"NSAIDs modulate clonal evolution in Barrett's esophagus"
Using *BEClonalEvolutionNSAID* for reproducing results

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1 Getting started

```
> source("http://www.bioconductor.org/biocLite.R")
> biocLite(c("cryptsim"))
```

2 Reading in data

3 System information

This analysis was carried out on a linux machine with 12GB of RAM using the following packages:

```
> sessionInfo()

R version 2.12.1 (2010-12-16)
Platform: i686-pc-linux-gnu (32-bit)

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=C              LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods
[7] base
```