Data analysis and classification

May 9, 2018

```
In [22]: import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plt
         import seaborn as sns

         from sklearn.preprocessing import StandardScaler
         from sklearn.preprocessing import MinMaxScaler
         from sklearn.metrics import f1_score
         from sklearn.metrics import precision_score
         from sklearn.metrics import accuracy_score
         from sklearn.metrics import auc
         from sklearn.metrics import roc_curve
         from sklearn.metrics import recall_score

         from sklearn.tree import DecisionTreeClassifier
         from sklearn.linear_model import LogisticRegression
         from sklearn import svm
         from sklearn.naive_bayes import GaussianNB
         from sklearn.naive_bayes import MultinomialNB
         from sklearn.gaussian_process import GaussianProcessClassifier
         from sklearn.gaussian_process.kernels import RBF
         from sklearn.gaussian_process.kernels import ConstantKernel as C

         from sklearn.model_selection import KFold
         import matplotlib.patches as mpatches
```

0.1 Importing the data

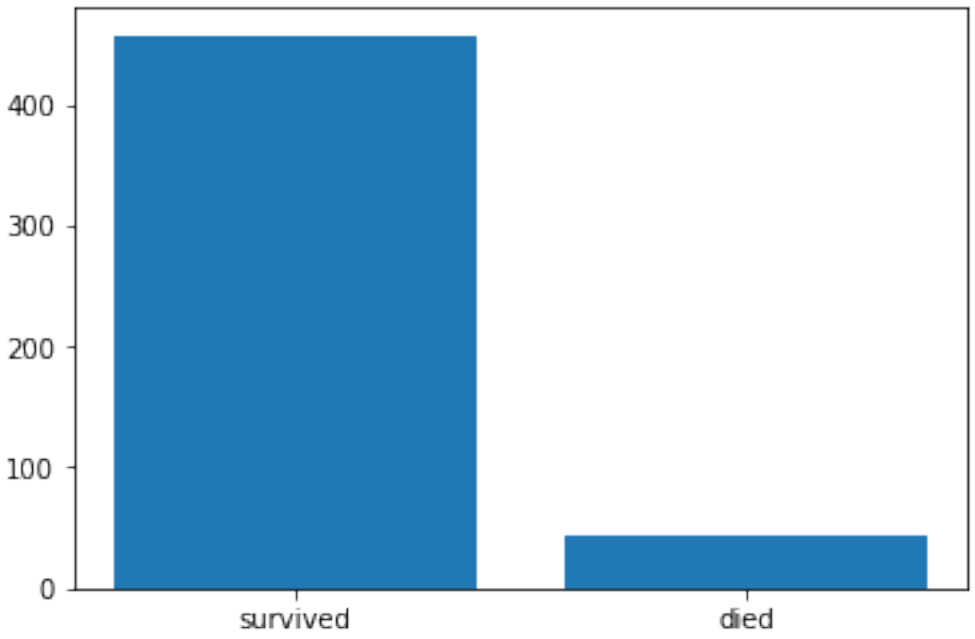
```
In [34]: data = pd.read_csv("neonatal_basic_data.csv")
         training_set = data[data['death']!=0]
         training_labels = training_set['death']
         training_data = training_set[['ga', 'bw']]
         test_set = data[data['death']==0]
         #test_labels = test_set['death']
         test_data = test_set[['ga', 'bw']]
```

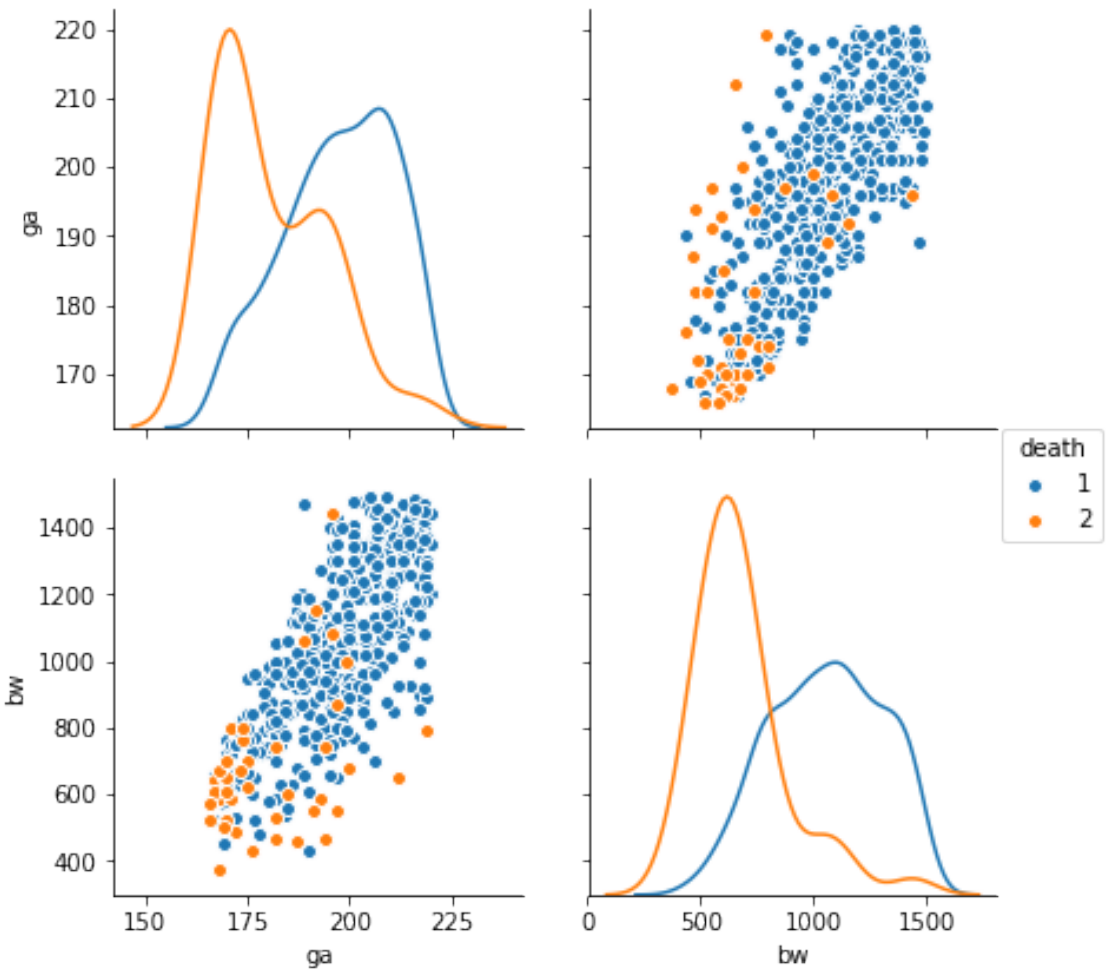
0.1.1 Scaling the data

```
In [35]: scaler = StandardScaler()
         training_data_stand = scaler.fit_transform(training_data)
         test_data_stand = scaler.fit_transform(test_data)

         minmaxscaler = MinMaxScaler()
         training_data_minmax = minmaxscaler.fit_transform(training_data)
         test_data_minmax = minmaxscaler.fit_transform(test_data)
```

0.2 Visualization of the class distribution

```
In [36]: labels = training_labels.as_matrix()
         classes, distribution = np.unique(labels, return_counts=True)
         plt.bar(classes, distribution)
         plt.xticks(classes, ["survived", "died"])
         plt.show()

         sns.pairplot(training_set[['ga', 'bw', 'death']]
                      , hue="death"
                      , vars=['ga', 'bw']
                      , diag_kind="kde"
                      #, kind="reg"
                      , size=3
                     )
         plt.show()
```

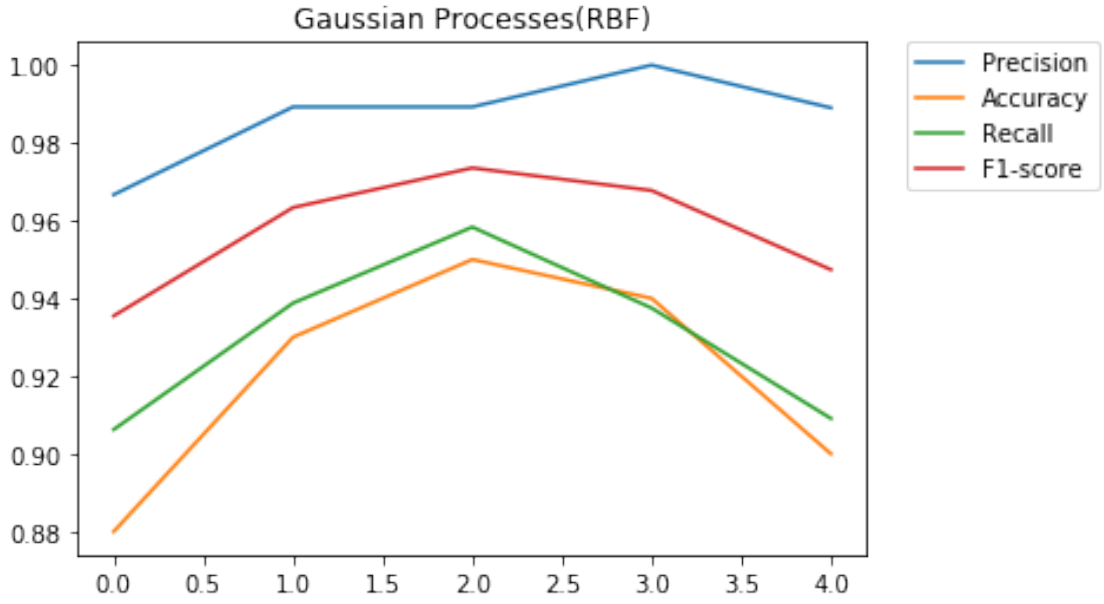




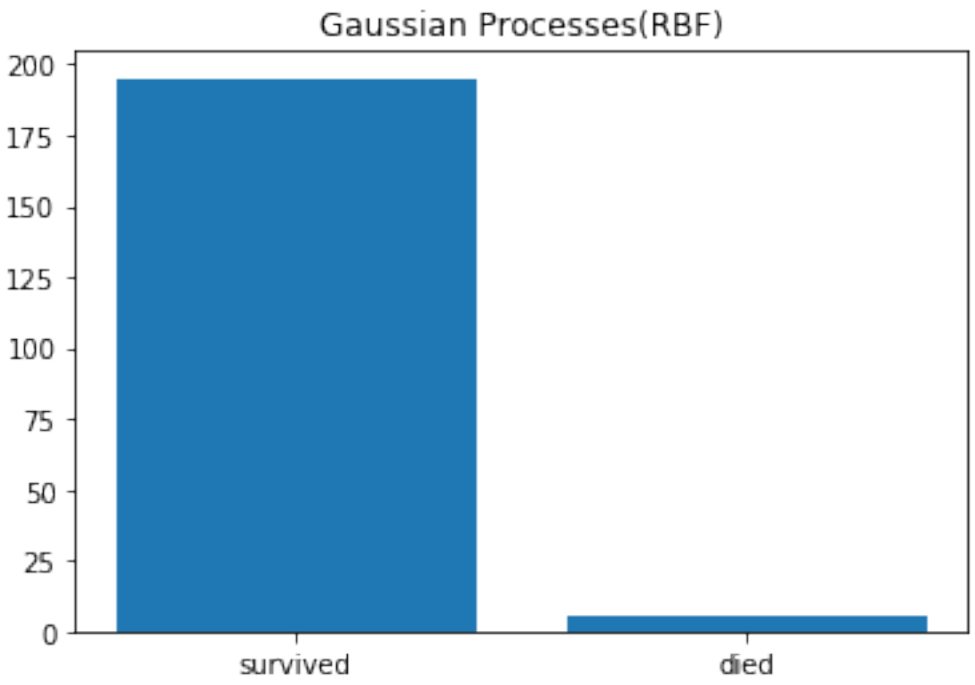

```
In [37]: #kernel = 1.0 * C(constant_value=1.0) + 1.0 * RBF(length_scale=1.0)
         kernel = 1.0 * RBF(length_scale=1.0)
         clfs = [(GaussianProcessClassifier(kernel=kernel, optimizer=None),"Gaussian Processes(R
                 , (svm.SVC(class_weight='balanced', kernel='rbf'),"SVM")
                 , (DecisionTreeClassifier(),"Decision tree")
                 , (LogisticRegression(),"Logistic regression")
                 , (GaussianNB(),"Gaussian naive Bayes")
                ]

         for clf, method_name in clfs:
             misclassif_lst = []
             precision_lst = []
             accuracy_lst = []
             recall_lst = []
             f1_lst = []
```

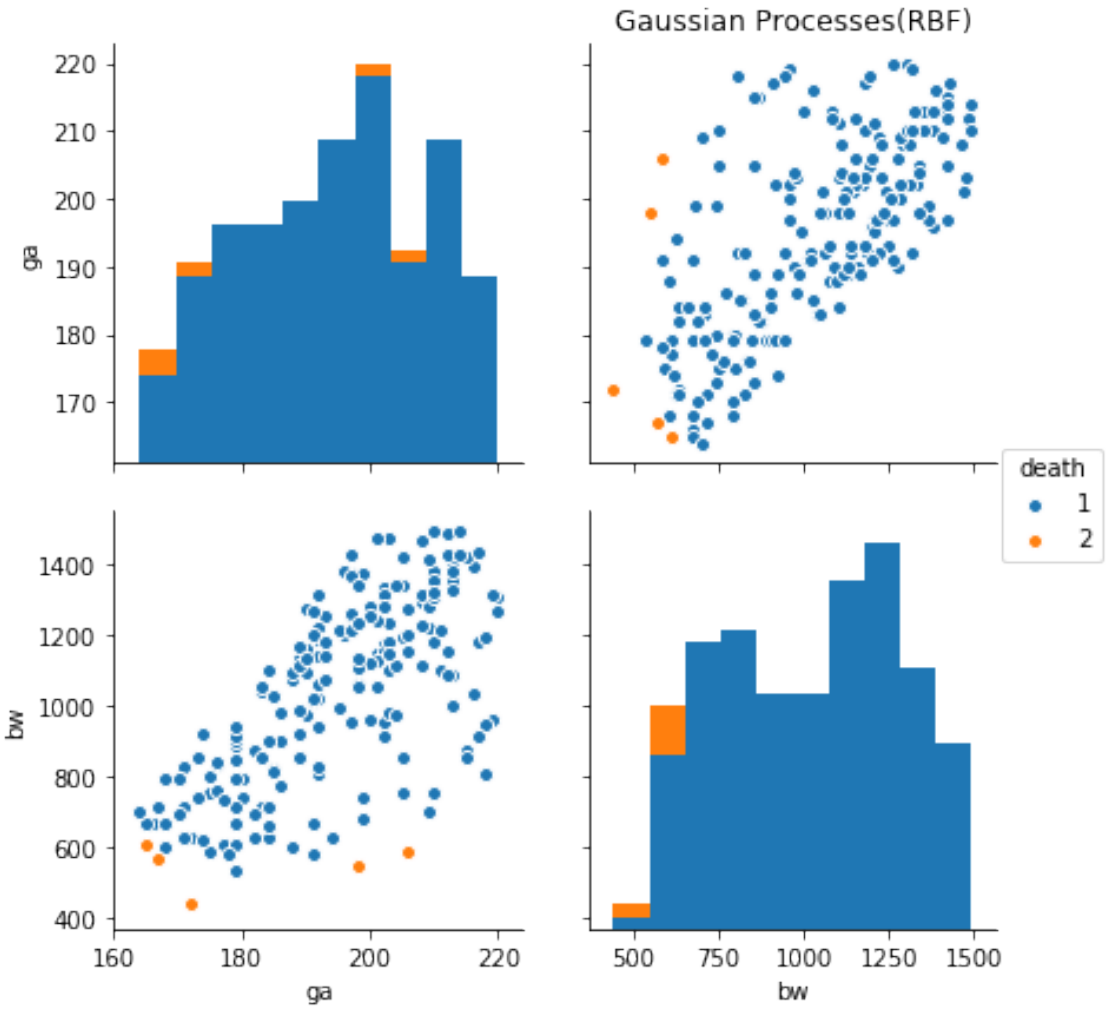
```
kf = KFold(n_splits=5)
for train_index, test_index in kf.split(training_data_stand):
    X_train, X_test = training_data_stand[train_index], training_data_stand[test_in
    y_train, y_test = training_labels[train_index], training_labels[test_index]
    clf.fit(X_train, y_train)
    y_pred = clf.predict(X_test)
    misclassif = np.sum(y_pred!=y_test)
    precision = precision_score(y_pred, y_test)
    accuracy = accuracy_score(y_pred, y_test)
    recall = recall_score(y_pred, y_test)
    f1 = f1_score(y_pred, y_test)

    misclassif_lst.append(misclassif)
    precision_lst.append(precision)
    accuracy_lst.append(accuracy)
    recall_lst.append(recall)

    f1_lst.append(f1)

plt.plot(range(5), precision_lst, label="Precision")
plt.plot(range(5), accuracy_lst, label="Accuracy")
plt.plot(range(5), recall_lst, label="Recall")
plt.plot(range(5), f1_lst, label="F1-score")
plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
plt.title(method_name)
plt.show()

print("Average on k-fold cross validation")
print("misclassif error:", np.mean(misclassif_lst))
print("precision:", np.mean(precision_lst))
print("accuracy:", np.mean(accuracy_lst))
print("recall:", np.mean(recall_lst))
print("f1:", np.mean(f1_lst))

clf.fit(training_data_stand, training_labels)
p = clf.predict(test_data_stand)

classes, distribution = np.unique(p, return_counts=True)
plt.bar(classes, distribution)
plt.title(method_name)
plt.xticks(classes, ["survived", "died"])
plt.show()

pred = pd.DataFrame(data={#'patientid':test_set['patientid'].as_matrix(),
                          'ga':test_set['ga'].as_matrix(), 'bw':test_set['bw'].a

if method_name=="Gaussian Processes(RBF)":
    gp_pred = pred
```

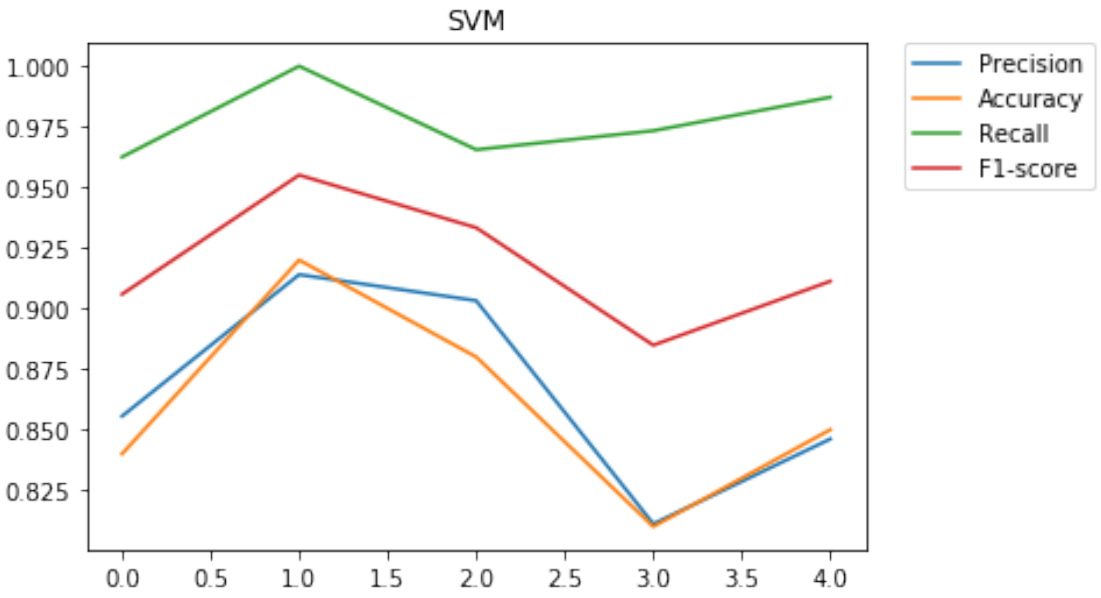
```
elif method_name=="SVM":
    svm_pred = pred
elif method_name=="Decision tree":
    dt_pred = pred
elif method_name=="Logistic regression":
    lr_pred = pred
elif method_name=="Gaussian naive Bayes":
    gnb_pred = pred

sns.pairplot(pred[['ga', 'bw', 'death']]
             , hue="death"
             , vars=['ga', 'bw']
             #, diag_kind="kde"
             #, kind="reg"
             , size=3
            )
plt.title(method_name)
plt.show()
```



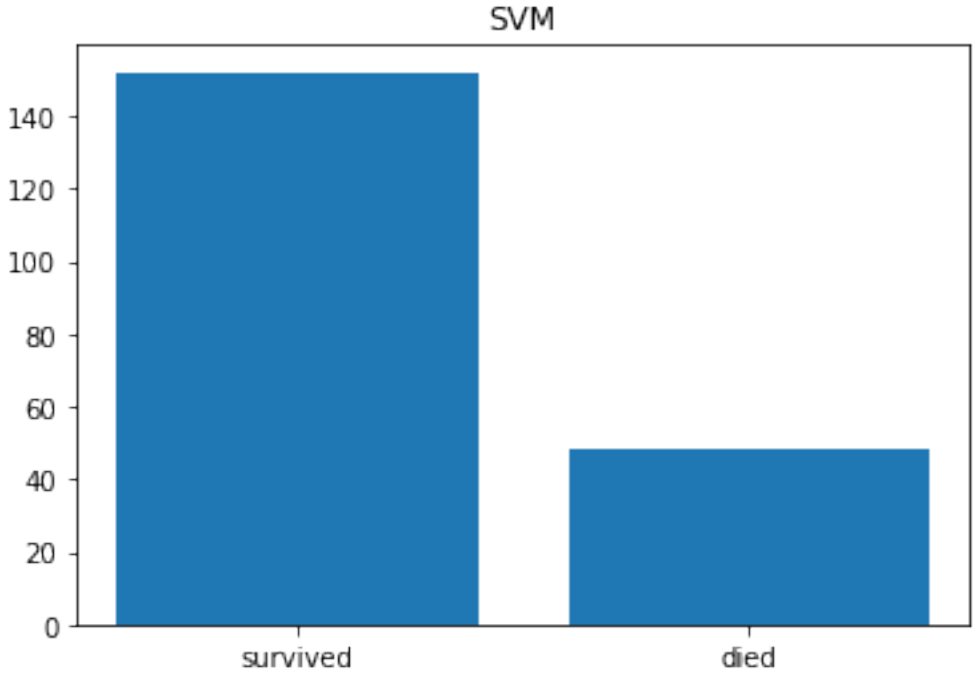

```
Average on k-fold cross validation
('misclassif error:', 8.0)
('precision:', 0.98683445586671392)
('accuracy:', 0.91999999999999993)
('recall:', 0.92998995052566491)
('f1:', 0.95749799727790652)
```

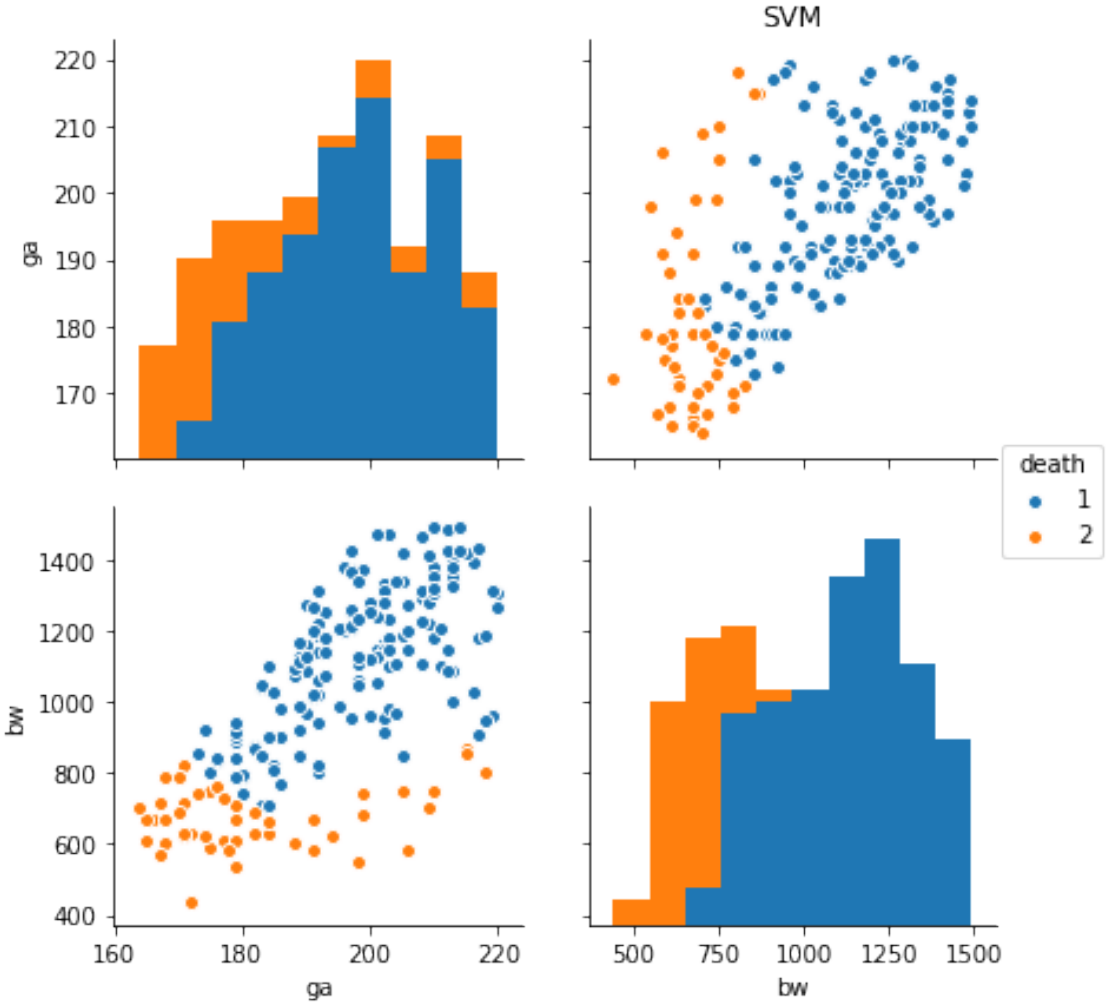

Gaussian Processes(RBF)
200
175
150
125
100
75
50
25
0
survived
died

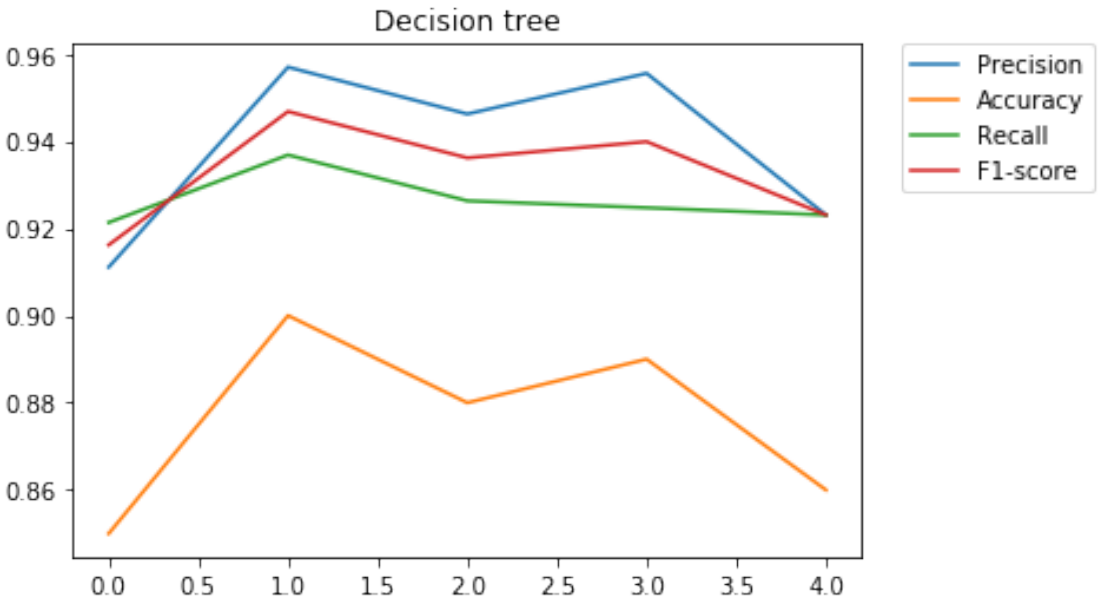

Gaussian Processes(RBF)
ga
bw
death
1
2
220
210
200
190
180
170
1400
1200
1000
800
600
400
160
180
200
220
500
750
1000
1250
1500



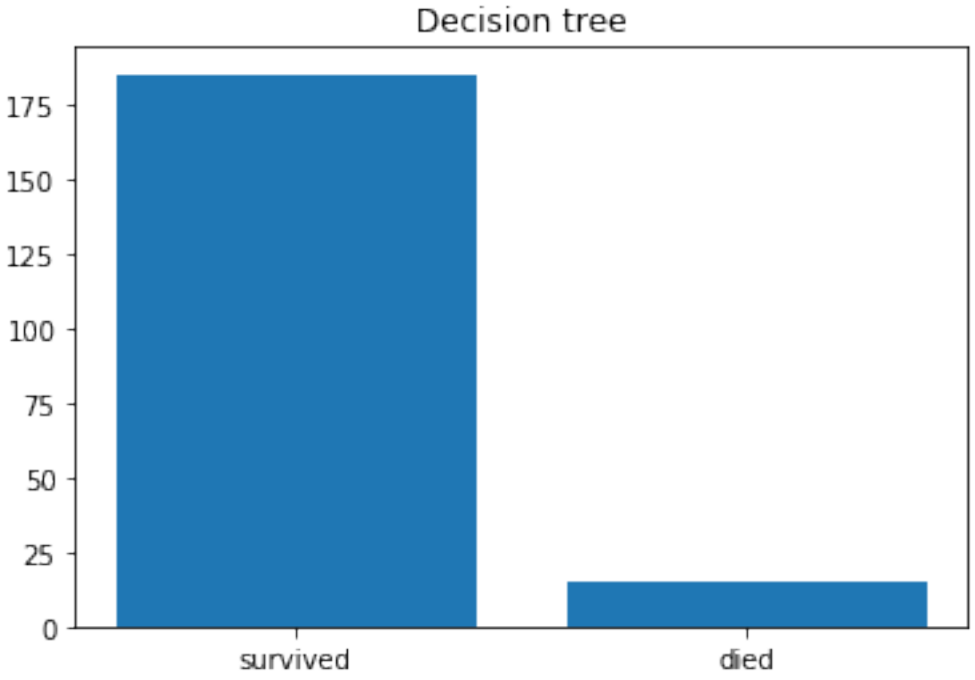

```
Average on k-fold cross validation
('misclassif error:', 14.0)
('precision:', 0.86600496277915617)
('accuracy:', 0.85999999999999999)
('recall:', 0.97770601237842614)
('f1:', 0.91807259088971416)
```

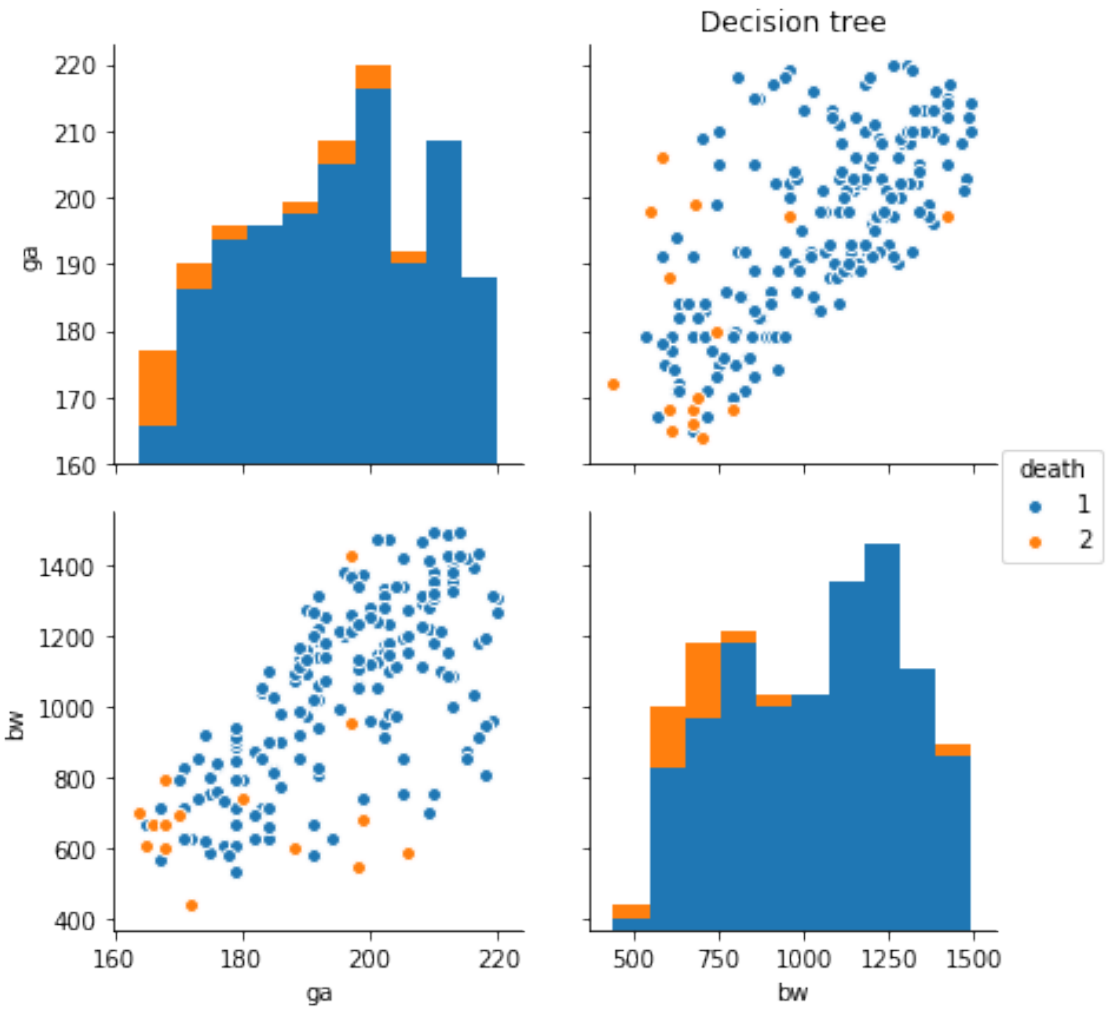


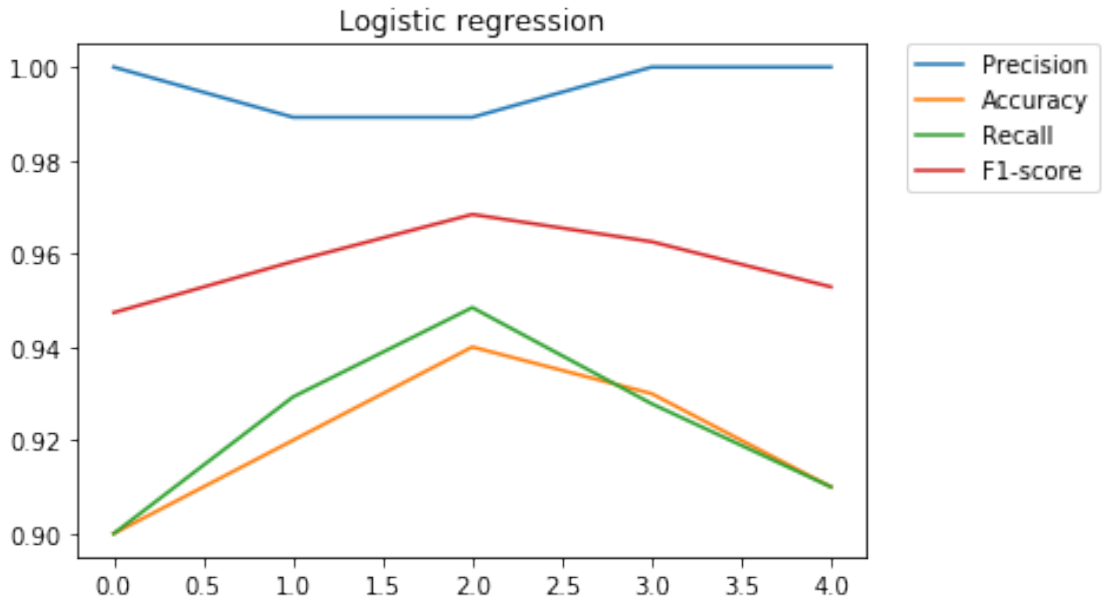

SVM
ga
bw
death
1
2
220
210
200
190
180
170
1400
1200
1000
800
600
400
160
180
200
220
500
750
1000
1250
1500



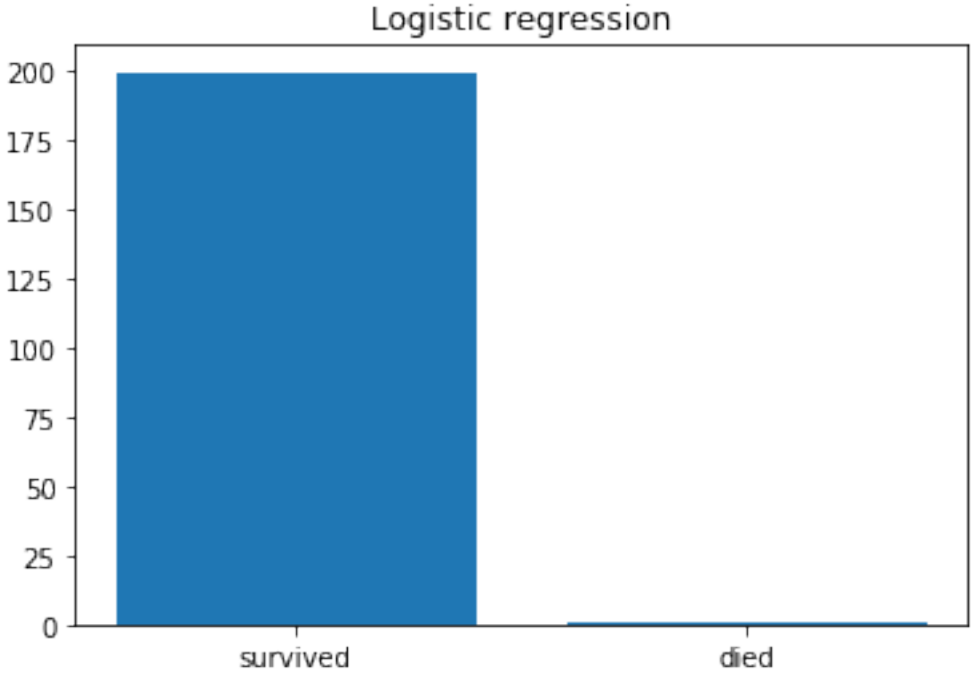

```
Average on k-fold cross validation
('misclassif error:', 12.4)
('precision:', 0.93859387923904047)
('accuracy:', 0.876)
('recall:', 0.92646286304324121)
('f1:', 0.93242949483642568)
```

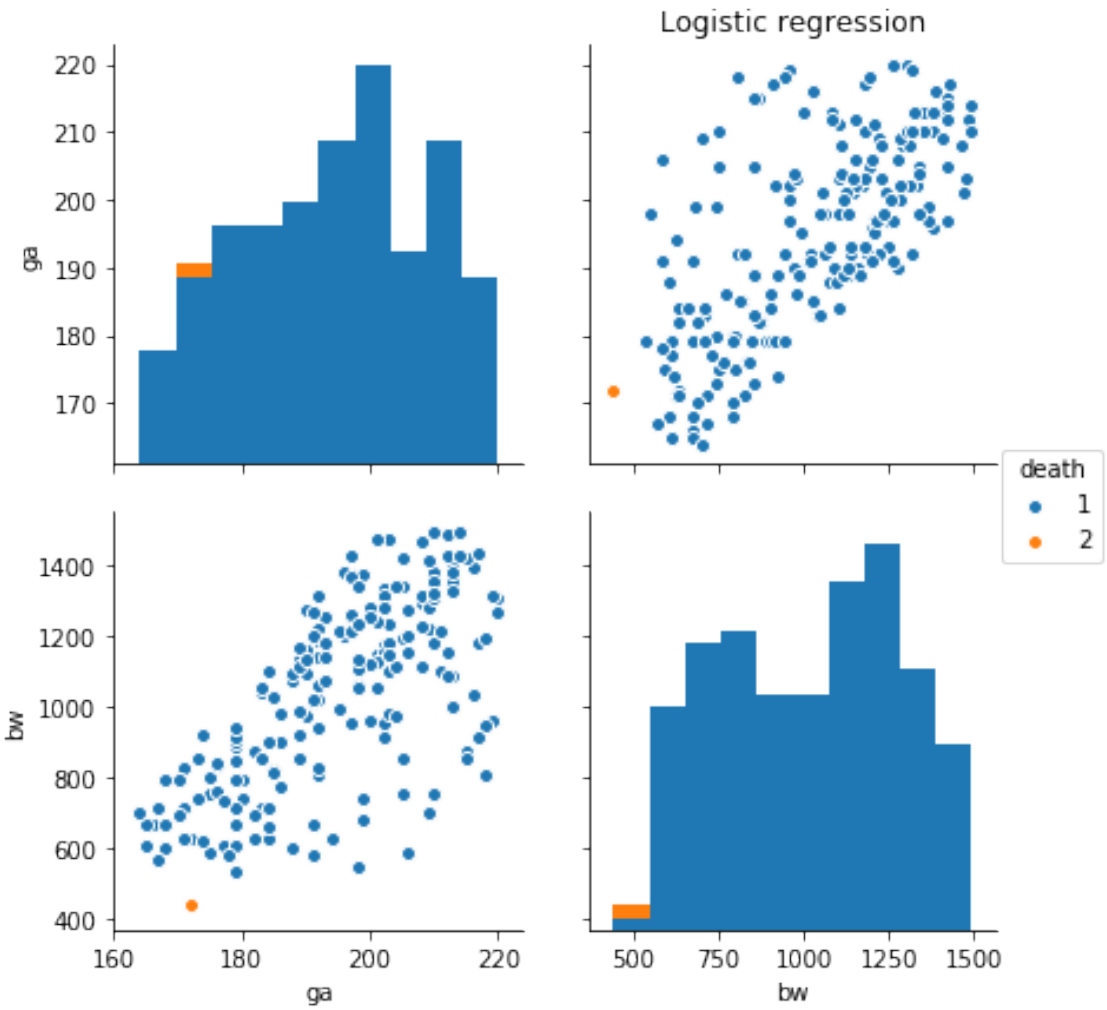


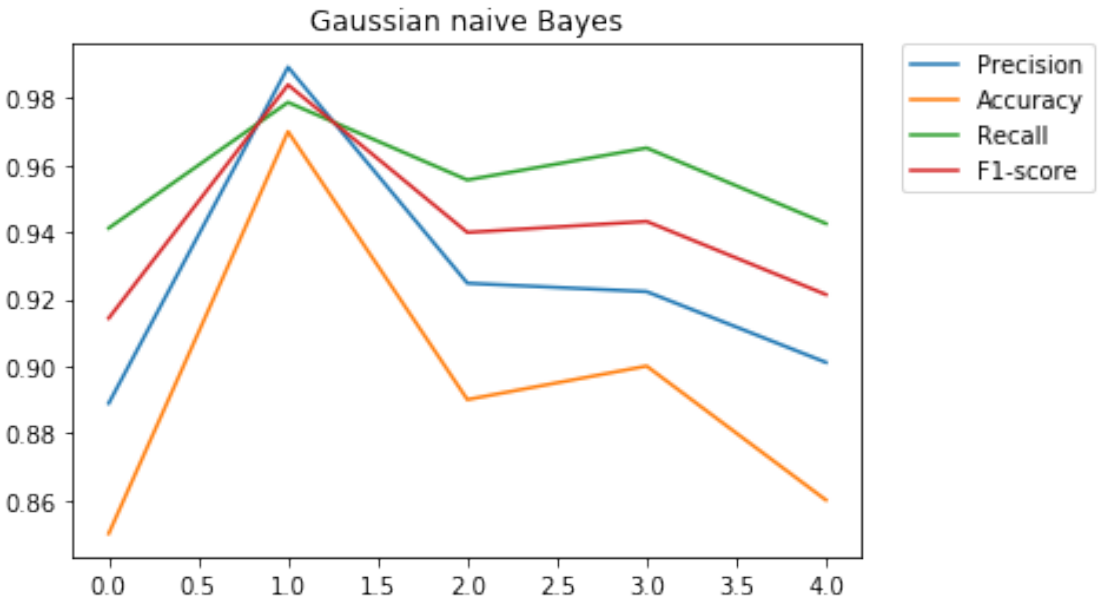

Decision tree
ga
bw
death
1
2
160
170
180
190
200
210
220
400
600
800
1000
1200
1400
500
750
1000
1250
1500



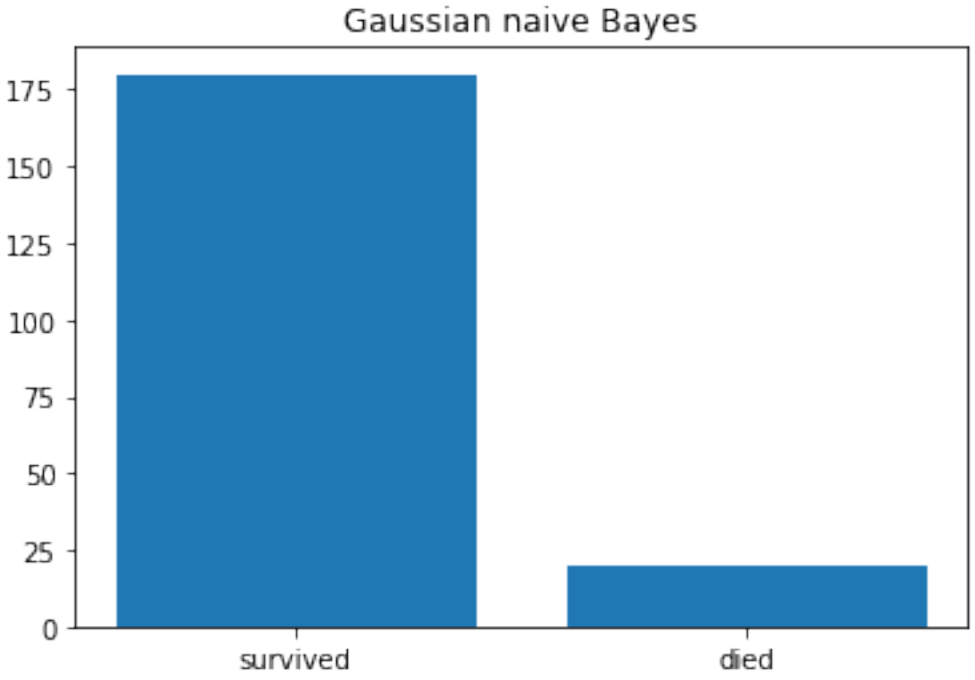

```
Average on k-fold cross validation
('misclassif error:', 8.0)
('precision:', 0.99569892473118282)
('accuracy:', 0.91999999999999993)
('recall:', 0.92311631781734893)
('f1:', 0.95791384661783252)
```

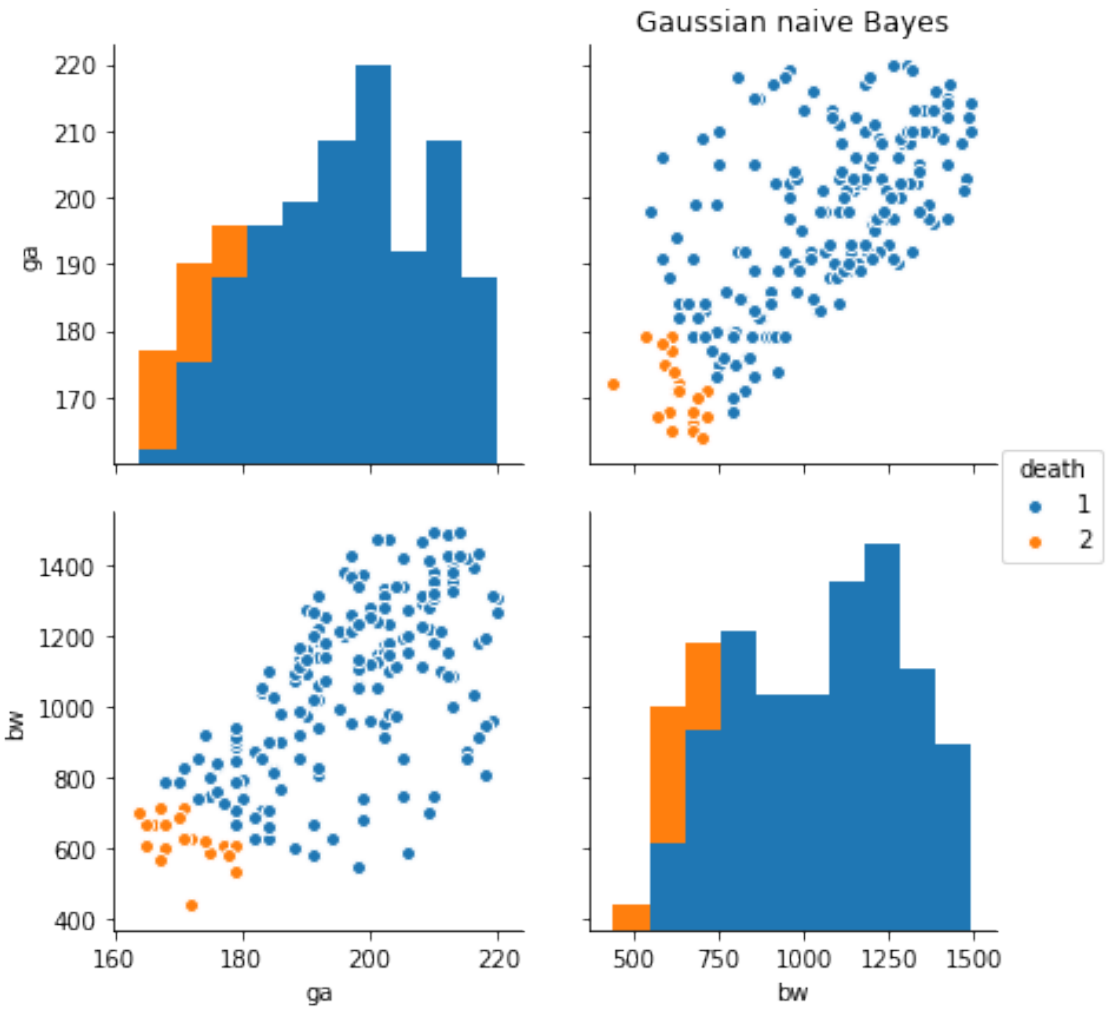



Logistic regression
ga
bw
death
1
2
220
210
200
190
180
170
1400
1200
1000
800
600
400
160
180
200
220
500
750
1000
1250
1500




```
Average on k-fold cross validation
('misclassif error:', 10.6)
('precision:', 0.92523770136673367)
('accuracy:', 0.89399999999999991)
('recall:', 0.95662008902021223)
('f1:', 0.94053275534162495)
```



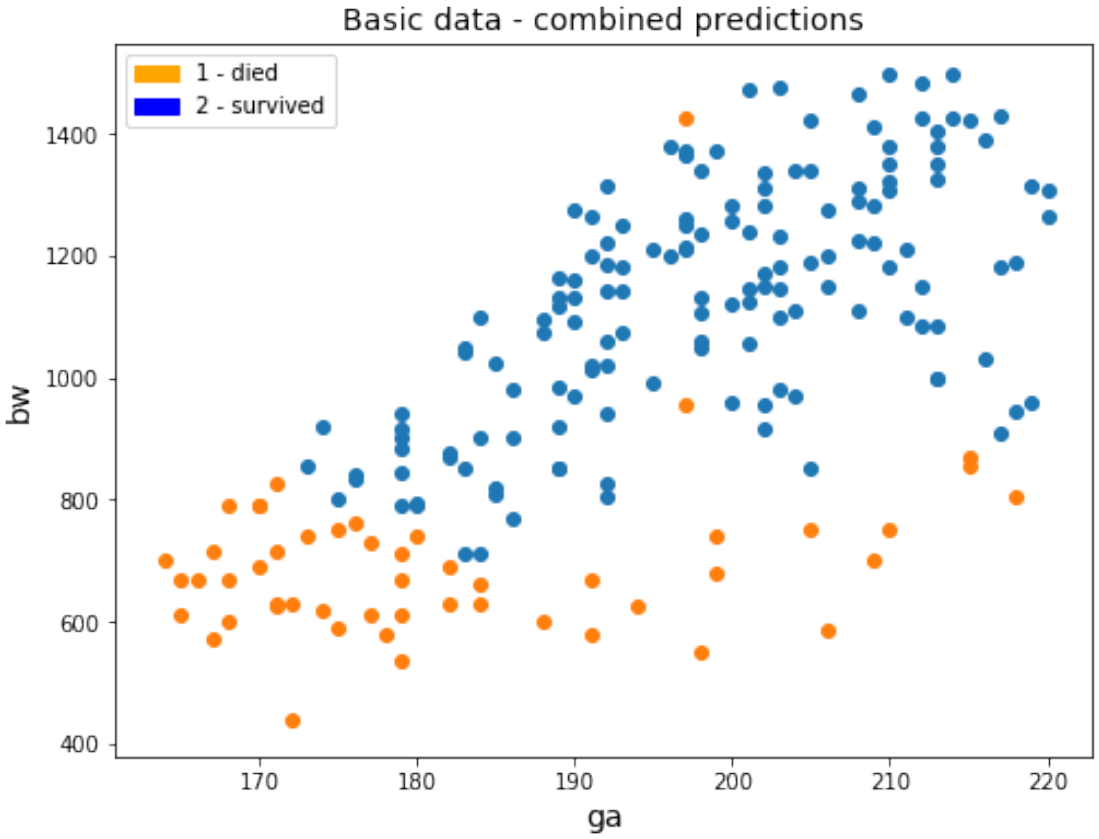


0.3 Mixing prediction

Final prediction are: - Survived: if all the models agree that the patient survived - Died: if at least one of the model classify the patient as died

```
In [39]: pred = pd.DataFrame(data={'patientid':test_set['patientid'].as_matrix(),
                                   'ga':test_set['ga'].as_matrix(), 'bw':test_set['bw'].as_ma
             , 'death_dt':dt_pred['death'], 'death_svm':svm_pred['death'], 'death_lr':lr_pred['d
             , 'death_gnb':gnb_pred['death'], 'death_gp':gp_pred['death']})

         died = pred.loc[(pred['death_lr'] == 2) | (pred['death_dt'] == 2) | (pred['death_svm']=
         survived = pred.loc[(pred['death_lr'] == 1) & (pred['death_dt'] == 1) & (pred['death_sv
         plt.figure(figsize=(8,6))
```

```
plt.scatter(survived['ga'], survived['bw'])
plt.scatter(died['ga'], died['bw'])
plt.xlabel("ga", fontsize=14)
plt.ylabel("bw", fontsize=14)

orange_patch = mpatches.Patch(color='orange', label='1 - died')
blue_patch = mpatches.Patch(color='blue', label='2 - survived')
plt.legend(handles=[orange_patch, blue_patch])
plt.title("Basic data - combined predictions", fontsize=14)
plt.show()
```



0.4 Time-series data classification

In [29]:
```
ts = pd.read_csv("timeseries.csv", names=['patientid','mean ABP_S','var ABP_S','slope A
training_data = ts[ts['patientid'].isin(data[data['death']!=0]['patientid'])]
training_data.drop(['patientid'], axis=1)
test_data = ts[ts['patientid'].isin(data[data['death']==0]['patientid'])]
test_data.drop(['patientid'], axis=1)
ts.shape
```

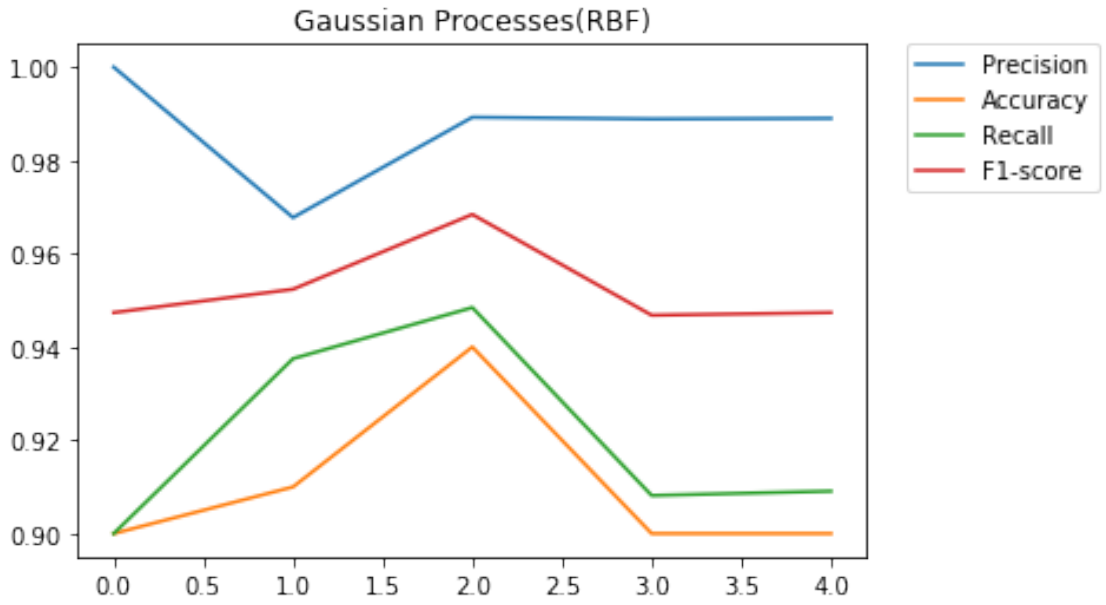
Out[29]:
```
(700, 21)
```

```
In [30]: scaler = StandardScaler()
         training_data_stand = scaler.fit_transform(training_data)
         test_data_stand = scaler.fit_transform(test_data)

         minmaxscaler = MinMaxScaler()
         training_data_minmax = minmaxscaler.fit_transform(training_data)
         test_data_minmax = minmaxscaler.fit_transform(test_data)
```

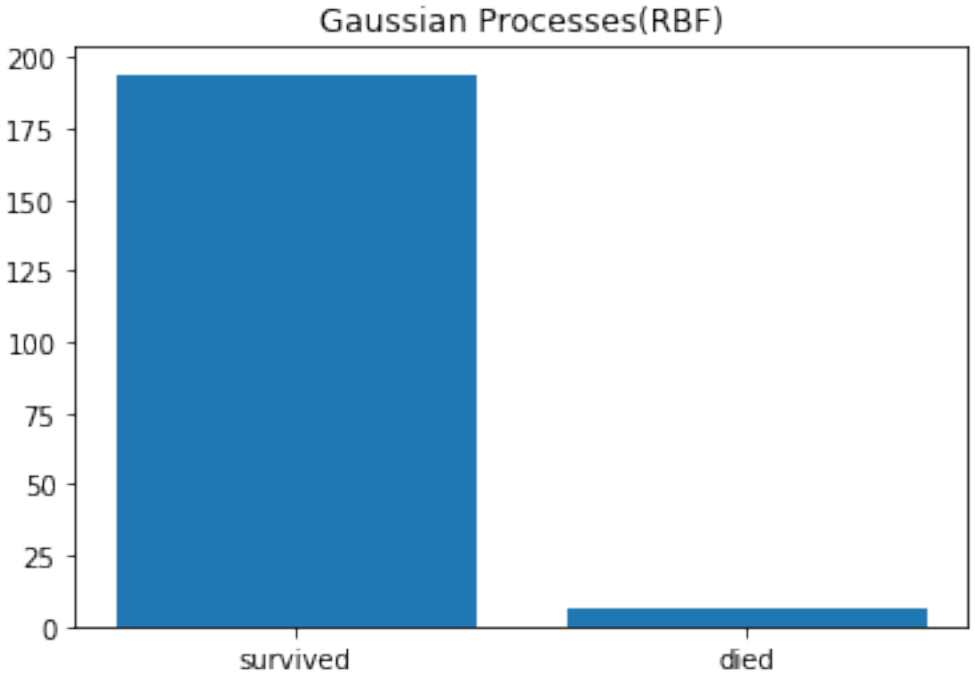
0.5 Evaluation of classifier via K-fold cross-validation

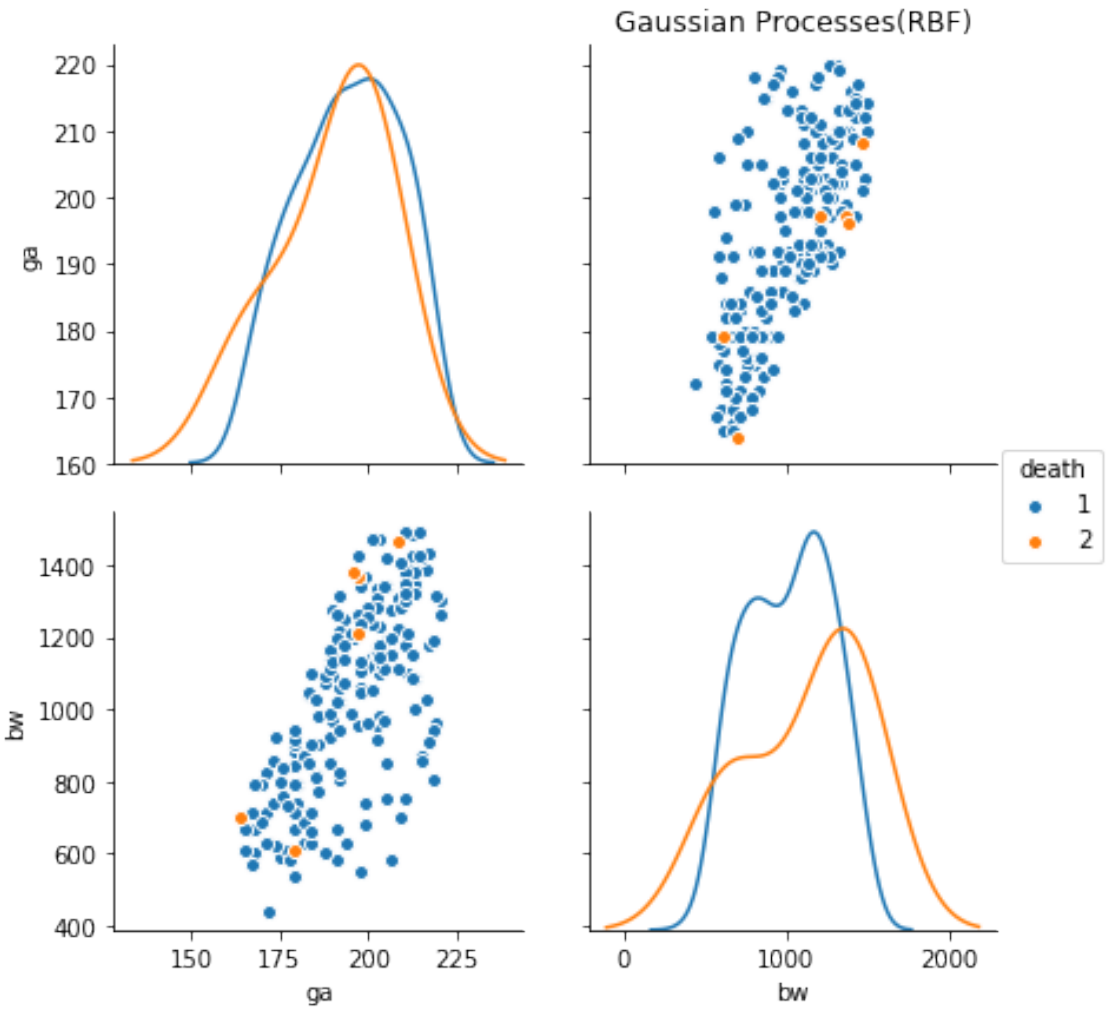
```
In [31]: for clf, method_name in clfs:
             misclassif_lst = []
             precision_lst = []
             accuracy_lst = []
             recall_lst = []
             f1_lst = []

             kf = KFold(n_splits=5)
             for train_index, test_index in kf.split(training_data_stand):
                 X_train, X_test = training_data_stand[train_index], training_data_stand[test_in
                 y_train, y_test = training_labels[train_index], training_labels[test_index]
                 clf.fit(X_train, y_train)
                 y_pred = clf.predict(X_test)
                 misclassif = np.sum(y_pred!=y_test)
                 precision = precision_score(y_pred, y_test)
                 accuracy = accuracy_score(y_pred, y_test)
                 recall = recall_score(y_pred, y_test)
                 f1 = f1_score(y_pred, y_test)

                 misclassif_lst.append(misclassif)
                 precision_lst.append(precision)
                 accuracy_lst.append(accuracy)
                 recall_lst.append(recall)

                 f1_lst.append(f1)

             plt.plot(range(5), precision_lst, label="Precision")
             plt.plot(range(5), accuracy_lst, label="Accuracy")
             plt.plot(range(5), recall_lst, label="Recall")
             plt.plot(range(5), f1_lst, label="F1-score")
             plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
             plt.title(method_name)
             plt.show()

             print("Average on k-fold cross validation")
             print("misclassif error:", np.mean(misclassif_lst))
             print("precision:", np.mean(precision_lst))
             print("accuracy:", np.mean(accuracy_lst))
```

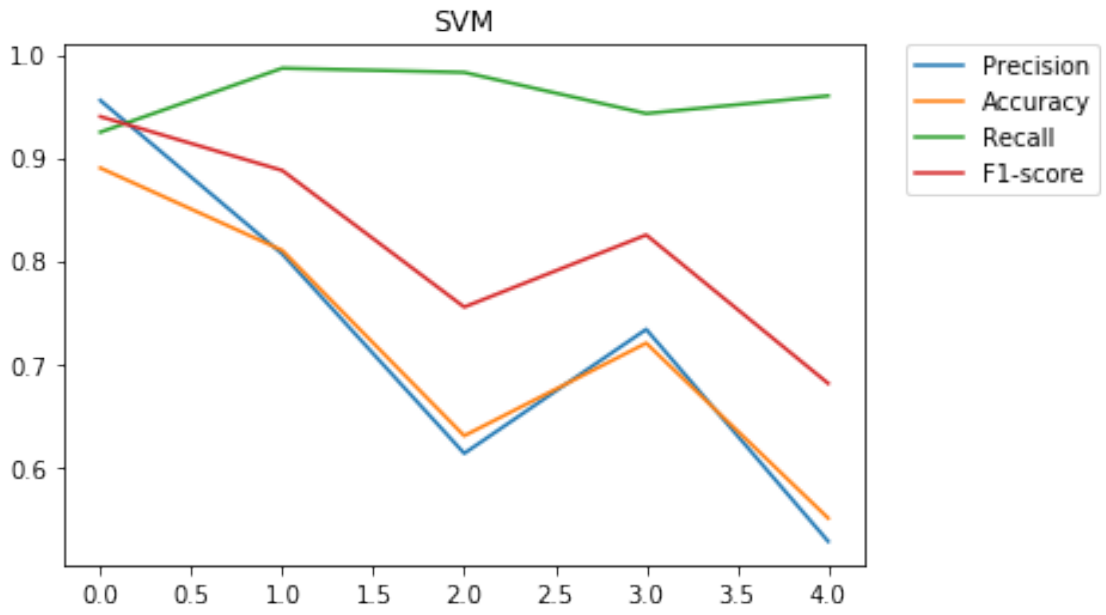
```
print("recall:", np.mean(recall_lst))
print("f1:", np.mean(f1_lst))

clf.fit(training_data_stand, training_labels)
p = clf.predict(test_data_stand)

classes, distribution = np.unique(p, return_counts=True)
plt.bar(classes, distribution)
plt.title(method_name)
plt.xticks(classes, ["survived", "died"])
plt.show()

pred = pd.DataFrame(data={#'patientid':test_set['patientid'].as_matrix(),
                          'ga':test_set['ga'].as_matrix(), 'bw':test_set['bw'].a

if method_name=="Gaussian Processes(RBF)":
    gp_pred = pred
elif method_name=="SVM":
    svm_pred = pred
elif method_name=="Decision tree":
    dt_pred = pred
elif method_name=="Logistic regression":
    lr_pred = pred
#elif method_name=="Gaussian naive Bayes":
#    gnb_pred = pred

sns.pairplot(pred[['ga', 'bw', 'death']]
             , hue="death"
             , vars=['ga', 'bw']
             , diag_kind="kde"
             #, kind="reg"
             , size=3
            )
plt.title(method_name)
plt.show()
```



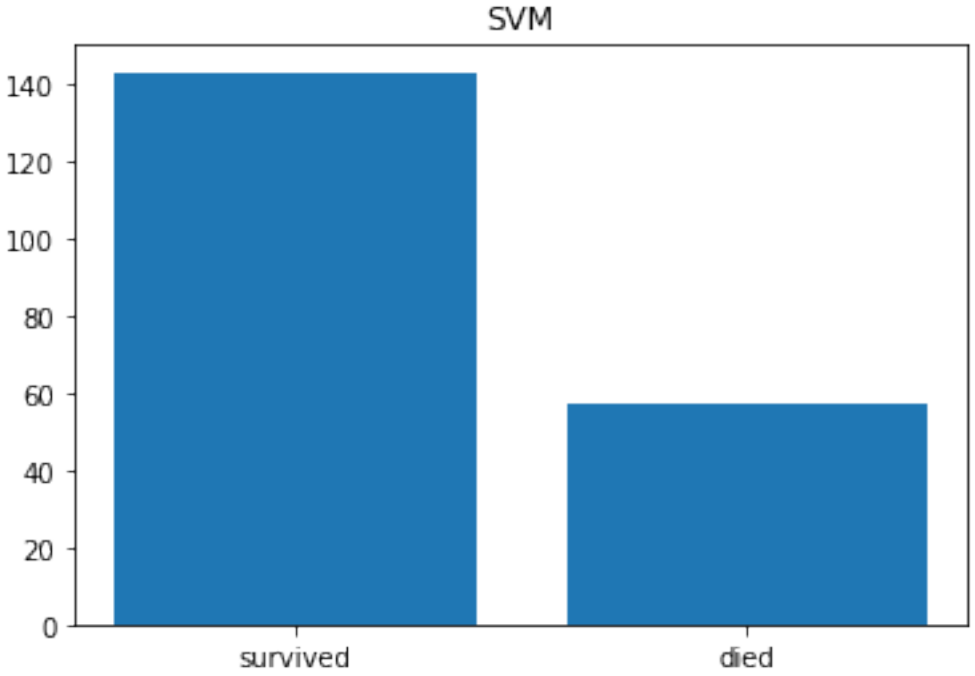

```
Average on k-fold cross validation
('misclassif error:', 9.0)
('precision:', 0.98697782504234122)
('accuracy:', 0.90999999999999992)
('recall:', 0.92064155652889068)
('f1:', 0.95246947155121853)
```

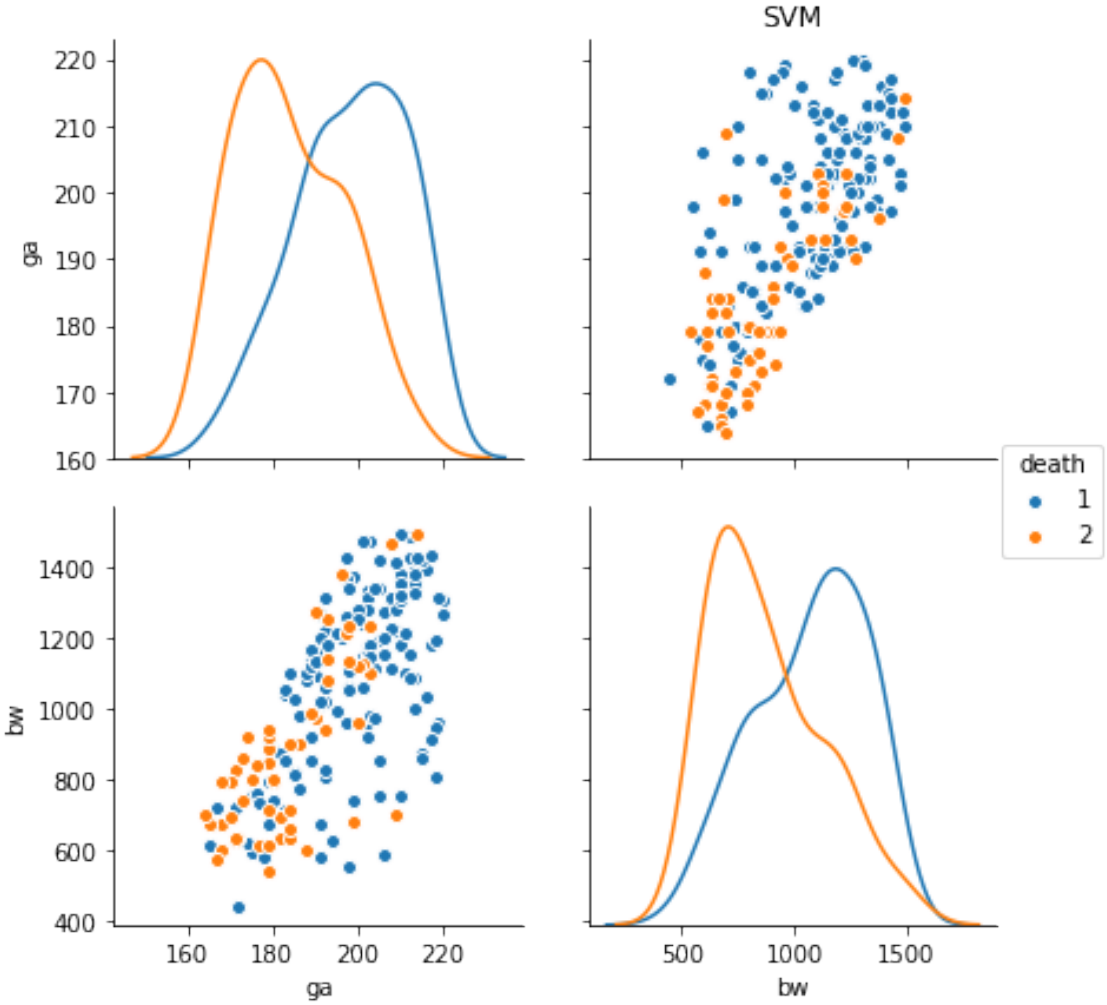



Gaussian Processes(RBF)
ga
bw
death
1
2
220
210
200
190
180
170
160
1400
1200
1000
800
600
400
150
175
200
225
0
1000
2000




```
Average on k-fold cross validation
('misclassif error:', 28.0)
('precision:', 0.72714325101421873)
('accuracy:', 0.71999999999999997)
('recall:', 0.95943781032113085)
('f1:', 0.81765652522531218)
```




SVM
ga
bw
death
1
2
160
170
180
190
200
210
220
400
600
800
1000
1200
1400
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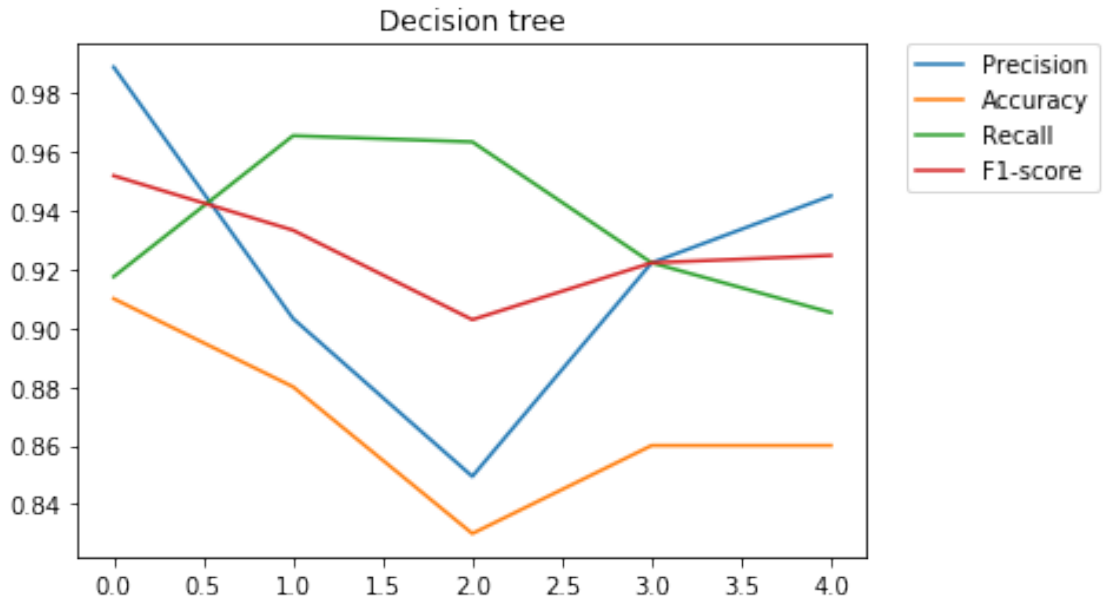
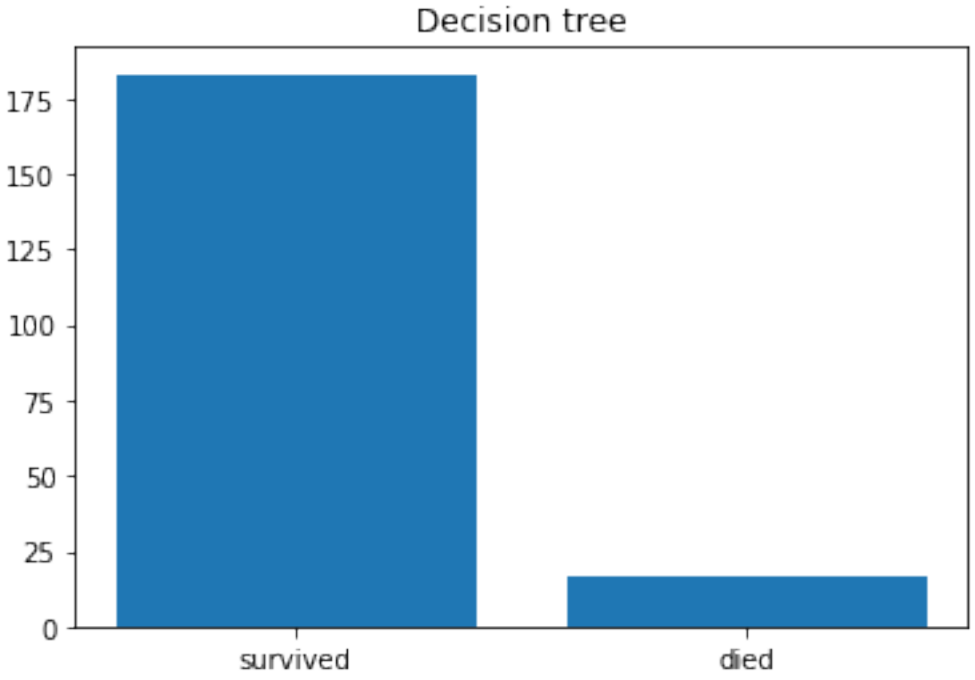
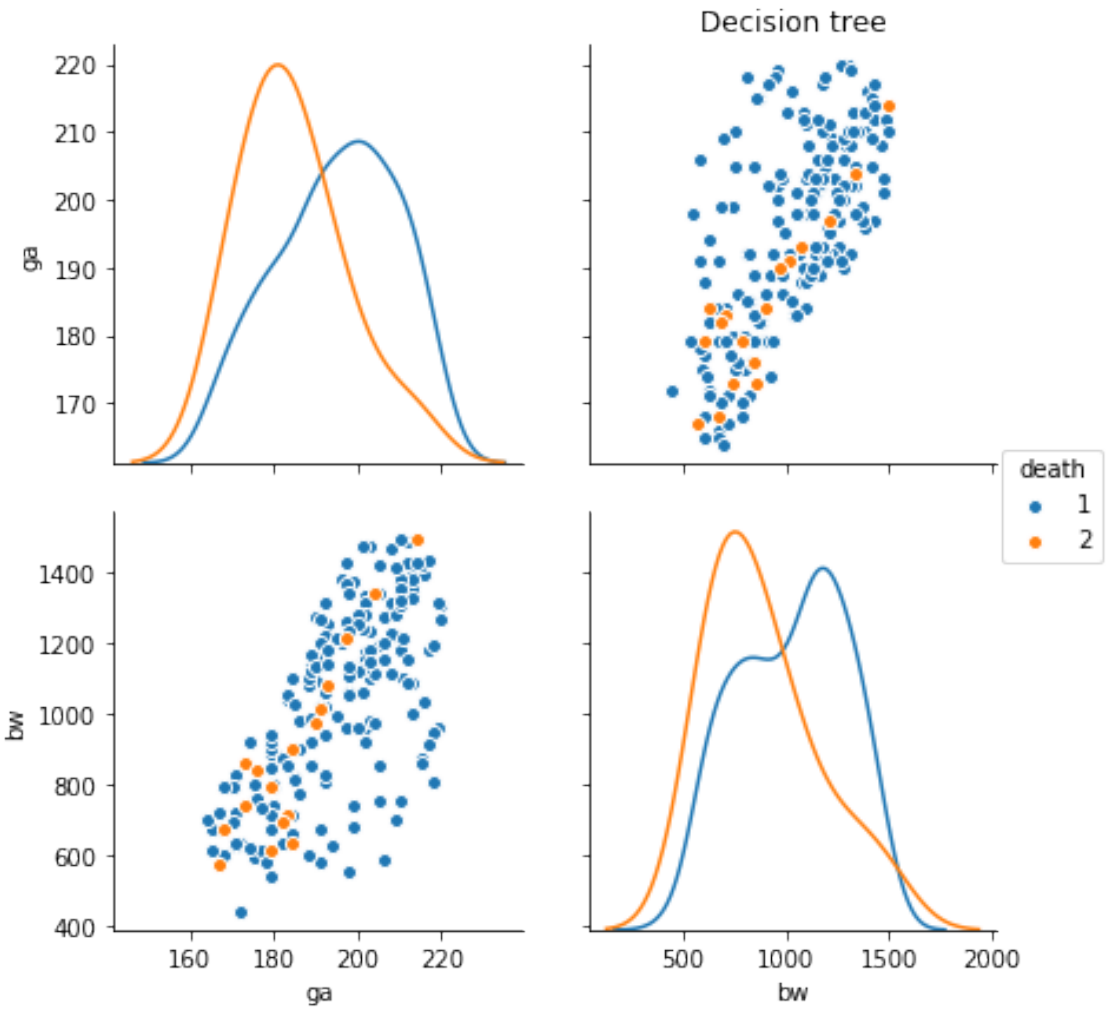
1500




```
Average on k-fold cross validation
('misclassif error:', 13.199999999999999)
('precision:', 0.92177084564181355)
('accuracy:', 0.86799999999999999)
('recall:', 0.93478860576769751)
('f1:', 0.92700310779248163)
```




Decision tree
ga
bw
death
1
2
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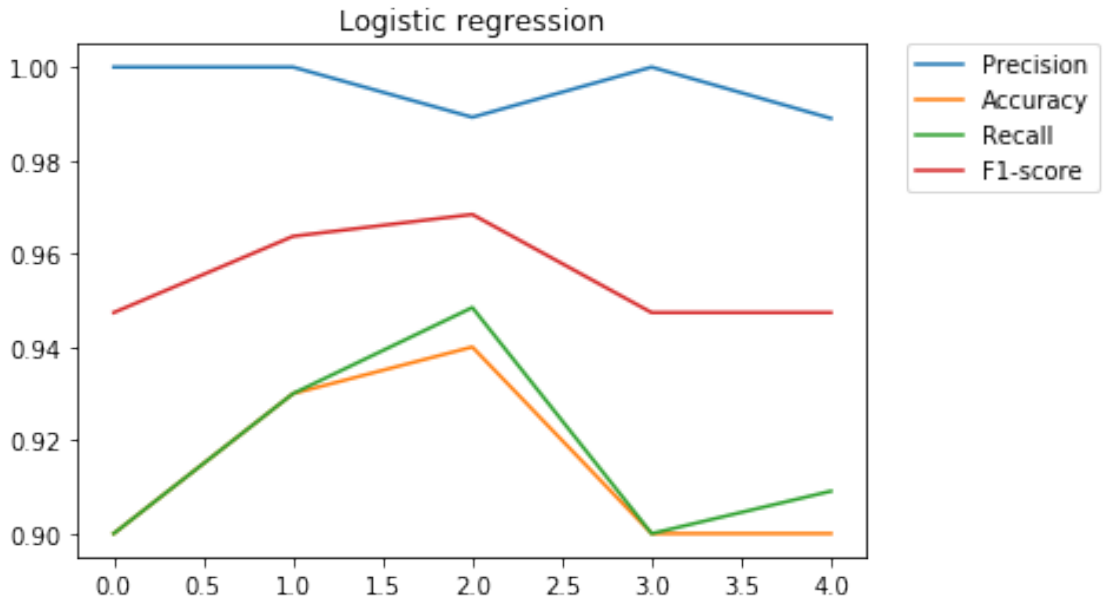
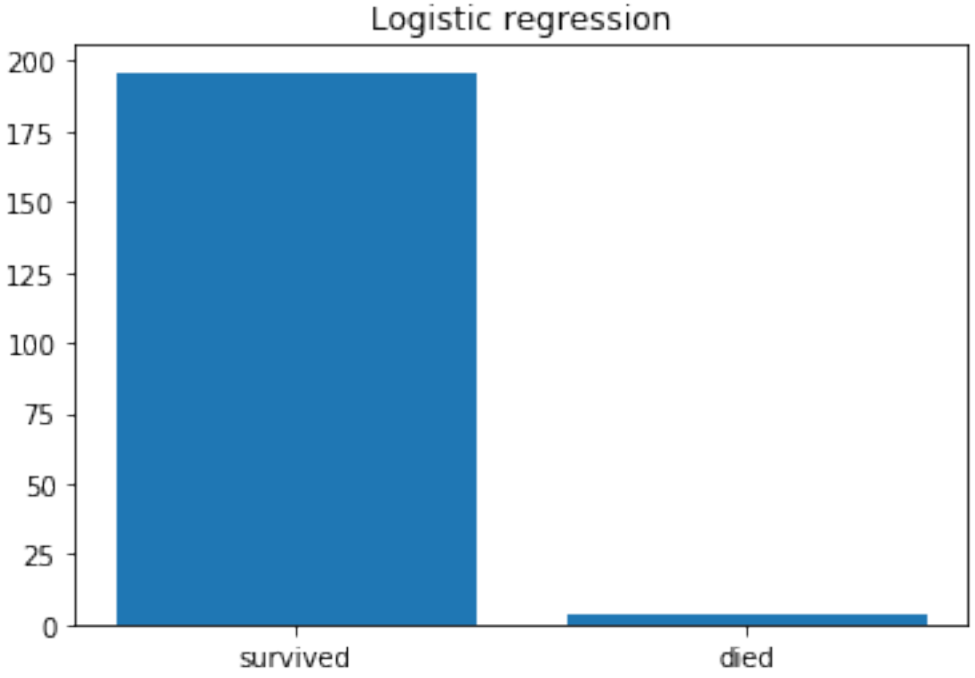
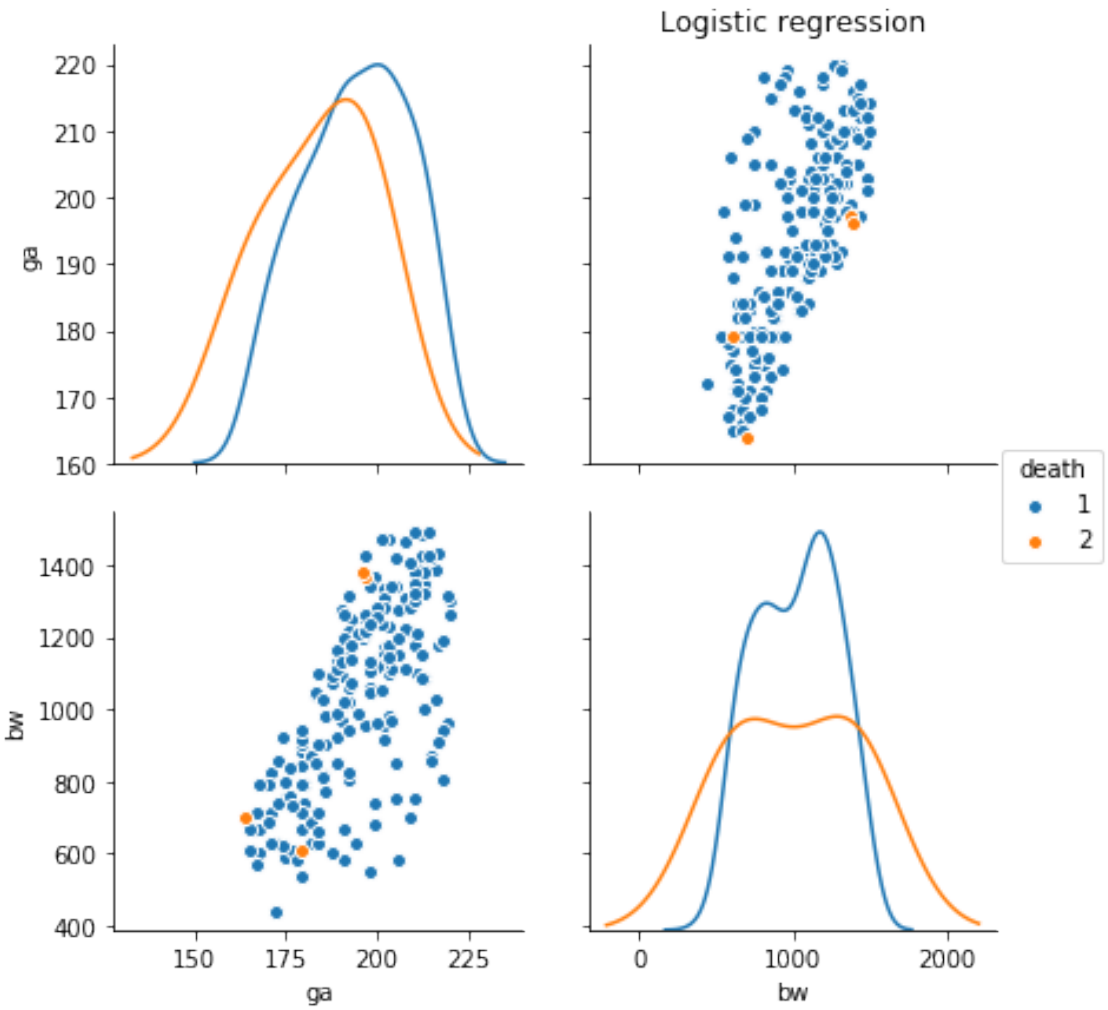



```
Average on k-fold cross validation
('misclassif error:', 8.5999999999999996)
('precision:', 0.99565166016778917)
('accuracy:', 0.91400000000000003)
('recall:', 0.91750890346766634)
('f1:', 0.9548513771475321)
```




Logistic regression
ga
bw
death
1
2
220
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200
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1200
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400
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225
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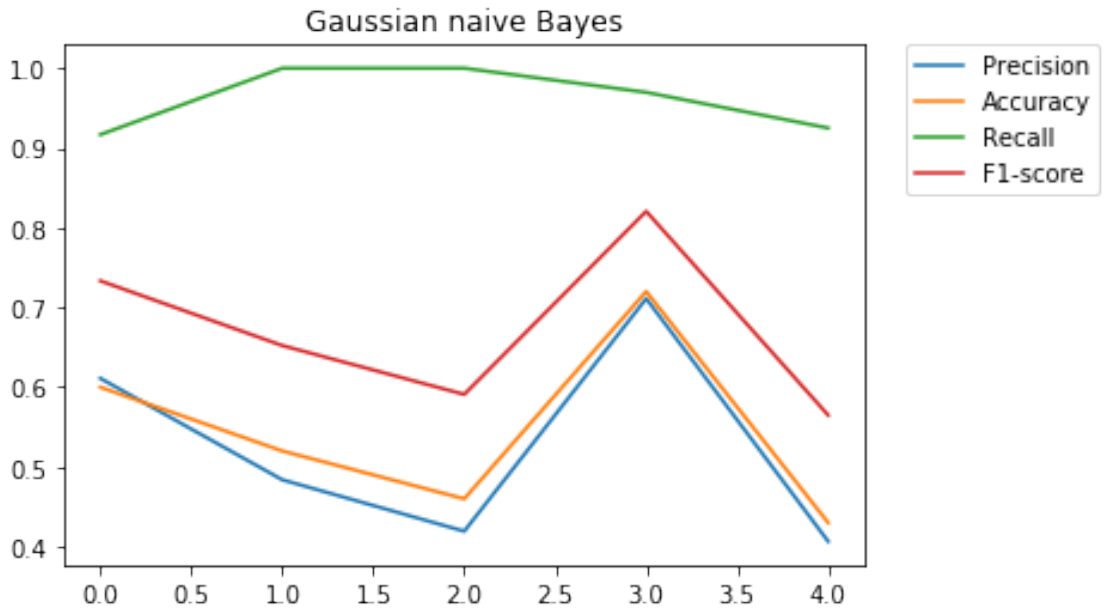
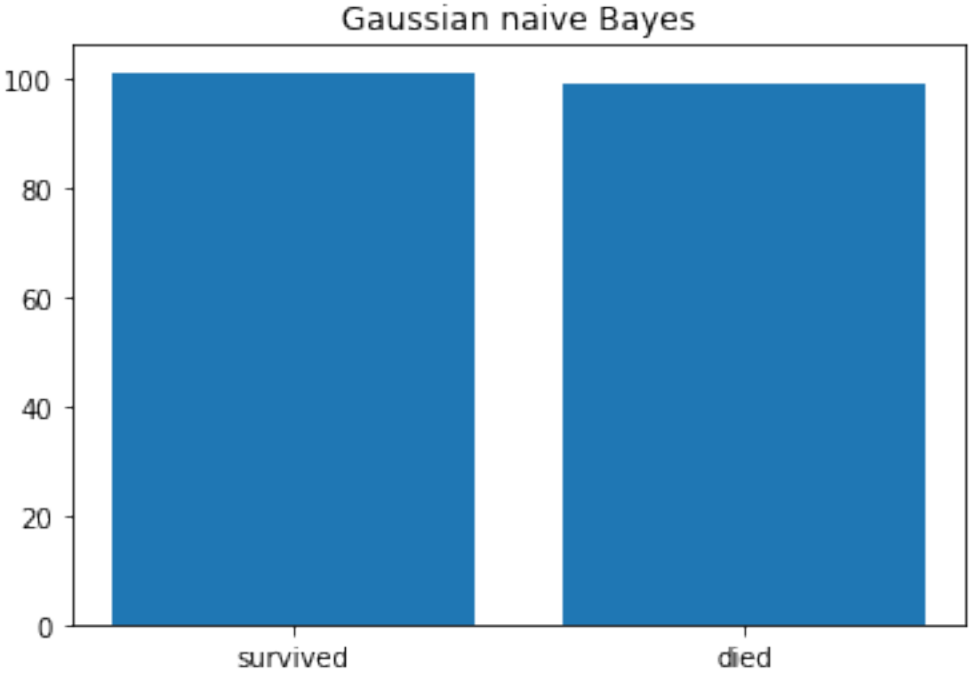
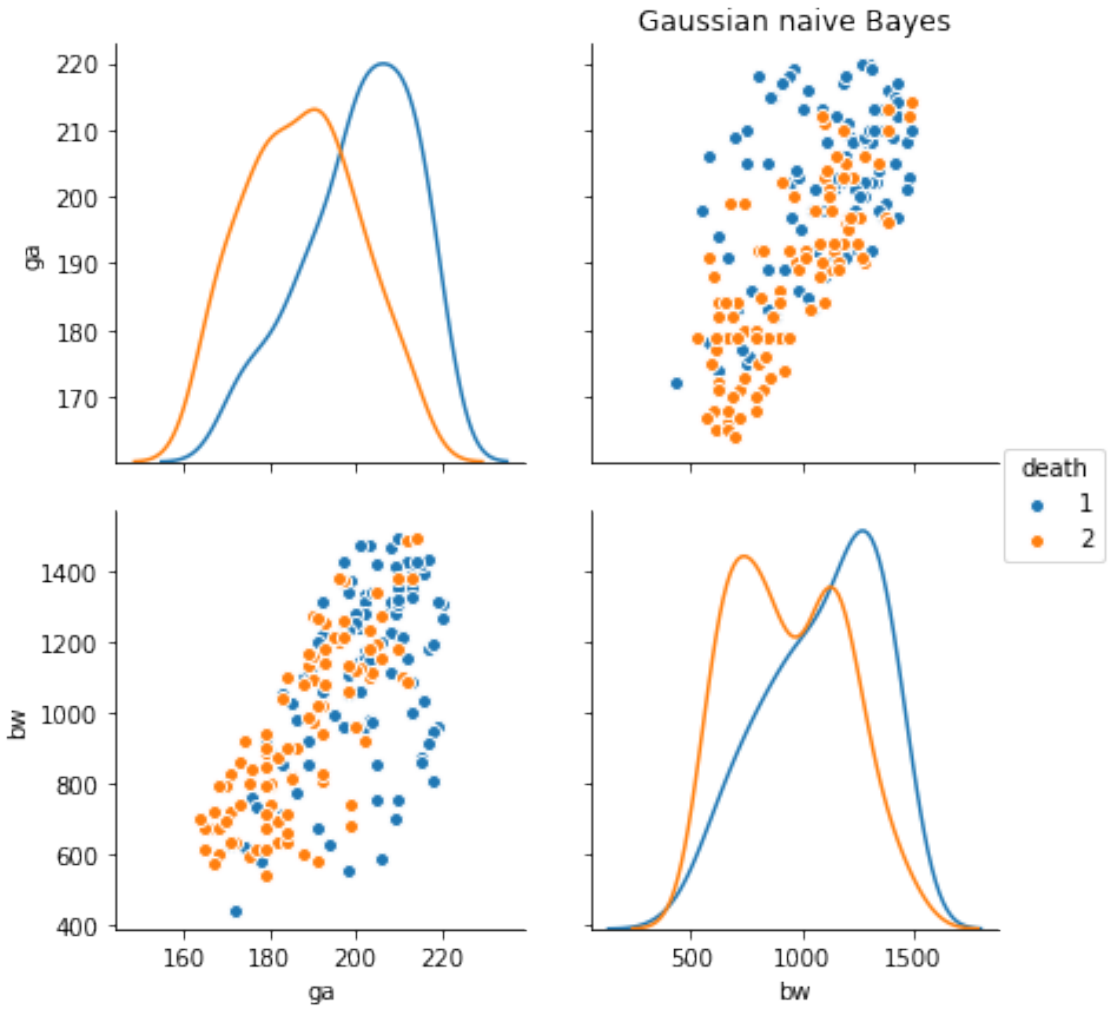


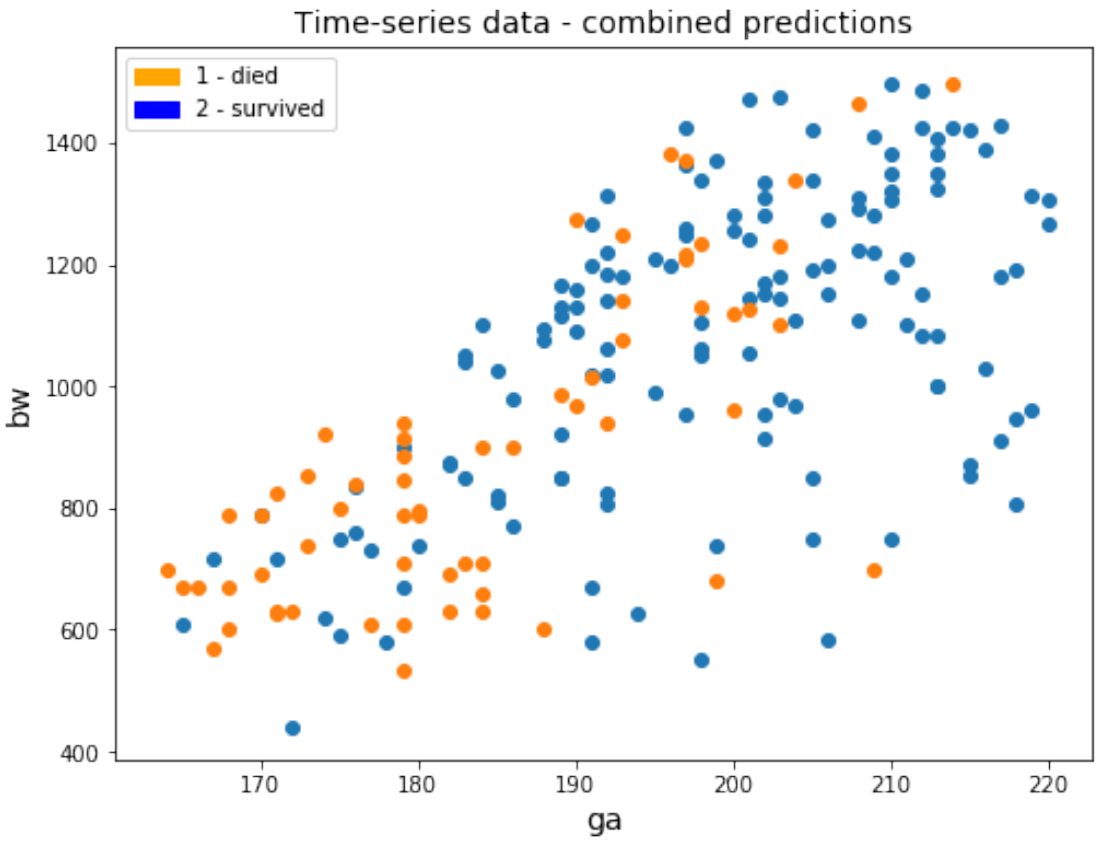

```
Average on k-fold cross validation
('misclassif error:', 45.399999999999999)
('precision:', 0.52640828705344833)
('accuracy:', 0.54600000000000004)
('recall:', 0.96227272727272728)
('f1:', 0.67236293079638576)
```






```
In [33]: pred = pd.DataFrame(data={'patientid':test_set['patientid'].as_matrix(),
                                   'ga':test_set['ga'].as_matrix(), 'bw':test_set['bw'].as_ma
             , 'death_dt':dt_pred['death'], 'death_svm':svm_pred['death']
             , 'death_lr':lr_pred['death'], 'death_gp':gp_pred['death']})

         died = pred.loc[(pred['death_dt'] == 2) | (pred['death_svm']==2) | (pred['death_gp'] ==
         survived = pred.loc[(pred['death_dt'] == 1) & (pred['death_svm']==1) & (pred['death_gp'
         plt.figure(figsize=(8,6))
         plt.scatter(survived['ga'], survived['bw'])
         plt.scatter(died['ga'], died['bw'])
         plt.xlabel("ga", fontsize=14)
         plt.ylabel("bw", fontsize=14)
```

```
orange_patch = mpatches.Patch(color='orange', label='1 - died')
blue_patch = mpatches.Patch(color='blue', label='2 - survived')
plt.legend(handles=[orange_patch, blue_patch])
plt.title("Time-series data - combined predictions", fontsize=14)
plt.show()
```



1 Combining time-series with basic data

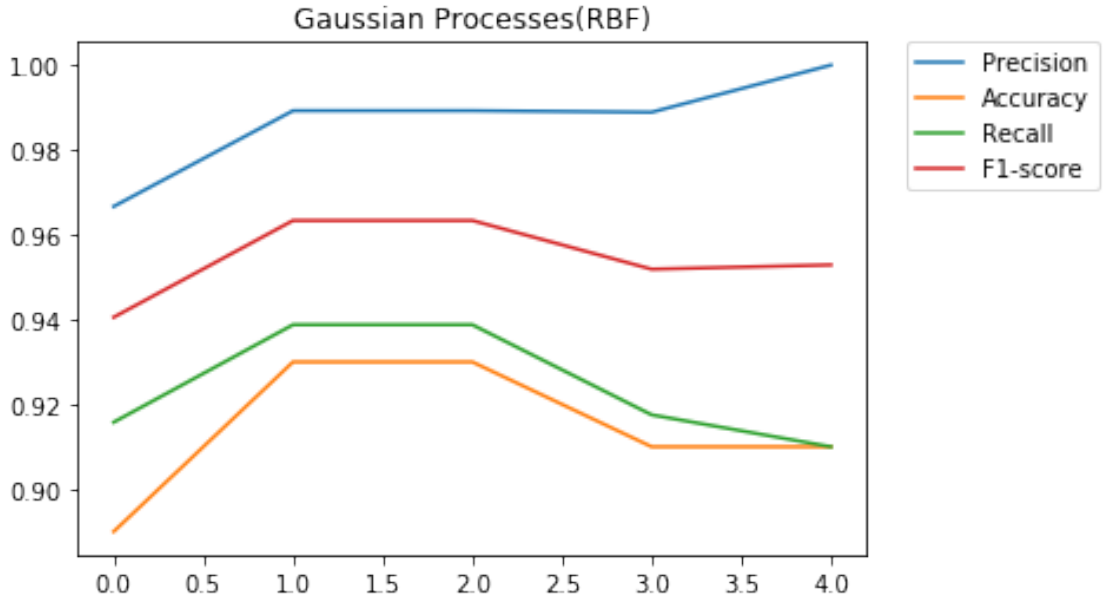
In [40]:
```
# ts, data
fulldata = data.merge(ts, on='patientid')
training_set = fulldata[fulldata['death']!=0]
training_labels = training_set['death']
training_data = training_set.drop(['patientid', 'death'], axis=1)
test_set = fulldata[fulldata['death']==0]
test_data = test_set.drop(['patientid', 'death'], axis=1)
```

In [41]:
```
scaler = StandardScaler()
training_data_stand = scaler.fit_transform(training_data)
test_data_stand = scaler.fit_transform(test_data)
```

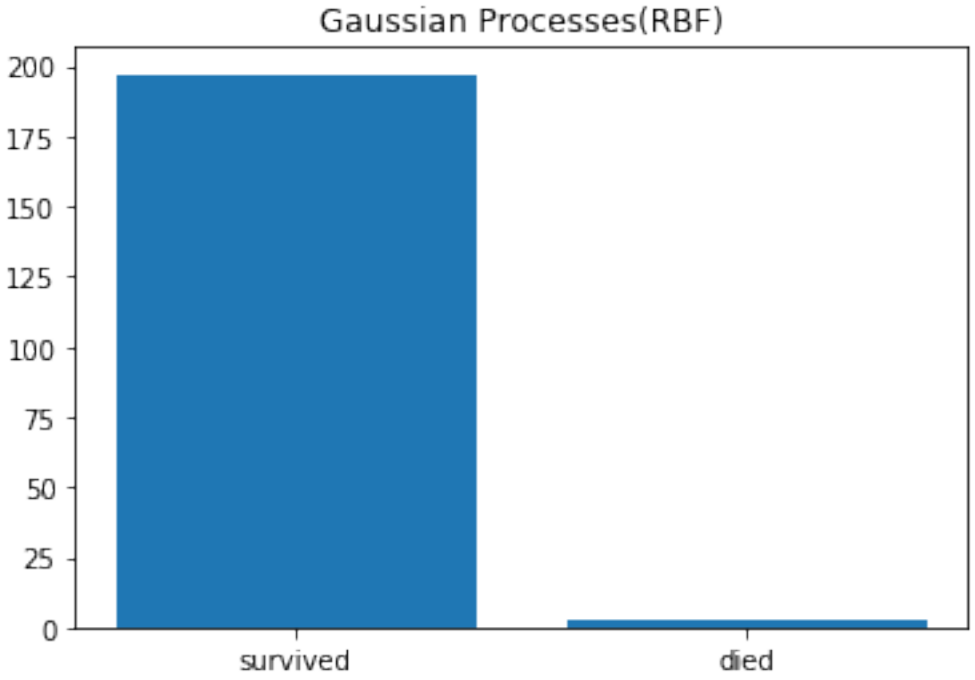
```
        minmaxscaler = MinMaxScaler()
        training_data_minmax = minmaxscaler.fit_transform(training_data)
        test_data_minmax = minmaxscaler.fit_transform(test_data)
```

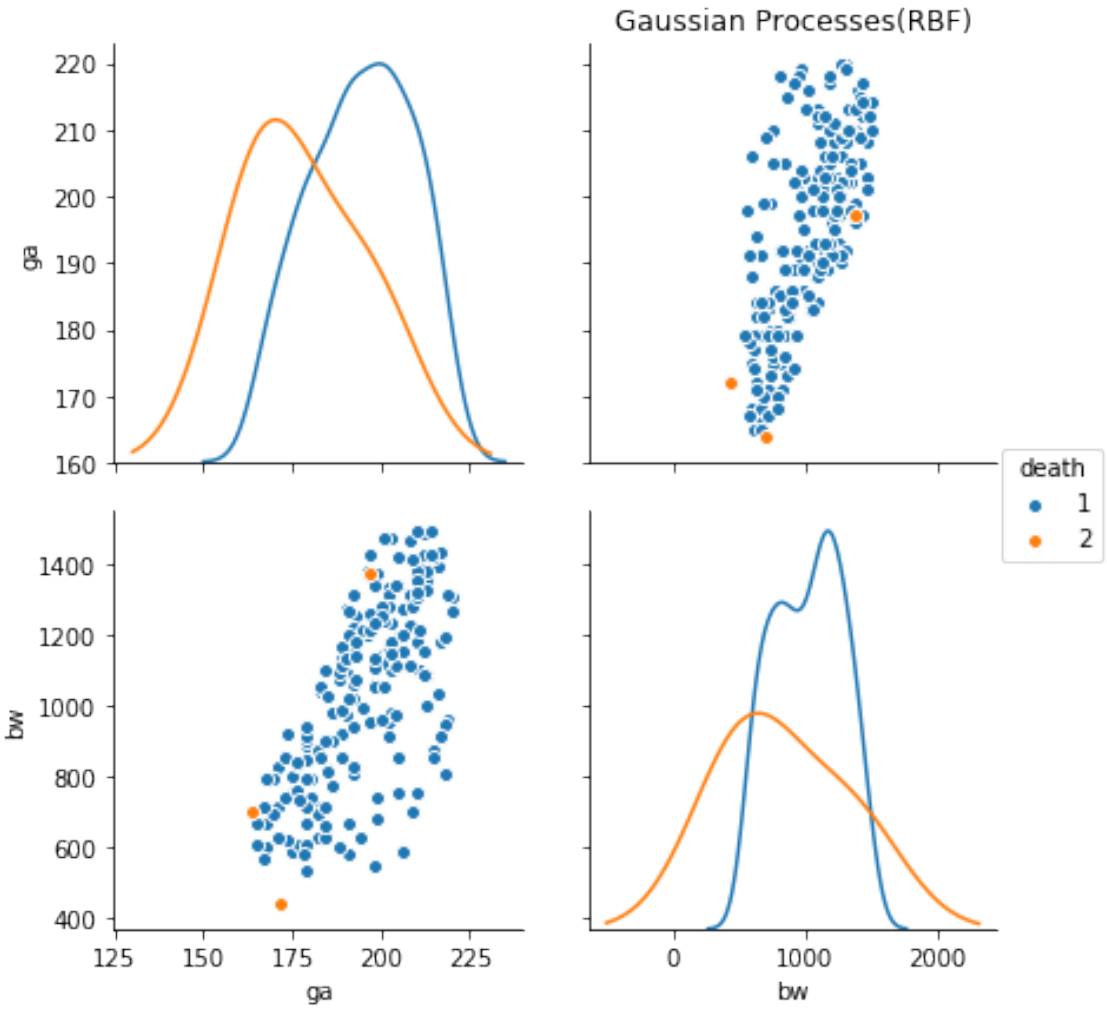
In [42]:
```
for clf, method_name in clfs:
    misclassif_lst = []
    precision_lst = []
    accuracy_lst = []
    recall_lst = []
    f1_lst = []

    kf = KFold(n_splits=5)
    for train_index, test_index in kf.split(training_data_stand):
        X_train, X_test = training_data_stand[train_index], training_data_stand[test_in
        y_train, y_test = training_labels[train_index], training_labels[test_index]
        clf.fit(X_train, y_train)
        y_pred = clf.predict(X_test)
        misclassif = np.sum(y_pred!=y_test)
        precision = precision_score(y_pred, y_test)
        accuracy = accuracy_score(y_pred, y_test)
        recall = recall_score(y_pred, y_test)
        f1 = f1_score(y_pred, y_test)

        misclassif_lst.append(misclassif)
        precision_lst.append(precision)
        accuracy_lst.append(accuracy)
        recall_lst.append(recall)

        f1_lst.append(f1)

    plt.plot(range(5), precision_lst, label="Precision")
    plt.plot(range(5), accuracy_lst, label="Accuracy")
    plt.plot(range(5), recall_lst, label="Recall")
    plt.plot(range(5), f1_lst, label="F1-score")
    plt.legend(bbox_to_anchor=(1.05, 1), loc=2, borderaxespad=0.)
    plt.title(method_name)
    plt.show()

    print("Average on k-fold cross validation")
    print("misclassif error:", np.mean(misclassif_lst))
    print("precision:", np.mean(precision_lst))
    print("accuracy:", np.mean(accuracy_lst))
    print("recall:", np.mean(recall_lst))
    print("f1:", np.mean(f1_lst))

    clf.fit(training_data_stand, training_labels)
    p = clf.predict(test_data_stand)
```

```
classes, distribution = np.unique(p, return_counts=True)
plt.bar(classes, distribution)
plt.title(method_name)
plt.xticks(classes, ["survived", "died"])
plt.show()

pred = pd.DataFrame(data={#'patientid':test_set['patientid'].as_matrix(),
                          'ga':test_set['ga'].as_matrix(), 'bw':test_set['bw'].a

if method_name=="Gaussian Processes(RBF)":
    gp_pred = pred
elif method_name=="SVM":
    svm_pred = pred
elif method_name=="Decision tree":
    dt_pred = pred
elif method_name=="Logistic regression":
    lr_pred = pred
#elif method_name=="Gaussian naive Bayes":
#    gnb_pred = pred

sns.pairplot(pred[['ga', 'bw', 'death']]
             , hue="death"
             , vars=['ga', 'bw']
             , diag_kind="kde"
             #, kind="reg"
             , size=3
            )
plt.title(method_name)
plt.show()
```



```
Average on k-fold cross validation
('misclassif error:', 8.5999999999999996)
('precision:', 0.98681003584229399)
('accuracy:', 0.91400000000000003)
('recall:', 0.92417325345764989)
('f1:', 0.95439867002540235)
```




Gaussian Processes(RBF)
ga
bw
death
1
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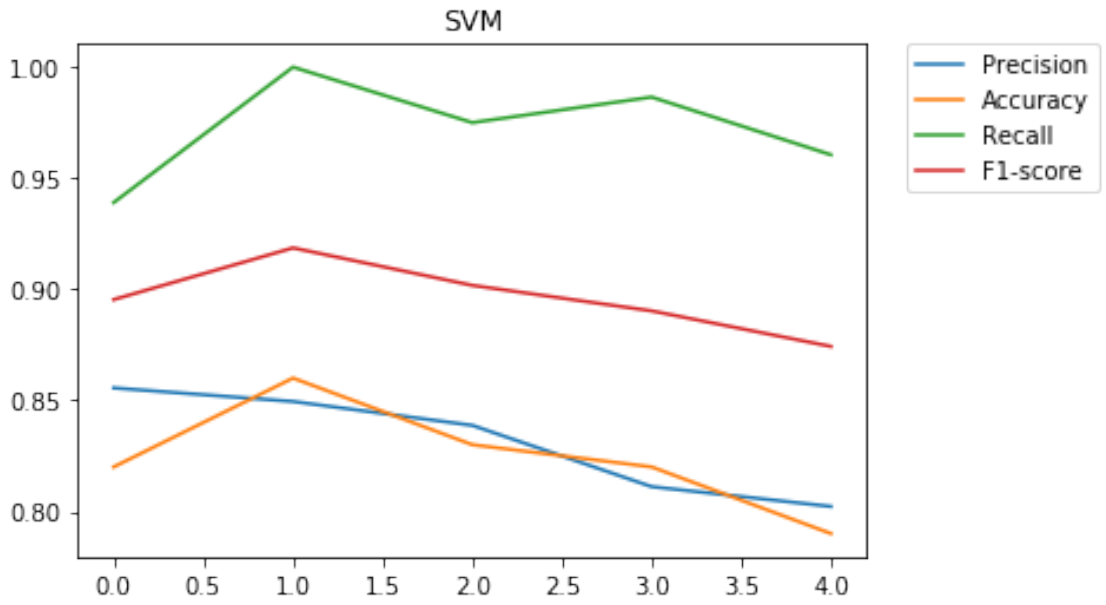
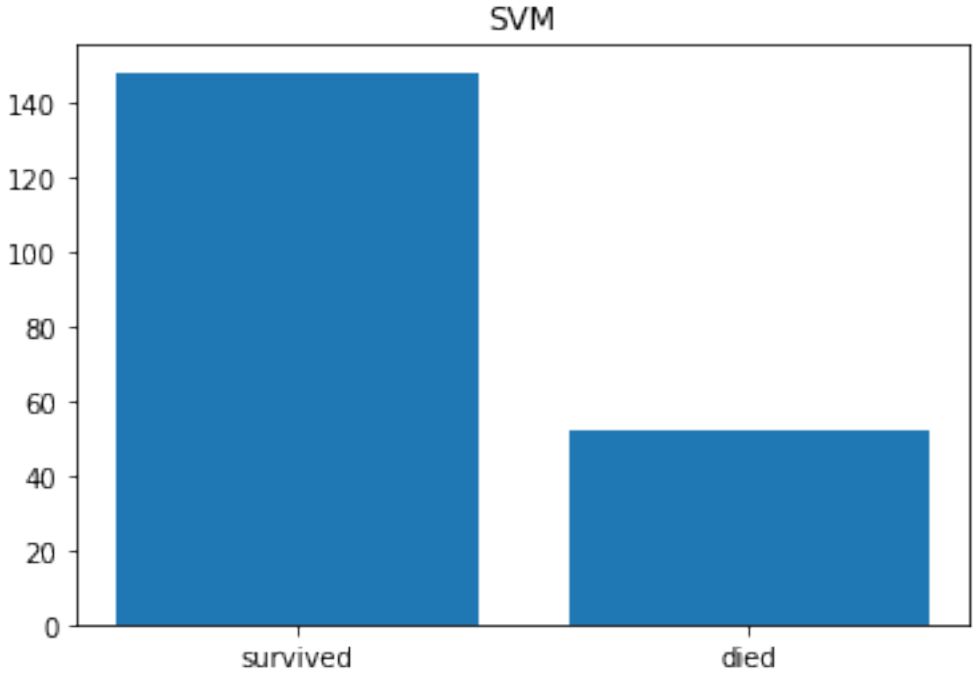
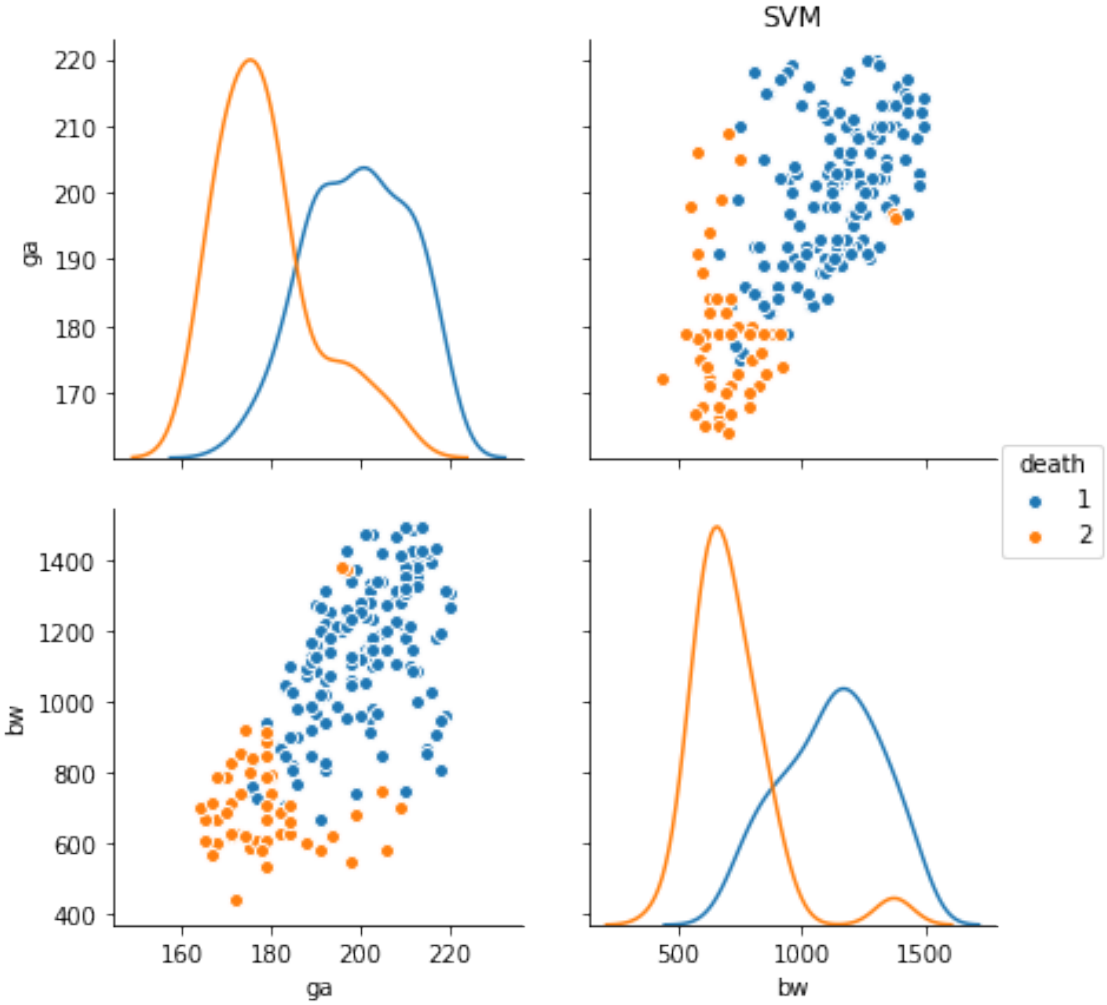
220
210
200
190
180
170
160
1400
1200
1000
800
600
400
125
150
175
200
225
0
1000
2000




```
Average on k-fold cross validation
('misclassif error:', 17.600000000000001)
('precision:', 0.83140730237504423)
('accuracy:', 0.82399999999999984)
('recall:', 0.97220743850397251)
('f1:', 0.89603659837266958)
```




SVM
ga
bw
death
1
2
220
210
200
190
180
170
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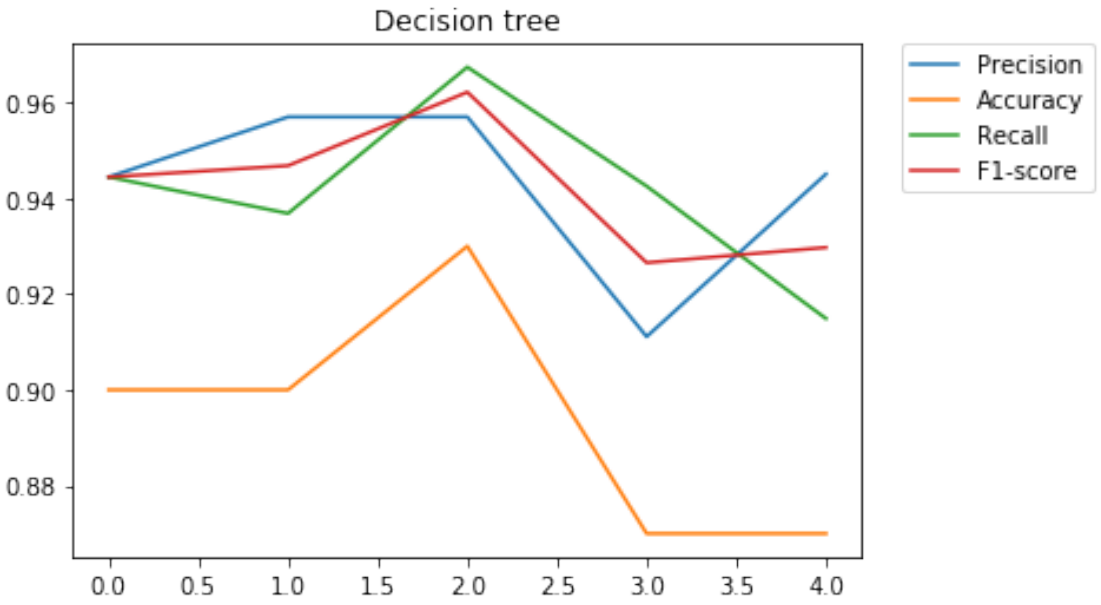
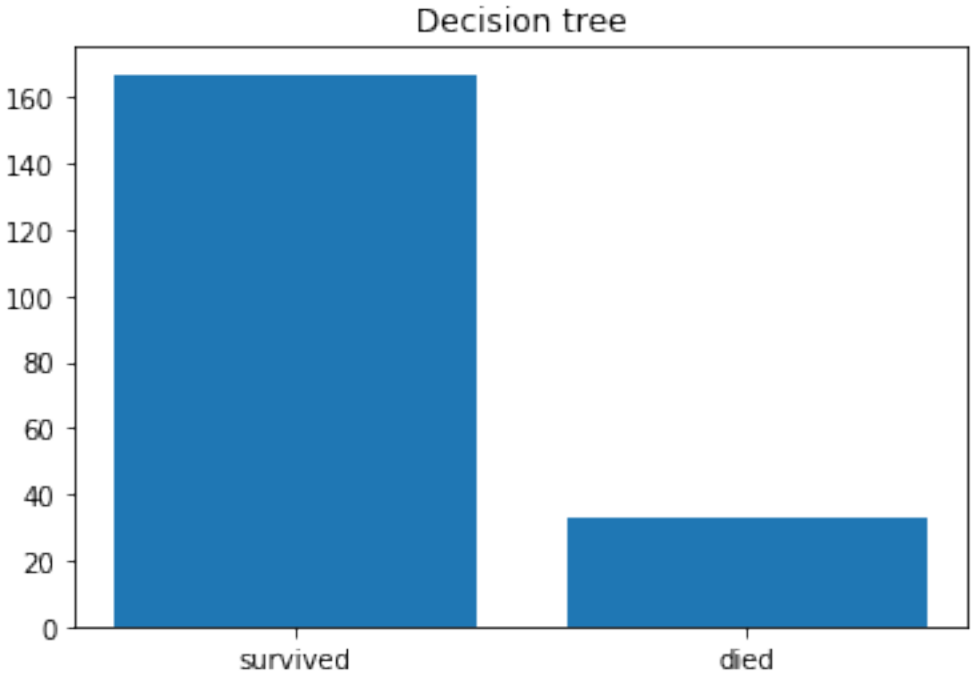
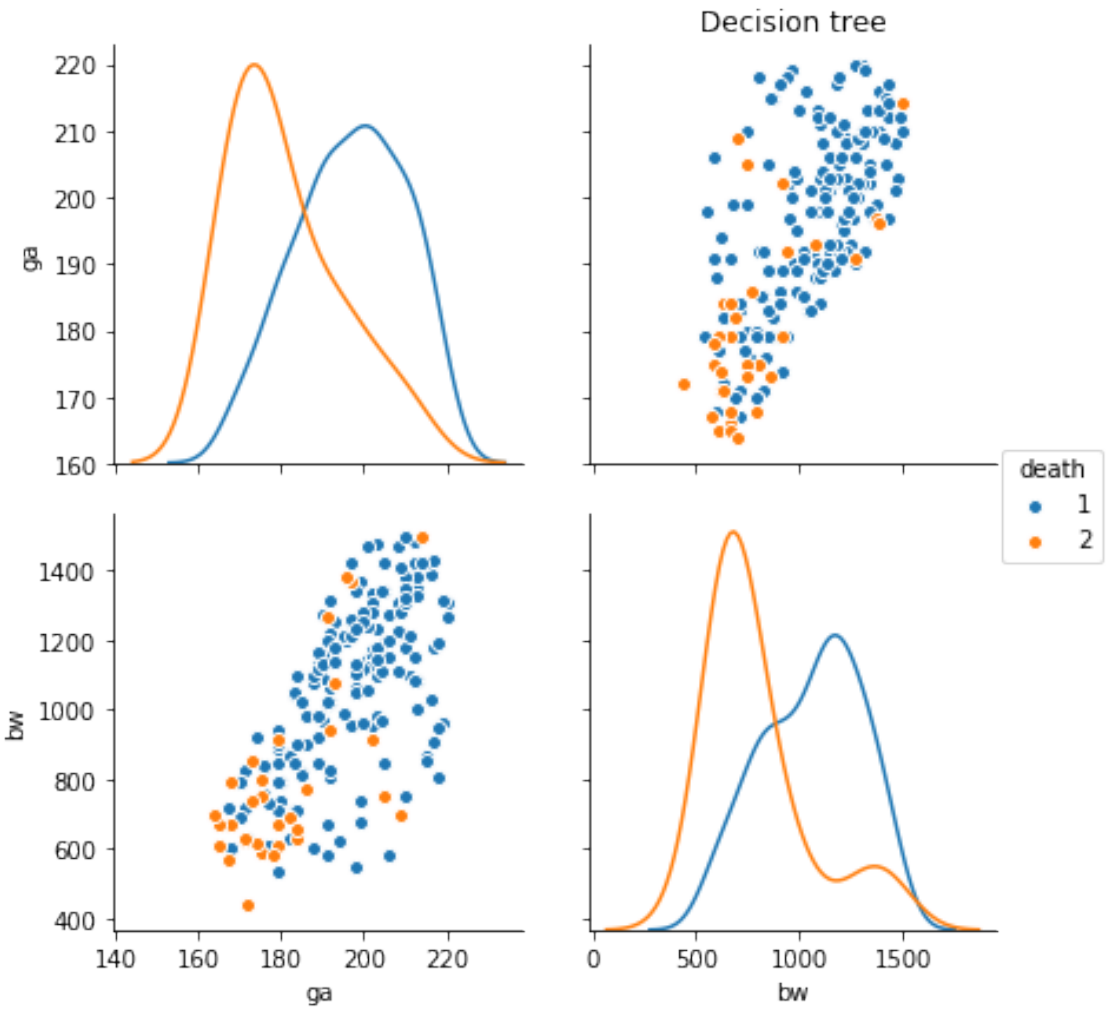



```
Average on k-fold cross validation
('misclassif error:', 10.6)
('precision:', 0.94291779904683126)
('accuracy:', 0.89399999999999991)
('recall:', 0.94122004134177784)
('f1:', 0.94193970385820369)
```




Decision tree
ga
bw
death
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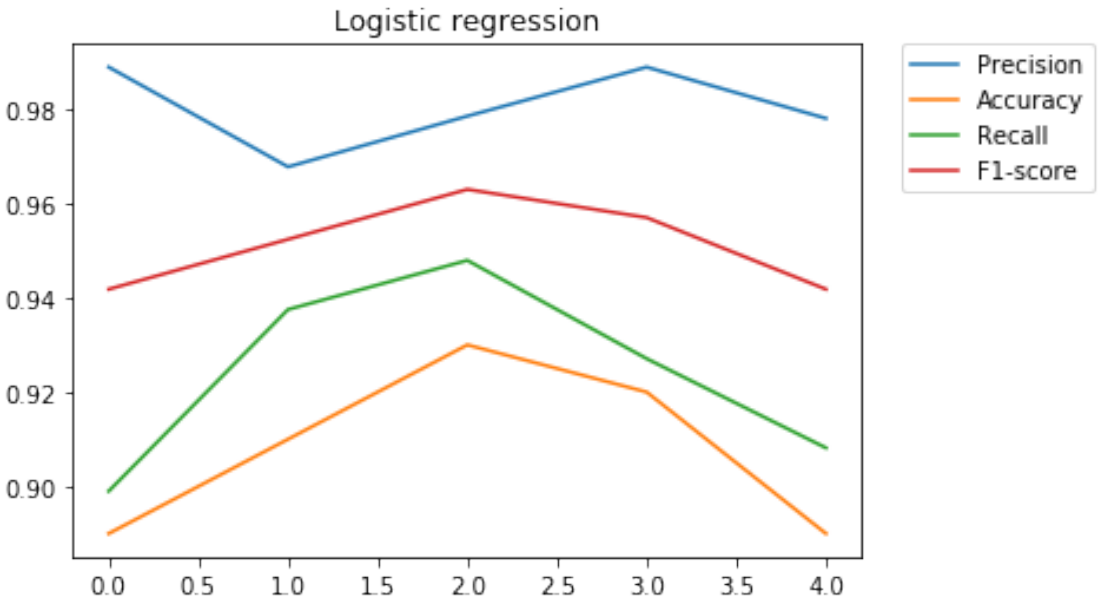
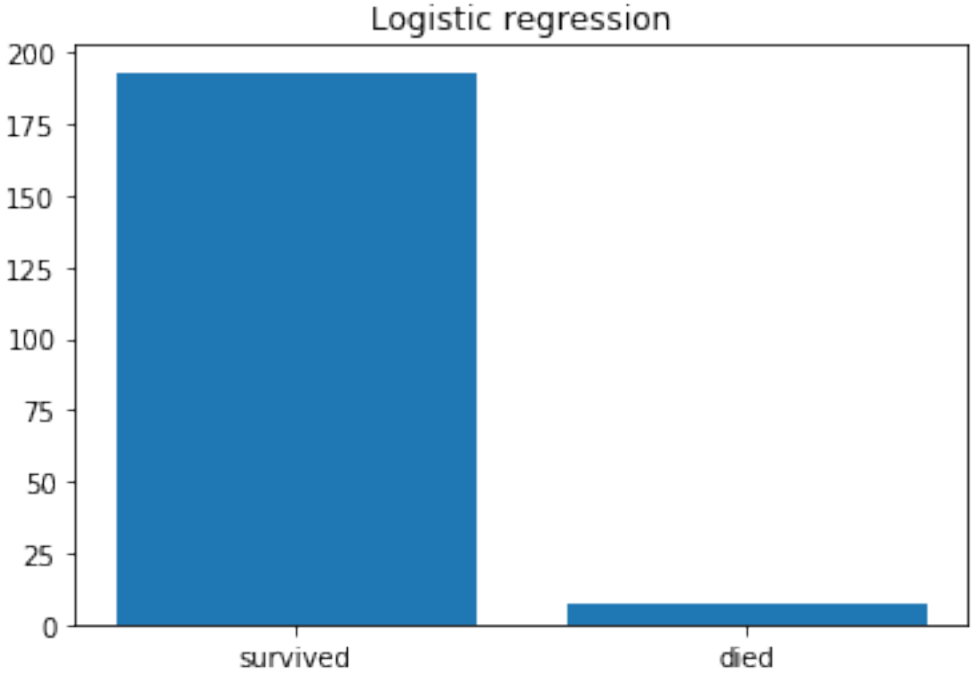
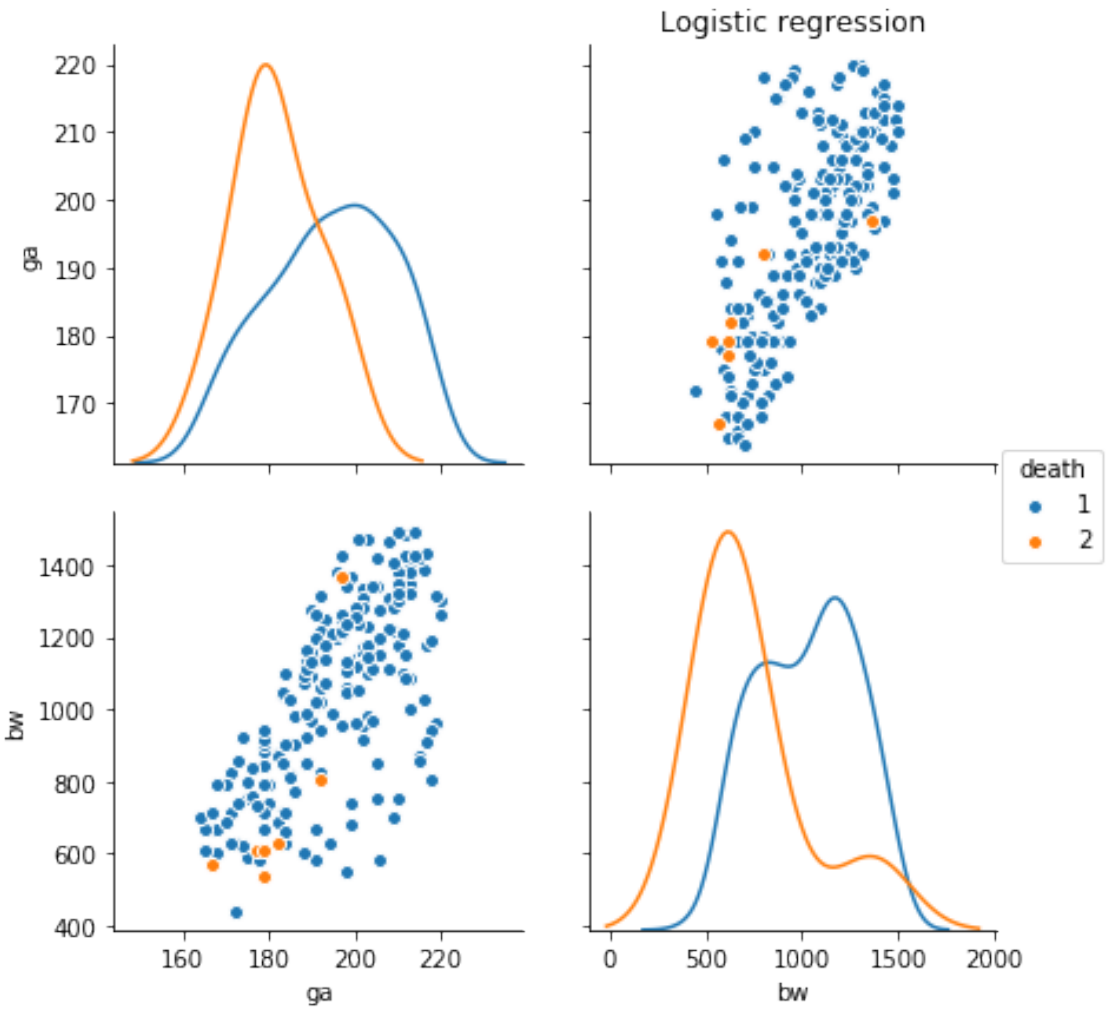



```
Average on k-fold cross validation
('misclassif error:', 9.1999999999999993)
('precision:', 0.98040726298790815)
('accuracy:', 0.90800000000000003)
('recall:', 0.92393063285920429)
('f1:', 0.95118620925072539)
```




Logistic regression
ga
bw
death
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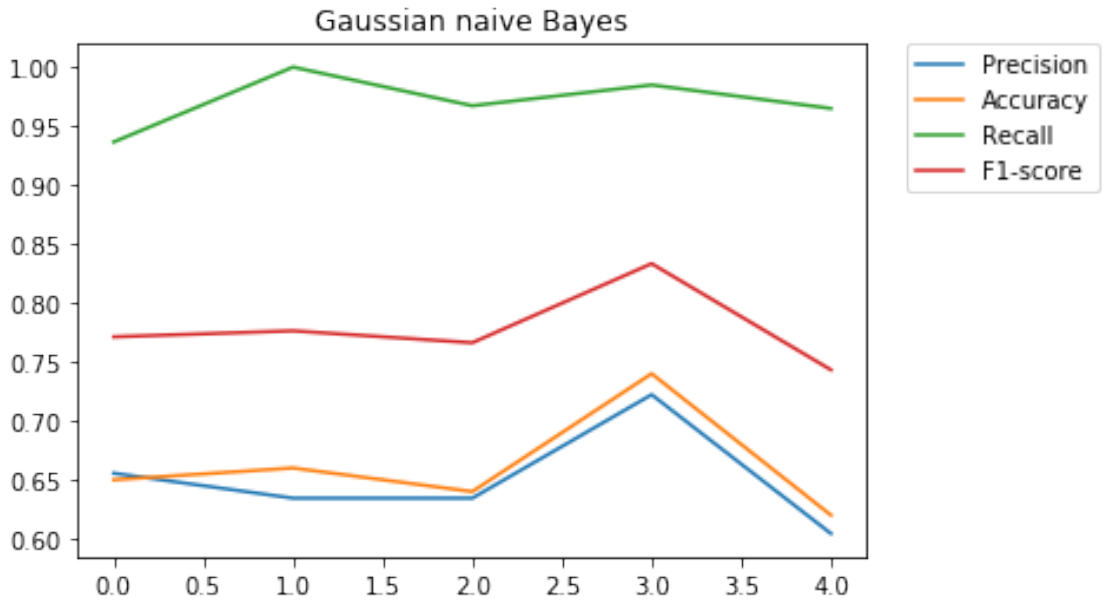
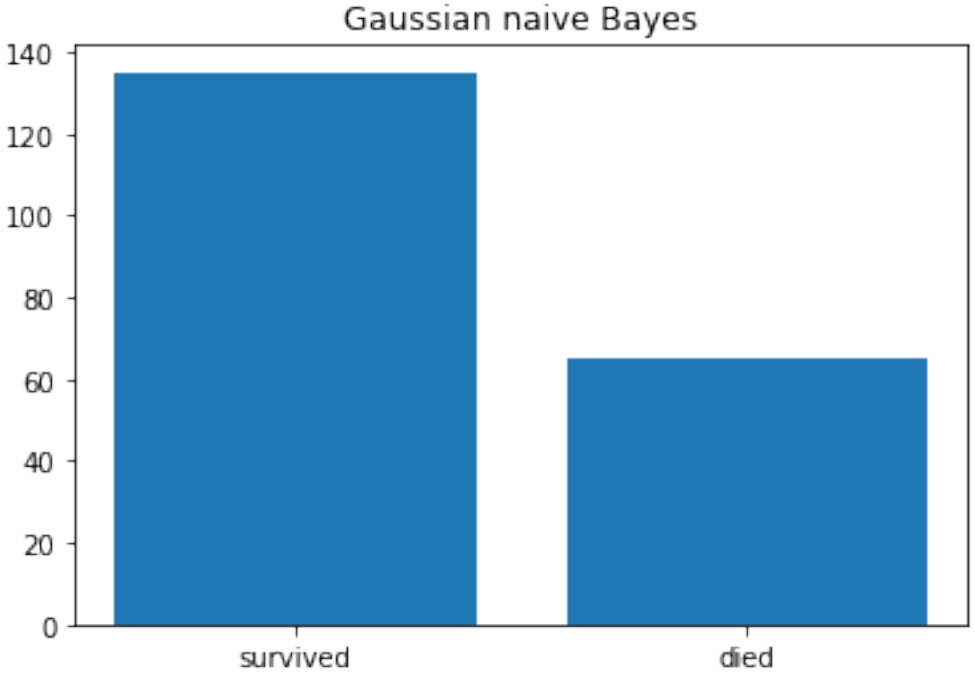
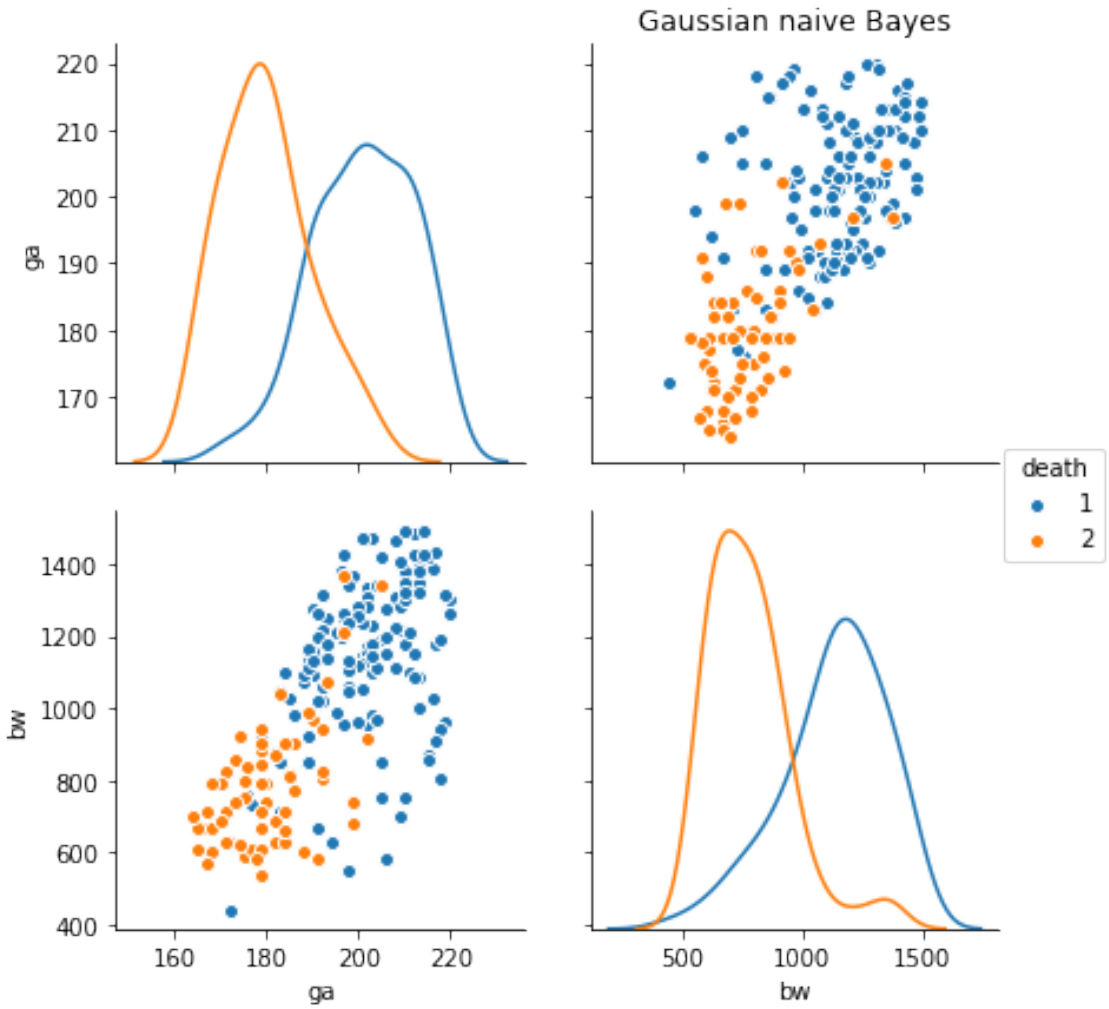



```
Average on k-fold cross validation
('misclassif error:', 33.799999999999997)
('precision:', 0.65019811729489152)
('accuracy:', 0.66200000000000014)
('recall:', 0.97069636336245479)
('f1:', 0.77807359246987728)
```

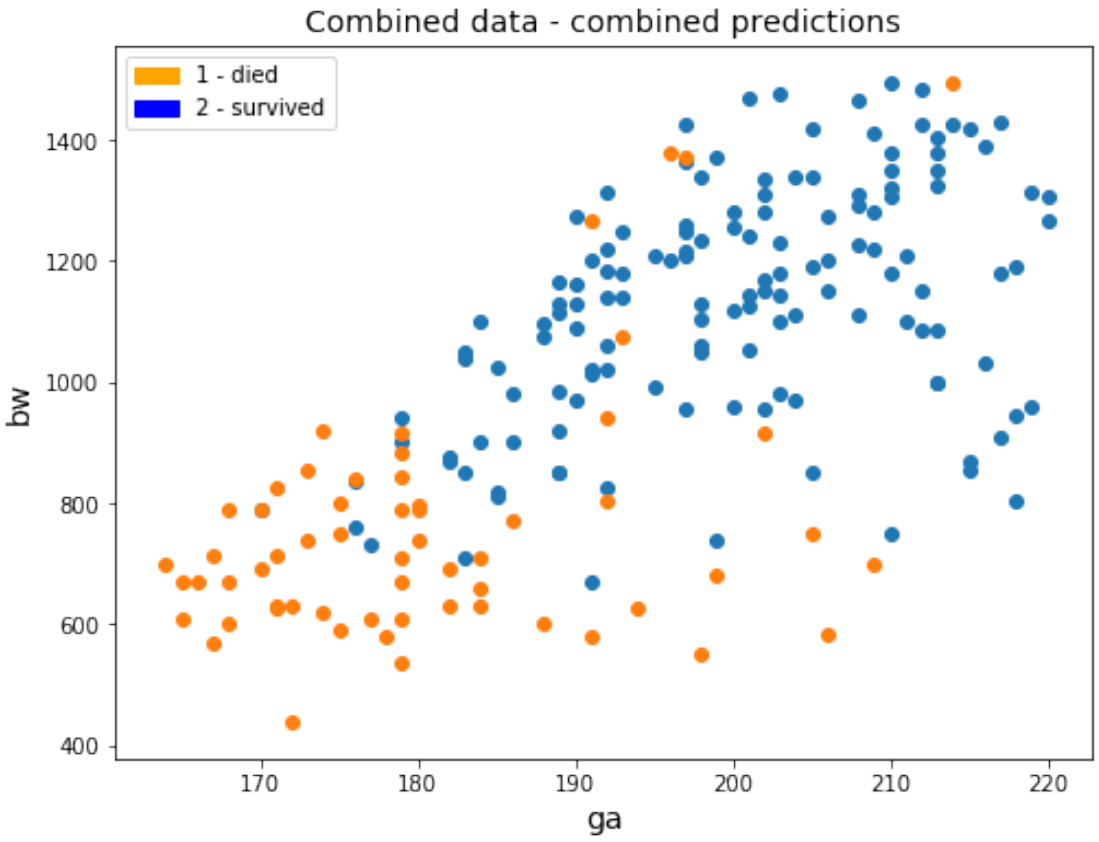





```
In [44]: pred = pd.DataFrame(data={'patientid':test_set['patientid'].as_matrix(),
                                   'ga':test_set['ga'].as_matrix(), 'bw':test_set['bw'].as_ma
             , 'death_dt':dt_pred['death'], 'death_svm':svm_pred['death']
             , 'death_lr':lr_pred['death'], 'death_gp':gp_pred['death']})

         died = pred.loc[(pred['death_dt'] == 2) | (pred['death_svm']==2) | (pred['death_gp'] ==
         survived = pred.loc[(pred['death_dt'] == 1) & (pred['death_svm']==1) & (pred['death_gp'
         plt.figure(figsize=(8,6))
         plt.scatter(survived['ga'], survived['bw'])
         plt.scatter(died['ga'], died['bw'])
         plt.xlabel("ga", fontsize=14)
         plt.ylabel("bw", fontsize=14)
```

```
orange_patch = mpatches.Patch(color='orange', label='1 - died')
blue_patch = mpatches.Patch(color='blue', label='2 - survived')
plt.legend(handles=[orange_patch, blue_patch])
plt.title("Combined data - combined predictions", fontsize=14)
plt.show()
```




```
In [49]: died["patientid"].as_matrix()
```

```
Out[49]: array([501, 502, 520, 522, 532, 533, 536, 540, 541, 542, 543, 547, 548,
                549, 551, 552, 563, 564, 566, 567, 574, 587, 590, 591, 592, 597,
                599, 604, 606, 607, 608, 609, 611, 613, 614, 615, 625, 627, 635,
                639, 640, 644, 648, 649, 652, 654, 659, 663, 665, 666, 669, 680,
                682, 685, 686, 688, 691, 693, 696, 697], dtype=object)
```