# **Burrows–Wheeler transform**

From Wikipedia, the free encyclopedia

The **Burrows–Wheeler transform (BWT**, also called **block-sorting compression**) rearranges a character string into runs of similar characters. This is useful for compression, since it tends to be easy to compress a string that has runs of repeated characters by techniques such as move-to-front transform and run-length encoding. More importantly, the transformation is **reversible**, without needing to store any additional data. The BWT is thus a "free" method of improving the efficiency of text compression algorithms, costing only some extra computation.

Contents	
■ 1 Description	
• 2 Example	
• 3 Explanation	
<ul> <li>4 Optimization</li> </ul>	
<ul> <li>5 Bijective variant</li> </ul>	
<ul> <li>6 Dynamic Burrows–Wheeler transform</li> </ul>	
<ul> <li>7 Sample implementation</li> </ul>	
8 BWT in bioinformatics	
9 References	
10 External links	

## Description

The Burrows–Wheeler transform is an algorithm used in data compression techniques such as bzip2. It was invented by Michael Burrows and David Wheeler in 1994 while Burrows was working at DEC Systems Research Center in Palo Alto, California.<sup>[1]</sup> It is based on a previously unpublished transformation discovered by Wheeler in 1983.

When a character string is transformed by the BWT, the transformation permutes the order of the characters. If the original string had several substrings that occurred often, then the transformed string will have several places where a single character is repeated multiple times in a row.

For example:

InputSIX.MIXED.PIXIES.SIFT.SIXTY.PIXIE.DUST.BOXESOutputTEXYDST.E.IXIXXXSSMPPS.B..E.S.EUSFXDIIOIIIT<sup>[2]</sup>

The output is easier to compress because it has many repeated characters. In this example the transformed string, there are a total of eight runs of identical characters: XX, II, XX, SS, PP, .., II, and III, which together make 17 out of the 44 characters.

### Example

The transform is done by sorting all rotations of the text into lexicographic order, by which we mean that the 8 rotations appear in the second column in a different order, in that the 8 rows have been sorted into lexicographical order. We then take as output the last column and the number k = 7 of the row that the non rotated row ends up in. For example, the text "^BANANA|" is transformed into "BNN^AA|A" through these steps (the red | character indicates the 'EOF' pointer):

Transformation				
Input	All rotations	Sorted into lexical order	Taking last column	Output last column
^BANANA	^BANANA     ^BANANA A   ^BANAN NA   ^BANA ANA   ^BAN NANA   ^BA ANANA   ^B BANANA   ^	ANANA   ^B ANA   ^BAN A   ^BANAN BANANA   ^ NANA   ^BA NA   ^BANA ^BANANA     ^BANANA	ANANA   ^ B ANA   ^ BAN A   ^ BANAN BANANA   ^ NANA   ^ BA NA   ^ BANA ^ BANANA     ^ BANANA	BNN^AA   A

The following pseudocode gives a simple (though inefficient) way to calculate the BWT and its inverse. It assumes that the input string s contains a special character 'EOF' which is the last character, occurs nowhere else in the text.

<pre>function BWT (string s)     create a table, rows are all possible rotations of s     sort rows alphabetically     return (last column of the table)</pre>	
<pre>function inverseBWT (string s) create empty table repeat length(s) times     // first insert creates first column     insert s as a column of table before first column of the table     sort rows of the table alphabetically    return (row that ends with the 'EOF' character)</pre>	

#### **Explanation**

To understand why this creates more-easily-compressible data, consider transforming a long English text frequently containing the word "the". Sorting the rotations of this text will group rotations starting with "he " together, and the last character of that rotation (which is also the character before the "he ") will usually be "t", so the result of the transform would contain a number of "t" characters along with the perhaps less-common exceptions (such as if it contains "Brahe ") mixed in. So it can be seen that the success of this transform depends upon one value having a high probability of occurring before a sequence, so that in general it needs fairly long samples (a few kilobytes at least) of appropriate data (such as text).

The remarkable thing about the BWT is not that it generates a more easily encoded output—an ordinary sort would do that—but that it is *reversible*, allowing the original document to be re-generated from the last column data.

The inverse can be understood this way. Take the final table in the BWT algorithm, and erase all but the last column. Given only this information, you can easily reconstruct the first column. The last column tells you all the characters in the text, so just sort these characters alphabetically to get the first column. Then, the first and last columns (of each row) together give you all *pairs* of successive characters in the document, where pairs are taken cyclically so that the last and first character form a pair. Sorting the list of pairs gives the first *and second* columns. Continuing in this manner, you can reconstruct the entire list. Then, the row with the "end of file" character at the end is the original text. Reversing the example above is done like this:

Inverse transformation		
	Input	
		ı
	BNN^AA A	

·i			
Add 1	Sort 1	Add 2	Sort 2
B N A A A A	A A B N N ^	BA NA ^B AN AN A	AN AN BA NA NA ^B ^
Add 3	Sort 3	Add 4	Sort 4
BAN NAN ^BA ANA ANA ANA ANA ANA ANA	ANA ANA A   ^ BAN NAN NA ABA   ^BA	BANA NANA ^BAN ANAN ANAN   ^BA A   ^B	ANAN ANA  A ^B BANA NANA NANA ^BAN  ^BA
Add 5	Sort 5	Add 6	Sort 6
BANAN NAI^B ^BANA ANANA ANAI^ I^BAN A ^BA	ANANA ANA   ^ A   ^BA BANAN NANA   NA   ^B ^BANA   ^BAN	BANANA NANA   ^ NA   ^BA BANAN ANANA   ANA   ^B   ^BANA A   ^BAN	ANANA  ^B A  ^BAN BANANA NANA  ^ NA  ^BA ^BANAN   ^BANA
Add 7	Sort 7	Add 8	Sort 8
BANANA   NANA   ^B NA   ^BAN ^BANANA   ^ ANA   ^BANAN   ^BANAN A   ^BANA	ANANA   ^ ANA   ^BA A   ^BANA BANANA   NANA   ^B NA   ^BAN ^BANANA   ^BANAN	BANANA   ^ NANA   ^BA NA   ^BANAN ^BANANA   ^B ANA   ^BA ANA   ^BANANA A   ^BANANA	ANANA   ^ B ANA   ^ BAN A   ^ BANAN BANANA   ^ BA NANA   ^ BANA ^ BANANA     ^ BANANA
Output			
^BANANA			

# Optimization

A number of optimizations can make these algorithms run more efficiently without changing the output. There is no need to represent the table in either the encoder or decoder. In the encoder, each row of the table can be represented by a single pointer into the strings, and the sort performed using the indices. Some care must be taken to ensure that the sort does not exhibit bad worst-case behavior: Standard library sort functions are unlikely to be appropriate. In the decoder, there is also no need to store the table, and in fact no sort is needed at all. In time proportional to the alphabet size and string length, the decoded string may be generated one character at a time from right to left. A "character" in the algorithm can be a byte, or a bit, or any other convenient size.

One may also make the observation that mathematically, the encoded string can be computed as a simple modification of the suffix array, and suffix arrays can be computed with linear time and memory. The BWT can be defined with regards to the suffix array SA of text T as (1-based indexing):

$$BWT[i] = egin{cases} T[SA[i]-1], & ext{if } SA[i] > 1 \ {}_{[3]} \ \$, & ext{otherwise} \end{cases}$$

There is no need to have an actual 'EOF' character. Instead, a pointer can be used that remembers where in a string the 'EOF' would be if it existed. In this approach, the output of the BWT must include both the transformed string, and the final value of the pointer. That means the BWT does expand its input slightly. The inverse transform then shrinks it back down to the original size: it is given a string and a pointer, and returns just a string.

A complete description of the algorithms can be found in Burrows and Wheeler's paper, or in a number of online sources.

# **Bijective variant**

When a bijective variant of the Burrows–Wheeler transform is performed on "^BANANA", you get ANNBAA^ without the need for a special character for the end of the string. A special character forces one to increase character space by one, or to have a separate field with a numerical value for an offset. Either of these features makes data compression more difficult. When dealing with short files, the savings are great percentage-wise.

The bijective transform is done by sorting all rotations of the Lyndon words. In comparing two strings of unequal length, one can compare the infinite periodic repetitions of each of these in lexicographic order and take the last column of the base-rotated Lyndon word. For example, the text "^BANANA|" is transformed into "ANNBAA^|" through these steps (the red | character indicates the EOF pointer) in the original string. The EOF character is unneeded in the bijective transform, so it is dropped during the transform and re-added to its proper place in the file.

The string is broken into Lyndon words so the words in the sequence are decreasing using the comparison method above. "^BANANA" becomes (^) (B) (AN) (AN) (A), but Lyndon words are combined into (^) (B) (ANAN) (A).

<b>Bijective transformation</b>				
Input All rotations		Sorted alphabetically by first letter	Last column of rotated Lyndon word	Output
^BANANA	BBBBBBBB (B) ANANANANA (ANAN) NANANANA (NANA) ANANANAN (ANAN) NANANANA (NANA) AAAAAAAA (A)	AAAAAAAA (A) ANANANAN (ANAN) ANANANAN (ANAN) BBBBBBBB (B) NANANANA (NANA) NANANANA (NANA)	AAAAAAAA (A) ANANANAN (ANAN) ANANANAN (ANAN) BBBBBBBB (B) NANANANA (NANA) NANANANA (NANA)	ANNBAA^



Add 3	Sort 3	Add 4	Sort 4
AAA NAN BBB ANA ANA ^^^	AAA ANA BBB NAN NAN ^^^	AAAA NANA BBBB ANAN ANAN ^^^^	AAAA ANAN BBBB NANA AAAA
	Out	tput	
^BANANA			

The above may be viewed as four cycles:

```
^{=}(^{)}(^{)}... = ^{-----}...
B = (B)(B)... = BBBB...
ANAN = (ANAN)(ANAN)... = ANANANAN...
A = (A)(A).. = AAAAA..
```

or 5 cycles WHERE ANAN broken into 2:

```
AN = (AN) (AN) \dots = ANANANAN
AN = (AN) (AN) \dots = ANANANAN
```

If a cycle is N character it will be repeated N times:

```
(^)
(B)
(ANAN)
(A)
```

or

(^) (B) (AN) (AN)

(A)

to get the

^BANANA

Since any rotation of the input string will lead to the same transformed string, the BWT cannot be inverted without adding an EOF marker to the input or, augmenting the output with information such as an index, making it possible to identify the input string from all its rotations.

There is a bijective version of the transform, by which the transformed string uniquely identifies the original. In this version, every string has a unique inverse of the same length.<sup>[4][5]</sup>

The fastest versions are linear in time and space.

The bijective transform is computed by factoring the input into a non-increasing sequence of Lyndon words; such a factorization exists in the Chen–Fox–Lyndon theorem,<sup>[6]</sup> and may be found in linear time.<sup>[7]</sup> The algorithm sorts the rotations of all the words; as in the Burrows–Wheeler transform, this produces a sorted sequence of *n* strings. The transformed string is then obtained by picking the final character of each string in this sorted list.

For example, applying the bijective transform gives:

Input	SIX.MIXED.PIXIES.SIFT.SIXTY.PIXIE.DUST.BOXES
Lyndon words	SIX.MIXED.PIXIES.SIFT.SIXTY.PIXIE.DUST.BOXES
Output	STEYDST.E.IXXIIXXSMPPXS.BEESUSFXDIOIIIIT

The bijective transform includes eight runs of identical characters. These runs are, in order: XX, II, XX, PP, ..., EE, ..., and IIII.

In total, 18 characters are used in these runs.

### **Dynamic Burrows–Wheeler transform**

When a text is edited, its Burrows–Wheeler transform will change. Salson *et al.*<sup>[8]</sup> propose an algorithm that deduces the Burrows–Wheeler transform of an edited text from that of the original text, doing a limited number of local reorderings in the original Burrows–Wheeler transform, which can be faster than constructing the Burrows–Wheeler transform of the edited text directly.

### Sample implementation

This Python implementation sacrifices speed for simplicity: the program is short, but takes more than the linear time that would be desired in a practical implementation.

Using the STX/ETX control codes to mark the start and end of the text, and using s[i:] + s[:i] to construct the *i*th rotation of *s*, the forward transform takes the last character of each of the sorted rows:

```
def bwt(s):
    """Apply Burrows-Wheeler transform to input string."""
    assert "\002" not in s and "\003" not in s, "Input string cannot contain STX and ETX characters"
    s = "\002" + s + "\003" # Add start and end of text marker
    table = sorted(s[i:] + s[:i] for i in range(len(s))) # Table of rotations of string
    last_column = [row[-1:] for row in table] # Last characters of each row
    return "".join(last_column) # Convert list of characters into string
```

The inverse transform repeatedly inserts r as the left column of the table and sorts the table. After the whole table is built, it returns the row that ends with ETX, minus the STX and ETX.

def ibwt(r):
 """Apply inverse Burrows-Wheeler transform."""
 table = [""] \* len(r) # Make empty table
 for i in range(len(r)):
 table = sorted(r[i] + table[i] for i in range(len(r))) # Add a column of r
 s = [row for row in table if row.endswith("\003")][0] # Find the correct row (ending in ETX)
 return s.rstrip("\003").strip("\002") # Get rid of start and end markers

Here is another, more efficient method for the inverse transform. Although more complex, it increases the speed greatly when decoding lengthy strings.

def ibwt(r, \*args):
 """Inverse Burrows-Wheeler transform. args is the original index \
 if it was not indicated by an ETX character."""
 firstCol = "".join(sorted(r))
 count = [0]\*256
 byteStart = [-1]\*256
 output = [""] \* len(r)
 shortcut = [None]\*len(r)

indexlist.append(index2)

return r, indexlist

'def ibwt(r,indexlist):

x = indexlist[0]
for \_ in r:

s = s + r[x] x = indexlist[x]

**BWT** in bioinformatics

s=**''** 

return s

References

Corporation

PMID 20529929.

sorting transform (PDF)

pp. 65–69, arXiv:0908.0239a.

# Join last characters of each row into string
r = ''.join([row[-1] for row in table\_sorted])

BWA.<sup>[12]</sup> and SOAP2<sup>[13]</sup>) that use the Burrows–Wheeler transform.

1. Burrows, Michael; Wheeler, David J. (1994), A

2. https://github.com/adrien-mogenet/scala-bwt/blob

3. Simpson, Jared T.; Durbin, Richard (2010-06-15).

using the FM-index". Bioinformatics. 26 (12):

i367-i373. doi:10.1093/bioinformatics/btq217.

5. Kufleitner, Manfred (2009), "On bijective variants

Žďárek, Jan, Prague Stringology Conference,

6. \*Lothaire, M. (1997), Combinatorics on words,

Schützenberger, M. P.; Choffrut, C.; Cori, R.;

Lyndon, Roger; Rota, Gian-Carlo. Foreword by

Roger Lyndon (2nd ed.), Cambridge University

7. Duval, Jean-Pierre (1983), "Factorizing words over

ISSN 0196-6774, Zbl 0532.68061.

**External links** 

/abs/0908.0239)

of the Burrows-Wheeler transform", in Holub, Jan;

Encyclopedia of Mathematics and Its Applications,

E.; Pirillo, G.; Foata, D.; Sakarovitch, J.; Simon, I.;

Press, p. 67, ISBN 0-521-59924-5, Zbl 0874.20040

an ordered alphabet", *Journal of Algorithms*, **4** (4): 363–381, doi:10.1016/0196-6774(83)90017-2,

17, Perrin, D.; Reutenauer, C.; Berstel, J.; Pin, J.

4. Gil, J.; Scott, D. A. (2009), A bijective string

"Efficient construction of an assembly string graph

Technical Report 124, Digital Equipment

/master/src/main/scala/me/algos

/bwt/BurrowsWheelerCodec.scala

ISSN 1367-4803. PMC 2881401 a.

block sorting lossless data compression algorithm,

```
#Generates shortcut lists
    for i in range(len(r)):
       shortcutIndex = ord(r[i])
        shortcut[i] = count[shortcutIndex]
        count[shortcutIndex] +=
        shortcutIndex = ord(firstCol[i])
       if byteStart[shortcutIndex] ==
                                      -1:
           byteStart[shortcutIndex] = i
    localIndex = (r.index("\003") if not args else args[0])
    for i in range(len(r)):
        #takes the next index indicated by the transformation vector
       nextByte = r[localIndex]
       output [len(r)-i-1] = nextByte
       shortcutIndex = ord(nextByte)
        #assigns localIndex to the next index in the transformation vector
       localIndex = byteStart[shortcutIndex] + shortcut[localIndex]
    return "".join(output).rstrip("\003").strip("\002")
         Here is a third one, more efficient and very simple method. It increases the speed greatly when decoding
lengthy strings. Although it needs an origin index list generated by bwt.
def bwt(s):
    """Apply Burrows-Wheeler transform to input string. Not indicated by a unique byte but use index lis
    # Table of rotations of string
    table = [s[i:] + s[:i] for i in range(len(s))]
    # Sorted table
    table_sorted = table[:]
    table_sorted.sort()
    # Get index list of ((every string in sorted table)'s next string in unsorted table)'s index in sort
    indexlist = []
    for t in table sorted:
       index1 = table.index(t)
       index1 = index1+1 if index1 < len(s)-1 else 0</pre>
       index2 = table_sorted.index(table[index1])
```

"""Inverse Burrows-Wheeler transform. Not indicated by a unique byte but use index list"""

The advent of next-generation sequencing (NGS) techniques at the end of the 2000s decade has led to another application of the Burrows–Wheeler transformation. In NGS, DNA is fragmented into small pieces, of which the first few bases are sequenced, yielding several millions of "reads", each 30 to 500 base pairs ("DNA characters") long. In many experiments, e.g., in ChIP-Seq, the task is now to align these reads to a reference genome, i.e., to the known, nearly complete sequence of the organism in question (which may be

up to several billion base pairs long). A number of alignment programs, specialized for this task, were published, which initially relied on hashing (e.g., Eland, SOAP,<sup>[9]</sup> or Maq<sup>[10]</sup>). In an effort to reduce the memory requirement for sequence alignment, several alignment programs were developed (Bowtie,<sup>[11]</sup>)

burrows.html) and project page (https://code.google.com/p/dcs-bwt-compressor/) for an open-source compression program and library based on the Burrows–Wheeler algorithm
MIT open courseware lecture on BWT (Foundations of Computational and Systems Biology) (https://www.youtube.com/watch?v=P3ORBMon8aw)

Retrieved from "https://en.wikipedia.org/w/index.php?title=Burrows–Wheeler\_transform& oldid=768908518"

Article by Mark Nelson on the BWT (http://marknelson.us/1996/09/01/bwt/)

version (http://encode.ru/attachment.php?attachmentid=959&d=1249146089)

Categories: Lossless compression algorithms | Transforms

- This page was last modified on 6 March 2017, at 13:33.
- Text is available under the Creative Commons Attribution-ShareAlike License; additional terms may apply. By using this site, you agree to the Terms of Use and Privacy Policy. Wikipedia® is a registered trademark of the Wikimedia Foundation, Inc., a non-profit organization.

Compression comparison of BWT based file compressors (http://compressionratings.com/bwt.html)

Yuta's openbwt-v1.5.zip contains source code for various BWT routines including BWTS for bijective

A Bijective String-Sorting Transform, by Gil and Scott (http://bijective.dogma.net/00yyy.pdf)

On Bijective Variants of the Burrows–Wheeler Transform, by Kufleitner (http://arxiv.org

Blog post (http://google-opensource.blogspot.com/2008/06/debuting-dcs-bwt-experimental-

- Salson M, Lecroq T, Léonard M, Mouchard L (2009). "A Four-Stage Algorithm for Updating a Burrows–Wheeler Transform". *Theoretical Computer Science*, **410** (43): 4350–4359
- doi:10.1016/j.tcs.2009.07.016.
  9. Li R; et al. (2008). "SOAP: short oligonucleotide alignment program". *Bioinformatics*. 24 (5): 713–714. doi:10.1093/bioinformatics/btn025. PMID 18227114.
- 10. Li H, Ruan J, Durbin R (2008-08-19). "Mapping short DNA sequencing reads and calling variants using mapping quality scores". *Genome Research*. 18 (11): 1851–1858. doi:10.1101/gr.078212.108. PMC 2577856 PMID 18714091.
- 11. Langmead B, Trapnell C, Pop M, Salzberg SL (2009). "Ultrafast and memory-efficient alignment of short DNA sequences to the human genome". *Genome Biology*. 10 (3): R25. doi:10.1186/gb-2009-10-3-r25. PMC 2690996. PMID 19261174.
- 12. Li H, Durbin R (2009). "Fast and accurate short read alignment with Burrows–Wheeler Transform". *Bioinformatics*. 25 (14): 1754–1760. doi:10.1093/bioinformatics/btp324. PMC 2705234
  A. PMID 19451168.
- 13. Li R; et al. (2009). "SOAP2: an improved ultrafast tool for short read alignment". *Bioinformatics*. 25 (15): 1966–1967. doi:10.1093/bioinformatics /btp336. PMID 19497933.
- (2009). "A Four-Stage Algorithm for Opdati Burrows–Wheeler Transform". *Theoretical Computer Science*. **410** (43): 4350–4359. doi:10.1016/j.tcs.2009.07.016.
  9. Li R; et al. (2008). "SOAP: short oligonucle alignment program". *Bioinformatics*. **24** (5):