

Package ‘illuminaio’

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Version 0.2.0

Title Parsing Illumina microarray output files

Description Tools for parsing Illumina’s microarray output files, including IDAT.

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Suggests RUnit, BiocGenerics, minfiData, hapmap370k

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biocViews Infrastructure, DataImport

R topics documented:

| | |
|----------|---|
| readBPM | 1 |
| readIDAT | 2 |

| | |
|--------------|----------|
| Index | 4 |
|--------------|----------|

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|---------|---|
| readBPM | <i>Low-level function to read BPM files</i> |
|---------|---|

Description

Reads BPM files (array design information) from Illumina arrays.

Usage

```
readBPM(file)
```

Arguments

file character string specifying BPM file to be read in

Value

A list.

Author(s)

Henrik Bengtsson

readIDAT

Low-level function to read IDAT files

Description

Reads intensity information for each bead type from a single IDAT file for Infinium II or Infinium HD platforms.

Usage

```
readIDAT(file)
```

Arguments

file character string specifying idat file to be read in.

Details

This function returns a list containing summarised intensities and other information extracted from a single .idat file.

Thanks to Keith Baggerly for providing the first version of this code.

There are two commonly encountered versions of IDAT. One version uses encryption to store data, and this function does not read encrypted IDAT files. This is the formatted usually produced by Illumina expression arrays. The other version is unencrypted files, which this function reads. This includes data from SNP arrays and DNA methylation arrays.

Search the Bioconductor archives for hints on how to read encrypted IDATs. We are considering merging that code into this package.

Value

A list which includes item `Quants` which contains average intensity (Mean), number of beads (NBeads) and a measure of variability (SD) for each bead type on the array.

Author(s)

Keith Baggerly, with modifications by Matt Ritchie, Henrik Bengtsson and Kasper Daniel Hansen

References

Ritchie ME, Carvalho BS, Hetrick KN, Tavar`e S, Irizarry RA. R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. *Bioinformatics*. 2009 Oct 1;25(19):2621-3.

Examples

```
if(require(minfiData)) {  
  idatDir <- system.file("extdata", "5723646052", package = "minfiData")  
  idatFile <- file.path(idatDir, "5723646052_R02C02_Grn.idat")  
  idat <- readIDAT(idatFile)  
  names(idat)  
  idat$Quants[1:5,]  
}
```

Index

*Topic **IO**

readBPM, [1](#)

readIDAT, [2](#)

readBPM, [1](#)

readIDAT, [2](#)