Package: idbrms (via r-universe)

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Contents

expose_idbrms_stan_fns 2	2
idbrm	2
idbrm.idbrms_convolution	3
idbrmfit	5
idbrms_stan_chunk	5
idbrms_version_stanvar	5
id_formula.idbrms_convolution	5
id_priors	1
id_priors.idbrms_convolution	3
id_stancode)
id_stancode.idbrms_convolution)
prepare 10)
prepare.idbrms_convolution	l
13	3

Index

expose_idbrms_stan_fns

Expose package stan functions in R

Description

This function exposes internal stan functions in R from a user supplied list of target files. Allows for testing of stan functions in R and potentially user use in R code.

Usage

```
expose_idbrms_stan_fns(files, dir, ...)
```

Arguments

files	A character vector indicating the target files
dir	A character string indicating the directory for the file
	Additional arguments passed to rstan::expose_stan_functions.

idbrm

Interface for infectious disease modelling using brms.

Description

Interface for infectious disease modelling using brms.

Usage

idbrm(data, formula, family, priors, custom_stancode, dry = FALSE, ...)

Arguments

data	A data frame as prepared for modelling using prepare with a class associated with the model prepared for.	
formula	A formula as defined using id_formula or as supported by brms::brm.	
family	A observation model family as defined in brms.	
priors	A list of priors as defined using brms or id_priors. Defaults to the the id_priors defined for the model class being fit.	
custom_stancode		
	A list of stanvars used to define custom stancode in brms. By default uses the code designed for the model class being fit (as specified using id_stancode).	
dry	Logical, defaults to TRUE. For testing purposes should just the stan code be output with not fitting done.	
	Additional arguments to pass to brms::brm.	

Author(s)

Sam Abbott

Examples

```
# define some example data
library(data.table)
dt <- data.table(
    region = "France", cases = seq(10, 500, by = 10),
    date = seq(as.Date("2020-10-01"), by = "days", length.out = 50)
    )
dt[, deaths := as.integer(shift(cases, 5) * 0.1)]
dt[is.na(deaths), deaths := 0]
dt <- prepare(
    dt, model = "convolution", location = "region",
    primary = "cases", secondary = "deaths",
    )
# fit the convolution model using a Poisson observation model
fit <- idbrm(data = dt, family = poisson(link = "identity"))</pre>
```

idbrm.idbrms_convolution

Delay Convolution Model

Description

A model that assumes that a secondary observations can be predicted using a convolution of a primary observation multipled by some scaling factor. An example use case of this model is to estimate the case fatality rate (with the primary observation being cases and the secondary observation being deaths) and then explore factors that influence it.

Usage

```
## S3 method for class 'idbrms_convolution'
idbrm(
    data,
    formula = id_formula(data),
    family = negbinomial(link = "identity"),
    priors = id_priors(data),
    custom_stancode = id_stancode(data),
    dry = FALSE,
    ...
)
```

Arguments

data	A data.frame as produced by prepare that must contain the date, location (as loc), primary (the data that the outcome is a convolution of) and secondary (the observation of interest. Should have class "idbrms_convolution".
formula	A formula as defined using id_formula or as supported by brms::brm.
family	A observation model family as defined in brms.
priors	A list of priors as defined using brms or id_priors. Defaults to the the id_priors defined for the model class being fit.
custom_stancode	
	A list of stanvars used to define custom stancode in brms. By default uses the code designed for the model class being fit (as specified using id_stancode).
dry	Logical, defaults to TRUE. For testing purposes should just the stan code be output with not fitting done.
	Additional parameters passed to brms::brm.

Value

A "brmsfit" object or stan code (if dry = TRUE).

Author(s)

Sam Abbott

Examples

```
# define some example data
library(data.table)
dt <- data.table(
    region = "France", cases = seq(10, 500, by = 10),
    date = seq(as.Date("2020-10-01"), by = "days", length.out = 50)
    )
dt[, deaths := as.integer(shift(cases, 5) * 0.1)]
dt[is.na(deaths), deaths := 0]
dt <- prepare(
    dt, model = "convolution", location = "region",
    primary = "cases", secondary = "deaths",
    )
# fit the convolution model using a Poisson observation model
fit <- idbrm(data = dt, family = poisson(link = "identity"))</pre>
```

idbrmfit

Description

Infectious disease modelling wrapper for brm

Usage

idbrmfit(formula, data, family, priors, custom_stancode, dry = FALSE, ...)

Arguments

formula	A brms model formula.	
data	A data frame.	
family	An observation model family as defined in brms.	
priors	A list of priors as defined using brms.	
custom_stancode		
	A list of stanvars used to define custom stancode in brms.	
dry	Logical, defaults to TRUE. For testing purposes should just the stan code be output with not fitting done.	
	Additional arguments to pass to brms::brm.	

Author(s)

Sam Abbott

idbrms_stan_chunk Read in a idbrms Stan code chunk

Description

Read in a idbrms Stan code chunk

Usage

```
idbrms_stan_chunk(path)
```

Arguments

path

The path within the "stan" folder of the installed idbrms package to the stan code chunk of interest.

Value

A character string containing the stan code chunk of interest.

Examples

idbrms_stan_chunk("functions/idbrms_convolve.stan")

idbrms_version_stanvar

Label a idbrms stan model with a version indicator

Description

Label a idbrms stan model with a version indicator

Usage

```
idbrms_version_stanvar()
```

Value

A brms stanvar chunk containing the package version used to build the stan code.

id_formula.idbrms_convolution

Define a formula for the convolution model

Description

Define a formula for the convolution model

Define a model specific formula

Usage

```
## S3 method for class 'idbrms_convolution'
id_formula(data, scale = ~1, cmean = ~1, lcsd = ~1, ...)
id_formula(data, ...)
```

id_priors

Arguments

data	A data.frame as produced by prepare that must contain the date, location (as loc), primary (the data that the outcome is a convolution of) and secondary (the observation of interest. Should have class "idbrms_convolution".
scale	Formula for the scaling of primary observations to secondary observations.
cmean	Formula for the convolution mean. Defaults to intercept only.
lcsd	Formula for the logged convolution standard deviation. Defaults to intercept only.
	Additional arguments for method.

Author(s)

Sam Abbott

Sam Abbott

id_priors

Define model specific priors

Description

Define model specific priors

Usage

id_priors(data, ...)

Arguments

data	A data frame as prepared for modelling using prepare with a class associated with the model prepared for.
	Additional arguments for method.

Author(s)

Sam Abbott

Description

Define priors for the delay convolution model

Usage

```
## S3 method for class 'idbrms_convolution'
id_priors(
    data,
    scale = c(round(log(0.1), 2), 1),
    cmean = c(2, 1),
    lcsd = c(-0.5, 0.25),
    ...
)
```

Arguments

data	A data.frame as produced by prepare that must contain the date, location (as loc), primary (the data that the outcome is a convolution of) and secondary (the observation of interest. Should have class "idbrms_convolution".
scale	Vector of length two defining the mean and the standard deviation of the normal prior for the scaling factor.
cmean	Vector of length two defining the mean and standard deviation of the log mean of the delay distribution.
lcsd	Vector of length two defining the mean and standard deviation of the log stan- dard deviation logged. the standard deviation to be greater than 0 on the uncon- strained scale.
	Additional arguments for method.

Author(s)

Sam Abbott

id_stancode

Description

Define model specific stancode

Usage

id_stancode(data, ...)

Arguments

data	A data frame as prepared for modelling using prepare with a class associated
	with the model prepared for.
	Additional arguments for method.

Author(s)

Sam Abbott

```
id_stancode.idbrms_convolution
```

Define stan code for a delay convolution model

Description

Define stan code for a delay convolution model

Usage

```
## S3 method for class 'idbrms_convolution'
id_stancode(data, ...)
```

Arguments

data	A data frame as produced by prepare that must contain the date, location (as
	loc), primary (the data that the outcome is a convolution of) and secondary (the
	observation of interest. Should have class "idbrms_convolution".
	Additional arguments for method.

Author(s)

Sam Abbott

prepare

Description

Prepare data for modelling with idbrm

Default method used when preparing data

Usage

prepare(data, ...)
Default S3 method:
prepare(data, model, ...)

Arguments

data	A dataframe to be used for modelling
	Additional arguments passed to model specific prepare functions
model	Character string, model type to prepare to use. Supported options are "convolu- tion".

Author(s)

Sam Abbott

Sam Abbott

Examples

```
# define some example data
library(data.table)
dt <- data.table(
    region = "France", cases = seq(10, 500, by = 10),
    date = seq(as.Date("2020-10-01"), by = "days", length.out = 50)
    )
dt <- dt[, deaths := as.integer(shift(cases, 5) * 0.1)]
dt <- dt[is.na(deaths), deaths := 0]
dt <- prepare(
    dt, model = "convolution", location = "region",
    primary = "cases", secondary = "deaths",
    )
dt[]
```

prepare.idbrms_convolution

Prepare data for fitting using a convolution model

Description

Prepare data for fitting using a convolution model

Usage

```
## S3 method for class 'idbrms_convolution'
prepare(
    data,
    location,
    primary,
    secondary,
    initial_obs = 14,
    max_convolution = 30,
    ...
)
```

Arguments

	data	A data frame containing at least two integer observations and a date variable.
	location	Character string, variable to use as the spatial location.
	primary	Character string, variable to use as the primary observation.
	secondary	Character string, variable to use as the secondary observation.
	initial_obs	Integer, number of observations to hold out from the likelihood. This is useful as initially the outcome will depend on primary data outside of the range of the training set and including this could bias the estimated delay distribution. Defaults to 14 days.
max_convolution		
		Integer defining the maximum index to use for the convolution. Defaults to 30 days.
		Additional arguments passed to model specific prepare functions

Author(s)

Sam Abbott

Examples

```
# define some example data
library(data.table)
dt <- data.table(
    region = "France", cases = seq(10, 500, by = 10),
```

```
date = seq(as.Date("2020-10-01"), by = "days", length.out = 50)
)
dt <- dt[, deaths := as.integer(shift(cases, 5) * 0.1)]
dt <- dt[is.na(deaths), deaths := 0]
dt <- prepare(
    dt, model = "convolution", location = "region",
    primary = "cases", secondary = "deaths",
    )
dt[]</pre>
```

Index

prepare, 10
prepare.idbrms_convolution, 11