

# Package ‘awst’

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**Title** Asymmetric Within-Sample Transformation

**Version** 1.16.0

**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

**biocViews** Normalization, GeneExpression, RNASeq, Software, Transcriptomics, Sequencing, SingleCell

**VignetteBuilder** knitr

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**Contents**

|                       |          |
|-----------------------|----------|
| awst . . . . .        | 2        |
| gene_filter . . . . . | 3        |
| <b>Index</b>          | <b>6</b> |

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

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**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)
```

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gene\_filter

*Gene filtering based on heterogeneity*

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### 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 <a href="#">awst</a> ).         |
| <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)
```

# Index

awst, [2](#), [4](#)

awst,matrix-method (awst), [2](#)

awst,SummarizedExperiment-method  
(awst), [2](#)

gene\_filter, [3](#)

gene\_filter,matrix-method  
(gene\_filter), [3](#)

gene\_filter,SummarizedExperiment-method  
(gene\_filter), [3](#)