Package: scifer (via r-universe)

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Type Package

Title Scifer: Single-Cell Immunoglobulin Filtering of Sanger Sequences

Version 1.7.3

URL https://github.com/rodrigarc/scifer

BugReports https://github.com/rodrigarc/scifer/issues

Description Have you ever index sorted cells in a 96 or 384-well plate and then sequenced using Sanger sequencing? If so, you probably had some struggles to either check the electropherogram of each cell sequenced manually, or when you tried to identify which cell was sorted where after sequencing the plate. Scifer was developed to solve this issue by performing basic quality control of Sanger sequences and merging flow cytometry data from probed single-cell sorted B cells with sequencing data. scifer can export summary tables, 'fasta' files, electropherograms for visual inspection, and generate reports.

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Encoding UTF-8

biocViews Preprocessing, QualityControl, SangerSeq, Sequencing, Software, FlowCytometry, SingleCell

Imports dplyr, rmarkdown, data.table, Biostrings, parallel, stats, plyr, knitr, ggplot2, gridExtra, DECIPHER, stringr, sangerseqR, kableExtra, tibble, scales, rlang, flowCore, methods, basilisk, reticulate, here, utils

RoxygenNote 7.2.3

VignetteBuilder knitr

Suggests fs, BiocStyle, testthat (>= 3.0.0)

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StagedInstall no

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/scifer

RemoteRef HEAD

RemoteSha a11fe5e3d4d8cb910dc54556f319cae302778dff

Contents

`df_to_fasta` *Fasta file creation from dataframe columns and/or vectors.*

Description

Fasta file creation from dataframe columns and/or vectors.

Usage

```
df_to_fasta(
  sequence_name,
  sequence_strings,
  file_name = "sequences.fasta",
  output_dir = NULL,
  save_fasta = TRUE
)
```

Arguments

`sequence_name`	Vector containing the names for each sequence, usually a column from a data.frame. eg. df$sequence_name
`sequence_strings`	Vector containing the DNA or RNA or AA sequences, usually a column from a data.frame. eg. df$sequences
`file_name`	Output file name to be saved as a fasta file
`output_dir`	Output directory for the fasta file. Default is the working directory
`save_fasta`	Logical argument, TRUE or FALSE, to indicate if fasta files should be saved. Default is TRUE.

Value

Saves a fasta file in the desired location, and also returns the stringset as BStringSet if saved as an object.

Examples

```
## Example with vectors, default for save_fasta ir TRUE
df_to_fasta(
    sequence_name = c("myseq1", "myseq2"),
    sequence_strings = c("GATCGAT", "ATCGTAG"),
    file_name = "my_sequences.fasta",
    output_dir = "",
    save_fasta = FALSE
)
```

`fcs_plot` *Plot flow data from index sorted cells*

Description

Plot flow data from index sorted cells

Usage

```
fcs_plot(processed_fcs_list = NULL)
```

Arguments

`processed_fcs_list`
: List generated using ‘fcs_processing()‘ containing two data.frames

Value

Returns a ggplot object with a traditional flow density plot with the sorted cells and the selected thresholds for the two probes used in fcs_processing().

Examples

```
index_sort_data <- fcs_processing(
    folder_path = system.file("/extdata/fcs_index_sorting",
                              package = "scifer"),
    compensation = TRUE, plate_wells = 96,
    probe1 = "Pre.F", probe2 = "Post.F",
    posvalue_probe1 = 600, posvalue_probe2 = 400
)

fcs_plot_obj <- fcs_plot(index_sort_data)
```

fcs_processing *Extract index sorting information from flow cytometry data*

Description

Extract index sorting information from flow cytometry data

Usage

```
fcs_processing(
  folder_path = "test/test_dataset/fcs_files/",
  compensation = TRUE,
  plate_wells = 96,
  probe1 = "Pre.F",
  probe2 = "Post.F",
  posvalue_probe1 = 600,
  posvalue_probe2 = 400
)
```

Arguments

folder_path	Folder containing all the flow data index filex (.fcs). Files should be named with their sample/plate ID. eg. "E11_01.fcs"
compensation	Logical argument, TRUE or FALSE, to indicate if the index files were compensated or not. If TRUE, it will apply its compensation prior assigning specificity
plate_wells	Type of plate used for single-cell sorting. eg. "96" or "384"
probe1	Name of the first channel used for the probe or the custom name assigned to the channel in the index file. eg. "FSC.A", "FSC.H", "SSC.A","DsRed.A", "PE.Cy5_5.A", "PE.Cy7.A","BV650.A", "BV711.A","Alexa.Fluor.700.A" "APC.Cy7.A","PerCP.Cy5.5.A
probe2	Name of the second channel used for the probe or the custom name assigned to the channel in the index file. eg. "FSC.A", "FSC.H", "SSC.A","DsRed.A", "PE.Cy5_5.A", "PE.Cy7.A","BV650.A", "BV711.A","Alexa.Fluor.700.A" "APC.Cy7.A","PerCP.Cy5.5.A
posvalue_probe1	Threshold used for fluorescence intensities to be considered as positive for the first probe
posvalue_probe2	Threshold used for fluorescence intensities to be considered as positive for the second probe

Value

If saved as an object, it returns a table containing all the processed flow cytometry index files, with their fluorescence intensities for each channel and well position.

Examples

```
index_sort_data <- fcs_processing(
    folder_path = system.file("/extdata/fcs_index_sorting",
                              package = "scifer"),
    compensation = TRUE, plate_wells = 96,
    probe1 = "Pre.F", probe2 = "Post.F",
    posvalue_probe1 = 600, posvalue_probe2 = 400
)
```

---

igblast *Run IgDiscover for IgBlast using basilisk, which enables the python environment for Igblast*

Description

Run IgDiscover for IgBlast using basilisk, which enables the python environment for Igblast

Usage

```
igblast(database = "path/to/folder", fasta = "path/to/file", threads = 1)
```

Arguments

database	Vector containing the database for VDJ sequences
fasta	Vector containing the sequences, usually a column from a data.frame. eg. df$sequences
threads	Variable containing the number of cores when computing in parallel, default threads = 1

Value

Creates a data frame with the Igblast analysis where each row is the tested sequence with columns containing the results for each sequence

Examples

```
## Example with test sequences
igblast(
    database = system.file("/inst/extdata/test_fasta/KIMDB_rm", package = "scifer"),

   fasta = system.file("/inst/extdata/test_fasta/test_igblast.txt", package = "scifer"),

    threads = 1
)
```

quality_report *Generate general and individualized reports*

Description

This function uses the other functions already described to create a HTML report based on sequencing quality. Besides the HTML reports, it also creates fasta files with all the sequences and individualized sequences, in addition to a csv file with the quality scores and sequences considered as good quality.

Usage

```
quality_report(
  folder_sequences = "path/to/sanger_sequences",
  outputfile = "QC_report.html",
  output_dir = "test/",
  processors = NULL,
  folder_path_fcs = NULL,
  plot_chromatogram = FALSE,
  raw_length = 343,
  trim_start = 65,
  trim_finish = 400,
  trimmed_mean_quality = 30,
  compensation = TRUE,
  plate_wells = "96",
  probe1 = "Pre.F",
  probe2 = "Post.F",
  posvalue_probe1 = 600,
  posvalue_probe2 = 400,
  cdr3_start = 100,
  cdr3_end = 150
)
```

Arguments

folder_sequences	Full file directory for searching all ab1 files in a recursive search method. It includes all files in subfolders
outputfile	Output file name for the report generation
output_dir	Output directory for all the different output files that are generated during the report
processors	Number of processors to use, you can set to NULL to detect automatically all available processors
folder_path_fcs	Full file directory for searching all flow cytometry index files, files with .fcs extensions, in a recursive search method

plot_chromatogram
: Logical argument, TRUE or FALSE, to indicate if chromatograms should be plotted or not. Default is FALSE

raw_length
: Minimum sequence length for filtering. Default is 343 for B cell receptors

trim_start
: Starting position where the sequence should start to have a good base call accuracy. Default is 65 for B cell receptors

trim_finish
: Last position where the sequence should have a good base call accuracy. Default is 400 for B cell receptors

trimmed_mean_quality
: Minimum Phred quality score expected for an average sequence. Default is 30, which means average of 99.9% base call accuracy

compensation
: Logical argument, TRUE or FALSE, to indicate if the index files were compensated or not. If TRUE, it will apply its compensation prior assigning specificities

plate_wells
: Type of plate used for single-cell sorting. eg. "96" or "384"

probe1
: Name of the first channel used for the probe or the custom name assigned to the channel in the index file. eg. "FSC.A", "FSC.H", "SSC.A","DsRed.A", "PE.Cy5_5.A", "PE.Cy7.A","BV650.A", "BV711.A","Alexa.Fluor.700.A" "APC.Cy7.A","PerCP.Cy5.5.A

probe2
: Name of the second channel used for the probe or the custom name assigned to the channel in the index file. eg. "FSC.A", "FSC.H", "SSC.A","DsRed.A", "PE.Cy5_5.A", "PE.Cy7.A","BV650.A", "BV711.A","Alexa.Fluor.700.A" "APC.Cy7.A","PerCP.Cy5.5.A

posvalue_probe1
: Threshold used for fluorescence intensities to be considered as positive for the first probe

posvalue_probe2
: Threshold used for fluorescence intensities to be considered as positive for the second probe

cdr3_start
: Expected CDR3 starting position, that depends on your primer set. Default is position 100

cdr3_end
: Expected CDR3 end position, that depends on your primer set. Default is position 150

Value

Saves HTML reports, fasta files, csv files

Examples

```
quality_report(
    folder_sequences = system.file("extdata/sorted_sangerseq",
                                   package = "scifer"),
    outputfile = "QC-report.html",
    output_dir = "~/test",
    folder_path_fcs = system.file("/extdata/fcs_index_sorting",
                                  package = "scifer"),
    processors = 1, compensation = TRUE, plate_wells = "96",
    probe1 = "Pre.F", probe2 = "Post.F",
    posvalue_probe1 = 600, posvalue_probe2 = 400,
```

```
    cdr3_start = 100,
    cdr3_end = 150
)
```

`scifer` *Scifer: Single-Cell Immunoglobulin Filtering of Sanger Sequences*

Description

Integrating index single-cell sorted files with Sanger sequencing per plates, combining single-cell sorted data (FACS) and specificity with Sanger sequencing information.

Author(s)

Rodrigo Arcoverde Cerveira <rodrigo.arcoverdi@gmail.com>

`secondary_peaks` *Check for secondary peaks in a sangerseq object*

Description

This function finds and reports secondary peaks in a sangerseq object. It returns a table of secondary peaks, and optionally saves an annotated chromatogram and a csv file of the peak locations.

Usage

```
secondary_peaks(
  s,
  ratio = 0.33,
  output.folder = NA,
  file.prefix = "seq",
  processors = NULL
)
```

Arguments

`s`	a sangerseq s4 object from the sangerseqR package
`ratio`	Ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are not.
`output.folder`	If output.folder is NA (the default) no files are written. If a valid folder is provided, two files are written to that folder: a .csv file of the secondary peaks (see description below) and a .pdf file of the chromatogram.
`file.prefix`	If output.folder is specified, this is the prefix which will be appended to the .csv and the .pdf file. The default is "seq".
`processors`	Number of processors to use, or NULL (the default) for all available processors

Value

A list with two elements:

1. secondary.peaks: a data frame with one row per secondary peak above the ratio, and three columns: "position" is the position of the secondary peak relative to the primary sequence; "primary.basecall" is the primary base call; "secondary.basecall" is the secondary basecall.

2. read: the input sangerseq s4 object after having the makeBaseCalls() function from sangerseqR applied to it. This re-calls the primary and secondary bases in the sequence, and resets a lot of the internal data.

Examples

```
## Read abif using sangerseqR package
s4_sangerseq <- sangerseqR::readsangerseq(
    system.file("/extdata/sorted_sangerseq/E18_C1/A1_3_IgG_Inner.ab1",
                package = "scifer")
)

## Summarise using summarise_abi_file()
processed_seq <- secondary_peaks(s4_sangerseq)
```

`summarise_abi_file` *Create a summary of a single ABI sequencing file*

Description

Create a summary of a single ABI sequencing file

Usage

```
summarise_abi_file(
  seq.abif,
  trim.cutoff = 1e-04,
  secondary.peak.ratio = 0.33,
  output.folder = NA,
  prefix = "seq",
  processors = NULL
)
```

Arguments

`seq.abif`	an abif.seq s4 object from the sangerseqR package
`trim.cutoff`	the cutoff at which you consider a base to be bad. This works on a logarithmic scale, such that if you want to consider a score of 10 as bad, you set cutoff to 0.1; for 20 set it at 0.01; for 30 set it at 0.001; for 40 set it at 0.0001; and so on. Contiguous runs of bases below this quality will be removed from the start and end of the sequence. Default is 0.0001.

`secondary.peak.ratio`
: the ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are not.

`output.folder`
: If output.folder is NA (the default) no files are written. If a valid folder is provided, two files are written to that folder: a .csv file of the secondary peaks (see description below) and a .pdf file of the chromatogram.

`prefix`
: If output.folder is specified, this is the prefix which will be appended to the .csv and the .pdf file. The default is "seq".

`processors`
: Number of processors to use, or NULL (the default) for all available processors

Value

A numeric vector including:

1. raw.length: the length of the untrimmed sequence, note that this is the sequence after conversion to a sangerseq object, and then the recalling the bases with MakeBaseCalls from the sangerseqR package
2. trimmed.length: the length of the trimmed sequence, after trimming using trim.mott from this package and the parameter supplied to this function
3. trim.start: the start position of the good sequence, see trim.mott for more details
4. trim.finish: the finish position of the good sequence, see trim.mott for more details
5. raw.secondary.peaks: the number of secondary peaks in the raw sequence, called with the secondary.peaks function from this package and the parameters supplied to this function
6. trimmed.secondary.peaks: the number of secondary peaks in the trimmed sequence, called with the secondary.peaks function from this package and the parameters supplied to this function
7. raw.mean.quality: the mean quality score of the raw sequence
8. trimmed.mean.quality: the mean quality score of the trimmed sequence
9. raw.min.quality: the minimum quality score of the raw sequence
10. trimmed.min.quality: the minimum quality score of the trimmed sequence

Examples

```
## Read abif using sangerseqR package
abi_seq <- sangerseqR::read.abif(
    system.file("/extdata/sorted_sangerseq/E18_C1/A1_3_IgG_Inner.ab1",
```

```
    package = "scifer")
)

## Summarise using summarise_abi_file()
summarise_abi_file(abi_seq)
```

`summarise_quality` *Generate a summary table containing quality measurements from sanger sequencing abi files*

Description

Generate a summary table containing quality measurements from sanger sequencing abi files

Usage

```
summarise_quality(
  folder_sequences = "input_folder",
  trim.cutoff = 0.01,
  secondary.peak.ratio = 0.33,
  processors = NULL
)
```

Arguments

`folder_sequences`	Folder containing all the sanger sequencing abi/ab1 files on subfolders. Each subfolder should have have a identifiable name, matching name with fcs data. eg. "E18_01", "E23_06". The first characters of the ab1 file name should be the well location. eg. "A1-sequence1.ab1", "F8_sequence-igg.ab1"
`trim.cutoff`	Cutoff at which you consider a base to be bad. This works on a logarithmic scale, such that if you want to consider a score of 10 as bad, you set cutoff to 0.1; for 20 set it at 0.01; for 30 set it at 0.001; for 40 set it at 0.0001; and so on. Contiguous runs of bases below this quality will be removed from the start and end of the sequence. Given the high quality reads expected of most modern ABI sequencers, the defualt is 0.0001.
`secondary.peak.ratio`	Ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated, while those below the ratio are not.
`processors`	Number of processors to use, or NULL (the default) for all available processors

Value

List containing two items: * summaries: contains all the summary results from the processed abi files, * quality_scores: contains all the Phred quality score for each position.

Examples

```
sf <- summarise_quality(
    folder_sequences = system.file("extdata/sorted_sangerseq",
                                   package = "scifer"),
    secondary.peak.ratio = 0.33,
    trim.cutoff = 0.01,
    processor = 1
)
```

Index