



Redes Neuronais Artificiais em Exames Clínicos

Computação Natural

CONTEÚDOS

- Análise e Preparação do Dataset
- Treino e Validação de Modelos de Aprendizagem
- Otimização de Parâmetros do Modelo
- Conclusão

ANÁLISE E PREPARAÇÃO DO DATASET

Atributo	Número de NaN
Age	5
Shape	31
Margin	48
Density	76
Severity	0

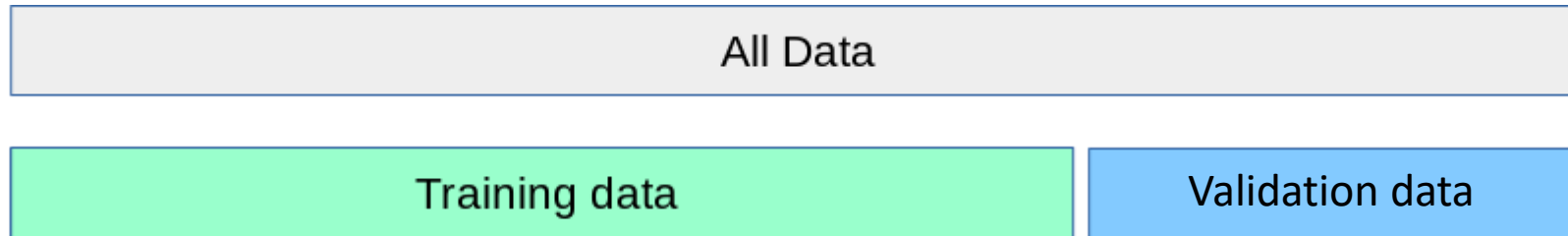
```
      age  shape  margin  density
0    67.0    3.0    5.0     3.0
2    58.0    4.0    5.0     3.0
3    28.0    1.0    1.0     3.0
8    57.0    1.0    5.0     3.0
10   76.0    1.0    4.0     3.0
```



Padronização

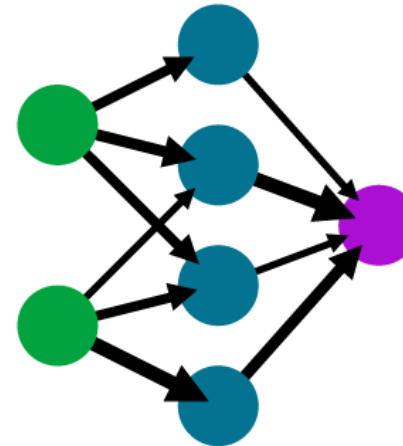
```
      age    shape    margin    density
0  0.765804  0.174460  1.395631  0.240313
2  0.151666  0.979883  1.395631  0.240313
3 -1.895458 -1.436386 -1.158927  0.240313
8  0.083429 -1.436386  1.395631  0.240313
10 1.379941 -1.436386  0.756992  0.240313
```

TREINO E VALIDAÇÃO DE MODELOS DE APRENDIZAGEM



TREINO E VALIDAÇÃO DE MODELOS DE APRENDIZAGEM

Split 1	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 2	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 3	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 4	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 5	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5



Score 1

Score 2

Score 3

Score 4

Score 5

Mean Score

Scores: $(\text{Accuracy} * 0.8) + (\text{Recall} * 0.2)$

OTIMIZAÇÃO DE PARÂMETROS DO MODELO



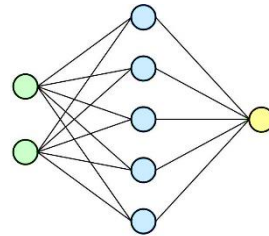
Algoritmos Genéticos

Representação do Problema:

- Número de camadas: 1 a 10 [1,2,...,10]
- Número de nodos: 2 a 128 [1,2,...,7]
- Learn Rate: 10^{-8} a 10^{-2} [2,3,...,8]
- Função de ativação: Relu ou Sigmoid [0,1]

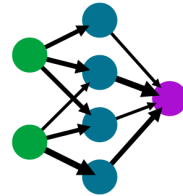
ITERAÇÃO DO ALGORITMO GENÉTICO

Split 1	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 2	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 3	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 4	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 5	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5



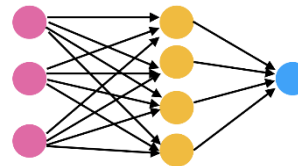
Mean Score 1

Split 1	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 2	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 3	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 4	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 5	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5



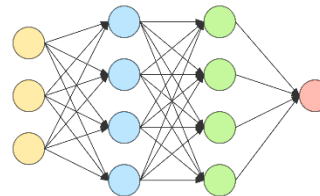
Mean Score 2

Split 1	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 2	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 3	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 4	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 5	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5



Mean Score 3

Split 1	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 2	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 3	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 4	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5
Split 5	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5



Mean Score 4

SELEÇÃO

(0.45) (0.37) (0.83) (0.42)
[Mean Score 1, Mean Score 2, Mean Score 3, Mean Score 4]

CRUZAMENTO

[[2, 4, 0.00000001, Relu], [4, 16, 0.001, Relu], [2, 4, 0.001, Relu], [4, 16, 0.00000001, Relu]]

MUTAÇÃO

[[2, 4, 0.00000001, Relu], [4, 16, 0.001, Relu], [2, 4, 0.001, **Relu**], [4, 16, 0.00000001, Relu]]

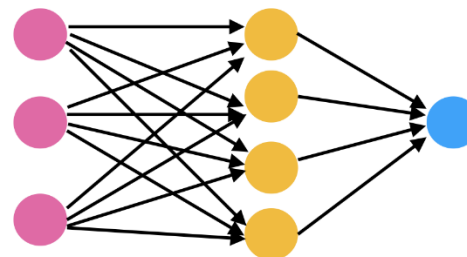


[[2, 4, 0.00000001, Relu], [4, 16, 0.001, Relu], [2, 4, 0.001, **Sigmoid**], [4, 16, 0.00000001, Relu]]

MELHOR ARQUITETURA

Training data

Test data



Final Score

The background features a large, light blue DNA double helix that curves across the frame. Overlaid on this are several smaller, darker blue molecular structures, including a detailed DNA segment in the upper left and various clusters of nodes connected by lines, resembling a network or chemical structure. The overall aesthetic is clean and scientific.

CONCLUSÃO



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