

Vectorizing the `DNAStr` function (work in progress)

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1 Introduction

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

Feel free to add your own comments.

2 `DNAStr` vs `XStringViews`

The `Biostrings2Classes` vignette presents a proposal for 2 new classes (*XString* and *XStringViews*) 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 `DNAStr` function to create a *DNAStr* object (a *DNAStr* object is just a particular case of an *XString* object):

```
> d <- DNAStr("TTGAAAA-CTC-N")
> is(d, "XString")
```

```
[1] TRUE
```

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

In *Biostrings* 1, the `DNASTring` function IS vectorized. Its vectorized form does the following: (1) concatenates 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 immediately obvious to the user, until he looks at the `offsets` slot.

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

3 The XStringViews 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 `XStringViews` generic function:

```
> v <- XStringViews(c("TTGAAAA-C", "TC-N"), "DNASTring")
> v
```

```
Views on a 13-letter DNASTring subject
subject: TTGAAAA-CTC-N
views:
      start end 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 <- XStringViews(hgu95av2probe$sequence, "DNASTring"))

      user  system elapsed
      0.17    0.00    0.17

> z
```

```
Views on a 5045000-letter DNASTring subject
subject: TGGCTCCTGCTGAGGTCCCCTTTCCGGCTG...CCCTCGTGCTCCTTGTC AACAGCGCACCCA
views:
      start      end width
[1]       1       25    25 [TGGCTCCTGCTGAGGTCCCCTTTCC]
[2]      26       50    25 [GGCTGTGAATTCCTGTACATATTC]
[3]      51       75    25 [GCTTCAATTCCATTATGTTTTAATG]
[4]      76      100    25 [GCCGTTTGACAGAGCATGCTCTGCG]
[5]     101     125    25 [TGACAGAGCATGCTCTGCGTTGTTG]
[6]     126     150    25 [CTCTGCGTTGTTGGTTTCACCAGCT]
[7]     151     175    25 [GGTTTCACCAGCTTCTGCCCTCACA]
```

```

      [8]      176      200      25 [TTCTGCCCTCACATGCACAGGGATT]
      [9]      201      225      25 [CCTCACATGCACAGGGATTTAACAA]
      ...      ...      ...      ...
[201792] 5044776 5044800      25 [GAGTGCCAATTCGATGATGAGTCAG]
[201793] 5044801 5044825      25 [ACACTGACACTTGTGCTCCTTGTC]
[201794] 5044826 5044850      25 [CAATTCGATGATGAGTCAGCAACTG]
[201795] 5044851 5044875      25 [GACTTCTGAGGAGATGGATAGCCT]
[201796] 5044876 5044900      25 [AGATGGATAGCCTTCTGTCAAAGCA]
[201797] 5044901 5044925      25 [ATAGCCTTCTGTCAAAGCATCATCT]
[201798] 5044926 5044950      25 [TTCTGTCAAAGCATCATCTCAACAA]
[201799] 5044951 5044975      25 [CAAAGCATCATCTCAACAAGCCCTC]
[201800] 5044976 5045000      25 [GTGCTCCTTGTC AACAGCGCACCCA]

```

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 into an *XStringViews* object

The `read.XStringViews` function can be used to load a FASTA file in an *XStringViews* object:

```

> file <- system.file("extdata", "someORF.fa", package = "Biostrings")
> orf <- read.XStringViews(file, subjectClass = "DNAString")
> orf

```

Views on a 26339-letter DNAString subject

subject: ACTTGTAATATATCTTTTATTTTCCGAGA...ACATAGGGCTAAGGAAGAAAAAAAATCAC

views:

```

      start   end width
[1]      1  5573  5573 [ACTTGTAATATATCTTTTATTT...TTATCGACCTTATTGTTGATAT]
[2]   5574 11398  5825 [TTCCAAGGCCGATGAATTCGACT...GTAAATTTTTTCTATTCTCTT]
[3]  11399 14385  2987 [CTTCATGTCAGCCTGCACTTCTG...GGTACTCATGTAGCTGCCTCAT]
[4]  14386 18314  3929 [CACTCATATCGGGGTCTTACTT...GTCCGAAACACGAAAAAAGTAC]
[5]  18315 20962  2648 [AGAGAAAGAGTTTCACTTCTTGA...TATAATTTATGTGTGAACATAG]
[6]  20963 23559  2597 [GTGTCCGGGCCTCGCAGGCGTTC...AGTTTTGGCAGAATGTACTTTT]
[7]  23560 26339  2780 [CAAGATAATGTCAAAGTTAGTGG...CTAAGGAAGAAAAAAAATCAC]

```

```

> names(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 SP07 SGDID:S0000007, Chr I from 134856-137635, Verified ORF"

```

6 Switching between DNA and RNA views

The `XStringViews` function can also be used to switch between “DNA” and “RNA” views on the same string:

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

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

```
> subject(orf)@shared
```

SharedRaw of length 26339 (data starting at address 0p65cc410)

```
> subject(orf2)@shared
```

SharedRaw of length 26339 (data starting at address 0p65cc410)