Machine Learning project: A classification task on heart conditions

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Acknowledgments (Dataset creators):

- 1. Hungarian Institute of Cardiology. Budapest: Andras Janosi, M.D.
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- 3. University Hospital, Basel, Switzerland: Matthias Pfisterer, M.D.
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- 5. David W. Aha (aha '@' ics.uci.edu) (714) 856-8779



Rationale & Objective

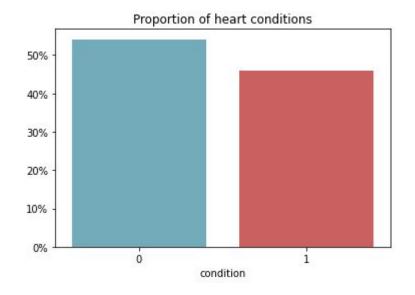
- Forming a deeper understanding of tree-based algorithms
- Developing a custom implementation of a Decision Tree (CART) and Random Forest algorithm
- Establishing a baseline and comparing it with the custom implementation
- Applying the algorithms to a relevant domain

The Dataset

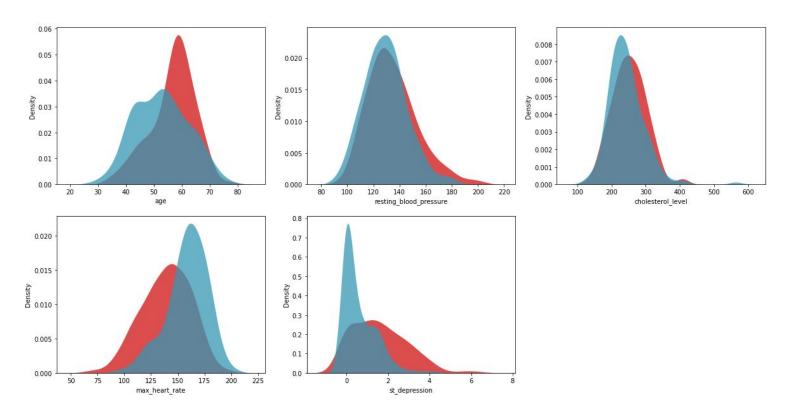
Dataset information

- Medical domain
- Cleveland Heart Disease dataset
- UCI Machine Learning Repository

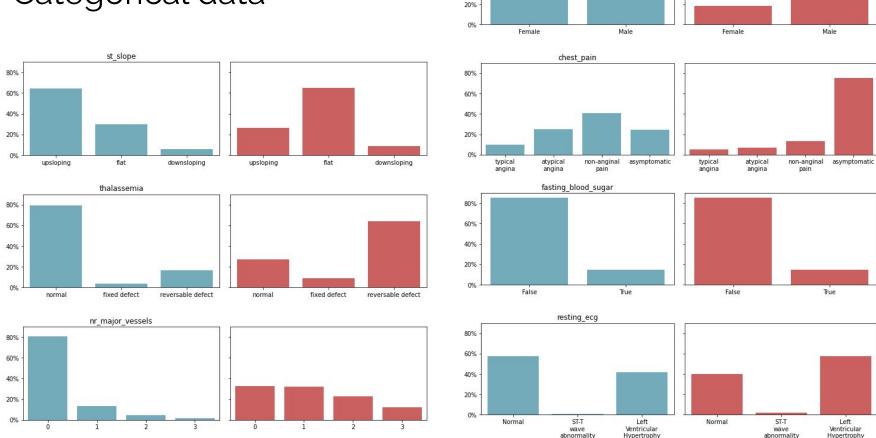
age	41
sex	2
chest_pain	4
resting_blood_pressure	50
cholesterol_level	152
fasting_blood_sugar	2
resting_ecg	3
max_heart_rate	91
exercise_induced_angina	2
st_depression	40
st_slope	3
nr_major_vessels	4
thalassemia	3
condition	2



Numerical data



Categorical data



sex

Male

pain

True

Left

Ventricular

Hypertrophy

80% 60%

40%

Data curation

Handling non-binary categorical data

- Categorical data can be problematic
- Encoding imposes an ordering that might not have been initially present
- Solution:
 - One-hot encoding

```
high_cardinality_cols = ['chest_pain', 'resting_ecg', 'st_slope', 'nr_major_vessels', 'thalassemia']
df = pd.get_dummies(df, columns=high_cardinality_cols, drop_first=True)
df
```

Data Curation - Handling missing values

- To build our models we cannot have missing values
- Solution:
 - Multiple imputation (by Chained Equations)

```
kernel = mf.KernelDataSet(df, save_all_iterations=True, random_state=42)
kernel.mice(5) # Nr of iterations
df = kernel.complete_data()

df.nr_major_vessels = df.nr_major_vessels.astype(int)
df.thalassemia = df.thalassemia.astype(int)
```

```
age sex 00 chest_pain 00 resting_blood_pressure 00 cholesterol_level 00 fasting_blood_sugar 00 resting_ecg 00 max_heart_rate 00 exercise_induced_angina 00 st_depression 00 st_slope 00 nr_major_vessels 00 chalassemia 00 condition 00 dtype: int64
```

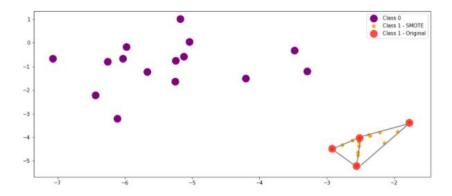
Feature Scaling

- Differing degrees of magnitude between features may affect the performance of some algorithms $X' = rac{X - \mu}{\sigma}$ $X' = rac{X - X_{min}}{X_{max} - X_{min}}$
- Solution:
 - Feature scaling
- Tree-based algorithms are unaffected by this problem, but feature scaling does not hurt them

```
cols to scale = ['age', 'resting_blood_pressure', 'cholesterol_level', 'max_heart_rate', 'st_depression']
ss = StandardScaler()
df[cols to scale] = ss.fit transform(df[cols to scale])
```

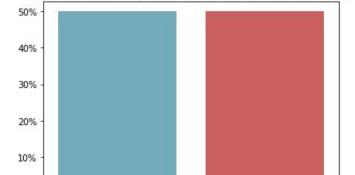
Train-Test split + SMOTE

- Unbalanced datasets are common in the medical domain
- An over-represented majority class may create bias when building a model
- Solution:
 - Oversampling (Synthesizing minority class examples)
 - Synthetic Minority Oversampling Technique (SMOTE)



SMOTE

```
oversample = SMOTE(random_state=42)
X_train_SMOTE, y_train_SMOTE = oversample.fit_resample(X_train, y_train)
oversampled_df = X_train_SMOTE.assign(condition = y_train_SMOTE)
condition_proportion(y_train_SMOTE, "Proportion of heart conditions (oversampled training data)")
print("Shape before SMOTE: " + str(X_train.shape))
print("Shape after SMOTE: " + str(X_train_SMOTE.shape))
```



condition

Proportion of heart conditions (oversampled training data)

CART

Development of an algorithm:

CART

- Classification and Regression Trees
- Builds binary trees
- Uses a greedy approach (recursive binary splitting) to create new nodes

```
def __init__(self, *,
             criterion = 'gini',
            max_depth = None,
            min_impurity_decrease = 0.0,
            min impurity split = None,
            min_samples_split = 2,
            max features = None,
            min_samples_leaf = 1):
    self.criterion = criterion
    self.max depth = max depth
   self.min_impurity_decrease = min_impurity decrease
    self.min impurity split = min impurity split
    self.min_samples_split = min_samples_split
    self.max features = max features
    self.min_samples_leaf = min_samples_leaf
    self.n classes = 0
    self.root = None
```

CART - The 'Partition' class

- Represents a single node in the tree
- Holds information about:
 - Left and Right child nodes
 - Feature and threshold used for splitting
 - Prediction (majority class)
 - Impurity

```
class Partition:
   def __init__(self,
                 split_feature,
                 split_value,
                 impurity_part,
                 impurity delta,
                 impurity_feature_example,
                 prediction.
                 counter):
        self.split feature = split feature
        self.split_value = split_value
        self.impurity_part = impurity_part
        self.impurity_delta = impurity_delta
        self.impurity_feature_example = impurity_feature_example
        self.prediction = prediction
        self.counter = counter
        self.left_part = None
        self.right_part = None
```

CART - Building the tree ('build_tree')

- Tree is built recursively from the top-down
- Split candidate that maximizes the reduction in impurity is selected at each step

```
split_feature, split_value, impurity_part, impurity_delta, impurity_feature_example = self.find_split(X, y)
curr part = Partition(split_feature, split_value, impurity part, impurity_delta, impurity_feature example, prediction, counter)
if(split feature is not None):
    # Temporarely create a merged df in order to filter features and classes together
   merged_df = np.append(X, np.vstack(y), axis=1)
    merged_df_left = merged_df[merged_df[:,split_feature] <= split_value]</pre>
    merged df right = merged df[merged df[:.split feature] > split value]
    curr part.left part = self.build tree(
        merged df left[:, :-1],
        merged_df_left[:, -1],
        depth) # Left
    curr part.right part = self.build tree(
        merged df right[:, :-1],
        merged_df_right[:, -1],
        depth) # Right
return curr part
```

CART - Stopping condition

- At a certain point nodes need to be turned into leaves
 - The partition is pure
 - No possible split can be imposed
 - The constraint imposed by an hyperparameter is broken
 - Maximum depth (`max_depth`)
 - Minimum reduction in impurity (`min_impurity_decrease`)
 - Minimum impurity (`min_impurity_split`)
 - Size of partition (`min_samples_split')
 - Size of child nodes (`min_samples_leaf')

CART - Searching a split candidate (`find_split`)

Nodes are analyzed in a feature-by-feature fashion

```
# Loop through all features
for feature in sampled_features:
    # Skip ahead if the feature has only one value
    if len(np.unique(X[:,feature])) == 1:
        continue

# Sort the examples in increasing order for the selected feature
    # Consider the midpoint between two (different) adjecent values as a possible split point
    feature_sorted, y_sorted = zip(*sorted(zip(X[:,feature], y), key=itemgetter(0)))

# Go through the sorted feature while keeping track of class occurences on each side (/partition)
    class_occ_left = Counter()
    for i in range(self.n_classes):
        class_occ_left[i] = 0 # Left partition starts as empty (all class counters are set to 0)

class_occ_right = class_occ_part.copy() # Same as occurences of each class in the partition
```

CART - Searching a split candidate (`find_split`)

- For every feature with `k` different values, we evaluate `k-1` split thresholds.
- Left & Right impurities are computed for each candidate

```
for example in range(1, size part):
    example class = v sorted[example-1]
   # Increment the example class on the left, decrement it on the right
   class_occ_left[example_class] += 1
    class occ right[example class] -= 1
   # Skip ahead if two adjacent values are equal
   if feature sorted[example] == feature sorted[example - 1]:
        continue
    size_left = example
   size right = size part - example
   # Skip if the threshold does not respect the min_samples_leaf parameter
   if(size_left < self.min_samples_leaf or size_right < self.min_samples_leaf):</pre>
        continue
    # Calculate the impurity of each side
    impurity left = self.calc impurity(class occ left, size left)
   impurity_right = self.calc_impurity(class_occ_right, size_right)
```

CART - Searching a split candidate (`find_split`)

- Eventually, the split candidate that maximizes the reduction in impurity from the current partition is returned
- Split candidate = Feature + threshold

```
# Weighted sum of impurities (with selected feature at current example)
curr_impurity_feature_example = ((size_left/size_part) * impurity_left) + ((size_right/size_part) * impurity_right)

# Reduction in impurity with current split
curr_impurity_delta = impurity_part - curr_impurity_feature_example

if(self.min_impurity_decrease and curr_impurity_delta < self.min_impurity_decrease):
    continue

if(curr_impurity_delta > impurity_delta):
    split_feature = feature
    split_value = (feature_sorted[example] + feature_sorted[example-1]) / 2
    impurity_delta = curr_impurity_delta
    impurity_feature_example = curr_impurity_feature_example
```

CART - Split strategy (`calc_impurity`)

- Two metrics to evaluate the impurity of a node
 - Gini Index & Information Gain (Entropy):

$$Gini(D) = 1 - \sum_{i=1}^{C} (p_i)^2$$
 $Entropy(D) = -\sum_{i=1}^{C} p_i log_2(p_i)$ $Gini_A(D) = \frac{size(D_1)}{size(D)} Gini(D_1) + \frac{size(D_2)}{size(D)} Gini(D_2)$ $Entropy_A(D) = \frac{size(D_1)}{size(D)} Entropy(D_1) + \frac{size(D_2)}{size(D)} Entropy(D_2)$ $\Delta Gini(A) = Gini(D) - Gini_A(D)$ $Gain(A) = Entropy(D) - Entropy_A(D)$

CART - Pruning

- Trees are low-bias, high-variance models
- Pruning helps the model to better generalize to unseen data
 - o Pre-pruning:
 - Stops the creation of some branches when the model is being built.
 - Controlled by parameters such as: `max_depth`, `min_impurity_decrease`,
 `min_impurity_split`, `min_samples_split` and `min_samples_leaf`
 - Post-pruning:
 - Removes sub-trees after the model has been built
 - Cost complexity pruning

CART - Predicting a class ('predict')

- Traverse the tree from root to leaf
- Use `split_feature` and `split_value` to decide whether to go left of right
- Use the `prediction` value at leaf to predict the class label

Development of an algorithm:

Random Forest

Random Forest

- Uses the CART implementation to perform ensemble learning
- Addresses the high-variance of trees with feature randomness and

bagging

```
def fit(self,
        Х,
       y):
   X, y = self.data_to_numpy(X, y)
    # Flush old forest
    if len(self.forest) > 0:
        self.forest = []
    self.n_classes = len(np.unique(y))
    for i in range(self.n_estimators):
        curr_tree = CustomDecisionTreeClassifier(criterion = self.criterion,
                                                 max depth = self.max depth,
                                                 min_impurity_decrease = self.min_impurity_decrease,
                                                 min impurity split = self.min impurity split,
                                                 min_samples_split = self.min_samples_split,
                                                  max_features = self.max_features,
                                                  min samples leaf = self.min samples leaf)
       if self.bootstrap:
            curr X, curr y = self.bootstrap sample(X, y, self.max samples)
            curr_tree.fit(curr_X, curr_y)
        else:
            curr_tree.fit(X, y)
        self.forest.append(curr_tree)
```

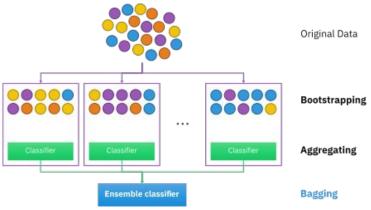
RF - Feature Randomness

- The search for a split candidate is limited to a random subset of features
- Feature sampling is done at the node level, NOT at the tree level

```
if(self.max_features == 'sqrt'):
    n=round(math.sqrt(X_cols))
elif(self.max_features == 'log2'):
    n=round(math.log2(X_cols))
elif((self.max_features is not None) and (self.max_features <= X_cols)):
    n=self.max_features
sampled_features = sorted(random.sample(range(0, X_cols), n))</pre>
```

RF - Bagging ('bootstrap_sample')

- Bagging = Bootstrap Aggregation
- Trees in the forest are built on slightly different datasets
- Obtained by performing sampling with replacement on the original data



RF - Predicting a class ('predict')

- Run the prediction on all trees in the forest
- Majority voting across all trees determines the prediction of the ensemble

Building the models

Preparation

Scoring function

Hyperparameter tuning function

Establishing a baseline (Sklearn implementation)

```
sklearn tree grid = {
    'criterion': ['gini', 'entropy'],
    'max depth': range(1.25).
    'min impurity decrease': [0.0, 0.1, 0.2],
    'min_samples_leaf': range(1,10),
    'min_samples_split': range(2,10)
sklearn tree params = get best estimator( param grid = sklearn tree grid,
                                          _estimator = DecisionTreeClassifier(random_state=42),
                                         X = X_train_SMOTE,
                                          y = y_train_SMOTE.to_numpy().flatten())
start time = time.time()
sklearn tree = DecisionTreeClassifier(**sklearn tree params, random state=42)
sklearn tree.fit(X train SMOTE, y train SMOTE.to numpy().flatten())
end time = time.time() - start time
score model(model = sklearn tree,
            X = X \text{ test,}
            y = y_test,
            library_name = 'Sklearn',
            algorithm_name = 'CART',
            fit time = end time)
```

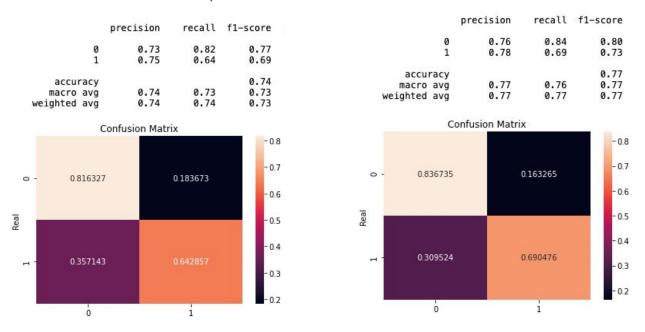
```
sklearn_forest_grid = {
    'max features': range(4,21).
    'n_estimators': [100, 200, 300, 400]
sklearn forest params = get best estimator( param grid = sklearn forest grid,
                                           estimator = RandomForestClassifier(random state=42),
                                           X = X train SMOTE,
                                           y = y_train_SMOTE.to_numpy().flatten(),
                                           _scoring='roc_auc')
start time = time.time()
sklearn forest = RandomForestClassifier(**sklearn forest params, random state=42)
sklearn forest.fit(X train SMOTE, v train SMOTE.to numpy().flatten())
end time = time.time() - start time
score model(model = sklearn forest,
            X = X_{test}
            y = y test,
            library_name = 'Sklearn',
            algorithm_name = 'Random Forest',
            fit time = end time)
```

Modelling using our custom implementations

Results

Decision Tree Classifier

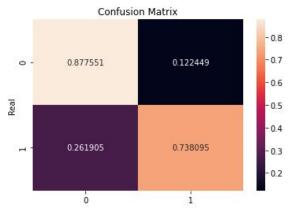
Sklearn vs Custom implementation



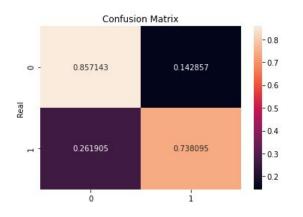
Random Forest Classifier

Sklearn vs Custom implementation

	precision	recall	f1-score
0	0.80	0.88	0.83
1	0.84	0.74	0.78
accuracy			0.81
macro avg	0.82	0.81	0.81
weighted avg	0.82	0.81	0.81

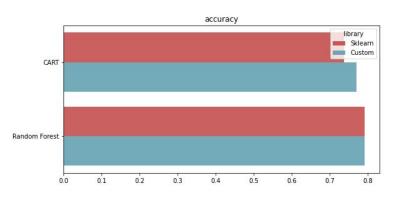


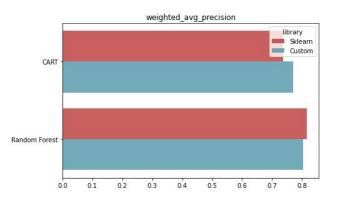
	precision	recall	f1-score
0	0.79	0.86	0.82
1	0.82	0.74	0.78
accuracy			0.80
macro avg	0.80	0.80	0.80
weighted avg	0.80	0.80	0.80

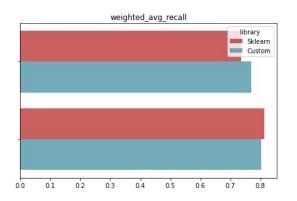


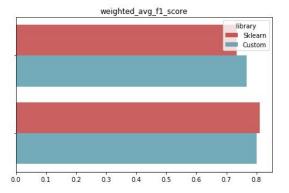
Results

 Comparable classification results across the board



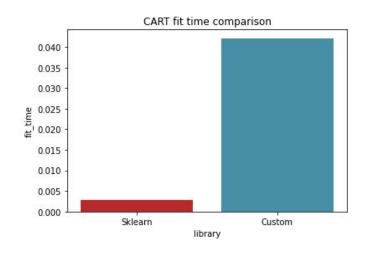


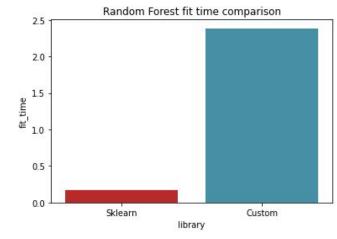




Results

 Execution time needed to build the model is higher than what is found in the Sklearn implementation





90 <u> </u>	library	algorithm	fit_time
0	Sklearn	CART	0.002825
1	Sklearn	Random Forest	0.172241
2	Custom	CART	0.042129
3	Custom	Random Forest	2.386401

Extra - CCP

Extra - Pruning with CCP

- Compute the effective alpha for all non-leaf nodes in the tree
- Nodes with the smallest alpha are the "weakest links"
 - They create trees that are redundant
 - The sub-trees they create will be pruned first

$$lpha_{effective}(t) = rac{R(t) - R(T_t)}{|T| - 1} \qquad \qquad R(T_t) = \sum_{i=1}^L R(t_i)$$

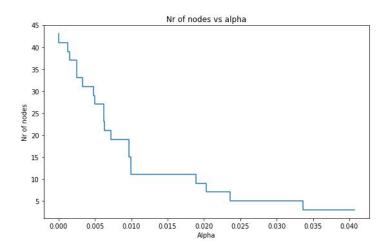
Extra - Pruning with CCP

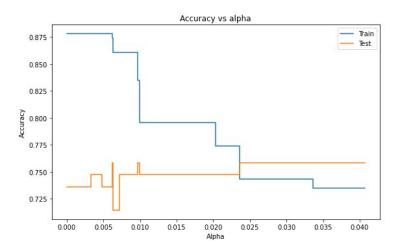
```
path = DecisionTreeClassifier(**sklearn_tree_params, random_state=42).cost_complexity_pruning_path(X_train_SMOTE, y_train_SMOTE)

# CCP alphas of subtrees + Sum of impurities of each subtree leaves
ccp_alphas, impurities = path.ccp_alphas, path.impurities

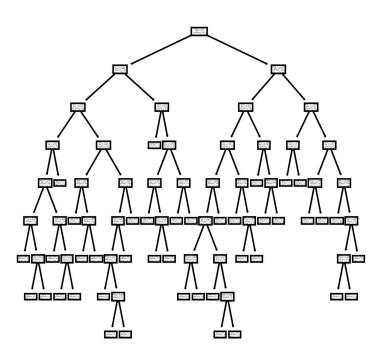
# Test the decision tree with all CCP alphas
clfs = []
for ccp_alpha in ccp_alphas:
    clf = DecisionTreeClassifier(**sklearn_tree_params, ccp_alpha=ccp_alpha, random_state=42)
    clf.fit(X_train_SMOTE, y_train_SMOTE)
    clfs.append(clf)

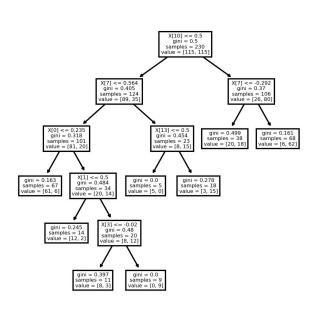
clfs = clfs[:-1]
ccp_alphas = ccp_alphas[:-1]
```





Extra - Pruning with CCP





Conclusions &

Future Work

What did we achieve?

- Pre-processed our dataset
- Developed a custom implementation of CART and RF
- Established a baseline with the Sklearn implementation of said algorithms
- Compared the results between the two version of the algorithm
- Experimented with CCP on the Decision Tree

What could we do next?

- Look at some optimization techniques to improve fit times
- Implement CCP in our custom algorithm
- Develop a tree-based regressor

Thank you!