

# Package ‘PredCRG’

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**Type** Package

**Title** Computational Prediction of Proteins Encoded by Circadian Genes

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**Author** Prabina Kumar Meher <meherprabin@yahoo.com>

**Maintainer** Prabina Kumar Meher <meherprabin@yahoo.com>

**Depends** R(>= 3.3.3)

**Imports** Biostrings, protr,Peptides, kernlab, e1071

**LazyData** TRUE

**Description** A computational model for predicting proteins encoded by circadian genes. The support vector machine has been employed with Laplace kernel for prediction of circadian proteins, where compositional, transitional and physico-chemical features were utilized as numeric features. User can predict for the test dataset using the proposed computational model. Besides, the user can also build their own training model using their training dataset, followed by prediction for the test set.

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

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model1

*Trained model with the Q1 dataset.*

---

### Description

The model1 is the trained model with the Q1 dataset using the developed approach.

### Usage

```
data("model1")
```

### Details

Here, 1558 sequences of pos\_Q1 and neg\_Q1 datasets were used for training. For prediction, support vector machine with Laplace kernel has been trained in which compositional, transitional and physico-chemical features are utilized.

### See Also

[PredCRG](#), [PredCRG\\_Enc](#), [PredCRG\\_training](#)

### Examples

```
library(kernlab)
data(test)
nam <- names(test)

#encoding of test set using compositional, transitional and physico-chemical features
enc <- PredCRG_Enc(test)

#predicting test set using model1 as CRG or non-CRG
pred <- predict(model1, newdata=enc[1:10,], type="response")

#predicting probabilities of the test sequences using model1
pred1 <- predict(model1, newdata=enc[1:10,], type="probabilities")

#combining predicted labels and probabilities
result <- data.frame(seq_name=nam[1:10], predicted_label=as.character(pred)
,predicted_probability=pred1[, "CRG"])

print(result)
```

---

model2

*Trained model with the Q2 dataset.*

---

### Description

The model2 is the trained model with the Q2 dataset using the developed approach.

### Usage

```
data("model2")
```

### Details

Here, 1596 sequences of pos\_Q2 and neg\_Q2 datasets were used for training. For prediction, support vector machine with Laplace kernel has been trained in which compositional, transitional and physico-chemical features are utilized.

### See Also

[PredCRG](#), [PredCRG\\_Enc](#), [PredCRG\\_training](#)

### Examples

```
library(kernlab)
data(test)
nam <- names(test)

#encoding of test set using compositional, transitional and physico-chemical features
enc <- PredCRG_Enc(test)

#predicting test set using model2 as CRG or non-CRG
pred <- predict(model2, newdata=enc[1:10,], type="response")

#predicting probabilities of the test sequences using model2
pred1 <- predict(model2, newdata=enc[1:10,], type="probabilities")

#combining predicted labels and probabilities
result <- data.frame(seq_name=nam[1:10], predicted_label=as.character(pred)
,predicted_probability=pred1[, "CRG"])

print(result)
```

---

`model3`*Trained model with the Q3 dataset.*

---

### Description

The model3 is the trained model with the Q3 dataset using the developed approach.

### Usage

```
data("model3")
```

### Details

Here, 1593 sequences of pos\_Q3 and neg\_Q3 datasets were used for training. For prediction, support vector machine with Laplace kernel has been trained in which compositional, transitional and physico-chemical features are utilized.

### See Also

[PredCRG](#), [PredCRG\\_Enc](#), [PredCRG\\_training](#)

### Examples

```
library(kernlab)
data(test)
nam <- names(test)

#encoding of test set using compositional, transitional and physico-chemical features
enc <- PredCRG_Enc(test)

#predicting test set using model3 as CRG or non-CRG
pred <- predict(model3, newdata=enc[1:10,], type="response")

#predicting probabilities of the test sequences using model3
pred1 <- predict(model3, newdata=enc[1:10,], type="probabilities")

#combining predicted labels and probabilities
result <- data.frame(seq_name=nam[1:10], predicted_label=as.character(pred)
,predicted_probability=pred1[, "CRG"])

print(result)
```

---

model4

*Trained model with the Q4 dataset.*

---

### Description

The model4 is the trained model with the Q4 dataset using the developed approach.

### Usage

```
data("model4")
```

### Details

Here, 1365 sequences of pos\_Q4 and neg\_Q4 datasets were used for training. For prediction, support vector machine with Laplace kernel has been trained in which compositional, transitional and physico-chemical features are utilized.

### See Also

[PredCRG](#), [PredCRG\\_Enc](#), [PredCRG\\_training](#)

### Examples

```
library(kernlab)
data(test)
nam <- names(test)

#encoding of test set using compositional, transitional and physico-chemical features
enc <- PredCRG_Enc(test)

#predicting test set using model4 as CRG or non-CRG
pred <- predict(model4, newdata=enc[1:10,], type="response")

#predicting probabilities of the test sequences using model4
pred1 <- predict(model4, newdata=enc[1:10,], type="probabilities")

#combining predicted labels and probabilities
result <- data.frame(seq_name=nam[1:10], predicted_label=as.character(pred)
,predicted_probability=pred1[, "CRG"])

print(result)
```

---

PredCRG

*Prediction of circadian proteins using the proposed PredCRG model.*

---

## Description

The user can predict the protein sequences as CRG (circadian protein) or non-CRG (non-circadian protein) with certain probability by supplying the test sequences.

## Usage

```
PredCRG(seq_data)
```

## Arguments

seq_data	Sequence dataset in FASTA format consisting of protein sequences with standard amino acid residues only. It must be an object of class <code>AAStringSet</code> which can be obtained by reading sequences with <code>readAAStringSet</code> available in <code>Biostings</code> package.
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## Details

The user has to supply only the `seq_data` for which the prediction is to be made.

## Value

A dataframe with three columns consisting of sequence name, predicted labels of sequences (CRG or non-CRG) and probabilities of prediction.

## Author(s)

Prabina Kumar Meher, ICAR-Indian Agricultural Statistics Research Institute, New Delhi-110012, INDIA

## See Also

[PredCRG\\_Enc](#), [PredCRG\\_training,model1](#), [model2](#), [model3](#), [model4](#)

## Examples

```
data(test)
tst <- test[1:10]
PredCRG(seq_data=tst)
```

---

PredCRG\_data

*Training dataset of the PredCRG model.*

---

## Description

The dataset that has been used to train the PredCRG model contains four sub-datasets (Q1, Q2, Q3 and Q4) which are prepared based on the homogeneity of sequence length. The positive sets of the sub-datasets are denoted as pos\_Q1, pos\_Q2, pos\_Q3 and pos\_Q4 respectively, whereas the negative sets as neg\_Q1, neg\_Q2, neg\_Q3 and neg\_Q4 respectively. Further, same number of sequences are there in both positive and negative sets in each sub-dataset. More clearly, 1588, 1596, 1593 and 1365 sequences are present for both positive and negative sets for Q1, Q2, Q3 and Q4 sub-datasets respectively. Further, the range of the length of the sequences for pos\_Q1, pos\_Q2, pos\_Q3 and pos\_Q4 are 39-221, 221-363, 363-538, 538-1000 amino acids respectively, and the range of the length of the sequences for neg\_Q1, neg\_Q2, neg\_Q3 and neg\_Q4 are 43-407, 407-485, 485-607 and 607-1000 amino acids respectively. In this dataset, only the Q1 sub-dataset is available due to constraint of space in CRAN. However, one can get all the four sub-datasets from GitHub repository ([https://github.com/meher861982/PredCRG\\_dataset](https://github.com/meher861982/PredCRG_dataset)).

## Usage

```
data("PredCRG_data")
```

## Format

The datasets are in `AAStringSet` format, which can be obtained by reading the FASTA file using `readAAStringSet` function available in Biostrings package.

## Details

The protein sequences encoded by the circadian genes constitutes the positive datasets, whereas a randomly selected dataset from the **Uniprot** for the clad *Viridi plantae* constitutes the negative dataset.

## Source

The circadian gene sequences are collected from the circadian gene database accessible at <http://cgdb.biocuckoo.org/>.

## See Also

[PredCRG](#), [PredCRG\\_Enc](#), [PredCRG\\_training,model1](#), [model2,model3,model4](#)

## Examples

```
data(PredCRG_data)

pos_Q1 <- PredCRG_data$pos_Q1 #positive set of Q1 dataset
```

```
neg_Q1 <- PredCRG_data$neg_Q1 #negative set of Q1 dataset
```

---

PredCRG\_Enc                    *Encoding of protein sequence data in to numeric feature vector based on PredCRG features.*

---

### Description

Before using the protein sequences for prediction using the proposed model, the sequences must be transformed into numeric feature vectors. The function PredCRG\_Enc will transform each protein sequences to a numeric vector of 62 observations, based on the compositional, physico-chemical and transitional features used in the PredCRG model.

### Usage

```
PredCRG_Enc(prot_seq)
```

### Arguments

prot\_seq                    Sequence dataset to be supplied as input, must be an object of class [AAStringSet](#)

### Details

The dataset must contains the protein sequences having standard amino acid residues only. The clas [AAStringSet](#) can be obtained by reading the FASTA file using [readAAStringSet](#) available in bioconductor package Biostrings.

### Value

A matrix of dimension n\*62, for n number of sequences.

### Author(s)

Prabina Kumar Meher, ICAR-Indian Agricultural Statistics Research Institute, New Delhi-110012, INDIA

### See Also

[PredCRG](#), [PredCRG\\_training](#), [model1](#), [model2](#), [model3](#), [model4](#)

### Examples

```
data(test)
enc <- PredCRG_Enc(test)#encoding of test sequence data
enc[1:5,1:5]
```



---

PredCRG_training	<i>Training of the PredCRG model using the user supplied sequence dataset.</i>
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---

### Description

User can build their own PredCRG model by using their own training dataset. User has to supply the protein sequence dataset of both positive and negative classes having standard amino acid residues only.

### Usage

```
PredCRG_training(pos_seq, neg_seq, kern)
```

### Arguments

pos_seq	circadian protein sequence dataset (also called positive dataset), must be an object of class <a href="#">AAStringSet</a> .
neg_seq	non-circadian protein sequence dataset (also called negative dataset), must be an object of class <a href="#">AAStringSet</a> .
kern	Type of kernel to be used. It may be laplace, linear, polynomial or RBF.

### Details

The sequences must of [AAStringSet](#) type can be obtained by reading the FASTA file of the sequences using function [readAAStringSet](#) available in Biostrings package.

### Value

Support Vector Machine object of class [ksvm](#)

### Author(s)

Prabina Kumar Meher, ICAR-Indian Agricultural Statistics Research Institute, New Delhi-110012, INDIA

### See Also

[PredCRG](#), [PredCRG\\_Enc](#), [model1](#), [model2](#), [model3](#), [model4](#)

### Examples

```
library(kernlab)
pos_Q1 <- PredCRG_data$pos_Q1
neg_Q1 <- PredCRG_data$neg_Q1

#training of the model using laplace kernel.
user_model <- PredCRG_training(pos_seq=pos_Q1[1:100], neg_seq=neg_Q1[1:100], kern="laplace")
```

```
data(test)
tst_enc <- PredCRG_Enc(test[1:10])#encoding of the test set
predict(user_model, tst_enc, type="response") #predicting the label of the test instances
predict(user_model, tst_enc, type="probabilities")#predicting the probability of the test instances

library(e1071)
#training of the model using RBF kernel.
user_model <- PredCRG_training(pos_seq=pos_Q1[1:100], neg_seq=neg_Q1[1:100], kern="RBF")
predict(user_model, tst_enc, probability=TRUE) #Predicting probability
predict(user_model, tst_enc) #Predicting labels
```

---

test	<i>Test dataset.</i>
------	----------------------

---

### Description

A test dataset containing 54 circadian protein sequences collected from literature. This dataset has been used as an independent test dataset for assessing the prediction accuracy of PredCRG model.

### Usage

```
data("test")
```

### See Also

[PredCRG](#), [PredCRG\\_Enc](#), [PredCRG\\_data](#)

### Examples

```
data(test)
PredCRG(test[1:10])
```

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