CPAT Documentation

Release 3.0.5

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CONTENTS

Warning: This documentation is for CPAT v3.0.0 or future versions. For documentation of CPAT v2.0.0 and older versions, please go to http://rna-cpat.sourceforge.net/

CHAPTER

ONE

CPAT V3.0.5 (01/24/2024)

Use "pyproject.toml" to replace "setup.py".

Note:

- `cpat.py` is now renamed to `cpat`. Similarly,
- `make_hexamer_tab.py` is renamed to `make_hexamer_tab`,
- `make_logitModel.py` is renamed to `make_logitModel`.
- To ensure compatibility with the previous pipelines, please add the following lines into your ~/.bashrc file.

```
alias cpat.py='cpat'
alias make_hexamer_tab.py='make_hexamer_tab'
alias make_logitModel.py='make_logitModel'
```

CHAPTER

TWO

CPAT V3.0.4 (05/26/2021)

Fix bug to read remote file for Python3.

CHAPTER

THREE

CPAT V3.0.3 (03/08/2021)

Update “cpat.py” to handle alternative start codens.

CHAPTER

FOUR

CPAT V3.0.2 (08/17/2020)

Update “make_logitModel.py” to make it compatible with “cpat.py”.

CHAPTER

FIVE

CPAT V3.0.1

Minor bug fixed regarding the output format.

CHAPTER

SIX

CPAT V3.0.0

For many transcripts, the longest ORF may not be the real ORF. For example, in human genome, the 2nd longest ORF of NM_198086 is the real ORF, and the 3rd longest ORF of NM_030915 is the real ORF. Version 3.0.0 is released to address this problem.

1) If model is provided, CPAT can be used as an ORFfinder. It gives exactly the same results as NCBI ORFfinder does.
2) Search for all ORF candidates. The number of ORF reported is controlled by `--min-orf` and `--top-orf`.
3) In addition to basic ORF information ("ORF frame", "ORF strand", "ORF start", "ORF end", "ORF sequence"), it also reports "coding probability" for each ORF.
4) The best ORF will be selected (controlled by `--best-orf`) either by **ORF length** or **coding probability**.

CHAPTER

SEVEN

INTRODUCTION

CPAT is a bioinformatics tool to predict RNA's coding probability based on the RNA sequence characteristics. To achieve this goal, CPAT calculates scores of these 4 linguistic features from a set of known protein-coding genes and another set of non-coding genes.

1) ORF size
2) ORF coverage
3) Fickett TESTCODE
4) Hexamer usage bias

CPAT will then builds a logistic regression model using these 4 features as predictor variables and the "protein-coding status" as the response variable. After evaluating the performance and determining the probability cutoff, the model can be used to predict the coding potential of new RNA sequences.

CHAPTER

EIGHT

INSTALLATION

8.1 Prerequisite

1) python3.5 or later version
2) numpy
3) pysam
4) R

8.2 install CPAT using pip3

```
$ pip3 install CPAT
$ pip3 install CPAT --upgrade  # if you already have CPAT v2.0 installed
```

Note:

- User need to download prebuilt logit model and hexamer table for human, mouse, zebrafish and fly. For other species, we provide scripts to build these models (see below).

CHAPTER

NINE

RUN CPAT ONLINE

https://wlcb.oit.uci.edu/cpat is hosted by Dr Wei Li's lab @ University of California Irvine.

Step1: Upload data to CPAT server. There are 3 different ways to uploada

- Upload BED or FASTA format files from local disk. Files can be regular or compressed (.gz, .Z. .z, .bz, .bz2, .bzip2).
- For small dataset, user can copy and paste data (in BED or FASTA format) directly to the text area.
- For larger dataset, user can save data in web server (http, https or ftp) first, then paste the data url to text area. For very large dataset, run CPAT locally.

Step2: Select Select Species assembly

Step3: Click Submit button

Note:

- This web server only supports Human (hg19), Mouse (mm9 and mm10), Fly (dm3) and Zebrafish (Zv9).
- When input file is BED format, the reference genome is required and the assembly version is important.
- When input file is FASTA format, the reference genome and the assembly version is ignored.

CHAPTER

TEN

RUN CPAT ON LOCAL COMPUTER

10.1 Input files

User needs to provide a gene file ('-g'), a logit model file ('-d'), a hexamer frequency table file ('-x') and specify the output file name('-o'). Gene file could be either in BED or FASTA format. If in BED format, user also needs to specify the reference genome sequence file ('-r').

10.2 Command line options

```
$ cpat -h
```

```
cpat  [options]

Options:
  --version             show program's version number and exit
  -h, --help            show this help message and exit
  -g GENE_FILE, --gene=GENE_FILE
                        Genomic sequnence(s) of RNA in FASTA
                        (https://en.wikipedia.org/wiki/FASTA_format) or
                        standard 12-column  BED
                        (https://genome.ucsc.edu/FAQ/FAQformat.html#format1)
                        format. It is recommended to use *short* and *unique*
                        sequence identifiers (such as Ensembl transcript id)
                        in FASTA and BED file. If this is a BED file,
                        reference genome ('-r/--ref') should be specified.
                        The input FASTA or BED file could be a regular text
                        file or compressed file (*.gz, *.bz2) or accessible
                        URL (http://, https://, ftp://). URL file cannot be a
                        compressed file.
  -o OUT_FILE, --outfile=OUT_FILE
                        The prefix of output files.
  -d LOGIT_MODEL, --logitModel=LOGIT_MODEL
                        Logistic regression model. The prebuilt models
                        for Human, Mouse, Fly, Zebrafish are availablel.
                        Run 'make_logitModel.py' to build logistic
                        regression model for your own training datset.
  -x HEXAMER_DAT, --hex=HEXAMER_DAT
                        The hexamer frequency table.                        The
                        prebuilt tables for Human, Mouse, Fly, Zebrafish
```

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```
                        are availablel. Run 'make_hexamer_tab.py' to make this
                        table for your own training dataset.
  -r REF_GENOME, --ref=REF_GENOME
                        Reference genome sequences in FASTA format.
                        Reference genome file will be indexed automatically
                        if the index file ( *.fai) does not exist. Will be
                        ignored if FASTA file was provided to '-g/--gene'.
  --antisense           Logical to determine whether to search for ORFs
                        from the anti-sense strand. *Sense strand* (or coding
                        strand) is DNA strand that carries the translatable
                        code in the 5 to 3 direction. default=False (i.e.
                        only search for ORFs from the sense strand)
  --start=START_CODONS  Start codon (use 'T' instead of 'U') used to
                        define the start of open reading frame (ORF).
                        default=ATG
  --stop=STOP_CODONS    Stop codon (use 'T' instead of 'U') used to
                        define the end of open reading frame (ORF). Multiple
                        stop codons are separated by ','. default=TAG, TAA,
                        TGA
  --min-orf=MIN_ORF_LEN
                        Minimum ORF length in nucleotides.
                        default=75
  --top-orf=N_TOP_ORF   Number of ORF candidates reported. RNAs may
                        have dozens of putative ORFs, in most cases, the real
                        ORF is ranked (by size) in the top several. It is not
                        necessary to calculate "Fickett score",
                        "Hexamer score" and "coding probability" for every
                        ORF. default=5
  --width=LINE_WIDTH    Line width of output ORFs in FASTA format.
                        default=100
  --log-file=LOG_FILE   Name of log file. default="CPAT_run_info.log"
  --best-orf=MODE       Criteria to select the best ORF: "l"=length,
                        selection according to the "ORF length";
                        "p"=probability, selection according to the
                        "coding probability". default="p"
  --verbose             Logical to determine if detailed running
                        information is printed to screen.
```

10.3 Examples

Use local FASTA file as input

```
$ cpat -x Human_Hexamer.tsv --antisense -d Human_logitModel.RData --top-orf=5 -g
Human_test_coding_mRNA.fa -o output1
```

Use a remote FASTA file as input

```
$ cpat -x Human_Hexamer.tsv --antisense -d Human_logitModel.RData --top-orf=5 -g https://
data.cyverse.org/dav-anon/iplant/home/liguow/CPAT/Human_test_coding_mRNA.fa -o output2
```

Use BED file as input. '-r' is required

```
$ cpat -x Human_Hexamer.tsv --antisense -d Human_logitModel.RData --top-orf=5 -g
Human_test_coding_mRNA_hg19.bed -r hg19.fa -o output3
```

10.4 Output

1. **output.ORF_seqs.fa**
   The top ORF sequences (at least 75 nucleotides long) in FASTA format.
2. **output.ORF_prob.tsv**
   ORF information (strand, frame, start, end, size, Fickett TESTCODE score, Hexamer score) and coding probability)
3. **output.ORF_prob.best.tsv**
   The information of the best ORF. This file is a subset of "output.ORF_prob.tsv"
4. **output.no_ORF.txt**
   Sequence IDs or BED entries with no ORF found. Should be considered as non-coding.
5. **output1.r**
   Rscript file.
6. **CPAT_run_info.log**
   The log file.

CHAPTER

ELEVEN

BUILD YOUR OWN HEXAMER TABLE

`make_hexamer_tab` calculates the in frame hexamer (6mer) frequency from CDS sequence in fasta format. A CDS is an mRNA sequence without the 3' UTR and 5' UTR regions. This table is required by `cpat` to calculate the hexamer usage score. Users can download prebuilt hexamer tables (Human, Mouse, Fly, Zebrafish) from here.

11.1 Usage

```
$ make_hexamer_tab -h
```

```
make_hexamer_tab  [options]

Options:
  --version             show program's version number and exit
  -h, --help            show this help message and exit
  -c CODING_FILE, --cod=CODING_FILE
                        Coding sequence (must be CDS without UTR, i.e.
                        from start coden to stop coden) in fasta format
  -n NONCODING_FILE, --noncod=NONCODING_FILE
                        Noncoding sequences in fasta format
```

11.2 Example

First, download these two files:

- Coding CDS sequences: Human_coding_transcripts_CDS.fa.gz
- Noncoding sequences: Human_noncoding_transcripts_RNA.fa.gz

Then, run:

```
$ make_hexamer_tab -c Human_coding_transcripts_CDS.fa.gz -n Human_noncoding_transcripts_RNA.
fa.gz >Human_Hexamer.tsv
```

11.3 Output

```
$ head Human_Hexamer.tsv
```

```
hexamer coding  noncoding
AAAAAA  0.0006471106736092786 0.001606589931772997
AAAAAC  0.00042092373222007566  0.0005113004850646316
AAAAAG  0.0008133623112408557 0.0006870944872085282
AAAAAT  0.0005917287586530271 0.0009504638599970318
AAAACA  0.0004934602747535982 0.00072569013848946 73
AAAACC  0.0004003805362324795 0.0003686803641407804
AAAACG  9.064420497619743e-05 0.00010448394168197091
AAAACT  0.00040683999476466 18 0.0004784022870680216
AAAAGA  0.0004286539039061299 0.000774026596998453
...
```

CHAPTER

TWELVE

BUILD YOUR OWN LOGIT MODEL

Build logistic regression model ("prefix.logit.RData") required by `cpat`. This program will output 3 files:

- prefix.feature.xls: A table contains features calculated from training datasets (coding and noncoding gene lists).
- prefix.logit.RData: logit model required by CPAT (if R was installed).
- prefix.make_logitModel.r: R script to build the above logit model.

Note: Users can download prebuilt logit models for Human, Mouse, Fly and Zebrafish.

12.1 Usage

```
make_logitModel  [options]

Options:
  --version             show program's version number and exit
  -h, --help            show this help message and exit
  -c CODING_FILE, --cgene=CODING_FILE
                        Genomic sequnences of protein-coding RNAs in
                        FASTA or standard 12-column BED format. It is
                        recommended to use *short* and *unique* sequence
                        identifiers (such as Ensembl transcript id) in
                        FASTA and BED file. The input FASTA or BED file
                        could be a regular text file or compressed file
                        (*.gz, *.bz2) or accessible URL (http://, https://,
                        ftp://). When BED file is provided, use the ORF
                        defined in the BED file (the 7th and 8th columns in
                        BED file define the positions of 'start codon,
                        and 'stop codon', respectively). When FASTA file
                        is provided, searching for the longet ORF. For
                        well annotated genome, we recommend using BED file
                        as input because the longest ORF predicted from
                        RNA sequence might not be the real ORF. If this is
                        a BED file, reference genome ('-r/--ref') should be
                        specified.
  -n NONCODING_FILE, --ngene=NONCODING_FILE
                        Genomic sequences of non-coding RNAs in FASTA or
                        standard 12-column BED format. It is recommended to
                        use *short* and *unique* sequence identifiers (such as
                        Ensembl transcript id) in FASTA and BED file. The
```

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```
                        input FASTA or BED file could be a regular text file
                        or compressed file (*.gz, *.bz2) or accessible URL
                        (http://, https://, ftp://). If this is a BED file,
                        reference genome ('-r/--ref') should be specified.
  -o OUT_FILE, --outfile=OUT_FILE
                        The prefix of output files.
  -x HEXAMER_DAT, --hex=HEXAMER_DAT
                        Hexamer frequency table. CPAT has prebuilt hexamer
                        frequency tables for Human, Mouse, Fly, Zebrafish. Run
                        'make_hexamer_tab.py' to generate this table.
  -r REF_GENOME, --ref=REF_GENOME
                        Reference genome sequences in FASTA format.
                        Ignore this option if mRNA sequences file was provided
                        to '-g'. Reference genome file will be indexed
                        automatically if the index file  *.fai) does not
                        exist.
  -s START_CODONS, --start=START_CODONS
                        Start codon (use 'T' instead of 'U') used to
                        define the start of open reading frame (ORF).
                        default=ATG
  -t STOP_CODONS, --stop=STOP_CODONS
                        Stop codon (use 'T' instead of 'U') used to
                        define the end of open reading frame (ORF).
                        Multiple stop codons are separated by ','.
                        default=TAG, TAA, TGA
  --min-orf=MIN_ORF_LEN
                        Minimum ORF length in nucleotides.
                        default=30
  --log-file=LOG_FILE   Name of log file.
                        default="make_logitModel_run_info.log"
  --verbose             Logical to determine if detailed running
                        information is printed to screen.
```

12.2 Example-1: FASTA as input

```
make_logitModel -x Human_Hexamer.tsv -c Human_coding_transcripts_mRNA.fa.gz -n
Human_noncoding_transcripts_RNA.fa.gz -o Human
```

```
2024-01-25 10:41:34 [INFO]  Start codons used: "ATG"
2024-01-25 10:41:34 [INFO]  Stop codons used: "TAG, TAA, TGA"
2024-01-25 10:41:34 [INFO]  Reading hexamer frequency table file: "Human_Hexamer.tsv"
2024-01-25 10:41:34 [INFO]  Process protein-coding RNA file: "Human_coding_transcripts_
↪mRNA.fa.gz"
2024-01-25 10:41:34 [INFO]  Protein-coding RNA file "Human_coding_transcripts_mRNA.fa.gz
↪" is in FASTA format
2024-01-25 10:42:12 [INFO]  Total 17984 coding sequences finished.
2024-01-25 10:42:12 [INFO]  Process non-coding RNA file: "Human_noncoding_transcripts_
↪RNA.fa.gz"
2024-01-25 10:42:12 [INFO]  Non-coding RNA file "Human_noncoding_transcripts_RNA.fa.gz"␣
↪is in FASTA format
```

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```
2024-01-25 10:42:20 [INFO]  Total 11519 non-coding sequences finished.
2024-01-25 10:42:20 [INFO]  Wrting to "Human.feature.xls"
2024-01-25 10:42:20 [INFO]  Making logistic regression model from "Human.feature.xls" ...
...
```

12.3 Example-2: BED as input

```
$ make_logitModel -x Human_Hexamer.tsv -c Human_coding_transcripts_hg19.bed -n
Human_noncoding_transcripts_hg19.bed -r /database/hg19.fa -o Human
```

```
2024-01-25 10:44:45 [INFO]  Start codons used: "ATG"
2024-01-25 10:44:45 [INFO]  Stop codons used: "TAG, TAA, TGA"
2024-01-25 10:44:45 [INFO]  Reading hexamer frequency table file: "Human_Hexamer.tsv"
2024-01-25 10:44:45 [INFO]  Process protein-coding RNA file: "Human_coding_transcripts_
↪hg19.bed"
2024-01-25 10:44:45 [INFO]  Protein-coding RNA file "Human_coding_transcripts_hg19.bed"␣
↪is in BED format
...
```

CHAPTER

THIRTEEN

USE CPAT TO DETECT ORF

When using CPAT to find ORFs, it will gives exactly the same results as NCBI ORFfinder.

13.1 Prepare data

Below is the mRNA sequence of protein-coding gene UQCR10. Copy and save it as "test.fa".

```
>NM_013387.4
GCGGTGGCGCGAGTTGGACTGTGAAGAAACATGGCGGCCGCGACGTTGAC
TTCGAAATTGTACTCCCTGCTGTTCCGCAGGACCTCCACCTTCGCCCTCA
CCATCATCGTGGGCGTCATGTTCTTCGAGCGCGCCTTCGATCAAGGCGCG
GACGCTATCTACGACCACATCAACGAGGGGAAGCTGTGGAAACACATCAA
GCACAAGTATGAGAACAAGTAGTTCCTTGGAGGCCCCCATCCAGGCCAGA
AGGACCAGGTCCACCCAGCAGCTGTTTGCCCAGAGCTGGAGCCTCAGCTT
GAAGATGATGCTCAAGGTACTCTTCATGGACCACCATTCGCTGTTGGCAA
GAAACGGCTTTACTTACAAAACAGACTCTTTACCTTCTGCTGTGTTTGAA
GTATGTTTAGTCAGCATGCTCAGGAAATAAATGTGAATTGCCCTTGAGAC
CTGCTTCTACATTGGTTGCTTTGTTAACTCTACCTGATCTTCACTTGTCA
GTAATTTGAGACCACTTCAAAGCCCTCTGCAAACACCCCAAAGGCAGAAT
CTGCTATTTTGAGTTTTCCATTAACTTCCAAAGAATTCTGGTTTTCAAAA
CAGGAGCCAGAGTTGGAGATATTACAGTCAACTTTGGCTTCTAAGCCAGT
AATTCCATTCTTAAATACCTCACTGTCTTGGCCATGGGGAAGCACTATGG
CCTCAGCTGGGGGAAAGACCCTGGCCTAGGGGTCTTAGCCACTCCCCACC
CTAGGGTATAGTTCAGGGGTATCCAATCCTTTGGCTTCCCTGGGCCATGT
TGGAAGAATTGTCTTGGGCCACACATAAAATACAGTAACCATAGCTGATG
AGCTAAAACAAAAAACAATGGTTTGTGCAAAAATCTCATAATGTTTTAAT
AAAGTTGAAGAATTTG
```

13.2 Run CPAT

The command to run cpat.py is as below:

```
$ cpat -x Human_Hexamer.tsv -d Human_logitModel.RData --top-orf=100 --antisense -g test.
fa -o output
```

Note:

- You must specify `--antisense`, otherwise, it will only search ORFs from the sense strand.

- You also specify `--top-orf` to a large number to report all the ORFs.
- The `--min-orf` is set to 75 by default, same as NCBI ORFfinder.

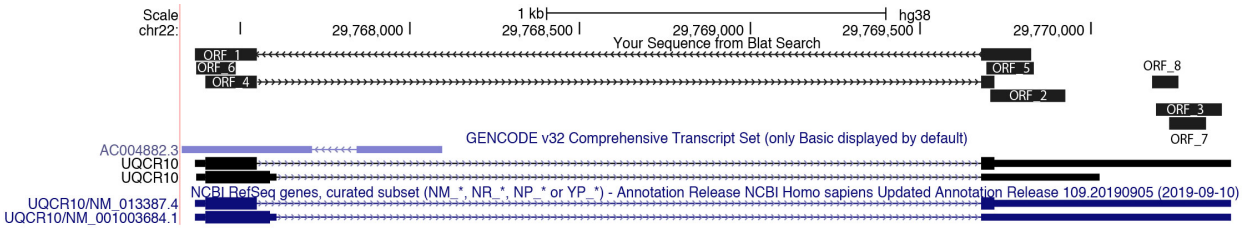
13.3 Check the results

A total of 8 ORFs were found (sorted by the ORF size, the 7th column). If you copy and paste the same sequence to NCBI ORFfinder web server, you will get **exactly the same** results.

```
$cat output.ORF_prob.tsv
```

```
ID      mRNA    ORF_strand      ORF_frame       ORF_start       ORF_end ORF     Fickett␣
↪Hexamer Coding_prob
NM_013387.4_ORF_1       916     -       2       327     1       327     1.103   0.
↪28998918917275         0.792763525921043
NM_013387.4_ORF_2       916     +       2       209     430     222     1.1605  0.
↪0674464550896935       0.271842476390681
NM_013387.4_ORF_3       916     -       1       889     695     195     0.9192  -0.
↪32000518247443        0.0113140534730678
NM_013387.4_ORF_4       916     +       1       31      222     192     1.2952  0.
↪600469985268255        0.915129459422605
NM_013387.4_ORF_5       916     -       1       337     197     141     1.1626  0.
↪133867810597757        0.185245402415541
NM_013387.4_ORF_6       916     -       3       119     3       117     1.2673  0.
↪442351820001225        0.618496534888714
NM_013387.4_ORF_7       916     -       3       842     735     108     0.5832  -0.
↪19401829042094        0.00290794398512764
NM_013387.4_ORF_8       916     +       3       684     761     78      0.7415  -0.
↪154613060436537       0.00454929869181486
```

CPAT offers **Fickett's TESTCODE score**, **Hexamer score**, and **coding probability** for each ORF. While the largest ORF is often the most probable for most mRNAs, it's not always the case. In the instance of NM_013387.4, the ORF_4 is the most likely to code for protein, evident from its highest coding probability, despite not being the largest ORF. This is confirmed through BLATing the 8 ORF sequences to the reference genome.



CHAPTER

FOURTEEN

HOW TO CHOOSE CUTOFF

Optimum cutoffs were determined from TG-ROC. For example, in human, coding probability (CP) cutoff >=0.364 indicates coding sequence, CP < 0.364 indicates noncoding sequence.

Table 1: Optimum cutoffs

Species	CP threshold	Sensitivity & Specificity
Human (*Homo sapiens*)	0.364	0.966
Mouse (*Mus musculus*)	0.44	0.955
Fly (*Drosophila melanogaster*)	0.39	0.963
Zebrafish (*Danio rerio*)	0.38	0.984

Here we provide the R code and the data that we used to generate Figure 3 **in our paper**. **Note the** ROCR **library is required to run our R code**.

1) Download R code and data from here

2) Put the R code and the data table in the same folder

```
$ ls
10Fold_CrossValidation.r       Human_train.dat
```

3) Run the R code from command line or console. The R code will perform 10-fold cross validation and generate Figure_3.

```
$ Rscript 10Fold_CrossValidation.r     # install ROCR before running this code

Loading required package: gplots
Attaching package: ‘gplots’
The following object is masked from ‘package:stats’:

    lowess

Loading required package: methods
Warning message:
package ‘gplots’ was built under R version 3.1.2
[1] "ID"      "mRNA"    "ORF"     "Fickett" "Hexamer" "Label"
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
```

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```
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
null device
          1
```

CHAPTER

FIFTEEN

HOW TO PREPARE TRAINING DATASET

We prebuild hexamer tables and logit models for human, mouse, fly and zebrafish. If you want to run CPAT for other species, you need to prepare your own training data.

- Optimal training datasets exhibit balance, where the count of coding sequences is approximately equal to that of noncoding sequences.
- In cases where the genome of your target species lacks sufficient annotation of 'coding' and 'noncoding' genes for constructing a training dataset, consider leveraging data from evolutionarily related species to build your model.

CHAPTER

SIXTEEN

EVALUATING PERFORMANCE

16.1 Figure-1

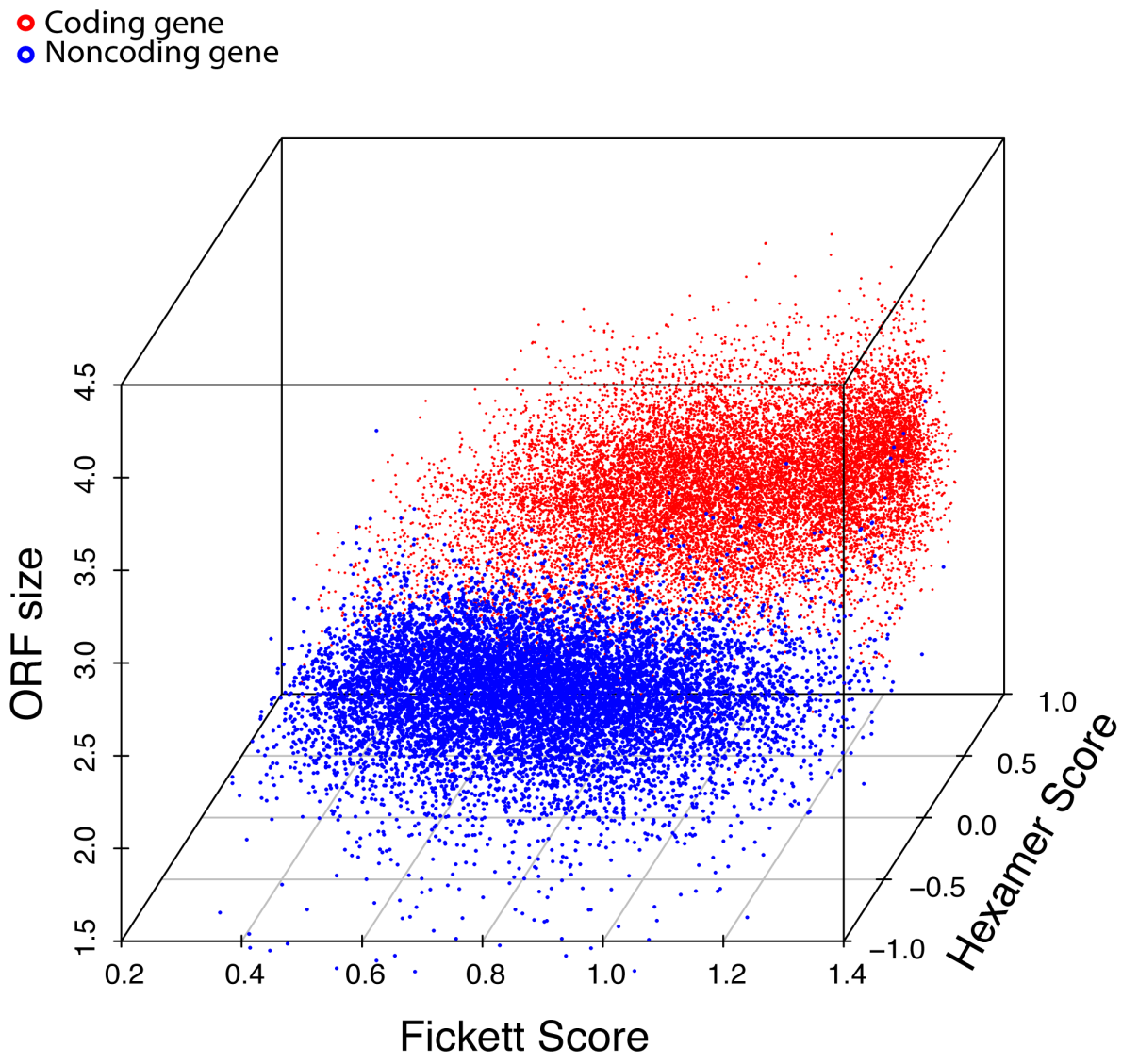
Combinatorial effects of 3 major features. 10,000 coding genes (red dots) and 10,000 noncoding genes (blue dots) are clearly separated into two clusters. (below figure)

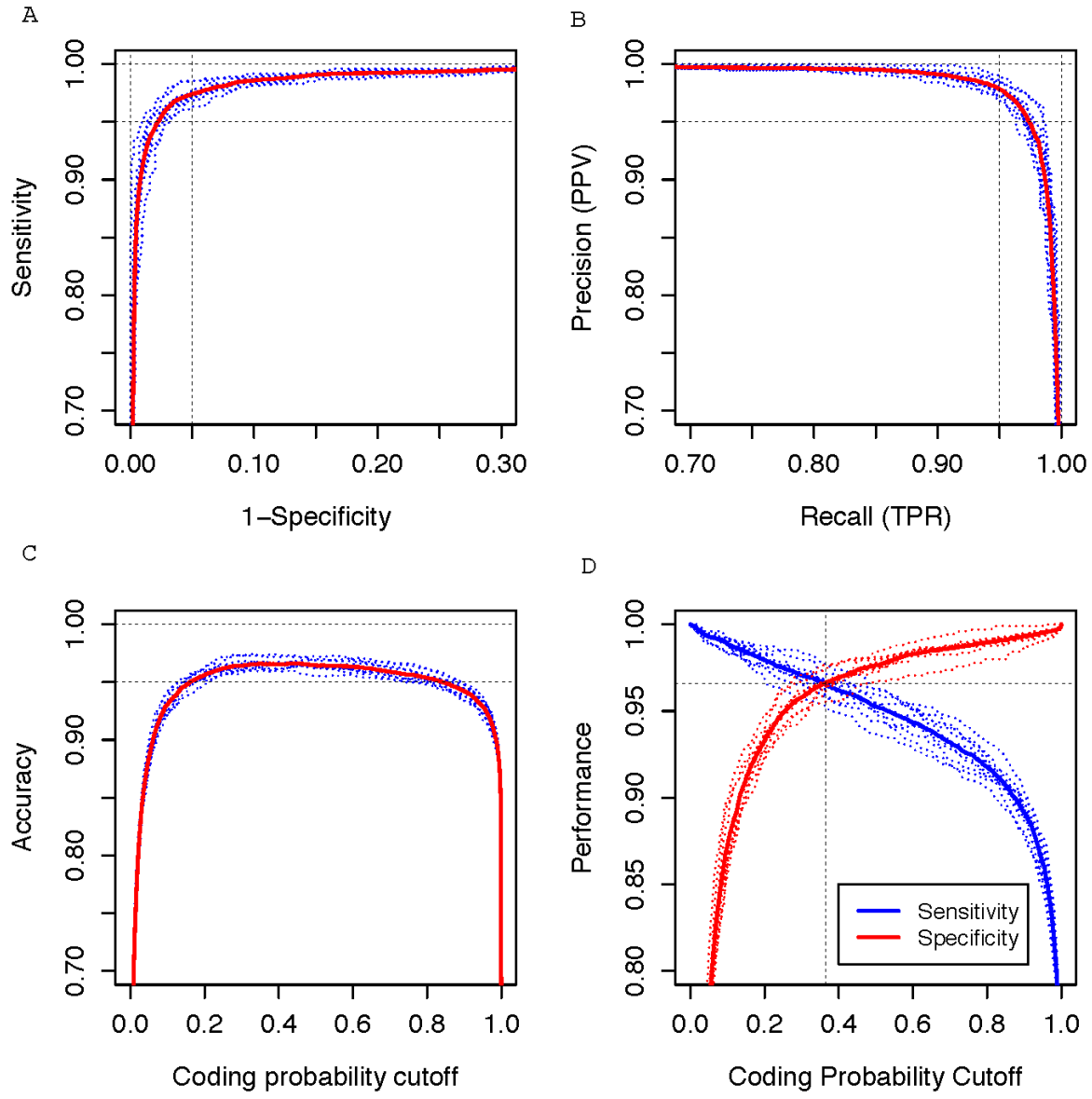
16.2 Figure-2

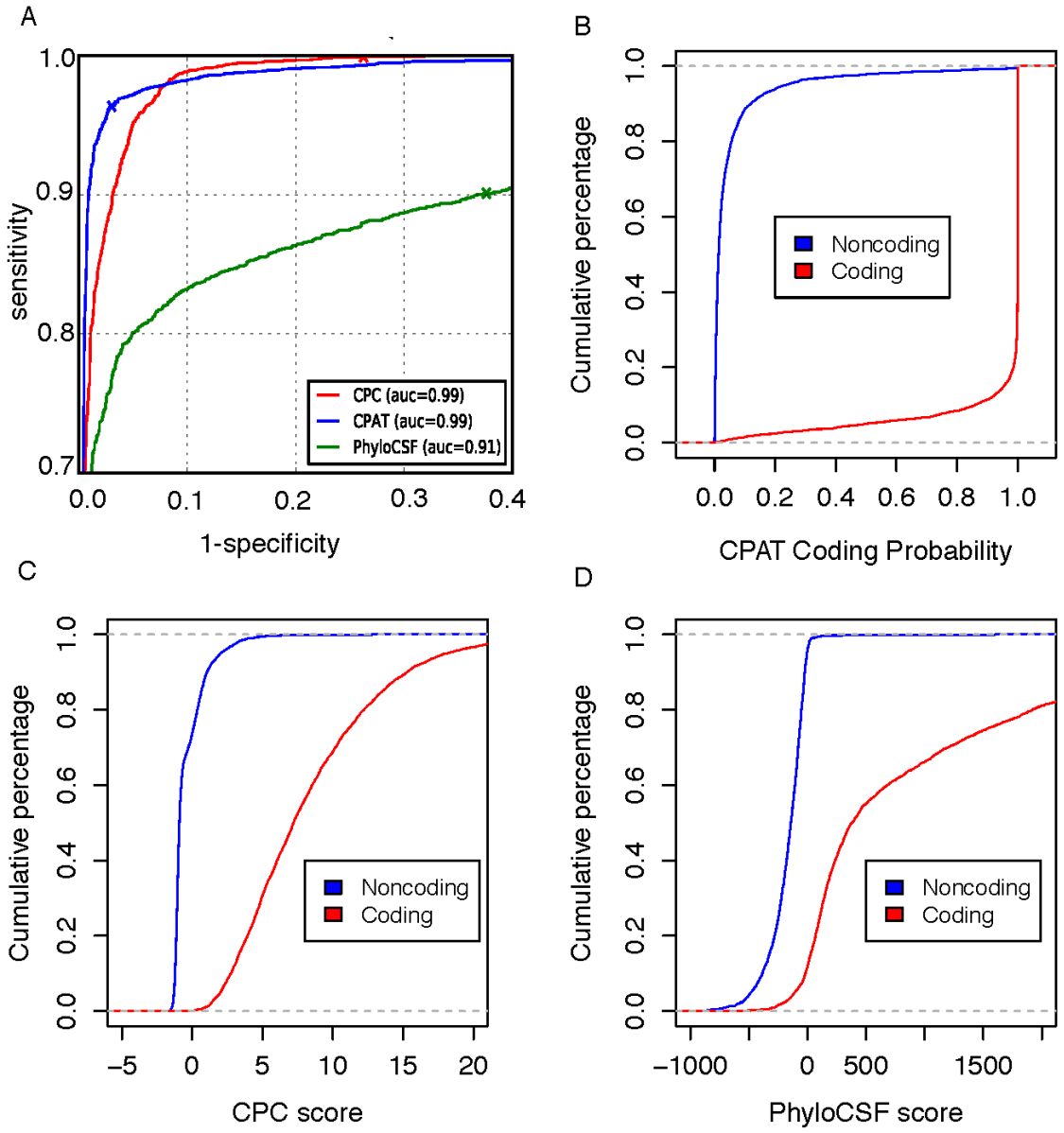
Performance evaluation was conducted using 10-fold cross-validation, considering a dataset comprising 10,000 coding genes and 10,000 noncoding genes. The blue dotted curves depict the results of individual 10-fold cross-validations, while the red solid curve represents the averaged curve across 10 validation runs. The evaluation metrics include: (A) ROC curve, (B) Precision-Recall (PR) curve, (C) Accuracy plotted against cutoff values, and (D) Two graphical ROC curves aimed at determining the optimum cutoff value.

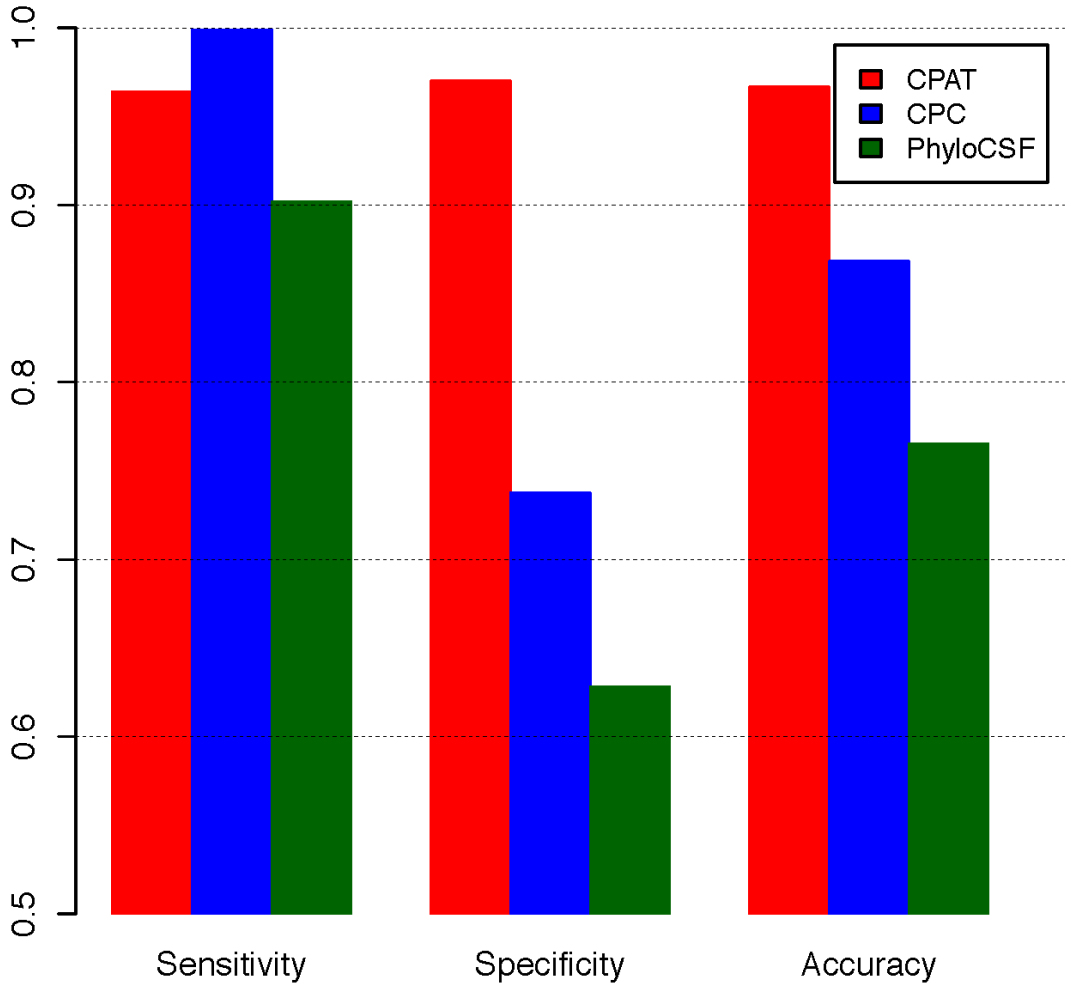
16.3 Figure-3

To compare CPAT with CPC and PhyloCSF, we build an independent testing dataset that composed of 4,000 high quality protein coding genes from Refseq annotation and 4,000 lincRNAs from Human lincRNA catalog (Cabili et al., 2011). All 8000 genes were not included in the training dataset of CPAT.


Coding gene
Noncoding gene
ORF size
1.5
2.0
2.5
3.0
3.5
4.0
4.5
0.2
0.4
0.6
0.8
1.0
1.2
1.4
Fickett Score
−1.0
−0.5
0.0
0.5
1.0
Hexamer Score


A
Sensitivity
1.00
0.90
0.80
0.70
0.00
0.10
0.20
0.30
1−Specificity
B
Precision (PPV)
1.00
0.90
0.80
0.70
0.70
0.80
0.90
1.00
Recall (TPR)
C
Accuracy
1.00
0.90
0.80
0.70
0.0
0.2
0.4
0.6
0.8
1.0
Coding probability cutoff
D
Performance
1.00
0.95
0.90
0.85
0.80
0.0
0.2
0.4
0.6
0.8
1.0
Coding Probability Cutoff
Sensitivity
Specificity


A
sensitivity
1-specificity
CPC (auc=0.99)
CPAT (auc=0.99)
PhyloCSF (auc=0.91)
B
Cumulative percentage
CPAT Coding Probability
Noncoding
Coding
C
Cumulative percentage
CPC score
Noncoding
Coding
D
Cumulative percentage
PhyloCSF score
Noncoding
Coding


1.0
0.9
0.8
0.7
0.6
0.5
CPAT
CPC
PhyloCSF
Sensitivity
Specificity
Accuracy

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REFERENCE

Wang, L., Park, H. J., Dasari, S., Wang, S., Kocher, J.-P., & Li, W. (2013). CPAT: Coding-Potential Assessment Tool using an alignment-free logistic regression model. Nucleic Acids Research, 41(6), e74. doi:10.1093/nar/gkt006

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Symbols