

# Package: ordPanel (via r-universe)

May 31, 2026

**Type** Package

**Title** Ordered Panel

**Version** 0.1.1

**Date** 2026-05-04

**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

**LazyData** true

**LazyDataCompression** xz

**URL** <https://github.com/tingtingzhan/ordPanel>,  
<https://tingtingzhan.quarto.pub/ordpanel/>,  
<https://tingtingzhan-ordpanel.netlify.app>

**Depends** R (>= 4.6.0)

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

**Suggests** testthat

**Config/testthat/edition** 3

**Config/roxygen2/version** 8.0.0

**Config/roxygen2/markdown** TRUE

**Config/pak/sysreqs**

libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev make libharfbuzz-dev libicu-dev libjpeg-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libssl-dev

**Repository** <https://tingtingzhan.r-universe.dev>

**Date/Publication** 2026-05-05 03:25:56 UTC

**RemoteUrl** <https://github.com/tingtingzhan/ordpanel>

**RemoteRef** HEAD

**RemoteSha** 44421910131605efdd903503b1be08ca41728ba8

## Contents

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

**Index** 10

---

ordPanel-package	<i>ordPanel: Ordered Panel</i>
------------------	--------------------------------

---

## 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.

**Author(s)**

**Maintainer:** Tingting Zhan <tingtingzhan@gmail.com> ([ORCID](#))

Authors:

- Tingting Zhan <tingtingzhan@gmail.com> ([ORCID](#))

Other contributors:

- Aejaz Sayeed ([ORCID](#)) [contributor]

**See Also**

Useful links:

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

---

[.panel

*Extract Rows of [panel](#)*

---

**Description**

Extract Rows of [panel](#)

**Usage**

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

**Arguments**

x	<a href="#">panel</a>
i	<a href="#">logical vector</a> , row indices
...	additional parameters, currently not in use

**Value**

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

---

autoplot.panellist	Visualize <a href="#">panellist</a> using Package <a href="https://CRAN.R-project.org/package=ggplot2">Rhrefhttps://CRAN.R-project.org/package=ggplot2</a> <b>ggplot2</b>
--------------------	---

---

### 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	<a href="#">panellist</a>
...	additional parameters, currently no use
which	<a href="#">character</a> scalar, 'oc' (default value) or (faux) 'roc'

### Value

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

---

panel	S4 Class <a href="#">panel</a>
-------	--------------------------------

---

### Description

S4 Class [panel](#)

### Usage

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

### Arguments

m1, m0	see detailed explanations in Section <b>Slots</b> . <ul style="list-style-type: none"> <li>• If both m1 and m0 are missing, then random <a href="#">logical matrix</a>-es will be generated;</li> <li>• If one-and-only-one of m1 and m0 is missing, then the function <code>panel()</code> will <a href="#">stop</a>.</li> </ul>
--------	---

**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](https://doi.org/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 <a href="#">panel</a>
...	additional parameters of the function <a href="#">consort_plot</a> , 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	<i>Flow-Charts of Ordered panellist</i>
----------------	---

---

**Description**

To create flow-charts for the creation 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](#), (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	<i>Show panel</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

To sort a [panel](#) by some 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 an **ordered** [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</i>
------	---

---

**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](#).

# Index

- \* **datasets**
  - pkg\_data, 6
  - [.panel, 3
- autolayer.panellist
  - (autoplot.panellist), 4
- autoplot.panellist, 4
- autoplot.panellist(), 4
  
- character, 4, 5
- consort\_plot, 5, 6
- cumsum0 (sum1), 9
- cumsum0(), 9
- cumsum1 (sum1), 9
- cumsum1(), 9
  
- data.frame, 5
  
- formula, 8
  
- ggplot, 4
  
- integer, 9
- invisible, 6, 7
  
- language, 8
- list, 5
- listof, 5
- logical, 3–5, 8
  
- matrix, 4, 5
  
- order, 8
- ordPanel (ordPanel-package), 2
- ordPanel-package, 2
  
- panel, 3, 4, 4–9
- panel(), 4, 5
- panel-class (panel), 4
- panellist, 4, 5, 7
- panellist(), 5
  
- patchwork, 7
- pkg\_data, 6
- plot.panel, 6
- plot.panel(), 6, 7
- plot.panellist, 7
- plot.panellist(), 7
  
- rownames, 5
  
- show, 7
- show, panel-method, 7
- sort\_by.panel, 8
- sort\_by.panel(), 8
- stop, 4
- subset, 8
- subset.panel, 8
- subset.panel(), 8
- sum0 (sum1), 9
- sum0(), 9
- sum1, 9
- sum1(), 9
  
- vector, 3, 5, 9
  
- wrap\_plots, 7
  
- zezulinski0 (pkg\_data), 6
- zezulinski1 (pkg\_data), 6