oneChannelGUI Package: What is new

Raffaele A Calogero, Francesca Cordero, Remo Sanges

April 3 2011

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 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 1.8.9

Fast parameter in GCRMA is set to FALSE.

2.3 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 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 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 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 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.

2.9 1.15.4

RNA-seq data need to be produced by SHRIMP RNAseq data loading can be now performed via Genominator package.

2.10 1.15.5

Low quality alignment data RNAseq data loading can be now performed via Genominator package.

2.11 1.15.7

The edgeR interface allows to handle covariates selection for exactTest.

2.12 1.15.10

Possibility to load mature miRNAs detected by aligning Illumina reads to Hs, Mm and Rn genomes using `http://web.bioinformatics.cicbiogune.es/microRNA/miRanalyser.php` web tool tab delimited files associated to mature miRNAs, containing sequencing counts can be directly loaded on oneChannelGUI Possibility to reformat the output produced by SHRIMP in the .bed and .logos files needed by oneChannelGUI for NGS data analysis.

2.13 1.15.14

Possibility to reformat primary data produced aligning Illumina reads to Hs genomes using MicroRazerS tool.

2.14 1.15.15

Possibility to load mature miRNAs detected by miRProf `http://srna-tools.cmp.uea.ac.uk/animal/cgi-bin/srna-tools.cgi` tab delimited files associated to mature miRNAs, containing sequencing counts can be directly loaded on oneChannelGUI

2.15 1.15.16

Possibility to load mature miRNAs detected by miRExpress `http://miRExpress.mbc.nctu.edu.tw` tab delimited files associated to mature miRNAs, containing sequencing counts can be directly loaded on oneChannelGUI

2.16 1.15.18

Possibility to load alignments generated with SHRIMP and mirBase precursors as reference tab delimited files can be directly loaded on oneChannelGUI

2.17 1.15.20

Adding the possibility to save the count matrix before ENSEMBL annotation addition, when miRbase is used as reference for SHRIMP detection of non-coding RNAs. It is notable that annotation addition will discard all microRNAs characterized by multiple entries on the genome.

2.18 1.17.1

Improving the loading of SHRIMP reformatted data generated mapping reads against microRNA precursors derived from miRbase. The latest version of a specifically re-

formatted verison of the miRbase precursors is available in oneChannelGUI. A specific reformatting function for sHRIMP output is available as part of oneChannelGUI release.

2.19 1.17.4

Adding an interface to baySeq package.

2.20 1.17.5

A function to download meV clustering software was added on the general tool menu. A function showing whihc external software is installed and connected to oneChannelGUI was added on the general tool menu.

2.21 1.17.6

RmiR interface is now provided to detect microRNA targets on the basis of expression data. An output compatible with RmiR package is now provided for baySeqinterface and limma.

2.22 1.17.7

A function to filter expression data upon the correlation existing with microRNA perturbation has been added. To run this analysis a time course experiment suitable for maSigPro analysis is needed. Expression data need to have at least 3 time points for samples transfected with a scrambled and with an Antagomir or a Mimic. The expression changes at the same time points used for microarray data are also needed to be measured for miRNA. miRNA expression data need to be saved as table deliminted file with two columns: column Name, which has to be organized exactly as the target file Name column,and a column named Value with expression of miRNA, e.g. deltaCt.

2.23 1.17.8

Cosie function was retired since data were based on hg18 and mm8 genomes release. Transcripts levels annotations and variant exons definition have been removed from the data dir and are downloadable togheter with the Affymentrix librarys for exon arrays. The procedure is transparents to users since as soon a exon array or gene array is going to be analysed the installation routine will download all necessary files.