

Package ‘FracFixR’

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Type Package

Title Compositional Statistical Framework for RNA Fractionation Analysis

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Description A compositional statistical framework for absolute proportion estimation between fractions in RNA sequencing data. 'FracFixR' addresses the fundamental challenge in fractionated RNA-seq experiments where library preparation and sequencing depth obscure the original proportions of RNA fractions. It reconstructs original fraction proportions using non-negative linear regression, estimates the ``lost" unrecoverable fraction, corrects individual transcript frequencies, and performs differential proportion testing between conditions. Supports any RNA fractionation protocol including polysome profiling, sub-cellular localization, and RNA-protein complex isolation.

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LazyData true

Depends R (>= 4.0.0)

Imports future.apply (>= 1.8.1), nnls (>= 1.4), ggplot2 (>= 3.3.5), dplyr (>= 1.0.7), RColorBrewer (>= 1.1-2), tidyr (>= 1.1.3), matrixStats (>= 0.60.0), aod (>= 1.3.1), stats, utils, future, grDevices

Suggests testthat (>= 3.0.0), knitr, rmarkdown

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DiffPropTest	<i>DiffPropTest: Statistical Testing for Differential Proportions</i>
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Description

Performs statistical testing to identify transcripts with significantly different proportions between conditions in specified fraction(s). Implements three test options: GLM (most powerful), Logit, and Wald.

Usage

```
DiffPropTest(NormObject, Conditions, Types, Test = c("GLM", "Logit", "Wald"))
```

Arguments

NormObject	Output from FracFixR() function
Conditions	Character vector of exactly 2 conditions to compare
Types	Character vector of fraction type(s) to analyze. Can be single fraction or multiple (will be combined)
Test	Statistical test to use: "GLM", "Logit", or "Wald"

Details

- GLM: Uses binomial generalized linear model (most statistically powerful)
- Logit: Faster alternative using logit transformation
- Wald: Beta-binomial Wald test for overdispersed count data

Value

Data frame with columns:

- transcript: transcript identifier
- mean_success_cond1/2: mean proportions in each condition
- mean_diff: difference in proportions
- log2FC: log2 fold change
- pval: p-value from statistical test
- padj: FDR-adjusted p-value

Examples

```
data(example_counts)
data(example_annotation)

# Run FracFixR
results <- FracFixR(example_counts, example_annotation, parallel=FALSE)
# Run differential testing
diff_results <- DiffPropTest(results,
                             Conditions = c("Control", "Treatment"),
                             Types = "Heavy_Polysome",
                             Test = "GLM")
```

example_annotation	<i>Example annotation data frame</i>
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Description

A data frame containing sample annotations for the example_counts matrix. Describes the experimental design with conditions, fraction types, and replicates.

Usage

```
example_annotation
```

Format

A data frame with 12 rows and 4 columns:

Sample Sample identifier matching column names in example_counts

Condition Experimental condition (Control or Treatment)

Type Fraction type (Total, Light_Polysome, or Heavy_Polysome)

Replicate Replicate identifier (Rep1 or Rep2)

Source

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Examples

```
data(example_annotation)
head(example_annotation)
table(example_annotation$Condition, example_annotation$Type)
```

example_counts	<i>Example RNA-seq count matrix</i>
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Description

A matrix containing simulated RNA-seq counts for 100 genes across 12 samples. The data simulates a polysome profiling experiment with two conditions (Control and Treatment) and three fractions (Total, Light_Polysome, Heavy_Polysome).

Usage

```
example_counts
```

Format

A numeric matrix with 100 rows (genes) and 12 columns (samples):

rows Gene identifiers (Gene1 to Gene100)

columns Sample identifiers (Sample1 to Sample12)

Source

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Examples

```
data(example_counts)
dim(example_counts)
head(example_counts[, 1:6])
```

FracFixR*FracFixR: Main Function for Fraction Correction*

Description

This is the core function that implements the FracFixR framework. It takes raw count data from total and fractionated samples and reconstructs the original fraction proportions through compositional modeling.

Usage

```
FracFixR(MatrixCounts, Annotation, parallel = TRUE)
```

Arguments

MatrixCounts	A numeric matrix of raw transcript/gene counts with: <ul style="list-style-type: none">• Rows: transcripts/genes (must have rownames)• Columns: samples (must have colnames matching Annotation\$Sample)
Annotation	A data.frame with required columns: <ul style="list-style-type: none">• Sample: sample identifiers matching column names in MatrixCounts• Condition: experimental condition (e.g., "Control", "Treatment")• Type: fraction type (must include at least one "Total")• Replicate: replicate identifier
parallel	A boolean indicating whether to use parallel processing of the transcripts (default=TRUE).

Details

The function works by:

1. Filtering transcripts based on presence in Total samples
2. For each condition and replicate, fitting NNLS regression
3. Estimating global fraction weights and individual transcript proportions
4. Calculating the "lost" unrecoverable fraction

Value

A list containing:

- OriginalData: filtered input count matrix
- Annotation: input annotation data
- Propestimates: matrix of proportion estimates
- Coefficients: data.frame of regression coefficients
- Fractions: data.frame of estimated fraction proportions
- plots: list of diagnostic plots

References

Cleynen et al. FracFixR: A compositional statistical framework for absolute proportion estimation between fractions in RNA sequencing data.

Examples

```
# Load example data
data(example_counts)
data(example_annotation)

# Run FracFixR
results <- FracFixR(example_counts, example_annotation, parallel=FALSE)

# View fraction proportions
print(results$Fractions)
```

PlotComparison

PlotComparison: Create Volcano Plot for Differential Results

Description

Generates avolcano plot showing transcripts with significant differential proportions between conditions.

Usage

```
PlotComparison(DiffPropResult, Conditions = NULL, Types = NULL, cutoff = NULL)
```

Arguments

DiffPropResult	Output from DiffPropTest() function
Conditions	Character vector of conditions being compared
Types	Character vector of fraction types analyzed
cutoff	Optional y-axis maximum for plot

Value

Volcano plot-type object

Examples

```
data(example_counts)
data(example_annotation)

# Run FracFixR
results <- FracFixR(example_counts, example_annotation, parallel=FALSE)
# Run differential testing
```

```
diff_results <- DiffPropTest(results,
                             Conditions = c("Control", "Treatment"),
                             Types = "Heavy_Polysome",
                             Test = "GLM")

# Create volcano plot
volcano <- PlotComparison(diff_results,
                          Conditions = c("Control", "Treatment"),
                          Types = "Heavy_Polysome")
```

PlotFractions

PlotFractions: Visualize Fraction Proportions

Description

Creates a stacked bar plot showing the distribution of RNA across fractions for each replicate, including the "lost" fraction.

Usage

```
PlotFractions(FracFixed)
```

Arguments

FracFixed Output from FracFixR() function

Value

ggplot2 object showing fraction proportions

Examples

```
data(example_counts)
data(example_annotation)

# Run FracFixR
results <- FracFixR(example_counts, example_annotation, parallel=FALSE)
# Create fraction plot
frac_plot <- PlotFractions(results)
# Save plot with ggsave("fractions.pdf", frac_plot, width = 10, height = 8)
```

polysome_annotation	<i>Polysome profiling annotation example</i>
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Description

An alternative annotation data frame for polysome profiling experiments with monosome and polysome fractions.

Usage

polysome_annotation

Format

A data frame with 12 rows and 4 columns:

- Sample** Sample identifier
- Condition** Experimental condition (Control or Stress)
- Type** Fraction type (Total, Monosome, or Polysome)
- Replicate** Replicate identifier (Rep1 or Rep2)

Source

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Examples

```
data(polysome_annotation)
head(polysome_annotation)
```

subcellular_annotation	<i>Subcellular fractionation annotation example</i>
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Description

An annotation data frame for subcellular fractionation experiments with nuclear and cytoplasmic fractions.

Usage

subcellular_annotation

Format

A data frame with 12 rows and 4 columns:

Sample Sample identifier

Condition Experimental condition (WT or Mutant)

Type Fraction type (Total, Nuclear, or Cytoplasmic)

Replicate Replicate identifier (Rep1 or Rep2)

Source

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Examples

```
data(subcellular_annotation)
head(subcellular_annotation)
```

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