

# Package ‘Wrench’

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**Depends** R (>= 3.5.0)

**Type** Package

**Title** Wrench normalization for sparse count data

**Version** 1.25.0

**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>

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

Obtain robust means. .

### Usage

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

### Arguments

res	result structure of wrench
estim.type	estimator type
...	other parameters

### Value

a chosen summary statistic

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`.getCondLogWeights`      *Log Postive-conditional weight computations for wrench estimators.*

---

**Description**

Log Postive-conditional weight computations for wrench estimators.

**Usage**

`.getCondLogWeights(res)`

**Arguments**

res                      result structure of wrench

**Value**

inverse variance weights when using positive conditional models.

---

`.getCondWeights`      *Postive-conditional weight computations for wrench estimators.*

---

**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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<code>.getHurdle</code>	<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**

<code>mat</code>	count matrix
<code>hdesign</code>	design matrix for the logistic; the default is usually sufficient.
<code>pres.abs.mod</code>	TRUE if glm regression is for presence or absence. FALSE if glm regression is for counts.
<code>thresh</code>	TRUE if numerically one/zero probability occurrences must be thresholded
<code>thresh.val</code>	if <code>thresh</code> is true, the numerically one/zero probability occurrences is thresholded to this value
<code>...</code>	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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<code>.getMargWeights</code>	<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

---

.getReference                    *This function generates the reference.*

---

**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

---

.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**

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

**Value**

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

---

`.getWeightedMean`      *Get weighted means for matrix*

---

**Description**

Get weighted means for matrix

**Usage**

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

**Arguments**

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

mat	input matrix
w	weights

**Value**

column-wise weighted means.

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

**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**

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