

# BCRANK: predicting binding site consensus from ranked DNA sequences

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## 1 Introduction

This document describes the **BCRANK** R package. **BCRANK**[1] is a method that takes a ranked list of genomic regions as input and outputs short DNA sequences that are overrepresented in some part of the list. The algorithm was developed for detecting transcription factor (TF) binding sites in a large number of enriched regions from high-throughput ChIP-chip or ChIP-seq experiments, but it can be applied to any ranked list of DNA sequences.

**BCRANK** uses a heuristic search strategy. First a score is computed for an initial short consensus sequence, typically selected at random. The score takes into account both the number of consensus occurrences and the rank of the genomic regions. Then all consensus sequences in a neighborhood of the start guess are evaluated and the one with highest score is kept as the starting point for the next iteration. Once the algorithm finds a local optimum, the algorithm is terminated and the locally optimal consensus is reported as a result. In order to increase the chance of detecting the globally optimal solution, the algorithm may be restarted several times using different random starting points. Alternatively, **BCRANK** can be used for assigning scores to previously established consensus sequences. The sections below describe in more detail how the neighborhood, scoring function and start guess are implemented.

The main aim of **BCRANK** is to predict the sequences that are bound by TF, and not necessarily to generate a perfect position weight matrix. Therefore **BCRANK** implements two penalties to give relatively higher scores to consensus sequences that are more likely to be bound by the TF. The effect of the penalties is that i) consensus sequences contain as few redundant bases as possible (i.e. not in *A, C, G, T*), and ii) the consensus should not be frequently occurring as a repetitive element in the input regions.

### 1.1 Neighborhood

In **BCRANK**, all consensus sequences are represented by IUPAC nucleotide symbols. The neighborhood of one consensus sequence  $s$  consists of all consensus sequences that can be generated from  $s$  by first adding one IUPAC letter N (representing any nucleotide) to either side of  $s$  and then flipping any base to any other IUPAC symbol. Since there are 15 symbols in total, a sequence of length  $l$  will have  $14 \cdot (l + 2)$  neighbors. After each search step any flanking Ns are removed from the highest scoring sequence in the neighborhood. The removal and additions of flanking Ns allows the algorithm to shorten and extend the predicted binding sites.

## 1.2 Scoring function

The score tells whether a given consensus sequence is overrepresented in some part of the ranked list or not. Starting from  $N$  ranked regions and a consensus sequence  $c$ , a binary vector of size  $N$  is created, with 1 at position  $i$  if  $c$  is occurring in sequence number  $i$ , and 0 if not. The reverse complement of  $c$  is also allowed to match. Then the cumulative sum of the match vector is computed and stored in a vector called  $A$ . The  $A$ -vector tells where in the ranked list most occurrences are located (see Figure 1).

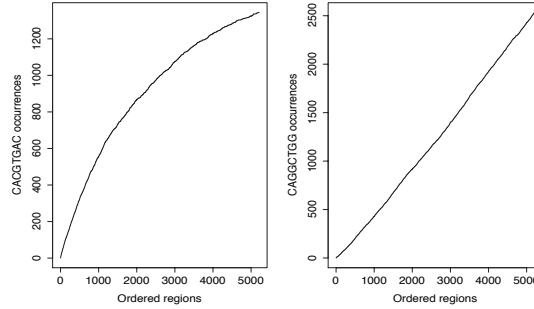


Figure 1:  $A$ -vectors for the two consensus sequences **CACGTGAC** (left) and **CAGGCTGG** (right). On the x-axis are the top 5211 regions from a whole genome ChIP-chip study on USF1 in human liver cells[2], ranked by their enrichment signal. The aim of **BCRANK** is to detect sequences that are biased towards some part of the list. Therefore **CACGTGAC** will get a higher score than **CAGGCTGG** even though it has a lower number of total occurrences. It is important to have enough number of ranked input regions to **BCRANK**, so this bias is observed for the correct binding motif. The established USF1 binding sequence is **CACGTG**.

To compute a score,  $A$  is compared to what it would look like if the genomic regions were randomly ordered. Therefore a large number  $R$  (the **reorderings** parameter to **bcrank()**) of random orderings of the input regions are generated, and a corresponding vector  $A_j$  is computed for each re-ordering  $1 \leq j \leq R$  as above. For each  $j$ , the difference  $D_j$  between  $A_j$  and  $A$  is estimated by the area between  $A$  and  $A_j$  (see Figure 2). When calculating  $D_j$ , the  $A$  and  $A_j$  vectors are first scaled so they range between 0 and 1.

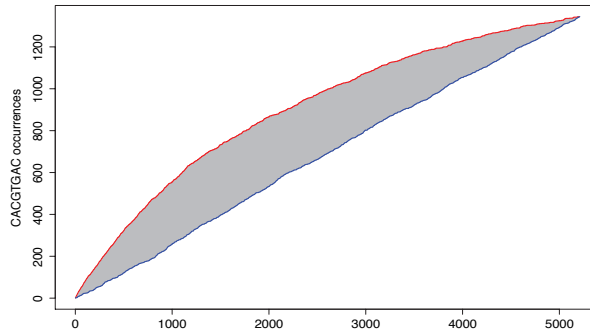


Figure 2: The vector  $A$  (red line) and a corresponding vector  $A_j$  (blue line) for **CACGTGAC** in the USF1 data. There is a clear bias towards the high scoring sequences as indicated by the red line. The significance of this bias can be estimated by comparing to the **CACGTGAC**-occurrences in randomly ordered regions, as indicated by the blue line.  $D_j$  corresponds to the grey area between the two lines.

$D_j$  will be close to zero when the consensus occurrences are distributed as expected by random

sampling. If on the other hand all  $D_j$  are far off from zero,  $c$  is biased towards some part of the list. Therefore the score is calculated as the t-statistic  $T$  for the  $D_j$  being drawn from a distribution centered around zero. Consensus sequences that are biased towards some part of the list will thus get high scores whereas consensus sequences with no bias will get low scores. Moreover, consensus sequences that are matching just a few regions will not get a high  $T$  even if it is matching only among the top ranked regions. This is because there will be a high variation within the  $D_j$  values which will result in a low  $T$ .

### 1.2.1 Penalties

The t-statistic gives consensus sequences that are biased towards some part of the list. But there may be other issues to take into account if the aim is to detect TFBS from ChIP-chip or ChIP-seq data. Therefore, BCRANK implements two penalties,  $P1$  and  $P2$ , with values between 0 and 1. The final scoring function is defined as:  $score = T \cdot P1 \cdot P2$ .

- $P1$  - Penalty on non-specific bases. Let  $l$  be the length of the consensus sequence and  $b$  the total number of fixed bases (A, C, G, T) in the sequence. If there are no fixed bases,  $b$  is set to 0.5. The penalty is then defined as  $P1 = b/l$ .
- $P2$  - Penalty on repetitive motifs. Let  $r_n, n \in 1, 2$  be the number of input DNA regions that contain at least  $n$  occurrences of the consensus. Then  $P2 = 1 - (r_2/r_1)$ .

## 1.3 Start guess

In case the algorithm is used for ab initio search, the initial guess is a randomly generated consensus of a specified length (the `length` parameter to `bcrank()`), with 10 bases as default. Multiple restarts with different random start guesses are usually required to increase the chance of finding the globally optimal solution. The number of restarts is determined by the `restarts` parameter.

BCRANK can also use start guesses passed to `bcrank()` by the `startguesses` parameter. By setting the `do.search` parameter to `FALSE`, BCRANK assigns scores for the given start guesses without performing any search.

## 1.4 Additional information

Some other important details:

- The algorithm is non-deterministic because of the random re-orderings when the score is calculated. This also implies that the same consensus sequence will get different BCRANK scores in the same data when run with different re-orderings. The variability in scores can be decreased by increasing the `reorderings` parameter
- The algorithm performs a breadth-first search, meaning that the highest scoring neighbor in the neighborhood is selected in each search step.
- The algorithm keeps track of all consensus sequences that have already been tested so the same sequence is not visited twice when performing a search.

## 2 BCRANK - An example run

The user is required to load the package using the `library()` command:

```
> library(BCRANK)
```

### 2.1 Sequence data

BCRANK takes a fasta file containing ranked sequences as input. The command below loads an example file containing 2500 ranked regions from a whole genome ChIP-chip experiment for the protein USF1 in the human liver cell line HepG2[2].

```
> fastaFile <- system.file("Exfiles/USF1_small.fa", package = "BCRANK")
```

### 2.2 Running BCRANK

The `bcrank()` function call below runs the BCRANK algorithm on the example USF1 data set. The `set.seed()` call sets seed for the random number generator for reproducibility.

```
> set.seed(0)
> BCRANKout <- bcrank(fastaFile, restarts=25)
```

Since it takes some time to run the algorithm, results can instead be loaded from a previous run on a larger USF1 data set containing the top 5211 regions:

```
> data(BCRANKout)
```

### 2.3 BCRANK output

An object of type `BCRANKresult` is returned:

```
> BCRANKout
```

An object of class "BCRANKresult"

Top 25 DNA motifs predicted by BCRANK:

	Consensus	Scores
1	GTCACGTG	316.34270
2	CACGTGAC	304.59499
3	CGCGGA	147.04100
4	GCGAST	135.22207
5	AHATAATAA	128.92440
6	GCGGNGCG	121.87198
7	TNCDGGGCG	119.76454
8	GCGGGGVNG	119.65945
9	CCGCGNTBY	118.77481
10	GDGCGGHGH	115.19679
11	TNCGCGNDG	112.95972
12	CGGGNGMGC	111.93052
13	GNNDCTGCS	111.12770
14	CGCGNNBCTBC	107.91403

15	CGGWSCVGA	93.88154
16	TNNCCAVCG	90.63345
17	GCACANAT	84.98763
18	KTNAGABCCT	84.08165
19	TATANBDAC	80.98513
20	AACAKADTDA	79.75340
21	CCVVDDGGACG	78.86994
22	CTCRATTGHT	74.67093
23	CTATKANYWMA	68.48067
24	CBCNCGHANTR	67.87154
25	KCRTKAHTDC	52.30902

Use methods `toptable(object)` and `fname(object)` to access object slots.

### 2.3.1 The BCRANKsearch object

Use the `toptable()` function to access information about each motif found by `bcrank`. It returns an object of type `BCRANKsearch`:

```
> topMotif <- toptable(BCRANKout, 1)
> topMotif
```

An object of class "BCRANKsearch"

Search path, starting from VGKTHVBRTB:

	Consensus	Score
1	VGKTHVBRTB	6.516874
2	CGKTHVBRTB	47.627369
3	CGKTHVBRTG	73.217992
4	CGKTCVBRTG	88.236721
5	CGKTCVCRTG	105.752733
6	GKTCVCRTG	142.234278
7	GKTCACRTG	188.156513
8	GGTCACRTG	235.594317
9	GGTCACGTG	255.725078
10	GTCACGTG	316.342696

Position weight matrix for search result (GTCACGTG):

	1	2	3	4	5	6	7	8
A	0	0	0	1	0	0	0	0
C	0	0	1	0	1	0	0	0
G	1	0	0	0	0	1	0	1
T	0	1	0	0	0	0	1	0

Use methods `searchPath(object)` and `pwm(object)` to access object slots.

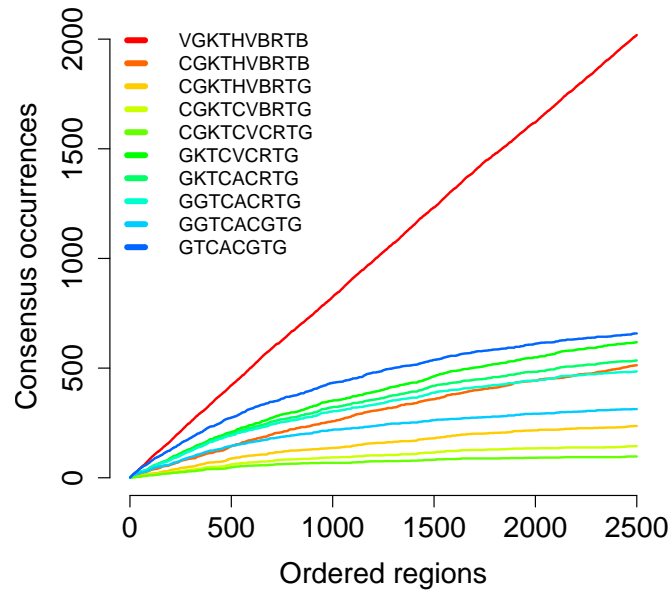
The `pwm()` function returns the position weight matrix for the search result. If `normalize` is set to `TRUE` each column will sum to 1.

```
> weightMatrix <- pwm(topMotif, normalize = FALSE)
> weightMatrix
```

	1	2	3	4	5	6	7	8
A	0	0	0	759	0	0	0	0
C	0	0	759	0	759	0	0	0
G	759	0	0	0	0	759	0	759
T	0	759	0	0	0	0	759	0

The search path can be visualized. For each consensus in the search path, the number of occurrences among the ranked regions are plotted. As seen in the figure, **BCRANK** searches for consensus sequences that don't give straight lines.

```
> plot(topMotif)
```



## References

- [1] Ameur, A., Rada-Iglesias, A., Komorowski, J., Wadelius, C. *Novel algorithm and ChIP-analysis identifies candidate functional SNPs*. Submitted
- [2] Rada-Iglesias, A., Ameur, A., Kapranov, P., Enroth, S., Komorowski, J., Gingeras, T. R., Wadelius, C. *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 Res. 2008 Jan 29