# narrowpeaksDiff: Analysis of differential variation across ChIP-seq experiments

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January, 2013

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## 1 Rationale

Under development.

## 2 Details

This document was written using:

```
R> sessionInfo()

R version 3.0.2 (2013-09-25)
Platform: x86_64-unknown-linux-gnu (64-bit)

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=C
 [5] LC_MONETARY=en_US.UTF-8    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] parallel  splines   stats     graphics  grDevices
[6] utils     datasets  methods   base

other attached packages:
```

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```
[1] rtracklayer_1.22.0   CSAR_1.14.0
[3] GenomicRanges_1.14.0 XVector_0.2.0
[5] IRanges_1.20.0       BiocGenerics_0.8.0
[7] NarrowPeaks_1.6.0

loaded via a namespace (and not attached):
 [1] BSgenome_1.30.0   Biostrings_2.30.0 Matrix_1.0-14
 [4] RCurl_1.95-4.1    Rsamtools_1.14.0  XML_3.98-1.1
 [7] bitops_1.0-6      fda_2.3.8         grid_3.0.2
[10] lattice_0.20-24   stats4_3.0.2      tools_3.0.2
[13] zlibbioc_1.8.0
```