

Sleep Apnea detection using Deep Learning Methodologies - Configuration Manual

MSc Research Project Data Analytics

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Programme:	Data Analytics		
Year:	2022		
Module:	MSc Research Project		
Supervisor:	Mr. Vladimir Milosavljevic		
Submission Due Date:	19/09/2022		
Project Title:	Sleep Apnea detection using Deep Learning Methodologies -		
	Configuration Manual		
Word Count:	XXX		
Page Count:	11		

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Sleep Apnea detection using Deep Learning Methodologies - Configuration Manual

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1 Introduction

The environmental setup utilized during the course of this research project "Sleep Apnea detection using Deep Learning Methodologies" is fully described in this configuration manual. This is followed by the walk-through of the implementation and the results. Section 2 covers hardware and software configurations used for development, Section 3 covers the data sources in the description, and Section 4 covers the implementation of the models.

2 System Specifications

2.1 Hardware specifications

Table 1 shows the details of the hardware used for the development of the model.

Table 1: Details of Hardware used				
Features	Versions			
Operating System	Microsoft Windows 10 Home			
Processor	Intel(R) Core(TM) i5-7200U CPU @ 2.50GHz			
System Type	64- bit Operating System, x64-based PC			
RAM	16 GB			
Hard Disk	1 TB			

2.2 Software specifications

This research was done on the Google Colabarotory environment for the development and execution of the models. The programming was done in the Python programming language. The latest python version is used in the Google Colab platform. The important libraries used for this research project are mentioned below.

- Matplotlib
- Numpy
- Tensorflow

- $\bullet~{\rm Keras}$
- wfdb
- sklearn

3 Data Sources

The Apnea-ECG database used for this research is publically available on the PhysioNet website. This dataset contains overnight polysomnography (PSG) data for 70 people. This data contains readings for heart rate in the form of single-lead ECG and respiratory signals including SpO2 data. Each recording comes with a number of files. Digitized ECGs (100 samples per second, 16 bits per sample) are stored in files with names of the kind rnn, dat. The accompanying signal files' names and formats are specified in the .hea files, which are (text) header files. The .apn files are (binary) annotation files, and each minute of each recording has an annotation for each minute indicating whether or not there was an apnea at that moment.

4 Implementation

The ECG signals were divided into one-minute sections and associated with their relevant annotation. The data for all the 70 persons available in the dataset were used in this research. Figure 1 shows all the libraries used in this research.



Figure 1: Libraries used in this research

4.1 Data Preprocessing

The dataset was loaded into Google drive and the drive was mounted into Google Colab to use the dataset. The signals present in the dataset are seven to ten hours long. The first minute of each signal is annotated as Normal(N) so the first minute is not considered. The one-minute signal sample is shown in Figure 2 for both annotations.



Figure 2: Sample for a part of the ECG signal

4.2 Data Transformation

The one-minute signals have a sampling frequency of 100 Hz was converted into spectogram using Fast Fourier transfer. These spectograms were then used to feed the neural network. The code used to create the spectogram is shown in Figure 3 along with the sample spectogram shown in Figure 4.



Figure 3: Code for spectogram



Figure 4: Spectogram for a part of signal

5 Model Implementation

5.1 Model 1 Baseline Convolution Neural Network

These components are used to visualize the better representation of each class. For data visualization, different techniques are used like principle component analysis. The spectrograms are converted into the Eigenvalues shown in Figure 6 which are further reshaped into the matrix.

```
In [5]: from sklearn.decomposition import PCA
               from math import ceil
              def eigenimages(full_mat, title, n_comp = 0.7, size = (64, 64)):
                     # fit PCA to describe n_comp * variability in the class
pca = PCA(n_components = n_comp, whiten = True)
pca.fit(full_mat)
                      print('Number of PC: ', pca.n_components_)
                      return pca
              def plot_pca(pca, size = (64, 64)):
    # plot eigenimpges in a grid
    n = pca.n_components_
    fig = plt.figure(figsize=(8, 8))
    r = int(n**.5)
    c = ceil(n/ r)
    fig.patch.set_facecolor('white')
    for in canae(n):
                     plt.show()
                  making n X m matrix
              # making in A important
def to_numpy_image(path, list_of_filename, size = (64, 64)):
    # iterating through each file
    for fn in list_of_filename:
        fp = path + fn
                           fp = path + fn
current_image = kimage.load_img(fp, target_size = size,
                                                                                  color_mode =
                                                                                                         'grayscale')
                            # covert image to a matrix
img_ts = kimage.img_to_array(current_image)
# turn that into a vector / 1D array
                            img_ts = [img_ts.ravel()]
try:
                                      concatenate different image
                            # Conclusive uryperent images
full_mat = np.concatenate((full_mat, img_ts))
except UnboundLocalError:
    # if not assigned yet, assign one
    full_mat = img_ts
                     return full_mat
               # list of files
              nophar_images = os.listdir(base_dir + "train/" + classes[1])
phar_images = os.listdir(base_dir + "train/" + classes[0])
```

Figure 5: Code to form PCA using Eigen

```
Number of PC: 11
```

Figure 6: Eigen Images for principle component

These principle components formed using Eigenvalues are shown in Figure 8 shows the average Eigen images for both Apnea and non-apnea type along with the difference between normal and apnea patient's averages.

AVERAGE IMAGES

```
def find_mean_img(full_mat, title, size = (64, 64)):
    # calculate the average
    mean_img = np.mean(full_mat, axis = 0)
    # reshape it back to a matrix
    mean_img = mean_img.reshape(size)
    plt.imshow(mean_img, vmin=0, vmax=255, cmap='Greys_r')
    plt.title(f'Average {title}')
    plt.axis('off')
    plt.show()
    return mean_img
# find the mean image of the pharyn images
phar_mean_img = find_mean_img(phar_images, classes[0])
# find the mean image of the no-pharyn images
nophar_mean_img = find_mean_img(nophar_images, classes[1])
```

Figure 7: Code to generate the average of Eigen images



Figure 8: Average of Eigen images and their differences

In the base convolution neural network model there is a total of 32 filters and channels. In the model, the output layer has one neuron and the sigmoid activation function because it is a binary classification problem. In the results, the output of the binary classification is one class versus the other class. Batch normalization is used in each layer for fast learning and enhanced generalization. Figure 9 below code is for the model building of baseline convolution neural network.

from te	nsorflow.keras import layers	
TH Reise	ore Rom	
K.clear	session()	
#Config	uring the model architecture	
def bui	ld_baseline():	
model	-Keras.Sequential(
C		
	# first convolution layer + Max pooling layer	
	layers.Conv20(32, (3, 3), activation="Pelu", padding="same",input_snape=(224, 224, 3)),	
	lavers MaxPaoline2D((2, 2))	
	# second convolution layer + max pooling lyger	
	leyers.Conv2D(64, (3, 3), pedding="seme", activation='relu'),	
	layers.BatchNormalization(),	
	layers.MaxPooling2D((2, 2)),	
	<pre>lavers (on/D(120 (2)) ondding="rame" artivation='relui)</pre>	
	layers, BatchNormalization().	
	lavers.MaxPooling2D((2, 2)).	
	# fourth convolution layer + max pooling layer	
	leyers.Conv2D(128, (3, 3), padding="some",activation='relu'),	
	leyers.BetchNormalization(),	
	layers.MaxPooling2D((2, 2)),	
	#A alphal average pooling layer	
	lavers.GlobalAveragePooling2D().	
	A Constant state of the state of a state of a state of a state of the	
	average Desperation and a set in a set	
12		
# compt	iling model	
Acces	te a Learning rate schedule	
10-50	hedule = keras.optimizers.schedules.ExponentialDecay(
ini	tial_learning_rate-le-5,	
dec	ay_steps=100,	
dec	ay_rate=0.9)	
#cont	lauring and compliing the model	
opt -	tf.keras.optimizers.Adam(learning_rate=lr_schedule)	
model	.compile(loss=loss_m, metrics=['eccurecy'], optimizer=opt)	
MC-CT-	colog the model	
Cotur		

Figure 9: Model building of Baseline convolution neural network

In Figure 9, while model compiling the Adams optimizer is used and the loss function is binary cross-entropy.

In [17]:	a# Relaxar B4H K.Clear_sesion() from tensorflow.compet.v1 import ConfigProto from tensorflow.compet.v1 import InteractiveSesion
	config = ConfigProto. config.gpu_options.allow_prowth = True session = InteractiveSesion(config=config)
	## create steps per epoch and validation steps ht_train_semples train_files ht_validation_semples tet_files
	## model_sourp.poths bestmodel_south = '''models/upstmodel_slappiz_'tetr(n_classes)+'class.N5' histor_path = ''.'.'.'models/trainsmodel_slappiz_'.tetr(n_classes)+'class.N5' histor_path = '''.'results/historiac(_classes)+'.log:
	 # <i>Callback for early stopping</i> callback - tf.keras.callbacks.EarlyStopping(monitor-'val_accuracy', patience-100, min_delta-ie-3, restore_best_weights=True)
	<pre>## Checkpoints and logs checkpoint = ModelCheckpoint(filepath=bestmodel_path, verbose=1, save_best_only=True) csu_bagger = CSVLogger(history_path)</pre>
	#start the training num_epochs = 1000 history = model_ffit(frain #emerator.
	<pre>step_pr_sec0^+ = n0_train_samples // BATCH_SIZE , validation_steps=n0_validation_samples // BATCH_SIZE, validation_steps=n0_validation_samples // BATCH_SIZE, vertost=1.</pre>
	<pre>callbacks=[callback,csv_logger, checkpoint]) model.save("./models/ohar-baseline.h5")</pre>

Figure 10: Code for Model training

In Figure 10 the model is trained for the 1000 epoch for train generator data and among them, the best model is saved. After the model training, the accuracy of the

model is increasing over time and it reaches 89%. The accuracy of the validation data is between 72-83%. The training loss continuously decreases.



Figure 11: Code of Results of baseline CNN



Figure 12: Accuracy and Loss graph of baseline CNN Model



Figure 13: Accuracy and Loss graph of baseline CNN Model with augmented data

5.2 Model 2 DenseNet121 with CNN

In the hybrid CNN model, a convolution neural network is designed on top of the DenseNet121 network as shown in Figure 14. For better results and accuracy the pretrained DenseNet121 model is designed with CNN. In the CNN model, the two convolutions 2D layers are used and concatenated in the next layer.



Figure 14: Model building of hybrid CNN model



Figure 15: Code for Model training of hybrid CNN model



Figure 16: Code for Results of baseline CNN



Figure 17: Code for Model training of hybrid CNN model

In the results of the model shown in Figure 17, the overfitting problem has been addressed to a great extent. After that, the fine-tuning of the model by freezing and unfreezing some of the layers, the accuracy on the train data came to a little less than 1.00 while the test accuracy came out to be 80%.

6 Evaluation

Accuracy is the ability of a classification model to accurately classify the data. In medical situations, it is crucial that an individual who is unwell be accurately classified; but, if some individuals who are not ill are also recorded as positive, there may be a problem. Therefore, it may be claimed that accuracy is more significant in medical instances. As many researchers in the past have used accuracy to show the effectiveness of various models

6.1 Baseline Convolution Neural Network

In the baseline convolution, neural network model the accuracy of the overall research is 73%, F1-score was 0.75. The Evaluation matrix and confusion matrix are shown in the Figure 19



Figure 18: Code to Generate the Classification Report of Model 1

		precision	recall	f1-score	support
	0.0	0.68	0.71	0.69	24
	1.0	0.77	0.74	0.75	31
accur	acy			0.73	55
macro	avg	0.72	0.73	0.72	55
weighted	avg	0.73	0.73	0.73	55

Figure 19: Classification Report of the Baseline Convolution Neural Network Model.

6.2 Baseline Convolution Neural Network after Data Augmentation

In this instance, the data was enhanced using a data augmentation technique before being fed to the CNN model. However, due to data augmentation's slight addition of noise to the signals data, accuracy fell to 69%. So, for the purpose of the final evaluation, the aforesaid model was used. The code for the generation of the confusion matrix is shown in Figure 20. The confusion matrix is shown in Figure 21.

45]:	import numpy as np
	import matplotlib.pyplot as plt
	import numpy as np
	import itertools
	def plot confusion matrix(cm
	target names.
	tile-'Confusion Matrix'
	cmap=None.
	pormalize=True):
	accuracy = np.trace(cm) / np.sum(cm).astype('float')
	misclass = 1 - accuracy
	if cman is None-
	<pre>cmap = plt.get cmap('Blues')</pre>
	<pre>plt.figure(figsize=(10, 8))</pre>
	plt.imshow(cm, interpolation='nearest', cmap=cmap)
	plt.title(title)
	plt.colorbar()
	if target names is not None.
	tick marks = no arange(len(target names))
	plt.xticks(tick marks, target pages, rotation=45)
	plt.vticks(tick marks, target names)
	if normalize:
	<pre>cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]</pre>
	thresh = cm max() / 1.5 if normalize else cm max() / 2
	for i i in itertools.product(range(cm.shanef0)), range(cm.shanef1));
	if normalize:
	<pre>plt.text(j, i, "{:0.4f}".format(cm[i, j]),</pre>
	horizontalalignment="center",
	color="white" if cm[i, j] > thresh else "black")
	else:
	<pre>plt.text(j, i, "{:,}".format(cm[i, j]),</pre>
	horizontalalignment="center",
	color="white" if cm[i, j] > thresh else "black")
	plt.tight_layout()
	plt.ylabel('True Label')
	<pre>plt.xlabel('Predicted Label\naccuracy={:0.4f}; misclass={:0.4f}'.format(accuracy, misclass))</pre>
	plt.show()
	tagget pager - clarger
	conjec_mones - closses of = confusion matrix(actuals, predicted)
	alot confuring matrix(of target name)

Figure 20: Code to Generate the Classification Report of Model 1 with Augmentation



Figure 21: Confusion Matrix of Model 1

6.3 DenseNet121 + CNN

The Hybrid Convolutional Neural Network with DenseNet121+CNN that was created for this research had a training accuracy of about 85% as shown in Figure 22, but after

some fine-tuning, it performed remarkably well. So, the refined model was taken into consideration for the initial assessment.

		precision	recall	f1-score	support
	0.0	0.86	0.73	0.79	26
	1.0	0.79	0.90	0.84	29
accur	acy			0.82	55
macro	avg	0.83	0.81	0.82	55
weighted	avg	0.82	0.82	0.82	55

Figure 22: Confusion Matrix of Model 2

6.4 DenseNet121+ CNN after fine-tuning

By briefly freezing and unfreezing some layers, the Hybrid CNN was adjusted. The final results were superior to the initial ones. Here, the validation accuracy was about 77%, and the training accuracy was over 99%. After adjustments, this model's total accuracy was 81.82% and its F1 score was 0.84. Figure 23, the additional evaluation metrics are displayed. According to the confusion matrix in Figure 22, 73.08% of people are actually classified as having apnea, and 89.66% of people are actually classed as not having apnea.



Figure 23: Confusion Matrix of Model 2