# Final Project - Deep Learning and Reinforcement Learning

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#### 1 Introduction

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Project available in: https://github.com/vcaitite/Coursera-IBM-Deep-Learning-Reinforcement-

Learning-Final-Project

### 1.1 Objectives

The objective of this work is to apply neural network models studied during the course to a practical problem regarding an available dataset publicly and involving recognition of the type of breast tumor (malignant or benign). The database was built by the University of Wisconsin Hospitals, Madison of Dr. William H. Wolberg [1].

#### 1.2 About Data

Basically the file containing the data contains 1 column of Id (just a identifier) followed by 9 columns containing the input vectors x, and finally, one last column containing the classification of the tumor corresponding to the y label of that sample. This dataset contains 699 samples. The table below shows the organization of the dataset.

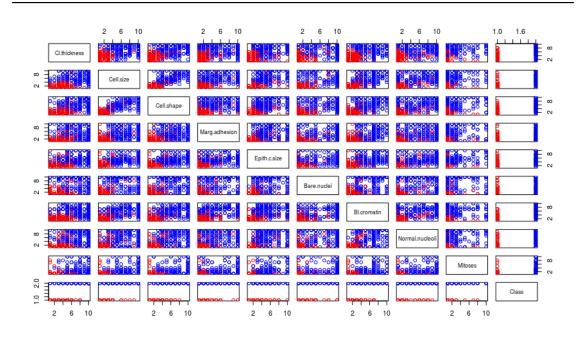
Attribute	Domain
1. Sample code number	id number
2. Clump Thickness	1 - 10
3. Uniformity of Cell Size	1 - 10
4. Uniformity of Cell Shape	1 - 10
5. Marginal Adhesion	1 - 10
6. Single Epithelial Cell Size	1 - 10
7. Bare Nuclei	1 - 10
8. Bland Chromatin	1 - 10
9. Normal Nucleoli	1 - 10
10. Mitoses	1 - 10
11. Class	benign or malignant

Dataset available in: https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Original)

#### 1.2.1 Importing Packages and Reading Data:

```
[85]: import warnings
      warnings.filterwarnings("ignore")
      import numpy as np
      import pandas as pd
      import matplotlib.pyplot as plt
      import seaborn as sns
      from sklearn.model_selection import train_test_split
      from sklearn.preprocessing import StandardScaler
      from sklearn.metrics import confusion_matrix, classification_report,_
       →precision_recall_curve, roc_auc_score, roc_curve, accuracy_score
      from sklearn.ensemble import RandomForestClassifier
      from sklearn.metrics import plot_confusion_matrix
      ## Import Keras objects for Deep Learning
      from keras.models import Sequential
      from keras.layers import Input, Dense, Flatten, Dropout, BatchNormalization,
       →LeakyReLU
      from keras.optimizers import Adam, SGD, RMSprop
[10]: path = "~/Documents/Online courses/Cousera/IBM Deep Learning and Reinforcement
      →Learning/final_project/project/database/BreastCancer.csv"
      df = pd.read_csv(path)
      print(df.shape)
      df.sample(5)
     (699, 11)
「10]:
                Id Cl.thickness Cell.size Cell.shape
                                                         Marg.adhesion \
      677
          1368267
                               5
                                          1
                                                      1
                                                                      1
      387 1114570
                               5
                                          3
                                                       3
                                                                      2
      9
           1033078
                               4
                                          2
                                                       1
                                                                      1
      399 1206314
                               1
                                          2
                                                       3
                                                                      1
                               4
                                          1
                                                       1
      638 1277792
                                                                      1
           Epith.c.size Bare.nuclei Bl.cromatin Normal.nucleoli Mitoses
                                                                               Class
      677
                      2
                                 1.0
                                                                              benign
                                                1
                                                                           1
      387
                      3
                                 1.0
                                                3
                                                                  1
                                                                              benign
                      2
                                                2
                                 1.0
                                                                  1
                                                                              benign
                                                                           1
      399
                      2
                                 1.0
                                                1
                                                                  1
                                                                              benign
                                                                           1
      638
                      2
                                                                  1
                                 1.0
                                                 1
                                                                              benign
```

In the table above, it's possible see 5 samples of the dataset and visualize the data organization. And in the Figure below, graphs were plotted considering only 2 dimensions at a time. As can be seen in the graphs, in general the data present a good spatial separation, which initially may indicate that the models will be able to perform a good classification. *This Figure was generated by the author using RStudio*.



Graphs considering 2 dimensions at a time.

## 1.3 Data Preprocessing

These data need to receive an initial treatment to eliminate missing data, represented by the string NA. In addition, the samples were labeled with a value of 0 (malignant) and 1 (benigno), and also the column referring to the identifiers was removed.

```
[11]: df=df.dropna()
      print(df.shape)
      (683, 11)
[12]: mapping = {'benign': 1, 'malignant': 0}
      df = df.replace({"Class": mapping})
[13]: del df['Id']
      df.sample(4)
[13]:
           Cl.thickness
                          Cell.size
                                      Cell.shape
                                                   Marg.adhesion
                                                                   Epith.c.size
      97
                       5
                                                1
                                                                1
                       2
      176
                                   1
                                                1
                                                                1
                                                                               2
      301
                                   1
                                                1
                                                                1
                                                                               2
                       1
      409
                       3
                                   1
                                                2
                                                                1
                                                                               2
                                       Normal.nucleoli
                                                        Mitoses
           Bare.nuclei Bl.cromatin
                                                                   Class
      97
                    1.0
                                    3
                                                      1
                                                                1
                                                                       1
```

```
    176
    1.0
    3
    1
    1
    1

    301
    1.0
    3
    1
    1
    1

    409
    1.0
    2
    1
    1
    1
```

#### 1.4 Split Data to Train, and Test (75%, 25%)

## 1.5 Normalizing the data

Shape of X\_test: (171, 9) Shape of y\_train: (512,) Shape of y\_test: (171,)

Before start the model part a good practice is normalize the data. This aids the training of neural nets by providing numerical stability.

```
[38]: normalizer = StandardScaler()
X_train_norm = normalizer.fit_transform(X_train)
X_test_norm = normalizer.transform(X_test)
```

#### 2 Model 1

### 2.1 Defining the Model

I will use the Sequential model to quickly build a neural network. This first network will be a single layer network. We have 9 variables, so we set the input shape to 9. The model defined below has a single hidden layer with 12 nodes with sigmoid activation. As the problem ia a binary classification, the final layer has just one node with a sigmoid activation.

```
[99]: # Define the Model
# Input size is 9-dimensional
# 1 hidden layer, 12 hidden nodes, sigmoid activation
# Final layer has just one node with a sigmoid activation (standard for binary
→ classification)

model_1 = Sequential()
model_1.add(Dense(12,input_shape = (9,),activation = 'sigmoid'))
```

```
model_1.add(Dense(1,activation='sigmoid'))
[100]: # This is a nice tool to view the model you have created and count the
     \rightarrowparameters
     model_1.summary()
    Model: "sequential_12"
    Layer (type)
                          Output Shape
    ______
    dense_38 (Dense)
                          (None, 12)
                                             120
    dense_39 (Dense)
                          (None, 1)
                                             13
    ______
    Total params: 133
    Trainable params: 133
```

## 2.2 Training and Testing the Model

Non-trainable params: 0

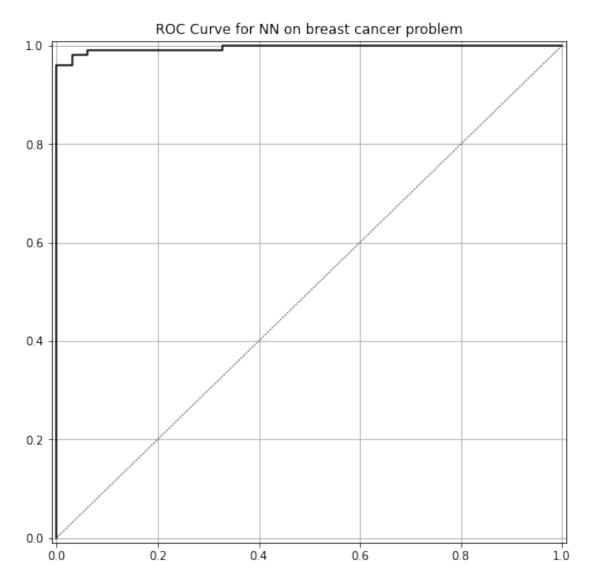
This first model will be trained with the Stochastic Gradient Descent with learning rate equals to 0.003. Others training parameters are: - epochs = 500 - batch\_size = 32

```
[26]: ## Like we did for the Random Forest, we generate two kinds of predictions
# One is a hard decision, the other is a probabilitistic score.

y_pred_class_nn_1 = model_1.predict_classes(X_test_norm)
y_pred_prob_nn_1 = model_1.predict(X_test_norm)
```

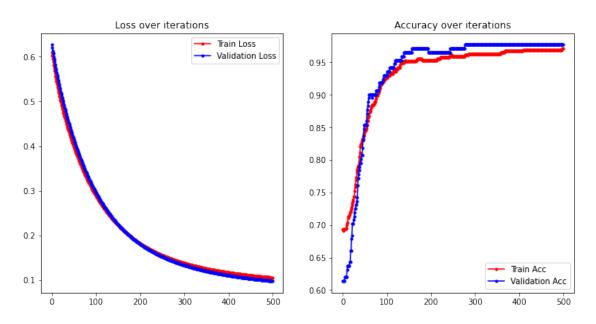
```
[27]: def plot_roc(y_test, y_pred, model_name):
    fpr, tpr, thr = roc_curve(y_test, y_pred)
    fig, ax = plt.subplots(figsize=(8, 8))
    ax.plot(fpr, tpr, 'k-')
    ax.plot([0, 1], [0, 1], 'k--', linewidth=.5) # roc curve for random model
    ax.grid(True)
```

accuracy is 0.977 roc-auc is 0.996

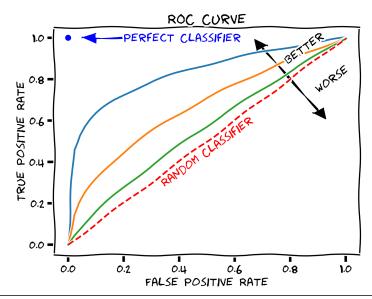


```
[28]: n = len(run_hist_1.history["loss"])
      fig = plt.figure(figsize=(12, 6))
      ax = fig.add_subplot(1, 2, 1)
      ax.plot(range(n), (run_hist_1.history["loss"]), 'r', marker='.', label="Train_"
       →Loss")
      ax.plot(range(n), (run_hist_1.history["val_loss"]), 'b', marker='.', __
       →label="Validation Loss")
      ax.legend()
      ax.set_title('Loss over iterations')
      ax = fig.add_subplot(1, 2, 2)
      ax.plot(range(n), (run_hist_1.history["accuracy"]), 'r', marker='.', label="Train_"
       →Acc")
      ax.plot(range(n), (run_hist_1.history["val_accuracy"]), 'b', marker='.', u
       ⇔label="Validation Acc")
      ax.legend(loc='lower right')
      ax.set_title('Accuracy over iterations')
```

#### [28]: Text(0.5, 1.0, 'Accuracy over iterations')



Above, the ROC curve and graphs showing the loss and accuracy over iterations were plotted. These last two allow us to observe the evolution of model training over iterations. The Receiver Operating Characteristic curve is created by plotting the true positive rate (TPR) against the false positive rate (FPR) at various threshold settings. In the next Figure you can see an illustration of how to analyze this curve.



The ROC space for a 'better' and 'worse' classifier. From: https://en.wikipedia.org/wiki/Receiver\_operating\_characteristic

As we can see, the result achieved by the generated ROC curve is very close to the point defined as "perfect classifier".

The final results obtained by this model were:

- accuracy is 0.977
- roc-auc is 0.996

And the Confusion Matrix of the classification can be seen below:

```
[88]: print('Confusion Matrix')
    print(confusion_matrix(y_test, y_pred_class_nn_1))
    print('Classification Report')
```

Confusion Matrix [[ 65 2] [ 2 102]]

Classification Report

```
[87]: target_names = ['Malignat', 'Benign']
print(classification_report(y_test, y_pred_class_nn_1,

→target_names=target_names))
```

	precision	recall	f1-score	support
Malignat Benign	0.97 0.98	0.97 0.98	0.97 0.98	67 104
accuracy			0.98	171

macro avg	0.98	0.98	0.98	171
weighted avg	0.98	0.98	0.98	171

#### 3 Model 2

#### 3.1 Defining the Model

Again, I will use the Sequential model to quickly build a neural network. This network will be a two hidden layers network. We have 9 variables, so we set the input shape to 9. The model defined below has 2 hidden layers, each with 7 nodes with ReLU activation. As the problem ia a binary classification, the final layer has just one node with a sigmoid activation.

```
[43]: model_2 = Sequential()
    model_2.add(Dense(7,input_shape = (9,),activation = 'relu'))
    model_2.add(Dense(7,activation='relu'))
    model_2.add(Dense(1,activation='sigmoid'))
    model_2.summary()
   Model: "sequential_9"
                                  Param #
   Layer (type) Output Shape
   ______
   dense_27 (Dense)
                       (None, 7)
                                         70
   dense_28 (Dense)
                      (None, 7)
                                         56
   dense_29 (Dense) (None, 1)
   _____
   Total params: 134
   Trainable params: 134
   Non-trainable params: 0
                   _____
```

### 3.2 Training and Testing the Model

This model will be trained with the Adam optimizer with learning rate equals to 0.003. Others training parameters are: - epochs = 50 - batch\_size = 32

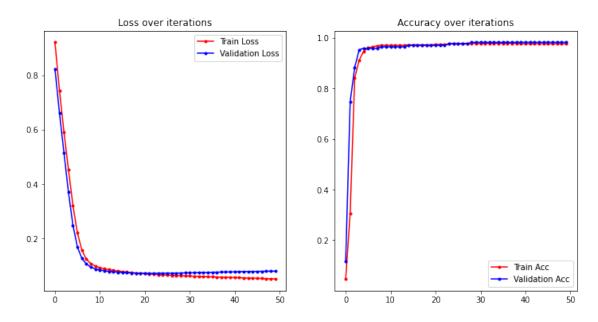
```
[102]: opt = Adam(learning_rate=0.003)
model_2.compile(opt, "binary_crossentropy", metrics=["accuracy"])
run_hist_2 = model_2.fit(X_train_norm, y_train, validation_data=(X_test_norm, y_test), epochs=50, verbose=0)

[46]: n = len(run_hist_2.history["loss"])
fig = plt.figure(figsize=(12, 6))
ax = fig.add_subplot(1, 2, 1)
```

```
ax.plot(range(n), (run_hist_2.history["loss"]),'r', marker='.', label="Train_\]
\[
\times_Loss"\)
ax.plot(range(n), (run_hist_2.history["val_loss"]),'b', marker='.',\]
\[
\times_label="Validation Loss"\)
ax.legend()
ax.set_title('Loss over iterations')

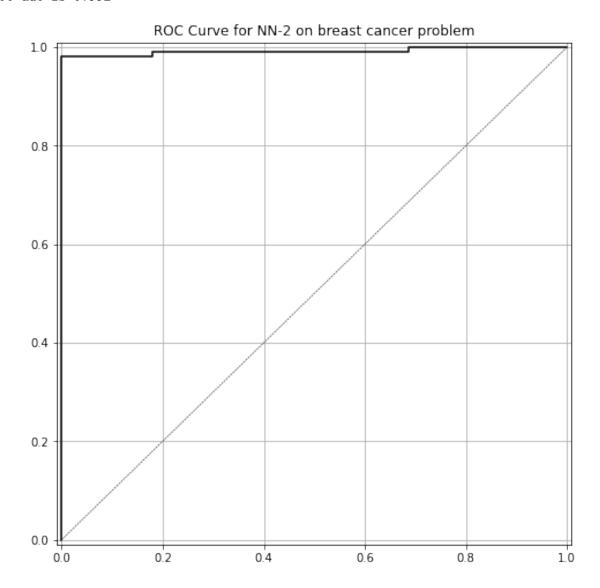
ax = fig.add_subplot(1, 2, 2)
ax.plot(range(n), (run_hist_2.history["accuracy"]),'r', marker='.', label="Train_\]
\[
\times_Acc"\)
ax.plot(range(n), (run_hist_2.history["val_accuracy"]),'b',marker='.',\]
\[
\times_label="Validation Acc"\)
ax.legend(loc='lower right')
ax.set_title('Accuracy over iterations')
```

#### [46]: Text(0.5, 1.0, 'Accuracy over iterations')



```
[47]: y_pred_class_nn_2 = model_2.predict_classes(X_test_norm)
y_pred_prob_nn_2 = model_2.predict(X_test_norm)
print('')
print('accuracy is {:.3f}'.format(accuracy_score(y_test,y_pred_class_nn_2)))
print('roc-auc is {:.3f}'.format(roc_auc_score(y_test,y_pred_prob_nn_2)))

plot_roc(y_test, y_pred_prob_nn_2, 'NN-2')
### END SOLUTION
```



As we can see, with this model we obtained even better results (accuracy equals to 0.982) than the last one.

```
[90]: print('Confusion Matrix')
  print(confusion_matrix(y_test, y_pred_class_nn_2))
  print('Classification Report')
```

```
Confusion Matrix
[[ 67 0]
 [ 3 101]]
Classification Report
```

```
[92]: target_names = ['Malignat', 'Benign']
print(classification_report(y_test, y_pred_class_nn_2,

→target_names=target_names))
```

	precision	recall	f1-score	support
Malignat	0.96	1.00	0.98	67
Benign	1.00	0.97	0.99	104
accuracy			0.98	171
macro avg	0.98	0.99	0.98	171
weighted avg	0.98	0.98	0.98	171

### 4 Model 3

## 4.1 Defining the model

In this last model, we will have a 3 hidden layers network. We have 9 variables, so we set the input shape to 9. The model defined below has 3 hidden layers: - Layer 1: 11 nodes with ReLU activation function. - Layers 2 and 3: 6 nodes with ReLU activation function.

As the problem ia a binary classification, the final layer has just one node with a sigmoid activation.

```
[53]: model_3 = Sequential()
model_3.add(Dense(11,input_shape = (9,),activation = 'relu'))
model_3.add(Dense(6,activation='relu'))
model_3.add(Dense(6,activation='relu'))
model_3.add(Dense(1,activation='sigmoid'))
model_3.summary()
```

Model: "sequential\_11"

Layer (type)	Output Shape	Param #
dense_34 (Dense)	(None, 11)	110
dense_35 (Dense)	(None, 6)	72
dense_36 (Dense)	(None, 6)	42
dense_37 (Dense)	(None, 1)	7
Total params: 231		

Trainable params: 231
Non-trainable params: 0

\_\_\_\_\_\_

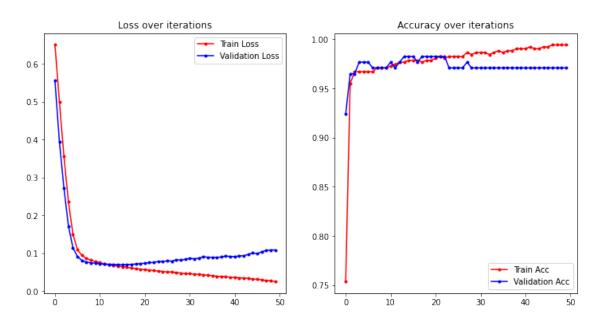
## 4.2 Training and Testing the Model

```
[103]: opt = Adam(learning_rate=0.003)
       model_3.compile(opt, "binary_crossentropy", metrics=["accuracy"])
       run_hist_3 = model_3.fit(X_train_norm, y_train, validation_data=(X_test_norm,_

y_test), epochs=50, verbose=0)
[57]: n = len(run_hist_3.history["loss"])
       fig = plt.figure(figsize=(12, 6))
       ax = fig.add_subplot(1, 2, 1)
       ax.plot(range(n), (run_hist_3.history["loss"]), 'r', marker='.', label="Train_"

Loss")
       ax.plot(range(n), (run_hist_3.history["val_loss"]), 'b', marker='.', __
        →label="Validation Loss")
       ax.legend()
       ax.set_title('Loss over iterations')
       ax = fig.add_subplot(1, 2, 2)
       ax.plot(range(n), (run_hist_3.history["accuracy"]), 'r', marker='.', label="Train_"
        →Acc")
       ax.plot(range(n), (run_hist_3.history["val_accuracy"]), 'b', marker='.', u
        →label="Validation Acc")
       ax.legend(loc='lower right')
       ax.set_title('Accuracy over iterations')
```

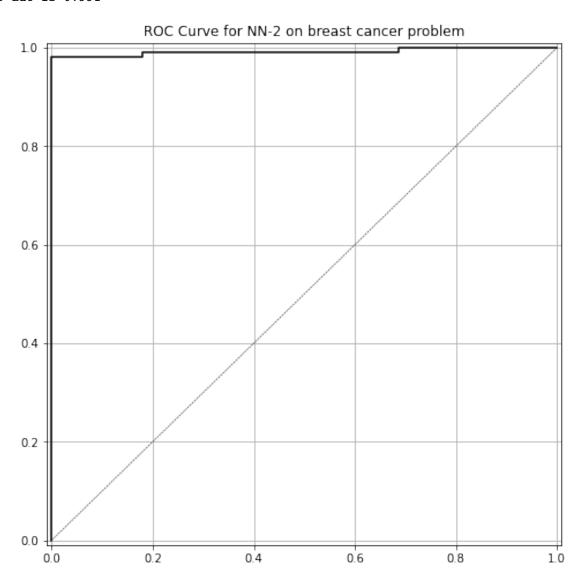
#### [57]: Text(0.5, 1.0, 'Accuracy over iterations')



While the training loss is still going down, it looks like the validation loss has gotten worse. This suggests that our network will not benefit from further training. Also was possible to see that this new network with more layers suffers more of overfitting.

```
[60]: y_pred_class_nn_3 = model_3.predict_classes(X_test_norm)
y_pred_prob_nn_3 = model_3.predict(X_test_norm)
print('')
print('accuracy is {:.3f}'.format(accuracy_score(y_test,y_pred_class_nn_3)))
print('roc-auc is {:.3f}'.format(roc_auc_score(y_test,y_pred_prob_nn_3)))
plot_roc(y_test, y_pred_prob_nn_2, 'NN-2')
```

accuracy is 0.971 roc-auc is 0.991



Like the other models, this one also achieved a satisfactory result, with an accuracy of approximately 0.97.

	precision	recall	f1-score	support
Malignat	0.96	0.97	0.96	67
Benign	0.98	0.97	0.98	104
accuracy			0.97	171
macro avg	0.97	0.97	0.97	171
weighted avg	0.97	0.97	0.97	171

# 5 Get a baseline performance using Random Forest

Just to get a baseline for the performance of our last classifiers we will train a Random Forest model with 200 trees on the training data and calculate the accuracy and roc\_auc\_score of the predictions..

```
[77]: ### BEGIN SOLUTION
## Train the RF Model
rf_model = RandomForestClassifier(n_estimators=200)
rf_model.fit(X_train, y_train)
```

[77]: RandomForestClassifier(n\_estimators=200)

```
[78]: # Make predictions on the test set - both "hard" predictions, and the scores

→ (percent of trees voting yes)

y_pred_class_rf = rf_model.predict(X_test)

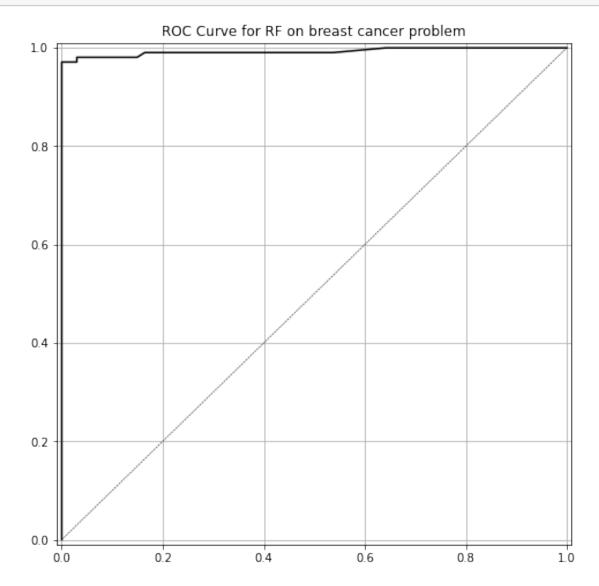
y_pred_prob_rf = rf_model.predict_proba(X_test)

print('accuracy is {:.3f}'.format(accuracy_score(y_test,y_pred_class_rf)))
```

```
print('roc-auc is {:.3f}'.format(roc_auc_score(y_test,y_pred_prob_rf[:,1])))
```

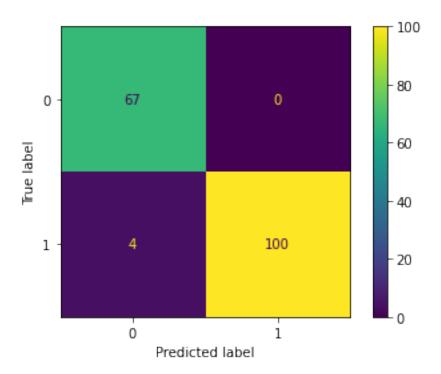
accuracy is 0.977 roc-auc is 0.990

[76]: plot\_roc(y\_test, y\_pred\_prob\_rf[:, 1], 'RF')



We obtained a result very similar to those achieved using the models based on Neural Networks.

```
[96]: plot_confusion_matrix(rf_model, X_test, y_test)
```



## 6 Conclusion

With this work, it was possible to practice the generation, training and testing of models based on Neural Networks. Possible next steps for this work could be:

- Perform a selection of attributes before starting model development.
- Test new classifier models using different machine learning techniques and match them with the models generated so far.
- Search for larger datasets on the topic.

## 7 References

 William H. Wolberg and O.L. Mangasarian: "Multisurface method of pattern separation for medical diagnosis applied to breast cytology", Proceedings of the National Academy of Sciences, U.S.A., Volume 87, December 1990, pp 9193-9196.