readat

Read and work with SomaLogic ADAT files

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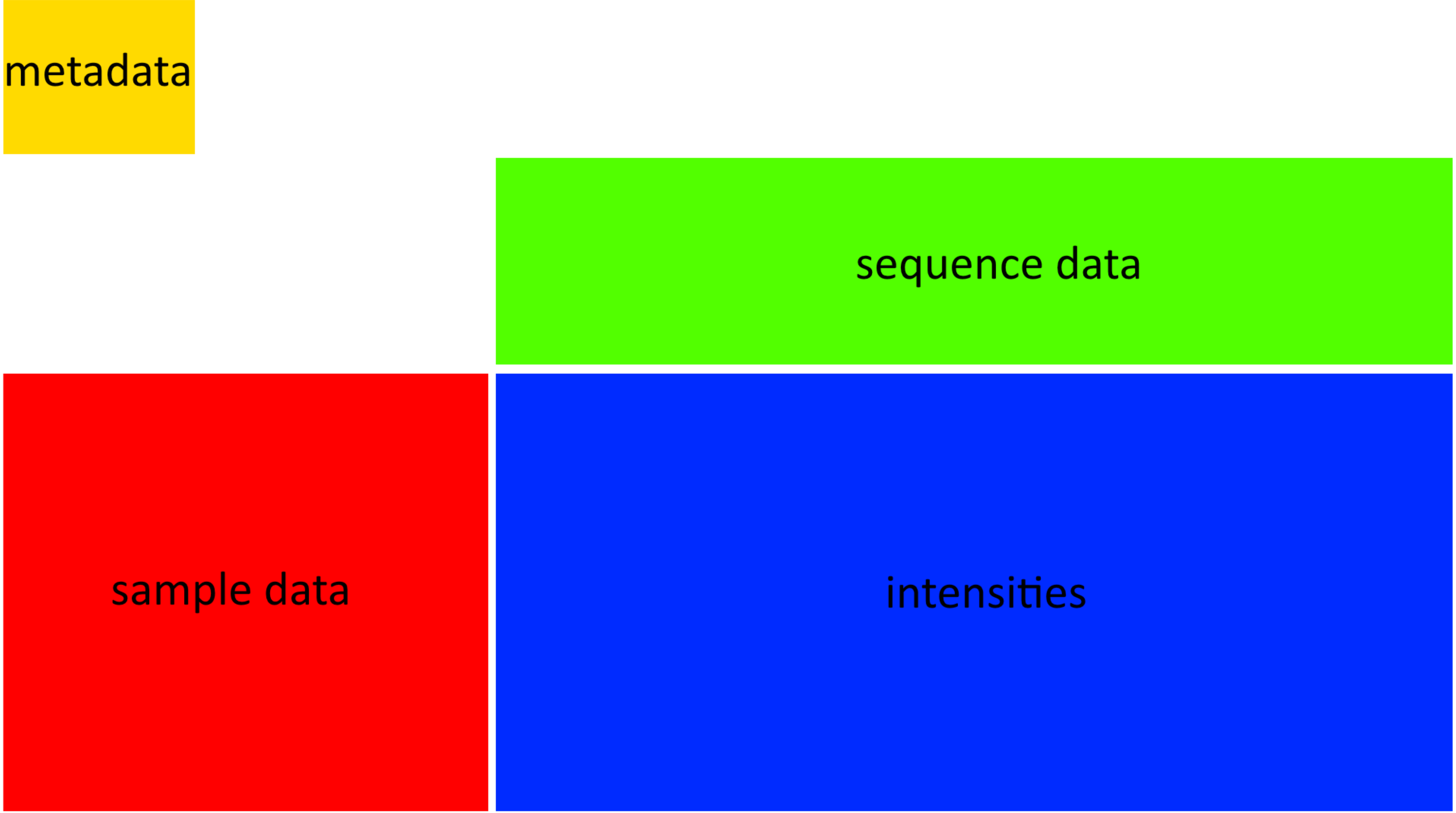


metadata

sequence data

sample data

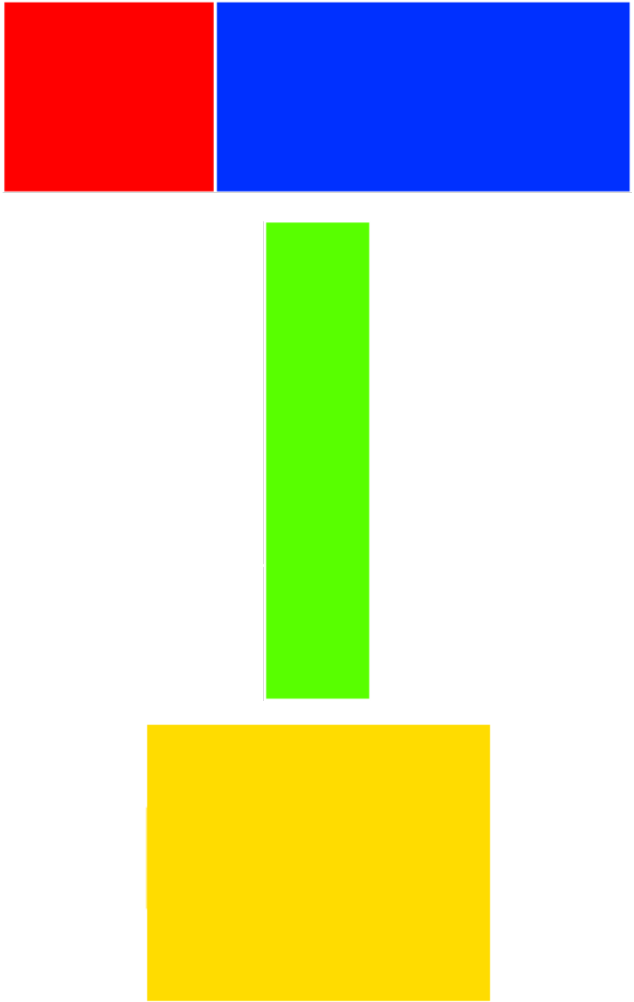
intensities

Reading data is easy:

```
somaData <- readAdat(adatFile)
```

How to store the data has a few answers:

```
class(somaData)
## [1] "WideSomaLogicData" "data.table" "data.frame"
```



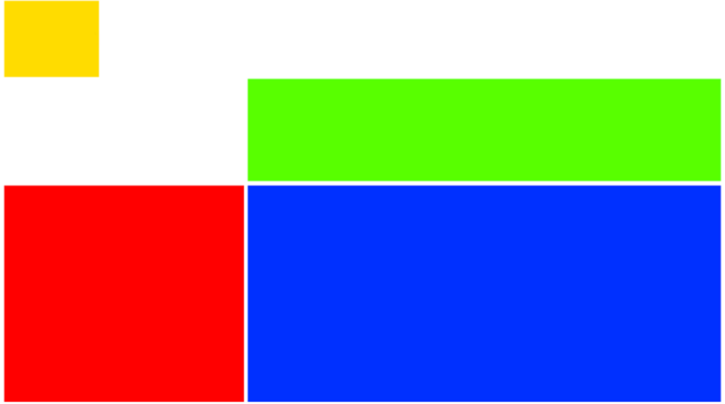
A data table of sample data and intensities

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

```
as.ExpressionSet(somaData)
as.SummarizedExperiment(somaData)
```

There are several useful ways of storing experimental data

readat supports 4 of them