CSE 572: Lab 6

In this lab, you will practice implementing feed-forward network and parameter tuning with k-fold cross valivation

nake changes to this notebook, click File > Save a copy to save your own version in your Google Drive or Github. Read the st ons below carefully. To execute the code, click on each cell below and press the SHIFT-ENTER keys simultaneously or by

a link to your Colab notebook, the .ipynb file, and a pdf of the executed notebook on Canvas.

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 Member 1
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Import libraries import tensorflow as tf import numpy as np import pandas as pd from tensorflow import keras from tensorflow.keras import layers

Feed-forward neural networks

Load the dataset

For this example, we will use the <u>Cleveland Heart Disease dataset</u>. Review the dataset documentation to learn more about the attributes and other aspects of the dataset. The dataset consists of a GSV file with 303 rows, Each row contains information about a patient. There are 14 attribute columns and one binary class column (1xrget) that reports whether or not a patient had a heart diseaset. We will train a feed-forwal neural network model to predict whether or not a given patient has a heart disease based on the attribute values.

Load the dataset data = pd.read_csv("http://storage.googleapis.com/download.tensorflow.org/data/heart.csv"

| | age | sex | cp | trestbps | chol | fbs | restecg | thalach | exang | oldpeak | slope | ca | thal | target |
|---|-----|-----|----|----------|------|-----|---------|---------|-------|---------|-------|----|------------|--------|
| 0 | 63 | - 1 | 1 | 145 | 233 | - 1 | 2 | 150 | 0 | 2,3 | 3 | 0 | fixed | 0 |
| 1 | 67 | 1 | 4 | 160 | 286 | 0 | 2 | 108 | 1 | 1.5 | 2 | 3 | normal | 1 |
| 2 | 67 | 1 | 4 | 120 | 229 | 0 | 2 | 129 | 1 | 2.6 | 2 | 2 | reversible | 0 |
| 3 | 37 | - 1 | 3 | 130 | 250 | D | 0 | 187 | 0 | 3.5 | 3 | 0 | normal | 0 |
| | | | | 400 | 204 | | | 470 | | | | | | |

(303, 14)

Split the dataset into three randomly-sampled subsets: training (60%), validation (20%), and test (20%). Use the seed variable for the

train, val, test = np.split(data.sample(frac=1, random_state=seed), [int(.6*len(data)), int(.8*len(data))])

Print the number of samples in each of the three subsets and the number of instances from each class. For example, for the training set you might print 'The training set has __instances (__heart disease,__ no disease)'

The training set has, 181, instances
- Heart disease: 48
- No heart disease: 333
The validation set has 61 instances
- Heart disease:, 18
- No heart disease:, 18
The test set has, 61, instances
Heart disease:, 77
No heart disease:, 17

Prepare the dataset

Before we can feed this dataset to our model for training and evaluation, we need to perform a few steps to get it ready

d Convert delatromes to Dataset dejects
def dataframe_To_dataset(de; shufrielrow):
df = df.copy()
a Remove the target column and store in a separate array
labels = df.popy('Larget')
ds = tf.dsta.Dataset.frow_larget(dict(df), labels))
if shuffle;
ds = df.shuffle(buffer stamlarset.)

train_ds_original = dataframe_to_dataset(train
val_ds_original = dataframe_to_dataset(val)
test_ds_original = dataframe_to_dataset(test)

The Dataset object yields a tuple containing the input feature vector and target (class value): (input, target). input is a dictionary of features and target is the value 0 or 1. The code below prints an example instance drawn from the training Dataset object.

Input: ('age': ctf.Tensor: shaper(), dtyperint64, numpy=35, 'sex': ctf.Tensor: shaper(), dtyperint64, numpy=35, 'ctf.Tensor: shaper(), dtyperint64, numpy=35, 'c

We can use the batch() function in keras to create batches from the full dataset for passing to the model. For the training dataset, we'll define a hyperparameter batch_size drive we'll set. For the validation and test sets, we will make the batch size equivalent to the size of the subsets to all samples in that should set are evaluated beth mire the dataset is evaluated by the most set.

batch_size = 32 train_ds = train_ds_original.batch(batch_size) val_ds = val_ds_original.batch(val.shape[0]) test_ds = test_ds_original.batch(test.shape[0])

There are seven categorical features in the dataset: sor, cp., fts., restrog, exang. ca, and thai. You can read more about what these features meen in the <u>dataset features meen in the dataset features meen in the dataset features meen in the dataset features meen in the same of the second of th</u>

def encode_categorical_feature(feature, name, dataset, is_string):
 from tensorflow.keras.layers import IntegerLookup
 from tensorflow.keras.layers import StringLookup

Create lookup layer to turn categorical features into 1-hot integer encodings if is string:
Lookup = StringLookup(output_mode="binary")

else: lookup = IntegerLookup(output_node="binary")

Prepare a Dataset that only yields the feature of interest feature_ds = dataset.map(lambda x, y: x[name]) feature_ds = feature_ds.map(lambda x: tf.expand_dims(x, -1))

Find the set of possible values and assign then a fixed integer index lookup.adapt(feature_ds)

The remaining features in the dataset (age, trestaps, chol., thalach, oldpeak, and slope) are all numerical measurements. You can read more about what these features mean in the dataset documentation. We don't need to encode the numerical features, but we do want to scale

```
them to the same range of values (e.g., using standardization or normalization). Below we define a function that uses the <u>Normalization()</u> layer to standardize the data (subtract the mean and divide by the standard deviation for each feature).
```

```
def normalize(feature, name, dataset):
    from tensorflow.keras.layers import Normalization
       # Create a Normalization layer for our feature
normalizer = Normalization()
      # Prepare a Dataset that only yields the feature of interest
feature_ds = dataset.map(lambda x, y: x[name])
feature_ds = feature_ds.map(lambda x: tf.expand_dims(x, -1))
       # Learn the statistics of the data
normalizer.adapt(feature_ds)
```

Now we can apply these functions to each of our features and return an encoded/preprocessed input layer. We first create tensor variables for each of the inputs, then apply the appropriate function, then concatenate all of these ainput layers for each feature together to form a single input feature layer.

```
_inputs [
kersa.lnput(shapec(1), name='so', dtype='int64'),
kersa.lnput(shapec(1), name='ny', dtype='int64'),
kersa.lnput(shapec(1), name='name', dtype='sring'),
kersa.lnput(shapec(1), name='name', dtype-'sring'),
kersa.lnput(shapec(1), name='name', dtype-'name', dtype-'sring'),
kersa.lnput(shapec(1), name='name', dtype-'name', dtype-
```

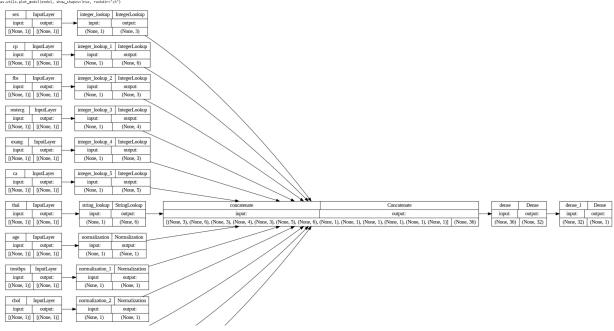
Now that we've prepared our dataset, we can construct our neural network model. We construct the model by composing Layer objects starting with the input typer (which we've already defined as **sture_layer*) and ending with the output layer (which will be the final output of the model). In this example, we will only use <u>Bensed</u> layers which are simple fully-connected feed-forward layers (i.e. each output from layer i.i. is connected by a weight variable to every neuron in layer 1). We will create a network with only one hidden layer (between the input and output layers).

The bense) layer object allows us to specify the activation function to use using the activation argument. In class, we talked about several activation functions including aigmoid, sign, and tank. Another commonly used activation functions in the rectified linear unit, or TRALL' function. Another commonly used activation function is the rectified linear unit, or TRALL' function, which has the equation a(z) = max(0, z). We will use $re_{\perp l} = max(0, z)$ with a cut activation function in this example for all layers except the final layer, which will use a stapeoid activation.

```
# Create a variable for the number or white, new and his inits = 32 
# Create a Bense layer and append it to the input layer 
hi layer = layers.Dense(hi_units, activation='relu')(feature_layer)
# Create an output layer with one output representing the likelihood of # heart disease and append it to the hidden layer output_layer - layers.Dense(1, activation-"signoid")(hi_layer)
  # Build the model specifying the input and output layer
model = keras.Model(inputs=all_inputs, outputs=output_layer)
```

We can plot our completed model to visualize the input, hidden, and output layers.

'rankdir='LR'' is to make the graph horizontal
keras.utils.plot_model(model, show_shapes=True, rankdir="LR")



Next we compile the model by specifying the optimization technique and loss function to be used in model training. We can also sp metric(s) that will be logged during training. We will use stochastic gradient descent (say) for the optimizer and brainary cose sertions as the loss function. We will log the accuracy metric futing training. We can also opedity the terminary sets phepapeamente here.

learning_rate = 0.01
model.compile(keras.optimizers.SGD(learning_rate=learning_rate), "binary_crossentropy", metrics=["accuracy"])

Train the model

vithat we've constructed and compiled our model, we can train the model using our training dataset. This is done in keras ction, which also gives us an option to provide the validation dataset which will be used to evaluate validation accuracy at

del result = model.fit(train ds. epochs=180, validation data=val ds)

```
6/6 [======
Epoch 10/100
   Epoch 11/100
6/6 [------
Epoch 12/100
```

```
--] - 0s 5ms/step - loss: 0.4598 - accuracy: 0.7624 - val_loss: 0.5120 - val_accuracy: 0.7849
      ============ | - 0s 5ms/step - loss: 0.4258 - accuracy: 0.7790 - val loss: 0.4798 - val accuracy: 0.7213
```

The fit() function returns a history attribute that gives the metrics recorded during training as a dictionary. We can print the dictionary keys to see which metrics were stored:

model_result.history.keys()

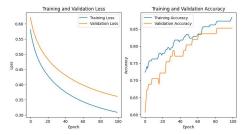
dict_keys(['loss', 'accuracy', 'val_loss', 'val_accuracy'])

Create a figure with two subplots. The first subplot should plot the training and validation loss (loss and val_loss) and the second subplot should plot the training and validation accuracy (accuracy and val_accuracy). Make sure you include the axis labels and a legend in each plot

Create a figure with two subplots
fig, (ax1, ax2) = plt.subplots(ncols=2, figsize=(10,5))

.plot(model_result.history['loss'], label='Training loss'), .plot(model_result.history['val_loss'], label='Validation Loss') .set_vlabel('tpoch') .set_vlabel('toss') .set_vlabel('toss') .set_vlabel('reining and Validation Loss')

plt.show()



Finally, we evaluate our trained model on the held-out test set. First we predict the outputs for the test data

preds = model.predict(test_ds)

The model output from the final sigmoid layer is a value between 0 and 1 representing the likelihood that a given sample patient has heart disease. To get the predicted classes, we predict 1 if the output was >= 0.5 and 0 otherwise.

pred_classes = [1 if p >= 0.5 else 0 for p in preds]

Compute and print the test accuracy.

Extract the training and validation accuracies from the results train_acc = train_res[1] val_acc = val_res[1] test_acc = test_res[1]

ice between the training and validation accuracies and the test accuracy. What do you think could explain

YOUR ANSWER HERE

- · Small validation/test set size
- Hyperparameter tuning with K-fold Cross Validation

✓ k-fold Cross validation

We will use 5-fold cross validation to train and evaluate our classifier. We will not do any model selection/hyperparameter tuning in this step, so we need to split our data into a training and test set.

To split the data into 3 folds we will shuffle the rows and then split them into k equal groups

Note: np.split raises error if indices_or_sections is
an integer and doesn't result in equal size splits
folds = np.split(data.sample(frac=1, random_state=seed), indices_or_sections=k)

| | age | sex | ср | trestbps | chol | fbs | restecg | thalach | exang | oldpeak | slope | ca | thal | target |
|----------------------|-----|-----|----|----------|------|-----|---------|---------|-------|---------|-------|----|--------|--------|
| 225 | 58 | 0 | 4 | 130 | 197 | 0 | 0 | 131 | 0 | 0.6 | 2 | 0 | normal | 0 |
| 201 | 43 | - 1 | 4 | 115 | 303 | 0 | 0 | 181 | 0 | 1.2 | 2 | 0 | normal | 0 |
| 52 | 53 | 0 | 4 | 130 | 264 | 0 | 2 | 143 | 0 | 0.4 | 2 | 0 | normal | 0 |
| 168 | 54 | 0 | 3 | 108 | 267 | 0 | 2 | 167 | 0 | 0.0 | - 1 | 0 | normal | 0 |
| 223 | 39 | 0 | 3 | 138 | 220 | 0 | 0 | 152 | 0 | 0.0 | 2 | 0 | normal | 0 |
| | | | | - | | | | | | | | | | |
| 247 | 59 | 1 | 0 | 164 | 176 | 1 | 0 | 90 | 0 | 1.0 | 1 | 2 | 1 | 0 |
| 288 | 57 | 0 | 4 | 128 | 303 | 0 | 2 | 159 | 0 | 0.0 | - 1 | 1 | normal | 0 |
| 156 | 62 | 0 | 4 | 150 | 244 | 0 | 0 | 154 | 1 | 1,4 | 2 | 0 | normal | 0 |
| 297 | 56 | 1 | 4 | 125 | 249 | 1 | 2 | 144 | 1 | 1.2 | 2 | 1 | normal | 0 |
| 252 | 57 | 0 | 1 | 130 | 236 | 0 | 0 | 174 | 0 | 0.0 | 1 | 1 | 2 | 0 |
| 75 rows × 14 columns | | | | | | | | | | | | | | |

YOUR CODE HERE

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                   Fold. 1. has. 101. instances (. 26. heart disease. 75 no disease)

    Train a Neural Network classifier

       eature layer = layers.concatenate(
   accuracies = []
for lr in learning_rate:
accuracies_per_param = []
                     # assign the folds to training and validation
train = pd.concat(folds[8:i] + folds[i:i])
val = folds[i]
train_ds_original = dataframe_to_dataset(train)
val_ds_original = dataframe_to_dataset(val, shuffle=False)
                     train_ds = train_ds_original.batch(32)
val_ds = val_ds_original.batch(val.shape[0])
                     model - create model(h1 units, 1r, h1 activation)
                     rodel_result = nodel.fit(train_ds, epochs=10, validation_data=val_ds)
                         pred_val = (pred_val >= 0.5).astype(int)
                     accuracies_per_param.append(accuracy_score(val['target'].values,pred_val))
         accuracies.append(accuracies_per_param)
                  | Topich 1/30 | 1-15 Step/step - loss: 0.8852 - accuracy: 0.7212 - val_loss: 0.8221 - val_accuracy: 0.3546 | 7/7 [ ... | 1-15 Step/step - loss: 0.8852 - accuracy: 0.7218 - val_accuracy: 0.3546 | 7/7 [ ... | 1-15 Step/step - loss: 0.8852 - accuracy: 0.3218 - val_accuracy: 0.3224 | val_accuracy: 0.3
                | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 
                                                                    7/7 [====-
1/1 [====-
Fooch 1/10
                                                                      Question 2: How many total combinations of the above hyperparameter choices are there?
   YOUR ANSWER HERE - The learning_rate list has 2 candidate values, And as the other hyperparameters are fixed, we get 2 combinations of
 Print the mean and standard deviation of the accuracy from cross validation for all hyperparams (across all k folds).
 print(accuracies)
acc_mean = np.mean(accuracies, axis=1)
acc_std = np.std(accuracies, axis=1)
                                                                                                                                                                  524, 8.7623762376237624], [0.801980198019802, 0.7623762376237624, 0.801980198
                                                    762376237624, 0.762376237623762

s Accucary Mean Accucary Std

1 0.762376 1.110223e-16

3 0.788779 1.866949e-02
   Question 3: If you increased the number of folds, do you expect the standard deviation of the accuracy across k folds to increase or decrease? Why?
```

https://colab.research.google.com/drive/1kpJrsvL_1mSbv_Hc6N0oWLV3t7i79eiO?authuser=1#scrollTo=FRqYpnKs743V&printMode=true