

# Package ‘SETA’

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**Title** Single Cell Ecological Taxonomic Analysis

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**Description**

This package provides functions for compositional analysis and visualization for single-cell data.

**License** GPL-3

**Encoding** UTF-8

**Depends** R (>= 4.0)

**Imports** methods, stats

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown, MASS, Matrix, Seurat,  
SummarizedExperiment, SingleCellExperiment

**VignetteBuilder** knitr

**biocViews** SingleCell

**RoxygenNote** 7.3.2

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setaALR	<i>Additive Log-Ratio Transform</i>
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## Description

Applies an ALR transform to a matrix of counts using a specified reference column.

## Usage

```
setaALR(counts, ref, pseudocount = 1)
```

## Arguments

<code>counts</code>	A matrix of counts.
<code>ref</code>	The reference column, specified either by name or by index.
<code>pseudocount</code>	Numeric. Added to avoid $\log(0)$ . Default is 1.

## Details

ALR transforms the data by taking  $\log(x_i/x_{ref})$  for each column  $i$  except the reference column. This is another way to map data from the simplex to a Euclidean space in compositional data analysis.

## Value

A list with:

**method** A string noting `ALR_ref=<ref>`.

**counts** A matrix of dimension `nrow(counts) x (ncol(counts) - 1)`.

## References

Aitchison, J. (1982). The Statistical Analysis of Compositional Data. *Journal of the Royal Statistical Society. Series B (Methodological)*, 44(2), 139-177.

## Examples

```
mat <- matrix(c(1,2,4,8), nrow=2, byrow=TRUE)
colnames(mat) <- c("A", "B")
out <- setaALR(mat, ref="A", pseudocount=0)
out$counts
```

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setaCLR	<i>Centered Log-Ratio Transform</i>
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**Description**

Applies a CLR transform to a matrix of counts. This transform is commonly used in compositional data analysis (CoDA) to project counts into a log-ratio space.

**Usage**

```
setaCLR(counts, pseudocount = 1)
```

**Arguments**

counts	A matrix of counts (rows = features, columns = samples).
pseudocount	Numeric. Added to all entries to avoid taking $\log(0)$ . Default is 1.

**Details**

The CLR transform is defined as  $\log(x/g(x))$  where  $g(x)$  is the geometric mean of each row (sample) in the log scale. A pseudocount helps avoid  $\log(0)$  - default is 1, as scRNA data can be sparse.

**Value**

A list with two elements:

**method** A string indicating the transform ("CLR").

**counts** A matrix of the same dimensions as the input after CLR transform.

**References**

Aitchison, J. (1982). The Statistical Analysis of Compositional Data. *Journal of the Royal Statistical Society. Series B (Methodological)*, 44(2), 139-177.

**Examples**

```
mat <- matrix(c(1,2,4,8), nrow=2, byrow=TRUE)
out <- setaCLR(mat, pseudocount=0)
out$counts
```

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setaCounts

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*Extract Taxonomic Counts from Various Single Cell Objects*


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## Description

Given a `SingleCellExperiment`, `Seurat`, or long-form `data.frame`, this function produces a type-by-sample matrix of cell counts. For `SingleCellExperiment` or `Seurat`, it looks for `type` and `sample` columns in the object-level metadata. For long-form data frames, it expects columns `bc`, `type`, and `sample`.

## Usage

```
setaCounts(obj)
```

## Arguments

`obj` Either a `SingleCellExperiment`, a `Seurat` object, or a `data.frame` with columns `bc`, `type`, and `sample`.

## Details

- **SingleCellExperiment:** Reads `colData(obj)` for `type` and `sample`.
- **Seurat:** Uses `obj@meta.data` for `type` and `sample`.
- **data.frame:** Duplicates (by `bc`) are removed so each cell is counted once.

If `type` or `sample` columns are missing, an error is thrown.

## Value

A matrix whose rows are cell types and whose columns are samples, with entries giving the count of unique barcodes per type-sample combination.

## Examples

```
# For a data.frame:
df <- data.frame(
  bc = paste0("cell", 1:10),
  type = sample(c("Tcell", "Bcell"), 10, TRUE),
  sample = sample(c("sample1", "sample2"), 10, TRUE)
)
cmat <- setaCounts(df)
cmat
```

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setaILR	<i>Isometric Log-Ratio Transform</i>
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**Description**

Applies an ILR transform to a matrix of counts, using a Helmert basis by default. Optionally includes a Box-Cox-like step on the log scale.

**Usage**

```
setaILR(counts, boxcox_p = 0, taxTree = NULL, pseudocount = 1)
```

**Arguments**

counts	A matrix of counts.
boxcox_p	Numeric. If nonzero, applies a Box-Cox-type transform to the log-values.
taxTree	Currently unused. Reserved for future taxonomic-balance approaches.
pseudocount	Numeric. Pseudocount to avoid log(0). Default is 1.

**Details**

The ILR transform is a key tool in compositional data analysis. By default, it uses a Helmert contrast matrix. The parameter `boxcox_p` allows an additional transform on the log-values, as described by whuber on <https://stats.stackexchange.com/questions/259208/how-to-perform-isometric-log-ratio-tr>

**Value**

A list with:

**method** A string indicating ILR with a Helmert basis (potentially noting `boxcox_p`).

**counts** A matrix of ILR-transformed values with `ncol(counts) - 1` columns.

**References**

Aitchison, J. (1982). The Statistical Analysis of Compositional Data. *Journal of the Royal Statistical Society. Series B (Methodological)*, 44(2), 139-177.

**Examples**

```
mat <- matrix(c(1,2,4,8), nrow=2, byrow=TRUE)
out <- setaILR(mat, boxcox_p=0)
out$counts
```

setaLatent

*Compute a Latent Space from Transformed Counts***Description**

Given an object produced by one of the seta\* transform functions (e.g., setaCLR), this function applies a dimension reduction method (PCA, PCoA, or NMDS) to the transform\_obj\$counts.

**Usage**

```
setaLatent(transform_obj, method = c("PCA", "PCoA", "NMDS"), dims = 2)
```

**Arguments**

transform_obj	A list returned by, e.g., setaCLR, setaILR, etc., containing a counts matrix.
method	A string specifying the dimension reduction method. One of "PCA", "PCoA", or "NMDS".
dims	Integer. Number of dimensions (components) to return. Default is 2.

**Details**

- **PCA**: Uses stats::prcomp on the rows of transform\_obj\$counts.
- **PCoA**: Computes a distance matrix via stats::dist, then applies classical multidimensional scaling (stats::cmdscale).
- **NMDS**: Uses MASS::isoMDS to compute non-metric MDS from the distance matrix.

Each method returns a data frame of coordinates in latentSpace, plus additional information specific to that method.

**Value**

A list containing:

**method** The chosen latent space method.

**latentSpace** A data frame of coordinates in the chosen latent space, with dims columns.

**loadings** For PCA, the loadings matrix. Otherwise NA.

**varExplained** Variance explained (for PCA or PCoA) or stress (for NMDS).

**Examples**

```
mat <- matrix(rpois(20, lambda=5), nrow=4) # small 4x5 matrix
colnames(mat) <- paste0("C", 1:5)
clr_out <- setaCLR(mat)
latent_pca <- setaLatent(clr_out, method="PCA", dims=2)
latent_pca$latentSpace
```

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setaLogCPM	<i>log2(CPM) Transform</i>
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### Description

Computes log2-based counts-per-million (CPM) for each column. Optionally uses provided size factors.

### Usage

```
setaLogCPM(counts, pseudocount = 1, size_factors = NULL, scale_factor = 1e+06)
```

### Arguments

counts	A matrix of counts.
pseudocount	Numeric. Added to counts to avoid $\log_2(0)$ . Default is 1.
size_factors	Optional numeric vector. If NULL, uses the column sums.
scale_factor	Numeric. The scaling factor for "per million" style. Default is 1e6.

### Details

A common RNA-seq transform is  $\log_2(\text{CPM} + 1)$ . This variant allows adjusting the pseudocount, size factors, and overall scale factor.

### Value

A list with:

**method** "logCPM".

**counts** A matrix of the same dimension, containing  $\log_2(\text{CPM} + \text{pseudocount})$ .

### Examples

```
mat <- matrix(1:4, nrow=2)
out <- setaLogCPM(mat)
out$counts
```

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setaPercent	<i>Percentage Transform</i>
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### Description

Converts columns (samples) of a counts matrix to percentages of their respective column sums.

### Usage

```
setaPercent(counts)
```

**Arguments**

**counts** A matrix of counts.

**Details**

Simple re-scaling for compositional-like interpretation in percentages. Useful for simplified Wilcoxon rank comparisons and such

**Value**

A list with:

**method** "percent".

**counts** A matrix of the same dimension, with each column summing to 100.

**Examples**

```
mat <- matrix(c(1,2,4,8), nrow=2, byrow=TRUE)
out <- setaPercent(mat)
out$counts
```

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setaTransform

*Wrapper for Common Compositional Transforms*

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**Description**

A convenience function that dispatches to one of the transforms: CLR, ALR, ILR, percent, or logCPM.

**Usage**

```
setaTransform(
  counts,
  method = c("CLR", "ALR", "ILR", "percent", "logCPM"),
  ref = NULL,
  taxTree = NULL,
  pseudocount = 1,
  size_factors = NULL
)
```

**Arguments**

**counts** A matrix of counts.

**method** Which transform to apply. One of "CLR", "ALR", "ILR", "percent", or "logCPM".

**ref** Reference column (only used if method="ALR").

**taxTree** Optional tree for ILR (not yet implemented).

**pseudocount** Numeric, used by CLR, ALR, ILR, logCPM. Default 1.

**size\_factors** For logCPM scaling. If NULL, uses column sums.



**Value**

A list as returned by the respective transform function.

**Examples**

```
mat <- matrix(c(1,2,4,8), nrow=2, byrow=TRUE)
setaTransform(mat, method="CLR")
setaTransform(mat, method="percent")
```

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