

# Package: Wrench (via r-universe)

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**Depends** R (>= 3.5.0)

**Type** Package

**Title** Wrench normalization for sparse count data

**Version** 1.30.0

**Description** Wrench is a package for normalization sparse genomic count data, like that arising from 16s metagenomic surveys.

**Imports** limma, matrixStats, locfit, stats, graphics

**License** Artistic-2.0

**LazyData** TRUE

**RoxygenNote** 6.1.0

**Suggests** knitr, rmarkdown, metagenomeSeq, DESeq2, edgeR

**VignetteBuilder** knitr

**biocViews** Normalization, Sequencing, Software

**URL** <https://github.com/HCBravoLab/Wrench>

**BugReports** <https://github.com/HCBravoLab/Wrench/issues>

**Repository** <https://bioc-release.r-universe.dev>

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<code>.estimSummary</code>	<i>Obtain robust means. .</i>
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### Description

Obtain robust means. .

### Usage

```
.estimSummary(res, estim.type = "s2.w.mean", ...)
```

### Arguments

<code>res</code>	result structure of wrench
<code>estim.type</code>	estimator type
<code>...</code>	other parameters

### Value

a chosen summary statistic

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<code>.getCondLogWeights</code>	<i>Log Postive-conditional weight computations for wrench estimators.</i>
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### Description

Log Postive-conditional weight computations for wrench estimators.

### Usage

```
.getCondLogWeights(res)
```

### Arguments

<code>res</code>	result structure of wrench
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### Value

inverse variance weights when using positive conditional models.

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.getCondWeights	<i>Postive-conditional weight computations for wrench estimators.</i>
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**Description**

Postive-conditional weight computations for wrench estimators.

**Usage**

```
.getCondWeights(res)
```

**Arguments**

res                    result structure of wrench

**Value**

positive conditional weights for each sample

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.getHurdle	<i>Obtains logistic fits for presence/absence and fitted probabilities of a zero occurring.</i>
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**Description**

This function is used to derive weights for feature-wise compositional estimates. Our (default) intention is to derive these based on average occurrences across the dataset, as just a function of sample depth, and not with particular relevance to groups.

**Usage**

```
.getHurdle(mat, hdesign = model.matrix(~-1 + log(colSums(mat))),
pres.abs.mod = TRUE, thresh = FALSE, thresh.val = 1e-08, ...)
```

**Arguments**

mat                    count matrix

hdesign                design matrix for the logistic; the default is usually sufficient.

pres.abs.mod        TRUE if glm regression is for presence or absence. FALSE if glm regression is for counts.

thresh                TRUE if numerically one/zero probability occurrences must be thresholded

thresh.val            if thresh is true, the numerically one/zero probability occurrences is thresholded to this value

...                    other parameters

**Value**

A list with components:

- pi0.fit - list with feature-wise glm.fit objects
- pi0 - matrix with fitted probabilities

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.getMargWeights	<i>Marginal weight computations for wrench estimators.</i>
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**Description**

Marginal weight computations for wrench estimators.

**Usage**

```
.getMargWeights(res, z.adj, ...)
```

**Arguments**

res	result structure of wrench
z.adj	TRUE if the result structure was generated with wrench with z.adj set to TRUE.
...	other parameters

**Value**

inverse marginal variances for robust mean computing

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.getReference	<i>This function generates the reference.</i>
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**Description**

This function generates the reference.

**Usage**

```
.getReference(mat, ref.est = "sw.means", ...)
```

**Arguments**

mat	count matrix; rows are features and columns are samples
ref.est	reference estimate method
...	other parameters

**Value**

the reference to be used for normalization

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.gets2                      *Obtain variances of logged counts.*

---

**Description**

Obtain variances of logged counts.

**Usage**

```
.gets2(mat, design = model.matrix(mat[1, ] ~ 1), plot = FALSE,  
      ebs2 = TRUE, smoothed = FALSE, ...)
```

**Arguments**

mat	count matrix; rows are features and columns are samples.
design	model matrix for the count matrix
plot	if the mean-variance trend function (the same as that of voom) needs to be plot.
ebs2	if regularization of variances needs to be performed.
smoothed	TRUE if all the variance estimates must be based on the mean-variance trend function.
...	other parameters

**Value**

a vector with variance estimates for logged feature-wise counts.

---

.getWeightedMean            *Get weighted means for matrix*

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**Description**

Get weighted means for matrix

**Usage**

```
.getWeightedMean(mat, w = rep(1, nrow(mat)))
```

**Arguments**

mat	input matrix
w	weights

**Value**

column-wise weighted means.

---

`.getWeightedMedian`      *Get weighted median for matrix*

---

### Description

Get weighted median for matrix

### Usage

```
.getWeightedMedian(mat, w = rep(1, nrow(mat)))
```

### Arguments

<code>mat</code>	input matrix
<code>w</code>	weights

### Value

column-wise weighted means.

---

wrench      *Normalization for sparse, under-sampled count data.*

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### Description

Obtain normalization factors for sparse, under-sampled count data that often arise with metagenomic count data.

### Usage

```
wrench(mat, condition, etype = "w.marg.mean", ebcf = TRUE,
        z.adj = FALSE, phi.adj = TRUE, detrend = FALSE, ...)
```

### Arguments

<code>mat</code>	count matrix; rows are features and columns are samples
<code>condition</code>	a vector with group information on the samples
<code>etype</code>	weighting strategy with the following options: <ul style="list-style-type: none"> <li>• <code>hurdle.w.mean</code>, the W1 estimator in manuscript.</li> <li>• <code>w.marg.mean</code>, the W2 estimator in manuscript. These are appropriately computed depending on whether <code>z.adj=TRUE</code> (see below)</li> <li>• <code>s2.w.mean</code>, weight by inverse of feature-variances of logged count data.</li> </ul>
<code>ebcf</code>	TRUE if empirical bayes regularization of ratios needs to be performed. Default recommended.

z.adj	TRUE if the feature-wise ratios need to be adjusted by hurdle probabilities (arises when taking marginal expectation). Default recommended.
phi.adj	TRUE if estimates need to be adjusted for variance terms (arises when considering positive-part expectations). Default recommended.
detrend	FALSE if any linear dependence between sample-depth and compositional factors needs to be removed. (setting this to TRUE reduces variation in compositional factors and can improve accuracy, but requires an extra assumption that no linear dependence between compositional factors and sample depth is present in samples).
...	other parameters

### Value

a list with components:

- *nf*, *normalization factors* for samples passed. Samples with zero total counts are removed from output.
- *ccf*, *compositional correction factors*. Samples with zero total counts are removed from output.
- *others*, a list with results from intermediate computations.
  - *qref*, reference chosen.
  - *design*, design matrix used for computation of positive-part parameters.
  - *s2*, feature-wise variances of logged count data.
  - *r*, (regularized) ratios of feature-wise proportions.
  - *radj*, adjustments made to the regularized ratios based on *z.adj* and *phi.adj* settings.

### Author(s)

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### Examples

```
#Obtain counts matrix and some group information
require(metagenomeSeq)
data(mouseData)
cntsMatrix <- MRcounts(mouseData)
group <- pData(mouseData)$diet
#Running wrench with defaults
W <- wrench( cntsMatrix, condition=group )
compositionalFactors <- W$ccf
normalizationFactors <- W$nf

#Introducing the above normalization factors for the most
# commonly used tools is shown below.

#If using metagenomeSeq
normalizedObject <- mouseData
normFactors(normalizedObject) <- normalizationFactors
```

```
#If using edgeR, we must pass in the compositional factors
require(edgeR)
edgerobj <- DGEList( counts=cntsMatrix,
                    group = as.matrix(group),
                    norm.factors=compositionalFactors )

#If using DESeq/DESeq2
require(DESeq2)
deseq.obj <- DESeqDataSetFromMatrix(countData = cntsMatrix,
                                   DataFrame(group),
                                   ~ group )
DESeq2::sizeFactors(deseq.obj) <- normalizationFactors
```

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