

From: Wen Yao <ywhzau@gmail.com>
Time: 2014/1/15 14:19
To: 'Michael Place'
Subject: **Re:** intansv

Dear Mike,

Thanks for your interest in intansv.

You should use this command:

```
bd <- readBreakDancer("/widomScratch1/mplace/results/breakDancer-  
analysis/data.ctx")
```

You can also enter "?system.file" in R to get the meaning of "system.file".

If you encounter any troubles in future using intansv, please contact me.

Regards,
Wen Yao

From: Michael Place [<mailto:>]
Time: 2014/1/15 5:16
To: ywhzau@gmail.com
Subject: intansv

Mr. Yao,

I am very interested in using your Bioconductor package.

But I keep getting the following error.

```
bd <- readBreakDancer(system.file  
("/widomScratch1/mplace/results/breakDancer-  
analysis/data.ctx",package="intansv"))  
Error in read.table(breakDancer, colClasses = bdColClass) :  
  no lines available in input  
In addition: Warning message:  
In file(file, "rt") :
```

file("") only supports open = "w+" and open = "w+b": using the former

The first few lines look like:

```
#Software: 1.4.3 (commit 1bd2363)
#Command: /usr/local/bin/breakdancer-max -d Jian_Ma-recal.ctx -h
Jian_Ma-recal.config
#Library Statistics:
#Jian_Ma-recal.bam    mean:903.92    std:352.8
uppercutoff:2080.3    lowercutoff:0    readlen:93.7    library:MCF7
reflen:3010700769    seqcov:13.2276    phycov:63.8029    1:546859
2:344368    4:265
#Chr1 Pos1 Orientation1 Chr2 Pos2 Orientation2 Type Size
Score num_Reads num_Reads_lib Allele_frequency Jian_Ma-
recal.bam
chr1 723721 82+91- chr1 726986 82+91- ITX -853 99
36 Jian_Ma-recal.bam|36 -nan NA
chr1 1074378 4+0- chr1 1076041 0+8- DEL 1208 61 4
Jian_Ma-recal.bam|4 0.923398 0.15
chr1 1223647 9+0- chr1 1225525 2+8- DEL 1351 99 8
Jian_Ma-recal.bam|8 0.99 0.02
chr1 1583700 7+18- chr1 1653477 34+14- ITX 65005 86
8 Jian_Ma-recal.bam|8 0.71 0.58
```

Would appreciate any suggestions.

Thank you,

Mike Place

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