

Configuration Manual

MSc Research Project
Data Analytics

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MSc Project Submission Sheet



School of Computing

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Lecturer: Dr. Catherine Mulwa

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Configuration Manual

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1 Introduction

This document provides a concise explanation of the manner in which the project to identify and detect brain tumours was implemented. This document contains every technology and technique required for implementation. We learn how to set up an environment for programming in part 2. Section 3 provides illustrations of various tools and software. Section 4 details how the project was executed out.

2 Environment set up

The configuration that was set up to implement the project are stated below:

1. Processor: Intel i7
2. Memory: 16GB RAM
3. Programming language: Python3
4. Python Environment: Google Colab, Jupyter Notebook

3 Softwares utilised

We have used Google Colab for training model and obtained accuracies for the models since there was limited availability of computer resources. Google Colab supports many libraries like PyTorch, TensorFlow, Keras, OpenCV which are necessary for the execution.



4 Implementation

4.1 Step 1: We have taken google colab into consideration for python code. Go to <https://colab.research.google.com/> url and sign in with your account.

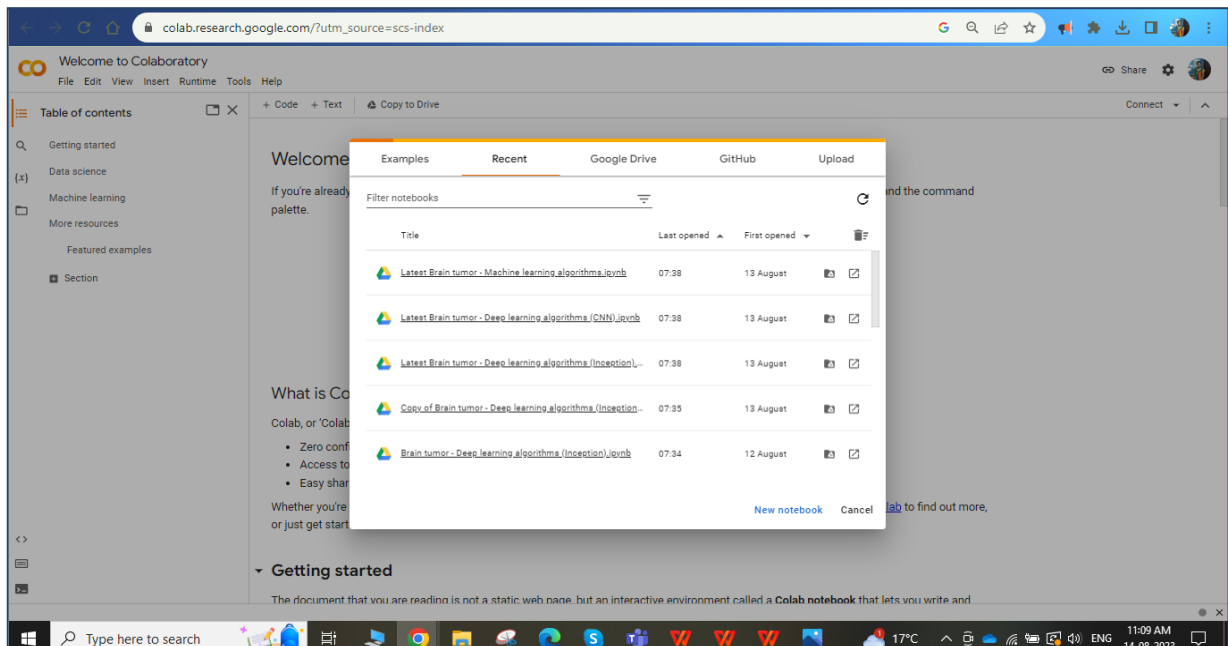


Fig 1 States the opening of Google Colab

4.2 step 2: Open the required programme for implementation - Machine learning - 'Latest Brain tumor - Machine learning algorithms.ipynb'

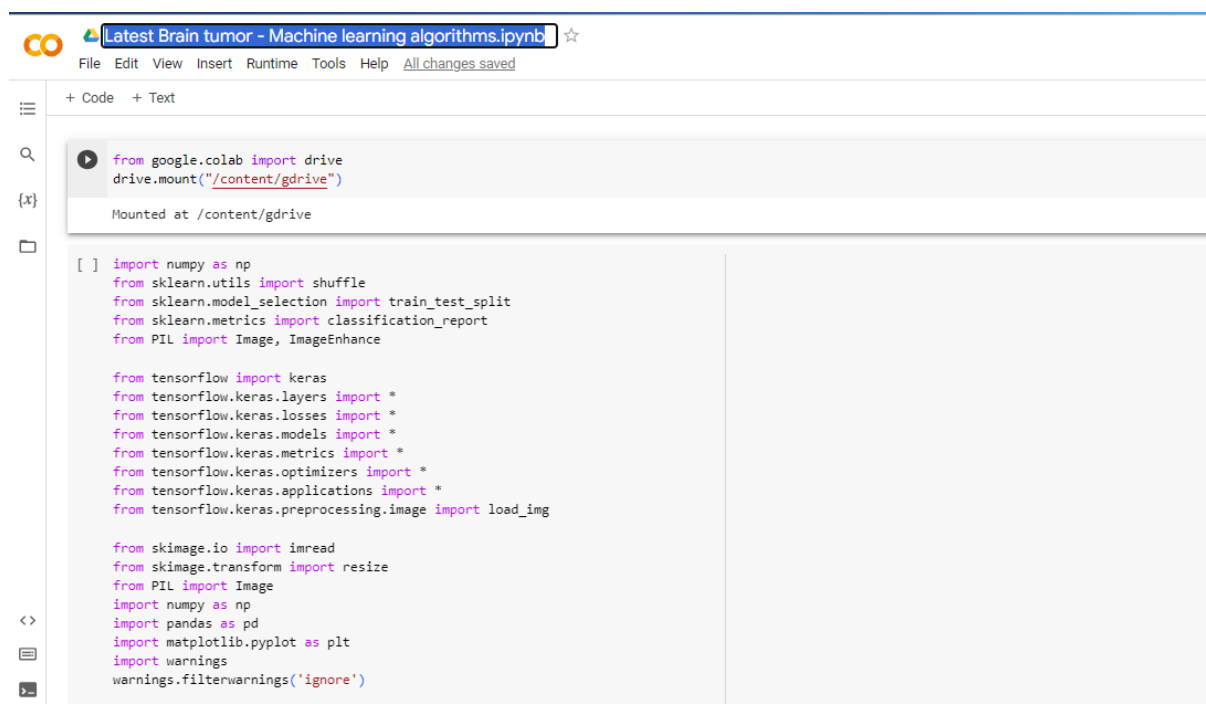


Fig 2 Shows the dataset been loaded from google drive and libraries are being imported

Parallely, open the program for CNN implementation by opening 'Latest Brain tumor - Deep learning algorithms (CNN).ipynb'

```

from google.colab import drive
drive.mount('/content/gdrive')

Mounted at /content/gdrive

[ ] import numpy as np
from sklearn.utils import shuffle
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report
from PIL import Image, ImageEnhance

from tensorflow import keras
from tensorflow.keras.layers import *
from tensorflow.keras.losses import *
from tensorflow.keras.models import *
from tensorflow.keras.metrics import *
from tensorflow.keras.optimizers import *
from tensorflow.keras.applications import *
from tensorflow.keras.preprocessing.image import load_img

from skimage.io import imread
from skimage.transform import resize
from PIL import Image
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')

import matplotlib.pyplot as plt
import seaborn as sns

from tqdm import tqdm
import os
import random

import os

```

Fig 3 Shows the dataset been loaded from drive and libraries are being imported

On the other side open the programme for Inception method with 'Latest Brain tumor - Deep learning algorithms (Inception).ipynb'

```

from google.colab import drive
drive.mount("/content/gdrive")

Mounted at /content/gdrive

[ ] import numpy as np
from sklearn.utils import shuffle
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report
from PIL import Image, ImageEnhance

from tensorflow import keras
from tensorflow.keras.layers import *
from tensorflow.keras.losses import *
from tensorflow.keras.models import *
from tensorflow.keras.metrics import *
from tensorflow.keras.optimizers import *
from tensorflow.keras.applications import *
from tensorflow.keras.preprocessing.image import load_img

from skimage.io import imread
from skimage.transform import resize
from PIL import Image
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')

```

Fig 4 Shows the dataset been loaded from drive and libraries are being imported

Similarly open the programme for implementation 'Latest Brain tumor - Deep learning algorithms (VGG).ipynb' and loading of the dataset using pandas libraries which is stored in google drive to access in google collab has been done for all the models.

```

from google.colab import drive
drive.mount("/content/gdrive")

Drive already mounted at /content/gdrive; to attempt to forcibly remount, call drive.mount("/content/gdrive", force_remount=True).

[ ] import numpy as np
    from sklearn.utils import shuffle
    from sklearn.model_selection import train_test_split
    from sklearn.metrics import classification_report
    from PIL import Image, ImageEnhance

    from tensorflow import keras
    from tensorflow.keras.layers import *
    from tensorflow.keras.losses import *
    from tensorflow.keras.models import *
    from tensorflow.keras.metrics import *
    from tensorflow.keras.optimizers import *
    from tensorflow.keras.applications import *
    from tensorflow.keras.preprocessing.image import load_img

    from skimage.io import imread
    from skimage.transform import resize
    from PIL import Image
    import numpy as np
    import pandas as pd
    import matplotlib.pyplot as plt
    import warnings
    warnings.filterwarnings('ignore')

```

Fig 5: Shows the dataset been loaded from drive and libraries are being imported

4.3 Step 4 Code in Google collab can be executed by using Run button



Fig 5: Shows to run the code

4.4 Step 4: Training the pretrained model with the test data and getting accuracies for CNN Method

```
[ ] print(classification_report(y_true, y_pred))
```

	precision	recall	f1-score	support
glioma	0.84	0.83	0.84	300
meningioma	0.75	0.74	0.75	306
notumor	0.94	0.92	0.93	405
pituitary	0.90	0.95	0.93	300
accuracy			0.87	1311
macro avg	0.86	0.86	0.86	1311
weighted avg	0.87	0.87	0.87	1311

```
[ ] accuracy = accuracy_score(y_true, y_pred)
```

```
[ ] accuracy
```

```
0.8657513348588863
```

Fig 6: Accuracy of the CNN models

```
] from sklearn.metrics import confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np

cm = confusion_matrix(y_true, y_pred)

# Define the font size
font_size = 20

# Plot the confusion matrix
plt.figure(figsize=(8,8))
sns.heatmap(cm, annot=True, cmap="Blues", fmt="d", xticklabels=unique_labels, yticklabels=unique_labels, annot_kws={"fontsize": font_size}, cbar=False)
plt.xlabel("Predicted Label", fontsize=font_size)
plt.ylabel("True Label", fontsize=font_size)
plt.xticks(fontsize=font_size)
plt.yticks(fontsize=font_size, rotation=0)
plt.show()
```

pituitary	250	47	0	3
meningioma	32	227	22	25

Fig 7: Confusion matrix for CNN

Training the pretrained model with the test data and getting accuracies for Machine learning Methods

```

Training NaiveBayes...
NaiveBayes trained in 6.90 seconds
Accuracy for NaiveBayes: 0.60
Classification Report for NaiveBayes:
      precision    recall  f1-score   support

 glioma           0.53     0.84     0.65     300
meningioma       0.34     0.23     0.28     306
 notumor         0.73     0.58     0.64     405
 pituitary       0.76     0.77     0.77     300

 accuracy              0.60     1311
 macro avg           0.59     0.61     0.58     1311
 weighted avg       0.60     0.60     0.59     1311

Confusion Matrix for NaiveBayes:
[[252  22   1  25]
 [127  71  87  21]
 [ 45 100 235  25]
 [ 55  13   1 231]]

```

Fig 8: Results for NaiveBayes

```

Training SVC...
SVC trained in 711.72 seconds
Accuracy for SVC: 0.82
Classification Report for SVC:
      precision    recall  f1-score   support

 glioma           0.76     0.79     0.77     300
meningioma       0.73     0.60     0.66     306
 notumor         0.88     0.91     0.90     405
 pituitary       0.87     0.95     0.91     300

 accuracy              0.82     1311
 macro avg           0.81     0.81     0.81     1311
 weighted avg       0.82     0.82     0.82     1311

Confusion Matrix for SVC:
[[236  50   0  14]
 [ 49 185  50  22]
 [ 20  10 370   5]
 [  5   9   0 286]]

```

Fig 9: Results for SVC

Training the pretrained model with the test data and getting accuracies for Inception Method

	precision	recall	f1-score	support
glioma	0.85	0.79	0.82	300
meningioma	0.76	0.74	0.75	306
notumor	0.95	0.94	0.94	405
pituitary	0.85	0.95	0.90	300
accuracy			0.86	1311
macro avg	0.85	0.86	0.85	1311
weighted avg	0.86	0.86	0.86	1311

Fig 10: Results for Inception

Training the pretrained model with the test data and getting accuracies for VGG Method

	precision	recall	f1-score	support
glioma	0.91	0.89	0.90	293
meningioma	0.86	0.85	0.86	297
notumor	0.97	0.97	0.97	396
pituitary	0.94	0.98	0.96	294
accuracy			0.93	1280
macro avg	0.92	0.92	0.92	1280
weighted avg	0.93	0.93	0.93	1280

Fig 11: VGG results

As seen by execution we have concluded that VGG has higher results with accuracy of 0.93.

References

www.tutorialspoint.com. (n.d.). Google Colab - What is Google Colab? - Tutorialspoint. [online] Available at: https://www.tutorialspoint.com/google_colab/what_is_google_colab.htm.