

# Algorithmic Bioinformatics Burrow-Wheeler Algorithm

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## Abstract

BLAST has been used for many years when aligning short reads against genomes but it is not fast enough any more. We describe BWA: A fast and accurate short read alignment with Burrows-Wheeler transform.

By Hang Le and Richard Durbin

## 1 Introduction

Given a query  $W$  with respect to a database(genome) BWA can, after some preprocessing, give back an exact match in time  $\mathcal{O}(|W|)$ .

### 1.1 Preprocessing

- Let  $\Sigma$  be an lexicographic alphabet, for example  $\Sigma = \{A, C, G, T\}$ , with  $\$$  being the smallest element, the rest can be in any order.
- Let  $X = x_0x_1 \dots x_{n-1}$  where  $x_i \in \Sigma$ ,  $0 \leq i \leq n-2$  and  $x_{n-1} = \$$ .
- We say that  $X[i] = x_i$ ,  $0 \leq i \leq n-1$ , is the  $i$ :th symbol of  $X$ ,  $X^{\geq i} = x_i \dots x_{n-1}$  is a suffix string of  $X$  and  $X^{\geq i, \leq j} = x_i \dots x_j$ .
- A suffix array(SA) for  $X$  is an array  $S$  where  $S[i]$  is the start position of the  $i$ :th smallest suffix of  $X$ .
- The Burrows-Wheeler Transform of  $X$  is defined as follows:

$$B[i] = \begin{cases} \$ & \text{if } S[i] = 0, \\ X(S[i] - 1) & \text{otherwise.} \end{cases}$$

- We also define the length of string  $X$  as  $|X|$  and therefore we have that  $|X| = |B| = n$ .

**Example**

Our genome = googol so  $X = \text{googol\$}$

<i>Positions</i>	<i>Suffixes</i>
0	googol\$
1	oogol\$g
2	ogol\$go
3	gol\$goo
4	ol\$goog
5	l\$googo
6	\$googol

Sorting  $\implies$

<i>i</i>	<i>S(i)</i>	<i>Suffixes</i>	<i>StartPositions</i>
0	6	\$googo	l
1	3	gol\$go	o
2	0	googol	\$
3	5	l\$goog	o
4	2	ogol\$g	o
5	4	ol\$goo	g
6	1	oogol\$	g

Here we have sorted the suffixes in lexicographical order.

The positions of the first symbols form the suffixarray  $S(i) = (6, 3, 0, 5, 2, 4, 1)$  and the concatenation of the last symbols of the circulated strings gives the BWT string  $B[i] = \text{lo$oogg}$ .

**End of example**

**Observe**

Each occurrence of  $W$  is in a interval of the Suffix Array  $S$ .

We will search for the so called  $SA$  interval of  $W$ .

**Definition 1.** The  $SA$  interval of  $W$  is  $[\underline{R}(W), \overline{R}(W)]$  where

$$\underline{R}(W) = \min\{k: W \text{ is a prefix of } X^{\geq S(k)}\} \tag{1}$$

$$\overline{R}(W) = \max\{k: W \text{ is a prefix of } X^{\geq S(k)}\} \tag{2}$$

**Observe**

All occurrences of  $W$  in  $X$  have startposition in

$$\{S(k) : \underline{R}(W) \leq k \leq \overline{R}(W)\}$$

Moreover  $\underline{R}(W) \leq \overline{R}(W)$  if and only if  $W$  occur in  $X$ .

**Theorem** (Ferragine, Manzini, 2000)

Let  $c(a) =$  The number of  $i$  such that  $X_i$  is lexicographically smaller than  $a \in \Sigma$   
and let

$O(a, i) =$  The number of occurrences of  $a$  in  $B^{\geq 0, \leq i}$   
then

$$\begin{aligned} \underline{R}(aW) &= c(a) + O(a, \underline{R}(W) - 1) + 1 \\ \overline{R}(aW) &= c(a) + O(a, \overline{R}(W)) \end{aligned}$$

Where  $aW$  is the symbol  $a$  concatenated to the string  $W$ .

For example if our original query was  $W = \text{ogo}$  then in the theorem above  $a = o$  and  $W = \text{go}$ .

In particular for the empty string  $\varepsilon$ , we have that  $\underline{R}(\varepsilon) = 0$  and  $\overline{R}(\varepsilon) = n - 1$

### Observations

(i) All suffixes starting with a symbol which is lexicographically smaller than  $a$  will appear before  $aW$

$$\Rightarrow \underline{R}(aW) \geq c(a)$$

(ii) Some suffixes in  $[0, \underline{R}(W) - 1]$  are preceded by an  $a$

$$\Rightarrow \underline{R}(aW) \geq c(a) + O(a, \underline{R}(W) - 1)$$

Moreover any suffixes preceding  $aW$  is of the type (i) or (ii) so

$$\Rightarrow \underline{R}(aW) = c(a) + O(a, \underline{R}(W) - 1)$$

(iii) The number of suffixes in  $\underline{R}(W), \overline{R}(W)$  that are preceded by  $a$  is

$$O(a, \overline{R}(W) - 1) - O(a, \underline{R}(W) - 1)$$

so

$$\overline{R}(W) = c(a) + O(a, \overline{R}(W))$$

## 1.2 Algorithm

We make a call like  $\text{ExRecur}(W, i, k, l)$  or  $\text{InexRecur}(W, i, z, k, l)$  where

- $W$  is our query
- $i = |W| - 1$
- $k, l$  is our SA-intervall so  $k = 0$  and  $l = n - 1$
- $z$  is a maximum allowing differences (mismatches or gaps)

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**Algorithm 1** *Calculate exact recursion*

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*Exrecur*( $W, i, k, l$ )

**if**  $i < 0$  **then**

**return**  $[k, l]$

**end if**

**if**  $k \leq 0$  **then**

$K \leftarrow C(W_i) + O(W_i, k - 1) + 1$

$l \leftarrow C(W_i) + O(W_i, l)$

**end if**

**return** *ExRecur*( $W, i - 1, k, l$ )

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**Algorithm 2** *Calculate inexact recursion*

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InexRecur( $W, i, z, k, l$ )
if  $z < 0$  then
  return  $\emptyset$ 
end if
if  $i < 0$  then
  return  $[k, l]$ 
end if;
 $I \leftarrow \emptyset$ 
for  $\sigma \in \{A, C, G, T\}$  do
   $k \leftarrow C(\sigma) + O(\sigma, k - 1) + 1$ 
   $l \leftarrow C(\sigma) + O(\sigma, l)$ 
  if  $k \leq 1$  then
     $I \leftarrow I \cup \text{InexRecur}(W, i, z - 1, k, l)$ 
    if  $\sigma = W_i$  then
       $I \leftarrow I \cup \text{InexRecur}(W, i - 1, z, k, l)$ 
    else
       $I \leftarrow I \cup \text{InexRecur}(W, i - 1, z - 1, k, l)$ 
    end if
  end if
end for
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