



Rab Protein Classification

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Goal of our project

Classify the Rabs into their group



```
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)

from sklearn.neighbors import NeighborsClassifier
n = 10
classifier = NeighborsClassifier(n_neighbors = n, metric = "minkowski", p=1)
classifier.fit(X_train, y_train)
y_pred = classifier.predict(X_test)

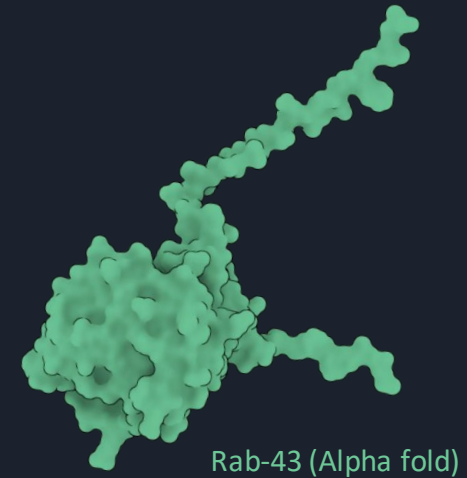
from sklearn.metrics import confusion_matrix, accuracy_score
cm = confusion_matrix(y_test, y_pred)
print("Matrice de confusion :")
print(cm)

from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix, accuracy_score

rf = RandomForestClassifier(n_estimators=100, random_state=42)
rf.fit(X_train, y_train)
y_pred = rf.predict(X_test)

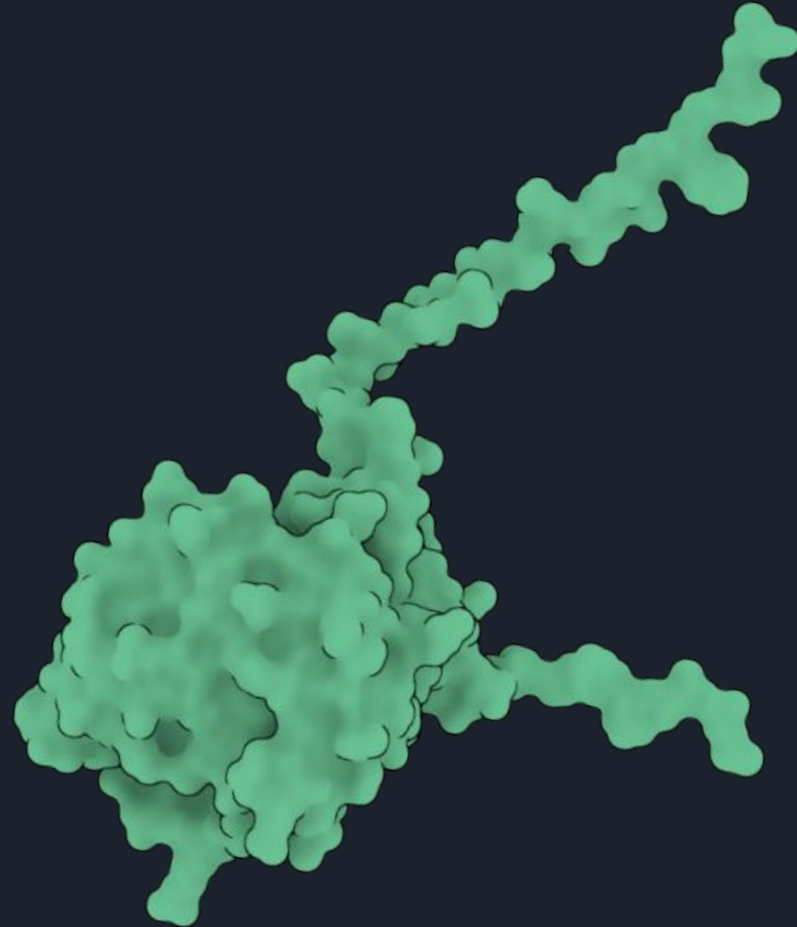
# Calculer et afficher la matrice de confusion et la précision
conf_matrix = confusion_matrix(y_test, y_pred)
accuracy = accuracy_score(y_test, y_pred)

print("Matrice de confusion :")
print(conf_matrix)
print("Précision : [accuracy]")
```





What are Rab proteins?



Rab-43 (Alpha fold)



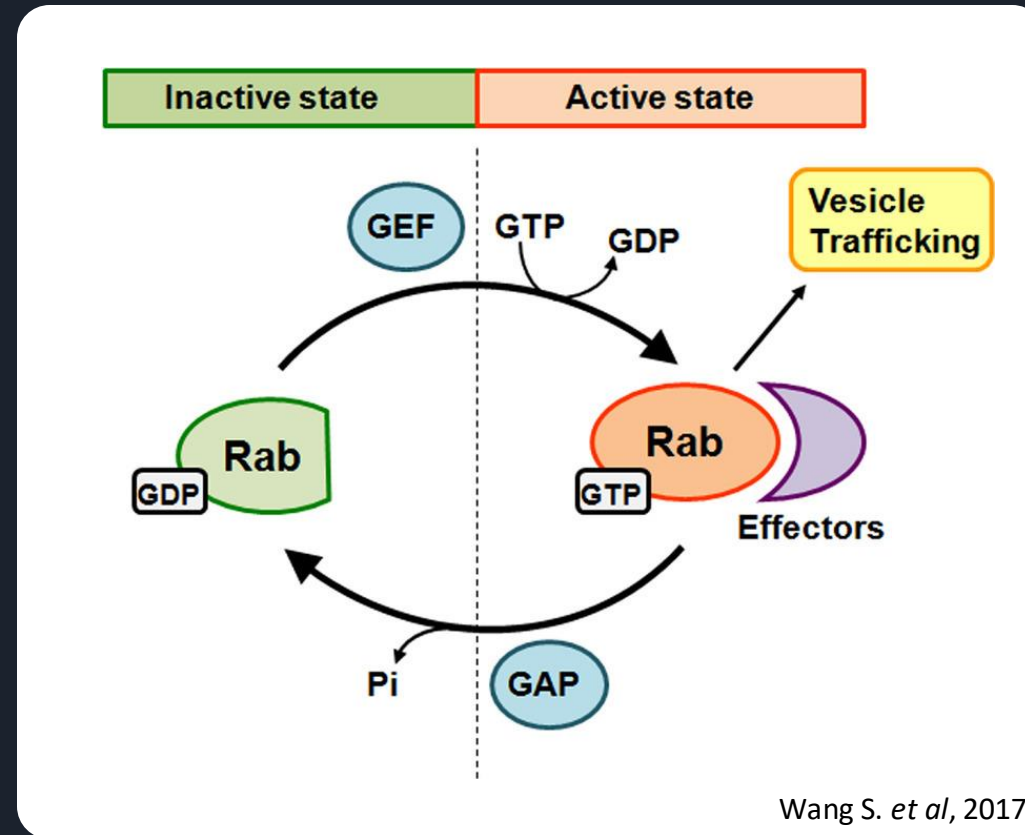
What are Rab proteins?

GTPase with functions in tethering in **vesicular trafficking**



What are Rab proteins?

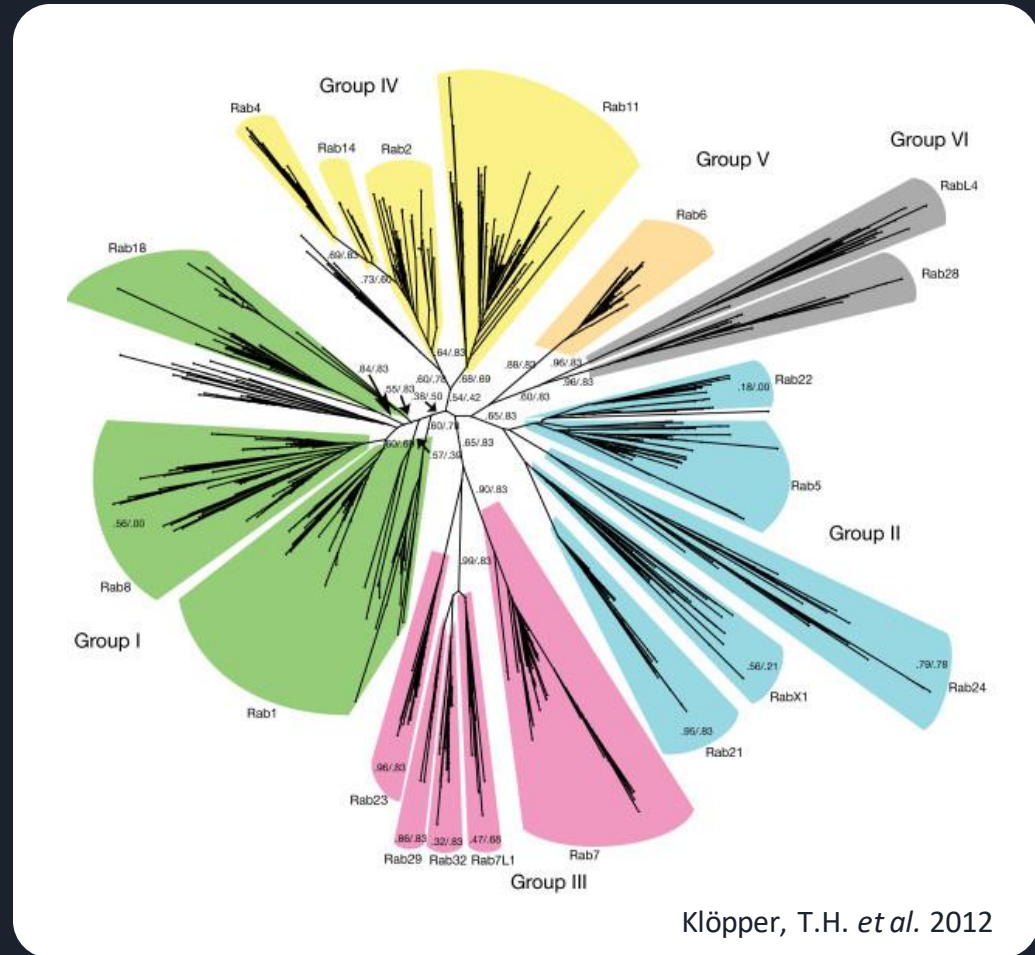
GTPase →
exchange GDP against
GTP to activate effectors





What are Rab proteins?

Large **family** of proteins





... and why study them?

Griscelli syndrome

- partial albinism
- immunological defects
- primary neurological dysfunctions

Choroideremia

- Blindness

Neurological disorders

Rab-associated
diseases

Pipeline and methods





What does our data look like?

```
>PoTr_Rab1C
MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDSYLESYISTI
GVDFKIRTVEQDGKTIKLQIWDTAGQERFRTITSSYYRGAH
GIIVVYDVTQESFNNVKQWLNEIDRYASENVNKLVLGNKC
DLTANKVVSYETAKAFADEIGIPFMETSAKNATNVEQAFMA
MAAEIKNRMASQPAMNNARPPTVQIRGQPVNQSGCCSS
>PaTe_Rab1_1
MSLQQEYDYLFKILLIGNSAVGKSSLLRFADNVFNESFLP
TIGVDFKIRTFDLNGKTVKLQIWDTAGQERFKITINSYYKG
AHGIILVYDVTDKQSFKDVENWLAEEVEKYANENVVRLVGN
KVDLESKREVTSEEGKELADSLNIRFIETSAKNSSNVEKAF
ITLANEIKAKVAKSSEAIIPVKTGPRITPDQQQNTVKDTGCC
>BrMa_Rab1
MVSINPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYI
STIGVDFKIRTIDLNGKTIKLQIWDTAGQERFRTITSSYYR
GAHGIIVVYDITDQESFNNVKQWLQEIDRYACENVNKLVLG
NKCDLIIRRAVEHSAAKEYADQLGIPFLETSAKSSTNVEQA
FLTMASEIKNRMGPIQQVGTGPSVRIGGSQPVNEKSGGCC
>CaA1_Ypt1
MNNEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTPDYISTI
GVDFKIRTIELDGKTIKLQIWDTAGQERFRTITSSYYRGAH
GIIIVYDVTQESFNNVKQWLQEIDRYATGGVMKLLVGNKA
DLSDKKIVEYTAAKEFADALDIPFLETSAKSSTNVEQAFYT
MARQIKAQMTNANAGNAANAKGKSNVNLRGESLTSNQSNS
CC
>PaTe_Rab1
MIKEYDYLFKLVIIIGNSGVGKSSLLRFADDQFSESYLTTI
GVDFRFRFLPIDGKNVKLQIWDTAGQERFRTITSAYYKGD
GIVMVYDVTQGSFDDIDKFWLHEVESYGEKNVQLLIIGNK
NDLDEQKQVETSKAEYCKSHNMLFMECSAKTADHVNN AFL
ELSRKLMAKK DASQP P K T T N T T S N A S Q Q S R G Q T N T N T Q Q
S K Q L S A G N T N Q K K Q K D G G C C
```

Number of Rab proteins per group



Unequal distribution



What did we do?

Protein sequences



Features



Machine Learning

```
>RAB 1
KVQKLSKTVIEVASLQNELATHL
HVQTQININVLDD
>RAB 2
KAEALRRTAVDIASLQSELATHL
QVQTQININ
>RAB 3
EVRQIEGRVVEISRLQEIFTEKVL
QQEAEIDSIHQ
```

Seq	Feat1	Feat2	Feat3
RAB 1	0.87	0.65	0.23
RAB 2	0.03	0.12	0.54
RAB 3	0.34	0.65	0.49

```
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train = sc.fit_transform(X_train)
X_test = sc.transform(X_test)

from sklearn.neighbors import KNeighborsClassifier
k = 11
classifier = KNeighborsClassifier(n_neighbors = k, metric = "minkowski", p=1)
classifier.fit(X_train, y_train)
y_pred = classifier.predict(X_test)

from sklearn.metrics import confusion_matrix, accuracy_score
print(confusion_matrix(y_test, y_pred))
print(accuracy_score(y_test, y_pred))

from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import confusion_matrix, accuracy_score

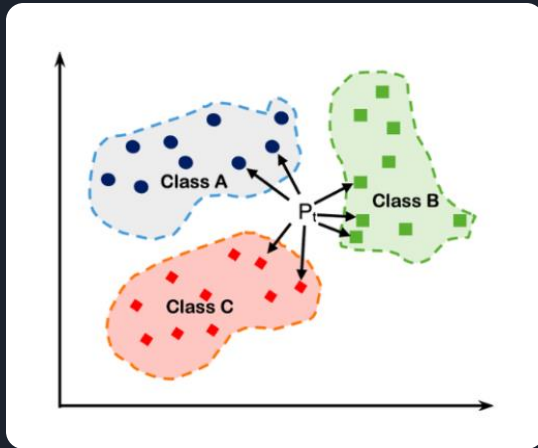
rf = RandomForestClassifier(n_estimators=100, random_state=42)
rf.fit(X_train, y_train)
y_pred = rf.predict(X_test)

# Calculer et afficher la matrice de confusion et la précision
conf_matrix = confusion_matrix(y_test, y_pred)
accuracy = accuracy_score(y_test, y_pred)

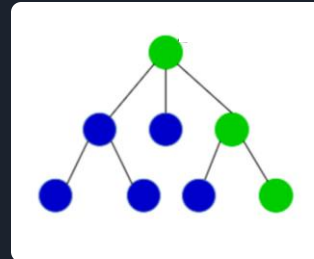
print("Matrice de confusion :\n", conf_matrix)
print("Precision : {accuracy}")
```



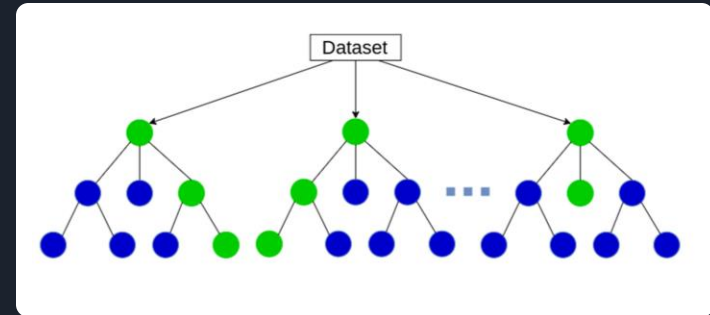
Methods used



KNN



Decision tree



Random forest

First feature: GAAC

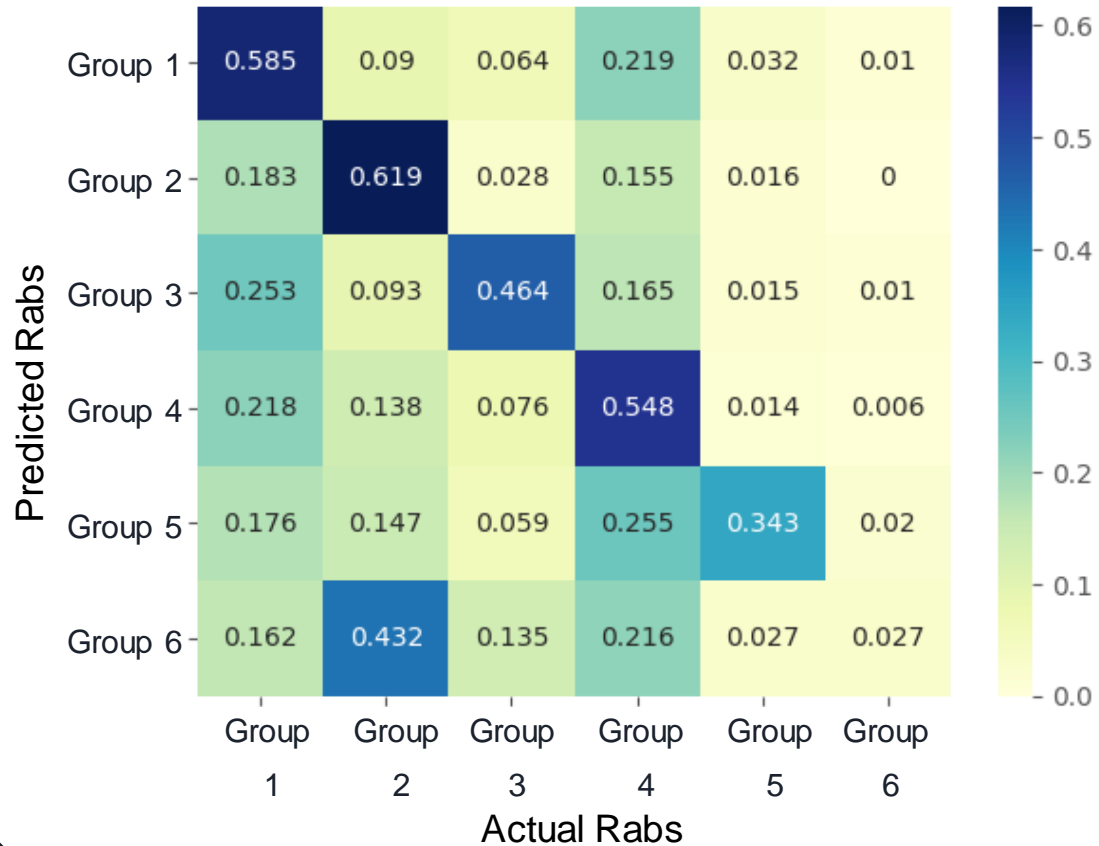
- GAAC = grouped amino acid composition
- **Physico-chemical** properties

	Aliphatic	Aromatic	Positively charged	Negatively charged	Uncharged
rab1	0,2	0,3	0,1	0,3	0,1
rab2	0,3	0,1	0,3	0,1	0,2
rab3	0,1	0,2	0,3	0,3	0,1



GAAC predictor using KNN

Confusion matrix from KNN model with $k = 5$ on Rab extracted GAAC features



Accuracy: 53%
Precision: 0.523
Recall: 0.526
F1-Score: 0.519

Second feature: CKSAAP

- CKSAAP = Composition of **k-spaced** amino acid pairs

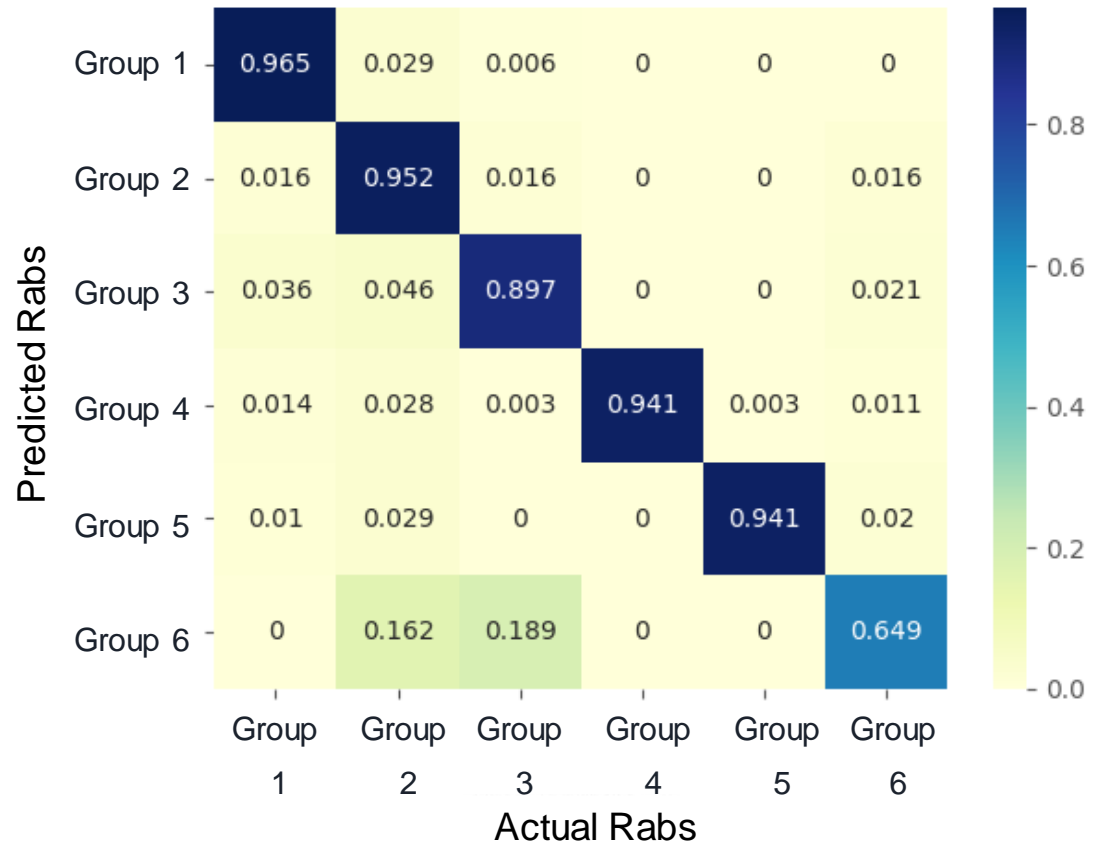
k	AA	LT
k=1	AxA	LxT
k=3	AxxxA	LxxxT
k=5	AxxxxxA	LxxxxxT

Protein sequence : DS**AWA**ELSGCIKT



CKSAAP predictor using **KNN**

Confusion matrix from KNN model with $k = 5$ on Rab extracted CKSAAP features

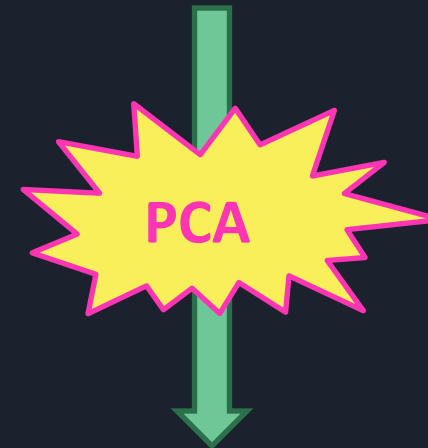


Accuracy: 94.7%

Precision: 0.950

Recall: 0.947

F1-Score: 0.945



Accuracy: 93.4%

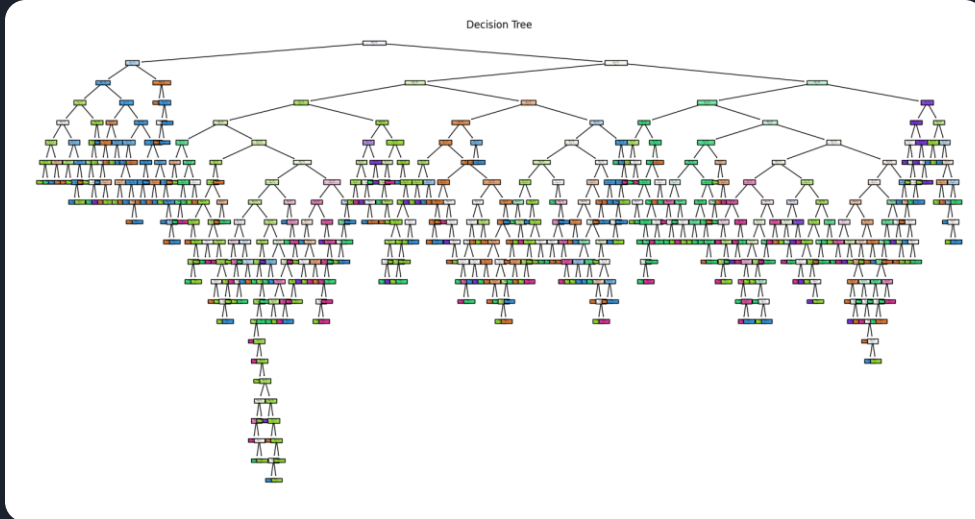
Precision: 0.936

Recall: 0.934

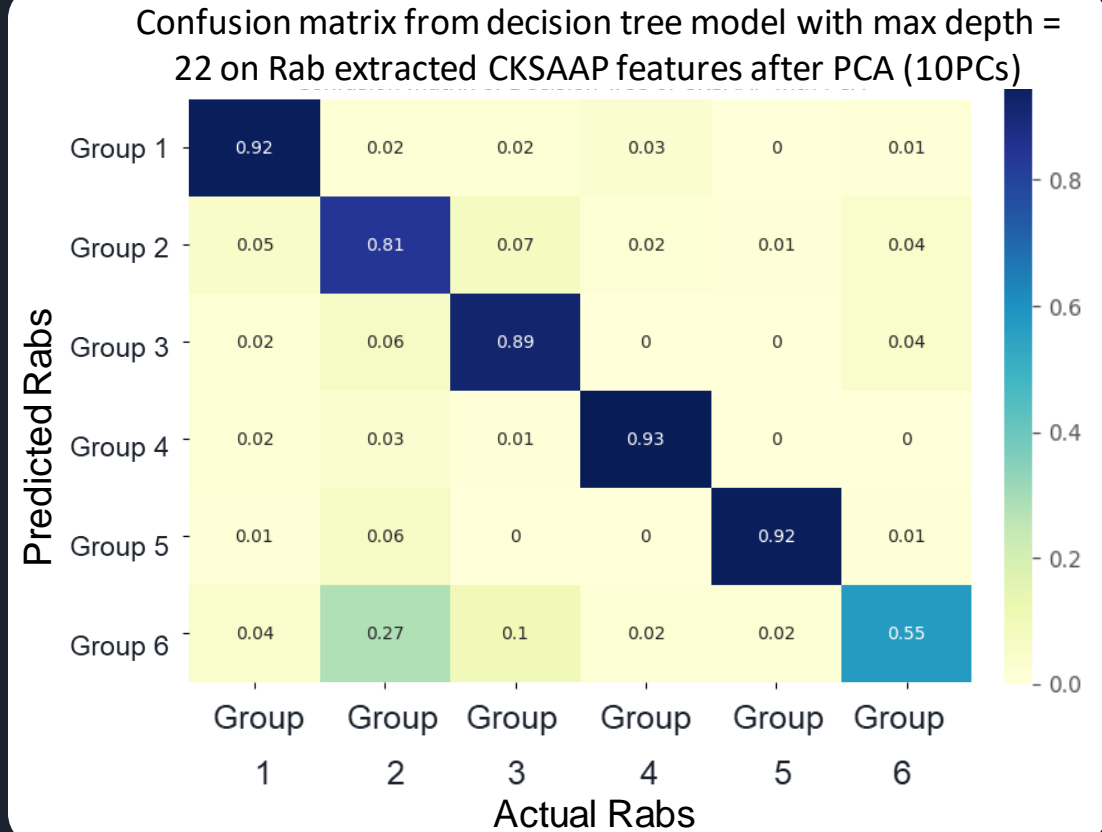
F1-Score: 0.934



CKSAAP predictor using **decision tree**



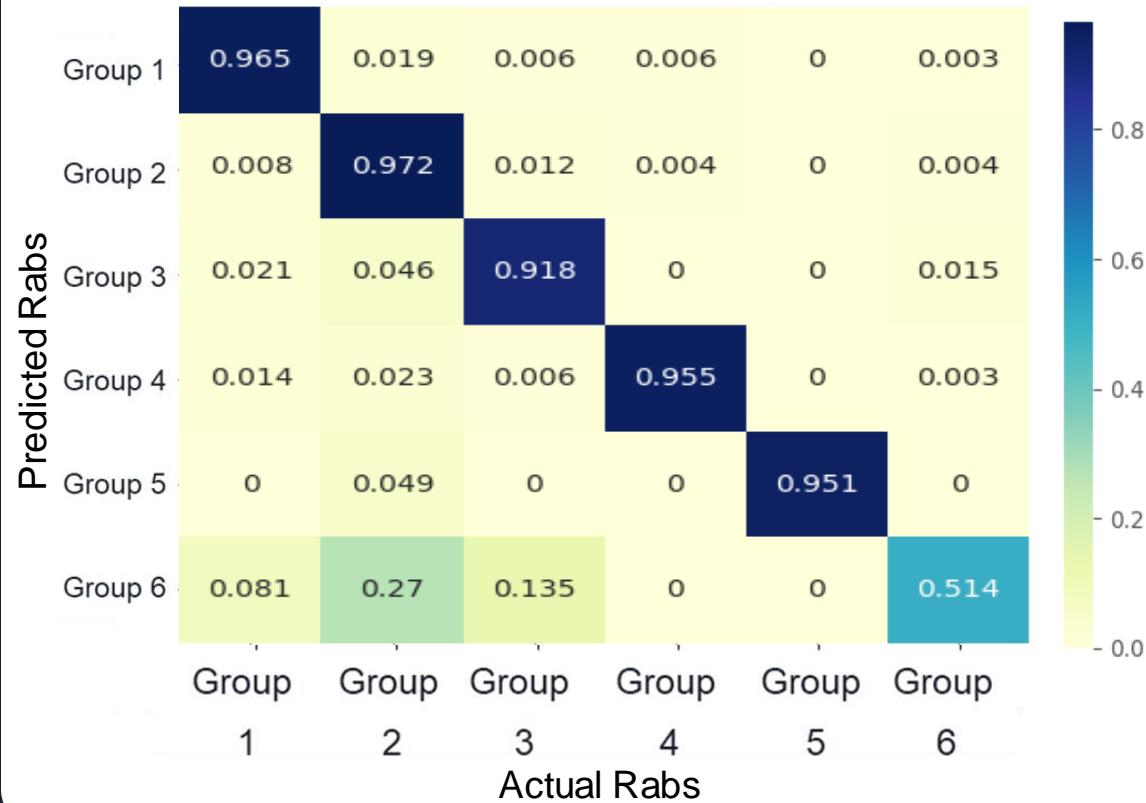
Accuracy: 89,28%
Precision: 0.839
Recall: 0.835
F-score: 0.837





CKSAAP predictor using random forest

Confusion matrix from random forest model with max on Rab extracted CKSAAP features after PCA (10PCs)



Accuracy : 94.2%

Precision : 0.942

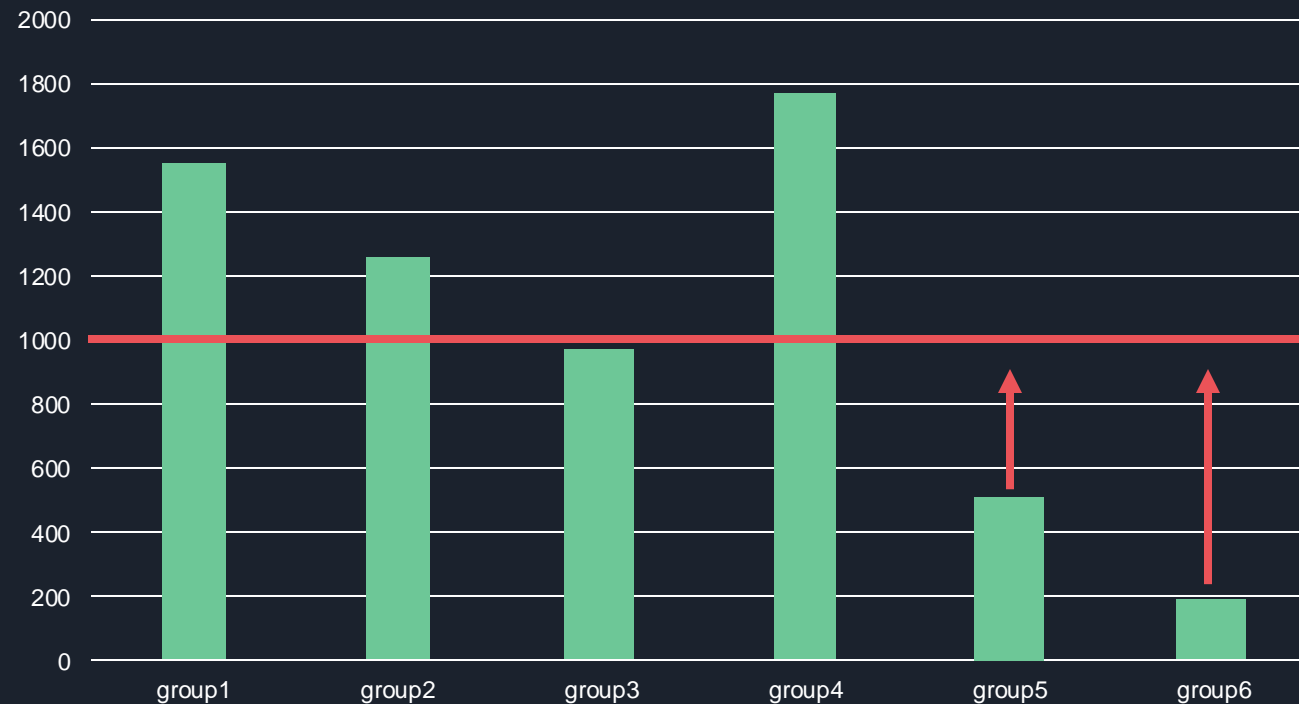
Recall : 0.941

F-score : 0.941



What is going on with group 6?

Number of Rab proteins per group



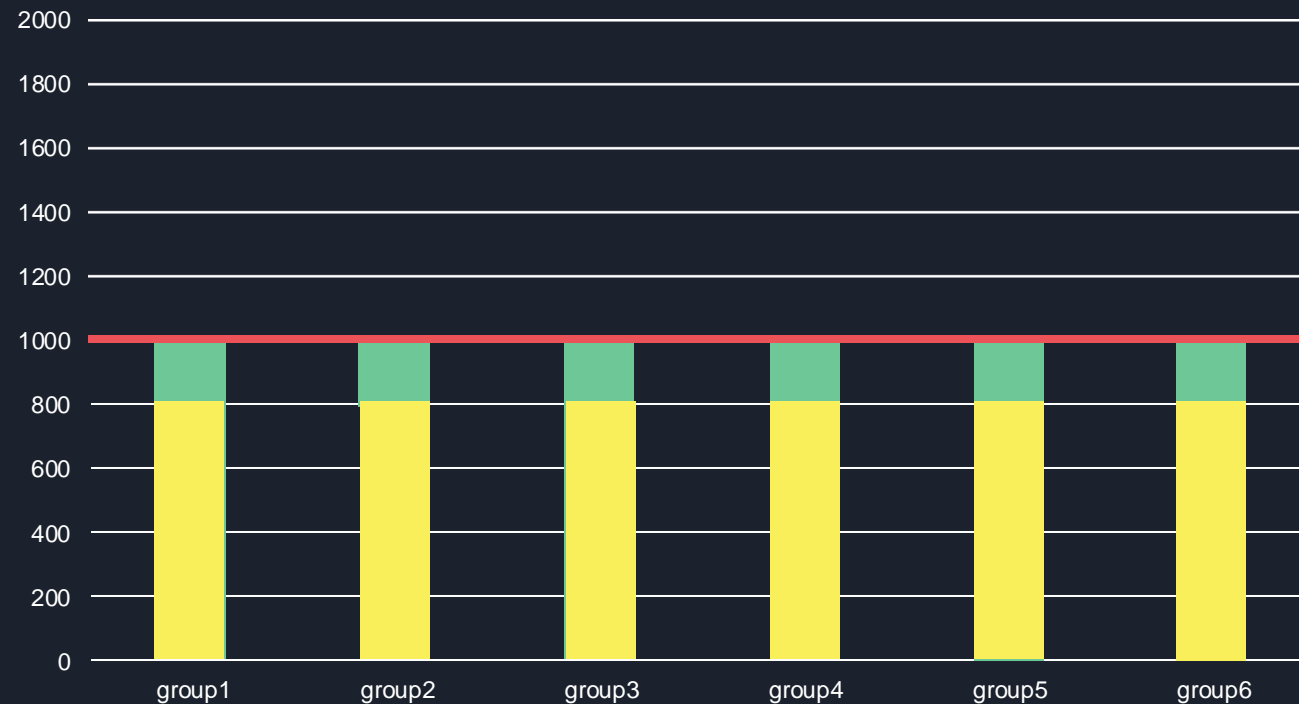
Oversampling:
Sample with replacement





What is going on with group 6?

Number of Rab proteins per group



Testing set

Training set

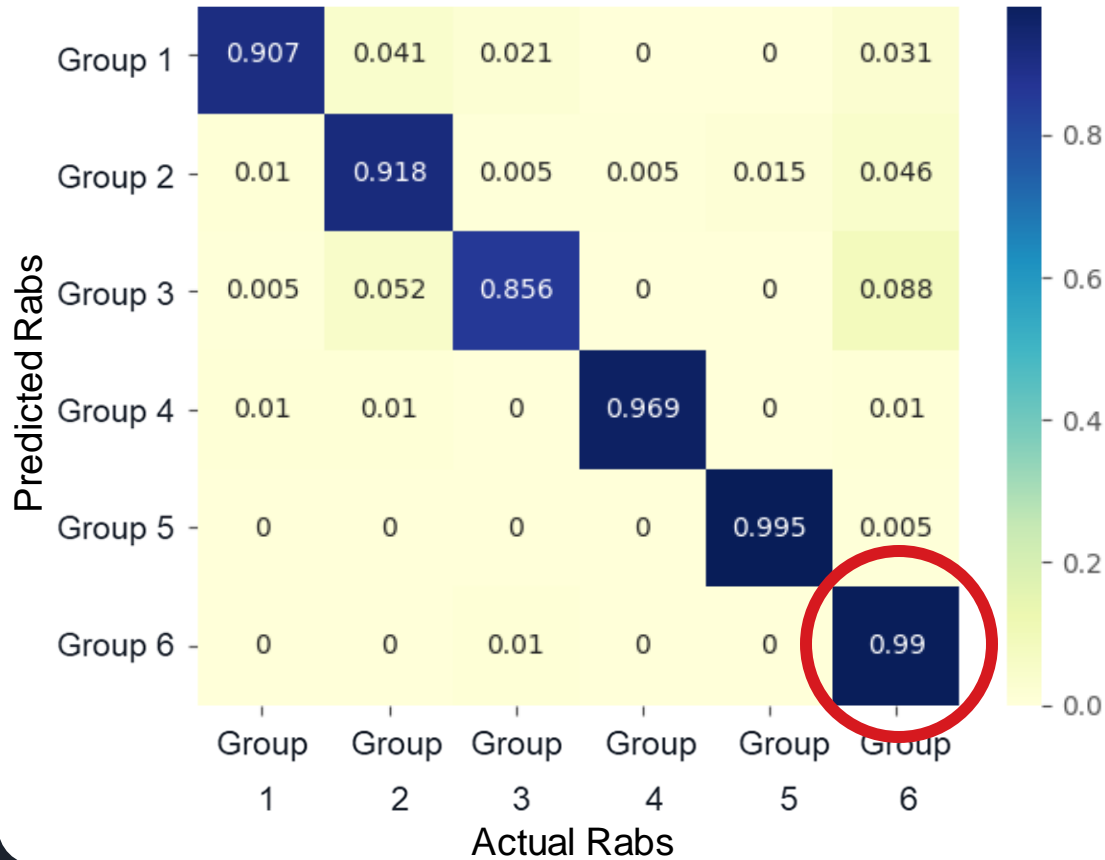
Oversampling:
Sample with replacement





CKSAAP with ~~resampling~~ *overfitting*

Confusion matrix from KNN model with $k = 5$ on Rab extracted CKSAAP after PCA (10PCs) with oversampling

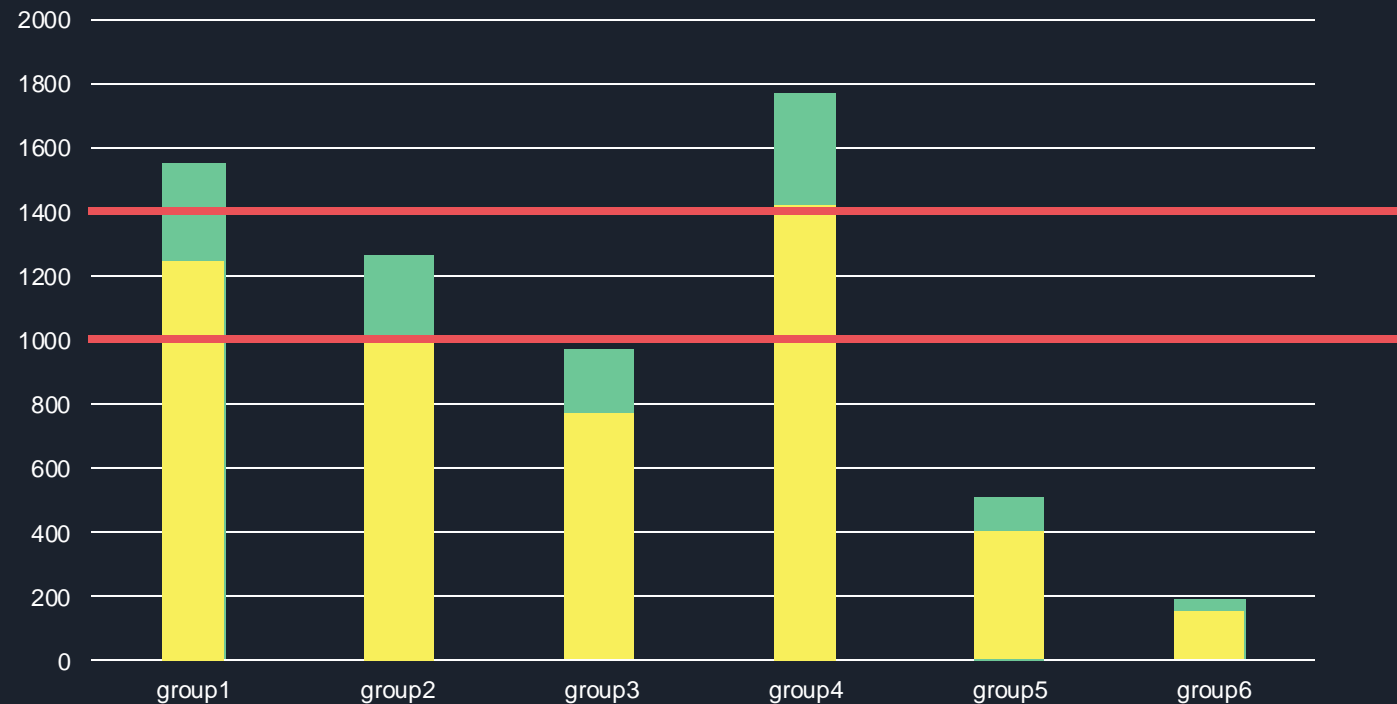




Improving sampling

Number of Rab proteins per group

Testing set
Training set

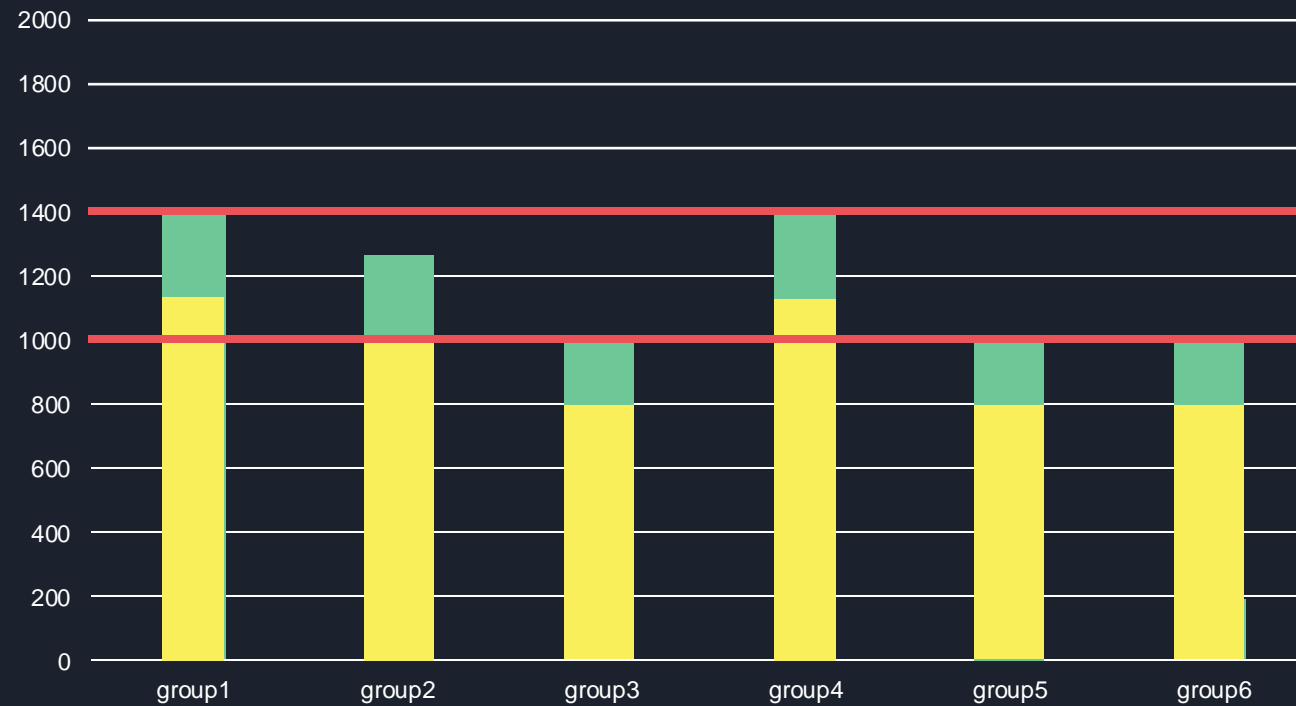




Improving sampling

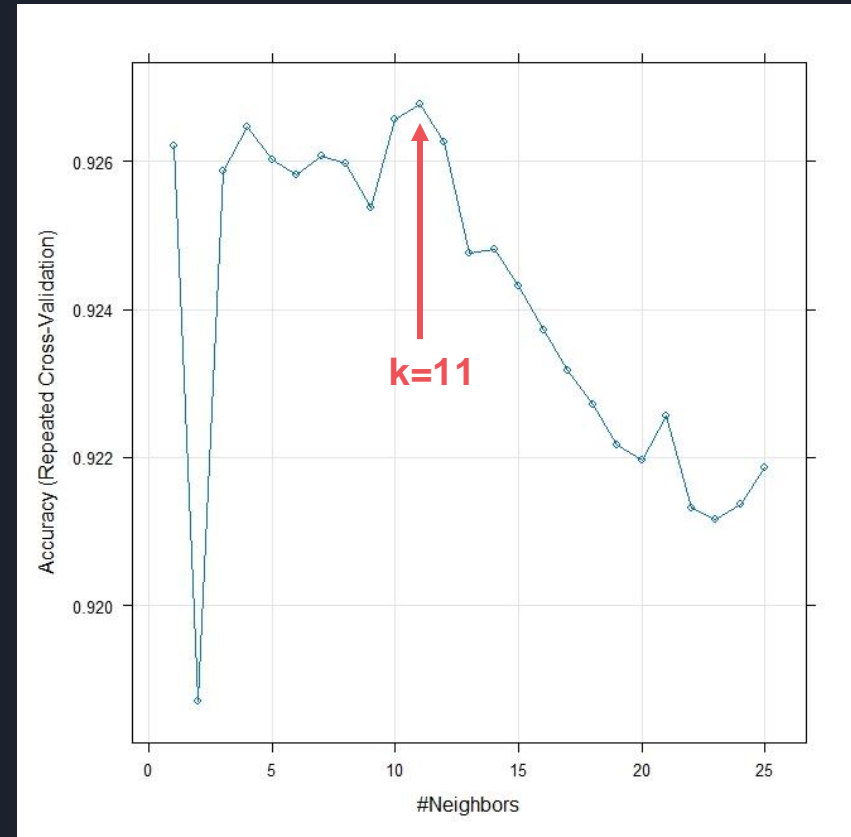
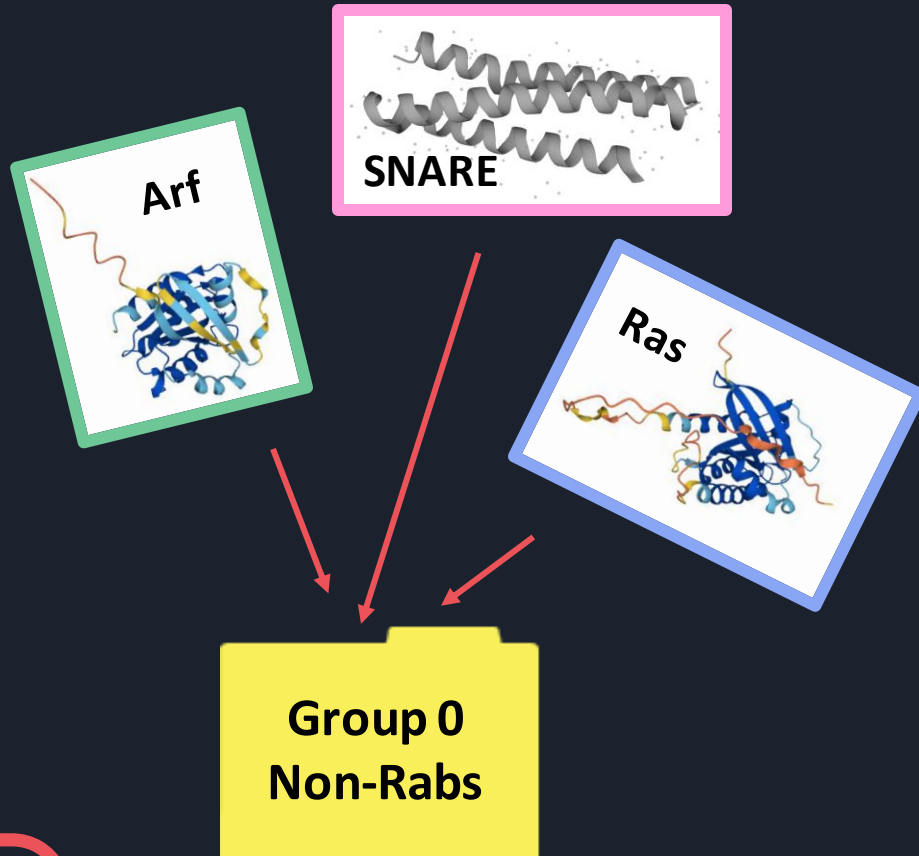
Number of Rab proteins per group

Testing set
Training set





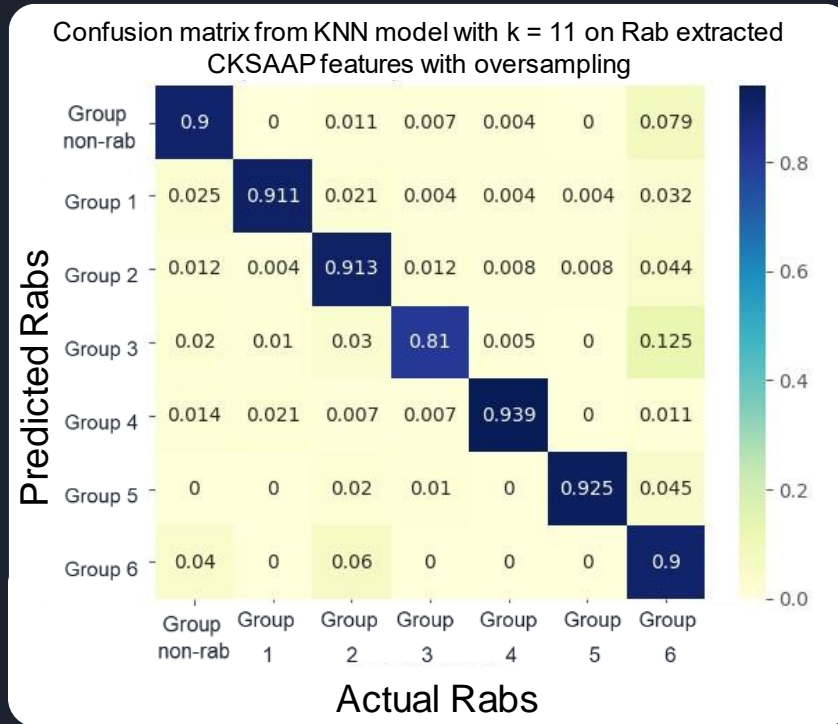
Improving the model





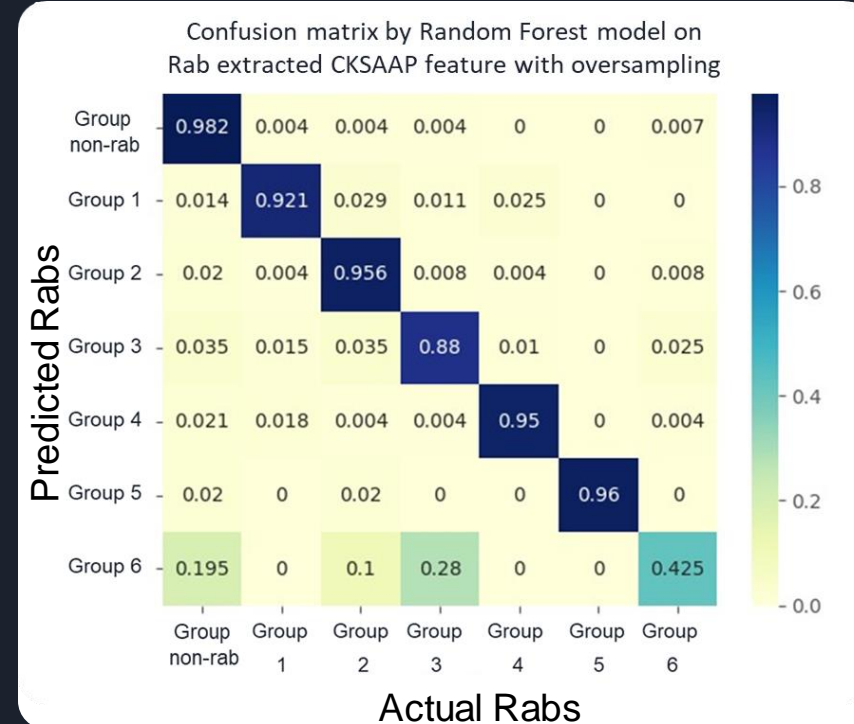
CKSAAP predictor with improved model

KNN



Accuracy: 90.2% Recall: 0.902
Precision: 0.912 F1-Score: 0.905

Random forest



Accuracy: 88.2% Recall: 0.882
Precision: 0.891 F1-Score: 0.874

Third feature: CTD

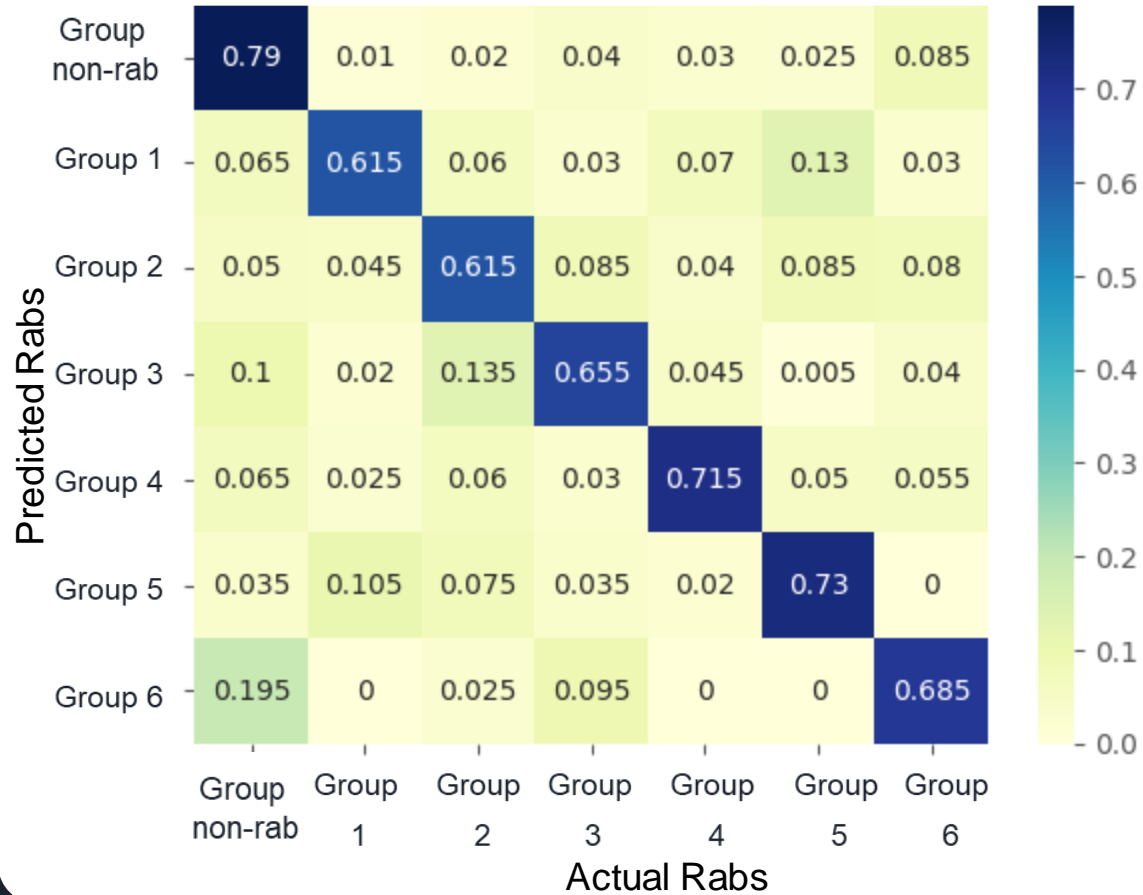
- **Physico-chemical** properties (CTD= Conjoint Triad Descriptors)

	Hydro-phobicity	Polarity	Van der Waals volume	Charge	...
rab1	0,212	0,66454	0,117	0,5888	
rab2	0,42588	0,1588	0,3665	0,05	
rab3	0,61	0,258	0,557	0,255	



CTD with KNN

Confusion matrix from KNN model with $k = 11$ on Rab extracted CTD after PCA (10PCs) feature with oversampling



Accuracy: 69%

Precision: 0.692

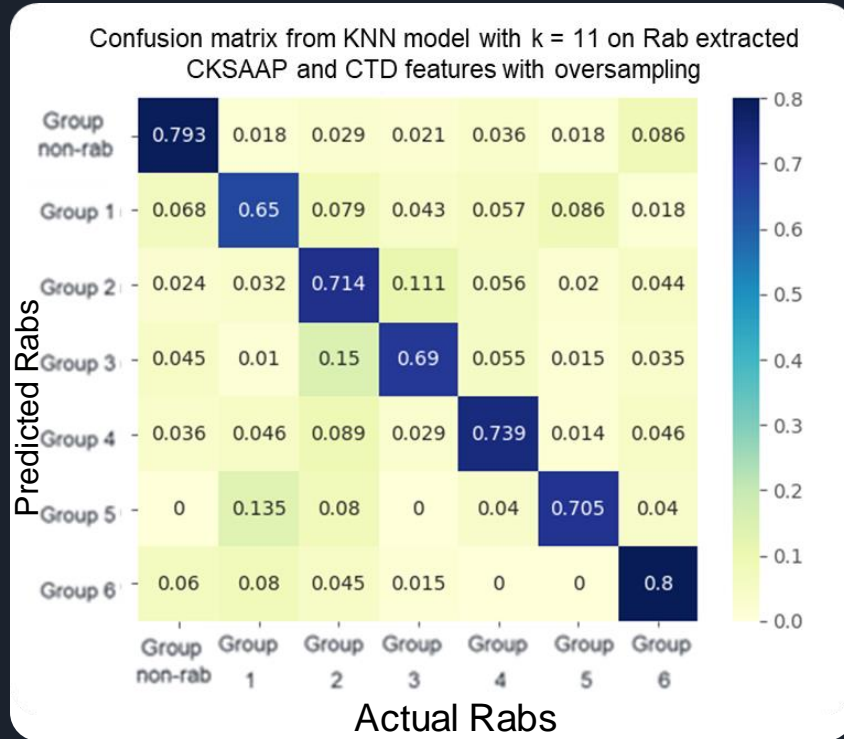
Recall: 0.686

F1-Score: 0.686



CKSAAP and CTD predictors combined

KNN



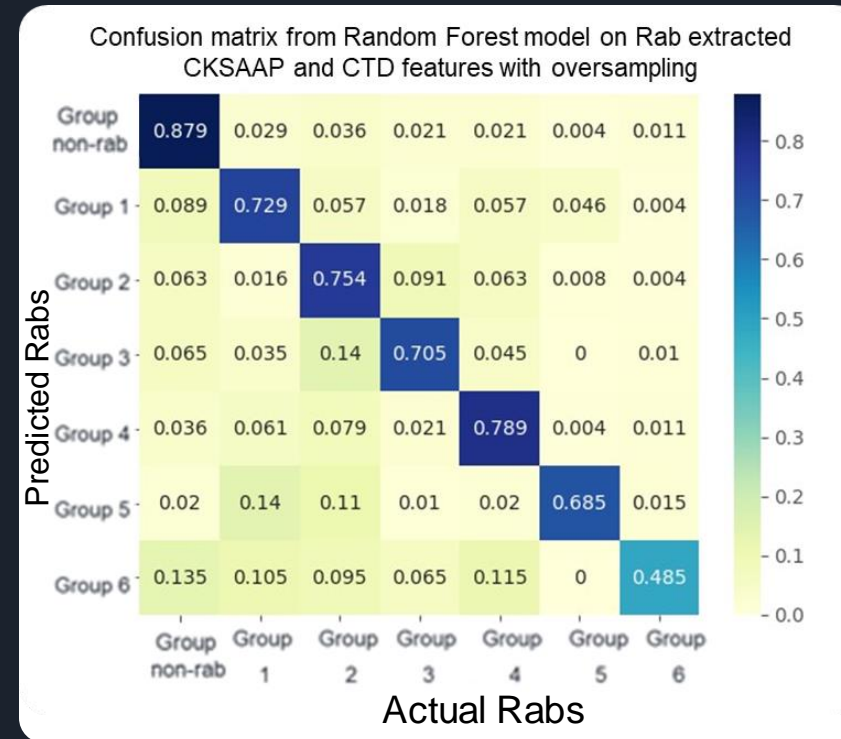
Accuracy: 73%

Precision: 0.731

Recall: 0.727

F1-Score: 0.727

Random forest



Accuracy: 73%

Precision: 0.747

Recall: 0.730

F1-Score: 0.728



Fourth feature: KSCT

- **Physico-chemical** properties (KSCT= K spaced conjoint triad)

	Hydro-phobicity	Polarity	Van der Waals volume	Charge	...
rab1	0,212	0,66454	0,11	0,5888	
rab2	0,02588	0,0588	0,3665	0,005	
rab3	0,6	0,258	0,557	0,255	

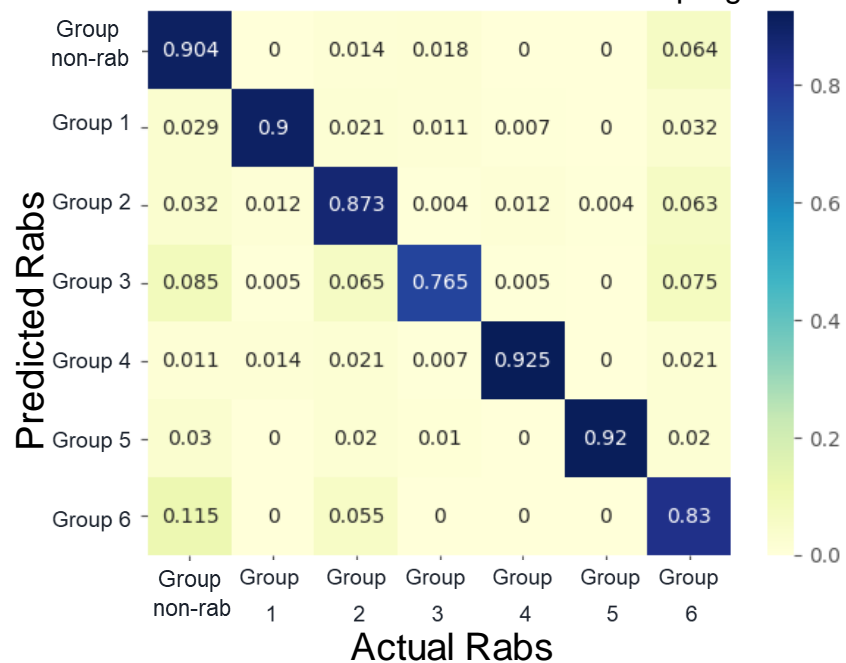




KSCT predictor

KNN

Confusion matrix from KNN model with $k = 11$ on Rab extracted KSCT feature with oversampling



Accuracy: 87.9%

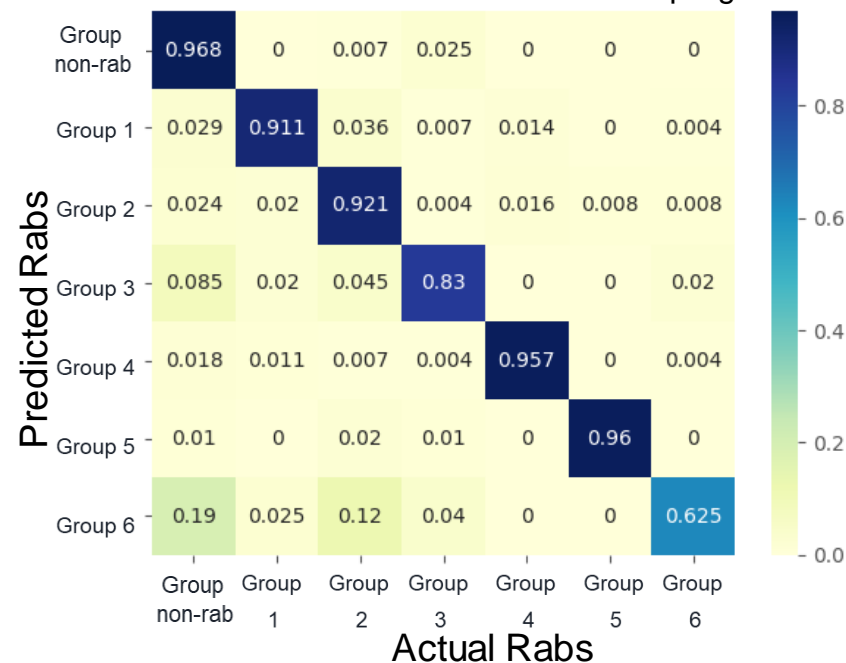
Precision: 0.888

Recall: 0.879

F1-Score: 0.881

Random forest

Confusion matrix from Random Forest model on Rab extracted KSCT feature with oversampling



Accuracy: 89.2%

Precision: 0.900

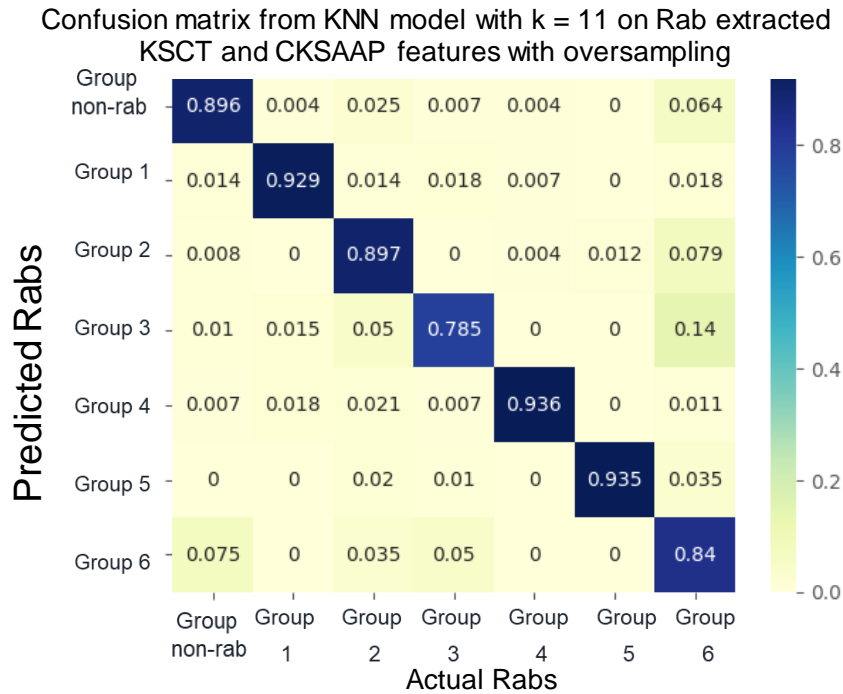
Recall: 0.892

F1-Score: 0.890



KSCT and CKSAAP predictors combined

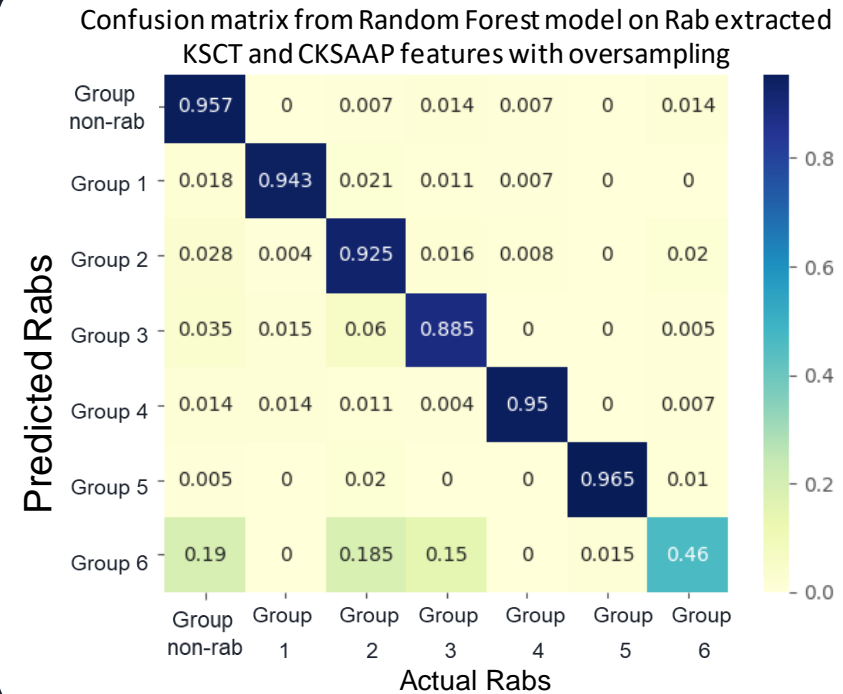
KNN



Accuracy: 89.3%
Precision: 0.901

Recall: 0.893
F1-Score: 0.895

Random forest

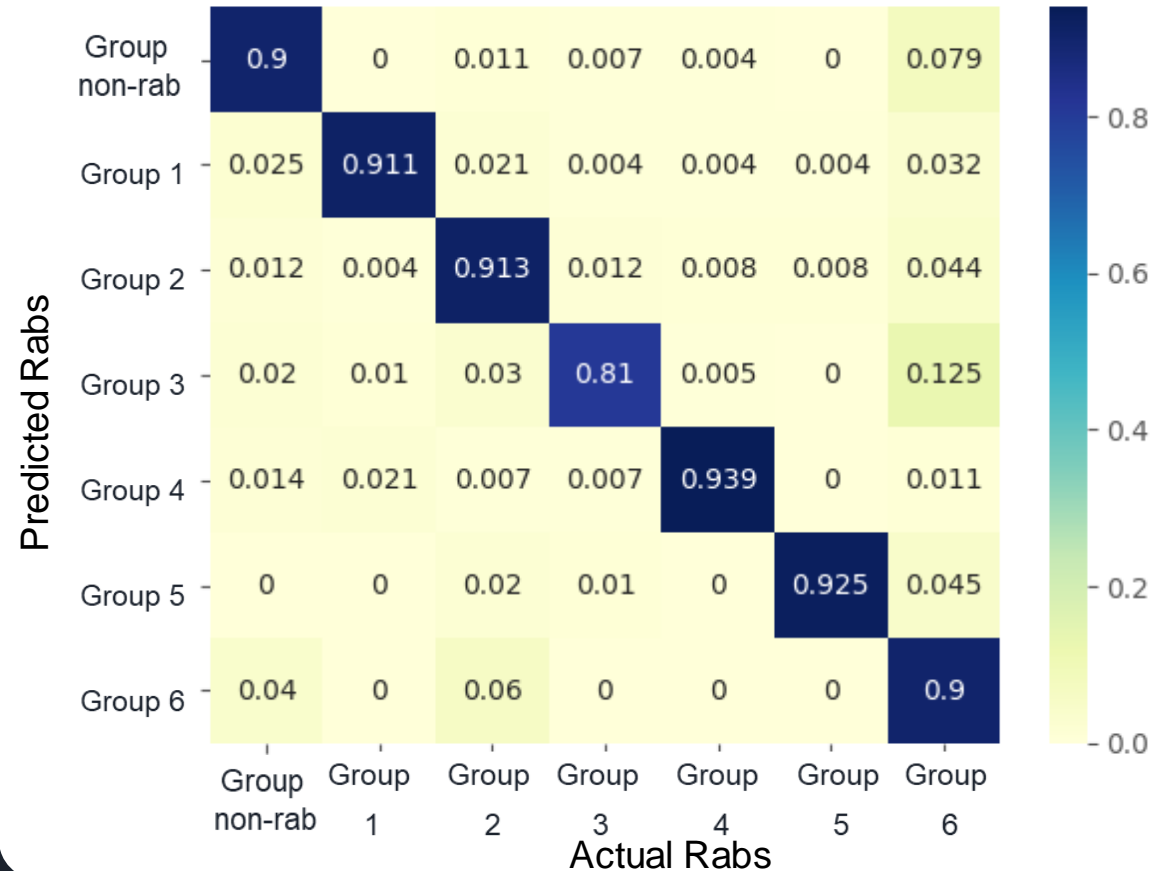


Accuracy: 88.2%
Precision: 0.888

Recall: 0.882
F1-Score: 0.876

Best of the best: CKSAAP with oversampling

Confusion matrix from KNN model with k = 11 on Rab extracted CKSAAP features with oversampling



Accuracy: 90.2%

Precision: 0.912

Recall: 0.902

F1-Score: 0.905

Take home messages

Best model: KNN with CKSAAP feature

Combos of features do not add to the model



Challenges



- **Unequal distribution** in classes
- **Unintuitive results**: best model is not a combination (?)
- **Lots of testing** and probing, limited time
- **Google colab**... not so easy to colab
- **Different kind of coding** but lots of help from our mentor and forums/Chat GPT





Feedback

- **Highly concentrated working period** blur lines between work and personal time
- **Grade disproportionately based on presentation**, rather than work done
- **Little time** between intermediate and final presentation but **helpful and inspiring**
- Very **helpful mentor**
- **Apply theory** seen in class on an interesting project
- Learned a lot about **coding and problem solving**



Thanks!

Questions?

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