# ANN(10,9,8)

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#### R Markdown

## 1st Qu.:5.125

1st Qu.:2.775

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

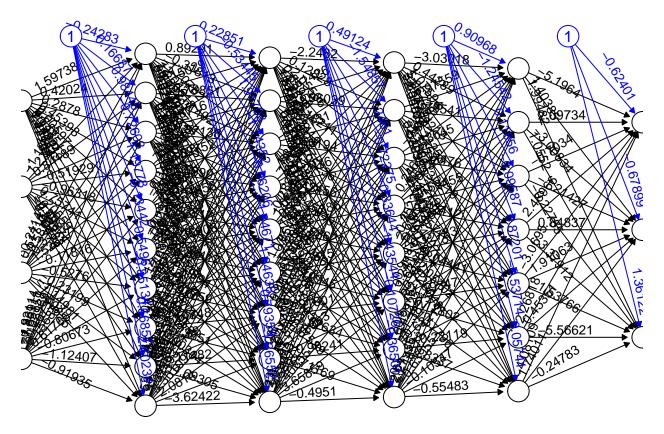
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
#load the necessary packages
install.packages(c("neuralnet","keras","tensorflow"), dependencies = T)
## Installing packages into '/cloud/lib/x86_64-pc-linux-gnu-library/4.4'
## (as 'lib' is unspecified)
library (neuralnet)
install.packages("tidyverse")
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.4'
## (as 'lib' is unspecified)
library(tidyverse)
## -- Attaching core tidyverse packages ------ tidyverse 2.0.0 --
## v dplyr
              1.1.4
                       v readr
                                    2.1.5
## v forcats 1.0.0
                        v stringr
                                    1.5.1
## v ggplot2 3.5.1
                                    3.2.1
                        v tibble
                        v tidyr
## v lubridate 1.9.3
                                    1.3.1
## v purrr
              1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::compute() masks neuralnet::compute()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                     masks stats::lag()
## i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become error
#data preparation
iris<-iris %>%mutate_if(is.character, as.factor)
#Sample of the dataset
set.seed(123)
iris_sample <- iris %>% sample_n(10)
summary(iris_sample)
                                                                       Species
    Sepal.Length
                    Sepal.Width
                                   Petal.Length Petal.Width
## Min. :4.300 Min. :2.500
                                   Min. :1.10
                                                 Min. :0.100
                                                                 setosa
```

1st Qu.:2.05 1st Qu.:0.450

versicolor:3

```
## Median: 5.650 Median: 3.000 Median: 4.50 Median: 1.350 virginica: 4
## Mean :5.670 Mean :3.010
                                   Mean :3.89 Mean :1.230
## 3rd Qu.:6.050 3rd Qu.:3.150
                                   3rd Qu.:5.10 3rd Qu.:1.875
## Max.
          :7.700 Max.
                          :3.800
                                   Max. :6.70 Max.
                                                        :2.200
# Train and test split
set.seed(254)
data_rows<-floor(0.80 * nrow(iris_sample))</pre>
data_rows
## [1] 8
train_indices<-sample(c(1:nrow(iris_sample)), data_rows)</pre>
train indices
## [1] 7 4 8 5 9 1 10 2
train_data<-iris_sample[train_indices, ]</pre>
train_data
      Sepal.Length Sepal.Width Petal.Length Petal.Width
                                                          Species
## 7
              5.5
                          2.5
                                       4.0
                                                  1.3 versicolor
              4.4
                          3.2
                                       1.3
## 4
                                                  0.2
                                                           setosa
## 8
              5.5
                          2.6
                                       4.4
                                                  1.2 versicolor
## 5
              5.9
                          3.0
                                       5.1
                                                  1.8 virginica
## 9
              5.8
                          2.7
                                       5.1
                                                  1.9 virginica
## 1
              4.3
                          3.0
                                       1.1
                                                  0.1
                                                           setosa
## 10
              6.1
                          3.0
                                       4.6
                                                  1.4 versicolor
## 2
              5.0
                          3.3
                                       1.4
                                                  0.2
                                                           setosa
test_data<-iris_sample[-train_indices,]</pre>
test_data
    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 3
             7.7
                         3.8
                                      6.7
                                                  2.2 virginica
## 6
             6.5
                         3.0
                                      5.2
                                                  2.0 virginica
#model training
model <-neuralnet (Species ~ Sepal.Length +Sepal.Width+Petal.Length +Petal.Width, data = train_data, hid
#plot the model
plot(model, rep = 'best')
```



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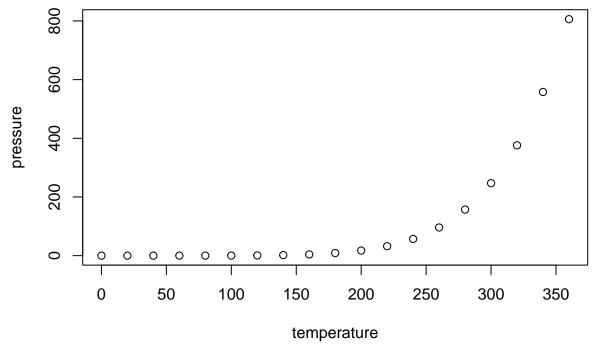
```
#predicting with the model
pred<-predict(model, test_data)</pre>
pred
##
            [,1]
                       [,2]
                                 [,3]
## 3 0.044703417 0.03193304 0.9721169
## 6 0.005014164 0.12700612 0.9698141
labels<-c("setosa", "versicolor", "virginca")</pre>
labels
## [1] "setosa"
                    "versicolor" "virginca"
#mapping prediction to labels
prediction_label<-data.frame(max.col(pred))%>%mutate(pred=labels[max.col.pred.])%>% select(2) %>%
unlist()
table(test_data$Species, prediction_label)
##
              prediction_label
##
               virginca
##
     setosa
##
     versicolor
                       0
     virginica
summary(test_data)
     Sepal.Length Sepal.Width Petal.Length
                                                 Petal.Width
##
                                                                     Species
         :6.5
                        :3.0 Min.
                                      :5.200
                                                Min. :2.00 setosa
   Min.
                 Min.
  1st Qu.:6.8 1st Qu.:3.2 1st Qu.:5.575
                                                1st Qu.:2.05 versicolor:0
```

```
Median:7.1
                  Median:3.4
                                 Median :5.950
                                                  Median :2.10
                                                                  virginica :2
##
##
    Mean
           :7.1
                  Mean
                          :3.4
                                 Mean
                                         :5.950
                                                  Mean
                                                          :2.10
                   3rd Qu.:3.6
                                 3rd Qu.:6.325
                                                  3rd Qu.:2.15
##
    3rd Qu.:7.4
   Max.
           :7.7
                          :3.8
                                 Max.
                                         :6.700
                                                  Max.
                                                          :2.20
##
                  Max.
#accuracy of the model
check= as.numeric(test_data$Species) == max.col(pred)
check
## [1] TRUE TRUE
accuracy<-(sum(check)/nrow(test_data))*100</pre>
print(accuracy)
```

## [1] 100

## **Including Plots**

You can also embed plots, for example:



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.