

# Configuration Manual

MSc Research Project  
Data Analytics

Deepika Kancharla  
Student ID: 23406739

School of Computing  
National College of Ireland

Supervisor: Hamilton Niculescu

**National College of Ireland**  
**MSc Project Submission Sheet**  
**School of Computing**



**Student Name:** Deepika Kancharla  
**Student ID:** 23406739  
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**Lecturer:** Hamilton Niculescu  
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# 1 Configuration Manual

## 1. System Requirements & Setup

All experiments in this research were executed using **Google Colab**, which provides a cloud-based environment suitable for large-scale data analysis and machine-learning experiments. The following hardware and software configurations were used to ensure full reproducibility of the results.

### 1.1 Hardware Configuration (Google Colab Runtime)

Google Colab provides virtualised hardware. During all modelling and analysis tasks, the following configuration was used:

- CPU:  $2 \times$  Intel(R) Xeon® Virtual CPU @ 2.20 GHz
- RAM: 12.7 GB
- Disk Storage: ~68 GB temporary runtime storage
- Runtime Type: Standard CPU Runtime

This configuration supports fast processing for large tabular datasets, scaling of feature-engineering pipelines, and efficient execution of machine-learning models such as Linear Regression and Random Forest.

### 1.2 Software Configuration

- Platform: Google Colaboratory (browser-based Jupyter environment)
- Operating System: Linux (Ubuntu 22.04 LTS backend)
- Programming Language: Python 3.10 (default Colab Python version)
- Development Environment: Google Colab Notebook

## 2. Core Libraries Used

### Data Handling & Processing

- pandas
- numpy

### Visualisation

- matplotlib
- seaborn

### Machine Learning Models

- scikit-learn
  - LabelEncoder
  - StandardScaler

- train\_test\_split
- LinearRegression
- RandomForestRegressor

#### Model Evaluation

- r2\_score
- mean\_absolute\_error
- mean\_squared\_error

These libraries support data collection through APIs, cleaning, preprocessing, modelling, prediction, and evaluation of booster uptake across countries.

### 3. Dataset Description

This study uses publicly available global COVID-19 datasets from multiple trusted sources, representing vaccination behaviour, booster uptake, hospitalisation indicators, and daily epidemiological updates.

#### 3.1 Dataset Sources

##### 3.1.1 Our World in Data (OWID)

Booster vaccination data & COVID-19 hospitalisation indicators

- COVID-19 hospitalisation data:  
<https://github.com/owid/covid-19-data/blob/master/public/data/hospitalizations/covid-hospitalizations.csv>
- Booster vaccination data:  
<https://ourworldindata.org/grapher/cumulative-covid-vaccine-booster-doses>

##### 3.1.2 World Health Organization (WHO)

Global daily epidemiological data

- <https://data.who.int/dashboards/covid19/data>

##### 3.1.3 Kaggle Dataset

COVID-19 global vaccination progress

- <https://www.kaggle.com/datasets/gpreda/covid-world-vaccination-progress>

#### 3.2 Dataset Usage in This Project

The following steps were applied to each dataset:

- Imported using pandas
- Merged on country and date
- Cleaned for missing values, duplicates, and inconsistent date formats
- Feature transformations applied:
  - Label encoding for categorical variables

- Scaling for numeric variables
- Target variable: daily booster uptake
- Predictor variables include:
  - Historical vaccination metrics
  - Epidemiological indicators
  - Hospitalisation & ICU occupancy rates
  - WHO daily case/death counts

The final merged dataset contained 4,991 country-date observations used for modelling.

## 4. How to Run the Project

This section explains how to reproduce the entire analysis pipeline on Google Colab.

### 4.1 Uploading the Notebook and Loading the Dataset

Step 1: Visit

<https://colab.research.google.com>

Step 2: Upload the provided notebook file – x23406739.ipynb

Step 3: Upload downloaded datasets (OWID, WHO, Kaggle CSV files)

Step 4: Load the datasets in the notebook using Pandas library.

### 4.2 Setting Up the Environment in Colab

All dependencies used in this project are available in Colab by default.

Import all required libraries:

```
import pandas as pd
import requests
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LinearRegression, LogisticRegression
from sklearn.ensemble import RandomForestRegressor
from sklearn.metrics import r2_score, mean_absolute_error, mean_squared
```

No additional installations are required.

### 4.3 Running the Notebook

Execute cells in sequence:

1. Load OWID, WHO, and Kaggle datasets
2. Merge datasets on country and date

3. Clean and preprocess data
4. Encode categorical variables
5. Split into training/test sets
6. Train Linear Regression model
7. Train Random Forest model
8. Evaluate each model using:
  - $R^2$
  - RMSE
  - MAE
9. Generate plots:
  - Correlation heatmap
  - Feature importance
  - Booster uptake prediction plots
  - Hospital/ICU vs predicted uptake scatterplots

#### 4.4 Accessing Results

Each execution cell outputs visual and numerical results including:

- Model performance metrics
- Predicted vs actual booster uptake graphs
- Feature importance ranking
- Scatterplots showing hospital/ICU occupancy trends

All outputs can be downloaded from Colab for reporting.

## 5. References

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