

From: Wen Yao <ywhzau@gmail.com>
Time: 2013/8/26 17:47
To: 'Dr. Xia Junhong'
Subject: Re: Re: Problem in installing intansv

Thanks. If you have any questions about "intansv", please contact me.

From: Dr. Xia Junhong [<mailto:>]
Time: 2013/8/26 17:20
To: Wen Yao
Subject: Re: Re: Problem in installing intansv

Dear Wen Yao,

I installed the program sucessfully according to your suggestion.

Thank you for your quick reply and good work!

Yours sincerely,
Junhong XIA
Research Fellow
Molecular Population Genetics Group,
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1 Research Link, National University of Singapore, 117604, Singapore

Tel: +65-68727406(O); +65-93911039(Mobile); Email: junhong@tll.org.sg

From: "Wen Yao" <ywhzau@gmail.com>
To: "Dr. Xia Junhong" <>
Sent: Monday, August 26, 2013 4:48:40 PM
Subject: Re: Problem in installing intansv

Dear Junhong,

Thanks for your interest in "intansv". Currently, intansv is not in the family of Bioconductor version 2.12. It will appear in the Bioconductor

version 2.13. I had no idea about the reason and I figured this out myself. So, you have to download the source of intansv and use the command "R CMD INSTALL intansv_0.99.2.tar.gz" to install it. Of course, you should have the dependence packages installed in advance. Use the function "biocLite" to install other packages could save you much time.

Any question is welcomed.

Best regards.

Wen Yao

From: Dr. Xia Junhong []
Time: 2013/8/26 15:58
To: ywhzau@gmail.com
Subject: Problem in installing intansv

Dear Wen Yao,
I am very interested in the program "intansv". However, I encountered one problem in installing the program in my linux system (Ubuntu). Below is the information during installation:

```
junhong@junhong-PowerEdge-T620:~/software\$ sudo R
```

```
R version 3.0.1 (2013-05-16) -- "Good Sport"  
Copyright (C) 2013 The R Foundation for Statistical Computing  
Platform: x86_64-pc-linux-gnu (64-bit)
```

```
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.
```

```
Natural language support but running in an English locale
```

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

```
> source("http://bioconductor.org/biocLite.R")
Bioconductor version 2.12 (BiocInstaller 1.10.3), ?biocLite for help
> biocLite("intansv")
BioC_mirror: http://bioconductor.org
Using Bioconductor version 2.12 (BiocInstaller 1.10.3), R version 3.0.1.
Installing package(s) 'intansv'
Warning message:
package aintansva is not available (for R version 3.0.1)
> library(intansv)
Error in library(intansv) : there is no package called aintansva
>
```

Do you know how to solve the problem? Thanks!

Yours sincerely,
Junhong XIA
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