# Model 2: Neural Network Based Model

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### **Importing Packages**

```
library(dplyr)
                      # for data manipulation
## Warning: package 'dplyr' was built under R version 4.1.3
##
## 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(keras)
                     # for fitting DNNs
## Warning: package 'keras' was built under R version 4.1.3
library(tfruns)
                      # for additional grid search & model training functions
## Warning: package 'tfruns' was built under R version 4.1.3
library(tensorflow)
## Warning: package 'tensorflow' was built under R version 4.1.3
library(tfestimators) # provides grid search & model training interface
## Warning: package 'tfestimators' was built under R version 4.1.3
## tfestimators is not recomended for new code. It is only compatible with Tensorflow version 1, and is
library(rsample)
## Warning: package 'rsample' was built under R version 4.1.3
library(tidyverse)
## Warning: package 'tidyverse' was built under R version 4.1.3
## -- Attaching packages -----
                                             ----- tidyverse 1.3.2 --
## v ggplot2 3.3.6
                      v purrr
                               0.3.4
                    v stringr 1.4.1
## v tibble 3.1.8
## v tidyr 1.2.1
                     v forcats 0.5.2
## v readr 2.1.3
```

Importing the dataset

The dataset used in this model is imported from radiomics data. It has 197 observations and 431 variables.

```
datard <- read csv("radiomics completedata.csv")</pre>
```

```
## Rows: 197 Columns: 431
## -- Column specification ------
## Delimiter: ","
## chr (1): Institution
## 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.
dim(datard)
```

## ## [1] 197 431

### **Data Pre-Processing**

#### Preprocessing the data

```
\#\#\#\# Checking for null and missing values
```

```
is.na(datard)
colSums(is.na(datard))
anyNA(datard)
```

## ## [1] FALSE

Based on the results, there is no missing values.

```
####Checking for normality
```

```
dp1 = datard%>%select_if(is.numeric)
datadl1 = lapply(dp1[,-1], shapiro.test)
r = lapply(datadl1, function(x)x$p.value) #Extracting p-value only
s=unlist(r) #to convert a list to vector
sum(s[s>0.05])
```

```
## [1] 0.1350113
r$Entropy_cooc.W.ADC
```

```
## [1] 0.1350113
```

Based on the results, there is only one variable who is normally distributed (i.e. Entropy\_cooc.W.ADC). All the rest are not normally distributed. Hence, we will try to normalize the data using orderNorm() function.

 $\#\#\#\#Normalizing\ the\ data$ 

```
datard_norm = datard[,c(3,5:length(names(datard)))]
datard_norm = apply(datard_norm,2,orderNorm)
datard_norm = lapply(datard_norm, function(x) x$x.t) #to transformed original data
datard_norm = datard_norm%>%as.data.frame()
```

Test again using shapiro-wilk's test.

```
datad12 = lapply(datard_norm, shapiro.test)
r2 = lapply(datad12, function(x) x$p.value)
s2 = unlist(r2)
sum(s2>0.05)
```

```
## [1] 428
```

Based on the results, the rest of the variables is now normally distributed.

Substituing the normalized values into the original data, we have

```
r3 = select(datard, c("Failure.binary", "Entropy_cooc.W.ADC"))
datard_n = cbind(r3,datard_norm)
```

## **Splitting**

Split the data into training (80%) and testing (30%).

```
datard_n<-datard_n %>%
    mutate(Failure.binary=ifelse(Failure.binary== "No",0,1))

set.seed(123)
rdsplit = initial_split(datard_n, prop = 0.8, strata = "Failure.binary")
rdtrain <- training(rdsplit)
rdtest <- testing(rdsplit)

train1 <- rdtrain[,-c(1,2)]%>%as.matrix.data.frame()
train2 <- rdtrain$Failure.binary
test1 <- rdtest[,-c(1,2)]%>%as.matrix.data.frame()
test2 <- rdtest$Failure.binary</pre>
```

## Reshaping the dataset

```
train1 <- array_reshape(train1, c(nrow(train1), ncol(train1)))
train1 <- train1

test1 <- array_reshape(test1, c(nrow(test1), ncol(test1)))
test1 <- test1

train2 <- to_categorical(train2, num_classes = 2)</pre>
```

```
## Loaded Tensorflow version 2.9.3
test2 <- to_categorical(test2, num_classes = 2)</pre>
```

#### Run the model

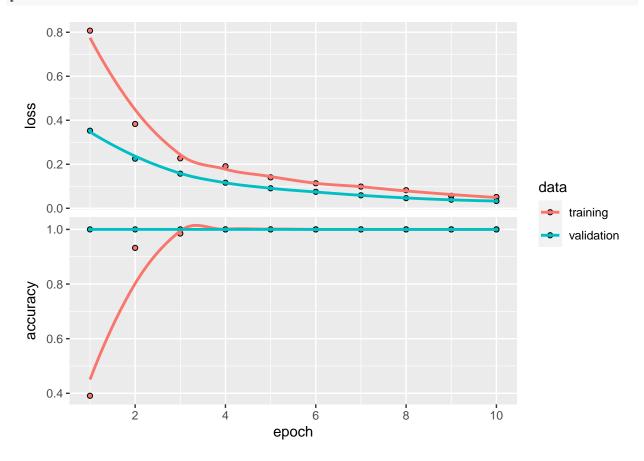
```
modeldl <- keras_model_sequential() %>%
   # Network architecture
  layer_dense(units = 256, activation = "sigmoid", input_shape = c(ncol(train1))) %>%
  layer_dropout(rate = 0.25) %>%
  layer_dense(units = 128, activation = "sigmoid") %>%
  layer dropout(rate = 0.25) %>%
  layer_dense(units = 128, activation = "sigmoid") %>%
  layer_dropout(rate = 0.25) %>%
  layer_dense(units = 64, activation = "sigmoid") %>%
  layer_dropout(rate = 0.25) %>%
  layer_dense(units = 64, activation = "sigmoid") %>%
  layer_dropout(rate = 0.25) %>%
  layer_dense(units = 2, activation = "softmax") %>%
# Backpropagation
 compile(
   loss = "categorical_crossentropy",
   optimizer = optimizer_rmsprop(),
   metrics = c("accuracy")
 )
modeldl
```

```
## Model: "sequential"
## Layer (type)
                              Output Shape
                                                      Param #
## dense_5 (Dense)
                              (None, 256)
                                                       109824
## dropout_4 (Dropout)
                              (None, 256)
                                                       0
## dense_4 (Dense)
                              (None, 128)
                                                       32896
## dropout_3 (Dropout)
                              (None, 128)
## dense_3 (Dense)
                              (None, 128)
                                                       16512
## dropout_2 (Dropout)
                              (None, 128)
## dense_2 (Dense)
                              (None, 64)
                                                       8256
## dropout_1 (Dropout)
                              (None, 64)
## dense_1 (Dense)
                              (None, 64)
                                                       4160
## dropout (Dropout)
                              (None, 64)
                                                       0
## dense (Dense)
                              (None, 2)
                                                       130
## -----
## Total params: 171,778
## Trainable params: 171,778
## Non-trainable params: 0
```

## Trained the model

```
#trained model history
fitdl <- modeldl %>%
```

```
fit(train1, train2,
      epochs = 10,
      batch_size = 128,
      validation_split = 0.15)
# Display output
fitdl
##
## Final epoch (plot to see history):
##
           loss: 0.05131
##
       accuracy: 1
       val_loss: 0.03279
##
## val_accuracy: 1
#plot the training and validation performance over 10 epochs
plot(fitdl)
```



# Evaluate the trained model using testing dataset

```
modeldl %>%
   evaluate(test1, test2)

## loss accuracy
## 0.03197459 1.00000000
```

```
dim(test1)
## [1] 40 428
dim(test2)
## [1] 40 2
Model prediction using testing dataset
modeldl %>%
 predict(test1) %>% `>`(0.5) %>% k_cast("int32")
## 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]
##
##
   [0 1]
   [0 1]
##
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   [0 1]
##
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##
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##
##
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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]], shape=(40, 2), dtype=int32)