Watson Studio: Heart Disease Modeling with Jupyter Notebooks

Introduction

In this lab, you use a Jupyter Notebook to train a model using the XGBoost library to classify whether a person has heart disease or not. In addition to training a model, the notebook also explains how to persist a trained model to the IBM Watson Machine Learning repository and deploy the model as a REST service.

To train and test the heart disease prediction model, you are using an open source data set published in the University of California, Irvine (UCI) Machine Learning Repository.

The notebook environment includes Python 3.6 runtime, XGBoost 0.82 and Scikit-Learn 0.20.

Objectives

Upon completing the lab, you will know how to:

- 1. Create a Jupyter notebook from a url.
- 2. Load a CSV file into Pandas DataFrame
- 3. Explore data using Pixiedust
- 4. Prepare data for training and evaluation.
- 5. Use Scikit Learn to create our ML pipeline. Use XGBoost to create, train, and evaluate our model.
- 6. Visualize the importance of features that were used to train the model.
- 7. Use cross validation to select optimal model hyperparameters based on a parameter grid
- 8. Persist the best model in the Watson Machine Learning model repository using Python client library.
- 9. Deploy the model for online scoring using the Python client library.

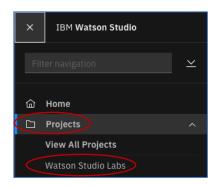
Lab Steps

Step 1 - Create a Jupyter Notebook

1. Click on the hamburger icon , then click on **Projects**, and then **Watson Studio Labs** (or whatever you named the project)



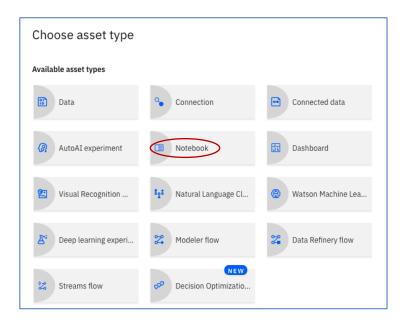
IBM Watson Studio



2. We are now going to create a notebook in our project. This notebook will be created from a url that points to the HeartDisease notebook in the github repository. Click the **Add to project** link.



3. Click on **Notebook**

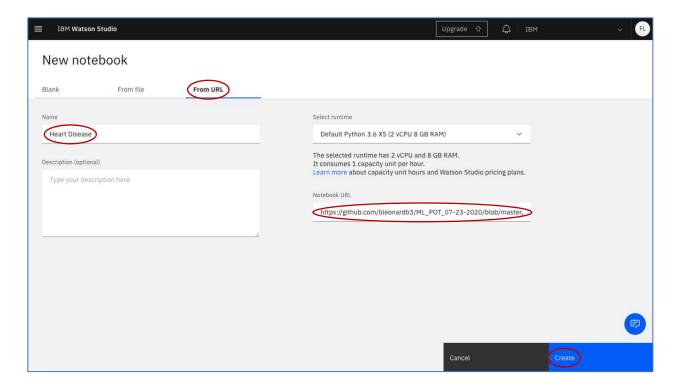


4. Click on **From URL** under **New Notebook**, enter **Heart Disease** for the **Name**, and optionally enter a **Description**. Leave the default for the **Runtime**.

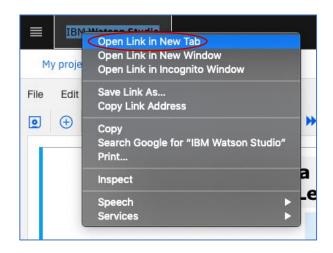
Cut and paste the following url into the Notebook URL field.

https://github.com/bleonardb3/ML_POT_07-23-2020/blob/master/Lab-5/Heart%20Disease.ipynb

Click Create Notebook.



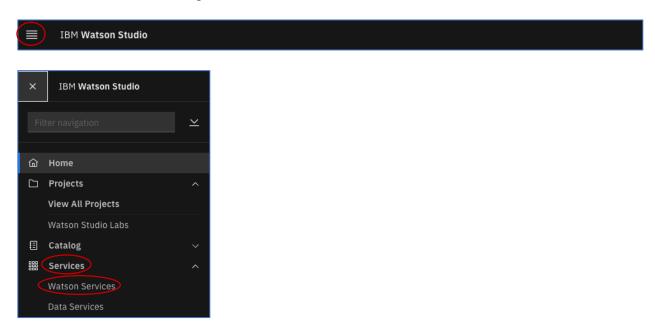
- 5. Before executing the code in the notebook, we need to do the following:
 - a. Obtain the credentials of the Watson Machine Learning service and copy those credentials into a designated notebook cell. We will need these credentials to work with the Watson Machine Learning API. The procedure to obtain the credentials will be described below.
- 6. Right-click on **IBM Watson Studio**, and the click on **Open Link in New Tab**.



7. Click on the new **Watson Studio** browser tab.



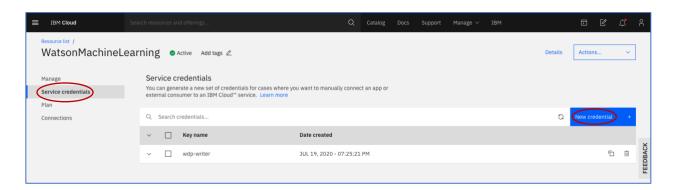
8. Click on the hamburger icon , and then **Services**, and **Watson Services**.



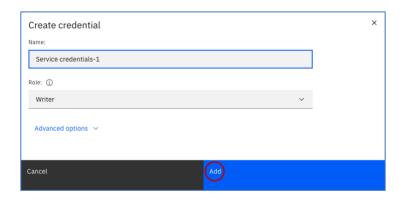
9. Hover over WatsonMachineLearning, click on the vertical ellipse on the right. ; and click on **Manage in IBM Cloud**.



10. A new browser tab will be created titled **Service Details – IBM Cloud.** This browser tab will be interfacing with the IBM Cloud user interface. Click on **Service credentials** and **New credential**.



11. Click on Add.



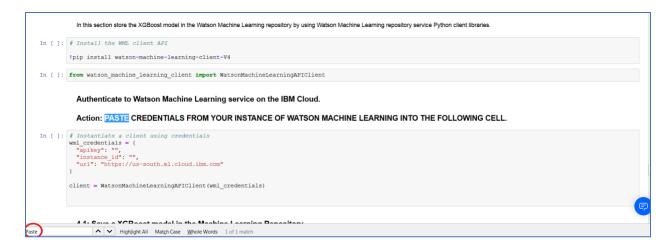
12. Click on ▼ next to View Credentials in the Service Credentials-1 row and click on the □ icon.



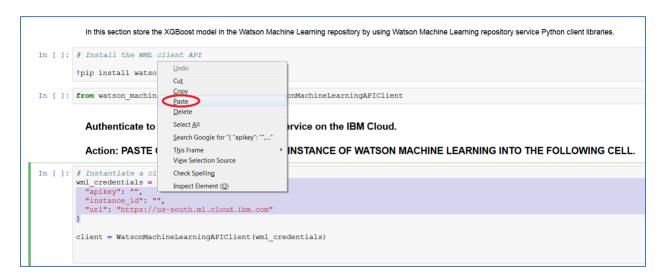
13. Click on the Heart Disease browser tab to go back to the notebook. Should be two browser tabs to the left of the **Service Details – IBM Cloud**.



14. Type Ctrl-F and type in Paste to find the notebook cell to paste in the credentials.



15. Highlight the text from the starting curly brace { to the ending curly brace }. Right-click on the highlighted text and click **Paste**.



16. The credentials should appear similar to below with different values.

17. Return to the top of the notebook, read through the documentation in the beginning and then select the first code cell.

	1. Setup
	Before you execute the sample code in this notebook, you must download the Heart Disease Data Set data in the Notebook's local filesystem
	Download Heart Disease Data Set to Notebook's local filesystem
	The Heart Disease Data Set is a freely available data set on the UCI Machine Learning Repository portal. The Heart Disease Data Set is hosted here.
	In order to download the data from LICI Machine Learning Repository, use the lager library. Use the following command to install the lager library. I pap install lager
In []:	pip install wget
	Now, the code in the cell below downloads the data set and saves it in the local fliesystem. The name of downloaded flie containing the data will be displayed in the output of this cell.
In []:	Laport wget
	link_to_data = 'http://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/processed.eleveland.data'
	# make sure no duplicates rm processed.cleveland*.data

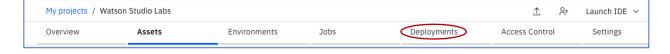
For those not familiar with Jupyter notebooks, read below.

A Jupyter notebook consists of a series of cells. These cells are of 2 types (1) documentation cells containing markdown, and (2) code cells (denoted by a bracket on the left of the cell) where you write Python code, R, or Scala code depending on the type of notebook. Code cells can be run by putting the cursor in the code cell and pressing **Shift>Enter>** on the keyboard. Alternatively, you can execute the cells by clicking on **Run icon** on the menu bar that will run the current cell (where the cursor is located) and then select the cell below. In this way, repeatedly clicking on **Run** executes all the cells in the notebook. When a code cell is executed the brackets on the left change to an asterisk '*' to indicate the code cell is executing. When completed, a sequence number appears. The output, if any, is displayed below the code cell.

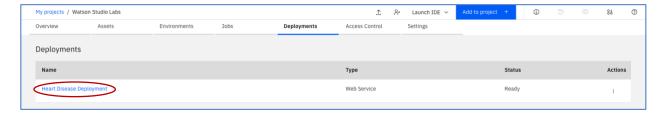
- 18. Execute each of the notebook cells in order (either by typing in **Shift>Enter>** or using the **Run** menu option). Read the notebook documentation to gain an understanding of the code that is executing. When all the cells in the notebook have been successfully executed, please return to this document, and continue with Step 21.
- 19. The notebook built, trained, saved, and deployed a machine learning model. Click Watson Studio Labs to exit out of the notebook.



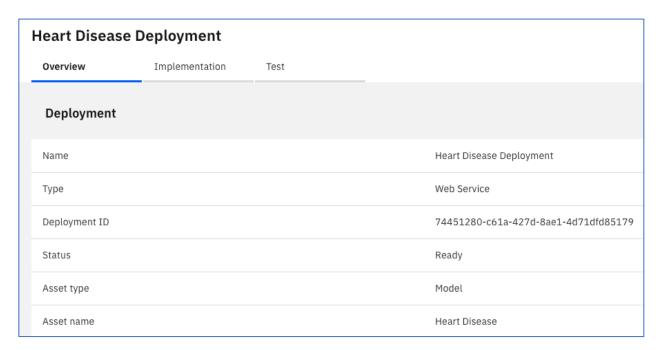
20. Click the **Deployments** tab.



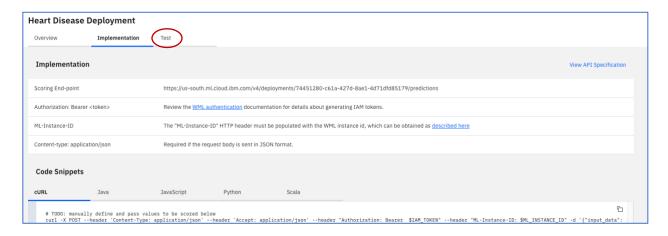
21. The deployment listed was generated programmatically from the notebook using the Watson Machine Learning APIs. It is a Web service deployment. Click on **Heart Disease Deployment.**



22. Click on **Implementation**.



23. The **Implementation** panel provides sample code in various programming languages and the scoring endpoint to be used when invoking the deployed model via a RESTful interface. Click on **Test**.

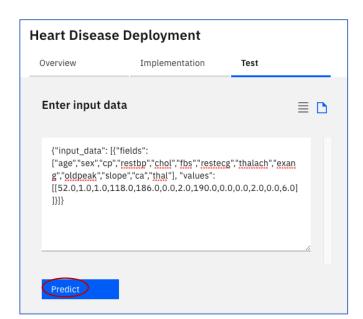


24. The **Test** panel enables testing the deployed model. Copy and then paste the following json where it says **Paste the request payload here.**

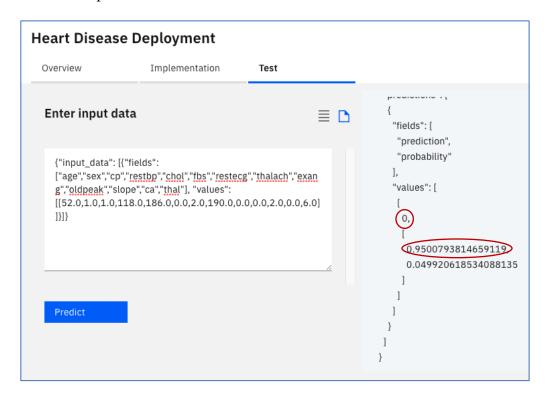
```
{"input_data": [{"fields":
    ["age", "sex", "cp", "restbp", "chol", "fbs", "restecg", "thalach", "exa
ng", "oldpeak", "slope", "ca", "thal"], "values":
    [[52.0,1.0,1.0,118.0,186.0,0.0,2.0,190.0,0.0,0.0,2.0,0.0,6.0]]}]
}
```



25. Click on **Predict**.



26. The prediction is no heart disease with a 95% confidence.



You have completed the Lab!

- ✓ Loaded a CSV file into Pandas DataFrame.
- ✓ Explored data using Pixiedust
- ✓ Prepared data for training and evaluation.
- ✓ Created, trained, and evaluated a XGBoost model.
- ✓ Visualized the importance of features that were used to train the model.
- ✓ Used cross validation to select optimal model hyperparameters based on a parameter grid
- ✓ Persisted the best model in Watson Machine Learning repository using the Python client library.
- ✓ Deployed the model for online scoring using the Python client library
- ✓ Visualized Deployment in the Watson Studio UI.
- ✓ Tested the deployment