From: Wen Yao <ywhzau@gmail.com>
Time: 2014/2/27 11:59
To: 'Rosenfeld, Jeffrey'
Subject: **Re**: INTANSV

Hi Jeff,

Yes. Currently intansv does not deal with CTX and ITS. Because CTX and ITS are more complex to predict. And the output of different programs differs in the output format. For example, BreakDancer doesn't give the jump direction of CTX (i.e. a piece of DNA jump from chromosome 1 to chromosome 2 or from chromosome 2 to chromosome 1) while DELLY gives the jump direction.

I will find more programs and intansv might support CTX and ITS in the next release.

Best regards,
Wen

From: Rosenfeld, Jeffrey [mailto:]
Time: 2014/2/27 11:34
To: Wen Yao
Subject: Re: INTANSV

Hi Wen,

    Thank you for the quick reply. Are you saying that intansv only works with DEL, INV and DUP, but does not deal with CTX and ITS?

Jeff

On Feb 26, 2014, at 9:02 PM, Wen Yao <ywhzau@gmail.com> wrote:

> Dear Jeff,

>
> Thanks for your interest in intansv.
>
> The reason why your command went wrong is because intansv can't find
> "C8.dance.txt". The example data were packaged with intansv and the
> function system.file were used to find the data packaged with an R
> package (for me, intansv). You can find the meaning of "system.file" by typing "?system.file"
> in R. So suppose "C8.dance.txt" is in "/home/jeff/C8.dance.txt", you
> should
> use:
> breakdancer <- readBreakDancer("/home/jeff/C8.dance.txt")
> But I find another problem in "C8.dance.txt ". I saw you were running
> BreakDancerMax 1.4.4-unstable version. The lines for the CTX output of
> C8.dance.txt have 11 columns while other lines have 12 columns. For
> now, you could remove lines for the CTX output before give it to
> readBreakDancer since intansv only deal with DEL, INV and DUP. What's
> more, the last line of "C8.dance.txt" should also be removed. I have
> modified "C8.dance.txt" and it is okay for intansv now. The modified
"C8.dance.txt " is in the attachment.
>
> I will update the example command and the documentation of intansv to
> make it not confusing. I will also make readBreakDancer more robust in
> the next release.
>
> If you encounter any problems or have any suggestions using intansv in
> the future, please contact me.
>
> Best regards,
>
> Wen
>
> -----Origin-----
> **From:** Rosenfeld, Jeffrey [[mailto:]](mailto:)
> **Time:** 2014/2/27 2:08
> **To:** ywhzau@gmail.com
> **Subject:** INTANSV

>
> Hi Wen,
>
> 	I am trying to get your package to work with my output from
> breakdancer, and I cannot seem to get it to take in my file. Using
> the attached file, I have tried:
>
> breakdancer <-
> readBreakDancer(system.file("C8.dance.txt",package="intansv"))
>
> and I get the following error:
> 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
>
> Thank you for the help,
>
> Jeff
>
>
> --
> Jeffrey Rosenfeld, Ph. D
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> History

>

> <C8.dance.noCTX.zip>