```
original dataset dir <- "~/Documents/R/train 2"
base dir <- "~/Documents/R/cats.vs.dogs"</pre>
dir.create(base dir)
train dir <- file.path(base dir, "train")</pre>
dir.create(train_dir)
validation_dir <- file.path(base_dir, "validation")</pre>
dir.create(validation dir)
test_dir <- file.path(base_dir, "test")</pre>
dir.create(test dir)
train_cats_dir <- file.path(train_dir, "cats")</pre>
dir.create(train cats dir)
train dogs dir <- file.path(train dir, "dogs")</pre>
dir.create(train dogs dir)
validation_cats_dir <- file.path(validation_dir, "cats")</pre>
dir.create(validation_cats_dir)
validation_dogs_dir <- file.path(validation_dir, "dogs")</pre>
dir.create(validation_dogs_dir)
test_cats_dir <- file.path(test_dir, "cats")</pre>
dir.create(test cats dir)
test_dogs_dir <- file.path(test_dir, "dogs")</pre>
dir.create(test dogs dir)
fnames <- paste0("cat.", 1:1000, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
      file.path(train cats dir))
##
   TRUE
##
   TRUE
##
   TRUE
##
   TRUE
   ##
TRUE
   ##
TRUE
   ##
TRUE
##
   TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
## [995] TRUE TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("cat.", 1001:1500, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(validation cats dir))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
```

```
fnames <- paste0("cat.", 1501:2000, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
 file.path(test_cats_dir))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("dog.", 1:1000, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(train_dogs_dir))
 ##
TRUE
TRUE
TRUE
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
TRUE
TRUE
TRUE
TRUE
TRUE
TRUE
TRUE
TRUE
## [995] TRUE TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("dog.", 1001:1500, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(validation dogs dir))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("dog.", 1501:2000, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
 file.path(test_dogs_dir))
##
TRUE TRUE
TRUE TRUE
```

Split the data into training, test and validation sets and verified the number of images in each.

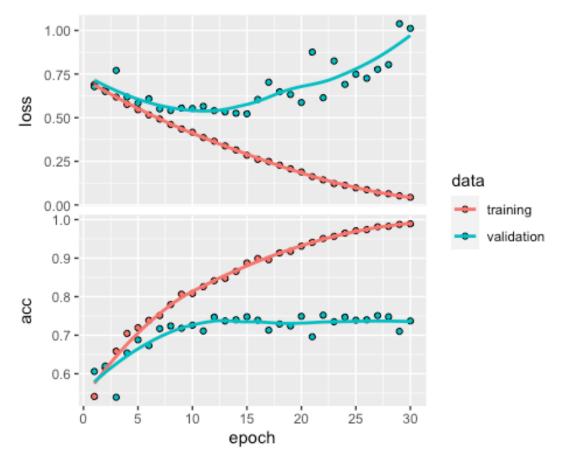
```
cat("total training cat images:", length(list.files(train cats dir)), "\n")
## total training cat images: 1000
cat("total training dog images:", length(list.files(train dogs dir)), "\n")
## total training dog images: 1000
cat("total validation cat images:", length(list.files(validation_cats_dir)),
"\n")
## total validation cat images: 500
cat("total validation dog images:", length(list.files(validation_dogs_dir)),
"\n")
## total validation dog images: 500
cat("total test cat images:", length(list.files(test cats dir)), "\n")
## total test cat images: 500
 cat("total test dog images:", length(list.files(test_dogs_dir)), "\n")
## total test dog images: 500
library(keras)
## Warning: package 'keras' was built under R version 4.1.2
model <- keras model sequential() %>%
  layer_conv_2d(filters = 32, kernel_size = c(3, 3), activation = "relu",
                input_shape = c(150, 150, 3)) %>%
  layer max pooling 2d(pool size = c(2, 2)) %>%
  layer_conv_2d(filters = 64, kernel_size = c(3, 3), activation = "relu") %>%
 layer_max_pooling_2d(pool_size = c(2, 2)) %>%
```

```
layer conv 2d(filters = 128, kernel size = c(3, 3), activation = "relu")
%>%
 layer_max_pooling_2d(pool_size = c(2, 2)) %>%
 layer_conv_2d(filters = 128, kernel_size = c(3, 3), activation = "relu")
%>%
 layer_max_pooling_2d(pool_size = c(2, 2)) %>%
 layer flatten() %>%
 layer_dense(units = 512, activation = "relu") %>%
 layer dense(units = 1, activation = "sigmoid")
## Loaded Tensorflow version 2.8.0
summary(model)
## Model: "sequential"
##
## Layer (type)
                                   Output Shape
                                                                Param
#
##
______
                                   (None, 148, 148, 32)
##
   conv2d_3 (Conv2D)
                                                                896
##
   max_pooling2d_3 (MaxPooling2D)
                                   (None, 74, 74, 32)
                                                                0
##
##
   conv2d_2 (Conv2D)
                                   (None, 72, 72, 64)
                                                                18496
##
##
                                   (None, 36, 36, 64)
## max_pooling2d_2 (MaxPooling2D)
##
## conv2d 1 (Conv2D)
                                   (None, 34, 34, 128)
                                                                73856
##
##
   max_pooling2d_1 (MaxPooling2D)
                                   (None, 17, 17, 128)
##
##
   conv2d (Conv2D)
                                   (None, 15, 15, 128)
                                                                147584
##
                                   (None, 7, 7, 128)
   max pooling2d (MaxPooling2D)
##
                                                                0
##
                                   (None, 6272)
## flatten (Flatten)
                                                                0
##
## dense_1 (Dense)
                                   (None, 512)
3211776
##
##
   dense (Dense)
                                   (None, 1)
                                                                513
##
##
______
## Total params: 3,453,121
```

```
## Trainable params: 3,453,121
## Non-trainable params: 0
##
model %>% compile(
 loss = "binary_crossentropy",
 optimizer = optimizer rmsprop(learning rate = 1e-4),
 metrics = c("acc")
)
train_datagen <- image_data_generator(rescale = 1/255)</pre>
validation_datagen <- image_data_generator(rescale = 1/255)</pre>
train_generator <- flow_images_from_directory(</pre>
 train_dir,
 train_datagen,
 target_size = c(150, 150),
 batch size = 20,
 class mode = "binary"
)
validation_generator <- flow_images_from_directory(</pre>
  validation_dir,
  validation_datagen,
 target_size = c(150, 150),
 batch_size = 20,
  class mode = "binary"
)
batch <- generator_next(train_generator)</pre>
str(batch)
## List of 2
## $ : num [1:20, 1:150, 1:150, 1:3] 0.886 0.31 0.235 0.918 0.882 ...
## $ : num [1:20(1d)] 0 1 0 0 1 1 1 1 1 1 ...
history <- model %>% fit_generator(
 train_generator,
 steps_per_epoch = 100,
 epochs = 30,
 validation data = validation generator,
 validation steps = 50
)
## Warning in fit_generator(., train_generator, steps_per_epoch = 100, epochs
## = 30, : `fit_generator` is deprecated. Use `fit` instead, it now accept
## generators.
```

Built and visualized the original model

```
model %>% save_model_hdf5("cats_and_dogs_small_1.h5")
plot(history)
## `geom_smooth()` using formula 'y ~ x'
```



Created

a second model using data augmentation.

```
model2 <- keras model sequential() %>%
  layer_conv_2d(filters = 32, kernel_size = c(3, 3), activation = "relu",
                input shape = c(150, 150, 3)) %>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer_conv_2d(filters = 64, kernel_size = c(3, 3), activation = "relu") %>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer_conv_2d(filters = 128, kernel_size = c(3, 3), activation = "relu")
%>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer_conv_2d(filters = 128, kernel_size = c(3, 3), activation = "relu")
%>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer flatten() %>%
  layer_dropout(rate = 0.5) %>%
  layer dense(units = 512, activation = "relu") %>%
  layer_dense(units = 1, activation = "sigmoid")
```

```
model2 %>% compile(
  loss = "binary crossentropy",
  optimizer = optimizer rmsprop(learning rate = 1e-4),
  metrics = c("acc")
)
datagen <- image_data_generator(</pre>
  rescale = 1/255,
  rotation_range = 40,
  width_shift_range = 0.2,
  height_shift_range = 0.2,
  shear range = 0.2,
  zoom_range = 0.2,
  horizontal_flip = TRUE
)
test_datagen <- image_data_generator(rescale = 1/255)</pre>
train_generator <- flow_images_from_directory(</pre>
  train dir,
  datagen,
  target_size = c(150, 150),
  batch size = 32,
  class_mode = "binary"
validation_generator <- flow_images_from_directory(</pre>
  validation dir,
  test_datagen,
  target_size = c(150, 150),
  batch size = 32,
  class mode = "binary"
)
history <- model2 %>% fit(
  train_generator,
  epochs = 30,
  validation data = validation generator,
base dir2 <- "~/Documents/R/cats.vs.dogs2"</pre>
dir.create(base_dir2)
train_dir2 <- file.path(base_dir2, "train")</pre>
dir.create(train_dir2)
validation_dir2 <- file.path(base_dir2, "validation")</pre>
dir.create(validation dir2)
test dir2 <- file.path(base dir2, "test")</pre>
dir.create(test_dir2)
```

```
train cats dir2 <- file.path(train dir2, "cats")</pre>
dir.create(train cats dir2)
train dogs dir2 <- file.path(train dir2, "dogs")
dir.create(train dogs dir2)
validation cats dir2 <- file.path(validation dir2, "cats")</pre>
dir.create(validation cats dir2)
validation_dogs_dir2 <- file.path(validation_dir2, "dogs")</pre>
dir.create(validation dogs dir2)
test_cats_dir2 <- file.path(test_dir2, "cats")</pre>
dir.create(test_cats_dir2)
test dogs dir2 <- file.path(test dir2, "dogs")
dir.create(test_dogs_dir2)
fnames <- paste0("cat.", 1:1300, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
    file.path(train cats dir2))
##
  TRUE
  ##
TRUE
  ##
TRUE
  ##
TRUE
  ##
TRUE
##
  TRUE
  ##
TRUE
  ##
TRUE
TRUE
TRUE
TRUE
TRUE
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
TRUE
TRUE
fnames <- paste0("cat.", 1001:1500, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
 file.path(validation cats dir2))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("cat.", 1501:2000, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(test cats dir2))
##
TRUE TRUE
```

```
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("dog.", 1:1300, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(train_dogs_dir2))
##
TRUE
##
TRUE
##
TRUE
TRUE
##
TRUE
##
TRUE
##
TRUE
##
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
fnames <- paste0("dog.", 1001:1500, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(validation dogs dir2))
TRUE TRUE
```

```
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("dog.", 1501:2000, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
 file.path(test dogs dir2))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
```

Increased the training data to 1300 images for a third model.

```
cat("total training cat images:", length(list.files(train_cats_dir2)), "\n")
## total training cat images: 1300
cat("total training dog images:", length(list.files(train_dogs_dir2)), "\n")
## total training dog images: 1300
cat("total validation cat images:", length(list.files(validation_cats_dir2)), "\n")
## total validation cat images: 500
```

```
cat("total validation dog images:", length(list.files(validation dogs dir2)),
"\n")
## total validation dog images: 500
cat("total test cat images:", length(list.files(test_cats_dir2)), "\n")
## total test cat images: 500
 cat("total test dog images:", length(list.files(test dogs dir2)), "\n")
## total test dog images: 500
model3 <- keras model sequential() %>%
  layer_conv_2d(filters = 32, kernel_size = c(3, 3), activation = "relu",
                input shape = c(150, 150, 3)) \%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer_conv_2d(filters = 64, kernel_size = c(3, 3), activation = "relu") %>%
  layer max pooling 2d(pool size = c(2, 2)) %>%
  layer conv 2d(filters = 128, kernel size = c(3, 3), activation = "relu")
%>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer_conv_2d(filters = 128, kernel_size = c(3, 3), activation = "relu")
%>%
  layer max pooling 2d(pool size = c(2, 2)) %>%
  layer_flatten() %>%
  layer_dense(units = 512, activation = "relu") %>%
  layer_dense(units = 1, activation = "sigmoid")
model3 %>% compile(
  loss = "binary crossentropy",
 optimizer = optimizer rmsprop(learning rate = 1e-4),
 metrics = c("acc")
)
train_datagen2 <- image_data_generator(rescale = 1/255)</pre>
validation datagen2 <- image data generator(rescale = 1/255)</pre>
train generator2 <- flow images from directory(
  train_dir2,
 train_datagen2,
 target size = c(150, 150),
 batch size = 20,
 class_mode = "binary"
)
validation generator2 <- flow images from directory(</pre>
  validation_dir2,
  validation_datagen2,
 target size = c(150, 150),
batch size = 20,
```

```
class mode = "binary"
)
history3 <- model3 %>% fit(
 train generator2,
 steps per epoch = 100,
 epochs = 30,
 validation data = validation generator2,
 validation steps = 50
)
base_dir3 <- "~/Documents/R/cats.vs.dogs3"</pre>
dir.create(base dir3)
train dir3 <- file.path(base dir3, "train")</pre>
dir.create(train_dir3)
validation dir3 <- file.path(base_dir3, "validation")</pre>
dir.create(validation dir3)
test_dir3 <- file.path(base_dir3, "test")</pre>
dir.create(test_dir3)
train cats dir3 <- file.path(train dir3, "cats")</pre>
dir.create(train_cats_dir3)
train dogs dir3 <- file.path(train dir3, "dogs")
dir.create(train_dogs_dir3)
validation cats_dir3 <- file.path(validation_dir3, "cats")</pre>
dir.create(validation_cats_dir3)
validation_dogs_dir3 <- file.path(validation_dir3, "dogs")</pre>
dir.create(validation dogs dir3)
test cats dir3 <- file.path(test dir3, "cats")
dir.create(test_cats_dir3)
test dogs dir3 <- file.path(test dir3, "dogs")
dir.create(test_dogs_dir3)
fnames <- paste0("cat.", 1:1800, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
        file.path(train cats dir3))
     ##
TRUE
##
    TRUE
##
    TRUE
    ##
TRUE
```

```
TRUE
##
TRUE
##
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
```

```
fnames <- paste0("cat.", 1001:1500, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
 file.path(validation_cats_dir3))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("cat.", 1501:2000, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(test_cats_dir3))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("dog.", 1:1800, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
 file.path(train dogs dir3))
 ##
TRUE
```

```
TRUE
##
TRUE
##
TRUE
TRUE
TRUE
##
TRUE
##
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
```

```
TRUE
TRUE
fnames <- paste0("dog.", 1001:1500, ".jpg")</pre>
file.copy(file.path(original dataset dir, fnames),
 file.path(validation dogs dir3))
##
TRUE TRUE
```

```
TRUE TRUE
## [496] TRUE TRUE TRUE TRUE TRUE
fnames <- paste0("dog.", 1501:2000, ".jpg")</pre>
file.copy(file.path(original_dataset_dir, fnames),
 file.path(test_dogs_dir3))
##
TRUE TRUE
```

```
TRUE TRUE
```

## [496] TRUE TRUE TRUE TRUE TRUE

Increased the training data to 1800 images for a fourth version of the model.

```
cat("total training cat images:", length(list.files(train_cats_dir3)), "\n")
## total training cat images: 1800
cat("total training dog images:", length(list.files(train_dogs_dir3)), "\n")
## total training dog images: 1800
cat("total validation cat images:", length(list.files(validation_cats_dir3)),
"\n")
## total validation cat images: 500
cat("total validation dog images:", length(list.files(validation_dogs_dir3)),
"\n")
## total validation dog images: 500
cat("total test cat images:", length(list.files(test cats dir3)), "\n")
## total test cat images: 500
 cat("total test dog images:", length(list.files(test dogs dir3)), "\n")
## total test dog images: 500
model4 <- keras model sequential() %>%
  layer_conv_2d(filters = 32, kernel_size = c(3, 3), activation = "relu",
                input_shape = c(150, 150, 3)) %>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer conv 2d(filters = 64, kernel size = c(3, 3), activation = "relu") %>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer conv 2d(filters = 128, kernel size = c(3, 3), activation = "relu")
%>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer conv 2d(filters = 128, kernel size = c(3, 3), activation = "relu")
%>%
  layer_max_pooling_2d(pool_size = c(2, 2)) %>%
  layer flatten() %>%
  layer_dense(units = 512, activation = "relu") %>%
  layer_dense(units = 1, activation = "sigmoid")
model4 %>% compile(
  loss = "binary crossentropy",
  optimizer = optimizer rmsprop(learning rate = 1e-4),
  metrics = c("acc")
)
train datagen3 <- image data generator(rescale = 1/255)</pre>
validation_datagen3 <- image_data_generator(rescale = 1/255)</pre>
```

```
train generator3 <- flow images from directory(
  train dir3,
  train_datagen3,
  target_size = c(150, 150),
  batch_size = 20,
  class_mode = "binary"
)
validation generator3 <- flow images from directory(</pre>
  validation_dir3,
  validation_datagen3,
  target_size = c(150, 150),
  batch size = 20,
  class_mode = "binary"
)
history4 <- model4 %>% fit(
  train_generator3,
  steps per epoch = 100,
  epochs = 30,
 validation_data = validation_generator3,
  validation steps = 50
)
```

This model with 1800 training images had the best performance overall.

Using a Pretrained model:

```
library(keras)
conv_base <- application_vgg16(</pre>
 weights = "imagenet",
 include_top = FALSE,
 input\_shape = c(150, 150, 3)
)
summary(conv_base)
## Model: "vgg16"
##
## Layer (type)
                                 Output Shape
                                                            Param
#
_______
===
## input_1 (InputLayer)
                                 [(None, 150, 150, 3)]
##
   block1 conv1 (Conv2D)
                                 (None, 150, 150, 64)
##
                                                            1792
##
```

```
##
   block1 conv2 (Conv2D)
                                    (None, 150, 150, 64)
                                                                  36928
##
##
   block1_pool (MaxPooling2D)
                                    (None, 75, 75, 64)
##
   block2_conv1 (Conv2D)
                                    (None, 75, 75, 128)
                                                                  73856
##
##
   block2 conv2 (Conv2D)
                                    (None, 75, 75, 128)
##
                                                                  147584
##
   block2 pool (MaxPooling2D)
##
                                    (None, 37, 37, 128)
##
   block3_conv1 (Conv2D)
                                    (None, 37, 37, 256)
##
                                                                  295168
##
## block3 conv2 (Conv2D)
                                    (None, 37, 37, 256)
                                                                  590080
##
##
   block3_conv3 (Conv2D)
                                    (None, 37, 37, 256)
                                                                  590080
##
## block3_pool (MaxPooling2D)
                                    (None, 18, 18, 256)
                                                                  0
##
## block4 conv1 (Conv2D)
                                    (None, 18, 18, 512)
1180160
##
## block4_conv2 (Conv2D)
                                    (None, 18, 18, 512)
2359808
## block4 conv3 (Conv2D)
                                    (None, 18, 18, 512)
2359808
##
## block4_pool (MaxPooling2D)
                                    (None, 9, 9, 512)
                                                                  0
##
## block5 conv1 (Conv2D)
                                    (None, 9, 9, 512)
2359808
##
## block5 conv2 (Conv2D)
                                    (None, 9, 9, 512)
2359808
##
## block5 conv3 (Conv2D)
                                    (None, 9, 9, 512)
2359808
##
## block5 pool (MaxPooling2D)
                                   (None, 4, 4, 512)
##
______
## Total params: 14,714,688
## Trainable params: 14,714,688
## Non-trainable params: 0
##
```

```
base dir4 <- "~/Documents/R/cats.vs.dogs4"</pre>
train dir4 <- file.path(base dir, "train")</pre>
validation_dir4 <- file.path(base_dir, "validation")</pre>
test dir4 <- file.path(base dir, "test")</pre>
datagen <- image data generator(rescale = 1/255)</pre>
batch size <- 20
extract_features <- function(directory, sample_count) {</pre>
  features \leftarrow array(0, dim = c(sample_count, 4, 4, 512))
  labels <- array(0, dim = c(sample_count))</pre>
  generator <- flow_images_from_directory(</pre>
    directory = directory,
    generator = datagen,
    target size = c(150, 150),
    batch_size = batch_size,
    class mode = "binary"
  )
  i <- 0
  while(TRUE) {
    batch <- generator next(generator)</pre>
    inputs_batch <- batch[[1]]</pre>
    labels_batch <- batch[[2]]</pre>
    features_batch <- conv_base %>% predict(inputs_batch)
    index_range <- ((i * batch_size)+1):((i + 1) * batch_size)</pre>
    features[index_range,,,] <- features_batch</pre>
    labels[index_range] <- labels_batch</pre>
    i < -i + 1
    if (i * batch_size >= sample_count)
      break
  }
  list(
    features = features,
    labels = labels
  )
}
train <- extract_features(train_dir4, 2000)</pre>
validation <- extract features(validation dir4, 1000)</pre>
test <- extract_features(test_dir4, 1000)</pre>
reshape features <- function(features) {</pre>
array_reshape(features, dim = c(nrow(features), 4 * 4 * 512))
```

```
train$features <- reshape features(train$features)</pre>
validation$features <- reshape_features(validation$features)</pre>
test$features <- reshape features(test$features)</pre>
model5 <- keras model sequential() %>%
  layer_dense(units = 256, activation = "relu",
              input_shape = 4 * 4 * 512) %>%
  layer_dropout(rate = 0.5) %>%
  layer_dense(units = 1, activation = "sigmoid")
model5 %>% compile(
  optimizer = optimizer_rmsprop(lr = 2e-5),
 loss = "binary_crossentropy",
 metrics = c("accuracy")
## Warning in backcompat fix rename lr to learning rate(...): the `lr`
argument has
## been renamed to `learning_rate`.
history5 <- model5 %>% fit(
  train$features, train$labels,
  epochs = 30,
  batch size = 20,
  validation data = list(validation$features, validation$labels)
)
```

The pretrained model performed well, but is still showing signs of overfitting.

Used the pretrained model with 1300 training images:

```
base_dir6 <- "~/Documents/R/cats.vs.dogs6"

datagen <- image_data_generator(rescale = 1/255)
batch_size <- 20

extract_features <- function(directory, sample_count) {

  features <- array(0, dim = c(sample_count, 4, 4, 512))
  labels <- array(0, dim = c(sample_count))

  generator <- flow_images_from_directory(
    directory = directory,
    generator = datagen,
    target_size = c(150, 150),
    batch_size = batch_size,
    class_mode = "binary"
  )

  i <- 0</pre>
```

```
while(TRUE) {
    batch <- generator next(generator)</pre>
    inputs_batch <- batch[[1]]</pre>
    labels_batch <- batch[[2]]</pre>
    features_batch <- conv_base %>% predict(inputs_batch)
    index_range <- ((i * batch_size)+1):((i + 1) * batch_size)</pre>
    features[index_range,,,] <- features_batch</pre>
    labels[index range] <- labels batch</pre>
    i < -i + 1
    if (i * batch size >= sample count)
      break
  }
 list(
    features = features,
    labels = labels
  )
}
train <- extract_features(train_dir2, 2600)</pre>
validation <- extract features(validation dir2, 1000)
test <- extract_features(test_dir2, 1000)</pre>
reshape features <- function(features) {</pre>
  array reshape(features, dim = c(nrow(features), 4 * 4 * 512))
train$features <- reshape features(train$features)</pre>
validation$features <- reshape features(validation$features)</pre>
test$features <- reshape_features(test$features)</pre>
model7 <- keras_model_sequential() %>%
  layer_dense(units = 256, activation = "relu",
               input_shape = 4 * 4 * 512) %>%
  layer_dropout(rate = 0.5) %>%
  layer dense(units = 1, activation = "sigmoid")
model7 %>% compile(
  optimizer = optimizer_rmsprop(lr = 2e-5),
 loss = "binary_crossentropy",
 metrics = c("accuracy")
)
## Warning in backcompat_fix_rename_lr_to_learning_rate(...): the `lr`
argument has
## been renamed to `learning_rate`.
history7 <- model7 %>% fit(
train$features, train$labels,
```

```
epochs = 30,
  batch size = 20,
  validation_data = list(validation$features, validation$labels)
)
Used the pretrained model with 1800 images:
```r
base_dir5 <- "~/Documents/R/cats.vs.dogs5"</pre>
datagen <- image_data_generator(rescale = 1/255)</pre>
batch_size <- 20
extract_features <- function(directory, sample_count) {</pre>
  features <- array(0, dim = c(sample_count, 4, 4, 512))</pre>
  labels <- array(0, dim = c(sample_count))</pre>
  generator <- flow_images_from_directory(</pre>
    directory = directory,
    generator = datagen,
    target_size = c(150, 150),
    batch size = batch size,
    class_mode = "binary"
  )
  i <- 0
  while(TRUE) {
    batch <- generator_next(generator)</pre>
    inputs batch <- batch[[1]]</pre>
    labels_batch <- batch[[2]]</pre>
    features_batch <- conv_base %>% predict(inputs_batch)
    index_range <- ((i * batch_size)+1):((i + 1) * batch_size)</pre>
    features[index_range,,,] <- features_batch</pre>
    labels[index_range] <- labels_batch</pre>
    i < -i + 1
    if (i * batch_size >= sample_count)
      break
  }
  list(
    features = features,
    labels = labels
  )
}
```

```
train <- extract_features(train_dir3, 3600)</pre>
validation <- extract features(validation dir3, 1000)</pre>
test <- extract features(test dir3, 1000)
reshape_features <- function(features) {</pre>
  array_reshape(features, dim = c(nrow(features), 4 * 4 * 512))
}
train$features <- reshape_features(train$features)</pre>
validation$features <- reshape_features(validation$features)</pre>
test$features <- reshape_features(test$features)</pre>
model6 <- keras model sequential() %>%
  layer_dense(units = 256, activation = "relu",
              input shape = 4 * 4 * 512) %>%
  layer_dropout(rate = 0.5) %>%
  layer_dense(units = 1, activation = "sigmoid")
model6 %>% compile(
  optimizer = optimizer_rmsprop(lr = 2e-5),
 loss = "binary_crossentropy",
 metrics = c("accuracy")
## Warning in backcompat fix rename lr to learning rate(...): the `lr`
argument has
## been renamed to `learning_rate`.
history6 <- model6 %>% fit(
 train$features, train$labels,
  epochs = 30,
 batch size = 20,
  validation data = list(validation$features, validation$labels)
)
```

This model resulted in the best performance overall.