

# Package ‘BCRANK’

September 23, 2012

**Title** Predicting binding site consensus from ranked DNA sequences

**Version** 1.18.0

**Date** 2010-08-25

**Depends** methods

**Author** Adam Ameur <Adam.Ameur@genpat.uu.se>

**Description** Functions and classes for de novo prediction of transcription factor binding consensus by heuristic search

**Maintainer** Adam Ameur <Adam.Ameur@genpat.uu.se>

**License** GPL-2

**LazyLoad** true

**Collate** AllClasses.R AllGenerics.R methods-BCRANKmatch.R  
methods-BCRANKsearch.R methods-BCRANKresult.R BCRANK.R

**Imports** Biostrings

**Suggests** seqLogo

**biocViews** SequenceMatching

## R topics documented:

bcrank . . . . .	2
BCRANKmatch-class . . . . .	3
BCRANKout . . . . .	4
BCRANKresult-class . . . . .	4
BCRANKsearch-class . . . . .	5
matchingSites . . . . .	6
<b>Index</b>	<b>7</b>

---

bcrank *BCRANK: predicting binding site consensus from ranked DNA sequences*

---

### Description

This function implements an algorithm for detection of short DNA sequences that are overrepresented in some part of the list. Starting from some initial consensus DNA sequence coded in IUPAC symbols, the method uses a heuristic search to improve the consensus until a local optimum is found. Individual predicted binding sites can be reported by the function [matchingSites](#).

### Usage

```
bcrank(fafile, startguesses=c(), restarts=10, length=10,
       reorderings=500, silent=FALSE, plot.progress=FALSE,
       do.search=TRUE, use.P1=FALSE, use.P2=TRUE, strip.desc=TRUE)
```

### Arguments

fafile	a ranked fasta file containing DNA sequences.
startguesses	a character vector with consensus sequences in IUPAC coding to be used as starting sequences in the search. If empty, random start guesses will be generated.
restarts	number restarts of the algorithm when using random start guesses.
length	length of random start guess.
reorderings	number of random reorderings of the DNA sequences performed when calculating score.
silent	reports progress status if FALSE.
plot.progress	if TRUE, the progress is displayed in a plot.
do.search	if FALSE, no search is performed. In that case the start guesses are assigned with scores and reported as results.
use.P1	Use penalty for bases other than A,C,G,T.
use.P2	Use penalty for motifs matching repetitive sequences.
strip.desc	An argument used by the function <a href="#">readFASTA()</a> . It specifies whether or not the ">" marking at the beginning of description lines should be removed.

### Value

The method returns an object of class [BCRANKresult-class](#).

### Author(s)

Adam Ameer, <adam.ameur@genpat.uu.se>

### References

Ameer, A., Rada-Iglesias, A., Komorowski, J., Wadelius, C. Identification of candidate regulatory SNPs by combination of transcription factor binding site prediction, SNP genotyping and haploChIP. *Nucleic Acids Res*, 2009, 37(12):e85.

**See Also**

[matchingSites](#), [BCRANKresult-class](#)

**Examples**

```
## Load example fasta file
fastaFile <- system.file("Exfiles/USF1_small.fa", package = "BCRANK")
## Run BCRANK
## Not run: BCRANKout <- bcrank(fastaFile, restarts=20)

## Show BCRANK results
toptable(BCRANKout)
## The top scoring result
topMotif <- toptable(BCRANKout,1)
## Plot BCRANK search path
plot(topMotif)
## Position Weight Matrix
pwm(topMotif, normalize=FALSE)
```

---

BCRANKmatch-class      *Class "BCRANKmatch"*

---

**Description**

Holds the [bcrank](#) score for one IUPAC consensus sequence. Several objects of this class are collected in a [BCRANKsearch-class](#) object

**Objects from the Class**

Objects are not intended to be created directly but as a result from running [bcrank](#).

**Slots**

**consensus:** consensus sequence in IUPAC coding  
**bcrankScore:** bcrank score for the consensus  
**matchVec:** vector with 0's (no match) and 1's (match) of same length as the ranked DNA sequences

**Methods**

**consensus** signature(object = "BCRANKmatch"): Returns the consensus sequence.  
**bcrankScore** signature(object = "BCRANKmatch"): Returns the bcrank score.  
**matchVector** signature(object = "BCRANKmatch"): Returns a vector with 0's (no match) and 1's (match) of same length and order as the ranked DNA sequences.

**Author(s)**

Adam Ameer, <adam.ameur@genpat.uu.se>

**See Also**

[bcrank](#), [BCRANKsearch-class](#)

---

BCRANKout

*BCRANK results for USF1 ChIP-chip data*


---

### Description

Results from running bcrank on USF1 whole genome ChIP-chip data for the human liver cell line HepG2.

### Usage

```
data(BCRANKout)
```

### Source

Data from whole genome ChIP-chip experiments on human liver cell line HepG2. (Rada-Iglesias, A., et al. 2007)

### References

Rada-Iglesias, A., et al. (2007) Whole-genome maps of USF1 and USF2 binding and histone H3 acetylation reveal new aspects of promoter structure and candidate genes for common human disorders. *Genome Research*, Accepted

### See Also

[bcrank](#)

---

BCRANKresult-class

*Class "BCRANKresult"*


---

### Description

Holds the results from running [bcrank](#). Contains a number of [BCRANKsearch-class](#) object, one for each restart of the bcrank search.

### Slots

**fname**: the name of the fasta file used for running bcrank.  
**toplist**: a list of BCRANKsearch-class objects, ranked by their scores.  
**funCall**: the function call that was made to bcrank.  
**nrSeqs**: number of sequences in the fasta input file.  
**restarts**: number of restarts used in the bcrank search.

### Methods

**fname** signature(object = "BCRANKmatch"): Returns the fasta file name.  
**toplist** signature(object = "BCRANKmatch", i=NULL): If i is NULL, returns a data frame containing consensus and score for the results for each restart of the bcrank search. Otherwise, the i'th BCRANKsearch-class object in the toplist is returned.

**Author(s)**

Adam Ameur, <adam.ameur@genpat.uu.se>

**See Also**

[bcrank](#), [BCRANKsearch-class](#),

---

BCRANKsearch-class     *Class "BCRANKsearch"*

---

**Description**

Holds the whole search path from a single [bcrank](#) run. Each individual search step is stored in a [BCRANKmatch-class](#) object. Several objects of this class are collected in a [BCRANKresult-class](#) object

**Objects from the Class**

Objects are not intended to be created directly but as a result from running [bcrank](#).

**Slots**

**searchPath**: a collection of [BCRANKmatch-class](#) objects, containing all [bcrank](#) search steps from a start guess to a locally optimal solution.

**final**: a [BCRANKmatch-class](#) object for the highest scoring consensus sequence (locally optimal solution) in this [bcrank](#) run.

**finalPWM**: position weight matrix for the highest scoring consensus sequence.

**finalNrMatch**: number of occurrences of the final consensus sequence in the fasta input file.

**nrIterations**: number of iterations required to move from the start guess to the final solution in this [bcrank](#) run.

**Methods**

**searchPath** signature(object = "BCRANKsearch", i=NULL): If i is NULL, returns a data frame containing consensus and score for the whole search path. Otherwise, the i'th [BCRANKmatch-class](#) object in the search path is returned.

**pwm** signature(object = "BCRANKsearch", normalize=TRUE): Returns the position weight matrix (pwm) for the highest scoring consensus in this [bcrank](#) run. Matrix positions are between 0 and 1 when normalize is TRUE. When FALSE, the number of matching sequences is reported.

**plot** signature(x = "BCRANKsearch", y = "missing"): A plot method for the searchPath.

**Author(s)**

Adam Ameur, <adam.ameur@genpat.uu.se>

**See Also**

[bcrank](#), [BCRANKmatch-class](#), [BCRANKresult-class](#)

---

matchingSites	<i>Report IUPAC consensus occurrences in a fasta file</i>
---------------	---

---

**Description**

This function reports all occurrences of a consensus sequence in a fasta file. It can be used to extract transcription factor binding sites predicted by BCRANK or other motif search methods.

**Usage**

```
matchingSites(fafile, motifSequence, revComp=TRUE, strip.desc=TRUE)
```

**Arguments**

fafile	a ranked fasta file containing DNA sequences.
motifSequence	a character vector in IUPAC coding representing a DNA sequence.
revComp	set to TRUE if the reverse complement also be matched.
strip.desc	An argument used by the function <a href="#">readFASTA()</a> . It specifies whether or not the ">" marking at the beginning of description lines should be removed.

**Value**

Returns a data frame with positions, strand and DNA sequence for the matching sites.

**Author(s)**

Adam Ameer, <adam.ameur@genpat.uu.se>

**References**

Ameer, A., Rada-Iglesias, A., Komorowski, J., Wadelius, C. Identification of candidate regulatory SNPs by combination of transcription factor binding site prediction, SNP genotyping and haploChIP. *Nucleic Acids Res*, 2009, 37(12):e85.

**See Also**

[bcrank](#)

# Index

## \*Topic **classes**

- BCRANKmatch-class, 3
- BCRANKresult-class, 4
- BCRANKsearch-class, 5

## \*Topic **datasets**

- BCRANKout, 4

## \*Topic **methods**

- bcrank, 2
- matchingSites, 6

bcrank, 2, 3–6

BCRANKmatch (BCRANKmatch-class), 3

BCRANKmatch-class, 3

BCRANKout, 4

BCRANKresult (BCRANKresult-class), 4

BCRANKresult-class, 4

bcrankScore (BCRANKmatch-class), 3

BCRANKsearch (BCRANKsearch-class), 5

BCRANKsearch-class, 5

consensus (BCRANKmatch-class), 3

fname (BCRANKresult-class), 4

matchingSites, 2, 3, 6

matchVector (BCRANKmatch-class), 3

plot,BCRANKsearch,missing-method  
(BCRANKsearch-class), 5

pwm (BCRANKsearch-class), 5

readFASTA(), 2, 6

searchPath (BCRANKsearch-class), 5

toptable (BCRANKresult-class), 4