

Package ‘trialr’

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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>; 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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BugReports <https://github.com/brockk/trialr/issues>

Suggests testthat, knitr, rmarkdown, ggridges, covr, DiagrammeR

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R topics documented:

trialr-package	3
as.data.frame.crm_fit	4
as.data.frame.efftox_fit	4
as.mcmc.list.crm_fit	5
as.mcmc.list.efftox_fit	5
as_tibble.augbin_2t_1a_fit	6
as_tibble.dose_finding_paths	6
augbin_2t_1a_fit	7
augbin_fit	8
binary_prob_success	8
careful_escalation	9
closest_to_target	10
crm_codified_dose_logistic	11
crm_dtpts	12
crm_fit-class	14
crm_params-class	15
crm_path_analysis	17
crm_prior_beliefs	19
crm_process	21
df_parse_outcomes	22
dose_finding_fit-class	23
dose_finding_path_node-class	23
efftox_analysis_to_df	24
efftox_contour_plot	25
efftox_dtpts	26
efftox_dtpts_to_dataframe	29
efftox_fit-class	30
efftox_get_tox	32
efftox_parameters_demo	33
efftox_params-class	34
efftox_parse_outcomes	35
efftox_path_analysis	36
efftox_process	38
efftox_simulate	38
efftox_solve_p	39
efftox_superiority	40
efftox_utility	41

efftox_utility_density_plot	42
parse_dose_finding_outcomes	42
parse_eff_tox_dose_finding_outcomes	44
peps2_get_data	45
peps2_process	47
plot.crm_fit	48
plot.efftox_fit	49
predict.augbin_2t_1a_fit	49
print.augbin_fit	50
print.crm_fit	51
print.efftox_fit	51
prior_predictive_augbin_2t_1a	52
prob_success	53
prob_tox_exceeds	54
ranBin2	55
rlkcorr	56
spread_paths	56
stan_augbin	57
stan_augbin_demo	60
stan_crm	60
stan_efftox	63
stan_efftox_demo	66
stan_hierarchical_response_thall	67
stan_peps2	69
summary.crm_fit	70
summary.efftox_fit	71
trialr_simulate	72
Index	74

trialr-package	<i>The 'trialr' package.</i>
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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. <http://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(crm_fit, ...)
```

Arguments

`crm_fit` 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(efftox_fit, ...)
```

Arguments

`efftox_fit` 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	<i>Class used by trialr to fit Wason & Seaman's Augmented Binary method in single arm trials with two post-baseline tumour assessments.</i>
------------------	--

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	<i>Class used by trialr to fit Wason & Seaman's Augmented Binary method.</i>
------------	---

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	<i>Calculate the binary probability of success.</i>
---------------------	---

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 $\text{logit}(p[i]) = \alpha + \beta x[i]$, where p is `prob_tox`.

Usage

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

Arguments

<code>prob_tox</code>	Numeric vector, seek codified doses that yield these probabilities of toxicity.
<code>alpha_mean</code>	Numeric, expected value of intercept.
<code>beta_mean</code>	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 <code>empiric</code> , <code>logistic</code> , <code>logistic_gamma</code> , or <code>logistic2</code> . 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 <code>cohort_sizes = c(2, 3)</code> .
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 resolve 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, 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.
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 <code>crm_params</code> containing data passed to <code>sampling</code> .
fit	An object of class <code>stanfit</code> , containing the posterior samples.
samples	An optional <code>data.frame</code> like object of samples.

Details

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

See Also

[stan_crm](#)

crm_params-class	<i>Container class for parameters to fit the CRM models in trialr.</i>
------------------	--

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	<i>Fit a CRM model to the incrementally observed outcomes on a trial pathway.</i>
-------------------	---

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

- a_0
- beta_mean
- beta_sd

Parameter requirements of logistic_gamma model

- a_0
- 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 opens up some nice opportunities
df <- as_tibble(paths)
df
# E.g. how did our view on the risk of toxicity at dose 2 evolve?
library(tidyr)
library(purrr)
library(dplyr)
```

```
df %>%
  mutate(prob_tox = fit %>% map('prob_tox')) %>%
  select(outcomes, dose_index, prob_tox) %>%
  unnest %>%
  filter(dose_index == 2)

## 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 analogous 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 <code>empiric</code> , <code>logistic</code> , <code>logistic_gamma</code> , or <code>logistic2</code> . 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 <code>rstan::stanmodel</code> , 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 represent 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

<code>node_id</code>	An integer representing the id of this node in a pathway.
<code>parent_node_id</code>	An integer representing the id of this node's parent in the pathway.
<code>depth</code>	An integer representing the depth of this node in the pathway, where the root has depth 0.
<code>outcomes</code>	A string representing the outcomes observed at the time of analysis. See df_parse_outcomes for a description of syntax and examples.
<code>next_dose</code>	An integer representing the dose recommended by the model for the next patient or cohort of patients.
<code>fit</code>	Object obtained from fitting the dose-finding model to outcomes.
<code>parent_fit</code>	Object obtained from fitting the dose-finding model to the outcomes of the parent node. Comparing to <code>fit</code> will often 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)
```

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 suppress.

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 suppress.
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. <code>seq(-3, 3, by = 0.2)</code> .

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 <code>cohort_sizes = c(2, 3)</code> .
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 <code>efftox_fit</code> 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 <code>rstan::sampling</code> .

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 <code>efftox_params</code> , a list of EffTox parameters. An example is yielded by <code>efftox_parameters_demo</code> .
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 <code>cohort_sizes = c(2, 3)</code> .
next_dose	the dose-level to be given to the immediately next cohort.
...	extra params passed to <code>rstan::sampling</code> .

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 <code>post_utility</code> ; 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 <code>utility</code> , 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 <code>prob_tox</code> and <code>prob_eff</code> (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 <code>efftox_params</code> containing data passed to <code>sampling</code> .
fit	An object of class <code>stanfit</code> , 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 hyperparameters 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, 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

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).
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.

See Also

[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 represent 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

<code>outcome_str</code>	A string representing the outcomes observed hitherto. See efftox_parse_outcomes for a description of syntax and examples. Alternatively, you may provide <code>doses_given</code> and <code>tox</code> parameters. See Details.
<code>verbose</code>	logical, TRUE to get log messages.
<code>...</code>	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 opens up some nice opportunities
df <- as_tibble(paths)
df
# E.g. how did our view on the event probabilities at dose 2 evolve?
library(tidyr)
library(purrr)
library(dplyr)
df %>%
  mutate(
    prob_tox = fit %>% map('prob_tox'),
    prob_eff = fit %>% map('prob_eff')
  ) %>%
  select(outcomes, dose_index, prob_tox, prob_eff) %>%
  unnest %>%
  filter(dose_index == 2)

## End(Not run)
```

efftox_process	<i>Process RStan samples from an EffTox model</i>
----------------	---

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 <code>rstan::stanmodel</code> , derived by fitting the trialr EffTox model.

Value

An instance of [efftox_fit](#).

efftox_simulate	<i>Run EffTox simulations</i>
-----------------	-------------------------------

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: $(\text{eff}_0, 0)$, $(1, \text{tox}_1)$ and $(\text{eff}_{\text{star}}, \text{tox}_{\text{star}})$

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 hyperparameters 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 <code>efftox_solve_p</code>
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

<code>fit</code>	An instance of <code>efftox_fit</code> .
<code>doses</code>	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 <code>doses = 1:3</code>

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')
```

`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 represent 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 represent 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 $\text{Dir}(\text{cohort_rho})$. <code>cohort_probs</code> or <code>cohort_rho</code> 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

```
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
)
```

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

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

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	<i>Predict probability of success for given tumour size measurements.</i>
--------------------------	---

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	<code>augbin_fit</code> object to print.
pars	parameters in model to summarise.
...	Extra parameters, passed onwards.

print.crm_fit	<i>Print crm_fit object.</i>
---------------	------------------------------

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	<i>Print efftox_fit object.</i>
------------------	---------------------------------

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.

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	<i>Calculate the probability of success.</i>
--------------	--

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

<code>x</code>	an R object of class "augbin_fit"
<code>...</code>	arguments passed to other methods
<code>y1_lower</code>	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to negative infinity.
<code>y1_upper</code>	numeric, maximum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 1 to baseline. Defaults to positive infinity.
<code>y2_lower</code>	numeric, minimum threshold to constitute success, scrutinising the log of the tumour size ratio comparing time 2 to baseline.
<code>y2_upper</code>	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 <code>fit\$tumour_size</code> .

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	<i>Calculate the probability that the rate of toxicity exceeds some threshold</i>
------------------	---

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

<code>nRep</code>	Number of simulated event pairs, positive integer.
<code>u</code>	Mean event probabilities, expressed as a vector of length 2. E.g. to simulate associated bivariate events with probabilities 80 $u = c(0.8, 0.3)$.
<code>psi</code>	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	<i>Sample LKJ correlation matrices.</i>
----------	---

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	dimension of matrix to sample.
eta	Distribution parameter

Value

matrix

spread_paths	<i>Spread the information in dose_finding_paths object to a wide data.frame format.</i>
--------------	---

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 dichotomisation 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 <code>tumour_size</code> and <code>non_shrinkage_failure</code> . NULL to fit the <code>augbin</code> variant for single-arm trials. NULL is the default.
model	Character string to denote the desired model. Currently, only <code>2t-1a</code> 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 <code>rstan::sampling</code> . The parameters required depend on the model form being fit. See sections below.
...	Extra parameters are passed to <code>rstan::sampling</code> . Commonly used options are <code>iter</code> , <code>chains</code> , <code>warmup</code> , <code>cores</code> , <code>control</code> . See sampling .

Value

an instance or subclass of type `augbin_fit`.

Single-arm model with two post-baseline assessments

The complete model form is:

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

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

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

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

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

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	<i>Simple helper function to demonstrate fitting of an Augmented Binary model.</i>
------------------	--

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	<i>Fit a CRM model</i>
----------	------------------------

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 tider 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:

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

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, alpha_mean,
            alpha_sd, beta_mean, beta_sd, gamma_mean, gamma_sd, zeta_mean, zeta_sd,
            eta_mean, eta_sd, psi_mean, psi_sd, 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).
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.
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 <code>rstan::sampling</code> . Commonly used options are <code>iter</code> , <code>chains</code> , <code>warmup</code> , <code>cores</code> , <code>control</code> . 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 attractiveness 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_fit stan_efftox_demo](#)

Examples

```
## Not run:
# This model is presented in Thall et al. (2014)
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,
  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)

# Shorthand for the above is:
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	<i>Fit the EffTox model presented in Thall et al. (2014)</i>
------------------	--

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 <code>rstan::sampling</code> . Commonly used options are <code>iter</code> , <code>chains</code> , <code>warmup</code> , <code>cores</code> , <code>control</code> . 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 <code>rstan::sampling</code> . Commonly used options are <code>iter</code> , <code>chains</code> , <code>warmup</code> , <code>cores</code> , and <code>control</code> .

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 $i = 1, \dots, N$. 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_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 <code>rstan::sampling</code> . Commonly used options are <code>iter</code> , <code>chains</code> , <code>warmup</code> , <code>cores</code> , and <code>control</code> .

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.

trialr_simulate	<i>Run a simulation study.</i>
-----------------	--------------------------------

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
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 outputs 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 intermittent 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)
```

Index

as.data.frame.crm_fit, 4
as.data.frame.efftox_fit, 4
as.mcmc.list.crm_fit, 5
as.mcmc.list.efftox_fit, 5
as_tibble.augbin_2t_1a_fit, 6
as_tibble.dose_finding_paths, 6
augbin_2t_1a_fit, 7
augbin_fit, 7, 8, 50, 58–60

binary_prob_success, 8

careful_escalation, 9
closest_to_target, 10
crm_codified_dose_logistic, 11
crm_dtpts, 12
crm_fit, 4, 5, 12, 20, 21, 23, 48, 51, 62, 63, 71
crm_fit (crm_fit-class), 14
crm_fit-class, 14
crm_params, 15, 21, 23
crm_params (crm_params-class), 15
crm_params-class, 15
crm_path_analysis, 13, 17
crm_prior_beliefs, 19
crm_process, 21

df_parse_outcomes, 12, 13, 17, 18, 22, 24, 61
dose_finding_fit, 10
dose_finding_fit
 (dose_finding_fit-class), 23
dose_finding_fit-class, 23
dose_finding_path_node, 13, 17, 18, 27, 36, 37
dose_finding_path_node
 (dose_finding_path_node-class), 23
dose_finding_path_node-class, 23

efftox_analysis_to_df, 24
efftox_contour_plot, 25
efftox_dtpts, 26, 30
efftox_dtpts_to_dataframe, 26, 29
efftox_fit, 4, 5, 23–25, 27, 38, 49, 51, 65–67, 71
efftox_fit (efftox_fit-class), 30
efftox_fit-class, 30
efftox_get_tox, 32
efftox_parameters_demo, 29, 30, 33, 38
efftox_params, 29–31, 33, 38
efftox_params (efftox_params-class), 34
efftox_params-class, 34
efftox_parse_outcomes, 26, 27, 35, 36, 37, 64–66
efftox_path_analysis, 27, 36
efftox_process, 38
efftox_simulate, 38
efftox_solve_p, 32, 39, 41
efftox_superiority, 40
efftox_utility, 41
efftox_utility_density_plot, 42

list, 13, 17, 36

mcmc.list, 5

parse_dose_finding_outcomes, 42
parse_eff_tox_dose_finding_outcomes, 44
peps2_get_data, 45, 48
peps2_process, 47
plot.crm_fit, 48
plot.efftox_fit, 49
predict.augbin_2t_1a_fit, 49
print.augbin_fit, 50
print.crm_fit, 51
print.efftox_fit, 51
prior_predictive_augbin_2t_1a, 52, 59, 60
prob_success, 49, 53
prob_tox_exceeds, 54
ranBin2, 55

rlkcorr, 56
rstan::sampling, 68, 70
rstan::stanfit, 68, 70

sampling, 15, 23, 31, 58–60, 63, 65, 66
spread_paths, 56
stan_augbin, 7, 8, 53, 57, 60
stan_augbin_demo, 60
stan_crm, 12, 13, 15, 17–21, 60, 71
stan_efftox, 25–27, 31, 35–37, 63, 67
stan_efftox_demo, 31, 35, 65, 66
stan_hierarchical_response_thall, 67
stan_peps2, 69
stanfit, 7, 8, 15, 23, 31
summary.crm_fit, 70
summary.efftox_fit, 71

tibble, 6, 50, 52, 54
trialr (trialr-package), 3
trialr-package, 3
trialr_simulate, 72