

# Configuration Manual

MSc Research Project MSCDAD SEP 23 B

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## **MSc Project Submission Sheet**

## **School of Computing**

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## Configuration Manual

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## 1 Introduction

The study conducted on liver segmentation tumor detection using Hybrid modelling, configuration steps are discussed below in detail. Each section covers the details like software used and hardware details and the data collection details. This also describes the execution details of the code in detail. By following the below steps the code can executed in a right way.

## 2 System hardware and software details

The study has used some specific requirements in terms of software and hardware which has clearly explained below:

#### The Hardware details:

RAM space: 32GB Hard Disk space: 1TB

Operating system: Windows 10 Processor: Intel i7, 12<sup>th</sup> Gen

#### The Software details:

Platform used (IDE): Kaggle Notebook

Language: Python 3.8 Database: Kaggle DB Browser: Google Chrome

I have used Jupyter Notebook to save the code from Kaggle to an executable format.

## 3 Steps to Run Project

The first step of running project is to import the dataset to the Kaggle environment and the dataset has been taken from the IRCAD website. The Kaggle account was created and the Kaggle GPO was used to run the project as the dataset was pretty heavy to run this in local machine or google colab.

#### a) Data Collection and loading

The was taken from the IRCAD website and was loaded to the Kaggle environment and shows like below:

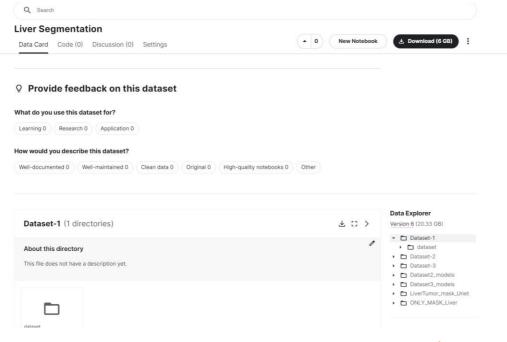


Fig 1: Data setting up in environment

#### b) Importing required libraries

The important libraries like NumPy, pandas, matplotlib etc are imported to the code for the later usage.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import os
import cv2
from plotly.subplots import make_subplots
import plotly.graph_objects as go
from sklearn import preprocessing
import random
import tensorflow as tf
import warnings
warnings.filterwarnings("ignore")
#!pip install visualkeras
import PIL
from PIL import Image
import numpy as np
import pandas as pd
import imageio
import imgaug as ia
import imgaug.augmenters as iaa
import numpy as np
import pandas as pd
```

Fig 2: Librairies importing

#### c) Loading the image and data into code

The image and the whole data were loaded in to the code and passed in to an array

```
Notebook Input Output Logs Comments (0) Settings
      def hasmask(y):
        return not np.any(y)
                                                                                                        N
      def classify_data(x,y):
         Y = []
         X=[]
         for i in tqdm(range(y.shape[0])):
             if hasmask(y[i,:,:]) == False:
                X.append(x[i,:,:])
                 Y.append(y[i,:,:])
         Y = np.array(Y)
         X = np.array(X)
         Y = Y.astype('float32')
         X = X.astype('float32')
         return X. Y
      def load_df(org):
         DIR = '../input/liver-segmentation/Dataset-1/dataset/3Dircadb1/3Dircadb1.1/'
         df = pd.DataFrame()
          for i in os.listdir(DIR+'PATIENT_DICOM/PATIENT_DICOM/'):
             df= df.append({
                 'Image':DIR+'PATIENT DICOM/PATIENT DICOM/'+i.
                  'Mask':DIR+'MASKS_DICOM/MASKS_DICOM/'+org+'/'+i,
                  'Mask_of_liver':DIR+'MASKS_DICOM/MASKS_DICOM/liver/'+i
             },ignore_index=True)
          return df
      df = load_df(organ)
      livertumor01
```

Fig 3: data loading

#### d) Pre-processing steps

In this step the array was loaded and checked if it is correctly loaded

```
def ld_dimcon(path):
   dicom = pydicom.read_file(path)
    data = dicom.pixel_array
    return data
def load_dataset(df):
   X = []
    Y = []
    for i in tqdm(df.index):
       X.append(ld_dimcon(df.iloc[i.0]))
       Y.append(ld_dimcon(df.iloc[i,1]))
       Y_liver.append(ld_dimcon(df.iloc[i,2]))
    X = np.array(X)
   Y_liver = np.array(Y_liver)
    {\tt print('With\ Empty\ masks', X.shape,\ Y.shape, Y\_liver.shape)}
    for i in range(5):
      ind = random.randint(0, X.shape[0] - 1)
       pltin(ind,X,Y,Y_liver)
    return \ X,Y,Y\_liver,df
{\tt X,Y,Y\_liver,df = load\_dataset(load\_df(organ))}
livertumor01
100%| 129/129 [00:04<00:00, 31.21it/s]
With Empty masks (129, 512, 512) (129, 512, 512) (129, 512, 512)
```

Fig 4: Array initlisation

```
In [8]:
    X.shape, Y.shape
Out[8]:
    ((129, 512, 512), (129, 512, 512))

In [9]:
    X = X.reshape(X.shape[0], X.shape[1], X.shape[2], 1)
    Y = Y.reshape(Y.shape[0], Y.shape[1], Y.shape[2], 1)
    X = np.float32(X)
    Y = np.float32(Y)

In [10]:
    X.shape, Y.shape
Out[10]:
    ((129, 512, 512, 1), (129, 512, 512, 1))
```

Fig 5: Vectorisation

#### e) Modelling steps

The Hybrid model is being developed here, as the below screenshot showing the application of InceptionV3 and U-Net with the application of the optimiser as well. The models also applied in the same way with U-Net and later GWO and PSO applied for the selected model.

```
Notebook Input Output Logs Comments (0) Settings
                           r with the system package manager. It is recommended to use a virtual environment instead: http
                         s://pip.pypa.io/warnings/venv
                                                                                                                                                                                                                                                                                                                               T
                                                                                                                                                                                                                                                                                                                         М
                         import segmentation_models as sm
                        BACKBONE = 'inceptionv3'
                        preprocess_input = sm.get_preprocessing(BACKBONE)
                        dim = 512
                         w,h =dim ,dim
                        BATCH SIZE = 8
                        CLASSES = ['Liver']
                        IR = 0.0001
                        EPOCHS = 40
                        preprocess_input = sm.get_preprocessing(BACKBONE)
                         # define network parameters
                        n_classes = 1 if len(CLASSES) == 1 else (len(CLASSES) + 1) # case for binary and multiclass segmenta
                         activation = 'sigmoid' if n_classes == 1 else 'softmax'
                         #create model
                         \verb|model = sm.Unet(BACKBONE,input\_shape=(w,h, 1),encoder\_weights=None, classes=n\_classes, activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activation=activati
                         tivation)
                         Segmentation Models: using `keras` framework.
In [13]: # define optomizer
                        optim = tf.keras.optimizers.Adam(LR)
                        # Segmentation models losses can be combined together by '+' and scaled by integer or float factor
                        dice_loss = sm.losses.DiceLoss()
                        focal_loss = sm.losses.BinaryFocalLoss() if n_classes == 1 else sm.losses.CategoricalFocalLoss()
```

Fig 6: Model appliaction of InceptionV3 in U-Net

#### f) Training of the model and graphs

```
# define optomizer
         optim = tf.keras.optimizers.Adam(LR)
          # Segmentation models losses can be combined together by '+' and scaled by integer or float factor
         dice_loss = sm.losses.DiceLoss()
         focal\_loss = sm.losses.BinaryFocalLoss() \ if \ n\_classes == 1 \ else \ sm.losses.CategoricalFocalLoss()
         total_loss = 0.9*dice_loss + (0.1 * focal_loss)
         # actulally total_loss can be imported directly from library, above example just show you how to manip
         ulate with losses
         # total_loss = sm.losses.binary_focal_dice_loss # or sm.losses.categorical_focal_dice_loss
         metrics = [sm.metrics.IOUScore(threshold=0.5), sm.metrics.FScore(threshold=0.5)]
         # compile keras model with defined optimozer, loss and metrics
         model.compile(optim, total_loss, metrics)
         from sklearn.model_selection import train_test_split
         X = np.float32(X)
         X = np.resize(X, (X.shape[0], dim, dim, 1))
         Y_dash = np.float32(Y)
         Y_dash = Y_dash/255
         Y_{dash} = np.resize(Y_{dash}, (Y_{dash.shape}[0], dim, dim, 1))
          X\_train, \ X\_test, \ y\_train, \ y\_test = train\_test\_split(X, \ Y\_dash, \ test\_size=0.20, \ random\_state=42) 
         X_{\text{train}}, X_{\text{valid}}, y_{\text{train}}, y_{\text{valid}} = train_test_split(X_{\text{train}}, y_{\text{train}}, test_size=0.15, random_state
         X_{\text{train.shape}}, X_{\text{valid.shape}}, X_{\text{test.shape}}, y_{\text{train.shape}}, y_{\text{valid.shape}}, y_{\text{test.shape}}
Out[13]:
                                                                                                                     N
                 from tensorflow.keras.models import model_from_json
                 model_json = model.to_json()
                 name = BACKBONE+'_D
                 with open(name+".json", "w") as json_file:
                     json_file.write(model_json)
                 model.save_weights(name+".h5")
                 import pandas as pd
                 hist_df = pd.DataFrame(history.history)
                 hist_df.to_csv(name+'.csv',index = False)
                 hist_df.tail()
```

Fig 7: Model training and graph

The model running is finished, and the later experiments are done based on the same manner to produce the outputs.