

# Package ‘jointCompRisk’

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**Type** Package

**Title** Joint Inference for Competing Risks Data Using Multiple Endpoints

**Version** 0.1.0

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**Description** Tools for competing risks trials that allow simultaneous inference on recovery and mortality endpoints. Provides data preparation helpers, standard cumulative incidence estimators (restricted mean time gained/lost), and severity weighted extensions that integrate longitudinal ordinal outcomes to summarise treatment benefit. Methods follow Wen, Wang, and Hu (2023) Biometrics 79(3):1635-1645 <[doi:10.1111/biom.13752](https://doi.org/10.1111/biom.13752)>.

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**Encoding** UTF-8

**LazyData** false

**Imports** dplyr, magrittr, stats, rlang, survival

**RoxygenNote** 7.3.2

**Depends** R (>= 3.5)

**Suggests** knitr, rmarkdown, readr, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**URL** <https://github.com/cathyzzzhang/jointCompRisk>

**BugReports** <https://github.com/cathyzzzhang/jointCompRisk/issues>

**NeedsCompilation** no

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**Repository** CRAN

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do_cif_analysis	<i>Run Standard CIF Analysis</i>
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Description

Given a prepped data list from [prep\\_data\\_cif](#), run the standard CIF analysis.

Usage

```
do_cif_analysis(prepped, tau = 15)
```

Arguments

- |         |   |
|---------|---|
| prepped | A list returned by <code>prep_data_cif()</code> , containing Treatment and Control. |
| tau     | Numeric, time horizon (e.g. 15 or 29).  |

Details

- RMLT1 uses parameters  $(a,b,c) = (0,1,0)$  for recovery/discharge analysis. - RMLT2 uses  $(a,b,c) = (0,0,1)$  for death analysis.

Value

A list with formatted results for RMLT1 and RMLT2.

---

```
do_weighted_cif_analysis
      Run Weighted CIF Analysis
```

---

### Description

Given the list from `prep_data_weighted_cif`, run Weighted RMLT1 (recovery/discharge) and Weighted RMLT2 (death) at a user-specified time horizon `tau`.

### Usage

```
do_weighted_cif_analysis(prepped, tau)
```

### Arguments

<code>prepped</code>	A list returned by <code>prep_data_weighted_cif()</code> .
<code>tau</code>	Numeric time horizon (e.g., 15 or 29).

### Details

- Weighted RMLT1 uses `eta=1` for recovery/discharge analysis. - Weighted RMLT2 uses `eta=2` for death analysis.

### Value

A list with formatted results for WRMLT1 and WRMLT2.

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<code>long_df</code>	<i>Longitudinal Severity Scores Dataset</i>
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### Description

Repeated measurements of ordinal severity scores over time for the same patients in the `main_df` dataset, with treatment-specific trajectory patterns.

### Usage

```
data(long_df)
```

### Format

A data frame with variable rows per patient:

**PersonID** Patient identifier matching ID in `main_df` (character)

**OrdinalScore** Severity score on 1-8 scale (numeric)

**RelativeDay** Study day (numeric) starting from day 0 (baseline)

## Details

Measurements are taken at scheduled visits: days 0 (baseline), 1, 3, 5, 7, 10, 14, 18, 21, 25, 28. The trajectory follows treatment-specific probabilities: treatment patients have 45 and 15 worsening probability, creating realistic differential clinical progression patterns.

## Source

Simulated data using treatment-specific random walk with boundaries

## Examples

```
data(long_df)
data(main_df)
head(long_df)
# See data for first patient
subset(long_df, PersonID == "Patient_001")
# Compare average scores by treatment
long_df %>%
  dplyr::left_join(main_df[,c("ID", "Treatment")], by=c("PersonID"="ID")) %>%
  dplyr::group_by(Treatment) %>%
  dplyr::summarise(mean_score = mean(OrdinalScore))
```

---

main_df	<i>Main Competing Risks Dataset Simulated clinical trial data with competing risks survival outcomes. This dataset follows the structure of Adaptive COVID-19 Treatment Trials (ACTT) with built-in treatment effects for demonstration purposes.</i>
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## Description

Main Competing Risks Dataset Simulated clinical trial data with competing risks survival outcomes. This dataset follows the structure of Adaptive COVID-19 Treatment Trials (ACTT) with built-in treatment effects for demonstration purposes.

## Usage

```
data(main_df)
```

## Format

A data frame with 150 rows and 7 variables:

**ID** Patient identifier (character)

**TimeToRecovery** Time to recovery event in days (numeric)

**TimeToDeath** Time to death event in days (numeric)

**RecoveryCensoringIndicator** Recovery censoring indicator (0=event observed, 1=censored)

**DeathCensoringIndicator** Death censoring indicator (0=event observed, 1=censored)

**BaselineScore** Baseline severity score, range 4-7 (numeric)

**Treatment** Treatment arm indicator (0=control, 1=treatment)

## Details

This is a simulated dataset created for demonstration purposes with realistic treatment effects built in: treatment group has 1.5× faster recovery times and 1.8× improved survival compared to control. The data represents a clinical trial with competing risks where patients can either recover or die, with administrative censoring at 30 days.

## Source

Simulated data based on Weibull distributions with treatment-specific parameters

## Examples

```
data(main_df)
head(main_df)
summary(main_df)
# Compare outcomes by treatment
tapply(main_df$TimeToRecovery, main_df$Treatment, summary)
tapply(main_df$TimeToDeath, main_df$Treatment, summary)
```

---

```
prep_data_cif
```

---

```
Prepare Data for Standard CIF
```

---

## Description

Cleans and prepares a single dataset for standard (competing risks) CIF analysis.

## Usage

```
prep_data_cif(
  data,
  ID = "USUBJID",
  TimeToRecovery = "TTRECOV",
  TimeToDeath = "TTDEATH",
  Recov_Censoring = "RECCNSR",
  Death_Censoring = "DTHCNSR",
  Treatment = "trt"
)
```

## Arguments

data	A data frame with columns for ID, time to recovery, time to death, recovery censor, death censor, and treatment indicator.
ID	Name of the patient ID column. Default is "USUBJID".
TimeToRecovery	Name of the time-to-recovery column. Default "TTRECOV".
TimeToDeath	Name of the time-to-death column. Default "TTDEATH".
Recov_Censoring	Name of the recovery-censor column. Default "RECCNSR" (0=event,1=censor).

Death\_Censoring      Name of the death-censor column. Default "DTHCNSR" (0=event,1=censor).

Treatment              Name of the treatment indicator column (0=control,1=treatment). Default "trt".

### Value

A list with:

- data.w: The processed data frame with columns cn, etime, estatus, etype2, Treatment.
- Treatment: Subset of data.w where Treatment==1.
- Control: Subset of data.w where Treatment==0.

---

```
prep_data_weighted_cif
```

*Prepare Data for Weighted CIF (Legacy Wrapper)*

---

### Description

Convenience wrapper that mirrors the original Part II data preparation workflow for weighted restricted mean analyses. The function now delegates to [prep\\_data\\_weighted\\_cif2](#) to provide consistent checks and support for arbitrary ordinal state definitions.

### Usage

```
prep_data_weighted_cif(
  data_main,
  data_long,
  wID_main = "USUBJID",
  wTimeToRecovery_main = "TTRECOV",
  wTimeToDeath_main = "TTDEATH",
  wRecov_Censoring_main = "RECCNSR",
  wDeath_Censoring_main = "DTHCNSR",
  wBaselineScore_main = "ordscr_bs",
  wTreatment_main = "trt",
  wID_long = "USUBJID",
  wADY_long = "ADYC",
  wScore_long = "ORDSCOR",
  wStates_death = c(4, 5, 6, 7),
  wWeights_death = c(2, 1.5, 1, 0.5),
  wStates_discharge = c(4, 5, 6, 7),
  wWeights_discharge = c(0.5, 1, 1.5, 2)
)
```

**Arguments**

data_main	A data.frame with ID, TTR, TTD, RECCNSR, DTHCNSR, baseline score, trt, etc.
data_long	A data.frame with repeated clinical scores over time (e.g. ADYC, ORDSCOR).
wID_main	Name of the patient ID column in the main dataset (default "USUBJID").
wTimeToRecovery_main	Name of the time-to-recovery column (default "TTRECOV").
wTimeToDeath_main	Name of the time-to-death column (default "TTDEATH").
wRecov_Censoring_main	Name of the recovery-censor column (default "RECCNSR").
wDeath_Censoring_main	Name of the death-censor column (default "DTHCNSR").
wBaselineScore_main	Name of the baseline ordinal column (default "ordscr_bs").
wTreatment_main	Name of the treatment indicator column (0=control,1=treatment). Default "trt".
wID_long	Name of the patient ID column in the long dataset (default "USUBJID").
wADY_long	Name of the day-since-treatment column in the long dataset (default "ADYC").
wScore_long	Name of the ordinal score column in the long dataset (default "ORDSCOR").
wStates_death	Vector of ordinal states for death weighting (default c(4,5,6,7)).
wWeights_death	Numeric weights, same length as wStates_death (default c(2,1.5,1,0.5)).
wStates_discharge	Vector of states for discharge weighting (default c(4,5,6,7)).
wWeights_discharge	Numeric weights, same length as wStates_discharge (default c(0.5,1,1.5,2)).

**Value**

See [prep\\_data\\_weighted\\_cif2](#).

---

```
prep_data_weighted_cif2
```

*Prepare Data for Weighted CIF*

---

**Description**

Prepares merged competing-risks and longitudinal severity data for weighted restricted mean analyses. The routine removes patients with zero follow-up or missing baseline severity, handles discharge-to-die cases, merges the longitudinal trajectory, and computes user-specified weighted time summaries for death-focused and discharge-focused analyses.

**Usage**

```

prep_data_weighted_cif2(
  data_main,
  data_long,
  wID_main = "USUBJID",
  wTimeToRecovery_main = "TTRECOV",
  wTimeToDeath_main = "TTDEATH",
  wRecov_Censoring_main = "RECCNSR",
  wDeath_Censoring_main = "DTHCNSR",
  wBaselineScore_main = "ordscr_bs",
  wTreatment_main = "trt",
  wID_long = "USUBJID",
  wADY_long = "ADYC",
  wScore_long = "ORDSCOR",
  wStates_death = c(4, 5, 6, 7),
  wWeights_death = c(2, 1.5, 1, 0.5),
  wStates_discharge = c(4, 5, 6, 7),
  wWeights_discharge = c(0.5, 1, 1.5, 2)
)

```

**Arguments**

<code>data_main</code>	A data.frame with ID, TTR, TTD, RECCNSR, DTHCNSR, baseline score, trt, etc.
<code>data_long</code>	A data.frame with repeated clinical scores over time (e.g. ADYC, ORDSCOR).
<code>wID_main</code>	Name of the patient ID column in the main dataset (default "USUBJID").
<code>wTimeToRecovery_main</code>	Name of the time-to-recovery column (default "TTRECOV").
<code>wTimeToDeath_main</code>	Name of the time-to-death column (default "TTDEATH").
<code>wRecov_Censoring_main</code>	Name of the recovery-censor column (default "RECCNSR").
<code>wDeath_Censoring_main</code>	Name of the death-censor column (default "DTHCNSR").
<code>wBaselineScore_main</code>	Name of the baseline ordinal column (default "ordscr_bs").
<code>wTreatment_main</code>	Name of the treatment indicator column (0=control,1=treatment). Default "trt".
<code>wID_long</code>	Name of the patient ID column in the long dataset (default "USUBJID").
<code>wADY_long</code>	Name of the day-since-treatment column in the long dataset (default "ADYC").
<code>wScore_long</code>	Name of the ordinal score column in the long dataset (default "ORDSCOR").
<code>wStates_death</code>	Vector of ordinal states for death weighting (default c(4,5,6,7)).
<code>wWeights_death</code>	Numeric weights, same length as wStates_death (default c(2,1.5,1,0.5)).
<code>wStates_discharge</code>	Vector of states for discharge weighting (default c(4,5,6,7)).
<code>wWeights_discharge</code>	Numeric weights, same length as wStates_discharge (default c(0.5,1,1.5,2)).



**Value**

A list containing:

- `data.ws.death` and `data.ws.discharge`: Full merged datasets with an added `wU` column for (death) or (discharge).
- `Treatment.death` and `Control.death`: Subsets for weighted WRMLT2 (death-focused).
- `Treatment.discharge` and `Control.discharge`: Subsets for weighted WRMLT1 (recovery-focused).

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