

# Package ‘GTEs’

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**Type** Package

**Title** Group Technical Effects

**Version** 1.0.0

**Language** en-US

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**Description** Implementation of the GTE (Group Technical Effects) model for single-cell data. GTE is a quantitative metric to assess batch effects for individual genes in single-cell data. For a single-cell dataset, the user can calculate the GTE value for individual features (such as genes), and then identify the highly batch-sensitive features. Removing these highly batch-sensitive features results in datasets with low batch effects.

**License** GPL-3

**Encoding** UTF-8

**Depends** R (>= 4.0.0)

**Imports** stats, Matrix, matrixStats, Rcpp, RcppEigen, dplyr

**LinkingTo** Rcpp (>= 1.0.8), RcppEigen

**RoxygenNote** 7.2.3

**NeedsCompilation** yes

**URL** <https://github.com/yzhou1999/GTEs>,  
<https://yzhou1999.github.io/GTEs/>

**BugReports** <https://github.com/yzhou1999/GTEs/issues>

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**Repository** CRAN

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group_onehot	<i>Compute one-hot matrix for given data frame and variable (s)</i>
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### Description

Compute one-hot matrix for given data frame and variable (s)

### Usage

```
group_onehot(x, ivar)
```

### Arguments

x	Input data frame.
ivar	Variable (s) for one-hot computation.

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Run.GroupTechEffects	<i>Compute the group technical effects.</i>
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### Description

Compute the group technical effects.

### Usage

```
Run.GroupTechEffects(X, meta, g_factor, b_factor, do.scale = FALSE)
```

### Arguments

X	Input data matrix.
meta	Input metadata (data.frame).
g_factor	Group variable (s).
b_factor	Batch variable (s).
do.scale	Whether to perform scaling.

**Value**

A list containing the overall GTE (`$OverallTechEffects`) and the GTE (`$GroupTechEffects`) of each subgroup under the group variable.

**Examples**

```
# X is a normalized expression matrix with rows as features and columns as cells.

# meta is a data.frame with columns containing metadata such as cell type, batch, etc.

data_file <- system.file("extdata", "example_data.rds", package = "GTEs")
example_data <- readRDS(data_file)
meta_file <- system.file("extdata", "example_meta.rds", package = "GTEs")
example_meta <- readRDS(meta_file)
GTE_ct <- Run.GroupTechEffects(example_data, example_meta,
                               g_factor = "CellType",
                               b_factor = "Batch")
```

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scale\_data

*Scale data matrix*

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**Description**

Scale data matrix

**Usage**

```
scale_data(
  data.x,
  do.center = TRUE,
  do.scale = TRUE,
  row.means = NULL,
  row.sds = NULL
)
```

**Arguments**

<code>data.x</code>	Input data matrix.
<code>do.center</code>	Whether center the row values. (default TRUE)
<code>do.scale</code>	Whether scale the row values. (default TRUE)
<code>row.means</code>	The provided row means to center. (default NULL)
<code>row.sds</code>	The provided row standard deviations to scale. (default NULL)

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Select.HBGs	<i>Select highly batch-sensitive genes (HBGs) under a group variable.</i>
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**Description**

Select highly batch-sensitive genes (HBGs) under a group variable.

**Usage**

```
Select.HBGs(GTE, bins = 0.1, gte.ratio = 0.95)
```

**Arguments**

GTE	GTE result.
bins	Bins.
gte.ratio	Ratio of selected HBGs to the total GTE.

**Value**

Identified HBGs.

**Examples**

```
# GTE is the result of Run.GroupTechEffects function.
data_file <- system.file("extdata", "GTE_ct.rds", package = "GTEs")
GTE_ct <- readRDS(data_file)
HBGs <- Select.HBGs(GTE_ct)
```

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select_hbgs	<i>Select HBGs using GTE vector.</i>
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**Description**

Select HBGs using GTE vector.

**Usage**

```
select_hbgs(gte, bins = 0.1, gte.ratio = 0.95, is.sort = TRUE)
```

**Arguments**

gte	Named GTE vector.
bins	Bins.
gte.ratio	Ratio of selected HBGs to overall GTE.
is.sort	Whether to sort genes by GTE from largest to smallest.

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