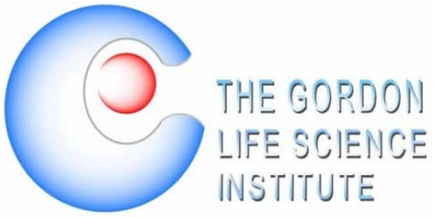
Pse-in-One 2.0: a web server for generating comprehensive modes of pseudo components of DNA, RNA, and protein sequences

Manual of stand-alone program of Pse-in-One-Analysis

2017-01-08

Home-page: http://bioinformatics.hitsz.edu.cn/Pse-in-One2.0/



Contents

1. Introduction

The **Pse-in-One 2.0** web server is an update version of **Pse-in-One** (1). **Pse-in-One 2.0** is able to generate totally 51 different modes of pseudo components for DNA, RNA, and protein sequences, including 20 modes for DNA sequences (**Table 1**), 14 modes for RNA sequences (**Table 2**), and 17 modes for protein sequences (**Table 3**). Compared with the old one, a total of 23 new pseudo component modes were added. In order to handle large dataset, the stand-alone program of **Pse-in-One 2.0** is given. Compared with the old version, a new facility called **Pse-in-One-Analysis** has been added, by which all the tedious jobs in developing a predictor, such as selecting optimal features and parameters as well as evaluating anticipated prediction quality, can be automatically fulfilled by the computer. Besides, to make the program lightweight and easy to use, 16 of the 23 newly-added modes were added to the standalone program. More details will be introduced in the following parts of this manual.

2. Installation

The **Pse-in-One 2.0** package can be run on Linux (64-bit) and Windows (64-bit) operating system. The full package and documents of **Pse-in-One 2.0** are available at http://bioinformatics.hitsz.edu.cn/Pse-in-One2.0/download. Before using **Pse-in-One 2.0**, the Python software should be first installed and configured. Python 2.7 64-bit is recommended, which can be downloaded from https://www.python.org.

After Python installed, the Python package Numpy (2) should be downloaded and installed from here: http://www.numpy.org/, or use the following command if Internet is accessible:
> pip install numpy

For Windows operating system, the Windows 7 or later versions are supported. The next step is the installation and configuration of LIBSVM (3). Extract the package to a directory. After un-zip the downloaded **Pse-in-One 2.0** package, make sure that the "libsvm.dll" is available in the directory "…\libsvm\windows"

For Linux operating system, the LIBSVM should be configured firstly. Un-zip the Pse-Analysis package to a folder, for example, "~/usr". Navigate to "~/usr/Pse-in-One 2.0/libsvm" directory, and type the command:
> make

After executing successfully, then navigate to "~/usr/ Pse-in-One 2.0/libsvm/python" directory, and type the command:
> make

If gnuplot has not been installed, use the following command lines to install gnuplot:
> sudo apt-get install gnuplot

Now, **Pse-in-One 2.0** is ready to use.

3. Function description

3.1 Directory structure

The main directory contains several Python files and folders. “nac.py”, “acc.py”, “pse.py” and “sc.py” are four executive Python scripts used for generating feature vectors based on the input sequence files and the selected feature extraction methods. “train.py” and “predict.py” are two executive scripts used for doing the analysis. The details of their functions will be introduced in the following sections. “const.py” contains the constants used in the scripts. “util.py” provides the useful functions used in the scripts and “util_sc.py” provides some specific functions used for “sc.py”. “libsvm” folder contains the LIBSVM package. The tool for drawing ROC curve is in the “gnuplot” folder. “docs” folder contains the related documents of Pse-in-One 2.0. In “data” folder, there are four subfolders: “example” folder contains the dataset files used in the example; “final_results” folder is used for storing the generated model file while the “gen_files” folder is used for storing the generated data files in the parameter selection process. The other files in the “data” folder are used for feature extraction methods. Modifications of these files are not suggested.

3.2 Feature extraction

3.2.1 Scripts

“nac.py”, “acc.py”, “pse.py” and “sc.py” are four executive Python scripts used for generating feature vectors based on the input sequence files and the selected feature extraction methods.
The “nac.py” is used for calculating the modes in the category nucleic acid composition or amino acid composition; the “acc.py” is used for calculating the modes in autocorrelation category. The “pse.py” is used for calculating the modes in the category pseudo nucleotide composition or pseudo amino acid composition. The “sc.py” is used for calculating the modes in predicted structure composition category.

3.2.2 Input and output

The input file for “nac.py”, “acc.py”, “pse.py” should be in a valid FASTA format that consists of a single initial line beginning with a greater-than symbol (“>”) in the first column, followed by lines of sequence data. The words right after the “>” symbol in the single initial line are optional and only used for the purpose of identification and description.
For “sc.py”, the input file should be in a valid FASTA format with the secondary structure as follows:

```
>example
GCAUCCGGGUUGAGGUAGUAGGUUGUAUGGUUUAGAGUUACACCCUGGG
AGUUAACUGUACAACCUUCUAGCUUUCCUUGGAGC
((.((((((..(((.(((.((((((((((((((..((.(..((...)).)..).)))))))))))))).))).)))..)))))))) (-31.60)
```

The output file formats support three choices that are suitable for downstream computational analyses, such as machine learning. The first and the default choice is the tab format. In this format, all data is separated by TABs. The second one is the LIBSVM’s sparse data format. For this format, each line contains an instance and is ended by a '\n' character, like <label> <index1>:<value1> <index2>:<value2> ... . The <label> is a category label of the sequence. The pair <index>:<value> gives a feature

(attribute) value: <index> is an integer starting from 1 and <value> is a real number. The third output format is the csv format. This format is similar to the tab format. The only difference is the separation characters between data are commas.

3.2.3 Physicochemical Properties Selection

The Physicochemical Properties Selection file is a text file that contains a list of property names used for generating the modes in categories: autocorrelation, pseudo nucleotide composition/ pseudo amino acid composition. For example, if you want to use the "Rise", "Tilt" and "Shift" of DNA dinucleotide for calculating, the Physicochemical Properties Selection file should be written as follows:

```
Rise
Tilt
Shift
```

After saving this file as "propChosen.txt" and specifying it using the command "-i propChosen.txt", or just "I propChosen.txt", the above three properties will be used in calculations. Meanwhile, you can also use the command "-a True" to select all the built-in physicochemical properties for the corresponding sequence type, which can be selected by using parameter DNA, RNA or PROTEIN.
The complete lists of physicochemical properties for DNA, RNA and protein sequences used in the stand-alone program are provided in **Table 4-12**.

3.2.4 User-defined Physicochemical Properties

In the user-defined physicochemical index files, each index should be represented in three lines. The first line must start with a greater-than symbol (">") in the first column. The words right after the ">" symbol in the single initial line are optional and only used for the purpose of identification and description of the index. The second line lists the names of the sequence compositions (i.e. amino acids, nucleotides, dinucleotides, or trinucleotides, etc), which should be sorted in the alphabet order, such as 'A' 'C' ... 'AA' 'AC'. All the elements in this line should be separated by TAB. The corresponding values of these sequence compositions are listed in the third line, which are separated by TAB.
For example, if you defined a physicochemical property "user_property", the user-defined physicochemical index file should be written as follows:

```
> user_property
A     C     …   AA AC …
0.21        0.12        …  0.37       0.15       …
```

After saving this file as "user_defined.txt" and specifying it using the command "-e user_defined.txt", or just "E user_defined.txt", the properties defined by user will be used in calculations.

3.3 Pse-in-One-Analysis

The facility **Pse-in-One-Analysis** includes two main scripts: "train.py" and "predict.py".

3.3.1 train.py

Basic functions

The "train.py" is used for training SVM-based predictors and evaluating their performance based on the input benchmark datasets. Both binary classification and multiclass classification are supported. There are three main processes of "train.py", including parameter selection, model training and cross validation. In the parameter selection process, the parameters of LIBSVM are optimized on the validation sets. In this process, the multiprocessing technique is employed to significantly reduce the computational cost. In the model training process, the LIBSVM package is employed to train the prediction models. Finally, in the cross validation process, the performance of the constructed predictors is evaluated by k-fold cross-validation, jackknife or independent dataset test which can be selected by users. For more details of these three processes, please refer to the "**Methods description**" section.

Input and output

The input files of "train.py" are at least two files of feature vectors in LIBSVM format generated by the feature extraction methods in "nac.py", "acc.py", "pse.py" and "sc.py". For binary classification problem, two files need to be input, storing the positive samples and the the negative samples, respectively. For multiclass classification, at least three files are needed. The output file is the trained SVM model listing the parameters used in the training process and the log information, for example:

```
c,128,g,0.5,b,0,bi_or_multi,0
svm_type c_svc
kernel_type rbf
gamma 0.5
nr_class 2
total_sv 2871
rho 33.5904
label 1 -1
nr_sv 1441 1430
SV
128 1:0.00108139 2:0.00108139 3:0.00108139 ……
……
```

3.3.2 predict.py

Basic functions

The "predict.py" predicts the unseen samples independent from the benchmark dataset based on the trained model generated by using "train.py". For binary classification, the performance of the constructed predictors is evaluated by five common performance measures, and the corresponding ROC curves can also be generated. For multiclass classification, only one measure is calculated. For more information of these functions, please refer to the "**Methods description**" section.

Input and output

The input file of "predict.py" is an independent file of feature vectors in LIBSVM format generated by feature extraction methods. If the label information of the samples is available, the performance measures of the predictors will be calculated based on the predicted labels and the input real labels, otherwise, the performance will not be

evaluated. One label should be listed in each line in the label file, for example:

```
+1
+1
+1
-1
-1
-1
……
```

The output of "predict.py" is a file containing the predicted labels in the same format as the input label file.

4. Commands

4.1 "nac.py" usage

Command line arguments for "nac.py":

Required	description
inputfile	The input file in FASTA format.
outputfile	The output file stored results.
{DNA, RNA, Protein}	The sequence type.
method	The method name of nucleic acid composition.

Optional	description
-h, --help	Show this help message and exit.
-k K	The k value of kmer.
-m M	For mismatch. The max value inexact matching. (m<k). (default = 1)
-delta	For subsequence method. The value of penalized factor. (0<=delta<=1). (default = 1)
-r {0,1}	Whether consider the reverse complement or not. 1 means True, 0 means False. (default = 0)
-f {tab, svm, csv}	The output format (default = tab). tab -- Simple format, delimited by TAB. svm - - The LIBSVM training data format. csv -- The format that can be loaded into a spreadsheet program.
-l	The libSVM output file label. For binary classification problem, the labels can only be '+1' or '-1' (default = "+1"); For multiclass classification problem, the labels can be set as an integer (default = "0").
-ps	The input positive source file in FASTA format for IDKmer. Only for IDKmer method.
-ns	The input negative source file in FASTA format for IDKmer. Only for IDKmer method.
-max_dis	The max distance value of DR and Distance Pair. Only for DR and Distance Pair methods(default = 3).

-cp	The reduced alphabet scheme. Choose one of the four: cp_13, cp_14, cp_19, cp_20. Only for Distance Pair method.
-multi	Whether binary classification or multiclass classification. 0: binary classification, default value. 1: multiclass classification.

4.2 “acc.py” usage

Command line arguments for “acc.py”:

Required	description
inputfile	The input file in FASTA format.
outputfile	The output file stored results.
{DNA, RNA, Protein}	The sequence type.
method	The method name of autocorrelation.

Optional	description
-h, --help	Show this help message and exit.
-lag LAG	The value of lag.
-i I	The index file user chosen.
-e E	The user-defined index file.
-all_index	Choose all physicochemical indices.
-no_all_index	Do not choose all physicochemical indices, default.
-f {tab, svm, csv}	The output format (default = tab). tab -- Simple format, delimited by TAB. svm -- The LIBSVM training data format. csv -- The format that can be loaded into a spreadsheet program.
-l	The libSVM output file label. For binary classification problem, the labels can only be '+1' or '-1' (default = “+1”); For multiclass classification problem, the labels can be set as an integer (default = “0”).
-lamada	The value of lamada. Only for MAC, GAC, NMBAC methods (default=1).
-oli	Choose one kind of Oligonucleotide: 0 represents dinucleotide, default; 1 represents trinucleotide.
-multi	Whether binary classification or multiclass classification. 0: binary classification, default value. 1: multiclass classification.

4.3 “pse.py” usage

Command line arguments for “pse.py”:

Required	description

inputfile	The input file in FASTA format.
outputfile	The output file stored results.
{DNA, RNA, Protein}	The sequence type.
method	The method name of pseudo components.

Optional	description
-h, --help	Show this help message and exit.
-lamada LAMADA	The value of lamada (default=2).
-w W	The value of weight (default=0.1).
-k K	The value of kmer, it works only with PseKNC method.
-e E	The user-defined index file, this parameter only needs to be set for PC-PseDNC-General, PC-PseTNC-General, SC-PseDNC-General, SC-PseTNC-General, PC- PseAAC-General or SC-PseAAC-General.
-all_index	Choose all physicochemical indices.
-no_all_index	Do not choose all physicochemical indices, default.
-f {tab, svm, csv}	The output format (default = tab). tab -- Simple format, delimited by TAB. svm -- The LIBSVM training data format. csv -- The format that can be loaded into a spreadsheet program.
-l	The libSVM output file label. For binary classification problem, the labels can only be '+1' or '-1' (default = "+1"); For multiclass classification problem, the labels can be set as an integer (default = "0").
-multi	Whether binary classification or multiclass classification. 0: binary classification, default value. 1: multiclass classification.

4.4 "sc.py" usage

Command line arguments for "sc.py":

Required	description
inputfile	The input file in FASTA format.
outputfile	The output file stored results.
{DNA, RNA, Protein}	The sequence type.
Method	The method name of predicted structure composition.

Optional	description
-h, --help	Show this help message and exit.
-k K	The number of k adjacent structure statuses (default=2). It works only with PseSSC method.
-n N	The maximum distance between structure statuses (default=0). It works only with PseDPC method.

-r R	The value of lambda, represents the highest counted rank (or tier) of the structural correlation along a RNA chain (default=2).
-w W	The weight factor used to adjust the effect of the correlation factors (default=0.1).
-f {tab, svm, csv}	The output format (default = tab). tab -- Simple format, delimited by TAB. svm -- The LIBSVM training data format. csv -- The format that can be loaded into a spreadsheet program.
-l	The libSVM output file label. For binary classification problem, the labels can only be '+1' or '-1' (default = "+1"); For multiclass classification problem, the labels can be set as an integer (default = "0").
-multi	Whether binary classification or multiclass classification. 0: binary classification, default value. 1: multiclass classification.

4.5 "train.py" usage

Command line arguments for "train.py":

required	description
files	The input files in LIBSVM format, generated by feature extraction methods mentioned above or **Pse-in-One 2.0** webserver. For binary classification, two files needed. For multiclass classification, at least three files needed.
-m M	The name of the trained SVM model.

Optional	description
-h, --help	Show this help message and exit.
-p {ACC,MCC,AUC}	The performance metric used for parameter selection. Default value is "ACC".
-v V	The cross validation mode. n: (an integer larger than 0) n-fold cross validation. j: (character "j") jackknife cross validation. i: (character 'i') independent test set method.
-i_files	The independent test dataset. If the parameter '-v' is specified as 'i', one or more independent test dataset files should be included. e.g. '-i_files test1.txt test2.txt'.

-c	The parameter cost of RBF kernel is usually represented as the c power of 2 and the value of c should be input here. Either one value or a range is acceptable. If users want to input a range, the format is like '-c 1 5 1': the first value is the lower bound, the second value is the upper bound and the third value is the step.
-g	The parameter gamma of RBF kernel is usually represented as the g power of 2 and the value of g should be input here. Either one value or a range is acceptable. If users want to input a range, the format is like '-g -1 5': the first value is the lower bound, the second value is the upper bound and the third value is the step. The default step is 1. Default value is -1.
-b {0,1}	Whether to train a SVC or SVR model for probability estimates, 0 or 1. Default value is 0.
-cpu CPU	The maximum number of CPU cores used for multiprocessing during parameter selection process. Default value is the number of all available CPU cores.

4.6 “predict.py” usage

Command line arguments for “predict.py”:

required	description
inputfiles	The input files in LIBSVM format, generated by feature extraction methods mentioned above or **Pse-in-One 2.0** webserver.
-m M	The name of the trained SVM model.

optional	description
-h, --help	Show this help message and exit.
-labels LABELS	The real label file. Optional.
-o O	The output file name listing the predicted labels. The default name is “output_labels.txt”.

4.7 Example

An example of using **Pse-in-One 2.0** to construct machine learning predictor for solving a specific task in bioinformatics is given.

Example: Reconstructing the predictor PseDNA-Pro for DNA binding protein identification based on the benchmark dataset (4), and evaluating its performance on an independent dataset (5) by using **Pse-in-One 2.0**.

The benchmark dataset contains 525 positive samples and 550 negative samples. There are 93 positive samples and 93 negative samples in the independent dataset. The

benchmark dataset and independent dataset are available at http://bioinformatics.hitsz.edu.cn/PseDNA-Pro/Resources/benchmark_dataset.pdf, and, http://journals.plos.org/plosone/article/asset?unique&id=info:doi/10.1371/journal.pone.0086703.s002, respectively.

In this example, the files "protein_pos.txt" and "protein_neg.txt" contain the positive dataset and negative dataset of the benchmark dataset, respectively. The samples of the independent dataset and their labels are stored in the files "protein_test.txt" and "labels.txt", respectively. All these four files are available in the "/data/example" folder.

Firstly, to construct the predictor PseDNA-Pro, extract features based on the benchmark dataset.
Convert the positive dataset "protein_pos.txt" into feature vectors in LIBSVM format, and save as an output file "pos_svm.txt":

```
python pse.py ./data/example/protein_pos.txt pos_svm.txt Protein PC-PseAAC -lamada  2 -w 0.05 -f svm
```

The content of the output file "pos_svm.txt" is as follows:

```
+1 1:0.04075964 2:0.01358655 3:0.0 4:0.08151929 5:0.04075964 6:0.0271731…
+1 1:0.29181499 2:0.19233261 3:0.0 4:0.0 5:0.0 6:0.19233261 …
+1 1:0.12355132 2:0.0 3:0.05615969 4:0.07862357 5:0.01123194 6:0.04492775…
……
```

Then convert the negative dataset "protein_neg.txt" into feature vectors in LIBSVM format, and save as an output file "neg_svm.txt":

```
python pse.py ./data/example/protein_neg.txt neg_svm.txt Protein PC-PseAAC -lamada  2 -w 0.05 -f svm -l -1
```

The content of the output file "neg_svm.txt" is as follows:

```
-1 1:0.06394096 2:0.06394096 3:0.05195203 4:0.02397786 5:0.04395941 …
-1 1:0.07606996 2:0.0 3:0.05071331 4:0.03728919 5:0.02535665 …
-1 1:0.04873717 2:0.01624572 3:0.03858359 4:0.05076788 5:0.0263993 …
……
```

After feature extraction, construct the predictor PseDNA-Pro based on "pos_svm.txt" and "neg_svm.txt":

```
python train.py pos_svm.txt neg_svm.txt -m protein.model -c 1 9 2 -g -3 1 2 -v 10
```

The output information is as follows:

```
Processing...
Parameter selection is in processing...

Iteration  c =  128  g =  0.125  finished.
Iteration  c =  8  g =  0.5  finished.
Iteration  c =  2  g =  0.125  finished.
Iteration  c =  32  g =  2  finished.
Iteration  c =  32  g =  0.5  finished.
Iteration  c =  8  g =  0.125  finished.
```

```
Iteration  c =  32  g =  0.125  finished.
Iteration  c =  512  g =  2  finished.
Iteration  c =  8  g =  2  finished.
Iteration  c =  512  g =  0.125  finished.
Iteration  c =  512  g =  0.5  finished.
Iteration  c =  128  g =  0.5  finished.
Iteration  c =  128  g =  2  finished.
Iteration  c =  2  g =  2  finished.
Iteration  c =  2  g =  0.5  finished.
The time cost for parameter selection is 2.24s
Parameter selection completed.

The optimal parameters for the dataset are: c =  7  g =  1


Model training is in processing...
The cross validation results are as follows:
ACC = 0.7488
MCC = 0.4964
AUC = 0.8190
Sn  = 0.7288
Sp  = 0.7683

The ROC curve has been saved. You can check it here:
/Pse-in-One 2.0/data/final_results/cross_validation.png

Model training completed.
The model has been saved. You can check it here:
/Pse-in-One 2.0/data/final_results/protein.model


Done.
Used time: 6.57s
```

The generated ROC curve is shown in **Fig. 1**.

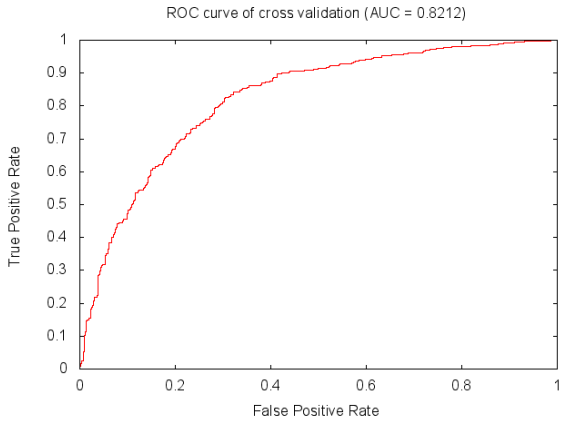


Fig .1. The ROC curve of cross validation.

Then, the performance of PseDNA-Pro can be further evaluated by using the independent dataset:
Firstly, convert the independent dataset “protein_test.txt” into feature vectors in

LIBSVM format, and save as an output file “test_svm.txt”:

```
python pse.py ./data/example/protein_test.txt test_svm.txt Protein PC-PseAAC -lamada  2 -w 0.05 -f svm
```

The content of the output file “pos_svm.txt” is as follows:

```
+1 1:0.09717009 2:0.0 3:0.04318671 4:0.04318671 5:0.02159335 …
+1 1:0.04954724 2:0.00707818 3:0.05662542 4:0.07078177 5:0.05662542 …
+1 1:0.05782654 2:0.01084248 3:0.05421239 4:0.06866902 5:0.04336991 …
……
```

After feature extraction, predict the independent dataset using the following commad:

```
python predict.py test_svm.txt -m protein.model -labels ./data/example/labels.txt
```

The output information is as follows:

```
Processing...
The parameters of RBF kernel:
c =  7  g =  1
The performance evaluations are as follows:

ACC = 0.6774
MCC = 0.3578
AUC = 0.7365
Sn  = 0.7419
Sp  = 0.6129

The ROC curve has been saved. You can check it here:
/Pse-in-One 2.0/data/final_results/predicted_roc.png

The predicted labels have been saved. You can check it here:
/Pse-in-One 2.0/data/final_results/output_labels.txt

Done.
Used time: 3.16s
```

As shown in this example, the PseDNA-Pro can be easily constructed based on the benchmark dataset by using the script “train.py”, and then evaluated on the independent dataset by using “predict.py”.

5. Methods description

5.1 Feature extraction

The **Pse-in-One 2.0** web server is able to generate totally 51 different modes of pseudo components for DNA, RNA, and protein sequences, including 20 modes for DNA sequences (**Table 1**), 14 modes for RNA sequences (**Table 2**), and 17 modes for protein sequences (**Table 3**). The detailed information of the 51 methods will be introduced in Pse-in-One 2.0 description document which can be downloaded from here: http://bioinformatics.hitsz.edu.cn/Pse-in-One2.0/static/download/Pse-in-One%202.0_description.pdf.

5.2 Parameter selection

In LIBSVM there are two parameters *c* and *g* which can determine the performance of the predictor. **Pse-in-One 2.0** is able to automatically optimize these parameters based on the best performance on the validation set by using the new facility **Pse-in-One-Analysis**. Users can input the range and step of the two parameters for optimizing. For more information of the input format, please refer to "**Commands**" section.
To improve the efficiency of this procedure, multiprocessing technique is applied, which significantly reduces the computational cost. One of the three performance measures, including Accuracy (ACC), Mathew's Correlation Coefficient (MCC) and Area Under roc Curve (AUC) can be used as the golden standard to optimize the parameters.

5.3 Model training

In the model training process, this model is trained based on LIBSVM with RBF kernel.
The trained SVM model and all the parameters are saved in a separate file, which will be used as the input for "predict.py".

5.4 Cross validation

Pse-in-One 2.0 provides three types of cross validation options, including k-fold cross validation, jackknife (leave-one-out cross validation) and independent dataset test, which can be chosen by the argument "-v". Please refer to "**Commands**" section for more details.
For binary classification, the performance of the predictor is measured by five common performance measures, including the accuracy (Acc), Mathew's Correlation Coefficient (MCC), Area Under roc Curve (AUC), sensitivity (Sn), and specificity (Sp). Furthermore, the ROC (Receiver Operating Characteristic) (6) curve will also be generated and saved in a PNG file.
For multiclass classification, only the performance measure of Acc is calculated since the other measures are not suitable for multiclass classification.

5.5 Sequence prediction

The "predict.py" is used to predict the unseen samples based on the model trained by using "train.py". The performance of the predictors can be further evaluated on the independent datasets. If the label information of the independent dataset is not available, the performance of the predictor will not be evaluated, and only the predicted labels are given. Otherwise, this script will output the predicted labels. For binary classification, the five performance measures (Acc, MCC, AUC, Sn, and Sp) will be calculated along with the corresponding ROC curve saved as a PNG file; for multiclass classification, only the performance measure Acc will be calculated.

Table 1. 20 modes of DNA sequences.

Category	Mode	Description
Nucleic acid Composition	Kmer	Basic kmer (7)
	RevKmer	Reverse complementary kmer(8,9)
	IDKmer	increment of diversity (10-12)
	Mismatch	The occurrences of kmers, allowing at most m mismatches (13-15)
	Subsequence	The occurences of kmers, allowing non-contiguous maches (13,15,16)
Autocorrelation	DAC	Dinucleotide-based auto covariance (17,18)
	DCC	Dinucleotide-based cross covariance (17,18)
	DACC	Dinucleotide-based auto-cross covariance (17,18)
	TAC	Trinucleotide-based auto covariance (17)
	TCC	Trinucleotide-based cross covariance (17)
	TACC	Trinucleotide-based auto-cross covariance (17)
	MAC	Moran autocorrelation (19,20)
	GAC	Geary autocorrelation (20,21)
	NMBAC	Normalized Moreau-Broto autocorrelation (20,22)
Pseudo nucleotide composition	PseDNC	Pseudo dinucleotide composition (23)
	PseKNC	Pseudo k-tuple nucleotide composition (24,25)
	PC-PseDNC-General	General parallel correlation pseudo dinucleotide composition (26)
	PC-PseTNC-General	General parallel correlation pseudo trinucleotide composition (26)
	SC-PseDNC-General	General series correlation pseudo dinucleotide composition (26)
	SC-PseTNC-General	General series correlation pseudo trinucleotide composition (26)

Table 2. 14 modes of RNA sequences.

Category	Mode	Description
Nucleic acid Composition	Kmer	Basic kmer (27)
	Mismatch	The occurrences of kmers, allowing at most m mismatches (13-15)
	Subsequence	The occurences of kmers, allowing non-contiguous maches (13,15,16)
Autocorrelation	DAC	Dinucleotide-based auto covariance (17,18,28)
	DCC	Dinucleotide-based cross covariance (17,18,28)
	DACC	Dinucleotide-based auto-cross covariance (17,18,28)
	MAC	Moran autocorrelation (19,20)
	GAC	Geary autocorrelation (20,21)
	NMBAC	Normalized Moreau-Broto autocorrelation (20,22)
Pseudo nucleotide composition	PC-PseDNC- General	General parallel correlation pseudo dinucleotide composition (18,20)
	SC-PseDNC-General	General series correlation pseudo dinucleotide composition (18,20)
Predicted Structure composition	Triplet	Local structure-sequence triplet element (29)
	PseSSC	Pseudo-structure status composition (30)
	PseDPC	Pseudo-distance structure status pair composition (31)

Table 3. 17 modes of protein sequences.

Category	Mode	Description
Amino acid composition	Kmer	Basic kmer (32)
	DR	Distance-based Residue (33)
	Distance Pair	PseAAC of Distance-Pairs and Reduced Alphabet (34)
Autocorrelation	AC	Auto covariance (17,28)
	CC	Cross covariance (17,28)
	ACC	Auto-cross covariance (17,28)
	PDT	Physicochemical distance transformation (35)
Pseudo amino acid composition	PC-PseAAC	Parallel correlation pseudo amino acid composition (36)
	SC-PseAAC	Series correlation pseudo amino acid composition (37)
	PC-PseAAC-General	General parallel correlation pseudo amino acid composition (36,38)
	SC-PseAAC-General	General series correlation pseudo amino acid composition (37,38)
Profile-based features	Top-n-gram	Select and combine the n most frequenct amino acids according to their frequencies. (32)
	PDT-Pofile	Profile-based Physicochemical distance transformation (35)
	DT	Distance-based Top-n-gram (33)
	AC-PSSM	Profile-based Auto covariance (17)
	CC-PSSM	Profile-based Cross covariance (17)
	ACC-PSSM	Profile-based Auto-cross covariance (17)

Table 4. The names of the 148 physicochemical indices for dinucleotides.

Base stacking	Protein induced deformability	B-DNA twist
Propeller twist	Duplex stability:(freeenergy)	Duplex tability(disruptenergy)
Protein DNA twist	Stabilising energy of Z-DNA	Aida_BA_transition
Breslauer_dS	Electron_interaction	Hartman_trans_free_energy
Lisser_BZ_transition	Polar_interaction	SantaLucia_dG
Sarai_flexibility	Stability	Stacking_energy
Sugimoto_dS	Watson-Crick_interaction	Twist
Shift	Slide	Rise
Twist stiffness	Tilt stiffness	Shift_rise
Twist_shift	Enthalpy1	Twist_twist
Shift2	Tilt3	Tilt1
Slide (DNA-protein complex)1	Tilt_shift	Twist_tilt
Roll_rise	Stacking energy	Stacking energy1
Propeller Twist	Roll11	Rise (DNA-protein complex)
Roll2	Roll3	Roll1
Slide_slide	Enthalpy	Shift_shift
Flexibility_slide	Minor Groove Distance	Rise (DNA-protein complex)1
Roll (DNA-protein complex)1	Entropy	Cytosine content
Major Groove Distance	Twist (DNA-protein complex)	Purine (AG) content
Tilt_slide	Major Groove Width	Major Groove Depth
Free energy6	Free energy7	Free energy4
Free energy3	Free energy1	Twist_roll
Flexibility_shift	Shift (DNA-protein complex)1	Thymine content
Tip	Keto (GT) content	Roll stiffness
Entropy1	Roll_slide	Slide (DNA-protein complex)
Twist2	Twist5	Twist4
Tilt (DNA-protein complex)1	Twist_slide	Minor Groove Depth
Persistance Length	Rise3	Shift stiffness
Slide3	Slide2	Slide1
Rise1	Rise stiffness	Mobility to bend towards minor groove
Dinucleotide GC Content	A-philicity	Wedge
DNA denaturation	Bending stiffness	Free energy5
Breslauer_dG	Breslauer_dH	Shift (DNA-protein complex)
Helix-Coil_transition	Ivanov_BA_transition	Slide_rise
SantaLucia_dH	SantaLucia_dS	Minor Groove Width
Sugimoto_dG	Sugimoto_dH	Twist1
Tilt	Roll	Twist7
Clash Strength	Roll_roll	Roll (DNA-protein complex)
Adenine content	Direction	Probability contacting nucleosome core
Roll_shift	Shift_slide	Shift1
Tilt4	Tilt2	Free energy8
Twist (DNA-protein complex)1	Tilt_rise	Free energy2
Stacking energy2	Stacking energy3	Rise_rise
Tilt_tilt	Roll4	Tilt_roll

Minor Groove Size	GC content	Inclination
Slide stiffness	Melting Temperature1	Twist3
Tilt (DNA-protein complex)	Guanine content	Twist6
Major Groove Size	Twist_rise	Rise2
Melting Temperature	Free energy	Mobility to bend towards major groove
Bend		

Table 5. The names of the 12 physicochemical indices for trinucleotides.

Bendability (DNAse)	Bendability (consensus)	Trinucleotide GC Content
Consensus_roll	Consensus-Rigid	Dnase I
MW-Daltons	MW-kg	Nucleosome
Nucleosome positioning	Dnase I-Rigid	Nucleosome-Rigid

Table 6. The names of the 90 physicochemical indices for dinucleotides.

Base stacking	Protein induced deformability	B-DNA twist
Dinucleotide GC Content	A-philicity	Propeller twist
Duplex stability-free energy	Duplex stability-disrupt energy	DNA denaturation
Bending stiffness	Protein DNA twist	Stabilising energy of Z-DNA
Aida_BA_transition	Breslauer_dG	Breslauer_dH
Breslauer_dS	Electron_interaction	Hartman_trans_free_energy
Helix-Coil_transition	Ivanov_BA_transition	Lisser_BZ_transition
Polar_interaction	SantaLucia_dG	SantaLucia_dH
SantaLucia_dS	Sarai_flexibility	Stability
Stacking_energy	Sugimoto_dG	Sugimoto_dH
Sugimoto_dS	Watson-Crick_interaction	Twist
Tilt	Roll	Shift
Slide	Rise	Stacking energy
Bend	Tip	Inclination
Major Groove Width	Major Groove Depth	Major Groove Size
Major Groove Distance	Minor Groove Width	Minor Groove Depth
Minor Groove Size	Minor Groove Distance	Persistance Length
Melting Temperature	Mobility to bend towards major groove	Mobility to bend towards minor groove
Propeller Twist	Clash Strength	Enthalpy
Free energy	Twist_twist	Tilt_tilt
Roll_roll	Twist_tilt	Twist_roll
Tilt_roll	Shift_shift	Slide_slide
Rise_rise	Shift_slide	Shift_rise
Slide_rise	Twist_shift	Twist_slide
Twist_rise	Tilt_shift	Tilt_slide
Tilt_rise	Roll_shift	Roll_slide
Roll_rise	Slide stiffness	Shift stiffness
Roll stiffness	Rise stiffness	Tilt stiffness
Twist stiffness	Wedge	Direction

Flexibility_slide	Flexibility_shift	Entropy

Table 7. The names of the 6 physicochemical indices for dinucleotides.

Twist	Tilt	Roll
Shift	Slide	Rise

Table 8. The names of the 22 physicochemical indices for dinucleotides.

Shift (RNA)	Hydrophilicity (RNA)
Hydrophilicity (RNA)	GC content
Purine (AG) content	Keto (GT) content
Adenine content	Guanine content
Cytosine content	Thymine content
Slide (RNA)	Rise (RNA)
Tilt (RNA)	Roll (RNA)
Twist (RNA)	Stacking energy (RNA)
Enthalpy (RNA)	Entropy (RNA)
Free energy (RNA)	Free energy (RNA)
Enthalpy (RNA)	Entropy (RNA)

Table 9. The names of the 11 physicochemical indices for dinucleotides.

Shift	Slide	Rise
Tilt	Roll	Twist
Stacking energy	Enthalpy	Entropy
Free energy	Hydrophilicity	

Table 10. The names of the 547 physicochemical indices for amino acids.

Hydrophobicity	Hydrophilicity	Mass
ARGP820102	ARGP820103	BEGF750101
BHAR880101	BIGC670101	BIOV880101
BROC820102	BULH740101	BULH740102
BUNA790103	BURA740101	BURA740102
CHAM820102	CHAM830101	CHAM830102
CHAM830105	CHAM830106	CHAM830107
CHOC760101	CHOC760102	CHOC760103
CHOP780201	CHOP780202	CHOP780203
CHOP780206	CHOP780207	CHOP780208
CHOP780211	CHOP780212	CHOP780213
CHOP780216	CIDH920101	CIDH920102
CIDH920105	COHE430101	CRAJ730101
DAWD720101	DAYM780101	DAYM780201
EISD840101	EISD860101	EISD860102
FASG760102	FASG760103	FASG760104
FAUJ880101	FAUJ880102	FAUJ880103
FAUJ880106	FAUJ880107	FAUJ880108
FAUJ880111	FAUJ880112	FAUJ880113
FINA910102	FINA910103	FINA910104
GEIM800102	GEIM800103	GEIM800104
GEIM800107	GEIM800108	GEIM800109
GOLD730101	GOLD730102	GRAR740101
GUYH850101	HOPA770101	HOPT810101
HUTJ700103	ISOY800101	ISOY800102
ISOY800105	ISOY800106	ISOY800107

JANJ780102	JANJ780103	JANJ790101
JOND750102	JOND920101	JOND920102
KANM800101	KANM800102	KANM800103
KARP850102	KARP850103	KHAG800101
KRIW790101	KRIW790102	KRIW790103
LEVM760101	LEVM760102	LEVM760103
LEVM760106	LEVM760107	LEVM780101
LEVM780104	LEVM780105	LEVM780106
LIFS790102	LIFS790103	MANP780101
MAXF760103	MAXF760104	MAXF760105
MEEJ800101	MEEJ800102	MEEJ810101
MEIH800102	MEIH800103	MIYS850101
NAGK730103	NAKH900101	NAKH900102
NAKH900105	NAKH900106	NAKH900107
NAKH900110	NAKH900111	NAKH900112
NAKH920102	NAKH920103	NAKH920104
NAKH920107	NAKH920108	NISK800101
OOBM770101	OOBM770102	OOBM770103
OOBM850101	OOBM850102	OOBM850103
PALJ810101	PALJ810102	PALJ810103
PALJ810106	PALJ810107	PALJ810108
PALJ810111	PALJ810112	PALJ810113
PALJ810116	PARJ860101	PLIV810101
PONP800103	PONP800104	PONP800105
PONP800108	PRAM820101	PRAM820102
PRAM900102	PRAM900103	PRAM900104
QIAN880101	QIAN880102	QIAN880103
QIAN880106	QIAN880107	QIAN880108
QIAN880111	QIAN880112	QIAN880113
QIAN880116	QIAN880117	QIAN880118
QIAN880121	QIAN880122	QIAN880123
QIAN880126	QIAN880127	QIAN880128
QIAN880131	QIAN880132	QIAN880133
QIAN880136	QIAN880137	QIAN880138
RACS770102	RACS770103	RACS820101
RACS820104	RACS820105	RACS820106
RACS820109	RACS820110	RACS820111
RACS820114	RADA880101	RADA880102
RADA880105	RADA880106	RADA880107
RICJ880102	RICJ880103	RICJ880104
RICJ880107	RICJ880108	RICJ880109
RICJ880112	RICJ880113	RICJ880114
RICJ880117	ROBB760101	ROBB760102
ROBB760105	ROBB760106	ROBB760107
ROBB760110	ROBB760111	ROBB760112
ROSG850101	ROSG850102	ROSM880101
SIMZ760101	SNEP660101	SNEP660102
SUEM840101	SUEM840102	SWER830101
TANS770103	TANS770104	TANS770105
TANS770108	TANS770109	TANS770110
VASM830103	VELV850101	VENT840101
WEBA780101	WERD780101	WERD780102
WOEC730101	WOLR810101	WOLS870101
YUTK870101	YUTK870102	YUTK870103

ZIMJ680101	ZIMJ680102	ZIMJ680103
AURR980101	AURR980102	AURR980103
AURR980106	AURR980107	AURR980108
AURR980111	AURR980112	AURR980113
AURR980116	AURR980117	AURR980118
ONEK900101	ONEK900102	VINM940101
VINM940104	MUNV940101	MUNV940102
MUNV940105	WIMW960101	KIMC930101
PARS000101	PARS000102	KUMS000101
KUMS000104	TAKK010101	FODM020101
NADH010103	NADH010104	NADH010105
MONM990201	KOEP990101	KOEP990102
CEDJ970103	CEDJ970104	CEDJ970105
FUKS010103	FUKS010104	FUKS010105
FUKS010108	FUKS010109	FUKS010110
AVBF000101	AVBF000102	AVBF000103
AVBF000106	AVBF000107	AVBF000108
MITS020101	TSAJ990101	TSAJ990102
WILM950101	WILM950102	WILM950103
GUOD860101	JURD980101	BASU050101
SUYM030101	PUNT030101	PUNT030102
GEOR030103	GEOR030104	GEOR030105
GEOR030108	GEOR030109	ZHOH040101
BAEK050101	HARY940101	PONJ960101
OLSK800101	KIDA850101	GUYH850102
GUYH850105	ROSM880104	ROSM880105
BLAS910101	CASG920101	CORJ870101
CORJ870104	CORJ870105	CORJ870106
MIYS990101	MIYS990102	MIYS990103
ENGD860101	FASG890101	TANS770101
ANDN920101	ARGP820101	TANS770106
BEGF750102	BEGF750103	VASM830101
BIOV880102	BROC820101	VHEG790101
BUNA790101	BUNA790102	WERD780103
CHAM810101	CHAM820101	WOLS870102
CHAM830103	CHAM830104	YUTK870104
CHAM830108	CHOC750101	ZIMJ680104
CHOC760104	CHOP780101	AURR980104
CHOP780204	CHOP780205	AURR980109
CHOP780209	CHOP780210	AURR980114
CHOP780214	CHOP780215	AURR980119
CIDH920103	CIDH920104	VINM940102
CRAJ730102	CRAJ730103	MUNV940103
DESM900101	DESM900102	MONM990101
EISD860103	FASG760101	KUMS000102
FASG760105	FAUJ830101	NADH010101
FAUJ880104	FAUJ880105	NADH010106
FAUJ880109	FAUJ880110	CEDJ970101
FINA770101	FINA910101	FUKS010101
GARJ730101	GEIM800101	FUKS010106
GEIM800105	GEIM800106	FUKS010111
GEIM800110	GEIM800111	AVBF000104
GRAR740102	GRAR740103	AVBF000109
HUTJ700101	HUTJ700102	COSI940101

ISOY800103	ISOY800104	WILM950104
ISOY800108	JANJ780101	BASU050102
JANJ790102	JOND750101	GEOR030101
JUKT750101	JUNJ780101	GEOR030106
KANM800104	KARP850101	ZHOH040102
KLEP840101	KRIW710101	DIGM050101
KYTJ820101	LAWE840101	GUYH850103
LEVM760104	LEVM760105	JACR890101
LEVM780102	LEVM780103	CORJ870102
LEWP710101	LIFS790101	CORJ870107
MAXF760101	MAXF760102	MIYS990104
MAXF760106	MCMT640101	TANS770102
MEEJ810102	MEIH800101	TANS770107
NAGK730101	NAGK730102	VASM830102
NAKH900103	NAKH900104	WARP780101
NAKH900108	NAKH900109	WERD780104
NAKH900113	NAKH920101	WOLS870103
NAKH920105	NAKH920106	ZASB820101
NISK860101	NOZY710101	ZIMJ680105
OOBM770104	OOBM770105	AURR980105
OOBM850104	OOBM850105	AURR980110
PALJ810104	PALJ810105	AURR980115
PALJ810109	PALJ810110	AURR980120
PALJ810114	PALJ810115	VINM940103
PONP800101	PONP800102	MUNV940104
PONP800106	PONP800107	BLAM930101
PRAM820103	PRAM900101	KUMS000103
PTIO830101	PTIO830102	NADH010102
QIAN880104	QIAN880105	NADH010107
QIAN880109	QIAN880110	CEDJ970102
QIAN880114	QIAN880115	FUKS010102
QIAN880119	QIAN880120	FUKS010107
QIAN880124	QIAN880125	FUKS010112
QIAN880129	QIAN880130	AVBF000105
QIAN880134	QIAN880135	YANJ020101
QIAN880139	RACS770101	PONP930101
RACS820102	RACS820103	KUHL950101
RACS820107	RACS820108	BASU050103
RACS820112	RACS820113	GEOR030102
RADA880103	RADA880104	GEOR030107
RADA880108	RICJ880101	ZHOH040103
RICJ880105	RICJ880106	WOLR790101
RICJ880110	RICJ880111	GUYH850104
RICJ880115	RICJ880116	COWR900101
ROBB760103	ROBB760104	CORJ870103
ROBB760108	ROBB760109	CORJ870108
ROBB760113	ROBB790101	MIYS990105
ROSM880102	ROSM880103	SNEP660104
SNEP660103		

Table 11. The names of the 3 physicochemical indices for amino acids.

Hydrophobicity	hydrophilicity	mass

Table 12. The names of the 2 physicochemical indices for amino acids.

Hydrophobicity	hydrophilicity

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