

# MATH 4322 Final Project Group 9

## Neural Network Model

```
library(readr)
library(NeuralNetTools)
```

Warning: package 'NeuralNetTools' was built under R version 4.3.3

```
library(nnet)
set.seed(35)

setwd("~/RStudio/Spring 2024/MATH 4322/Project/MATH4322")
cardio.data <- read_delim("cardio_train.csv", delim = ";",
                          escape_double = FALSE, trim_ws = TRUE)
```

Rows: 70000 Columns: 13

-- Column specification -----  
Delimiter: ";"

dbl (13): id, age, gender, height, weight, ap\_hi, ap\_lo, cholesterol, gluc, ...

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.

```
cardio.data$gender = as.factor(cardio.data$gender)
cardio.data$cholesterol = as.factor(cardio.data$cholesterol)
cardio.data$gluc = as.factor(cardio.data$gluc)
cardio.data$smoke = as.factor(cardio.data$smoke)
cardio.data$alco = as.factor(cardio.data$alco)
cardio.data$active = as.factor(cardio.data$active)
```

```

cardio.data$cardio = as.factor(cardio.data$cardio)

sample = sample(1 : nrow(cardio.data), floor(nrow(cardio.data) * 0.8))
cardio.train = cardio.data[sample, ]
cardio.test = cardio.data[-sample, ]

cardio.model = nnet(cardio ~ . - id - gender, data = cardio.train,
                    size = 6, rang = 0.5, decay = 5e-2, maxit = 5000)

```

```

# weights: 85
initial value 39022.927542
iter 10 value 38814.263045
iter 20 value 38643.556537
iter 30 value 38619.193201
iter 40 value 38599.346136
iter 50 value 36518.868686
iter 60 value 33905.075190
iter 70 value 33593.251770
iter 80 value 33294.114889
iter 90 value 32249.152366
iter 100 value 31962.110688
iter 110 value 31514.126189
iter 120 value 31401.592821
iter 130 value 30969.960281
iter 140 value 30942.104981
iter 150 value 30906.273917
iter 160 value 30885.923042
iter 170 value 30711.736212
iter 180 value 30656.327509
iter 190 value 30620.581492
iter 200 value 30577.575309
iter 210 value 30552.096076
iter 220 value 30538.342087
iter 230 value 30529.178590
iter 240 value 30526.349646
iter 250 value 30518.701286
iter 260 value 30510.719464
iter 270 value 30472.858266
iter 280 value 30454.156349
iter 290 value 30441.490266
iter 300 value 30427.124792
iter 310 value 30409.836919

```

```
iter 320 value 30377.488109
iter 330 value 30362.476826
iter 340 value 30343.864594
iter 350 value 30334.529335
iter 360 value 30329.206365
iter 370 value 30325.401306
iter 380 value 30315.604903
iter 390 value 30298.275813
iter 400 value 30279.330848
iter 410 value 30274.533158
iter 420 value 30273.247609
iter 430 value 30272.060312
iter 440 value 30271.366855
iter 450 value 30270.638513
iter 460 value 30270.316483
iter 470 value 30270.096038
iter 480 value 30269.520857
iter 490 value 30267.257482
iter 500 value 30266.472018
iter 510 value 30266.124146
iter 520 value 30265.729148
iter 530 value 30265.277089
iter 540 value 30265.184041
iter 540 value 30265.183814
iter 540 value 30265.183803
final value 30265.183803
converged
```

```
print(cardio.model)
```

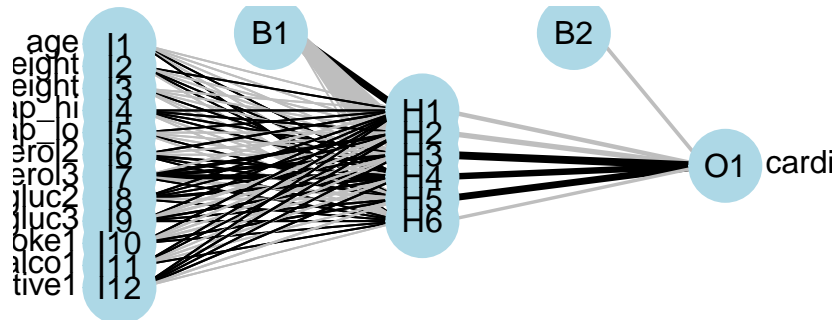
a 12-6-1 network with 85 weights

inputs: age height weight ap\_hi ap\_lo cholesterol2 cholesterol3 gluc2 gluc3 smoke1 alco1 act.

output(s): cardio

options were - entropy fitting decay=0.05

```
plotnet(cardio.model)
```



```
summary(cardio.model)
```

a 12-6-1 network with 85 weights

options were - entropy fitting decay=0.05

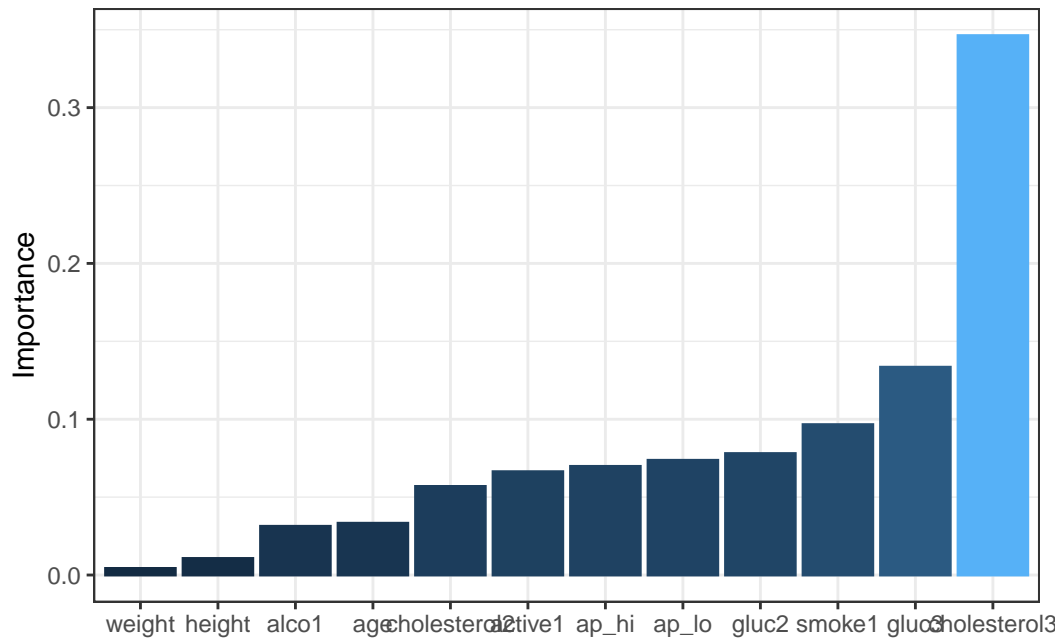
b->h1	i1->h1	i2->h1	i3->h1	i4->h1	i5->h1	i6->h1	i7->h1	i8->h1	i9->h1
6.54	0.00	0.01	-0.01	0.05	0.00	0.41	-0.35	0.31	0.26
i10->h1	i11->h1	i12->h1							
0.44	0.27	0.19							
b->h2	i1->h2	i2->h2	i3->h2	i4->h2	i5->h2	i6->h2	i7->h2	i8->h2	i9->h2
-14.86	0.00	-0.01	-0.01	0.18	0.00	-0.05	1.78	0.02	-1.21
i10->h2	i11->h2	i12->h2							
-0.33	0.07	0.47							
b->h3	i1->h3	i2->h3	i3->h3	i4->h3	i5->h3	i6->h3	i7->h3	i8->h3	i9->h3
-13.31	0.00	-0.01	0.00	0.14	0.00	-0.02	1.93	0.02	-1.05
i10->h3	i11->h3	i12->h3							
-0.36	-0.04	0.20							
b->h4	i1->h4	i2->h4	i3->h4	i4->h4	i5->h4	i6->h4	i7->h4	i8->h4	i9->h4
-8.07	0.00	0.00	0.02	0.04	-0.01	0.55	3.44	1.27	0.48
i10->h4	i11->h4	i12->h4							
-0.61	-0.24	0.27							
b->h5	i1->h5	i2->h5	i3->h5	i4->h5	i5->h5	i6->h5	i7->h5	i8->h5	i9->h5
-0.41	0.00	0.01	0.00	-0.02	0.03	0.25	-1.93	-0.54	0.19

```

i10->h5 i11->h5 i12->h5
  0.50   -0.03   -0.43
b->h6 i1->h6 i2->h6 i3->h6 i4->h6 i5->h6 i6->h6 i7->h6 i8->h6 i9->h6
  0.00   0.03  -0.01   0.00  -0.05  -0.07   0.00   0.00   0.00   0.00
i10->h6 i11->h6 i12->h6
  0.00   0.00   0.00
b->o h1->o h2->o h3->o h4->o h5->o h6->o
-2.20 -3.08 -4.15  7.27  5.53  6.03 -1.75

```

```
garson(cardio.model)
```



```

cardio.train.predict = predict(cardio.model, cardio.train, type = "class")
cardio.train.values = cardio.train$cardio
cardio.test.predict = predict(cardio.model, cardio.test, type = "class")
cardio.test.values = cardio.test$cardio

cardio.train.table = table(cardio.train.values, cardio.train.predict)
cardio.train.table

```

```

          cardio.train.predict
cardio.train.values    0     1

```

```
0 21537 6477
1 8356 19630
```

```
cardio.test.table = table(cardio.test.values, cardio.test.predict)
cardio.test.table
```

```
      cardio.test.predict
cardio.test.values  0    1
0 5386 1621
1 2073 4920
```