

# Package: cdtmbnma (via r-universe)

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**Type** Package

**Title** Component, Dose, and Time Network Meta-Analysis with  
Dose-Dependent Interactions

**Version** 0.2.1

**Date** 2026-07-10

**Description** Bayesian component model-based network meta-analysis for treatment combinations with explicit component dose-response and dose-dependent interaction surfaces. The main interface fits single-timepoint arm-level networks with continuous or binary outcomes, any number of components, additive, bilinear, or saturating pairwise interactions, study-level random effects, and prediction at unobserved dose combinations. A stage-one longitudinal interface fits a two-component exponential time-course model with a bilinear interaction on the asymptote. Estimation uses 'Stan' through 'cmdstanr' or 'rstan'. Methods are described in Welton et al. (2009)  [<doi:10.1093/aje/kwp014>](https://doi.org/10.1093/aje/kwp014), Mawdsley et al. (2016)  [<doi:10.1002/psp4.12091>](https://doi.org/10.1002/psp4.12091), Wicha et al. (2017)  [<doi:10.1038/s41467-017-01929-y>](https://doi.org/10.1038/s41467-017-01929-y), and Pedder et al. (2019)  [<doi:10.1002/jrsm.1351>](https://doi.org/10.1002/jrsm.1351).

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**Encoding** UTF-8

**Depends** R (>= 4.1.0)

**Imports** posterior, stats, graphics, grDevices, utils

**Suggests** cmdstanr, rstan, testthat (>= 3.0.0), knitr, rmarkdown, loo

**Additional\_repositories** <https://stan-dev.r-universe.dev>

**SystemRequirements** A working Stan backend through cmdstanr/CmdStan or rstan.

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**Config/testthat/edition** 3

**NeedsCompilation** no  
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|                  |                                                        |
|------------------|--------------------------------------------------------|
| cdtmbnma-package | <i>Component, Dose, and Time Network Meta-Analysis</i> |
|------------------|--------------------------------------------------------|

---

Description

Bayesian component model-based network meta-analysis for treatment combinations with explicit component dose-response and dose-dependent interaction surfaces. The main model supports single-timepoint arm-level networks with continuous or binary outcomes. A stage-one interface supports a two-component exponential time-course model for repeated arm means.

## Details

The single-timepoint workflow is `cdt_data()` followed by `cdt_fit()`, or the one-call wrapper `cdtmbnma()`. Estimation uses Stan through either **cmdstanr** or **rstan**. Fitted objects have `summary()`, `coef()`, `plot()`, and `predict()` methods.

## Interaction surfaces

**none** Additive component effects.

**bilinear** One parameter per component pair; the interaction grows with the product of normalised component doses.

**gpdi** A saturating general pharmacodynamic interaction surface.

## Author(s)

Tyler Pitre

---

antihtn\_factorial\_template

*Amlodipine-Anchored Hypertension Factorial Extraction Template*

---

## Description

Reads the package's antihypertensive factorial extraction form or data dictionary.

## Usage

```
antihtn_factorial_template(type = c("extraction", "dictionary"))
```

## Arguments

`type` Either "extraction" or "dictionary".

## Value

A data frame.

---

|          |                                                   |
|----------|---------------------------------------------------|
| cdt_data | <i>Assemble a Component Dose-Response Network</i> |
|----------|---------------------------------------------------|

---

## Description

Turns an arm-level data frame into the design consumed by `cdt_fit()`. Every component named in components must have a dose column, and zero means the component is absent from that arm.

## Usage

```
cdt_data(data, study, components, outcome = c("continuous", "binary"),
  y = NULL, se = NULL, sd = NULL, n = NULL,
  events = NULL, n_binary = NULL, ref = NULL,
  dstar = NULL, interactions = NULL)
```

## Arguments

|                  |                                                                                              |
|------------------|----------------------------------------------------------------------------------------------|
| data             | A data frame with one row per study arm.                                                     |
| study            | Name of the column identifying the study.                                                    |
| components       | Character vector of component dose column names. A value of zero marks the component absent. |
| outcome          | Either "continuous" or "binary".                                                             |
| y                | For a continuous outcome, the arm mean column.                                               |
| se               | For a continuous outcome, the arm standard error column. Supply this or both sd and n.       |
| sd, n            | For a continuous outcome, columns of arm standard deviation and sample size.                 |
| events, n_binary | For a binary outcome, event-count and sample-size columns.                                   |
| ref              | Optional column flagging exactly one within-study reference arm per study.                   |
| dstar            | Optional named numeric vector of dose-normalisation references for the bilinear surface.     |
| interactions     | NULL, or a list of length-2 character vectors naming component pairs to model.               |

## Value

An object of class `cdt_data`.

## Examples

```
df <- data.frame(study = c("s1", "s1", "s1"), A = c(0, 1, 1),
  B = c(0, 0, 1), y = c(0, -1, -2), se = c(1, 1, 1))
d <- cdt_data(df, study = "study", components = c("A", "B"),
  outcome = "continuous", y = "y", se = "se")
d
```

---

|             |                                            |
|-------------|--------------------------------------------|
| cdt_extdata | <i>Read an Installed Package Data File</i> |
|-------------|--------------------------------------------|

---

**Description**

Reads a CSV file installed with the package.

**Usage**

```
cdt_extdata(name)
```

**Arguments**

|      |                              |
|------|------------------------------|
| name | Filename under inst/extdata. |
|------|------------------------------|

**Value**

A data frame.

---

|         |                                                            |
|---------|------------------------------------------------------------|
| cdt_fit | <i>Fit a Component Dose-Response Network Meta-Analysis</i> |
|---------|------------------------------------------------------------|

---

**Description**

Compiles the Stan model on first use and samples the posterior.

**Usage**

```
cdt_fit(data, interaction = c("bilinear", "none", "gpdi"),
  priors = cdt_priors(), newdata = NULL, backend = "auto", chains = 4,
  iter_warmup = 1000, iter_sampling = 1000, adapt_delta = 0.95,
  seed = 1, refresh = 0, ...)
```

**Arguments**

|                                    |                                                                                               |
|------------------------------------|-----------------------------------------------------------------------------------------------|
| data                               | A cdt_data object.                                                                            |
| interaction                        | Interaction surface: "bilinear", "none", or "gpdi".                                           |
| priors                             | A named list from cdt_priors().                                                               |
| newdata                            | Optional data frame of component-dose combinations for Stan generated-quantities predictions. |
| backend                            | One of "auto", "cmdstanr", or "rstan".                                                        |
| chains, iter_warmup, iter_sampling | Sampler settings.                                                                             |
| adapt_delta                        | Target acceptance probability passed to the Stan backend.                                     |
| seed                               | Random seed.                                                                                  |
| refresh                            | Console refresh interval.                                                                     |
| ...                                | Passed to the backend sampler.                                                                |

## Details

The additive model uses `interaction = "none"`. The bilinear model uses one interaction parameter per co-occurring component pair. The "gpdi" model uses a saturating surface adapted from the general pharmacodynamic interaction model.

## Value

An object of class `cdtmbnma`.

## Examples

```
sv <- sacval_example()
d <- cdt_data(sv, "study", c("d_sac", "d_val"), outcome = "continuous",
             y = "y", se = "se", dstar = c(d_sac = 200, d_val = 320))

# Fitting needs a Stan backend, and the Stan model is compiled on first use.
if (requireNamespace("rstan", quietly = TRUE)) {
  fit <- cdt_fit(d, interaction = "bilinear", backend = "rstan",
               chains = 2, iter_warmup = 500, iter_sampling = 500)
  summary(fit)
}
```

---

cdt\_priors

---

*Prior Settings for Single-Timepoint Models*


---

## Description

Creates prior hyperparameters for `cdt_fit()`.

## Usage

```
cdt_priors(emax_sd = 10, logED50_mean = log(50), logED50_sd = 1,
          int_sd = 5, ref_sd = 10, omega_sd = 2)
```

## Arguments

|                                                     |                                                                     |
|-----------------------------------------------------|---------------------------------------------------------------------|
| <code>emax_sd</code>                                | Prior standard deviation for component Emax values.                 |
| <code>logED50_mean</code> , <code>logED50_sd</code> | Prior mean and standard deviation for log half-maximal dose values. |
| <code>int_sd</code>                                 | Prior standard deviation for interaction parameters.                |
| <code>ref_sd</code>                                 | Prior standard deviation for per-study reference levels.            |
| <code>omega_sd</code>                               | Half-normal prior scale for the random-effect standard deviation.   |

## Value

A named list of prior hyperparameters.

---

|               |                                                                     |
|---------------|---------------------------------------------------------------------|
| cdt_time_data | <i>Assemble a Two-Component Longitudinal Component-Dose Network</i> |
|---------------|---------------------------------------------------------------------|

---

**Description**

Builds data for the two-component exponential time-course model.

**Usage**

```
cdt_time_data(data, study, arm, time, components, y, se = NULL,
              sd = NULL, n = NULL, ref = NULL, dstar = NULL)
```

**Arguments**

|            |                                                                        |
|------------|------------------------------------------------------------------------|
| data       | A long data frame with one row per study-arm-time observation.         |
| study      | Name of the study column.                                              |
| arm        | Name of the arm column.                                                |
| time       | Name of the follow-up time column.                                     |
| components | Character vector naming exactly two component dose columns.            |
| y, se      | Outcome mean and standard error columns.                               |
| sd, n      | Optional standard deviation and sample-size columns used to derive se. |
| ref        | Optional column flagging the reference arm.                            |
| dstar      | Optional named numeric vector of two dose-normalisation references.    |

**Value**

An object of class `cdt_time_data`.

---

|              |                                                        |
|--------------|--------------------------------------------------------|
| cdt_time_fit | <i>Fit the Two-Component Component-Dose-Time Model</i> |
|--------------|--------------------------------------------------------|

---

**Description**

Fits the stage-one longitudinal Stan model with an exponential time-course.

**Usage**

```
cdt_time_fit(data, priors = cdt_time_priors(), newdata = NULL,
             backend = "auto", chains = 4, iter_warmup = 1000,
             iter_sampling = 1000, adapt_delta = 0.95, seed = 1,
             refresh = 0, ...)
```

**Arguments**

|                                    |                                                         |
|------------------------------------|---------------------------------------------------------|
| data                               | A cdt_time_data object.                                 |
| priors                             | A named list from cdt_time_priors().                    |
| newdata                            | Optional data frame of two-component dose combinations. |
| backend                            | One of "auto", "cmdstanr", or "rstan".                  |
| chains, iter_warmup, iter_sampling | Sampler settings.                                       |
| adapt_delta                        | Target acceptance probability.                          |
| seed                               | Random seed.                                            |
| refresh                            | Console refresh interval.                               |
| ...                                | Passed to the backend sampler.                          |

**Value**

An object of class cdt\_timefit.

---

|                 |                                                               |
|-----------------|---------------------------------------------------------------|
| cdt_time_priors | <i>Prior Settings for the Two-Component Time-Course Model</i> |
|-----------------|---------------------------------------------------------------|

---

**Description**

Creates prior hyperparameters for cdt\_time\_fit().

**Usage**

```
cdt_time_priors(ref_E_sd = 5, ref_lograte_mean = -3,
  ref_lograte_sd = 1, emax_sd = 10, logED50_mean = 0,
  logED50_sd = 1, eta_sd = 5, rate_sd = 1,
  omega_E_sd = 2, omega_k_sd = 0.5)
```

**Arguments**

|                                  |                                                                           |
|----------------------------------|---------------------------------------------------------------------------|
| ref_E_sd                         | Prior standard deviation for study-specific reference asymptotes.         |
| ref_lograte_mean, ref_lograte_sd | Prior mean and standard deviation for study-specific reference log rates. |
| emax_sd                          | Prior standard deviation for component Emax values.                       |
| logED50_mean, logED50_sd         | Prior mean and standard deviation for log half-maximal dose values.       |
| eta_sd                           | Prior standard deviation for the bilinear interaction.                    |
| rate_sd                          | Prior standard deviation for component log-rate dose effects.             |
| omega_E_sd, omega_k_sd           | Half-normal prior scales for random-effect standard deviations.           |

**Value**

A named list of prior hyperparameters.



**Description**

Convenience wrapper that builds the design with `cdt_data()` and fits it with `cdt_fit()`.

**Usage**

```
cdtmbnma(data, study, components, outcome = c("continuous", "binary"),
  y = NULL, se = NULL, sd = NULL, n = NULL,
  events = NULL, n_binary = NULL, ref = NULL,
  dstar = NULL, interactions = NULL,
  interaction = c("bilinear", "none", "gpdi"),
  priors = cdt_priors(), newdata = NULL, backend = "auto", chains = 4,
  iter_warmup = 1000, iter_sampling = 1000, adapt_delta = 0.95,
  seed = 1, refresh = 0, ...)
```

**Arguments**

`data`, `study`, `components`, `outcome`, `y`, `se`, `sd`, `n`, `events`, `n_binary`, `ref`, `dstar`,  
`interactions`

Passed to `cdt_data()`.

`interaction`, `priors`, `newdata`, `backend`, `chains`, `iter_warmup`,  
`iter_sampling`, `adapt_delta`, `seed`, `refresh`, ...

Passed to `cdt_fit()`.

**Value**

An object of class `cdtmbnma`.

**Examples**

```
# Fitting needs a Stan backend, and the Stan model is compiled on first use.
if (requireNamespace("rstan", quietly = TRUE)) {
  fit <- cdtmbnma(sacval_example(), study = "study",
    components = c("d_sac", "d_val"), outcome = "continuous",
    y = "y", se = "se", backend = "rstan",
    chains = 2, iter_warmup = 500, iter_sampling = 500)
  summary(fit)
}
```

---

|                  |                                                              |
|------------------|--------------------------------------------------------------|
| coef.cdt_timefit | <i>Extract Long-Term Coefficients from a Time-Course Fit</i> |
|------------------|--------------------------------------------------------------|

---

**Description**

Extracts long-term component coefficient summaries.

**Usage**

```
## S3 method for class 'cdt_timefit'
coef(object, ...)
```

**Arguments**

|        |                              |
|--------|------------------------------|
| object | A fitted cdt_timefit object. |
| ...    | Unused.                      |

**Value**

A data frame with Emax and ED50 summaries for the two components.

---

|               |                                       |
|---------------|---------------------------------------|
| coef.cdtmbnma | <i>Extract Component Coefficients</i> |
|---------------|---------------------------------------|

---

**Description**

Extracts component dose-response coefficient summaries.

**Usage**

```
## S3 method for class 'cdtmbnma'
coef(object, ...)
```

**Arguments**

|        |                           |
|--------|---------------------------|
| object | A fitted cdtmbnma object. |
| ...    | Unused.                   |

**Value**

A data frame with posterior summaries for component Emax and ED50 values.

---

|                   |                                                    |
|-------------------|----------------------------------------------------|
| copd_bgf_template | <i>COPD BGF Triple-Therapy Extraction Template</i> |
|-------------------|----------------------------------------------------|

---

**Description**

Reads the package's COPD BGF extraction form or data dictionary.

**Usage**

```
copd_bgf_template(type = c("extraction", "dictionary"))
```

**Arguments**

|      |                                      |
|------|--------------------------------------|
| type | Either "extraction" or "dictionary". |
|------|--------------------------------------|

**Value**

A data frame.

---

|               |                                            |
|---------------|--------------------------------------------|
| plot.cdtmbnma | <i>Plot Component Dose-Response Curves</i> |
|---------------|--------------------------------------------|

---

**Description**

Draws marginal component dose-response curves with posterior credible bands.

**Usage**

```
## S3 method for class 'cdtmbnma'  
plot(x, ngrid = 60, probs = c(0.025, 0.975), ...)
```

**Arguments**

|       |                                      |
|-------|--------------------------------------|
| x     | A fitted cdtmbnma object.            |
| ngrid | Number of dose points per curve.     |
| probs | Two quantiles for the credible band. |
| ...   | Passed to plot().                    |

**Value**

Invisibly, a list of plotted grids.

---

|                     |                                                         |
|---------------------|---------------------------------------------------------|
| predict.cdt_timefit | <i>Predict Long-Term Effects from a Time-Course Fit</i> |
|---------------------|---------------------------------------------------------|

---

**Description**

Computes long-term asymptotic relative effects for the stage-one longitudinal model.

**Usage**

```
## S3 method for class 'cdt_timefit'
predict(object, newdata, probs = c(0.025, 0.975), ...)
```

**Arguments**

|         |                                                                     |
|---------|---------------------------------------------------------------------|
| object  | A fitted cdt_timefit object.                                        |
| newdata | Data frame carrying the two component-dose columns used in fitting. |
| probs   | Quantiles for credible intervals.                                   |
| ...     | Unused.                                                             |

**Value**

A data frame with doses, posterior mean, posterior standard deviation, and requested quantiles.

---

|                  |                                                                |
|------------------|----------------------------------------------------------------|
| predict.cdtmbnma | <i>Predict Relative Effects at Component-Dose Combinations</i> |
|------------------|----------------------------------------------------------------|

---

**Description**

Computes posterior relative effects against the all-zero reference at arbitrary component-dose combinations.

**Usage**

```
## S3 method for class 'cdtmbnma'
predict(object, newdata, probs = c(0.025, 0.975), ...)
```

**Arguments**

|         |                                                                 |
|---------|-----------------------------------------------------------------|
| object  | A fitted cdtmbnma object.                                       |
| newdata | Data frame carrying the component dose columns used in fitting. |
| probs   | Quantiles for credible intervals.                               |
| ...     | Unused.                                                         |

**Value**

A data frame with doses, posterior mean, posterior standard deviation, and requested quantiles.

---

sacval\_example

*Sacubitril and Valsartan Blood-Pressure Dose Plane*


---

**Description**

Reads the package's sacubitril/valsartan example data.

**Usage**

```
sacval_example()
```

**Value**

A data frame with columns study, arm, d\_sac, d\_val, n, y, sd, se, and sd\_source.

**Examples**

```
head(sacval_example())
```

---

summary.cdt\_timefit

*Summarise a Two-Component Time-Course Fit*


---

**Description**

Summarises key structural parameters in a cdt\_timefit object.

**Usage**

```
## S3 method for class 'cdt_timefit'
summary(object, ...)
```

**Arguments**

|        |                              |
|--------|------------------------------|
| object | A fitted cdt_timefit object. |
| ...    | Unused.                      |

**Value**

A data frame of posterior summaries and convergence diagnostics.

---

|                  |                                 |
|------------------|---------------------------------|
| summary.cdtmbnma | <i>Summarise a cdtmbnma Fit</i> |
|------------------|---------------------------------|

---

**Description**

Summarises the structural parameters of a cdtmbnma fit.

**Usage**

```
## S3 method for class 'cdtmbnma'  
summary(object, ...)
```

**Arguments**

|        |                           |
|--------|---------------------------|
| object | A fitted cdtmbnma object. |
| ...    | Unused.                   |

**Value**

A data frame of posterior summaries and convergence diagnostics.

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