

# Package ‘awst’

December 18, 2024

**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.

**License** MIT + file LICENSE

**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

**git\_url** <https://git.bioconductor.org/packages/awst>

**git\_branch** devel

**git\_last\_commit** d18c8ed

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-12-18

**Author** Davide Risso [aut, cre, cph] (ORCID:  
<<https://orcid.org/0000-0001-8508-5012>>),  
Stefano Pagnotta [aut, cph] (ORCID:  
<<https://orcid.org/0000-0002-8298-9777>>)

**Maintainer** Davide Risso <risso.davide@gmail.com>

## Contents

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

---

|      |  |
|------|--|
| 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

|                         |  |
|-------------------------|--|
| x                       | a matrix of transformed gene expression counts (typically the results of <a href="#">awst</a> ).         |
| from                    | the minimum value from which to start binning data.  |
| to                      | the maximum value for the binning of the data.   |
| nBins                   | the number of bins.  |
| heterogeneity_threshold | the threshold used for the filtering.  |
| awst_values             | 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](#)