

**From:** Wen Yao <ywhzau@gmail.com>  
**Time:** 2013/9/7 17:03  
**To:** 'Guo-dong Wang'  
**Subject:** Re: HELP: I can not install intansv

Dear Guodong,

I am sorry for the late response. I was traveling in the last few days and had no access to the internet.

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 the dependence packages could save you much time. Any question is welcomed.

Best regards.

Wen Yao

**From:** Guo-dong Wang [<mailto:>]  
**Time:** 2013/9/5 16:12  
**To:** [ywhzau@gmail.com](mailto:ywhzau@gmail.com)  
**Subject:** HELP: I can not install intansv

Dear Wen Yao

Thank you very much developing the intansv for annotating the SV.

Right now, I encounter problems when installing it as follows:

```
> source("http://bioconductor.org/biocLite.R")
Bioconductor version 2.12 (BiocInstaller 1.10.3), ?biocLite for help
> biocLite()
> 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 'intansv' is not available (for R version 3.0.1)

Could you give me some suggestion? Thank you very much!

Best Regards  
Guo-Dong

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All knowledge is, in final analysis, history.  
All sciences are, in the abstract, mathematics.  
All judgements are, in their rationale, statistics.

C.R. Rao; Statistics and Truth: Putting Chance to Work

By discouraging investigations with no obvious immediate payoff, it  
shortchanges the future.

Martin Davis; Engines of Logic: Mathematicians and the Origin of  
the Computer

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