Atrial Fibrillation Classification

The goal of this exercise is to train different conventional classification models to discriminate between atrial fibrillation and normal sinus rhythm from a sequence of interbeat intervals. We use interbeat intervals extracted from the Long Term AF Database (https://physionet.org/content/ltafdb/1.0.0/).

We will train the following models on windows of interbeat intervals:

- Decision tree
- Support vector machine (SVM)
- Naive Bayes

The models will be trained on simple features derived from each window of interbeat intervals.

First, we import all the required packages, define global constants, and seed the random number generators to obtain reproducible results.

In [1]:
```
%matplotlib widget


import operator
import pathlib
import warnings
import IPython.display
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import sklearn.metrics
import sklearn.model_selection
from sklearn.pipeline import make_pipeline
from sklearn.preprocessing import StandardScaler
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import f_regression
from sklearn.feature_selection import SelectFromModel
from sklearn.linear_model import Lasso
import seaborn as sns


DATA_FILE = pathlib.Path('../data/ltafdb_intervals.npz')
LOG_DIRECTORY = pathlib.Path('../logs/af_classification')
```

Then, we load the windows of interbeat intervals and the corresponding labels. We also load the record identifiers. They will help to avoid using intervals from the same record for both training and testing.

In [2]:
```
def load_data():
    with np.load(DATA_FILE) as data:
```

```
        intervals = data['intervals']
        labels = data['labels']
        identifiers = data['identifiers']
    return intervals, labels, identifiers


intervals, labels, identifiers = load_data()
targets = (labels == 'atrial_fibrillation').astype('float32')[:, None]
window_size = intervals.shape[1]

print(f'Number of windows: {intervals.shape[0]}')
print(f'Window size: {window_size}')
print(f'Window labels: {set(labels)}')
```

```
Number of windows: 25064
Window size: 32
Window labels: {'atrial_fibrillation', 'normal_sinus_rhythm'}
```

Here are a few examples of windows of interbeat intervals.

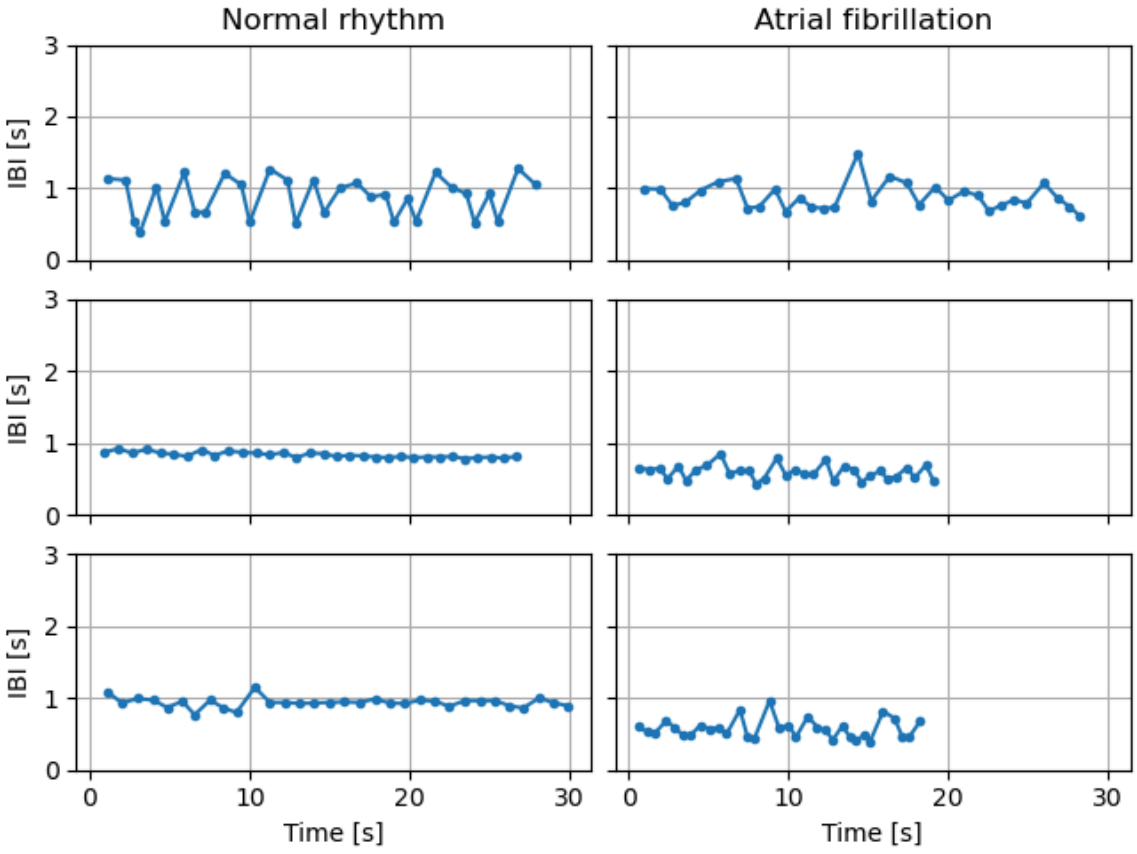
In [3]:
```
def plot_interval_examples(intervals, targets, n_examples=3):
    normal_indices = np.random.choice(np.flatnonzero(targets == 0.0), n_examples
    af_indices = np.random.choice(np.flatnonzero(targets == 1.0), n_examples, re

    def plot_intervals(ax, index):
        ax.plot(np.cumsum(intervals[index]), intervals[index], '.-')
        ax.grid(True)

    fig, axes = plt.subplots(n_examples, 2, sharex='all', sharey='all', squeeze=
    for i in range(n_examples):
        plot_intervals(axes[i, 0], normal_indices[i])
        plot_intervals(axes[i, 1], af_indices[i])
    plt.setp(axes, ylim=(0.0, 3.0))
    plt.setp(axes[-1, :], xlabel='Time [s]')
    plt.setp(axes[:, 0], ylabel='IBI [s]')
    axes[0, 0].set_title('Normal rhythm')
    axes[0, 1].set_title('Atrial fibrillation')


plot_interval_examples(intervals, targets)
```

Figure



The next step is to split the dataset into subsets for training, validation, and testing stratified by labels.

In [4]:
```
def split_data(identifiers, intervals, targets):
    splitter = sklearn.model_selection.StratifiedGroupKFold(n_splits=5)
    indices = list(map(operator.itemgetter(1), splitter.split(intervals, targets
    i_train = np.hstack(indices[:-2])
    i_val = indices[-2]
    i_test = indices[-1]

    assert not (set(identifiers[i_train]) & set(identifiers[i_val]))
    assert not (set(identifiers[i_train]) & set(identifiers[i_test]))
    assert not (set(identifiers[i_val]) & set(identifiers[i_test]))
    assert set(identifiers[i_train]) | set(identifiers[i_val]) | set(identifiers

    return i_train, i_val, i_test


i_train, i_val, i_test = split_data(identifiers, intervals, targets)


def build_summary(subsets, targets):
    data = []
    for subset, y in zip(subsets, targets):
        data.append({
            'subset': subset,
            'total_count': y.size,
            'normal_count': np.sum(y == 0.0),
            'af_count': np.sum(y == 1.0),
            'normal_proportion': np.mean(y == 0.0),
            'af_proportion': np.mean(y == 1.0),
```

```
        })
    return pd.DataFrame(data)


IPython.display.display(build_summary(('training', 'validation', 'testing'), (ta
```

	subset	total_count	normal_count	af_count	normal_proportion	af_proportion
0	training	15000	6919	8081	0.461267	0.538733
1	validation	4964	2365	2599	0.476430	0.523570
2	testing	5100	2311	2789	0.453137	0.546863

To better understand the dataset, we extract two features from each window of interbeat intervals: the mean and the standard deviation. We then plot these two features for the two classes.

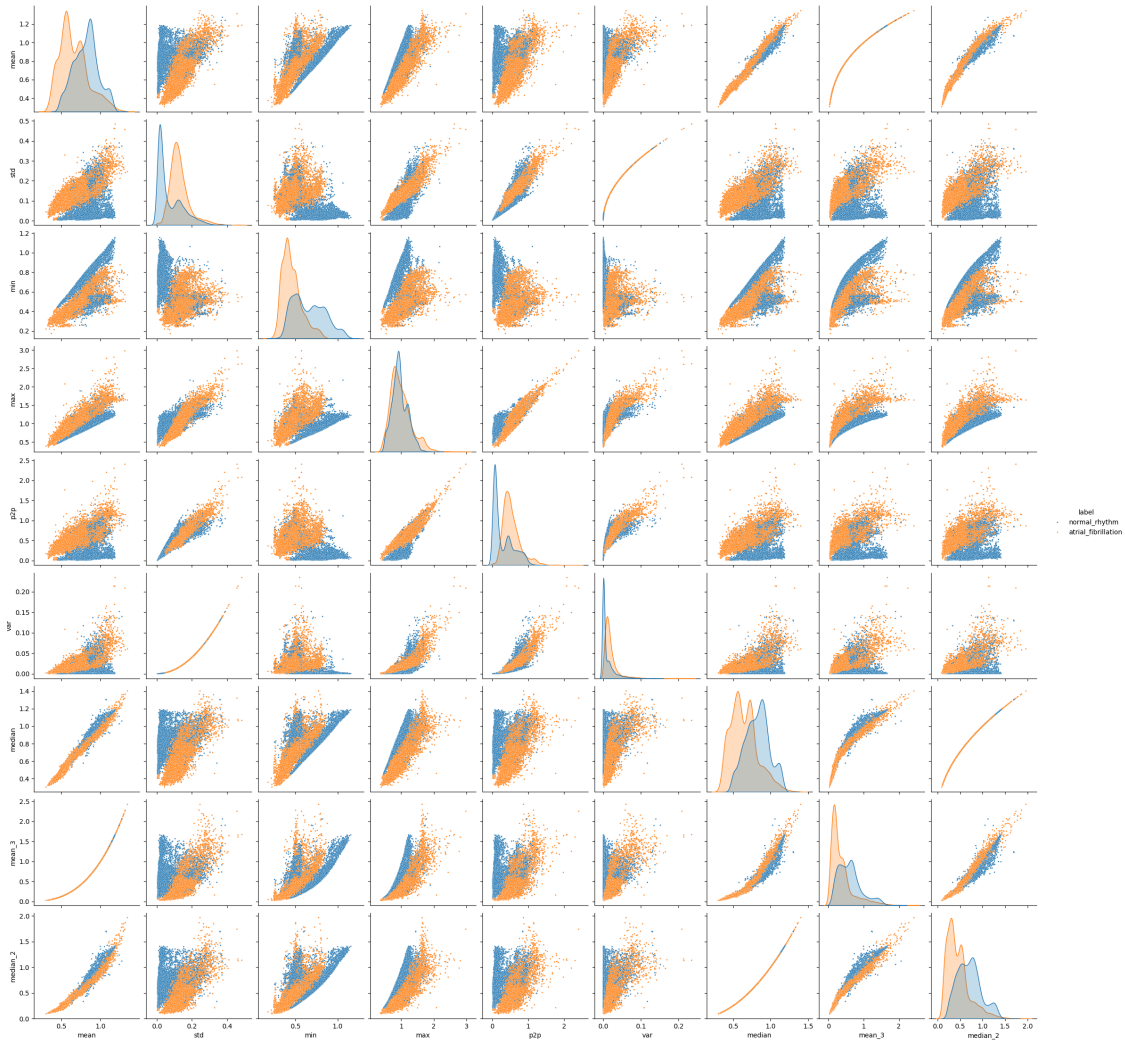
In [5]:
```
f_mean = np.mean(intervals, axis=1)
f_std = np.std(intervals, axis=1)
f_min = np.min(intervals, axis=1)
f_max = np.max(intervals, axis=1)
f_median = np.median(intervals, axis=1)
features = pd.DataFrame({
    'mean': f_mean,
    'std': f_std,
    'min': f_min,
    'max': f_max,
    'p2p': f_max - f_min,
    'var': np.power(f_std, 2),
    'median': f_median,
    'mean_3': np.power(f_mean, 3),
    'median_2': np.power(f_median, 2),

})


def plot_features(f, y):
    data = f.copy()
    data['label'] = y.ravel()
    data['label'] = data['label'].map({0.0: 'normal_rhythm', 1.0: 'atrial_fibril
    sns.pairplot(data, hue='label', plot_kws={'s': 4})


plot_features(features.iloc[i_train], targets[i_train])
```

Figure



It is also possible to select the most relevant features using various methods. Here, we define implement three fature selection techniques: lasso, univariate, hybrid.

In [6]:
```
class FeatureSelector:

    def __init__(self, method, numbers):
        self.method = method.lower()
        self.numbers = numbers

    def apply(self, features, targets):
        features_names = [column for column in features.columns if column not in
        features_selection = features.copy()
        features_selection.insert(0, 'reference', targets)
        features_selection = features_selection.dropna(axis=0, how='any', inplac
        ranks = self.rank_features(features_selection[features_names],
                                   features_selection['reference'],
                                   self.method)
        del features_selection
        return self.select_features(ranks, self.numbers)

    @staticmethod
    def select_features(ranks, feature_num):
        ranks.sort_values(by='ranks', axis=0, ascending=False, inplace=True,
                          kind='quicksort', ignore_index=True)
        return ranks['feature_names'].iloc[: feature_num].tolist()
```

```
    @staticmethod
    def rank_features(features, reference, method):
        def univariate_selection(data, ref):
            selector = SelectKBest(f_regression, k="all")
            scores = selector.fit(data, ref).scores_
            return scores / np.nansum(scores)

        def lasso_selection(data, ref):
            alphas = np.arange(0.01, 0.3, 0.01)
            coefficients = np.empty([len(alphas), data.shape[1]])
            for row, alpha in enumerate(alphas):
                selector = SelectFromModel(Lasso(alpha=alpha), prefit=False)
                coefficients[row, :] = selector.fit(data, ref).estimator_.coef_
            coefficients = np.abs(coefficients)
            real_ranks = np.nansum(coefficients, axis=0)
            return real_ranks / np.nansum(real_ranks)

        if method == 'lasso':
            ranks = lasso_selection(features, reference)
        elif method == 'univariate':
            ranks = univariate_selection(features, reference)
        elif method == 'hybrid':
            rank_lasso = lasso_selection(features, reference)
            rank_univariate = univariate_selection(features, reference)
            rank_combined = rank_lasso + rank_univariate
            ranks = rank_combined / np.nansum(rank_combined)
        else:
            raise TypeError("Feature selection method is not supported")
        return pd.DataFrame({
            'feature_names': features.columns,
            'ranks': ranks,
        })

feature_selection_method = 'lasso'
feature_selection_numbers = 5
features_list = FeatureSelector(feature_selection_method, feature_selection_numb
print(f"Selected features:{features_list}")
```

```
Selected features:['median_2', 'p2p', 'mean', 'std', 'min']
```

To classify atrial fibrillation and normal rhythm, we define the following models: Decision Tree, SVM, and Naive Bayes. To this end, we define a model builder class which provides a method to build the models.

In [7]:
```
class ModelBuilder:

    def __init__(self, config):
        self.config = config['model']

    def apply(self):
        return eval(f"self._build_{self.config['name']}()")

    def _build_tree(self, max_depth=5):
        if 'max_depth' in self.config.keys():
            max_depth = self.config['max_depth']
        return make_pipeline(
            StandardScaler(),
            DecisionTreeClassifier(max_depth=max_depth))
```

```
    def _build_svm(self, kernel='rbf', gamma='scale', regularization=1):
        if 'kernel' in self.config.keys():
            kernel = self.config['kernel']
        if 'gamma' in self.config.keys():
            gamma = self.config['gamma']
        if 'regularization' in self.config.keys():
            regularization = self.config['regularization']
        return make_pipeline(
            StandardScaler(),
            SVC(kernel=kernel, gamma=gamma, C=regularization,
                probability=True))

    def _build_bayes(self, var_smoothing=1e-09):
        if 'var_smoothing' in self.config.keys():
            var_smoothing = self.config['var_smoothing']
        return make_pipeline(
            StandardScaler(),
            GaussianNB(var_smoothing=var_smoothing))
```

Now, we define a class for the training of the models.

In [8]:
```
class ModelTrainer:

    def __init__(self, config):
        self.config = config['feature']

    def apply(self, model, features, reference, i_train):
        features_list = self._get_features_list(list(features.columns))
        features_train = features.copy()
        features_train.insert(0, 'reference', reference)
        features_train = features_train.iloc[i_train].copy()
        features_train = features_train.dropna(axis=0, how='any', inplace=False,
                                               subset=features_list + ['reference'
        return model.fit(
            features_train[features_list].values, features_train['reference'].va

    def _get_features_list(self, current_features):
        if 'all' in self.config['list']:
            features_list = [feature for feature in current_features
                             if feature not in self.config['exclusion'] + ['refe
        else:
            features_list = [feature for feature in
                             self.config['list']
                             if feature in current_features and feature not
                             in self.config['exclusion'] + ['reference']]
        return features_list
```

We also define a class to apply the trained models on the test data.

In [9]:
```
class ModelTester:

    def __init__(self, config):
        self.config = config['feature']

    def apply(self, model, features):
        features_list = self._get_features_list(list(features.columns))
        inx = np.logical_not(
            np.sum(np.isnan(features[features_list]), 1).astype(bool))
```

```
        detections = np.zeros_like(inx)
        detections[:] = np.nan
        detections[inx] = model.predict(features[features_list].values[inx])
        return pd.DataFrame({'prediction': detections})

    def _get_features_list(self, current_features):
        if 'all' in self.config['list']:
            features_list = [feature for feature in current_features
                             if feature not in self.config['exclusion'] + ['refe
        else:
            features_list = [feature for feature in self.config['list']
                             if feature in current_features and feature not
                             in self.config['exclusion'] + ['reference']]
        return features_list
```

In order to evaluate the results of the models, we define an Evaluator class as follows:

In [10]:
```
class Evaluator:

    def __init__(self):
        pass

    def apply(self, result, reference, i_train, i_test):
        result_bool = result.astype(bool)
        reference_bool = reference.astype(bool)
        metrics = []
        for subset, indices in (('train', i_train), ('test', i_test)):
            metrics.append({
                'subset': subset,
                **self.compute_performance_parameters(result_bool[indices], refe
            })
        return pd.DataFrame(metrics)

    @staticmethod
    def compute_performance_parameters(result, reference):
        def zero_division(a, b):
            if b != 0:
                return np.round(a / b, 2)
            else:
                return 0.00
        result_not = np.logical_not(result)
        reference_not = np.logical_not(reference)
        tp = np.sum(result[reference])
        fn = np.sum(result_not[reference])
        tn = np.sum(result_not[reference_not])
        fp = np.sum(result[reference_not])
        return {
            'tp': tp,
            'fn': fn,
            'tn': tn,
            'fp': fp,
            'sensitivity': zero_division(tp, tp + fn),
            'specificity': zero_division(tn, tn + fp),
            'accuracy': zero_division(tp + tn, tp + tn + fn + fp),
            'precision': zero_division(tp, tp + fp)
        }
```

The final step before training and evaluating the models is to define the configurations of the different models.

We will train the models with the following configurations:

- Decision tree without features selection
  - Using all the features
  - max_depth: 3
- Decision tree with features selection
  - Using the selected features
  - max_depth: 3
- SVM without features selection
  - Using all the features
  - kernel: rbf
  - gamma: scale
  - regularization: 1
- SVM with features selection
  - Using the selected features
  - kernel: rbf
  - gamma: scale
  - regularization: 1
- Naive Bayes without features selection
  - Using all the features
  - var_smoothing: 1e-09
- Naive Bayes with features selection
  - Using the selected features
  - var_smoothing: 1e-09

In [11]:
```
exclude_features = []
configs = {
    'decision_tree_all_features': {
        'feature': {
            'list': 'all',
            'exclusion': exclude_features,
            'selection_method': [],
            'selection_numbers': np.nan,
        },
        'model': {
            'name': 'tree',
            'max_depth': 15,
        },
    },
    'decision_tree_selected_features': {
        'feature': {
            'list': features_list,
            'exclusion': exclude_features,
            'selection_method': feature_selection_method,
            'selection_numbers': feature_selection_numbers,
        },
        'model': {
```

```
            'name': 'tree',
            'max_depth': 15,
        },
    },
    'svm_all_features': {
        'feature': {
            'list': 'all',
            'exclusion': exclude_features,
            'selection_method': [],
            'selection_numbers': np.nan,
        },
        'model': {
            'name': 'svm',
            'kernel': 'rbf',
            'gamma': 'scale',
            'regularization': 1,
        },
    },
    'svm_selected_features': {
        'feature': {
            'list': features_list,
            'exclusion': exclude_features,
            'selection_method': feature_selection_method,
            'selection_numbers': feature_selection_numbers,
        },
        'model': {
            'name': 'svm',
            'kernel': 'rbf',
            'gamma': 'scale',
            'regularization': 1,
        },
    },
    'bayes_all_features': {
        'feature': {
            'list': 'all',
            'exclusion': exclude_features,
            'selection_method': [],
            'selection_numbers': np.nan,
        },
        'model': {
            'name': 'bayes',
            'var_smoothing': 1e-09,
        },
    },
    'bayes_selected_features': {
        'feature': {
            'list': features_list,
            'exclusion': exclude_features,
            'selection_method': feature_selection_method,
            'selection_numbers': feature_selection_numbers,
        },
        'model': {
            'name': 'bayes',
            'var_smoothing': 1e-09,
        },
    },
}
```

Now, we are ready to train the models.

In [16]:
```
models = {}
for name, config in configs.items():
    print(f' * Training {name!r} model')
    model = ModelBuilder(config).apply()
    models[name] = ModelTrainer(config).apply(model, features, targets, i_train)
```

```
* Training 'decision_tree_all_features' model
* Training 'decision_tree_selected_features' model
* Training 'svm_all_features' model
* Training 'svm_selected_features' model
* Training 'bayes_all_features' model
* Training 'bayes_selected_features' model
```

Here, we evaluate the trained models on the features.

In [17]:
```
output = {}
for name, config in configs.items():
    print(f' * Applying {name!r} model')
    output[name] = ModelTester(config).apply(models[name], features)
```

```
* Applying 'decision_tree_all_features' model
* Applying 'decision_tree_selected_features' model
* Applying 'svm_all_features' model
* Applying 'svm_selected_features' model
* Applying 'bayes_all_features' model
* Applying 'bayes_selected_features' model
```

Now that all models are trained we can evaluate them on the subsets for training, validation, and testing.

In [14]:
```
metrics = []
for name, config in configs.items():
    print(f'Evaluating {name!r} model')
    performance = Evaluator().apply(output[name]['prediction'].values, targets[:
    performance.insert(0, 'model', name)
    metrics.append(performance)
print("\n*** Performance report ***\n")
metrics = pd.concat(metrics, axis=0, ignore_index=True)
metrics = metrics.set_index(['model', 'subset'])
index = metrics.index.get_level_values(0).unique()
columns = pd.MultiIndex.from_product([metrics.columns, metrics.index.get_level_v
metrics = metrics.unstack().reindex(index=index, columns=columns)
IPython.display.display(metrics)
```

```
Evaluating 'decision_tree_all_features' model
Evaluating 'decision_tree_selected_features' model
Evaluating 'svm_all_features' model
Evaluating 'svm_selected_features' model
Evaluating 'bayes_all_features' model
Evaluating 'bayes_selected_features' model

*** Performance report ***
```

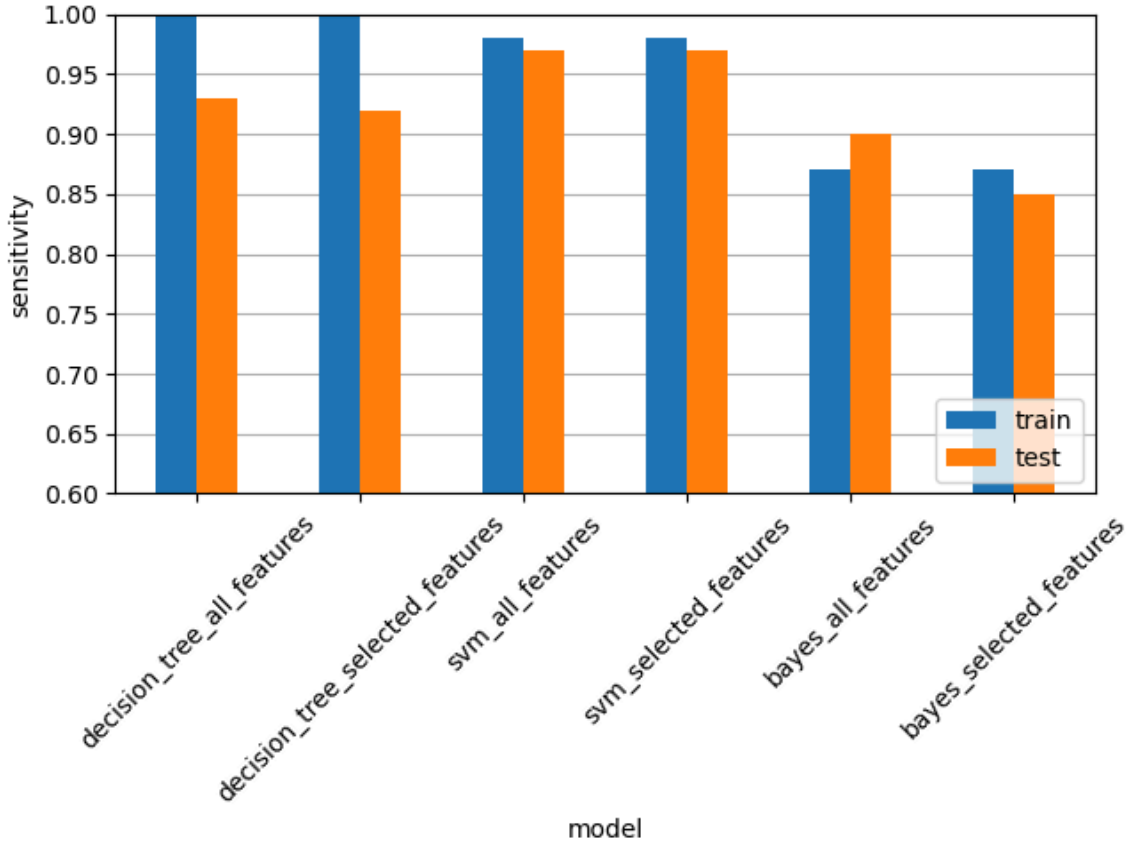
	tp		fn		tn		fp		sensitivit	
subset	train	test	train	test	train	test	train	test	train	tes
model										
decision_tree_all_features	8041	2595	40	194	6807	2220	112	91	1.00	0.9
decision_tree_selected_features	8055	2578	26	211	6813	2207	106	104	1.00	0.9
svm_all_features	7888	2709	193	80	6282	2227	637	84	0.98	0.9
svm_selected_features	7890	2715	191	74	6290	2235	629	76	0.98	0.9
bayes_all_features	7064	2501	1017	288	4826	1948	2093	363	0.87	0.9
bayes_selected_features	7009	2380	1072	409	4792	2002	2127	309	0.87	0.8

We can also plot the different metrics.

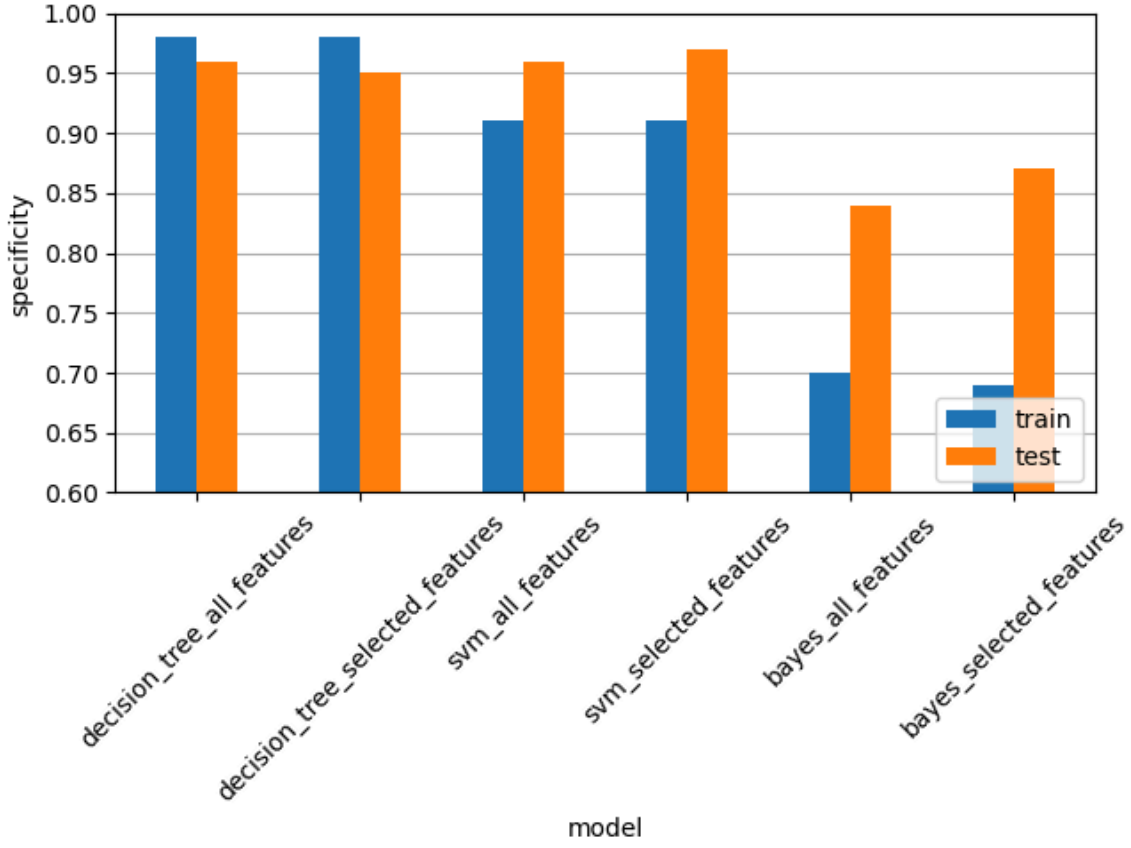
In [15]:
```
def plot_metrics(data):
    for metric in data.columns.get_level_values(0).unique():
        if metric in ['count', 'tp', 'tn', 'fp', 'fn']:
            continue
        df = data[metric]
        plt.figure(constrained_layout=True)
        plt.gca().set_axisbelow(True)
        df.plot(kind='bar', ylabel=metric, ax=plt.gca())
        plt.grid(axis='y')
        plt.ylim(0.6, 1.0)
        plt.legend(loc='lower right')
        plt.gca().xaxis.set_tick_params(rotation=45)


plot_metrics(metrics)
```

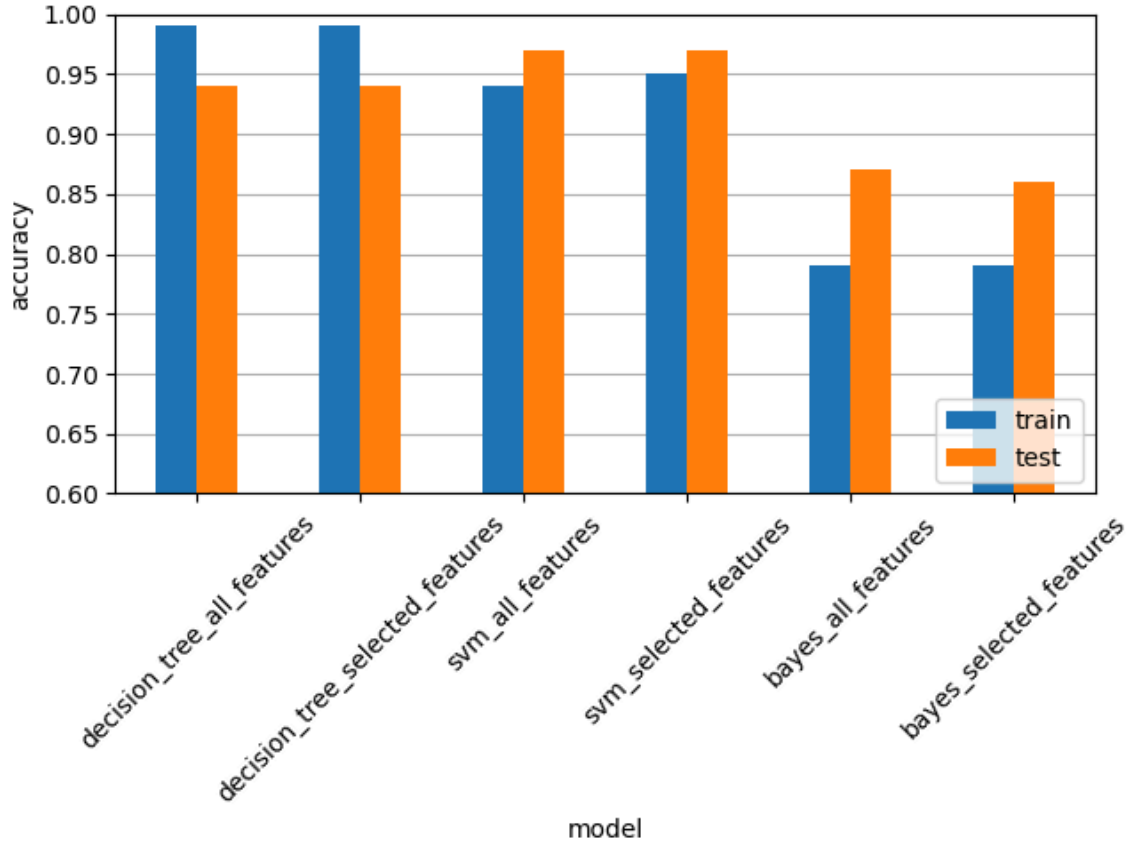
Figure



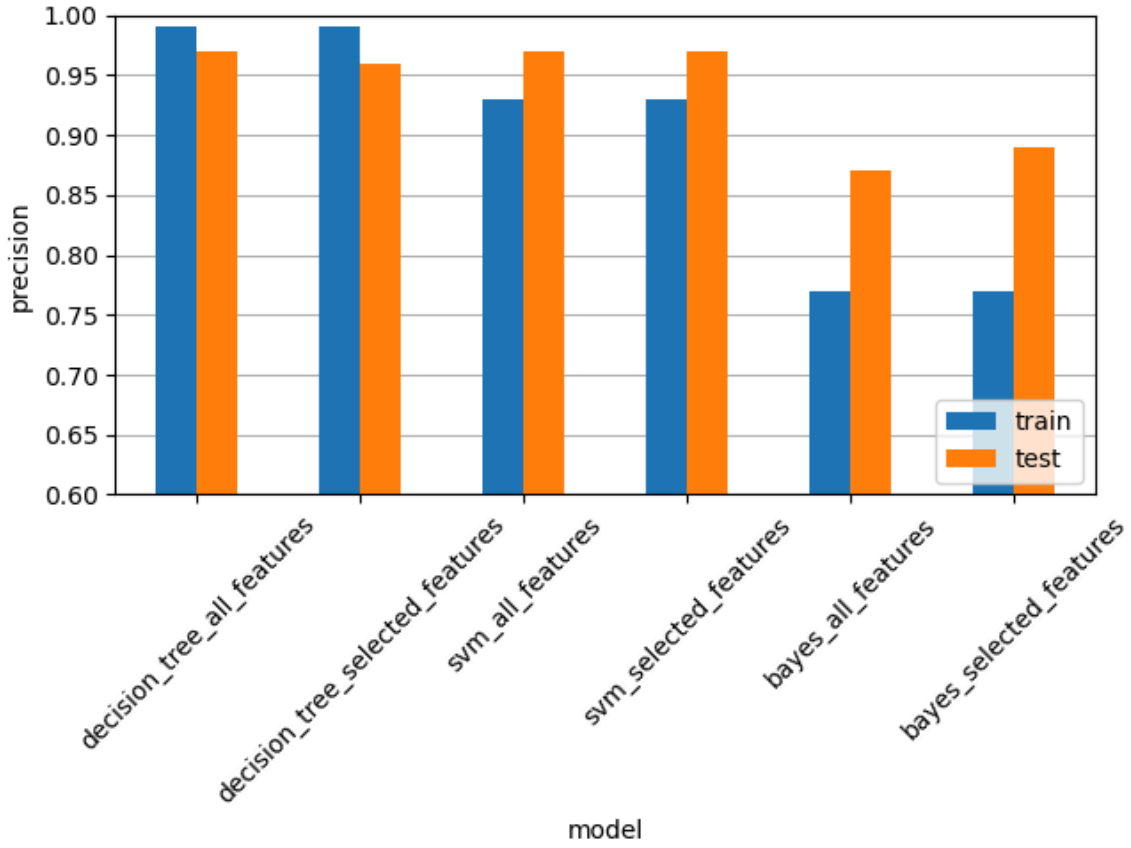
Figure



Figure



Figure



1.6 Problems

P6. If you want to select a set of features manually, which features would you choose and why?

Our first step is to choose features that have the least correlation between two of them. Therefore, we will choose either std or var, mean_3 or mean, median or median_2 as all of these variables have the most correlation between each other. Their plots are just a line. Then to choose between these different variables, we look at their correlation with the other variables. At the end, between these 6 variables, we choose std, mean_3 and median_2. We can draw a straight line between the two types of dot (normal rhythm and atrial fibrilation) that separate the most of the dots in p2p and min so we choose them. Finally, our final selected features are : std, min, p2p, mean_3 and median_2.

P7. Do the automatically selected features match your manually selected features? Explain the reasons for any similarities and/or differences.

As for the P2, both feature selection results are different. And for similar reasons these 2 process rely on a chosen feature selection method that will impact the number and the nature of the features.

Moreover like the P2, in the real life those two processes are usually done with different methods that are compared to each other and furthermore compared to the real life problem where the decision is made knowing the feature effect on what we want to study.

P8. Do you see any signs of overfitting and/or underfitting of the models? Why?

The score of one for the sensitivity of decision tree models in the training set is clearly a sign of overfitting because it means that the model could have a tendency to classify more in one category than the other.

The really low specificity score for the Bayes models on the training set compared to the test set is a sign of underfitting which is confirmed by the low accuracy score of these models on the training set (compared to the test set and overall). The precision presents the same flaws as well, which is coherent.

P9. Considering all conditions, which model will you finally choose to detect atrial fibrillation? Why?

The model showing the less an overfitting/underfitting patterns, having the better accuracy and precision on the test set is the SVM one. However, it is the most complex computationally speaking so if we needed a less costly one, despite its overfitting patterns, the decision tree one could work.