Métricas para os Modelos

Avaliando a qualidade da modelagem

Métricas

Regressão

- Mean Absolute Error (MAE)
- Mean Squared Error (MSE)
- Root Mean Squared Error (RMSE)
- R^2 (R-Squared)

Clusterização

- Rand index
- Mutual Information based scores
- Homogeneity, completeness and V-measure
- Fowlkes-Mallows scores
- Silhouette Coefficient
- Calinski-Harabasz Index
- Contingency Matrix
- Pair Confusion Matrix

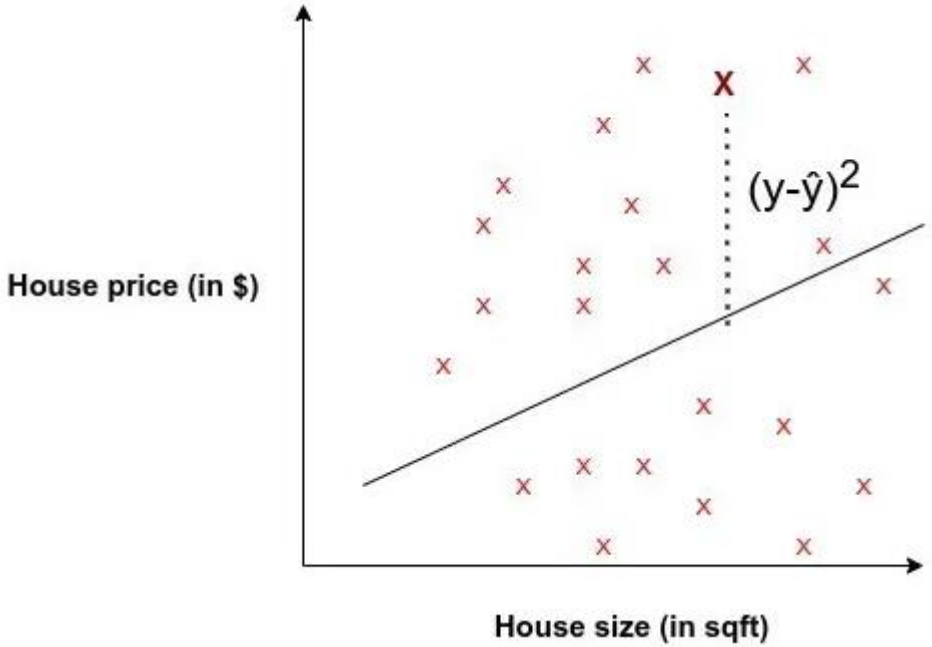
Classificação

- Accuracy
- Confusion Matrix (not a metric but fundamental to others)
- Precision and Recall
- F1-score
- AU-ROC

Fonte: https://neptune.ai/blog/performance-metrics-in-machine-learning-complete-guide
https://scikit-learn.org/stable/modules/clustering.html#clustering-performance-evaluation

Mean Squared Error

$$MSE = \frac{1}{N}\sum_{j=1}^{N}(y_j - \check{y}_j)^2$$



Fonte: https://neptune.ai/blog/performance-metrics-in-machine-learning-complete-guide

Índice de exatidão (acurácia)

A porcentagem do quanto o método acertou dentro do conjunto total de amostras na base de dados

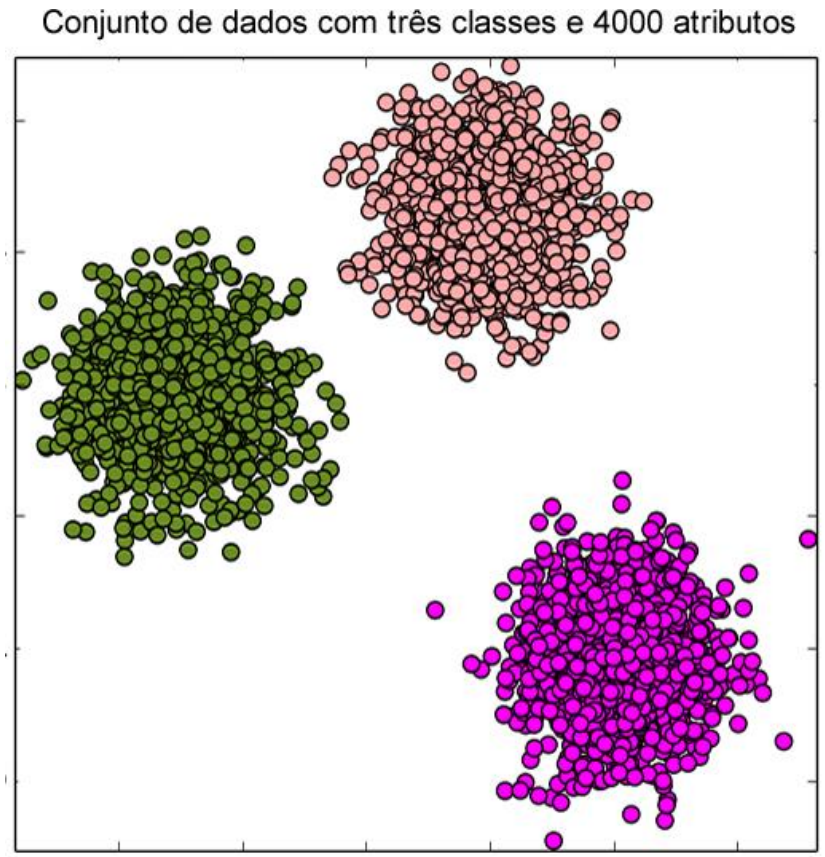
$$Exatidão = \frac{\sum_{i=1}^{m} A_{nn}}{\sum_{i=1}^{m} \sum_{j=1}^{m} A_{ij}}$$

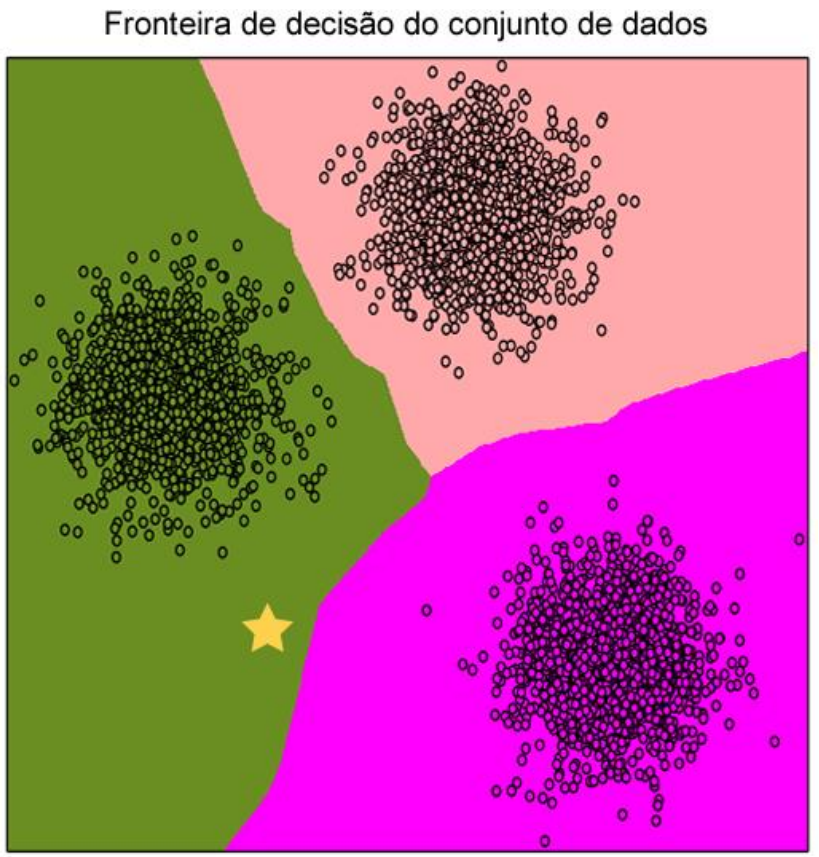
Matriz de Confusão

Classes	1	2	3	4	Amostras incluídas (comissionadas)	Total de amostras na linha	Erro de comissão (%)
1	33	4	2	1	7	40	17,5
2	2	35	3	0	5	40	12,5
3	0	3	34	3	6	40	15
4	0	1	2	37	3	40	7,5

Amostras omitidas	2	8	7	4
Total de amostras na coluna	35	43	41	41
Erro de omissão (%)	5,7	19	17	10

Fronteiras de decisão





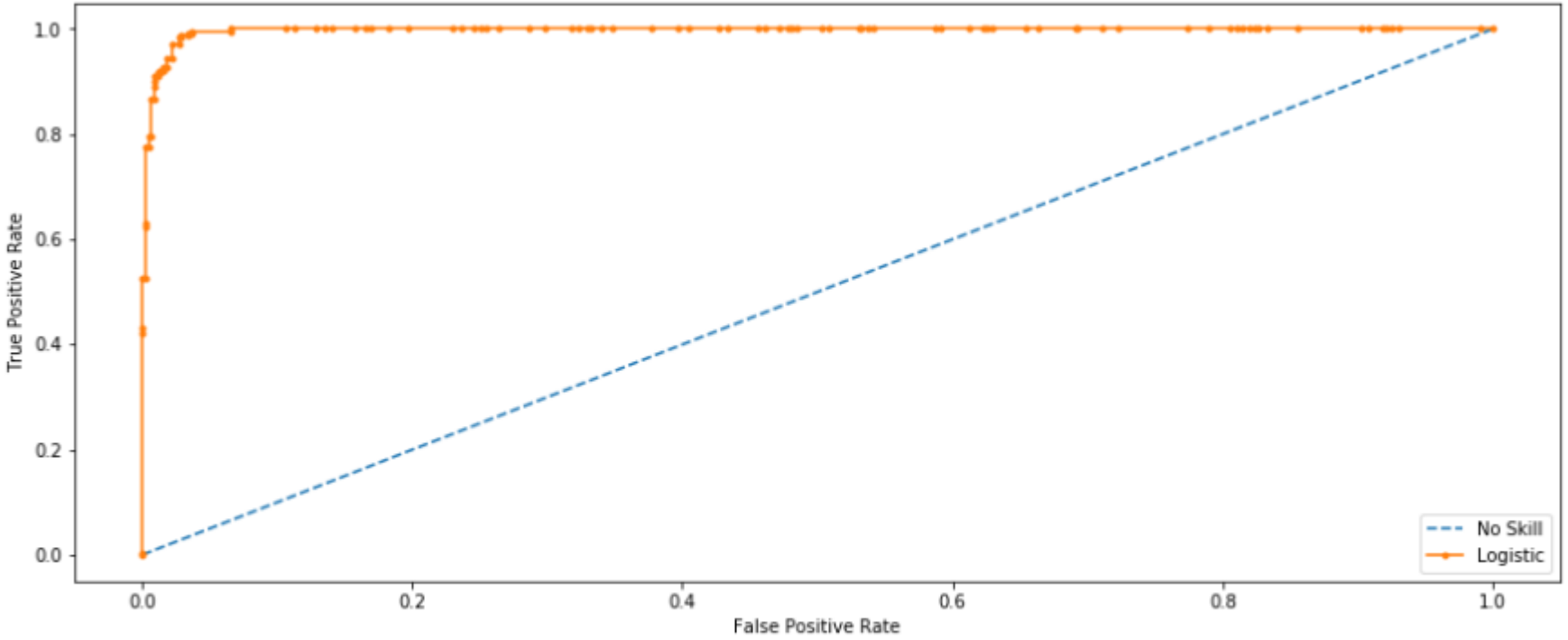
F1-score

$$F_1 = \frac{2}{\frac{1}{precision} + \frac{1}{recall}}$$

$$R = \frac{TP}{TP+FN} = \frac{\text{Cancer patients correctly identified}}{\text{Cancer patients correctly identified+incorrectly labelled non-cancer patients as cancerous}}$$

$$P = \frac{TP}{TP+FP} = \frac{\text{Cancer patients correctly identified}}{\text{Cancer patients correctly identified+incorrectly labelled cancer patients as non-cancerous}}$$

AU-ROC



No Skill: ROC AUC=0.500

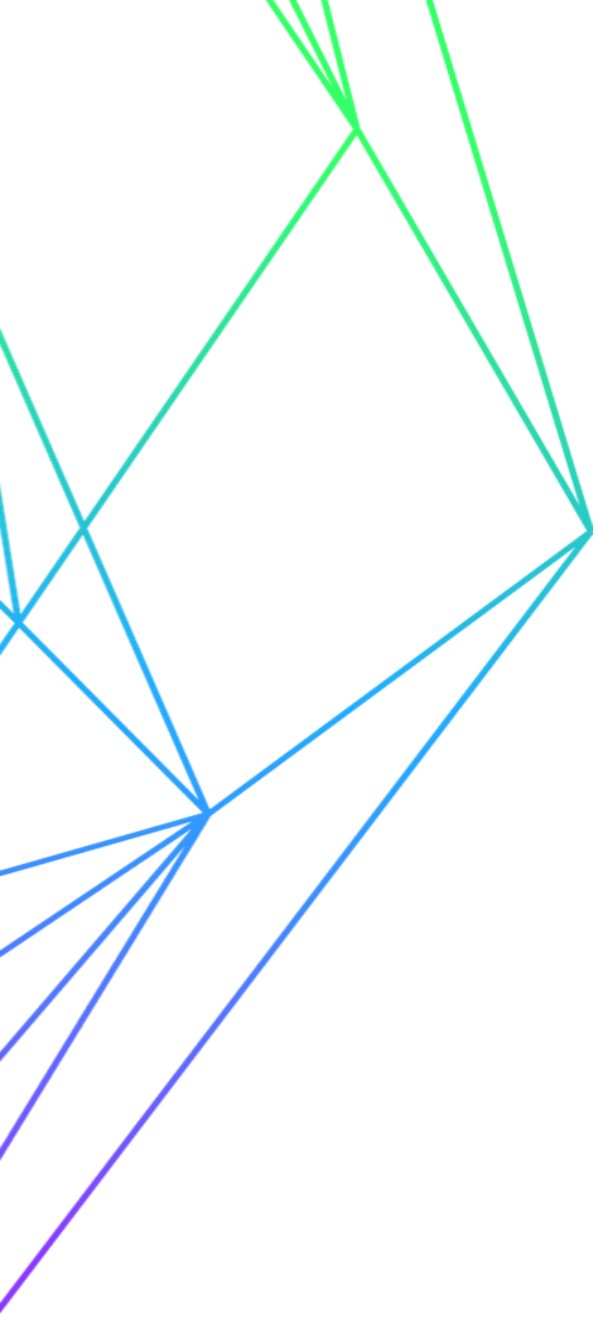
Logistic: ROC AUC=0.996

$$TPR = \frac{TP}{TP+FN} \qquad FPR = \frac{FP}{FP+TN}$$

Índice Rand Corrigido

Um mais usados para validação externa de agrupamentos e determina a similaridade de partições.

varia no intervalo [-1,1], onde quanto mais próximo de 1 mais similares são as partições comparadas



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