In [1]: in i	mporting all the important libraries mport pathlib mport tensorflow as tf mport matplotlib.pyplot as plt mport numpy as np mport pandas as pd mport os
In [2]: ## # #6 In [3]: ## # dd dd In [4]: #in p. in In [5]: bin in U In [7]: ## O # V In [7]: ## O # V In [7]: ## O # In [7]: ## In [7]: ## O # In [7]: ## In [
St. In [3]: ## d. d. In [4]: #in p. in p. In [5]: b. in in Un In [7]: ## O. # Un For Un Un In [7]: ## O. # Un In [7]:	<pre>import PIL from tensorflow import keras from tensorflow.keras import layers from tensorflow.keras.models import Sequential ## If you are using the data by mounting the google drive, use the following: ## from google.colab import drive ## drive.mount('/content/gdrive') ##Ref:https://towardsdatascience.com/downloading-datasets-into-google-drive-via-google-colab-bcb1b30b</pre>
in product of the pro	this assignment uses a dataset of about 2357 images of skin cancer types. The dataset contains 9 sub-directories in each train and test subdirectories. The 9 sub-directories contains the images of 9 skin cancer types respectively. **Defining the path for train and test images** **Todo: Update the paths of the train and test dataset* **Lata_dir_train = pathlib.Path("Skin cancer ISIC The International Skin Imaging Collaboration/Train/") **Lata_dir_test = pathlib.Path("Skin cancer ISIC The International Skin Imaging Collaboration/Test/")
C D n [5]: b in in U [31]: # # o # t Fo U: Fo U:	checking how many image files are present in train and test datasets by counting number of jpg file mage_count_train = len(list(data_dir_train.glob('*/*.jpg'))) print(image_count_train) mage_count_test = len(list(data_dir_test.glob('*/*.jpg'))) print(image_count_test) 239 18
[31]: ## (31]: ## (4) (5) (6) (7) (8) (9) (9) (9) (9) (1) (1) (1) (1	coad using keras.preprocessing et's load these images off disk using the helpful image_dataset_from_directory utility. Create a dataset efine some parameters for the loader:
Fo U: ## ## U: ## U: ## U: ## U: ## U: ## U: ## ##	mg_height = 180 mg_width = 180 See 80% of the images for training, and 20% for validation. ## Write your train dataset here ## Note use seed=123 while creating your dataset using tf.keras.preprocessing.image_dataset_from_dire ## Note, make sure your resize your images to the size img_height*img_width, while writting the datas rain ds = tf.keras.preprocessing.image dataset from directory(
Fo U:	<pre>directory= data_dir_train, labels='inferred', label_mode='int', batch_size = batch_size, validation_split=0.2, subset="training", image_size=(img_height, img_width), seed = 123) ound 2239 files belonging to 9 classes. sing 1792 files for training. ## Write your validation dataset here ## Note use seed=123 while creating your dataset using tf.keras.preprocessing.image dataset from dire</pre>
n [6.	with Note, make sure your resize your images to the size img_height*img_width, while writting the datastal_ds = tf.keras.preprocessing.image_dataset_from_directory(directory= data_dir_train, labels='inferred', label_mode='int', batch_size=batch_size, validation_split=0.2, subset="validation", image_size=(img_height, img_width), seed = 123) ound 2239 files belonging to 9 classes. sing 447 files for validation.
# # c. p.	List out all the classes of skin cancer and store them in a list. You can find the class names in the class_names attribute on these datasets. These correspond to the directory names in alphabetical order. class_names = train_ds.class_names crint(class_names) 'actinic keratosis', 'basal cell carcinoma', 'dermatofibroma', 'melanoma', 'nevus', 'pigmented benig keratosis', 'seborrheic keratosis', 'squamous cell carcinoma', 'vascular lesion']
Ton [9]: ii	<pre>dodo, create a code to visualize one instance of all the nine classes present in the dataset mport matplotlib.pyplot as plt if your code goes here, you can use training or validation data to visualize clt.figure(figsize = (10,10)) for i in range(len(class_names)): filtered_ds = train_ds.filter(lambda x, 1: tf.math.equal(1[0], i))</pre>
	<pre>for image, label in filtered_ds.take(1): ax = plt.subplot(3, 3, i+1) plt.imshow(image[0].numpy().astype('uint8')) plt.title(class_names[label.numpy()[0]]) plt.axis('off') actinic keratosis</pre>
	melanoma nevus pigmented benign keratosis
	seborrheic keratosis squamous cell carcinoma vascular lesion
di	the <code>image_batch</code> is a tensor of the shape (32, 180, 180, 3). This is a batch of 32 images of shape <code>180x180x3</code> (the last imension refers to color channels RGB). The <code>label_batch</code> is a tensor of the shape (32,), these are corresponding labels to the 32 mages.
[10]: A	Dataset.cache() keeps the images in memory after they're loaded off disk during the first epoch. Dataset.prefetch() overlaps data preprocessing and model execution while training. Dataset.prefetch() overlaps data preprocessing and model execution while training. Dataset.prefetch() overlaps data preprocessing and model execution while training. Dataset.prefetch() overlaps data preprocessing and model execution while training. Dataset.prefetch() overlaps data preprocessing and model execution while training. Dataset.prefetch() overlaps data preprocessing and model execution while training. Dataset.prefetch() overlaps data preprocessing and model execution while training. Dataset.prefetch() overlaps data preprocessing and model execution while training.
[11]: #	codo: Create a CNN model. which can accurately detect 9 classes present in the dataset. Use Layers.experimental.preprocessing.Rescaling to normalize pixel values between (0,1). The RGB channel values are in [0, 255] range. This is not ideal for a neural network. Here, it is good to standardize values to be in the [0, 1] ### Your code goes here tum_class = 9 todel = Sequential([layers.experimental.preprocessing.Rescaling(scale = 1./255,input shape=(img height, img width, 3))
]	<pre>layers.Conv2D(16,3,padding='same',activation= 'relu'), layers.MaxPooling2D(), layers.Conv2D(32,3,padding='same',activation= 'relu'), layers.MaxPooling2D(), layers.Conv2D(64,3,padding='same',activation= 'relu'), layers.MaxPooling2D(), layers.Flatten(), layers.Platten(), layers.Dense(128,activation = 'relu'), layers.Dense(num_class)</pre>
C [12]: #	Compile the model Choose an appropirate optimiser and loss function for model training ### Todo, choose an appropirate optimiser and loss function Hodel.compile(optimizer='adam', Loss= tf.keras.losses.SparseCategoricalCrossentropy(from_logits=True), metrics=['accuracy'])
Mo	<pre>Wiew the summary of all layers codel.summary() codel: "sequential" ayer (type)</pre>
CCC ma	ax_pooling2d (MaxPooling2D) (None, 90, 90, 16) 0 onv2d_1 (Conv2D) (None, 90, 90, 32) 4640 ax_pooling2d_1 (MaxPooling2 (None, 45, 45, 32) 0 onv2d_2 (Conv2D) (None, 45, 45, 64) 18496 ax_pooling2d_2 (MaxPooling2 (None, 22, 22, 64) 0 latten (Flatten) (None, 30976) 0
	ense (Dense) (None, 128) 3965056 ense_1 (Dense) (None, 9) 1161 =================================
[14]: e ₁ h.	<pre>Train the model pochs = 20 istory = model.fit(train_ds, validation_data=val_ds, epochs=epochs) poch 1/20 6/56 [====================================</pre>
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E; 50 1 E; 50 1 E; 50 1	poch 5/20 6/56 [====================================
1 Ep 50 1 Ep 50 1 Ep 50 1	.4972 - val_accuracy: 0.5347 poch 9/20 6/56 [====================================
1 E _I 5 2 E _I 5 1 E _I	.8188 - val_accuracy: 0.5481 poch 13/20 6/56 [====================================
5 (2 E ₁ 5 (2 E ₁ 5 (6/56 [====================================
2 E ₁ 50 2 V	.3151 - val_accuracy: 0.5347 poch 20/20 6/56 [====================================
ej p. p. p. p. p. p. p.	<pre>oss = history.history['loss'] ral_loss = history.history['val_loss'] pochs_range = range(epochs) rlt.figure(figsize=(8, 8)) rlt.subplot(1, 2, 1) rlt.plot(epochs_range, acc, label='Training Accuracy') rlt.plot(epochs_range, val_acc, label='Validation Accuracy') rlt.legend(loc='lower right') rlt.title('Training and Validation Accuracy')</pre>
p. p. p. p. p.	<pre>clt.subplot(1, 2, 2) clt.plot(epochs_range, loss, label='Training Loss') clt.plot(epochs_range, val_loss, label='Validation Loss') clt.legend(loc='upper right') clt.title('Training and Validation Loss') clt.show() Training and Validation Accuracy Training and Validation Loss Training Loss Trainin</pre>
(0.9 - Validation Loss 0.8 - 2.0 - 1.5 - 1
(0.6 -
	Validation Accuracy Valida
va va in su [16]: #	's clearly visible that the model has overfit as training accuracy could rach a maximum of 0.93 which is much higher than the maximum alidation accuracy, 0.56. Hence, we need to do appropriate data augmentation so that there will be agreeable overlap between training a alidation accuracies. Since colorspace transformation, random erasing, kernal filters and mixing images methods all can cause loss of attegrity of the image in our case of melanoma detection and hence lower the accuracy of model, geometric transformations would be the uitable data augmentation to do. Todo, after you have analysed the model fit history for presence of underfit or overfit, choose an accordance data augumentation strategy.
[17]: ##	<pre># Your code goes here tata_augmentation = tf.keras.Sequential([layers.experimental.preprocessing.RandomFlip("horizontal_and_vertical"), layers.experimental.preprocessing.RandomRotation(0.1),) # Todo, visualize how your augmentation strategy works for one instance of training image. # Your code goes here plt.figure(figsize=(10, 10)) # For images, in train ds.take(1):</pre>
[45]: ##	Create the model, compile and train the model # You can use Dropout layer if there is an evidence of overfitting in your findings # Your code goes here um_class = 9 odel = Sequential([data_augmentation, layers.experimental.preprocessing.Rescaling(1./255 , input_shape=(img_height, img_width, 3)), layers.Conv2D(16, 3, padding='same', activation='relu'), layers.MaxPooling2D(), layers.Conv2D(32, 3, padding='same', activation='relu'), layers.MaxPooling2D(), layers.MaxPooling2D(), layers.MaxPooling2D(), layers.Dropout(0.1), layers.Platten(), layers.Platten(), layers.Dense(128, activation='relu'),
[46]: #	<pre>layers.Dense(num_class)) Compiling the model # Your code goes here todel.compile(optimizer='adam',</pre>
[47]: #h.	<pre>Training the model # Your code goes here, note: train your model for 20 epochs istory = model.fit(train_ds, validation_data=val_ds, epochs= 20) poch 1/20 6/56 [====================================</pre>
8 (E _I 5 (E _I 5 (E _I 5 (681 - val_accuracy: 0.3535 poch 2/20 6/56 [====================================
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E ₁ 50 33 V	<pre>883 - val_accuracy: 0.5101 poch 20/20 6/56 [====================================</pre>
ej p.	<pre>oss = history.history['loss'] ral_loss = history.history['val_loss'] pochs_range = range(epochs) rlt.figure(figsize=(8, 8)) rlt.subplot(1, 2, 1) rlt.plot(epochs_range, acc, label='Training Accuracy') rlt.plot(epochs_range, val_acc, label='Validation Accuracy') rlt.legend(loc='lower right') rlt.title('Training and Validation Accuracy')</pre>
p p p p	clt.subplot(1, 2, 2) clt.plot(epochs_range, loss, label='Training Loss') clt.plot(epochs_range, val_loss, label='Validation Loss') clt.legend(loc='upper right') clt.title('Training and Validation Loss') clt.show() Training and Validation Accuracy Training and Validation Loss Validation Loss Validation Loss
(0.50 - 0.45 - 0.45 - 0.40 - 1.6 -
(0.40 - 0.35 - 0.30 - 0.25 - Training Accuracy Validation Accuracy
in Ti fro	odo: Write your findings after the model fit, see if there is an evidence of model overfit or underfit. Do you think there is some improvement now as compared to the previous model run? The model is performing better now, and overfitting is handled after data augmentation and addition of drop out layer, which is evidenced om the similar accuracy values of train and validations sets, which are 0.61 and 0.54 respectively.
[22]: #	context: Many times real life datasets can have class imbalance, one class can have proportionately higher number of samples ompared to the others. Class imbalance can have a detrimental effect on the final model quality. Hence as a sanity check it ecomes important to check what is the distribution of classes in the data. ## Your code goes here. for i in range(9): print(class_names[i]) path = class_names[i]+'/*.jpg' image_count_train = len(list(data_dir_train.glob(path)))
1: ba 3: da 9: ma 4:	print(image_count_train) ctinic keratosis 14 asal cell carcinoma 76 ermatofibroma
3! p: 4! se 7' so 1! va	igmented benign keratosis 62 eborrheic keratosis 7 quamous cell carcinoma 81 ascular lesion 39
- 1 se	which class has the least number of samples? eborrheic keratosis Which classes dominate the data in terms proportionate number of samples? igmented benign keratosis
[23]: # [49]: po	codo: Rectify the class imbalance context: You can use a python package known as Augmentor (https://augmentor.readthedocs.io/en/master/) to add more amples across all classes so that none of the classes have very few samples. In the list = [] In the class names:
d.	-
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2 2 2 2 2 7 7	2. Define a number of operations to perform on this data set using your Pipeline object. 3. Execute these operations by calling the Pipeline's sample() method. ath_to_training_dataset="D:/Master of AI/IIITB EPG/Assignments/CNN_assignment/Skin cancer ISIC The Invariant Invar
[51]: p	re.
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