In [1]:	Introduction to Scikit-Learn (sklearn)  This notebook demonstrates some of the most useful functions of the beautiful Scikit-Learn library.  What we're going to cover:  1. An end-to-end Scikit-Learn workflow 2. Getting the data ready 3. Choose the right estimator/algorithm for our problems 4. Fit the model/algorithm and use it to make predictions on our data 5. Evaluating a model 6. Improve a model 7. Save and load a trained model 8. Putting it all together!  import pandas as pd import numpy as np import matplotlib.pyplot as plt
<pre>In [2]: Out[2]:</pre>	# 1. Get the data ready heart_disease = pd.read_csv("heart-disease.csv") heart_disease     age   sex   cp   trestbps   chol   fbs   restecg   thalach   exang   oldpeak   slope   ca   thal   target   0   63   1   3   145   233   1   0   150   0   2.3   0   0   1   1   1   37   1   2   130   250   0   1   187   0   3.5   0   0   2   1   2   41   0   1   130   204   0   0   172   0   1.4   2   0   2   1
In [3]:	3 56 1 1 120 236 0 1 178 0 0.8 2 0 2 1  4 57 0 0 120 354 0 1 163 1 0.6 2 0 2 1
In [4]: Out[4]:	<pre>from sklearn.ensemble import RandomForestClassifier  clf = RandomForestClassifier()  # we'll keep the default hyperparameters for now clf.get_params()  {'bootstrap': True,    'ccp_alpha': 0.0,    'class_weight': None,    'criterion': 'gini',    'max_depth': None,    'max_features': 'auto',    'max_leaf_nodes': None,    'max_samples': None,    'min_impurity_decrease': 0.0,    'min_impurity_split': None,    'min_samples_leaf': 1,    'min_samples_leaf': 2,    'min_weight_fraction_leaf': 0.0,    'n_estimators': 100,    'n_jobs': None,    'oob_score': False,</pre>
In [6]:	<pre>'random_state': None, 'verbose': 0, 'warm_start': False}  # 3. Fit the model to the training data from sklearn.model_selection import train_test_split  X_train, X_test, y_train, y_test = train_test_split(X, y,</pre>
<pre>In [8]: Out[8]:</pre>	<pre>y_preds array([0, 1, 0, 1, 1, 0, 0, 1, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0,</pre>
In [10]:	clf.score(X_test, y_test)  0.8688524590163934  # use some other evaluation metrics from sklearn.metrics import classification_report, confusion_matrix, accuracy_score  print(classification_report(y_test, y_preds))  precision recall f1-score support  0 0.92 0.79 0.85 29 1 0.83 0.94 0.88 32  accuracy 0.87 61 macro avg 0.88 0.87 0.87 61
Out[12]:  In [13]: Out[13]:	<pre>weighted avg    0.87    0.87    0.87    61  confusion_matrix(y_test, y_preds)  array([[23, 6],         [ 2, 30]], dtype=int64)  accuracy_score(y_test, y_preds)  0.8688524590163934  # 5. Improve the mode1 # Try different amount of n_estimators</pre>
	<pre>np.random.seed(42) for i in range(10, 100, 10):     print(f"Trying model with {i} estimators")     clf = RandomForestClassifier(i).fit(X_train, y_train)      print(f"Model accuracy on test set: {clf.score(X_test, y_test) * 100:.2f}%")     print("")  Trying model with 10 estimators Model accuracy on test set: 85.25%  Trying model with 20 estimators Model accuracy on test set: 80.33%  Trying model with 30 estimators Model accuracy on test set: 85.25%</pre>
	Trying model with 40 estimators Model accuracy on test set: 85.25%  Trying model with 50 estimators Model accuracy on test set: 85.25%  Trying model with 60 estimators Model accuracy on test set: 88.52%  Trying model with 70 estimators Model accuracy on test set: 86.89%  Trying model with 80 estimators Model accuracy on test set: 85.25%  Trying model with 90 estimators Model accuracy on test set: 85.25%
In [16]:	<pre># 6. Save a model and load it import pickle pickle.dump(clf, open("random_forest_m1.pkl", "wb"))  loaded_model = pickle.load(open("random_forest_m1.pkl", 'rb')) loaded_model.score(X_test, y_test)  0.8524590163934426  1. Getting the data ready</pre>
In [17]: Out[17]:	Three main things we have to do:  1. Split the data into features and labels (usually x and y)  • then split them into train set and test set  2. Converting non-numerical values to numerical values (feature encoding)  3. Filling (imputing) or disregarding missing values  heart_disease.head()   age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal target  0 63 1 3 145 233 1 0 150 0 2.3 0 0 1 1  1 37 1 2 130 250 0 1 187 0 3.5 0 0 2 1
	2 41 0 1 130 204 0 0 172 0 1.4 2 0 2 1 3 56 1 1 120 236 0 1 178 0 0.8 2 0 2 1 4 57 0 0 120 354 0 1 163 1 0.6 2 0 2 1  1.1 Split the data into features and labels  X = heart_disease.drop("target", axis=1) # features y = heart_disease["target"] # labels  Split features and labels into training and test sets
In [20]:	<pre># Split the data into training and test sets from sklearn.model_selection import train_test_split  test_size = 0.2 X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=test_size)  X_train.shape, X_test.shape, y_train.shape, y_test.shape # X_train # 242: 80% of the dataset # 13: number of lables (columns)  ((242, 13), (61, 13), (242,), (61,))  1.2 Converting non-numerical values</pre>
In [21]: Out[21]:	For this, we need another dataset  \[ \text{car_sales} = \text{pd.read_csv("car-sales-extended.csv")}} \]  \[ \text{Make Colour Odometer (KM) Doors Price} \]  \[ \text{0 Honda White 35431 4 15323}} \]  \[ \text{1 BMW Blue 192714 5 19943}} \]  \[ \text{2 Honda White 84714 4 28343}} \]  \[ \text{3 Toyota White 154365 4 13434}} \]  \[ \text{4 Nissan Blue 181577 3 14043}} \]
	<pre>Colour</pre>
In [24]:	<pre># Build machine learning model from sklearn.ensemble import RandomForestRegressor  try:     model = RandomForestRegressor()     model.fit(X_train, y_train)     model.score(X_test, y_test) except ValueError as e:     print(f"ValueError: {e}")  ValueError: could not convert string to float: 'Toyota'</pre> ValueError: could not convert string to float
	<pre># Turn the categories into numbers from sklearn.preprocessing import OneHotEncoder from sklearn.compose import ColumnTransformer  categorical_features = ["Make", "Colour",</pre>
Out[25]:  In [26]: Out[26]:	0.00000e+00, 3.54310e+04], [1.00000e+00, 0.00000e+00, 0.00000e+00,, 0.00000e+00, 1.00000e+00, 1.92714e+05], [0.00000e+00, 1.00000e+00, 0.00000e+00,, 1.00000e+00, 0.00000e+00, 8.47140e+04],, [0.00000e+00, 0.00000e+00, 1.00000e+00,, 1.00000e+00, 0.00000e+00, 6.66040e+04], [0.00000e+00, 1.00000e+00, 0.00000e+00,, 1.00000e+00, 0.00000e+00, 2.15883e+05], [0.00000e+00, 0.00000e+00, 0.00000e+00,, 1.00000e+00, 0.00000e+00, 2.48360e+05]])
In [27]: Out[27]:	0 Honda       White       35431       4         1 BMW       Blue       192714       5         2 Honda       White       84714       4         3 Toyota       White       154365       4         4 Nissan       Blue       181577       3         pd. DataFrame (transformed_X) . head()         0 1 2 3 4 5 6 7 8 9 10 11       12         0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.
	1 1.0 0.0 0.0 1.0 1.0 1.0 0.0 1.0 0.0 1.0 0.0 1.0 1
In [28]: Out[28]:	1. transforms the feature Make into a vector of size 3 filled with zeros.  • Say that the first zero represents Honda, the second Toyota and the third BMW  2. for each entry (row), it changes 0 into 1 in the slot that corresponds to the actual categorical feature.  • Say that the entry was a Toyota, then the vector would be [0,1,0]  from IPython.display import YouTubeVideo YouTubeVideo('v_4KWmkwmsU', start=69)  One-hot Encoding explained
In [29]:	<pre>dummies = pd.get_dummies(X)</pre>
Out[29]: In [30]:	Odometer (KM)         Doors         Make_BMW         Make_Honda         Make_Nissan         Make_Toyota         Colour_Black         Colour_Blue         Colour_Green         Colour_Red         Colour_Red         Colour_Sulphane           0         35431         4         0         1         0 </th
Out[30]:	model.fit(X_train, y_train) model.score(X_test, y_test)  0.3235867221569877   1.3 Missing values  We have two options for handling missing data:  1. Fill the missing data (imputation) 2. Remove the samples with missing data  Let's import another dataset that has missing values.
<pre>In [31]: Out[31]:</pre>	car_sales_missing = pd.read_csv("car-sales-extended-missing-data.csv")  Make Colour Odometer (KM) Doors Price  Henda White 35431.0 4.0 15323.0  Honda White 192714.0 5.0 19943.0  Honda White 84714.0 4.0 28343.0  Toyota White 154365.0 4.0 13434.0  Nissan Blue 181577.0 3.0 14043.0  From the head of the DataFrame, it doesn't seem like we have missing values.  We can calculate how many there are in this way.
<pre>In [32]: Out[32]: In [33]:</pre>	<pre>car_sales_missing.isna().sum()  Make</pre>
<pre>In [34]: Out[34]:</pre>	<pre># Fill the "Colour" column car_sales_missing["Colour"].fillna("missing", inplace=True)  # Fill the "Odometer" column car_sales_missing["Odometer (KM)"].fillna(car_sales_missing["Odometer (KM)"].mean(),</pre>
<pre>In [35]: Out[35]:</pre>	Odometer (KM) 0 Doors 0 Price 50 dtype: int64  Option 2: Fill missing data with Scikit-learn  car_sales_missing2 = pd.read_csv("car-sales-extended-missing-data.csv") car_sales_missing2.head()  Make Colour Odometer(KM) Doors Price  O Honda White 35431.0 4.0 15323.0  1 BMW Blue 192714.0 5.0 19943.0
<pre>In [36]: Out[36]: In [37]:</pre>	Colour 50 Odometer (KM) 50 Doors 50 Price 50 dtype: int64
	<pre># don't have the "Price" value (our label), so we # just drop them car_sales_missing2.dropna(subset=["Price"], inplace=True)  # Split into X &amp; y X = car_sales_missing2.drop("Price", axis=1) y = car_sales_missing2["Price"]  # Fill missing values with Scikit-learn from sklearn.impute import SimpleImputer from sklearn.compose import ColumnTransformer  # Fill categorical values with "missing" and # numerical values with mean cat_imp = SimpleImputer(strategy="constant", fill_value="missing")</pre>
	<pre>door_imp = SimpleImputer(strategy="constant", fill_value=4) num_imp = SimpleImputer(strategy="mean")  # Define columns cat_features = ["Make", "Colour"] door_feature = ["Doors"] num_features = ["Odometer (KM)"]  # Create an imputer (something that fills missing data) imputer = ColumnTransformer([</pre>
	Colour 0 Odometer (KM) 0
In [41]:	
	**Regression** - predicting a number     **Classification** - predicting wether a sample is one thing or another (healthy, ill)  To help us choose the correct estimator, Scikit-learn has offered a flowchart to base upon.  Classification    Scikit-learn   Scikit-learn   Scikit-learn   Scikit-learn   Scikit-learn   Scikit-learn   Start   Start
	Bayes No NOT YES Samples Samples
In [42]: In [43]:	# <img src="./sklearn-ml-map.png"/> 2.1 Picking a machine learning model for a regression problem  # Import built-in Boston housing dataset from sklearn.datasets import load_boston
In [44]: Out[44]:	boston_dict = load_boston()  boston_df = pd.DataFrame(boston_dict["data"],
<pre>In [45]: Out[45]: In [46]:</pre>	# How many samples do we have? len(boston_df)  506  Following the Sklearn guidelines, we'll pick Ridge Regression model  from sklearn.linear_model import Ridge  # Setup numpy seed seed = 46 np.random.seed(seed)
Out[46]:	<pre># Create the data X = boston_df.drop("target", axis=1) y = boston_df["target"]  # Split into train and test X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  # Instantiate Ridge model model = Ridge() model.fit(X_train, y_train)  # Check the score on test data model.score(X_test, y_test)  0.794636752603225</pre> This test worked quite fine But what if Ridge wasn't working as expected?
In [47]:	This test worked quite fine. But what if Ridge wasn't working as expected?  And if we wanted to improve these results?  Scikit-learn suggests us another class of models: EnsembleRegressor.  The most famous and used is RandomForest  from sklearn.ensemble import RandomForestRegressor  # Setup numpy seed seed = 46 np.random.seed(seed)  # Create the data X = boston_df.drop("target", axis=1) y = boston_df["target"]  # Split into train and test
Out[47]:	<pre># Split into train and test X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2) # Instantiate RandomForest rf = RandomForestRegressor() rf.fit(X_train, y_train) # Check the score on test data rf.score(X_test, y_test)  0.8827430393207987  Using the same random seed, we've already improved our result by quite a margin!  2.2 Picking a machine learning model for a classification problem</pre>
<pre>In [48]: Out[48]: In [49]:</pre>	heart_disease = pd.read_csv("heart-disease.csv") heart_disease.head()    age   sex   cp   trestbps   chol   fbs   restecg   thalach   exang   oldpeak   slope   ca   thal   target     0   63   1   3   145   233   1   0   150   0   2.3   0   0   1   1     1   37   1   2   130   250   0   1   187   0   3.5   0   0   2   1     2   41   0   1   130   204   0   0   172   0   1.4   2   0   2   1     3   56   1   1   120   236   0   1   178   0   0.8   2   0   2   1     4   57   0   0   120   354   0   1   163   1   0.6   2   0   2   1
<pre>In [49]: Out[49]: In [50]:</pre>	<pre>len(heart_disease)  303  Following the Sklearn guidelines, we'll pick LinearSVC  from sklearn.svm import LinearSVC  # Setup random seed seed = 42 np.random.seed(seed)  # Make the data X = heart_disease.drop("target", axis=1) y = heart_disease["target"]</pre>
Out[50]:	
	ConvergenceWarning: Liblinear failed to converge, increase the number of iterations.  This warning tells us to increase the parameter max_iter (default 1000) when istantiating the LinearSVC class. We'll skip this for the moment.  Just as before, we're now interested in seeing another algorithm in action to see if we can improve our results.  Let's use **RandomForestClassifier**  from sklearn.ensemble import RandomForestClassifier  # Setup random seed seed = 42
	<pre>seed = 42 np.random.seed(seed)  # Make the data X = heart_disease.drop("target", axis=1) y = heart_disease["target"]  # Split the data X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  # Istantiate RandomForestClassifier clf = RandomForestClassifier() clf.fit(X_train, y_train)  # Evaluate the RandomForestClassifier clf.score(X_test, y_test)</pre>
Out[51]:	0.8524590163934426  In this case, they performed quite similar.  3. Fit the model on our data and use it to make predictions  3.1 Fit the model to the data  Different names for:  • X = features, feature variables, data • y = labels, targets, target variables
In [52]:	<pre>from sklearn.ensemble import RandomForestClassifier  # Setup random seed seed = 42 np.random.seed(seed)  # Make the data X = heart_disease.drop("target", axis=1) y = heart_disease["target"]  # Split the data X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  # Istantiate RandomForestClassifier clf = RandomForestClassifier()</pre>
In [53]:	clf.fit(X_train, y_train);  We've seen this line of code multiple times, but what does it actually do?  First, let's remind us how is our data structured.

;	<pre>Two ways to make predictions:  1. predict() function 2. predict_proba()  To predict a value, the model needs an input with the exact same features and labels.  3.2.1: predict()  try:     clf_predict(pp_array([1.4.2.6.2]))</pre>
3 6	<pre>clf.predict(np.array([1,4,2,6,2])) except ValueError as e:     print(f"ValueError: {e}")  ValueError: Expected 2D array, got 1D array instead: array=[1. 4. 2. 6. 2.]. Reshape your data either using array.reshape(-1, 1) if your data has a single feature or array e(1, -1) if it contains a single sample.  # since the model has never seen X_test # let's use this as an example clf.predict(X_test)</pre>
	array([0, 1, 1, 0, 1, 1, 1, 0, 0, 1, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
;	<ul> <li>clf.score(X_test, y_test)</li> <li>sklearn.metrics.accuracy_score(y_test, y_preds)</li> </ul> 3.2.2: predict_proba() Returns probabilities of a classification label What? Run the code.
ć	clf.predict_proba(X_test[:5])  array([[0.89, 0.11],
	predict_proba() gives us the probability of a classification label, meaning that the return value is expressed as the probabe **n**th value is either 0 or 1, "black" or "white", "ill" or "healthy".  Let's take the first result: [0.89, 0.11], meaning that it has been classified as  • 0 with 89% chance and  • 1 with 11% chance
-	4. Evaluating a model  Three ways to evaluate models/estimators:  1. Estimator score() method 2. Statistical estimators 3. The scoring parameter 4. Scikit-learn metric functions  from sklearn.ensemble import RandomForestClassifier
	<pre>seed = 45 np.random.seed(seed)  X = heart_disease.drop("target", axis=1) y = heart_disease["target"]  X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  clf = RandomForestClassifier() clf.fit(X_train, y_train);</pre>
	4.1 Evaluating a model using the score() method  clf.score(X_test, y_test)  0.8360655737704918  4.2 -clf Classification model evaluation metrics  1. Accuracy
	<pre>2. Area under ROC curve 3. Confusion matrix 4. Classification report  from sklearn.model_selection import cross_val_score from sklearn.ensemble import RandomForestClassifier  seed = 89 np.random.seed(seed)  X = heart_disease.drop("target", axis=1) y = heart_disease["target"]</pre>
	<pre>X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  clf = RandomForestClassifier() clf.fit(X_train, y_train);  4.2.1 Accuracy  np.mean(cross_val_score(clf, X, y, cv=5)) 0.8283060109289618</pre>
	4.2.2 Area under ROC curve  ROC curves are a comparison of a model's true positive rate (tpr) versus a model's false positive rate (fpr).  Because of this, we only truly care about what our model predicts to be positive (or 1).  from sklearn.metrics import roc_curve  # Make predictions with probabilities y_probs = clf.predict_proba(X_test)
	<pre># Extract the probabilities of event "positive" y_probs_positive = y_probs[:, 1] y_probs_positive[10:]  array([0.38, 0.26, 0.51, 0.22, 0.32, 0.98, 0.78, 0.2, 0.67, 0.01, 0.76,</pre>
	<pre>fpr, tpr, thresholds = roc_curve(y_test, y_probs_positive)  # Create a function to plot ROC curves import matplotlib.pyplot as plt  def plot_roc_curve(fpr, tpr):     # plot roc curve     plt.plot(fpr, tpr, color="orange", label="ROC")     # plot line with no predictive power (baseline)     plt.plot([0,1], [0,1], color="darkblue", linestyle="", label="Guessing")      plt.xlabel("False positive rate (fpr)")     plt.ylabel("True positive rate (fpr)")</pre>
	<pre>plt.ylabel("True positive rate (tpr)") plt.title("Receiver Operating Characteristic (ROC) curve") plt.legend()  plt.show()  plot_roc_curve(fpr, tpr)  Receiver Operating Characteristic (ROC) curve  10 ROC</pre>
	91 0.6 0.0 0.2 0.4 0.6 0.8 1.0 False positive rate (fpr)
	# Evaluate the Area Under the Curve (AUC) score  from sklearn.metrics import roc_auc_score  roc_auc_score(y_test, y_probs_positive)  0.9043956043956044  4.2.3 Confusion matrix  A confusion matrix is a quick way to compare the labels a model predicts and the actual labels it was supposed to predict.
	In essence, giving you and idea of where the model is getting confused.  from sklearn.metrics import confusion_matrix  # predictions on the test data y_preds = clf.predict(X_test) # creating the confusion matrix conf_mat = confusion_matrix(y_test, y_preds) conf_mat  array([[21, 5],
	<pre>[ 5, 30]], dtype=int64)  # having a better view at the matrix pd.crosstab(y_test, y_preds,</pre>
	<pre># Having a colored view using Seaborn's heatmap() import seaborn as sb  def plot_conf_mat():     # Set the font scale     # sb.set(font_scale=1.5)     fig, ax = plt.subplots(figsize=(3,3))     ax = sb.heatmap(conf_mat,</pre>
	annot=True, # adds annotations cbar=False, # removes the colorbar ) plt.xlabel("True label") plt.ylabel("Predicted label")  plot_conf_mat()
4	4.2.4 Classification report  from sklearn.metrics import classification_report
	print(classification_report(y_test, y_preds))  precision recall f1-score support  0 0.81 0.81 0.81 26 1 0.86 0.86 0.86 35  accuracy 0.84 61 macro avg 0.83 0.83 0.83 61 weighted avg 0.84 0.84 0.84 61
	Classification report analysis  Precision - Indicates the proportion of positive identifications (model predicted class 1) which were actually correct. A model which produces no false positives has a precision of 1.0.  Recall - Indicates the proportion of actual positives which were correctly classified. A model which produces no false negatives has a recall of 1.0.  F1 score - A combination of precision and recall. A perfect model achieves an F1 score of 1.0.  Support - The number of samples each metric was calculated on.  Accuracy - The accuracy of the model in decimal form. Perfect accuracy
-	Accuracy - The accuracy of the model in decimal form. Perfect accuracy is equal to 1.0.      Accuracy - The accuracy of the model in decimal form. Perfect accuracy is equal to 1.0.      Accuracy - The accuracy of the model in decimal form. Perfect accuracy is equal to 1.0.      Accuracy - The accuracy of the model in decimal form. Perfect accuracy is equal to 1.0.      Accuracy - The accuracy of the model in decimal form. Perfect accuracy is equal to 1.0.      Macro avg - Short for macro average, the average precision, recall and F1 score between classes. Macro avg doesn't class imbalance into effort, so if you do have class imbalances, pay attention to this metric.      Weighted avg - Short for weighted average, the weighted average precision, recall and F1 score between classes. Weighted means each metric is calculated with respect to how many samples there are in each class. This metric will favour the majority class (e.g. will give a high value when one class out performs another due to having more samples).  To summarize classification metrics:  Accuracy is a good measure to start with if all classes are balanced (e.g. same amount of samples which are labelled with
4	<ul> <li>Precision and recall become more important when classes are imbalanced</li> <li>If false positive predictions are worse than false negatives, aim for higher precision</li> <li>If false negative predictions are worse than false positives, aim for higher recall</li> <li>F1-score is a combination of precision and recall</li> <li>4.2 -reg Regression model evaluation metrics</li> <li>1. R² or coefficient of determination</li> <li>2. Mean absolute error (MAE)</li> </ul>
1	3. Mean squared error (MSE)
	<pre>seed = 562 np.random.seed(seed)  X = boston_df.drop("target", axis=1) y = boston_df["target"]  X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  model = RandomForestRegressor() model.fit(X_train, y_train);</pre>
1	<pre># This returns exactely that! model.score(X_test, y_test)  0.9125088209795402  Another way to calculate this is by using the r2_score() method  from sklearn.metrics import r2_score  # Fill an array with y_test mean y test mean = np.full(len(y test), y test.mean())</pre>
	r2_score(y_test, y_test_mean) # score is 0 because it was tested on # the mean of the test targets.  0.0  r2_score(y_test, y_test) # score is 1 because it perfectely # predicted itself.  1.0
	4.2.2 Mean absolute error (MAE)  Average of the absolute differences between predicted values and actual values.  from sklearn.metrics import mean_absolute_error  y_preds = model.predict(X_test)  mean_absolute_error(y_test, y_preds)
	<pre># Let's visualize the data first mae_df = pd.DataFrame({     "actual values": y_test,     "predicted values": y_preds }) mae_df.head(8)  actual values predicted values</pre>
	151       19.6       19.283         390       15.1       14.813         284       32.2       31.709         348       24.5       27.481         172       23.1       20.456         306       33.4       34.805         320       23.8       23.616         143       15.6       13.260
	mae_df["differences"] = mae_df["predicted values"] - mae_df["actual values"]           actual values         predicted values         differences           151         19.6         19.283         -0.317           390         15.1         14.813         -0.287           284         32.2         31.709         -0.491           348         24.5         27.481         2.981
	172       23.1       20.456       -2.644         306       33.4       34.805       1.405         320       23.8       23.616       -0.184         143       15.6       13.260       -2.340         # Mean Absolute Error manually calculated       np.mean (np.abs (mae_df["differences"]))         2.0864117647058826
1	4.2.3 Mean squared error (MSE)  Average of the squared differences between predicted values and actual values.  from sklearn.metrics import mean_squared_error  mean_squared_error(y_test, y_preds)  8.117253647058815  # Mean Squared Error manually calculated  np.mean(np.square(mae_df["differences"]))
	8.117253647058815  4.3 -clf Using the scoring parameter  from sklearn.model_selection import cross_val_score from sklearn.ensemble import RandomForestClassifier  seed = 89 np.random.seed(seed)
	<pre>X = heart_disease.drop("target", axis=1) y = heart_disease["target"] X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  clf = RandomForestClassifier() clf.fit(X_train, y_train);  cross_val_score(clf,  # estimator</pre>
Č	Cross validation  Secting Note: Page 11 April 11 April 12
	Split  80 patient records  Training split (80%)  Test split (20%)  Model is trained on training data, and evaluated on the test data.  Model is trained on 5 different versions of training data, and
1	k-fold cross-validation splits the data in training data and testing data in k possible combinations.  The result of cross_val_score() is an array of length k that represents the score of each different "version" of the data. that we didn't "luckily split" our data so that there were easy-to-find patterns in the training data.  cv_acc = cross_val_score(clf, X, y, cv=5, scoring="accuracy") print(f"The cross-validated accuracy is: {np.mean(cv_acc)*100:.2f}%")  The cross-validated accuracy is: 80.17%
	<pre>cv_prec = cross_val_score(clf, X, y, cv=5, scoring="precision") print(f"The cross-validated precision is: {np.mean(cv_prec)*100:.2f}%") The cross-validated precision is: 83.93%  cv_recall = cross_val_score(clf, X, y, cv=5, scoring="recall") print(f"The cross-validated recall is: {np.mean(cv_recall)*100:.2f}%") The cross-validated recall is: 83.64%  cv_f1 = cross_val_score(clf, X, y, cv=5, scoring="f1")</pre>
	<pre>print(f"The cross_val_score(clf, x, y, cv=s, scoring="ff") print(f"The cross-validated F1 is: {np.mean(cv_f1)*100:.2f}%")  4.3 -reg Using the scoring parameter  from sklearn.model_selection import cross_val_score from sklearn.ensemble import RandomForestRegressor  seed = 62 np.random.seed(seed)</pre>
	<pre>X = boston_df.drop("target", axis=1) y = boston_df["target"]  model = RandomForestRegressor()  # R^2 np.random.seed(seed) cv_r2 = cross_val_score(model, X, y, cv=5, scoring=None) np.mean(cv_r2)</pre>
	# Mean Absolute Error  np.random.seed(seed)  cv_mae = cross_val_score(model, X, y, cv=5, scoring="neg_mean_absolute_error")  np.mean(cv_mae)  -2.9538927586876325  # Mean Squared Error  np.random.seed(seed)  cv_mse = cross_val_score(model, X, y, cv=5, scoring="neg_mean_squared_error")
•	
	<pre>X = heart_disease.drop("target", axis=1) y = heart_disease["target"]  X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  clf = RandomForestClassifier() clf.fit(X_train, y_train);  # Make predictions using our model y_preds = clf.predict(X_test)</pre>
(	<pre># Evaluate the classifier using different functions print("Classifier metrics on the test set\n") print(f"Accuracy: \t{accuracy_score(y_test, y_preds)*100:.2f}%") print(f"Precision: \t{precision_score(y_test, y_preds)*100:.2f}%") print(f"Recall: \t{recall_score(y_test, y_preds)*100:.2f}%") print(f"F1: \t\t{f1_score(y_test, y_preds)*100:.2f}%")  Classifier metrics on the test set  Accuracy: 83.61% Precision: 83.33% Recall: 88.24%</pre>
	Recall: 88.24% F1: 85.71%  4.4 -reg Using Scikit-learn functions  from sklearn.metrics import r2_score, mean_absolute_error, mean_squared_error  seed = 621 np.random.seed(seed)  X = boston_df.drop("target", axis=1)
	<pre>y = boston_df["target"]  X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)  model = RandomForestRegressor()  model.fit(X_train, y_train);  # Make predictions using our model  y_preds = model.predict(X_test)  # Evaluate the regressor using different functions  print("Regression metrics on the test set\n")</pre>
	<pre>print(f"R^2: \t{r2_score(y_test, y_preds)*100:.2f}%") print(f"MAE: \t{mean_absolute_error(y_test, y_preds):.3f}") print(f"MSE: \t{mean_squared_error(y_test, y_preds):.3f}")  Regression metrics on the test set  R^2: 82.97% MAE: 2.405 MSE: 13.448</pre>
١	<ul> <li>5. Improving a model</li> <li>When improving a model, we call the first predictions baseline predictions and the first model baseline model.</li> <li>On the subsequent iterations, we try to improve on these. There are two main ways:</li> <li>1. From a data perspective <ul> <li>Could we collect more data? (more data is generally better)</li> <li>Could we improve the data? (more info for each sample)</li> </ul> </li> <li>From a model perspective <ul> <li>Could we use a more complex model?</li> <li>Could we improve the current model by tuning the hyperparameters?</li> </ul> </li> </ul>
	<pre>from sklearn.ensemble import RandomForestClassifier  clf = RandomForestClassifier()  # see the model's hyperparameters clf.get_params()  {'bootstrap': True,   'ccp_alpha': 0.0,</pre>
	<pre>'class_weight': None, 'criterion': 'gini', 'max_depth': None, 'max_features': 'auto', 'max_leaf_nodes': None, 'max_samples': None, 'min_impurity_decrease': 0.0, 'min_impurity_split': None, 'min_samples_leaf': 1, 'min_samples_split': 2, 'min_weight_fraction_leaf': 0.0, 'n_estimators': 100, 'n_estimators': None</pre>
•	'n_jobs': None, 'oob_score': False, 'random_state': None, 'verbose': 0, 'warm_start': False)  You can adjust the hyperparameters in three ways:  1. By hand 2. Randomly with **RandomSearchCV** 3. Exhaustively with **GridSearchCV**
I	5.1 Tuning hyperparameters by hand  Let's make three sets of data: training, validation and testing.  We're now going to try and adjust:  max_depth max_features min_samples_leaf
•	_
	recall = recall_score(y_true, y_preds)
	This time, since we need three sets of data, we have to manually split it.  seed = 724 np.random.seed(seed)  # Shuffle the data heart_disease_shuffled = heart_disease.sample(frac=1)  # Set the split percentages train_split = round(0.7 * len(heart_disease_shuffled)) valid_split = round(train_split + 0.15 * len(heart_disease_shuffled))
	<pre># Make baseline predictions on validation data y_val_preds = clf.predict(X_val)  baseline_metrics = evaluate_preds(y_val, y_val_preds)  {'accuracy': 0.689, 'precision': 0.545, 'recall': 0.75, 'f1': 0.632}  Let's now create a second classifier and test it with different hyperparameters  seed = 724</pre>
	<pre>seed = 724 np.random.seed(seed)  clf2 = RandomForestClassifier(n estimators=600)</pre>
	<pre>clf2.fit(X_train, y_train)  y_val_preds2 = clf2.predict(X_val)  baseline_metrics2 = evaluate_preds(y_val, y_val_preds2)  # doesn't change that much in this case, worse actually  {'accuracy': 0.644, 'precision': 0.5, 'recall': 0.688, 'f1': 0.579}</pre>
	<pre>clf2.fit(X_train, y_train)  y_val_preds2 = clf2.predict(X_val)  baseline_metrics2 = evaluate_preds(y_val, y_val_preds2)  # doesn't change that much in this case, worse actually</pre>

In [105]: from sklearn.model\_selection import RandomizedSearchCV # create a dict having keys=hyperparam # we want to tune and values=list of # possible values we want to try grid = { "n estimators": [100,200,500,1000,1200], "max depth": [None, 5, 10, 20, 30], "max\_features": ["auto", "sqrt"], "min\_samples\_split": [2,4,6], "min\_samples\_leaf": [1,2,4] seed = 724np.random.seed(seed) X = heart disease shuffled.drop("target", axis=1) y = heart disease shuffled["target"] X train, X test, y train, y test = train test split(X, y, test size=0.2) clf = RandomForestClassifier(n jobs=1) # Setup RandomizedSearchCV rs clf = RandomizedSearchCV( estimator=clf, param distributions=grid, n iter=10, # number of models to try # number of k cross-validations verbose=2, n iter is the most important parameter in this case: it represents how many random configurations will be taken into consideration. It will randomly choose one value per hyperparameter and test the model with that configuration. In [106]: | # Fit the RandomizedSearchCV rs\_clf.fit(X\_train, y\_train); # Total number of fits: n iter \* cv Fitting 5 folds for each of 10 candidates, totalling 50 fits [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20 [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20, tot al=0.1s[CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20 [Parallel(n jobs=1)]: Using backend SequentialBackend with 1 concurrent workers. [Parallel(n\_jobs=1)]: Done 1 out of 1 | elapsed: 0.0s remaining: [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20, tot [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20 [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20, tot al=0.1s[CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20 [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20, tot [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20 [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=auto, max\_depth=20, tot [CV] n estimators=100, min samples split=2, min samples leaf=2, max features=sqrt, max depth=None [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None, t otal= 0.1s[CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None, t [CV] n estimators=100, min samples split=2, min samples leaf=2, max features=sqrt, max depth=None [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None, t otal= 0.1s[CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None, t otal= 0.1s[CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None [CV] n\_estimators=100, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=None, t [CV] n\_estimators=1000, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=30 [CV] n\_estimators=1000, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=30, to [CV] n estimators=1000, min samples split=2, min samples leaf=1, max features=sqrt, max depth=30 [CV] n estimators=1000, min samples split=2, min samples leaf=1, max features=sqrt, max depth=30, to [CV] n\_estimators=1000, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=30 [CV] n\_estimators=1000, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=30, to [CV] n\_estimators=1000, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=30 [CV] n estimators=1000, min samples split=2, min samples leaf=1, max features=sqrt, max depth=30, to [CV] n\_estimators=1000, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=30 [CV] n\_estimators=1000, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=30, to [CV] n estimators=500, min samples split=2, min samples leaf=1, max features=sqrt, max depth=10 [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10, tot [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10 [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10, tot al= [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10 [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10, tot [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10 [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10, tot al= [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10 [CV] n\_estimators=500, min\_samples\_split=2, min\_samples\_leaf=1, max\_features=sqrt, max\_depth=10, tot [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10 [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10, to [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10 [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10, to [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10 [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10, to [CV] n estimators=1000, min samples split=6, min samples leaf=4, max features=auto, max depth=10 [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10, to 1.1s [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10 [CV] n\_estimators=1000, min\_samples\_split=6, min\_samples\_leaf=4, max\_features=auto, max\_depth=10, to [CV] n\_estimators=1200, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=auto, max\_depth=10 [CV] n\_estimators=1200, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=auto, max\_depth=10, to [CV] n\_estimators=1200, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=auto, max\_depth=10 [CV] n estimators=1200, min samples split=2, min samples leaf=2, max features=auto, max depth=10, to [CV] n\_estimators=1200, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=auto, max\_depth=10 [CV] n\_estimators=1200, min\_samples\_split=2, min\_samples\_leaf=2, max\_features=auto, max\_depth=10, to [CV] n estimators=1200, min samples split=2, min samples leaf=2, max features=auto, max depth=10 [CV] n estimators=1200, min samples split=2, min samples leaf=2, max features=auto, max depth=10, to 1.3s [CV] n estimators=1200, min samples split=2, min samples leaf=2, max features=auto, max depth=10 [CV] n estimators=1200, min samples split=2, min samples leaf=2, max features=auto, max depth=10, to [CV] n\_estimators=500, min\_samples\_split=4, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=30 [CV] n estimators=500, min samples split=4, min samples leaf=2, max features=sqrt, max depth=30, tot [CV] n\_estimators=500, min\_samples\_split=4, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=30 [CV] n\_estimators=500, min\_samples\_split=4, min\_samples\_leaf=2, max\_features=sqrt, max\_depth=30, tot al= 0.5s [CV] n estimators=500, min samples split=4, min samples leaf=2, max features=sqrt, max depth=30 [CV] n estimators=500, min samples split=4, min samples leaf=2, max features=sqrt, max depth=30, tot al= [CV] n estimators=500, min samples split=4, min samples leaf=2, max features=sqrt, max depth=30 [CV] n estimators=500, min samples split=4, min samples leaf=2, max features=sqrt, max depth=30, tot [CV] n estimators=500, min samples split=4, min samples leaf=2, max features=sqrt, max depth=30 [CV] n estimators=500, min samples split=4, min samples leaf=2, max features=sqrt, max depth=30, tot al= [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5 [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5, tota 0.7s[CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5 [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5, tota 0.6s [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5 [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5, tota [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5 [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5, tota [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5 [CV] n estimators=500, min samples split=6, min samples leaf=1, max features=sqrt, max depth=5, tota l= 0.6s [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10 [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10, to [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10 [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10, to [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10 [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10, to [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10 [CV] n\_estimators=1200, min\_samples\_split=6, min\_samples\_leaf=1, max\_features=auto, max\_depth=10, to [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10 [CV] n estimators=1200, min samples split=6, min samples leaf=1, max features=auto, max depth=10, to tal= 1.3s [CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30 [CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30, to [CV] n\_estimators=1200, min\_samples\_split=2, min\_samples\_leaf=4, max\_features=sqrt, max\_depth=30 [CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30, to tal = 1.3s[CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30 [CV] n\_estimators=1200, min\_samples\_split=2, min\_samples\_leaf=4, max\_features=sqrt, max\_depth=30, to [CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30 [CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30, to [CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30 [CV] n estimators=1200, min samples split=2, min samples leaf=4, max features=sqrt, max depth=30, to tal= 1.3s[Parallel(n jobs=1)]: Done 50 out of 50 | elapsed: 41.3s finished In [107]: | # Show the combination that resulted # in best cross-validation results rs clf.best params Out[107]: {'n estimators': 1200, 'min samples split': 2, 'min samples leaf': 2, 'max features': 'auto', 'max\_depth': 10} From now on, when we call predict() or score(), the best hyperparameters will be used. In [108]: | rs\_y\_preds = rs\_clf.predict(X\_test) # Evaluate the predictions using our custom function rs\_metrics = evaluate\_preds(y\_test, rs\_y\_preds) {'accuracy': 0.951, 'precision': 0.975, 'recall': 0.951, 'f1': 0.963} 5.3 Tuning hyperparameters with GridSearchCV In [109]: # Our current grid grid Out[109]: {'n\_estimators': [100, 200, 500, 1000, 1200], 'max depth': [None, 5, 10, 20, 30], 'max\_features': ['auto', 'sqrt'], 'min\_samples\_split': [2, 4, 6], 'min\_samples\_leaf': [1, 2, 4]} GridSearchCV is a brute-force algorithm. This means it will try every single possible combination. With large datasets and many hyperparameter options, this will take a really long time. Thus, we'll reduce our hyperparameter options. In [110]: grid2 = {'n estimators': [100, 200, 500], 'max\_depth': [None], 'max\_features': ['auto', 'sqrt'], 'min samples split': [6], 'min\_samples\_leaf': [1, 2] In [111]: from sklearn.model\_selection import GridSearchCV seed = 8915np.random.seed(seed) X = heart disease shuffled.drop("target", axis=1) y = heart disease shuffled["target"] X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size=0.2) clf = RandomForestClassifier(n jobs=1) # Setup GridSearchCV gs clf = GridSearchCV( estimator=clf, param\_grid=grid2, # number of k cross-validations cv=5, verbose=2, In [112]: | gs\_clf.fit(X\_train, y\_train); Fitting 5 folds for each of 12 candidates, totalling 60 fits [CV] max depth=None, max features=auto, min samples leaf=1, min samples split=6, n estimators=100 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100, t [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100 [Parallel(n jobs=1)]: Using backend SequentialBackend with 1 concurrent workers. [Parallel(n\_jobs=1)]: Done 1 out of 1 | elapsed: 0.0s remaining: [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100, t [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100, t otal= 0.1s[CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100, t otal= 0.1s[CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=100, t [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200, t [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200, t [CV] max depth=None, max features=auto, min samples leaf=1, min samples split=6, n estimators=200 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200, t otal= 0.2s[CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200, t otal= 0.2s[CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200 [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, min\_samples\_split=6, n\_estimators=200, t [CV] max\_depth=None, max\_features=auto, min\_samples\_leaf=1, 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min\_samples\_leaf=2, min\_samples\_split=6, n\_estimators=500, t [CV] max\_depth=None, max\_features=sqrt, min\_samples\_leaf=2, min\_samples\_split=6, n\_estimators=500 [CV] max\_depth=None, max\_features=sqrt, min\_samples\_leaf=2, min\_samples\_split=6, n\_estimators=500, t [CV] max\_depth=None, max\_features=sqrt, min\_samples\_leaf=2, min\_samples\_split=6, n\_estimators=500 [CV] max\_depth=None, max\_features=sqrt, min\_samples\_leaf=2, min\_samples\_split=6, n\_estimators=500, t otal= 0.5s[Parallel(n\_jobs=1)]: Done 60 out of 60 | elapsed: 17.7s finished In [113]: gs\_clf.best\_params\_ Out[113]: {'max\_depth': None, 'max\_features': 'auto', 'min\_samples\_leaf': 2, 'min samples split': 6, 'n\_estimators': 100} In [114]: gs\_y\_preds = gs\_clf.predict(X\_test) # evaluate the predictions gs\_metrics = evaluate\_preds(y\_test, gs\_y\_preds) {'accuracy': 0.869, 'precision': 0.868, 'recall': 0.917, 'f1': 0.892} Let's now compare our different models metrics. In [115]: compare\_metrics\_df = pd.DataFrame({ "baseline": baseline\_metrics, "clf2": baseline metrics2, "random search": rs metrics, "grid search": gs\_metrics compare\_metrics\_df.plot.bar(figsize=(10,8)); 1.0 random\_search grid search 0.8 0.6 0.4 0.2 0.0 6. Save and load a trained model Two ways to save and load a trained model: 1. pickle module 2. joblib module 6.1 Saving and loading using pickle In [116]: import pickle # Save a model pickle.dump(gs clf, open("gs random forest classifier.pkl", 'wb')) In [117]: # Load a model gs clf loaded = pickle.load(open("gs random forest classifier.pkl", 'rb')) gs clf loaded Out[117]: GridSearchCV(cv=5, estimator=RandomForestClassifier(n jobs=1), param grid={'max depth': [None], 'max features': ['auto', 'sqrt'], 'min samples leaf': [1, 2], 'min samples split': [6], 'n estimators': [100, 200, 500]}, verbose=2) In [118]: # Test if it worked pickled y preds = gs clf loaded.predict(X test) evaluate\_preds(y\_test, pickled\_y\_preds); {'accuracy': 0.869, 'precision': 0.868, 'recall': 0.917, 'f1': 0.892} 6.2 Saving and loading using joblib In [119]: import joblib # Save a model joblib.dump(gs clf, filename="gs random forest classifier.jbl") Out[119]: ['gs\_random\_forest\_classifier.jbl'] In [120]: # Load a model gs clf loaded = joblib.load(filename="gs random forest classifier.jbl") gs clf loaded Out[120]: GridSearchCV(cv=5, estimator=RandomForestClassifier(n jobs=1), param\_grid={'max\_depth': [None], 'max\_features': ['auto', 'sqrt'], 'min samples leaf': [1, 2], 'min samples split': [6], 'n estimators': [100, 200, 500]}, verbose=2) In [121]: # Test if it worked joblib y preds = gs clf loaded.predict(X test) evaluate\_preds(y\_test, joblib\_y\_preds); {'accuracy': 0.869, 'precision': 0.868, 'recall': 0.917, 'f1': 0.892} 6.3 Which one should you use? According to the <u>Scikit-learn model perstistence</u> documentation: it may be better to use joblib's replacement of pickle ( dump & load ), which is more efficient on objects that carry large numpy arrays internally as is often the case for fitted scikit-learn estimators 7. Putting it all together Steps we want to do (in one cell): 1. Fill missing data 2. Convert data to numbers 3. Build a model on the data In [122]: import pandas as pd import numpy as np from sklearn.compose import ColumnTransformer from sklearn.pipeline import Pipeline from sklearn.impute import SimpleImputer from sklearn.preprocessing import OneHotEncoder # Modelling from sklearn.ensemble import RandomForestRegressor from sklearn.model\_selection import train\_test\_split, GridSearchCV seed = 689np.random.seed(seed) # Import data and drop rows with missing data car\_sales = pd.read\_csv("./car-sales-extended-missing-data.csv") car sales.dropna(subset=["Price"], inplace=True) # Define different features and transformer pipeline categorical features = ["Make", "Colour"] categorical\_transformer = Pipeline(steps=[ ("imputer", SimpleImputer(strategy="constant", fill\_value="missing")), ("onehot", OneHotEncoder(handle unknown="ignore")) ]) door feature = ["Doors"] door transformer = Pipeline(steps=[ ("imputer", SimpleImputer(strategy="constant", fill value=4)), ]) numeric\_features = ["Odometer (KM)"] numeric\_transformer = Pipeline(steps=[ ("imputer", SimpleImputer(strategy="mean")), ]) # Setup preprocessing steps (fill missing values, then convert to numbers) preprocessor = ColumnTransformer(transformers=[ ("cat", categorical transformer, categorical features), ("door", door\_transformer, door\_feature), ("num", numeric\_transformer, numeric\_features), ]) # Create a preprocessing and modelling Pipeline model = Pipeline(steps=[ ("preprocessor", preprocessor), ("model", RandomForestRegressor()) ]) # Split data X = car sales.drop("Price", axis=1) y = car sales["Price"] X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size=0.2) # Fit and score the model model.fit(X\_train, y\_train) model.score(X test, y test) Out[122]: 0.22006217452053511