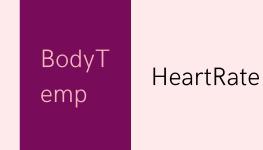


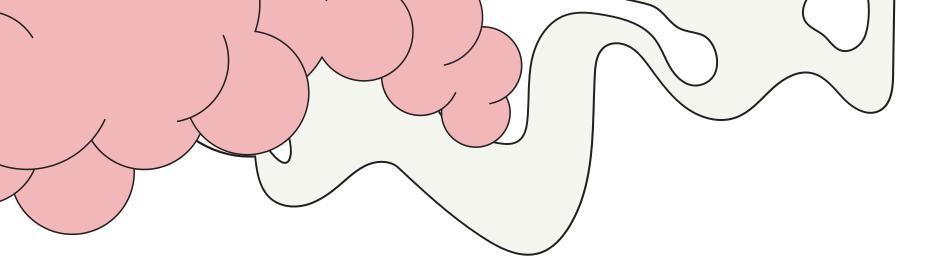
### Conheça a Base

- Simples
- Possui 1014 instâncias e 7 Features
- <u>Link</u>









## Pré-Processamento

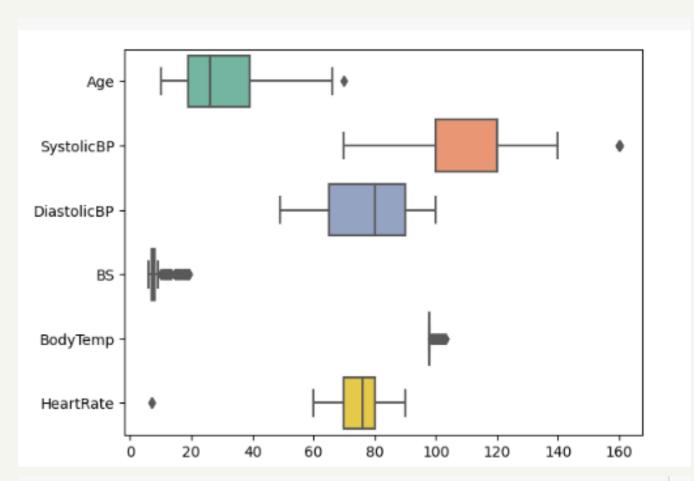
**Dados Faltantes** 

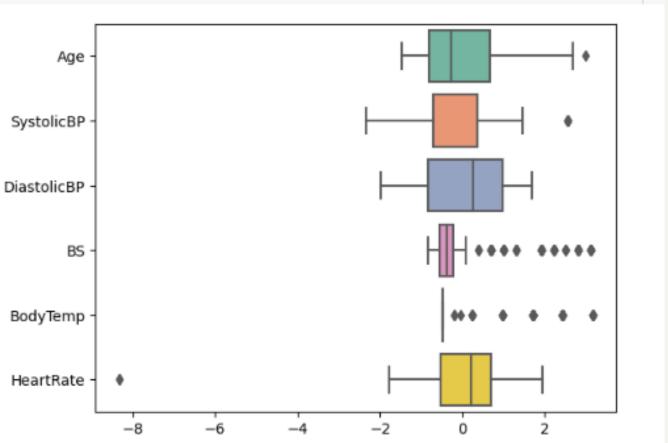
```
[ ] print(data.isnull().sum())
```

```
Age 0
SystolicBP 0
DiastolicBP 0
BS 0
BodyTemp 0
HeartRate 0
RiskLevel 0
dtype: int64
```

# Normalização

Dados com escalas diferentes interferiram nos resultados dos algoritmos.







#### Outliers

O z-score nos dá uma ideia do quanto um determinado ponto está afastado da média dos dados. Mede quantos desvios padrão abaixo ou acima da média populacional os dados estão

x: observação

 $\mu$ : média

 $\sigma$ : desvio padrão

```
outliers=[]
def find_outliers(data_set):
    corte_dp =3
    media = np.mean(data_set)
    dp =np.std(data_set)
    for dado in data_set:
        z_score = (dado - media)/dp
        if np.abs(z_score) > corte_dp:
            outliers.append(dado)
    #print('Os outliers são: ', outliers)
    return outliers
outliersBodyTemp = find_outliers(data['BodyTemp'])
outliersHearthRate = find_outliers(data['HeartRate'
outliersBodyTemp
outliersHearthRate
```



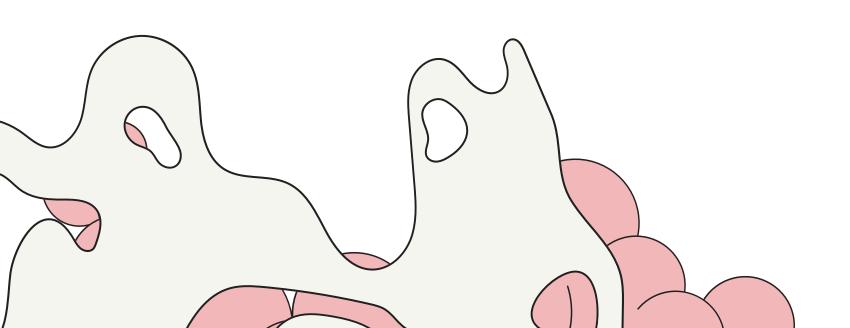
# Report

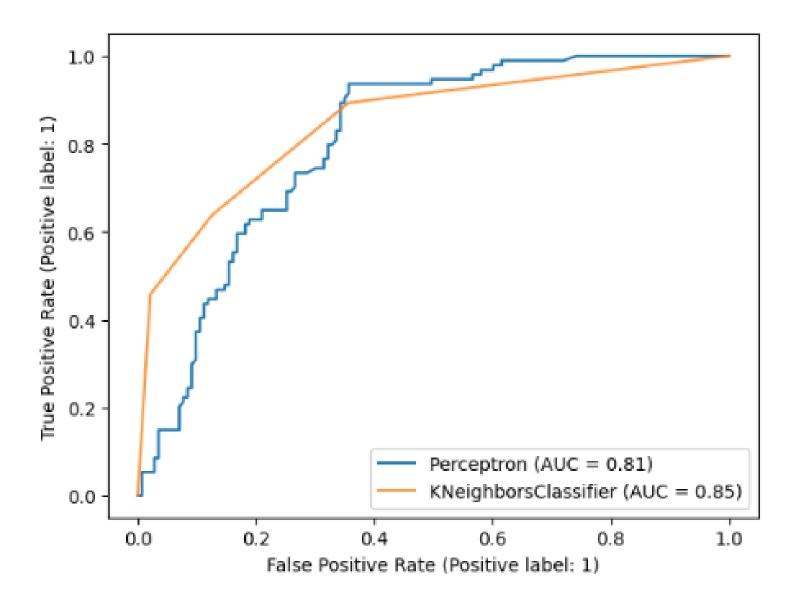
	precision	espec	recall	f1	acuraccy
k=3	0 - 0.79 1- 0.77	0.87	0 - 0.87 1 - 0.64	0 - 0.83 1 - 0.70	0.78
k=5	0 - 0.81 1 - 0.74	0.84	0 - 0.84 1 - 0.70	0 - 0.82 1- 0.72	0.78
k=7	0 - 0.81 1 - 0.68	0.78	0 - 0.78 1 - 0.72	0 - 0.79 1 - 0.70	0.75

# Report

	precision	espec	recall	f1	acuraccy
eta=0.4 max_iter=25 random_state=23	0 - 0.94 1- 0.62	0.63	0 - 0.63 1 - 0.94	0 - 0.75 1 - 0.75	0.75
eta = 0.5 max_iter=25 random_state=33	0 - 0.74 1 - 0.68	0.82	0 - 0.83 1 - 0.55	0 - 0.78 1- 0.61	0.72
eta = 0.6 max_iter=25 random_state=27	0 - 0.74 1 - 0.62	0.82	0 - 0.76 1 - 0.59	0 - 0.75 1 - 0.60	0.69

#### Curva ROC











RNA score 0.6440677966101696

KNN score 0.768361581920904



RNA score 0.673788832284487

KNN score 0.7570472480271702



RNA score 0.689215291750503

KNN score 0.7810261569416499