Image Process and Feature Matching

Dataset in use: https://www.kaggle.com/datasets/cashutosh/gender-classification-dataset/data (https://www.kaggle.com/datasets/cashutosh/gender-classification-dataset/data)

```
In [1]: import os
        import cv2
        import glob
        import random
        import pickle
        import logging
        import numpy as np
        from tqdm import tqdm
        from sklearn import metrics
        from skimage import feature
        from sklearn.svm import SVC
        import matplotlib.pyplot as plt
        from sklearn.cluster import KMeans
In [2]: import warnings
        warnings.filterwarnings("ignore")
In [3]: | def metric report(actual, predicted):
            acc = metrics.accuracy_score(actual, predicted)
            precision = metrics.precision_score(actual, predicted)
            recall = metrics.recall score(actual, predicted)
            f1 = metrics.f1_score(actual, predicted)
            return (acc, precision, recall, f1)
In [4]: |ext='jpg'
In [5]: def image_reader(file_path, in_use, ext=ext):
            images = []
            files = os.listdir(file_path)
            random.shuffle(files)
            files = files[:int(len(files)*in use)]
            for file in tqdm(files, desc = 'Reading Images'):
                if file.endswith(ext):
                    img_path = os.path.join(file_path, file)
                    img = cv2.imread(img_path, 0)
                    images.append(img)
            return images
        male_dir = './dataset/Training/male'
        female_dir = './dataset/Training/female'
        male_test_dir = './dataset/Validation/male'
        female_test_dir = './dataset/Validation/female'
```

```
train_male_images = image_reader(male_dir, 0.25)
In [7]:
        train_female_images = image_reader(female_dir, 0.25)
        Reading Images: 100%
                                                                                   5941/59
        41 [00:14<00:00, 409.49it/s]
        Reading Images: 100%
                                                                                   5810/58
        10 [00:15<00:00, 373.75it/s]
In [8]: | test_male_images = image_reader(male_test_dir, 0.1)
        test_female_images = image_reader(female_test_dir, 0.1)
        Reading Images: 100%
                                                                                     580/5
        80 [00:01<00:00, 337.18it/s]
        Reading Images: 100%
                                                                                     584/5
        84 [00:01<00:00, 336.50it/s]
```

Local Binary Patterns

```
In [10]: def single_image_pipeline(img, desc, male_hist_path, female_hist_path):
    lbp_hist = desc.describe(img)
    lbp_hist = lbp_hist.astype(np.float32)

male_lbp_hist = np.load(male_hist_path).astype(np.float32)
female_lbp_hist = np.load(female_hist_path).astype(np.float32)

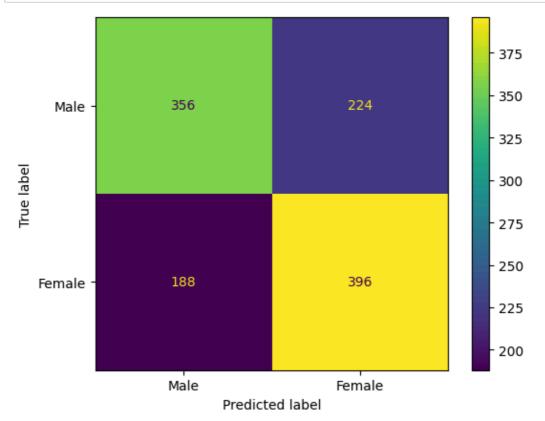
male_distance = cv2.compareHist(lbp_hist, male_lbp_hist, cv2.HISTCMP_CORREL)
female_distance = cv2.compareHist(lbp_hist, female_lbp_hist, cv2.HISTCMP_CORREL
# HISTCMP_INTERSECT, HISTCMP_CORREL, HISTCMP_BHATTACHARYYA, HISTCMP_HELLINGER,
return 0 if male_distance >= female_distance else 1
```

```
In [11]: desc = LocalBinaryPatterns(20, 5)
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```
In [12]:
         Male-Female LBP histogramlari elde edilir ve kaydedilir.
         male_histograms = [desc.describe(img) for img in tqdm(train_male_images, desc="Com
         female_histograms = [desc.describe(img) for img in tqdm(train_female_images, desc=
         np.save('male_lbp_histograms.npy', male_histograms)
         np.save('female_lbp_histograms.npy', female_histograms)
         male lbp hist = np.mean(male histograms, axis=0)
         female_lbp_hist = np.mean(female_histograms, axis=0)
         np.save('male_lbp_hist.npy', male_lbp_hist)
         np.save('female_lbp_hist.npy', female_lbp_hist)
Out[12]: '\nmale_histograms = [desc.describe(img) for img in tqdm(train_male_images, desc
         ="Computing LBP histogram - Male")]\nfemale_histograms = [desc.describe(img) for
         img in tqdm(train female images, desc="Computing LBP histogram - Female")]\n\nnp.
         save(\'male_lbp_histograms.npy\', male_histograms)\nnp.save(\'female_lbp_histogra
         ms.npy\', female_histograms)\n\nmale_lbp_hist = np.mean(male_histograms, axis=0)
         \nfemale_lbp_hist = np.mean(female_histograms, axis=0)\n\nnp.save(\'male_lbp_his
         t.npy\', male_lbp_hist)\nnp.save(\'female_lbp_hist.npy\', female_lbp_hist)\n'
In [13]: predictions male = []
         for img in test_male_images:
             predictions_male.append(single_image_pipeline(img, desc, 'male_lbp_hist.npy',
In [14]: | predictions_female = []
         for img in test_female_images:
             predictions_female.append(single_image_pipeline(img, desc, 'male_lbp_hist.npy'
         actual = np.hstack( (np.zeros(len(predictions male)), np.ones(len(predictions fema
In [15]:
         predicted = np.hstack( (predictions_male, predictions_female) )
In [16]: metric report(actual, predicted)
Out[16]: (0.6460481099656358, 0.6387096774193548, 0.678082191780822, 0.6578073089700996)
```

confusion matrix = metrics.confusion matrix(actual, predicted)

In [17]:



```
In [19]: # Asagidaki img_path degiskenine istenen goruntulerin pathi verilir ve lbp ile gene
img_path = './test_images/064943.jpg.jpg'
img = cv2.imread(img_path, 0)
actual = int(os.path.basename(img_path).startswith('1'))

pred = single_image_pipeline(img, desc, 'male_lbp_hist.npy', 'female_lbp_hist.npy'
if actual == pred:
    print('Gender Detected!')
```

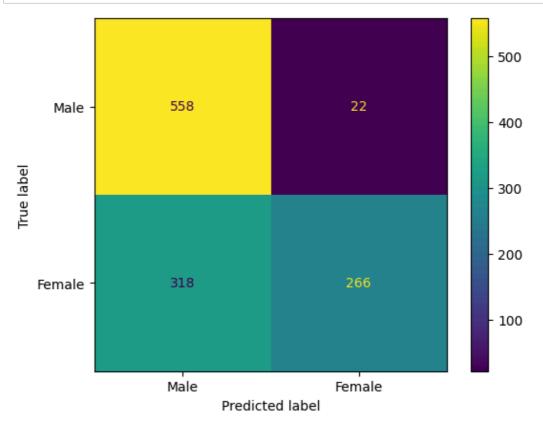
Gender Detected!

Histogram of Oriented Gradients (HoG)

```
In [20]: hog = cv2.HOGDescriptor()
```

```
In [21]: def hog_pattern_extractor(hog: cv2.HOGDescriptor, images, ext=ext, r_shape=(64, 12)
             data = []
             for img in tqdm(images):
                 img_resized = cv2.resize(img, r_shape)
                 hist = hog.compute(img_resized)
                 hist = hist.flatten()
                 data.append(hist)
             return data
In [22]: def single image pipeline hog(img, hog, male hist path, female hist path, r shape=
             img_resized = cv2.resize(img, r_shape)
             hist = hog.compute(img_resized)
             hist = hist.astype(np.float32)
             male hog hist = np.load(male hist path).astype(np.float32)
             female_hog_hist = np.load(female_hist_path).astype(np.float32)
             male distance = cv2.compareHist(hist, male hog hist, cv2.HISTCMP INTERSECT)
             female_distance = cv2.compareHist(hist, female_hog_hist, cv2.HISTCMP_INTERSECT
             # HISTCMP_INTERSECT, HISTCMP_CORREL, HISTCMP_BHATTACHARYYA, HISTCMP_HELLINGER,
             return 0 if male_distance >= female_distance else 1
In [23]: |male_histograms = hog_pattern_extractor(hog, train_male_images)
         female_histograms = hog_pattern_extractor(hog, train_female_images)
         male_hog_hist = np.mean(male_histograms, axis=0)
         female hog hist = np.mean(female histograms, axis=0)
         np.save('male hog hist.npy', male hog hist)
         np.save('female_hog_hist.npy', female_hog_hist)
         100%
                                                                                   5941/594
         1 [00:01<00:00, 4204.88it/s]
                                                                                   5810/581
         100%
         0 [00:01<00:00, 4270.13it/s]
In [24]: | actual, predicted = [], []
         for img in test_male_images:
             actual.append(0)
             predicted.append(single_image_pipeline_hog(img, hog, 'male_hog_hist.npy', 'fem
In [25]: | for img in test_female_images:
             actual.append(1)
             predicted.append(single_image_pipeline_hog(img, hog, 'male_hog_hist.npy', 'fem
In [26]: metric_report(actual, predicted)
Out[26]: (0.7079037800687286,
          0.9236111111111112,
          0.4554794520547945,
          0.6100917431192661)
```

```
In [27]: confusion_matrix = metrics.confusion_matrix(actual, predicted)
```



```
In [29]: # Asagidaki img_path degiskenine istenen goruntulerin pathi verilir ve hog ile gene
img_path = './test_images/064943.jpg.jpg'
img = cv2.imread(img_path, 0)
actual = int(os.path.basename(img_path).startswith('1'))

pred = single_image_pipeline_hog(img, hog, 'male_hog_hist.npy', 'female_hog_hist.n

if actual == pred:
    print('Gender Detected!')
```

Gender Detected!