

Package ‘SCAN.UPC’

March 26, 2013

Encoding UTF-8

Type Package

Title Single-channel array normalization (SCAN)

Version 1.0.0

Author Stephen R. Piccolo and W. Evan Johnson

Maintainer Stephen R. Piccolo <stephen.piccolo@hsc.utah.edu>

Description SCAN is a microarray normalization method to facilitate personalized-medicine workflows. Rather than processing microarray samples as groups, which can introduce biases and present logistical challenges, SCAN normalizes each sample individually by modeling and removing probe- and array-specific background noise using only data from within each array. (The Universal Probability of expression Codes (UPC) method is an extension of SCAN and will be added to this package soon.)

License MIT

Depends R (>= 2.14.0), Biobase (>= 2.6.0), oligo, Biostrings

Suggests pd.hg.u95a

Imports utils, methods

biocViews Software, Microarray, Preprocessing

URL <http://bioconductor.org>, <http://jlab.bu.edu/software/scan-upc>

R topics documented:

SCAN	2
Index	4

SCAN

*Single-Channel Array Normalization (SCAN)***Description**

This function is used to normalize single-channel expression microarrays via the SCAN method. In raw form, such microarray data come in the form of Affymetrix .CEL files.

Usage

```
SCAN(ceFilePattern, outFilePath = NA, probeSummaryPackage = NA,
     probeLevelOutDirPath = NA, verbose = TRUE)
```

Arguments

ceFilePattern	Absolute or relative path to the input file to be processed. To process multiple files, wildcard characters can be used (e.g., "*.CEL"). This is the only required parameter.
outFilePath	Absolute or relative path where the output file will be saved. This is optional.
probeSummaryPackage	An R package that specifies alternative probe/gene mappings. This is optional. See note below for more details.
probeLevelOutDirPath	Absolute or relative path to a directory where probe-level normalized values can be saved. This is optional. By default, the probe-level values will be discarded after they have been summarized. However, if the user has a need to repeatedly process the same file (perhaps to try various probe/gene mappings), this option can be useful because SCAN will retrieve previously normalized values if a probe-level file exists, rather than renormalize the raw data. The user should be aware that probe-level files may consume a considerable amount of disk space.
verbose	Whether to output more detailed status information as files are normalized. Default is TRUE.

Value

An ExpressionSet object that contains a row for each probeset/gene/transcript and a column for each input file.

Note

By default, SCAN uses the default mappings between probes and genes that have been provided by the manufacturer. However, these mappings may be outdated or may include problematic probes (for example, those that cross hybridize). The default mappings also may produce multiple summary values per gene. Alternative mappings, such as those provided by the BrainArray resource (see http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/genomic_curated_CDF.asp), allow SCAN to produce a single value per gene and to use updated gene definitions. Users can specify alternative mappings using the probeSummaryPackage parameter. If specified, this package must conform to the standards of the AnnotationDbi package. The BrainArray packages can be downloaded from http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/CDF_download.asp. When using BrainArray, be sure to download the R source package for probe-level mappings (see vignette for more information).

Author(s)

Stephen R. Piccolo

References

Piccolo SR, Sun Y, Campbell JD, Lenburg ME, Bild AH, and Johnson WE. A single-sample microarray normalization method to facilitate personalized-medicine workflows. *Genomics*, 2012.

Examples

```
# Download an example CEL file and save it as a temporary local file
celFilePath = file.path(tempdir(), "Vignette_Example.CEL.gz")
download.file("http://www.ncbi.nlm.nih.gov/geo/suppl/?acc=GSM555237&file=GSM555237.CEL.gz", celFilePath)

# Normalize a CEL file
normalized = SCAN(celFilePath)

# Normalize a CEL file and save output to a file
normalized = SCAN(celFilePath, "output_file.txt")

## Not run:
# Normalize a CEL file and summarize at the gene level using BrainArray
# mappings for Entrez Gene
probeFilePath = file.path(tempdir(), "hgu95ahsentrezgprobe_15.0.0.tar.gz")
download.file("http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/15.0.0/entrezg.download/hg
install.packages(probeFilePath, repos=NULL, type="source")
library(hgu95ahsentrezgprobe)
normalized = SCAN(celFilePath, probeSummaryPackage=hgu95ahsentrezgprobe)

## End(Not run)
```

Index

SCAN, [2](#)