Disclaimer and acknowledgement

Author: H. NIU

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The notebook was partly borrowed, adpated and function-added for needs from https://github.com/IntelliHQ/CardiacArrestMortality_ANZICS (https://github.com/IntelliHQ/CardiacArrestMortality_ANZICS), which holds the copyright and credits on that code. This is acknowledged the LICENSE with that repo is not copied along. I greatly appreciate the authors of that code for their efforts.

In [1]:
```
!python -V
```

```
Python 3.7.3
```

In [2]:
```
import pickle
import random
import pandas as pd
import numpy as np
import scipy.stats as stats
import sklearn
import matplotlib

from sklearn.base import BaseEstimator, TransformerMixin, ClassifierMixin
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline, FeatureUnion

from sklearn.model_selection import train_test_split

from sklearn.metrics import accuracy_score, confusion_matrix, roc_curve, auc
#from sklearn.metrics.scorer import make_scorer

from lime.lime_tabular import LimeTabularExplainer
import matplotlib.pyplot as plt

pd.set_option('display.max_columns', None)

print('Numpy version:', np.__version__)
print('Pandas version:', pd.__version__)
print('sklearn version:', sklearn.__version__)
print('matplotlib version:', matplotlib.__version__)
```

```
Numpy version: 1.19.5
Pandas version: 0.25.1
sklearn version: 1.0
matplotlib version: 3.4.3
```

In [3]:
```
#Imports
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import itertools

#scikit-learn package (https://pypi.org/project/scikit-learn)
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, roc_curve, auc
#from sklearn.metrics.scorer import make_scorer

#eli5 package (https://eli5.readthedocs.io/en/latest)
import eli5
from eli5.sklearn import PermutationImportance

#lime package (https://github.com/marcotcr/lime)
import lime
import lime.lime_tabular

#shap package (https://github.com/slundberg/shap)
import shap
```

In [4]:
```
# %matplotlib inline
plt.style.use('ggplot')
plt.rcParams['figure.figsize'] = 12, 8
plt.rcParams['xtick.labelsize'] = 12
plt.rcParams['ytick.labelsize'] = 12
plt.rcParams['axes.titlesize'] = 18
```

Making machine learning pipleline

LIME explainers take in the original raw data for model explanation (for human understandable explainations), so the target model has to include the preprocessing steps. So the following pipleline is largely a repeat of what's done in the preprocessing and omitting the model fitting steps.

In [5]:
```
df = pd.read_excel(r'C:\Users\neo\Huijie\Code\Predicting CA Mortality\Data\1

df.head()
```

Out[5]:

	Gender	Age_value	BMI_value	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CA
0	Female	46.0	23.738662	0	0	
1	Male	72.0	24.341758	0	0	
2	Male	56.0	24.034610	0	0	
3	Female	64.0	29.048656	0	0	
4	Male	68.0	28.081633	0	0	

In [6]:

```
df['Age']='<12'
#df['Age']='>=65'
df.loc[(df['Age_value'] >= 12) & (df['Age_value'] < 40), 'Age'] = '12~40'
#df.loc[(df['Age_value'] < 40), 'Age'] = '<40'
df.loc[(df['Age_value'] >= 40) & (df['Age_value'] < 65), 'Age'] = '40~65'
df.loc[(df['Age_value'] >= 65), 'Age'] = '>=65'
#df.loc[(df['Age_value'] <=5), 'Age'] = '<=5'

df['BMI']='Underweight'
df.loc[(df['BMI_value'] >= 19) & (df['BMI_value'] < 24), 'BMI'] = 'Ideal'
df.loc[(df['BMI_value'] >= 24) & (df['BMI_value'] < 28), 'BMI'] = 'Overweigh
df.loc[(df['BMI_value'] >= 28), 'BMI'] = 'Obese'

#df['ASA']='I-III'
#df.loc[(df['ASA_PS'] >= 4), 'ASA'] = 'IV-V'
df['ASA']='I'
df.loc[(df['ASA_PS'] >= 2) & (df['ASA_PS'] < 3), 'ASA'] = 'II'
df.loc[(df['ASA_PS'] >= 3) & (df['ASA_PS'] < 4), 'ASA'] = 'III'
df.loc[(df['ASA_PS'] >= 4) & (df['ASA_PS'] < 5), 'ASA'] = 'IV'
df.loc[(df['ASA_PS'] >= 5), 'ASA'] = 'V'

#df['Hemorrhage']='0'
df['Hemorrhage'] = '<200'
df.loc[(df['Hemorrhage_ml'] >= 200) & (df['Hemorrhage_ml'] < 800), 'Hemorrha
df.loc[(df['Hemorrhage_ml'] >= 800), 'Hemorrhage'] = '>=800'

#df['Blood_transfusion']='0'
df['Blood_transfusion'] = '<200'
df.loc[(df['Blood_transfusion_ml'] >= 200) & (df['Blood_transfusion_ml'] < 8
df.loc[(df['Blood_transfusion_ml'] >= 800), 'Blood_transfusion'] = '>=800'

df['Epinephrine']='0'
df.loc[(df['Epinephrine_mg'] > 0) & (df['Epinephrine_mg'] <= 5), 'Epinephrin
df.loc[(df['Epinephrine_mg'] > 5), 'Epinephrine'] = '>5'

df['Atropine']='0'
df.loc[(df['Atropine_mg'] > 0) & (df['Atropine_mg'] <= 0.65), 'Atropine'] =
df.loc[(df['Atropine_mg'] > 0.65), 'Atropine'] = '>0.65'

df['Amiodarone']='0'
#df.loc[(df['Amiodarone_g'] > 0) & (df['Amiodarone_g'] <= 0.11), 'Amiodarone
df.loc[(df['Amiodarone_g'] > 0), 'Amiodarone'] = '0.04~0.3'

df['Ephedrine']='0'
#df.loc[(df['Ephedrine_mg'] > 0) & (df['Ephedrine_mg'] <= 6), 'Ephedrine'] =
df.loc[(df['Ephedrine_mg'] > 0), 'Ephedrine'] = '6~15'

df['Methoxamine']='0'
#df.loc[(df['Methoxamine_mg'] > 0) & (df['Methoxamine_mg'] <= 3), 'Methoxami
df.loc[(df['Methoxamine_mg'] > 0), 'Methoxamine'] = '1~35'

#df['CPR']='0'
#df.loc[(df['CPR_min'] > 0) & (df['CPR_min'] < 30), 'CPR'] = '<=30'
df.loc[(df['CPR_min'] < 30), 'CPR'] = '<30'
df.loc[(df['CPR_min'] >= 30) & (df['CPR_min'] < 60), 'CPR'] = '30~60'
df.loc[(df['CPR_min'] >= 60), 'CPR'] = '>=60'
```

```
57
58
59 df2=df[["Gender","Age","BMI","Comorbidity_diabetes","Comorbidity_hypertensio
60 "Comorbidity_pulmonary","Comorbidity_hepatic","Comorbidity_renal","Comorbidi
61 "Comorbidity_tumor","Surgical_type","Emergency","Trauma","Anaesthetic_type",
62 "ASA","Timing_arrest","Defibrillate","Cause_arrest","Hemorrhage","Blood_tran
63 "Epinephrine","Atropine","Amiodarone","Ephedrine","Methoxamine","CPR","Died"
64
65 df2.head()
66 df2.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 29 columns):
Gender                       150 non-null object
Age                          150 non-null object
BMI                          150 non-null object
Comorbidity_diabetes         150 non-null int64
Comorbidity_hypertension     150 non-null int64
Comorbidity_CAD              150 non-null int64
Comorbidity_pulmonary        150 non-null int64
Comorbidity_hepatic          150 non-null int64
Comorbidity_renal            150 non-null int64
Comorbidity_neurological     150 non-null int64
Comorbidity_tumor            150 non-null int64
Surgical_type                150 non-null object
Emergency                    150 non-null int64
Trauma                       150 non-null int64
Anaesthetic_type             150 non-null object
Operative_position           150 non-null object
ASA                          150 non-null object
Timing_arrest                150 non-null object
Defibrillate                 150 non-null int64
Cause_arrest                 150 non-null object
Hemorrhage                   150 non-null object
Blood_transfusion            150 non-null object
Epinephrine                  150 non-null object
Atropine                     150 non-null object
Amiodarone                   150 non-null object
Ephedrine                    150 non-null object
Methoxamine                  150 non-null object
CPR                          150 non-null object
Died                         150 non-null int64
dtypes: int64(12), object(17)
memory usage: 34.1+ KB
```

In [7]:
```
df=df2
X=df
X['Gender'] = X.Gender.map({'Male':1, 'Female':0}) # M -> 1, F -> 0
X['Age'] = X.Age.map({'<12':0,'12~40':1,'40~65':2,'>=65':3}) #
X['BMI'] = X.BMI.map({'Underweight':0, 'Ideal':1,'Overweight':2,'Obese':3})
X['ASA'] = X.ASA.map({'I':0, 'II':1, 'III':2,'IV':3,'V':4}) #
X['Hemorrhage'] = X.Hemorrhage.map({'<200':0, '200~800':1,'>=800':2}) #
X['Blood_transfusion'] = X.Blood_transfusion.map({'<200':0, '200~800':1,'>=8
X['Epinephrine'] = X.Epinephrine.map({'0':0, '<=5':1,'>5':2}) #
X['Atropine'] = X.Atropine.map({'0':0, '<=0.65':1,'>0.65':2}) #
X['Amiodarone'] = X.Amiodarone.map({'0':0, '0.04~0.3':1}) #
X['Ephedrine'] = X.Ephedrine.map({'0':0, '6~15':1}) #
X['Methoxamine'] = X.Methoxamine.map({'0':0, '1~35':1}) #
X['CPR'] = X.CPR.map({'<30':0,'30~60':1,'>=60':2}) #
X['Surgical_type'] = X.Surgical_type.map({'Abdominal':0, 'Neurosurgery':1,'O
        # Abdominal->0, Neurosurgery->1,Thoracic->3,Throat->4,Others->5
X['Anaesthetic_type'] = X.Anaesthetic_type.map({'General':1, 'Local':0}) # G
X['Operative_position'] = X.Operative_position.map({'Left lateral decubitus'
                                                    'Lithotomy':3,'Su
X['Timing_arrest'] = X.Timing_arrest.map({'Induction':0, 'Intubation':1,'Sur
X['Cause_arrest'] = X.Cause_arrest.map({'Anesthesia':0, 'Comorbidity':1,'Sur
df=X
```

In [8]:
```
def split_train_test(data, test_ratio):
    shuffled_indices = np.random.permutation(len(data))
    test_set_size = int(len(data) * test_ratio)
    test_indices = shuffled_indices[:test_set_size]
    train_indices = shuffled_indices[test_set_size:]
    return data.iloc[train_indices], data.iloc[test_indices]
```

In [9]:
```
#Now split the data into training and test set(85-15 split)
data_train, data_test = train_test_split(df, test_size=.25,
                                         stratify=df.Gender, random_state=0)
```

In [10]:
```
data_train.head()
```

Out[10]:

	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comor
85	1	2	1	0	1	0	
105	0	2	3	0	0	0	
65	0	1	1	0	0	1	
142	1	2	3	0	1	1	
149	1	2	2	0	1	1	

Data preprocessing

In [11]:
```
categorical_vars = ["Gender","Age","BMI","Comorbidity_diabetes","Comorbidity
"Comorbidity_pulmonary","Comorbidity_hepatic","Comorbidity_renal","Comorbidi
"Comorbidity_tumor","Surgical_type","Emergency","Trauma","Anaesthetic_type",
"ASA","Timing_arrest","Defibrillate","Cause_arrest","Hemorrhage","Blood_tran
"Epinephrine","Atropine","Amiodarone","Ephedrine","Methoxamine","CPR"]

categorical_var_idxs = [idx for idx, _ in enumerate(list(data_train.columns)
print(categorical_var_idxs)
```

```
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21,
22, 23, 24, 25, 26, 27]
```

In [12]:
```
categorical_vars2 = ["Gender","Age","BMI","Comorbidity_diabetes","Comorbidit
"Comorbidity_pulmonary","Comorbidity_hepatic","Comorbidity_renal","Comorbidi
"Comorbidity_tumor","Surgical_type","Emergency","Trauma","Anaesthetic_type",
"ASA","Timing_arrest","Defibrillate","Cause_arrest","Hemorrhage","Blood_tran
"Epinephrine","Atropine","Amiodarone","Ephedrine","Methoxamine","CPR","Died"

categorical_var_idxs2 = [idx for idx, _ in enumerate(list(data_train.columns
print(categorical_var_idxs2)
```

```
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21,
22, 23, 24, 25, 26, 27, 28]
```

In [13]:
```
# to make a custom transformer to fit into a pipeline
class Vars_selector(BaseEstimator, TransformerMixin):
    '''Return a subset of variables in a numpy array based on indecies'''
    def __init__(self, var_idxs):
        '''var_idxs is a list of categorical variables indecies'''
        self.var_idxs = var_idxs

    def fit(self, X, y=None):
        return self

    def transform(self, X):
        '''returns a dataframe with selected variables'''
        return np.array(X)[:, self.var_idxs]
```

In [14]:
```
class Cat_vars_encoder(BaseEstimator, TransformerMixin):
    '''Return the transformed categorical variables based on indecies'''
    def fit(self, X, y=None):
        return self

    def transform(self, X):
        # arf column index
        # arf_idx = categorical_vars.index('arf')
        # X[:, arf_idx] = np.array(pd.Series(X[:, arf_idx]).map({1:1, 2:0}))
        return X
```

Transform data in a pipeline

In [15]:
```
# categorical variables preprocessing
cat_vars_pipeline = Pipeline([
    ('selector', Vars_selector(categorical_var_idxs)),
    ('encoder', Cat_vars_encoder())
])
```

In [16]:
```
# categorical variables preprocessing
cat_vars_pipeline2 = Pipeline([
    ('selector', Vars_selector(categorical_var_idxs2)),
    ('encoder', Cat_vars_encoder())
])
```

In [17]:
```
continuous_vars = [] #['Age', 'BMI', 'Hemorrhage_ml', 'Blood_transfusion', '
       #'Amiodarone_g', 'Ephedrine_mg', 'Methoxamine_mg', 'CPR_min']
```

To transform the variables in one step.

In [18]:
```
preproc_pipeline = FeatureUnion(transformer_list=[
    ('cat_pipeline', cat_vars_pipeline)
    #,('cont_pipeline', cont_vars_pipeline)
])


preproc_pipeline2 = FeatureUnion(transformer_list=[
    ('cat_pipeline', cat_vars_pipeline2)
    #,('cont_pipeline', cont_vars_pipeline)
])
```

In [19]:
```
data_train_X = pd.DataFrame(preproc_pipeline.fit_transform(data_train),
                            columns=categorical_vars + continuous_vars)

data_train_X2 = pd.DataFrame(preproc_pipeline2.fit_transform(data_train),
                            columns=categorical_vars2 + continuous_vars)
```

In [20]:
```
data_test_X = pd.DataFrame(preproc_pipeline2.fit_transform(data_test),
                            columns=categorical_vars2 + continuous_vars)

data_test_X.head()
```

Out[20]:

	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comorbi
0	0	2	0	0	0	1	
1	0	1	1	0	0	0	
2	0	2	2	0	0	0	
3	0	1	2	0	1	1	
4	1	2	2	0	1	1	

In [21]:
```
print(data_train_X2.shape)
```

```
(112, 29)
```

Making explanation

1. A feature importance explainer

https://machinelearningmastery.com/calculate-feature-importance-with-python/ (https://machinelearningmastery.com/calculate-feature-importance-with-python/)

To restore the models and fit them into pipeline.

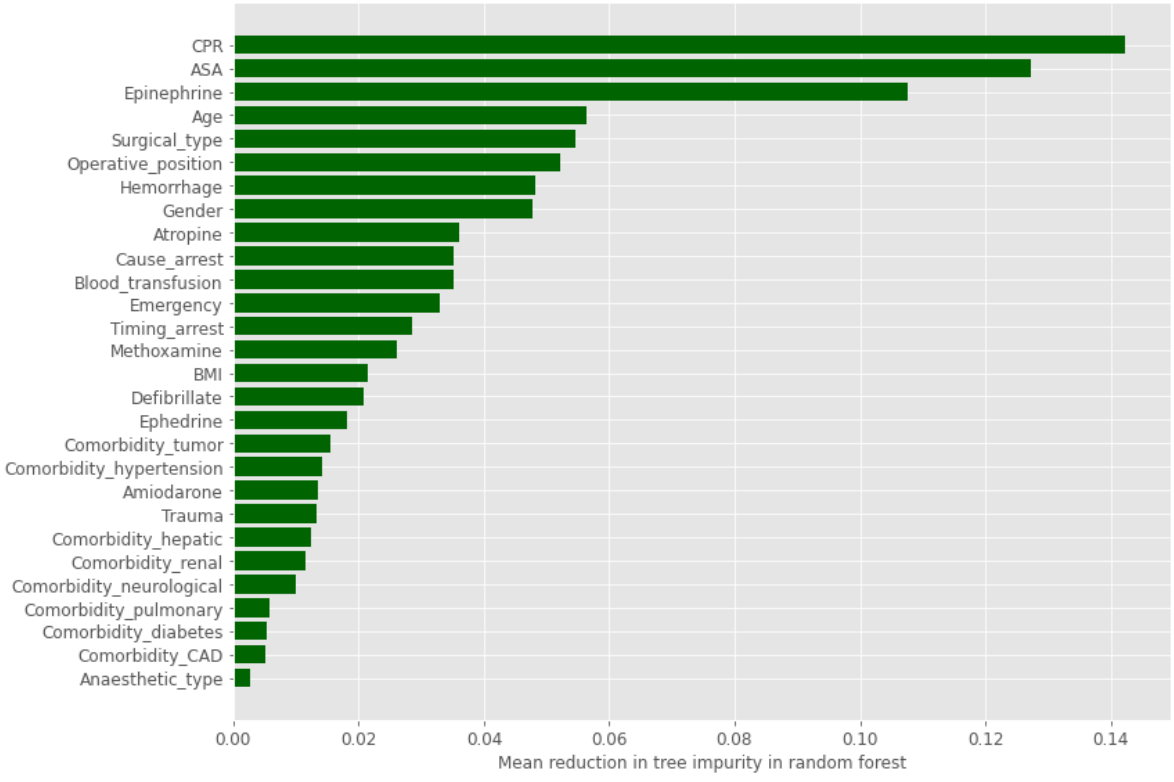
In [22]:
```
with open(r'C:\Users\neo\Huijie\Code\Predicting CA Mortality\Models\rf_clf_f
    rf_clf = pickle.load(f)
model=rf_clf
```

```
Trying to unpickle estimator DecisionTreeClassifier from version 0.24.0 when us
ing version 1.0. This might lead to breaking code or invalid results. Use at yo
ur own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maintai
nability-limitations (https://scikit-learn.org/stable/modules/model_persistenc
e.html#security-maintainability-limitations)
Trying to unpickle estimator RandomForestClassifier from version 0.24.0 when us
ing version 1.0. This might lead to breaking code or invalid results. Use at yo
ur own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maintai
nability-limitations (https://scikit-learn.org/stable/modules/model_persistenc
e.html#security-maintainability-limitations)
```

In [23]:
```
#data=data_train.drop('Died',1)
data=data_train_X
```

In [24]:

```
import matplotlib.patches as patches
import matplotlib.colors as colors
import math


# Feature importance dataframe
imp_df = pd.DataFrame({'feature': data.columns.values,
                       'importance': model.feature_importances_})

# Reorder by importance
ordered_df = imp_df.sort_values(by='importance')
imp_range=range(1,len(imp_df.index)+1)

## Barplot with confidence intervals
height = ordered_df['importance']
bars = ordered_df['feature']
y_pos = np.arange(len(bars))

# Create horizontal bars
plt.barh(y_pos, height, color='darkgreen')

# Create names on the y-axis
plt.yticks(y_pos, bars)

plt.xlabel("Mean reduction in tree impurity in random forest")

plt.tight_layout()


# Show graphic
plt.show()
```



In [25]:

```
# Feature importance based on TRAINING set

perm_test = PermutationImportance(model, scoring=make_scorer(roc_auc_score),
                                  n_iter=50, random_state=0, cv="prefit")

# fit and see the permuation importances
perm_test.fit(data, data_train['Died'])

imp_df = eli5.explain_weights_df(perm_test)
label_df = pd.DataFrame({'feature': [ "x" + str(i) for i in range(len(data.c
imp_df = pd.merge(label_df, imp_df, on='feature', how='inner', validate="one

# Reorder by importance
ordered_df = imp_df.sort_values(by='weight')
imp_range=range(1,len(imp_df.index)+1)


## Barplot with confidence intervals

height = ordered_df['weight']
bars = ordered_df['feature_name']
ci = 1.96 * ordered_df['std']
y_pos = np.arange(len(bars))

# Create horizontal bars
plt.barh(y_pos, height, xerr=ci, color='darkgreen')

# Create names on the y-axis
plt.yticks(y_pos, bars)

plt.xlabel("Permutation feature importance training set (decrease in AUC)")
plt.tight_layout()

# Show graphic
plt.show()

```

```
X has feature names, but RandomForestClassifier was fitted without feature na
mes
X has feature names, but RandomForestClassifier was fitted without feature na
mes
X has feature names, but RandomForestClassifier was fitted without feature na
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X has feature names, but RandomForestClassifier was fitted without feature na
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X has feature names, but RandomForestClassifier was fitted without feature na
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X has feature names, but RandomForestClassifier was fitted without feature na
mes
```

```
X has feature names, but RandomForestClassifier was fitted without feature na
```

2. Preparing a LIME explainer

To restore the models and fit them into pipeline.

In [26]:
```
with open(r'C:\Users\neo\Huijie\Code\Predicting CA Mortality\Models\ensemble_
    ensemble_clf = pickle.load(f)
```

```
Trying to unpickle estimator LogisticRegression from version 0.24.0 when usin
g version 1.0. This might lead to breaking code or invalid results. Use at yo
ur own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator DecisionTreeClassifier from version 0.24.0 when
 using version 1.0. This might lead to breaking code or invalid results. Use
 at your own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator RandomForestClassifier from version 0.24.0 when
 using version 1.0. This might lead to breaking code or invalid results. Use
 at your own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator DecisionTreeRegressor from version 0.24.0 when u
sing version 1.0. This might lead to breaking code or invalid results. Use at
your own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator DummyClassifier from version 0.24.0 when using v
ersion 1.0. This might lead to breaking code or invalid results. Use at your
 own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator GradientBoostingClassifier from version 0.24.0 w
hen using version 1.0. This might lead to breaking code or invalid results. U
se at your own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator SVC from version 0.24.0 when using version 1.0.
 This might lead to breaking code or invalid results. Use at your own risk. F
or more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator AdaBoostClassifier from version 0.24.0 when usin
g version 1.0. This might lead to breaking code or invalid results. Use at yo
ur own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
Trying to unpickle estimator LabelEncoder from version 0.24.0 when using vers
ion 1.0. This might lead to breaking code or invalid results. Use at your own
risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
```

```
ence.html#security-maintainability-limitations)
Trying to unpickle estimator VotingClassifier from version 0.24.0 when using
 version 1.0. This might lead to breaking code or invalid results. Use at you
r own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maint
ainability-limitations (https://scikit-learn.org/stable/modules/model_persist
ence.html#security-maintainability-limitations)
```

In [27]:

```
## for ensemble_clf:
class Ensemble_clf(BaseEstimator, ClassifierMixin):
    def fit(self, X, y=None):
        return ensemble_clf
    def predict_proba(self, X):
        return ensemble_clf.predict_proba(X)
```

In [28]:

```
## for ensemble_clf
ensemble_pipeline = Pipeline([
    ('preprocessing', FeatureUnion(transformer_list=[
                            ('cat_pipeline', cat_vars_pipeline)
                        ])),
    ('ensemble_clf', Ensemble_clf())
])
```

In [29]:
```
1 ensemble_pipeline.fit(data_train)
```

Out[29]:
```
Pipeline(steps=[('preprocessing',
                 FeatureUnion(transformer_list=[('cat_pipeline',
                                                 Pipeline(steps=[('selector',
                                                                  Vars_selector
(var_idxs=[0,

1,

2,

3,

4,

5,

6,

7,

8,

9,

10,

11,

12,

13,

14,

15,

16,

17,

18,

19,

20,

21,

22,

23,

24,
```

```
25,

26,

27])),
                                                                ('encoder',
                                                                 Cat_vars_enco
der())]))])),
                ('ensemble_clf', Ensemble_clf())])
```

Preparing a LIME explainer

Because LIME takes only float numpy array of the original dataset, to provide a human understandable explanation, it needs to know the mapping from the encoded value to original value for the categorical variables.

This is accomplished through the categorical_names argument. This is a dictionary of a list of values mapped to the index of the (categorical) variable column.

In [30]:

```
# make the categorical original values mapping
## the order of the names should correspond to their (int) encoded values
### This is required for LIME, because LIME uses these to index the categori
categorical_vals = '''Gender=Female,Male
Age=<12,12~40,40~65,>65
BMI= Underweight,Ideal,Overweight,Obese
Comorbidity_diabetes=F,T
Comorbidity_hypertension=F,T
Comorbidity_CAD=F,T
Comorbidity_pulmonary=F,T
Comorbidity_hepatic=F,T
Comorbidity_renal=F,T
Comorbidity_neurological=F,T
Comorbidity_tumor=F,T
Surgical_type=Abdominal,Neurosurgery,Orthopedics,Thoracic,Throat,Others
Emergency=F,T
Trauma=F,T
Anaesthetic_type=Local,General
Operative_position=Left lateral decubitus, Right lateral decubitus,Prone,Lit
ASA=I,II,III,IV,V
Timing_arrest=Induction,Intubation,Surgery,Unknown
Defibrillate=F,T
Cause_arrest=Anesthesia,Comorbidity,Surgery,Unknown
Hemorrhage=<200ml,200~800ml,>800ml
Blood_transfusion=<200ml,200~800ml,>800ml
Epinephrine=0,0~5mg,>5mg
Atropine=0,<0.65mg,>0.65mg
Amiodarone=0,0.04~0.3g
Ephedrine=0,6~15mg
Methoxamine=0,1~35mg
CPR=<30min,30~60min,>60min'''.split('\n')

categorical_names = {}
for val in categorical_vals:
    categorical_names[categorical_var_idxs[categorical_vars.index(val.split(
```

In [31]:
```
categorical_names
```

Out[31]:
```
{0: ['Female', 'Male'],
 1: ['<12', '12~40', '40~65', '>65 '],
 2: [' Underweight', 'Ideal', 'Overweight', 'Obese'],
 3: ['F', 'T'],
 4: ['F', 'T'],
 5: ['F', 'T'],
 6: ['F', 'T'],
 7: ['F', 'T'],
 8: ['F', 'T'],
 9: ['F', 'T'],
 10: ['F', 'T'],
 11: ['Abdominal',
  'Neurosurgery',
  'Orthopedics',
  'Thoracic',
  'Throat',
  'Others'],
 12: ['F', 'T'],
 13: ['F', 'T'],
 14: ['Local', 'General'],
 15: ['Left lateral decubitus',
  ' Right lateral decubitus',
  'Prone',
  'Lithotomy',
  'Supine'],
 16: ['I', 'II', 'III', 'IV', 'V'],
 17: ['Induction', 'Intubation', 'Surgery', 'Unknown'],
 18: ['F', 'T'],
 19: ['Anesthesia', 'Comorbidity', 'Surgery', 'Unknown'],
 20: ['<200ml', '200~800ml', '>800ml '],
 21: ['<200ml', '200~800ml', '>800ml '],
 22: ['0', '0~5mg', '>5mg '],
 23: ['0', '<0.65mg', '>0.65mg'],
 24: ['0', '0.04~0.3g '],
 25: ['0', '6~15mg'],
 26: ['0', '1~35mg'],
 27: ['<30min', '30~60min', '>60min']}
```

LIME perturbs the training sample to build a locally linear model to approximate the target model at the test point.

In [32]:
```
explainer = LimeTabularExplainer(
    data_train.iloc[:, :-1].values, # remove the target variable from the tr
    class_names=['Died','Survived'],
    feature_names=list(data_train.columns),
    categorical_features=categorical_var_idxs,
    categorical_names=categorical_names,
    verbose=True
)
```

In [33]:
```
#https://stackoverflow.com/questions/60178732/problem-fixing-future-warning-

    #test_sample = data_test.ix[data_test.Died == (not survived), :-1]
    #test_sample = data_test.loc[data_test.Died == (not survived)][:-1]
```

In [34]:
```
def get_test_sample(model, died=True, correct=True, seed=42, count=1):
    '''
    Return one random sample from test set based on the selection criteria.

    parameters:
      model - the model which is tested for
      survived - select survived sample
      correct - select the sample which the model prediected correctly
    '''
    test_sample = data_test.ix[data_test.Died == (not died), :-1]
    prediction = model.predict_proba(test_sample)

    if (died and correct) or (not died and not correct):
        ids = np.argwhere((prediction[:,0] > prediction[:,1]))
    elif (died and not correct) or (not died and correct):
        ids = np.argwhere((prediction[:,0] <= prediction[:,1]))
    if count == 1:
        idx = random.Random(seed).choice(ids)
    else:
        ids = ids.reshape(len(ids)).tolist()
        idx = random.Random(seed).sample(ids, count)

    return test_sample.iloc[idx,:]
```

In [35]:
```
def plot_vertical_bar(explaination, title='Local explanation for class died'
    exp_list = explaination.as_list()
    tags, values, colors = [],[],[]
    for i in range(len(exp_list)):
        tags.append(exp_list[i][0])
        values.append(exp_list[i][1])
        if(exp_list[i][1] > 0):
            colors.append('r')
        else:
            colors.append('g')

    fig, ax = plt.subplots()

    y_pos = np.arange(len(tags))

    ax.barh(y_pos, values, align='center',
            color=colors, ecolor='black')
    ax.set_yticks(y_pos)
    ax.set_yticklabels(tags)
    ax.invert_yaxis()  # labels read top-to-bottom
    ax.set_title(title)
```

In [36]:
```
def score_compare(x, y, threshold = 0.5):
    if x < threshold and y < threshold:
        return 'True Negative'
    elif x < threshold and y > threshold:
        return 'False Negative'
    elif x > threshold and y > threshold:
        return 'True Positive'
    elif x > threshold and y < threshold:
        return 'False Positive'
```

Correct, True Negative, patient survived

In [37]:
```
test_sample_died_correct = get_test_sample(ensemble_pipeline, died=True, cor
test_sample_died_correct
```

```
.ix is deprecated. Please use
.loc for label based indexing or
.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

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-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)
```

Out[37]:

	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comorb
17	0	3	2	0	1	1	

In [38]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_died_correct)
score = 1-round(result[0,0],2)
score
```

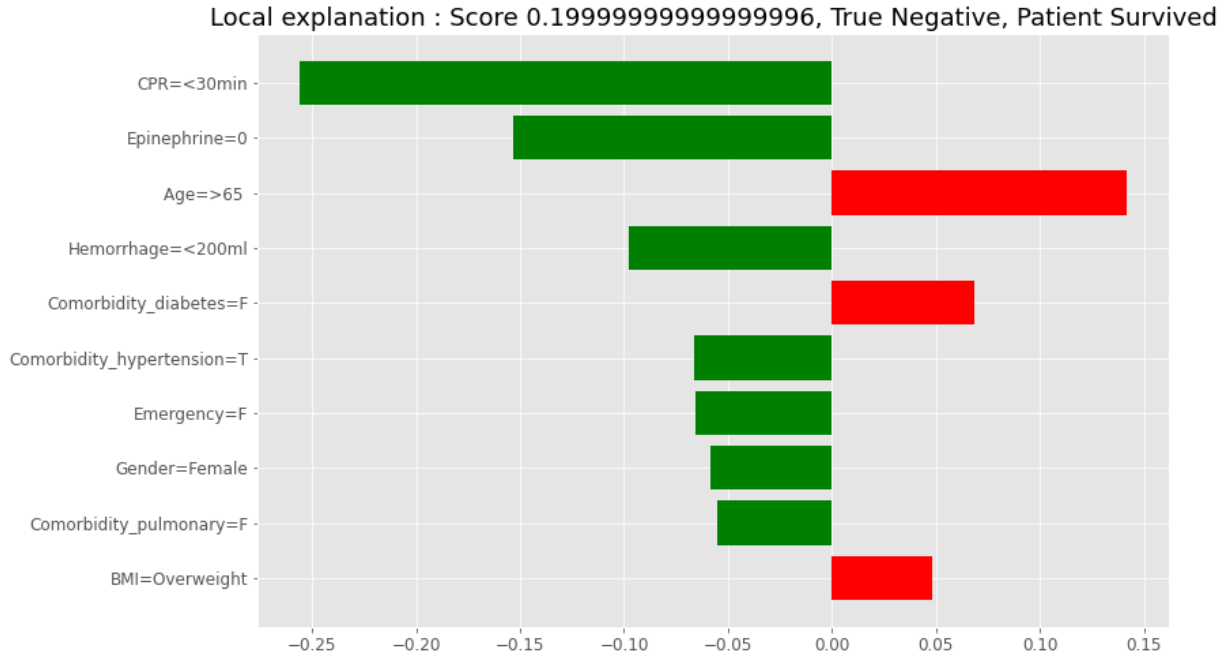
Out[38]: 0.19999999999999996

Let's see how LIME explainer (with default settings) explains it.

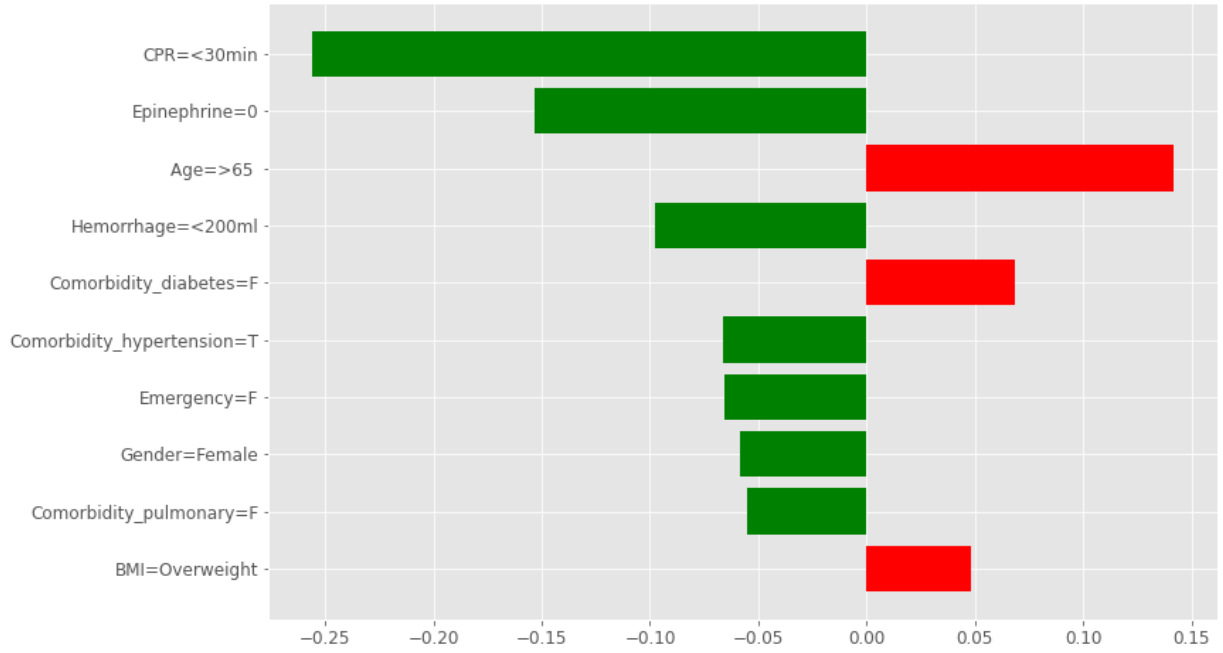
In [39]:
```
1 explaination = explainer.explain_instance(test_sample_died_correct.values.ra
```

```
Intercept 0.7589152534734966
Prediction_local [0.26636104]
Right: 0.20438393533185692
```

In [40]:
```
1 outcome = 0
2 outcome_title = 'Survived'
3 plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```



In [41]:
```
outcome = 0
outcome_title = 'Survived'
#plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient
plot_vertical_bar(explaination, ''.format(score, score_compare(score, outcom
```



In [42]:
```
test_sample_died_correct = get_test_sample(ensemble_pipeline, seed=43) #, su
test_sample_died_correct
```

```
.ix is deprecated. Please use
.loc for label based indexing or
.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

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.loc for label based indexing or
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See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)
```

Out[42]:

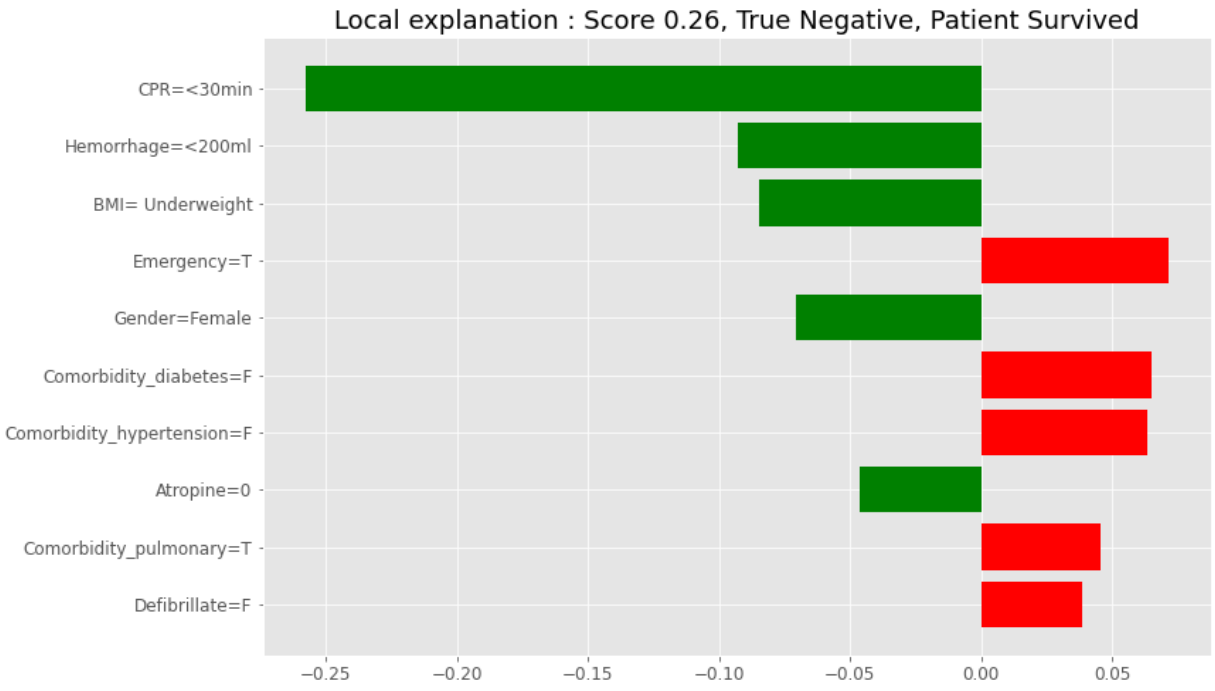
	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comor
139	0	2	0	0	0	1	

In [43]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_died_correct)
score = 1-round(result[0,0],2)
score
```

Out[43]: 0.26

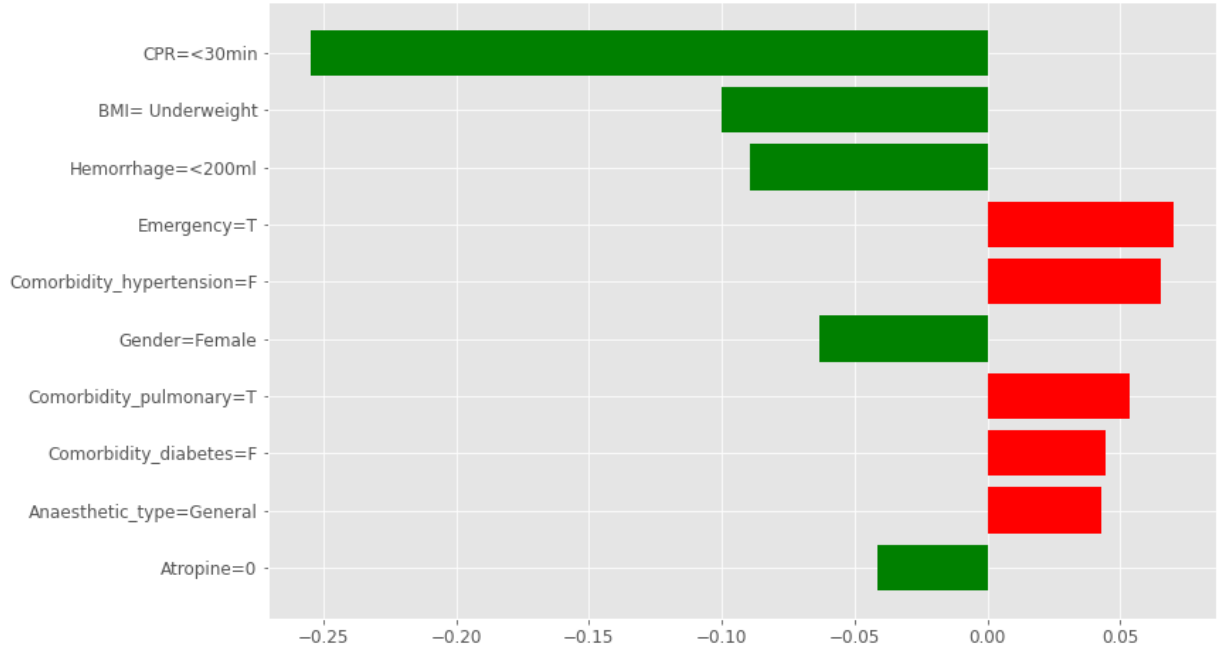
In [44]:
```
explaination = explainer.explain_instance(test_sample_died_correct.values.ra
print(explaination)
outcome = 0
outcome_title = 'Survived'
plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```

```
Intercept 0.6035533371112072
Prediction_local [0.33570023]
Right: 0.26366191167685205
<lime.explanation.Explanation object at 0x000000C8B3A919E8>
```



In [45]:
```
explaination = explainer.explain_instance(test_sample_died_correct.values.ra
print(explaination)
outcome = 0
outcome_title = 'Survived'
plot_vertical_bar(explaination, ''.format(score, score_compare(score, outcom
```

```
Intercept 0.5931771988539475
Prediction_local [0.32067057]
Right: 0.26366191167685205
<lime.explanation.Explanation object at 0x000000C8B4EFF9B0>
```



Correct, True Positive, patient died

In [46]:
```
test_sample_died_correct = get_test_sample(ensemble_pipeline, died=False, co
test_sample_died_correct
```

```
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.loc for label based indexing or
.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

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.loc for label based indexing or
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See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)
```

Out[46]:

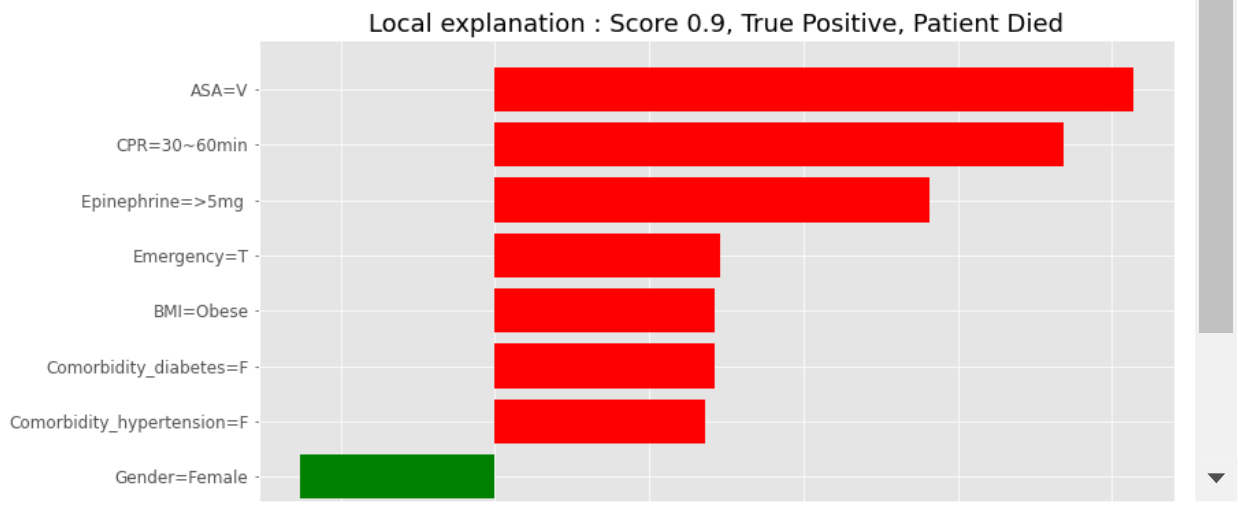
	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comor
104	0	1	3	0	0	1	

In [47]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_died_correct)
score = 1-round(result[0,0],2)
score
```

Out[47]: 0.9

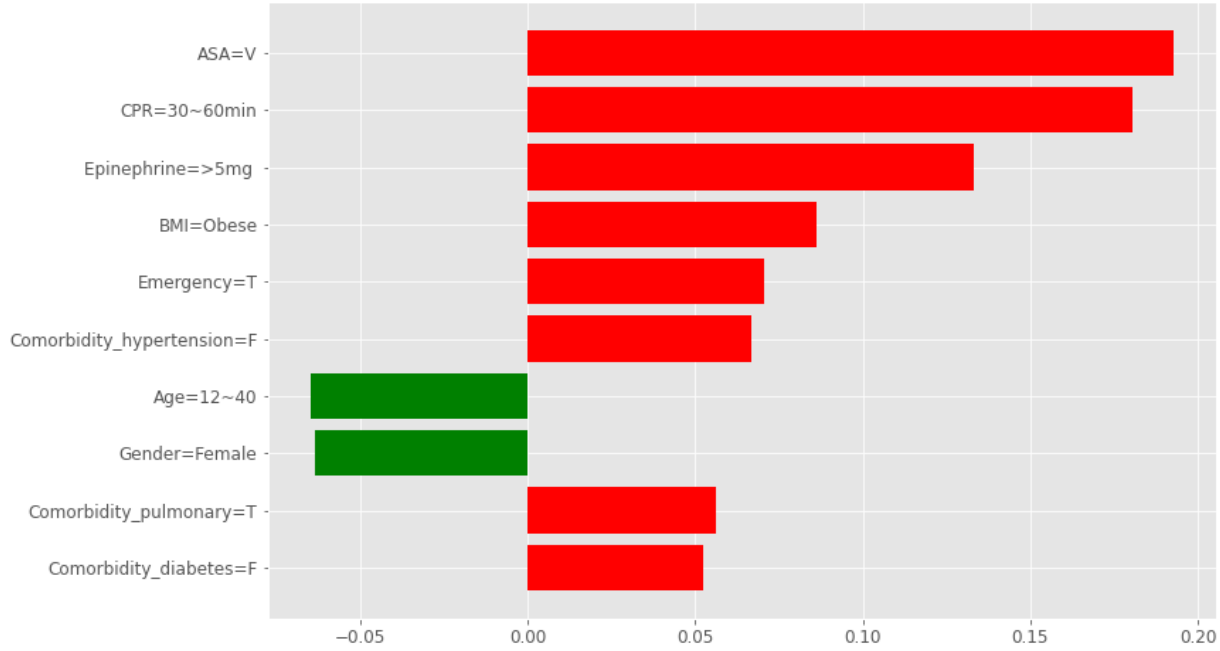
In [48]:
```
explaination = explainer.explain_instance(test_sample_died_correct.values.ra
print(explaination)
outcome = 1
outcome_title = 'Died'
plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```

```
Intercept 0.25696037453462417
Prediction_local [1.00166513]
Right: 0.8997209131124573
<lime.explanation.Explanation object at 0x000000C8B24E2160>
```



In [49]:
```
explaination = explainer.explain_instance(test_sample_died_correct.values.ra
print(explaination)
outcome = 1
outcome_title = 'Died'
plot_vertical_bar(explaination, ''.format(score, score_compare(score, outcom
```

```
Intercept 0.2808745369165182
Prediction_local [0.99104523]
Right: 0.8997209131124573
<lime.explanation.Explanation object at 0x000000C8B4DE6978>
```



In [50]:
```
test_sample_died_correct = get_test_sample(ensemble_pipeline, died=False, se
test_sample_died_correct
```

```
.ix is deprecated. Please use
.loc for label based indexing or
.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

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See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)
```

Out[50]:

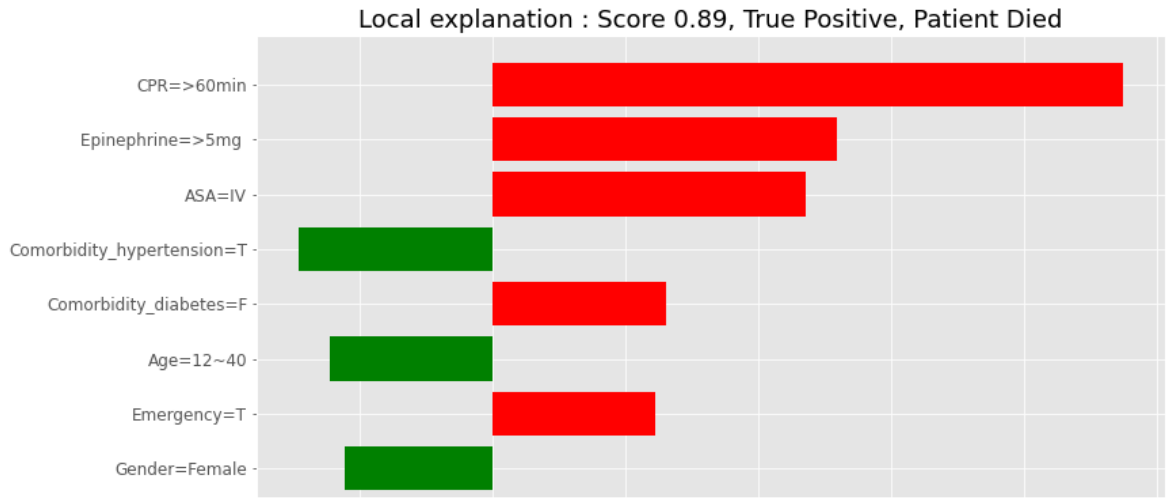
	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comor
100	0	1	2	0	1	1	

In [51]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_died_correct)
score = 1-round(result[0,0],2)
score
```

Out[51]: 0.89

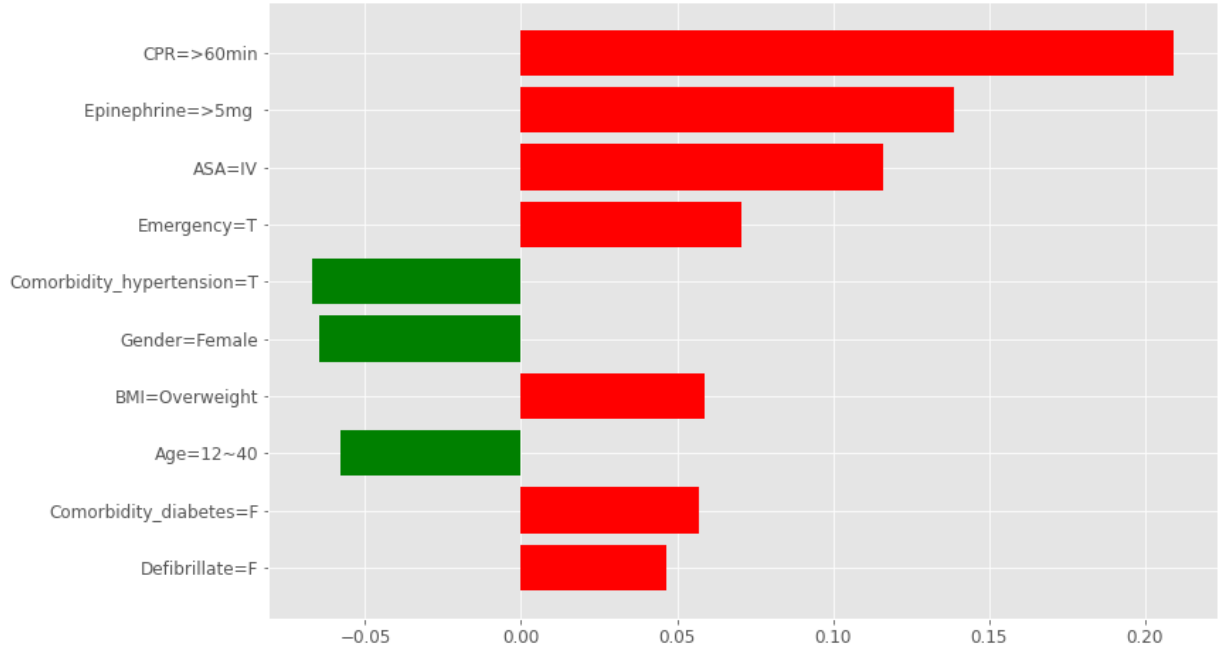
In [52]:
```
explaination = explainer.explain_instance(test_sample_died_correct.values.ra
print(explaination)
outcome = 1
outcome_title = 'Died'
plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```

```
Intercept 0.3926734633053218
Prediction_local [0.90741066]
Right: 0.8863784910412932
<lime.explanation.Explanation object at 0x000000C8B4E7D588>
```



In [53]:
```
explaination = explainer.explain_instance(test_sample_died_correct.values.ra
print(explaination)
outcome = 0
outcome_title = 'survived'
plot_vertical_bar(explaination, ''.format(score, score_compare(score, outcom
```

```
Intercept 0.3841302201029104
Prediction_local [0.89185997]
Right: 0.8863784910412932
<lime.explanation.Explanation object at 0x000000C8B4E3DA58>
```



Incorrect, False Negative, patient died

In [54]:
```
test_sample_died_correct = get_test_sample(ensemble_pipeline, died=False, co
test_sample_incorrect
```

```
.ix is deprecated. Please use
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.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

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-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
<ipython-input-54-bdb0d0cc47fa> in <module>
      1 test_sample_died_correct = get_test_sample(ensemble_pipeline, died=Fals
e, correct=False, seed=42, count=1)
----> 2 test_sample_incorrect

NameError: name 'test_sample_incorrect' is not defined
```

In [ ]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_incorrect)
score = 1-round(result[0,0],2)
score
```

In [ ]:
```
explaination = explainer.explain_instance(test_sample_incorrect.values.ravel
print(explaination)
outcome = 1
outcome_title = 'Died'
plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```

In [ ]:
```
explaination = explainer.explain_instance(test_sample_incorrect.values.ravel
print(explaination)
outcome = 1
outcome_title = 'Died'
plot_vertical_bar(explaination, ''.format(score, score_compare(score, outcom
```

In [ ]:
```
test_sample_died_correct = get_test_sample(ensemble_pipeline, died=False, co
test_sample_incorrect
```

In [ ]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_incorrect)
score = 1-round(result[0,0],2)
score
```

In [ ]:
```
explaination = explainer.explain_instance(test_sample_incorrect.values.ravel
print(explaination)
outcome = 1
outcome_title = 'Died'
plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```

Incorrect, False Positive, patient survived

In [55]:
```
test_sample_incorrect = get_test_sample(ensemble_pipeline, correct=False, di
test_sample_incorrect
```

```
.ix is deprecated. Please use
.loc for label based indexing or
.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

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-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)
```

Out[55]:

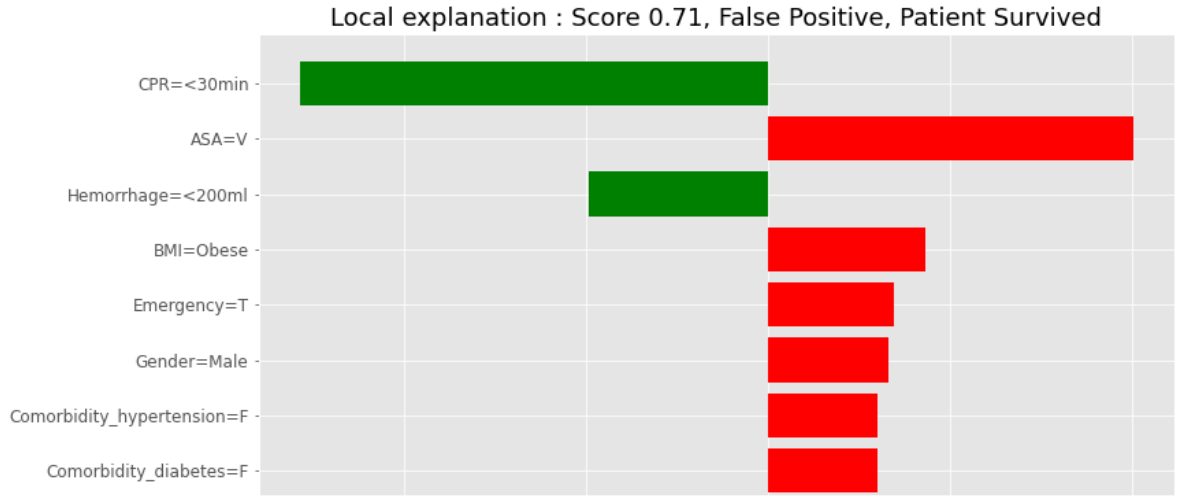
	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comorb
19	1	2	3	0	0	1	

In [56]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_incorrect)
score = 1-round(result[0,0],2)
score
```

Out[56]: 0.71

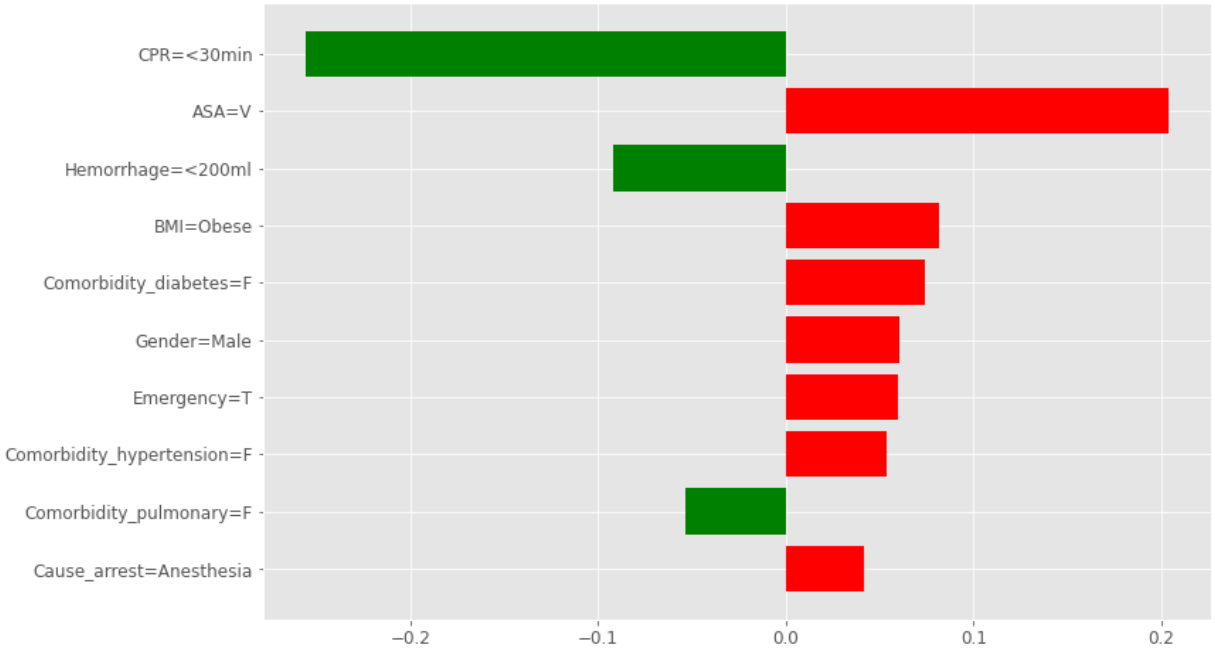
In [57]:
```
explaination = explainer.explain_instance(test_sample_incorrect.values.ravel
print(explaination)
outcome = 0
outcome_title = 'Survived'
plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```

```
Intercept 0.5335559116085485
Prediction_local [0.72396846]
Right: 0.7144154525359052
<lime.explanation.Explanation object at 0x000000C8B39BBD68>
```



In [58]:
```
explaination = explainer.explain_instance(test_sample_incorrect.values.ravel
print(explaination)
outcome = 0
outcome_title = 'Survived'
#plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient
plot_vertical_bar(explaination, ''.format(score, score_compare(score, outcom
```

```
Intercept 0.5379357467805043
Prediction_local [0.71395739]
Right: 0.7144154525359052
<lime.explanation.Explanation object at 0x000000C8B391D978>
```



In [59]:
```
test_sample_incorrect = get_test_sample(ensemble_pipeline, correct=False, di
test_sample_incorrect
```

```
.ix is deprecated. Please use
.loc for label based indexing or
.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)

.ix is deprecated. Please use
.loc for label based indexing or
.iloc for positional indexing

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ix-indexer
-is-deprecated (http://pandas.pydata.org/pandas-docs/stable/user_guide/indexin
g.html#ix-indexer-is-deprecated)
```

Out[59]:

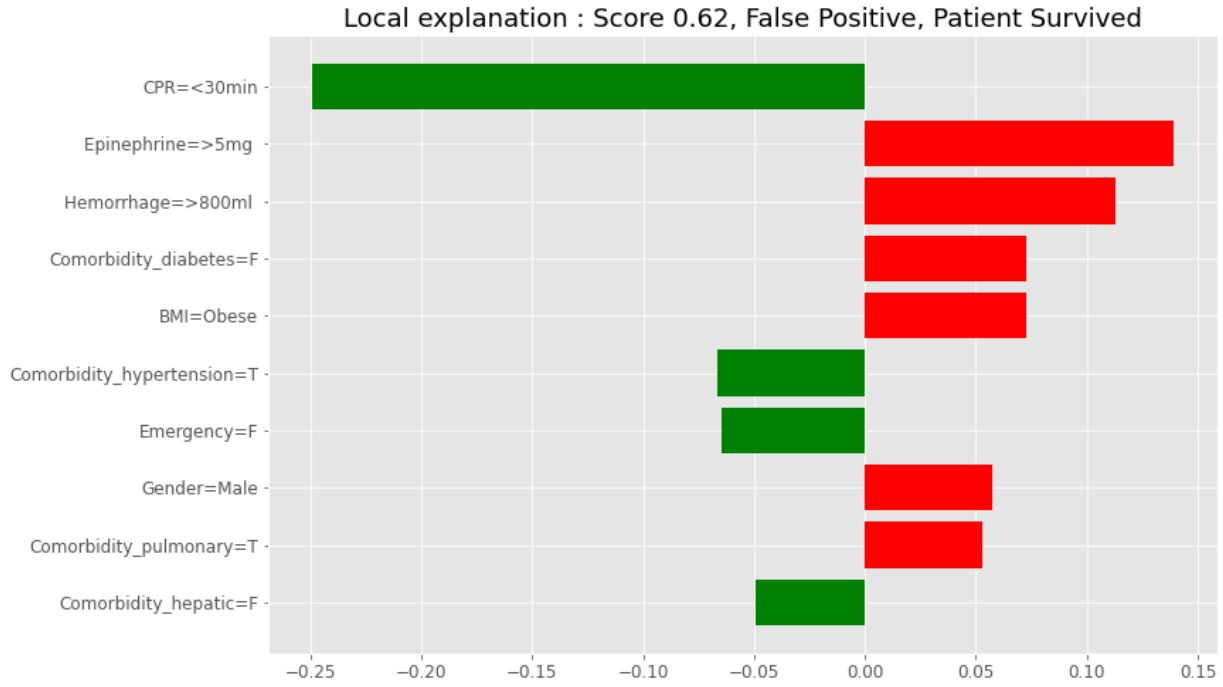
	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comor
126	1	2	3	0	1	1	

In [60]:
```
# prediction
result = ensemble_pipeline.predict_proba(test_sample_incorrect)
score = 1-round(result[0,0],2)
score
```

Out[60]: 0.62

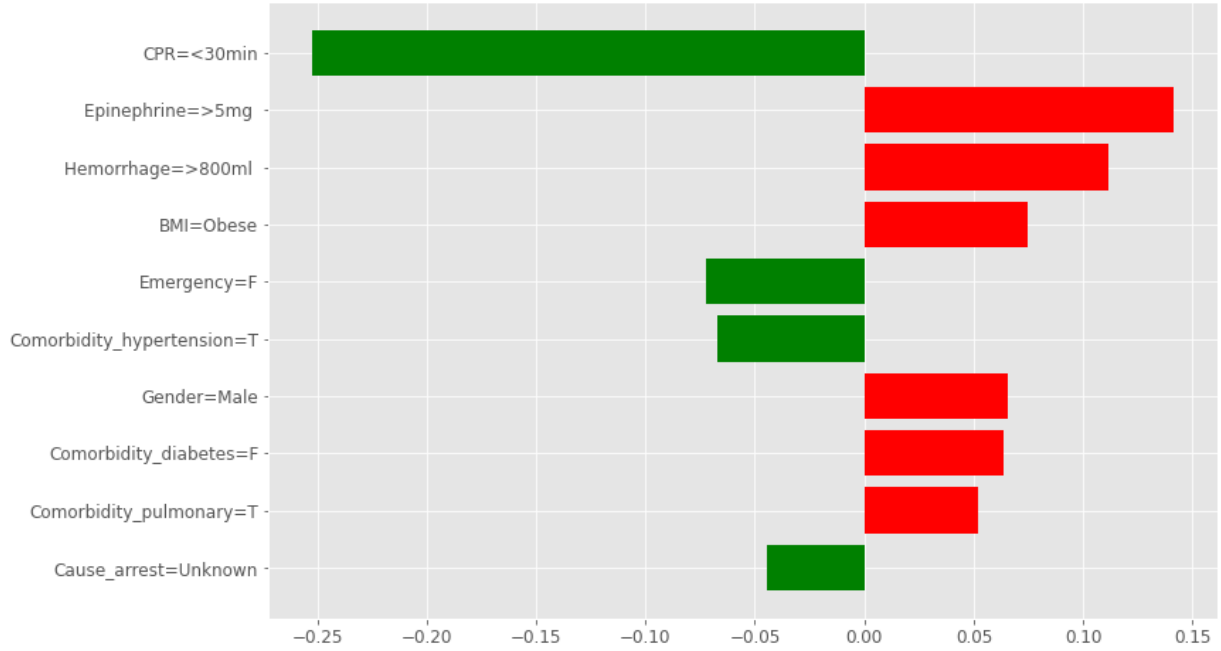
In [61]:
```
explaination = explainer.explain_instance(test_sample_incorrect.values.ravel
print(explaination)
outcome = 0
outcome_title = 'Survived'
plot_vertical_bar(explaination, 'Local explanation : Score {}, {}, Patient {
```

```
Intercept 0.5646545897255475
Prediction_local [0.64332151]
Right: 0.6166866999359815
<lime.explanation.Explanation object at 0x000000C8B24B3518>
```



In [62]:
```
explaination = explainer.explain_instance(test_sample_incorrect.values.ravel
print(explaination)
outcome = 1
outcome_title = 'died'
plot_vertical_bar(explaination, ''.format(score, score_compare(score, outcom
```

```
Intercept 0.5442164456791525
Prediction_local [0.61693366]
Right: 0.6166866999359815
<lime.explanation.Explanation object at 0x000000C8B20F66D8>
```

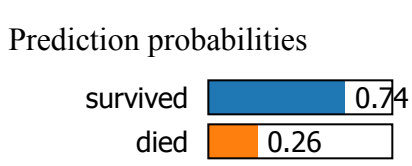


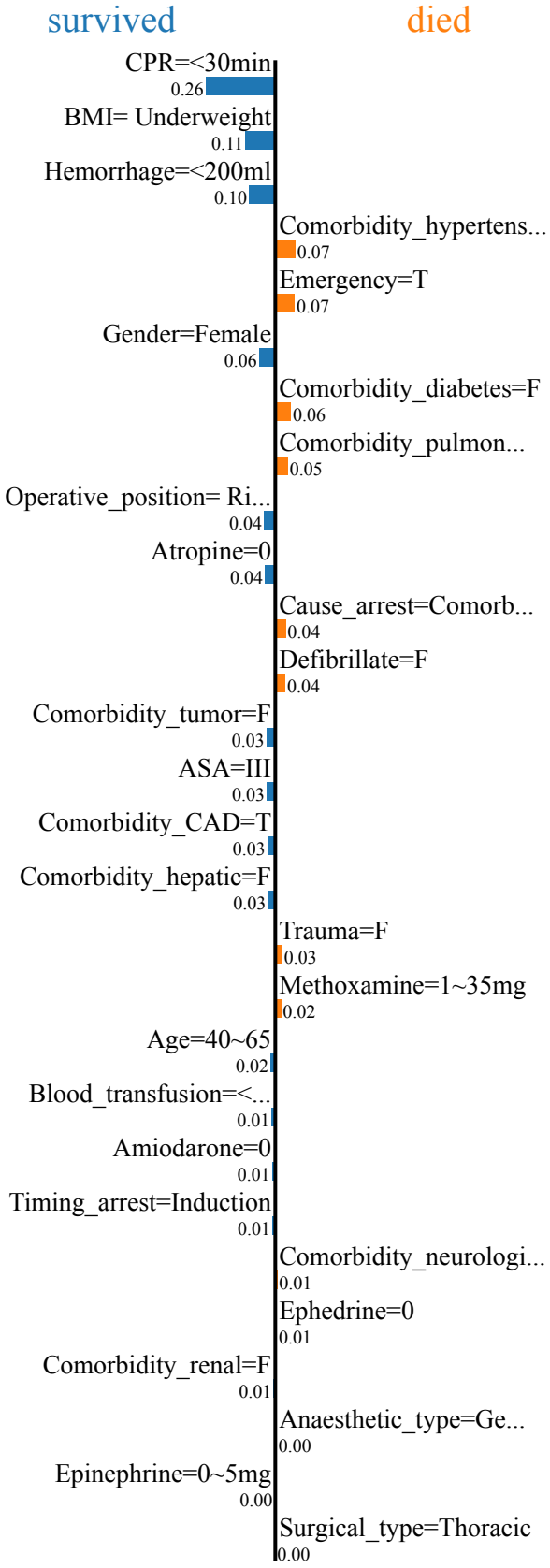
Overall explanation by LIME

In [63]:

```
#model =rf_clf
model=ensemble_clf

RANDOM_STATE=123

explainer = LimeTabularExplainer(
    data_train.iloc[:, :-1].values, # remove the target variable from the tr
    class_names=['survived','died'],
    feature_names=list(data_train.columns),
    categorical_features=categorical_var_idxs,
    categorical_names=categorical_names,
    mode="classification",
    verbose=True,
    random_state=RANDOM_STATE)


##LIME

#Explain samples in test set
X_explain = data_test.iloc[:, :-1]
#data_test.drop('Died',1)

#Explaining first subject in test set using all 30 features
exp = explainer.explain_instance(X_explain.values[0,:],model.predict_proba,
#Plot local explanation
plt = exp.as_pyplot_figure()
plt.tight_layout()
exp.show_in_notebook(show_table=True)
```

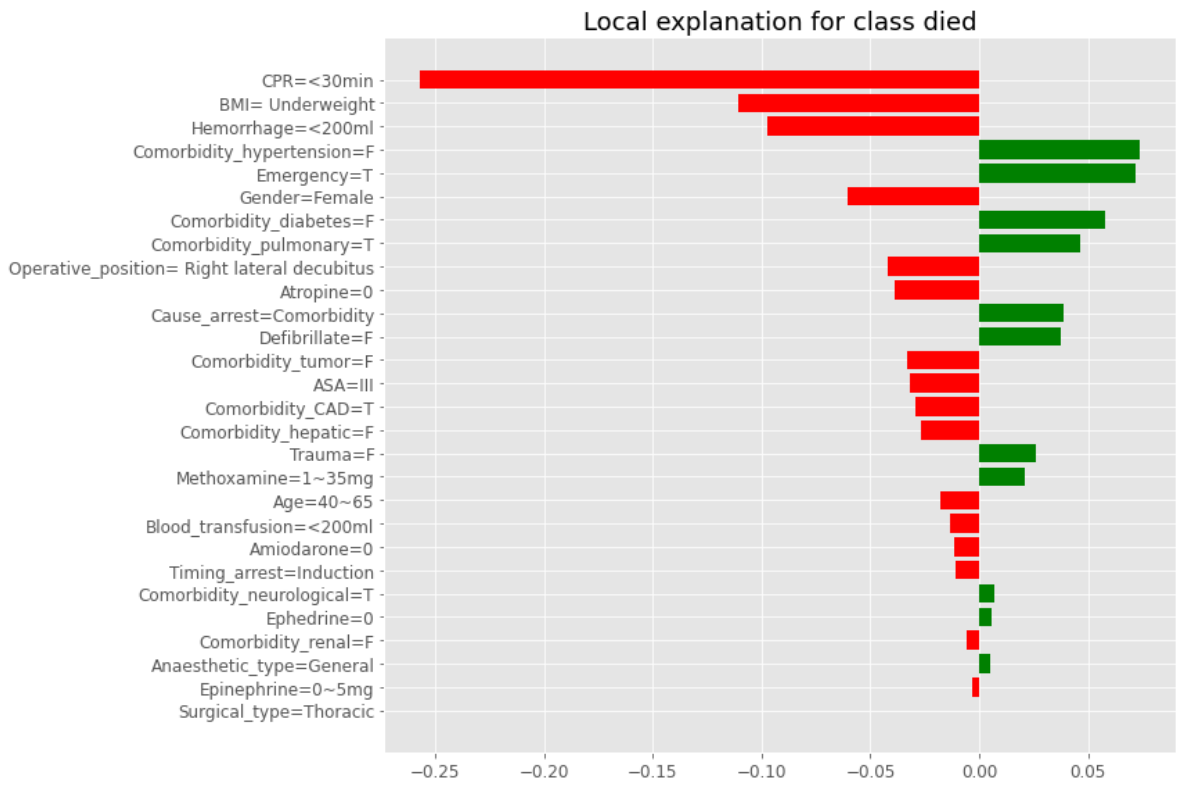
```
Intercept 0.6523716191933714
Prediction_local [0.25479006]
Right: 0.2636619116768521
```





Feature	Value
CPR=<30min	True
BMI= Underweight	True
Hemorrhage=<200ml	True

Comorbidity_hypertension=F	True
Emergency=T	True
Gender=Female	True
Comorbidity_diabetes=F	True
Comorbidity_pulmonary=T	True



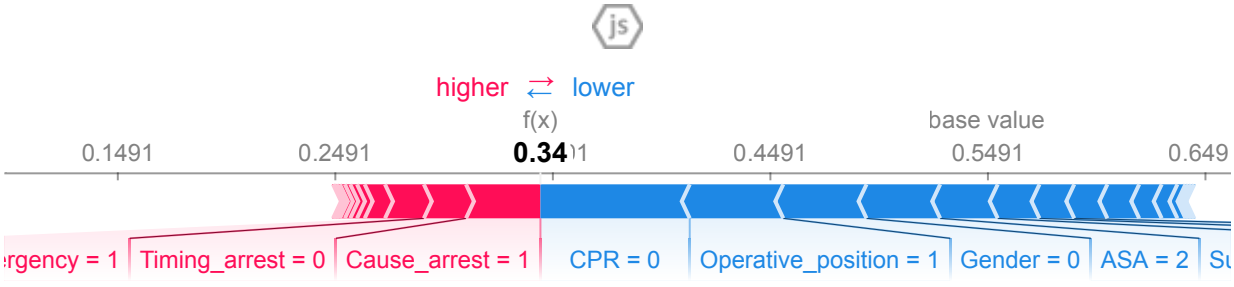
3. Preparing a SHAP explainer

In [64]:
```
with open(r'C:\Users\neo\Huijie\Code\Predicting CA Mortality\Models\rf_clf_f
    rf_clf = pickle.load(f)
model=rf_clf
```

```
Trying to unpickle estimator DecisionTreeClassifier from version 0.24.0 when us
ing version 1.0. This might lead to breaking code or invalid results. Use at yo
ur own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maintai
nability-limitations (https://scikit-learn.org/stable/modules/model_persistenc
e.html#security-maintainability-limitations)
Trying to unpickle estimator RandomForestClassifier from version 0.24.0 when us
ing version 1.0. This might lead to breaking code or invalid results. Use at yo
ur own risk. For more info please refer to:
https://scikit-learn.org/stable/modules/model_persistence.html#security-maintai
nability-limitations (https://scikit-learn.org/stable/modules/model_persistenc
e.html#security-maintainability-limitations)
```

In [65]:
```
#We can also use Shapley force plots to give us additional information on a

# explain the model's predictions on test set using SHAP values
# same syntax works for xgboost, LightGBM, CatBoost, and some scikit-learn m
explainer = shap.TreeExplainer(model)

# shap_values consists of a list of two matrices of dimension samplesize x #
# The first matrix uses average nr of benign samples as base value
# The second matrix which is used below uses average nr of malignant samples
shap_values = explainer.shap_values(X_explain)


# Interactive visualization of the explanation of the first subject
# in the test set (X_explain).
# It shows the relative contribution of features to get from the base value
# samples(average value)
# to the output value (1 in case of malignant sample)
# the numbers at the bottom show the actual values for this sample.
shap.initjs() #initialize javascript in cell
shap.force_plot(explainer.expected_value[1], shap_values[1][0,:], X_explain.
```

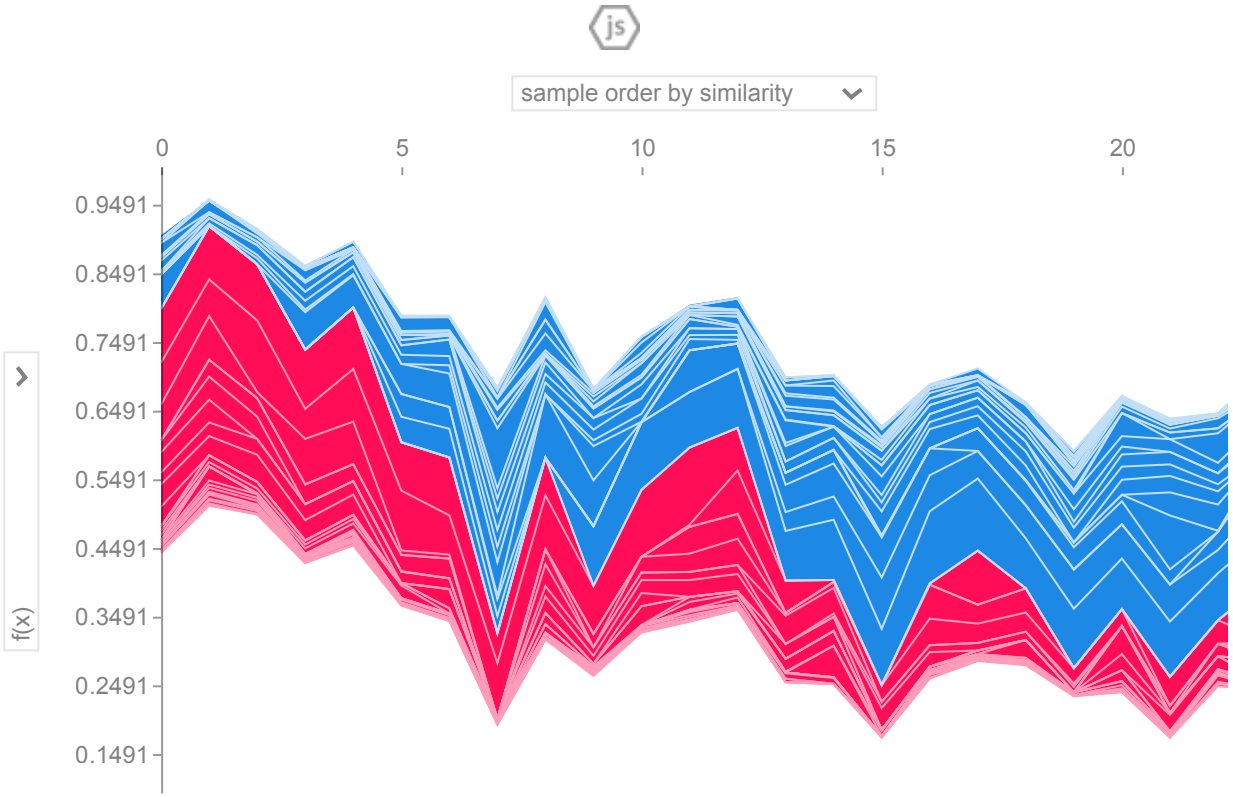
Out[65]:



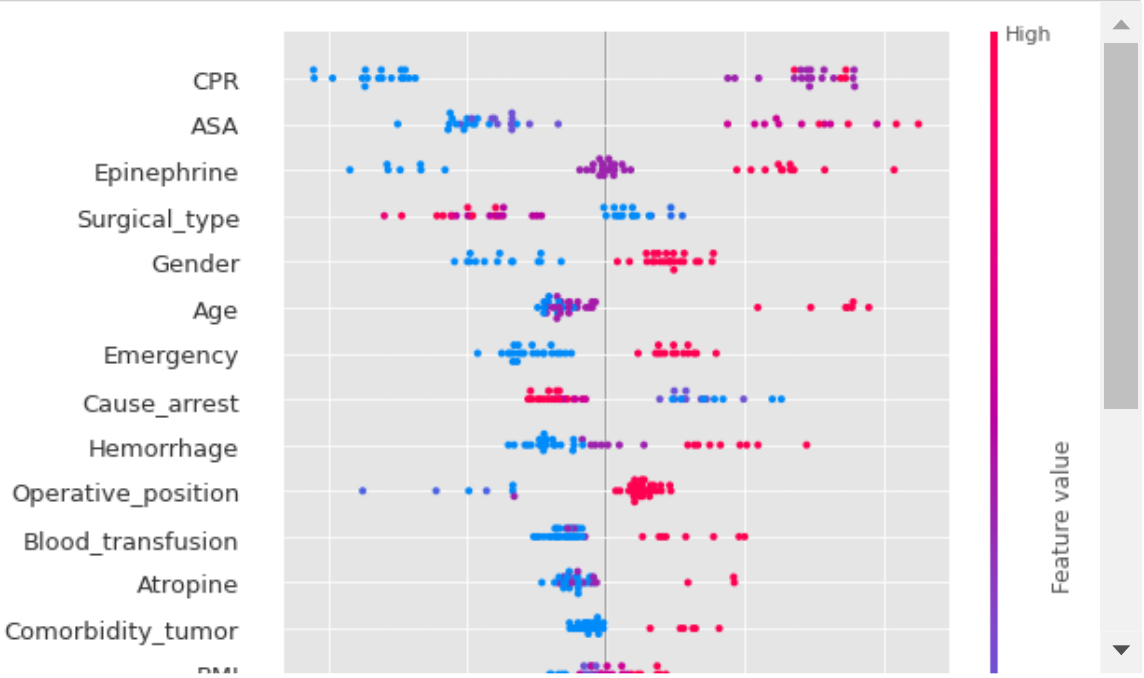
In [66]:

```
#Interactive visualization of all sample/feature Shapley values
#It is possible to show the relative contribution of individual features for
# samples on the y-axis as well.
shap.initjs()
shap.force_plot(explainer.expected_value[1], shap_values[1], X_explain)
```

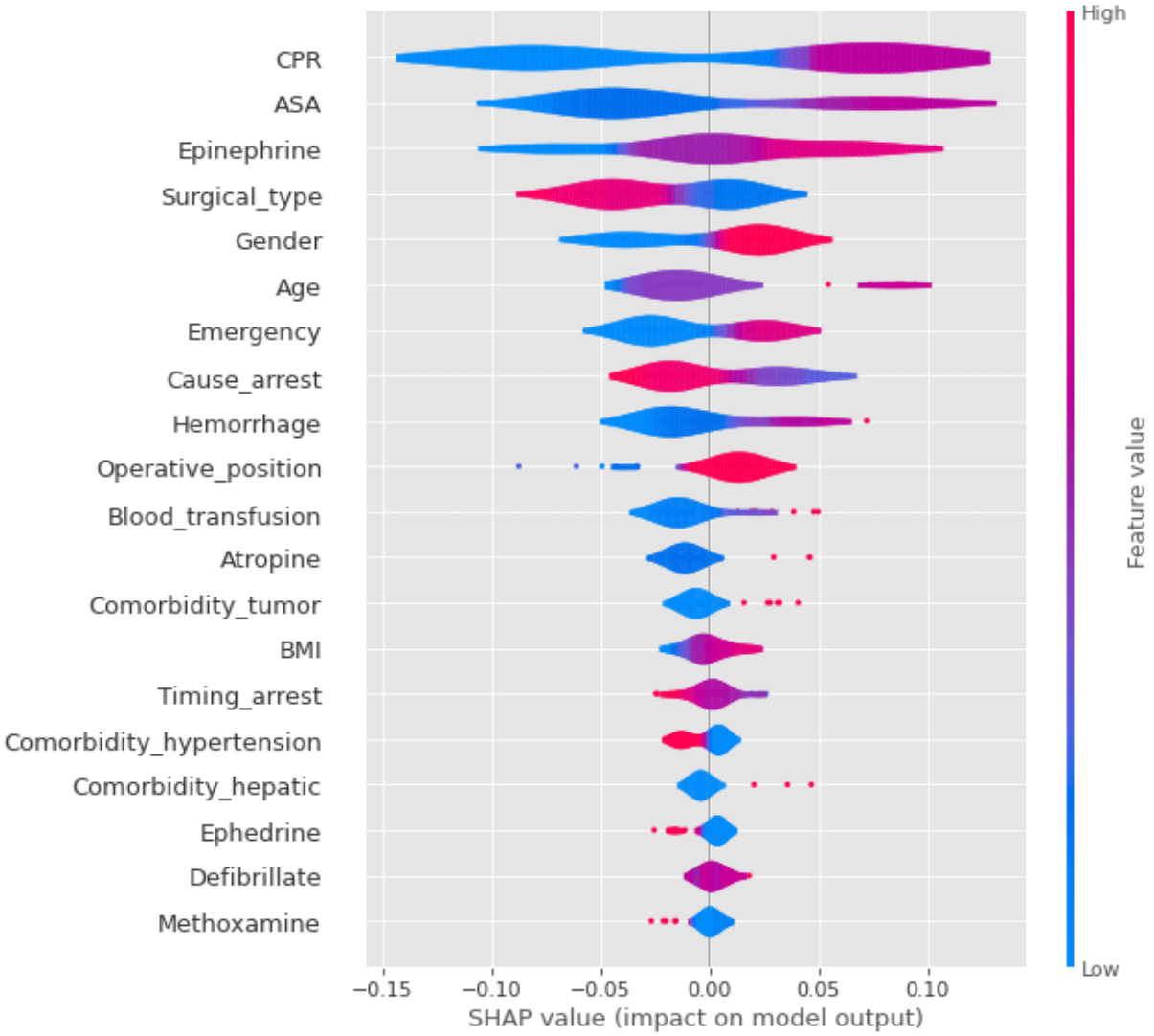
Out[66]:



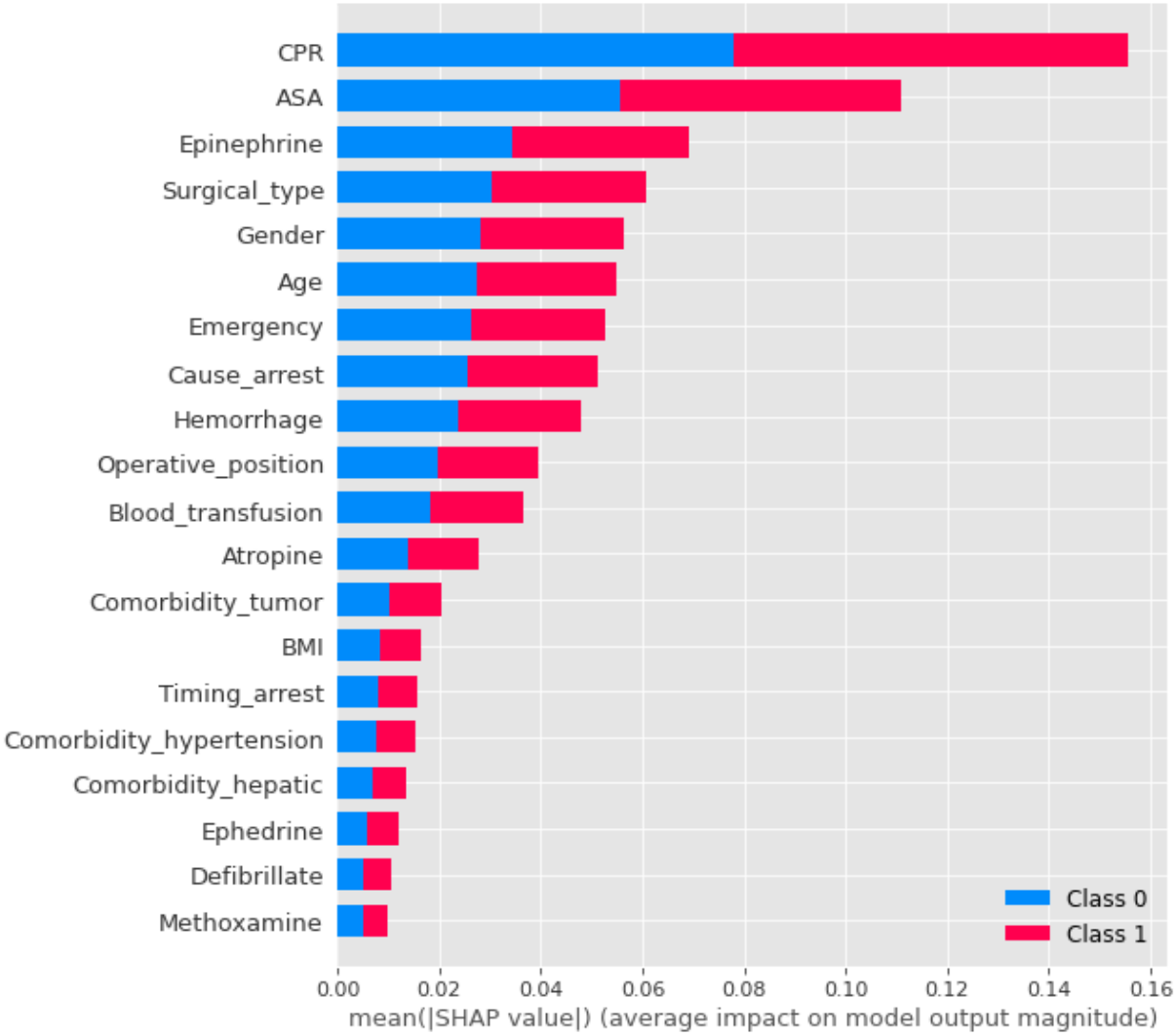
In [67]:
```
#A summary plot with the shapley value (feature importance)
shap.summary_plot(shap_values[1], X_explain)
```



In [68]:
```
#Same as above, but with violin plots to better see the distribution of shap
shap.summary_plot(shap_values[1], X_explain, plot_type="violin")
```



In [69]:
```
shap.summary_plot(shap_values, X_explain, plot_type="bar", show=False)
plt.tight_layout()
plt.savefig('test.png', dpi=300)
```



4. Partial Dependence Plots

Partial Dependency Plots (DPD) show the effect a feature has on the outcome of a predictive based model. It marginalizes the model output over the distribution of features in order to extract the importance of the feature of interest. This importance calculation is based on an important assumption, namely that the feature of interest is not correlated with all other features (except for the target). The reason for this is that it will show data points that are likely to be impossible. For example, weight and height are correlated but the PDP might show the effect of a large weight and very small height on the target while that combination is highly unlikely. This can be partially resolved by showing a rug at the bottom of your PDP.

https://lmc2179.github.io/posts/pdp.html (https://lmc2179.github.io/posts/pdp.html)

In [70]:
```
from pdpbox import pdp
import seaborn as sns
```

In [71]:
```
#data=data_train.drop('Died',1)
df_pdp=data_train_X
```

In [72]:
```
with open(r'C:\Users\neo\Huijie\Code\Predicting CA Mortality\Models\rf_clf_f
    rf_clf = pickle.load(f)
model=rf_clf
```

4.0 Correlation - One-hot Encoding

Below the correlation matrix is shown between features to give an indication of whether the assumption of independence is violated or not. From these features one can conclude that there seems to be no violation seeing as features are not highly correlated. Here we look into the one-hot encoded features.

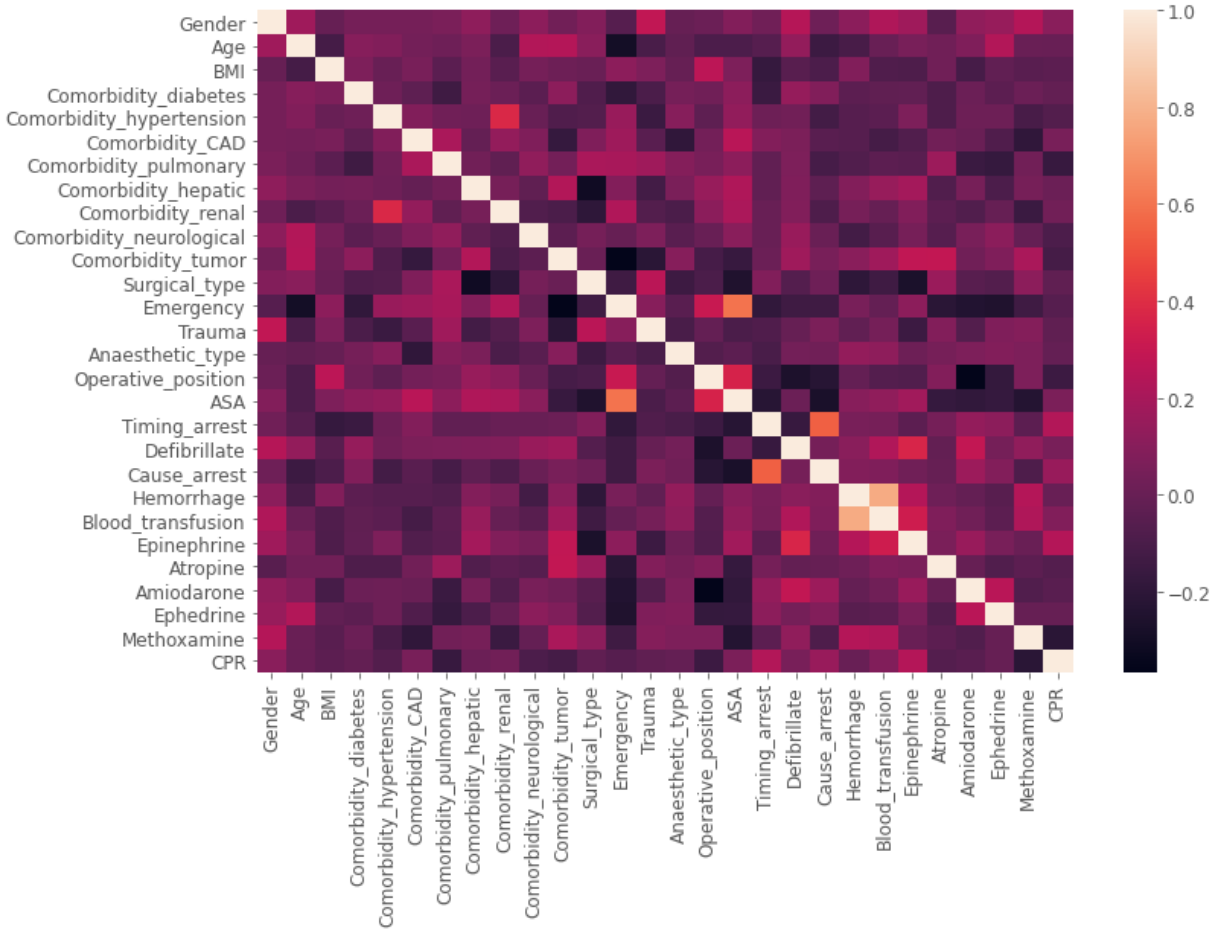
In [73]:
```
df_pdp.head()
```

Out[73]:

	Gender	Age	BMI	Comorbidity_diabetes	Comorbidity_hypertension	Comorbidity_CAD	Comorbi
0	1	2	1	0	1	0	
1	0	2	3	0	0	0	
2	0	1	1	0	0	1	
3	1	2	3	0	1	1	
4	1	2	2	0	1	1	

In [74]:
```
# calculate the correlation matrix
corr = df_pdp.corr()

# plot the heatmap
sns.heatmap(corr,
        xticklabels=corr.columns,
        yticklabels=corr.columns)
```

Out[74]: <AxesSubplot:>



Then I simply extract the features that have the highest absolute correlation by unstacking the correlation matrix and quicksorting it.

In [75]:
```
c = df_pdp.corr().abs()
s = c.unstack()
so = s.sort_values(kind="quicksort")
df_corr = pd.DataFrame(so).reset_index().dropna()
df_corr.columns = ['feature1', 'feature2', 'r']
df_corr = df_corr[df_corr.r < 1].sort_values('r', ascending=False)
df_corr.head(10)
```

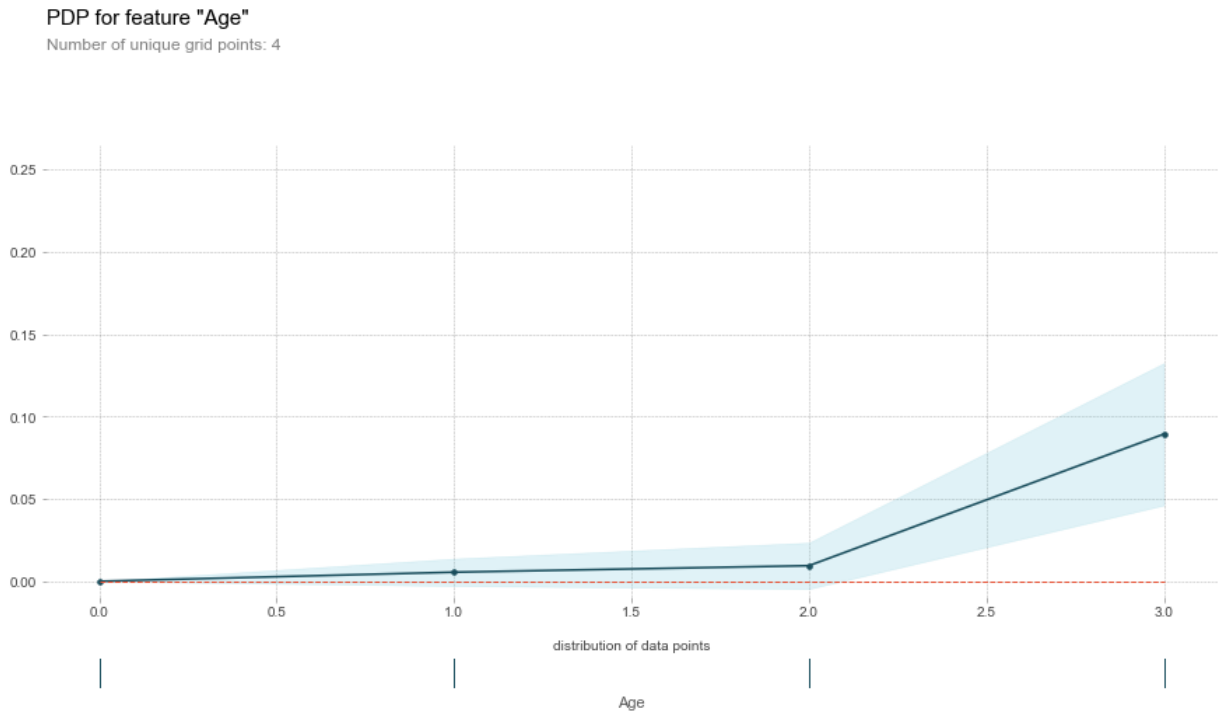
Out[75]:

	feature1	feature2	r
755	Hemorrhage	Blood_transfusion	0.774969
754	Blood_transfusion	Hemorrhage	0.774969
753	ASA	Emergency	0.595407
752	Emergency	ASA	0.595407
751	Timing_arrest	Cause_arrest	0.542557
750	Cause_arrest	Timing_arrest	0.542557
749	Comorbidity_hypertension	Comorbidity_renal	0.378397
748	Comorbidity_renal	Comorbidity_hypertension	0.378397
747	Operative_position	Amiodarone	0.367689
746	Amiodarone	Operative_position	0.367689

4.1 PDP - Single feature

The PDP plot for the feature "Age" shows that until the age of 50 there is a higher chance of earning more as a persons age increases. However, after the age of 50 we see this trend going the other direction, namely that age has a negative effect on the likelihood of earning more.

In [76]:
```
pdp_fare = pdp.pdp_isolate(
    model=rf_clf, dataset=df_pdp[df_pdp.columns[0:28]], model_features=df_pd
)
fig, axes = pdp.pdp_plot(pdp_fare, 'Age', plot_pts_dist=True)
```



In [ ]:
```
1
```