

# Package ‘prebs’

April 5, 2014

**Title** Probe region expression estimation for RNA-seq data for improved microarray comparability

**Description** The prebs package aims at making RNA-sequencing (RNA-seq) data more comparable to microarray data. The comparability is achieved by summarizing sequencing-based expressions of probe regions using a modified version of RMA algorithm. The pipeline takes mapped reads in BAM format as an input and produces either gene expressions or original microarray probe set expressions as an output.

**Version** 1.2.1

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**Depends** R (>= 2.14.0), Rsamtools (>= 1.13.1), affy

**Imports** parallel, methods, stats, GenomicRanges (>= 1.13.3), IRanges

**Suggests** prebsdata, hgu133plus2cdf, hgu133plus2probe

**License** Artistic-2.0

**biocViews** Microarray, RNAseq, Sequencing, Bioinformatics, GeneExpression, Preprocessing

**Collate** 'PREBS.R'

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calc_prebs	<i>Calculate PREBS values</i>
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### Description

calc\_prebs calculates PREBS values for given set of BAM files.

### Usage

```
calc_prebs(bam_files, probe_mapping_file,
           cdf_name = NULL, cluster = NULL, output_eset = TRUE)
```

### Arguments

bam_files	A vector containing .bam files.
probe_mapping_file	A file containing probe mappings in the genome.
cdf_name	A name of CDF package to use in RMA algorithm. If cdf_name=NULL, the package name is inferred from the name of probe_mapping_file ("HGU133Plus2_Hs_ENSG_mapping.txt" -> "hgu133plus2hsensgcdf")
cluster	A cluster object created using "makeCluster" function from "parallel" package. If cluster=NULL, no parallelization is used.
output_eset	If set to TRUE, the output of calc_prebs will be ExpressionSet object. Otherwise, the output will be a data frame.

### Details

calc\_prebs is the main function of prebs package that implements the whole pipeline. The function takes mapped reads in BAM format and probe sequence mappings as an input. The output depends on output\_eset option. If output\_eset=TRUE then calc\_prebs returns ExpressionSet object (ExpressionSet object is defined in affy package). Otherwise it returns a data frame containing PREBS values.

For running calc\_prebs with custom CDF, the custom CDF package has to be downloaded and installed from Custom CDF website: <http://brainarray.mbni.med.umich.edu/CustomCDF>

For running calc\_prebs with manufacturer's CDF, the manufacturer's CDF package can be installed from Bioconductor, for example: `biocLite("GenomicRanges"); biocLite("hgu133plus2cdf")`

For a detailed input specification, please refer to the prebs vignette.

### Value

ExpressionSet object or a data frame containing PREBS values

## Examples

```

if (require(prebsdata)) {
  # Get full paths to data files in \code{prebsdata} package
  bam_file1 <- system.file(file.path("sample_bam_files", "input1.bam"), package="prebsdata")
  bam_file2 <- system.file(file.path("sample_bam_files", "input2.bam"), package="prebsdata")
  bam_files <- c(bam_file1, bam_file2)
  custom_cdf_mapping1 <- system.file(file.path("custom-cdf", "HGU133Plus2_Hs_ENSG_mapping.txt"),
                                     package="prebsdata")
  custom_cdf_mapping2 <- system.file(file.path("custom-cdf", "HGU133A2_Hs_ENSG_mapping.txt"),
                                     package="prebsdata")
  manufacturer_cdf_mapping <- system.file(file.path("manufacturer-cdf", "HGU133Plus2_mapping.txt"),
                                          package="prebsdata")

  if (interactive()) {
    # Run PREBS using custom CDF without parallelization
    prebs_values <- calc_prebs(bam_files, custom_cdf_mapping1)
    head(exprs(prebs_values))

    # Run PREBS using custom CDF with parallelization
    library(parallel)
    N_CORES = 2
    CLUSTER <- makeCluster(N_CORES)
    prebs_values <- calc_prebs(bam_files, custom_cdf_mapping1, cluster=CLUSTER)
    stopCluster(CLUSTER)

    # Run PREBS using another custom CDF
    prebs_values <- calc_prebs(bam_files, custom_cdf_mapping2)

    # Run PREBS and return data frame instead of ExpressionSet object
    prebs_values <- calc_prebs(bam_files, custom_cdf_mapping1, output_eset=FALSE)
    head(prebs_values)
  }

  # Run PREBS using Manufacturers CDF (outputs probe set expressions)
  prebs_values <- calc_prebs(bam_files, manufacturer_cdf_mapping)
  head(exprs(prebs_values))

  # Same as above, but state CDF package name explicitly
  prebs_values <- calc_prebs(bam_files, manufacturer_cdf_mapping, cdf_name="hgu133plus2cdf")
}

```

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```
prebs
```

```
PREBS package
```

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## Description

The prebs package aims at making RNA-sequencing (RNA-seq) data more comparable to microarray data. The comparability is achieved by summarizing sequencing-based expressions of probe regions using a modified version of RMA algorithm. The pipeline takes mapped reads in BAM format as an input and produces either gene expressions or original microarray probe set expressions as an output.

**Details**

The package has only one public function: `calc_prebs`. Type `help(calc_prebs)` for more information on the usage.

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