**AI Exam Process Steps with Functions:**

A close up of a device

Description automatically generated

1. **Initial steps**
   1. **Load your dataset**
   2. **Examine it and get rid of anything that doesn’t apply**
      1. *examine\_df(df)*
      2. *distribution\_plot(df,column\_name)*
      3. *joint\_plot(df,x,y)*
      4. *pair\_plot(df)*
   3. **Split the dataset into the input and output variables**
      1. *separate\_components(df, column\_of\_y)*
2. **Pre-processing**

Can be either done using first fit() then transform() function or fit\_transform()

* 1. **Rescale data(Normalization)**

Important for optimization algorithms that use gradient descent and regressions that weigh inputs(regression/neural networks or with clustering – k-means)

* + 1. *rescale (X)*
  1. **Standardize data (1 to 0)**

Assumes Gaussian distribution but different means and standard deviation. 0 means mean and 1 means standard distribution. Most relevant for linear, log regreassion and LDA(linear discriminant analysis)

* + 1. *standardize(X)*
  1. **Normalize data (Each row equals 1)**

Normalize by row so that each row length 1. Useful for algorithms that weigh input values as a whole such as Neural Networks and distance algorithms(K-nn)

* + 1. *normalize(X)*
  1. **Binarize data (on binary threshold)**

Transform data based on binary threshold. Used when adding a new feature often.

* + 1. *binarize(X)*
  1. **Label Encoding**

Changing name of column

* + 1. *encode(df, name\_of\_column, new\_name)*
  1. **Dummy encoding**

Create dummy variables for each class to avoid order when in reality only encoding

* + 1. *get\_dummies(df, column\_name)*

1. **Feature Selection**

Quality of model determined by data features. Select those features that contribute most to the variable of interest. It reduces overfitting through reducing redundancy. Improves accuracy by creating a more accurate model. Reduces time needed to train by excluding irrelevant features.

* 1. **Univariate Selection**

Uses statistical test mostly with KBest to determine most relevant attributes using statistical test

* + 1. *univariate\_chi(x, y, df, target\_var, k=4(default))*
  1. **Recursive feature elimination**

Recursively removes attributes and builds models with remaining. Model accuracy as guidance on which combination of attributes contributes the most.

* + 1. *recursive\_elimination(x, y, df, target\_var, k=3(default))*
  1. **PCA – Principal Component Analysis**

Data reduction method with linear algebra through compressing several dimensions into principal components. Cannot explain them once comporessed.

Method combines highly correlated variables together to form smaller number of an artificial set of variables called “principal components” that account for most variance in the data.

* + 1. *pca(x, k=3(default))*
  1. **Tree Classifier**

Can be used to estimate importance of feature to refine the model and to make decision beteen explainability and accuracy. Many trees with variations to get accurate result

* + 1. *Extra\_trees(x,y,df,target\_var, estimators=100(default))*

1. **Model Evaluation**

Two reasons for evaluation:

Decide which interventions are effective

Get concrete knowledge on how accurate they are and to what extent we can trust them

We cannot use data we used for training the model to assess it. Two approaches to mitigate it – 1) use Train-Test Split works well with a lot of data 2) sampling techniques to augment the amount of data available

1. **Train and test set**

Split dataset into 70-30 or 80-20 split. Simple, fast and good for large datasets. We have to ensure variance is similar. If not, might not be good predictor.

* 1. *test\_split(x,y,test\_size, seed=7(default))*

1. **K-fold Cross-validation**

Used to reduce variance of using test-train-split. Divide data into folds and train multiple times. Dataset must be large to accommodate process

* 1. *k\_fold\_cross\_val(x,y,splits=10(default))*

1. **Leave one-out cross-validation**

As many folds as point. Prediciton will be done for each point separately. Standard deviation has more variance than with kfold and more computational expense

* 1. *leave\_one\_out(x,y)*

1. **Repeated random test-train splits**

Repeatedly takes train-test split. Results might look promising but are not realistic as same data is used over and over again.

* 1. *repeated\_test\_train(x,y, test\_size,repetitions=10)*

1. **Performance Metrics**

Metric against which model will be tuned, hyperparameters will be selected and algorithm will be evaluated

Classification Problem: Attributes are numeric and binary classification problem

Regression problem: Regression problems as continuous relationship assessement

**Classification Metrics:**

* 1. **Accuracy**

Ratio of (correct predictions/all predictions). Only suitable if classes are balanced and errors in each similarly important (wrong cancer diagnosis vs. no diagnosis of ill)

* + 1. *precision\_recall(x,y,test\_size)*
  1. **Logarithmic Loss**

Evaluates predictions of probabilities on a scalar between 0 and 1 as confidence measure.

* + 1. *k\_fold\_cross\_val(x,y, scoring = ‘neg\_log\_loss’)*
  1. **Area under ROC curve**

Ability of model to discriminate between positive and negative classes. AUC of 1 means perfect model:   
Sensitivity: True positive (positive values correctly classified)  
Specificity: True negative (negative values correctly classified)

* + 1. *area\_under\_roc(x,y,test\_size)*
  1. **Confusion Matrix**

Presentation of accuracy of the model in its four classes(TP, TN, FP,FN).

* + 1. *con\_matrix(x,y,test\_size=0.3)*
  1. **Classification Report**

Report to summarize many of the accuracy measures  
a) Precision = TP/TP+FP  
b) Recall = TP/TP+FN  
c) F1-Score = 2 x Precision x Recall / Precision + Recall (good for uneven distribution of classes)  
d) Support – number of elements of each class in Y-Teset  
e) Averages

* + 1. *class\_report(x,y, test\_size=0.3)*

**Regression Metrics:**

1. **Mean Absolute Error (MAE)**

Sum of absolute differences between values and prediction. 0 is perfect fit.

* 1. *mean\_abs\_error(X,Y)*

1. **Mean Square Error(MSE)**

Square value of absolute differences. Maximize score.

* 1. *mean\_squared\_error(X,Y)*

1. **R2**

Explained variance by regression

* 1. *r\_2(X,Y)*

1. **Clustering**

Unsupervised learning technique. Not one single solution. Clusters depend on point of view and question we try to answer. Finding best number of clusters, checking goodness and multidimensional clusters as some of the challenges we have. Additionally, as we are dealing with distances, all variables have to be rescaled from 0 to 1.

In some cases, clustering coincides with classification. When we know class, we can apply measures such as accuracy. Otherwise, it is hard to assess accuracy.

* 1. **Rescale and fit to columns**

Columns have to be rescaled and with column title

* + 1. *scale\_cluster\_df(x)*
  1. **Elbow Method**

Used to identify optimal number of clusters that minimize intra-cluster distance.

* + 1. *elbow(x,y)*
  1. **Silhouette Visualization**

Checking goodness of clusters. Measures mean intra-cluster distance relative to nearest clusters providing an appreciation of compactness.

* + 1. *Silhouette\_visual(x\_scaled)*
  1. **Inter-cluster distance**

The further apart centroids are the better

* + 1. *inter\_cluster\_dist(x\_scaled)*
  1. **Accuracy clustering**We can determine accuracy of cluster if we know classes.
     1. *accuracy\_clustering(x\_scaled, y)*
  2. **Silhouette score**Measure of how similar object is to own cluster compared to other clusters. Ranges from +1 to -1 and high value indicates that object is well matched to own cluster. If low or negative, too many or too few clusters chosen.
     1. *silh\_sco(x\_scaled, model)*
  3. **Centroid rescaling for meaning**

Centroids can only be interpreted if we rescale them from 0 to 1 range to their original ranges. On this basis we can interpret them.

* + 1. *centroid\_meaning(model, x, x\_scaled)*
  1. **Agglomerative Hierarchical Clustering**

Start with every point as one cluster and agglomerate with next closest point to a cluster until entire data set is a cluster