# 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 1.8.8

Bioconductor BeadStudio 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 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 hugene 10 stprobeset.db, mogene 10 stprobeset.db and ragene 10 stprobeset.db for GENE 1.0 ST arrays is trad of the internal annotation based on Affymetrix data.

### 2.7 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 1.15.1

Two groups linear model analysis with batch effect was added.