

# EigenFaces

1. Didn't make any change in the best parameters, it returned that the best C value is 1000 in both cases.
2. `SVC(C=1000.0, cache_size=200, class_weight='balanced', coef0=0.0, decision_function_shape='ovr', degree=3, gamma=0.0001, kernel='rbf', max_iter=-1, probability=False, random_state=None, shrinking=True, tol=0.001, verbose=False).`  
*The value of C did not change.*
3. -
4. The performance decreases as the number of components increase. As the number of eigenfaces increased it will make it harder for the classifier. Since svm uses quadratic solver then it works better with smaller dataset
5. -
6. The performance decreased from 87% to 82%
7. Some of the Images have different poses than the funnelled one
8. Runtime:
  - a. cpu runtime: 115.009 seconds
  - b. gpu runtime: 91.114 seconds
  - c. tpu runtime: 116.308 seconds

## Classification of cancer gene expressions

### Score vs the Number of Components:

The classifier shower higher scores for the number of components values between 105 and 115. The PCA ideally tries to get the minimal number of components that

results in retaining a high percentage of the variance. Using a number of components equal to the number of features, provides higher score, at the cost of using more dimensions.

## One-vs-One or One-vs-All SVM:

One-Versus-All SVM was used so that the number of classifiers would be 14 instead of  $[(14 * (14-1)) / 2] = 91$  classifiers in case of One-vs-One.

## Hierarchical clustering:

The homogeneity metric score varied according linkage type of the hierarchical clustering:

1. Average linkage: 0.35
2. Ward linkage: 0.52
3. Complete Linkage: 0.43

This means that the best clusters were produced by ward linkage, however, it still did poorly in classifying the data.