

Package ‘awst’

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Title Asymmetric Within-Sample Transformation

Version 1.15.0

Description We propose an Asymmetric Within-Sample Transformation (AWST) to regularize RNA-seq read counts and reduce the effect of noise on the classification of samples. AWST comprises two main steps: standardization and smoothing. These steps transform gene expression data to reduce the noise of the lowly expressed features, which suffer from background effects and low signal-to-noise ratio, and the influence of the highly expressed features, which may be the result of amplification bias and other experimental artifacts.

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Encoding UTF-8

RoxygenNote 7.1.1

URL <https://github.com/drisso/awst>

BugReports <https://github.com/drisso/awst/issues>

Imports stats, methods, SummarizedExperiment

Suggests airway, ggplot2, testthat, EDASeq, knitr, BiocStyle, RefManageR, sessioninfo, rmarkdown

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|------|--|
| awst | <i>Asymmetric Within-Sample Transformation</i> |
|------|--|

Description

This function implements the asymmetric within-sample transformation described in Risso and Pagnotta (2019). The function includes two steps: a standardization step and a asymmetric win-sorization step. See details.

Usage

```
## S4 method for signature 'matrix'
awst(x, poscount = FALSE, full_quantile = FALSE, sigma0 = 0.075, lambda = 13)

## S4 method for signature 'SummarizedExperiment'
awst(
  x,
  poscount = FALSE,
  full_quantile = FALSE,
  sigma0 = 0.075,
  lambda = 13,
  expr_values = "counts",
  name = "awst"
)
```

Arguments

| | |
|---------------|---|
| x | a matrix of (possibly normalized) RNA-seq read counts or a ‘SummarizedExperiment’. |
| poscount | a logical value indicating whether positive counts only should be used for the standardization step. |
| full_quantile | a logical value indicating whether the data have been normalized with the full-quantile normalization. In this case, computations can be sped up. |
| sigma0 | a multiplicative constant to be applied to the smoothing function. |
| lambda | a parameter that controls the growth rate of the smoothing function. |
| expr_values | integer scalar or string indicating the assay that contains the matrix to use as input. |

name string specifying the name of the assay to be used to store the results of the transformation.

Details

The standardization step is based on a log-normal distribution of the high-intensity genes. Optionally, only positive counts can be used in this step (this option is especially useful for single-cell data). The winsorization step is controlled by two parameters, `sigma0` and `lambda`, which control the growth rate of the winsorization function.

Value

if 'x' is a matrix, it returns a matrix of transformed values, with genes in rows and samples in column. If 'x' is a 'SummarizedExperiment', it returns a 'SummarizedExperiment' with the transformed value in the 'name' slot.

Methods (by class)

- `matrix`: the input is a matrix of (possibly normalized) counts
- `SummarizedExperiment`: the input is a `SummarizedExperiment` with (possibly normalized) counts in one of its assays.

References

Risso and Pagnotta (2019). Within-sample standardization and asymmetric winsorization lead to accurate classification of RNA-seq expression profiles. Manuscript in preparation.

Examples

```
x <- matrix(data = rpois(100, lambda=5), ncol=10, nrow=10)
awst(x)
```

gene_filter

Gene filtering based on heterogeneity

Description

This function filters out genes that show a low heterogeneity, as measured by Shannon's entropy.

Usage

```
## S4 method for signature 'matrix'
gene_filter(
  x,
  from = min(x, na.rm = TRUE),
  to = max(x, na.rm = TRUE),
  nBins = 20,
```

```

    heterogeneity_threshold = 0.1
  )

  ## S4 method for signature 'SummarizedExperiment'
  gene_filter(
    x,
    from = min(assay(x, awst_values), na.rm = TRUE),
    to = max(assay(x, awst_values), na.rm = TRUE),
    nBins = 20,
    heterogeneity_threshold = 0.1,
    awst_values = "awst"
  )

```

Arguments

| | |
|--------------------------------------|--|
| <code>x</code> | a matrix of transformed gene expression counts (typically the results of <code>awst</code>). |
| <code>from</code> | the minimum value from which to start binning data. |
| <code>to</code> | the maximum value for the binning of the data. |
| <code>nBins</code> | the number of bins. |
| <code>heterogeneity_threshold</code> | the threshold used for the filtering. |
| <code>awst_values</code> | integer scalar or string indicating the assay that contains the awst-transformed values to use as input. |

Details

Shannon's entropy is computed on the categorized data after AWST transformation. Those genes that show a lower entropy than the predefined threshold are deemed to carry too low information to be useful for the classification of the samples, and are hence removed.

Value

if 'x' is a matrix, it returns a filtered matrix. If 'x' is a 'SummarizedExperiment', it returns a filtered 'SummarizedExperiment'

Methods (by class)

- `matrix`: the input is a matrix of awst-transformed values.
- `SummarizedExperiment`: the input is a `SummarizedExperiment` with awst-transformed values in one of its assays.

References

Risso and Pagnotta (2019). Within-sample standardization and asymmetric winsorization lead to accurate classification of RNA-seq expression profiles. Manuscript in preparation.

Examples

```
set.seed(222)
x <- matrix(rpois(75, lambda=5), ncol=5, nrow=15)
a <- awst(x)
gene_filter(a)
```

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