MODEL 2 NEURAL NETWORK-BASED CLASSIFICATION MODEL

REY P. PENDANG

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```
# Helper packages
library(dplyr)
                     # for data wrangling
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
      filter, lag
## The following objects are masked from 'package:base':
##
      intersect, setdiff, setequal, union
library(tidyverse)
                     # for filtering
## -- Attaching packages -----
## v ggplot2 3.4.0
                    v purrr 0.3.5
## v tibble 3.1.8 v stringr 1.4.1
          1.2.1
## v tidyr
                     v forcats 0.5.2
## v readr
          2.1.3
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
library(readr)
                     # load dataset
library(rsample)
                     # for creating validation splits
library(bestNormalize) # for normalizing the dataset
library(keras)
                    # for fitting DNNs
library(tfruns)
                     # for additional grid search
library(tfestimators) # provides grid search & model training interface
```

Load the data set

library(tensorflow)

The data frame output of data reprocessing converted into to "csv", which will be used for entire project.

tfestimators is not recomended for new code. It is only compatible with Tensorflow version 1, and is

```
dt <- read_csv("normalRad.CSV")</pre>
```

```
## Rows: 197 Columns: 431
## -- Column specification -------
## Delimiter: ","
        (1): Institution
## chr
## dbl (430): Failure.binary, Failure, Entropy_cooc.W.ADC, GLNU_align.H.PET, Mi...
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
View(dt)
head(dt)
## # A tibble: 6 x 431
    Institution Failure.~1 Failure Entro~2 GLNU_~3 Min_h~4 Max_h~5 Mean_~6 Varia~7
                     <dbl>
                             <dbl>
                                     <dbl>
                                            <dbl>
                                                    <dbl>
                                                            <dbl>
                                                                    <dbl>
## 1 A
                             1.15
                                     12.9 -0.433 -0.270 -0.257
                                                                   -0.192 0.0509
## 2 A
                         1 - 0.533
                                     12.2 -1.02
                                                    0.671 0.405
                                                                    0.490 0.687
## 3 A
                             2.24
                                      12.8
                                            0.179 - 1.41 - 1.57
                                                                   -1.53 -1.57
## 4 A
                         1 -0.140
                                      13.5
                                            2.00
                                                   -0.218 0.0764 -0.153 0.0127
## 5 A
                                            0.153 -1.06 -1.15
                            0.787
                                      12.6
                                                                   -1.45 -1.91
## 6 A
                         1 - 2.80
                                      13.2
                                            0.391 -1.57 -1.91
                                                                   -1.72 -1.84
## # ... with 422 more variables: Standard_Deviation_hist.PET <dbl>,
      Skewness_hist.PET <dbl>, Kurtosis_hist.PET <dbl>, Energy_hist.PET <dbl>,
      Entropy_hist.PET <dbl>, AUC_hist.PET <dbl>, H_suv.PET <dbl>,
## #
      Volume.PET <dbl>, X3D_surface.PET <dbl>, ratio_3ds_vol.PET <dbl>,
## #
      ratio_3ds_vol_norm.PET <dbl>, irregularity.PET <dbl>,
## #
      tumor_length.PET <dbl>, Compactness_v1.PET <dbl>, Compactness_v2.PET <dbl>,
## #
      Spherical disproportion.PET <dbl>, Sphericity.PET <dbl>, ...
```

Check for null and missing values

[1] O

```
Using sum(is.n()).function, We can determine if any missing values in our data.

#The result shows either True or False. If True, omit the missing values using na.omit()

#[1] FALSE

#Thus, our data has no missing values.

sum(is.na(dt))
```

Split the data into training (80%) and testing (20%)

```
dt<-dt %>%
  mutate(Failure.binary=ifelse(Failure.binary== "No",0,1))
dt=dt[,-1]
set.seed(123) # for reproducibility
split = initial_split(dt,prop = 0.8 ,strata = "Failure.binary")
churn_train <- training(split)
churn_test <- testing(split)</pre>
```

```
X_train <- churn_train[,-c(1,2)]%>%as.matrix.data.frame()
X_test <- churn_test[,-c(1,2)]%>%as.matrix.data.frame()
y_train <- churn_train$Failure.binary
y_test <- churn_test$Failure.binary</pre>
```

Reshape the data set

```
X_train <- array_reshape(X_train, c(nrow(X_train), ncol(X_train)))
X_train <- X_train

X_test <- array_reshape(X_test, c(nrow(X_test), ncol(X_test)))
X_test <- X_test

y_train <- to_categorical(y_train, num_classes = 2)

## Loaded Tensorflow version 2.9.3

y_test <- to_categorical(y_test, num_classes = 2)</pre>
```

Run the model

with the R function **keras_mod_sequential()** of keras package, allows us to create our network with a layering approach. First, we initiated our sequential feedforward DNN architecture with *keras_model_sequential()* and then added some dense layers. Hence, we created five hidden layers with 256, 128, 128, 64 and 64 neurons, we added the *sigmoid* activation function. Followed by an output layer with 2 nodes and specified activation = *softmax*.

```
model <- keras model sequential() %>%
  layer_dense(units = 256, activation = "sigmoid", input_shape = c(ncol(X_train))) %>%
  layer_dropout(rate = 0.2) %>%
  layer_dense(units = 128, activation = "sigmoid") %>%
  layer_dropout(rate = 0.2) %>%
  layer_dense(units = 128, activation = "sigmoid") %>%
  layer_dropout(rate = 0.2) %>%
  layer_dense(units = 64, activation = "sigmoid") %>%
  layer_dropout(rate = 0.2) %>%
  layer_dense(units = 64, activation = "sigmoid") %>%
  layer_dropout(rate = 0.2) %>%
  layer_dense(units = 2, activation = "softmax")%>%
 compile(
   loss = "categorical_crossentropy",
   optimizer = optimizer_rmsprop(),
   metrics = c("accuracy")
```

Model compile approach

```
model %>% compile(
  loss = "categorical_crossentropy",
  optimizer = optimizer_adam(),
```

```
metrics = c("accuracy")
)
```

Training the model

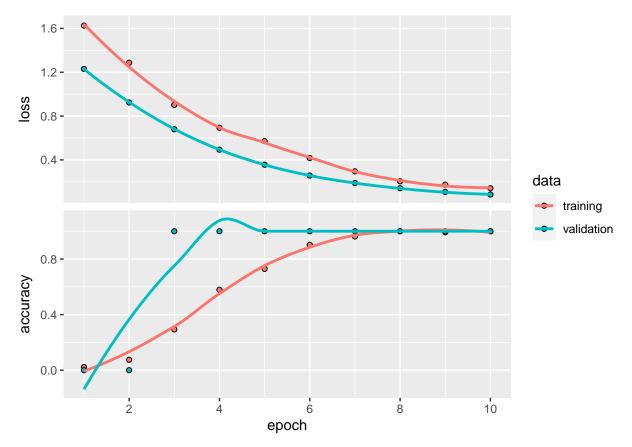
Already built a fundamental mod; all that remains is to feed it some data to train on. To achieve this, we input our training data and mod into a fit() function.

An epoch indicates how many times the algorithm views the entire dataset. Therefore, an epoch has ended whenever the algorithm has viewed all of the samples in the data set. Since a single epoch would be too large to transmit to the computer all at once, we divide it in several smaller batches.

```
trainm <- model %>%
  fit(X_train, y_train, epochs = 10, batch_size = 128, validation_split = 0.15)

trainm

##
## Final epoch (plot to see history):
## loss: 0.1416
## accuracy: 1
## val_loss: 0.08408
## val_accuracy: 1
plot(trainm)
```



Evaluate the trained model using testing dataset

```
model %>%
  evaluate(X_test, y_test)

## loss accuracy
## 0.08298509 1.00000000

dim(X_test)

## [1] 40 428

dim(y_test)

## [1] 40 2
```

Model prediction using testing dataset

```
%>% predict(X_test) %>% `>`(0.8) %>% k_cast("int32")
model
## tf.Tensor(
## [[0 1]
   [0 1]
##
##
   [0 1]
   [0 1]
##
##
   [0 1]
##
   [0 1]
##
   [0 1]
##
    [0 1]
##
   [0 1]
##
   [0 1]
##
   [0 1]
    [0 1]
##
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   [0 1]
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   [0 1]
    [0 1]
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   [0 1]
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   [0 1]
   [0 1]
##
   [0 1]
##
    [0 1]
##
##
   [0 1]
## [0 1]
## [0 1]
```

```
## [0 1]
## [0 1]
## [0 1]
## [0 1]
## [0 1]
## [0 1]
## [0 1]], shape=(40, 2), dtype=int32)
```