# oneChannelGUI Package: What is new 

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## 1 oneChannelGUI Reference

```
oneChannelGUI: a graphical interface to Bioconductor tools,
designed for life scientists who are not
familiar with R language.
Sanges R, Cordero F, Calogero RA.
Bioinformatics. 2007 Dec 15;23, 24, 3406-8.
```


## 2 Updates

## $2.1 \quad 1.8 .8$

Bioconductor BeadStudion V3: report generated by BeadStudio V3 can be loaded in oneChannelGUI. BeadStudio V3 report MUST be a SAMPLE PROBE PROFILE containing at least

AVG_Signal

## $2.2 \quad 1.8 .9$

Fast parameter in GCRMA is set to FALSE.

## $2.3 \quad 1.10 .7$

Revised annotation for variant exons has been added. After statistical detection of putative splicing. It is now possible to select only exon-level probesets associated to non-costitutive exons, i.e. those exons associated only to a to a subset of isoforms.

## $2.4 \quad 1.10 .8$

Added Cosie method to correct SI index: Gaidatzis et al. Nucleic Acids Research, 2009, pg. 1. Since intcor function from metaArray package has a bug it was sobstituted by intCor from MergeMaid package. Alternative splicing events can be visualized on the UCSC Genome Browser via rtracklayer.

## $2.5 \quad 1.10 .9$

Starting from the work of Shah and Pallas work BMC Bioinformatics. 2009 Jan 20;10:26. Limma routines available for gene-level analysis were implemented at exon-level to detect alternative splicing events.

## $2.6 \quad 1.11 .17$

Using Bioconductor hugene10stprobeset.db, mogene10stprobeset.db and ragene10stprobeset.db for GENE 1.0 ST arrays istrad of the internal annotaiton based on Affymetrix data.

## $2.7 \quad 1.13 .4$

Exon-level annotation is provided by three external packages: HuExExonProbesetLocationHg19, MoExExonProbesetLocation, RaExExonProbesetLocation. oneChannelGUI is now providing a basic interface to the secondary analysis of Next Generation Sequencing data. The inteface is designed for ncRNAs quantification analysis.

## $2.8 \quad 1.15 .1$

Two groups linear model analysis with batch effect was added.

