af_classification

December 5, 2024

1 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.

[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.

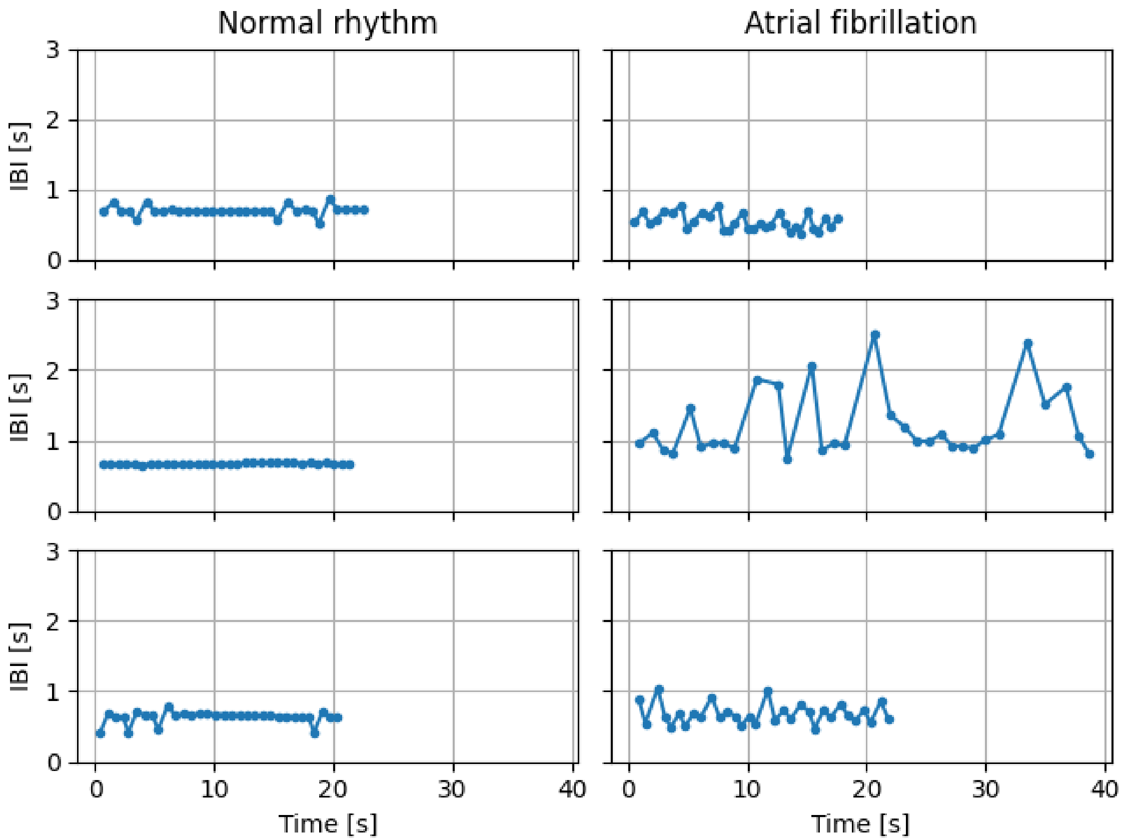
[2]:
```
def load_data():
    with np.load(DATA_FILE) as data:
        intervals = data['intervals']
        labels = data['labels']
        identifiers = data['identifiers']
    return intervals, labels, identifiers


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.

[3]:
```
def plot_interval_examples(intervals, targets, n_examples=3):
    normal_indices = np.random.choice(np.flatnonzero(targets == 0.0),␣
↪n_examples, replace=False)
    af_indices = np.random.choice(np.flatnonzero(targets == 1.0), n_examples,␣
↪replace=False)

    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=False, constrained_layout=True)
    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)
```



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

[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, identifiers)))
    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]))
```

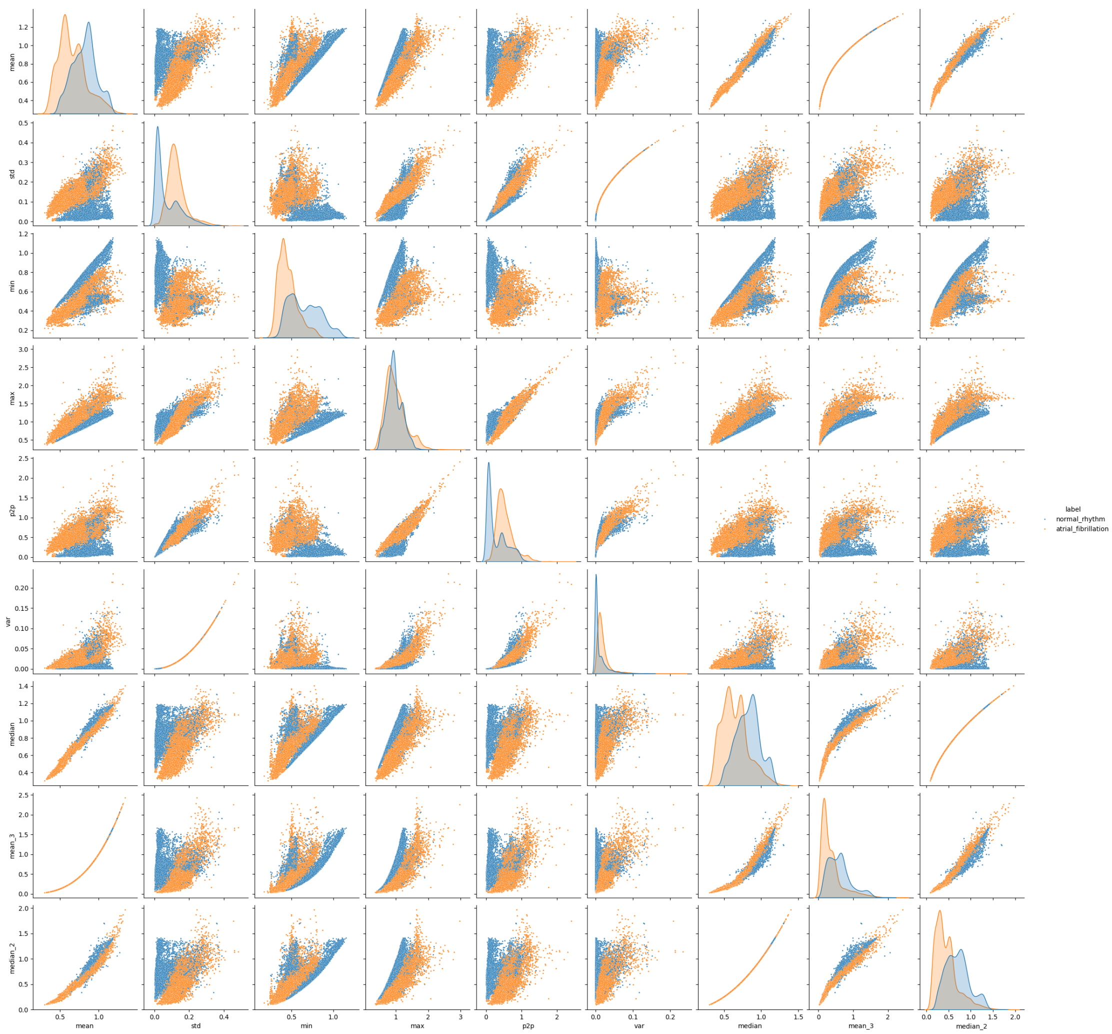
```
    assert set(identifiers[i_train]) | set(identifiers[i_val]) |␣
↪set(identifiers[i_test]) == set(identifiers)

    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'),␣
↪(targets[i_train], targets[i_val], targets[i_test])))
```

```
       subset  total_count  normal_count  af_count  normal_proportion  \
0    training        15000          6919      8081           0.461267
1  validation         4964          2365      2599           0.476430
2     testing         5100          2311      2789           0.453137

   af_proportion
0       0.538733
1       0.523570
2       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.

[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_fibrillation'})
    sns.pairplot(data, hue='label', plot_kws={'s': 4})


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



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

[6]:
```python
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 ['reference']]
        features_selection = features.copy()
        features_selection.insert(0, 'reference', targets)
```

```python
        features_selection = features_selection.dropna(axis=0, how='any',␣
↪inplace=False)
        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_numbers).apply(features.iloc[i_train], targets[i_train])
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.

[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.

[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'].
↪values)

    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'] +␣
↪['reference']]
        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.

[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'] +␣
↪['reference']]
        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
```

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

[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],␣
↪reference_bool[indices]),
            })
        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

[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.

[12]:
```
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.

[13]:
```
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.

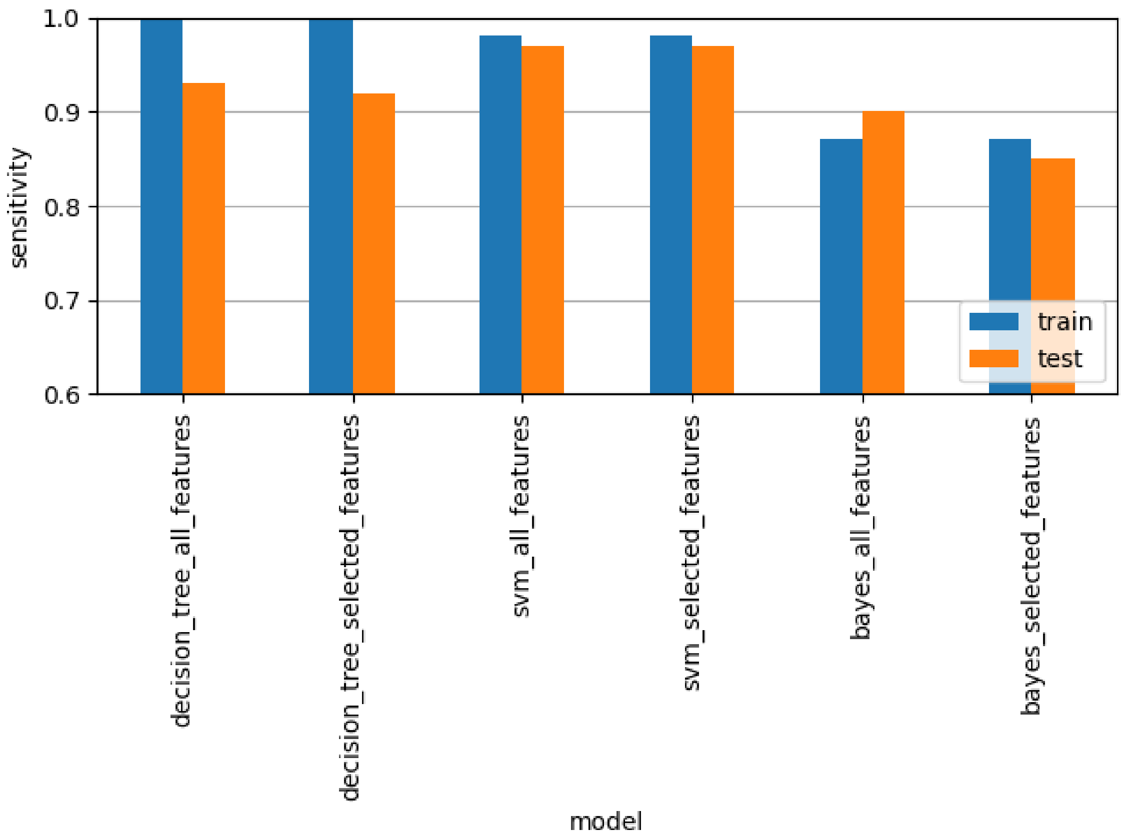
```
[14]: metrics = []
for name, config in configs.items():
    print(f'Evaluating {name!r} model')
    performance = Evaluator().apply(output[name]['prediction'].values, targets[:
 ↪, 0], i_train, i_test)
    performance.insert(0, 'model', name)
    metrics.append(performance)
print("\n*** Performance 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_values(1).unique()])
metrics = metrics.unstack().reindex(index=index, columns=columns)
IPython.display.display(metrics)
```

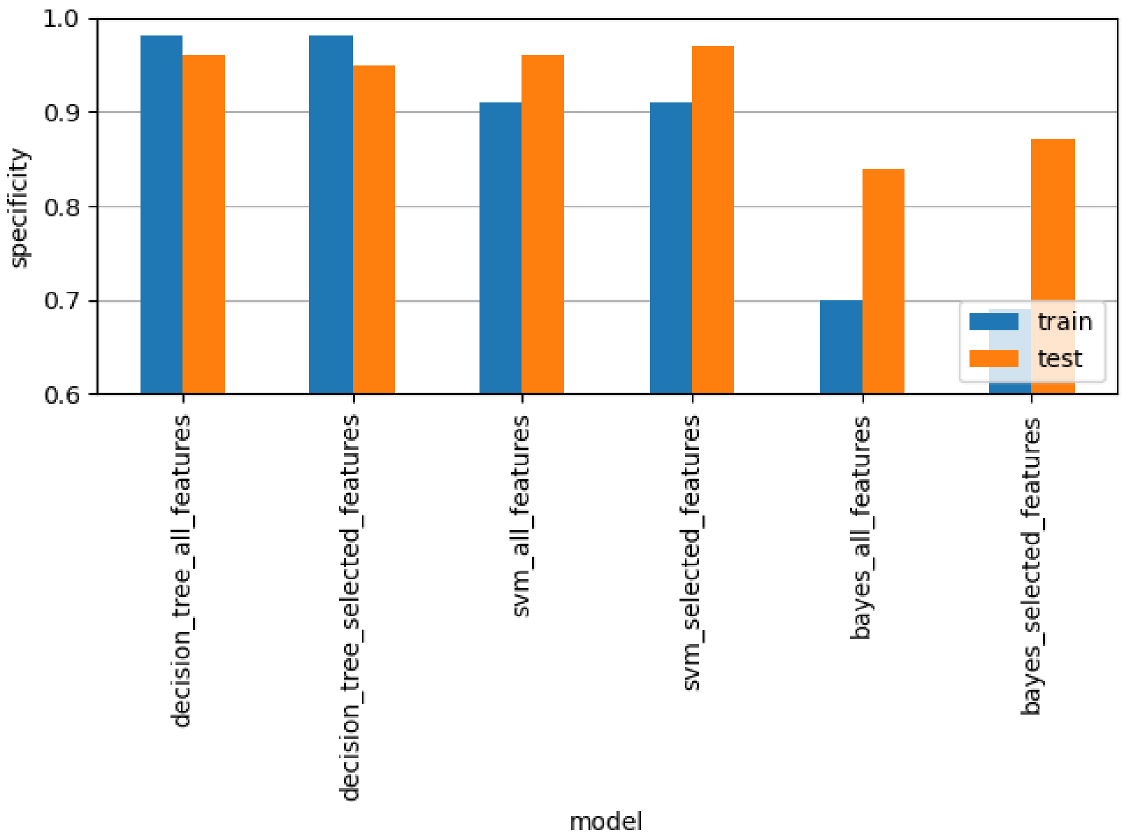
```
Evaluating 'decision_tree_all_features' model
Evaluating 'decision_tree_selected_features' model
Evaluating 'svm_all_features' model
Evaluating 'svm_selected_features' model
Evaluating 'bayes_all_features' model
Evaluating 'bayes_selected_features' model

*** Performance report ***


                                   tp          fn          tn          fp       \
subset                          train  test train  test train  test train  test
model
decision_tree_all_features       8047  2593    34   196  6805  2218   114    93
decision_tree_selected_features  8055  2578    26   211  6813  2194   106   117
svm_all_features                 7888  2709   193    80  6282  2227   637    84
svm_selected_features            7890  2715   191    74  6290  2235   629    76
bayes_all_features               7064  2501  1017   288  4826  1948  2093   363
bayes_selected_features          7009  2380  1072   409  4792  2002  2127   309

                                sensitivity       specificity       accuracy  \
subset                                train  test       train  test    train
model
decision_tree_all_features             1.00  0.93        0.98  0.96     0.99
decision_tree_selected_features        1.00  0.92        0.98  0.95     0.99
svm_all_features                       0.98  0.97        0.91  0.96     0.94
svm_selected_features                  0.98  0.97        0.91  0.97     0.95
bayes_all_features                     0.87  0.90        0.70  0.84     0.79
bayes_selected_features                0.87  0.85        0.69  0.87     0.79

                                      precision
subset                           test     train  test
```

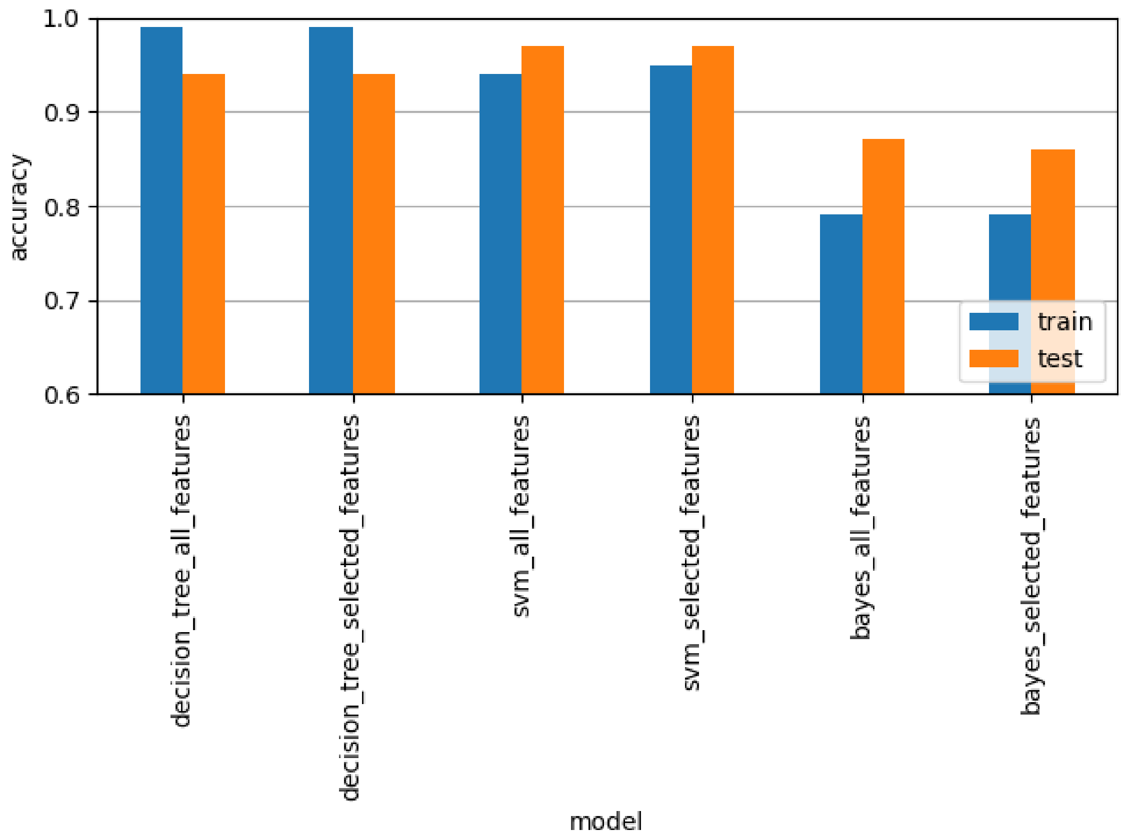
```
model
decision_tree_all_features       0.94      0.99  0.97
decision_tree_selected_features  0.94      0.99  0.96
svm_all_features                 0.97      0.93  0.97
svm_selected_features            0.97      0.93  0.97
bayes_all_features               0.87      0.77  0.87
bayes_selected_features          0.86      0.77  0.89
```

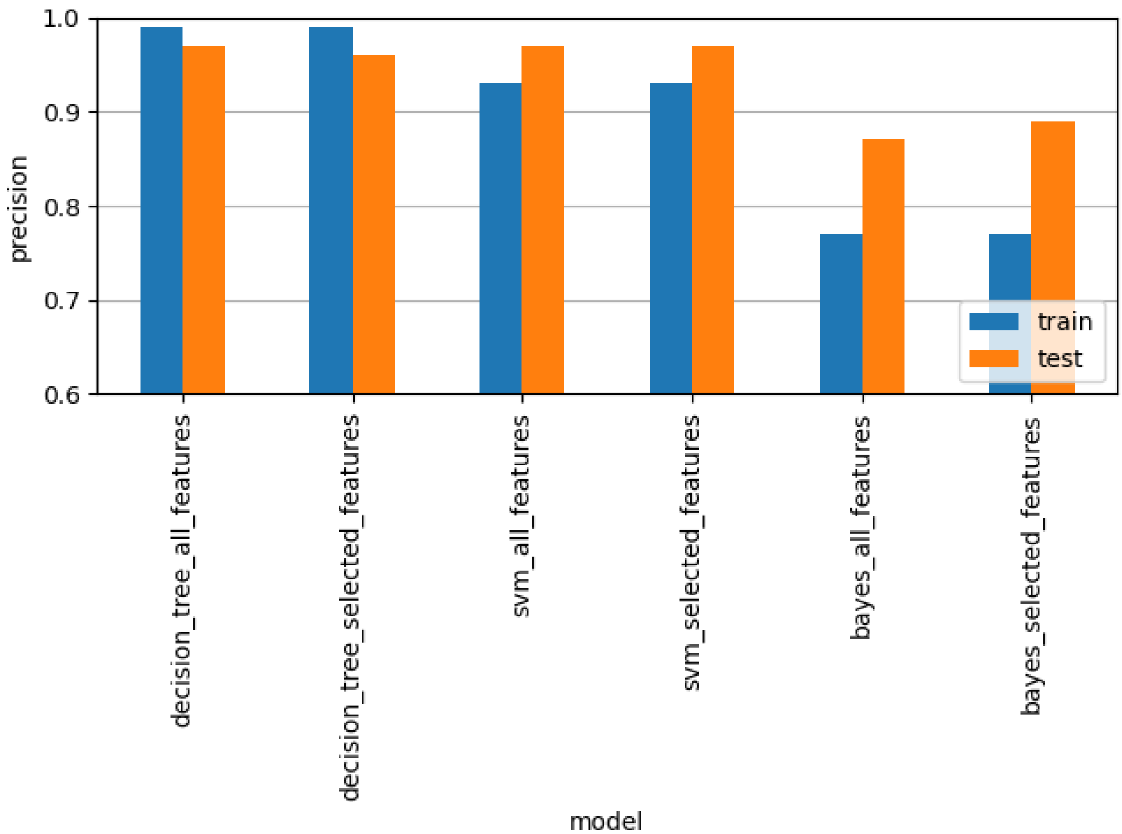
We can also plot the different metrics.

[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=90)


plot_metrics(metrics)
```


1.0
0.9
0.8
0.7
0.6
sensitivity
train
test
decision_tree_all_features
decision_tree_selected_features
svm_all_features
svm_selected_features
bayes_all_features
bayes_selected_features
model


1.0
0.9
0.8
0.7
0.6
specificity
train
test
decision_tree_all_features
decision_tree_selected_features
svm_all_features
svm_selected_features
bayes_all_features
bayes_selected_features
model


1.0
0.9
0.8
0.7
0.6
accuracy
train
test
decision_tree_all_features
decision_tree_selected_features
svm_all_features
svm_selected_features
bayes_all_features
bayes_selected_features
model



2 Exercise Questions

2.1 Question 6

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

Answer

Using the criteria written down in Question 1, one would first look for features that have their class density distribution well separated from one another (in simpler terms, the graphs on the diagonal where the orange plot overlaps the blue one as less as possible), and then choose the features that have low correlations with one another.

Using these facts, a wise choice of features would be mean, std and p2p.

2.2 Question 7

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

Answer

The results are again quite similar between the manually and automatically selected features.

The automatic selection used “LASSO” feature selection, which works by introducing a penalty term into the regression model that shrinks the coefficients of less important features towards zero, effectively removing them from the model. The similarities are that in both cases the correlation of the features with the target classes, as well as the correlations between them. However, Lasso takes it a bit further as it considers the correlation between multiple features. So it can find potential relations that would not appear on the two-dimensional pair plot representation. On the other hand, manually, you might rule out certain features that have no physiological meaning, which Lasso cannot do.

2.3 Question 8

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

Answer

Over-fitting is highlighted by the test error being much higher than the training error. Looking at Figure 5, the decision tree classifier is such a case of over-fitting, regardless of the feature selection, indicating that the model has been trained for too long, becoming a bit too specific to the training data and performing worse on unseen data.

Under-fitting occurs when both test and train errors are high. Looking at Figure 5, such a case is shown for the Bayes model, again regardless of the feature selection, this indicates that the model is too simplistic to capture the underlying patter in the data. A possible reason for this bad performance might be the fact that the Bayes model assumes independance between the features.

2.4 Question 9

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

Answer

Considering all conditions, it is clear that the Naive Bayes model is not the right choice, as it performs significantly worse that the other two models.

In this case, the best model to use would be the SVM with only selected features. Even though both models have similar performances (same accuracy, specificity, …), the one with less features is also faster in terms of computation time. Moreover, the sensitivity metric is the most important one to consider as it has much worse consequences to miss positive cases than to falsely identify someone as positive in this case. Furthermore, this model does not show any sign of over-/under-fitting. Therefore SVM with only selected features is the best model to choose.