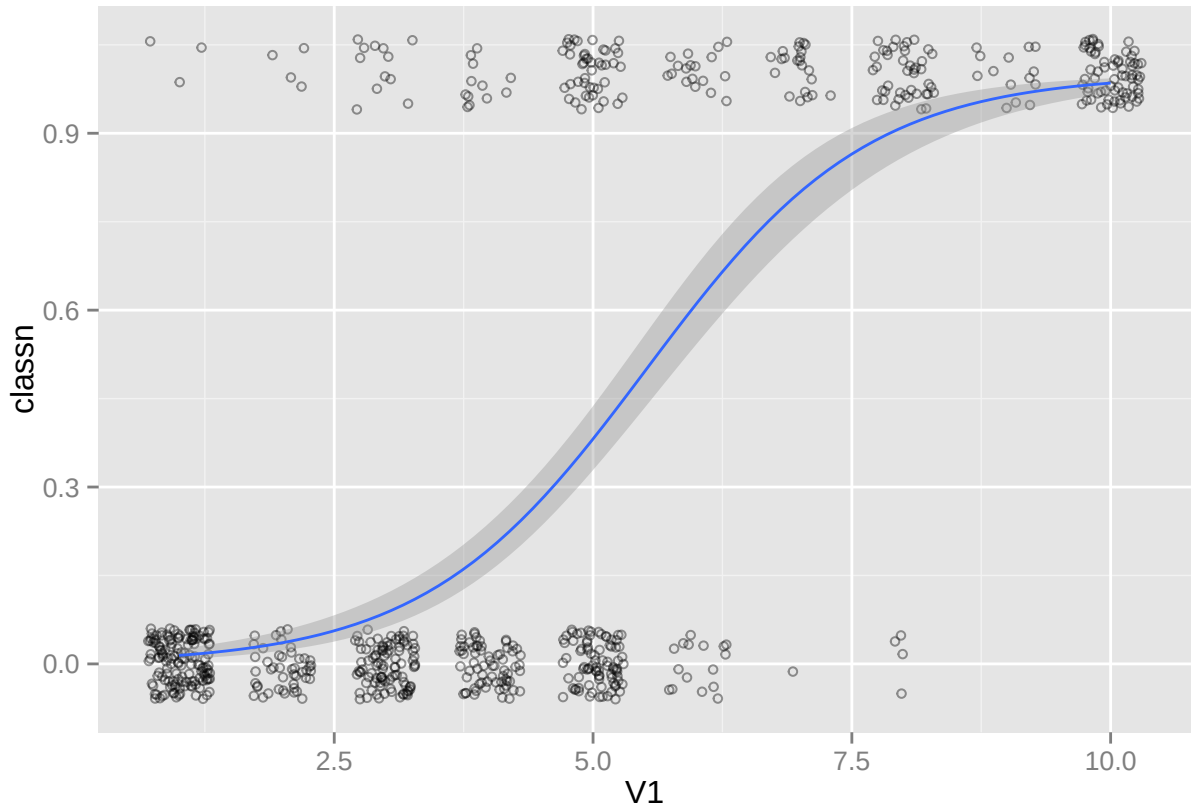


Another common type of model fit is a logistic regression.

```
library( MASS) # For the data set
b <- biopsy
b$classn[ b$class =="benign"] <- 0
b$classn[ b$class =="malignant"] <- 1
head(b)
```

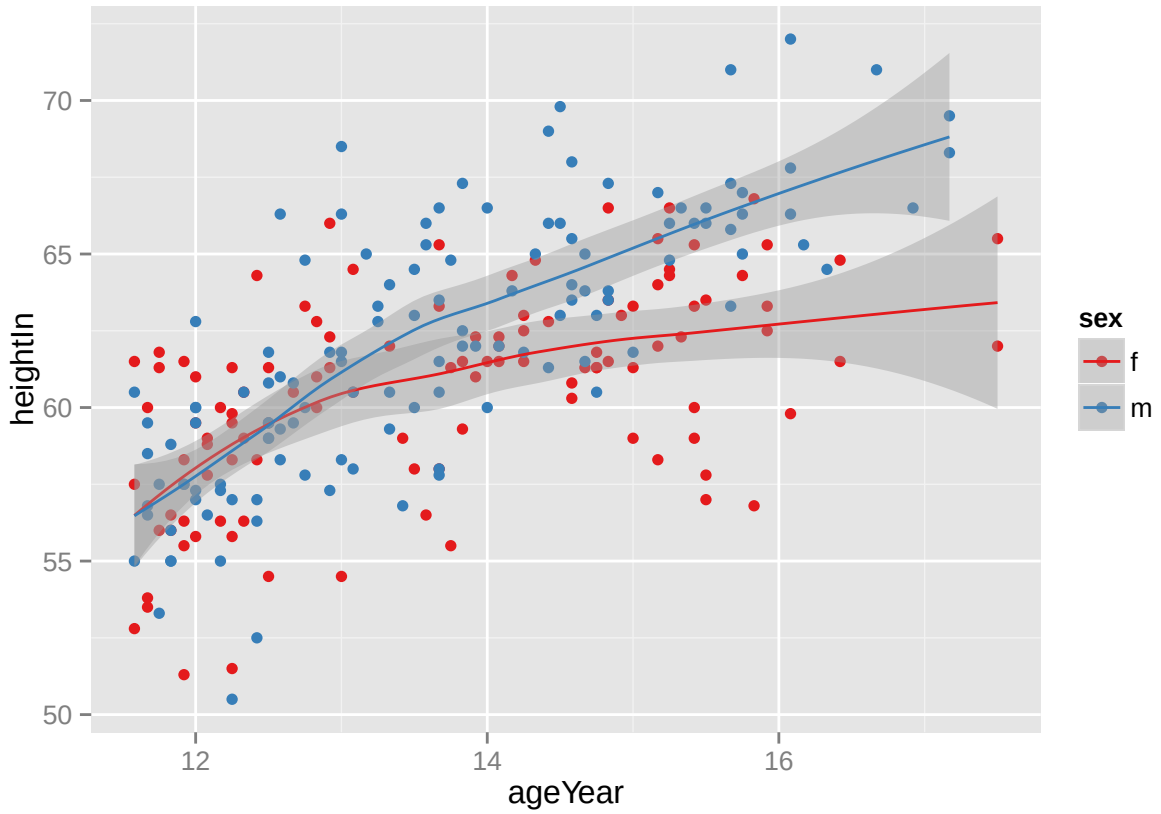
```
##        ID V1 V2 V3 V4 V5 V6 V7 V8 V9     class classn
## 1 1000025  5  1  1  1  2  1  3  1  1    benign      0
## 2 1002945  5  4  4  5  7 10  3  2  1    benign      0
## 3 1015425  3  1  1  1  2  2  3  1  1    benign      0
## 4 1016277  6  8  8  1  3  4  3  7  1    benign      0
## 5 1017023  4  1  1  3  2  1  3  1  1    benign      0
## 6 1017122  8 10 10  8  7 10  9  7  1 malignant      1
```

```
# we'll just look at the relationship of V1 (clump thickness) and the class of the tumor.
ggplot( b, aes( x = V1, y = classn)) +
  geom_point( position = position_jitter( width = 0.3, height = 0.06), alpha = 0.4, shape = 21, size =
  stat_smooth( method = glm, family = binomial)
```

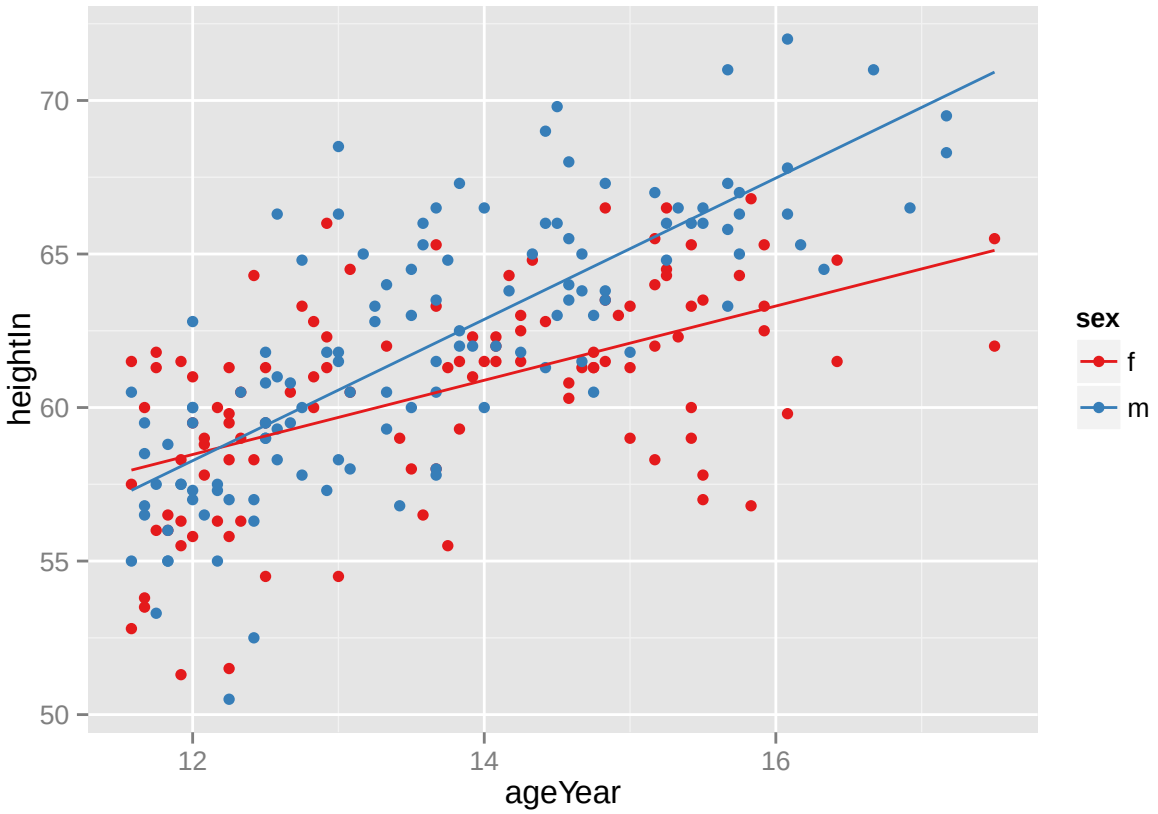



```
# If your scatter plot has points grouped by a factor, using colour or shape, one fit line will be draw
sps <- ggplot( heightweight, aes( x = ageYear, y = heightIn, colour = sex)) +
  geom_point() +
  scale_colour_brewer( palette ="Set1")
sps + geom_smooth()
```

```
## geom_smooth: method="auto" and size of largest group is <1000, so using loess. Use 'method = x' to cl
```




```
# If you want the lines to extrapolate from the data
sps +
  geom_smooth( method = lm, se = FALSE, fullrange = TRUE)
```



7. If you want the lines to extrapolate from the data

You have already created a fitted regression model object for a data set, and you want to plot the lines for that model.

```
model <- lm( heightIn ~ ageYear + I(ageYear^2), heightweight)
model
```

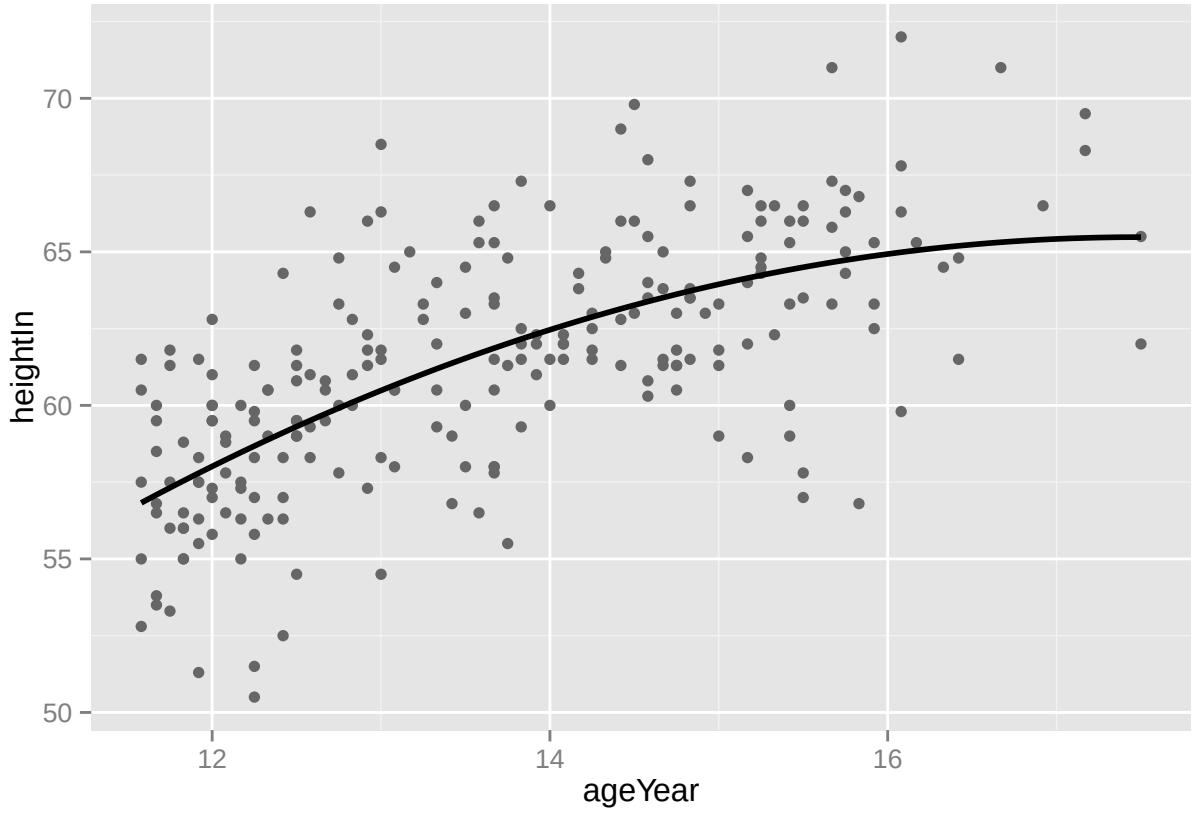
```
##
## Call:
## lm(formula = heightIn ~ ageYear + I(ageYear^2), data = heightweight)
##
## Coefficients:
##  (Intercept)       ageYear  I(ageYear^2)
##     -10.3136        8.6673       -0.2478
```

```
# Create a data frame with ageYear column, interpolating across range
xmin <- min( heightweight$ageYear)
xmax <- max( heightweight$ageYear)
predicted <- data.frame( ageYear = seq( xmin, xmax, length.out = 100))
predicted$heightIn <- predict( model, predicted)
head(predicted)
```

```
##    ageYear heightIn
## 1 11.58000 56.82624
## 2 11.63980 57.00047
```

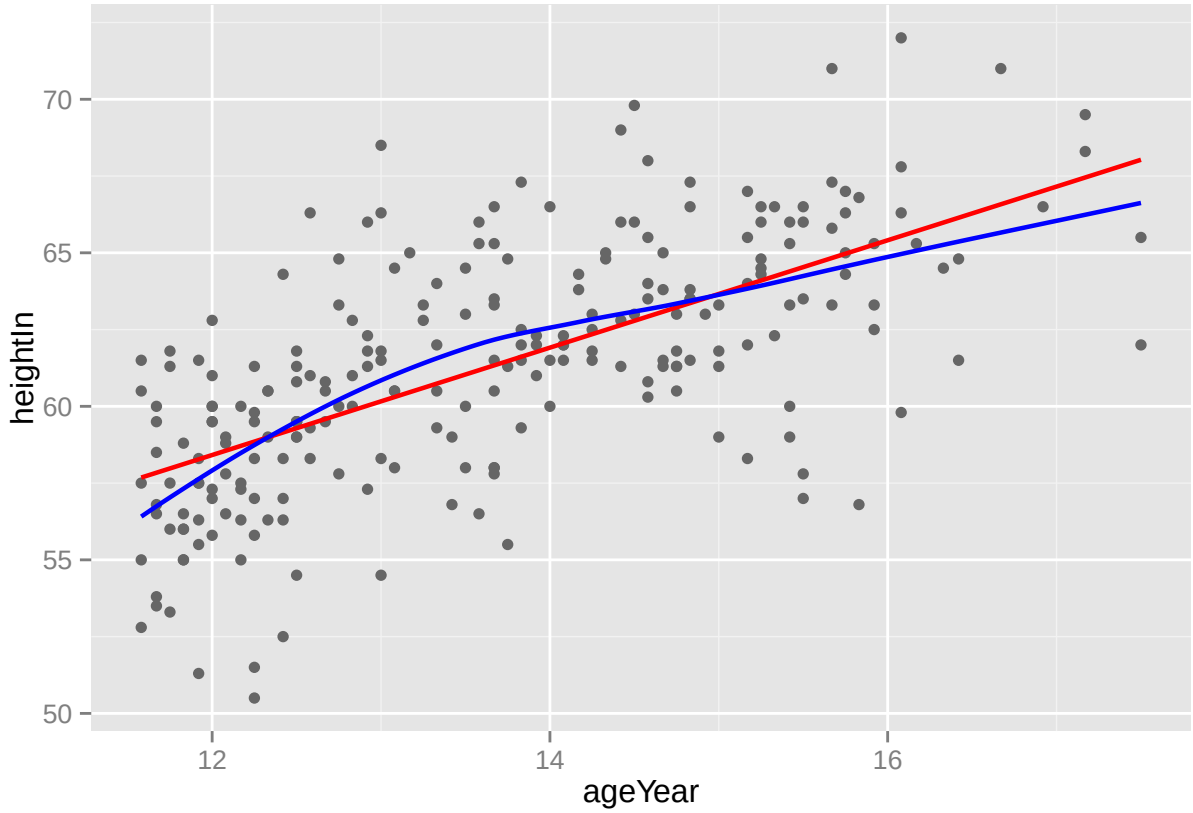
```
## 3 11.69960 57.17294
## 4 11.75939 57.34363
## 5 11.81919 57.51255
## 6 11.87899 57.67969
```

```
# We can now plot the data points along with the values predicted from the model
sp <- ggplot( heightweight, aes( x = ageYear, y = heightIn)) +
  geom_point( colour ="grey40")

sp + geom_line( data = predicted, size = 1)
```




```
# Given a model, predict values of yvar from xvar
# This supports one predictor and one predicted variable
# xrange: If NULL, determine the x range from the model object. If a vector with
# two numbers, use those as the min and max of the prediction range.
# samples: Number of samples across the x range.
# ...: Further arguments to be passed to predict()
predictvals <- function( model, xvar, yvar, xrange = NULL, samples = 100, ...) {
  # If xrange isn't passed in, determine xrange from the models.
  # Different ways of extracting the x range, depending on model type
  if (is.null(xrange)) {
    if (any( class( model) %in% c("lm", "glm")))
      xrange <- range( model $ model[[ xvar]])
    else if (any( class( model) %in% "loess")) xrange <- range( model $ x)
    }
  newdata <- data.frame( x = seq( xrange[1], xrange[2], length.out = samples))
  names( newdata) <- xvar
```

```
  newdata[[ yvar]] <- predict( model, newdata = newdata, ...)
  newdata
  }

modlinear <- lm( heightIn ~ ageYear, heightweight)
modloess <- loess( heightIn ~ ageYear, heightweight)

lm_predicted <- predictvals( modlinear, "ageYear", "heightIn")
loess_predicted <- predictvals( modloess, "ageYear", "heightIn")

sp +
  geom_line( data = lm_predicted, colour ="red", size =.8) +
  geom_line( data = loess_predicted, colour ="blue", size =.8)
```



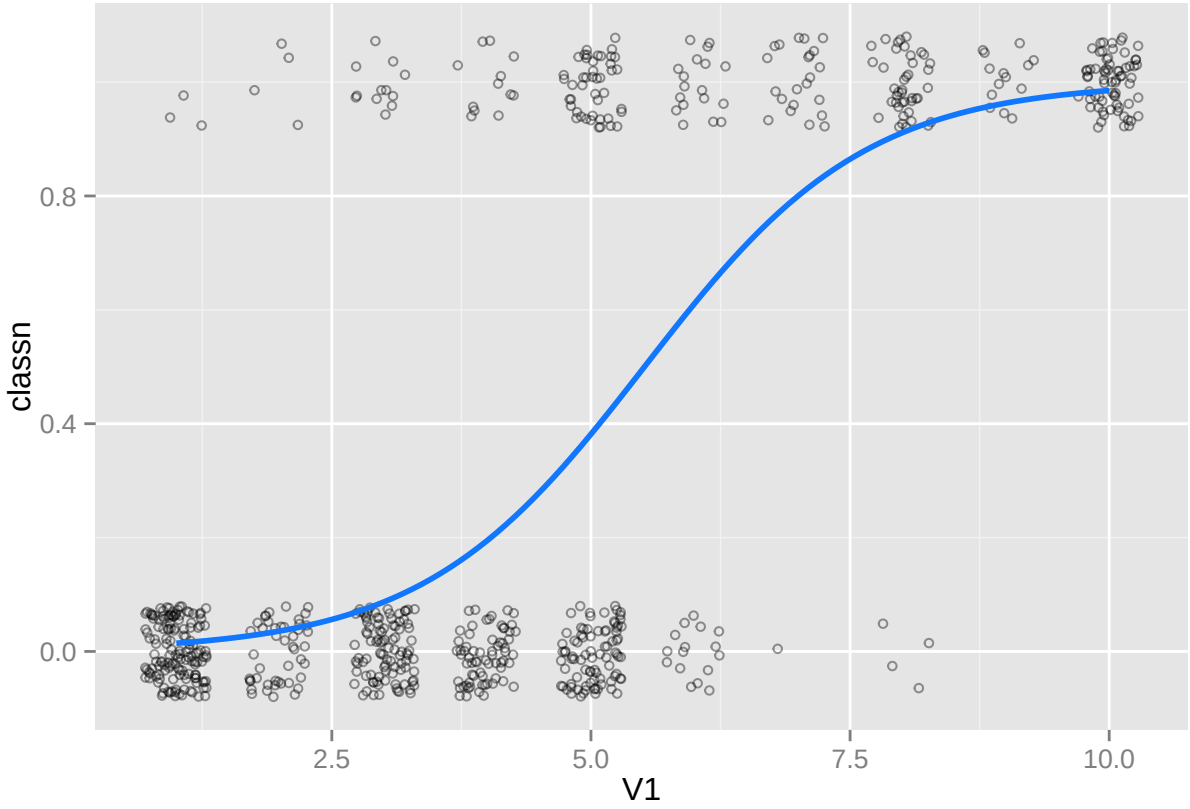
For glm models that use a nonlinear link function, you need to specify type =" response"

```
library( MASS) # For the data set
b <- biopsy
b$classn[ b$class =="benign"] <- 0
b$classn[ b$class =="malignant"] <- 1
head(b)
```

```
##        ID V1 V2 V3 V4 V5 V6 V7 V8 V9     class classn
## 1 1000025  5  1  1  1  2  1  3  1  1    benign      0
## 2 1002945  5  4  4  5  7 10  3  2  1    benign      0
## 3 1015425  3  1  1  1  2  2  3  1  1    benign      0
## 4 1016277  6  8  8  1  3  4  3  7  1    benign      0
```

```
## 5 1017023  4  1  1  3  2  1  3  1  1    benign      0
## 6 1017122  8 10 10  8  7 10  9  7  1 malignant      1
```

```
# glm model
fitlogistic <- glm( classn ~ V1, b, family = binomial)

# Get predicted values
glm_predicted <- predictvals( fitlogistic, "V1", "classn", type ="response")

ggplot( b, aes( x = V1, y = classn)) +
  geom_point( position = position_jitter( width =.3, height =.08), alpha = 0.4, shape = 21, size = 1.5)
  geom_line( data = glm_predicted, colour ="#1177FF", size = 1)
```



8. Adding Fitted Lines from Multiple Existing Models

With the heightweight data set, we'll make a linear model with lm() for each of the levels of sex, and put those model objects in a list. The model building is done with a function, make_model()

```
make_model <- function( data) {
  lm( heightIn ~ ageYear, data)
  }
models <- dlply( heightweight, "sex", .fun = make_model) # Print out the list of two lm objects, f and
models
```

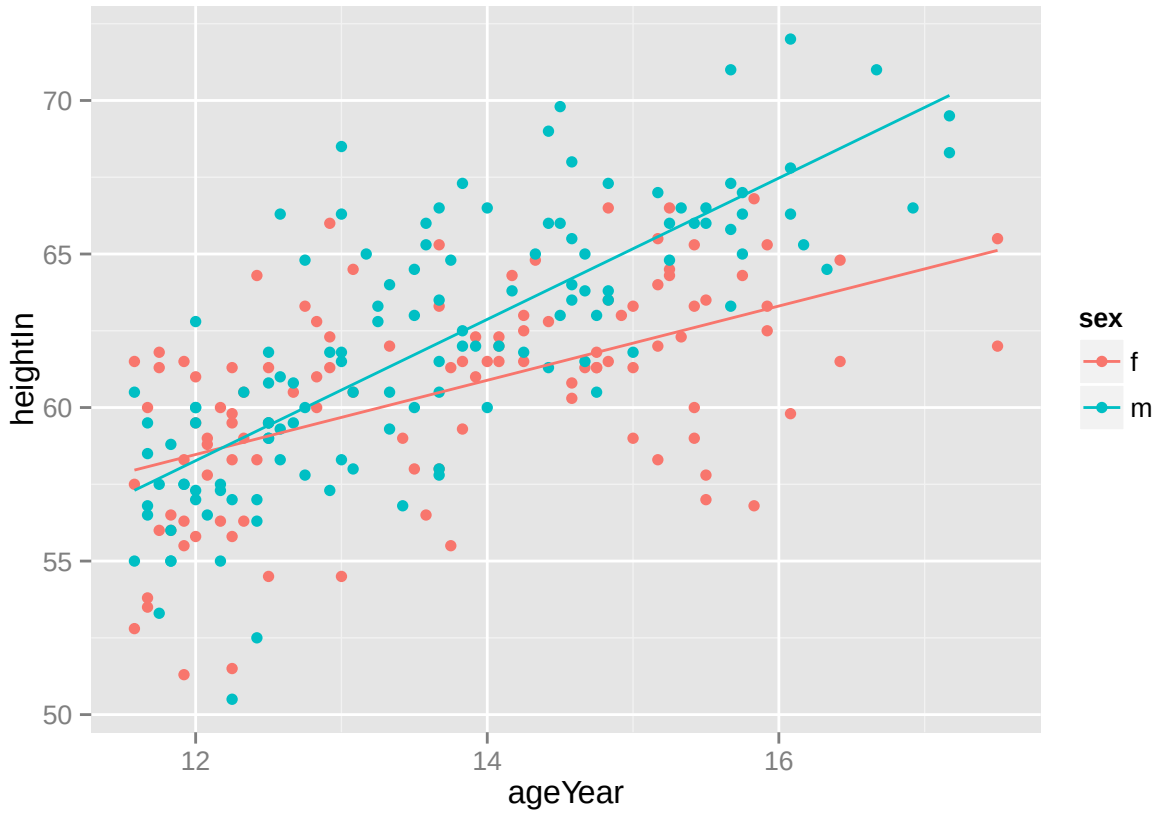
```
## $f
##
```

```
## Call:
## lm(formula = heightIn ~ ageYear, data = data)
##
## Coefficients:
## (Intercept)      ageYear
##      43.963        1.209
##
##
## $m
##
## Call:
## lm(formula = heightIn ~ ageYear, data = data)
##
## Coefficients:
## (Intercept)      ageYear
##      30.658        2.301
##
##
## attr(,"split_type")
## [1] "data.frame"
## attr(,"split_labels")
##   sex
## 1   f
## 2   m
```

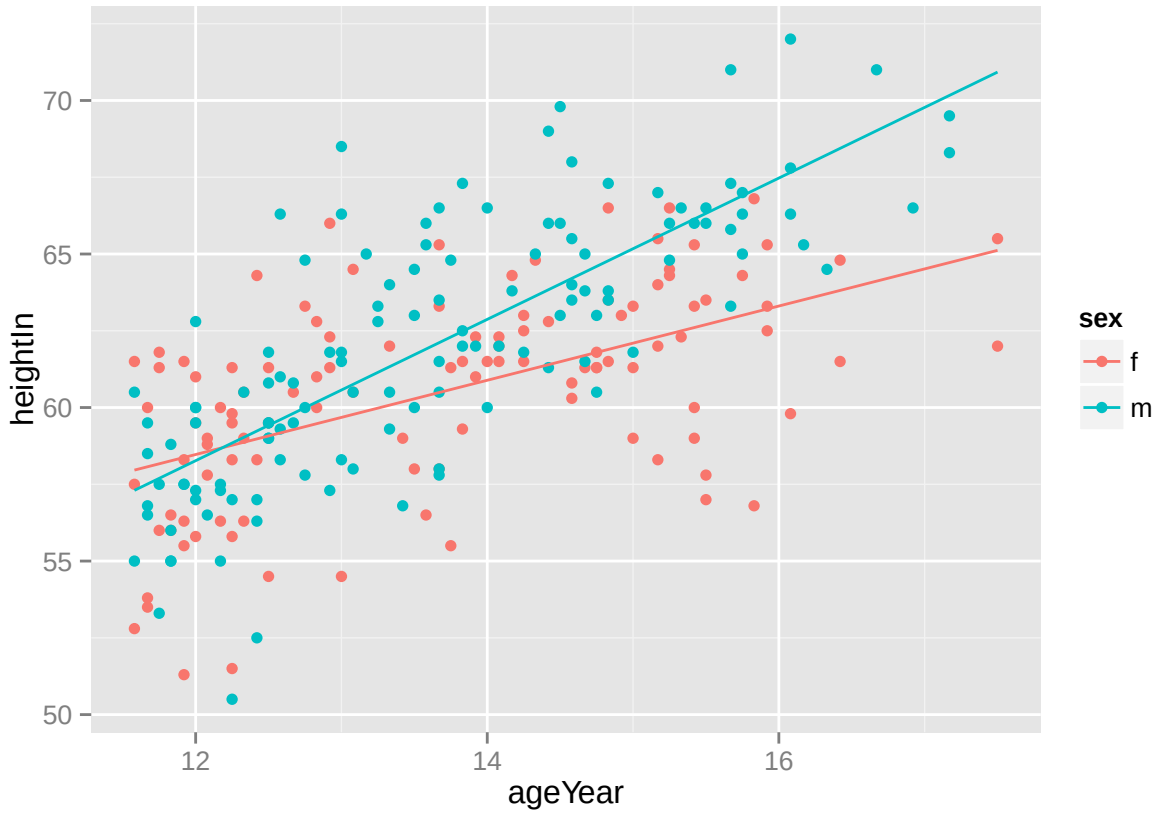
```
# Now that we have the list of model objects, we can run predictvals() to get predicted values from eac
predvals <- ldply( models, .fun = predictvals, xvar ="ageYear", yvar ="heightIn")
head(predvals)
```

```
##   sex  ageYear heightIn
## 1   f 11.58000 57.96250
## 2   f 11.63980 58.03478
## 3   f 11.69960 58.10707
## 4   f 11.75939 58.17936
## 5   f 11.81919 58.25165
## 6   f 11.87899 58.32394
```

```
# Finally, we can plot the data with the predicted values
ggplot( heightweight, aes( x = ageYear, y = heightIn, colour = sex)) +
  geom_point() +
  geom_line( data = predvals)
```




```
predvals <- ldply( models, .fun = predictvals, xvar ="ageYear", yvar ="heightIn",
                   xrange = range( heightweight$ageYear))
ggplot( heightweight, aes( x = ageYear, y = heightIn, colour = sex)) +
  geom_point() + geom_line( data = predvals)
```

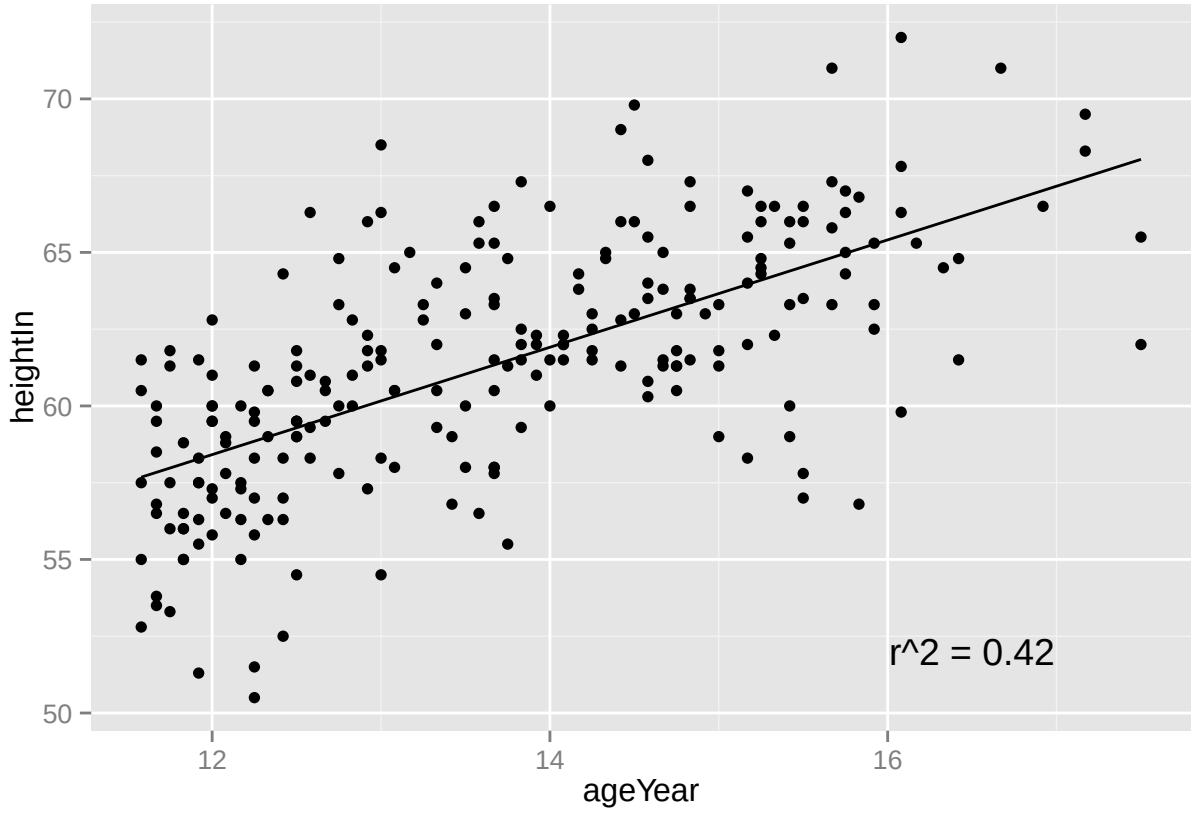


9. Adding Annotations with Model Coefficients

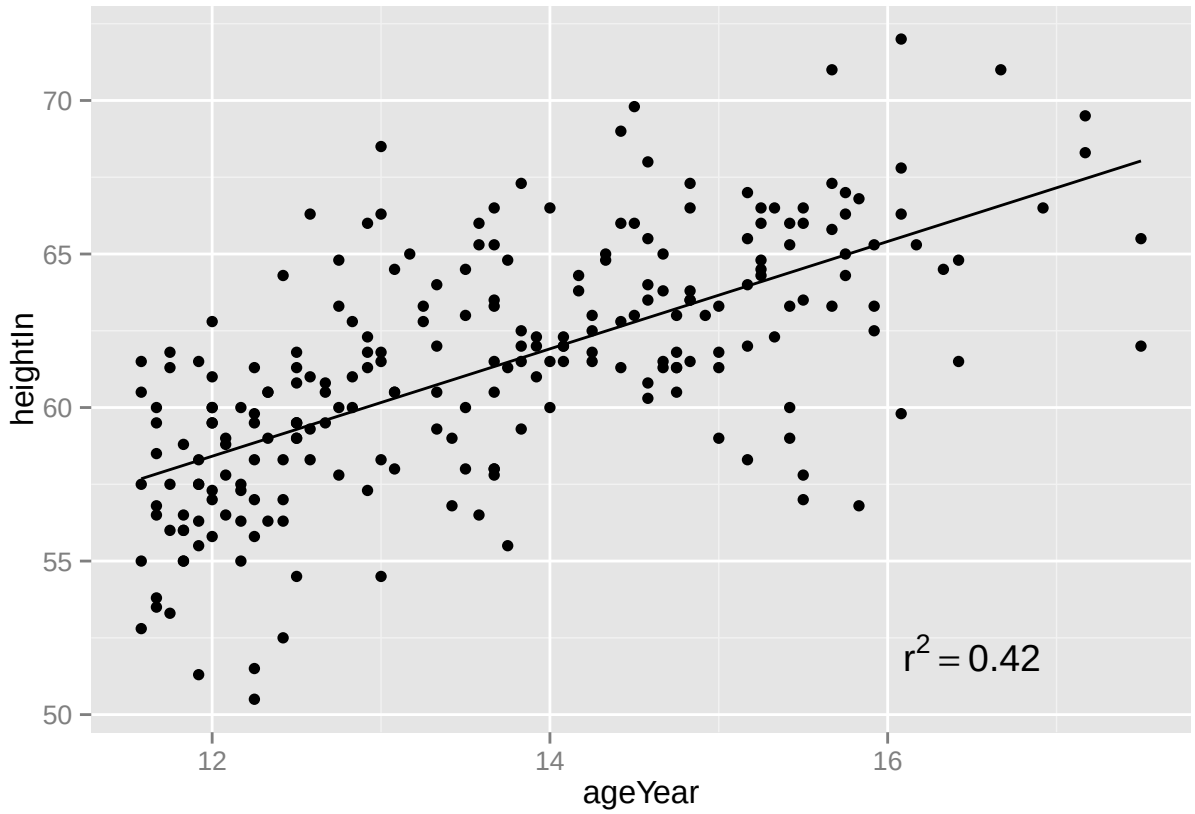
```
model <- lm( heightIn ~ ageYear, heightweight)
summary( model)
```

```
##
## Call:
## lm(formula = heightIn ~ ageYear, data = heightweight)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.3517 -1.9006  0.1378  1.9071  8.3371
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  37.4356     1.8281   20.48   <2e-16 ***
## ageYear       1.7483     0.1329   13.15   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.989 on 234 degrees of freedom
## Multiple R-squared:  0.4249, Adjusted R-squared:  0.4225
## F-statistic: 172.9 on 1 and 234 DF,  p-value: < 2.2e-16
```

```r
# First generate prediction data
pred <- predictvals( model, "ageYear", "heightIn")
sp <- ggplot( heightweight, aes( x = ageYear, y = heightIn)) +
  geom_point() + geom_line( data = pred)

##
sp +
  annotate("text", label ="r^2 = 0.42", x = 16.5, y = 52)
```




```r
##
sp +
  annotate("text", label ="r^2 == 0.42", parse = TRUE, x = 16.5, y = 52)
```



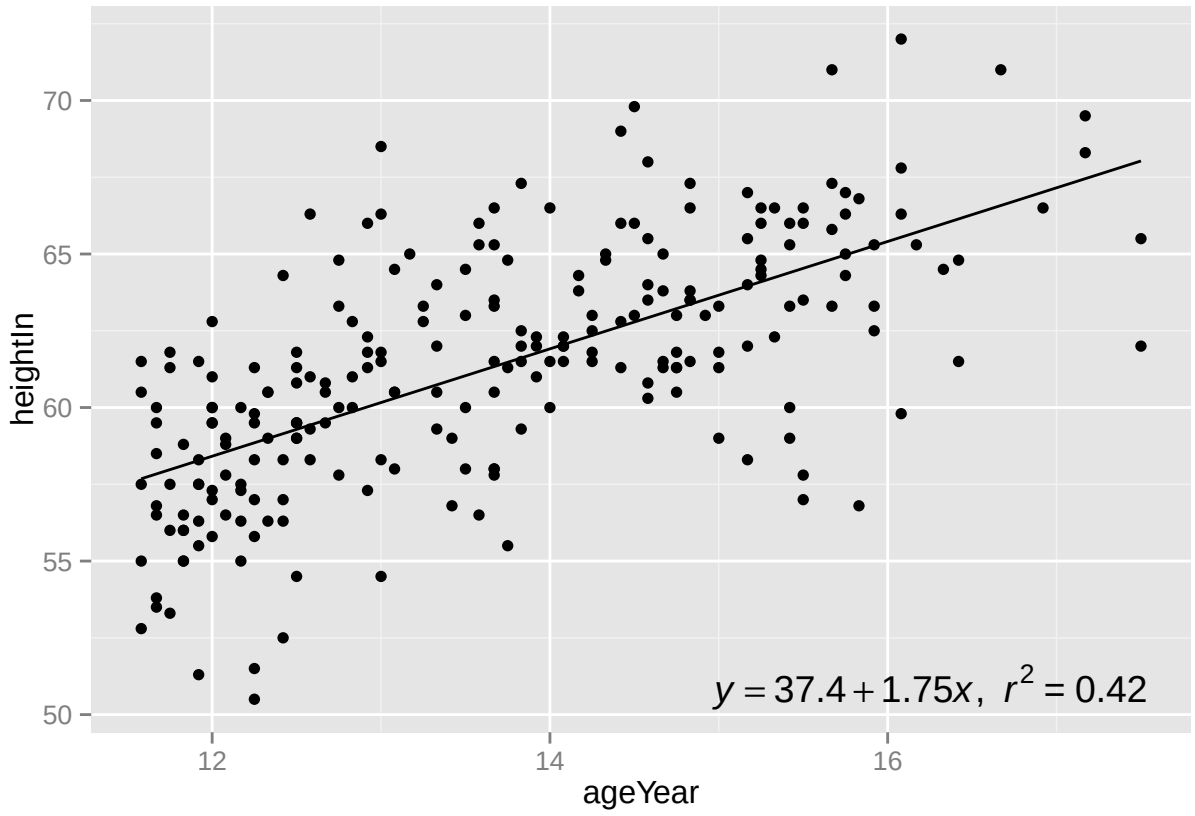

```
## It's possible to automatically extract values from the model object and build an expression
eqn <- as.character(
  as.expression( substitute( italic( y) == a + b * italic( x) * "," ~~ italic(r)^2 ~ "=" ~ r2,
                             list( a = format( coef( model)[1], digits = 3),
                                   b = format( coef( model)[2], digits = 3),
                                   r2 = format( summary(model)$r.squared,
                                                digits = 2) ))))
eqn
```

```
## [1] "italic(y) == \"37.4\" + \"1.75\" * italic(x) * \",\" ~ ~italic(r)^2 ~ \"=\" ~ \"0.42\""
```

```
# Parsing turns it into an expression
parse( text = eqn)
```

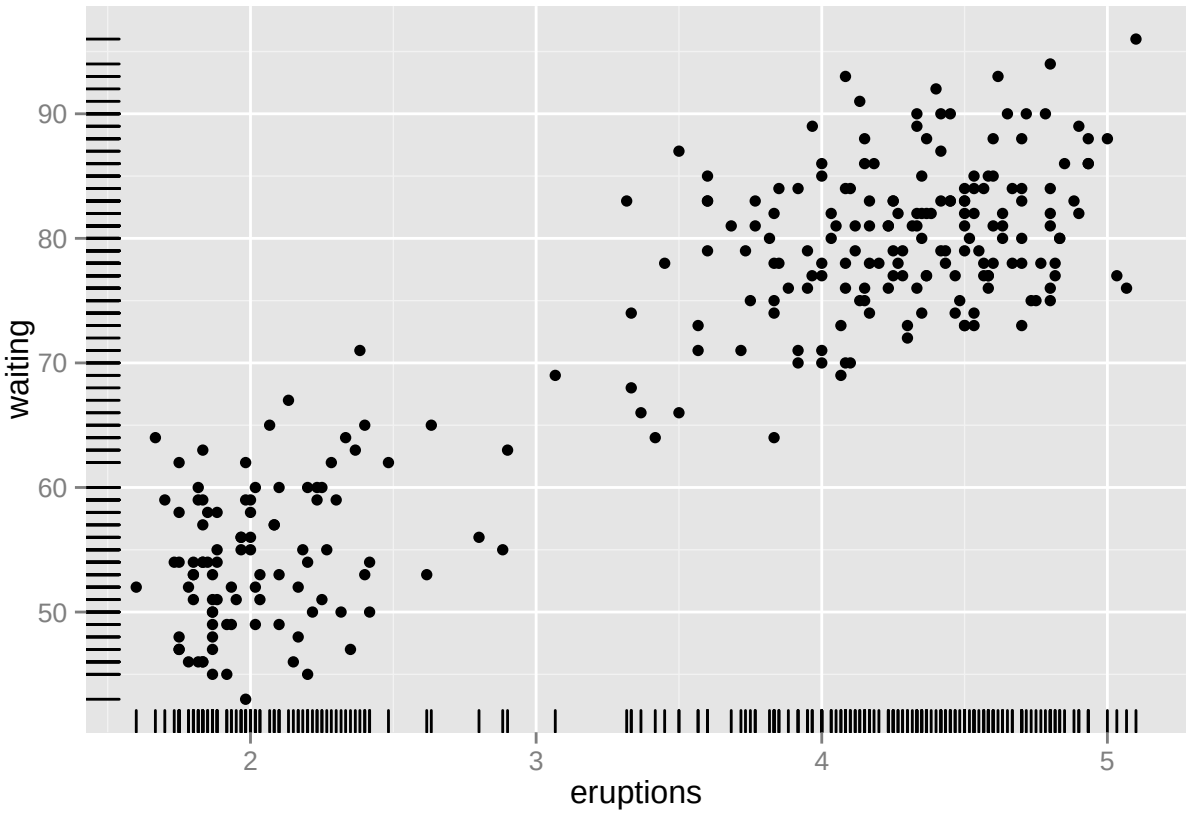
```
## expression(italic(y) == "37.4" + "1.75" * italic(x) * "," ~ ~italic(r)^2 ~
##     "=" ~ "0.42")
```

```
# Now that we have the expression string, we can add it to the plot.
sp + annotate("text", label = eqn, parse = TRUE, x = Inf, y =-Inf, hjust = 1.1, vjust =-.5)
```

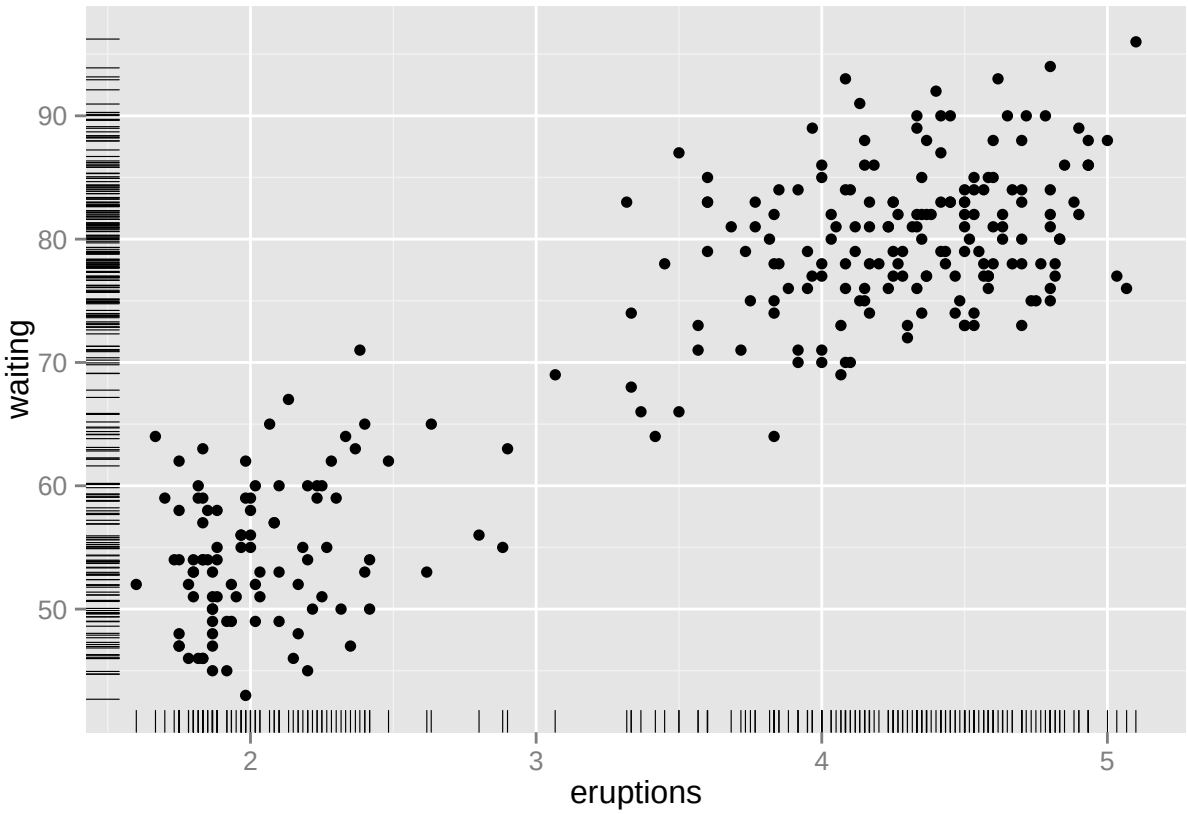


10. Adding Marginal Rugs to a Scatter Plot

```
ggplot( faithful, aes( x = eruptions, y = waiting)) +
  geom_point() +
  geom_rug()
```




```
# To reduce the overplotting, we can jitter the line positions and make them slightly thinner by specif
ggplot( faithful, aes( x = eruptions, y = waiting)) +
  geom_point() +
  geom_rug( position ="jitter", size =.2)
```



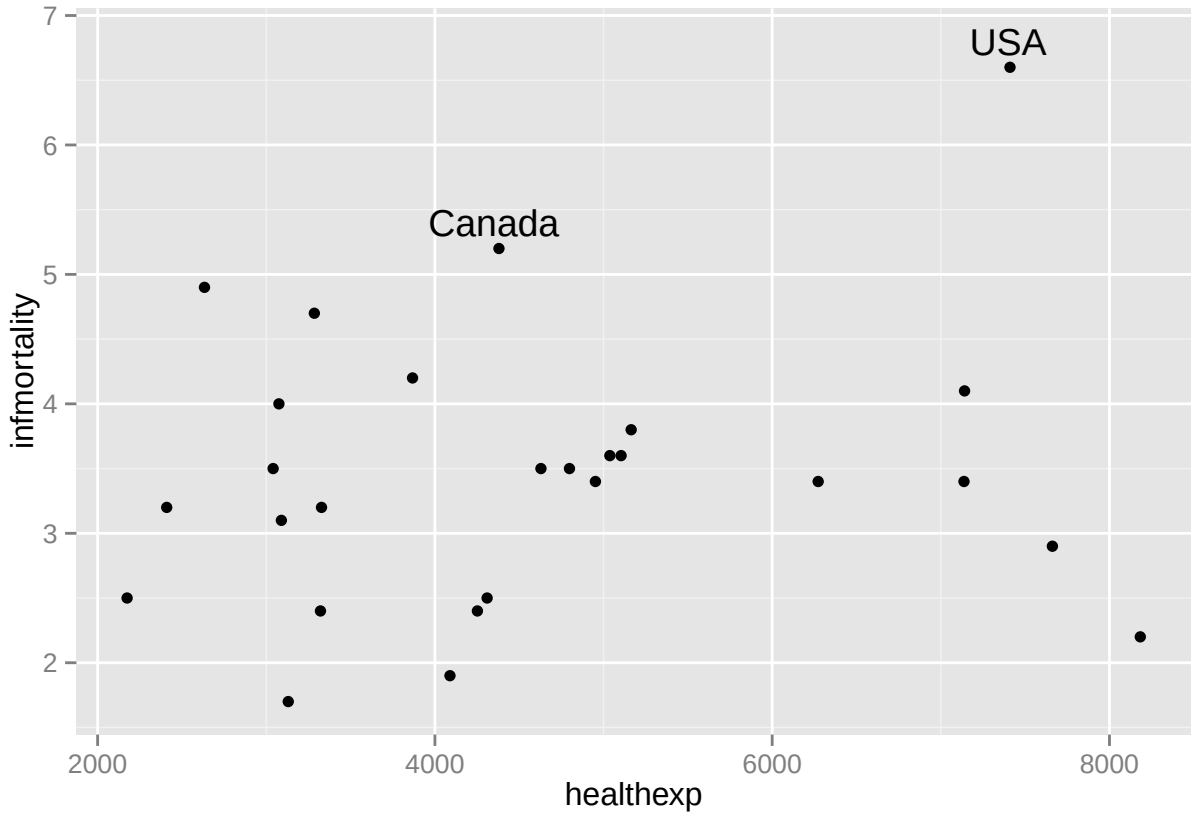
11. Labeling Points in a Scatter Plot

```
# we'll just take the subset of countries that spent more than $ 2000 USD per capita:
subset( countries, Year == 2009 & healthexp > 2000)
```

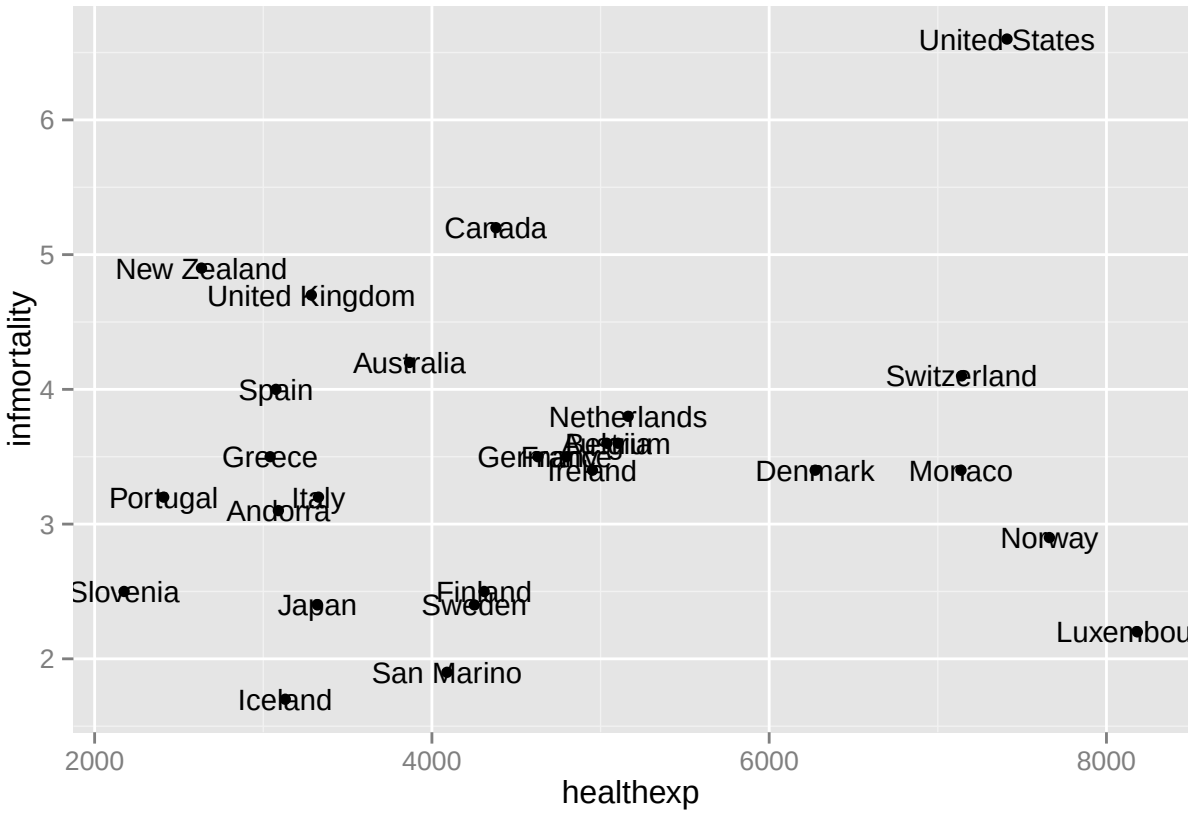
```
##                Name Code Year       GDP laborrate healthexp infmortality
## 254         Andorra  AND 2009        NA        NA  3089.636          3.1
## 560       Australia  AUS 2009  42130.82      65.2  3867.429          4.2
## 611         Austria  AUT 2009  45555.43      60.4  5037.311          3.6
## 968         Belgium  BEL 2009  43640.20      53.5  5104.019          3.6
## 1733         Canada  CAN 2009  39599.04      67.8  4379.761          5.2
## 2702        Denmark  DNK 2009  55933.35      65.4  6272.729          3.4
## 3365        Finland  FIN 2009  44576.73      60.9  4309.604          2.5
## 3416         France  FRA 2009  40663.05      56.1  4797.966          3.5
## 3671        Germany  DEU 2009  40658.58      59.8  4628.769          3.5
## 3824         Greece  GRC 2009  28936.48      53.7  3040.734          3.5
## 4436        Iceland  ISL 2009  37972.24      77.5  3130.391          1.7
## 4691        Ireland  IRL 2009  49737.93      63.6  4951.845          3.4
## 4844          Italy  ITA 2009  35073.32      49.1  3327.630          3.2
## 4946          Japan  JPN 2009  39456.44      59.5  3321.466          2.4
## 5864     Luxembourg  LUX 2009 106252.24      55.5  8182.855          2.2
## 6680         Monaco  MCO 2009 172676.34        NA  7137.390          3.4
## 7088    Netherlands  NLD 2009  48068.35      66.1  5163.740          3.8
## 7190    New Zealand  NZL 2009  29352.45      68.6  2633.625          4.9
## 7445         Norway  NOR 2009  78408.71      66.9  7661.610          2.9
```

```
## 7955        Portugal  PRT 2009  22029.87      62.5  2409.661          3.2
## 8312      San Marino  SMR 2009        NA        NA  4089.271          1.9
## 8822        Slovenia  SVN 2009  24101.26      58.9  2174.718          2.5
## 9077           Spain  ESP 2009  31891.39      58.6  3075.013          4.0
## 9536          Sweden  SWE 2009  43406.17      64.8  4251.976          2.4
## 9587     Switzerland  CHE 2009  63524.65      66.9  7140.729          4.1
## 10454 United Kingdom  GBR 2009  35163.41      62.2  3285.050          4.7
## 10505  United States  USA 2009  45744.56      65.0  7410.163          6.6
```

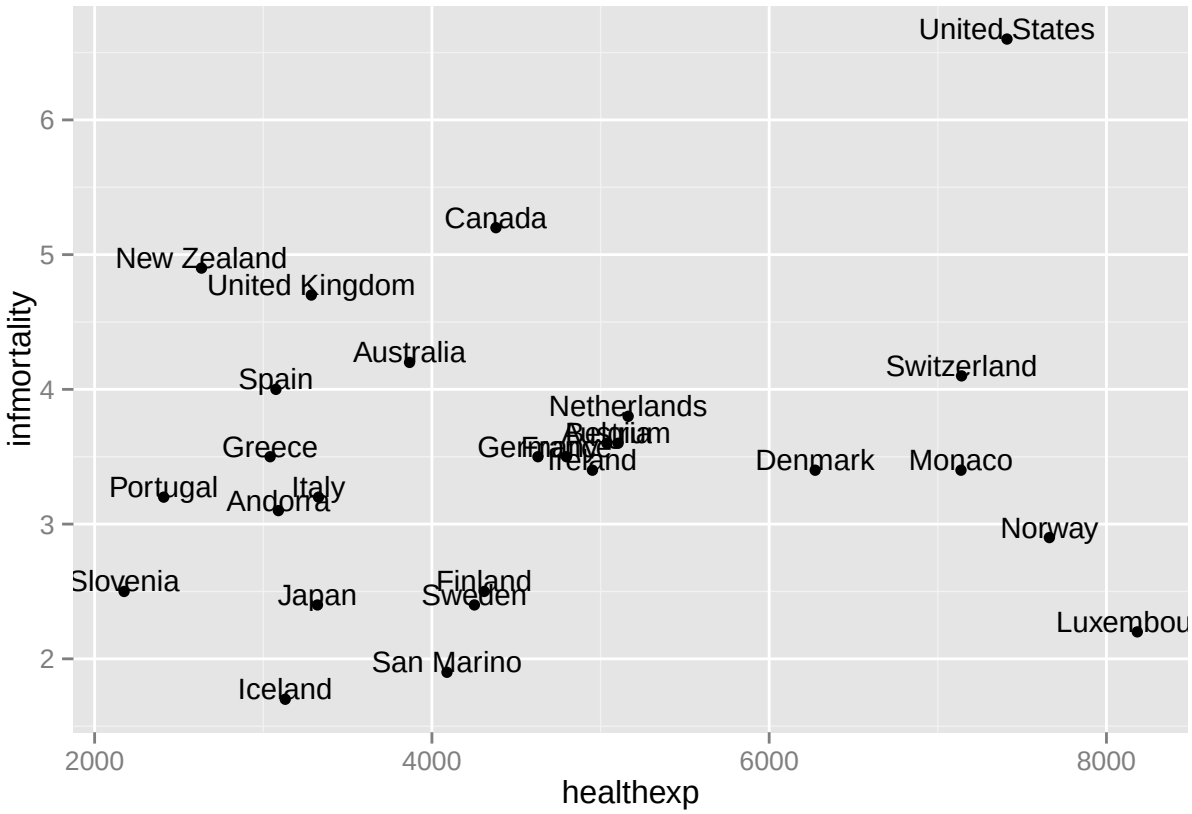
```
# To manually add annotations, use annotate(),
sp <- ggplot( subset( countries, Year == 2009 & healthexp > 2000), aes( x = healthexp, y = infmortality)
  geom_point()

sp +
  annotate("text", x = 4350, y = 5.4, label ="Canada") +
  annotate("text", x = 7400, y = 6.8, label ="USA")
```



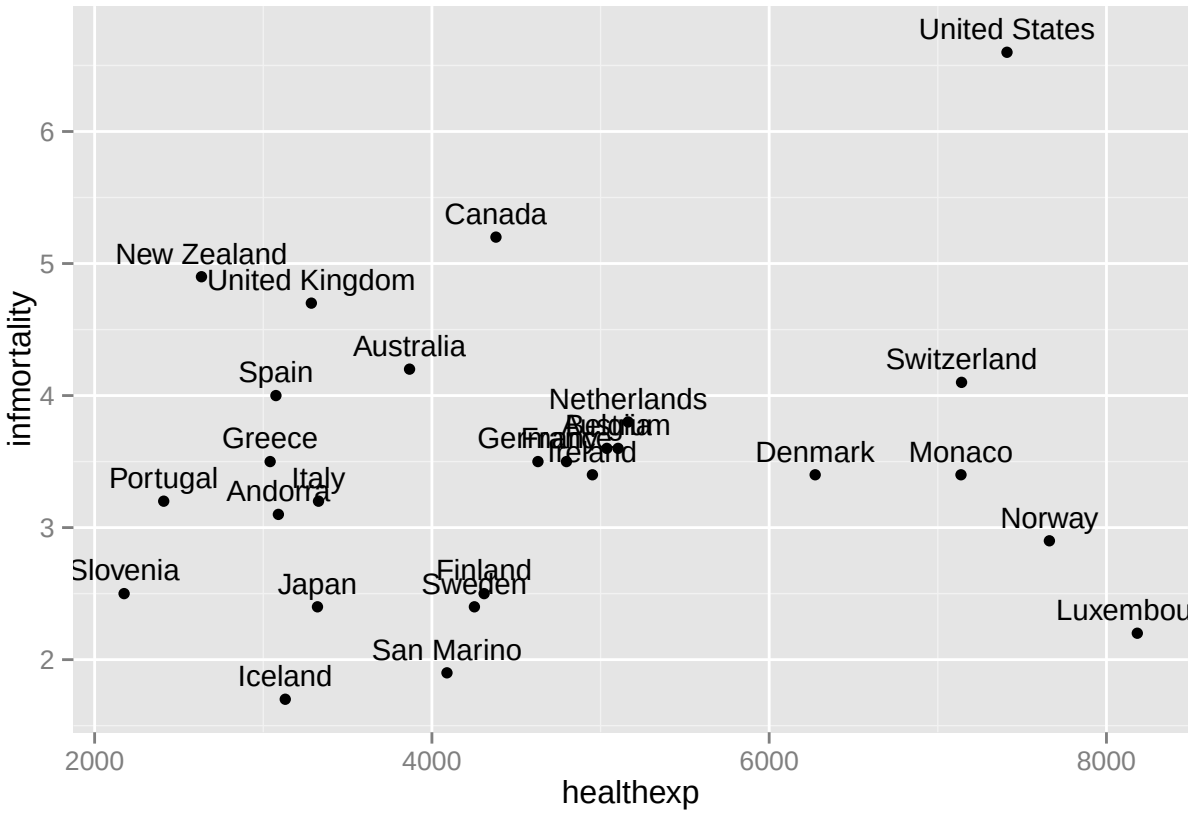

```
# To automatically add the labels from your data we use geom_text() and map a column that is a factor o
sp +
  geom_text( aes( label = Name), size = 4)
```



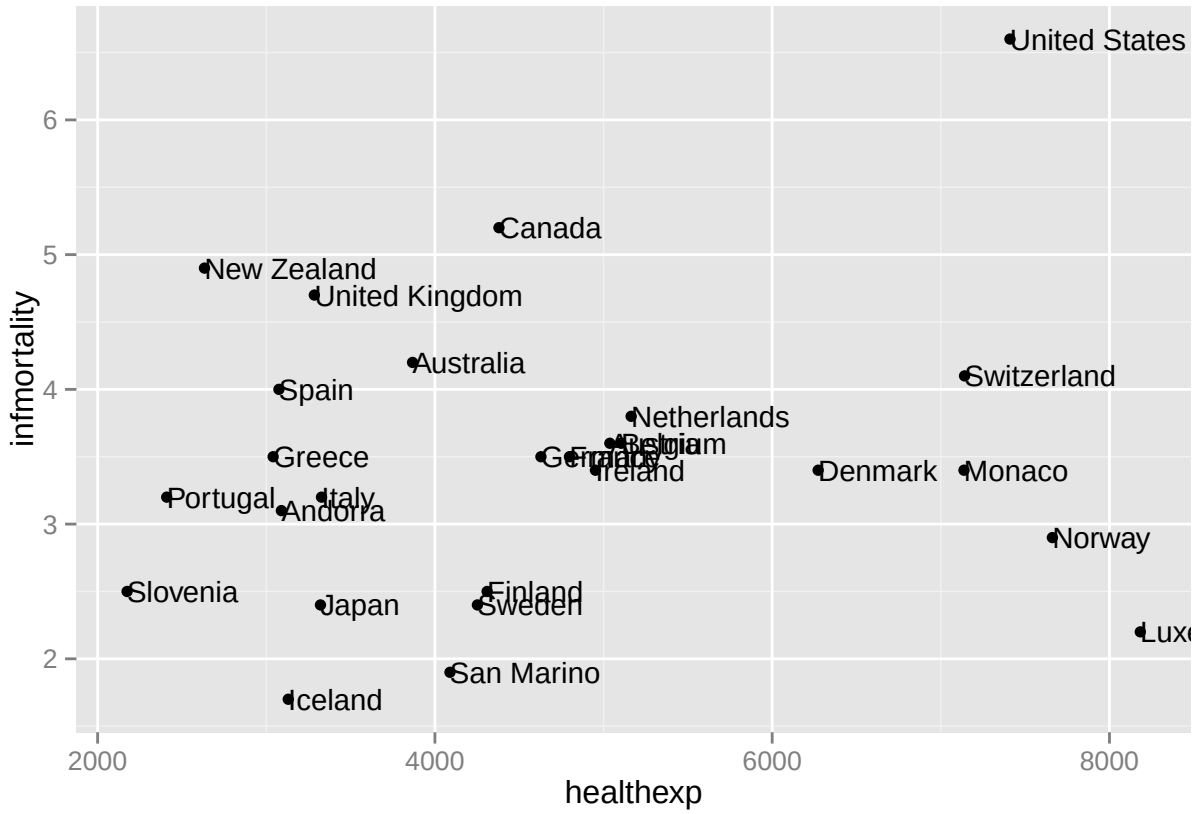

```
sp +
  geom_text( aes( label = Name), size = 4, vjust = 0)
```



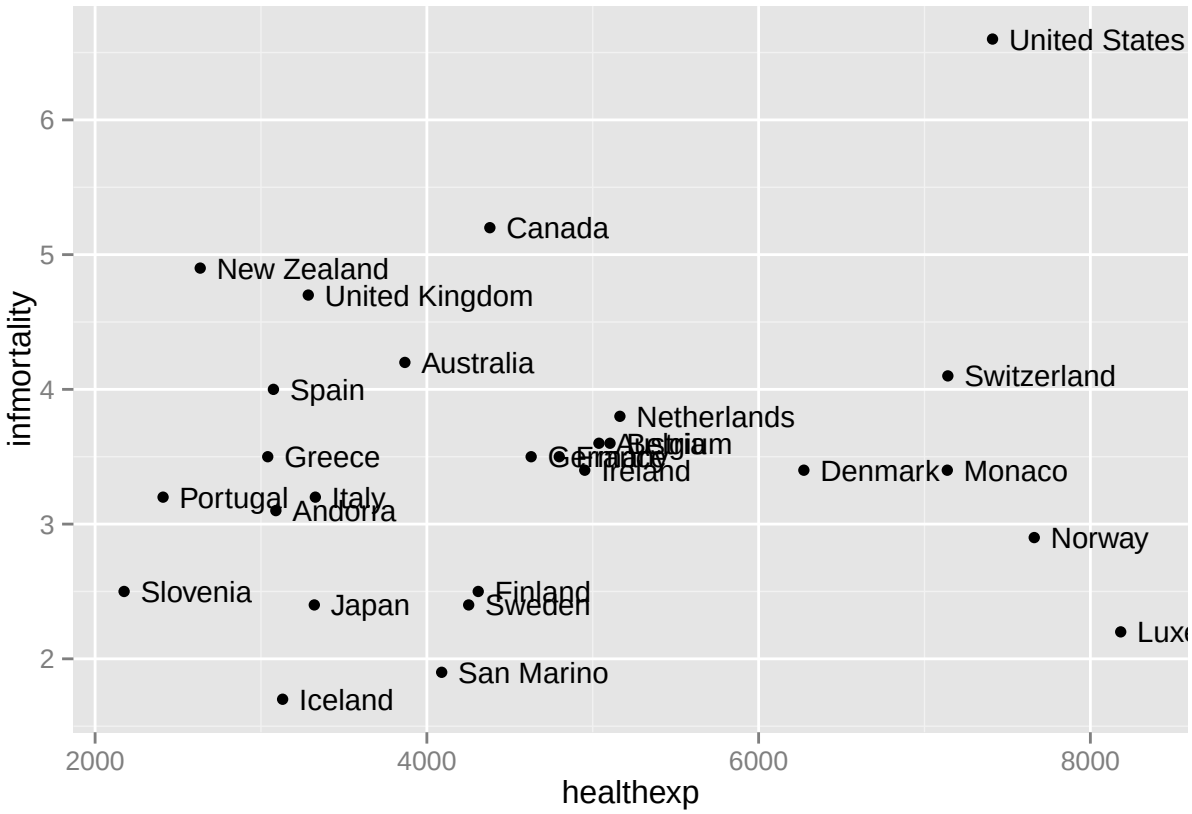

```
# Add a little extra to y
sp +
  geom_text( aes( y = infmortality +.1, label = Name), size = 4, vjust = 0)
```




```
sp +
  geom_text( aes( label = Name), size = 4, hjust = 0)
```




```
sp +
  geom_text( aes( x = healthexp + 100, label = Name), size = 4, hjust = 0)
```

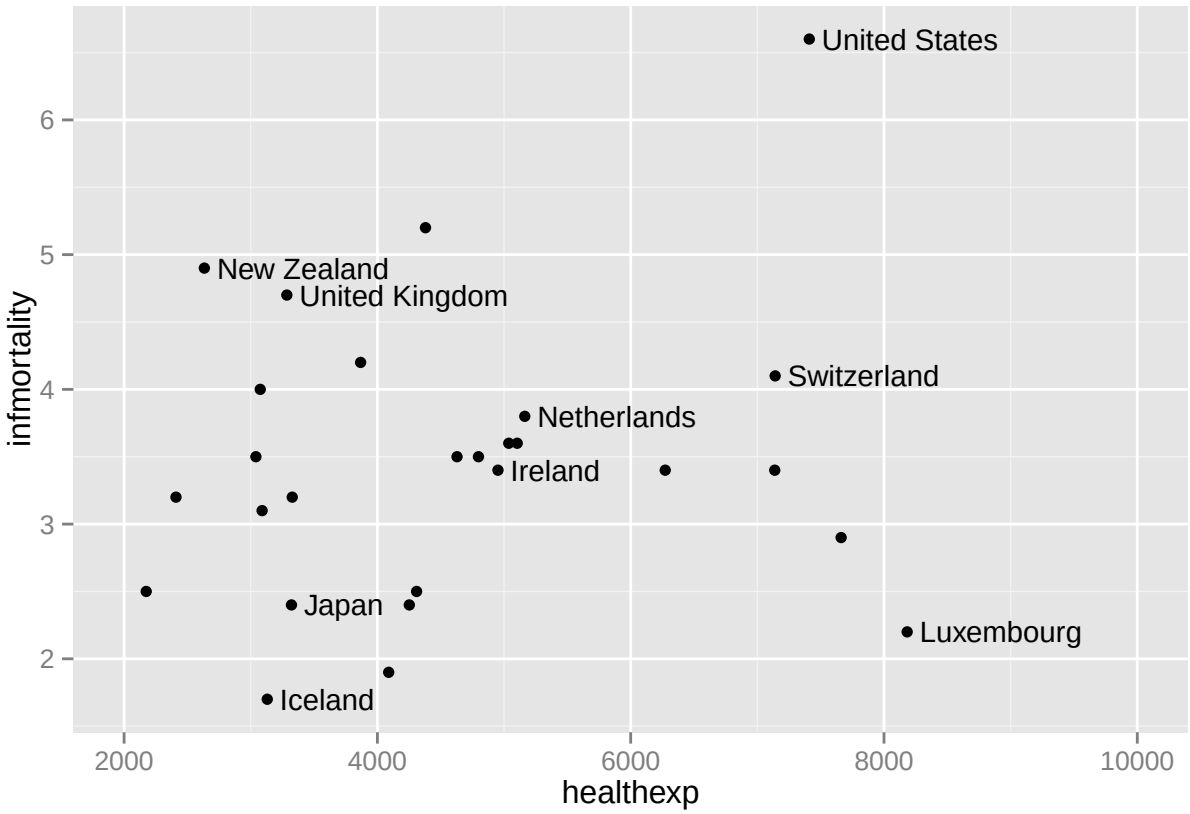



```
# you can add a new column to your data frame containing just the labels you want.
cdat <- subset( countries, Year == 2009 & healthexp > 2000)
cdat$Name1 <- cdat$Name
idx <- cdat$Name1 %in% c(" Canada", "Ireland", "United Kingdom", "United States", "New Zealand", "Icela
head(idx)
```

```
## [1] FALSE FALSE FALSE FALSE FALSE FALSE
```

```
# Then we'll use that Boolean vector to overwrite all the other entries in Name1 with NA:
cdat$Name1[!idx] <- NA

# Now we can make the plot
ggplot( cdat, aes( x = healthexp, y = infmortality)) +
  geom_point() +
  geom_text( aes( x = healthexp + 100, label = Name1), size = 4, hjust = 0) +
  xlim( 2000, 10000)
```

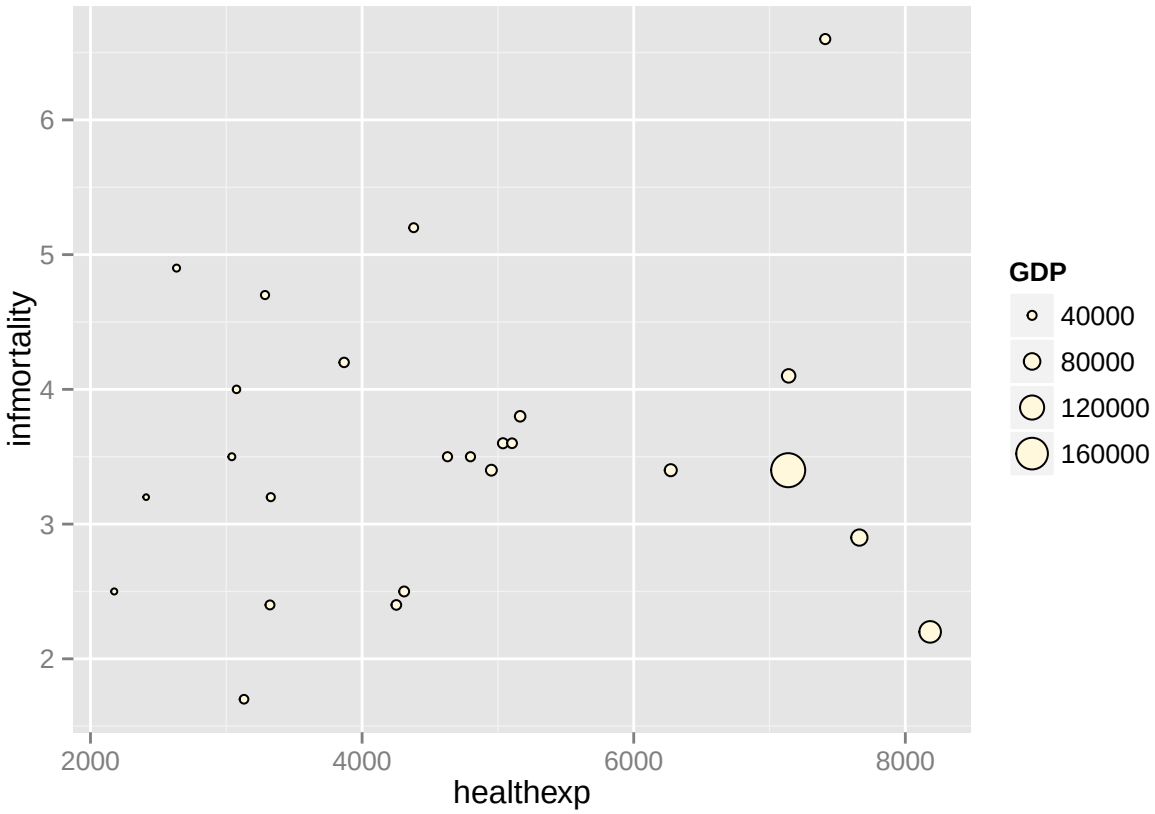
```
## Warning: Removed 18 rows containing missing values (geom_text).
```



12. Creating a Balloon Plot

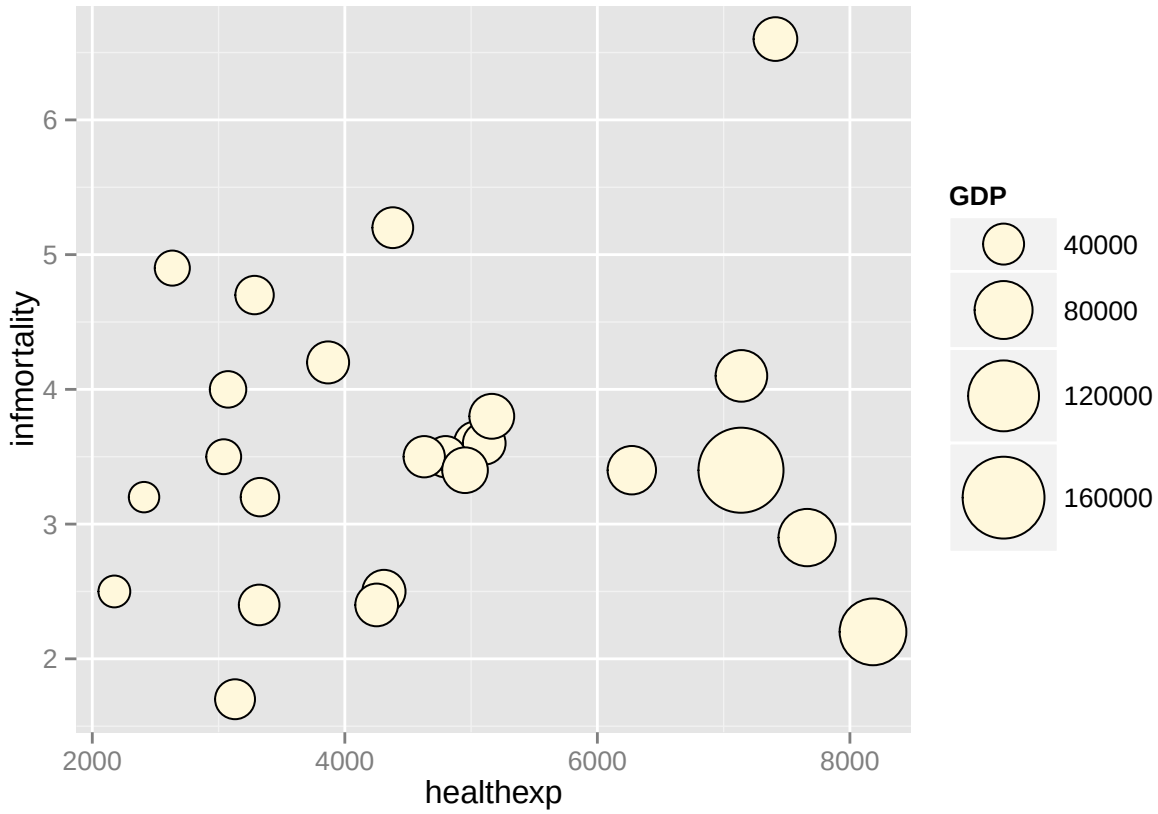
```
p <- ggplot( cdat, aes( x = healthexp, y = infmortality, size = GDP)) +
  geom_point( shape = 21, colour ="black", fill ="cornsilk")

# GDP mapped to radius (default with scale_size_continuous)
p
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```

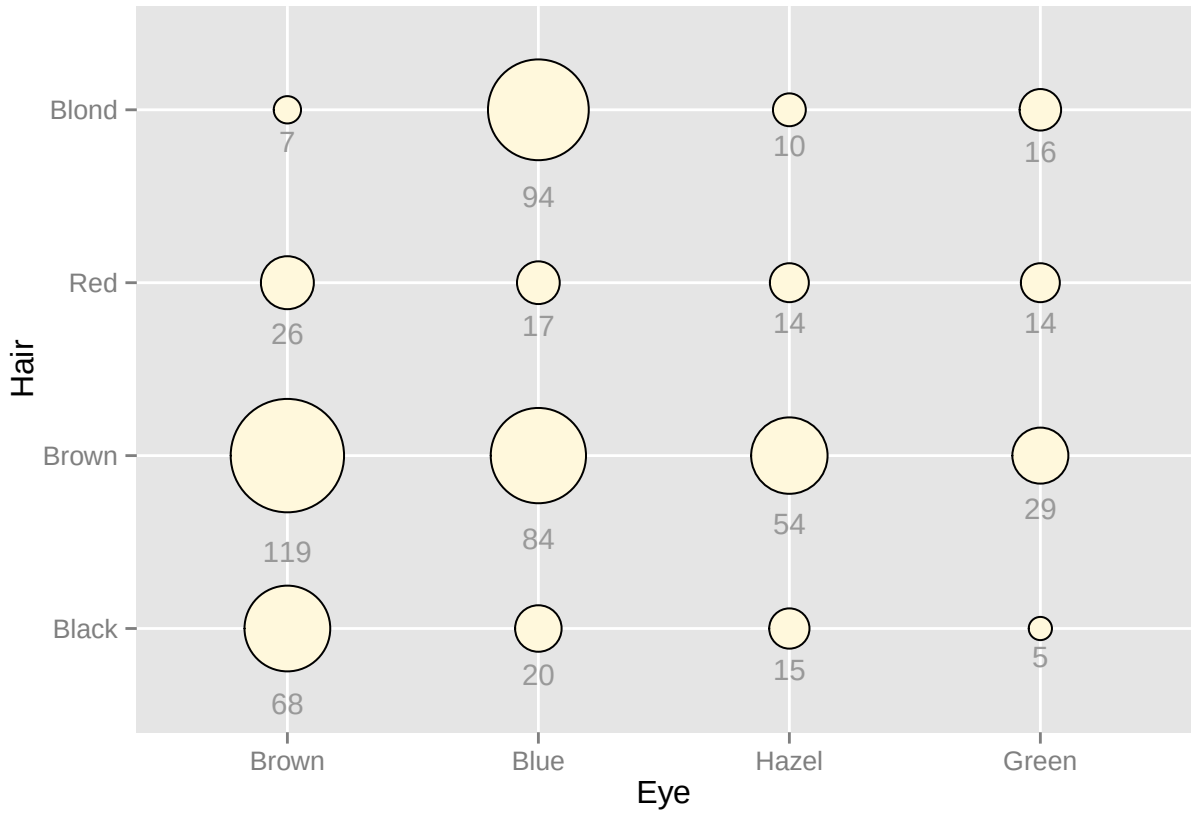



```
# GDP mapped to area instead, and larger circles
p + scale_size_area( max_size = 15)
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```




```
# Add up counts for male and female
hec <- HairEyeColor[,,"Male"] + HairEyeColor[,,"Female"]

# Convert to long format
library( reshape2)
hec <- melt( hec, value.name ="count")

ggplot( hec, aes( x = Eye, y = Hair)) +
  geom_point( aes( size = count), shape = 21, colour ="black", fill ="cornsilk") +
  scale_size_area( max_size = 20, guide = FALSE) +
  geom_text( aes( y = as.numeric(Hair)-sqrt(count)/ 22, label = count), vjust = 1, colour ="grey60", si
```

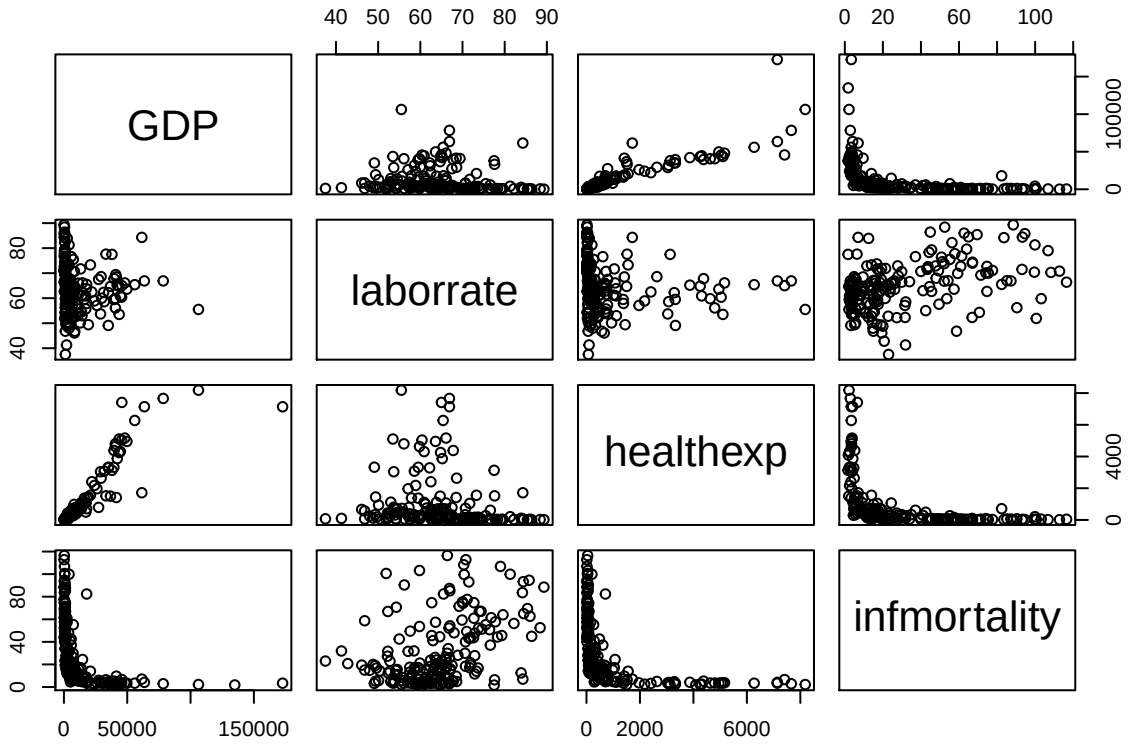


13. Making a Scatter Plot Matrix

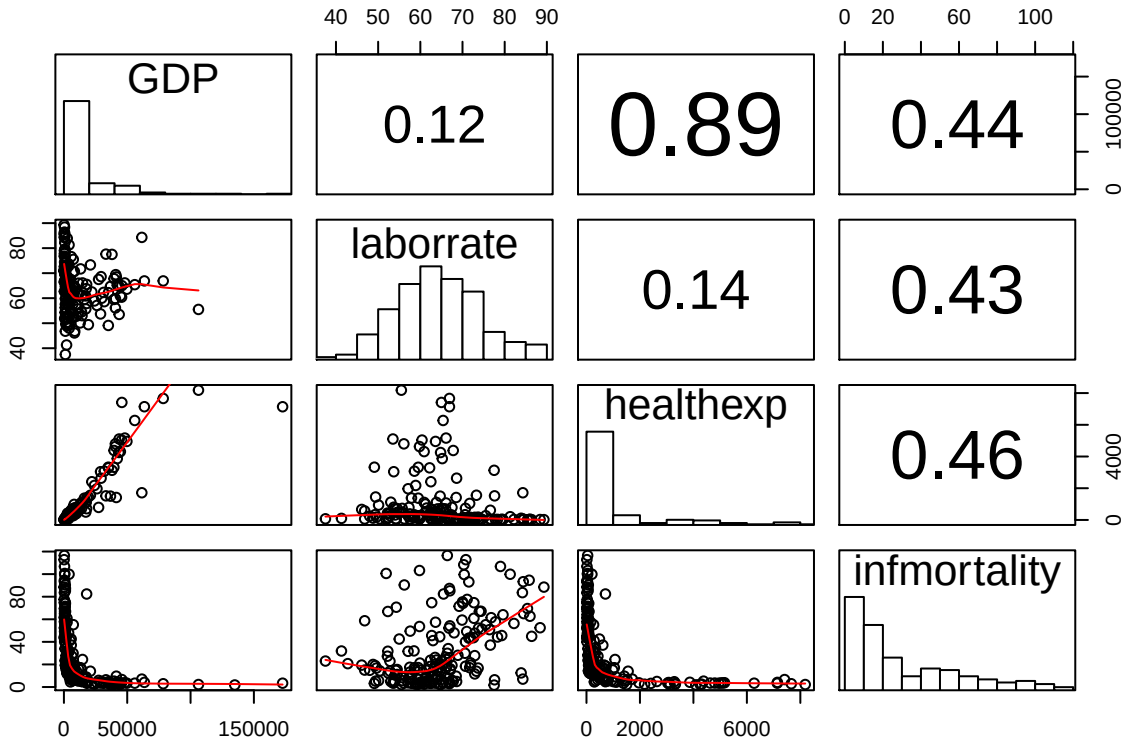
```
c2009 <- subset( countries, Year == 2009, select = c( Name, GDP, laborrate, healthexp, infmortality))
head(c2009)
```

```
##                Name      GDP laborrate  healthexp infmortality
## 50      Afghanistan       NA      59.8   50.88597        103.2
## 101         Albania 3772.605      59.5  264.60406         17.2
## 152         Algeria 4022.199      58.5  267.94653         32.0
## 203 American Samoa       NA        NA         NA           NA
## 254         Andorra       NA        NA 3089.63589          3.1
## 305          Angola 4068.576      81.3  203.80787         99.9
```

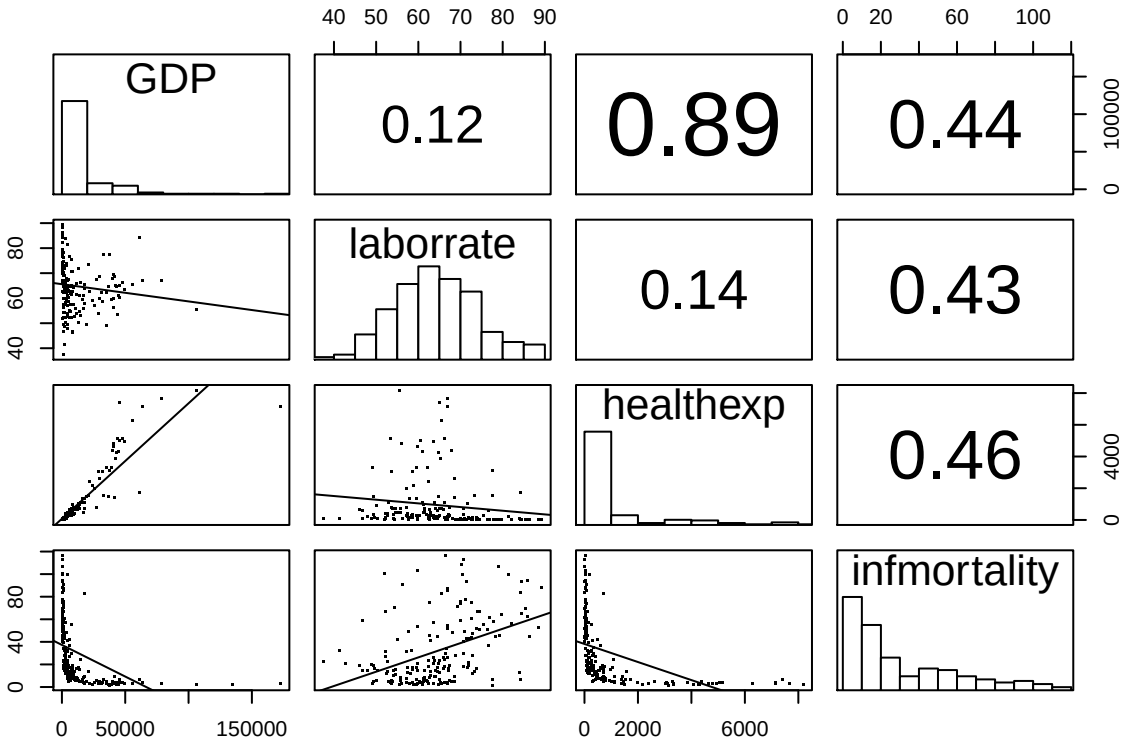
```
# make the scatter plot matrix
pairs( c2009[, 2: 5])
```




```
panel.cor <- function( x, y, digits = 2, prefix ="", cex.cor, ...) {
  usr <- par("usr")
  on.exit( par(usr))
  par( usr = c( 0, 1, 0, 1))
  r <- abs( cor( x, y, use ="complete.obs"))
  txt <- format( c( r, 0.123456789), digits = digits)[1]
  txt <- paste( prefix, txt, sep ="")
  if( missing( cex.cor)) cex.cor <- 0.8 / strwidth(txt)
  text( 0.5, 0.5, txt, cex = cex.cor * (1 + r) / 2)
  }

panel.hist <- function( x, ...) {
  usr <- par("usr")
  on.exit( par(usr))
  par( usr = c( usr[1:2], 0, 1.5) )
  h <- hist( x, plot = FALSE)
  breaks <- h$breaks
  nB <- length(breaks)
  y <- h$counts
  y <- y/max( y)
  rect( breaks[-nB], 0, breaks[-1], y, col ="white", ...)
  }

pairs( c2009[,2:5], upper.panel = panel.cor,
       diag.panel = panel.hist,
       lower.panel = panel.smooth)
```




```
# It may be more desirable to use linear regression lines instead of LOWESS lines.
panel.lm <- function (x, y, col = par("col"), bg = NA, pch = par("pch"), cex = 1, col.smooth = "black",
  points( x, y, pch = pch, col = col, bg = bg, cex = cex)
  abline( stats::lm( y ~ x), col = col.smooth, ...)
  }

pairs( c2009[, 2:5], pch =".",
       upper.panel = panel.cor,
       diag.panel = panel.hist,
       lower.panel = panel.lm)
```


GDP
0.12
0.89
0.44
laborrate
0.14
0.43
healthexp
0.46
infmortality
40 50 60 70 80 90
0 20 60 100
0 100000
40 60 80
0 4000
0 40 80
0 50000 150000
0 2000 6000