demo-rfiw-t2-tri-subject

February 4, 2020

1 Demo for RFIW-2020 (Task 2): Tri-Subject Verification

1.1 Overview

Analysis and evaluation demo for tri-subject verification.

Here are a few tricks using pandas in the Recognizing Families In the Wild (RFIW) data challenge. Specifically, in the tri-subject verification task (Task-II).

We will evaluate pairs and perform analysis on the features used for assessment. Specifically, we will - Load all features into dictionary. - Evaluate according to verification protocol. - Calculate verification accuracies for the different relationship pair-types, along with the averaged accuracy. - Generate a ROC curve. - Visualize score distributions for KIN and NON-KIN for the different relationship types.

It is assumed features are extracted in are stored with the same name a image files, except as PKL files. The demo loads all features into a dictionary with keys set as the image (face) name and path (i.e., FID/MID/faceID), but with the extension omitted. Thus, modifications can easily be made in data loading cell to fit the scheme in place if different.

For this, faces were encoded using SphereFace trained on MSCeleb in Pytorch (though any features can be plugged in).

No fine-tuning or special tricks were employed. This is solely to demonstrate a few simple steps for evaluation, followed by easy to generate, yet appealing and insightful, visualizations of the feature embeddings.

[3]:
```
import numpy as np
import pandas as pd
import seaborn as sns



import matplotlib.pyplot as plt
from sklearn.metrics import roc_auc_score, roc_curve
```

[4]:
```
%matplotlib inline
# set styles for figures
sns.set(style="white", rc={"axes.facecolor": (0, 0, 0, 0)})
sns.set_style('whitegrid', {'font.family': 'serif',
                            'font.serif' : 'Times New Roman', 'fontsize': 18})
```

Prepare file paths

[14]:
```
dir_root = '../../data/rfiw2020-data/'

dir_data = dir_root + 'trisubject_verification/'
f_test_ref = dir_data + 'test_triples_reference.csv'
f_val_ref = dir_data + 'val_triplets_reference.csv'

dir_features = f'{dir_root}/FIDs-features/'
```

Load CSV files, feature file paths, and determine relationship types

[15]:
```
df_val = pd.read_csv(f_val_ref)

# get all unique relationship types in DF
relationship_types = df_val.tag.unique()
print('Processing {} pairs of {} relationship types'.format(len(df_val),␣
 ↪len(relationship_types)))

df_test = pd.read_csv(f_test_ref)

f_feats = np.unique(df_val.If.to_list() +
                    df_val.Im.to_list() + df_val.Ic.to_list())
```

```
Processing 3568 pairs of 2 relationship types
```

Load features

[16]:
```
feats = {f: pd.read_pickle(dir_features + f.replace('.jpg', '.pkl')) for f in␣
 ↪f_feats}
```

Determine cosine score for each pair. Do Father-Child and Mother-Child independently. Then, we will fuse scores as the average of the two.

[17]:
```
# score all feature pairs, because L2 norm applied on features dot is same as␣
 ↪cosine sim
df_val['score_fc'] = df_val.apply(lambda x: np.dot(feats[x.If], feats[x.Ic].T),␣
 ↪axis=1)
df_val['score_mc'] = df_val.apply(lambda x: np.dot(feats[x.Im], feats[x.Ic].T),␣
 ↪axis=1)

df_val['score'] = df_val.apply(lambda x: (x.score_fc + x.score_mc)/2, axis=1)
```

[18]:
```
df_val.head()
```

[18]:
```
                           If                           Im  \
0   F0007/MID1/P00073_face2.jpg  F0007/MID2/P00078_face2.jpg
1   F0007/MID1/P00073_face2.jpg  F0007/MID2/P00081_face1.jpg
2  F0007/MID1/P00077_face12.jpg  F0007/MID2/P00074_face0.jpg
```

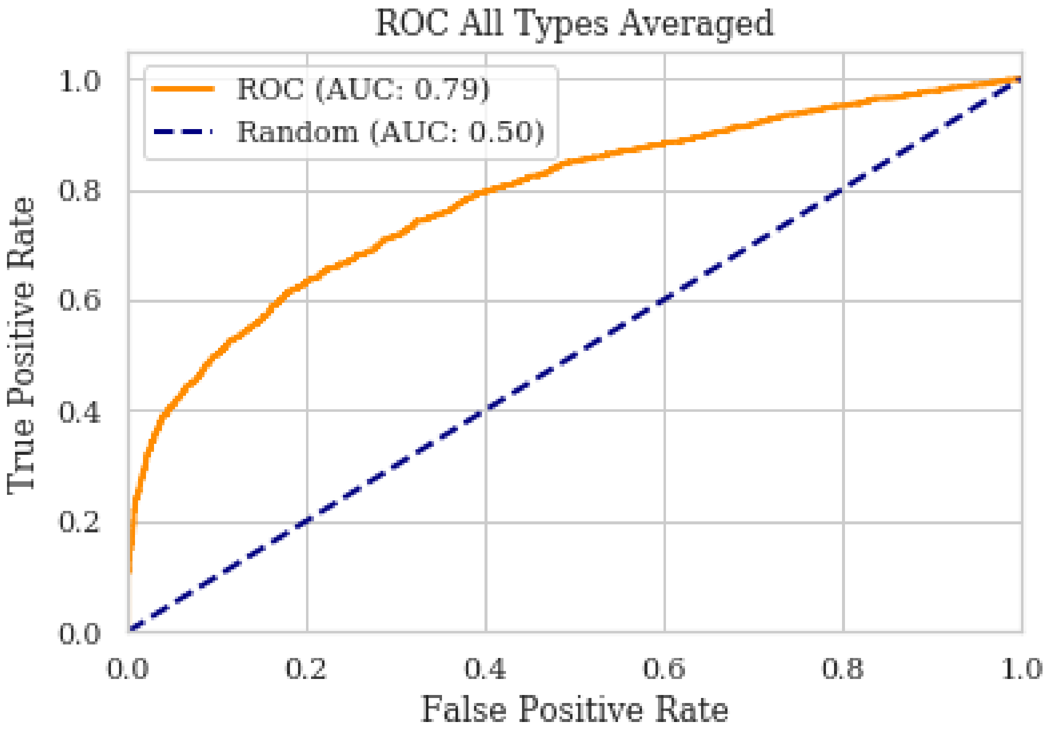
```
3  F0007/MID1/P00077_face12.jpg  F0007/MID2/P11277_face2.jpg
4   F0007/MID1/P00079_face1.jpg  F0007/MID2/P00074_face0.jpg

                            Ic  label  tag    FID           F           M  \
0  F0007/MID6/P00074_face1.jpg      1  FMD  F0007  F0007/MID1  F0007/MID2
1  F0007/MID6/P00073_face3.jpg      1  FMD  F0007  F0007/MID1  F0007/MID2
2  F0007/MID4/P00074_face5.jpg      1  FMD  F0007  F0007/MID1  F0007/MID2
3  F0007/MID5/P00076_face0.jpg      1  FMD  F0007  F0007/MID1  F0007/MID2
4  F0007/MID4/P00074_face5.jpg      1  FMD  F0007  F0007/MID1  F0007/MID2

            C  count  reversed_weights  score_fc  score_mc     score
0  F0007/MID6      4          0.002803 -0.028150  0.004090 -0.012030
1  F0007/MID6      4          0.002803  0.153014  0.265303  0.209159
2  F0007/MID4      4          0.002803  0.165362  0.115922  0.140642
3  F0007/MID5      4          0.002803  0.140530  0.380819  0.260674
4  F0007/MID4      4          0.002803  0.114652  0.115922  0.115287
```

[19]:
```python
df_val.tail()
```

[19]:
```
                               If                           Im  \
3563  F0999/MID1/P10554_face0.jpg  F0999/MID4/P10558_face0.jpg
3564  F0999/MID1/P10554_face0.jpg  F0999/MID4/P10558_face0.jpg
3565  F0999/MID1/P10554_face0.jpg  F0999/MID4/P10552_face1.jpg
3566  F1004/MID2/P13032_face0.jpg  F1004/MID1/P13035_face0.jpg
3567  F1004/MID2/P13033_face0.jpg  F1004/MID1/P13033_face2.jpg

                                Ic  label  tag    FID           F           M  \
3563   F0123/MID6/P01278_face1.jpg      0  FMS  F0999  F0999/MID1  F0999/MID4
3564   F0422/MID1/P04454_face3.jpg      0  FMS  F0999  F0999/MID1  F0999/MID4
3565   F0438/MID6/P04637_face1.jpg      0  FMS  F0999  F0999/MID1  F0999/MID4
3566   F0283/MID5/P03026_face0.jpg      0  FMS  F1004  F1004/MID2  F1004/MID1
3567  F0826/MID3/P08740_face10.jpg      0  FMS  F1004  F1004/MID2  F1004/MID1

               C  count  reversed_weights  score_fc  score_mc     score
3563  F0123/MID6      5          0.002242  0.044601 -0.154332 -0.054866
3564  F0422/MID1      5          0.002242  0.063158 -0.086713 -0.011777
3565  F0438/MID6      5          0.002803 -0.079974 -0.026765 -0.053370
3566  F0283/MID5      5          0.000561  0.136953  0.021686  0.079320
3567  F0826/MID3      5          0.000561 -0.013962  0.037142  0.011590
```

[20]:
```python
df_val['label']=df_val['label'].astype(np.uint)
fpr, tpr, threshold = roc_curve(df_val['label'], df_val['score'])

auc = roc_auc_score(df_val['label'], df_val['score'])
```

[21]:
```python
plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC (AUC: %0.2f)' % auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--', label='Random (AUC:
↪ 0.50)')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC All Types Averaged')
plt.legend(loc="best")
plt.show()
```

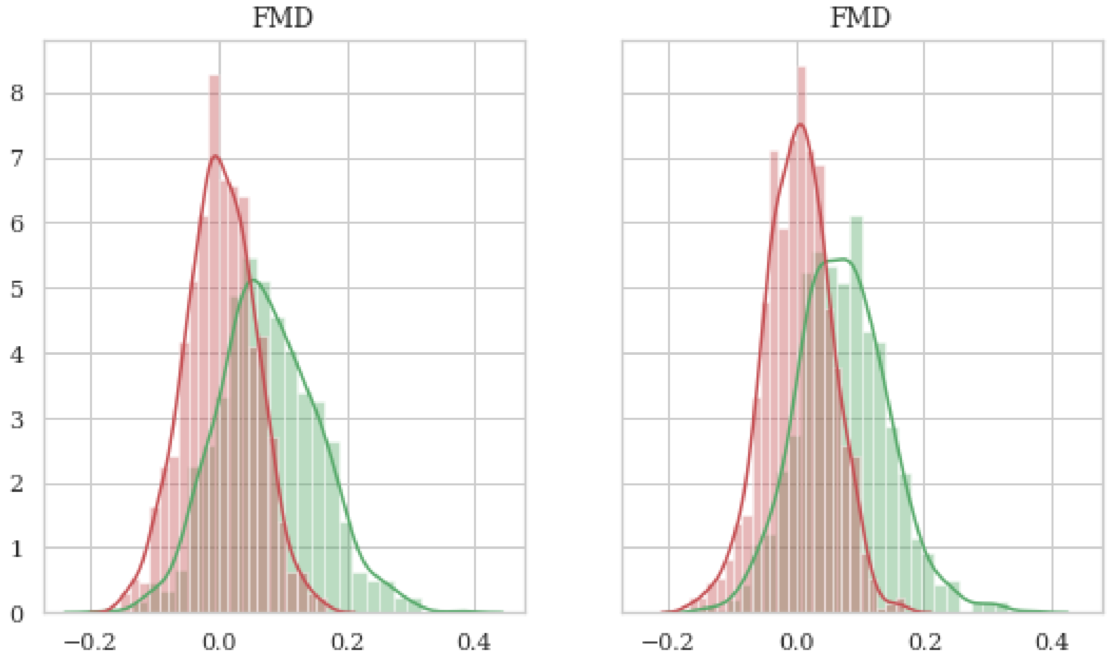


Next plot signal detection models (SDM) for each relationship type. From this, the distribution of scores as a function of label (i.e., KIN vs NON-KIN) can be compared.

[24]:
```
sns.despine(left=True)

f, axs = plt.subplots(1, 2,figsize=(9,5), sharex=True, sharey=True)

for i in range(len(relationship_types)):
    df_cur = df_val.loc[df_val.tag == relationship_types[i],['score', 'label']]
    sns.distplot(df_cur.loc[df_cur.label==1,'score'],hist=True,␣
↪label='True',ax=axs[i],color='g')
    sns.distplot(df_cur.loc[df_cur.label==0,'score'],␣
↪hist=True,label='False',ax=axs[i],color='r')
```

```
    axs[i].set_title(relationship_types[0])
    axs[i].set_xlabel('')

axs[0].set_ylabel('Frequency')
```

```
<Figure size 432x288 with 0 Axes>
```



Similar to SDM, but let's look at boxen plots as means of another visualization of two-class separability.