

From: Wen Yao <ywhzau@gmail.com>
Time: 2014/4/26 16:24
To: 'Phil Ross'
Subject: Re: Re: intansv
Attachment: intansv_1.4.1.tar.gz

Hi Phil,

The intansv package you downloaded from the Bioconductor was 1.4.0 since it need some time for the svn to take effect. The *svAnnotation* in 1.4.1 won't throw out warnings.

The geneAnnotation went wrong because your gff file doesn't contain UTR elements (The organism you are working on probably is not animal or plant). And I had fixed this bug.

The *plotChromosome* went wrong because your gff file contains chromosome whose length is shorter than the default window size (1 Mb). And I had fixed this bug.

The *plotRegion* went wrong because your *structuralVariation* doesn't contain Inversions. I had fixed that bug.

And the command you use *plotRegion* should be:

*plotRegion(structuralVariation, **gffAnnotation**, "Pf3D7_01_v3", 1, 115601)*

The attachment file is the modified intansv package.

If you encounter any problem using intansv, please contact me.

Best,
Wen

From: Phil Ross [[mailto:](#)]
Time: 2014/4/26 2:00
To: Wen Yao
Subject: Re: Re: intansv

Hi Wen,

In addition I am currently trying to run this software on a Mac (as you can see from the sessionInfo() output) but we have another person in the lab running the package on a windows machine. Do you think that would have anything to do with it?

Best,
Phil

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Sent with [Sparrow](#)

On Friday, April 25, 2014 at 1:09 PM, Phil Ross wrote:

Hi Wen,

I was able to update to the latest version (1.4.0 as listed at bioconductor.org) and now svAnnotation runs wile outputting only warnings (see below).

However geneAnnotation and the plot functions still aren' t working...

```
> ga <- llply(structuralVariation, geneAnnotation,  
genomeAnnotation=gffAnnotation)  
Error in `$.data.frame`(`*tmp*`, "type", value = "utr") :  
  replacement has 1 row, data has 0  
> sa <- llply(structuralVariation, svAnnotation,  
genomeAnnotation=gffAnnotation)  
Warning messages:  
1: In `$.data.frame`(structuralVariationAnno, chr) :  
  Name partially matched in data frame
```

```

2: In `$.data.frame`(structuralVariationAnno, chr) :
  Name partially matched in data frame
> plotChromosome(genome, structuralVariation)
Error: wrong sign in 'by' argument
> plotRegion(structuralVariation, genome, "Pf3D7_01_v3", 1, 115601)
Error in (function (classes, fdef, mtable) :
  unable to find an inherited method for function 'Rle' for
signature "NULL", "missing"

```

I' ll attach the script of commands I' m running and the data files
I' m using in this email.

Let me know what you might think the problem is!

Also here is my session info:

```

R version 3.1.0 (2014-04-10)
Platform: x86_64-apple-darwin13.1.0 (64-bit)

```

```

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-
8/en_US.UTF-8

```

attached base packages:

```

[1] parallel stats    graphics grDevices utils    datasets methods
base

```

other attached packages:

```

[1] rtracklayer_1.24.0 intansv_1.4.0    GenomicRanges_1.16.2
GenomeInfoDb_1.1.2 IRanges_1.22.3
[6] ggbio_1.12.0      ggplot2_0.9.3.1 plyr_1.8.1
BiocGenerics_0.10.0 BiocInstaller_1.14.1

```

loaded via a namespace (and not attached):

```

[1] AnnotationDbi_1.26.0 BatchJobs_1.2    BBmisc_1.6
Biobase_2.24.0
[5] BiocParallel_0.6.0 biomaRt_2.20.0   Biostrings_2.32.0

```

biovizBase_1.12.0
 [9] *bitops_1.0-6* *brew_1.0-6* *BSgenome_1.32.0*
 cluster_1.15.2
 [13] *codetools_0.2-8* *colorspace_1.2-4* *DBI_0.2-7*
 dichromat_2.0-0
 [17] *digest_0.6.4* *fail_1.2* *foreach_1.4.2*
 Formula_1.1-1
 [21] *GenomicAlignments_1.0.0* *GenomicFeatures_1.16.0* *grid_3.1.0*
 gridExtra_0.9.1
 [25] *gtable_0.1.2* *Hmisc_3.14-4* *iterators_1.0.7*
 lattice_0.20-29
 [29] *latticeExtra_0.6-26* *MASS_7.3-31* *munzell_0.4.2*
 proto_0.3-10
 [33] *RColorBrewer_1.0-5* *Rcpp_0.11.1* *RCurl_1.95-4.1*
 reshape2_1.4
 [37] *Rsamtools_1.16.0* *RSQLite_0.11.4* *scales_0.2.4*
 sendmailR_1.1-2
 [41] *splines_3.1.0* *stats4_3.1.0* *stringr_0.6.2*
 survival_2.37-7
 [45] *tools_3.1.0* *VariantAnnotation_1.10.0* *XML_3.98-1.1*
 XVector_0.4.0
 [49] *zlibbioc_1.10.0*

Best,
Phil

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On Wednesday, April 23, 2014 at 9:16 AM, Wen Yao wrote:

Dear Phil,

The formatting of your gff file does cause problem. The line containing "supercontig" should be removed. And the sequences at the tail of the file is also not needed for intansv (won't be a problem). I had made a new gff file and sent you as an attachment.

Besides, I found a small bug in the svAnnotation function. I had created a new version of intansv (version 1.4.1). You can download the new version and I hope that will help you out.

If you encounter any problem using intansv, please contact me.

Regards,
Wen

From: Phil Ross [<mailto:>]
Time: 2014/4/21 22:15
To: Wen Yao
Subject: Re: intansv

Hi Wen,

Thanks for helping us out! Here is a Dropbox link to the gff file we're interested in using!

https://www.dropbox.com/s/cpaqi7kxdkqli4h/PlasmoDB-9.3_Pfalciparum3D7.gff

So you think the formatting is the issue?

Best,
Phil

Best,
Phil

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On Saturday, April 19, 2014 at 9:25 AM, wrote:

Dear Phil,

Thanks for your interest in intansv.

I wasn't in the Bioc mailing list (and joined it a minute ago).

You can send your gff file to me and i will check where the problem occurred.

Best regards,
Wen

Attachments:

- PlasmoDB-9.3_Pfalciparum3D7.gff.gz

Attachments:

- wen.zip