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# An Intelligent Prototype for the Characterization of Myocardial Infarction Blood and Analysis on the Efficacy of Streptokinase using Spectral Data

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**ABSTRACT**

Myocardial Infarction (MI) or Acute Myocardial Infarction (AMI), commonly known as a heart attack, is the interruption of blood supply to part of the heart, causing heart cells to die. This is most commonly due to occlusion (blockage) of a coronary artery following the rupture of a vulnerable atherosclerotic plaque, which is an unstable collection of lipids and white blood cells in the wall of an artery. The resulting ischemia and oxygen shortage if left untreated for a sufficient period of time can cause damage or death (infarction) of heart muscle tissue (myocardium). Streptokinase (SK), a protein secreted by several species of streptococci can bind and activate human plasminogen. SK is used as an effective and inexpensive clot-dissolving medication in some cases of MI (heart attack) and pulmonary embolism. Though investigations on characterisation of MI blood and analysis on the efficacy of the drug Streptokinase have been done by many, not much work is done on automation of this investigation. The goal of this study is to train the prototype (Neural Network [NN]) to identify whether the given blood sample is MI blood or not and also to examine prospectively the effect of Streptokinase in MI patients using the prototype which is already trained to identify the MI blood.

**Key words:** Myocardial Infarction, Blood, Streptokinase, Spectral data.

## INTRODUCTION

Myocardial Infarction (MI) or Acute Myocardial Infarction (AMI), commonly known as a heart attack, is the interruption of blood supply to part of the heart, causing heart cells to die. This is most commonly due to occlusion (blockage) of a coronary artery following the rupture of a vulnerable atherosclerotic plaque, which is an unstable collection of lipids and white blood cells in the wall of an artery. The resulting ischemia and oxygen shortage if left untreated for a sufficient period of time can cause damage or death (infarction) of heart muscle tissue (myocardium). Streptokinase (SK), a protein secreted by several species of streptococci can bind and activate human plasminogen. SK is used as an effective and inexpensive clot-dissolving medication in some cases of MI (heart attack) (Sikri and Bardia, 2007) and pulmonary embolism (Meneveau et al., 1997). Though investigation on characterisation of MI blood and analysis on the efficacy of the drug Streptokinase have been done by many, not much work is done on automation of this investigations.

The goal of this study is to train the prototype (Neural Network [NN]) to identify whether the given blood sample is MI blood or not, across the dose range on R1, R2, R3 and R4 where R1, R2, R3, R4 are Intensity Ratio Parameters. R1 is given by $A_{2960}/A_{2870}$ which is due to asymmetric and symmetric stretching vibrations of the methyl group of the lipids. R2 is given by $A_{1651}/A_{1546}$ which is due to the ratio of intensities of amide-I and amide-II bands of the amino acids and hence proteins. R3 is given by $A_{1402}/A_{1305}$ which is due to the ratio of the intensities of asymmetric and symmetric deformations of the methyl groups of proteins and lipids. R4 is given by $A_{1245}/A_{1170}$ which is due to P-O stretching of lipid phosphate and C-O stretching of glucose (Sailatha, 2007) and also to examine prospectively the effect of Streptokinase in MI patients using the prototype which is already trained to identify the MI blood (Djodilatchoumy et al., 2008).

## EXPERIMENTAL

For characterization of MI blood, three-layered feed forward back propagation network is used. The prototype consists of 3 layers namely (i) input layer, (ii) hidden layer (iii) output layer with 1 neuron. The value of the output neuron varies from 0 to 1(value 0 indicates the most healthy blood and value 1 indicates the most diseased blood). Two ml of blood samples were collected from 14 healthy subjects and 14 MI patients from Railway Hospital, Perambur, Chennai, India. Then, FTIR spectra of blood sera of the collected 28 samples were recorded and fed as input to train the prototype (Ronald et al., 2000). The training sample numbers 1-7 and 15-21 represent the healthy group and training sample numbers 8-14 and 22-28 belong to the diseased group (Table 3).

The prototype has 4 neurons in the input layer each corresponding to R1, R2, R3 and R4. Then it is trained by varying the number of neurons in the hidden layer. The $Weight_{IH}$ x – y which is the strength/weight of the connection between unit x in the input layer and unit y in the hidden layer and $Weight_{HO}$ x – y which is the weight of the connection between unit x in the hidden layer and unit y in the output layer are calculated and are given in Table 1.

The efficacy of the drug Streptokinase in myocardial infarction patients is calculated using the prototype that is already trained to characterize the MI blood across the dose range on R1, R2, R3 and R4 where R1, R2, R3, R4 are Intensity Ratio Parameters.

**Table 1**

| Weight | Value |
|---|---|
| $Weight_{IH}$ 1 – 1 | -1.928881 |
| $Weight_{IH}$ 1 – 2 | -2.027387 |
| $Weight_{IH}$ 1 – 3 | -2.242503 |
| $Weight_{IH}$ 1 – 4 | 2.128931 |
| $Weight_{IH}$ 2– 1 | -0.794969 |
| $Weight_{IH}$ 2 – 2 | -1.434592 |
| $Weight_{IH}$ 2 – 3 | -1.553051 |
| $Weight_{IH}$ 2 – 4 | 1.719043 |
| $Weight_{IH}$ 3 – 1 | -1.316888 |
| $Weight_{IH}$ 3 - 2 | -1.041491 |
| $Weight_{IH}$ 3 – 3 | -1.137544 |
| $Weight_{IH}$ 3 – 4 | 1.843226 |
| $Weight_{IH}$ 4 – 1 | -1.188237 |
| $Weight_{IH}$ 4 – 2 | -1.195751 |
| $Weight_{IH}$ 4 – 3 | -1.643424 |
| $Weight_{IH}$ 4 – 4 | 2.308789 |
| $Weight_{OH}$ 1 – 1 | -4.063186 |
| $Weight_{OH}$ 2– 1 | -4.417873 |
| $Weight_{OH}$ 3 – 1 | -5.280274 |
| $Weight_{OH}$ 4 – 1 | 6.734867 |

To study the efficacy of the drug Streptokinase, 14 patients from Railways Headquarters Hospital, Perambur, Chennai, India who were suffering from myocardial infarction were chosen. Before the drug therapy, their blood

**Table 2**

| No. of neurons in hidden layer | No. of iterations |
|---|---|
| 1 | 1,37,687 |
| 2 | 90,094 |
| 3 | 48,562 |
| 4 | 36,820 |
| 5 | 69,664 |

**Table 3: Testing - Training Samples**

| Sample No. | R1 | R2 | R3 | R4 | Output |
|---|---|---|---|---|---|
| 1 | 1.105600 | 1.298800 | 1.213500 | 1.122800 | 0.215999 |
| 2 | 1.089600 | 1.208000 | 1.177400 | 1.145800 | 0.104777 |
| 3 | 1.085300 | 1.208800 | 1.161100 | 1.129000 | 0.028938 |
| 4 | 1.088200 | 1.215400 | 1.131900 | 1.081800 | 0.028938 |
| 5 | 1.102500 | 1.252400 | 1.164100 | 1.157900 | 0.276985 |
| 6 | 1.097500 | 1.292400 | 1.206000 | 1.156400 | 0.273763 |
| 7 | 1.095500 | 1.294200 | 1.120000 | 1.101200 | 0.202628 |
| 8 | 1.307000 | 1.410200 | 1.297000 | 1.306400 | 0.998714 |
| 9 | 1.288000 | 1.385700 | 1.309200 | 1.281900 | 0.999667 |
| 10 | 1.283300 | 1.516000 | 1.272100 | 1.275800 | 0.998677 |
| 11 | 1.294100 | 1.410900 | 1.418700 | 1.308600 | 0.998738 |
| 12 | 1.297600 | 1.353800 | 1.312800 | 1.280400 | 0.998655 |
| 13 | 1.301200 | 1.402500 | 1.284000 | 1.289800 | 0.998684 |
| 14 | 1.285800 | 1.386500 | 1.293700 | 1.294200 | 0.998663 |
| 15 | 1.106800 | 1.227800 | 1.186000 | 1.149800 | 0.252727 |
| 16 | 1.106000 | 1.274800 | 1.187700 | 1.168000 | 0.236171 |
| 17 | 1.095800 | 1.255900 | 1.155600 | 1.170200 | 0.333663 |
| 18 | 1.102200 | 1.233400 | 1.140200 | 1.114600 | 0.046600 |
| 19 | 1.100800 | 1.212200 | 1.201000 | 1.140200 | 0.215674 |
| 20 | 1.087200 | 1.225100 | 1.172800 | 1.111300 | 0.042576 |
| 21 | 1.101400 | 1.201200 | 1.192400 | 1.124000 | 0.110757 |
| 22 | 1.289600 | 1.374500 | 1.413400 | 1.277900 | 0.998694 |
| 23 | 1.283300 | 1.516000 | 1.302300 | 1.281800 | 0.998700 |
| 24 | 1.295300 | 1.410900 | 1.344400 | 1.343000 | 0.998736 |
| 25 | 1.395300 | 1.416100 | 1.321800 | 1.281200 | 0.998715 |
| 26 | 1.289000 | 1.604700 | 1.388800 | 1.320000 | 0.998749 |
| 27 | 1.304500 | 1.488400 | 1.403400 | 1.367400 | 0.998757 |
| 28 | 1.291200 | 1.407800 | 1.421400 | 1.312000 | 0.998736 |

**Table 4: Testing – Random Samples**

```
Random Sample  : 1
Give the input(R1)        -  1.0051
Give the input(R2)        -  10981
Give the input(R3)        -  1.0131
Give the input(R4)        -  1.0221
      Result  :  .028938
Random Sample  : 2
Give the input(R1)        -  1.3171
Give the input(R2)        -  1.4101
Give the input(R3)        -  1.2171
Give the input(R4)        -  1.3171
        Result :  .998641
```

**Table 5**

| Sample No. | R1 | R2 | R3 | R4 | Output |
|---|---|---|---|---|---|
| | | | **Pre** | | |
| 1 | 1.307000 | 1.410200 | 1.297000 | 1.306400 | 0.998714 |
| 2 | 1.288000 | 1.385700 | 1.309200 | 1.281900 | 0.998667 |
| 3 | 1.283300 | 1.516000 | 1.272100 | 1.275800 | 0.998667 |
| 4 | 1.294100 | 1.410900 | 1.418700 | 1.308600 | 0.998738 |
| 5 | 1.297600 | 1.353800 | 1.312800 | 1.280400 | 0.998655 |
| 6 | 1.301200 | 1.402500 | 1.284000 | 1.289800 | 0.998684 |
| 7 | 1.285800 | 1.386500 | 1.293700 | 1.294200 | 0.998663 |
| 8 | 1.289600 | 1.374500 | 1.413400 | 1.277900 | 0.998694 |
| 9 | 1.283300 | 1.516000 | 1.302300 | 1.281800 | 0.998700 |
| 10 | 1.295300 | 1.410900 | 1.344400 | 1.343000 | 0.998736 |
| 11 | 1.395300 | 1.416100 | 1.321800 | 1.281200 | 0.998715 |
| 12 | 1.289000 | 1.604700 | 1.388800 | 1.320000 | 0.998749 |
| 13 | 1.304500 | 1.488400 | 1.403400 | 1.367400 | 0.998757 |
| 14 | 1.291200 | 1.407800 | 1.421400 | 1.312000 | 0.998735 |
| | | | **Post** | | |
| 1 | 1.153300 | 1.110400 | 1.105900 | 1.187600 | 0.851018 |
| 2 | 1.157300 | 1.157400 | 1.111600 | 1.120900 | 0.400218 |
| 3 | 1.131200 | 1.126500 | 1.207900 | 1.121400 | 0.478169 |
| 4 | 1.161100 | 1.108700 | 1.169400 | 1.155000 | 0.743316 |
| 5 | 1.150100 | 1.110400 | 1.151500 | 1.117800 | 0.321348 |
| 6 | 1.028000 | 1.197500 | 1.150200 | 1.087600 | 0.028938 |
| 7 | 1.153300 | 1.127700 | 1.174400 | 1.174800 | 0.835720 |
| 8 | 1.164300 | 1.128400 | 1.160400 | 1.115700 | 0.480435 |
| 9 | 1.118500 | 1.076500 | 1.040900 | 1.182300 | 0.521794 |
| 10 | 1.130100 | 1.130700 | 1.110800 | 1.172200 | 0.546842 |
| 11 | 1.164200 | 1.138200 | 1.122200 | 1.095000 | 0.479285 |
| 12 | 1.085300 | 1.126400 | 1.187200 | 1.158100 | 0.228588 |
| 13 | 1.084400 | 1.107800 | 1.167200 | 1.222200 | 0.698815 |
| 14 | 1.020000 | 1.093200 | 1.186000 | 1.104200 | 0.067779 |

samples were collected and FTIR spectra of blood sera of the collected samples were recorded. Then the recorded spectral data were fed as input to the prototype and the output were noted down. (pre-treatment).

The selected 14 patients were prescribed with Streptokinase for a period of three months. A final check up was performed over a period of 3 months, after the treatment was initiated. To find the efficacy of the above said drug, the FTIR spectra were recorded after 3 months and the spectral data were fed as input to the prototype and the output were noted down. (post-treatment) (Sailatha, 2007).

## RESULTS AND DISCUSSION

Fixing the value of the learning parameters to 0.9, the network is trained by varying the number of neurons in the hidden layer. It is found that the prototype is trained effectively with 4 neurons in the hidden layer (36,820 iterations) which is shown in Table 2. The results secured by using this prototype confirmed beyond the doubt

that the training samples and random samples are correctly identified which is shown in Table 3 and Table 4 respectively.

The output of pre-treatment (Pre) and post-treatment (Post) are given in Table 5. The percentage of efficacy of the drug is calculated using the formula (Pre-Post) / Pre * 100 and the results are given in 6. It is concluded from the result that streptokinase therapy reduces the disease by 52.21%. The value of mean and standard deviation (SD) of the normal, pre-treatment and post-treatment states are summarized in Table 7. The significance of the results is also verified statistically using t-test which is shown in Table 8.

**Table 6**

| Sample No. | Efficacy – Streptokinase |
|---|---|
| 1 | 14.788551 |
| 2 | 59.924732 |
| 3 | 52.119339 |
| 4 | 25.574493 |
| 5 | 67.821918 |
| 6 | 97.102381 |
| 7 | 16.316121 |
| 8 | 51.893676 |
| 9 | 47.752690 |
| 10 | 45.246529 |
| 11 | 52.009833 |
| 12 | 77.112577 |
| 13 | 30.031496 |
| 14 | 93.213491 |

**Table 7**

| | Healthy Subjects | Pre Treatment | Post Treatment |
|---|---|---|---|
| Mean | .276443 | .998705 | .495908 |
| SD | .260744 | .000033 | .221212 |

**Table 8**

$H_0$ : There is no change due to treatment using Streptokinase
$H_1$ : There is a change due to treatment using Streptokinase

| Sample No. (n) | Output before Treatment (x) | Output after Treatment (y) | d = y-x | $d^2$ |
|---|---|---|---|---|
| 1 | 0.998714 | 0.851018 | -0.147696 | 0.021814 |
| 2 | 0.998667 | 0.400218 | -0.598449 | 0.358141 |
| 3 | 0.998667 | 0.478169 | -0.520498 | 0.270918 |
| 4 | 0.998738 | 0.743316 | -0.255422 | 0.065240 |
| 5 | 0.998655 | 0.321348 | -0.677307 | 0.458745 |
| 6 | 0.998684 | 0.028938 | -0.969746 | 0.940407 |
| 7 | 0.998663 | 0.835720 | -0.162943 | 0.026550 |
| 8 | 0.998694 | 0.480435 | -0.518259 | 0.268592 |
| 9 | 0.998700 | 0.521794 | -0.476906 | 0.227439 |
| 10 | 0.998736 | 0.546842 | -0.451894 | 0.204208 |
| 11 | 0.998715 | 0.479285 | -0.519430 | 0.269807 |
| 12 | 0.998749 | 0.228588 | -0.770161 | 0.593148 |
| 13 | 0.998757 | 0.698815 | -0.299942 | 0.089965 |
| 14 | 0.998735 | 0.067779 | -0.930956 | 0.866679 |

mean of d = -0.0.521401
standard deviation = 0.247218
The test statistics, t = 7.604374
No. of degrees of freedom $nd_f$ = 14-1 =13$d_f$
Table value of t for 13$d_f$ at 5% level of significance = 2.160
Conclusion : Since the table value is less than the calculated value, $H_0$ is rejected. Hence there is a change due to treatment.

## CONCLUSION

NNs are being used in the detection of various diseases such as hyperlipidemia, chronic renal failure, head and neck squamous cell carcinoma and a variety of health-related indices can also be monitored. (Ronald et al., 2000, Djodilatchoumy et al., 2008) The onset of a particular medical condition could be associated with a very complex combination of changes on a subset of the variables being monitored in medicines. NNs have been used to recognize this predictive pattern, so that the appropriate treatment can be prescribed. FTIR spectroscopy allows accurate lipids concentration determination. Since our NN is trained to distinguish the MI blood with the fine details of FTIR spectra, it can improve the diagnostic accuracy and rate of MI treatment at a faster rate with more accuracy. It can also be used to analyze the efficacy of the drug Streptokinase.

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