

Common Statistical Techniques in R

May 14, 2019

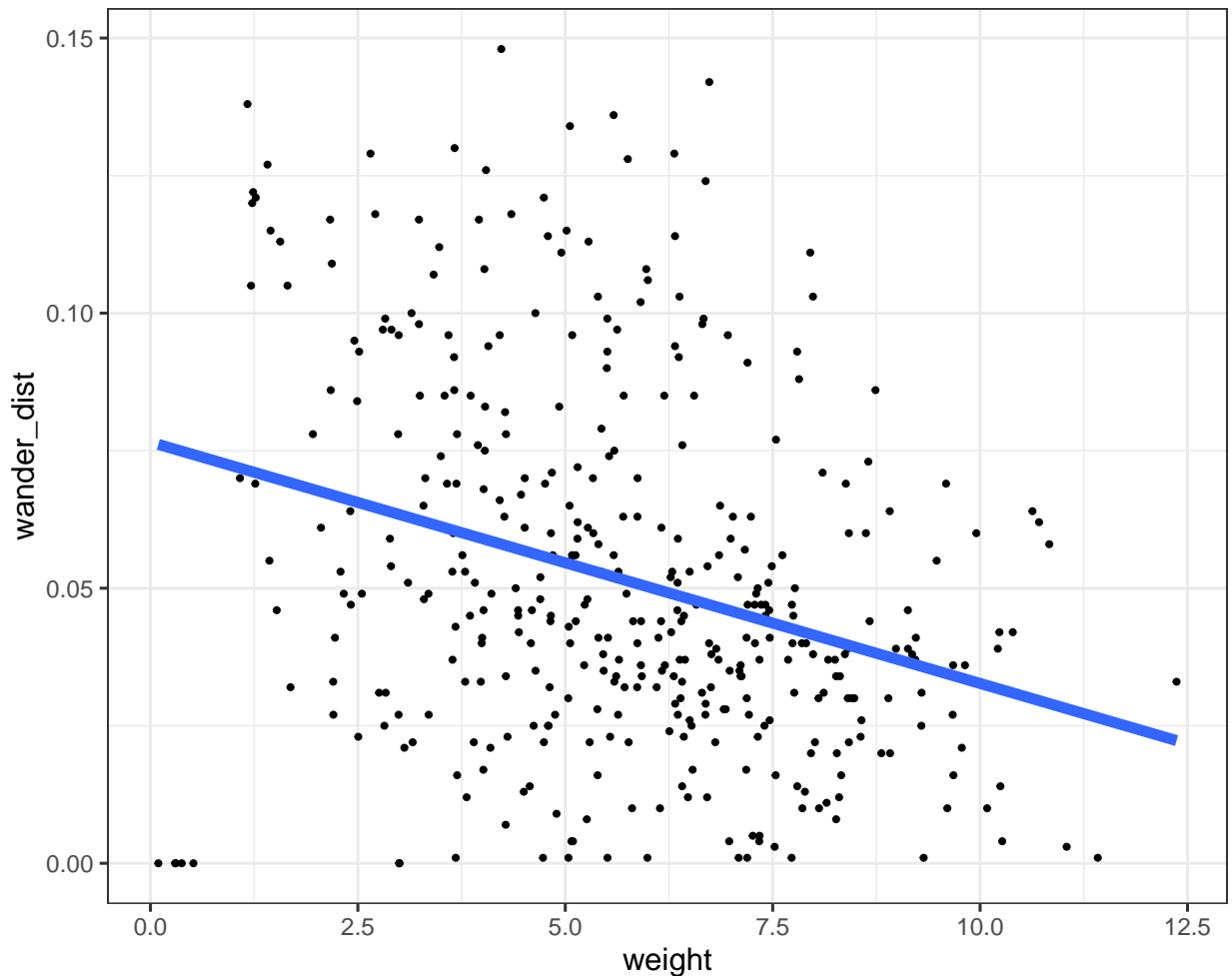
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0.1 Learning Objectives

- To become familiar with common statistical functions available in R
 - Linear Regression
 - Logistic Regression
 - K-Means Clustering
-

0.1.1 Simple Linear Regression



Linear regression is one of the most commonly used methods in all of statistics. It is used for a large variety of applications and offers highly interpretable results. It was the first regression method discovered and belongs to one of the most important families of models, generalized linear models.

Simple linear regression estimates the linear relationship between two variables, an outcome variable y , and an explanatory variable x .

To fit a linear regression in R , we can use the `lm()` function (think *linear model*). We use the formula notation, $y \sim x$ where y is the name of your outcome variable, and x is the name of your explanatory variable, both are unquoted. The easiest way to view the results interactively is with the `summary()` function.

```
weight_fit <- lm(formula = wander_dist ~ weight, data = cats)
summary(weight_fit)
```

Call:

```
lm(formula = wander_dist ~ weight, data = cats)
```

```

Residuals:
      Min       1Q   Median       3Q      Max
-0.076139 -0.019173 -0.004538  0.018240  0.094993

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.0765553   0.0042990   17.808  <2e-16 ***
weight      -0.0043866   0.0006988   -6.278   9e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.0316 on 398 degrees of freedom
Multiple R-squared:  0.09009,    Adjusted R-squared:  0.08781
F-statistic: 39.41 on 1 and 398 DF,  p-value: 9.003e-10

```

In this case, the `summary` function returns an object that provides a lot of interesting information when printed out. It also stores that information as part of the object, things like the terms used in the model, the coefficients of the model estimates, and the residuals of the model. This is nice if we want to do something programmatic with the results.

0.1.2 Multiple Linear Regression

We aren't restricted to just one explanatory variable in linear regression. We can test the effect of a linear relationship between multiple explanatory variables *simultaneously*. In the `lm` function, we just add extra variable names in the formula separated by `+`'s.

```
wander_fit <- lm(formula = wander_dist ~ weight + age, data = cats)
summary(wander_fit)
```

```

Call:
lm(formula = wander_dist ~ weight + age, data = cats)

Residuals:
      Min       1Q   Median       3Q      Max
-0.083498 -0.019287 -0.002461  0.017039  0.068823

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.046857   0.004724   9.918  <2e-16 ***
weight      -0.014260   0.001119  -12.747  <2e-16 ***
age          0.017581   0.001661   10.587  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.02794 on 397 degrees of freedom

```

Multiple R-squared: 0.2904, Adjusted R-squared: 0.2868
F-statistic: 81.24 on 2 and 397 DF, p-value: < 2.2e-16

0.1.3 Challenge

Fit a model predicting `wander_dist` and include `weight`, `age`, and `fixed` as predictors.
What is the estimate for the effect of being `fixed` on the wandering distance?

```
wander_fit <- lm(formula = wander_dist ~ weight + age + fixed, data = cats)
summary(wander_fit)
```

Call:

```
lm(formula = wander_dist ~ weight + age + fixed, data = cats)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-0.091273	-0.018117	-0.001609	0.017690	0.071914

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.054592	0.005074	10.760	< 2e-16 ***
weight	-0.014130	0.001101	-12.836	< 2e-16 ***
age	0.017582	0.001633	10.764	< 2e-16 ***
fixed	-0.011700	0.003083	-3.796	0.00017 ***

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

Residual standard error: 0.02748 on 396 degrees of freedom

Multiple R-squared: 0.3153, Adjusted R-squared: 0.3101

F-statistic: 60.79 on 3 and 396 DF, p-value: < 2.2e-16

If an explanatory variable is not binary (coded as 0s or 1s), we can still include it in the model. The `lm` function understands factors to be categorical variables automatically and will output the estimates with a reference category.

```
wander_fit <- lm(formula = wander_dist ~ weight + age + factor(coat) + sex, data = cats)
summary_fit <- summary(wander_fit)
summary_fit['coefficients']
```

\$coefficients

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.043847799	0.005622582	7.7985172	5.719688e-14
weight	-0.014196808	0.001125488	-12.6139100	7.470796e-31
age	0.017760029	0.001675466	10.6000533	2.978738e-23
factor(coat)brown	0.006257836	0.004003785	1.5629800	1.188642e-01
factor(coat)calico	-0.001345917	0.005120491	-0.2628492	7.928049e-01

```
factor(coat)maltese 0.005543267 0.005907650 0.9383201 3.486577e-01
factor(coat)tabby 0.001579503 0.004265994 0.3702545 7.113928e-01
sexmale -0.002616410 0.002870695 -0.9114206 3.626340e-01
```

0.1.4 Challenge

What command will return the r-squared value from the `summary_lm_fit` object after running these commands:

```
wander_fit <- lm(formula = wander_dist ~ weight + age + fixed, data = cats)
summary_lm_fit <- summary(wander_fit)
```

The `lm` function also can estimate interactions between explanatory variables. This is useful if we think that the linear relationship between our outcome `y` and a variable `x1` is *different* depending on the variable `x2`. This can be accomplished by connecting two variables in the formula with a `*` instead of a `+`.

0.1.5 Challenge

Fit a linear regression model estimating the relationship between the outcome, wandering distance (`wander_dist`) and explanatory variables age (`age`), weight (`weight`), with an interaction between age and weight. What is the coefficient associated with the interaction between age and weight?

```
wander_fit <- lm(formula = wander_dist ~ weight * age, data = cats)
summary(wander_fit)
```

Call:

```
lm(formula = wander_dist ~ weight * age, data = cats)
```

Residuals:

```
      Min       1Q   Median       3Q      Max
-0.070356 -0.019174 -0.002753  0.019351  0.066527
```

Coefficients:

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.0176044  0.0096232   1.829 0.068094 .
weight       -0.0086451  0.0019568  -4.418 1.29e-05 ***
age           0.0241292  0.0024971   9.663 < 2e-16 ***
weight:age    -0.0011310  0.0003255  -3.474 0.000569 ***
---
```

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

Residual standard error: 0.02756 on 396 degrees of freedom

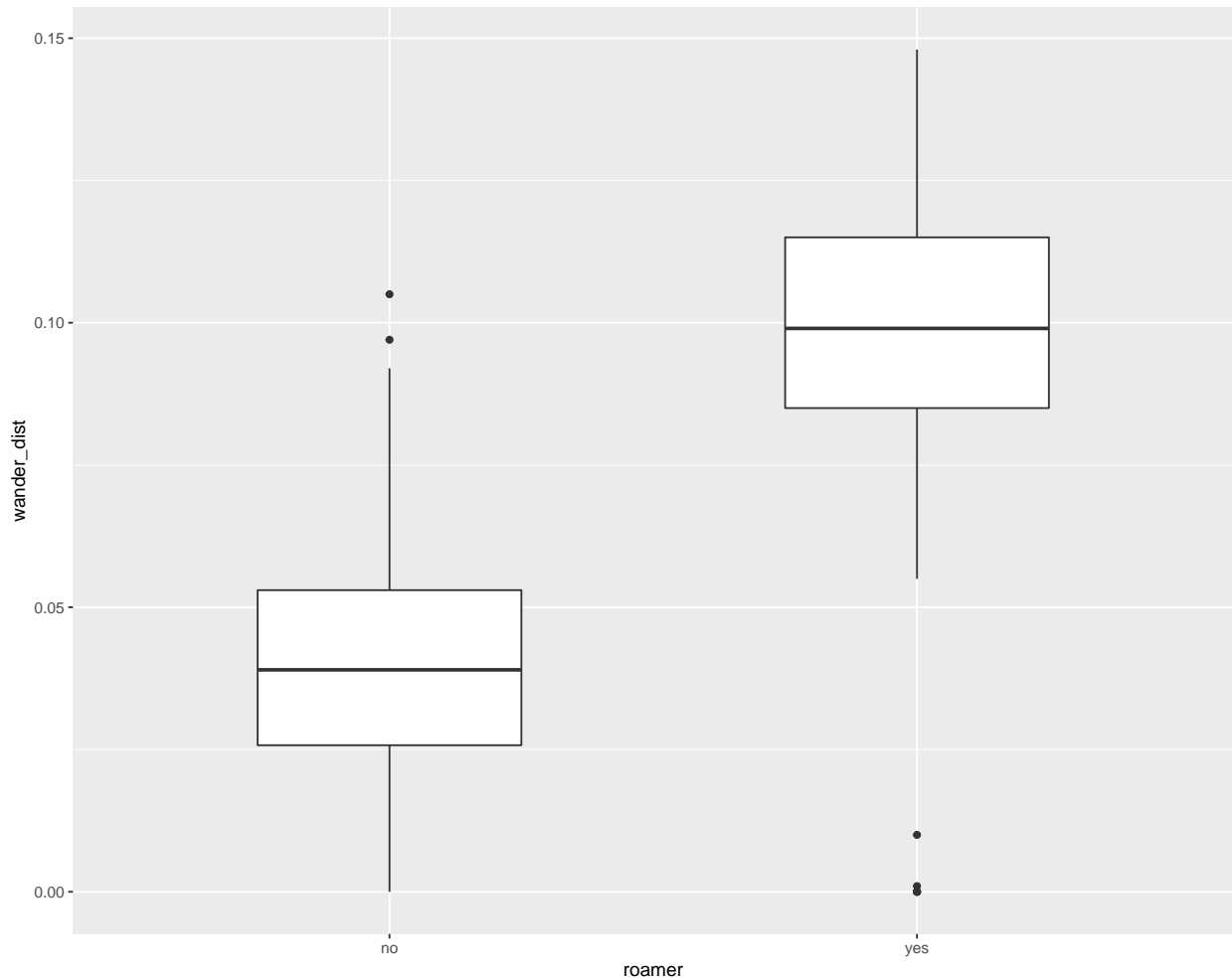
Multiple R-squared: 0.3114, Adjusted R-squared: 0.3062

F-statistic: 59.69 on 3 and 396 DF, p-value: < 2.2e-16

0.2 Logistic Regression

If we are analyzing a binary outcome, we can use *logistic regression*. Logistic regression uses the linear model framework, but makes different assumptions about the distribution of the outcome. So we can look for associations between binary outcome variables and multiple explanatory variables.

```
ggplot(cats, aes(x = roamer, y = wander_dist)) +  
  geom_boxplot(width = 0.5)
```



For logistic regression, we use the `glm` function. It takes formula and data arguments like the `lm` function, but we also need to specify a family. For logistic, we pass `binomial` as the family, which tells the `glm` function that we have a binary outcome, and we want to use the logit link function.

```
roamer_fit <- glm(formula = roamer ~ wander_dist, data = cats, family = binomial )
```

We can use the `summary` function to extract important information from the object that `glm` returns, just like with the `lm` function

```
glm_summary <- summary(roamer_fit)
glm_summary
```

Call:

```
glm(formula = roamer ~ wander_dist, family = binomial, data = cats)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.9068	-0.3812	-0.2234	-0.0767	3.4678

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-6.0103	0.5634	-10.668	<2e-16 ***
wander_dist	72.8672	7.4867	9.733	<2e-16 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 421.53 on 399 degrees of freedom
 Residual deviance: 212.89 on 398 degrees of freedom
 AIC: 216.89

Number of Fisher Scoring iterations: 6

0.2.1 Challenge

```
roamer_fit <- glm(formula = roamer ~ wander_dist + weight, data = cats, family = binomial )
summary(roamer_fit)
```

Call:

```
glm(formula = roamer ~ wander_dist + weight, family = binomial,
    data = cats)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2674	-0.3752	-0.1984	-0.0728	3.6661

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.44909	0.75765	-5.872	4.3e-09 ***
wander_dist	68.99577	7.57569	9.108	< 2e-16 ***
weight	-0.25096	0.09484	-2.646	0.00814 **

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

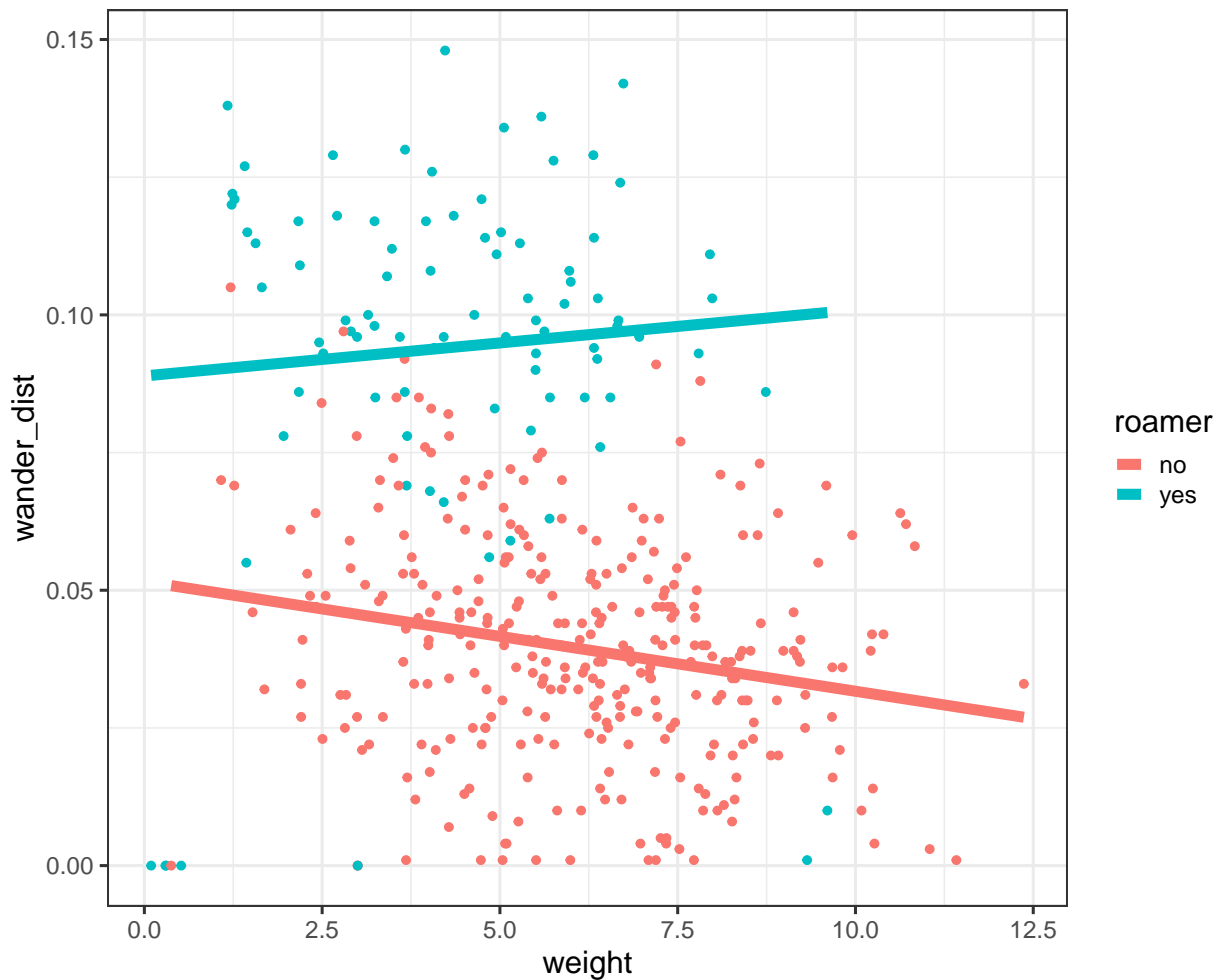
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 421.53 on 399 degrees of freedom
Residual deviance: 205.44 on 397 degrees of freedom
AIC: 211.44

Number of Fisher Scoring iterations: 6

We can look at the effects of multiple covariates on our binary outcome with logistic regression, just like with linear regression. We just add as many variable names as we'd like to the right side of the formula argument, separated by + symbols.

```
ggplot(cats, aes(x = weight, y = wander_dist, color = roamer)) +  
  geom_point(size = 2) +  
  geom_smooth(method = 'lm', se = FALSE, size = 3) +  
  theme_bw(base_size = 18)
```




```
# cats$roamer <- relevel(cats$roamer, ref = 'yes')
roamer_fit <- glm(formula = roamer ~ wander_dist + weight, data = cats, family = binomial )
glm_summary <- summary(roamer_fit)
glm_summary
```

Call:

```
glm(formula = roamer ~ wander_dist + weight, family = binomial,
    data = cats)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2674	-0.3752	-0.1984	-0.0728	3.6661

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.44909	0.75765	-5.872	4.3e-09 ***
wander_dist	68.99577	7.57569	9.108	< 2e-16 ***
weight	-0.25096	0.09484	-2.646	0.00814 **

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 421.53 on 399 degrees of freedom
 Residual deviance: 205.44 on 397 degrees of freedom
 AIC: 211.44

Number of Fisher Scoring iterations: 6

```
names(glm_summary)
```

[1] "call"	"terms"	"family"	"deviance"
[5] "aic"	"contrasts"	"df.residual"	"null.deviance"
[9] "df.null"	"iter"	"deviance.resid"	"coefficients"
[13] "aliased"	"dispersion"	"df"	"cov.unscaled"
[17] "cov.scaled"			

```
glm_summary$coefficients
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.4490855	0.75764856	-5.872229	4.299754e-09
wander_dist	68.9957683	7.57569390	9.107518	8.428814e-20
weight	-0.2509641	0.09484151	-2.646141	8.141576e-03

```
glm_summary$null.deviance
```

```
[1] 421.5264
```

```
glm_summary$deviance
```

```
[1] 205.4406
```

```
glm_summary$aic
```

```
[1] 211.4406
```

We can also use the model objects to predict on unobserved values. We just need to pass a data frame with all of the terms used in the original model to the `predict` function. The `predict` function will return values in a few different ways. The default value of the `type` argument is “link” and will return things on the same scale as the linear predictors. This is often not what we want. If we pass “response” to the `type` argument, we’ll get predicted values on the same scale as the response. In the logistic case, this is the predicted probability.

```
new_cats <- data.frame(wander_dist = c(0.15, 0.10, 0.05),  
                      weight = c(2, 6, 12))
```

```
new_cats
```

```
  wander_dist weight  
1         0.15     2  
2         0.10     6  
3         0.05    12
```

```
predicted_logit <- predict(object = roamer_fit, newdata = new_cats)  
predicted_logit
```

```
      1      2      3  
5.3983516 0.9447069 -4.0108658
```

```
predicted_probs <- predict(object = roamer_fit, newdata = new_cats, type = 'response')  
predicted_probs
```

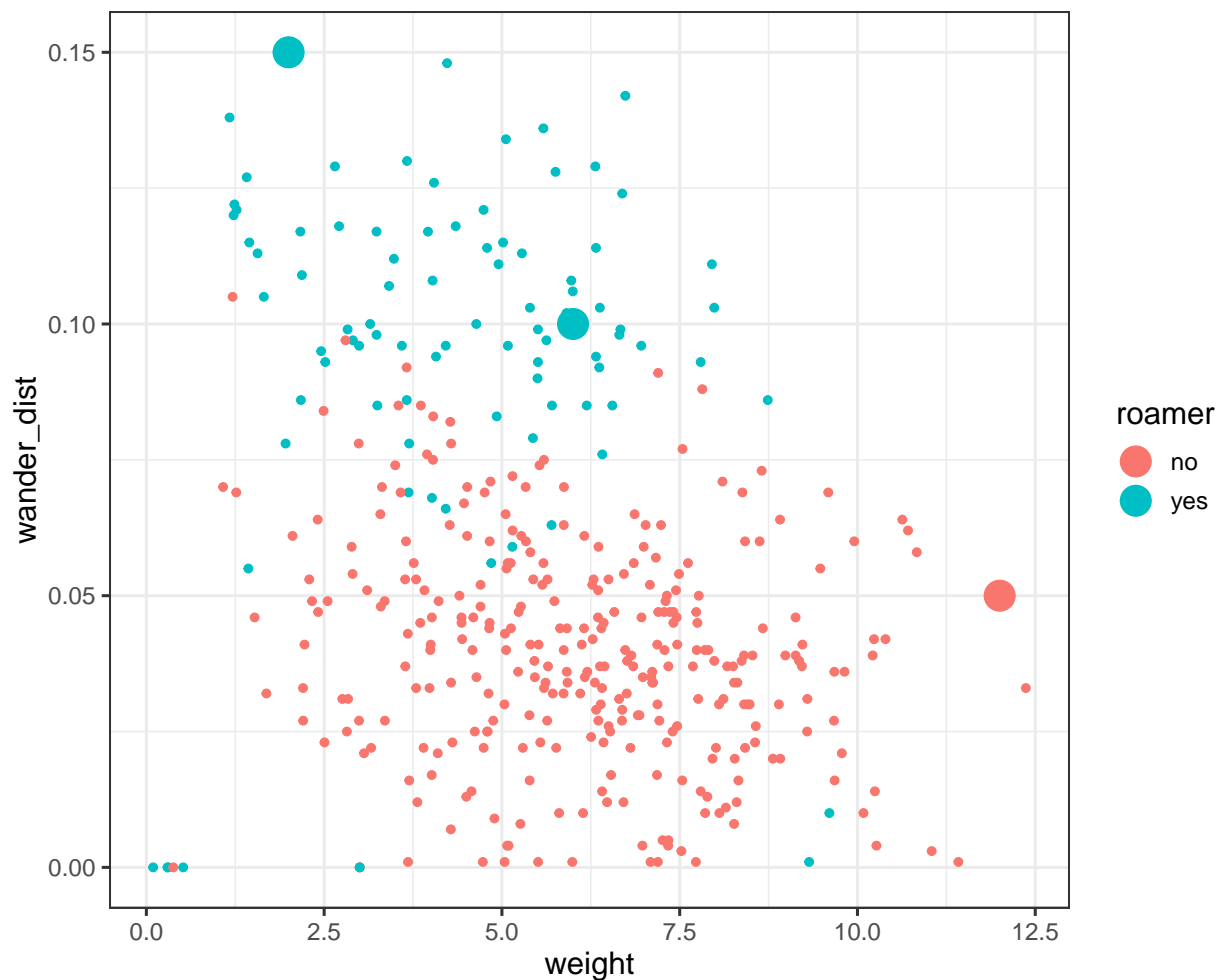
```
      1      2      3  
0.99549634 0.72004946 0.01779529
```

We can then predict whether each cat is a roamer or not based on the predicted probability from our model. We need to assign a cut-off probability.

```
new_cats$predicted_prob <- predicted_probs
```

```
new_cats <- new_cats %>% mutate(roamer = ifelse(predicted_prob > 0.5, 'yes', 'no'))
```

```
ggplot(cats, aes(x = weight, y = wander_dist, color = roamer, group = roamer)) +  
  geom_point(size = 2) +  
  geom_point(data = new_cats, aes(x = weight, y = wander_dist, color = roamer), size = 8) +  
  theme_bw(base_size = 18)
```



0.3 K-means Clustering

Another popular machine learning technique is k-means clustering. It seeks to group your data into a fixed number of clusters based on a measure of distance. An important pre-processing step to clustering is the center and scale your data.

```
cats <- cats %>%  
  mutate(scale_weight = scale(weight),  
         scale_wander = scale(wander_dist),  
         scale_age = scale(age))
```

We use the `kmeans` function to perform the clustering, and need to pass it a data frame, the number of centers we want, and another argument `nstart`, which helps get around some numerical issues if the algorithm gets stuck in a local extrema.

```
cats_cluster <-  
  kmeans(x = cats %>% select(scale_weight, scale_wander, scale_age),
```

```

        centers = 3,
        nstart = 20)
str(cats_cluster)

```

List of 9

```

$ cluster      : int [1:400] 2 2 2 2 3 1 2 3 3 2 ...
$ centers      : num [1:3, 1:3] -0.654 -0.621 0.902 -0.479 1.416 ...
..- attr(*, "dimnames")=List of 2
.. ..$ : chr [1:3] "1" "2" "3"
.. ..$ : chr [1:3] "scale_weight" "scale_wander" "scale_age"
$ totss       : num 1197
$ withinss    : num [1:3] 163 144 187
$ tot.withinss: num 494
$ betweenss   : num 703
$ size        : int [1:3] 135 99 166
$ iter        : int 3
$ ifault      : int 0
- attr(*, "class")= chr "kmeans"

```

```
cats_cluster$centers
```

```

      scale_weight scale_wander scale_age
1  -0.6537444    -0.4787674 -0.8643999
2  -0.6208415     1.4159815 -0.1528717
3   0.9019205    -0.4551119  0.7941463

```

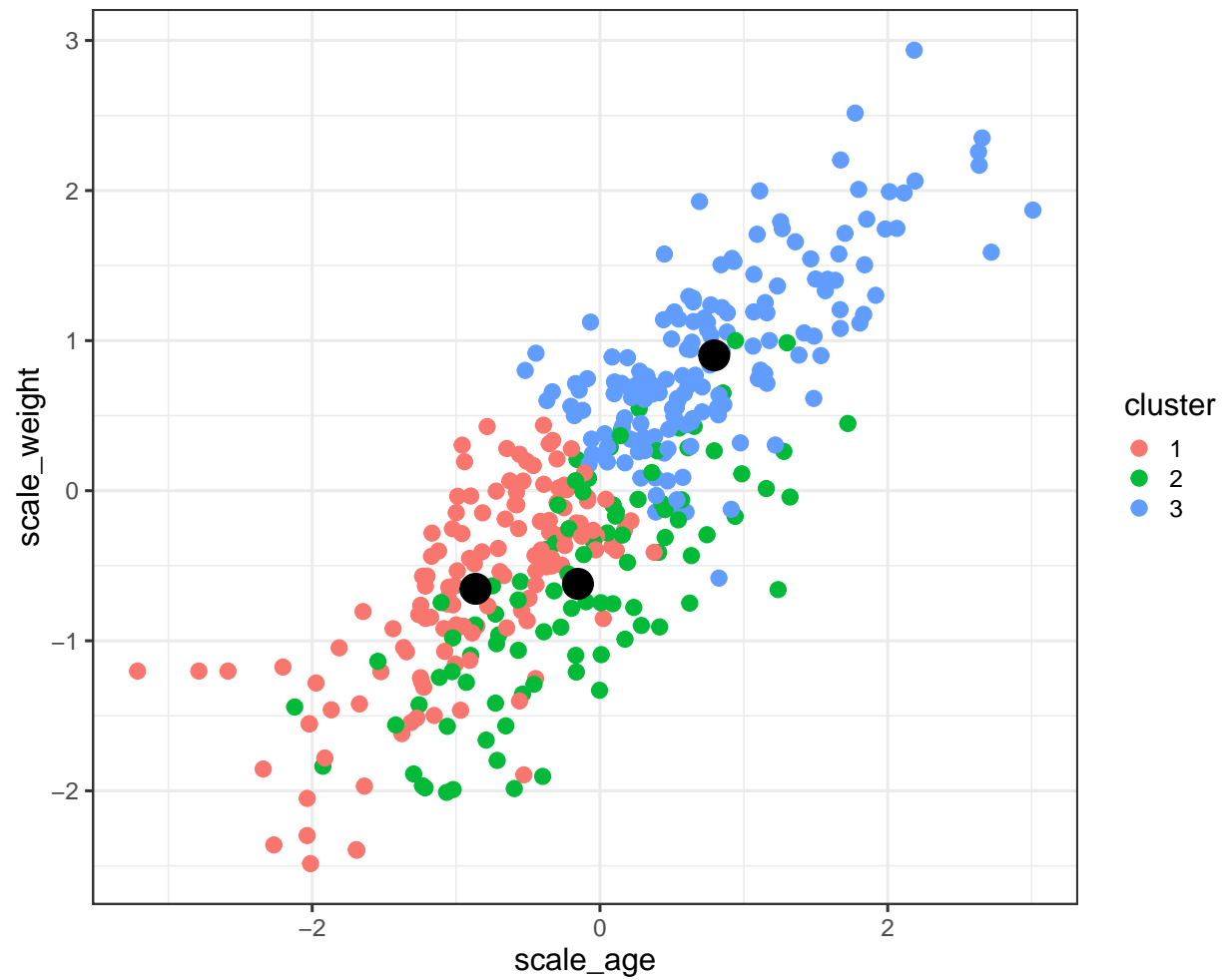
We can use ggplot to visualize the clusters.

```

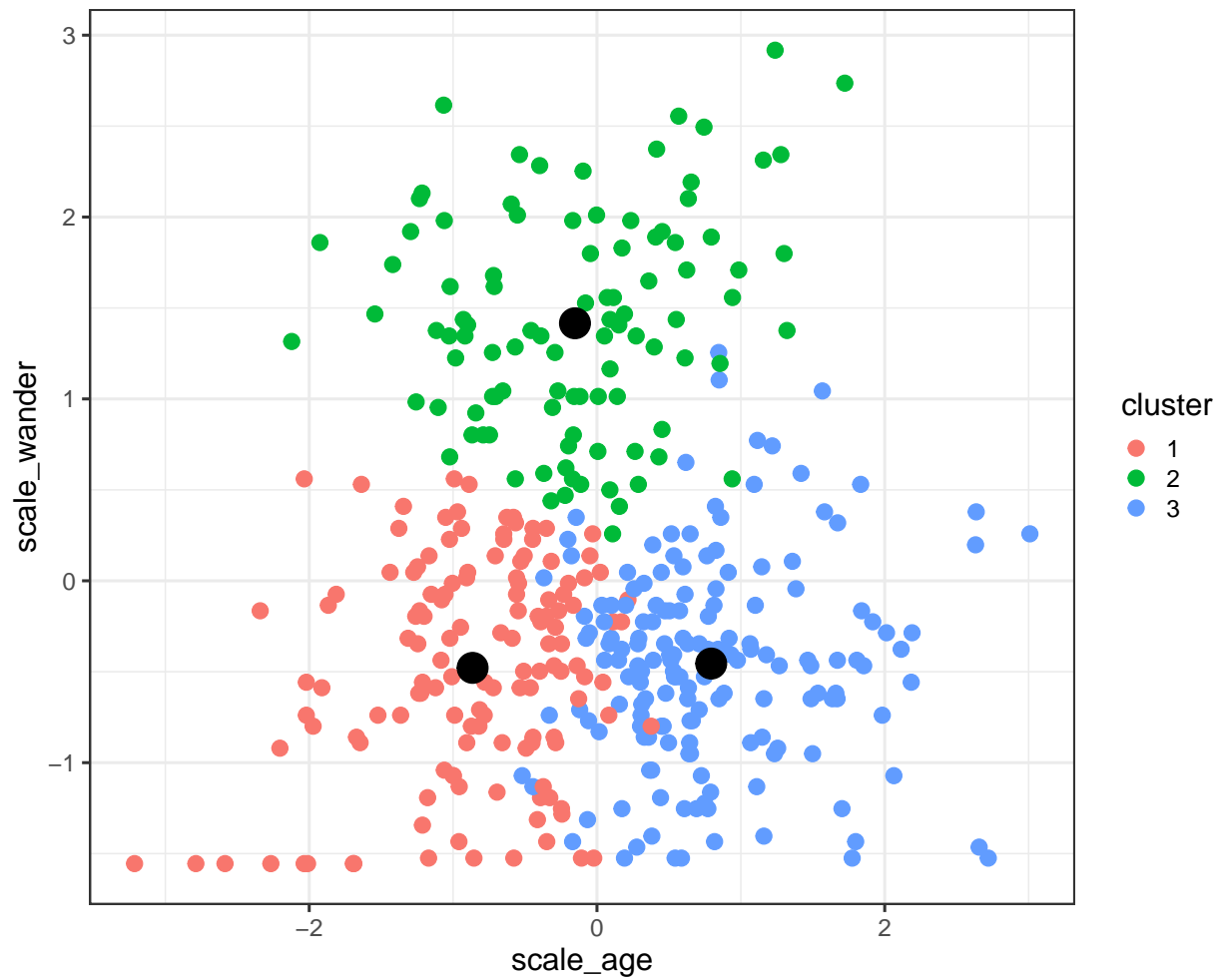
cats$cluster <- factor(cats_cluster$cluster)
cluster_centers <- as.data.frame(cats_cluster$centers)

ggplot(data = cats) +
  geom_point(aes(x = scale_age, y = scale_weight, color = cluster), size = 4) +
  geom_point(data = cluster_centers, aes(x = scale_age, y = scale_weight), color = 'black', size = 100) +
  theme_bw(base_size = 18)

```



```
ggplot(data = cats) +
  geom_point(aes(x = scale_age, y = scale_wander, color = cluster), size = 4) +
  geom_point(data = cluster_centers, aes(x = scale_age, y = scale_wander), color = 'black', size = 10) +
  theme_bw(base_size = 18)
```



```
ggplot(data = cats) +
  geom_point(aes(x = scale_weight, y = scale_wander, color = cluster), size = 4) +
  geom_point(data = cluster_centers, aes(x = scale_weight, y = scale_wander), color = 'black',
    theme_bw(base_size = 18)
```

