

Appliability of basic machine learning algorithms for breast cancer diagnosis based on geometric characteristics of cell nuclei

Description of the data set

In this notebook I am going to analyze a data set containing geometric characteristics found in samples of breast mass. The data set also contains a classification of each sample as benign (sample was taken from breast tissue that does not contain) or malignant (sample was taken from breast tissue that contains cancer).

Research questions

The research questions I would like to answer using this data set are:

1. Using data similar to data in this data set, would it be possible to accurately detect breast cancer with basic machine learning algorithms like the ones introduced in the Python for Data Science course?
2. How do these basic algorithms perform in comparison with more advanced machine learning techniques?
3. Is it possible to determine which of the features are important to the classification, and which ones have little or no contribution?

Research methods

To answer my first research question, I am going to pick three or four basic machine learning algorithms, train them with a portion of the data in the data set, and use the rest of the data to test their accuracy. I am also going to try different values for input parameters like the maximum node count of the decision tree and see which values result in the best accuracy.

To answer the second research question, I will examine existing notebooks on <https://www.kaggle.com> (<https://www.kaggle.com>) in which other people have described their results with the same data set using more advanced techniques like Artificial Neural Networks.

To answer the third research question, I will first examine feature distribution plots and try to predict which features should turn out to be most important to the algorithms and then compare my predictions with feature importance values calculated by the models.

First, I am going to explore the data set and make myself familiar with the data, its shape, the size of the data set and data quality. Next, I am going to

Exploring the data set

The data set was retrieved from <https://www.kaggle.com/uciml/breast-cancer-wisconsin-data> (<https://www.kaggle.com/uciml/breast-cancer-wisconsin-data>).

In [1]:

```
import pandas as pd
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
```

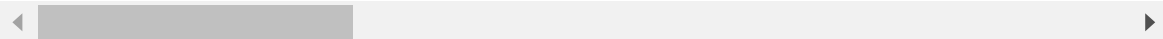
In [2]:

```
df = pd.read_csv('breast_cancer_classification.csv')
df.head()
```

Out[2]:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothnes
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

5 rows × 33 columns



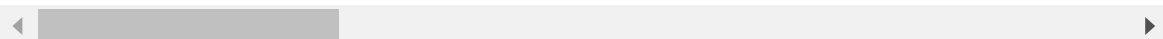
In [3]:

```
df.describe()
```

Out[3]:

	id	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	569.0
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	0.0
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	0.0
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	0.0
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	0.0
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	0.0
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	0.1
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	0.1

8 rows × 32 columns



In [4]:

```
df.isnull().any()
```

Out[4]:

```
id                False
diagnosis         False
radius_mean       False
texture_mean      False
perimeter_mean    False
area_mean         False
smoothness_mean   False
compactness_mean  False
concavity_mean    False
concave points_mean False
symmetry_mean     False
fractal_dimension_mean False
radius_se         False
texture_se        False
perimeter_se      False
area_se           False
smoothness_se     False
compactness_se    False
concavity_se      False
concave points_se False
symmetry_se       False
fractal_dimension_se False
radius_worst      False
texture_worst     False
perimeter_worst   False
area_worst        False
smoothness_worst  False
compactness_worst False
concavity_worst   False
concave points_worst False
symmetry_worst    False
fractal_dimension_worst False
Unnamed: 32       True
dtype: bool
```

In [5]:

```
df = df.drop(df.columns[32], axis=1)
```

In [6]:

```
df.isnull().any()
```

Out[6]:

```
id                False
diagnosis         False
radius_mean       False
texture_mean      False
perimeter_mean    False
area_mean         False
smoothness_mean   False
compactness_mean  False
concavity_mean    False
concave points_mean False
symmetry_mean     False
fractal_dimension_mean False
radius_se         False
texture_se        False
perimeter_se      False
area_se          False
smoothness_se     False
compactness_se    False
concavity_se      False
concave points_se False
symmetry_se       False
fractal_dimension_se False
radius_worst      False
texture_worst     False
perimeter_worst   False
area_worst        False
smoothness_worst  False
compactness_worst False
concavity_worst   False
concave points_worst False
symmetry_worst    False
fractal_dimension_worst False
dtype: bool
```

In [7]:

```
features = df.columns
features
```

Out[7]:

```
Index(['id', 'diagnosis', 'radius_mean', 'texture_mean', 'perimeter_mean',
       'area_mean', 'smoothness_mean', 'compactness_mean', 'concavity_mean',
       'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',
       'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_se',
       'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_se',
       'fractal_dimension_se', 'radius_worst', 'texture_worst',
       'perimeter_worst', 'area_worst', 'smoothness_worst',
       'compactness_worst', 'concavity_worst', 'concave points_worst',
       'symmetry_worst', 'fractal_dimension_worst'],
      dtype='object')
```

In [8]:

```
features = features.drop(['id', 'diagnosis'])  
features
```

Out[8]:

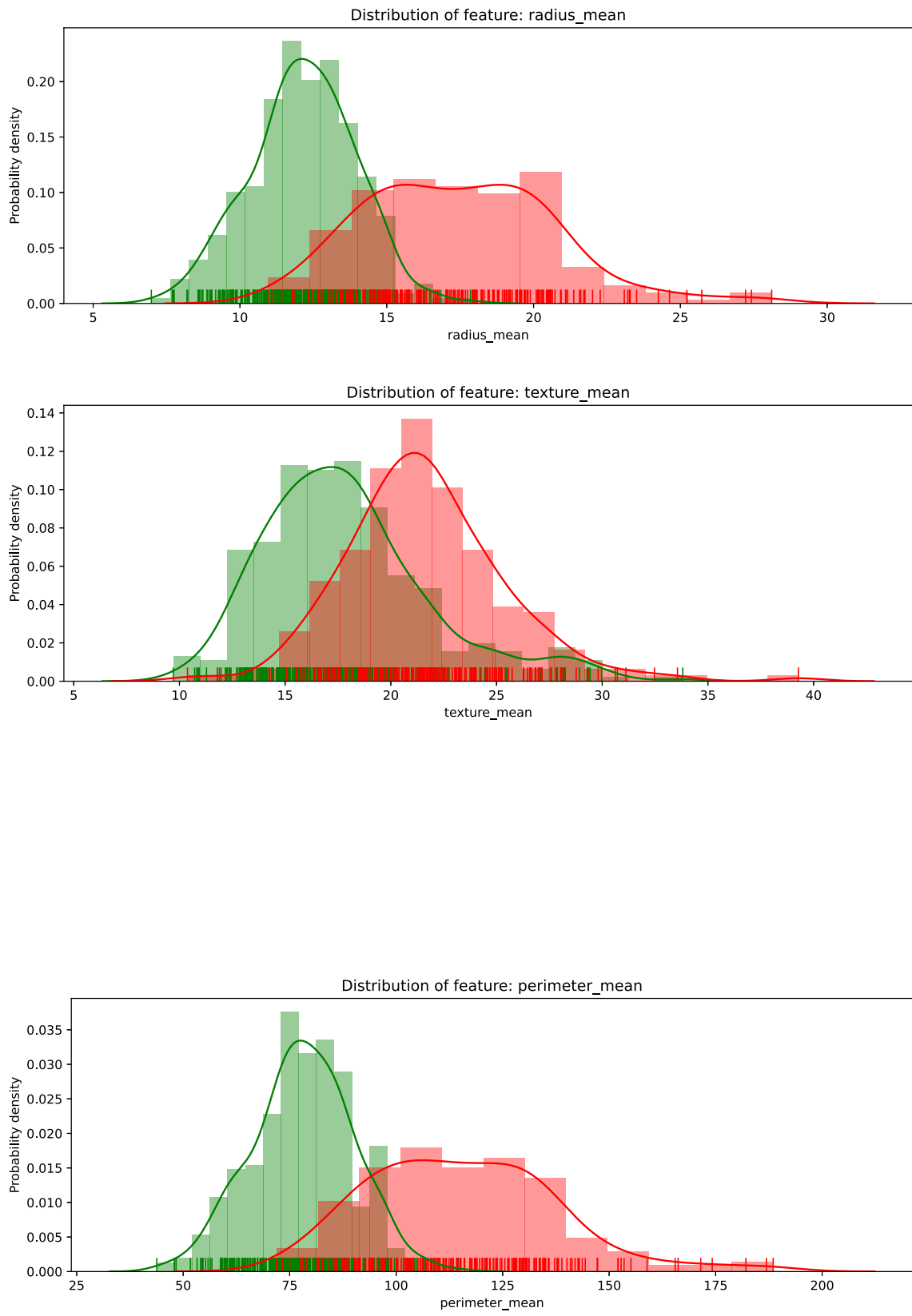
```
Index(['radius_mean', 'texture_mean', 'perimeter_mean', 'area_mean',  
      'smoothness_mean', 'compactness_mean', 'concavity_mean',  
      'concave points_mean', 'symmetry_mean', 'fractal_dimension_mean',  
      'radius_se', 'texture_se', 'perimeter_se', 'area_se', 'smoothness_s  
e',  
      'compactness_se', 'concavity_se', 'concave points_se', 'symmetry_s  
e',  
      'fractal_dimension_se', 'radius_worst', 'texture_worst',  
      'perimeter_worst', 'area_worst', 'smoothness_worst',  
      'compactness_worst', 'concavity_worst', 'concave points_worst',  
      'symmetry_worst', 'fractal_dimension_worst'],  
      dtype='object')
```

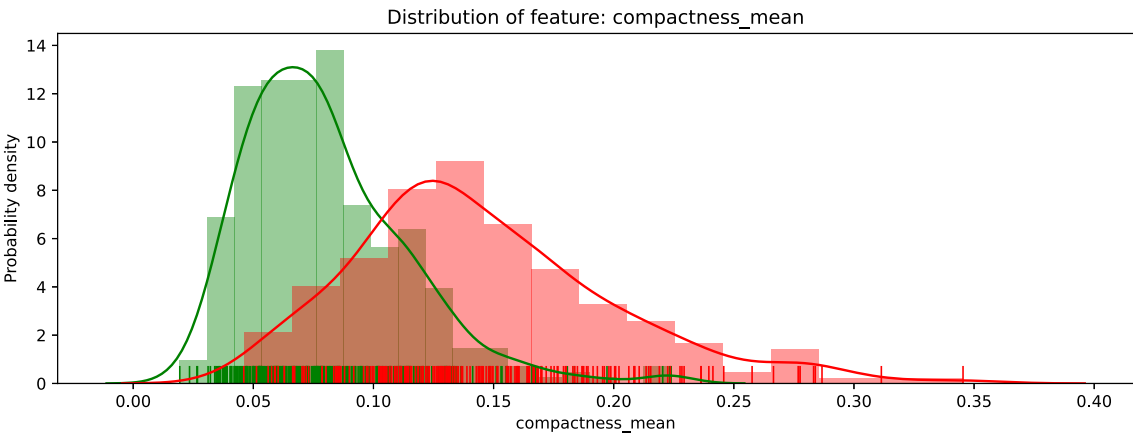
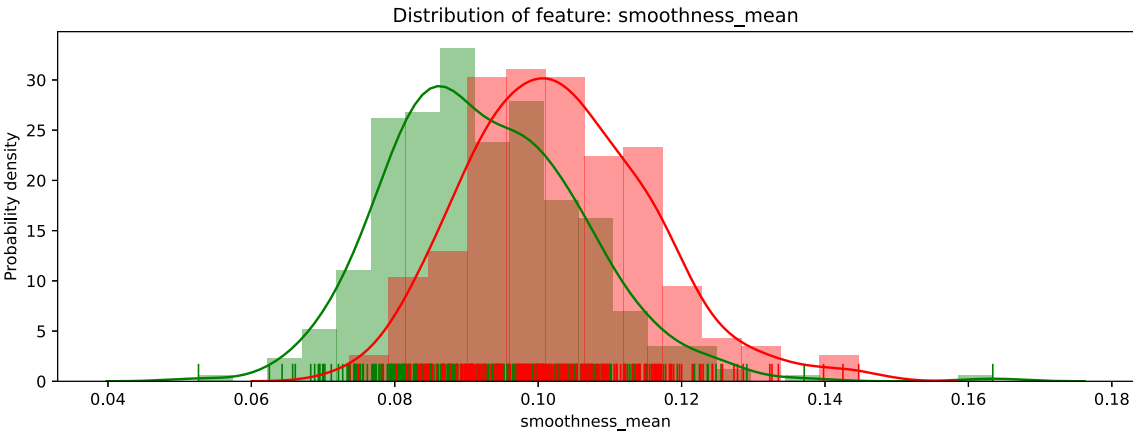
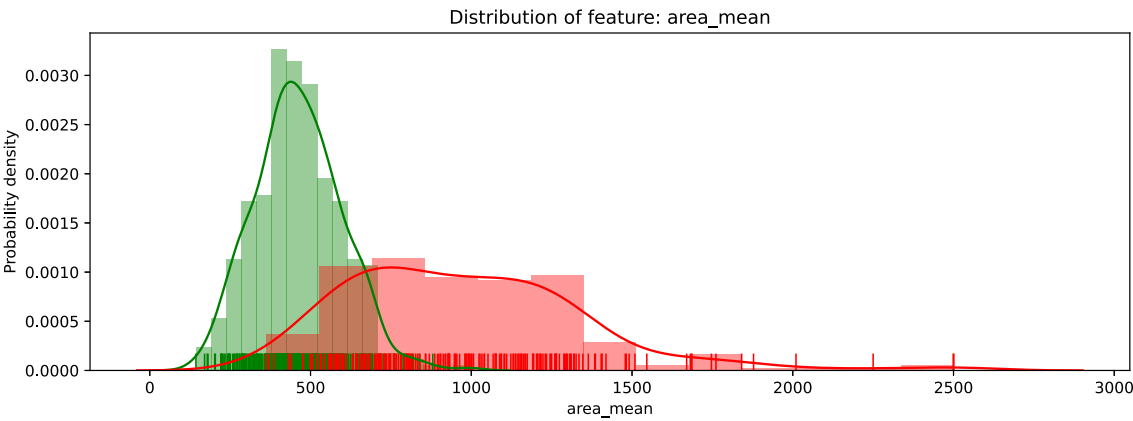
In [9]:

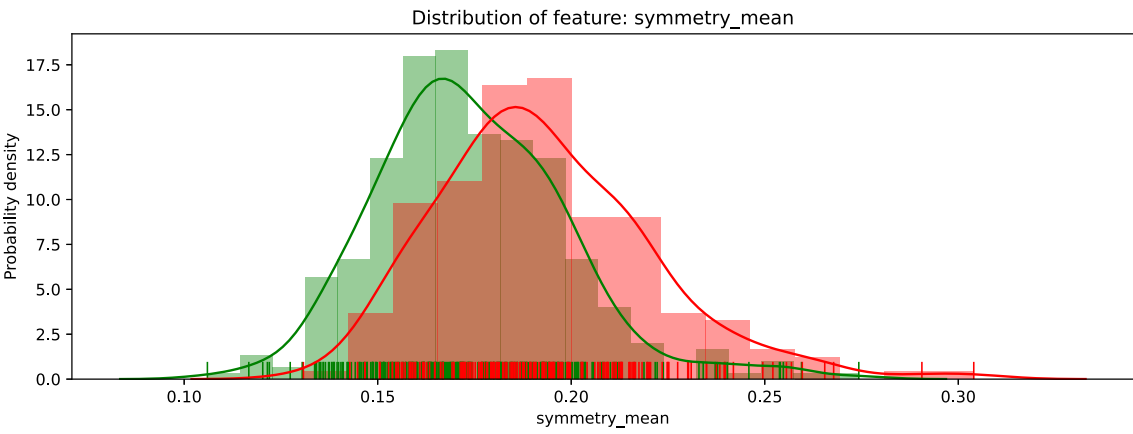
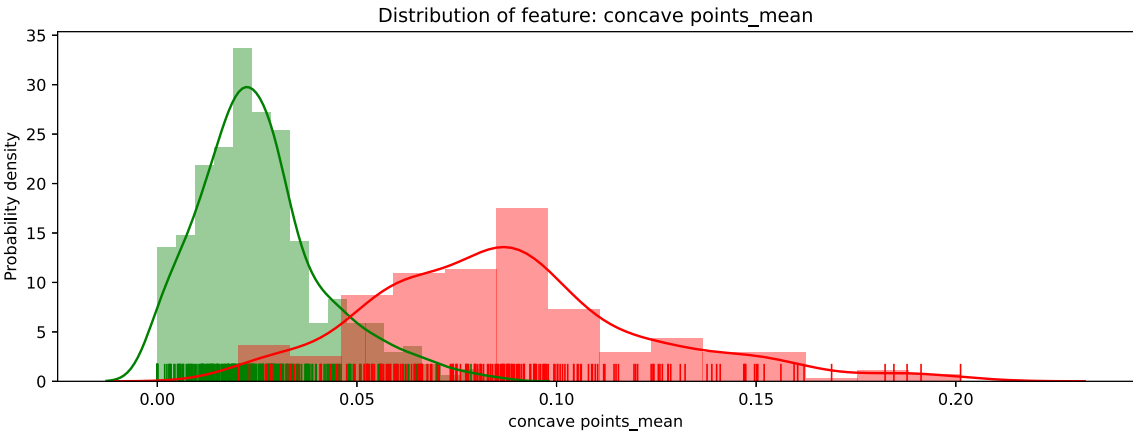
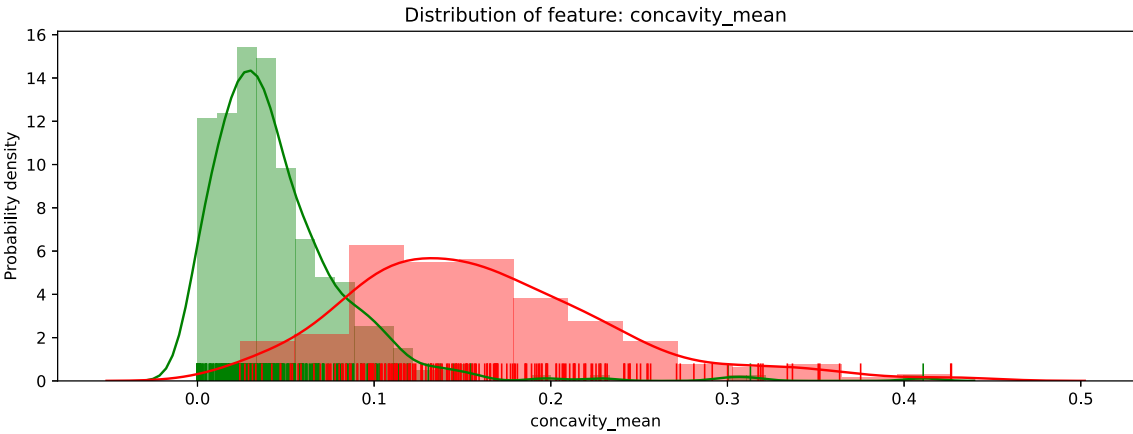
```
import matplotlib.pyplot as plt
import matplotlib.gridspec as gridspec
import seaborn as sns

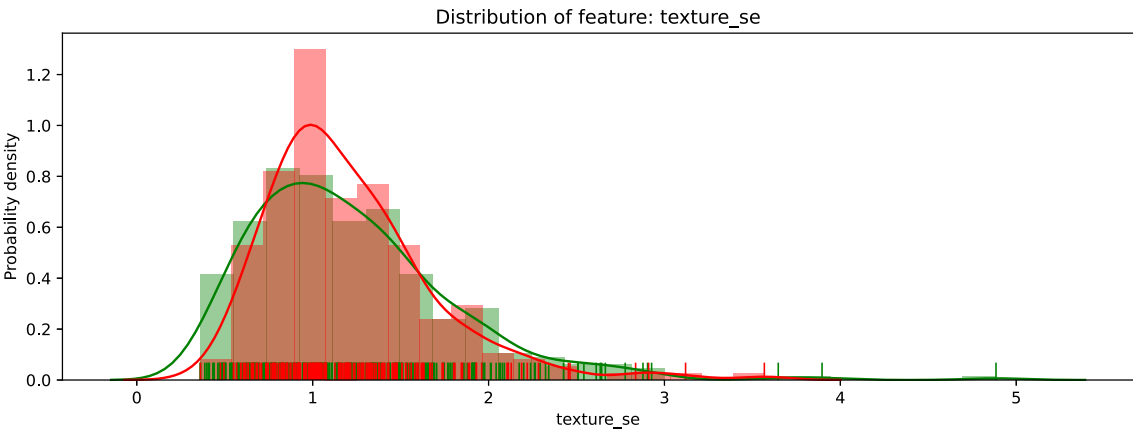
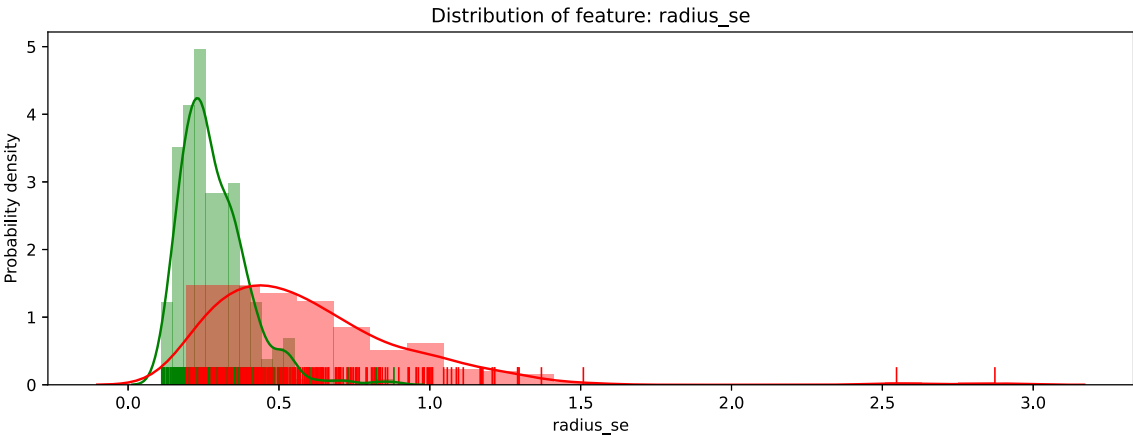
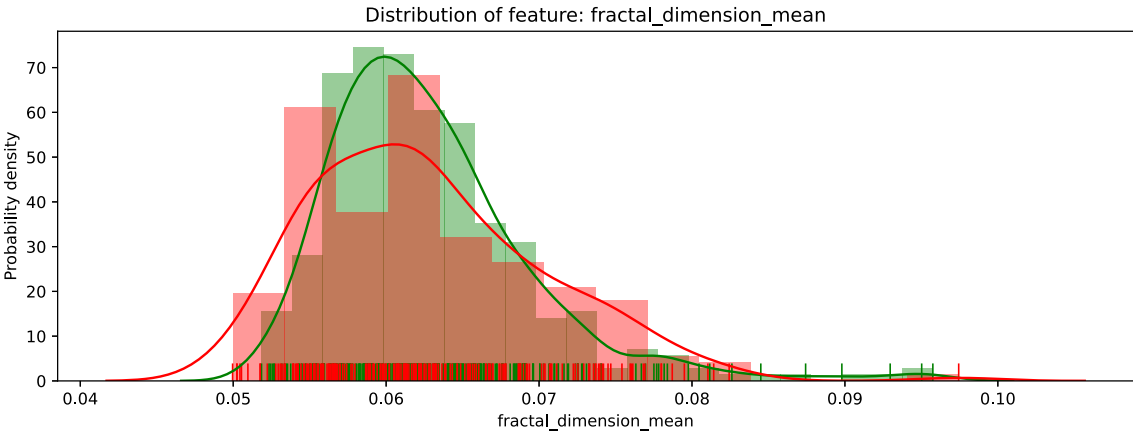
features = df.iloc[:,2:].columns
plt.suptitle('Title')
for i, f in enumerate(df[features]):
    plt.figure(figsize=(12, 4))
    ax = plt.subplot(1, 1, 1)
    sns.distplot(df[f][df.diagnosis == 'B'], rug=True, color='green')
    sns.distplot(df[f][df.diagnosis == 'M'], rug=True, color='red')
    ax.set_xlabel(str(f))
    ax.set_ylabel('Probability density')
    ax.set_title('Distribution of feature: ' + str(f))
plt.show()
```

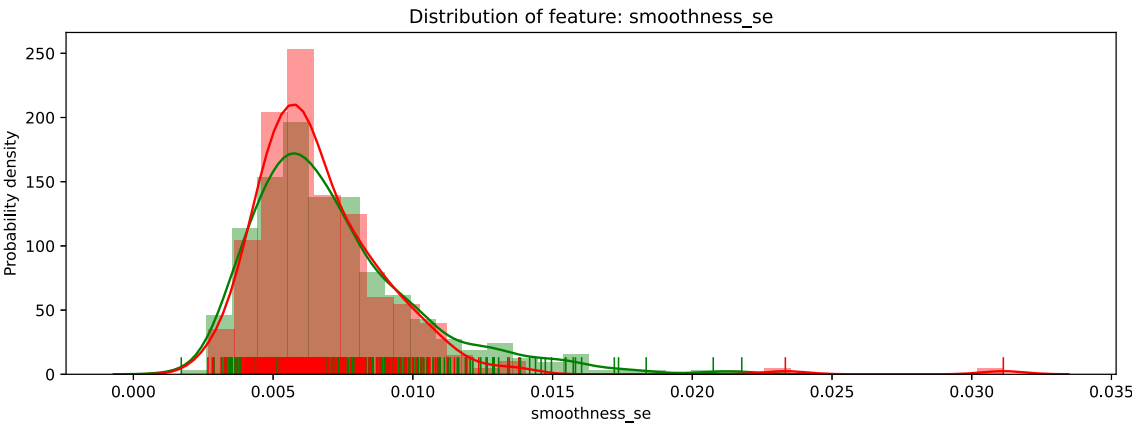
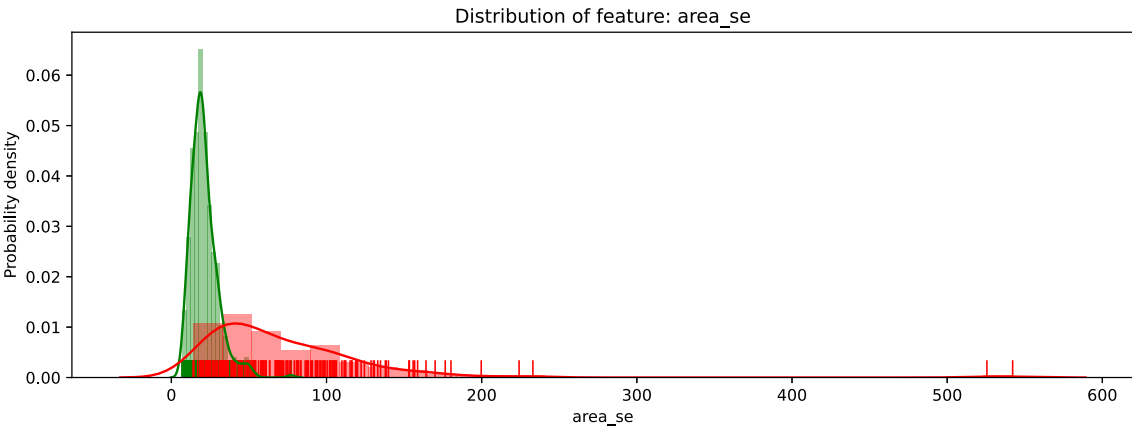
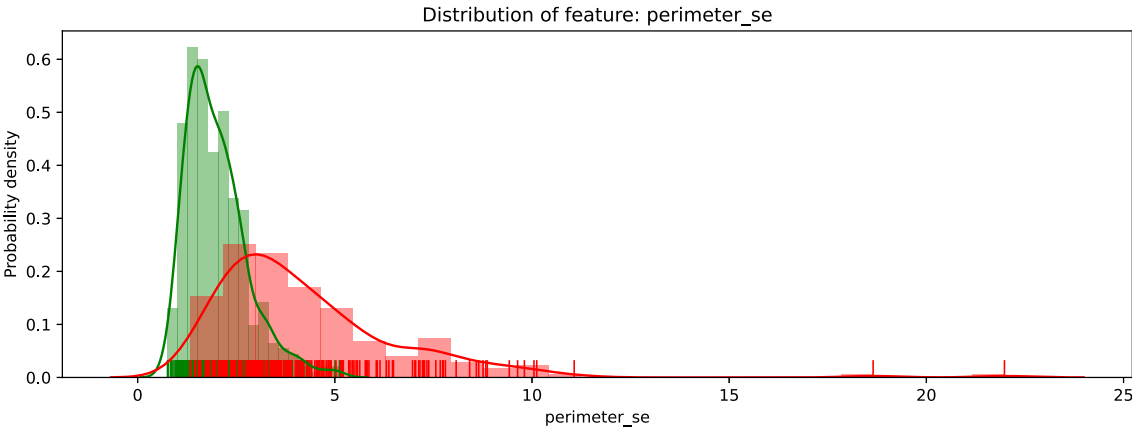
<Figure size 432x288 with 0 Axes>

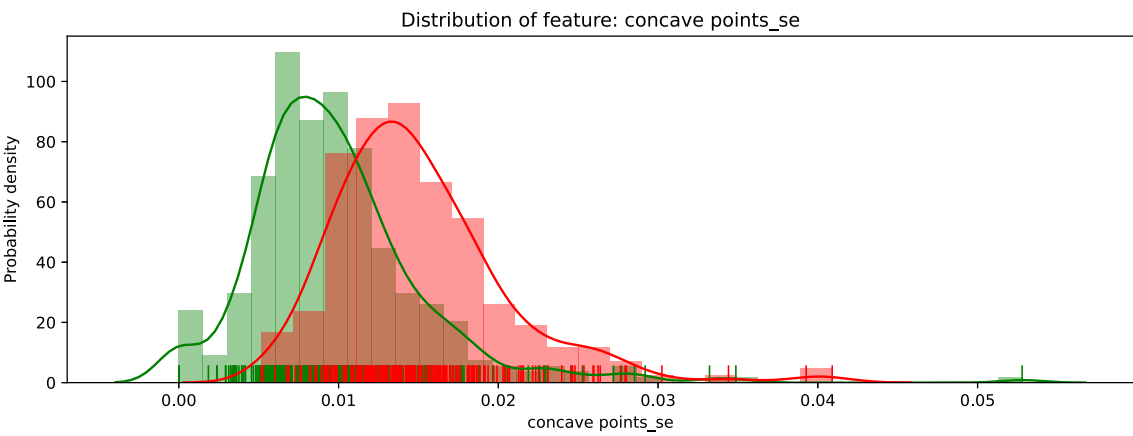
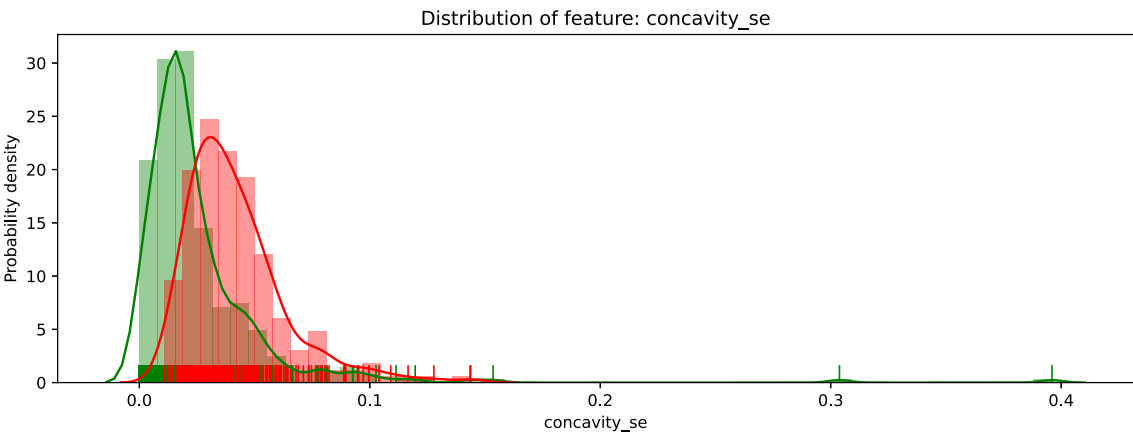
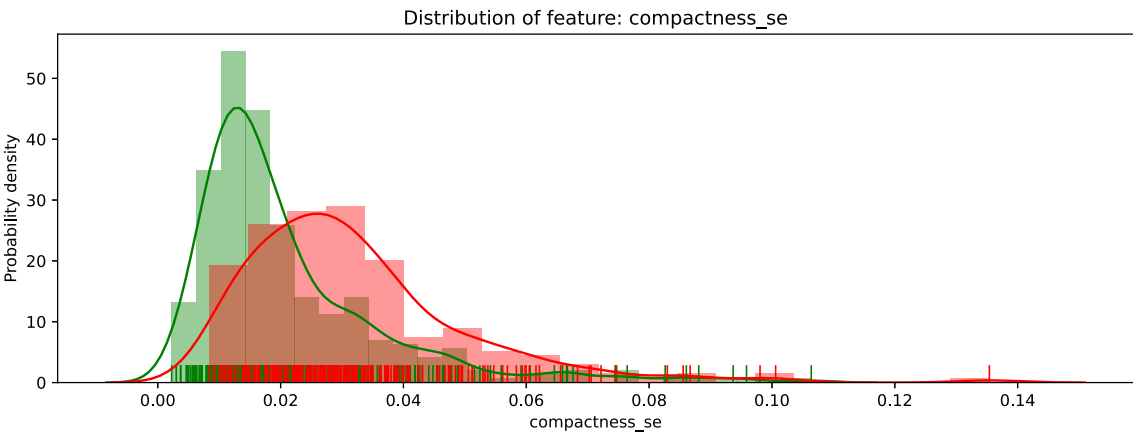


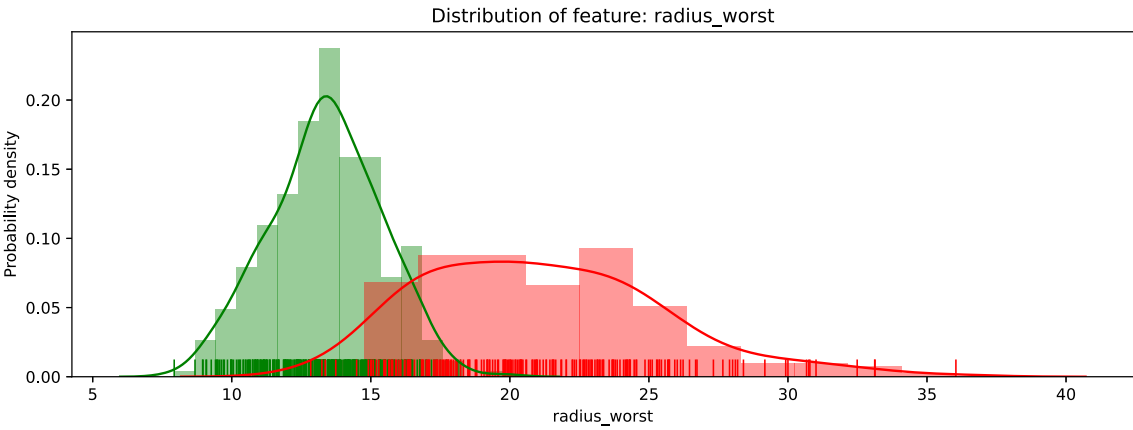
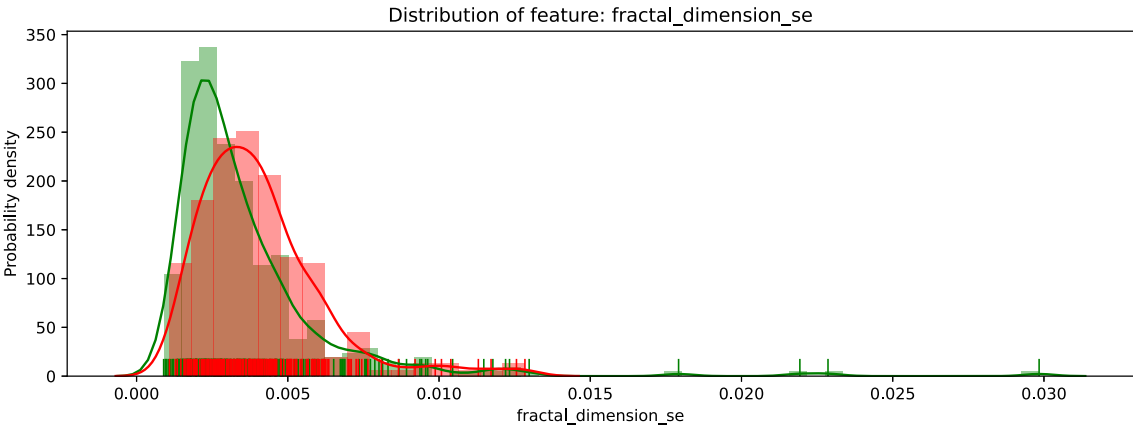
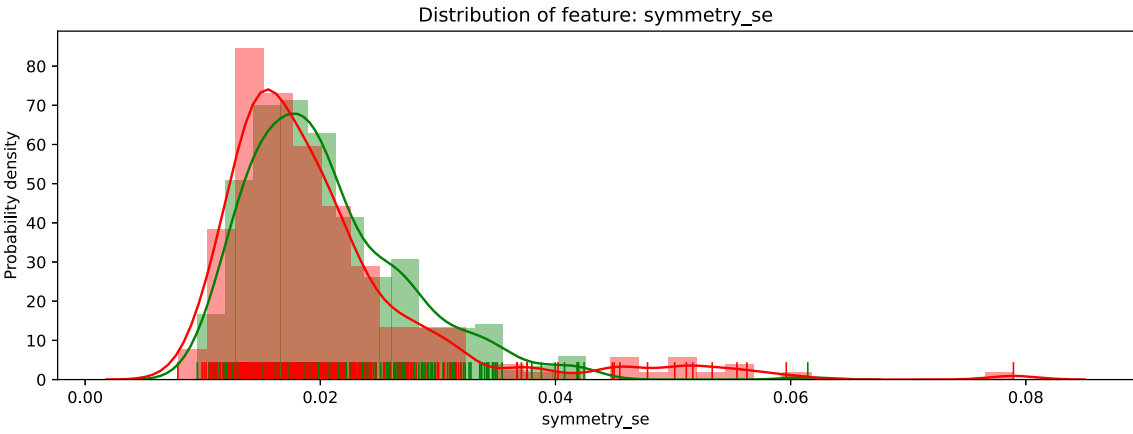


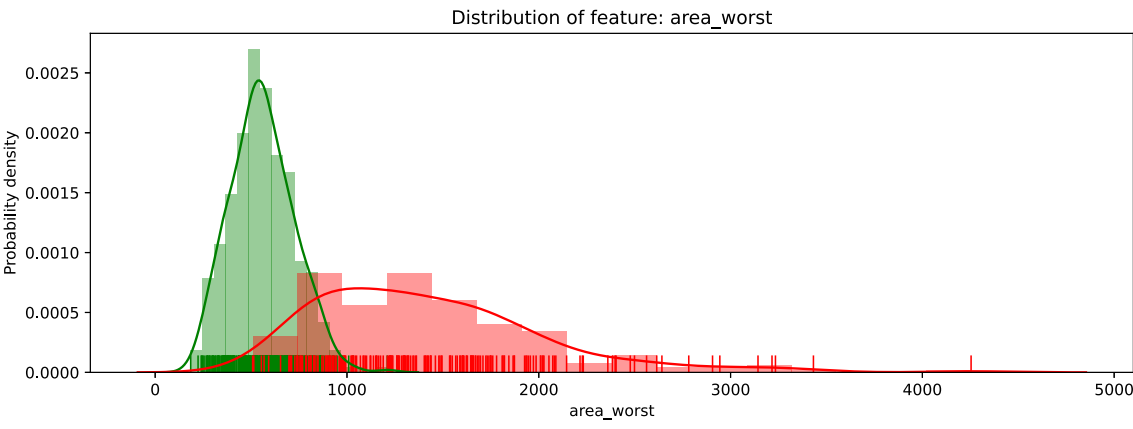
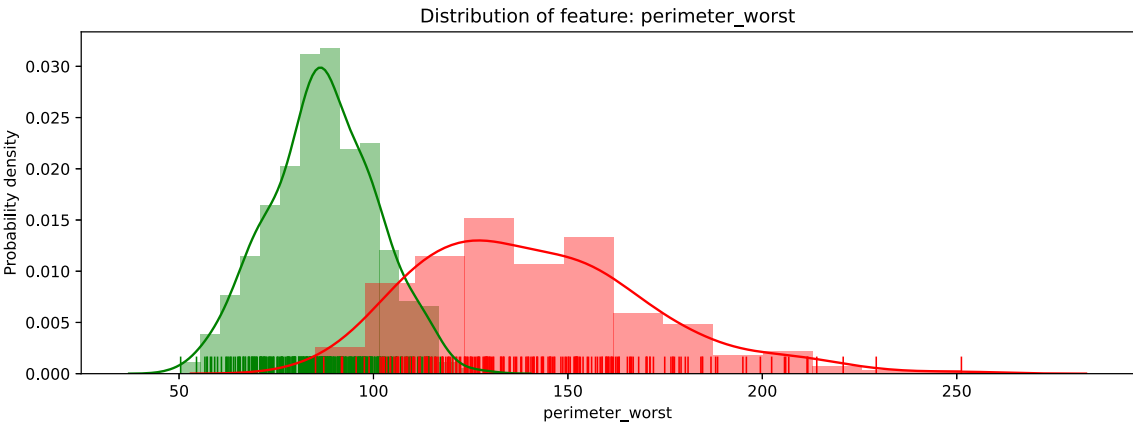
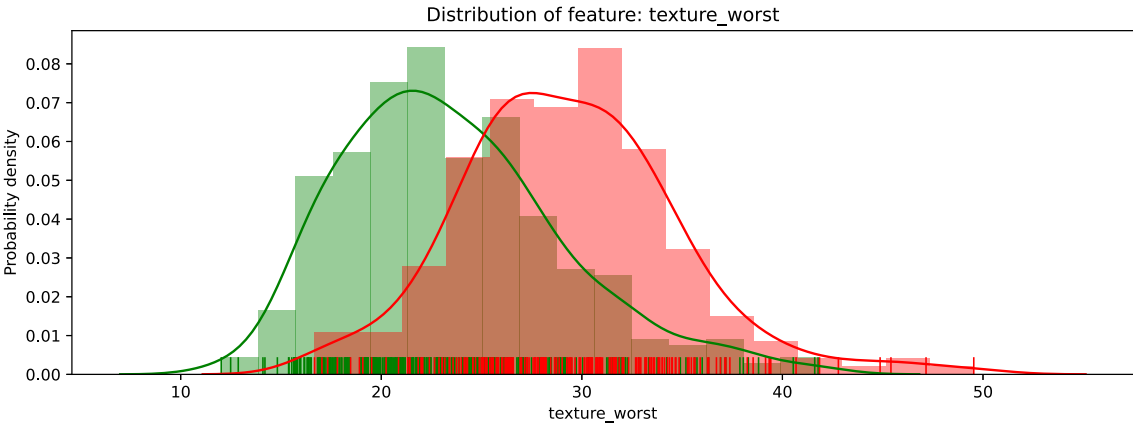


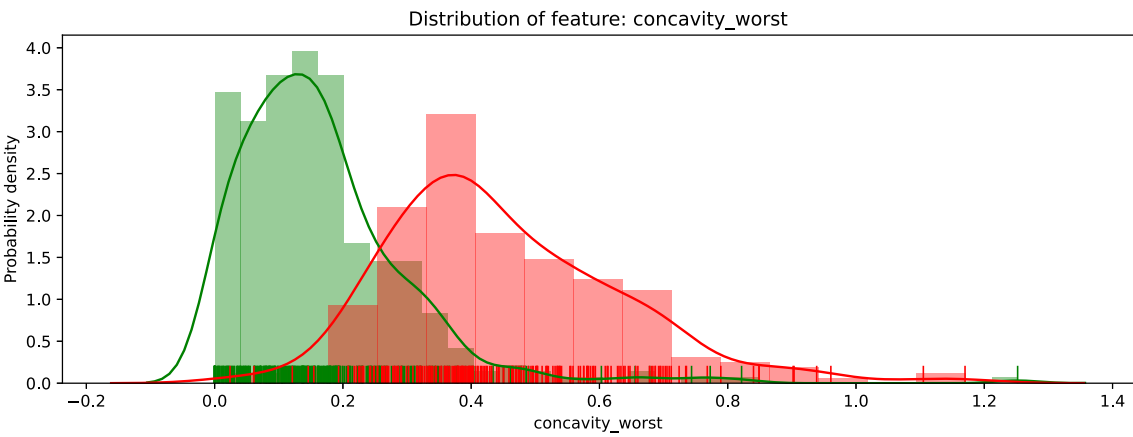
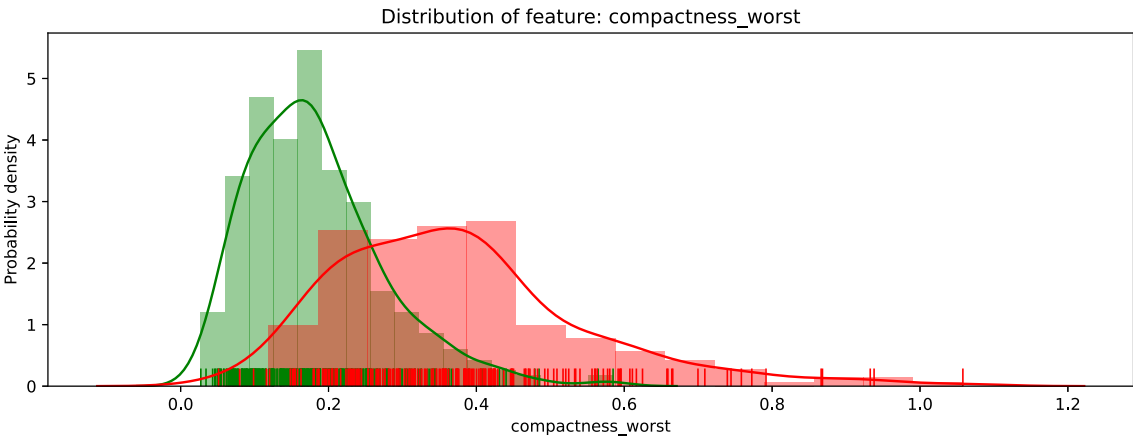
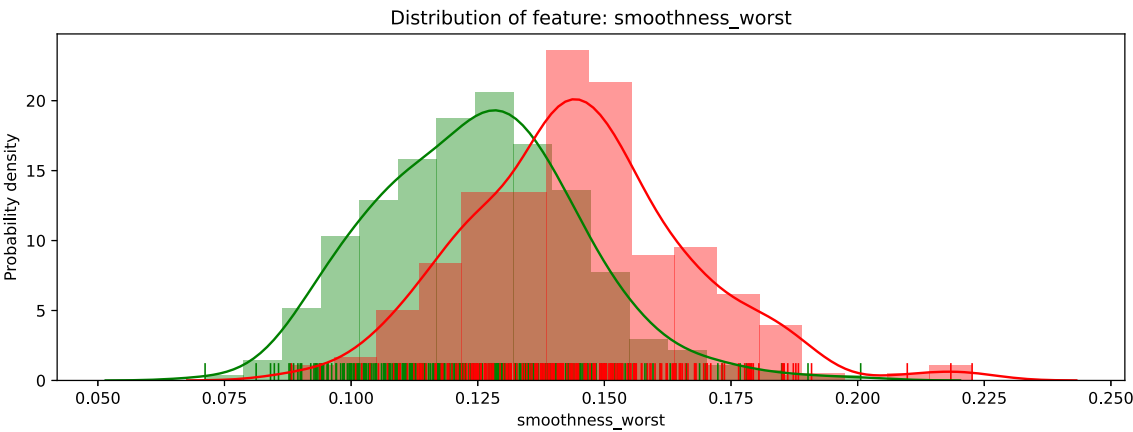


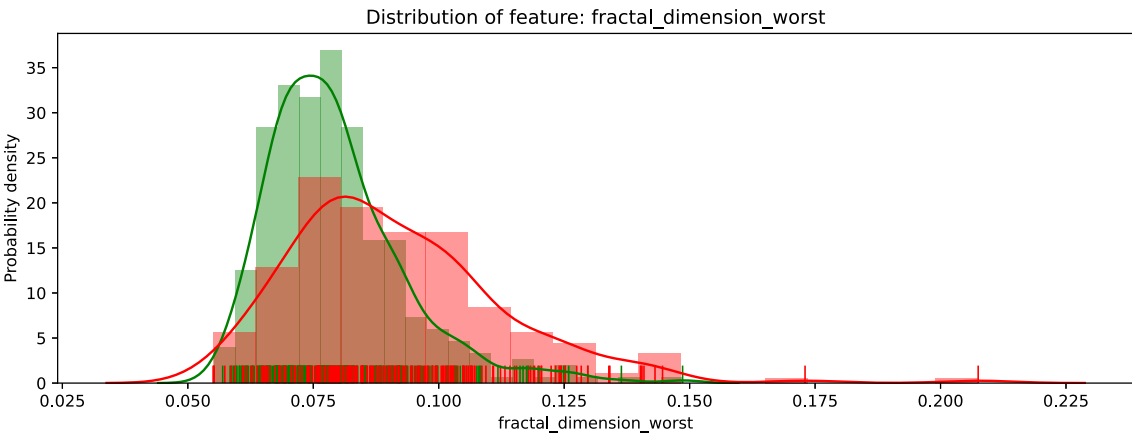
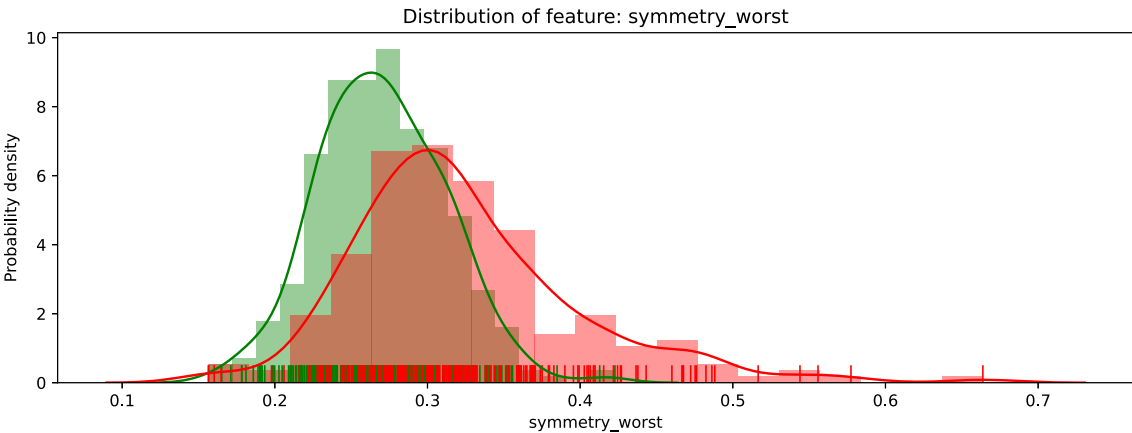
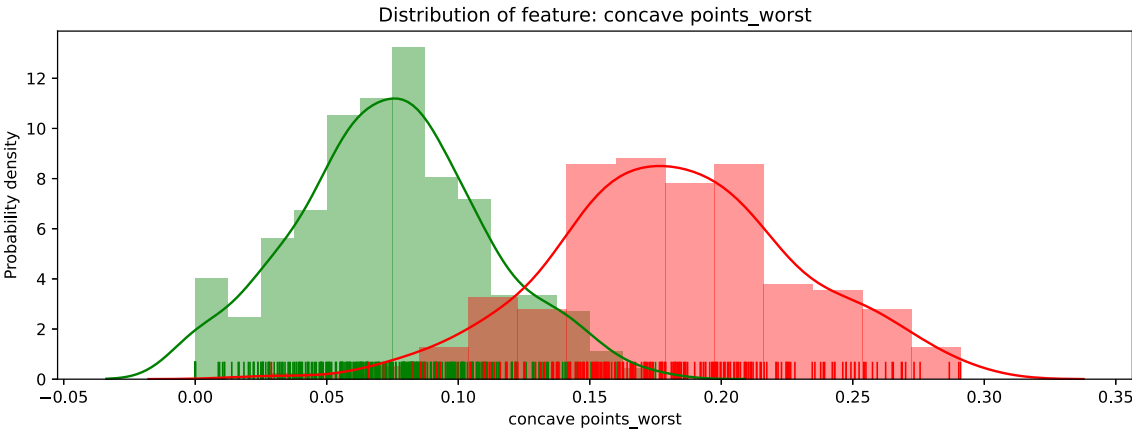










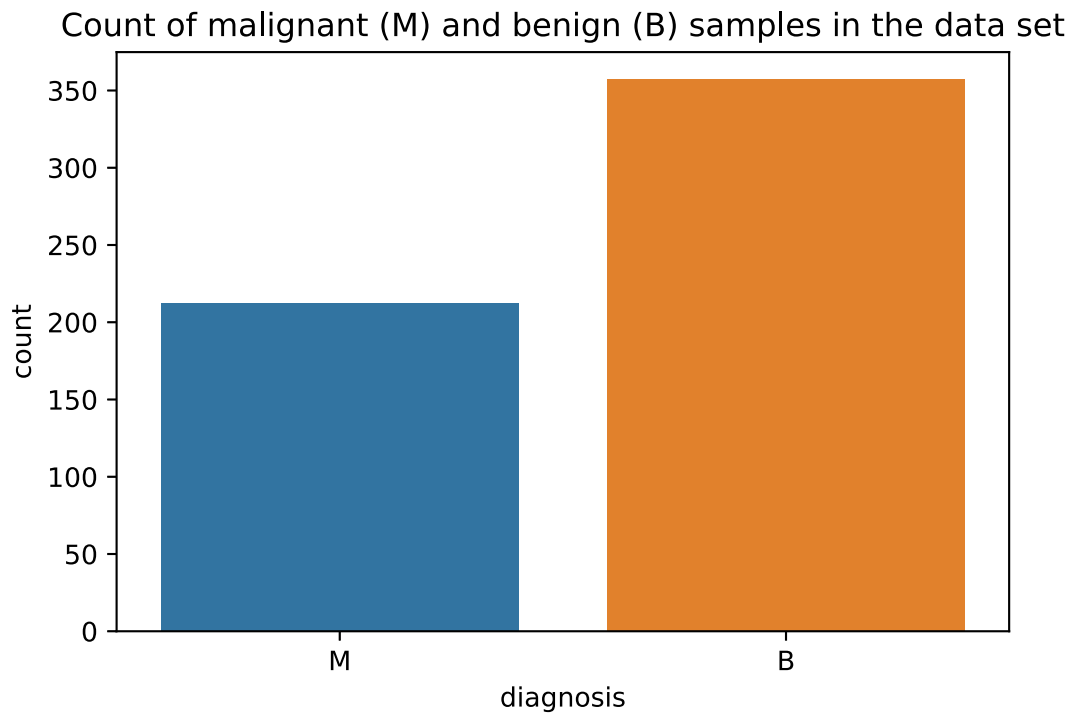


In [10]:

```
ax = sns.countplot(df['diagnosis'], label = "Occurrences")  
plt.title("Count of malignant (M) and benign (B) samples in the data set")
```

Out[10]:

Text(0.5, 1.0, 'Count of malignant (M) and benign (B) samples in the data set')



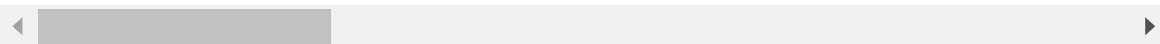
In [11]:

```
X = df[features]
X
```

Out[11]:

	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactne
0	17.99	10.38	122.80	1001.0	0.11840	
1	20.57	17.77	132.90	1326.0	0.08474	
2	19.69	21.25	130.00	1203.0	0.10960	
3	11.42	20.38	77.58	386.1	0.14250	
4	20.29	14.34	135.10	1297.0	0.10030	
...	
564	21.56	22.39	142.00	1479.0	0.11100	
565	20.13	28.25	131.20	1261.0	0.09780	
566	16.60	28.08	108.30	858.1	0.08455	
567	20.60	29.33	140.10	1265.0	0.11780	
568	7.76	24.54	47.92	181.0	0.05263	

569 rows × 30 columns



In [12]:

```
Y = df['diagnosis']
```

In [13]:

```
X = StandardScaler().fit_transform(X)
X
```

Out[13]:

```
array([[ 1.09706398, -2.07333501,  1.26993369, ...,  2.29607613,
         2.75062224,  1.93701461],
       [ 1.82982061, -0.35363241,  1.68595471, ...,  1.0870843 ,
        -0.24388967,  0.28118999],
       [ 1.57988811,  0.45618695,  1.56650313, ...,  1.95500035,
         1.152255  ,  0.20139121],
       ...,
       [ 0.70228425,  2.0455738 ,  0.67267578, ...,  0.41406869,
        -1.10454895, -0.31840916],
       [ 1.83834103,  2.33645719,  1.98252415, ...,  2.28998549,
         1.91908301,  2.21963528],
       [-1.80840125,  1.22179204, -1.81438851, ..., -1.74506282,
        -0.04813821, -0.75120669]])
```

In [14]:

```
X_train, X_test, y_train, y_test = train_test_split(X, Y, test_size=0.33, random_state=7383)
print(len(X_train))
print(len(X_test))
print(len(y_train))
print(len(y_test))
```

381

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381

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Application of basic machine learning algorithms

In [15]:

```
scores = []
for i in range(2, 20):
    classifier = DecisionTreeClassifier(max_leaf_nodes=i, random_state=123)
    predictions = classifier.fit(X_train, y_train).predict(X_test)
    score = accuracy_score(y_true = y_test, y_pred = predictions)
    scores.append(dict(score=score, classifier=classifier))
    print('With ' + str(i) + 'nodes is score: ' + str(score))

max_score = max(s['score'] for s in scores)
best_classifier = next(s for s in scores if s['score'] == max_score)['classifier']
print('Feature importances:')
imp_dict = zip (features, best_classifier.feature_importances_)
imp_dict = sorted(imp_dict, key = lambda t: t[1])
for f, i in imp_dict:
    print(f + ': ' + str(i))
print('Max score: ' + str(max_score))
```

```
With 2nodes is score: 0.9095744680851063
With 3nodes is score: 0.925531914893617
With 4nodes is score: 0.9414893617021277
With 5nodes is score: 0.9361702127659575
With 6nodes is score: 0.9361702127659575
With 7nodes is score: 0.9361702127659575
With 8nodes is score: 0.9361702127659575
With 9nodes is score: 0.9308510638297872
With 10nodes is score: 0.925531914893617
With 11nodes is score: 0.925531914893617
With 12nodes is score: 0.925531914893617
With 13nodes is score: 0.925531914893617
With 14nodes is score: 0.925531914893617
With 15nodes is score: 0.925531914893617
With 16nodes is score: 0.9202127659574468
With 17nodes is score: 0.9042553191489362
With 18nodes is score: 0.9042553191489362
With 19nodes is score: 0.9042553191489362
Feature importances:
radius_mean: 0.0
texture_mean: 0.0
perimeter_mean: 0.0
area_mean: 0.0
smoothness_mean: 0.0
compactness_mean: 0.0
concavity_mean: 0.0
concave points_mean: 0.0
symmetry_mean: 0.0
fractal_dimension_mean: 0.0
radius_se: 0.0
texture_se: 0.0
perimeter_se: 0.0
area_se: 0.0
smoothness_se: 0.0
compactness_se: 0.0
concavity_se: 0.0
concave points_se: 0.0
symmetry_se: 0.0
fractal_dimension_se: 0.0
radius_worst: 0.0
perimeter_worst: 0.0
smoothness_worst: 0.0
compactness_worst: 0.0
concavity_worst: 0.0
symmetry_worst: 0.0
fractal_dimension_worst: 0.0
texture_worst: 0.06198140435134387
concave points_worst: 0.12598114750037204
area_worst: 0.8120374481482842
Max score: 0.9414893617021277
```

In [16]:

```
scores = []
for i in range(2, 20):
    classifier = RandomForestClassifier(max_leaf_nodes=i)
    predictions = classifier.fit(X_train, y_train).predict(X_test)
    score = accuracy_score(y_true = y_test, y_pred = predictions)
    scores.append(dict(score=score, classifier=classifier))
    print('With ' + str(i) + 'nodes is score: ' + str(score))

max_score = max(s['score'] for s in scores)
best_classifier = next(s for s in scores if s['score'] == max_score)['classifier']
print('Feature importances:')
imp_dict = zip (features, best_classifier.feature_importances_)
imp_dict = sorted(imp_dict, key = lambda t: t[1])
for f, i in imp_dict:
    print(f + ': ' + str(i))
print('Max score: ' + str(max_score))
rfc = best_classifier
```

```
With 2nodes is score: 0.9202127659574468
With 3nodes is score: 0.9414893617021277
With 4nodes is score: 0.9521276595744681
With 5nodes is score: 0.9414893617021277
With 6nodes is score: 0.9627659574468085
With 7nodes is score: 0.9574468085106383
With 8nodes is score: 0.9521276595744681
With 9nodes is score: 0.9574468085106383
With 10nodes is score: 0.9627659574468085
With 11nodes is score: 0.9627659574468085
With 12nodes is score: 0.9627659574468085
With 13nodes is score: 0.9680851063829787
With 14nodes is score: 0.9627659574468085
With 15nodes is score: 0.9680851063829787
With 16nodes is score: 0.9627659574468085
With 17nodes is score: 0.9680851063829787
With 18nodes is score: 0.9627659574468085
With 19nodes is score: 0.9627659574468085
Feature importances:
symmetry_se: 0.0029504800389258887
smoothness_mean: 0.0030968062684194617
compactness_se: 0.00328462254770653
fractal_dimension_worst: 0.003439161756059001
fractal_dimension_mean: 0.0038299257456068402
concavity_se: 0.0038422706962367623
texture_se: 0.0040181991191703004
concave points_se: 0.004621914551159907
smoothness_se: 0.004916791050718517
fractal_dimension_se: 0.004994991931322467
symmetry_mean: 0.005059165720012492
compactness_mean: 0.007553693867938604
smoothness_worst: 0.007623544755808637
symmetry_worst: 0.007941398442551586
compactness_worst: 0.0117430899405953
radius_se: 0.012089140339998286
texture_mean: 0.013432121420938196
texture_worst: 0.015263839515334438
perimeter_se: 0.015596444622860495
concavity_worst: 0.025311817377956597
area_mean: 0.0306070729403948
concave points_mean: 0.044910959648023364
perimeter_mean: 0.05515154488563485
radius_mean: 0.058659120273257113
area_se: 0.05955916991080493
concavity_mean: 0.06595506328161753
concave points_worst: 0.12213140759542765
perimeter_worst: 0.12836355178700246
area_worst: 0.13539900343410682
radius_worst: 0.13865368653441035
Max score: 0.9680851063829787
```

In [17]:

```

classifier = GaussianNB()
predictions = classifier.fit(X_train, y_train).predict(X_test)
score = accuracy_score(y_true = y_test, y_pred = predictions)
print(str(score))
from sklearn.inspection import permutation_importance
imps = permutation_importance(classifier, X_test, y_test)
print(imps.importances_mean)

```

0.9468085106382979

```

[ 6.38297872e-03  1.06382979e-03  7.44680851e-03  1.06382979e-02
 0.00000000e+00 -2.22044605e-17 -3.19148936e-03  9.57446809e-03
 0.00000000e+00  0.00000000e+00  1.27659574e-02  0.00000000e+00
 1.17021277e-02  5.31914894e-02 -7.44680851e-03 -4.25531915e-03
-1.06382979e-03 -1.06382979e-03  0.00000000e+00 -2.22044605e-17
 8.51063830e-03  1.06382979e-03  6.38297872e-03  2.76595745e-02
 0.00000000e+00 -4.25531915e-03 -3.19148936e-03  6.38297872e-03
 0.00000000e+00 -4.25531915e-03]

```

In [18]:

```

classifier = KNeighborsClassifier()
predictions = classifier.fit(X_train, y_train).predict(X_test)
score = accuracy_score(y_true = y_test, y_pred = predictions)
print(str(score))

```

0.9680851063829787

Comparison of the accuracy the used basic algorithms with more sophisticated machine learning algorithms

Basic algorithms examined in this project

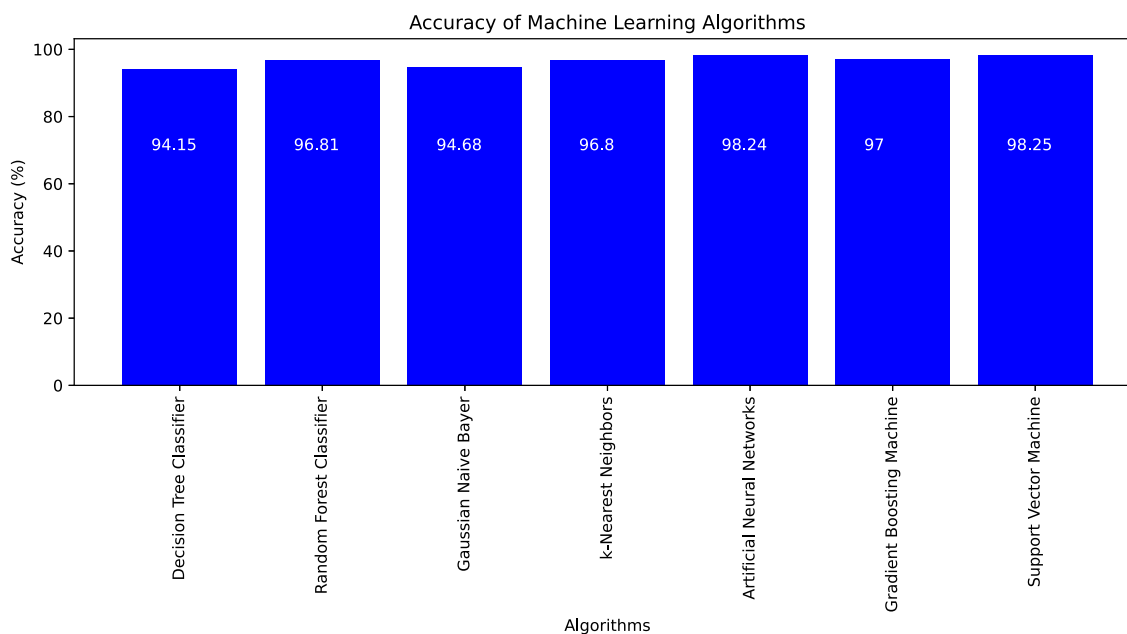
- Decision Tree Classifier (DTC): 94.15%
- Random Forest Classifier (RFC): 96.81%
- Gaussian Naive Bayes (GNB): 94.68%
- k-Nearest Neighbors (KNN): 96,80% ### Advanced algorithms examined by others
- Artificial Neural Networks (ANN): 98.24% <https://www.kaggle.com/thebrownviking20/intro-to-keras-with-breast-cancer-data-ann> (<https://www.kaggle.com/thebrownviking20/intro-to-keras-with-breast-cancer-data-ann>)
- Gradient Boosting Machine (GBM): 97% <https://www.kaggle.com/gpreda/breast-cancer-prediction-from-cytopathology-data> (<https://www.kaggle.com/gpreda/breast-cancer-prediction-from-cytopathology-data>)
- Support Vector Machine (SVM): 98.25% <https://www.kaggle.com/faressayah/support-vector-machine-pca-tutorial-for-beginner> (<https://www.kaggle.com/faressayah/support-vector-machine-pca-tutorial-for-beginner>)

In [19]:

```
algorithm_accuracy = {  
    'Decision Tree Classifier': 94.15,  
    'Random Forest Classifier': 96.81,  
    'Gaussian Naive Bayes': 94.68,  
    'k-Nearest Neighbors': 96.80,  
    'Artificial Neural Networks': 98.24,  
    'Gradient Boosting Machine': 97,  
    'Support Vector Machine': 98.25  
}  
  
plt.figure(figsize=(12, 4))  
  
for index, value in enumerate(algorithm_accuracy.values()):  
    plt.text(index - 0.2, 70, str(value), color='white')  
  
plt.title('Accuracy of Machine Learning Algorithms')  
plt.xticks(rotation=90)  
plt.xlabel('Algorithms')  
plt.ylabel('Accuracy (%)')  
plt.bar(algorithm_accuracy.keys(), algorithm_accuracy.values(), color='b')
```

Out[19]:

<BarContainer object of 7 artists>



Most important features

Looking at the distribution graphs, the following features appeared as the most important ones to me for the classification problem because they have the smallest overlapping areas for benign and malignant samples:

- `cancavity_mean`
- `concave points_mean`
- `radius_worst`
- `perimeter_worst`
- `area_worst`
- `cancavity_worst`
- `concave points_worst`

This is how the classifiers weighed the feature importance: The Decision Tree Classifier found only three features being important for classification and ignored the other features:

- `texture_worst`: 0.06198140435134387
- `concave points_worst`: 0.12598114750037204
- `area_worst`: 0.8120374481482842

The Random Forest Classifier weighed these features as most important:

- `radius_mean`: 0.05872515489464252
- `area_mean`: 0.06469903094642988
- `perimeter_mean`: 0.0665823176981204
- `concave points_worst`: 0.09296126521373517
- `radius_worst`: 0.11300785482788624
- `perimeter_worst`: 0.12171853874149956
- `area_worst`: 0.15396899594687236

The other two classification algorithms have no concept of feature importance

In [27]:

```

imp_dict = zip (features, rfc.feature_importances_)
imp_list = sorted(imp_dict, key = lambda t:(t[1], t[0]))
features = []
importances = []
for i in imp_list:
    features += [i[0]]
    importances += [i[1]]
plt.figure(figsize=(12, 6))

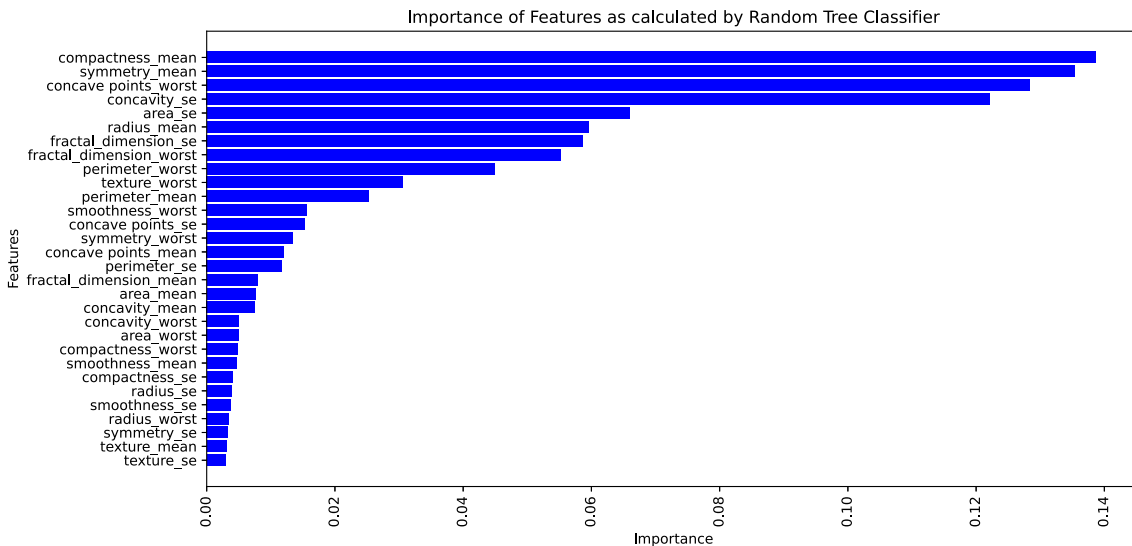
# for index, value in enumerate(imp_dict_sorted.values()):
#     plt.text(index - 0.2, 70, str(value), color='white')

plt.title('Importance of Features as calculated by Random Tree Classifier')
plt.xticks(rotation=90)
plt.xlabel('Importance')
plt.ylabel('Features')
plt.barh(features, importances, color='b')

```

Out[27]:

<BarContainer object of 30 artists>



In []: