Vectorizing the `DNAString` function (work in progress)

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1 Introduction

This is a short tour on the `DNAString` function vectorization feature.

Feel free to add your own comments.

2 `DNAString` vs `BStringViews`

The `Biostrings2Classes` vignette presents a proposal for 2 new classes (*BString* and *BStringViews*) as a replacement for the *BioString* class currently defined in the *Biostrings* 1 (*Biostrings* v 1.4.x) package.

It also shows how to use the `DNAString` function to create a *DNAString* object (a *DNAString* object is just a particular case of a *BString* object):

```
> d <- DNAString("TTGAAAA-CTC-N")
```

However this function is NOT vectorized: it always returns a *DNAString* object (which can only represent a *single* string).

In *Biostrings* 1, the `DNAString` function IS vectorized. Its vectorized form does the following: (1) concats the elements of its `src` argument into a single big string, (2) stores the offsets of all these elements in the `offsets` slot.

This behaviour is not immediatly obvious to the user, until he looks at the `offsets` slot.

It always returns a *BioString* object (with has as many values as the number of elements passed in the `src` argument).

3 The `BStringViews` generic function

The feature described in the previous section (provided by the vectorized form of the `DNAString` function in *Biostrings* 1) is provided in *Biostrings* 2 via the `BStringViews` generic function:

```
> v <- BStringViews(c("TTGAAAA-C", "TC-N"), "DNAString")
> v

  Views on a 13-letter DNAString subject
Subject: TTGAAAA-CTC-N
Views:
    first last width
[1]     1    9     9 |TTGAAAA-C|
[2]    10   13     4 |TC-N|
```

4 Performance

The following example was provided by Wolfgang:

```
> library(hgu95av2probe)

> system.time(z <- BStringViews(hgu95av2probe$sequence, "DNAString"))

[1] 8.130 0.090 8.398 0.000 0.000

> z

  Views on a 4977100-letter DNAString subject
Subject: TCTCCTTTGCTGAGGCCTCCAGCTTAGGCCTCCA...GTGAAACCCAGCCTGGCCAACATGGTGAAACCC
Views:
           first    last width
     [1]       1      25    25 |TCTCCTTTGCTGAGGCCTCCAGCTT|
     [2]      26      50    25 |AGGCCTCCAGCTTCAGGCAGGCCAA|
     [3]      51      75    25 |CCAGCTTCAGGCAGGCCAAGGCCTT|
     [4]      76     100    25 |AGCTCAGGTGGCCCCAGTTCAATCT|
     [5]     101     125    25 |AGTTCTGGAATGGAAGGGTTCTGGC|
     [6]     126     150    25 |TAGGGACTCAGGGCCATGCCTGCCC|
     [7]     151     175    25 |TTCCCTGAAGGAACATTCCTTAGTC|
     [8]     176     200    25 |GAAGGAACATTCCTTAGTCTCAAGG|
     [9]     201     225    25 |CTTAGTCTCAAGGGCTAGCATCCCT|
     ...     ...     ...   ... ...
[199076] 4976876 4976900    25 |TTCAAGACCAGCCTGGCCAACATGG|
[199077] 4976901 4976925    25 |TCAAGACCAGCCTGGCCAACATGGT|
```

```
[199078] 4976926 4976950    25 |CAAGACCAGCCTGGCCAACATGGTG|
[199079] 4976951 4976975    25 |AAGACCAGCCTGGCCAACATGGTGA|
[199080] 4976976 4977000    25 |AGACCAGCCTGGCCAACATGGTGAA|
[199081] 4977001 4977025    25 |GACCAGCCTGGCCAACATGGTGAAA|
[199082] 4977026 4977050    25 |ACCAGCCTGGCCAACATGGTGAAAC|
[199083] 4977051 4977075    25 |CCAGCCTGGCCAACATGGTGAAACC|
[199084] 4977076 4977100    25 |CAGCCTGGCCAACATGGTGAAACCC|
```

With *Biostrings* 1, the call to `DNAString(hgu95av2probe$sequence)` takes about 20 minutes... (the implementation of the vectorization feature is quadratic in time, as reported by Wolfgang).

5 Loading a FASTA file in a *BStringViews* object

The `BStringViews` function can be used to load a FASTA file in a *BStringViews* object:

```
> srcpath <- system.file("Exfiles", "someORF.fsa", package = "Biostrings")
> f <- file(srcpath)
> orf <- BStringViews(f, "DNAString")
> close(f)
> orf

  Views on a 26339-letter DNAString subject
Subject: ACTTGTAAATATATCTTTTATTTTCCGAGAGGAA...TATACATAGGGCTAAGGAAGAAAAAAAAATCAC
Views:
    first  last width
[1]     1  5573  5573 |ACTTGTAAATATATCTTTTATTTTCC...ACGCTTATCGACCTTATTGTTGATAT|
[2]  5574 11398  5825 |TTCCAAGGCCGATGAATTCGACTCTT...CAGAGTAAATTTTTTTCTATTCTCTT|
[3] 11399 14385  2987 |CTTCATGTCAGCCTGCACTTCTGGGT...CGATGGTACTCATGTAGCTGCCTCAT|
[4] 14386 18314  3929 |CACTCATATCGGGGGTCTTACTTCCC...ACGTGTCCCGAAACACGAAAAAGTAC|
[5] 18315 20962  2648 |AGAGAAAGAGTTTCACTTCTTGATTA...AAAATATAATTTATGTGTGAACATAG|
[6] 20963 23559  2597 |GTGTCCGGGCCTCGCAGGCGTTCTAC...TTCAAGTTTTGGCAGAATGTACTTTT|
[7] 23560 26339  2780 |CAAGATAATGTCAAAGTTAGTGGTCG...AGGGCTAAGGAAGAAAAAAAAATCAC|

> desc(orf)

[1] ">YAL001C TFC3 SGDID:S0000001, Chr I from 152168-146596, reverse complement, Verified ORF
[2] ">YAL002W VPS8 SGDID:S0000002, Chr I from 142709-148533, Verified ORF"
[3] ">YAL003W EFB1 SGDID:S0000003, Chr I from 141176-144162, Verified ORF"
[4] ">YAL005C SSA1 SGDID:S0000004, Chr I from 142433-138505, reverse complement, Verified ORF
[5] ">YAL007C ERP2 SGDID:S0000005, Chr I from 139347-136700, reverse complement, Verified ORF
[6] ">YAL008W FUN14 SGDID:S0000006, Chr I from 135916-138512, Verified ORF"
[7] ">YAL009W SPO7 SGDID:S0000007, Chr I from 134856-137635, Verified ORF"
```

6 Switching between DNA and RNA views

The `BStringViews` function can also be used to switch between "DNA" and "RNA" views on the same string:

```
> orf2 <- BStringViews(orf, "RNAString")
```

These conversions are very fast because no string data needs to be copied:

```
> orf[[0]]@data

26339-byte buffer (starting at address 0x546e3c8)

> orf2[[0]]@data

26339-byte buffer (starting at address 0x546e3c8)
```