

3.1 million

Dogs enter shelters each year.

2 million

Of those dogs are adopted each year.

34%

Of dogs were purchased from breeders.

Prediction Goal

How likely is a dog to be adopted?

Allow shelters to predict available capacity based on how quickly a dog is to be adopted.



Raw Data

- Id: Unique identification code for the dogs
- Organization id: Unique identification code for shelter
- URL: link to dogs on Petfinder
- Type: type of animal (all dog)
- Special: species of animal (all dog)
- Breeds: primary, secondary, and tertiary breeds for each dog *
- Colors: primary, secondary, and tertiary colors of each dog *
- Age: Age of dog (Baby, Young, Adult, or Senior) *
- Gender: gender of the dog (male or female) *
- Coat: coat pattern of dog (Curly, long, medium, none, short, wire) *
- Size: how big the dog is (Small, Medium, Large, Extra Large) *
- Environment: what type of environment the dog came from
- Name: Name of the dog
- Description: Brief description of the dog
- Organization_animal_id: The ID of the dog from the shelter organization
- Photos: link to photos of the dogs
- Status Change Date: Date status became "adopted" or "adoptable"
- Neutered: Status of if the dog is spayed or neutered *
- Status: Whether the dog had been adopted or is available for adoption *
- Attributes: Whether the dog was house trained or have special needs

Summary of Cleaning

```
adogs1 <- read_csv("datasets/pet-adoption.csv")</pre>
adogs1[c('primary_breed', 'other_breeds')] <- str_split_fixed(adogs1$breeds, ',', 2)</pre>
adogs1[c('p','p1_breed' )] <- str_split_fixed(adogs1$primary_breed, ':', 2)</pre>
adogs1$p1_breed<-gsub("'","",adogs1$p1_breed)</pre>
adogs1[c('breed', 'breed_other')] <- str_split_fixed(adogs1$p1_breed, '/', 2)</pre>
adogs1[c('primary_color', 'other_colors')] <- str_split_fixed(adogs1$colors, ',', 2)
adogs1$primary_color<-gsub("'","",adogs1$primary_color)</pre>
adogs1[c('p1','p1_color')] <- str_split_fixed(adogs1$primary_color, ':', 2)</pre>
adogs1[c('c', 'c_other')] <- str_split_fixed(adogs1$p1_color, '/', 2)</pre>
adogs1[c('color', 'c1_other')] <- str_split_fixed(as.character(adogs1$c), '\\s*\\([\\\)', 2)</pre>
adogs1[c('spayed_n', 'other')] <- str_split_fixed(adogs1$attributes, ',', 2)</pre>
adogs1[c('n','neutered')] <- str_split_fixed(adogs1$spayed_n, ':', 2)</pre>
adogs1$neutered<-gsub("'","",adogs1$neutered)</pre>
view(adogs1)
```

```
glimpse(adogs1)
adoas1 <-
  adoas1 %>%
  mutate(age = as.factor(age),
         gender = as.factor(gender),
         color = as.factor(color).
         breed = as.factor(breed).
         coat = as.factor(coat).
         size = as.factor(size),
         neutered = as.factor(neutered),
         adopted = as.factor(status))
#There are 90 factors for breed, I am going to make this the top 12. Also recoded
adopted variable to make it easier to interpret.
adogs1 <-
  mutate(breed = fct_lump_n(breed, n = 12).
         adopted = fct_recode(adopted.
                              "not adopted" = "adoptable".
                              "adopted" = "adopted"))
#Also needed to create a dummy variable in order to calculate RMSE
adopted_dummy = ifelse(adoqs1$adopted == "adopted", 1, 0)
adogs1 <- cbind(adogs1, adopted_dummy)</pre>
```

- Create tidy data
- Factor variables
- Create necessary dummy variables

Summary Statistics

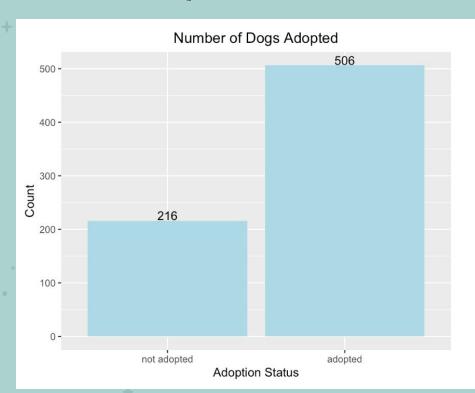
Variable	N	Mean
id	722	48552589.717
type	722	
Dog	722	100%
species	722	
Dog	722	100%
age	722	
Adult	283	39.2%
Baby	196	27.1%
Senior	59	8.2%
Young	184	25.5%
gender	722	
Female	340	47.1%
Male	382	52.9%
size	722	
Extra Large	7	1%
Large	163	22.6%
Medium	405	56.1%
Small	147	20.4%
coat	722	
Curly	1	0.1%
Long	17	2.4%
	17 87	2.4% 12%
Long		
Long Medium	87	12%

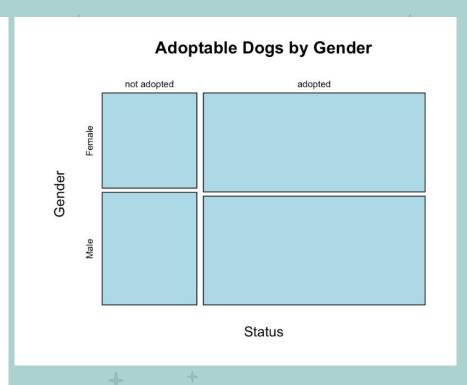
status	722	
adoptable	216	29.9%
adopted	506	70.1%
distance	722	
None	722	100%
p	722	
{'primary'	722	100%
breed	722	
Australian Cattle Dog	17	2.4%
Beagle	22	3%
Chihuahua	46	6.4%
Dachshund	19	2.6%
German Shepherd Dog	35	4.8%
Hound	30	4.2%
Husky	21	2.9%
Labrador Retriever	68	9.4%
Mixed Breed	55	7.6%
Pit Bull Terrier	53	7.3%
Shepherd	29	4%
Terrier	57	7.9%
Other	270	37.4%

		A
color	722	
Apricot	15	2.1%
Bicolor	22	3%
Black	131	18.1%
Brindle	41	5.7%
Brown	29	4%
Golden	11	1.5%
Gray	11	1.5%
Harlequin	1	0.1%
Merle	10	1.4%
None	309	42.8%
Red	27	3.7%
Tricolor	42	5.8%
White	50	6.9%
Yellow	23	3.2%
neutered	722	
False	187	25.9%
True	535	74.1%
adopted	722	
not adopted	216	29.9%
adopted	506	70.1%

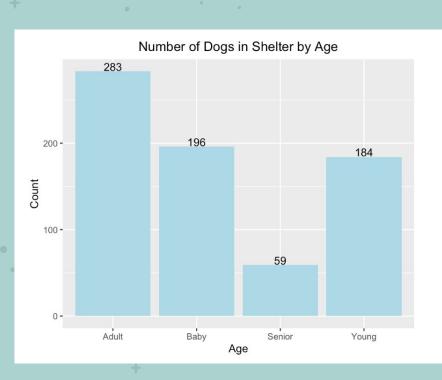
> dim(adogs1) [1] 722 46

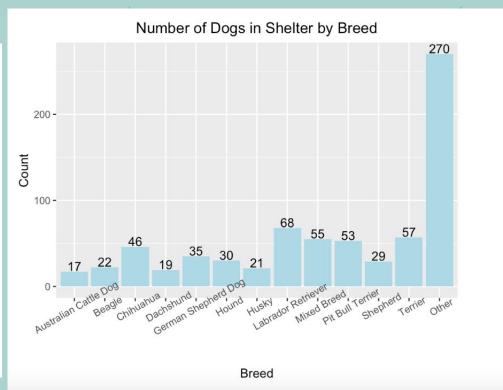
Summary Plots





Summary Plots





+ 01 Logistic Regression



	•				
Coefficients:					
	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	13.80393	1455.39862	0.009	0.992432	
ageBaby	1.00862	0.29976	3.365	0.000766	***
ageSenior	-0.75769	0.40042	-1.892	0.058461	
ageYoung	0.52825	0.28414	1.859	0.063014	
genderMale	-0.16056	0.22701	-0.707	0.479391	
breed Beagle	1.02629	0.92899	1.105	0.269274	
breed Chihuahua	1.71217	0.90460	1.893	0.058392	
breed Dachshund	0.84425	0.97976	0.862	0.388861	
breed German Shepherd Dog	2.70944	0.90743	2.986	0.002828	**
breed Hound	2.12929	0.92585		0.021458	*
breed Husky	3.01298	1.06244	2.836	0.004570	**
breed Labrador Retriever	3.13762	0.87019		0.000311	***
breed Mixed Breed	0.95048			0.220827	
breed Pit Bull Terrier	0.54331			0.486878	
breed Shepherd	2.38954			0.006686	**
breed Terrier	1.51226			0.067541	
breedOther	1.96124			0.007821	**
color Bicolor	-0.65814			0.612314	
color Black	-1.76008	1.17951	-1.492	0.135642	
color Brindle	-1.45536			0.240807	
color Brown	-1.19856			0.350373	
color Golden	-0.89142			0.535939	
color Gray	-2.30221			0.108438	
color Harlequin		1455.39803		0.993418	
color Merle	-1.47451			0.310560	
color None	-1.11462			0.345094	
color Red	-0.82409	1.32138	-0.624	0.532851	

color Tricolor	-0.73135	1.27650	-0.573	0.566691	
color White	-1.57929	1.21435	-1.301	0.193420	
color Yellow	-1.08215	1.37186	-0.789	0.430215	
coatLong	-15.80553	1455.39774	-0.011	0.991335	
coatMedium	-14.86165	1455.39764	-0.010	0.991853	
coatNone	-15.58108	1455.39764	-0.011	0.991458	
coatShort	-14.70247	1455.39763	-0.010	0.991940	
coatWire	-0.67720	1563.53367	0.000	0.999654	
sizeLarge	1.10849	0.99077	1.119	0.263216	
sizeMedium	1.58534	0.98253	1.614	0.106628	
sizeSmall	2.72804	1.03434	2.637	0.008353	×
neutered True	-0.09598	0.26544	-0.362	0.717651	

Exponentiated coefficients

(Intercept) 988484.6382817833219 aenderMale 0.8516659710242 breed German Shepherd Dog 15.0208753947324 breed Mixed Breed 2.5869477598844 breedOther 7.1081222010399 color Brown 0.3016294778639 color Merle 0.2288912502817 color White 0.2061212385977 coatNone 0.0000001710900 sizeMedium 4.8809693598390

ageBaby 2.7418265869967 breed Beagle 2.7907018237932 breed Hound 8.4088709214552 breed Pit Bull Terrier 1.7216967118967 color Bicolor 0.5178115159064 color Golden 0.4100747733220 color None 0.3280395462218 color Yellow 0.3388648432662 coatShort 0 0000004119065 sizeSmall

15.3029345697051

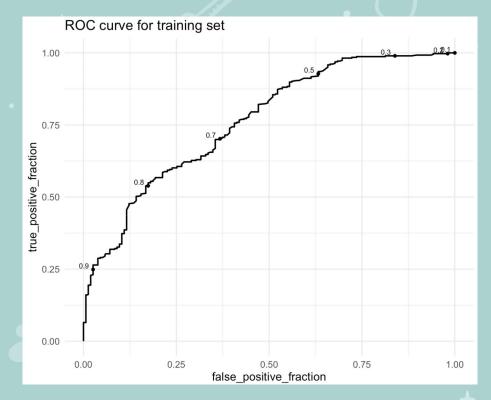
ageSenior 0.4687492541337 breed Chihuahua 5.5409939985475 20.3480359578264 breed Shepherd 10.9084792664178 color Black 0.1720308431929 color Gray 0.1000376413772 color Red 0.4386342753229 coatLong 0.0000001366927 coatWire 0.5080378344903 neutered True 0.9084783581152

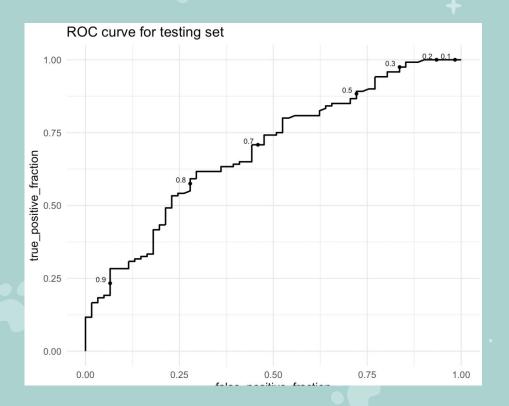
breed Dachshund 2.3262276465154 breed Husky breed Labrador Retriever 23.0488746708371 breed Terrier 4.5369611282032 color Brindle 0.2333155557025 color Harlequin 163633.9504383301537 color Tricolor 0.4812600727971 coatMedium 0.0000003512919 sizeLarge 3.0297868682695

ageYoung

1.6959538631584

- Small dogs have a 1430% probability of being adopted relative to extra large dogs.
- Large dogs have 203% probability of being adopted
- Popular dog breeds like labrador retrievers, german shepherds, and huskies have over a 1400% probability of being adopted relative to the australian cattle doq.
- Less popular breeds like pit bulls have a 72% probability of being adopted relative to australian cattle dogs







calc_auc(results_test)



0.7622764

AUC <dbl>

0.6891393



```
adogs1_train <- training(adogs1_split)</pre>
adogs1_test <- testing(adogs1_split)</pre>
enet_mod1 <- cva.glmnet(adopted ~ age + gender + color + breed + coat + size + neutered,
                       data = adogs1,
                       alpha = seq(0,1, by = 0.05),
                       family = "binomial")
                                                                                                                                       get_alpha <- function(fit) {</pre>
 alpha <- fit$alpha
 error <- sapply(fit$modlist,
                  function(mod) {min(mod$cvm)})
                                                                                                                                       0
 alpha[which.min(error)]
                                                                                                                                   0
                                                                                      .124
                                                                                                                                0
                                                                                 CV loss
                                                                                                                            0
                                                                                                                         0
get_model_params <- function(fit) {</pre>
                                                                                                                     0
                                                                                      1.123
 alpha <- fit$alpha
                                                                                                                  0
 lambdaMin <- sapply(fit$modlist, `[[`, "lambda.min")</pre>
                                                                                                               0
 lambdaSE <- sapply(fit$modlist, `[[`, "lambda.1se")</pre>
                                                                                             0
                                                                                                           0
 error <- sapply(fit$modlist, function(mod) {min(mod$cvm)})</pre>
                                                                                      1.122
 best <- which.min(error)</pre>
                                                                                                        0
 data.frame(alpha = alpha[best], lambdaMin = lambdaMin[best],
                                                                                                    0
             lambdaSE = lambdaSE[best], eror = error[best])
                                                                                                 0
                                                                                            0.0
                                                                                                          0.2
                                                                                                                        0.4
                                                                                                                                      0.6
                                                                                                                                                    0.8
                                                                                                                                                                  1.0
# extract the best alpha value and model parameters
best_alpha <- get_alpha(enet_mod1)</pre>
print(best_alpha)
                                                                                                                              alpha
get_model_params(enet_mod1)
minlossplot(enet_mod1,
                                                                                      lambdaMin
            cv.type = "min")
                                                          alpha
                                                                                                                       lambdaSE
                                                                                                                                                           eror
                                                           0.05
                                                                                      0.06873802
                                                                                                                       0.3342456
                                                                                                                                                     1.121505
```

1 row

adogs1_split <- initial_split(adogs1)</pre>

```
dog_mod <- cv.glmnet(adopted ~ age + gender + color + breed + coat + size + neutered,</pre>
                       data = adogs1_train,
                      alpha = 0.
                      family = "binomial")
coefpath(doa_mod)
print(dog_mod$lambda.min)
print(dog_mod$lambda.1se)
coef(dog_mod, s = dog_mod$lambda.min) %>%
  round(3)
# print coefficient using lambda.1se
coef(dog_mod, s = dog_mod$lambda.1se) %>%
  round(3)
dog_coefs <- tibble(</pre>
  `varnames` = rownames(coef(dog_mod, s = dog_mod$lambda.1se)),
  `ridge_min` = coef(dog_mod, s = dog_mod$lambda.min) %>%
    round(3) %>% as.matrix() %>% as.data.frame(),
  `ridge_1se` = coef(dog_mod, s = dog_mod$lambda.1se) %>%
    round(3) %>% as.matrix() %>% as.data.frame()
print(dog_coefs)
plot(dog_mod)
```

lambda.min

[1] 0.122627

lambda.1se

[1] 0.8651092

(Intercept)	1.10
ageAdult	-0.32
ageBaby	0.41
ageSenior	-0.48
ageYoung	0.13
genderFemale	0.04
genderMale	-0.04
color Apricot	0.70

color Bicolor
color Black
color Brindle
color Golden
color Gray
color Harlequin
color Merle
color Red
color Tricolor
color White
color Yellow

breed American Bulldog breed Australian Cattle Dog breed Australian Shepherd

-0.470

-1.522

0.183

0.728

-0.336

0.333

0.102

0.663

0.741

-0.648

-0.877

1.165

0.221

0.380

0.015

-0.097

breed Beagle breed Border Collie

breed Boxer

breed Collie

breed Hound

breed Husky

breed Cattle Dog

breed Chihuahua

breed Dachshund

breed Mixed Breed

breed Retriever

breed Shepherd

breed Shih Tzu

breed Terrier

breedOther

breed German Shepherd Dog

breed Labrador Retriever

breed Pit Bull Terrier

lambda.min

0.136 0.045		
	coatCurly coatLong coatMedium coatNone coatShort coatWire	-0.530 0.153 -0.274 0.216 1.372
0.831 -0.191 -0.071 0.291 0.275 -0.093 0.250 0.124	sizeExtra Large sizeLarge sizeMedium sizeSmall neutered False neutered True	-1.385 -0.388 -0.067 0.578 -0.038 0.038
-0.758 1.207 -0.432 0.933		A

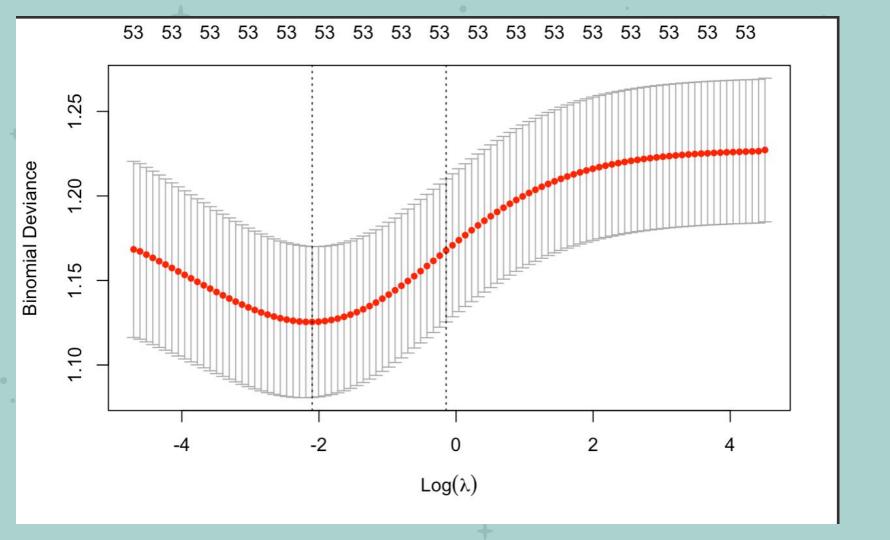
	cept)	0.577
ageAdı	ult	-0.172
ageBał	ру	0.197
ageSer	nior	-0.142
ageYou	ung	0.057
gender	⁻ Female	0.025
gendei		-0.025
	Apricot	0.253
	Bicolor	0.131
	Black	-0.049
	Brindle	-0.025
	Brown	0.020
	Golden	0.034
color		-0.155
color	Harlequin	0.337
	Merle	-0.018
color	None	-0.056
color		0.113
	Tricolor	0.138
	White	-0.028
	Yellow	0.128
reed	American Bulldog	-0.002
	Australian Cattle Dog	-0.279
	Australian Shepherd	0.423
	Beagle	-0.140
	Border Collie	0.330
	Boxer	-0.198
	Cattle Dog	-0.606
	Chihuahua	0.150
	Collie	0.273
	Dachshund	-0.081
	German Shepherd Dog	0.086
	Hound	0.084
	Husky	0.247
	Labrador Retriever	0.296
	Mixed Breed	-0.279
	Pit Bull Terrier	-0.424
	Retriever	0.416
reed	Shepherd	0.088
	Shih Tzu	0.181
	Terrier	0.069
reed(Other	-0.042

(Intercept)

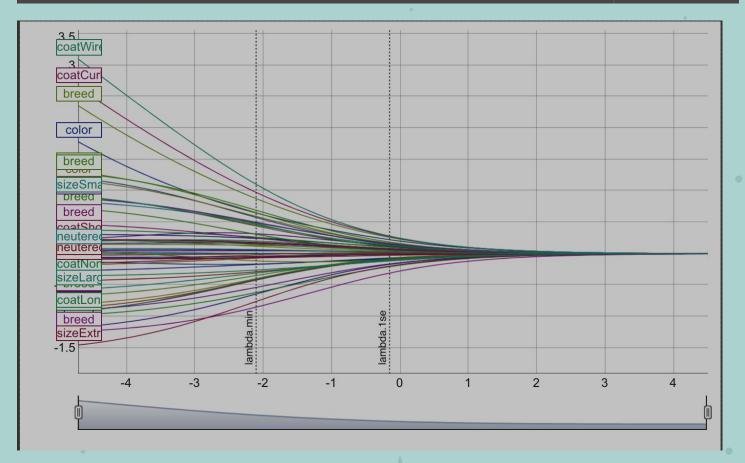
0.977

lambda.1se

coatCurly	
coatLong	-0.171
coatMedium	0.070
coatNone	-0.142
coatShort	0.117
coatWire	0.424
sizeExtra Large	-0.613
sizeLarge	-0.167
sizeMedium	-0.015
sizeSmall	0.229
neutered False	-0.022
neutered True	0.022



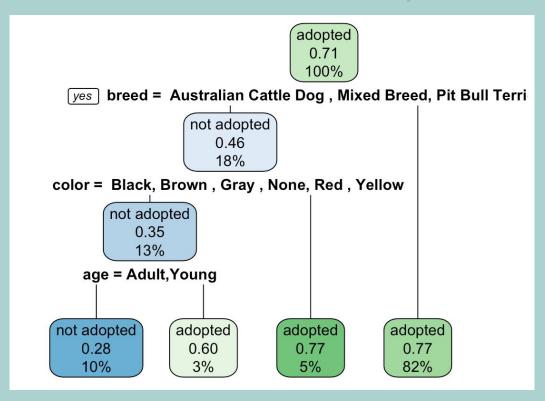
```
devtools::install_github("jaredlander/coefplot")
library('coefplot')
coefpath(dog_mod)
```





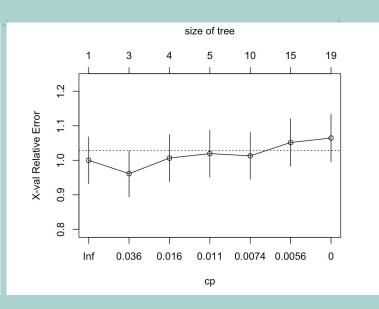
Basic Decision Tree

- Each node shows the predicted class, predicted probability of adoption, and the percentage of observations in that node
- Any breed that is not an Australian Cattle Dog, Mixed Breed, or Pit Bull have a 77% of being adopted



Cross-Validation

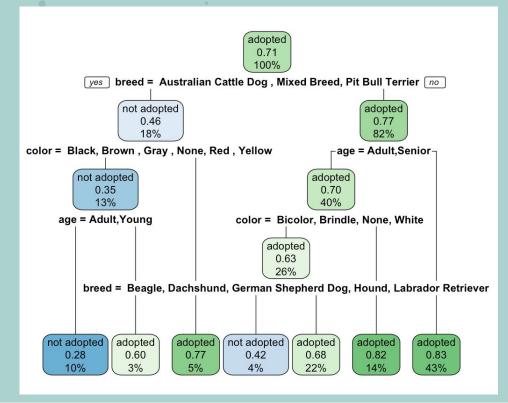
```
library('rpart')
adogs1 rpart <- rpart(adopted ~ age + gender + color + breed + coat + size + neutered,
                      data = adogs1 train,
                      control = list(cp = 0,
                                     minsplit = 10,
                                     maxdepth = 10))
adogs1 rpart$cptable
              CP nsplit rel error
                                     xerror
                                                  xstd
     0.067741935
                      0 1.0000000 1.0000000 0.06784677
   2 0.019354839
                      2 0.8645161 0.9612903 0.06703565
   3 0.012903226
                      3 0.8451613 1.0064516 0.06797705
   4 0.008602151
                      4 0.8322581 1.0193548 0.06823349
## 5 0.006451613
                      9 0.7677419 1.0129032 0.06810596
## 6 0.004838710
                     14 0.7354839 1.0516129 0.06885086
                     18 0.7161290 1.0645161 0.06908847
## 7 0.000000000
plotcp(adogs1_rpart)
```



Cross validation shows the optimal number of splits to minimize error is 18.

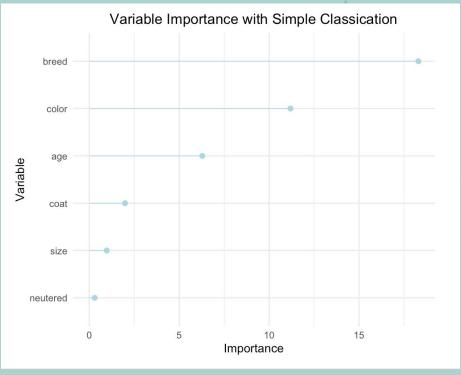
More Complex Tree

- Included the optimal split
- Same top node split, but more in depth



Variable Importance

 Breed is the most important variable followed by color and age



```
adogs1_rpart$variable.importance
## breed color age
## 18.2958261 11.1866218 6.2818963

coat size neutered
1.9883553 0.9698528 0.3025540
```

```
adogs1_rpart$variable.importance %>%
   data.frame() %>%
   rownames_to_column(var = "Feature") %>%
   rename(Overall = '.') %>%
   ggplot(aes(x = fct_reorder(Feature, Overall), y = Overall)) +
   geom_pointrange(aes(ymin = 0, ymax = Overall), color = "lightblue", size = .3) +
   theme_minimal() +
   coord_flip() +
   labs(x = "Variable", y = "Importance", title = "Variable Importance with Simple Classicatio
n") +
   theme(plot.title = element_text(hjust = 0.5))
```

Root Mean Squared Error

- RMSE = 0.5759
- This means that the model is relatively accurate at predicting adoption
- Could still be improved

Comparison

01

Logistic Regression

Test AUC = .6891

Model is slightly overfit since the training AUC is higher than the test AUC 02

Ridge

Finding the best lambda



03

Decision Tree

RMSE = 0.5759

Model is decent at predicting which dogs with be adopted. More interpretable



Conclusion

We recommend shelters implement the use of a decision tree to predict probability of adoption. The model was pretty accurate and it is the most interpretable.

