Package ‘ordPanel’

May 9, 2026

Type Package

Title Ordered Panel

Version 0.1.1

Date 2026-03-18

Description The ordered panel methodology (Zezulinski et al 2025 <doi:10.1159/000545366>) provides a structured framework for identifying and organizing sets of biomarkers, such as genetic variants, that distinguish between positive and negative subjects in a study when only a training cohort is available. This approach is particularly useful in situations where an independent validation cohort does not yet exist, rendering conventional performance metrics such as the receiver operating characteristic (ROC) curve and area under the ROC curve (AUC) inappropriate or potentially misleading. The methodology emphasizes transparent construction and evaluation of ordered signatures of biomarkers, allowing investigators to examine operating characteristics without establishing predictive performance.

License GPL-2

Encoding UTF-8

Language en-US

RoxygenNote 7.3.3

LazyData true

LazyDataCompression xz

URL `https://github.com/tingtingzhan/ordPanel`,
`https://tingtingzhan-ordpanel.netlify.app`

Depends R (>= 4.5.0)

Imports cli, flextable, ggplot2, methods, consort, patchwork, scales

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

Author Tingting Zhan [aut, cre] (ORCID:
<`https://orcid.org/0000-0001-9971-4844`>),
Aejaz Sayeed [ctb] (ORCID: <`https://orcid.org/0000-0001-6900-7524`>)

Maintainer Tingting Zhan <`tingtingzhan@gmail.com`>

Repository CRAN

Date/Publication 2026-03-19 07:20:02 UTC

Contents

`ordPanel-package` *ordPanel: Ordered Panel*

Description

The ordered panel methodology (Zezulinski et al 2025 doi:10.1159/000545366) provides a structured framework for identifying and organizing sets of biomarkers, such as genetic variants, that distinguish between positive and negative subjects in a study when only a training cohort is available. This approach is particularly useful in situations where an independent validation cohort does not yet exist, rendering conventional performance metrics such as the receiver operating characteristic (ROC) curve and area under the ROC curve (AUC) inappropriate or potentially misleading. The methodology emphasizes transparent construction and evaluation of ordered signatures of biomarkers, allowing investigators to examine operating characteristics without establishing predictive performance.

Author(s)

Maintainer: Tingting Zhan <`tingtingzhan@gmail.com`> (ORCID)

Other contributors:

- Aejaz Sayeed (ORCID) [contributor]

See Also

Useful links:

- `https://github.com/tingtingzhan/ordPanel`
- `https://tingtingzhan-ordpanel.netlify.app`

`autoplot.panellist` *Visualize panellist using Package* R*hrefhttps://CRAN.R-project.org/package=ggplot2***ggplot2**

Description

Visualize panellist using Package **ggplot2**

Usage

```
## S3 method for class 'panellist'
autoplot(object, ...)

## S3 method for class 'panellist'
autolayer(object, which = c("oc", "roc"), ...)
```

Arguments

`object`	panellist
`...`	additional parameters, currently no use
`which`	character scalar, `'oc'` (default value) or (faux) `'roc'`

Value

The `S3` method `autoplot.panellist()` returns a ggplot object.

`panel` `S4` *Class panel*

Description

`S4` Class panel

Usage

```
panel(m1 = zezulinski1, m0 = zezulinski0)
```

Arguments

`m1, m0`	see detailed explanations in Section **Slots**. • If both `m1` and `m0` are missing, then random logical matrix-es will be generated; • If one-and-only-one of `m1` and `m0` is missing, then the function `panel()` will stop.

Value

The function `panel()` returns an R object of `S4` class panel.

Slots

- `m1,m0` logical matrix-es, true and false positives, respectively. In other words, the variants tested positive in the positive and negative subjects (patients), respectively. Rows are different variants. Columns are different subjects. The rownames of `m0` and `m1` must be the same.
- `id` list of character vectors
- `ordered` logical scalar, whether this is an ordered panel
- `label` (optional) character scalar, a human-friendly description of the panel
- `consort` (optional) data.frame to create a consort_plot

`panellist` panellist

Description

To combine multiple panels.

Usage

```
panellist(...)
```

Arguments

`...`	one or more panels

Value

The function `panellist()` returns an `S3` object of `panellist`, which inherits from the classes listof and list.

`pkg_data` *Data Sets in Package* **ordPanel**

Description

Data sets used as examples in package **ordPanel**.

Usage

```
zezulinski1

zezulinski0
```

Format

An object of class `matrix` (inherits from `array`) with 12877 rows and 50 columns.

An object of class `matrix` (inherits from `array`) with 12877 rows and 31 columns.

References

doi:10.1159/000545366

`plot.panel` *Flow-Chart of Ordered panel*

Description

To create a flow-chart for the creation of an ordered panel.

Usage

```
## S3 method for class 'panel'
plot(x, ...)
```

Arguments

`x`	an ordered panel
`...`	additional parameters of the function consort_plot, except for `data`, `orders` and `side_box`

Value

The function `plot.panel()` returns

- an R object of class `'consort'` (returned from the function consort_plot), if the input panel has a non-default `@consort` slot;
- an invisible `NULL`-value, if the input panel has a default `@consort` slot.

`plot.panellist` *Flow-Charts of Ordered panellist*

Description

To create flow-charts for the creation of an ordered panellist.

Usage

```
## S3 method for class 'panellist'
plot(x, ...)
```

Arguments

`x`	an ordered panellist
`...`	additional parameters for the function wrap_plots, **not** for the function `plot.panel()`

Value

The function `plot.panellist()` returns

- a patchwork, (returned from the function wrap_plots), if the input panellist has at least one panel with a non-default `@consort` slot;
- an invisible `NULL`-value, if all panels in the input panellist have a default `@consort` slot.

`show,panel-method` *Show panel*

Description

Show panel

Usage

```
## S4 method for signature 'panel'
show(object)
```

Arguments

`object`	panel

Value

The show method of panel class does not have a returned value.

`sort_by.panel` *Sort panel by Given Criterion*

Description

To sort a panel by some given criterion.

Usage

```
## S3 method for class 'panel'
sort_by(x, y, ...)
```

Arguments

`x`	panel
`y`	one-sided formula
`...`	additional parameters of order

Value

The `S3` method `sort_by.panel()` returns an **ordered** panel.

`subset.panel` *Select a subset of panel*

Description

Select a subset of panel

Usage

```
## S3 method for class 'panel'
subset(x, subset, append.label = FALSE, ...)
```

Arguments

`x`	panel
`subset`	R language object
`append.label`	logical scalar (default value `FALSE`), whether to append the subset-criterion to `x@label`
`...`	additional parameters, currently not in use

Value

The `S3` method `subset.panel()` returns an R object of `S4` class panel.

`sum1` *Number of True & False Positives*

Description

Number of True & False Positives

Usage

```
sum1(x)

sum0(x)

cumsum1(x)

cumsum0(x)
```

Arguments

`x`	panel

Value

The functions `sum1()` and `sum0()` return a integer vector.

The functions `cumsum1()` and `cumsum0()` return a non-decreasing integer vector.

`[.panel` *Extract Rows of panel*

Description

Extract Rows of panel

Usage

```
## S3 method for class 'panel'
x[i, ...]
```

Arguments

`x`	panel
`i`	logical vector, row indices
`...`	additional parameters, currently not in use

Value

The `S3` method `[.panel()` returns a panel.

Index