

Package ‘ShortRead’

April 5, 2014

Type Package

Title Classes and methods for high-throughput short-read sequencing data.

Version 1.20.0

Author Martin Morgan, Michael Lawrence, Simon Anders

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

Description Base classes, functions, and methods for representation of high-throughput, short-read sequencing data.

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LazyLoad yes

Depends methods, BiocGenerics (>= 0.1.0), IRanges (>= 1.19.34), GenomicRanges (>= 1.13.43), Biostrings (>= 2.29.18), lattice, Rsamtools (>= 1.13.1)

Imports Biobase, hwriter, zlibbioc, latticeExtra

Enhances Rmpi, parallel

Suggests biomaRt, RUnit, GenomicFeatures, yeastNagalakshmi

LinkingTo IRanges, XVector, Biostrings

biocViews DataImport, Sequencing, HighThroughputSequencing, QualityControl

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ShortReadBase-package *Base classes and methods for high-throughput short-read sequencing data.*

Description

Base classes, functions, and methods for representation of high-throughput, short-read sequencing data.

Details

See packageDescription(ShortRead)

Author(s)

Maintainer: Martin Morgan <mtmorgan@fhcrc.org>

`.QA-class` *Virtual class for representing quality assessment results*

Description

Classes derived from `.QA-class` represent results of quality assurance analyses. Details of derived class structure are found on the help pages of the derived classes.

Objects from the Class

Objects from the class are created by ShortRead functions, in particular `qa`.

Extends

Class "`.ShortReadBase`", directly.

Methods

Methods defined on this class include:

rbind signature(...="list"): rbind data frame objects in All objects of ... must be of the same class; the return value is an instance of that class.

show signature(object = "SolexaExportQA"): Display an overview of the object contents.

Author(s)

Martin Morgan <mtmmorgan@fhcrc.org>

See Also

Specific classes derived from .QA

Examples

```
getClass(".QA", where=getNamespace("ShortRead"))
```

accessors

Accessors for ShortRead classes

Description

These functions and generics define ‘accessors’ (to get and set values) for objects in the **ShortRead** package; methods defined in other packages may have additional meaning.

Usage

```
## SRVector
vclass(object, ...)
## ShortRead / ShortReadQ
sread(object, ...)
id(object, ...)
## AlignedRead
chromosome(object, ...)
position(object, ...)
alignQuality(object, ...)
alignData(object, ...)
## Solexa
experimentPath(object, ...)
dataPath(object, ...)
scanPath(object, ...)
imageAnalysisPath(object, ...)
baseCallPath(object, ...)
analysisPath(object, ...)
```

```
## SolexaSet
solexaPath(object, ...)
laneDescription(object, ...)
laneNames(object, ...)
```

Arguments

object An object derived from class `ShortRead`. See help pages for individual objects, e.g., [ShortReadQ](#). The default is to extract the contents of a slot of the corresponding name (e.g., `slot sread`) from object.

... Additional arguments passed to the accessor. The default definitions do not make use of additional arguments.

Value

Usually, the value of the corresponding slot, or other simple content described on the help page of object.

Author(s)

Martin Morgan

Examples

```
sp <- SolexaPath(system.file(extdata, package=ShortRead))
experimentPath(sp)
basename(analysisPath(sp))
```

AlignedDataFrame *AlignedDataFrame constructor*

Description

Construct an `AlignedDataFrame` from a data frame and its metadata

Usage

```
AlignedDataFrame(data, metadata, nrow = nrow(data))
```

Arguments

data A data frame containing alignment information.

metadata A data frame describing the columns of data, and with number of rows of metadata corresponding to number of columns of data. . The data frame must contain a column `labelDescription` providing a verbose description of each column of data.

nrow An optional argument, to be used when data is not provided, to construct an `AlignedDataFrame` with the specified number of rows.

Value

An object of [AlignedDataFrame](#).

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

AlignedDataFrame-class

"AlignedDataFrame" representing alignment annotations as a data frame

Description

This class extends [AnnotatedDataFrame](#). It is a data frame and associated metadata (describing the columns of the data frame). The main purpose of this class is to contain alignment data in addition to the central information of [AlignedRead](#).

Objects from the Class

Objects from the class are created by calls to the [AlignedDataFrame](#) function.

Slots

data: Object of class "data.frame" containing the data. See [AnnotatedDataFrame](#) for details.

varMetadata: Object of class "data.frame" describing columns of data. See [AnnotatedDataFrame](#) for details.

dimLabels: Object of class character describing the dimensions of the [AnnotatedDataFrame](#). Used internally; see [AnnotatedDataFrame](#) for details.

.__classVersion__: Object of class "Versions" describing the version of this object. Used internally; see [AnnotatedDataFrame](#) for details.

Extends

Class "[AnnotatedDataFrame](#)", directly. Class "[Versioned](#)", by class "[AnnotatedDataFrame](#)", distance 2.

Methods

This class inherits methods `pData` (to retrieve the underlying data frame) and `varMetadata` (to retrieve the metadata) from [AnnotatedDataFrame](#).

Additional methods include:

append signature(`x = "AlignedDataFrame"`, `values = "AlignedDataFrame"`): append values after `x`. `varMetadata` of `x` and `y` must be identical; `pData` and `varMetadata` are appended using `rbind`.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[AnnotatedDataFrame](#)

AlignedRead

Construct objects of class "AlignedRead"

Description

This function constructs objects of [AlignedRead](#). It will often be more convenient to create AlignedRead objects using parsers such as [readAligned](#).

Usage

```
AlignedRead(sread, id, quality, chromosome, position, strand,
            alignQuality,
            alignData = AlignedDataFrame(nrow = length(sread)))
```

Arguments

sread	An object of class DNASTringSet, containing the DNA sequences of the short reads.
id	An object of class BStringSet, containing the identifiers of the short reads. This object is the same length as sread.
quality	An object of class BStringSet, containing the ASCII-encoded quality scores of the short reads. This object is the same length as sread.
chromosome	A factor describing the particular sequence within a set of target sequences (e.g. chromosomes in a genome assembly) to which each short read aligns.
position	A integer vector describing the (base pair) position at which each short read begins its alignment.
strand	A factor describing the strand to which the short read aligns.
alignQuality	A numeric vector describing the alignment quality.
alignData	An AlignedDataFrame with number of rows equal to the length of sread, containing additional information about alignments.

Value

An object of class [AlignedRead](#).

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[AlignedRead](#).

AlignedRead-class	<i>"AlignedRead" class for aligned short reads</i>
-------------------	--

Description

This class represents and manipulates reads and their genomic alignments. Alignment information includes genomic position, strand, quality, and other data.

Objects from the Class

Objects of this class can be created from a call to the [AlignedRead](#) constructor, or more typically by parsing appropriate files (e.g., [readAligned](#)).

Slots

chromosome Object of class "factor" the particular sequence within a set of target sequences (e.g. chromosomes in a genome assembly) to which each short read aligns.

position Object of class "integer" the (base-pair) position in the genome to which the read is aligned. AlignedRead objects created by [readAligned](#) use 1-based indexing, with alignments reported in 'left-most' coordinates, as described in the vignette.

strand Object of class "factor" the strand of the alignment.

alignQuality Object of class "numeric" representing an alignment quality score.

alignData Object of class "AlignedDataFrame" additional alignment information.

quality Object of class "BStringSet" representing base-call read quality scores.

sread Object of class "DNAStrngSet" DNA sequence of the read.

id Object of class "BStringSet" read identifier.

Extends

Class "[ShortReadQ](#)", directly. Class "[ShortRead](#)", by class "[ShortReadQ](#)", distance 2. Class "[.ShortReadBase](#)", by class "[ShortReadQ](#)", distance 3.

Methods

See [accessors](#) for additional functions to access slot content, and [ShortReadQ](#), [ShortRead](#) for inherited methods. Additional methods include:

[signature(x = "AlignedRead", i = "ANY", j = "missing")]: This method creates a new [AlignedRead](#) object containing only those reads indexed by i. chromosome is recoded to contain only those levels in the new subset.

append signature(x = "AlignedRead", values = "AlignedRead"): append values after x. chromosome and strand must be factors with the same levels. See methods for ShortReadQ, AlignedDataFrame for details of how these components of x and y are appended.

coerce signature(from = "PairwiseAlignments", to = "AlignedRead"):

signature(from = "AlignedRead", to = "RangesList"): signature(from = "AlignedRead", to = "RangedData")

signature(from = "AlignedRead", to = "GRanges"): signature(from = "AlignedRead", to = "GAlignments")

signature(from = "AlignedRead", to = "GappedReads"):

Invoke these methods with, e.g., as(from, "AlignedRead") to coerce objects of class from to class "AlignedRead".

Coercion from AlignedRead to [RangesList](#), [RangedData](#) or [GRanges](#) assumes that position(from) uses a 'leftmost' (see coverage on this page) coordinate system. Since [Ranges](#) objects cannot store NA values, reads with NA in the position, width, chromosome or (in the case of [GRanges](#)) strand vectors are dropped.

chromosome signature(object = "AlignedRead"): access the chromosome slot of object.

position signature(object = "AlignedRead"): access the position slot of object.

strand signature(object = "AlignedRead"): access the strand slot of object.

coverage signature(x = "AlignedRead", shift = 0L, width = NULL, weight = 1L, ..., coords = c("leftmost",

Calculate coverage across reads present in x.

shift must be either 0L or a named integer vector with names including all levels(chromosome(x)).

It specifies how the reads in x should be (horizontally) shifted *before* the coverage is computed.

width must be either NULL or a named vector of non-negative integers with names including all levels(chromosome(x)). In the latter case, it specifies for each chromosome the end of the chromosome region over which coverage is to be calculated *after* the reads have been shifted. Note that this region always starts at chromosome position 1. If width is NULL, it ends at the rightmost chromosome position covered by at least one read.

weight must be 1L for now (weighting the reads is not supported yet, sorry).

coords specifies the coordinate system used to record position. Both systems number base pairs from left to right on the 5' strand. leftmost indicates the eland convention, where position(x) is the left-most (minimum) base pair, regardless of strand. fiveprime is the MAQ convention, where position(x) is the coordinate of the 5' end of the aligned read.

extend indicates the number of base pairs to extend the read. Extension is in the 3' direction, measured from the 3' end of the aligned read.

The return value of coverage is a SimpleRleList object.

%in% signature(x = "AlignedRead", table = "RangesList"):

Return a length(x) logical vector indicating whether the chromosome, position, and width of x overlap (see [IRanges](#) [overlap](#)) with ranges in table. Reads for which chromosome(), position(), or width() return NA *never* overlap with table. This function assumes that positions are in 'leftmost' coordinates, as defined in coverage.

srrorder signature(x = "AlignedRead", ..., withSread=TRUE):

srrank signature(x = "AlignedRead", ..., withSread=TRUE):

srsort signature(x = "AlignedRead", ..., withSread=TRUE):

srduplicated signature(x = "AlignedRead", ..., withSread=TRUE):

Order, rank, sort, and find duplicates in AlignedRead objects. Reads are sorted by chromosome, strand, position, and then (if withSread=TRUE) sread; less fine-grained sorting can be accomplished with, e.g., `x[srorder(sread(x))]`. `sruplicated` behaves like `duplicated`, i.e., the first copy of a duplicate is FALSE while the remaining copies are TRUE.

show `signature(object = "AlignedRead")`: provide a compact display of the AlignedRead content.

detail `signature(x = "AlignedRead")`: display `alignData` in more detail.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[readAligned](#)

Examples

```
showMethods(class="AlignedRead", where=getNamespace("ShortRead"))
dirPath <- system.file(extdata, maq, package=ShortRead)
(aln <- readAligned(dirPath, out.aln.1.txt, type="MAQMapView"))
coverage(aln)[[1]]
cvg <- coverage(aln, shift=c(ChrA=10L))
## remove 0 coverage on left ends
ltrim0 <- function(x) {
  i <- !cumprod(runValue(x) == 0)
  Rle(runValue(x)[i], runLength(x)[i])
}
endoapply(cvg, ltrim0)
## demonstration of show() and detail() methods
show(aln)
detail(aln)
```

alphabetByCycle

Summarize short read nucleotide or quality scores by cycle

Description

`alphabetByCycle` summarizes short read nucleotides or qualities by cycle, e.g., returning the number of occurrences of each nucleotide A, T, G, C across all reads from 36 cycles of a Solexa lane.

Usage

```
alphabetByCycle(stringSet, alphabet, ...)
```

Arguments

stringSet	A R object representing the collection of reads or quality scores to be summarized.
alphabet	The alphabet (character vector of length 1 strings) from which the sequences in stringSet are composed. Methods often define an appropriate alphabet, so that the user does not have to provide one.
...	Additional arguments, perhaps used by methods defined on this generic.

Details

The default method requires that stringSet extends the `XStringSet` class of **Biostrings**.

The following method is defined, in addition to methods described in class-specific documentation:

alphabetByCycle signature(stringSet = "BStringSet"): this method uses an alphabet spanning all ASCII characters, codes 1:255.

Value

A matrix with number of rows equal to the length of alphabet and columns equal to the maximum width of reads or quality scores in the string set. Entries in the matrix are the number of times, over all reads of the set, that the corresponding letter of the alphabet (row) appeared at the specified cycle (column).

Author(s)

Martin Morgan

See Also

The IUPAC alphabet in Biostrings.

http://www.bioperl.org/wiki/FASTQ_sequence_format for the BioPerl definition of fastq.

Solexa documentation 'Data analysis - documentation : Pipeline output and visualisation'.

Examples

```
showMethods("alphabetByCycle")

sp <- SolexaPath(system.file(extdata, package=ShortRead))
rfq <- readFastq(analysisPath(sp), pattern="s_1_sequence.txt")
alphabetByCycle(sread(rfq))

abcq <- alphabetByCycle(quality(rfq))
dim(abcq)
## high scores, first and last cycles
abcq[64:94,c(1:5, 32:36)]
```

alphabetScore	<i>Efficiently calculate the sum of quality scores across bases</i>
---------------	---

Description

This generic takes a [QualityScore](#) object and calculates, for each read, the sum of the encoded nucleotide probabilities.

Usage

```
alphabetScore(object, ...)
```

Arguments

object	An object of class QualityScore .
...	Additional arguments, currently unused.

Value

A vector of numeric values of length equal to the length of object.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

BAMQA-class	<i>Quality assessment from BAM files</i>
-------------	--

Description

This class contains a list-like structure with summary descriptions derived from visiting one or more BAM files.

Objects from the Class

Objects of the class are usually produced by a [qa](#) method, with the argument type="BAM".

Slots

`.srlist`: Object of class "list", containing data frames or lists of data frames summarizing the results of qa.

Extends

Class "[SRList](#)", directly. Class "[.QA](#)", directly. Class "[.SRUtil](#)", by class "SRList", distance 2. Class "[.ShortReadBase](#)", by class ".QA", distance 2.

Methods

Accessor methods are inherited from the [SRList](#) class.

report signature(x="BAMQA", ..., dest=tempfile(), type="html"): produces an html file summarizing QA results.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[qa](#).

Examples

```
showClass("BAMQA")
```

BowtieQA-class

Quality assessment summaries from Bowtie files

Description

This class contains a list-like structure with summary descriptions derived from visiting one or more Bowtie files.

Objects from the Class

Objects of the class are usually produced by a [qa](#) method, with the argument type="Bowtie".

Slots

`.srlist`: Object of class "list", containing data frames or lists of data frames summarizing the results of qa.

Extends

Class "[SRList](#)", directly. Class "[.QA](#)", directly. Class "[.SRUtil](#)", by class "SRList", distance 2. Class "[.ShortReadBase](#)", by class ".QA", distance 2.

Methods

Accessor methods are inherited from the [SRList](#) class.

report signature(x="BowtieQA", ..., dest=tempfile(), type="html"): produces an html file summarizing the QA results.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[qa](#).

Examples

```
showClass("BowtieQA")
```

clean	<i>Remove sequences with ambiguous nucleotides from short read classes</i>
-------	--

Description

Short reads may contain ambiguous base calls (i.e., IUPAC symbols different from A, T, G, C). This generic removes all sequences containing 1 or more ambiguous bases.

Usage

```
clean(object, ...)
```

Arguments

object	An object for which clean methods exist; see below to discover these methods.
...	Additional arguments, perhaps used by methods.

Details

The following method is defined, in addition to methods described in class-specific documentation:

clean signature(*x* = "DNAStrngSet"): Remove all sequences containing non-base (A, C, G, T) IUPAC symbols.

Value

An instance of `class(object)`, containing only sequences with non-redundant nucleotides.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
showMethods(clean)
```

countLines	<i>Count lines in all (text) files in a directory whose file name matches a pattern</i>
------------	---

Description

countLines visits all files in a directory path dirPath whose base (i.e., file) name matches pattern. Lines in the file are counted as the number of new line characters.

Usage

```
countLines(dirPath, pattern=character(0), ..., useFullName=FALSE)
```

Arguments

dirPath	A character vector (or other object; see methods defined on this generic) giving the directory path (relative or absolute) of files whose lines are to be counted.
pattern	The (grep -style) pattern describing files whose lines are to be counted. The default (character(0)) results in line counts for all files in the directory.
...	Additional arguments, passed internally to list.files. See list.files .
useFullName	A logical(1) indicating whether elements of the returned vector should be named with the base (file) name (default; useFullName=FALSE) or the full path name (useFullName=TRUE).

Value

A named integer vector of line counts. Names are paths to the files whose lines have been counted, excluding dirPath.

Author(s)

Martin Morgan

Examples

```
sp <- SolexaPath(system.file(extdata, package=ShortRead))
countLines(analysisPath(sp))
countLines(experimentPath(sp), recursive=TRUE)
countLines(experimentPath(sp), recursive=TRUE, useFullName=TRUE)
```

 deprecated *Deprecated and defunct functions*

Description

These functions were introduced but are now deprecated or defunct.

Usage

```
basePath(object, ...)
pileup(start, fraglength, chrlength, dir = strand( "+" ),
        readlength = fraglength, offset = 1)
```

Arguments

object	For basePath, and object of class ExperimentPath.
...	Additional arguments.
start	A vector with the start positions of each read on the reference sequence. All reads must correspond to the same reference sequence.
fraglength	A vector of the same length as 'start' with the lengths of all the fragments. Alternatively, a single integer, specifying one constant length to assume for all tags.
chrlength	The length of the reference sequence. You may use the function readBfaToc to extract this information from the .bfa file.
dir	A factor with level "-" and "+" of the same length as 'start', specifying whether the fragment extends to the right (towards higher index values, '+') or to the left (towards lower index values, '-') beyond the read. See below for more explanation.
readlength	The length of the reads, either as a vector of the same length as 'start' or as a single number. This parameter makes sense only if 'dir' is used, too. If not specified, read lengths and fragment lengths are taken to be the same.
offset	The index of the first base pair in the result vector. The default is 1, i.e. assumes that the 'start' positions are in 1-based chromosome coordinates.

Value

pileup	an integer vector of length 'chrlength', each element counting how many fragments map to this basepair.
--------	---

Note

(the following refers to the pileup function)

1. This function is not suitable for paired-end reads.
2. If the arguments 'dir' and 'readlength' are not used, the fragments are assumed to start at the positions given in 'start' and extend to the right by the number of basepairs given in fraglength. If

'dir' and 'readlength' are supplied then the interval starting at 'start' and extending to the right by the number of base pairs given in 'readlength' marks the position of the read, which is one end of the fragment. If 'dir' is '+', it is taken as the left end and the fragment will be extended to the right to have the total length given by 'fraglength'. If 'dir' is '-', the end is taken as the right end and is extended to the left. Note that in the latter case, the 'start' position does mark the border between read and rest of fragment, not an actual 'end' of the fragment. If you are confused now, look at the examples below.

3. Sorry for the inconsequent use of 'width' and 'length' in a seemingly interchangeable fashion.

Author(s)

Simon Anders, EMBL-EBI, <sanders@fs.tum.de>

Examples

Not run:

Example 1: Assuming that lane is an AlignedRead object containing aligned reads from a Solexa lane, you may get a pile-up representation of chromosome 13 as follows

```
chr13length <- 114142980 # the length of human chromosome 13
pu <- pileup(position(lane)[chromosome(lane)=="13"],
             width(lane), chr13length )
```

Example 2: Even though the width of the reads (as reported by width(lane)) is only 24, these 24 bp are just one end of a longer fragment. Assuming that all fragments have been sonicated to about the same length, say 150 bp, we may get a better pile-up representation by:

```
pu2 <- pileup(position(lane)[chromosome(lane)=="13"], 150,
              chr13length, strand(lane)[chromosome(lane)=="13"],
              width(lane) )
```

End(Not run)

dustyScore

Summarize low-complexity sequences

Description

dustyScore identifies low-complexity sequences, in a manner inspired by the dust implementation in BLAST.

Usage

```
dustyScore(x, batchSize=NA, ...)
```

Arguments

x	A DNASTringSet object, or object derived from ShortRead, containing a collection of reads to be summarized.
batchSize	NA or an integer(1) vector indicating the maximum number of reads to be processed at any one time.
...	Additional arguments, not currently used.

Details

The following methods are defined:

dustyScore signature(x = "DNASTringSet"): operating on an object derived from class DNASTringSet.

dustyScore signature(x = "ShortRead"): operating on the sread of an object derived from class ShortRead.

The dust-like calculations used here are as implemented at <https://stat.ethz.ch/pipermail/bioc-sig-sequencing/2009-February/000170.html>. Scores range from 0 (all triplets unique) to the square of the width of the longest sequence (poly-A, -C, -G, or -T).

The batchSize argument can be used to reduce the memory requirements of the algorithm by processing the x argument in batches of the specified size. Smaller batch sizes use less memory, but are computationally less efficient.

Value

A vector of numeric scores, with length equal to the length of x.

Author(s)

Herve Pages (code); Martin Morgan

References

Morgulis, Getz, Schaffer and Agarwala, 2006. WindowMasker: window-based masker for sequenced genomes, Bioinformatics 22: 134-141.

See Also

The WindowMasker supplement defining dust ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/windowmasker/windowmasker_suppl.pdf

Examples

```
sp <- SolexaPath(system.file(extdata, package=ShortRead))
rfq <- readFastq(analysisPath(sp), pattern="s_1_sequence.txt")
range(dustyScore(rfq))
```

ExperimentPath-class *"ExperimentPath" class representing a file hierarchy of data files*

Description

Short read technologies often produce a hierarchy of output files. The content of the hierarchy varies. This class represents the root of the file hierarchy. Specific classes (e.g., [SolexaPath](#)) represent different technologies.

Objects from the Class

Objects from the class are created by calls to the constructor:

```
ExperimentPath(experimentPath)
```

experimentPath character(1) object pointing to the top-level directory of the experiment; see specific technology classes for additional detail.

verbose=FALSE (optional) logical vector which, when TRUE results in warnings if paths do not exist.

All paths must be fully-specified.

Slots

ExperimentPath has one slot, containing a fully specified path to the corresponding directory (described above).

basePath See above.

The slot is accessed with experimentPath.

Extends

Class "[.ShortReadBase](#)", directly.

Methods

Methods include:

show signature(object = "ExperimentPath"): briefly summarize the file paths of object.

detail signature(x = "ExperimentPath"): summarize file paths of x.

Author(s)

Michael Lawrence

Examples

```
showClass("ExperimentPath")
```

FastqFile-class *Sampling and streaming records from fastq files*

Description

FastqFile represents a path and connection to a fastq file. FastqFileList is a list of such connections.

FastqSampler draws a subsample from a fastq file. yield is the method used to extract the sample from the FastqSampler instance; a short illustration is in the example below. FastqSamplerList is a list of FastqSampler elements.

FastqStreamer draws successive subsets from a fastq file, a short illustration is in the example below. FastqStreamerList is a list of FastqStreamer elements.

Usage

```
## FastqFile and FastqFileList
FastqFile(con, ...)
FastqFileList(..., class="FastqFile")
## S3 method for class ShortReadFile
open(con, ...)
## S3 method for class ShortReadFile
close(con, ...)
## S4 method for signature FastqFile
readFastq(dirPath, pattern=character(), ...)

## FastqSampler and FastqStreamer
FastqSampler(con, n=1e6, readerBlockSize=1e8, verbose=FALSE,
             ordered = FALSE)
FastqSamplerList(..., n=1e6, readerBlockSize=1e8, verbose=FALSE,
                 ordered = FALSE)
FastqStreamer(con, n, readerBlockSize=1e8, verbose=FALSE)
FastqStreamerList(..., n, readerBlockSize=1e8, verbose=FALSE)
yield(x, ...)
```

Arguments

con, dirPath	A character string naming a connection, or (for con) an R connection (e.g., file, gzfile).
n	For FastqSampler, the size of the sample (number of records) to be drawn. For FastqStreamer a numeric(1) (set to 1e6 when n is missing) providing the number of successive records to be returned on each yield, or an IRanges -class delimiting the (1-based) indices of records returned by each yield; entries in n must have non-zero width and must not overlap.
readerBlockSize	The number of bytes or characters to be read at one time; smaller readerBlockSize reduces memory requirements but is less efficient.

verbose	Display progress.
ordered	logical(1) indicating whether sampled reads should be returned in the same order as they were encountered in the file.
x	An instance from the FastqSampler or FastqStreamer class.
...	Additional arguments. For FastqFileList, FastqSamplerList, or FastqStreamerList, this can either be a single character vector of paths to fastq files, or several instances of the corresponding FastqFile, FastqSampler, or FastqStreamer objects.
pattern	Ignored.
class	For developer use, to specify the underlying class contained in the FastqFileList.

Objects from the class

Available classes include:

FastqFile A file path and connection to a fastq file.

FastqFileList A list of FastqFile instances.

FastqSampler Uniformly sample records from a fastq file.

FastqStreamer Iterate over a fastq file, returning successive parts of the file.

Methods

The following methods are available to users:

`readFastq, FastqFile-method`: see also [?readFastq](#).

`writeFastq, ShortReadQ, FastqFile-method`: see also [?writeFastq](#), [?"writeFastq, ShortReadQ, FastqFile-method"](#)

`yield`: Draw a single sample from the instance. Operationally this requires that the underlying data (e.g., file) represented by the Sampler instance be visited; this may be time consuming.

See Also

[readFastq](#), [writeFastq](#), [yield](#).

Examples

```
sp <- SolexaPath(system.file(extdata, package=ShortRead))
fl <- file.path(analysisPath(sp), "s_1_sequence.txt")

f <- FastqFile(fl)
rfq <- readFastq(f)

f <- FastqSampler(fl, 50)
yield(f) # sample of size n=50
yield(f) # independent sample of size 50
close(f)

## Return sample as ordered in original file
f <- FastqSampler(fl, 50, ordered=TRUE)
```

```

yield(f)
close(f)

f <- FastqStreamer(fl, 50)
yield(f)    # records 1 to 50
yield(f)    # records 51 to 100
close(f)

## iterating over an entire file
f <- FastqStreamer(fl, 50)
while (length(fq <- yield(f))) {
  ## do work here
  print(length(fq))
}
close(f)

## iterating over IRanges
rng <- IRanges(c(50, 100, 200), width=10:8)
f <- FastqStreamer(fl, rng)
while (length(fq <- yield(f))) {
  print(length(fq))
}
close(f)

## Internal fields, methods, and help; for developers
ShortRead::FastqSampler_g$methods()
ShortRead::FastqSampler_g$fields()
ShortRead::FastqSampler_g$help("yield")

```

filterFastq

Filter fastq from one file to another

Description

filterFastq filters reads from source to destination file(s) applying a filter to reads in each file. The filter can be a function or FilterRules instance; operations are done in a memory-efficient manner.

Usage

```

filterFastq(files, destinations, ..., filter = FilterRules(),
            yieldSize = 1000000L)

```

Arguments

files	a character vector of valid file paths.
destinations	a character vector of destinations of the same length as files. destinations must not already exist.
...	Additional arguments, perhaps used by a filter function.

filter	A simple function taking as it's first argument a ShortReadQ instance and returning a modified ShortReadQ instance (e.g., with records or nucleotides removed), or a FilterRules instance specifying which records are to be removed.
yieldSize	Number of fastq records processed in each call to filter; increase this for (marginally) more efficient I/O at the expense of increased memory use.

Author(s)

Martin Morgan mtmorgan@fhcrc.org

Examples

```
## path to a convenient fastq file
sp <- SolexaPath(system.file(extdata, package=ShortRead))
fl <- file.path(analysisPath(sp), "s_1_sequence.txt")

## filter reads to keep those with GC < 0.7
fun <- function(x) {
  gc <- alphabetFrequency(sread(x), baseOnly=TRUE)[c("G", "C")]
  x[rowSums(gc) / width(x) < .7]
}
filterFastq(fl, tempfile(), filter=fun)

## trimEnds,character-method uses filterFastq internally
trimEnds(fl, "V", destinations=tempfile())
```

GappedReads-class *GappedReads objects*

Description

The GappedReads class extends the [GAlignments](#) class defined in the GenomicRanges package. A GappedReads object contains all the information contained in a [GAlignments](#) object plus the sequences of the queries. Those sequences can be accessed via the `qseq` accessor.

Constructor

`readGappedReads(file, format="BAM", use.names=FALSE, ...)`: Read a file as a GappedReads object. Like with the `readGAlignments` constructor, by default (i.e. `use.names=FALSE`) the resulting object has no names. If `use.names` is `TRUE`, then the names are constructed from the query template names (QNAME field in a SAM/BAM file).

Note that this function is just a front-end that delegates to the format-specific back-end function specified via the `format` argument. The `use.names` argument and any extra argument are passed to the back-end function. Only the BAM format is supported for now. Its back-end is the `readGappedReadsFromBam` function defined in the Rsamtools package. See [?readGappedReadsFromBam](#) for more information (you might need to install and load the Rsamtools package first).

Accessors

In the code snippets below, `x` is a `GappedReads` object.

`qseq(x)`: Extracts the sequences of the queries as a `DNAStrngSet` object.

Author(s)

H. Pages and P. Aboyoun

References

<http://samtools.sourceforge.net/>

See Also

[GAlignments-class](#), [readGappedReadsFromBam](#)

Examples

```
greads_file <- system.file("extdata", "ex1.bam", package="Rsamtools")
greads <- readGappedReads(greads_file)
greads
qseq(greads)
```

Intensity-class	<i>"Intensity", "IntensityInfo", and "IntensityMeasure" base classes for short read image intensities</i>
-----------------	---

Description

The `Intensity`, `IntensityMeasure`, and `IntensityInfo` classes represent and manipulate image intensity measures. Instances from the class may also contain information about measurement errors, and additional information about the reads from which the intensities are derived.

`Intensity`, and `IntensityMeasure`, are virtual classes, and cannot be created directly. Classes derived from `IntensityMeasure` (e.g., `ArrayIntensity`) and `Intensity` (e.g., `SolexaIntensity`) are used to represent specific technologies.

Objects from the Class

`ArrayIntensity` objects can be created with calls of the form `ArrayIntensity(array(0, c(1, 2, 3)))`.

Objects of derived classes can be created from calls such as the `SolexaIntensity` constructor, or more typically by parsing appropriate files (e.g., [readIntensities](#)).

Slots

Class Intensity has slots:

readInfo: Object of class "IntensityInfo" containing columns for the lane, tile, x, and y coordinates of the read.

intensity: Object of class "IntensityMeasure" containing image intensity data for each read and cycle.

measurementError: Object of class "IntensityMeasure" containing measures of image intensity uncertainty for each read and cycle.

.hasMeasurementError: Length 1 logical variable indicating whether intensity standard errors are included (internal use only).

Classes IntensityInfo and IntensityMeasure are virtual classes, and have no slots.

Extends

These classes extend "[.ShortReadBase](#)", directly.

Methods

Methods and accessor functions for Intensity include:

readInfo signature(object = "Intensity"): access the readInfo slot of object.

intensity signature(object = "Intensity"): access the intensity slot of object.

measurementError signature(object = "Intensity"): access the nse slot of object, or signal an error if no standard errors are available.

dim signature(object = "Intensity"): return the dimensions (e.g., number of reads by number of cycles) represented by object.

show signature(object = "Intensity"): provide a compact representation of the object.

Subsetting "[" is available for the IntensityMeasure class; the drop argument to "[" is ignored.

Subsetting with "[[" is available for the ArrayIntensity class. The method accepts three arguments, corresponding to the read, base, and cycle(s) to be selected. The return value is the array (i.e., underlying data values) corresponding to the selected indices.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[readIntensities](#)

Examples

```
showMethods(class="Intensity", where=getNamespace("ShortRead"))
example(readIntensities)
```

MAQMapQA-class

Quality assessment summaries from MAQ map files

Description

This class contains a list-like structure with summary descriptions derived from visiting one or more MAQMap files.

Objects from the Class

Objects of the class are usually produced by a [qa](#) method.

Slots

`.srlist`: Object of class "list", containing data frames or lists of data frames summarizing the results of qa.

Extends

Class "[SRList](#)", directly. Class "[.QA](#)", directly. Class "[.SRUtil](#)", by class "SRList", distance 2. Class "[.ShortReadBase](#)", by class ".QA", distance 2.

Methods

Accessor methods are inherited from the [SRList](#) class.

report signature(`x="MAQMapQA"`, ..., `dest=tempfile()`, `type="html"`): produces an html file summarizing the QA results.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[qa](#).

Examples

```
showClass("MAQMapQA")
```

qa *Perform quality assessment on short reads*

Description

This function is a common interface to quality assessment functions available in ShortRead. Results from this function may be displayed in brief, or integrated into reports using, e.g., [report](#).

Usage

```
qa(dirPath, ...)
## S4 method for signature character
qa(dirPath, pattern=character(0),
   type=c("SolexaExport", "SolexaRealign", "Bowtie", "MAQMap",
          "MAQMapShort", "fastq", "BAM"),
   ...)
## S4 method for signature list
qa(dirPath, ...)
```

Arguments

dirPath	A character vector or other object (e.g., SolexaPath ; see <code>showMethods</code> , below) locating the data for which quality assessment is to be performed. See help pages for defined methods (by evaluating the example code, below) for details of available methods.
pattern	A character vector limiting the files in <code>dirPath</code> to be processed, as with list.files . Care should be taken to specify <code>pattern</code> to avoid reading unintended files.
type	The type of file being parsed; must be a character vector of length 1, selected from one of the types enumerated in the parameter.
...	Additional arguments used by methods.

`sample=TRUE`: Logical(1) indicating whether QA should be performed on a sample (default size 1000000) drawn from each FASTQ file, or from the entire file.

`n`: The number of reads to sample when processing FASTQ files.

`fapply`, `reduce`: Influence how evaluation occurs when this function is run with the **Rmpi** or **parallel** packages; see [srapply](#).

`Lpattern`, `Rpattern`: A character vector or XString object to be matched to the left end of a sequence. If either `Lpattern` or `Rpattern` are provided, `trimLRPatterns` is invoked to produce a measure of adapter contamination. Mismatch rates are 0.1 on the left and 0.2 on the right, with a minimum overlap of 10 nt.

Details

The most common use of this function provides a directory path and pattern identifying FASTQ files for quality assessment. The default is then to create a quality assessment report based on a random sample of $n=1000000$ reads from each file.

The following methods are defined, in addition to those on S4 formal classes documented elsewhere:

`qa, character-method` Quality assessment is performed on all files in directory `dirPath` whose file name matches `pattern`. The type of analysis performed is based on the `type` argument. Use `SolexaExport` when all files matching `pattern` are `Solexa_export.txt` files. Use `SolexaRealign` for `Solexa_realign.txt` files. Use `Bowtie` for Bowtie files. Use `MAQMapShort` for MAQ map files produced by MAQ versions below 0.70 and `MAQMap` for more recent output. Use `fastq` for collections of fastq-format files. Use `BAM` for `.bam` files; see the `param` argument in [readAligned](#) for information on how to influence reads included in the `qa` summary. Quality assessment details vary depending on data source.

`qa, list-method` `dirPath` is a list of objects, all of the same class and typically derived from `ShortReadQ`, on which quality assessment is performed. All elements of the list must have names, and these should be unique.

Value

An object derived from class `.QA`. Values contained in this object are meant for use by [report](#)

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[.QA](#), [SolexaExportQA](#) [MAQMapQA](#) [FastqQA](#) [BAMQA](#)

Examples

```
sp <- SolexaPath(system.file("extdata", package = "ShortRead"))
qa1 <- qa(sp)
fq <- file.path(analysisPath(sp), pattern="s_1_sequence.txt")
qa2 <- qa(readFastq(fq), basename(fq)) # name fastq files

## create report from a random sample of each file
qas0 <- Map(function(fl, nm) {
  fq <- FastqSampler(fl)
  qa(yield(fq), nm)
}, fq, sub(".txt", "", basename(fq)))
qa3 <- do.call(rbind, qas0)

showMethods("qa", where=getNamespace("ShortRead"))
```

QA-class

*(Updated) classes for representing quality assessment results***Description**

Classes derived from .QA-class represent results of quality assurance analyses.

Objects from the Class

Users create instances of many of these classes by calling the corresponding constructors, as documented on the help page for `qa2`. Classes constructed in this way include `QACollate`, `QAFastqSource`, `QAAdapterContamination`, `QAFrequentSequence`, `QANucleotideByCycle`, `QANucleotideUse`, `QAQualityByCycle`, `QAQualityUse`, `QAReadQuality`, and `QASequenceUse`.

The classes `QASource`, `QAFiltered`, `QAFlagged` and `QASummary` are generated internally, not by users.

Extends

`.QA2` extends class "`.ShortReadBase`", directly.

`QASummary` is a virtual class extending `.QA2`; all user-creatable classes extend `QASummary`.

`QASource` extends `QASummary`. All classes used to represent raw data input (`QAFastqSource`) extend `QASource`.

`QAData` is a reference class, used to contain a single instance of the fastq used in all QA Summary steps.

`QACollate` extends `.QA2`. It contains a `SimpleList` instance with zero or more `QASummary` elements.

`QA` extends `.QA2`, and contains a `SimpleList` of zero or more `QASummary` elements. This class represents the results of the `qa2` analysis.

Methods

Methods defined on this class include:

qa2 signature(`object="QACollate"`, `state`, ..., `verbose=FALSE`) creates a QA report from the elements of `QACollate`. Methods on `qa2` for objects extending class `QASummary` summarize QA statistics for that class, e.g., `qa2`, `QAFrequentSequences-method` implements the calculations required to summarize frequently used sequences, using data in `state`.

report signature(`x="QA"`, ...) creates an HTML report. Methods on `report` for objects extending class `QASummary` are responsible for creating the html snippet for that QA component.

flag signature(`object=".QA2"`, ..., `verbose=FALSE`) implements criteria to flag individual lanes as failing quality assessment. NOTE: `flag` is not fully implemented.

rbind signature(...=`"QASummary"`): `rbind` multiple summary elements of the same class, as when these have been created by separately calculating statistics on a number of fastq files.

show signature(`object = "SolexaExportQA"`): Display an overview of the object contents.

Author(s)

Martin Morgan <mtmmorgan@fhcrc.org>

See Also

Specific classes derived from .QA2

Examples

```
getClass(".QA2", where=getNamespace("ShortRead"))
```

qa2

(Updated) quality assessment reports on short reads

Description

This page summarizes an updated approach to quality assessment reports in ShortRead.

Usage

```
## Input source for short reads
QAFastqSource(con = character(), n = 1e+06, readerBlockSize = 1e+08,
  flagNSequencesRange = NA_integer_, ...,
  html = system.file("template", "QASources.html", package="ShortRead"))
QAData(seq = ShortReadQ(), filter = logical(length(seq)), ...)

## Possible QA elements
QAFrequentSequence(useFilter = TRUE, addFilter = TRUE,
  n = NA_integer_, a = NA_integer_, flagK=.8, reportSequences = FALSE,
  ...)
QANucleotideByCycle(useFilter = TRUE, addFilter = TRUE, ...)
QANucleotideUse(useFilter = TRUE, addFilter = TRUE, ...)
QAQualityByCycle(useFilter = TRUE, addFilter = TRUE, ...)
QAQualityUse(useFilter = TRUE, addFilter = TRUE, ...)
QAReadQuality(useFilter = TRUE, addFilter = TRUE,
  flagK = 0.2, flagA = 30L, ...)
QASequenceUse(useFilter = TRUE, addFilter = TRUE, ...)
QAAdapterContamination(useFilter = TRUE, addFilter = TRUE,
  Lpattern = NA_character_, Rpattern = NA_character_,
  max.Lmismatch = 0.1, max.Rmismatch = 0.2, min.trim = 9L, ...)

## Order QA report elements
QACollate(src, ...)

## perform analysis
qa2(object, state, ..., verbose=FALSE)
```

```

## Outputs from qa2
QA(src, filtered, flagged, ...)
QAFiltered(useFilter = TRUE, addFilter = TRUE, ...)
QAFlagged(useFilter = TRUE, addFilter = TRUE, ...)

## Summarize results as html report
## S4 method for signature QA
report(x, ..., dest = tempfile(), type = "html")

## additional methods; flag is not fully implemented
flag(object, ..., verbose=FALSE)

## S4 method for signature QASummary
rbind(..., deparse.level = 1)

```

Arguments

con	character(1) file location of fastq input, as used by FastqSampler.
n	integer(1) number of records to input, as used by FastqStreamer (QAFastqSource). integer(1) number of sequences to tag as 'frequent' (QAFrequentSequence).
readerBlockSize	integer(1) number of bytes to input, as used by FastqStreamer.
flagNSequencesRange	integer(2) minimum and maximum reads above which source files will be flagged as outliers.
html	character(1) location of the HTML template for summarizing this report element.
seq	ShortReadQ representation of fastq data.
filter	logical() vector with length equal to seq, indicating whether elements of seq are filtered (TRUE) or not.
useFilter, addFilter	logical(1) indicating whether the QA element should be calculating using the filtered (useFilter=TRUE) or all reads, and whether reads failing the QA element should be added to the filter used by subsequent steps (addFilter = TRUE) or not.
a	integer(1) count of number of sequences above which a read will be considered 'frequent' (QAFrequentSequence).
flagK, flagA	flagK numeric(1) between 0 and 1 indicating the fraction of frequent sequences greater than or equal to n or a above which a fastq file will be flagged (QAFrequentSequence). flagK numeric{1} between 0 and 1 and flagA integer(1) indicating that a run should be flagged when the fraction of reads with quality greater than or equal to flagA falls below threshold flagK.
reportSequences	logical(1) indicating whether frequent sequences are to be reported.
Lpattern, Rpattern, max.Lmismatch, max.Rmismatch, min.trim	Parameters influencing adapter identification, see matchPattern .

src	The source, e.g., QAFastqSource, on which the quality assessment report will be based.
object	An instance of class derived from QA on which quality metrics will be derived; for end users, this is usually the result of QACollate..
state	The data on which quality assessment will be performed; this is not usually necessary for end-users.
verbose	logical(1) indicating whether progress reports should be reported.
filtered, flagged	Primarily for internal use, instances of QAFiltered and QAFlagged.
x	An instance of QA on which a report is to be generated.
dest	character(1) providing the directory in which the report is to be generated.
type	character(1) indicating the type of report to be generated; only “html” is supported.
deparse.level	see rbind .
...	Additional arguments, e.g., html to specify the location of the html source to use as a template for the report.

Details

Use QACollate to specify an order in which components of a QA report are to be assembled. The first argument is the data source (e.g., QAFastqSource).

Functions related to data input include:

QAFastqSource defines the location of fastq files to be included in the report. con is used to construct a [FastqSampler](#) instance, and records are processed using qa2, QAFastqSource-method.

QAData is a class for representing the data during the QA report generation pass; it is primarily for internal use.

Possible elements in a QA report are:

QAFrequentSequence identifies the most-commonly occurring sequences. One of n or a can be non-NA, and determine the number of frequent sequences reported. n specifies the number of most-frequent sequences to filter, e.g., n=10 would filter the top 10 most commonly occurring sequences; a provides a threshold frequency (count) above which reads are filtered. The sample is flagged when a fraction flagK of the reads are filtered.

reportSequences determines whether the most commonly occurring sequences, as determined by n or a, are printed in the html report.

QANucleotideByCycle reports nucleotide frequency as a function of cycle.

QAQualityByCycle reports average quality score as a function of cycle.

QAQualityUse summarizes overall nucleotide qualities.

QAReadQuality summarizes the distribution of read qualities.

QASequenceUse summarizes the cumulative distribution of reads occurring 1, 2, ... times.

QAAdapterContamination reports the occurrence of ‘adapter’ sequences on the left and / or right end of each read.

Value

An object derived from class `.QA`. Values contained in this object are meant for use by [report](#)

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[QA](#).

Examples

```
sp <- SolexaPath(system.file(extdata, package=ShortRead))
fl <- file.path(analysisPath(sp), "s_1_sequence.txt")
fls <- c(fl, fl)

coll <- QACollate(QAFastqSource(fls), QAReadQuality(),
  QAAdapterContamination(), QANucleotideUse(),
  QAQualityUse(), QASequenceUse(),
  QAFrequentSequence(n=10), QANucleotideByCycle(),
  QAQualityByCycle())
x <- qa2(coll, verbose=TRUE)
res <- report(x)
if (interactive())
  browseURL(res)

## Not run: ## parallel evaluation
options(srapply_fapply="parallel")
coll <- QACollate(QAFastqSource(fls), qaFastqTemplate)
x2 <- qa2(coll, verbose=TRUE)
browseURL(res2 <- report(x2))

## End(Not run)
```

QualityScore

Construct objects indicating read or alignment quality

Description

Use these functions to construct quality indicators for reads or alignments. See [QualityScore](#) for details of object content and methods available for manipulating them.

Usage

```
NumericQuality(quality = numeric(0))  
IntegerQuality(quality = integer(0))  
MatrixQuality(quality = new("matrix"))  
FastqQuality(quality, ...)  
SFastqQuality(quality, ...)
```

Arguments

quality	An object used to initialize the data structure. Appropriate objects are indicated in the constructors above for Numeric, Integer, and Matrix qualities. For FastqQuality and SFastqQuality, methods are defined for BStringSet , character, and missing.
...	Additional arguments, currently unused.

Value

Constructors return objects of the corresponding class derived from [QualityScore](#).

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[QualityScore](#), [readFastq](#), [readAligned](#)

Examples

```
nq <- NumericQuality(rnorm(20))  
nq  
quality(nq)  
quality(nq[10:11])
```

QualityScore-class *Quality scores for short reads and their alignments*

Description

This class hierarchy represents quality scores for short reads. [QualityScore](#) is a virtual base class, with derived classes offering different ways of representing qualities. Methods defined on [QualityScore](#) are implemented in all derived classes.

Objects from the Class

Objects from the class are created using constructors (e.g., `NumericQuality`) named after the class name.

Defined classes are as follows:

QualityScore Virtual base class; instances cannot be instantiated.

NumericQuality A single numeric vector, where values represent quality scores on an arbitrary scale.

IntegerQuality A integer numeric vector, where values represent quality scores on an arbitrary scale.

MatrixQuality A rectangular matrix of quality scores, with rows representing reads and columns cycles. The content and interpretation of row and column entries is arbitrary; the rectangular nature implies quality scores from equal-length reads.

FastqQuality 'fastq' encoded quality scores stored in a `BStringSet` instance. Base qualities of a single read are represented as an ASCII character string. The integer-valued quality score of a single base is encoded as its ASCII equivalent plus 33. The precise definition of the integer-valued quality score is unspecified, but is usually a Phred score; the meaning can be determined from the source of the quality scores. Multiple reads are stored as a `BStringSet`, and so can be of varying lengths.

SolexaQuality As with `FastqQuality`, but with integer qualities encoded as ASCII equivalent plus 64.

Extends

Class "`.ShortReadBase`", directly.

Methods

The following methods are defined on all `QualityScore` and derived classes:

[signature(x = "QualityScore", i = "ANY", j = "missing")

[signature(x = "MatrixQuality", i = "ANY", j = "missing"):

Subset the object, with index `i` indicating the reads for which quality scores are to be extracted. The class of the result is the same as the class of `x`. It is an error to provide any argument other than `i`.

[[signature(x = "QualityScore", i = "ANY", j = "ANY"):

Subset the object, returning the quality score (e.g., numeric value) of the `i`th read.

[[signature(x = "MatrixQuality", i = "ANY", j = "ANY"):

Returns the vector of quality scores associated with the `i`th read.

dim signature(x = "MatrixQuality"):

The integer(2) dimension (e.g., number of reads, read width) represented by the quality score.

length signature(x = "QualityScore"):

length signature(x = "MatrixQuality"):

The integer(1) length (e.g., number of reads) represented by the quality score. Note that length of `MatrixQuality` is the number of rows of the corresponding matrix, and not the length of the corresponding numeric vector.

append signature(x = "QualityScore", values = "QualityScore"): append values after x.

width signature(x = "QualityScore"):

width signature(x = "NumericQuality"):

width signature(x = "MatrixQuality"):

width signature(x = "FastqQuality"):

A numeric vector with length equal to the number of quality scores, and value equal to the number of quality scores for each read. For instance, a [FastqQuality](#) will have widths equal to the number of nucleotides in the underlying short read.

show signature(object = "QualityScore"):

show signature(object = "NumericQuality"):

show signature(object = "FastqQuality"):

provide a brief summary of the object content.

detail signature(x = "QualityScore"):

provide a more detailed view of object content.

The following methods are defined on specific classes:

alphabet signature(x = "FastqQuality", ...): Return a character vector of valid quality characters.

encoding signature(x = "FastqQuality", ...), signature(x = "SFastqQuality", ...): Returns a named character vector of integer encodings.

alphabetFrequency signature(stringSet = "FastqQuality"):

Apply [alphabetFrequency](#) to quality scores, returning a matrix as described in [alphabetFrequency](#).

alphabetByCycle signature(stringSet = "FastqQuality"):

Apply [alphabetByCycle](#) to quality scores, returning a matrix as described in [alphabetByCycle](#).

alphabetScore signature(object = "FastqQuality"):

alphabetScore signature(object = "SFastqQuality"):

Apply [alphabetScore](#) (i.e., summed base quality, per read) to object.

coerce signature(from = "FastqQuality", to = "numeric"):

coerce signature(from = "FastqQuality", to = "matrix"):

coerce signature(from = "FastqQuality", to = "PhredQuality"):

coerce signature(from = "SFastqQuality", to = "matrix"):

coerce signature(from = "SFastqQuality", to = "SolexaQuality"):

Use `as(from, "matrix")` and similar to coerce objects of class `from` to class `to`, using the quality encoding implied by the class. When `to` is "matrix", the result is a matrix of type `integer` with number of columns equal to the maximum width of `from`; elements `i, j` with `j > width(from)[i]` have value `NA_integer_`. The result always represents the integer encoding of the corresponding quality string.

narrow signature(x = "FastqQuality", start = NA, end = NA, width = NA, use.names = TRUE): 'narrow' quality so that scores are between start and end bases, according to [narrow](#) in the `IRanges` package.

trimTailw signature(object="FastqQuality", k="integer", a="character", halfwidth="integer", ..., range) trim trailing nucleotides when a window of width $2 * halfwidth + 1$ contains k or more quality scores falling at or below a.

trimTails signature(object="FastqQuality", k="integer", a="character", successive=FALSE, ..., ranges=FA) trim trailing scores if k scores fall below the quality encoded by a. If successive=FALSE, the k'th failing score and all subsequent scores are trimmed. If successive=TRUE, failing scores must occur successively; the sequence is trimmed from the first of the successive failing score.

srorder signature(x = "FastqQuality"):

srrank signature(x = "FastqQuality"):

srduplicated signature(x = "FastqQuality"):

Apply [srsort](#), srorder, srrank, and srduplicated to quality scores, returning objects as described on the appropriate help page.

Integer representations of SFastqQuality and FastqQuality can be obtained with `as(x, "matrix")`.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[NumericQuality](#) and other constructors.

Examples

```
names(slot(getClass("QualityScore"), "subclasses"))
encoding(FastqQuality())
encoding(SFastqQuality())
```

readAligned

Read aligned reads and their quality scores into R representations

Description

Import files containing aligned reads into an internal representation of the alignments, sequences, and quality scores. Most methods (see ‘details’ for exceptions) read all files into a single R object.

Usage

```
readAligned(dirPath, pattern=character(0), ...)
```

Arguments

dirPath	A character vector (or other object; see methods defined on this generic) giving the directory path (relative or absolute; some methods also accept a character vector of file names) of aligned read files to be input.
pattern	The (grep -style) pattern describing file names to be read. The default (character(0)) results in (attempted) input of all files in the directory.
...	Additional arguments, used by methods. When dirPath is a character vector, the argument type must be provided. Possible values for type and their meaning are described below. Most methods implement filter=srFilter(), allowing objects of SRFilter to selectively returns aligned reads.

Details

There is no standard aligned read file format; methods parse particular file types.

The readAligned, character-method interprets file types based on an additional type argument. Supported types are:

type="SolexaExport" This type parses .*_export.txt files following the documentation in the Solexa Genome Alignment software manual, version 0.3.0. These files consist of the following columns; consult Solexa documentation for precise descriptions. If parsed, values can be retrieved from [AlignedRead](#) as follows:

Machine see below
Run number stored in alignData
Lane stored in alignData
Tile stored in alignData
X stored in alignData
Y stored in alignData
Multiplex index see below
Paired read number see below
Read sread
Quality quality
Match chromosome chromosome
Match contig alignData
Match position position
Match strand strand
Match description Ignored
Single-read alignment score alignQuality
Paired-read alignment score Ignored
Partner chromosome Ignored
Partner contig Ignored
Partner offset Ignored
Partner strand Ignored
Filtering alignData

The following optional arguments, set to FALSE by default, influence data input

withMultiplexIndex When TRUE, include the multiplex index as a column multiplexIndex in alignData.

withPairedReadNumber When TRUE, include the paired read number as a column pairedReadNumber in alignData.

withId When TRUE, construct an identifier string as 'Machine_Run:Lane:Tile:X:Y#multiplexIndex/pairedReadNumber'. The substrings '#multiplexIndex' and '/pairedReadNumber' are not present if withMultiplexIndex=FALSE or withPairedReadNumber=FALSE.

withAll A convenience which, when TRUE, sets all with* values to TRUE.

Note that not all paired read columns are interpreted. Different interfaces to reading alignment files are described in [SolexaPath](#) and [SolexaSet](#).

type="SolexaPrealign" See [SolexaRealign](#)

type="SolexaAlign" See [SolexaRealign](#)

type="SolexaRealign" These types parse s_L_TTTT_prealign.txt, s_L_TTTT_align.txt or s_L_TTTT_realign.txt files produced by default and eland analyses. From the Solexa documentation, align corresponds to unfiltered first-pass alignments, prealign adjusts alignments for error rates (when available), realign filters alignments to exclude clusters failing to pass quality criteria.

Because base quality scores are not stored with alignments, the object returned by readAligned scores all base qualities as -32.

If parsed, values can be retrieved from [AlignedRead](#) as follows:

Sequence stored in sread

Best score stored in alignQuality

Number of hits stored in alignData

Target position stored in position

Strand stored in strand

Target sequence Ignored; parse using [readXStringColumns](#)

Next best score stored in alignData

type="SolexaResult" This parses s_L_eland_results.txt files, an intermediate format that does not contain read or alignment quality scores.

Because base quality scores are not stored with alignments, the object returned by readAligned scores all base qualities as -32.

Columns of this file type can be retrieved from [AlignedRead](#) as follows (description of columns is from Table 19, Genome Analyzer Pipeline Software User Guide, Revision A, January 2008):

Id Not parsed

Sequence stored in sread

Type of match code Stored in alignData as matchCode. Codes are (from the Eland manual): NM (no match); QC (no match due to quality control failure); RM (no match due to repeat masking); U0 (best match was unique and exact); U1 (best match was unique, with 1 mismatch); U2 (best match was unique, with 2 mismatches); R0 (multiple exact matches found); R1 (multiple 1 mismatch matches found, no exact matches); R2 (multiple 2 mismatch matches found, no exact or 1-mismatch matches).

Number of exact matches stored in alignData as nExactMatch

Number of 1-error mismatches stored in alignData as nOneMismatch

Number of 2-error mismatches stored in alignData as nTwoMismatch

Genome file of match stored in chromosome

Position stored in position

Strand (direction of match) stored in strand

'N' treatment stored in alignData, as NCharacterTreatment. '.' indicates treatment of 'N' was not applicable; 'D' indicates treatment as deletion; 'I' indicates treatment as insertion

Substitution error stored in alignData as mismatchDetailOne and mismatchDetailTwo. Present only for unique inexact matches at one or two positions. Position and type of first substitution error, e.g., 11A represents 11 matches with 12th base an A in reference but not read. The reference manual cited below lists only one field (mismatchDetailOne), but two are present in files seen in the wild.

type="MAQMap", records=-1L Parse binary map files produced by MAQ. See details in the next section. The records option determines how many lines are read; -1L (the default) means that all records are input. For type="MAQMap", dir and pattern must match a single file.

type="MAQMapShort", records=-1L The same as type="MAQMap" but for map files made with Maq prior to version 0.7.0. (These files use a different maximum read length [64 instead of 128], and are hence incompatible with newer Maq map files.). For type="MAQMapShort", dir and pattern must match a single file.

type="MAQMapView" Parse alignment files created by MAQ's 'mapview' command. Interpretation of columns is based on the description in the MAQ manual, specifically

...each line consists of read name, chromosome, position, strand, insert size from the outer coordinates of a pair, paired flag, mapping quality, single-end mapping quality, alternative mapping quality, number of mismatches of the best hit, sum of qualities of mismatched bases of the best hit, number of 0-mismatch hits of the first 24bp, number of 1-mismatch hits of the first 24bp on the reference, length of the read, read sequence and its quality.

The read name, read sequence, and quality are read as XStringSet objects. Chromosome and strand are read as factors. Position is numeric, while mapping quality is numeric. These fields are mapped to their corresponding representation in AlignedRead objects.

Number of mismatches of the best hit, sum of qualities of mismatched bases of the best hit, number of 0-mismatch hits of the first 24bp, number of 1-mismatch hits of the first 24bp are represented in the AlignedRead object as components of alignData.

Remaining fields are currently ignored.

type="Bowtie" Parse alignment files created with the Bowtie alignment algorithm. Parsed columns can be retrieved from [AlignedRead](#) as follows:

Identifier id

Strand strand

Chromosome chromosome

Position position; see comment below

Read sread; see comment below

Read quality quality; see comments below

Similar alignments alignData, 'similar' column; Bowtie v. 0.9.9.3 (12 May, 2009) documents this as the number of other instances where the same read aligns against the same reference characters as were aligned against in this alignment. Previous versions marked this as 'Reserved'

Alignment mismatch locations alignData 'mismatch', column

NOTE: the default quality encoding changes to FastqQuality with **ShortRead** version 1.3.24. This method includes the argument qualityType to specify how quality scores are encoded. Bowtie quality scores are 'Phred'-like by default, with qualityType=FastqQuality, but can be specified as 'Solexa'-like, with qualityType=SFastqQuality.

Bowtie outputs positions that are 0-offset from the left-most end of the + strand. ShortRead parses position information to be 1-offset from the left-most end of the + strand.

Bowtie outputs reads aligned to the - strand as their reverse complement, and reverses the quality score string of these reads. ShortRead parses these to their original sequence and orientation.

type="SOAP" Parse alignment files created with the SOAP alignment algorithm. Parsed columns can be retrieved from [AlignedRead](#) as follows:

id id

seq sread; see comment below

qual quality; see comment below

number of hits alignData

a/b alignData (pairedEnd)

length alignData (alignedLength)

+/- strand

chr chromosome

location position; see comment below

types alignData (typeOfHit: integer portion; hitDetail: text portion)

This method includes the argument qualityType to specify how quality scores are encoded. It is unclear from SOAP documentation what the quality score is; the default is 'Solexa'-like, with qualityType=SFastqQuality, but can be specified as 'Phred'-like, with qualityType=FastqQuality.

SOAP outputs positions that are 1-offset from the left-most end of the + strand. ShortRead preserves this representation.

SOAP reads aligned to the - strand are reported by SOAP as their reverse complement, with the quality string of these reads reversed. ShortRead parses these to their original sequence and orientation.

type="BAM" Parse BAM files produced by samtools and other third party programs. This method includes the argument param=ScanBamParam(). The ScanBamParam object is recycled for all files. The which and flag arguments to ScanBamParam() can be used to influence which reads in the BAM file are parsed; see [ScanBamParam](#). The following values override user settings (issuing a warning if contradictory values are provided):

simpleCigar=TRUE Reads aligned with indels are ignored; this is required for representation in [AlignedRead](#).

reverseComplement=TRUE By default, BAM stores reads as they are aligned to the reference genome, whereas [AlignedRead](#) stores them as they are prior to alignment; this flag converts reads from the BAM to [AlignedRead](#) format.

what=c("qname", "flag", "rname", "strand", "pos", "mapq", "seq", "qual") These BAM fields are mapped to corresponding fields in AlignedRead.

BAM fields are mapped to AlignedRead as:

```

qname id
seq sread
qual quality
strand strand
rname chromosome
pos position
mapq alignQuality
flag alignData

```

Value

A single R object (e.g., `AlignedRead`) containing alignments, sequences and qualities of all files in `dirPath` matching pattern. There is no guarantee of order in which files are read.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>, Simon Anders <anders@ebi.ac.uk> (MAQ map)

See Also

The `AlignedRead` class.

Genome Analyzer Pipeline Software User Guide, Revision A, January 2008.

The MAQ reference manual, <http://maq.sourceforge.net/maq-manpage.shtml#5>, 3 May, 2008.

The Bowtie reference manual, <http://bowtie-bio.sourceforge.net>, 28 October, 2008.

The SOAP reference manual, <http://soap.genomics.org.cn/soap1>, 16 December, 2008.

The BAM file format specification, <http://samtools.sourceforge.net>.

Examples

```

sp <- SolexaPath(system.file("extdata", package="ShortRead"))
ap <- analysisPath(sp)
## ELAND_EXTENDED
(aln0 <- readAligned(ap, "s_2_export.txt", "SolexaExport"))
## PhageAlign
(aln1 <- readAligned(ap, "s_5_.*_realign.txt", "SolexaRealign"))

## MAQ
dirPath <- system.file(extdata, maq, package=ShortRead)
list.files(dirPath)
## First line
readLines(list.files(dirPath, full.names=TRUE)[[1]], 1)
countLines(dirPath)
## two files collapse into one
(aln2 <- readAligned(dirPath, type="MAQMapView"))

```

```
## select only chr1-5.fa, + strand
filt <- compose(chromosomeFilter("chr[1-5].fa"),
               strandFilter("+"))
(aln3 <- readAligned(sp, "s_2_export.txt", filter=filt))
```

readBaseQuality *Read short reads and their quality scores into R representations*

Description

readBaseQuality reads all base call files in a directory dirPath whose file name matches seqPattern and all quality score files whose name matches prbPattern, returning a compact internal representation of the sequences, and quality scores in the files. Methods read all files into a single R object.

Usage

```
readBaseQuality(dirPath, ...)
## S4 method for signature character
readBaseQuality(dirPath, seqPattern=character(0),
                prbPattern=character(0), type=c("Solexa"), ...)
```

Arguments

dirPath	A character vector (or other object; see methods defined on this generic) giving the directory path (relative or absolute) of files to be input.
seqPattern	The (grep -style) pattern describing base call file names to be read. The default (character(0)) results in (attempted) input of all files in the directory.
prbPattern	The (grep -style) pattern describing quality score file names to be read. The default (character(0)) results in (attempted) input of all files in the directory.
type	The type of file to be parsed. Supported types include: Solexa: parse reads and their qualities from _seq.txt and _prb.txt-formatted files, respectively.
...	Additional arguments, perhaps used by methods.

Value

A single R object (e.g., [ShortReadQ](#)) containing sequences and qualities of all files in dirPath matching seqPattern and prbPattern respectively. There is no guarantee of order in which files are read.

Author(s)

Patrick Aboyoun <paboyoun@fhcrc.org>

See Also

A [ShortReadQ](#) object.

[readXStringColumns](#), [readPrb](#)

Examples

```
sp <- SolexaPath(system.file("extdata", package="ShortRead"))
readBaseQuality(sp, seqPattern="s_1.*_seq.txt", prbPattern="s_1.*_prb.txt")
```

readBfaToc

Get a list of the sequences in a Maq .bfa file

Description

As [coverage](#) needs to know the lengths of the reference sequences, this function is provided which extracts this information from a .bfa file (Maq's "binary FASTA" format).

Usage

```
readBfaToc( bfafile )
```

Arguments

`bfafile` The file name of the .bfa file.

Value

An integer vector with one element per reference sequence found in the .bfa file, each vector element named with the sequence name and having the sequence length as value.

Author(s)

Simon Anders, EMBL-EBI, <sanders@fs.tum.de>

(Note: The C code for this function incorporates code from Li Heng's MAQ software, (c) Li Heng and released by him under GPL 2.

readFasta

*Read and write FASTA files to or from ShortRead objects***Description**

readFasta reads all FASTA-formated files in a directory dirPath whose file name matches pattern pattern, returning a compact internal representation of the sequences and quality scores in the files. Methods read all files into a single R object; a typical use is to restrict input to a single FASTA file.

writeFasta writes an object to a single file, using mode="w" (the default) to create a new file or mode="a" append to an existing file. Attempting to write to an existing file with mode="w" results in an error.

Usage

```
readFasta(dirPath, pattern = character(0), ...,
          nrec=-1L, skip=0L)
## S4 method for signature character
readFasta(dirPath, pattern = character(0), ...,
          nrec=-1L, skip=0L)
writeFasta(object, file, mode="w", ...)
## S4 method for signature DNASTringSet
writeFasta(object, file, mode="w", ...)
```

Arguments

dirPath	A character vector giving the directory path (relative or absolute) or single file name of FASTA files to be read.
pattern	The (grep -style) pattern describing file names to be read. The default (character(0)) results in (attempted) input of all files in the directory.
object	An object to be output in fasta format.
file	A length 1 character vector providing a path to a file to the object is to be written to.
mode	A length 1 character vector equal to either 'w' or 'a' to write to a new file or append to an existing file, respectively.
...	Additional arguments used by methods or, for writeFasta, writeXStringSet .
nrec	See ?readDNASTringSet .
skip	See ?readDNASTringSet .

Value

readFasta returns a [DNASTringSet](#). containing sequences and qualities contained in all files in dirPath matching pattern. There is no guarantee of order in which files are read.

writeFasta is invoked primarily for its side effect, creating or appending to file file. The function returns, invisibly, the length of object, and hence the number of records written. There is a writeFasta method for any class derived from [ShortRead](#).

Author(s)

Martin Morgan

Examples

```
showMethods("readFasta")

showMethods("writeFasta")

f1 <- system.file("extdata", "someORF.fa", package="Biostrings")

rfa <- readFasta(f1)
sread(rfa)
id(rfa)

sp <- SolexaPath(system.file(extdata, package=ShortRead))
rfq <- readFastq(analysisPath(sp), pattern="s_1_sequence.txt")

file <- tempfile()
writeFasta(rfq, file)
readLines(file, 8)

writeFasta(sread(rfq), file) # no ids
```

`readFastq`*Read and write FASTQ-formatted files*

Description

`readFastq` reads all FASTQ-formatted files in a directory `dirPath` whose file name matches `pattern`, returning a compact internal representation of the sequences and quality scores in the files. Methods read all files into a single R object; a typical use is to restrict input to a single FASTQ file.

`writeFastq` writes an object to a single file, using `mode="w"` (the default) to create a new file or `mode="a"` append to an existing file. Attempting to write to an existing file with `mode="w"` results in an error.

Usage

```
readFastq(dirPath, pattern=character(0), ...)
## S4 method for signature character
readFastq(dirPath, pattern=character(0), ..., withIds=TRUE)

writeFastq(object, file, mode="w", full=FALSE, ...)
```


Value

readFastq returns a single R object (e.g., `ShortReadQ`) containing sequences and qualities contained in all files in `dirPath` matching `pattern`. There is no guarantee of order in which files are read.

writeFastq is invoked primarily for its side effect, creating or appending to file `file`. The function returns, invisibly, the length of object, and hence the number of records written.

Author(s)

Martin Morgan

See Also

The IUPAC alphabet in Biostrings.

http://www.bioperl.org/wiki/FASTQ_sequence_format for the BioPerl definition of fastq.

Solexa documentation ‘Data analysis - documentation : Pipeline output and visualisation’.

Examples

```
showMethods(readFastq)
showMethods(writeFastq)

sp <- SolexaPath(system.file(extdata, package=ShortRead))
rfq <- readFastq(analysisPath(sp), pattern="s_1_sequence.txt")
sread(rfq)
id(rfq)
quality(rfq)

## SolexaPath method knows where FASTQ files are placed
rfq1 <- readFastq(sp, pattern="s_1_sequence.txt")
rfq1

file <- tempfile()
writeFastq(rfq, file)
readLines(file, 8)
```

readIntensities

Read Illumina image intensity files

Description

readIntensities reads image ‘intensity’ files (such as Illumina’s `_int.txt` and (optionally) `_nse.txt`) into a single object.

Usage

```
readIntensities(dirPath, pattern=character(0), ...)
```


Arguments

dirPath	Directory path or other object (e.g., SolexaPath) for which methods are defined.
pattern	A length 1 character vector representing a regular expression to be combined with dirPath, as described below, to match files to be summarized.
...	Additional arguments used by methods.

Details

Additional methods are defined on specific classes, see, e.g., [SolexaPath](#).

The readIntensities, character-method contains an argument type that determines how intensities are parsed. Use the type argument to readIntensities, character-method, as described below. All readIntensities, character methods accepts the following arguments:

withVariability: Include estimates of variability (i.e., from parsing _nse files).

verbose: Report on progress when starting to read each file.

The supported types and their signatures are:

type="RtaIntensity" Intensities are read from Illumina _cif.txt and _cnf.txt-style files. The signature for this method is

```
dirPath, pattern=character(0), ..., type="RtaIntensity", lane=integer(0), cycles=integer(0),
cycleNames=sprintf("C      tileNames=sprintf("s_      posNames=sprintf("s_
withVariability=TRUE, verbose=FALSE
```

lane: integer(1) identifying the lane in which cycles and tiles are to be processed.

cycles: integer() enumerating cycles to be processed.

cycleIteration: integer(1) identifying the iteration of the base caller to be summarized

tiles: integer() enumerating tile numbers to be summarized.

laneName, cycleNames, tileNames, posNames: character() vectors identifying the lane and cycle directories, and the 'pos' and tile file names (excluding the '.cif' or '.cnf' extension) to be processed.

The dirPath and pattern arguments are combined as list.files(dirPath, pattern), and must identify a single directory. Most uses of this function will focus on a single tile (specified with, e.g., tiles=1L); the laneName, cycleNames, tileNames, and posNames parameters are designed to work with the default Illumina pipeline and do not normally need to be specified.

type="IparIntensity" Intensities are read from Solexa _pos.txt, _int.txt.p, _nse.txt.p-style file triplets. The signature for this method is

```
dirPath, pattern=character(0), ..., type="IparIntensity", intExtension="_int.txt.p.gz",
Files to be parsed are determined as, e.g., paste(pattern, intExtension, sep="").
```

type="SolexaIntensity" Intensities are read from Solexa _int.txt and _nse.txt-style files.

The signature for this method is

```
dirPath, pattern=character(0), ..., type="SolexaIntensity", intExtension="_int.txt", nse
Files to be parsed are determined as, e.g., paste(pattern, intExtension, sep="").
```

Value

An object derived from class [Intensity](#).

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>, Michael Muratet <mmuratet@hudsonalpha.org> (RTA).

Examples

```
f1 <- system.file("extdata", package="ShortRead")
sp <- SolexaPath(f1)
int <- readIntensities(sp)
int
intensity(int)[1,,] # one read
intensity(int)[[1:2,,]] # two reads, as array
head(rowMeans(intensity(int))) # treated as array
head(pData(readInfo(int)))

## Not run: ## RTA Lane 2, cycles 1:80, cycle iteration 1, tile 3
int <- readIntensities("Data/Intensities", type="RtaIntensity",
                      lane=2, cycles=1:80, tiles=3)

## End(Not run)
```

readPrb

Read Solexa prb files as fastq-style quality scores

Description

readPrb reads all `_prb.txt` files in a directory into a single object. Most methods (see details) do this by identifying the maximum base call quality for each cycle and read, and representing this as an ASCII-encoded character string.

Usage

```
readPrb(dirPath, pattern = character(0), ...)
```

Arguments

dirPath	Directory path or other object (e.g., SolexaPath for which methods are defined).
pattern	Regular expression matching names of <code>_prb</code> files to be summarized.
...	Additional arguments, e.g., to sapply , used during evaluation.

Details

The `readPrb`, `character-method` contains an argument `as` that determines the value of the returned object, as follows.

`as="SolexaEncoding"` The ASCII encoding of the maximum per cycle and read quality score is encoded using Solexa conventions.

`as="FastqEncoding"` The ASCII encoding of the maximum per cycle and read quality score is encoded using Fastq conventions, i.e., `!` has value 0.

`as="IntegerEncoding"` The maximum per cycle and read quality score is returned as a in integer value. Values are collated into a matrix with number of rows equal to number of reads, and number of columns equal to number of cycles.

`as="array"` The quality scores are *not* summarized; the return value is an integer array with dimensions corresponding to reads, nucleotides, and cycles.

Value

An object of class `QualityScore`, or an integer matrix.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
f1 <- system.file("extdata", package="ShortRead")
sp <- SolexaPath(f1)
readPrb(sp, "s_1.*_prb.txt") # all tiles to a single file
```

readQseq

Read Solexa qseq files as fastq-style quality scores

Description

`readQseq` reads all files matching `pattern` in a directory into a single `ShortReadQ`-class object. Information on machine, lane, tile, x, and y coordinates, filtering status, and read number are not returned (although filtering status can be used to selectively include reads as described below).

Usage

```
readQseq(dirPath, pattern = character(0), ...,
         as=c("ShortReadQ", "DataFrame", "XDataFrame"),
         filtered=FALSE,
         verbose=FALSE)
```

Arguments

dirPath	Directory path or other object (e.g., SolexaPath) for which methods are defined.
pattern	Regular expression matching names of _qseq files to be summarized.
...	Additional argument, passed to I/O functions.
as	character(1) indicating the class of the return type. "XDataFrame" is included for backward compatibility, but is no longer supported.
filtered	logical(1) indicating whether to include only those reads passing Solexa filtering?
verbose	logical(1) indicating whether to report on progress during evaluation.

Value

An object of class [ShortReadQ](#).

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
f1 <- system.file("extdata", package="ShortRead")
sp <- SolexaPath(f1)
readQseq(sp)
```

readXStringColumns *Read one or more columns into XStringSet (e.g., DNAStrngSet) objects*

Description

This function allows short read data components such as DNA sequence, quality scores, and read names to be read in to XStringSet (e.g., DNAStrngSet, BStringSet) objects. One or several files of identical layout can be specified.

Usage

```
readXStringColumns(dirPath, pattern=character(0),
                  colClasses=list(NULL),
                  nrows=-1L, skip=0L,
                  sep = "\t", header = FALSE, comment.char="#")
```

Arguments

dirPath	A character vector giving the directory path (relative or absolute) of files to be read.
pattern	The (grep -style) pattern describing file names to be read. The default (character(0)) reads all files in dirPath. All files are expected to have identical numbers of columns.
colClasses	A list of length equal to the number of columns in a file. Columns with corresponding colClasses equal to NULL are ignored. Other entries in colClasses are expected to be character strings describing the base class for the XStringSet. For instance a column of DNA sequences would be specified as "DNAStrng". The column would be parsed into a DNAStrngSet object.
nrows	A length 1 integer vector describing the maximum number of XString objects to read into the set. Reads may come from more than one file when dirPath and pattern parse several files and nrow is greater than the number of reads in the first file.
skip	A length 1 integer vector describing how many lines to skip at the start of each file.
sep	A length 1 character vector describing the column separator.
header	A length 1 logical vector indicating whether files include a header line identifying columns. If present, the header of the first file is used to name the returned values.
comment.char	A length 1 character vector, with a single character that, when appearing at the start of a line, indicates that the entire line should be ignored. Currently there is no way to use comment characters in other than the first position of a line.

Value

A list, with each element containing an XStringSet object of the type corresponding to the non-NULL elements of colClasses.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
## valid character strings for colClasses
names(slot(getClass("XString"), "subclasses"))

dirPath <- system.file(extdata, maq, package=ShortRead)

colClasses <- rep(list(NULL), 16)
colClasses[c(1, 15, 16)] <- c("BString", "DNAStrng", "BString")

## read one file
readXStringColumns(dirPath, "out.aln.1.txt", colClasses=colClasses)
```

```
## read all files into a single object for each column
res <- readXStringColumns(dirPath, colClasses=colClasses)
```

renewable

Renew (update) a ShortRead object with new values

Description

Use `renew` to update an object defined in **ShortRead** with new values. Discover update-able classes and values with `renewable`.

Usage

```
renewable(x, ...)
renew(x, ...)
```

Arguments

<code>x</code>	For <code>renewable</code> : missing, <code>character(1)</code> , or a class defined in the ShortRead package. For <code>renew</code> : an instance of a class defined in the ShortRead package.
<code>...</code>	For <code>renewable</code> , ignored. For <code>renew</code> , named arguments identifying which parts of <code>x</code> are to be renewed.

Details

When invoked with no arguments `renewable` returns a character vector naming classes that can be renewed.

When invoked with a `character(1)` or an instance of a **ShortRead** class, a list of the names and values of the elements that can be renewed. When `x` is a character vector naming a virtual class, then each element of the returned list is a non-virtual descendant of that class that can be used in renewal. This is not fully recursive.

`renew` is always invoked with the `x` argument being an instance of a class identified by `renewable()`. Remaining arguments are name-value pairs identifying the components of `x` that are to be renewed (updated). The name-value pairs must be consistent with `renewable(x)`. The resulting object is checked for validity. Multiple components of the object can be updated in a single call to `renew`, allowing comparatively efficient complex transformations.

Value

`renewable()` returns a character vector of renewable classes.

`renewable(x)` returns a named list. The names correspond to renewable classes, and the elements of the list correspond to renewable components of the class.

`renew(x, ...)` returns an object of the same class as `x`, but with components of `x` replaced by the named values of `...`

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
## discovery
renewable()
renewable("AlignedRead")
renewable("QualityScore") ## instantiable classes

## example data
sp <- SolexaPath(system.file("extdata", package="ShortRead"))
ap <- analysisPath(sp)
filt <- chromosomeFilter("chr[[:digit:]]+.fa")
aln <- readAligned(ap, "s_2_export.txt", "SolexaExport",
                  filter=filt)

## renew chromosomes from chr1.fa to chr1, etc
labels <- sub("\\.fa", "", levels(chromosome(aln)))
renew(aln, chromosome=factor(chromosome(aln), labels=labels))

## multiple changes -- update chromosome, offset position
renew(aln, chromosome=factor(chromosome(aln), labels=labels),
      position=1L+position(aln))

## oops! invalid instances cannot be constructed
try(renew(aln, position=1:10))
```

report

Summarize quality assessment results into a report

Description

This generic function summarizes results from evaluation of [qa](#) into a report. Available report formats vary depending on the data analysed.

Usage

```
report(x, ..., dest=tempfile(), type="html")
report_html(x, dest, type, ...)
```

Arguments

x An object returned by [qa](#), usually derived from class [.QA](#)

... Additional arguments used by specific methods.

All methods with `type="html"` support the argument `cssFile`, which is a named, length 1 character vector. The value is a path to a CSS file to be incorporated into

	the report (e.g., <code>system.file("template", "QA.css", package="ShortRead")</code>). The name of <code>cssFile</code> is the name of the CSS file as seen by the html report (e.g., "QA.css").
	See specific methods for details on additional . . . arguments.
<code>dest</code>	The output destination for the final report. For <code>type="html"</code> this is a directory; for (deprecated) <code>type="pdf"</code> this is a file.
<code>type</code>	A text string defining the type of report; available report types depend on the type of object <code>x</code> ; usually this is "html".

Details

`report_html` is meant for use by package authors wishing to add methods for creating HTML reports; users should always invoke `report`.

The following methods are defined:

- `x="BAMQA", ..., dest=tempfile(), type="html"` Produce an HTML-based report from an object of class [BAMQA](#).
- `x="BowtieQA", ..., dest=tempfile(), type="html"` Produce an HTML-based report from an object of class [BowtieQA](#).
- `x="FastqQA", ..., dest=tempfile(), type="html"` Produce an HTML-based report from an object of class [FastqQA](#).
- `x="MAQMapQA", ..., dest=tempfile(), type="html"` Produce an HTML-based report from an object of class [MAQMapQA](#).
- `x="SolexaExportQA", ..., dest=tempfile(), type="html"` Produce an HTML-based report from an object of class [SolexaExportQA](#).
- `x="SolexaExportQA", ..., dest=tempfile(), type="pdf"` (Deprecated) Produce an PDF report from an object of class [SolexaExportQA](#).
- `x="SolexaPath", ..., dest=tempfile(), type="html"` Produce an HTML report by first visiting all `_export.txt` files in the `analysisPath` directory of `x` to create a [SolexaExportQA](#) instance.
- `x="SolexaPath", ..., dest=tempfile(), type="pdf"` (Deprecated) Produce an PDF report by first visiting all `_export.txt` files in the `analysisPath` directory of `x` to create a [SolexaExportQA](#) instance.
- `x="ANY", ..., dest=tempfile(), type="ANY"` This method is used internally

Value

This function is invoked for its side effect; the return value is the name of the directory or file where the report was created.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[SolexaExportQA](#)

Examples

```
showMethods("report")

## default CSS file
cssFile <- c(QA.css=system.file("template", "QA.css",
                               package="ShortRead"))
noquote(readLines(cssFile))
```

RochePath-class	<i>"RochePath" class representing a Roche (454) experiment location</i>
-----------------	---

Description

This class represents the directory location where Roche (454) result files (fasta sequences and qualities) can be found.

Objects from the Class

Objects from the class are created with the RochePath constructor:

```
RochePath(experimentPath = NA_character_, readPath = experimentPath, qualPath = readPath, ..., verbose)
```

experimentPath character(1) or [RochePath](#) pointing to the top-level directory of a Roche experiment.

readPath character() of directories (typically in experimentPath) containing sequence (read) information. The default selects all directories matching `list.files(experimentPath, "run")`.

qualPath character() of directories (typically in experimentPath) containing quality information. The default selects all directories matching `list.files(experimentPath, "run")`.

verbose logical(1) indicating whether invalid paths should be reported interactively.

Slots

RocheSet has the following slots:

readPath: Object of class "character", as described in the constructor, above.

qualPath: Object of class "character", as described in the constructor, above.

basePath: Object of class "character", containing the experimentPath.

Extends

Class "[ExperimentPath](#)", directly. Class "[.Roche](#)", directly. Class "[.ShortReadBase](#)", by class "[ExperimentPath](#)", distance 2. Class "[.ShortReadBase](#)", by class "[.Roche](#)", distance 2.

Methods

RochePath has the following methods or functions defined:

readFasta signature(`dirPath = "RochePath"`, `pattern=".\.fna$"`, `sample = 1`, `run = 1`, ...):
Read sequences from files matching `list.files(dirPath, pattern)` (when `dirPath="character"`)
or `list.files(readPath(dir)[run], pattern)[sample]`. The result is a `DNAStringSet`.

readQual signature(`dirPath = "RochePath"`, `reads=NULL`, `pattern=".\.qual$"`, `sample=1`, `run=1`, ...):
Read quality scores from files matching `list.files(qualPath(dirPath)[run])[sample]`.
Non-null reads is used as an (optional) template for parsing quality scores.

readFastaQual signature(`dirPath = "RochePath"`, `fastaPattern = ".\.fna$"`, `qualPattern = ".\.qual$"`, ...):
read sequences and quality scores into a `ShortReadQ` instance.

readFastaQual signature(`dirPath = "character"`, `fastaPattern = ".\.fna$"`, `qualPattern = ".\.qual$"`, ...):
wrapper for method above, coercing `dirPath` to a `RochePath` via `RochePath(dirPath)`.

readBaseQuality signature(`dirPath = "RochePath"`, ...): Reads in base and quality information. Currently delegates to `readFastaQual`, above, but will do more after `RochePath` supports more file types.

read454 signature(`dirPath = "RochePath"`, ...): Pass arguments on to `readFastaQual`, documented above.

readPath signature(`object = "RochePath"`): return the contents of the `readPath` slot.

runNames signature(`object = "RochePath"`): return the basenames of `readPath(object)`.

RocheSet signature(`path = "RochePath"`): create a `RocheSet` from `path`.

Additional methods include:

show signature(`object = "RochePath"`): Briefly summarize the experiment path locations.

detail signature(`x = "RochePath"`): Provide additional detail on the Roche path. All file paths are presented in full.

Author(s)

Michael Lawrence <mflawrence@fhcrc.org>

See Also

[ExperimentPath](#).

Examples

```
showClass("RochePath")
```

RocheSet-class	<i>Roche (454) experiment-wide data container</i>
----------------	---

Description

This class is meant to coordinate all data in a Roche (454) experiment. See [SRSet](#) for additional details.

Objects from the Class

Create objects from this class using one of the RocheSet methods documented below

Slots

sourcePath: Object of class "RochePath" The file system location of the data used in this experiment.

readIndex: Object of class "integer" indexing reads included in the experiment; see [SRSet](#) for details on data representation in this class.

readCount: Object of class "integer" containing the number of reads associated with each sample; see [SRSet](#) for details on data representation in this class.

phenoData: Object of class "AnnotatedDataFrame" with as many rows as there are samples, containing information on experimental design.

readData: Object of class "AnnotatedDataFrame" containing as many rows as there are reads, containing information on each read in the experiment.

Extends

Class "[SRSet](#)", directly. Class "[.Roche](#)", directly. Class "[.ShortReadBase](#)", by class "[SRSet](#)", distance 2. Class "[.ShortReadBase](#)", by class "[.Roche](#)", distance 2.

Methods

No methods defined with class "RocheSet" in the signature; see [SRSet](#) for inherited methods.

Author(s)

Michael Lawrence <mflawrence@fhcrc.org>

See Also

[SRSet](#)

Examples

```
showClass("RocheSet")
```

RtaIntensity

Construct objects of class "RtaIntensity"

Description

[RtaIntensity](#) objects contain Illumina image intensity measures created by the RTA pipeline. It will often be more convenient to create this object using [readIntensities](#).

Usage

```
RtaIntensity(intensity=array(0, c(0, 0, 0)),
             measurementError=array(0, c(0, 0, 0)),
             readInfo=SolexaIntensityInfo(
               lane=integer()[seq_len(nrow(intensity))]),
             ...)
```

Arguments

<code>intensity</code>	A matrix of image intensity values. Successive columns correspond to nucleotides A, C, G, T; four successive columns correspond to each cycle. Typically, derived from "_int.txt" files.
<code>measurementError</code>	As <code>intensity</code> , but measuring standard error. Usually derived from "_nse.txt" files.
<code>readInfo</code>	An object of class <code>AnnotatedDataFrame</code> , containing information described by <code>RtaIntensityInfo</code> .
<code>...</code>	Additional arguments, not currently used.

Value

An object of class [RtaIntensity](#).

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[RtaIntensity](#), [readIntensities](#).

Examples

```
rta <- RtaIntensity(array(runif(60), c(5,4,3)))
intensity(rta)
## subsetting, access, and coercion
as(intensity(rta)[1:2,,], "array")
```

RtaIntensity-class *Class "RtaIntensity"*

Description

Subclass of [Intensity](#) for representing image intensity data from the Illumina RTA pipeline.

Objects from the Class

Objects can be created by calls to `RtaIntensity` or more usually `readIntensities`.

Slots

Object of `RtaIntensity` have slots:

`readInfo`: Object of class `"RtaIntensityInfo"` representing information about each read.

`intensity`: Object of class `"ArrayIntensity"` containing an array of intensities with dimensions read, base, and cycle. Nucleotide are A, C, G, T for each cycle.

`measurementError`: Object of class `"ArrayIntensity"` containing measurement errors for each read, cycle, and base, with dimensions like that for `intensity`.

`.hasMeasurementError`: Object of class `"ScalarLogical"` used internally to indicate whether measurement error information is included.

Extends

Class `"SolexaIntensity"`, directly.

Class `"Intensity"`, by class `"SolexaIntensity"`, distance 2.

Class `".ShortReadBase"`, by class `"SolexaIntensity"`, distance 3.

Methods

Class `"RtaIntensity"` inherits accessor, subsetting, and display methods from class `SolexaIntensity`.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[SolexaIntensity](#), [readIntensities](#)

Examples

```
showClass("RtaIntensity")
showMethods(class="RtaIntensity", where=getNamespace("ShortRead"))
```

ShortRead-class *"ShortRead" class for short reads*

Description

This class provides a way to store and manipulate, in a coordinated fashion, uniform-length short reads and their identifiers.

Objects from the Class

Objects from this class are created by readFasta, or by calls to the constructor ShortRead, as outlined below.

Slots

sread: Object of class "DNAStrngSet" containing IUPAC-standard, uniform-length DNA strings represent short sequence reads.

id: Object of class "BStringSet" containing identifiers, one for each short read.

Extends

Class "[.ShortReadBase](#)", directly.

Methods

Constructors include:

ShortRead signature(sread = "DNAStrngSet", id = "BStringSet"): Create a ShortRead object from reads and their identifiers. The length of id must match that of sread.

ShortRead signature(sread = "DNAStrngSet", id = "missing"): Create a ShortRead object from reads, creating empty identifiers.

ShortRead signature(sread = "missing", id = "missing", ...): Create an empty ShortRead object.

Methods include:

sread signature(object = "AlignedRead"): access the sread slot of object.

id signature(object = "AlignedRead"): access the id slot of object.

[signature(x = "ShortRead", i = "ANY", j = "missing"): This method creates a new ShortRead object containing only those reads indexed by i. Additional methods on '[,ShortRead' do not provide additional functionality, but are present to limit inappropriate use.

append signature(x = "ShortRead", values = "ShortRead"): append the sread and id slots of values after the corresponding fields of x.

narrow signature(x = "ShortRead", start = NA, end = NA, width = NA, use.names = TRUE): 'narrow' sread so that sequences are between start and end bases, according to [narrow](#) in the IRanges package.

length signature(x = "ShortRead"): returns a integer(1) vector describing the number of reads in this object.

width signature(x = "ShortRead"): returns an integer() vector of the widths of each read in this object.

srorder signature(x = "ShortRead"):

srrank signature(x = "ShortRead"):

srsort signature(x = "ShortRead"):

srduplicated signature(x = "ShortRead"): Order, rank, sort, and find duplicates in ShortRead objects based on sread(x), analogous to the corresponding functions order, rank, sort, and duplicated, ordering nucleotides in the order ACGT.

srdistance signature(pattern="ShortRead", subject="ANY"): Find the edit distance between each read in pattern and the (short) sequences in subject. See [srdistance](#) for allowable values for subject, and for additional details.

trimLRPatterns signature(Lpattern = "", Rpattern = "", subject = "ShortRead", max.Lmismatch = 0, max.Rmismatch = 0):

Remove left and / or right flanking patterns from sread(subject), as described in [trimLRPatterns](#).

Classes derived from ShortRead (e.g., [ShortReadQ](#), [AlignedRead](#)) have corresponding base quality scores trimmed, too. The class of the return object is the same as the class of subject, except when ranges=TRUE when the return value is the ranges to use to trim 'subject'.

alphabetByCycle signature(stringSet = "ShortRead"): Apply [alphabetByCycle](#) to the sread component of stringSet, returning a matrix as described in [alphabetByCycle](#).

tables signature(x= "ShortRead", n = 50): Apply [tables](#) to the sread component of x, returning a list summarizing frequency of reads in x.

clean signature(object="ShortRead"): Remove all reads containing non-nucleotide ("N", "-") symbols.

show signature(object = "ShortRead"): provides a brief summary of the object, including its class, length and width.

detail signature(x = "ShortRead"): provides a more extensive summary of this object, displaying the first and last entries of sread and id.

writeFasta signature(object, file, ...): write object to file in fasta format. See [writeXStringSet](#) for ... argument values.

Author(s)

Martin Morgan

See Also

[ShortReadQ](#)

Examples

```
showClass("ShortRead")
showMethods(class="ShortRead", where=getNamespace("ShortRead"))
```

ShortRead-deprecated *Deprecated functions from the ShortRead package*

Description

These functions are deprecated, and will become defunct.

Usage

```
uniqueFilter(withSread=TRUE, .name="UniqueFilter")
```

Arguments

withSread	A logical(1) indicating whether uniqueness includes the read sequence (withSread=TRUE) or is based only on chromosome, position, and strand (withSread=FALSE)
.name	An optional character(1) object used to over-ride the name applied to default filters.

Details

See [srFilter](#) for details of ShortRead filters.

uniqueFilter selects elements satisfying !srduplicated(x) when withSread=TRUE, and !(duplicated(chromosome(x)) duplicated(strand(x))) when withSread=FALSE.

The behavior when withSread=TRUE can be obtained with occurrenceFilter(withSread=TRUE). The behavior when withSread=FALSE can be obtained using a custom filter

ShortReadQ-class *"ShortReadQ" class for short reads and their quality scores*

Description

This class provides a way to store and manipulate, in a coordinated fashion, the reads, identifiers, and quality scores of uniform-length short reads.

Objects from the Class

Objects from this class are the result of [readFastq](#), or can be constructed from DNASTringSet, QualityScore, and BStringSet objects, as described below.

Slots

Slots sread and id are inherited from [ShortRead](#). An additional slot defined in this class is:

quality: Object of class "BStringSet" representing a quality score (see [readFastq](#) for some discussion of quality score).

Extends

Class "[ShortRead](#)", directly. Class "[.ShortReadBase](#)", by class "ShortRead", distance 2.

Methods

Constructors include:

ShortReadQ signature(sread = "DNAStrngSet", quality = "QualityScore", id = "BStringSet"):

ShortReadQ signature(sread = "DNAStrngSet", quality = "BStringSet", id = "BStringSet"):

Create a ShortReadQ object from reads, their quality scores, and identifiers. When quality is of class BStringSet, the type of encoded quality score is inferred from the letters used in the scores. The length of id and quality must match that of sread.

ShortReadQ signature(sread = "DNAStrngSet", quality = "QualityScore", id = "missing"):

ShortReadQ signature(sread = "DNAStrngSet", quality = "BStringSet", id = "missing"):

Create a ShortReadQ object from reads and their quality scores, creating empty identifiers. When quality is of class BStringSet, the type of encoded quality score is inferred from the letters used in the scores.

ShortReadQ signature(sread = "missing", quality = "missing", id = "missing", ...):

Create an empty ShortReadQ object.

See [accessors](#) for additional functions to access slot content, and [ShortRead](#) for inherited methods. Additional methods include:

quality inherited from signature(object = "ANY"): access the quality slot of object.

coerce signature(from = "SFastqQuality", to = "QualityScaledDNAStrngSet"):

(Use as(from, "QualityScaledDNAStrngSet")) coerce objects of class from to class to, using the quality encoding implied by quality(from). See [QualityScore](#) for supported quality classes and their coerced counterparts.

writeFastq signature(object = "ShortReadQ", file = "character", ...):

writeFastq signature(object = "ShortReadQ", file = "FastqFile", ...): Write object to file in fastq format. See [writeFastq](#) for additional arguments mode and full.

[signature(x = "ShortReadQ", i = "ANY", j = "missing"): This method creates a new ShortReadQ object containing only those reads indexed by i. Additional methods on '[,ShortRead' do not provide additional functionality, but are present to limit inappropriate use.

append signature(x = "ShortReadQ", values = "ShortRead"): append the sread, quality and id slots of values after the corresponding fields of x.

narrow signature(x = "ShortReadQ", start = NA, end = NA, width = NA, use.names = TRUE):

narrow sread and quality so that sequences are between start and end bases, according to [narrow](#) in the IRanges package.

trimTailw signature(object="ShortReadQ", k="integer", a="character", halfwidth="integer", ..., ranges= trim trailing nucleotides when a window of width 2 * halfwidth + 1 contains k or more quality scores falling at or below a.

trimTails signature(object="ShortReadQ", k="integer", a="character", successive=FALSE, ..., ranges=FALSE) trim trailing nucleotides if k nucleotides fall below the quality encoded by a. If successive=FALSE, the k'th failing nucleotide and all subsequent nucleotides are trimmed. If successive=TRUE, failing nucleotides must occur successively; the sequence is trimmed from the first of the successive failing nucleotides.

alphabetByCycle signature(stringSet = "ShortReadQ"): Apply [alphabetByCycle](#) to the sread component, the quality component, and the combination of these two components of stringSet, returning a list of matrices with three elements: "sread", "quality", and "both".

alphabetScore signature(object = "ShortReadQ"): See [alphabetScore](#) for details.

qa signature(dirPath = "ShortReadQ", lane="character", ..., verbose=FALSE): Perform quality assessment on the ShortReadQ object using lane to identify the object and returning an instance of [ShortReadQA](#). See [qa](#)

detail signature(x = "ShortReadQ"): display the first and last entries of each of sread, id, and quality entries of object.

Author(s)

Martin Morgan

See Also

[readFastq](#) for creation of objects of this class from fastq-format files.

Examples

```
showClass("ShortReadQ")
showMethods(class="ShortReadQ", where=getNamespace("ShortRead"),
            inherit=FALSE)
showMethods(class="ShortRead", where=getNamespace("ShortRead"),
            inherit=FALSE)

sp <- SolexaPath(system.file(extdata, package=ShortRead))
rfq <- readFastq(analysisPath(sp), pattern="s_1_sequence.txt")
quality(rfq)
quality(trimTails(rfq, 2, "H", successive=TRUE))
```

ShortReadQA-class

Quality assessment of fastq files and ShortReadQ objects

Description

These classes contains a list-like structure with summary descriptions derived from visiting one or more fastq files, or from a [ShortReadQ](#) object.

Objects from the Class

Objects of the class are usually produced by a [qa](#) method.

Slots

`.srlist`: Object of class "list", containing data frames or lists of data frames summarizing the results of `qa`.

Extends

Class "`SRList`", directly. Class "`.QA`", directly. Class "`.SRUtil`", by class "`SRList`", distance 2. Class "`.ShortReadBase`", by class "`.QA`", distance 2.

Methods

Accessor methods are inherited from the `SRList` class.

Additional methods defined on this class are:

report signature(`x="FastqQA"`, ..., `dest=tempfile()`, `type="html"`): produces HTML files summarizing QA results. `dest` should be a directory.

report signature(`x="ShortReadQA"`, ..., `dest=tempfile()`, `type="html"`): produces HTML files summarizing QA results. `dest` should be a directory.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[qa](#).

Examples

```
showClass("FastqQA")
```

Snapshot-class

Class "Snapshot"

Description

A `Snapshot`-class to visualize genomic data from BAM files with zoom and pan functionality.

Usage

```
Snapshot(files, range, ...)
```

Arguments

<code>files</code>	A character() or BamFileList specifying the file(s) to be visualized.
<code>range</code>	A GRanges object specifying the range to be visualized.
<code>...</code>	Additional, optional, arguments to be passed to the Snapshot initialize function. Arguments include: <ul style="list-style-type: none"> functions: A SnapshotFunctionList of functions, in addition to built-in 'fine_coverage', 'coarse_coverage', 'multifine_coverage', to be used for visualization. currentFunction: character(1) naming the function, from functions to be used for data input and visualization. The default chooses a function based on the scale at which the data is being visualized. annTrack: Annotation track. If built-in visualization functions are to be used, annTrack should be a GRanges instance and the first column of its elementMetadata would be used to annotate the range. fac: Character(1) indicating which factor used for grouping the sample files. The factor should be included in the elementMetadata of files, otherwise ignored. Used only to visualize multiple files. .auto_display: logical(1) indicating whether the visualization is to be updated when show is invoked. .debug logical(1) indicating whether debug messages are to be printed.

Methods

zoom	signature(x = "Snapshot"): Zoom (in or out) the current plot.
pan	signature(x = "Snapshot"): Pan (right or left) the current plot.
togglefun	signature(x = "Snapshot"): Toggle the current functions which imported records are to be immediately evaluated. Note that the active range will be changed to the current active window.
togglep	signature(x = "Snapshot"): Toggle the panning effects.
togglez	signature(x = "Snapshot"): Toggle the zooming effects.

Accessors

show	signature(object = "Snapshot"): Display a Snapshot object.
files	signature(x = "Snapshot"): Get the files field (object of class BamFileList) of a Snapshot object.
functions	signature(x = "Snapshot"): Get the functions field (object of SnapshotFunctionList) of a Snapshot object.
view	signature(x = "Snapshot"): Get the view field (object of SpTrellis) of a Snapshot object.
vrange	signature(x = "Snapshot"): Get the .range field (object of GRanges) of a Snapshot object.
getTrellis	signature(x = "Snapshot"): Get the trellis object, a field of the SpTrellis object.

Fields

- .debug: Object of class function to display messages while in debug mode
- .auto_display: Object of class logical to automatically display the coverage plot.
- .range: Object of class GRanges indicating which ranges of records to be imported from BAM fields.
- .zin: Object of class logical indicating whether the current zooming effect is zoom in.
- .pright: Object of class logical indicating whether the current panning effect is right.
- .data: Object of class data.frame containing coverage a position is represented for each strand and BAM file.
- .data_dirty: Object of class logical indicating whether to re-evaluate the imported records.
- .initial_functions: Object of class SnapshotFunctionList available by the Snapshot object.
- .current_function: Object of class character of the function the imported recorded are currently evaluated and visualized.
- annTrack: Default to NULL if not intended to visualize the annotation track. If default visualization function(s) is intended to be used to plot the annotation, annTrack has to be a GRanges instance.
- functions: Object of class SnapshotFunctionList of customized functions to evaluate and visualize the imported records.
- files: Object of class BamFileList to be imported.
- view: Object of class SpTrellis that is essentially a reference class wrapper of Trellis objects.

Class-Based Methods

- display(): Display the current Snapshot object.
- pan(): Pan (right or left) the current plot.
- zoom(): Zoom (in or out) the current plot.
- toggle(zoom, pan, currentFunction): Toggle zooming, panning effects or the currentFunction in which the imported records are to be evaluated and visualized.

Author(s)

Martin Morgan and Chao-Jen Wong <cwon2@fhcrc.org>

See Also

[SpTrellis](#)

Examples

```
## example 1: Importing specific ranges of records

file <- system.file("extdata", "SRR002051.chrI-V.bam",
                    package="yeastNagalakshmi")
which <- GRanges("chrI", IRanges(1, 2e5))
```

```

s <- Snapshot(file, range=which)

## methods
zoom(s) # zoom in
## zoom in to a specific region
zoom(s, range=GRanges("chrI", IRanges(7e4, 7e4+8000)))
pan(s) # pan right
togglez(s) # change effect of zooming
zoom(s) # zoom out
togglep(s) # change effect of panning
pan(s)

## accessors
functions(s)
vrange(s)
show(s)
ignore.strand(s)
view(s) ## extract the spTrellis object
getTrellis(s) ## extract the trellis object

## example 2: ignore strand
s <- Snapshot(file, range=which, ignore.strand=TRUE)

##
## example 3: visualizing annotation track
##

library(GenomicFeatures)

getAnnGR <- function(txdb, which) {
  ex <- exonsBy(txdb, by="gene")
  seqlevels(ex, force=TRUE) <- seqlevels(which)
  r <- range(ex)
  gr <- unlist(r)
  values(gr)[["gene_id"]] <- rep.int(names(r), times=elementLengths(r))
  gr
}

txdbFile <- system.file("extdata", "sacCer2_sgdGene.sqlite",
                        package="yeastNagalakshmi")
# txdb <- makeTranscriptDbFromUCSC(genome="sacCer2",
#                                  tablename="sgdGene")
txdb <- loadDb(txdbFile)
which <- GRanges("chrI", IRanges(1, 2e5))
gr <- getAnnGR(txdb, which)
## note that the first column of the elementMetadata annotates of the
## range of the elements.
gr

s <- Snapshot(file, range=which, annTrack=gr)
annTrack(s)
## zoom in to an interesting region
zoom(s, range=GRanges("chrI", IRanges(7e4, 7e4+8000)))

```

```

togglez(s) ## zoom out
zoom(s)

pan(s)

## example 4, 5, 6: multiple BAM files with multicoarse_covarage
## and multifine_coverage view.

## Resolution does not automatically switch for views of multiple
## files. It is important to note if width(which) < 10,000, use
## multifine_coverage. Otherwise use multicoarse_coverage
file <- system.file("extdata", "SRR002051.chrI-V.bam",
                    package="yeastNagalakshmi")
which <- GRanges("chrI", IRanges(1, 2e5))
s <- Snapshot(c(file, file), range=which,
              currentFunction="multicoarse_coverage")

## grouping files and view by multicoarse_coverage
bfiles <- BamFileList(c(a=file, b=file))
values(bfiles) <- DataFrame(sampleGroup=factor(c("normal", "tumor")))
values(bfiles)
s <- Snapshot(bfiles, range=which,
              currentFunction="multicoarse_coverage", fac="sampleGroup")

## grouping files and view by multifine_coverage
which <- GRanges("chrI", IRanges(7e4, 7e4+8000))
s <- Snapshot(bfiles, range=which,
              currentFunction="multifine_coverage", fac="sampleGroup")

```

SnapshotFunction-class

Class "SnapshotFunction"

Description

A class to store custom reader and viewer functions for the [Snapshot](#) class.

Usage

```

SnapshotFunction(reader, viewer, limits, ...)
reader(x, ...)
viewer(x, ...)
limits(x, ...)

```

Arguments

reader	A function for reading data. The function must take a single argument (a Snapshot instance) and return a data.frame summarizing the file.
--------	---

viewer	A function for visualizing the data. The function must accept the <code>data.frame</code> created by <code>reader</code> , and return an <code>SpTrellis</code> object representing the view.
limits	An <code>integer(2)</code> indicating the minimum and maximum number of nucleotides the <code>SnapshotFunction</code> is intended to visualize. For instance, a ‘fine-scale’ viewer displaying a pileup might be appropriate at between 1000 and 50000 nucleotides.
x	An instance of <code>SnapshotFunction</code>
...	Additional arguments, currently unused.

Fields

reader: Object of class `function` for reading data from BAM files and returning a `data.frame`.
viewer: Object of class `function` for visualization that returns an `SpTrellis` object.
limits: Object of class `integer` for the limits of ranges to be visualized.

Author(s)

Martin Morgan and Chao-Jen Wong

See Also

[Snapshot](#)

Examples

```
## internally defined function
reader(ShortRead:::.fine_coverage)
viewer(ShortRead:::.fine_coverage)
limits(ShortRead:::.fine_coverage)
```

SolexaExportQA-class *Quality assessment summaries from Solexa export and realign files*

Description

This class contains a list-like structure with summary descriptions derived from visiting one or more Solexa ‘export’ or ‘realign’ files.

Objects from the Class

Objects of the class are usually produced by a `qa` method.

Slots

.srlist: Object of class “list”, containing data frames or lists of data frames summarizing the results of `qa`.

Extends

Class "[SRList](#)", directly. Class "[.QA](#)", directly. Class "[.SRUtil](#)", by class "SRList", distance 2. Class "[.ShortReadBase](#)", by class ".QA", distance 2.

Methods

Accessor methods are inherited from the [SRList](#) class.

Additional methods defined on this class are:

report signature(`x="SolexaExportQA", ..., dest=tempfile(), type="html"`): produces HTML files summarizing QA results. `dest` should be a directory.

report signature(`x="SolexaExportQA", ..., dest=tempfile(), type="pdf"`): (deprecated; use `type="html"` instead) produces a pdf file summarizing QA results. `dest` should be a file.

report signature(`x="SolexaRealignQA", ..., dest=tempfile(), type="html"`): produces HTML files summarizing QA results. `dest` should be a directory.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[qa](#).

Examples

```
showClass("SolexaExportQA")
```

SolexaIntensity	<i>Construct objects of class "SolexaIntensity" and "SolexaIntensityInfo"</i>
-----------------	---

Description

This function constructs objects of [SolexaIntensity](#) and [SolexaIntensityInfo](#). It will often be more convenient to create these objects using parsers such as [readIntensities](#).

Usage

```
SolexaIntensity(intensity=array(0, c(0, 0, 0)),
               measurementError=array(0, c(0, 0, 0)),
               readInfo=SolexaIntensityInfo(
                 lane=integer(nrow(intensity))),
               ...)
SolexaIntensityInfo(lane=integer(0),
                   tile=integer(0)[seq_along(lane)],
                   x=integer(0)[seq_along(lane)],
                   y=integer(0)[seq_along(lane)])
```

Arguments

intensity	A matrix of image intensity values. Successive columns correspond to nucleotides A, C, G, T; four successive columns correspond to each cycle. Typically, derived from "_int.txt" files.
measurementError	As intensity, but measuring standard error. Usually derived from "_nse.txt" files.
readInfo	An object of class AnnotatedDataFrame, containing information described by SolexaIntensityInfo.
lane	An integer vector giving the lane from which each read is derived.
tile	An integer vector giving the tile from which each read is derived.
x	An integer vector giving the tile-local x coordinate of the read from which each read is derived.
y	An integer vector giving the tile-local y coordinate of the read from which each read is derived.
...	Additional arguments, not currently used.

Value

An object of class [SolexaIntensity](#), or SolexaIntensityInfo.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[SolexaIntensity](#).

SolexaIntensity-class *Classes "SolexaIntensity" and "SolexaIntensityInfo"*

Description

Instances of [Intensity](#) and [IntensityInfo](#) for representing image intensity data from Solexa experiments.

Objects from the Class

Objects can be created by calls to SolexaIntensityInfo or SolexaIntensity, or more usually readIntensities.

Slots

Object of `SolexaIntensity` have slots:

`readInfo`: Object of class `"SolexaIntensityInfo"` representing information about each read.

`intensity`: Object of class `"ArrayIntensity"` containing an array of intensities with dimensions read, base, and cycle. Nucleotide are A, C, G, T for each cycle.

`measurementError`: Object of class `"ArrayIntensity"` containing measurement errors for each read, cycle, and base, with dimensions like that for `intensity`.

`.hasMeasurementError`: Object of class `"ScalarLogical"` used internally to indicate whether measurement error information is included.

Object of `SolexaIntensityInfo`

data Object of class `"data.frame"`, inherited from `AnnotatedDataFrame`.

varMetadata Object of class `"data.frame"`, inherited from `AnnotatedDataFrame`.

dimLabels Object of class `"character"`, inherited from `AnnotatedDataFrame`.

`.__classVersion__` Object of class `"Versions"`, inherited from `AnnotatedDataFrame`.

.init Object of class `"ScalarLogical"`, used internally to indicate whether the user initialized this object.

Extends

Class `SolexaIntensity`:

Class `"Intensity"`, directly. Class `".ShortReadBase"`, by class `"Intensity"`, distance 2.

Class `SolexaIntensityInfo`:

Class `"AnnotatedDataFrame"`, directly Class `"IntensityInfo"`, directly Class `"Versioned"`, by class `"AnnotatedDataFrame"`, distance 2 Class `".ShortReadBase"`, by class `"IntensityInfo"`, distance 2 Class `"IntensityInfo"`, directly.

Methods

Class `"SolexaIntensity"` inherits accessor and display methods from class `Intensity`. Additional methods include:

[`signature(x = "SolexaIntensity", i="ANY", j="ANY", k="ANY")`:

Selects the `ith` read, `jth` nucleotide, and `kth` cycle. Selection is coordinated across `intensity`, `measurement error`, and `read information`.

Class `"SolexaIntensityInfo"` inherits accessor, subsetting, and display methods from class `IntensityInfo` and `AnnotatedDataFrame`.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[readIntensities](#)

Examples

```
showClass("SolexaIntensity")
sp <- SolexaPath(system.file(extdata, package=ShortRead))
int <- readIntensities(sp)
int # SolexaIntensity
readInfo(int) # SolexaIntensityInfo
int[1:5,,] # read 1:5
```

SolexaPath-class	<i>"SolexaPath" class representing a standard output file hierarchy</i>
------------------	---

Description

Solexa produces a hierarchy of output files. The content of the hierarchy varies depending on analysis options. This class represents a standard class hierarchy, constructed by searching a file hierarchy for appropriately named directories.

Objects from the Class

Objects from the class are created by calls to the constructor:

```
SolexaPath(experimentPath, dataPath=.solexaPath(experimentPath, "Data"),
```

experimentPath character(1) object pointing to the top-level directory of a Solexa run, e.g., /home/solexa/user/080220_HWI-EAS88_0004. This is the only required argument

dataPath (optional) Solexa 'Data' folder .

scanPath (optional) Solexa GoldCrest image scan path.

imageAnalysisPath (optional) Firecrest image analysis path.

baseCallPath (optional) Bustard base call path.

analysisPath (optional) Gerald analysis pipeline path.

... Additional arguments, unused by currently implemented methods.

verbose=FALSE (optional) logical vector which, when TRUE results in warnings if paths do not exist.

All paths must be fully-specified.

Slots

SolexaPath has the following slots, containing either a fully specified path to the corresponding directory (described above) or NA if no appropriate directory was discovered.

basePath See experimentPath, above.

dataPath See above.

scanPath See above.

imageAnalysisPath See above.

baseCallPath See above.

analysisPath See above.

Extends

Class ".Solexa", directly. Class ".ShortReadBase", by class ".Solexa", distance 2.

Methods

Transforming methods include:

readIntensities signature(dirPath = "SolexaPath", pattern=character(0), run, ...):
Use imageAnalysisPath(sp)[run] as the directory path(s) and pattern=character(0) as the pattern for discovering Solexa intensity files. See [readIntensities, character-method](#) for additional parameters.

readPrb signature(dirPath = "SolexaPath", pattern=character(0), run, ...):
Use baseCallPath(dirPath)[run] as the directory path(s) and pattern=character(0) as the pattern for discovering Solexa 'prb' files, returning a [SFastqQuality](#) object containing the maximum qualities found for each base of each cycle.
The ... argument may include the named argument as. This influences the return value, as explained on the [readPrb, character-method](#) page.

readFasta signature(dirPath, pattern = character(0), ..., nrec=-1L, skip=0L):
Use analysisPath(dirPath)[run] as the directory path(s) for discovering fasta-formatted files, returning a [ShortRead](#) object. The default method reads *all* files into a single object.

readFastq signature(dirPath = "SolexaPath", pattern = ".*_sequence.txt", run, ..., qualityType="SFastqQ"):
Use analysisPath(dirPath)[run] as the directory path(s) and pattern=".*_sequence.txt" as the pattern for discovering fastq-formatted files, returning a [ShortReadQ](#) object. The default method reads *all* sequence files into a single object.

readBaseQuality signature(dirPath = "SolexaPath", seqPattern = ".*_seq.txt", prbPattern = "s_[1-8]_prb"):
Use baseCallPath(dirPath)[run] as the directory path(s) and seqPattern=".*_seq.txt" as the pattern for discovering base calls and prbPattern=".*_prb.txt" as the pattern for discovering quality scores. Note that the default method reads *all* base call and quality score files into a single object; often one will want to specify a pattern for each lane.

readQseq signature(directory="SolexaPath", pattern=".*_qseq.txt.*", run, ..., filtered=FALSE):
Use analysisPath(dirPath)[run] as the directory path and pattern=".*_qseq.txt.*" as the pattern for discovering read and quality scores in Solexa 'qseq' files. Data from *all* files are read into a single object; often one will want to specify a pattern for each lane. Details are as for [readQseq, character-method](#).

readAligned signature(`dirPath = "SolexaPath"`, `pattern = ".*_export.txt.*"`, `run, ...`, `filter=srFilter()`)

Use `analysisPath(dirPath)[run]` as the directory path and `pattern=".*_export.txt"` as the pattern for discovering Eland-aligned reads in the Solexa 'export' file format. Note that the default method reads *all* aligned read files into a single object; often one will want to specify a pattern for each lane. Use an object of [SRFilter](#) to select specific chromosomes, strands, etc.

qa signature(`dirPath="SolexaPath"`, `pattern="character(0)"`, `run, ...`):

Use `analysisPath(dirPath)[run]` as the directory path(s) and `pattern=".*_export.txt"` as the pattern for discovering Solexa export-formatted files, returning a [SolexaExportQA](#) object summarizing quality assessment. If `Rmpi` or `parallel` has been initiated, quality assessment calculations are distributed across available nodes or cores (one node per export file.)

report signature(`x, ...`, `dest=tempfile()`, `type="pdf"`): Use `qa(x, ...)` to generate quality assessment measures, and use these to generate a quality assessment report at location `dest` of type `type` (e.g., 'pdf').

SolexaSet signature(`path = "SolexaPath"`): create a [SolexaSet](#) object based on `path`.

Additional methods include:

show signature(`object = "SolexaPath"`): briefly summarize the file paths of `object`. The `experimentPath` is given in full; the remaining paths are identified by their leading characters.

detail signature(`x = "SolexaPath"`): summarize file paths of `x`. All file paths are presented in full.

Author(s)

Martin Morgan

Examples

```
showClass("SolexaPath")
showMethods(class="SolexaPath", where=getNamespace("ShortRead"))
sf <- system.file("extdata", package="ShortRead")
sp <- SolexaPath(sf)
sp
readFastq(sp, pattern="s_1_sequence.txt")
## Not run:
nfiles <- length(list.files(analysisPath(sp), "s_[1-8]_export.txt"))
library(Rmpi)
mpi.spawn.Rslaves(nslaves=nfiles)
report(qa(sp))

## End(Not run)
## Not run:
nfiles <- length(list.files(analysisPath(sp), "s_[1-8]_export.txt"))
library(parallel)
options(srapply_fapply="parallel")
report(qa(sp))

## End(Not run)
```

SolexaSet-class	<i>"SolexaSet" coordinating Solexa output locations with sample annotations</i>
-----------------	---

Description

This class coordinates the file hierarchy produced by the Solexa ‘pipeline’ with annotation data contained in an [AnnotatedDataFrame](#) (defined in the **Biobase** package).

Objects from the Class

Objects can be created from the constructor:

```
SolexaSet(path, ...).
```

path A character(1) vector giving the fully-qualified path to the root of the directory hierarchy associated with each Solexa flow cell, or an object of class [SolexaPath](#) (see [SolexaPath](#) for this method).

... Additional arguments, especially [laneDescription](#), an [AnnotatedDataFrame](#) describing the content of each of the 8 lanes in the Solexa flow cell.

Slots

SolexaSet has the following slots:

solexaPath: Object of class "SolexaPath".

laneDescription: Object of class "AnnotatedDataFrame", containing information about the samples in each lane of the flow cell.

Extends

Class "[.Solexa](#)", directly. Class "[.ShortReadBase](#)", by class ".Solexa", distance 2.

Methods

solexaPath signature(object = "SolexaSet"): Return the directory paths present when this object was created as a [SolexaPath](#).

laneNames signature(object = "SolexaSet"): Return the names of each lane in the flow cell, currently names are simply 1:8.

show signature(object = "SolexaSet"): Briefly summarize the experiment path and lane description of the Solexa set.

detail signature(x = "SolexaSet"): Provide additional detail on the Solexa set, including the content of `solexaPath` and the `pData` and `varMetadata` of `laneDescription`.

Methods transforming SolexaSet objects include:

readAligned signature(dirPath = "SolexaSet", pattern = ".*_export.txt", run, ..., filter=srFilter()):

Use analysisPath(solexaPath(dirPath))[run] as the directory path(s) and pattern=".*_export.txt" as the pattern for discovering Eland-aligned reads in the Solexa 'export' file format. Note that the default method reads *all* aligned read files into a single object; often one will want to specify a pattern for each lane. Use an object of [SRFilter](#) to select specific chromosomes, strands, etc.

Author(s)

Martin Morgan

Examples

```
showClass("SolexaSet")
showMethods(class="SolexaSet", where=getNamespace("ShortRead"))
## construct a SolexaSet
sf <- system.file("extdata", package="ShortRead")
df <- data.frame(Sample=c("Sample 1", "Sample 2", "Sample 3", "Sample
                        4", "Center-wide control", "Sample 6", "Sample
                        7", "Sample 8"),
                Genome=c(rep("hg18", 4), "phi_plus_SNPs.txt",
                        rep("hg18", 3)))
dfMeta <- data.frame(labelDescription=c("Type of sample",
                                       "Alignment genome"))
adf <- new("AnnotatedDataFrame", data=df, varMetadata=dfMeta)
SolexaSet(sf, adf)
```

SpTrellis-class

Class "SpTrellis"

Description

A reference class to manage the trellis graphics related component of the [Snapshot](#) functionality for visualization of genomic data.

Usage

```
SpTrellis(trellis, debug_enabled=FALSE)
```

Arguments

trellis A trellis object for storing the plot of the genome area being visualized.

debug_enabled logical(1) indicating whether class methods should report debugging information to the user.

Fields

trellis: Object of class `trellis` for storing the plot information.

debug_enabled logical(1) indicating whether class methods should report debugging information to the user.

Methods

zi signature(x="SpTrellis"): zoom in
zo signature(x="SpTrellis"): zoom out
right signature(x="SpTrellis"): shift to the right
left signature(x="SpTrellis"): shift to the left
restore signature(x="SpTrellis"): restore to the original plot
show signature(x="SpTrellis"): show the current plot
update signature(x="SpTrellis"): update the trellis parameters of the SpTrellis object.

Author(s)

Chao-Jen cwon2@fhcrc.org

See Also

[Snapshot](#)

Examples

```
col <- c("#66C2A5", "#FC8D62")
x = numeric(1000)
x[sample(1000, 100)] <- abs(rnorm(100))
df <- data.frame(x = c(x, -x), pos = seq(1, 1e5, length.out=1000),
                group = rep(c("positive", "negative"), each=1000))
cv <- xyplot(x ~ pos, df, group=group, type="s",
            col=col, main="yeast chrI:1 - 2e5",
            ylab="Coverage", xlab="Coordinate",
            scales=list(y=list(tck=c(1,0)),
                       x=list(rot=45, tck=c(1,0), tick.number=20)),
            panel=function(...) {
                panel.xyplot(...)
                panel.grid(h=-1, v=20)
                panel.abline(a=0, b=0, col="grey")
            })
s <- SpTrellis(cv)
s
zi(s)
zi(s)
left(s)
right(s)
zo(s)
restore(s)
```

spViewPerFeature *Tools to visualize genomic data*

Description

Use Snapshot-class to visualize a specific region of genomic data

Usage

```
spViewPerFeature(GRL, name, files, ignore.strand=FALSE,
                 multi.levels = FALSE, fac=character(0L), ...)
```

Arguments

GRL	Object GRangeList containing annotation of genomic data. It can be generated by applying exonsBy() or transcriptsBy() to a TranscriptDb instance. See examples below.
name	Character(1) specifying which element in GRL to be visualized.
files	Character() or BamFileList specifying the file(s) to be visualized. If multiple files, local metadata of the files can be hold by setting a DataFrame (values(files) <- DataFrame(...)). See examples below.
ignore.strand	Logical(1) indicating whether to ignore the strand of the genomic data.
multi.levels	Logical(1) indicating whether to plot the coverage of multiple files on different panels. If FALSE, the mean coverage of multiple files would be plotted.
fac	Character(1) indicating which column of local metadata (elementMetadata()) should be used to group the samples. Ignore
...	Arguments used for creating a Snapshot object.

Value

A Snapshot instance

Author(s)

Chao-Jen Wong <cwon2@fhcrc.org>

See Also

[Snapshot](#)

Examples

```
## Example 1
library(GenomicFeatures)
txdbFile <- system.file("extdata", "sacCer2_sgdGene.sqlite",
                        package="yeastNagalakshmi")

## either use a txdb file queried from UCSC or use existing TxDb packages.
txdb <- loadDb(txdbFile)

grl <- exonsBy(txdb, by="gene")
file <- system.file("extdata", "SRR002051.chrI-V.bam",
                    package="yeastNagalakshmi")
s <- spViewPerFeature(GRL=grl, name="YAL001C", files=file)

## Example 2
## multi-files: using BamFileList and setting up the DataFrame
## holding the phenotype data

bfiles <- BamFileList(c(a=file, b=file))
values(bfiles) <- DataFrame(sampleGroup=factor(c("normal", "tumor")))
values(bfiles)

s <- spViewPerFeature(GRL=grl, name="YAL001C",
                     files=bfiles, multi.levels=TRUE, fac="sampleGroup")
```

srapply

Apply-like function for distribution across MPI-based clusters.

Description

This lapply like function evaluates locally or, if **Rmpi** or **parallel** is loaded (and **Rmpi** workers spawned) and `options(srapply_fapply)` set appropriately (see below), across nodes in a cluster. Errors in evaluation of FUN generate warnings; results are trimmed to exclude results where the error occurs.

Usage

```
srapply(X, FUN, ..., fapply = .fapply(), reduce = .reduce(),
        USE.NAMES = FALSE, verbose = FALSE)
```

Arguments

X Tasks to be distributed. X should be an object for which lapply or sapply are defined (more precisely, `mpi.parLapply`, `mpi.parSapply`, or `mclapply`). Performance is best when these objects are relatively small, e.g., file names, compared to the work to be done on each by FUN.

FUN	A function to be applied to each element of <i>X</i> . The function must have ... or named argument <code>verbose</code> in its signature. It is best if it makes no reference to variables other than those in its argument list. or in loaded packages (the ShortRead package is available on remote nodes).
...	Additional arguments, passed to FUN.
fapply	An optional argument defining an lapply-like function to be used in partitioning <i>X</i> . See details, below.
reduce	Optional function accepting a list (the result of fapply and summarizing this. The default reports errors in function evaluation as warnings, returning the remaining values as elements of a list. See details below for additional hints.
USE.NAMES	If TRUE and if <i>X</i> is character, use <i>X</i> as names for the result unless it had names already.
verbose	Report whether evaluation is local or mpi-based; also forwarded to FUN, allowing detailed reports from remote instances.

Details

The default value for `fapply` is available with `ShortRead::fapply()`. It tests `getOption("srapply_fapply")` for value "Rmpi" or "parallel".

If **Rmpi** is indicated, `fapply` ensures that **ShortRead** is required on all workers, and then invokes `mpi.parLapply` with arguments *X*, FUN, ..., and `verbose`. The function FUN is wrapped so that errors are returned as objects of class `SRError` with type `RemoteError`. If no workers are available, the code evaluates FUN so that errors are reported as with remote evaluation.

If **parallel** is indicated, `fapply` invokes `mclapply` with arguments as for `mpi.parLapply`.

Custom reduce functions might be written as `reduce=function(lst) unlist(lst, use.names=TRUE)`.

Value

The returned value depends on the value of `reduce`, but by default is a list with elements containing the results of FUN applied to each of *X*. Evaluations resulting in an error have been removed, and a warning generated.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
## ... or verbose required in argument,
srapply(1:10, function(i, ...) i)
## collapse result to vector
srapply(1:10, function(i, ...) i, reduce=unlist)
x <- srapply(1:10, function(i, ...) {
  if (runif(1)<.2) stop("oops") else i
})
length(x) ## trimmed to exclude errors
```

`srdistance`*Edit distances between reads and a small number of short references*

Description

`srdistance` calculates the edit distance from each read in `pattern` to each read in `subject`. The underlying algorithm [pairwiseAlignment](#) is only efficient when both reads are short, and when the number of subject reads is small.

Usage

```
srdistance(pattern, subject, ...)
```

Arguments

<code>pattern</code>	An object of class <code>DNAStrngSet</code> containing reads whose edit distance is desired.
<code>subject</code>	A short character vector, <code>DNAStrng</code> or (small) <code>DNAStrngSet</code> to serve as reference.
<code>...</code>	additional arguments, forward to <code>srapply</code> .

Details

The underlying algorithm performs pairwise alignment from each read in `pattern` to each sequence in `subject`. The return value is a list of numeric vectors of distances, one list element for each sequence in `subject`. The vector in each list element contains for each read in `pattern` the edit distance from the read to the corresponding subject. The weight matrix and gap penalties used to calculate the distance are structured to weight base substitutions and single base insert/deletions equally. Edit distance between known and ambiguous (e.g., N) nucleotides, or between ambiguous nucleotides, are weighted as though each possible nucleotide in the ambiguity were equally likely.

Value

A list of length equal to that of `subject`. Each element is a numeric vector equal to the length of `pattern`, with values corresponding to the minimum distance between between the corresponding `pattern` and `subject` sequences.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[pairwiseAlignment](#)

Examples

```
sp <- SolexaPath(system.file("extdata", package="ShortRead"))
aln <- readAligned(sp, "s_2_export.txt")
polyA <- polyn("A", 35)
polyT <- polyn("T", 35)

d1 <- srdistance(clean(sread(aln)), polyA)
d2 <- srdistance(sread(aln), polyA)
d3 <- srdistance(sread(aln), c(polyA, polyT))
```

srduplicated

Order, sort, and find duplicates in XStringSet objects

Description

These generics order, rank, sort, and find duplicates in short read objects, including fastq-encoded qualities. `srrorder`, `srrank` and `srsort` differ from the default functions `rank`, `order` and `sort` in that sorting is based on an internally-defined order rather than, e.g., the order implied by `LC_COLLATE`.

Usage

```
srrorder(x, ...)
srrank(x, ...)
srsort(x, ...)
srduplicated(x, ...)
```

Arguments

`x` The object to be sorted, ranked, ordered, or to have duplicates identified; see the examples below for objects for which methods are defined.

`...` Additional arguments available for use by methods; usually ignored.

Details

Unlike `sort` and friends, the implementation does not preserve order of duplicated elements. Like `duplicated`, one element in each set of duplicates is marked as `FALSE`.

`srrank` settles ties using the “min” criterion described in [rank](#), i.e., identical elements are ranked equal to the rank of the first occurrence of the sorted element.

The following methods are defined, in addition to methods described in class-specific documentation:

srsort signature(`x = "XStringSet"`):

srrorder signature(`x = "XStringSet"`):

srduplicated signature(`x = "XStringSet"`):

Apply `srrorder`, `srrank`, `srsort`, `srduplicated` to `XStringSet` objects such as those returned by [sread](#).

srsort signature(x = "ShortRead"):

srorder signature(x = "ShortRead"):

srduplicated signature(x = "ShortRead"):

Apply srorder, srrank, srsort, srduplicated to [XStringSet](#) objects to the sread component of [ShortRead](#) and derived objects.

Value

The functions return the following values:

srorder	An integer vector the same length as x, containing the indices that will bring x into sorted order.
srrank	An integer vector the same length as x, containing the rank of each sequence when sorted.
srsort	An instance of x in sorted order.
srduplicated	A logical vector the same length as x indicating whether the indexed element is already present. Note that, like duplicated, subsetting x using the result returned by !srduplicated(x) includes one representative from each set of duplicates.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
showMethods("srsort")
showMethods("srorder")
showMethods("srduplicated")

sp <- SolexaPath(system.file(extdata, package=ShortRead))
rfq <- readFastq(analysisPath(sp), pattern="s_1_sequence.txt")

sum(srduplicated(sread(rfq)))
srsort(sread(rfq))
srsort(quality(rfq))
```

srFilter

Functions for user-created and built-in ShortRead filters

Description

These functions create user-defined (srFilter) or built-in instances of [SRFilter](#) objects. Filters can be applied to objects from [ShortRead](#), returning a logical vector to be used to subset the objects to include only those components satisfying the filter.

Usage

```

srFilter(fun, name = NA_character_, ...)
## S4 method for signature missing
srFilter(fun, name=NA_character_, ...)
## S4 method for signature function
srFilter(fun, name=NA_character_, ...)

compose(filt, ..., .name)

idFilter(regex=character(0), fixed=FALSE, exclude=FALSE,
         .name="idFilter")
chromosomeFilter(regex=character(0), fixed=FALSE, exclude=FALSE,
                 .name="ChromosomeFilter")
positionFilter(min=-Inf, max=Inf, .name="PositionFilter")
strandFilter(strandLevels=character(0), .name="StrandFilter")
occurrenceFilter(min=1L, max=1L,
                 withSread=c(TRUE, FALSE, NA),
                 duplicates=c("head", "tail", "sample", "none"),
                 .name=.occurrenceName(min, max, withSread,
                                       duplicates))
nFilter(threshold=0L, .name="CleanNFilter")
polynFilter(threshold=0L, nuc=c("A", "C", "T", "G", "other"),
            .name="PolyNFilter")
dustyFilter(threshold=Inf, batchSize=NA, .name="DustyFilter")
srdistanceFilter(subject=character(0), threshold=0L,
                 .name="SRDistanceFilter")
alignQualityFilter(threshold=0L, .name="AlignQualityFilter")
alignDataFilter(expr=expression(), .name="AlignDataFilter")

```

Arguments

fun	An object of class function to be used as a filter. fun must accept a single named argument x, and is expected to return a logical vector such that x[fun(x)] selects only those elements of x satisfying the conditions of fun
name	A character(1) object to be used as the name of the filter. The name is useful for debugging and reference.
filt	A SRFilter object, to be used with additional arguments to create a composite filter.
.name	An optional character(1) object used to over-ride the name applied to default filters.
regex	Either character(0) or a character(1) regular expression used as grep(regex, chromosome(x)) to filter based on chromosome. The default (character(0)) performs no filtering
fixed	logical(1) passed to grep, influencing how pattern matching occurs.
exclude	logical(1) which, when TRUE, uses regex to exclude, rather than include, reads.

min	numeric(1)
max	numeric(1). For positionFilter, min and max define the closed interval in which position must be found $\text{min} \leq \text{position} \leq \text{max}$. For occurrenceFilter, min and max define the minimum and maximum number of times a read occurs after the filter.
strandLevels	Either character(0) or character(1) containing strand levels to be selected. ShortRead objects have standard strand levels NA, "+", "-", "*", with NA meaning strand information not available and "*" meaning strand information not relevant.
withSread	A logical(1) indicating whether uniqueness includes the read sequence (withSread=TRUE), is based only on chromosome, position, and strand (withSread=FALSE), or only the read sequence (withSread=NA), as described for occurrenceFilter below..
duplicates	Either character{1}, a function name, or a function taking a single argument. Influence how duplicates are handled, as described for occurrenceFilter below.
threshold	A numeric(1) value representing a minimum (srdistanceFilter, alignQualityFilter) or maximum (nFilter, polynFilter, dustyFilter) criterion for the filter. The minima and maxima are closed-interval (i.e., $x \geq \text{threshold}$, $x \leq \text{threshold}$ for some property x of the object being filtered).
nuc	A character vector containing IUPAC symbols for nucleotides or the value "other" corresponding to all non-nucleotide symbols, e.g., N.
batchSize	NA or an integer(1) vector indicating the number of DNA sequences to be processed simultaneously by dustyFilter. By default, all reads are processed simultaneously. Smaller values use less memory but are computationally less efficient.
subject	A character() of any length, to be used as the corresponding argument to srdistance .
expr	A expression to be evaluated with <code>pData(alignData(x))</code> .
...	Additional arguments for subsequent methods; these arguments are not currently used.

Details

srFilter allows users to construct their own filters. The fun argument to srFilter must be a function accepting a single argument x and returning a logical vector that can be used to select elements of x satisfying the filter with `x[fun(x)]`

The signature (`fun="missing"`) method creates a default filter that returns a vector of TRUE values with length equal to `length(x)`.

compose constructs a new filter from one or more existing filter. The result is a filter that returns a logical vector with indices corresponding to components of x that pass all filters. If not provided, the name of the filter consists of the names of all component filters, each separated by " o ".

The remaining functions documented on this page are built-in filters that accept an argument x and return a logical vector of `length(x)` indicating which components of x satisfy the filter.

idFilter selects elements satisfying `grep(regex, id(x), fixed=fixed)`.

chromosomeFilter selects elements satisfying `grep(regex, chromosome(x), fixed=fixed)`.

positionFilter selects elements satisfying `min <= position(x) <= max`.

strandFilter selects elements satisfying `match(strand(x), strand, nomatch=0) > 0`.

occurrenceFilter selects elements that occur `>=min` and `<=max` times. `withSread` determines how reads will be treated: `TRUE` to include the sread, chromosome, strand, and position when determining occurrence, `FALSE` to include chromosome, strand, and position, and `NA` to include only sread. The default is `withSread=TRUE`. `duplicates` determines how reads with more than `max` reads are treated. `head` selects the first `max` reads of each set of duplicates, `tail` the last `max` reads, and `sample` a random sample of `max` reads. `none` removes all reads represented more than `max` times. The user can also provide a function (as used by `tapply`) of a single argument to select amongst reads.

nFilter selects elements with fewer than `threshold` N symbols in each element of `sread(x)`.

polynFilter selects elements with fewer than `threshold` copies of any nucleotide indicated by `nuc`.

dustyFilter selects elements with high sequence complexity, as characterized by their `dustyScore`. This emulates the `dust` command from WindowMaker software. Calculations can be memory intensive; use `batchSize` to process the argument to `dustyFilter` in batches of the specified size.

srDistanceFilter selects elements at an edit distance greater than `threshold` from all sequences in `subject`.

alignQualityFilter selects elements with `alignQuality(x)` greater than `threshold`.

alignDataFilter selects elements with `pData(alignData(x))` satisfying `expr`. `expr` should be formulated as though it were to be evaluated as `eval(expr, pData(alignData(x)))`.

Value

srFilter returns an object of `SRFilter`.

Built-in filters return a logical vector of `length(x)`, with `TRUE` indicating components that pass the filter.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[SRFilter](#).

Examples

```
sp <- SolexaPath(system.file("extdata", package="ShortRead"))
aln <- readAligned(sp, "s_2_export.txt") # Solexa export file, as example

# a chromosome 5 filter
filt <- chromosomeFilter("chr5.fa")
aln[filt(aln)]
# filter during input
readAligned(sp, "s_2_export.txt", filter=filt)
```

```

# x- and y- coordinates stored in alignData, when source is SolexaExport
xy <- alignDataFilter(expression(abs(x-500) > 200 & abs(y-500) > 200))
aln[xy(aln)]

# both filters as a single filter
chr5xy <- compose(filt, xy)
aln[chr5xy(aln)]

# both filters as a collection
filters <- c(filt, xy)
subsetByFilter(aln, filters)
summary(filters, aln)

# read, chromosome, strand, position tuples occurring exactly once
aln[occurrenceFilter(withSread=TRUE, duplicates="none")(aln)]
# reads occurring exactly once
aln[occurrenceFilter(withSread=NA, duplicates="none")(aln)]
# chromosome, strand, position tuples occurring exactly once
aln[occurrenceFilter(withSread=FALSE, duplicates="none")(aln)]

# custom filter: minimum calibrated base call quality >20
goodq <- srFilter(function(x) {
  apply(as(quality(x), "matrix"), 1, min, na.rm=TRUE) > 20
}, name="GoodQualityBases")
goodq
aln[goodq(aln)]

```

SRFilter-class

"SRFilter" for representing functions operating on ShortRead objects

Description

Objects of this class are functions that, when provided an appropriate object from the ShortRead package, return logical vectors indicating which parts of the object satisfy the filter criterion.

A number of filters are built-in (described below); users are free to create their own filters, using the `srFilter` function.

Objects from the Class

Objects can be created through `srFilter` (to create a user-defined filter) or through calls to constructors for predefined filters, as described on the `srFilter` page.

Slots

.Data: Object of class "function" taking a single named argument `x` corresponding to the ShortRead object that the filter will be applied to. The return value of the filter function is expected to be a logical vector that can be used to subset `x` to include those elements of `x` satisfying the filter.

name: Object of class "ScalarCharacter" representing the name of the filter. The name is useful for suggesting the purpose of the filter, and for debugging failed filters.

Extends

Class "[function](#)", from data part. Class "[.SRUtil](#)", directly. Class "[OptionalFunction](#)", by class "function", distance 2. Class "[PossibleMethod](#)", by class "function", distance 2.

Methods

srFilter signature(fun = "SRFilter"): Return the function representing the underlying filter; this is primarily for interactive use to understanding filter function; usually the filter is invoked as a normal function call, as illustrated below

name signature(x = "SRFilter"): Return, as a ScalarCharacter, the name of the function.

show signature(object = "SRFilter"): display a brief summary of the filter

coerce signature(from = "SRFilter", to = "FilterRules"): Coerce a filter to a [FilterRules](#) object of length one.

c signature(x = "SRFilter", ...): Combine filters into a single [FilterRules](#) object.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

[srFilter](#) for predefined and user-defined filters.

Examples

```
## see ?srFilter
```

SRFilterResult-class *"SRFilterResult" for SRFilter output and statistics*

Description

Objects of this class are logical vectors indicating records passing the applied filter, with an associated data frame summarizing the name, input number of records, records passing filter, and logical operation used for all filters in which the result participated.

Usage

```
SRFilterResult(x = logical(), name = NA_character_,
  input = length(x), passing = sum(x), op = NA_character_)
## S4 method for signature SRFilterResult,SRFilterResult
Logic(e1, e2)
## S4 method for signature SRFilterResult
name(x, ...)
stats(x, ...)
## S4 method for signature SRFilterResult
show(object)
```

Arguments

<code>x</code> , <code>object</code> , <code>e1</code> , <code>e2</code>	For <code>SRFilterResult</code> , <code>logical()</code> indicating records that passed filter or, for others, an instance of <code>SRFilterResult</code> class.
<code>name</code>	<code>character()</code> indicating the name by which the filter is to be referred. Internally, <code>name</code> , <code>input</code> , <code>passing</code> , and <code>op</code> may all be vectors representing columns of a <code>data.frame</code> summarizing the application of successive filters.
<code>input</code>	<code>integer()</code> indicating the length of the original input.
<code>passing</code>	<code>integer()</code> indicating the number of records passing the filter.
<code>op</code>	<code>character()</code> indicating the logical operation, if any, associated with this filter.
<code>...</code>	Additional arguments, unused in methods documented on this page.

Objects from the Class

Objects can be created through `SRFilterResult`, but these are automatically created by the application of `srFilter` instances.

Slots

`.Data`: Object of class "logical" indicating records that passed the filter.

`name`: Object of class "ScalarCharacter" representing the name of the filter whose results are summarized. The name is either the actual name of the filter, or a combination of filter names and logical operations when the outcome results from application of several filters in a single logical expression.

`stats`: Object of class "data.frame" summarizing the name, input number of records, records passing filter, and logical operation used for all filters in which the result participated. The `data.frame` rows correspond either to single filters, or to logical combinations of filters.

Extends

Class "`logical`", from data part. Class "`.SRUtil`", directly. Class "`vector`", by class "logical", distance 2. Class "`atomic`", by class "logical", distance 2. Class "`vectorORfactor`", by class "logical", distance 3.

Methods

Logic signature(e1 = "SRFilterResult", e2 = "SRFilterResult"): logic operations on filters.

! signature(x = "SRFilterResult"): Negate the outcome of the current filter results

name signature(x = "SRFilterResult"): The name of the filter that the results are based on.

stats signature(x = "SRFilterResult"): a data.frame as described in the 'Slots' section of this page.

show signature(object = "SRFilterResult"): summary of filter results.

Author(s)

Martin Morgan <mailto:mtmorgan@fhcrc.org>

See Also

[srFilter](#)

Examples

```
fa <- srFilter(function(x) x %% 2 == 0, "Even")
fb <- srFilter(function(x) x %% 2 == 1, "Odd")
```

```
x <- 1:10
fa(x) | fb(x)
fa(x) & fb(x)
!(fa(x) & fb(x))
```

SRSet-class

A base class for Roche experiment-wide data

Description

This class coordinates phenotype (sample) and sequence data, primarily as used on the Roche platform.

Conceptually, this class has reads from a single experiment represented as a long vector, ordered by sample. The readCount slot indicates the number of reads in each sample, so that the sum of readCount is the total number of reads in the experiment. The readIndex field is a light-weight indicator of which reads from all those available that are currently referenced by the SRSet.

Objects from the Class

Objects of this class are not usually created directly, but instead are created by a derived class, e.g., [RocheSet](#).

Slots

sourcePath: Object of class "ExperimentPath", containing the directory path where sequence files can be found.

readIndex: Object of class "integer" indicating specific sequences included in the experiment.

readCount: Object of class "integer" containing the number of reads in each sample included in the experiment. The sum of this vector is the total number of reads.

phenoData: Object of class "AnnotatedDataFrame" describing each sample in the experiment. The number of rows of phenoData equals the number of elements in readCount.

readData: Object of class "AnnotatedDataFrame" containing annotations on all reads.

Extends

Class "[.ShortReadBase](#)", directly.

Methods

experimentPath signature(object = "SRSet"): return the [ExperimentPath](#) associated with this object.

phenoData signature(object = "SRSet"): return the [phenoData](#) associated with this object.

readCount signature(object="SRSet"):

readIndex signature(object="SRSet"):

readData signature(object="SRSet"):

sourcePath signature(object="SRSet"): Retrieve the corresponding slot from object.

show signature(object = "SRSet"): display the contents of this object.

detail signature(x = "SRSet"): provide more extensive information on the object.

Author(s)

Michael Lawrence <mflawrence@fhcrc.org>

Examples

```
showClass("SRSet")
```

 SRUtil-class

 ".SRUtil" and related classes

Description

These classes provide important utility functions in the **ShortRead** package, but may occasionally be seen by the user and are documented here for that reason.

Objects from the Class

Utility classes include:

- `.SRUtil-class` a virtual base class from which all utility classes are derived.
- `SRError-class` created when errors occur in **ShortRead** package code.
- `SRWarn-class` created when warnings occur in **ShortRead** package code
- `SRList-class` representing a list (heterogeneous collection) of objects.
- `SRVector-class` representing a vector (homogeneous collection, i.e., all elements of the same class) of objects.

Objects from these classes are not normally constructed by the user. However, constructors are available, as follows.

`SRError(type, fmt, ...)`, `SRWarn(type, fmt, ...)`:

type character(1) vector describing the type of the error. `type` must come from a pre-defined list of types.

fmt a `sprintf`-style format string for the message to be reported with the error.

... additional arguments to be interpolated into `fmt`.

`SRList(...)`

... elements of any type or length to be placed into the `SRList`. If the length of **...** is 1 and the argument is a list, then the list itself is placed into `SRList`.

`SRVector(..., vclass)`

... elements all satisfying an `is` relationship with `vclass`, to be placed in `SRVector`.

vclass the class to which all elements in **...** belong. If `vclass` is missing and `length(list(...))` is greater than zero, then `vclass` is taken to be the class of the first argument of **...**

`SRVector` errors:

SRVectorClassDisagreement this error occurs when not all arguments **...** satisfy an `'is'` relationship with `vclass`.

Slots

`SRError` and `SRWarn` have the following slots defined:

.type: Object of class "character" containing the type of error or warning. `.type` must come from a pre-defined list of types, see, e.g., `ShortRead:::SRError_types`.

.message: Object of class "character" containing a detailed message describing the error or warning.

`SRList` has the following slot defined:

.srlist: Object of class "list" containing the elements in the list.

`SRVector` extends `SRList`, with the following additional slot:

vclass: Object of class "character" naming the type of object all elements of `SRVector` must be.

Methods

Accessors are available for all slots, and have the same name as the slot, e.g., `vclass` to access the `vclass` slot of `SRVector`. Internal slots (those starting with `'` also have accessors, but these are not exported e.g., `ShortRead::: .type`).

`SRList` has the following methods:

- length** signature(`x = "SRList"`): return the (`integer(1)`) length of the `SRList`.
- names** signature(`x = "SRList"`): return a character vector of list element names. The length of the returned vector is the same as the length of `x`.
- names<-** signature(`x = "SRList"`, `value = "character"`): assign value as names for members of `x`.
- [** signature(`x = "SRList"`, `i = "ANY"`, `j = "missing"`): subset the list using standard R list subset paradigms.
- [[** signature(`x = "SRList"`, `i = "ANY"`, `j = "missing"`): select element `'i'` from the list, using standard R list selection paradigms.
- lapply** signature(`X = "SRList"`, `FUN="ANY"`): apply a function to all elements of `X`, with additional arguments interpreted as with [lapply](#).
- sapply** signature(`X = "SRList"`): apply a function to all elements of `X`, simplifying the result if possible. Additional arguments interpreted as with [sapply](#).
- show** signature(`object = "SRList"`): display an informative summary of the object content, including the length of the list represented by object.
- detail** signature(`x = "SRList"`): display a more extensive version of the object, as one might expect from printing a standard list in R.

`SRVector` inherits all methods from `SRList`, and has the following additional methods:

- show** signature(`object = "SRVector"`): display an informative summary of the object content, e.g., the vector class (`vclass`) and length.
- detail** signature(`x = "SRVector"`): display a more extensive version of the object, as one might expect from a printing a standard R list.

Author(s)

Martin Morgan

Examples

```
getClass(".SRUtil", where=getNamespace("ShortRead"))
ShortRead:::SRError_types
ShortRead:::SRWarn_types

detail(SRList(1:5, letters[1:5]))

tryCatch(SRVector(1:5, letters[1:5]),
         SRVectorClassDisagreement=function(err) {
           cat("caught:", conditionMessage(err), "\n")
         })
```

tables	<i>Summarize XStringSet read frequencies</i>
--------	--

Description

This generic summarizes the number of times each sequence occurs in an `XStringSet` instance.

Usage

```
tables(x, n=50, ...)
```

Arguments

x	An object for which a tables method is defined.
n	An integer(1) value determining how many named sequences will be present in the top portion of the return value.
...	Additional arguments available to methods

Details

Methods of this generic summarize the frequency with which each read occurs. There are two components to the summary. The reads are reported from most common to least common; typically a method parameter controls how many reads to report. Methods also return a pair of vectors describing how many reads were represented 1, 2, ... times.

The following methods are defined, in addition to methods described in class-specific documentation:

tables signature(x= "XStringSet", n = 50): Apply tables to the XStringSet x.

Value

A list of length two.

top	A named integer vector. Names correspond to sequences. Values are the number of times the corresponding sequence occurs in the XStringSet. The vector is sorted in decreasing order; methods typically include a parameter specifying the number of sequences to return.
distribution	a data.frame with two columns. n0ccurrences is the number of times any particular sequence is represented in the set (1, 2, ...). nReads is the number of reads with the corresponding occurrence.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
showMethods("tables")
sp <- SolexaPath(system.file("extdata", package="ShortRead"))
aln <- readAligned(sp)
tables(sread(aln), n=6)
xyplot(log10(nReads)~log10(nOccurrences),
       tables(sread(aln))$distribution)
```

trimTails

Trim ends of reads based on nucleotides or qualities

Description

These generic functions remove leading or trailing nucleotides or qualities. `trimTails` and `trimTailw` remove low-quality reads from the right end using a sliding window (`trimTailw`) or a tally of (successive) nucleotides falling at or below a quality threshold (`trimTails`). `trimEnds` takes an alphabet of characters to remove from either left or right end.

Usage

```
## S4 methods for ShortReadQ, FastqQuality, or SFastqQuality
trimTailw(object, k, a, halfwidth, ..., ranges=FALSE)
trimTails(object, k, a, successive=FALSE, ..., ranges=FALSE)
trimEnds(object, a, left=TRUE, right=TRUE, relation=c("<=", "=="),
         ..., ranges=FALSE)

## S4 method for signature BStringSet
trimTailw(object, k, a, halfwidth, ..., alphabet, ranges=FALSE)
## S4 method for signature BStringSet
trimTails(object, k, a, successive=FALSE, ...,
         alphabet, ranges=FALSE)

## S4 method for signature character
trimTailw(object, k, a, halfwidth, ..., destinations, ranges=FALSE)
## S4 method for signature character
trimTails(object, k, a, successive=FALSE, ..., destinations, ranges=FALSE)
## S4 method for signature character
trimEnds(object, a, left=TRUE, right=TRUE, relation=c("<=", "=="),
         ..., destinations, ranges=FALSE)
```

Arguments

object	An object (e.g., <code>ShortReadQ</code> and derived classes; see below to discover these methods) or character vector of fastq file(s) to be trimmed.
k	integer(1) describing the number of failing letters required to trigger trimming.

a	For trimTails and trimTailw, a character(1) with nchar(a) == 1L giving the letter at or below which a nucleotide is marked as failing. For trimEnds a character() with all nchar() == 1L giving the letter at or below which a nucleotide or quality scores marked for removal.
halfwidth	The half width (cycles before or after the current; e.g., a half-width of 5 would span 5 + 1 + 5 cycles) in which qualities are assessed.
successive	logical(1) indicating whether failures can occur anywhere in the sequence, or must be successive. If successive=FALSE, then the k'th failed letter and subsequent are removed. If successive=TRUE, the first succession of k failed and subsequent letters are removed.
left, right	logical(1) indicating whether trimming is from the left or right ends.
relation	character(1) selected from the argument values, i.e., "<=" or "==" indicating whether all letters at or below the alphabet(object) are to be removed, or only exact matches.
...	Additional arguments, perhaps used by methods.
destinations	For object of type character(), an equal-length vector of destination files. Files must not already exist.
alphabet	character() (ordered low to high) letters on which quality scale is measured. Usually supplied internally (user does not need to specify). If missing, then set to ASCII characters 0-127.
ranges	logical(1) indicating whether the trimmed object, or only the ranges satisfying the trimming condition, be returned.

Details

trimTailw starts at the left-most nucleotide, tabulating the number of cycles in a window of $2 * \text{halfwidth} + 1$ surrounding the current nucleotide with quality scores that fall at or below a. The read is trimmed at the first nucleotide for which this number $\geq k$. The quality of the first or last nucleotide is used to represent portions of the window that extend beyond the sequence.

trimTails starts at the left-most nucleotide and accumulates cycles for which the quality score is at or below a. The read is trimmed at the first location where this number $\geq k$. With successive=TRUE, failing qualities must occur in strict succession.

trimEnds examines the left, right, or both ends of object, marking for removal letters that correspond to a and relation. The trimEnds, ShortReadQ-method trims based on quality.

ShortReadQ methods operate on quality scores; use sread() and the ranges argument to trim based on nucleotide (see examples).

character methods transform one or several fastq files to new fastq files, applying trim operations based on quality scores; use filterFastq with your own filter argument to filter on nucleotides.

Value

An instance of class(object) trimmed to contain only those nucleotides satisfying the trim criterion or, if ranges=TRUE an IRanges instance defining the ranges that would trim object.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
showMethods(trimTails)

sp <- SolexaPath(system.file(extdata, package=ShortRead))
rfq <- readFastq(analysisPath(sp), pattern="s_1_sequence.txt")

## remove leading / trailing quality scores <= I
trimEnds(rfq, "I")
## remove leading / trailing Ns
rng <- trimEnds(sread(rfq), "N", relation=="=", ranges=TRUE)
narrow(rfq, start(rng), end(rng))
## remove leading / trailing Gs or Cs
trimEnds(rfq, c("G", "C"), relation=="=")
```

Utilites

Utilities for common, simple operations

Description

These functions perform a variety of simple operations.

Usage

```
polyn(nucleotides, n)
```

Arguments

nucleotides	A character vector with all elements having exactly 1 character, typically from the IUPAC alphabet.
n	An integer(1) vector.

Details

polyn returns a character vector with each element having n characters. Each element contains a single nucleotide. Thus polyn("A", 5) returns AAAAA.

Value

polyn returns a character vector of length length(nucleotide)

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

Examples

```
polyn(c("A", "N"), 35)
```

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