

# Package ‘ordPanel’

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**Type** Package

**Title** Ordered Panel

**Version** 0.1.0

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**Description** The ordered panel methodology (Zezulinski et al 2025 <[doi:10.1159/000545366](https://doi.org/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), flextable, ggplot2

**Imports** cli, methods, consort, matrixStats, patchwork, scales

**NeedsCompilation** no

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## Contents

ordPanel-package . . . . .	2
append_label . . . . .	3
as_flextable.panel . . . . .	3
as_flextable.panellist . . . . .	4
autoplot.panellist . . . . .	4
ordPanel_bib . . . . .	5
panel . . . . .	5
panellist . . . . .	6
pkg_data . . . . .	6
plot.panel . . . . .	7
plot.panellist . . . . .	8
show,panel-method . . . . .	8
sort_by.panel . . . . .	9
subset.panel . . . . .	9
sum1 . . . . .	10
[.panel . . . . .	10

<b>Index</b>	<b>11</b>
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ordPanel-package	<i>ordPanel: Ordered Panel</i>
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### Description

The ordered panel methodology (Zezulinski et al 2025 [doi:10.1159/000545366](https://doi.org/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.

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### See Also

Useful links:

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

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append_label	<i>Append to @label of <a href="#">panel</a></i>
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---

**Description**

Append to @label of [panel](#)

**Usage**

```
append_label(x, info)
```

**Arguments**

x	<a href="#">panel</a>
info	<a href="#">character</a> scalar

**Value**

The function [append\\_label\(\)](#) returns an [panel](#) object.

**Note**

There is no generic function `labels<-` in package **base**.  
The function [comment<-](#) is not an S3 generic.

---

as_flextable.panel	<i>Convert <a href="#">panel</a> into <a href="#">flextable</a></i>
--------------------	---------------------------------------------------------------------

---

**Description**

Convert [panel](#) into [flextable](#)

**Usage**

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

**Arguments**

x	<a href="#">panel</a>
...	additional parameters, currently of no use

**Value**

The S3 method [as\\_flextable.panel\(\)](#) returns a [flextable](#).

---

`as_flextable.panellist`

*Convert a [panellist](#) into [flextable](#)*

---

### Description

Convert a [panellist](#) into [flextable](#)

### Usage

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

### Arguments

`x`                    [panellist](#)  
`...`                additional parameters, currently of no use

### Value

The S3 method `as_flextable.panellist()` returns a [flextable](#).

### Note

The S3 method `as_flextable.panellist()` may be eventually deprecated.

---

`autoplot.panellist`    Visualize [panellist](#) using Package [Rhrefhttps://CRAN.R-project.org/package=ggplot2](https://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.

---

ordPanel_bib	<i>Bibliography in package <b>ordPanel</b></i>
--------------	------------------------------------------------

---

**Description**

Bibliography in package **ordPanel**

**Usage**

```
.zezulinski25(key = "Zezulinski25", ...)
```

**Arguments**

key, ... additional parameters of the function `bibentry`

**Value**

The function `.zezulinski25()` returns a `bibentry` object.

---

panel	<i>S4 Class <code>panel</code></i>
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---

**Description**

S4 Class `panel`

**Usage**

```
panel(m1, m0)
```

**Arguments**

m1, m0 see **Slots**

**Value**

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

**Slots**

- m1 [logical matrix](#), true positives, i.e., variants tested positive in the positive subjects (patients). Rows are different variants. Columns are different subjects. The [rownames](#) of m0 and m1 must be the same
- m0 [logical matrix](#), false positives, i.e., variants tested positive in the negative subjects (patients). Rows are different variants. Columns are different subjects. The [rownames](#) of m0 and m1 must be the same.
- id [list](#) of [character vectors](#)
- label (optional) [character](#) scalar, a human-friendly description of the [panel](#)
- consort (optional) [data.frame](#) to create a [consort\\_plot](#)

---

panellist	panellist
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**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	<i>Data Sets in Package <b>ordPanel</b></i>
----------	---------------------------------------------

---

**Description**

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

**Usage**

```
m1
```

```
m0
```

### 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](https://doi.org/10.1159/000545366)

### Examples

```
# data used in  
.zezulinski25()
```

---

<code>plot.panel</code>	<i>CONSORT-Like Flow-Chart of Ordered <a href="#">panel</a></i>
-------------------------	-----------------------------------------------------------------

---

### Description

To create a CONSORT-Like flow-chart of an ordered [panel](#).

### Usage

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

### Arguments

<code>x</code>	an ordered <a href="#">panel</a>
<code>...</code>	additional parameters of the function <a href="#">consort_plot</a> , except for <code>data</code> , <code>orders</code> and <code>side_box</code>

### Value

The function `plot.panel()` returns an R object of class `'consort'`.

---

plot.panellist	<i>CONSORT-Like Flow-Chart of Ordered <a href="#">panellist</a></i>
----------------	---------------------------------------------------------------------

---

### Description

To create a CONSORT-Like flow-chart of an ordered [panellist](#).

### Usage

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

### Arguments

x	an ordered <a href="#">panellist</a>
...	additional parameters for the function <a href="#">wrap_plots</a> , <b>not</b> for the function <a href="#">plot.panel()</a>

### Value

The function [plot.panellist\(\)](#) returns a [patchwork](#).

---

show,panel-method	<i>Show <a href="#">panel</a></i>
-------------------	-----------------------------------

---

### Description

Show [panel](#)

### Usage

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

### Arguments

object	<a href="#">panel</a>
--------	-----------------------

### Value

The [show](#) method of [panel](#) class does not have a returned value.

---

sort_by.panel	<i>Sort <a href="#">panel</a> by Given Criterion</i>
---------------	------------------------------------------------------

---

**Description**

Sort [panel](#) by Given Criterion

**Usage**

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

**Arguments**

x	<a href="#">panel</a>
y	one-sided <a href="#">formula</a>
...	additional parameters of <a href="#">order</a>

**Value**

The S3 method [sort\\_by.panel\(\)](#) returns a [panel](#).

---

subset.panel	<i>Select a <a href="#">subset</a> of <a href="#">panel</a></i>
--------------	-----------------------------------------------------------------

---

**Description**

Select a [subset](#) of [panel](#)

**Usage**

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

**Arguments**

x	<a href="#">panel</a>
subset	R <a href="#">language</a> object
append.label	<a href="#">logical</a> scalar (default value FALSE), whether to append the subset-criterion to <code>x@label</code>
...	additional parameters, currently not in use

**Value**

The S3 method [subset.panel\(\)](#) returns an R object of S4 class [panel](#).

---

sum1	<i>Number of True &amp; False Positives, per variant</i>
------	----------------------------------------------------------

---

**Description**

Number of True & False Positives, per variant

**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 **strictly** increasing [integer vector](#).

---

[.panel	<i>Extract Rows of <a href="#">panel</a></i>
---------	----------------------------------------------

---

**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

## \* datasets

pkg\_data, 6  
.zezulinski25 (ordPanel\_bib), 5  
.zezulinski25(), 5  
[.panel, 10  
append\_label, 3  
append\_label(), 3  
as\_flextable.panel, 3  
as\_flextable.panel(), 3  
as\_flextable.panellist, 4  
as\_flextable.panellist(), 4  
autolayer.panellist  
    (autoplot.panellist), 4  
autoplot.panellist, 4  
autoplot.panellist(), 5  
bibentry, 5  
character, 3, 4, 6  
comment<-, 3  
consort\_plot, 6, 7  
cumsum0 (sum1), 10  
cumsum0(), 10  
cumsum1 (sum1), 10  
cumsum1(), 10  
data.frame, 6  
flextable, 3, 4  
formula, 9  
ggplot, 5  
integer, 10  
language, 9  
list, 6  
listof, 6  
logical, 6, 9, 10  
m0 (pkg\_data), 6

m1 (pkg\_data), 6  
matrix, 6  
order, 9  
ordPanel (ordPanel-package), 2  
ordPanel-package, 2  
ordPanel\_bib, 5  
panel, 3, 5, 5, 6–10  
panel(), 5  
panel-class (panel), 5  
panellist, 4, 6, 8  
panellist(), 6  
patchwork, 8  
pkg\_data, 6  
plot.panel, 7  
plot.panel(), 7, 8  
plot.panellist, 8  
plot.panellist(), 8  
rownames, 6  
show, 8  
show, panel-method, 8  
sort\_by.panel, 9  
sort\_by.panel(), 9  
subset, 9  
subset.panel, 9  
subset.panel(), 9  
sum0 (sum1), 10  
sum0(), 10  
sum1, 10  
sum1(), 10  
vector, 6, 10  
wrap\_plots, 8