Remaking the Bioinformatics article

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To redo the analysis from the article, first install the bams package and its dependencies:

```
> options(repos=c(getOption("repos"),"http://www.bioconductor.org/packages/release/bioc"))
> install.packages("bams",dep=TRUE)
```

All of the article source files can then be found in the `bams/article` directory, which you can find by executing the following code in R:

```
> system.file("article",package="bams")
```

Normally the file `bams/article/zzz.stats.RData` should be present. This file saves the results of running all the smoothing algorithms on all the copy number profiles, then quantifying which smoothing models are consistent with the annotation data. To remake the article starting from these saved results, simply type `make` in the `bams/article` directory, which should create `HOCKING-model-selection-breakpoint-annotations.pdf`

If you are interested in redoing the smoothing algorithms, you can do so by removing the `zzz.stats.RData` file as well. Then, when you type `make`, the code in `bams/article/make.all.stats.R` will be used to first remake a `smooth` directory (by default in your home directory) which will contain results of the smoothing models for each profile. But this will take A LONG TIME.

To speed up this process, you can redo the smoothing models for each profile in parallel, if you have access to a cluster with the command line program `qsub`. Try installing the `bams` package on the cluster, then executing the code in `bams/article/smoothing-commands.R`, which should use the cluster to make a `smooth` directory with result files. Then from the cluster, execute the code in `bams/article/make.all.stats.R` to remake zzz.stats.RData, copy this file to the `bams/article` directory, and type `make`.