Package: trialr (via r-universe)

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Title Clinical Trial Designs in 'rstan'

Description A collection of clinical trial designs and methods, implemented in 'rstan' and R, including: the Continual Reassessment Method by O'Quigley et al. (1990) <doi:10.2307/2531628>; EffTox by Thall & Cook (2004) <doi:10.1111/j.0006-341X.2004.00218.x>; the two-parameter logistic method of Neuenschwander, Branson & Sponer (2008) <doi:10.1002/sim.3230>; and the Augmented Binary method by Wason & Seaman (2013) <doi:10.1002/sim.5867>; and more. We provide functions to aid model-fitting and analysis. The 'rstan' implementations may also serve as a cookbook to anyone looking to extend or embellish these models. We hope that this package encourages the use of Bayesian methods in clinical trials. There is a preponderance of early phase trial designs because this is where Bayesian methods are used most. If there is a method you would like implemented, please get in touch.

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trialr-package *The 'trialr' package.*

Description

trialr collects in one place Bayesian clinical trial designs and methods. Models are implemented in Stan and helper functions are provided in R.

References

Stan Development Team (2018). RStan: the R interface to Stan. R package version 2.18.2. https://mc-stan.org/

as.data.frame.crm_fit *Convert crm_fit object to* data.frame.

Description

Convert crm_fit object to data.frame.

Usage

```
## S3 method for class 'crm_fit'
as.data.frame(x, ...)
```

Arguments

x	crm_fit object to convert.
...	Extra parameters, passed onwards.

Value

A data.frame

as.data.frame.efftox_fit *Convert efftox_fit object to* data.frame.

Description

Convert efftox_fit object to data.frame.

Usage

```
## S3 method for class 'efftox_fit'
as.data.frame(x, ...)
```

Arguments

x	efftox_fit object to convert.
...	Extra parameters, passed onwards.

Value

A data.frame

as.mcmc.list.crm_fit *Convert* crm_fit *to instance of* mcmc.list

Description

This function allows trialr to use tidybayes functions.

Usage

```
## S3 method for class 'crm_fit'
as.mcmc.list(x, ...)
```

Arguments

x	Object of class crm_fit
...	Extra variables that are passed onwards.

Value

Object of class mcmc.list

`as.mcmc.list.efftox_fit` *Convert* `efftox_fit` *to instance of* `mcmc.list`

Description

This function allows trialr to use tidybayes functions.

Usage

```
## S3 method for class 'efftox_fit'
as.mcmc.list(x, ...)
```

Arguments

`x`	Object of class `efftox_fit`
`...`	Extra variables that are passed onwards.

Value

Object of class `mcmc.list`

`as_tibble.augbin_2t_1a_fit` *Cast* `augbin_2t_1a_fit` *object to* `tibble`.

Description

Cast `augbin_2t_1a_fit` object to `tibble`.

Usage

```
## S3 method for class 'augbin_2t_1a_fit'
as_tibble(x, ...)
```

Arguments

`x`	Object of class `augbin_2t_1a_fit`.
`...`	Extra args passed onwards.

Value

Object of class `tibble`

`as_tibble.dose_finding_paths` *Cast* `dose_finding_paths` *object to* `tibble`.

Description

Cast `dose_finding_paths` object to `tibble`.

Usage

```
## S3 method for class 'dose_finding_paths'
as_tibble(x, ...)
```

Arguments

`x`	Object of class `dose_finding_paths`.
`...`	Extra args passed onwards.

Value

Object of class `tibble`

`augbin_2t_1a_fit` *Class used by* **trialr** *to fit Wason & Seaman's Augmented Binary method in single arm trials with two post-baseline tumour assessments.*

Description

Class used by **trialr** to fit Wason & Seaman's Augmented Binary method in single arm trials with two post-baseline tumour assessments.

Usage

```
augbin_2t_1a_fit(num_patients, tumour_size, non_shrinkage_failure, fit)
```

Arguments

`num_patients`	Integer, the number of patients analysed.
`tumour_size`	matrix-like object containing tumour size measures, with rows representing patients and columns representing chronological assessment points. Column one is baseline.
`non_shrinkage_failure`	matrix-like object containing logical indicators of non-shrinkage failure, with rows representing patients and columns representing chronological assessment points.
`fit`	An object of class `stanfit`, containing the posterior samples.

References

Wason JMS, Seaman SR. Using continuous data on tumour measurements to improve inference in phase II cancer studies. Statistics in Medicine. 2013;32(26):4639-4650. doi:10.1002/sim.5867

Eisenhauer EA, Therasse P, Bogaerts J, et al. New response evaluation criteria in solid tumours: Revised RECIST guideline (version 1.1). European Journal of Cancer. 2009;45(2):228-247. doi:10.1016/j.ejca.2008.10.026

See Also

`augbin_fit` `stan_augbin`

`augbin_fit` *Class used by* **trialr** *to fit Wason & Seaman's Augmented Binary method.*

Description

Class used by **trialr** to fit Wason & Seaman's Augmented Binary method.

Usage

```
augbin_fit(num_patients, tumour_size, non_shrinkage_failure, fit)
```

Arguments

`num_patients`	Integer, the number of patients analysed.
`tumour_size`	matrix-like object containing tumour size measures, with rows representing patients and columns representing chronological standardised assessment points. Column one is baseline.
`non_shrinkage_failure`	matrix-like object containing logical indicators of non-shrinkage failure, with rows representing patients and columns representing chronological standardised assessment points.
`fit`	An object of class `stanfit`, containing the posterior samples.

References

Wason JMS, Seaman SR. Using continuous data on tumour measurements to improve inference in phase II cancer studies. Statistics in Medicine. 2013;32(26):4639-4650. doi:10.1002/sim.5867

Eisenhauer EA, Therasse P, Bogaerts J, et al. New response evaluation criteria in solid tumours: Revised RECIST guideline (version 1.1). European Journal of Cancer. 2009;45(2):228-247. doi:10.1016/j.ejca.2008.10.026

See Also

`stan_augbin`

`binary_prob_success` *Calculate the binary probability of success.*

Description

Calculate the binary probability of success.

Calculate the binary probability of success from an augbin_2t_1a_fit object.

Usage

```
binary_prob_success(x, ...)

## S3 method for class 'augbin_2t_1a_fit'
binary_prob_success(
  x,
  y1_lower = -Inf,
  y1_upper = Inf,
  y2_lower = -Inf,
  y2_upper = log(0.7),
  conf.level = 0.95,
  ...
)
```

Arguments

`x`	an R object of class `"augbin_fit"`
`...`	arguments passed to other methods
`y1_lower`	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to negative infinity.
`y1_upper`	numeric, maximum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to positive infinity.
`y2_lower`	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 2 to baseline.
`y2_upper`	numeric, maximum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 2 to baseline. Defaults to log(0.7).
`conf.level`	confidence level for interval.

Value

a `data.frame`-like object

Examples

```
## Not run:
fit <- stan_augbin_demo()
binary_prob_success(fit, y2_upper = log(0.7))

## End(Not run)
```

`careful_escalation` *Dose selection function that practices careful escalation.*

Description

Dose selection function that avoids dose-skipping in escalation and advocates stopping when there is sufficient evidence that the risk of toxicity at a reference dose exceeds some threshold.

Usage

```
careful_escalation(
  dose_finding_fit,
  tox_threshold,
  certainty_threshold,
  reference_dose = 1,
  start_dose = 1
)
```

Arguments

`dose_finding_fit`	Instance of `dose_finding_fit`.
`tox_threshold`	numeric, the toxicity threshold.
`certainty_threshold`	numeric, the required confidence that the risk of toxicity exceeds ‘tox_threshold‘ to advocate stopping.
`reference_dose`	the integer index of the reference dose. 1 by default, i.e. the lowest dose-level.
`start_dose`	the integer index of the desired starting dose. 1 by default. This is required for the function to give the desired answer when no patients have yet been treated.

Value

an integer dose-level

Examples

```
## Not run:
# CRM example
fit <- stan_crm('1N 2N 3T', skeleton = c(0.1, 0.2, 0.35, 0.6),
                target = 0.2, model = 'empiric', beta_sd = 1,
                seed = 123)

## End(Not run)
```

`closest_to_target` *Get index of element in vector with value closest to a target*

Description

Get index of element in vector with value closest to a target

Usage

```
closest_to_target(vector, target)
```

Arguments

`vector`	Identify element in this numeric vector
`target`	numeric target

Value

an integer indexing `vector`

Examples

```
closest_to_target(c(0.1, 0.2, 0.3), 0.05)  # 1
closest_to_target(c(0.1, 0.2, 0.3), 0.22)  # 2
closest_to_target(c(0.1, 0.2, 0.3), -0.05) # 1
closest_to_target(c(0.1, 0.2, 0.3), 8) # 3
```

crm_codified_dose_logistic *Calculate codified CRM doses.*

Description

Calculate the codified CRM doses that map to probability of toxicity `prob_tox` in a logistic model with expected values for intercept and gradient. I.e. find $x[i]$ such that $logit(p[i]) = \alpha + \beta x[i]$, were p is `prob_tox`.

Usage

```
crm_codified_dose_logistic(prob_tox, alpha_mean, beta_mean)
```

Arguments

`prob_tox`	Numeric vector, seek codified doses that yield these probabilities of toxicity.
`alpha_mean`	Numeric, expected value of intercept.
`beta_mean`	Numeric, expected value of gradient with respect to dose.

Value

Numeric vector of codified doses.

Examples

```
skeleton <- c(0.05, 0.1, 0.2, 0.5)
crm_codified_dose_logistic(skeleton, 1, 0)
crm_codified_dose_logistic(skeleton, 3, 0.5)
```

crm_dtps *Calculate dose-transition pathways for a CRM study*

Description

Calculate dose-transition pathways (DTPs, Yap et al, 2017) for a dose-finding trial using the continual reassessment method (CRM) design. DTPs are a glimpse into the future for an in-progress trial. They tell us what the model would advise for all feasible future outcomes. They can be used in the design stages to detect possible undesirable behaviour. They can be used during the trial to aid planning and understanding.

Usage

```
crm_dtps(
  skeleton,
  target,
  model,
  cohort_sizes,
  previous_outcomes = "",
  next_dose = NULL,
  user_dose_func = NULL,
  verbose = FALSE,
  i_am_patient = FALSE,
  ...
)
```

Arguments

skeleton	a vector of the prior guesses of toxicity at doses. This should be a monotonically-increasing vector of numbers between 0 and 1.
target	the target toxicity probability, a number between 0 and 1. This value would normally be one of the values in skeleton, but that is not a requirement.
model	Character string to denote desired model. One of empiric, logistic, logistic_gamma, or logistic2. The choice of model determines which extra parameters are required by .... See Details.
cohort_sizes	vector of future cohort sizes, i.e. positive integers. E.g. To calculate paths for the the next cohort of two followed by another cohort of three, use cohort_sizes = c(2, 3).
previous_outcomes	Outcomes observed hitherto in the syntax required by df_parse_outcomes.
next_dose	optional, integer (1-based) dose-level to be given to the next cohort. If omitted, the dose suggested by the model is used.
user_dose_func	optional delegate for deciding dose. A function that takes a crm_fit as the sole argument and returns the integer (1-based) dose-level to be given next, or NA to show that no dose should be chosen and the trial stopped. This function gives the user the opportunity to build in custom behaviour to tailor the dose selection decision in response to the insights garnered by the fit model, or recommend that a trial path be halted immediately. If omitted, the dose ordinarily chosen by the model is used. An example is given below.
verbose	logical, TRUE to get log messages.
i_am_patient	logical. The number of paths to analyse grows faster than linearly in the number of future cohorts to resolve. Fitting many models by MCMC can take a long time. This function will not proceed unless you signify your patience when the number of paths to reolve exceeds 100.
...	Extra parameters passed to stan_crm.

Details

Different model choices require that different parameters are provided. See below.

Value

A list of dose_finding_path_node objects.

Parameter requirements of empiric model

- beta_sd

Parameter requirements of logistic model

- a0
- beta_mean
- beta_sd

Parameter requirements of logistic_gamma model

- a0
- beta_shape
- beta_inverse_scale

Parameter requirements of logistic2 model

- alpha_mean
- alpha_sd
- beta_mean
- beta_sd

Author(s)

Kristian Brock

References

Yap C, Billingham LJ, Cheung YK, Craddock C, O'Quigley J. Dose transition pathways: The missing link between complex dose-finding designs and simple decision-making. Clinical Cancer Research. 2017;23(24):7440-7447. doi:10.1158/1078-0432.CCR-17-0582

See Also

df_parse_outcomes, stan_crm, crm_path_analysis, dose_finding_path_node

Examples

```
## Not run:
target <- 0.25
skeleton <- c(0.05, 0.15, 0.25, 0.4, 0.6)

# Run DTPs for the first two cohorts of two for new a trial:
paths <- crm_dtps(skeleton = skeleton, target = target, model = 'empiric',
```

```
                  cohort_sizes = c(2, 2), next_dose = 3, beta_sd = 1)
length(paths)  # 13

library(tibble)
df <- as_tibble(paths)
df


# Run DTPs for the next cohort of three in a trial that has already treated
# six patients, seeing some toxicity at dose-level 3:
paths2 <- crm_dtps(skeleton = skeleton, target = target, model = 'empiric',
                   cohort_sizes = c(3), previous_outcomes = '2NNN 3TTN',
                   beta_sd = 1)
length(paths2)  # 5
as_tibble(paths2)
# We see that de-escalation to dose-level 2 should occur now, and that any
# further toxicity will result in advice for further de-escalation to
# dose-level 1.


# An example with a custom dose selection function
paths3 <- crm_dtps(skeleton = skeleton, target = target, model = 'empiric',
                   cohort_sizes = c(3, 3), previous_outcomes = '2NN 3TN',
                   next_dose = 2, beta_sd = 1,
                   user_dose_func = function(x) {
                     careful_escalation(x, tox_threshold = target + 0.1,
                                        certainty_threshold = 0.7)
                   }, seed = 123, refresh = 0)
spread_paths(as_tibble(paths3) %>% select(-fit, -parent_fit, -dose_index))
# Stopping is recommended when the dose selection function returns NA.

## End(Not run)
```

`crm_fit-class` *Class of model fit by* **trialr** *using the CRM dose-finding design.*

Description

Class of model fit by **trialr** using the CRM dose-finding design.

Usage

```
crm_fit(
  dose_indices,
  num_patients,
  doses,
  tox,
  weights,
  prob_tox,
  median_prob_tox,
```

```
  prob_mtd,
  recommended_dose,
  dat,
  fit,
  samples = NULL
)
```

Arguments

dose_indices	A vector of integers representing the dose-levels under consideration.
num_patients	Integer, the number of patients analysed.
doses	vector of integers representing the dose given to the patients.
tox	vector of integers representing the toxicity status of the patients.
weights	Vector of numeric weights for the observations for patients 1:num_patients, thus facilitating the TITE-CRM design.
prob_tox	The posterior mean probabilities of toxicity at doses 1:n; a vector of numbers between 0 and 1.
median_prob_tox	The posterior median probabilities of toxicity at doses 1:n; a vector of numbers between 0 and 1.
prob_mtd	The posterior probability that each dose is the MTD, by the chosen model; a vector of numbers between 0 and 1. This probability reflects the uncertainty remaining in the parameter distributions, whereas prob_tox and median_prob_tox do not.
recommended_dose	An integer representing the dose-level that is recommended for the next patient or cohort. Contrast to modal_mtd_candidate.
dat	Object crm_params containing data passed to sampling.
fit	An object of class stanfit, containing the posterior samples.
samples	An optional data.frame like object of samples.

Details

See methods(class = "crm_fit") for an overview of available methods.

See Also

stan_crm

`crm_params-class` *Container class for parameters to fit the CRM models in trialr.*

Description

Container class for parameters to fit the CRM models in trialr.

Usage

```
crm_params(
  skeleton,
  target,
  a0 = NULL,
  alpha_mean = NULL,
  alpha_sd = NULL,
  beta_mean = NULL,
  beta_sd = NULL,
  beta_shape = NULL,
  beta_inverse_scale = NULL
)
```

Arguments

`skeleton`	a vector of the prior guesses of toxicity at doses. This should be a monotonically-increasing vector of numbers between 0 and 1.
`target`	the target toxicity probability, a number between 0 and 1. This value would normally be one of the values in `skeleton`, but that is not a requirement.
`a0`	Value of fixed intercept parameter. Only required for certain models. See Details.
`alpha_mean`	Prior mean of intercept variable for normal prior. Only required for certain models. See Details.
`alpha_sd`	Prior standard deviation of intercept variable for normal prior. Only required for certain models. See Details.
`beta_mean`	Prior mean of gradient variable for normal prior. Only required for certain models. See Details.
`beta_sd`	Prior standard deviation of slope variable for normal prior. Only required for certain models. See Details.
`beta_shape`	Prior shape parameter of slope variable for gamma prior. Only required for certain models. See Details.
`beta_inverse_scale`	Prior inverse scale parameter of slope variable for gamma prior. Only required for certain models. See Details.

Details

Different model parameterisations require that difference parameter values are specified.

Parameter requirements of `empiric` model

- `beta_sd`

Parameter requirements of `logistic` model

- `a0`
- `beta_mean`
- `beta_sd`

Parameter requirements of `logistic_gamma` model

- `a0`
- `beta_shape`
- `beta_inverse_scale`

Parameter requirements of `logistic2` model

- `alpha_mean`
- `alpha_sd`
- `beta_mean`
- `beta_sd`

See Also

`stan_crm`

`crm_path_analysis` *Fit a CRM model to the incrementally observed outcomes on a trial pathway.*

Description

Fit a continuous reassessment method (CRM) model to the outcomes cumulatively observed at the end of each cohort in a trial pathway. E.g. if the trial pathway is 1NN 2NN 3NT, we have three cohorts of two patients. This function will fit the model to the following four states: before any patients have been evaluated; after 1NN; after 1NN 2NN; and finally after 1NN 2NN 3NT. This allows us to analyse how the trial model is evolving in its estimation as trial data is accumulated.

Usage

```
crm_path_analysis(outcome_str, skeleton, target, model, verbose = FALSE, ...)
```

Arguments

outcome_str	A string representing the outcomes observed hitherto. See df_parse_outcomes for a description of syntax and examples. Alternatively, you may provide doses_given and tox parameters. See Details.
skeleton	a vector of the prior guesses of toxicity at doses. This should be a monotonically-increasing vector of numbers between 0 and 1.
target	the target toxicity probability, a number between 0 and 1. This value would normally be one of the values in skeleton, but that is not a requirement.
model	Character string to denote desired model. One of empiric, logistic, logistic_gamma, or logistic2. The choice of model determines which extra parameters are required by .... See Details.
verbose	logical, TRUE to get log messages.
...	Extra parameters passed to stan_crm.

Details

Different model choices require that different parameters are provided. See below.

Value

A list of dose_finding_path_node objects.

Parameter requirements of empiric model

- beta_sd

Parameter requirements of logistic model

- a0
- beta_mean
- beta_sd

Parameter requirements of logistic_gamma model

- a0
- beta_shape
- beta_inverse_scale

Parameter requirements of logistic2 model

- alpha_mean
- alpha_sd
- beta_mean
- beta_sd

Author(s)

Kristian Brock

See Also

df_parse_outcomes, stan_crm, dose_finding_path_node

Examples

```
## Not run:
# CRM example
target <- 0.25
skeleton <- c(0.05, 0.15, 0.25, 0.4, 0.6)
paths <- crm_path_analysis(
  outcome_str = '1NNN 2NTN 2NNN',
  skeleton = skeleton, target = target, model = 'empiric',
  beta_sd = 1, seed = 123, refresh = 0)
length(paths)  # 4
names(paths)[1]  # ""
names(paths)[2]  # "1NNN"
names(paths)[3]  # "1NNN 2NTN"
names(paths)[4]  # "1NNN 2NTN 2NNN"
# Each node is an analysis fit to the cumulative outcomes
# Converting to a tibble presents some nice tidyverse-related opportunities
library(tibble)
df <- as_tibble(paths)
df

## End(Not run)
```

---

crm_prior_beliefs *Get the prior beliefs for a CRM trial scenario.*

Description

Infer the prior beliefs consistent with the parameters and model form for a CRM dose-finding trial. This function could be interpreted as fitting the model to no data, thus examining the beliefs on dose-toxicity that are suggested by the parameter priors alone. This function provides the task analagous to stan_crm before any data has been collected.

Usage

```
crm_prior_beliefs(
  skeleton,
  target,
  model = c("empiric", "logistic", "logistic_gamma", "logistic2"),
  a0 = NULL,
  alpha_mean = NULL,
```

```
  alpha_sd = NULL,
  beta_mean = NULL,
  beta_sd = NULL,
  beta_shape = NULL,
  beta_inverse_scale = NULL,
  ...
)
```

Arguments

skeleton	a vector of the prior guesses of toxicity at doses. This should be a monotonically-increasing vector of numbers between 0 and 1.
target	the target toxicity probability, a number between 0 and 1. This value would normally be one of the values in skeleton, but that is not a requirement.
model	Character string to denote desired model. One of empiric, logistic, logistic_gamma, or logistic2. The choice of model determines which parameters are required. See Details.
a0	Value of fixed intercept parameter. Only required for certain models. See Details.
alpha_mean	Prior mean of intercept variable for normal prior. Only required for certain models. See Details.
alpha_sd	Prior standard deviation of intercept variable for normal prior. Only required for certain models. See Details.
beta_mean	Prior mean of gradient variable for normal prior. Only required for certain models. See Details.
beta_sd	Prior standard deviation of slope variable for normal prior. Only required for certain models. See Details.
beta_shape	Prior shape parameter of slope variable for gamma prior. Only required for certain models. See Details.
beta_inverse_scale	Prior inverse scale parameter of slope variable for gamma prior. Only required for certain models. See Details.
...	extra parameters passed to stan_crm.

Details

Different model choices require that different parameters are provided. See below.

Value

An object of class crm_fit

Parameter requirements of empiric model

- beta_sd

Parameter requirements of `logistic` model

- `a0`
- `beta_mean`
- `beta_sd`

Parameter requirements of `logistic_gamma` model

- `a0`
- `beta_shape`
- `beta_inverse_scale`

Parameter requirements of `logistic2` model

- `alpha_mean`
- `alpha_sd`
- `beta_mean`
- `beta_sd`

Author(s)

Kristian Brock

References

O'Quigley, J., Pepe, M., & Fisher, L. (1990). Continual reassessment method: a practical design for phase 1 clinical trials in cancer. Biometrics, 46(1), 33-48. https://www.jstor.org/stable/2531628

Cheung, Y.K. (2011). Dose Finding by the Continual Reassessment Method. CRC Press. ISBN 9781420091519

See Also

`stan_crm` `crm_fit`

Examples

```
skeleton <- c(0.05, 0.1, 0.15, 0.33, 0.5)
target <- 0.33

prior_fit1 <- crm_prior_beliefs(skeleton, target, model = 'empiric',
                                beta_sd = sqrt(1.34))
prior_fit2 <- crm_prior_beliefs(skeleton, target, model = 'logistic_gamma',
                                a0 = 3, beta_shape = 1,
                                beta_inverse_scale = 2)
```

crm_process *Process RStan samples from a CRM model.*

Description

Internal function to process rstan samples from a CRM model to make inferences about dose-toxicity and which dose should be recommended next. Typically, this function is not required to be called explicitly by the user because `stan_crm` will call it implicitly.

Usage

```
crm_process(dat, fit)
```

Arguments

`dat`	An instance of `crm_params`, a list of CRM parameters.
`fit`	An instance of `rstan::stanmodel`, derived by fitting one of the trialr CRM models.

Value

An instance of `crm_fit`.

df_parse_outcomes *Parse a string of dose-finding trial outcomes to binary vector notation.*

Description

Parse a string of dose-finding trial outcomes to the binary vector notation required by Stan for model invocation. The outcome string describes the doses given and outcomes observed. The format of the string is the pure phase I analogue to that described in Brock et al. (2017). The letters T and N are used to represents patients that experienced (T)oxicity and (N)o toxicity. These letters are concatenated after numerical dose-levels to convey the outcomes of cohorts of patients. For instance, `2NNT` represents a cohort of three patients that were treated at dose-level 2, one of whom experienced toxicity, and two that did not. The results of cohorts are separated by spaces. Thus, `2NNT 1NN` extends our previous example, where the next cohort of two were treated at dose-level 1 and neither experienced toxicity. See examples.

Usage

```
df_parse_outcomes(outcome_string, as.list = TRUE)
```

Arguments

`outcome_string`	character string, conveying doses given and outcomes observed.
`as.list`	TRUE (the default) to return a `list`; FALSE to return a `data.frame`

Value

If `as.list == TRUE`, a list with elements `tox`, `doses` and `num_patients`. These elements are congruent with those of the same name in `crm_params`, for example. If `as.list == FALSE`, a data.frame with columns `tox` and `doses`.

References

Brock, K., Billingham, L., Copland, M., Siddique, S., Sirovica, M., & Yap, C. (2017). Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology, 17(1), 112. https://doi.org/10.1186/s12874-017-0381-x

Examples

```
x = df_parse_outcomes('1NNN 2NTN 3TTT')
x$num_patients  # 9
x$doses         # c(1, 1, 1, 2, 2, 2, 3, 3, 3)
x$tox           # c(0, 0, 0, 0, 1, 0, 1, 1, 1)
sum(x$tox)      # 4
```

---

dose_finding_fit-class

Class of dose-finding model fit by **trialr** *using Stan.*

Description

Class of dose-finding model fit by **trialr** using Stan.

Usage

```
dose_finding_fit(
  dose_indices,
  num_patients,
  doses,
  tox,
  prob_tox,
  median_prob_tox,
  recommended_dose,
  dat,
  fit
)
```

Arguments

`dose_indices`	A vector of integers representing the dose-levels under consideration.
`num_patients`	Integer, the number of patients analysed.
`doses`	vector of integers representing the dose given to the patients.

tox	vector of integers representing the toxicity status of the patients.
prob_tox	The posterior mean probabilities of toxicity at doses 1:n; a vector of numbers between 0 and 1.
median_prob_tox	The posterior median probabilities of toxicity at doses 1:n; a vector of numbers between 0 and 1.
recommended_dose	An integer representing the dose-level that is recommended for the next patient or cohort.
dat	Object crm_params containing data passed to sampling.
fit	An object of class stanfit, containing the posterior samples.

See Also

crm_fit, efftox_fit

`dose_finding_path_node-class` *Class to hold the elements of a single dose-finding analysis residing in a pathway of analyses.*

Description

A pathway in a dose-finding trial is a series of successive analyses. For instance, the model will likely be fit to all of the outcomes observed at the end of the first cohort, the second cohort, etc. This class holds the elements reflecting the analysis, and the place of this analysis in the pathway.

Usage

```
dose_finding_path_node(
  node_id,
  parent_node_id,
  depth,
  outcomes,
  next_dose,
  fit,
  parent_fit
)
```

Arguments

node_id	An integer representing the id of this node in a pathway.
parent_node_id	An integer representing the id of this node's parent in the pathway.
depth	An integer representing the depth of this node in the pathway, where the root has depth 0.

outcomes	A string representing the outcomes observed at the time of analysis. See df_parse_outcomes for a description of syntax and examples.
next_dose	An integer representing the dose recommended by the model for the next patient or cohort of patients.
fit	Object obtained from fitting the dose-finding model to outcomes.
parent_fit	Object obtained from fitting the dose-finding model to the outcomes of the parent node. Comparing to fit will oten be valuable.

Value

Instance of class dose_finding_path_node

Examples

```
## Not run:
parent_outcomes <- '1NNN'
outcomes <- '1NNN 2NNT'
target <- 0.25
skeleton <- c(0.05, 0.15, 0.25, 0.4, 0.6)
parent_fit <- stan_crm(outcome_str = parent_outcomes, skeleton = skeleton,
                       target = target, model = 'empiric', beta_sd = 1)
fit <- stan_crm(outcome_str = outcomes, skeleton = skeleton,
                target = target, model = 'empiric', beta_sd = 1)
dose_finding_path_node(node_id = 2, parent_node_id = 1, depth = 1,
                       outcomes = outcomes, next_dose = fit$recommended_dose,
                       fit = fit, parent_fit = parent_fit)

## End(Not run)
```

---

eff_at_dose *Get the number of efficacy events seen at the doses under investigation.*

Description

Get the number of efficacy events seen at the doses under investigation.

Usage

```
eff_at_dose(x, dose, ...)

## S3 method for class 'efftox_fit'
eff_at_dose(x, dose = NULL, ...)
```

Arguments

x	An R object of class "dose_finding_fit"
dose	Optional integer, at which dose-level? Omit to get data on all doses.
...	arguments passed to other methods

Value

integer vector

Examples

```
## Not run:
# EffTox example
x <- stan_efftox_demo(outcome_str = '1N 2E')
eff_at_dose(fit)            # c(0, 1, 0, 0)
eff_at_dose(fit, dose = 2)  # 1
eff_at_dose(fit, dose = 3)  # 0

## End(Not run)
```

`efftox_analysis_to_df` *EffTox analysis to data.frame*

Description

Convenient function to turn an `efftox_fit` into a `data.frame`.

Usage

```
efftox_analysis_to_df(x)
```

Arguments

x	An instance of `efftox_fit`

Value

a `data.frame`

See Also

`stan_efftox`

Examples

```
fit <- stan_efftox_demo(outcome_str = '1N 2E 3B')
df <- efftox_analysis_to_df(fit)
df
```

`efftox_contour_plot` *Plot EffTox utility contours*

Description

Plot EffTox utility contours. The probability of efficacy is on the x-axis and toxicity on the y-axis. The zero-utility curve is plotted bolder. The three "hinge points" are plotted as blue triangles. Optional Prob(Efficacy) vs Prob(Toxicity) points can be added; these are shown as red numerals, enumerated in the order provided.

Usage

```
efftox_contour_plot(
  fit,
  use_ggplot = FALSE,
  prob_eff = fit$prob_eff,
  prob_tox = fit$prob_tox,
  num_points = 1000,
  util_vals = seq(-3, 3, by = 0.2)
)
```

Arguments

`fit`	An instance of `efftox_fit`.
`use_ggplot`	logical, TRUE to use ggplot2. Defaults to FALSE to use standard R graphics.
`prob_eff`	vector of numbers between 0 and 1, containing the efficacy probabilities of extra points to add to the plot as points, e.g. the posterior mean efficacy probabilities of the doses under investigation. Paired with prob_tox, thus they should be the same length. Defaults to the values fitted by the model. Use NULL to supress.
`prob_tox`	vector of numbers between 0 and 1, containing the toxicity probabilities of extra points to add to the plot as points, e.g. the posterior mean toxicity probabilities of the doses under investigation. Paired with prob_eff, thus they should be the same length. Defaults to the values fitted by the model. Use NULL to supress.
`num_points`	integer for number of points to calculate on each curve. The default is 1000 and this should be plenty.
`util_vals`	A contour is plotted for each of these utility values. The default is contours spaced by 0.2 between from -3 and 3, i.e. `seq(-3, 3, by = 0.2)`.

Value

if `use_ggplot = TRUE`, an instance of `ggplot`; else no object is returned. Omit assignment in either case to just view the plot.

See Also

`stan_efftox`

Examples

```
fit <- stan_efftox_demo(outcome_str = '1N 2E 3B')
efftox_contour_plot(fit)
title('EffTox utility contours')
# The same with ggplot2
efftox_contour_plot(fit, use_ggplot = TRUE) +
                    ggplot2::ggtitle('EffTox utility contours')
```

`efftox_dtps` *Calculate dose-transition pathways for an EffTox study*

Description

Calculate dose-transition pathways for an EffTox study. The function `efftox_dtps_to_dataframe` performs a similar function, but is much less-flexible.

Usage

```
efftox_dtps(
  cohort_sizes,
  previous_outcomes = "",
  next_dose = NULL,
  user_dose_func = NULL,
  verbose = FALSE,
  i_am_patient = FALSE,
  ...
)
```

Arguments

`cohort_sizes`	vector of future cohort sizes, i.e. positive integers. E.g. To calculate paths for the the next cohort of two followed by another cohort of three, use `cohort_sizes = c(2, 3)`.
`previous_outcomes`	Outcomes observed hitherto in the syntax required by `efftox_parse_outcomes`.
`next_dose`	the dose-level to be given to the immediately next cohort.
`user_dose_func`	optional delegate for deciding dose. A function that takes a `efftox_fit` as the sole argument and returns the integer (1-based) dose-level to be given next, or NA to show that no dose should be chosen and the trial stopped. This function gives the user the opportunity to build in custom behaviour to tailor the dose selection decision in response to the insights garnered by the fit model, or recommend that a trial path be halted immediately. If omitted, the dose ordinarily chosen by the model is used. An example is given below.
`verbose`	logical, TRUE to get progress messages.
`i_am_patient`	logical, TRUE to show your tolerance for waiting for over 100 models to fit. Set to FALSE by default.
`...`	extra params passed to `rstan::sampling`.

Value

dose pathways in a `data.frame`.

References

Yap C, Billingham LJ, Cheung YK, Craddock C, O'Quigley J. Dose transition pathways: The missing link between complex dose-finding designs and simple decision-making. Clinical Cancer Research. 2017;23(24):7440-7447. doi:10.1158/1078-0432.CCR-17-0582

Brock K, Billingham L, Copland M, Siddique S, Sirovica M, Yap C. Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology. 2017;17(1):112. doi:10.1186/s12874-017-0381-x

See Also

`efftox_parse_outcomes`, `stan_efftox`, `efftox_path_analysis`, `dose_finding_path_node`

Examples

```
## Not run:
# Calculate paths for the first cohort of 3 in Thall et al 2014 example
paths1 <- efftox_dtps(cohort_sizes = c(3), next_dose = 1,
                      real_doses = c(1.0, 2.0, 4.0, 6.6, 10.0),
                      efficacy_hurdle = 0.5, toxicity_hurdle = 0.3,
                      p_e = 0.1, p_t = 0.1,
                      eff0 = 0.5, tox1 = 0.65,
                      eff_star = 0.7, tox_star = 0.25,
                      alpha_mean = -7.9593, alpha_sd = 3.5487,
                      beta_mean = 1.5482, beta_sd = 3.5018,
                      gamma_mean = 0.7367, gamma_sd = 2.5423,
                      zeta_mean = 3.4181, zeta_sd = 2.4406,
                      eta_mean = 0, eta_sd = 0.2,
                      psi_mean = 0, psi_sd = 1, seed = 123)



# Calculate paths for the next two cohorts of 2, in an in-progress trial
# Warning: this create 100 paths. It will run for a minute or two.
paths2 <- efftox_dtps(cohort_sizes = c(2, 2),
                      previous_outcomes = '1NN 2EE',
                      next_dose = 1,
                      real_doses = c(1.0, 2.0, 4.0, 6.6, 10.0),
                      efficacy_hurdle = 0.5, toxicity_hurdle = 0.3,
                      p_e = 0.1, p_t = 0.1,
                      eff0 = 0.5, tox1 = 0.65,
                      eff_star = 0.7, tox_star = 0.25,
                      alpha_mean = -7.9593, alpha_sd = 3.5487,
                      beta_mean = 1.5482, beta_sd = 3.5018,
                      gamma_mean = 0.7367, gamma_sd = 2.5423,
                      zeta_mean = 3.4181, zeta_sd = 2.4406,
                      eta_mean = 0, eta_sd = 0.2,
                      psi_mean = 0, psi_sd = 1, seed = 123,
```

```
                      i_am_patient = TRUE)

# Paths can be converted to a tibble
library(tibble)
library(dplyr)
df <- as_tibble(paths2)
df %>% print(n = 200)

# And shaped in a wide format
spread_paths(df %>% select(-fit, -parent_fit, -dose_index)) %>%
  print(n = 100)
# Incredibly, there are 100 ways these two cohorts of two can end up.



# An example with a custom dose selection function.
# Define a function to select the maximal utility dose, no matter what.
# Note: this diverges from the original authors' intentions; we provide this
# for illustration only!
max_utility_dose <- function(efftox_fit) {
  return(which.max(efftox_fit$utility))
}
# Fit the paths, providing the user_dose_func parameter
# Warning: this create 100 paths. It will run for a minute or two.
paths3 <- efftox_dtps(cohort_sizes = c(2, 2),
                      previous_outcomes = '1NN 2EE',
                      next_dose = 1,
                      real_doses = c(1.0, 2.0, 4.0, 6.6, 10.0),
                      efficacy_hurdle = 0.5, toxicity_hurdle = 0.3,
                      p_e = 0.1, p_t = 0.1,
                      eff0 = 0.5, tox1 = 0.65,
                      eff_star = 0.7, tox_star = 0.25,
                      alpha_mean = -7.9593, alpha_sd = 3.5487,
                      beta_mean = 1.5482, beta_sd = 3.5018,
                      gamma_mean = 0.7367, gamma_sd = 2.5423,
                      zeta_mean = 3.4181, zeta_sd = 2.4406,
                      eta_mean = 0, eta_sd = 0.2,
                      psi_mean = 0, psi_sd = 1,
                      user_dose_func = max_utility_dose,
                      seed = 123, i_am_patient = TRUE)

# We can see where the dose-selections differ at the second future cohort
# by joining these paths to those calculated in the previous example:
left_join(
  as_tibble(paths2)%>%
    select(.node, .parent, .depth, outcomes, model_dose = next_dose),
  as_tibble(paths3) %>%
    select(.node, user_dose = next_dose),
  by = '.node'
) %>% spread_paths() %>%
  filter(model_dose2 != user_dose2)
# They differ in many places. The user defined functions sometimes selects
# higher doses; sometimes lower.
```

```
## End(Not run)
```

`efftox_dtps_to_dataframe` *Calculate dose-transition pathways for an EffTox study*

Description

Calculate dose-transition pathways for an EffTox study. Note that TODO TODO TODO

Usage

```
efftox_dtps_to_dataframe(dat, cohort_sizes, next_dose, ...)
```

Arguments

`dat`	An instance of `efftox_params`, a list of EffTox parameters. An example is yielded by `efftox_parameters_demo`.
`cohort_sizes`	vector of future cohort sizes, i.e. positive integers. E.g. To calculate paths for the the next cohort of two followed by another cohort of three, use `cohort_sizes = c(2, 3)`.
`next_dose`	the dose-level to be given to the immediately next cohort.
`...`	extra params passed to `rstan::sampling`.

Value

dose pathways in a `data.frame`.

References

Brock K, Billingham L, Copland M, Siddique S, Sirovica M, Yap C. Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology. 2017;17(1):112. doi:10.1186/s12874-017-0381-x

See Also

`efftox_dtps`, `efftox_params`, `efftox_parameters_demo`

Examples

```
# Calculate the paths for the first cohort of 3 in Thall et al 2014 example
dat <- efftox_parameters_demo()
## Not run:
dtps1 <- efftox_dtps_to_dataframe(dat = dat, cohort_sizes = c(3),
                                  next_dose = 1)

## End(Not run)
# To calculate future paths in a partially-observed trial
dat <- efftox_parameters_demo()
dat$doses = array(c(1,1,1))
dat$eff = array(c(0,0,0))
dat$tox = array(c(1,1,1))
dat$num_patients = 3
## Not run:
dtps2 <- efftox_dtps_to_dataframe(dat = dat, cohort_sizes = c(3),
                                  next_dose = 1)

## End(Not run)
```

---

efftox_fit-class *Class of model fit by* **trialr** *using the EffTox dose-finding design.*

Description

Phase I/II dose-finding trials, i.e. those that search for a dose my efficacy and toxicity outcomes search for the optimal biological dose (OBD), rather than the maximum tolerated dose (MTD) that is typically sought be traditional toxicity-only dose-finding.

Usage

```
efftox_fit(
  dose_indices,
  num_patients,
  doses,
  tox,
  eff,
  prob_tox,
  prob_eff,
  median_prob_tox,
  median_prob_eff,
  prob_acc_tox,
  prob_acc_eff,
  utility,
  post_utility,
  prob_obd,
  acceptable,
```

```
  recommended_dose,
  dat,
  fit
)
```

Arguments

dose_indices	A vector of integers representing the dose-levels under consideration.
num_patients	Integer, the number of patients analysed.
doses	vector of integers representing the dose given to the patients.
tox	vector of integers representing the toxicity status of the patients.
eff	vector of integers representing the efficacy status of the patients.
prob_tox	The posterior mean probabilities of toxicity at doses 1:n; a vector of numbers between 0 and 1.
prob_eff	The posterior mean probabilities of efficacy at doses 1:n; a vector of numbers between 0 and 1.
median_prob_tox	The posterior median probabilities of toxicity at doses 1:n; a vector of numbers between 0 and 1.
median_prob_eff	The posterior mean probabilities of efficacy at doses 1:n; a vector of numbers between 0 and 1.
prob_acc_tox	The posterior mean probabilities that toxicity at the doses is acceptable, i.e. that it is less than the maximum toxicity threshold; a vector of numbers between 0 and 1.
prob_acc_eff	The posterior mean probabilities that efficacy at the doses is acceptable, i.e. that it exceeds the minimum acceptable efficacy threshold; a vector of numbers between 0 and 1.
utility	The utilities of doses 1:n, calculated by plugging the posterior mean probabilities of efficacy and toxicity into the utility formula, as advocated by Thall & Cook. Contrast to post_utility; a vector of numbers.
post_utility	The posterior mean utilities of doses 1:n, calculated from the posterior distributions of the utilities. This is in contrast to utility, which uses plug-in posterior means of efficacy and toxicity, as advocated by Thall & Cook; a vector of numbers.
prob_obd	The posterior probability that each dose is the optimal biological dose (OBD); a vector of numbers between 0 and 1. This probability reflects the uncertainty remaining in the parameter distributions, whereas prob_tox and prob_eff (etc) do not.
acceptable	A vector of logical values to indicate whether doses 1:n are acceptable, according to the rules for acceptable efficacy & toxicity, and rules on not skipping untested doses.
recommended_dose	An integer representing the dose-level recommended for the next patient or cohort; or NA if stopping is recommended.
dat	Object efftox_params containing data passed to sampling.
fit	An object of class stanfit, containing the posterior samples.

Details

See `methods(class = "efftox_fit")` for an overview of available methods.

See Also

`stan_efftox` `stan_efftox_demo`

---

efftox_get_tox *Get the Prob(Tox) for Prob(Eff) and utility pairs*

Description

Get the probability of toxicity for probability-of-efficacy and utility pairs

Usage

```
efftox_get_tox(eff, util, p, eff0, tox1)
```

Arguments

`eff`	Probability of efficacy; number between 0 and 1
`util`	Utility score; number
`p`	p-index of EffTox utility contours. Use `efftox_solve_p`
`eff0`	Efficacy probability required when toxicity is impossible; a number between 0 and 1
`tox1`	Toxicity probability permitted when efficacy is guaranteed; a number between 0 and 1

Value

Probability(s) of toxicity

Note

Various ways of vectorising the function are demonstrated in the examples

See Also

`efftox_solve_p`

Examples

```
p <- efftox_solve_p(0.5, 0.65, 0.7, 0.25)

prob_tox <- efftox_get_tox(0.7, 0, p, eff0 = 0.5, tox1 = 0.65)
round(prob_tox, 2) == 0.25

prob_tox <- efftox_get_tox(0.7, seq(-0.5, 0.25, by = 0.25), p, eff0 = 0.5,
                           tox1 = 0.65)
round(prob_tox, 2) == c(0.57, 0.41, 0.25, 0.09)

prob_tox <- efftox_get_tox(c(0.5, 0.7, 0.8), 0.25, p, eff0 = 0.5, tox1 = 0.65)
round(prob_tox, 2) == c(NaN, 0.09, 0.22)

prob_tox <- efftox_get_tox(c(0.5, 0.7, 0.8), c(-1, 0, 1), p, eff0 = 0.5,
                           tox1 = 0.65)
round(prob_tox, 2) == c(0.63, 0.25, NaN)
```

`efftox_parameters_demo` *Get parameters to run the EffTox demo*

Description

Get parameters to run the EffTox demo. These match those used to demonstrate EffTox in Thall et al. 2014.

Usage

```
efftox_parameters_demo()
```

Value

a `list` of parameters, described in `efftox_params`

References

Thall, Herrick, Nguyen, Venier & Norris. 2014, Effective sample size for computing prior hyper-parameters in Bayesian phase I-II dose-finding

See Also

`efftox_params`

Examples

```
dat <- efftox_parameters_demo()
names(dat)
dat$real_doses == c(1, 2, 4, 6.6, 10)
```

`efftox_params-class` *Container class for parameters to fit the EffTox model in trialr.*

Description

Container class for parameters to fit the EffTox model in trialr.

Usage

```
efftox_params(
  real_doses,
  efficacy_hurdle,
  toxicity_hurdle,
  p_e,
  p_t,
  eff0,
  tox1,
  eff_star,
  tox_star,
  priors
)
```

Arguments

`real_doses`	a vector of numbers.The doses under investigation. They should be ordered from lowest to highest and be in consistent units. E.g., to conduct a dose-finding trial of doses 10mg, 20mg and 50mg, use c(10, 20, 50).
`efficacy_hurdle`	Minimum acceptable efficacy probability. A number between 0 and 1.
`toxicity_hurdle`	Maximum acceptable toxicity probability. A number between 0 and 1.
`p_e`	Certainty required to infer a dose is acceptable with regards to being probably efficacious; a number between 0 and 1.
`p_t`	Certainty required to infer a dose is acceptable with regards to being probably tolerable; a number between 0 and 1.
`eff0`	Efficacy probability required when toxicity is impossible; a number between 0 and 1 (see Details).
`tox1`	Toxicity probability permitted when efficacy is guaranteed; a number between 0 and 1 (see Details).
`eff_star`	Efficacy probability of an equi-utility third point (see Details).
`tox_star`	Toxicity probability of an equi-utility third point (see Details).
`priors`	instance of class `efftox_priors`, the hyperparameters for normal priors on the six model parameters.

See Also

efftox_priors get_efftox_priors stan_efftox stan_efftox_demo

---

efftox_parse_outcomes *Parse a string of EffTox outcomes to binary vector notation.*

Description

Parse a string of EffTox outcomes to the binary vector notation required by Stan for model invocation. The outcome string describes the doses given and outcomes observed. The format of the string is described in Brock et al. (2017). The letters E, T, N and B are used to represents patients that experienced (E)fficacy only, (T)oxicity only, (B)oth efficacy and toxicity, and (N)either. These letters are concatenated after numerical dose-levels to convey the outcomes of cohorts of patients. For instance, `2ETB` represents a cohort of three patients that were treated at dose-level 2, and experienced efficacy, toxicity and both events, respectively. The results of cohorts are separated by spaces. Thus, `2ETB 1NN` extends our previous example, where the next cohort of two were treated at dose-level 1 and both patients experienced neither efficacy nor toxicity. See examples.

We present the notation in the EffTox setting but it is applicable in general seamless phase I/II dose-finding scenarios.

Usage

```
efftox_parse_outcomes(outcome_string, as.list = TRUE)
```

Arguments

`outcome_string`	character string, conveying doses given and outcomes observed.
`as.list`	TRUE (be default) to return a `list`; FALSE to return a `data.frame`

Value

If `as.list == TRUE`, a list with elements `eff`, `tox`, `doses` and `num_patients`. These elements are congruent with those of the same name in `efftox_params`. If `as.list == FALSE`, a data.frame with columns `eff`, `tox`, and `doses`.

References

Brock, K., Billingham, L., Copland, M., Siddique, S., Sirovica, M., & Yap, C. (2017). Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology, 17(1), 112. https://doi.org/10.1186/s12874-017-0381-x

Examples

```
x = efftox_parse_outcomes('1NNE 2EEN 3TBB')
x$num_patients == 9
x$eff == c(0, 0, 1, 1, 1, 0, 0, 1, 1)
sum(x$tox) == 3
```

`efftox_path_analysis` *Fit an EffTox model to the incrementally observed outcomes on a trial pathway.*

Description

Fit a EffTox model to the outcomes cumulatively observed at the end of each cohort in a trial pathway. E.g. if the trial pathway is 1EN 2NN 3BT, we have three cohorts of two patients. This function will fit the model to the following four states: before any patients have been evaluated; after 1EN; after 1EN 2NN; and finally after 1EN 2NN 3BT. This allows us to analyse how the trial model is evolving in its estimation as trial data is accumulated.

Usage

```
efftox_path_analysis(outcome_str, verbose = FALSE, ...)
```

Arguments

`outcome_str`	A string representing the outcomes observed hitherto. See `efftox_parse_outcomes` for a description of syntax and examples. Alternatively, you may provide `doses_given` and `tox` parameters. See Details.
`verbose`	logical, TRUE to get log messages.
`...`	All other parameters are passed to `stan_efftox`.

Value

A `list` of `dose_finding_path_node` objects.

Author(s)

Kristian Brock

See Also

`efftox_parse_outcomes`, `stan_efftox`, `dose_finding_path_node`

Examples

```
## Not run:
# EffTox example
paths <- efftox_path_analysis(
  outcome_str = '1NNN 2NEN 3NEB',
  real_doses = c(1.0, 2.0, 4.0, 6.6, 10.0),
  efficacy_hurdle = 0.5, toxicity_hurdle = 0.3,
  p_e = 0.1, p_t = 0.1,
  eff0 = 0.5, tox1 = 0.65,
  eff_star = 0.7, tox_star = 0.25,
  alpha_mean = -7.9593, alpha_sd = 3.5487,
```

```
  beta_mean = 1.5482, beta_sd = 3.5018,
  gamma_mean = 0.7367, gamma_sd = 2.5423,
  zeta_mean = 3.4181, zeta_sd = 2.4406,
  eta_mean = 0, eta_sd = 0.2,
  psi_mean = 0, psi_sd = 1, seed = 123, refresh = 0)

length(paths)  # 4
names(paths)[1]  # ""
names(paths)[2]  # "1NNN"
names(paths)[3]  # "1NNN 2NEN"
names(paths)[4]  # "1NNN 2NEN 3NEB"
# Each node is an analysis fit to the cumulative outcomes
# Converting to a tibble presents some nice tidyverse-related opportunities
library(tibble)
df <- as_tibble(paths)
df

## End(Not run)
```

`efftox_priors` *Simple class to hold prior hyperparameters for the EffTox model.*

Description

Simple class to hold prior hyperparameters for the EffTox model.

Usage

```
efftox_priors(
  alpha_mean,
  alpha_sd,
  beta_mean,
  beta_sd,
  gamma_mean,
  gamma_sd,
  zeta_mean,
  zeta_sd,
  eta_mean,
  eta_sd,
  psi_mean,
  psi_sd
)
```

Arguments

`alpha_mean`	The prior normal mean of the intercept term in the toxicity logit model. A number.
`alpha_sd`	The prior normal standard deviation of the intercept term in the toxicity logit model. A number.

beta_mean	The prior normal mean of the slope term in the toxicity logit model. A number.
beta_sd	The prior normal standard deviation of the slope term in the toxicity logit model. A number.
gamma_mean	The prior normal mean of the intercept term in the efficacy logit model. A number.
gamma_sd	The prior normal standard deviation of the intercept term in the efficacy logit model. A number.
zeta_mean	The prior normal mean of the slope term in the efficacy logit model. A number.
zeta_sd	The prior normal standard deviation of the slope term in the efficacy logit model. A number.
eta_mean	The prior normal mean of the squared term coefficient in the efficacy logit model. A number.
eta_sd	The prior normal standard deviation of the squared term coefficient in the efficacy logit model. A number.
psi_mean	The prior normal mean of the association term in the combined efficacy-toxicity model. A number.
psi_sd	The prior normal standard deviation of the association term in the combined efficacy-toxicity model. A number.

Value

list-like, instance of class `efftox_priors`.

Author(s)

Kristian Brock <kristian.brock@gmail.com>

References

Thall, P., & Cook, J. (2004). Dose-Finding Based on Efficacy-Toxicity Trade-Offs. Biometrics, 60(3), 684-693.

Thall, P., Herrick, R., Nguyen, H., Venier, J., & Norris, J. (2014). Effective sample size for computing prior hyperparameters in Bayesian phase I-II dose-finding. Clinical Trials, 11(6), 657-666. https://doi.org/10.1177/1740774514547397

Examples

```
# The priors used in Thall et al. (2014)
p <- efftox_priors(alpha_mean = -7.9593, alpha_sd = 3.5487,
                   beta_mean = 1.5482, beta_sd = 3.5018,
                   gamma_mean = 0.7367, gamma_sd = 2.5423,
                   zeta_mean = 3.4181, zeta_sd = 2.4406,
                   eta_mean = 0, eta_sd = 0.2,
                   psi_mean = 0, psi_sd = 1)
# The class exists simply to hold these twelve values.
```

efftox_process *Process RStan samples from an EffTox model*

Description

Internal function to process rstan samples from an EffTox model to make inferences about dose-acceptability, dose-utility and which dose should be recommended next.

Usage

```
efftox_process(dat, fit)
```

Arguments

dat	An instance of efftox_params, a list of EffTox parameters. An example is yielded by efftox_parameters_demo.
fit	An instance of rstan::stanmodel, derived by fitting the trialr EffTox model.

Value

An instance of efftox_fit.

efftox_simulate *Run EffTox simulations*

Description

Run EffTox simulations for assumed true efficacy and toxicity curves.

Usage

```
efftox_simulate(
  dat,
  num_sims,
  first_dose,
  true_eff,
  true_tox,
  cohort_sizes,
  ...
)
```

Arguments

dat	An instance of efftox_params, a list of EffTox parameters. An example is yielded by efftox_parameters_demo.
num_sims	integer, number of simulated iterations
first_dose	integer, the dose-level to give to patient 1, e.g. 1 for the lowest dose.
true_eff	the true probabilities of efficacy at the doses under investigation; a vector of numbers between 0 and 1.
true_tox	the true probabilities of toxicity at the doses under investigation; a vector of numbers between 0 and 1.
cohort_sizes	a vector of integer cohort sizes. A dose decision is made when each cohort is completed and the next cohort is treated at the recommended dose. To conduct a trial using at most 20 patients, where dose is re-evaluated after every second patient, use rep(2, 10). To conduct a trial of 8 patients where dose is re-evaluated after each single patient, use rep(1, 8). Cohort size need not be uniform. E.g. c(rep(1, 5), rep(3, 10)) represents a trial where the dose is re-evaluated after each patient for the first 5 patients, and then after every third patient for a further 30 patients.
...	Extra parameters provided via the ellipsis are passed to stan::sampling

Value

A list with named elements recommended_dose, efficacies, toxicities, and doses_given.

Examples

```
dat <- efftox_parameters_demo()
set.seed(123)
# Let's say we want to use only 2 chains. Extra args are passed to stan
## Not run:
sims <- efftox_simulate(dat, num_sims = 10, first_dose = 1,
                        true_eff = c(0.20, 0.40, 0.60, 0.80, 0.90),
                        true_tox = c(0.05, 0.10, 0.15, 0.20, 0.40),
                        cohort_sizes = rep(3, 13),
                        chains = 2)
table(sims$recommended_dose) / length(sims$recommended_dose)
table(unlist(sims$doses_given)) / length(unlist(sims$doses_given))
table(unlist(sims$doses_given)) / length(sims$recommended_dose)

## End(Not run)
# In real life, we would run thousands of iterations, not 10.
# This is an example.
```

`efftox_solve_p` *Calculate the p-index for EffTox utility contours*

Description

Calculate the p-index for EffTox utility contours so that the neutral utility contour intersects the following points in the Prob(Efficacy) - Prob(Toxicity) plane: (`eff0`, 0), (1, `tox1`) and (`eff_star`, `tox_star`)

Usage

```
efftox_solve_p(eff0, tox1, eff_star, tox_star)
```

Arguments

`eff0`	Efficacy probability required when toxicity is impossible; a number between 0 and 1
`tox1`	Toxicity probability permitted when efficacy is guaranteed; a number between 0 and 1
`eff_star`	Efficacy probability of an equi-utility third point
`tox_star`	Toxicity probability of an equi-utility third point

Value

The p-index

References

Thall, Herrick, Nguyen, Venier & Norris. 2014, Effective sample size for computing prior hyper-parameters in Bayesian phase I-II dose-finding

Examples

```
efftox_solve_p(0.5, 0.65, 0.7, 0.25)
```

efftox_superiority *Get dose-superiority matrix in EffTox*

Description

Get a dose-superiority matrix from an EffTox dose analysis. EffTox seeks to choose the dose with the highest utility, thus superiority is inferred by posterior utility. The item in row i, col j is the posterior probability that the utility of dose j exceeds that of dose i.

Usage

```
efftox_superiority(fit)
```

Arguments

fit	An instance of efftox_fit.

Value

n by n matrix, where n is number of doses under investigation. The item in row i, col j is the posterior probability that the utility of dose j exceeds that of dose i.

Examples

```
fit <- stan_efftox_demo('1N 2E 3B')
sup_mat <- efftox_superiority(fit)
```

efftox_utility *Get the utility of efficacy & toxicity probability pairs*

Description

Get the utility of efficacy & toxicity probability pairs

Usage

```
efftox_utility(p, eff0, tox1, prob_eff, prob_tox)
```

Arguments

p	p-index of EffTox utility contours. Use efftox_solve_p
eff0	Efficacy probability required when toxicity is impossible; a number between 0 and 1
tox1	Toxicity probability permitted when efficacy is guaranteed; a number between 0 and 1
prob_eff	Probability of efficacy; number between 0 and 1
prob_tox	Probability of toxicity; number between 0 and 1

Value

Utility value(s)

See Also

efftox_solve_p

Examples

```
p <- efftox_solve_p(0.5, 0.65, 0.7, 0.25)

u <- efftox_utility(p, 0.5, 0.65, prob_eff = 0.7, prob_tox = 0.25)
round(u, 4) == 0

u <- efftox_utility(p, 0.5, 0.65, prob_eff = c(0.6, 0.7, 0.8),
                    prob_tox = c(0.1, 0.2, 0.3))
round(u, 2) == c(0.04, 0.08, 0.12)
```

---

efftox_utility_density_plot

Plot densities of EffTox dose utilities

Description

Plot densities of EffTox dose utilities. Optionally plot only a subset of the doses by specifying the doses parameter. This function requires ggplot2 be installed.

Usage

```
efftox_utility_density_plot(fit, doses = NULL)
```

Arguments

fit	An instance of efftox_fit.
doses	optional, vector of integer dose-levels to plot. E.g. to plot only dose-levels 1, 2 & 3 (and suppress the plotting of any other doses), use doses = 1:3

Value

an instance of ggplot. Omit assignment to just view the plot.

Note

This function requires that ggplot2 be installed.

Examples

```
fit <- stan_efftox_demo('1N 2E 3B')
efftox_utility_density_plot(fit) + ggplot2::ggtitle('My doses')  # Too busy?
# Specify subset of doses to make plot less cluttered
efftox_utility_density_plot(fit, doses = 1:3) + ggplot2::ggtitle('My doses')
```

`get_efftox_priors` *Get normal prior hyperparameters for the EffTox model.*

Description

Get normal prior hyperparameters for the EffTox model using the algorithm presented in Thall et al. (2014) that targets a family of priors with a pre-specified effective sample size (ESS).

Usage

```
get_efftox_priors(
  doses = NULL,
  scaled_doses = NULL,
  pi_T,
  ess_T,
  pi_E,
  ess_E,
  num_samples = 10^4,
  seed = 123
)
```

Arguments

`doses`	A vector of numbers, the doses under investigation. They should be ordered from lowest to highest and be in consistent units. E.g. to conduct a dose-finding trial of doses 10mg, 20mg and 50mg, use c(10, 20, 50). Specify `doses` or `scaled_doses`.
`scaled_doses`	Optional, vector of numbers, representing the scaled doses under investigation. Thall et al. advocate `scaled_doses = log(doses) - mean(log(doses))`, and that is what we use here. Specify `doses` or `scaled_doses`.
`pi_T`	Vector of prior expectations of probabilities of toxicity at the doses. Should be congruent to `doses` or `scaled_doses`.
`ess_T`	Numerical, sought total effective sample size for priors on parameters in the toxicity sub-model. Thall et al. (2014) advocate values in (0.3, 1.0) but stress that stress-testing with values outside this range may be necessary.
`pi_E`	Vector of prior expectations of probabilities of efficacy at the doses. Should be congruent to `doses` or `scaled_doses`.

ess_E	Numerical, sought total effective sample size for priors on parameters in the efficacy sub-model. Thall et al. (2014) advocate values in (0.3, 1.0) but stress that stress-testing with values outside this range may be necessary.
num_samples	Number of samples to draw from priors. The default 10^4 seems to be a nice compromise between accuracy and speed. Orders of magnitude larger take a long time to run.
seed	Optional seed. This process involves randomness so seeds are used for repeatable results.

Value

An instance of class efftox_priors.

References

Thall, P., Herrick, R., Nguyen, H., Venier, J., & Norris, J. (2014). Effective sample size for computing prior hyperparameters in Bayesian phase I-II dose-finding. Clinical Trials, 11(6), 657-666. https://doi.org/10.1177/1740774514547397

Examples

```
## Not run:
# Reproduce the priors calculated in Thall et al. (2014)
p <- get_efftox_priors(
  doses = c(1.0, 2.0, 4.0, 6.6, 10.0),
  pi_T = c(0.02, 0.04, 0.06, 0.08, 0.10), ess_T = 0.9,
  pi_E = c(0.2, 0.4, 0.6, 0.8, 0.9), ess_E = 0.9
)
p
# These are close to the published example. They do not match exactly because
# the process of deriving them is iterative.

## End(Not run)
```

---

n_at_dose *Get the number of patients treated at the doses under investigation.*

Description

Get the number of patients treated at the doses under investigation.

Usage

```
n_at_dose(x, dose, ...)

## S3 method for class 'dose_finding_fit'
n_at_dose(x, dose = NULL, ...)
```

Arguments

x	An R object of class "dose_finding_fit"
dose	Optional integer, at which dose-level? Omit to get data on all doses.
...	arguments passed to other methods

Value

integer vector

Examples

```
## Not run:
# CRM example
target <- 0.2
fit <- stan_crm('1N 2N 3T', skeleton = c(0.1, 0.2, 0.35, 0.6),
                target = target, model = 'empiric', beta_sd = sqrt(1.34),
                seed = 123)
n_at_dose(fit)            # c(1, 1, 1, 0)
n_at_dose(fit, dose = 3)  # 1

## End(Not run)
```

---

parse_dose_finding_outcomes

Parse a string of dose-finding trial outcomes.

Description

Parse a string of dose-finding trial outcomes

Parse a string of dose-finding trial outcomes to a list. The outcome string describes the doses given, outcomes observed and the timing of analyses that recommend a dose. The format of the string is the pure phase I analogue to that described in Brock _et al_. (2017). The letters T and N are used to represents patients that experienced (T)oxicity and (N)o toxicity. These letters are concatenated after numerical dose-levels to convey the outcomes of cohorts of patients. For instance, `2NNT` represents a cohort of three patients that were treated at dose-level 2, one of whom experienced toxicity, and two that did not. The results of cohorts are separated by spaces and it is assumed that a dose-finding decision takes place at the end of a cohort. Thus, `2NNT 1NN` builds on our previous example, where the next cohort of two were treated at dose-level 1 and neither of these patients experienced toxicity. See examples.

Usage

```
parse_dose_finding_outcomes(outcome_string)
```

Arguments

outcome_string	character representing doses given, outcomes observed, and timing of analyses. See Description.

Value

a list with a slot for each cohort. Each cohort slot is itself a list, containing elements: * `dose`, the integer dose delivered to the cohort; * `outcomes`, a character string representing the `T` or `N` outcomes for the patients in this cohort.

References

Brock, K., Billingham, L., Copland, M., Siddique, S., Sirovica, M., & Yap, C. (2017). Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology, 17(1), 112. https://doi.org/10.1186/s12874-017-0381-x

Examples

```
x = parse_dose_finding_outcomes('1NNN 2NNT 3TT')
length(x)
x[[1]]$dose
x[[1]]$outcomes
x[[2]]$dose
x[[2]]$outcomes
x[[3]]$dose
x[[3]]$outcomes
```

`parse_eff_tox_dose_finding_outcomes`
Parse a string of phase I/II dose-finding trial outcomes.

Description

Parse a string of phase I/II dose-finding trial outcomes. Phase I/II trials conduct dose-finding by efficacy and toxicity outcomes.

Parse a string of phase I/II dose-finding outcomes to a list. The outcome string describes the doses given, efficacy and toxicity outcomes observed and the timing of analyses that recommend a dose. The format of the string is described in Brock _et al_. (2017). The letters E, T, N & B are used to represents patients that experienced (E)fficacy, (T)oxicity, (N)either and (B)oth. These letters are concatenated after numerical dose-levels to convey the outcomes of cohorts of patients. For instance, `2NET` represents a cohort of three patients that were treated at dose-level 2, one of whom experienced toxicity only, one that experienced efficacy only, and one that had neither. The results of cohorts are separated by spaces and it is assumed that a dose-finding decision takes place at the end of a cohort. Thus, `2NET 1NN` builds on our previous example, where the next cohort of two were treated at dose-level 1 and neither of these patients experienced either event. See examples.

Usage

```
parse_eff_tox_dose_finding_outcomes(outcome_string)
```

Arguments

outcome_string	character representing doses given, outcomes observed, and timing of analyses. See Description.

Value

a list with a slot for each cohort. Each cohort slot is itself a list, containing elements: * dose, the integer dose delivered to the cohort; * outcomes, a character string representing the E, T N or B outcomes for the patients in this cohort.

References

Brock, K., Billingham, L., Copland, M., Siddique, S., Sirovica, M., & Yap, C. (2017). Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology, 17(1), 112. https://doi.org/10.1186/s12874-017-0381-x

Examples

```
x = parse_eff_tox_dose_finding_outcomes('1NEN 2ENT 3TB')
length(x)
x[[1]]$dose
x[[1]]$outcomes
x[[2]]$dose
x[[2]]$outcomes
x[[3]]$dose
x[[3]]$outcomes
```

---

peps2_get_data *Get data to run the PePS2 trial example*

Description

Get data to run the BEBOP model in the PePS2 trial. The trial investigates pembrolizumab in non-small-cell lung cancer. Patients may be previously treated (PT) or treatment naive (TN). Pembro response rates in lung cancer have been shown to increase with PD-L1 tumour proportion score. PD-L1 score is measured at baseline. Each patient belongs to one of the Low, Medium or High categories. These two baseline variables stratify the patient population and are used as predictive variables to stratify the analysis. The BEBOP model studies co-primary efficacy and toxicity outcomes in the presence of predictive data. Thus, PePS2 studies efficacy and toxicity in 6 distinct cohorts: TN Low, TN Medium, TN High, PT Low, PT Medium, PT High. The design admits all-comers and does not target specific sample sizes in the individual cohorts. Hyperprior parameters have defaults to match those used in PePS2, but all may be overridden. The returned object includes randomly-sampled outcomes, as well as parameters to run the model. These are all combined in the same list object for passing to RStan, as is the convention. See the accompanying vignette for a full description.

Usage

```
peps2_get_data(
  num_patients,
  cohort_probs = NULL,
  prob_eff,
  prob_tox,
  eff_tox_or,
  cohort_rho = c(15.7, 21.8, 12.4, 20.7, 18, 11.4),
  alpha_mean = -2.2,
  alpha_sd = 2,
  beta_mean = -0.5,
  beta_sd = 2,
  gamma_mean = -0.5,
  gamma_sd = 2,
  zeta_mean = -0.5,
  zeta_sd = 2,
  lambda_mean = -2.2,
  lambda_sd = 2,
  psi_mean = 0,
  psi_sd = 1
)
```

Arguments

num_patients	Total number of patients to use, positive integer.
cohort_probs	Probabilities that a patient belongs to each of the 6 cohorts, in the order given above; a vector of numbers between 0 and 1 that add up to 1. cohort_probs or cohort_rho must be specified.
prob_eff	Probabilities of efficacy in each of the 6 cohorts, in the order given above; a vector of numbers between 0 and 1
prob_tox	Probabilities of toxicity in each of the 6 cohorts, in the order given above; a vector of numbers between 0 and 1
eff_tox_or	Measure of strength of association between efficacy and toxicity, in each of the 6 cohorts, in the order given above; a vector of numbers. Use 1 for no association; numbers increasingly greater than 1 for stronger positive associations, and numbers less than 1 for stronger negative associations
cohort_rho	Concentration parameters for cohort membership, in the order given above, using a Dirichlet distribution. This leads to randomly- sampled cohort sizes distributed Dir(cohort_rho). cohort_probs or cohort_rho must be specified.
alpha_mean	The prior mean of alpha. Alpha is the efficacy model intercept.
alpha_sd	The prior standard deviation of alpha. Alpha is the efficacy model intercept.
beta_mean	The prior mean of beta. Beta is the efficacy model term for being previously treated.
beta_sd	The prior standard deviation of beta. Beta is the efficacy model term for being previously treated.

gamma_mean	The prior mean of gamma. Gamma is the efficacy model term for being PD-L1 score = Low.
gamma_sd	The prior standard deviation of gamma. Gamma is the efficacy model term for being PD-L1 score = Low.
zeta_mean	The prior mean of zeta. Zeta is the efficacy model term for being PD-L1 score = Medium.
zeta_sd	The prior standard deviation of zeta. Zeta is the efficacy model term for being PD-L1 score = Medium.
lambda_mean	The prior mean of lambda. Lambda is the toxicity model intercept.
lambda_sd	The prior standard deviation of lambda. Lambda is the toxicity model intercept.
psi_mean	The prior mean of psi. Psi is the joint model association parameter.
psi_sd	The prior standard deviation of psi. Psi is the joint model association parameter.

Value

a `list` of parameters

Examples

```
## Not run:
set.seed(123)
dat <- peps2_get_data(num_patients = 60,
                      prob_eff = c(0.167, 0.192, 0.5, 0.091, 0.156, 0.439),
                      prob_tox = rep(0.1, 6),
                      eff_tox_or = rep(1, 6))
fit <- stan_peps2(
  eff = dat$eff,
  tox = dat$tox,
  cohorts = dat$cohorts
)

## End(Not run)
```

---

peps2_process *Process RStan samples from a BEBOP model fit to PePS2 data*

Description

Process RStan samples from a BEBOP model fit to PePS2 data. This step lets us make inferences about whether the modelled efficacy and toxicity probabilities suggest the treatment is acceptable in each of the cohorts under study. The parameters have default values to match those used in the PePS2 trial. See the accompanying vignette for a full description.

Usage

```
peps2_process(
  fit,
  min_eff = 0.1,
  max_tox = 0.3,
  eff_cert = 0.7,
  tox_cert = 0.9
)
```

Arguments

fit	An instance of rstan::stanmodel, derived by fitting data to the BEBOP in PePS2 model. Use stan_peps2.
min_eff	The lower efficacy probability threshold; a number between 0 and 1.
max_tox	The upper toxicity probability threshold; a number between 0 and 1.
eff_cert	Certainty required to infer the treatment is acceptable with regards to being probably efficacious; a number between 0 and 1.
tox_cert	Certainty required to infer the treatment is acceptable with regards to being probably tolerable; a number between 0 and 1.

Value

a list with the following items:

- ProbEff, the posterior mean probability of efficacy in the 6 cohorts.
- ProbAccEff, the posterior mean probability that the probability of efficacy exceeds min_eff, in the 6 cohorts.
- ProbTox, the posterior mean probability of toxicity in the 6 cohorts.
- ProbAccTox, the posterior mean probability that the probability of toxicity is less than max_tox, in the 6 cohorts.
- Accept, a vector of logical values to show whether treatment should be accepted in the 6 cohorts. Treatment is acceptable when it is probably efficacious and probably not toxic, with respect to the described rules.
- alpha, the posterior mean estimate of alpha.
- beta, the posterior mean estimate of beta.
- gamma, the posterior mean estimate of gamma.
- zeta, the posterior mean estimate of zeta.
- lambda, the posterior mean estimate of lambda.
- psi, the posterior mean estimate of psi.

See Also

peps2_get_data

Examples

```
set.seed(123)
fit <- stan_peps2(
  eff = c(0, 1, 0, 1, 0, 0),
  tox = c(0, 0, 1, 1, 0, 0),
  cohorts = c(3, 1, 1, 4, 5, 6)
)
decision <- peps2_process(fit)
decision$Accept
decision$ProbEff
decision$ProbAccEff
```

---

plot.crm_fit *Plot an crm_fit*

Description

Plot an crm_fit

Usage

```
## S3 method for class 'crm_fit'
plot(x, pars = "prob_tox", ...)
```

Arguments

x	crm_fit object to plot.
pars	Parameters to plot. Plots utility scores by default.
...	Extra parameters, passed onwards.

Value

A plot

---

plot.efftox_fit *Plot an efftox_fit*

Description

Plot an efftox_fit

Usage

```
## S3 method for class 'efftox_fit'
plot(x, pars = "utility", ...)
```

Arguments

x	efftox_fit object to plot.
pars	Parameters to plot. Plots utility scores by default.
...	Extra parameters, passed onwards.

Value

A plot

---

predict.augbin_2t_1a_fit

Predict probability of success for given tumour size measurements.

Description

This method simply forwards to prob_success.

Usage

```
## S3 method for class 'augbin_2t_1a_fit'
predict(
  object,
  y1_lower = -Inf,
  y1_upper = Inf,
  y2_lower = -Inf,
  y2_upper = log(0.7),
  probs = c(0.025, 0.975),
  newdata = NULL,
  ...
)
```

Arguments

object	Object of class augbin_2t_1a_fit.
y1_lower	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to negative infinity.
y1_upper	numeric, maximum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to positive infinity.
y2_lower	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 2 to baseline.
y2_upper	numeric, maximum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 2 to baseline. Defaults to log(0.7).
probs	pair of probabilities to use to calculate the credible interval for the probability of success.

newdata	data for which to infer the probability of success. A dataframe-like object with baseline tumour sizes in first column, and first and second post-baseline tumour sizes in columns 2 and 3. Omitted by default. When omitted, newdata is set to be the object$tumour_size.
...	Extra args passed onwards.

Value

Object of class tibble

---

print.augbin_fit *Print augbin_fit object.*

Description

Print augbin_fit object.

Usage

```
## S3 method for class 'augbin_fit'
print(
  x,
 pars = c("alpha", "beta", "gamma", "Omega", "sigma", "alphaD1", "gammaD1", "alphaD2",
    "gammaD2"),
  ...
)
```

Arguments

x	augbin_fit object to print.
pars	parameters in model to summarise.
...	Extra parameters, passed onwards.

---

print.crm_fit *Print crm_fit object.*

Description

Print crm_fit object.

Usage

```
## S3 method for class 'crm_fit'
print(x, ...)
```

Arguments

x	crm_fit object to print.
...	Extra parameters, passed onwards.

---

print.efftox_fit *Print efftox_fit object.*

Description

Print efftox_fit object.

Usage

```
## S3 method for class 'efftox_fit'
print(x, ...)
```

Arguments

x	efftox_fit object to convert.
...	Extra parameters, passed onwards.

---

print.nbg_fit *Print nbg_fit object.*

Description

Print nbg_fit object.

Usage

```
## S3 method for class 'nbg_fit'
print(x, ...)
```

Arguments

x	nbg_fit object to print.
...	Extra parameters, passed onwards.

`prior_predictive_augbin_2t_1a` *Sample data from the Augmented Binary model prior predictive distribution.*

Description

Sample data from the prior predictive distributions of the two-period, single arm Augmented Binary model, subject to chosen prior parameters.

Usage

```
prior_predictive_augbin_2t_1a(
  num_samps,
  alpha_mean,
  alpha_sd,
  beta_mean,
  beta_sd,
  gamma_mean,
  gamma_sd,
  sigma_mean,
  sigma_sd,
  omega_lkj_eta,
  alpha_d1_mean,
  alpha_d1_sd,
  gamma_d1_mean,
  gamma_d1_sd,
  alpha_d2_mean,
  alpha_d2_sd,
  gamma_d2_mean,
  gamma_d2_sd
)
```

Arguments

`num_samps`	Number of samples.
`alpha_mean`	Prior mean of alpha parameter.
`alpha_sd`	Prior sd of alpha parameter.
`beta_mean`	Prior mean of beta parameter.
`beta_sd`	Prior sd of beta parameter.
`gamma_mean`	Prior mean of gamma parameter.
`gamma_sd`	Prior sd of gamma parameter.
`sigma_mean`	Prior mean of sigma parameter.
`sigma_sd`	Prior sd of sigma parameter.

omega_lkj_eta	Prior eta parameter for LKJ prior on covariance matrix of log tumour sizes.
alpha_d1_mean	Prior mean of alpha_D1 parameter.
alpha_d1_sd	Prior sd of alpha_D1 parameter.
gamma_d1_mean	Prior mean of gamma_D1 parameter.
gamma_d1_sd	Prior sd of gamma_D1 parameter.
alpha_d2_mean	Prior mean of alpha_D2 parameter.
alpha_d2_sd	Prior sd of alpha_D2 parameter.
gamma_d2_mean	Prior mean of gamma_D2 parameter.
gamma_d2_sd	Prior sd of gamma_D2 parameter.

Value

Object of class tibble

See Also

stan_augbin

Examples

```
prior_predictive_augbin_2t_1a(num_samps = 1000,
                              alpha_mean = 0, alpha_sd = 1,
                              beta_mean = 0, beta_sd = 1,
                              gamma_mean = 0, gamma_sd = 1,
                              sigma_mean = 0, sigma_sd = 1,
                              omega_lkj_eta = 1,
                              alpha_d1_mean = 0, alpha_d1_sd = 1,
                              gamma_d1_mean = 0, gamma_d1_sd = 1,
                              alpha_d2_mean = 0, alpha_d2_sd = 1,
                              gamma_d2_mean = 0, gamma_d2_sd = 1)
```

---

prob_success *Calculate the probability of success.*

Description

Calculate the probability of success.

Calculate the probability of success for an augbin_2t_1a_fit object.

Usage

```
prob_success(x, ...)

## S3 method for class 'augbin_2t_1a_fit'
prob_success(
  x,
  y1_lower = -Inf,
  y1_upper = Inf,
  y2_lower = -Inf,
  y2_upper = log(0.7),
  probs = c(0.025, 0.975),
  newdata = NULL,
  ...
)
```

Arguments

x	an R object of class "augbin_fit"
...	arguments passed to other methods
y1_lower	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to negative infinity.
y1_upper	numeric, maximum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to positive infinity.
y2_lower	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 2 to baseline.
y2_upper	numeric, maximum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 2 to baseline. Defaults to log(0.7).
probs	pair of probabilities to use to calculate the credible interval for the probability of success.
newdata	data for which to infer the probability of success. A dataframe-like object with baseline tumour sizes in first column, and first and second post-baseline tumour sizes in columns 2 and 3. Omitted by default. When omitted, newdata is set to be the fit$tumour_size.

Value

Object of class tibble

Examples

```
## Not run:
fit <- stan_augbin_demo()
prob_success(fit, y2_upper = log(0.7))

## End(Not run)
```

`prob_tox_exceeds` *Calculate the probability that the rate of toxicity exceeds some threshold*

Description

Calculate the probability that the rate of toxicity exceeds some threshold

Calculate the probability that the rate of toxicity exceeds some threshold

Usage

```
prob_tox_exceeds(x, ...)

## S3 method for class 'dose_finding_fit'
prob_tox_exceeds(x, threshold, ...)
```

Arguments

`x`	an R object of class `"dose_finding_fit"`
`...`	arguments passed to other methods
`threshold`	numeric, threshold value.

Value

numerical vector of probabilities

numerical vector of probabilities

Examples

```
## Not run:
# CRM example
target <- 0.2
fit <- stan_crm('1N 2N 3T', skeleton = c(0.1, 0.2, 0.35, 0.6),
                target = target, model = 'empiric', beta_sd = sqrt(1.34),
                seed = 123)
prob_tox_exceeds(fit, target)

## End(Not run)
```

ranBin2 *Sample pairs of correlated binary events*

Description

This function is reproduced from the `binarySimCLF` package on CRAN. The original package appears no longer to be maintained. View the original source at: https://github.com/cran/binarySimCLF/blob/master/R/ranBin2.

Usage

```
ranBin2(nRep, u, psi)
```

Arguments

`nRep`	Number of simulated event pairs, positive integer.
`u`	Mean event probabilities, expressed as a vector of length 2. E.g. to simulate associated bivariate events with probabilities 80 `u = c(0.8, 0.3)`.
`psi`	Odds ratio, number. This parameter controls the strength of association. Use `psi = 1` for no association. Values greater than 1 correspond to increasingly positive association between the two events, and vice-versa.

Value

Matrix of events represented as 0s and 1s, with `nRep` rows and 2 columns. The first column is the incidence of event 1.

Examples

```
probs <- c(0.8, 0.3)
s <- ranBin2(1000, probs, psi=0.2)  # 1000 pairs of outcomes
cor(s)  # Negatively correlated because psi < 1
colMeans(s)  # Event rates as expected
```

rlkjcorr *Sample LKJ correlation matrices.*

Description

This function was copied from Richard McElreath's rethinking package hosted at https://github.com/rmcelreath/rethinking. In turn, he appears to have copied it from Ben Bolker's rLKJ function from the emdbook package, although I cannot find it there (else I would have imported it).

Usage

```
rlkjcorr(n, K, eta = 1)
```

Arguments

n	Number of matrices to sample.
K	dimenstion of matrix to sample.
eta	Distribution parameter

Value

matrix

---

spread_paths *Spread the information in dose_finding_paths object to a wide data.frame format.*

Description

Spread the information in dose_finding_paths object to a wide data.frame format.

Usage

```
spread_paths(df = NULL, dose_finding_paths = NULL, max_depth = NULL)
```

Arguments

df	Optional `data.frame` like that returned by as_tibble(dose_finding_paths). Columns .depth, .node, .parent are required. All other columns are spread with a suffix reflecting depth.
dose_finding_paths	Optional instance of dose_finding_paths. Required if ‘df‘ is null.
max_depth	integer, maximum depth of paths to traverse.

Value

A data.frame

Examples

```
## Not run:
target <- 0.25
skeleton <- c(0.05, 0.15, 0.25, 0.4, 0.6)
paths <- crm_dtps(skeleton = skeleton, target = target, model = 'empiric',
                  cohort_sizes = c(1, 1), next_dose = 3, beta_sd = 1)
spread_paths(dose_finding_paths = paths)

df <- as_tibble(paths)
spread_paths(df)
spread_paths(df %>% select(-fit, -parent_fit, -dose_index))

## End(Not run)
```

`stan_augbin` *Fit Wason & Seaman's Augmented Binary model for tumour response.*

Description

Phase II clinical trials in oncology commonly assess response as a key outcome measure. Patients achieve a RECIST response if their tumour size post-baseline has changed in size by some threshold amount and they do not experience non-shrinkage failure. An example of non-shrinkage failure is the appearance of new lesions. As a dichtotomisation of the underlying continuous tumour size measurement, RECIST response is inefficient. Wason & Seaman introduced the Augmented Binary method to incorporate mechanisms for non-shrinkage failure whilst modelling the probability of response based on the continuous tumour size measurements. See model-specific sections below, and the references.

Usage

```
stan_augbin(
  tumour_size,
  non_shrinkage_failure,
  arm = NULL,
  model = c("2t-1a"),
  prior_params = list(),
  ...
)
```

Arguments

`tumour_size`	matrix-like object containing tumour size measures, with rows representing patients and columns representing chronological standardised assessment points. Column one is baseline.
`non_shrinkage_failure`	matrix-like object containing logical indicators of non-shrinkage failure, with rows representing patients and columns representing chronological standardised assessment points.
`arm`	optional vector of integers representing the allocated treatment arms for patients, assumed in the same order as `tumour_size` and `non_shrinkage_failure`. NULL to fit the augbin variant for single-arm trials. NULL is the default.
`model`	Character string to denote the desired model. Currently, only `2t-1a` is supported, representing the model variant with two post-baseline assessments in a single arm trial. Multi-period and multi-arm versions will be added in future releases. The model choice determines the prior parameters that must be provided. See sections below.
`prior_params`	list of prior parameters. These are combined with the data and passed to `rstan::sampling`. The parameters required depend on the model form being fit. See sections below.
`...`	Extra parameters are passed to `rstan::sampling`. Commonly used options are `iter`, `chains`, `warmup`, `cores`, `control`. See `sampling`.

Value

an instance or subclass of type augbin_fit.

Single-arm model with two post-baseline assessments

The complete model form is:

$$(y_{1i}, y_{2i})^T \sim N((\mu_{1i}, \mu_{2i})^T, \Sigma)$$

$$\mu_{1i} = \alpha + \gamma z_{0i}$$

$$\mu_{2i} = \beta + \gamma z_{0i}$$

$$logit(Pr(D_{1i} = 1|Z_{0i})) = \alpha_{D1} + \gamma_{D1} z_{0i}$$

$$logit(Pr(D_{2i} = 1|D_{1i} = 0, Z_{0i}, Z_{1i})) = \alpha_{D2} + \gamma_{D2} z_{1i}$$

where z_{0i}, z_{1i}, z_{2i} are tumour sizes at baseline, period 1, and period 2, for patient i; y_{1i}, y_{2i} are the log-tumour-size ratios with respect to baseline; D_{1i}, D_{2i} are indicators of non-shrinkage failure; and Σ is assumed to be unstructured covariance matrix, with associated correlation matrix having an LKJ prior.

The following prior parameters are required:

- alpha_mean & alpha_sd for normal prior on α.
- beta_mean & beta_sd for normal prior on β.
- gamma_mean & gamma_sd for normal prior on γ.
- sigma_mean & sigma_sd for normal priors on diagonal elements of Σ;
- omega_lkj_eta for a LKJ prior on the two-period correlation matrix associated with Sigma. omega_lkj_eta = 1 is uniform, analogous to a Beta(1,1) prior on a binary probability.
- alpha_d1_mean & alpha_d1_sd for normal prior on α_{D1}.
- gamma_d1_mean & gamma_d1_sd for normal prior on γ_{D1}.
- alpha_d2_mean & alpha_d2_sd for normal prior on α_{D2}.
- gamma_d2_mean & gamma_d2_sd for normal prior on γ_{D2}.

Author(s)

Kristian Brock

References

Wason JMS, Seaman SR. Using continuous data on tumour measurements to improve inference in phase II cancer studies. Statistics in Medicine. 2013;32(26):4639-4650. doi:10.1002/sim.5867

Eisenhauer EA, Therasse P, Bogaerts J, et al. New response evaluation criteria in solid tumours: Revised RECIST guideline (version 1.1). European Journal of Cancer. 2009;45(2):228-247. doi:10.1016/j.ejca.2008.10.026

See Also

augbin_fit prior_predictive_augbin_2t_1a sampling

Examples

```
priors <- list(alpha_mean = 0, alpha_sd = 1,
               beta_mean = 0, beta_sd = 1,
               gamma_mean = 0, gamma_sd = 1,
               sigma_mean = 0, sigma_sd = 1,
               omega_lkj_eta = 1,
               alpha_d1_mean = 0, alpha_d1_sd = 1,
               gamma_d1_mean = 0, gamma_d1_sd = 1,
               alpha_d2_mean = 0, alpha_d2_sd = 1,
               gamma_d2_mean = 0, gamma_d2_sd = 1)
# Scenario 1 of Table 1 in Wason & Seaman (2013)
N <- 50
sigma <- 1
delta1 <- -0.356
mu <- c(0.5 * delta1, delta1)
Sigma = matrix(c(0.5 * sigma^2, 0.5 * sigma^2, 0.5 * sigma^2, sigma^2),
               ncol = 2)
alphaD <- -1.5
gammaD <- 0
set.seed(123456)
y <- MASS::mvrnorm(n = N, mu, Sigma)
z0 <- runif(N, min = 5, max = 10)
z1 <- exp(y[, 1]) * z0
z2 <- exp(y[, 2]) * z0
d1 <- rbinom(N, size = 1, prob = gtools::inv.logit(alphaD + gammaD * z0))
d2 <- rbinom(N, size = 1, prob = gtools::inv.logit(alphaD + gammaD * z1))
tumour_size <- data.frame(z0, z1, z2) # Sizes in cm
non_shrinkage_failure <- data.frame(d1, d2)
# Fit
## Not run:
fit <- stan_augbin(tumour_size, non_shrinkage_failure,
                   prior_params = priors, model = '2t-1a', seed = 123)

## End(Not run)
```

`stan_augbin_demo` *Simple helper function to demonstrate fitting of an Augmented Binary model.*

Description

This function exist mostly to demonstrate things you can do to instances of `augbin_fit` without having to paste into each example the not inconsiderable blob of code to sample outcomes and fit the model.

Usage

```
stan_augbin_demo()
```

Value

instance of augbin_fit

See Also

stan_augbin augbin_fit prior_predictive_augbin_2t_1a sampling

Examples

```
## Not run:
fit <- stan_augbin_demo()
# I told you it was simple.

## End(Not run)
```

---

stan_crm *Fit a CRM model*

Description

Fit a continual reassessment method (CRM) model for dose-finding using Stan for full Bayesian inference. There are several likelihood and prior combinations supported. See model-specific sections below.

Usage

```
stan_crm(
  outcome_str = NULL,
  skeleton,
  target,
  model = c("empiric", "logistic", "logistic_gamma", "logistic2"),
  a0 = NULL,
  alpha_mean = NULL,
  alpha_sd = NULL,
  beta_mean = NULL,
  beta_sd = NULL,
  beta_shape = NULL,
  beta_inverse_scale = NULL,
  doses_given = NULL,
  tox = NULL,
  weights = NULL,
  ...
)
```

Arguments

outcome_str	A string representing the outcomes observed hitherto. See df_parse_outcomes for a description of syntax and examples. Alternatively, you may provide doses_given and tox parameters. See Details.
skeleton	a vector of the prior guesses of toxicity at doses. This should be a monotonically-increasing vector of numbers between 0 and 1.
target	the target toxicity probability, a number between 0 and 1. This value would normally be one of the values in skeleton, but that is not a requirement.
model	Character string to denote desired model. One of empiric, logistic, logistic_gamma, or logistic2. The choice of model determines which parameters are required. See Details.
a0	Value of fixed intercept parameter. Only required for certain models. See Details.
alpha_mean	Prior mean of intercept variable for normal prior. Only required for certain models. See Details.
alpha_sd	Prior standard deviation of intercept variable for normal prior. Only required for certain models. See Details.
beta_mean	Prior mean of gradient variable for normal prior. Only required for certain models. See Details.
beta_sd	Prior standard deviation of slope variable for normal prior. Only required for certain models. See Details.
beta_shape	Prior shape parameter of slope variable for gamma prior. Only required for certain models. See Details.
beta_inverse_scale	Prior inverse scale parameter of slope variable for gamma prior. Only required for certain models. See Details.
doses_given	A optional vector of dose-levels given to patients 1:num_patients, where 1=lowest dose, 2=second dose, etc. Only required when outcome_str is not provided.
tox	An optional vector of toxicity outcomes for patients 1:num_patients, where 1=toxicity and 0=no toxicity. Only required when outcome_str is not provided.
weights	An optional vector of numeric weights for the observations for patients 1:num_patients, thus facilitating the TITE-CRM design. Can be used with outcome_str, or with doses_given and tox. It is generally tidier to specify doses_given, tox and weights when a TITE-CRM analysis is desired.
...	Extra parameters are passed to rstan::sampling. Commonly used options are iter, chains, warmup, cores, and control.

Details

The quickest and easiest way to fit a CRM model to some observed outcomes is to describe the outcomes using **trialr**'s syntax for dose-finding outcomes. See df_parse_outcomes for full details and examples.

Different model choices require that different parameters are provided. See sections below.

Value

An object of class `crm_fit`

The `empiric` model

The model form is:
$F(x_i, \beta) = x_i^{\exp \beta}$
and the required parameters are:

- `beta_sd`

The `logistic` model

The model form is:
$F(x_i, \beta) = 1/(1 + \exp(-a_0 - \exp(\beta)x_i))$
and the required parameters are:

- `a0`
- `beta_mean`
- `beta_sd`

The `logistic_gamma` model

The model form is:
$F(x_i, \beta) = 1/(1 + \exp(-a_0 - \exp(\beta)x_i))$
and the required parameters are:

- `a0`
- `beta_shape`
- `beta_inverse_scale`

The `logistic2` model

The model form is:
$F(x_i, alpha, \beta) = 1/(1 + \exp(-\alpha - \exp(\beta)x_i))$
and the required parameters are:

- `alpha_mean`
- `alpha_sd`
- `beta_mean`
- `beta_sd`

Author(s)

Kristian Brock

References

O'Quigley, J., Pepe, M., & Fisher, L. (1990). Continual reassessment method: a practical design for phase 1 clinical trials in cancer. Biometrics, 46(1), 33-48. https://www.jstor.org/stable/2531628

Cheung, Y.K. (2011). Dose Finding by the Continual Reassessment Method. CRC Press. ISBN 9781420091519

See Also

crm_fit sampling

Examples

```
## Not run:
# CRM example
fit1 <- stan_crm('1N 2N 3T', skeleton = c(0.1, 0.2, 0.35, 0.6),
                 target = 0.2, model = 'empiric', beta_sd = sqrt(1.34),
                 seed = 123)

fit2 <- stan_crm('1NNN 2NNN 3TTT', skeleton = c(0.1, 0.2, 0.35, 0.6),
                 target = 0.2, model = 'logistic', a0 = 3, beta_mean = 0,
                 beta_sd = sqrt(1.34), seed = 123)

# The seed is passed to the Stan sampler. The usual Stan sampler params like
# cores, iter, chains etc are passed on too via the ellipsis operator.

# TITE-CRM example, p.124 of Dose Finding by the CRM, Cheung (2010)
fit3 <-stan_crm(skeleton = c(0.05, 0.12, 0.25, 0.40, 0.55), target = 0.25,
                doses_given = c(3, 3, 3, 3),
                tox = c(0, 0, 0, 0),
                weights = c(73, 66, 35, 28) / 126,
                model = 'empiric', beta_sd = sqrt(1.34), seed = 123)
fit3$recommended_dose

## End(Not run)
```

---

stan_efftox *Fit an EffTox model*

Description

Fit an EffTox model using Stan for full Bayesian inference.

Usage

```
stan_efftox(
  outcome_str = NULL,
  real_doses,
  efficacy_hurdle,
```

```
  toxicity_hurdle,
  p_e,
  p_t,
  eff0,
  tox1,
  eff_star,
  tox_star,
  priors = NULL,
  alpha_mean = NULL,
  alpha_sd = NULL,
  beta_mean = NULL,
  beta_sd = NULL,
  gamma_mean = NULL,
  gamma_sd = NULL,
  zeta_mean = NULL,
  zeta_sd = NULL,
  eta_mean = NULL,
  eta_sd = NULL,
  psi_mean = NULL,
  psi_sd = NULL,
  doses_given = NULL,
  eff = NULL,
  tox = NULL,
  ...
)
```

Arguments

outcome_str	A string representing the outcomes observed hitherto. See efftox_parse_outcomes for a description of syntax and examples. Alternatively, you may provide doses_given, eff and tox parameters. See Details.
real_doses	A vector of numbers, the doses under investigation. They should be ordered from lowest to highest and be in consistent units. E.g. to conduct a dose-finding trial of doses 10mg, 20mg and 50mg, use c(10, 20, 50).
efficacy_hurdle	Minimum acceptable efficacy probability. A number between 0 and 1.
toxicity_hurdle	Maximum acceptable toxicity probability. A number between 0 and 1.
p_e	Certainty required to infer a dose is acceptable with regards to being probably efficacious; a number between 0 and 1.
p_t	Certainty required to infer a dose is acceptable with regards to being probably tolerable; a number between 0 and 1.
eff0	Efficacy probability required when toxicity is impossible; a number between 0 and 1 (see Details).
tox1	Toxicity probability permitted when efficacy is guaranteed; a number between 0 and 1 (see Details).
eff_star	Efficacy probability of an equi-utility third point (see Details).

tox_star	Toxicity probability of an equi-utility third point (see Details).
priors	instance of class efftox_priors, the hyperparameters for normal priors on the six model parameters.
alpha_mean	Optional, the prior normal mean of the intercept term in the toxicity logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
alpha_sd	Optional, the prior normal standard deviation of the intercept term in the toxicity logit model. A number.You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
beta_mean	Optional, the prior normal mean of the slope term in the toxicity logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
beta_sd	Optional, the prior normal standard deviation of the slope term in the toxicity logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
gamma_mean	Optional, The prior normal mean of the intercept term in the efficacy logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
gamma_sd	Optional, the prior normal standard deviation of the intercept term in the efficacy logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
zeta_mean	Optional, the prior normal mean of the slope term in the efficacy logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
zeta_sd	Optional, the prior normal standard deviation of the slope term in the efficacy logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
eta_mean	Optional, the prior normal mean of the squared term coefficient in the efficacy logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
eta_sd	Optional, the prior normal standard deviation of the squared term coefficient in the efficacy logit model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
psi_mean	Optional, the prior normal mean of the association term in the combined efficacy-toxicity model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
psi_sd	Optional, the prior normal standard deviation of the association term in the combined efficacy-toxicity model. A number. You should prioritise specifying this value via priors but this option is provided for backwards-compatibility.
doses_given	A optional vector of dose-levels given to patients 1:num_patients, where 1=lowest dose, 2=second dose, etc. Only required when outcome_str is not provided.
eff	An optional vector of efficacy outcomes for patients 1:num_patients, where 1=efficacy and 0=no efficacy. Only required when outcome_str is not provided.

tox	An optional vector of toxicity outcomes for patients 1:num_patients, where 1=toxicity and 0=no toxicity. Only required when outcome_str is not provided.
...	Extra parameters are passed to rstan::sampling. Commonly used options are iter, chains, warmup, cores, control. sampling.

Details

The quickest and easiest way to fit an EffTox model to some observed outcomes is to describe the outcomes using **trialr**'s syntax for efficacy-toxicity dose-finding outcomes. See efftox_parse_outcomes for full details and examples.

Utility or attractivess scores are calculated in EffTox using L^p norms. Imagine the first quadrant of a scatter plot with prob_eff along the x-axis and prob_tox along the y-axis. The point (1, 0) (i.e. guaranteed efficacy & no toxicity) is the holy grail. The neutral contour intersects the points (eff0, 0), (1, tox1) and (eff_star, tox_star). A unique curve intersects these three points and identifies a value for p, the exponent in the L^p norm. On this neutral- utility contour, scores are equal to zero. A family of curves with different utility scores is defined that are "parallel" to this neutral curve. Points with probabilities of efficacy and toxicity that are nearer to (1, 0) will yield greater scores, and vice-versa.

Value

An object of class efftox_fit

Author(s)

Kristian Brock <kristian.brock@gmail.com>

References

Thall, P., & Cook, J. (2004). Dose-Finding Based on Efficacy-Toxicity Trade-Offs. Biometrics, 60(3), 684-693.

Thall, P., Herrick, R., Nguyen, H., Venier, J., & Norris, J. (2014). Effective sample size for computing prior hyperparameters in Bayesian phase I-II dose-finding. Clinical Trials, 11(6), 657-666. https://doi.org/10.1177/1740774514547397

Brock, K., Billingham, L., Copland, M., Siddique, S., Sirovica, M., & Yap, C. (2017). Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology, 17(1), 112. https://doi.org/10.1186/s12874-017-0381-x

See Also

efftox_priors get_efftox_priors efftox_fit stan_efftox_demo

Examples

```
## Not run:
# This model is presented in Thall et al. (2014).
p <- efftox_priors(alpha_mean = -7.9593, alpha_sd = 3.5487,
                   beta_mean = 1.5482, beta_sd = 3.5018,
                   gamma_mean = 0.7367, gamma_sd = 2.5423,
```

```
                  zeta_mean = 3.4181, zeta_sd = 2.4406,
                  eta_mean = 0, eta_sd = 0.2,
                  psi_mean = 0, psi_sd = 1)
mod1 <- stan_efftox('1N 2E 3B',
                    real_doses = c(1.0, 2.0, 4.0, 6.6, 10.0),
                    efficacy_hurdle = 0.5, toxicity_hurdle = 0.3,
                    p_e = 0.1, p_t = 0.1,
                    eff0 = 0.5, tox1 = 0.65,
                    eff_star = 0.7, tox_star = 0.25,
                    priors = p,
                    seed = 123)

# The above is a longhad version of:
mod2 <- stan_efftox_demo('1N 2E 3B', seed = 123)

# the seed is passed to the Stan sampler. The usual Stan sampler params like
# cores, iter, chains etc are passed on too via the ellipsis operator.

## End(Not run)
```

`stan_efftox_demo` *Fit the EffTox model presented in Thall et al. (2014)*

Description

Fit the EffTox model presented in Thall et al. (2014) using Stan for full Bayesian inference.

Usage

```
stan_efftox_demo(outcome_str, ...)
```

Arguments

`outcome_str`	A string representing the outcomes observed hitherto. See `efftox_parse_outcomes` for a description of syntax and examples. Alternatively, you may provide `doses_given`, `eff` and `tox` parameters. See Details.
`...`	Extra parameters are passed to `rstan::sampling`. Commonly used options are `iter`, `chains`, `warmup`, `cores`, `control`. `sampling`.

Value

An object of class `efftox_fit`

Author(s)

Kristian Brock <kristian.brock@gmail.com>

References

Thall, P., & Cook, J. (2004). Dose-Finding Based on Efficacy-Toxicity Trade-Offs. Biometrics, 60(3), 684-693.

Thall, P., Herrick, R., Nguyen, H., Venier, J., & Norris, J. (2014). Effective sample size for computing prior hyperparameters in Bayesian phase I-II dose-finding. Clinical Trials, 11(6), 657-666. https://doi.org/10.1177/1740774514547397

Brock, K., Billingham, L., Copland, M., Siddique, S., Sirovica, M., & Yap, C. (2017). Implementing the EffTox dose-finding design in the Matchpoint trial. BMC Medical Research Methodology, 17(1), 112. https://doi.org/10.1186/s12874-017-0381-x

See Also

`efftox_fit` `stan_efftox`

Examples

```
## Not run:
# This model is presented in Thall et al. (2014)
mod2 <- stan_efftox_demo('1N 2E 3B', seed = 123)

# The seed is passed to the Stan sampler. The usual Stan sampler params like
# cores, iter, chains etc are passed on too via the ellipsis operator.

## End(Not run)
```

---

stan_hierarchical_response_thall

Fit the hierarchical response model described by Thall et al. *(2003).*

Description

Fit the hierarchical response model to exchangeable groups described by Thall *et al.* (2003).

Usage

```
stan_hierarchical_response_thall(
  group_responses,
  group_sizes,
  mu_mean,
  mu_sd,
  tau_alpha,
  tau_beta,
  ...
)
```

Arguments

group_responses	vector of integers, number of responses in each group
group_sizes	vector of integers, number of patients in each group
mu_mean	mean parameter of normal prior distribution on mu. See details.
mu_sd	standard deviation parameter of normal prior distribution on mu. See details.
tau_alpha	parameter alpha of inverse gamma prior distribution on tau. See details.
tau_beta	beta parameter of inverse gamma prior distribution on tau. See details.
...	Extra parameters are passed to `rstan::sampling`. Commonly used options are `iter`, `chains`, `warmup`, `cores`, and `control`.

Details

Thall *et al.* (2003) describe hierarchical methods for analysing treatment effects of a common intervention in several sub-types of a disease. The treatment effects are assumed to be different but exchangeable and correlated. Observing efficacy in one cohort, for example, increases one's expectations of efficacy in others. They demonstrate the hierarchical approach in a trial with binary response outcomes and in another with time-to-event outcomes. This function fits their model for binary response outcomes.

Let the probability of response in group i be $\pi[i]$ for $i = 1, ..., N$. They assume a logistic model so that $\theta_i = \log \pi_i/(1 - \pi_i)$ is the log-odds of response in group i. They assume that $\theta_i \sim N(\mu, \sigma^2)$.

The authors implemented their model in BUGS. As is the convention in BUGS, the authors define normal distributions by a precision parameter τ as opposed to the standard deviation parameter σ used here. We have re-specified their model to comply with the Stan convention of using standard deviation. The authors use a normal prior on μ, and a gamma prior on τ, equivalent to an inverse gamma prior on $\tau^{-1} = \sigma^2$.

The authors provide WinBUGS code in their publication. We implement their model here in Stan.

Value

Object of class `rstan::stanfit` returned by `rstan::sampling`

References

Thall, Wathen, Bekele, Champlin, Baker, and Benjamin. 2003. "Hierarchical Bayesian approaches to phase II trials in diseases with multiple subtypes." Statistics in Medicine 22 (5): 763–80. https://doi.org/10.1002/sim.1399.

See Also

`rstan::stanfit`, `rstan::sampling`

Examples

```
## Not run:
# Example from p.778 of Thall et al. (2003)
mod0 <- stan_hierarchical_response_thall(
  group_responses = c(0, 0, 1, 3, 5, 0, 1, 2, 0, 0),
```

```
  group_sizes = c(0, 2 ,1, 7, 5, 0, 2, 3, 1, 0),
  mu_mean = -1.3863,
  mu_sd = sqrt(1 / 0.1),
  tau_alpha = 2,
  tau_beta = 20)

## End(Not run)
```

---

stan_nbg *Fit a Neuenschwander, Branson & Gsponer logit dose-finding model*

Description

Fit Neuenschwander, Branson & Gsponer logit model for dose-finding using Stan for full Bayesian inference.

Usage

```
stan_nbg(
  outcome_str = NULL,
  real_doses,
  d_star,
  target,
  alpha_mean = NULL,
  alpha_sd = NULL,
  beta_mean = NULL,
  beta_sd = NULL,
  doses_given = NULL,
  tox = NULL,
  weights = NULL,
  ...
)
```

Arguments

outcome_str	A string representing the outcomes observed hitherto. See df_parse_outcomes for a description of syntax and examples. Alternatively, you may provide doses_given and tox parameters. See Details.
real_doses	A vector of numbers, the doses under investigation. They should be ordered from lowest to highest and be in consistent units. E.g. to conduct a dose-finding trial of doses 10mg, 20mg and 50mg, use c(10, 20, 50).
d_star	d_star, numeric reference dose-level. The linear covariate in this logit model is dose / d_star.
target	the target toxicity probability, a number between 0 and 1.
alpha_mean	Prior mean of intercept variable for normal prior. See Details.

alpha_sd	Prior standard deviation of intercept variable for normal prior. See Details.
beta_mean	Prior mean of gradient variable for normal prior. See Details.
beta_sd	Prior standard deviation of slope variable for normal prior. See Details.
doses_given	A optional vector of dose-levels given to patients 1:num_patients, where 1=lowest dose, 2=second dose, etc. Only required when outcome_str is not provided.
tox	An optional vector of toxicity outcomes for patients 1:num_patients, where 1=toxicity and 0=no toxicity. Only required when outcome_str is not provided.
weights	An optional vector of numeric weights for the observations for patients 1:num_patients, thus facilitating a time-to-event (TITE) design. Can be used with outcome_str, or with doses_given and tox. It is generally tidier to specify doses_given, tox and weights when a TITE-analysis is desired.
...	Extra parameters are passed to rstan::sampling. Commonly used options are iter, chains, warmup, cores, and control.

Details

The quickest and easiest way to fit this model to some observed outcomes is to describe the outcomes using **trialr**'s syntax for dose-finding outcomes. See df_parse_outcomes for full details and examples.

The two-parameter model form is:

$F(x_i, \alpha, \beta) = 1/(1 + \exp -(\alpha + \exp(\beta) log(x_i/d_s tar)))$

and the required parameters are:

- alpha_mean
- alpha_sd
- beta_mean
- beta_sd

Value

An object of class nbg_fit, which inherits behaviour from crm_fit.

Author(s)

Kristian Brock <kristian.brock@gmail.com>

References

Neuenschwander, B., Branson, M., & Gsponer, T. (2008). Critical aspects of the Bayesian approach to phase I cancer trials. Statistics in Medicine, 27, 2420–2439. https://doi.org/10.1002/sim

See Also

crm_fit sampling

Examples

```
## Not run:
# Non-TITE example:
fit1 <- stan_nbg('1NNN 2NNN 3TTT', real_doses = c(10, 20, 50, 100, 200),
                 d_star = 200, target = 0.25,
                 alpha_mean = -1, alpha_sd = 2,
                 beta_mean = 0, beta_sd = 1,
                 seed = 123)
fit1$recommended_dose

# The seed is passed to the Stan sampler. The usual Stan sampler params like
# cores, iter, chains etc are passed on too via the ellipsis operator.

# TITE-CRM example
fit2 <-stan_nbg(real_doses = c(10, 20, 50, 100, 200), d_star = 200,
                target = 0.25,
                doses_given = c(3, 3, 3, 3),
                tox = c(0, 0, 0, 0),
                weights = c(73, 66, 35, 28) / 126,
                alpha_mean = -1, alpha_sd = 2,
                beta_mean = 0, beta_sd = 1,
                seed = 123)
fit2$recommended_dose

## End(Not run)
```

`stan_peps2` *Fit the P2TNE model developed for the PePS2 trial to some outcomes.*

Description

The PePS2 trial investigates pembrolizumab in non-small-cell lung cancer. Patients may be previously treated (PT) or treatment naive (TN). Response rates in lung cancer have been shown to increase with PD-L1 tumour proportion score. PD-L1 score is measured at baseline. Each patient belongs to one of the categories <1 stratify the patient population and are used as predictive variables to stratify the analysis. The BEBOP model studies co-primary efficacy and toxicity outcomes in the presence of predictive data. Thus, PePS2 studies efficacy and toxicity in 6 distinct cohorts: TN Low, TN Medium, TN High, PT Low, PT Medium, PT High. The design admits all-comers and does not target specific sample sizes in the individual cohorts. Hyperprior parameters have defaults to match those used in PePS2, but all may be overridden. The returned object includes randomly-sampled outcomes, as well as parameters to run the model. These are all combined in the same list object for passing to RStan, as is the convention. See the accompanying vignette for a full description.

Usage

```
stan_peps2(
  eff,
```

```
  tox,
  cohorts,
  alpha_mean = -2.2,
  alpha_sd = 2,
  beta_mean = -0.5,
  beta_sd = 2,
  gamma_mean = -0.5,
  gamma_sd = 2,
  zeta_mean = -0.5,
  zeta_sd = 2,
  lambda_mean = -2.2,
  lambda_sd = 2,
  psi_mean = 0,
  psi_sd = 1,
  ...
)
```

Arguments

eff	A vector of efficacy outcomes for the patients, where 1=efficacy and 0=no efficacy.
tox	A vector of toxicity outcomes for the patients, where 1=toxicity and 0=no toxicity.
cohorts	A vector of integers from 1 to 6, denoting the cohorts to which the patients belong.
alpha_mean	The prior mean of alpha. Alpha is the efficacy model intercept.
alpha_sd	The prior standard deviation of alpha. Alpha is the efficacy model intercept.
beta_mean	The prior mean of beta. Beta is the efficacy model term for being previously treated.
beta_sd	The prior standard deviation of beta. Beta is the efficacy model term for being previously treated.
gamma_mean	The prior mean of gamma. Gamma is the efficacy model term for being PD-L1 score = Low.
gamma_sd	The prior standard deviation of gamma. Gamma is the efficacy model term for being PD-L1 score = Low.
zeta_mean	The prior mean of zeta. Zeta is the efficacy model term for being PD-L1 score = Medium.
zeta_sd	The prior standard deviation of zeta. Zeta is the efficacy model term for being PD-L1 score = Medium.
lambda_mean	The prior mean of lambda. Lambda is the toxicity model intercept.
lambda_sd	The prior standard deviation of lambda. Lambda is the toxicity model intercept.
psi_mean	The prior mean of psi. Psi is the joint model association parameter.
psi_sd	The prior standard deviation of psi. Psi is the joint model association parameter.
...	Extra parameters are passed to `rstan::sampling`. Commonly used options are `iter`, `chains`, `warmup`, `cores`, and `control`.

Value

Object of class rstan::stanfit returned by rstan::sampling

Examples

```
## Not run:
fit <- stan_peps2(
  eff = c(0, 1, 0, 1, 0, 0),
  tox = c(0, 0, 1, 1, 0, 0),
  cohorts = c(3, 1, 1, 4, 5, 6)
)

## End(Not run)
```

---

summary.crm_fit *Obtain summary of an crm_fit*

Description

Obtain summary of an crm_fit

Usage

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

Arguments

object	crm_fit object to summarise.
...	Extra parameters, passed onwards.

Value

A summary object.

See Also

stan_crm

summary.efftox_fit *Obtain summary of an efftox_fit*

Description

Obtain summary of an efftox_fit

Usage

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

Arguments

object	efftox_fit object to summarise.
...	Extra parameters, passed onwards.

Value

A summary object.

total_weight_at_dose *Get the total weight of patient outcomes at the doses under investigation.*

Description

Get the total weight of patient outcomes at the doses under investigation.

Usage

```
total_weight_at_dose(x, dose, ...)

## Default S3 method:
total_weight_at_dose(x, dose = NULL, ...)
```

Arguments

x	An R object of class "dose_finding_fit"
dose	Optional integer, at which dose-level? Omit to get data on all doses.
...	arguments passed to other methods

Value

numerical vector

Examples

```
## Not run:
# CRM example
fit <- stan_crm(skeleton = c(0.1, 0.2, 0.35, 0.6), target = 0.2,
                model = 'empiric', beta_sd = sqrt(1.34), seed = 123,
                doses = c(1, 1, 2, 2, 2),
                tox   = c(0, 0, 0, 0, 0),
                weights = c(1, 1, 0.9, 0.1, 0.1))

total_weight_at_dose(fit)            # c(2, 1.1, 0, 0)
total_weight_at_dose(fit, dose = 2)  # 1.1

## End(Not run)
```

`tox_at_dose` *Get the number of toxicity events seen at the doses under investigation.*

Description

Get the number of toxicity events seen at the doses under investigation.

Usage

```
tox_at_dose(x, dose, ...)

## S3 method for class 'dose_finding_fit'
tox_at_dose(x, dose = NULL, ...)
```

Arguments

`x`	An R object of class `"dose_finding_fit"`
`dose`	Optional integer, at which dose-level? Omit to get data on all doses.
`...`	arguments passed to other methods

Value

integer vector

Examples

```
## Not run:
# CRM example
target <- 0.2
fit <- stan_crm('1N 2N 3T', skeleton = c(0.1, 0.2, 0.35, 0.6),
                target = target, model = 'empiric', beta_sd = sqrt(1.34),
                seed = 123)
tox_at_dose(fit)            # c(0, 0, 1, 0)
tox_at_dose(fit, dose = 3)  # 1

## End(Not run)
```

`trialr_simulate` *Run a simulation study.*

Description

This function is a fairly flexible way of running simulation studies in trialr, and beyond. It essentially uses delegates to perform this pattern:

```
for i in 1:N:
  data = get_data_func()
  fit = fit_model_func(data)
  if summarise_func is null:
    sims[i] = fit
  else
    sims[i] = summarise_func(data, fit)
  end
loop
return sims
```

Usage

```
trialr_simulate(
  N,
  get_data_func,
  fit_model_func,
  summarise_func = NULL,
  num_logs = 10,
  num_saves = NULL,
  save_func = NULL
)
```

Arguments

`N`	integer, number of simulated iterations to run.
`get_data_func`	Function that takes no parameters and returns a sampled dataset to be analysed. I.e. the call signature is f().
`fit_model_func`	Function that accepts the output of `get_data_func` as the sole parameter and fits the model or performs the analysis, returning an object of arbitrary type.
`summarise_func`	Optional. If provided, this function should accept the ouputs of `get_data_func` and `fit_model_func` as parameters 1 & 2 and perform some post-fit processing or simplification. The result of this call is the output from iteration i. If omitted, the fit object from `fit_model_func` is simply used as the output from iteration i.
`num_logs`	Number of log messages to receive about progress. NULL to suppress logging. E.g. if N=100 and num_logs=10, you will get log messages when i=10, 20, 30, etc.

num_saves — Number of interimittent saves to attempt. NULL to suppress saving E.g. if N=100 and num_saves=10, the save_func delegate will be called after iteration i=10, 20, 30, etc.

save_func — Optional. Function that takes the interim list of simulated objects as the sole parameter and saves them somehow. This, combined with num_saves, allows periodic saving of in-progress results to avoid complete data loss if the simulation study fails for some reason.

Value

list of length N. The items in the list are as returned by summarise_func or fit_model_func.

Examples

```
get_data_func <- function() {
  group_sizes <- rbinom(n = 5, size = 50, prob = c(0.1, 0.3, 0.3, 0.2, 0.1))
  group_responses <- rbinom(n = 5, size = group_sizes,
                            prob = c(0.2, 0.5, 0.2, 0.2, 0.2))
  list(
    group_responses = group_responses, group_sizes = group_sizes,
    mu_mean = gtools::logit(0.1), mu_sd = 1, tau_alpha = 2, tau_beta = 20
  )
}
fit_model_func <- function(data) {
  data <- append(data, list(refresh = 0))
  do.call(stan_hierarchical_response_thall, args = data)
}
summarise_func <- function(data, fit) {
  # Probability that estimate response rate exceeds 30%
  unname(colMeans(as.data.frame(fit, 'prob_response') > 0.3))
}
## Not run:
sims <- trialr_simulate(N = 20, get_data_func, fit_model_func, summarise_func)
# Posterior probabilities that the response rate in each cohort exceeds 30%:
do.call(rbind, sims)
# Cohorts are in columns; simulated iterations are in rows.

## End(Not run)
```

---

weights_at_dose *Get the weights of patient outcomes at the doses under investigation.*

Description

Get the weights of patient outcomes at the doses under investigation.

Usage

```
weights_at_dose(x, dose, ...)

## Default S3 method:
weights_at_dose(x, dose = NULL, ...)

## S3 method for class 'crm_fit'
weights_at_dose(x, dose = NULL, ...)
```

Arguments

x	An R object of class "dose_finding_fit"
dose	Optional integer, at which dose-level? Omit to get data on all doses.
...	arguments passed to other methods

Value

list if dose omitted, numerical vector if dose provided.

Examples

```
## Not run:
# CRM example
fit <- stan_crm(skeleton = c(0.1, 0.2, 0.35, 0.6), target = 0.2,
                model = 'empiric', beta_sd = sqrt(1.34), seed = 123,
                doses = c(1, 1, 2, 2, 2),
                tox   = c(0, 0, 0, 0, 0),
                weights = c(1, 1, 0.9, 0.1, 0.1))
l <- weights_at_dose(fit)

length(l)  # 4
l[[1]]  # c(1, 1)
l[[2]]  # c(0.9, 0.1, 0.1)
l[[3]]  # c()

weights_at_dose(fit, dose = 2)  # c(0.9, 0.1, 0.1)

## End(Not run)
```

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