readat

Read and work with SomaLogic ADAT files

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Reading data is easy:

somaData <- readAdat(ADatFile)
How to store the data has a few answers:

class(somaData)
## [1] "WideSomaLogicData" "data.table" "data.frame"
A data table of sample data and intensities

An attribute containing a data table of sequence data

An attribute containing a list of metadata
Melting to long form is convenient for dplyr or ggplot2 workflows

longSomaData <- melt(somaData)
class(longSomaData)
## [1] "LongSomaLogicData" "data.table" "data.frame"
Conversion to ExpressionSets and SummarizedExperiments is supported

```r
as.ExpressionSet(somaData) as.SummarizedExperiment(somaData)
```
There are several useful ways of storing experimental data. readat supports 4 of them.