Theoretical and practical metagenomic approaches to viral discovery

Practical Session: Random Forest Classifier and viral application

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Discussion

How to: Implement the Random Forest Classifier



```
from sklearn.ensemble import RandomForestClassifier
from sklearn import datasets
# we know this already...
```

with open ('virus.csv', 'r') as inputStream:



. . .

RANDOM FOREST

```
from sklearn.ensemble import RandomForestClassifier
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# we know this already...
with open('virus.csv', 'r') as inputStream:
...

# create the classifier object
# n_estimators: number of trees for the forest
# max_depth: maximum depth of one tree
for E RandomForestClassifier(n_estimators=100, max_depth=2)
from sklearn.ensemble import RandomForestClassifier(n_estimators=100, max_depth=2)
from sklearn.ensemble import RandomForestClassifier
```



Training our model to identify viral elements



WE WANT TO IDENTIFY VIRAL PRE-MIRNAS

Our task:

In the mirbase database are currently around 320 viral pre-miRNAs. We want to use them in to train a machine learning model that can distinguish between viral pre-miRNAs and other sequences.



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- a file with our negative data
- some utilities we need (reading the data, ...)



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- ► Features?



EXERCISE



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Your task

Have a look at the rf_classifier.py script. Try to understand as much of it as possible.

Then, create a Random Forest Classifier and train the model with the data — precursor.fa and negative_set.fa



Let us discuss our results



```
1 # first we need to translate the sequences into something
2 # that can be used by the machine learning algorithm:
```



Discussion

```
# first we need to translate the sequences into something
# that can be used by the machine learning algorithm:

import numpy as np
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4  import numpy as np
5  # read in the data
7  trainingsData = read_training_set(positive, negative)
```



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that can be used by the machine learning algorithm:

import numpy as np

# read in the data
trainingsData = read_training_set(positive, negative)

# transform the sequence into features
trainingSet, targets = transform data(trainingsData)
```



```
def transform_data(data):
    # this will be our data structure
    trainingSet = []
    targets = []
```



FUNCTION DEFINITIONS

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def transform_data(data):
    # this will be our data structure
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    targets = []

# iterate over all sequences
for dataPoint in data:
# sequence = dataPoint[0]
# group = dataPoint[1]
# extract the features
length = len(sequence)
...
```



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          sequence = dataPoint[0]
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          # extract the features
          length = len(sequence)
11
12
          . . .
13
14
          # store everything in our array
          vector = [length, ...]
15
          trainingSet.append(vector)
16
          targets.append(group)
17
18
```



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VIRUS BIOINFORMATICS

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          trainingSet.append(vector)
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          targets.append(group)
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19
        # return the data within a numpy array
20
        return(np.array(trainingSet, dtype=float), targets)
```

PERFORMANCE OF OUR MODEL

```
# we know this already. we split the data into training and test sets
   data training, data test, target training, target test =
        train test split(trainingSet, targets, test size=0.2)
     creating the random forest classifier and already fitting the training data
   rfc = RandomForestClassifier(n estimators=100, max depth=2).
         fit(data_training, target_training)
     prediction of the test set
   prediction = rfc.predict(data_test)
10
     output the confusion matrix to evaluate the model
   print()
11
   print(metrics.confusion matrix(target test, prediction))
12
   print (metrics.accuracy_score(target_test, prediction))
13
```



COFFEE BREAK



