Package 'geostan'

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Title Bayesian Spatial Analysis

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URL https://connordonegan.github.io/geostan/

BugReports https://github.com/ConnorDonegan/geostan/issues

Description

For spatial data analysis; provides exploratory spatial analysis tools, spatial regression, spatial econometric, and disease mapping models, model diagnostics, and special methods for inference with small area survey data (e.g., the America Community Survey (ACS)) and censored population health monitoring data. Models are pre-specified using the Stan programming language, a platform for Bayesian inference using Markov chain Monte Carlo (MCMC). References: Carpenter et al. (2017) <doi:10.18637/jss.v076.i01>; Donegan (2021) <doi:10.31219/osf.io/3ey65>; Donegan (2022) <doi:10.21105/joss.04716>; Donegan, Chun and Hughes (2020) <doi:10.1016/j.spasta.2020.100450>; Donegan, Chun and Griffith (2021) <doi:10.3390/ijerph18136856>; Morris et al. (2019) <doi:10.1016/j.sste.2019.100301>.

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`geostan-package` *The geostan R package.*

Description

Bayesian spatial modeling powered by Stan. **geostan** provides access to a variety of hierarchical spatial models using the R formula interface, supporting a complete spatial analysis workflow with a suite of spatial analysis tools. It is designed primarily for public health and social science research but is generally applicable to modeling areal or network data. Unique features of the package include its spatial measurement error model (for inference with small area estimates such as those from the American Community Survey), its fast proper conditional autoregressive (CAR) and simultaneous autoregressive (SAR) models (SEM and SLM), and its eigenvector spatial filtering (ESF) models. The package also supports spatial regression with raster layers.

Author(s)

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- Amy Tims [contributor]

References

Carpenter, B., Gelman, A., Hoffman, M.D., Lee, D., Goodrich, B., Betancourt, M., Brubaker, M., Guo, J., Li, P., Riddell, A., 2017. Stan: A probabilistic programming language. Journal of statistical software 76. doi:10.18637/jss.v076.i01.

Donegan, C., Y. Chun and A. E. Hughes (2020). Bayesian estimation of spatial filters with Moran's Eigenvectors and hierarchical shrinkage priors. *Spatial Statistics*. doi:10.1016/j.spasta.2020.100450 (open access: doi:10.31219/osf.io/fah3z).

Donegan, Connor and Chun, Yongwan and Griffith, Daniel A. (2021). Modeling community health with areal data: Bayesian inference with survey standard errors and spatial structure. *Int. J. Env. Res. and Public Health* 18 (13): 6856. doi:10.3390/ijerph18136856. Supplementary material: https://github.com/ConnorDonegan/survey-HBM.

Donegan, Connor (2021). Building spatial conditional autoregressive models in the Stan programming language. *OSF Preprints*. doi:10.31219/osf.io/3ey65.

Donegan, Connor (2022) geostan: An R package for Bayesian spatial analysis. *The Journal of Open Source Software*. 7, no. 79: 4716. doi:10.21105/joss.04716.

Gabry, J., Goodrich, B. and Lysy, M. (2020). rstantools: Tools for developers of R packages interfacing with Stan. R package version 2.1.1 https://mc-stan.org/rstantools/.

Morris, M., Wheeler-Martin, K., Simpson, D., Mooney, S. J., Gelman, A., & DiMaggio, C. (2019). Bayesian hierarchical spatial models: Implementing the Besag York Mollié model in stan. Spatial and spatio-temporal epidemiology, 31, 100301. doi:10.1016/j.sste.2019.100301.

Stan Development Team (2019). RStan: the R interface to Stan. R package version 2.19.2. https://mc-stan.org

See Also

Useful links:

- https://connordonegan.github.io/geostan/
- Report bugs at https://github.com/ConnorDonegan/geostan/issues

---

`aple` *Spatial autocorrelation estimator*

Description

The approximate-profile likelihood estimator for the spatial autocorrelation parameter from a simultaneous autoregressive (SAR) model (Li et al. 2007).

Usage

```
aple(x, w, digits = 3)
```

Arguments

`x`	Numeric vector of values, length `n`. This will be standardized internally with `scale(x)`.
`w`	An `n x n` row-standardized spatial connectivity matrix. See shape2mat.
`digits`	Number of digits to round results to.

Details

The `APLE` is an estimate of the spatial autocorrelation parameter one would obtain from fitting an intercept-only SAR model. Note, the `APLE` approximation is not reliable when the number of observations is large.

Value

the APLE estimate, a numeric value.

Source

Li, Honfei and Calder, Catherine A. and Cressie, Noel (2007). Beyond Moran's I: testing for spatial dependence based on the spatial autoregressive model. Geographical Analysis: 39(4): 357-375.

See Also

mc, moran_plot, lisa, sim_sar

Examples

```
library(sf)
data(georgia)
w <- shape2mat(georgia, "W")
x <- georgia$ICE
aple(x, w)
```

---

as.matrix.geostan_fit *Extract samples from a fitted model*

Description

Extract samples from the joint posterior distribution of parameters.

Usage

```
## S3 method for class 'geostan_fit'
as.matrix(x, ...)

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

## S3 method for class 'geostan_fit'
as.array(x, ...)
```

Arguments

x	A fitted model object of class geostan_fit.
...	Further arguments passed to rstan methods for for as.data.frame, as.matrix, or as.array

Value

A matrix, data frame, or array of MCMC samples is returned.

Examples

```
data(georgia)
A <- shape2mat(georgia, "B")

fit <- stan_glm(deaths.male ~ offset(log(pop.at.risk.male)),
                C = A,
                data = georgia,
                family = poisson(),
                chains = 1, iter = 600) # for speed only


s <- as.matrix(fit)
dim(s)

a <- as.matrix(fit, pars = "intercept")
dim(a)

# Or extract the stanfit object
S <- fit$stanfit
print(S, pars = "intercept")
samples <- as.matrix(S)
dim(samples)
```

---

auto_gaussian *Auto-Gaussian family for CAR models*

Description

create a family object for the auto-Gaussian CAR or SAR specification

Usage

```
auto_gaussian(type)
```

Arguments

type	Optional; either "CAR" for conditionally specified auto-model or "SAR" for the simultaneously specified auto-model. The type is added internally by `stan_car` or `stan_sar` when needed.

Value

An object of class `family`

See Also

`stan_car`

Examples

```
cp = prep_car_data(shape2mat(georgia))
fit <- stan_car(log(rate.male) ~ 1,
                data = georgia,
                car_parts = cp,
                family = auto_gaussian(),
                chains = 2, iter = 700) # for speed only
print(fit)
```

---

edges *Edge list*

Description

Creates a list of connected nodes following the graph representation of a spatial connectivity matrix.

Usage

```
edges(C, unique_pairs_only = TRUE, shape)
```

Arguments

C	A connectivity matrix where connection between two nodes is indicated by non-zero entries.
unique_pairs_only	By default, only unique pairs of nodes (i, j) will be included in the output.
shape	Optional spatial object (geometry) to which C refers. If given, the function returns an sf object.

Details

This is used internally for stan_icar, can be helpful for creating the scaling factor for BYM2 models fit with stan_icar, and can be used for visualizing a spatial connectivity matrix.

Value

If shape is missing, this returns a data.frame with three columns. The first two columns (node1 and node2) contain the indices of connected pairs of nodes; only unique pairs of nodes are included (unless unique_pairs_only = FALSE). The third column (weight) contains the corresponding matrix element, C[node1, node2].

If shape is provided, the results are joined to an sf object so the connections can be visualized.

See Also

shape2mat, prep_icar_data, stan_icar

Examples

```
data(sentencing)
C <- shape2mat(sentencing)
nbs <- edges(C)
head(nbs)

## similar to:
head(Matrix::summary(C))
head(Matrix::summary(shape2mat(georgia, "W")))

## add geometry for plotting
library(sf)
E <- edges(C, shape = sentencing)
g1 = st_geometry(E)
g2 = st_geometry(sentencing)
plot(g1, lwd = .2)
plot(g2, add = TRUE)
```

`eigen_grid` *Eigenvalues of a spatial weights matrix: for spatial regression with raster data*

Description

Approximate eigenvalues for the row-standardized spatial connectivity matrix W of a regular tessellation, e.g., remotely sensed imagery.

Usage

```
eigen_grid(row = 5, col = 5)
```

Arguments

`row`	Number of rows in the raster dataset
`col`	Number of columns in the raster dataset

Details

Uses Equation 5 from Griffith (2000) to calculate the eigenvalues for a row-standardized spatial weights matrix; this is valid for a regular tessellation (rectangular grid or raster). The rook criteria is used to define adjacency.

The purpose is to calculate eigenvalues of the spatial weights matrix for the CAR and SAR models, enabling spatial regression with large raster data sets. This function is used internally by `prep_sar_data2` and `prep_car_data2`. For more details, see: `vignette("raster-regression", package = "geostan")`.

Value

Returns the eigenvalues of the row-standardized spatial weights matrix (a numeric vector length `row * col`).

Source

Griffith, Daniel A. (2000). Eigenfunction properties and approximations of selected incidence matrices employed in spatial analyses. *Linear Algebra and its Applications* 321 (1-3): 95-112. doi:10.1016/S00243795(00)000318.

See Also

`prep_sar_data2`, `prep_car_data2`

Examples

```
e <- eigen_grid(row = 50, col = 95)
print(head(e, 25))
```

---

expected_mc *Expected value of the residual Moran coefficient*

Description

Expected value for the Moran coefficient of model residuals under the null hypothesis of no spatial autocorrelation.

Usage

```
expected_mc(X, C)
```

Arguments

`X`	model matrix, including column of ones.
`C`	Connectivity matrix.

Value

Returns a numeric value.

Source

Chun, Yongwan and Griffith, Daniel A. (2013). Spatial statistics and geostatistics. Sage, p. 18.

Examples

```
data(georgia)
C <- shape2mat(georgia)
X <- model.matrix(~ college, georgia)
expected_mc(X, C)
```

`georgia` *Georgia all-cause, sex-specific mortality, ages 55-64, years 2014-2018*

Description

A simple features (sf) object for Georgia counties with sex- and age-specific deaths and populations at risk (2014-2018), plus select estimates (with standard errors) of county characteristics. Standard errors of the ICE were calculated using the Census Bureau's variance replicate tables.

Usage

```
georgia
```

Format

A simple features object with county geometries and the following columns:

GEOID Six digit combined state and county FIPS code

NAME County name

ALAND Land area

AWATER Water area

population Census Bureau 2018 county population estimate

white Percent White, ACS 2018 five-year estimate

black Percent Black, ACS 2018 five-year estimate

hisp Percent Hispanic/Latino, ACS 2018 five-year estimate

ai Percent American Indian, ACS 2018 five-year estimate

deaths.male Male deaths, 55-64 yo, 2014-2018

pop.at.risk.male Population estimate, males, 55-64 yo, years 2014-2018 (total), ACS 2018 five-year estimate

pop.at.risk.male.se Standard error of the pop.at.risk.male estimate

deaths.female Female deaths, 55-64 yo, 2014-2018

pop.at.risk.female Population estimate, females, 55-64 yo, years 2014-2018 (total), ACS 2018 five-year estimate

pop.at.risk.female.se Standard error of the pop.at.risk.female estimate

ICE Index of Concentration at the Extremes

ICE.se Standard error of the ICE estimate, calculated using variance replicate tables

income Median household income, ACS 2018 five-year estimate

income.se Standard error of the income estimate

college Percent of the population age 25 or higher than has a bachelors degree of higher, ACS 2018 five-year estimate

college.se Standard error of the college estimate

insurance Percent of the population with health insurance coverage, ACS 2018 five-year estimate

insurance.se Standard error of the insurance estimate

rate.male Raw (crude) age-specific male mortality rate, 2014-2018

rate.female Raw (crude) age-specific female mortality rate, 2014-2018

geometry simple features geometry for county boundaries

Source

Centers for Disease Control and Prevention, National Center for Health Statistics. Underlying Cause of Death 1999-2018 on CDC Wonder Online Database. 2020. Available online: https://wonder.cdc.gov/ (accessed on 19 October 2020).

Donegan, Connor and Chun, Yongwan and Griffith, Daniel A. (2021). "Modeling community health with areal data: Bayesian inference with survey standard errors and spatial structure." *Int. J. Env. Res. and Public Health* 18 (13): 6856. DOI: 10.3390/ijerph18136856 Data and code: https://github.com/ConnorDonegan/survey-HBM.

Kyle Walker and Matt Herman (2020). tidycensus: Load US Census Boundary and Attribute Data as 'tidyverse' and 'sf'-Ready Data Frames. R package version 0.11. https://CRAN.R-project.org/package=tidycensus

US Census Bureau. Variance Replicate Tables, 2018. Available online: https://www.census.gov/programs-surveys/acs/data/variance-tables.2018.html (accessed on 19 October 2020).

Examples

```
data(georgia)
head(georgia)

library(sf)
plot(georgia[,'rate.female'])
```

---

get_shp *Download shapefiles*

Description

Given a url to a shapefile in a compressed .zip file, download the file and unzip it into a folder in your working directory.

Usage

```
get_shp(url, folder = "shape")
```

Arguments

url	url to download a shapefile.
folder	what to name the new folder in your working directory containing the shapefile

Value

A folder in your working directory with the shapefile; filepaths are printed to the console.

Examples

```
library(sf)
url <- "https://www2.census.gov/geo/tiger/GENZ2019/shp/cb_2019_us_state_20m.zip"
folder <- tempdir()
print(folder)
get_shp(url, folder)
states <- sf::st_read(folder)
head(states)
```

---

gr *The Geary Ratio*

Description

An index for spatial autocorrelation. Complete spatial randomness (lack of spatial pattern) is indicated by a Geary Ratio (GR) of 1; positive autocorrelation moves the index towards zero, while negative autocorrelation will push the index towards 2.

Usage

```
gr(x, w, digits = 3, na.rm = FALSE, warn = TRUE)
```

Arguments

x	Numeric vector of length n. By default, this will be standardized using the scale function.
w	An n x n spatial connectivity matrix. See shape2mat.
digits	Number of digits to round results to.
na.rm	If na.rm = TRUE, observations with NA values will be dropped from both x and w.
warn	If FALSE, no warning will be printed to inform you when observations with NA values have been dropped, or if any observations without neighbors have been found.

Details

The Geary Ratio is an index of spatial autocorrelation. The numerator contains a series of sums of squared deviations, which will be smaller when each observation is similar to its neighbors. This term makes the index sensitive to local outliers, which is advantageous for detecting such outliers and for measuring negative autocorrelation. The denominator contains the total sum of squared deviations from the mean value. Hence, under strong positive autocorrelation, the GR approaches zero. Zero spatial autocorrelation is represented by a GR of 1. Negative autocorrelation pushes the GR above 1, towards 2.

$$GR = \frac{n-1}{2K}\frac{M}{D}$$

$$M = \sum_i \sum_j w_{i,j}(x_i - x_j)^2$$

$$D = \sum_i (x_i - \overline{x})^2$$

Observations with no neighbors are removed before calculating the GR. (The alternative would be for those observations to contribute zero to the numerator—but zero is not a neutral value, it represents strong positive autocorrelation.)

Value

Returns the Geary ratio (a single numeric value).

Source

Chun, Yongwan, and Daniel A. Griffith. Spatial Statistics and Geostatistics: Theory and Applications for Geographic Information Science and Technology. Sage, 2013.

Geary, R. C. "The contiguity ratio and statistical mapping." The Incorporated Statistician 5, no. 3 (1954): 115-127_129-146.

Unwin, Antony. "Geary's Contiguity Ratio." The Economic and Social Review 27, no. 2 (1996): 145-159.

Examples

```
data(georgia)
x <- log(georgia$income)
w <- shape2mat(georgia, "W")
gr(x, w)
```

lg *Local Geary*

Description

A local indicator of spatial association based on the Geary Ratio (Geary's C) for exploratory spatial data analysis. Large values of this statistic highlight local outliers, that is, values that are not like their neighbors.

Usage

```
lg(x, w, digits = 3, scale = TRUE, na.rm = FALSE, warn = TRUE)
```

Arguments

x	Numeric vector of length n. By default, this will be standardized using the scale function.
w	An n x n spatial connectivity matrix. See shape2mat.
digits	Number of digits to round results to.
scale	If TRUE, then x will automatically be standardized using scale(x, center = TRUE, scale = TRUE).
na.rm	If na.rm = TRUE, observations with NA values will be dropped from both x and w.
warn	If FALSE, no warning will be printed to inform you when observations with NA values have been dropped, or if any observations without neighbors have been found.

Details

Local Geary's C is found in the numerator of the Geary Ratio (GR). For the i^{th} observation, the local Geary statistic is

$$C_i = \sum_j w_{i,j} * (x_i - x_j)^2$$

Hence, local Geary values will be largest for those observations that are most unlike their neighboring values. If a binary connectivity matrix is used (rather than row-standardized), then having many neighbors can also increase the value of the local Geary statistic. For most purposes, the row-standardized spatial weights matrix may be the more appropriate choice.

Value

The function returns a vector of numeric values, each value being a local indicator of spatial association (or dissimilarity), ordered as x.

Source

Anselin, Luc. "Local indicators of spatial association—LISA." Geographical analysis 27, no. 2 (1995): 93-115.

Chun, Yongwan, and Daniel A. Griffith. Spatial Statistics and Geostatistics: Theory and Applications for Geographic Information Science and Technology. Sage, 2013.

Examples

```
library(ggplot2)
data(georgia)
x <- log(georgia$income)
w <- shape2mat(georgia, "W")
lisa <- lg(x, w)
hist(lisa)
ggplot(georgia) +
  geom_sf(aes(fill = lisa)) +
scale_fill_gradient(high = "navy",
                    low = "white")
 ## or try: scale_fill_viridis()
```

---

lisa *Local Moran's I*

Description

A local indicator of spatial association (LISA) based on Moran's I (the Moran coefficient) for exploratory data analysis.

Usage

```
lisa(x, w, type = TRUE, scale = TRUE, digits = 3)
```

Arguments

x	Numeric vector of length n.
w	An n x n spatial connectivity matrix. See shape2mat. If w is not row standardized (all(Matrix::rowSums(w) == 1)), it will automatically be row-standardized.
type	Return the type of association also (High-High, Low-Low, High-Low, and Low-High)? Defaults to FALSE.
scale	If TRUE, then x will automatically be standardized using scale(x, center = TRUE, scale = TRUE). If FALSE, then the variate will be centered but not scaled, using scale(x, center = TRUE, scale = FALSE).
digits	Number of digits to round results to.

Details

The values of `x` will automatically be centered first with `z = scale(x, center = TRUE, scale = scale)` (with user control over the `scale` argument). The LISA values are the product of each `z` value with the weighted sum of their respective surrounding value:

$$I_i = z_i \sum_j w_{ij} z_j$$

(or in R code: `lisa = z * (w %*% z)`). These are for exploratory analysis and model diagnostics.

An above-average value (i.e. positive z-value) with positive mean spatial lag indicates local positive spatial autocorrelation and is designated type "High-High"; a low value surrounded by high values indicates negative spatial autocorrelation and is designated type "Low-High", and so on.

This function uses Equation 7 from Anselin (1995). Note that the `spdep` package uses Formula 12, which divides the same value by a constant term $\sum_i z_i^2/n$. So the `geostan` version can be made equal to the `spdep` version by dividing by that value.

Value

If `type = FALSE` a numeric vector of lisa values for exploratory analysis of local spatial autocorrelation. If `type = TRUE`, a `data.frame` with columns `Li` (the lisa value) and `type`.

Source

Anselin, Luc. "Local indicators of spatial association—LISA." Geographical Analysis 27, no. 2 (1995): 93-115.

See Also

`moran_plot`, `mc`, `aple`, `lg`, `gr`

Examples

```
library(ggplot2)
library(sf)
data(georgia)
w <- shape2mat(georgia, "W")
x <- georgia$ICE
li = lisa(x, w)
head(li)
ggplot(georgia, aes(fill = li$Li)) +
  geom_sf() +
  scale_fill_gradient2()
```

log_lik *Extract log-likelihood*

Description

Extract log-likelihood

Usage

```
log_lik(object, array = FALSE, ...)

## S3 method for class 'geostan_fit'
log_lik(object, array = FALSE, ...)
```

Arguments

object	A geostan_fit model
array	Return results as an array, one matrix per MCMC chain?
...	Other arguments (not used)

Value

A matrix (or array) of MCMC samples for the log-likelihood: the casewise probability of the data conditional on estimated parameter values.

See Also

waic dic

make_EV *Prepare data for spatial filtering*

Description

Prepare data for spatial filtering

Usage

```
make_EV(C, nsa = FALSE, threshold = 0.2, values = FALSE)
```

Arguments

C	A binary spatial weights matrix. See shape2mat.
nsa	Logical. Default of nsa = FALSE excludes eigenvectors capturing negative spatial autocorrelation. Setting nsa = TRUE will result in a candidate set of EVs that contains eigenvectors representing positive and negative SA.
threshold	Defaults to threshold=0.2 to exclude eigenvectors representing spatial autocorrelation levels that are less than threshold times the maximum possible Moran coefficient achievable for the given spatial connectivity matrix. If theshold = 0, all eigenvectors will be returned (however, the eigenvector of constants (with eigenvalue of zero) will be dropped automatically).
values	Should eigenvalues be returned also? Defaults to FALSE.

Details

Returns a set of eigenvectors related to the Moran coefficient (MC), limited to those eigenvectors with |MC| > threshold if nsa = TRUE or MC > threshold if nsa = FALSE, optionally with corresponding eigenvalues.

Value

A data.frame of eigenvectors for spatial filtering. If values=TRUE then a named list is returned with elements eigenvectors and eigenvalues.

Source

Daniel Griffith and Yongwan Chun. 2014. "Spatial Autocorrelation and Spatial Filtering." in M. M. Fischer and P. Nijkamp (eds.), *Handbook of Regional Science.* Springer.

See Also

stan_esf, mc

Examples

```
library(ggplot2)
data(georgia)
C <- shape2mat(georgia, style = "B")
EV <- make_EV(C)
head(EV)

ggplot(georgia) +
  geom_sf(aes(fill = EV[,1])) +
  scale_fill_gradient2()
```

mc *The Moran coefficient (Moran's I)*

Description

The Moran coefficient, a measure of spatial autocorrelation (also known as Global Moran's I)

Usage

```
mc(x, w, digits = 3, warn = TRUE, na.rm = FALSE)
```

Arguments

x	Numeric vector of input values, length n.
w	An n x n spatial connectivity matrix. See shape2mat.
digits	Number of digits to round results to.
warn	If FALSE, no warning will be printed to inform you when observations with zero neighbors or NA values have been dropped.
na.rm	If na.rm = TRUE, observations with NA values will be dropped from both x and w.

Details

The formula for the Moran coefficient (MC) is

$$MC = \frac{n}{K} \frac{\sum_i \sum_j w_{ij}(y_i - \overline{y})(y_j - \overline{y})}{\sum_i (y_i - \overline{y})^2}$$

where n is the number of observations and K is the sum of all values in the spatial connectivity matrix W, i.e., the sum of all row-sums: $K = \sum_i \sum_j w_{ij}$.

If any observations with no neighbors are found (i.e. `any(Matrix::rowSums(w) == 0)`) they will be dropped automatically and a message will print stating how many were dropped. (The alternative would be for those observations to have a spatial lage of zero, but zero is not a neutral value.)

Value

The Moran coefficient, a numeric value.

Source

Chun, Yongwan, and Daniel A. Griffith. Spatial Statistics and Geostatistics: Theory and Applications for Geographic Information Science and Technology. Sage, 2013.

Cliff, Andrew David, and J. Keith Ord. Spatial processes: models & applications. Taylor & Francis, 1981.

See Also

moran_plot, lisa, aple, gr, lg

Examples

```
library(sf)
data(georgia)
w <- shape2mat(georgia, style = "W")
x <- georgia$ICE
mc(x, w)
```

`me_diag` *Measurement error model diagnostics*

Description

Visual diagnostics for spatial measurement error models.

Usage

```
me_diag(
  fit,
  varname,
  shape,
  probs = c(0.025, 0.975),
  plot = TRUE,
  mc_style = c("scatter", "hist"),
  size = 0.25,
  index = 0,
  style = c("W", "B"),
  w = shape2mat(shape, match.arg(style), quiet = TRUE),
  binwidth = function(x) 0.5 * sd(x)
)
```

Arguments

`fit`	A `geostan_fit` model object as returned from a call to one of the `geostan::stan_*` functions.
`varname`	Name of the modeled variable (a character string, as it appears in the model formula).
`shape`	An object of class `sf` or another spatial object coercible to `sf` with `sf::st_as_sf`.
`probs`	Lower and upper quantiles of the credible interval to plot.
`plot`	If `FALSE`, return a list of `ggplots` and a `data.frame` with the raw data values alongside a posterior summary of the modeled variable.

mc_style	Character string indicating how to plot the Moran coefficient for the delta values: if mc = "scatter", then moran_plot will be used with the marginal residuals; if mc = "hist", then a histogram of Moran coefficient values will be returned, where each plotted value represents the degree of residual autocorrelation in a draw from the join posterior distribution of delta values.
size	Size of points and lines, passed to geom_pointrange.
index	Integer value; use this if you wish to identify observations with the largest n=index absolute Delta values; data on the top n=index observations ordered by absolute Delta value will be printed to the console and the plots will be labeled with the indices of the identified observations.
style	Style of connectivity matrix; if w is not provided, style is passed to shape2mat and defaults to "W" for row-standardized.
w	An optional spatial connectivity matrix; if not provided, one will be created using shape2mat.
binwidth	A function with a single argument that will be passed to the binwidth argument in geom_histogram. The default is to set the width of bins to 0.5 * sd(x).

Value

A grid of spatial diagnostic plots for measurement error models comparing the raw observations to the posterior distribution of the true values. Includes a point-interval plot of raw values and modeled values; a Moran scatter plot for delta = z - x where z are the survey estimates and x are the modeled values; and a map of the delta values (take at their posterior means).

Source

Donegan, Connor and Chun, Yongwan and Griffith, Daniel A. (2021). "Modeling community health with areal data: Bayesian inference with survey standard errors and spatial structure." *Int. J. Env. Res. and Public Health* 18 (13): 6856. DOI: 10.3390/ijerph18136856 Data and code: https://github.com/ConnorDonegan/survey-HBM.

See Also

sp_diag, moran_plot, mc, aple

Examples

```
library(sf)
data(georgia)
## binary adjacency matrix
A <- shape2mat(georgia, "B")
## prepare data for the CAR model, using WCAR specification
cars <- prep_car_data(A, style = "WCAR")
## provide list of data for the measurement error model
ME <- prep_me_data(se = data.frame(college = georgia$college.se),
                   car_parts = cars)
## sample from the prior probability model only, including the ME model
fit <- stan_glm(log(rate.male) ~ college,
                ME = ME,
```

```
                data = georgia,
                prior_only = TRUE,
                iter = 1e3, # for speed only
                chains = 2, # for speed only
                refresh = 0 # silence some printing
                )

## see ME diagnostics
me_diag(fit, "college", georgia)
## see index values for the largest (absolute) delta values
 ## (differences between raw estimate and the posterior mean)
me_diag(fit, "college", georgia, index = 3)
```

`moran_plot` *Moran scatter plot*

Description

Plots a set of values against their spatially lagged values and gives the Moran coefficient as a measure of spatial autocorrelation.

Usage

```
moran_plot(
  x,
  w,
  xlab = "x (centered)",
  ylab = "Spatial Lag",
  pch = 20,
  col = "darkred",
  size = 2,
  alpha = 1,
  lwd = 0.5,
  na.rm = FALSE
)
```

Arguments

`x`	A numeric vector of length n.
`w`	An n x n spatial connectivity matrix.
`xlab`	Label for the x-axis.
`ylab`	Label for the y-axis.
`pch`	Symbol type.
`col`	Symbol color.
`size`	Symbol size.

alpha	Symbol transparency.
lwd	Width of the regression line.
na.rm	If na.rm = TRUE, any observations of x with NA values will be dropped from x and from w.

Details

For details on the symbol parameters see the documentation for geom_point.

If any observations with no neighbors are found (i.e. any(Matrix::rowSums(w) == 0)) they will be dropped automatically and a message will print stating how many were dropped.

Value

Returns a gg plot, a scatter plot with x on the horizontal and its spatially lagged values on the vertical axis (i.e. a Moran scatter plot).

Source

Anselin, Luc. "Local indicators of spatial association—LISA." Geographical analysis 27, no. 2 (1995): 93-115.

See Also

mc, lisa, aple

Examples

```
data(georgia)
x <- georgia$income
w <- shape2mat(georgia, "W")
moran_plot(x, w)
```

---

n_eff *Effective sample size*

Description

An approximate calculation for the effective sample size for spatially autocorrelated data. Only valid for approximately normally distributed data.

Usage

```
n_eff(n, rho)
```

Arguments

n	Number of observations.
rho	Spatial autocorrelation parameter from a simultaneous autoregressive model.

Details

Implements Equation 3 from Griffith (2005).

Value

Returns effective sample size n*, a numeric value.

Source

Griffith, Daniel A. (2005). Effective geographic sample size in the presence of spatial autocorrelation. Annals of the Association of American Geographers. Vol. 95(4): 740-760.

See Also

sim_sar, aple

Examples

```
n_eff(100, 0)
n_eff(100, 0.5)
n_eff(100, 0.9)
n_eff(100, 1)

rho <- seq(0, 1, by = 0.01)
plot(rho, n_eff(100, rho),
     type = 'l',
     ylab = "Effective Sample Size")
```

---

n_nbs *Count neighbors in a connectivity matrix*

Description

Count neighbors in a connectivity matrix

Usage

```
n_nbs(C)
```

Arguments

C	A connectivity matrix

Value

A vector with the number of non-zero values in each row of C

Examples

```
data(sentencing)
C <- shape2mat(sentencing)
sentencing$Ni <- n_nbs(C)
```

`posterior_predict` *Sample from the posterior predictive distribution*

Description

Draw samples from the posterior predictive distribution of a fitted `geostan` model.

Usage

```
posterior_predict(
  object,
  S,
  summary = FALSE,
  width = 0.95,
  approx = TRUE,
  K = 20,
  preserve_order = FALSE,
  seed
)
```

Arguments

`object`	A `geostan_fit` object.
`S`	Optional; number of samples to take from the posterior distribution. The default, and maximum, is the total number of samples stored in the model.
`summary`	Should the predictive distribution be summarized by its means and central quantile intervals? If `summary = FALSE`, an `S` x `N` matrix of samples will be returned. If `summary = TRUE`, then a `data.frame` with the means and `100*width` credible intervals is returned.
`width`	Only used if `summary = TRUE`, to set the quantiles for the credible intervals. Defaults to `width = 0.95`.
`approx`	For SAR models only; `approx = TRUE` uses an approximation method for the inverse of matrix `(I - rho * W)`.
`K`	For SAR models only; number of matrix powers to for the matrix inverse approximation (used when `approx = TRUE`). High values of rho (especially > 0.9) require larger K for accurate approximation.
`preserve_order`	If `TRUE`, the order of posterior draws will remain fixed; the default is to permute the MCMC samples so that (with small sample size `S`) each successive call to `posterior_predict` will return a different sample from the posterior probability distribution.

seed — A single integer value to be used in a call to set.seed before taking samples from the posterior distribution.

Details

This method returns samples from the posterior predictive distribution of the model (at the observed values of covariates, etc.). The predictions incorporate uncertainty of all parameter values (used to calculate the expected value of the model, for example) plus the error term (the model's description of the amount of variability of observations around the expected value). If the model includes measurement error in the covariates, this source of uncertainty (about X) is passed into the posterior predictive distribution as well.

For SAR models (and all other models), the observed outcomes are *not* used to formulate the posterior predictive distribution. The posterior predictive distribution for the SLM (see stan_sar) is given by

$$(I - \rho W)^{-1}(\mu + \epsilon).$$

The SDLM is the same but includes spatially-lagged covariates in mu. The approx = FALSE method for SAR models requires a call to Matrix::solve(I - rho * W) for each MCMC sample; the approx = TRUE method uses an approximation based on matrix powers (LeSage and Pace 2009). The approximation will deteriorate if ρ^K is not near zero, so use with care.

Value

A matrix of size S x N containing samples from the posterior predictive distribution, where S is the number of samples drawn and N is the number of observations. If summary = TRUE, a data.frame with N rows and 3 columns is returned (with column names mu, lwr, and upr).

Source

LeSage, James, & Robert kelley Pace (2009). *Introduction to Spatial Econometrics*. Chapman and Hall/CRC.

Gelman, A., J. B.Carlin, H. S. Stern, D. B. Dunson, A. Vehtari, & D. B. Rubin, D. B. (2014). *Bayesian data analysis* (3rd ed.). CRC Press.

McElreath, Richard (2016). *Statistical Rethinking: A Bayesian Course with Examples in R and Stan*. CRC Press, Ch. 3.

Examples

```
E <- sentencing$expected_sents
sentencing$log_E <- log(E)
 fit <- stan_glm(sents ~ offset(log_E),
                 re = ~ name,
                 data = sentencing,
                 family = poisson(),
                 chains = 2, iter = 600) # for speed only


 yrep <- posterior_predict(fit, S = 65)
 plot(density(yrep[1,] / E ))
 for (i in 2:nrow(yrep)) lines(density(yrep[i,] / E), col = 'gray30')
```

```
 lines(density(sentencing$sents / E), col = 'darkred', lwd = 2)

sars <- prep_sar_data2(row = 9, col = 9)
W <- sars$W
y <- sim_sar(rho = .9, w = W)
fit <- stan_sar(y ~ 1, data = data.frame(y=y), sar = sars,
                iter = 650, quiet = TRUE)
yrep <- posterior_predict(fit, S = 15)
```

`predict.geostan_fit` *Predict method for* `geostan_fit` *models*

Description

Obtain predicted values from a fitted model by providing new covariate values.

Usage

```
## S3 method for class 'geostan_fit'
predict(
  object,
  newdata,
  alpha = as.matrix(object, pars = "intercept"),
  center = object$x_center,
  summary = TRUE,
  type = c("link", "response"),
  add_slx = FALSE,
  approx = FALSE,
  K = 15,
  ...
)
```

Arguments

`object`	A fitted model object of class `geostan_fit`.
`newdata`	A data frame in which to look for variables with which to predict. Note that if the model formula includes an offset term, `newdata` must contain the offset column (see examples below). If covariates in the model were centered using the `centerx` argument, the `predict.geostan_fit` method will automatically center the predictors in `newdata` using the values stored in `object$x_center`. If `newdata` is missing, the fitted values of the model will be returned.
`alpha`	An N-by-1 matrix of MCMC samples for the intercept; this is provided by default. If used, note that the intercept needs to be provided on the scale of the linear predictor. This argument might be used if there is a need to incorporate the spatial trend term (as a spatially-varying intercept).

center	Optional vector of numeric values or a logical scalar to pass to scale. Defaults to using object$x_center. If the model was fit using centerx = TRUE, then covariates were centered and their mean values are stored in object$x_center and the predict method will use them automatically to center newdata; if the model was fit with centerx = FALSE, then object$x_center = FALSE and newdata will not be centered.
summary	If FALSE, a matrix containing samples from the posterior distribution at each observation is returned. The default, TRUE, will summarize results by providing an estimate (mean) and credible interval (formed by taking quantiles of the MCMC samples).
type	By default, results from predict are on the scale of the linear predictor (type = "link"). The alternative (type = "response") is on the scale of the response variable. For example, the default return values for a Poisson model on the log scale, and using type = "response" will return the original scale of the outcome variable (by exponentiating the log values).
add_slx	Logical. If add_slx = TRUE, any spatially-lagged covariates that were specified through the 'slx' argument (of the model fitting function, e.g., stan_glm) will be added to the linear predictor. The spatial lag terms will be calculated internally using object$C, the spatial weights matrix used to fit the model. Hence, newdata must have N = object$N rows. Predictions from spatial lag models (SAR models of type 'SLM' and 'SDLM') always include the SLX terms (i.e., any value passed to add_slx will be overwritten with TRUE).
approx	For SAR models of type 'SLM' or 'SDLM' only; use an approximation for matrix inversion? See details below.
K	Number of matrix powers to use with approx.
...	Not used

Details

The primary purpose of the predict method is to explore marginal effects of covariates. The uncertainty present in these predictions refers to uncertainty in the expected value of the model. The expectation does not include the error term of the model (nb: one expects actual observations to form a cloud of points around the expected value). By contrast, posterior_predict returns the complete (posterior) predictive distribution of the model (the expectation plus noise).

The model formula will be taken from object$formula, and then a model matrix will be created by passing newdata to the model.frame function (as in: model.frame(object$formula, newdata). Parameters are taken from as.matrix(object, pars = c("intercept", "beta")).

The examples illustrate how to use the function in most cases.

Special considerations apply to models with spatially-lagged covariates and a spatially-lagged dependent variable (i.e., the 'SLM' and 'SDLM' models fit by stan_sar).

Spatial lag of X:

Spatially-lagged covariates which were included via the slx argument will, by default, not be included in the predicted values. (The user can have greater control by manually adding the spatially-lagged covariate to the main model formula.) The slx term will be be included in predictions if add_slx = TRUE or if the fitted model is a SAR model of type 'SLM' or 'SDLM'. In

either of those cases, newdata must have the same number of rows as were used to fit the original data.

Spatial lag of Y:

The typical 'marginal effect' interpretation of the regression coefficients does not hold for the SAR models of type 'SLM' or 'SDLM'. For details on these 'spillover effects', see LeSage and Pace (2009), LeSage (2014), and impacts.

Predictions for the spatial lag model (SAR models of type 'SLM') are equal to:

$$(I - \rho W)^{-1} X\beta$$

where $X\beta$ contains the intercept and covariates. Predictions for the spatial Durbin lag model (SAR models of type 'SDLM') are equal to:

$$(I - \rho W)^{-1}(X\beta + WX\gamma)$$

where $WX\gamma$ are spatially lagged covariates multiplied by their coefficients. For this reason, the predict.geostan_fit method requires that newdata have as many rows as the original data (so that nrow(newdata) == nrow(object$C)); the spatial weights matrix will be taken from object$C.

The inverse of the matrix $(I - \rho W)$ can be time consuming to compute (especially when iterating over MCMC samples). You can use approx = TRUE to approximate the inverse using a series of matrix powers. The argument K controls how many powers to use for the approximation. As a rule, higher values of ρ require larger K to obtain accuracy. Notice that ρ^K should be close to zero for the approximation to hold. For example, for $\rho = .5$ a value of $K = 8$ may suffice ($0.5^8 = 0.004$), but larger values of ρ require higher values of K.

Generalized linear models:

In generalized linear models (such as Poisson and Binomial models) marginal effects plots on the response scale may be sensitive to the level of other covariates in the model and to geographic location (given a spatially-varying mean value). If the model includes a spatial autocorrelation component (for example, you used a spatial CAR, SAR, or ESF model, or used the re argument for random effects), by default these terms will be fixed at zero for the purposes of calculating marginal effects. If you want to change this, you can introduce a varying intercept manually using the alpha argument.

Value

If summary = FALSE, a matrix of samples is returned. If summary = TRUE (the default), a data frame is returned.

Source

Goulard, Michael, Thibault Laurent, and Christine Thomas-Agnan (2017). About predictions in spatial autoregressive models: optimal and almost optimal strategies. *Spatial Economic Analysis* 12 (2-3): 304-325.

LeSage, James (2014). What Regional Scientists Need to Know about Spatial Econometrics. *The Review of Regional Science* 44: 13-32 (2014 Southern Regional Science Association Fellows Address).

LeSage, James, & Robert kelley Pace (2009). *Introduction to Spatial Econometrics*. Chapman and Hall/CRC.

Examples

```
data(georgia)
georgia$income <- georgia$income / 1e3

fit <- stan_glm(deaths.male ~ offset(log(pop.at.risk.male)) + log(income),
                data = georgia,
                re = ~ GEOID,
                centerx = TRUE,
                family = poisson(),
                chains = 2, iter = 600) # for speed only

# note: pop.at.risk.male=1 leads to offset of log(pop.at.risk.male)=0
# so that the predicted values are rates
newdata <- data.frame(
             income = seq(min(georgia$income),
                          max(georgia$income),
                           length.out = 200),
             pop.at.risk.male = 1)

preds <- predict(fit, newdata, type = "response")
head(preds)
plot(preds$income,
     preds$mean * 10e3,
     type = "l",
     ylab = "Deaths per 10,000",
     xlab = "Income ($1,000s)")

# here the predictions are rates per 10,000
newdata$pop.at.risk.male <- 10e3
preds <- predict(fit, newdata, type = "response")
head(preds)

# plot range
y_lim <- c(min(preds$`2.5%`), max(preds$`97.5%`))

# plot line
plot(preds$income,
    preds$mean,
    type = "l",
    ylab = "Deaths per 10,000",
    xlab = "Income ($1,000s)",
    ylim = y_lim,
    axes = FALSE)

# add shaded cred. interval
x <- c(preds$income, rev(preds$income))
y <- c(preds$`2.5%`, rev(preds$`97.5%`))
polygon(x = x, y = y,
       col = rgb(0.1, 0.2, 0.3, 0.3),
       border = NA)

# add axes
```

```
yat = seq(0, 300, by = 20)
axis(2, at = yat)

xat = seq(0, 200, by = 10)
axis(1, at = xat)

# show county incomes
rug(georgia$income)
```

`prep_car_data` *Prepare data for the CAR model*

Description

Prepare data for the CAR model

Usage

```
prep_car_data(
  A,
  style = c("WCAR", "ACAR", "DCAR"),
  k = 1,
  gamma = 0,
  lambda = TRUE,
  stan_fn = ifelse(style == "WCAR", "wcar_normal_lpdf", "car_normal_lpdf"),
  quiet = FALSE
)
```

Arguments

A	Binary adjacency matrix; for style = DCAR, provide a symmetric matrix of distances instead. The distance matrix should be sparse, meaning that most distances should be zero (usually obtained by setting some threshold distance beyond which all are zero).
style	Specification for the connectivity matrix (C) and conditional variances (M); one of "WCAR", "ACAR", or "DCAR".
k	For style = DCAR, distances will be raised to the -k power (d^-k).
gamma	For style = DCAR, distances will be offset by gamma before raising to the -kth power.
lambda	If TRUE, return eigenvalues required for calculating the log determinant of the precision matrix and for determining the range of permissible values of rho. These will also be printed with a message if lambda = TRUE.
stan_fn	Two computational methods are available for CAR models using stan_car: car_normal_lpdf and wcar_normal_lpdf. For WCAR models, either method will work but wcar_normal_lpdf is faster. To force use car_normal_lpdf when style = 'WCAR', provide stan_fn = "car_normal_lpdf".
quiet	Controls printing behavior. By default, quiet = FALSE and the range of permissible values for the spatial dependence parameter is printed to the console.

Details

The CAR model is:

```
Normal(Mu, Sigma), Sigma = (I - rho * C)^-1 * M * tau^2,
```

where `I` is the identity matrix, `rho` is a spatial autocorrelation parameter, `C` is a connectivity matrix, and `M * tau^2` is a diagonal matrix with conditional variances on the diagonal. `tau^2` is a (scalar) scale parameter.

In the WCAR specification, `C` is the row-standardized version of `A`. This means that the non-zero elements of `A` will be converted to `1/N_i` where `N_i` is the number of neighbors for the `i`th site (obtained using `Matrix::rowSums(A)`. The conditional variances (on the diagonal of `M * tau^2`), are also proportional to `1/N_i`.

The ACAR specification is from Cressie, Perrin and Thomas-Agnon (2005); also see Cressie and Wikle (2011, p. 188) and Donegan (2021).

The DCAR specification is inverse distance-based, and requires the user provide a (sparse) distance matrix instead of a binary adjacency matrix. (For `A`, provide a symmetric matrix of distances, not inverse distances!) Internally, non-zero elements of `A` will be converted to: `d_{ij} = (a_{ij} + gamma)^(-k)` (Cliff and Ord 1981, p. 144; Donegan 2021). Default values are `k=1` and `gamma=0`. Following Cressie (2015), these values will be scaled (divided) by their maximum value. For further details, see the DCAR_A specification in Donegan (2021).

For inverse-distance weighting schemes, see Cliff and Ord (1981); for distance-based CAR specifications, see Cressie (2015 [1993]), Haining and Li (2020), and Donegan (2021).

Details on CAR model specifications can be found in Table 1 of Donegan (2021).

Value

A list containing all of the data elements required by the CAR model in `stan_car`.

Source

Cliff A, Ord J (1981). Spatial Processes: Models and Applications. Pion.

Cressie N (2015 [1993]). Statistics for Spatial Data. Revised edition. John Wiley & Sons.

Cressie N, Perrin O, Thomas-Agnan C (2005). "Likelihood-based estimation for Gaussian MRFs." Statistical Methodology, 2(1), 1–16.

Cressie N, Wikle CK (2011). Statistics for Spatio-Temporal Data. John Wiley & Sons.

Donegan, Connor (2021). Spatial conditional autoregressive models in Stan. *OSF Preprints*. doi:10.31219/osf.io/3ey65.

Haining RP, Li G (2020). Modelling Spatial and Spatio-Temporal Data: A Bayesian Approach. CRC Press.

Examples

```
data(georgia)

## use a binary adjacency matrix
```

```
A <- shape2mat(georgia, style = "B")

## WCAR specification
cp <- prep_car_data(A, "WCAR")
1 / range(cp$lambda)

## ACAR specification
cp <- prep_car_data(A, "ACAR")

## DCAR specification (inverse-distance based)
A <- shape2mat(georgia, "B")
D <- sf::st_distance(sf::st_centroid(georgia))
A <- D * A
cp <- prep_car_data(A, "DCAR", k = 1)
```

`prep_car_data2` *Prepare data for the CAR model: raster analysis*

Description

Prepare a list of data required for the CAR model; this is for working with (large) raster data files only. For non-raster analysis, see prep_car_data.

Usage

```
prep_car_data2(row = 100, col = 100, quiet = FALSE)
```

Arguments

`row`	Number of rows in the raster
`col`	Number of columns in the raster
`quiet`	Controls printing behavior. By default, `quiet = FALSE` and the range of permissible values for the spatial dependence parameter is printed to the console.

Details

Prepare input data for the CAR model when your dataset consists of observations on a regular (rectangular) tessellation, such as a raster layer or remotely sensed imagery. The rook criteria is used to determine adjacency. This function uses Equation 5 from Griffith (2000) to generate approximate eigenvalues for a row-standardized spatial weights matrix from a P-by-Q dimension regular tessellation.

This function can accommodate very large numbers of observations for use with `stan_car`; for large N data, it is also recommended to use `slim = TRUE` or the `drop` argument. For more details, see: `vignette("raster-regression", package = "geostan")`.

Value

A list containing all of the data elements required by the CAR model in `stan_car`.

Source

Griffith, Daniel A. (2000). Eigenfunction properties and approximations of selected incidence matrices employed in spatial analyses. *Linear Algebra and its Applications* 321 (1-3): 95-112. doi:10.1016/S00243795(00)000318.

See Also

prep_sar_data2, prep_car_data, stan_car.

Examples

```
row = 100
col = 120
car_dl <- prep_car_data2(row = row, col = col)
```

---

prep_icar_data *Prepare data for ICAR models*

Description

Given a symmetric n x n connectivity matrix, prepare data for intrinsic conditional autoregressive models in Stan. This function may be used for building custom ICAR models in Stan. This is used internally by stan_icar.

Usage

```
prep_icar_data(C, scale_factor = NULL)
```

Arguments

C	Connectivity matrix
scale_factor	Optional vector of scale factors for each connected portion of the graph structure. If not provided by the user it will be fixed to a vector of ones.

Details

This is used internally to prepare data for stan_icar models. It can also be helpful for fitting custom ICAR models outside of geostan.

Value

list of data to add to Stan data list:

k number of groups

group_size number of nodes per group

n_edges number of connections between nodes (unique pairs only)

node1 first node

node2 second node. (`node1[i]` and `node2[i]` form a connected pair)

weight The element `C[node1, node2]`.

group_idx indices for each observation belonging each group, ordered by group.

m number of disconnected regions requiring their own intercept.

A n-by-m matrix of dummy variables for the component-specific intercepts.

inv_sqrt_scale_factor By default, this will be a k-length vector of ones. Placeholder for user-specified information. If user provided `scale_factor`, then this will be `1/sqrt(scale_factor)`.

comp_id n-length vector indicating the group membership of each observation.

Source

Besag, Julian, Jeremy York, and Annie Mollié. 1991. "Bayesian Image Restoration, with Two Applications in Spatial Statistics." Annals of the Institute of Statistical Mathematics 43 (1): 1–20.

Donegan, Connor. Flexible Functions for ICAR, BYM, and BYM2 Models in Stan. Code Repository. 2021. Available online: https://github.com/ConnorDonegan/Stan-IAR/ (accessed Sept. 10, 2021).

Freni-Sterrantino, Anna, Massimo Ventrucci, and Håvard Rue. 2018. "A Note on Intrinsic Conditional Autoregressive Models for Disconnected Graphs." Spatial and Spatio-Temporal Epidemiology 26: 25–34.

Morris, Mitzi, Katherine Wheeler-Martin, Dan Simpson, Stephen J Mooney, Andrew Gelman, and Charles DiMaggio. 2019. "Bayesian Hierarchical Spatial Models: Implementing the Besag York Mollié Model in Stan." Spatial and Spatio-Temporal Epidemiology 31: 100301.

Riebler, Andrea, Sigrunn H Sørbye, Daniel Simpson, and Håvard Rue. 2016. "An Intuitive Bayesian Spatial Model for Disease Mapping That Accounts for Scaling." Statistical Methods in Medical Research 25 (4): 1145–65.

See Also

`edges`, `shape2mat`, `stan_icar`, `prep_car_data`

Examples

```
data(sentencing)
C <- shape2mat(sentencing)
icar.data.list <- prep_icar_data(C)
```

prep_me_data *Prepare data for spatial measurement error models*

Description

Prepares the list of data required for geostan's (spatial) measurement error models. Given a data frame of standard errors and any optional arguments, the function returns a list with all required data for the models, filling in missing elements with default values.

Usage

```
prep_me_data(
  se,
  car_parts,
  prior,
  logit = rep(FALSE, times = ncol(se)),
  bounds = c(-Inf, Inf)
)
```

Arguments

se	Data frame of standard errors; column names must match (exactly) the variable names used in the model formula.
car_parts	A list of data required for spatial CAR models, as created by prep_car_data; optional. If omitted, the measurement error model will be a non-spatial Student's t model.
prior	A named list of prior distributions (see priors). If none are provided, default priors will be assigned. The list of priors may include the following parameters:

df If using a non-spatial ME model, the degrees of freedom (df) for the Student's t model is assigned a gamma prior with default parameters of `gamma2(alpha = 3, beta = 0.2)`. Provide values for each covariate in `se`, listing the values in the same order as the columns of `se`.

location The prior for the location parameter (mu) is a normal (Gaussian) distribution (the default being `normal(location = 0, scale = 100)`). To adjust the prior distributions, provide values for each covariate in `se`, listing the values in the same order as the columns of se.

scale The prior for the scale parameters is Student's t, and the default parameters are `student_t(df = 10, location = 0, scale = 40)`. To adjust, provide values for each covariate in `se`, listing the values in the same order as the columns of se.

car_rho The CAR model, if used, has a spatial autocorrelation parameter, `rho`, which is assigned a uniform prior distribution. You must specify values that are within the permissible range of values for `rho`; these are automatically printed to the console by the prep_car_data function.

logit	Optional vector of logical values (TRUE, FALSE) indicating if the latent variable should be logit-transformed. Only use for rates. This keeps rates between zero and one and may improve modeling of skewed variables (e.g., the poverty rate).
bounds	Rarely needed; an optional numeric vector of length two providing the upper and lower bounds, respectively, of the variables (e.g., a magnitudes must be greater than 0). If not provided, they will be set to c(-Inf, Inf) (i.e., unbounded).

Value

A list of data as required for (spatial) ME models. Missing arguments will be filled in with default values, including prior distributions.

See Also

se_log

Examples

```
data(georgia)

## for a non-spatial prior model for two covariates
se <- data.frame(ICE = georgia$ICE.se,
                 college = georgia$college.se)
ME <- prep_me_data(se)

## see default priors
print(ME$prior)

## set prior for the scale parameters
ME <- prep_me_data(se,
                   prior = list(scale = student_t(df = c(10, 10),
                                                  location = c(0, 0),
                                                  scale = c(20, 20))))

## for a spatial prior model (often recommended)
A <- shape2mat(georgia, "B")
cars <- prep_car_data(A)
ME <- prep_me_data(se,
                   car_parts = cars)
```

---

prep_sar_data *Prepare data for a simultaneous autoregressive (SAR) model*

Description

Given a spatial weights matrix W, this function prepares data for the simultaneous autoregressive (SAR) model (a.k.a spatial error model (SEM)) in Stan. This is used internally by stan_sar, and may also be used for building custom SAR models in Stan.

Usage

```
prep_sar_data(W, quiet = FALSE)
```

Arguments

W	Spatial weights matrix, typically row-standardized.
quiet	Controls printing behavior. By default, quiet = FALSE and the range of permissible values for the spatial dependence parameter is printed to the console.

Details

This is used internally to prepare data for stan_sar models. It can also be helpful for fitting custom SAR models in Stan (outside of geostan), as described in the geostan vignette on custom spatial models.

Value

Return's a list of data required as input for geostan's SAR models, as implemented in Stan. The list contains:

ImW_w Numeric vector containing the non-zero elements of matrix $(I - W)$.

ImW_v An integer vector containing the column indices of the non-zero elements of $(I - W)$.

ImW_u An integer vector indicating where in ImW_w a given row's non-zero values start.

nImW_w Number of entries in ImW_w.

Widx Integer vector containing the indices corresponding to values of -W in ImW_w (i.e. non-diagonal entries of $(I - W)$).

nW Integer length of Widx.

eigenvalues_w Eigenvalues of W matrix.

n Number of rows in W.

W Sparse matrix representation of W

rho_min Minimum permissible value of ρ (1/min(eigenvalues_w)).

rho_max Maximum permissible value of ρ (1/max(eigenvalues_w).

The function will also print the range of permissible ρ values to the console (unless quiet = TRUE).

See Also

shape2mat, stan_sar, prep_car_data, prep_icar_data

Examples

```
data(georgia)
W <- shape2mat(georgia, "W")
sar_dl <- prep_sar_data(W)
```

prep_sar_data2 *Prepare data for SAR model: raster analysis*

Description

Prepares a list of data required for using the SAR model; this is for working with (large) raster data files. For non-raster analysis, see prep_sar_data.

Usage

```
prep_sar_data2(row, col, quiet = FALSE)
```

Arguments

row	Number of rows in the raster
col	Number of columns in the raster
quiet	Controls printing behavior. By default, quiet = FALSE and the range of permissible values for the spatial dependence parameter is printed to the console.

Details

Prepare data for the SAR model when your raw dataset consists of observations on a regular tessellation, such as a raster layer or remotely sensed imagery. The rook criteria is used to determine adjacency. This function uses Equation 5 from Griffith (2000) to calculate the eigenvalues for a row-standardized spatial weights matrix of a P-by-Q dimension regular tessellation.

This function can accommodate very large numbers of observations for use with stan_sar; for large N data, it is also recommended to use slim = TRUE or the drop argument. For details, see: vignette("raster-regression", package = "geostan").

Value

A list containing all of the data elements required by the SAR model in stan_sar.

Source

Griffith, Daniel A. (2000). Eigenfunction properties and approximations of selected incidence matrices employed in spatial analyses. *Linear Algebra and its Applications* 321 (1-3): 95-112. doi:10.1016/S00243795(00)000318.

See Also

prep_car_data2, prep_sar_data, stan_sar.

Examples

```
row = 100
col = 120
sar_dl <- prep_sar_data2(row = row, col = col)
```

`print.geostan_fit` *print or plot a fitted geostan model*

Description

Print a summary of model results to the R console, or plot posterior distributions of model parameters.

Usage

```
## S3 method for class 'geostan_fit'
print(x, probs = c(0.025, 0.2, 0.5, 0.8, 0.975), digits = 3, pars = NULL, ...)

## S3 method for class 'geostan_fit'
plot(x, pars, plotfun = "hist", fill = "steelblue4", ...)
```

Arguments

`x`	A fitted model object of class `geostan_fit`.
`probs`	Argument passed to `quantile`; which quantiles to calculate and print.
`digits`	number of digits to print
`pars`	parameters to include; a character string (or vector) of parameter names.
`...`	additional arguments to `rstan::plot` or `rstan::print.stanfit`.
`plotfun`	Argument passed to `rstan::plot`. Options include histograms ("hist"), MCMC traceplots ("trace"), and density plots ("dens"). Diagnostic plots are also available such as Rhat statistics ("rhat"), effective sample size ("ess"), and MCMC autocorrelation ("ac").
`fill`	fill color for histograms and density plots.

Value

The print methods writes text to the console to summarize model results. The plot method resturns a `ggplot` (from `rstan::plot` for stanfit objects).

Examples

```
data(georgia)
georgia$income <- georgia$income/1e3

fit <- stan_glm(deaths.male ~ offset(log(pop.at.risk.male)) + log(income),
                centerx = TRUE,
                data = georgia,
                family = poisson(),
                chains = 2, iter = 600) # for speed only


# print and plot results
print(fit)
plot(fit)
```

---

priors *Prior distributions*

Description

Prior distributions

Usage

```
uniform(lower, upper, variable = NULL)

normal(location = 0, scale, variable = NULL)

student_t(df = 10, location = 0, scale, variable = NULL)

gamma2(alpha, beta, variable = NULL)

hs(global_scale = 1, slab_df = 10, slab_scale, variable = "beta_ev")
```

Arguments

lower, upper	lower and upper bounds of the distribution
variable	A reserved slot for the variable name; if provided by the user, this may be ignored by **geostan**.
location	Location parameter(s), numeric value(s)
scale	Scale parameter(s), positive numeric value(s)
df	Degrees of freedom, positive numeric value(s)
alpha	shape parameter, positive numeric value(s)
beta	inverse scale parameter, positive numeric value(s)
global_scale	Control the (prior) degree of sparsity in the horseshoe model (0 < global_scale < 1).

slab_df	Degrees of freedom for the Student's t model for large coefficients in the horseshoe model (slab_df > 0).
slab_scale	Scale parameter for the Student's t model for large coefficients in the horseshoe model (slab_scale > 0).

Details

The prior distribution functions are used to set the values of prior parameters.

Users can control the values of the parameters, but the distribution (model) itself is fixed. The intercept and regression coefficients are given Gaussian prior distributions and scale parameters are assigned Student's t prior distributions. Degrees of freedom parameters are assigned gamma priors, and the spatial autocorrelation parameter in the CAR model, rho, is assigned a uniform prior. The horseshoe (hs) model is used by stan_esf.

Note that the variable argument is used internally by geostan, and any user provided values will be ignored.

Parameterizations:

For details on how any distribution is parameterized, see the Stan Language Functions Reference document: https://mc-stan.org/users/documentation/.

The horseshoe prior:

The horseshoe prior is used by stan_esf as a prior for the eigenvector coefficients. The horseshoe model encodes a prior state of knowledge that effectively states, 'I believe a small number of these variables may be important, but I don't know which of them is important.' The horseshoe is a normal distribution with unknown scale (Polson and Scott 2010):

```
beta_j ~ Normal(0, tau^2 * lambda_j^2)
```

The scale parameter for this prior is the product of two terms: lambda_j^2 is specific to the variable beta_j, and tau^2 is known as the global shrinkage parameter.

The global shrinkage parameter is assigned a half-Cauchy prior:

```
tau ~ Cauchy(0, global_scale * sigma)
```

where global_scale is provided by the user and sigma is the scale parameter for the outcome variable; for Poisson and binomial models, sigma is fixed at one. Use global_scale to control the overall sparsity of the model.

The second part of the model is a Student's t prior for lambda_j. Most lambda_j will be small, since the model is half-Cauchy:

```
lambda_j ~ Cauchy(0, 1)
```

This model results in most lambda_j being small, but due to the long tails of the Cauchy distribution, strong evidence in the data can force any particular lambda_j to be large. Piironen and Vehtari (2017) adjust the model so that those large lambda_j are effectively assigned a Student's t model:

```
Big_lambda_j ~ Student_t(slab_df, 0, slab_scale)
```

This is a schematic representation of the model; see Piironen and Vehtari (2017) or Donegan et al. (2020) for details.

Value

An object of class `prior` which will be used internally by **geostan** to set parameters of prior distributions.

Student's t:

Return value for `student_t` depends on the input; if no arguments are provided (specifically, if the scale parameter is missing), this will return an object of class 'family'; if at least the scale parameter is provided, `student_t` will return an object of class `prior` containing parameter values for the Student's t distribution.

Source

Donegan, C., Y. Chun and A. E. Hughes (2020). Bayesian estimation of spatial filters with Moran's Eigenvectors and hierarchical shrinkage priors. *Spatial Statistics*. doi:10.1016/j.spasta.2020.100450 (open access: doi:10.31219/osf.io/fah3z).

Polson, N.G. and J.G. Scott (2010). Shrink globally, act locally: Sparse Bayesian regularization and prediction. *Bayesian Statistics* 9, 501-538.

Piironen, J and A. Vehtari (2017). Sparsity information and regularization in the horseshoe and other shrinkage priors. In *Electronic Journal of Statistics*, 11(2):5018-5051.

Examples

```
# normal priors for k=2 covariates
data(georgia)
prior <- list()
k <- 2
prior$beta <- normal(location = rep(0, times = k),
                     scale = rep(4, times = k))
prior$intercept <- normal(-5, 5)
print(prior)
fit <- stan_glm(deaths.male ~ offset(log(pop.at.risk.male)) + log(income) + college,
                # re = ~ GEOID,
                centerx = TRUE,
                data = georgia,
                family = poisson(),
                prior = prior,
                chains = 2, iter = 600) # for speed only
print(fit)


# setting (hyper-) priors in ME models
se <- data.frame(insurance = georgia$insurance.se)
prior <- list()
prior$df <- gamma2(3, 0.2)
prior$location <- normal(50, 50)
prior$scale <- student_t(12, 10, 20)
print(prior)
ME <- prep_me_data(se = se, prior = prior)
fit <- stan_glm(log(rate.male) ~ insurance,
                data = georgia,
```

```
 centerx = TRUE,
 ME = ME,
chains = 2, iter = 600) # for speed only
```

`residuals.geostan_fit` *Extract residuals, fitted values, or the spatial trend*

Description

Extract model residuals, fitted values, or spatial trend from a fitted `geostan_fit` model.

Usage

```
## S3 method for class 'geostan_fit'
residuals(object, summary = TRUE, rates = TRUE, detrend = TRUE, ...)

## S3 method for class 'geostan_fit'
fitted(object, summary = TRUE, rates = TRUE, trend = TRUE, ...)

spatial(object, summary = TRUE, ...)

## S3 method for class 'geostan_fit'
spatial(object, summary = TRUE, ...)
```

Arguments

`object`	A fitted model object of class `geostan_fit`.
`summary`	Logical; should the values be summarized by their mean, standard deviation, and quantiles (`probs = c(.025, .2, .5, .8, .975)`) for each observation? Otherwise, a matrix containing samples from the posterior distributions is returned.
`rates`	For Poisson and Binomial models, should the fitted values be returned as rates, as opposed to raw counts? Defaults to `TRUE`; see the `Details` section for more information.
`detrend`	For auto-normal models (CAR and SAR models with Gaussian likelihood only); if `detrend = FALSE`, the residuals will equal `y - Mu`, where `Mu` does not contain the implicit spatial trend. If `detrend = TRUE` (the default), the residuals will equal `Resid = y - Mu - Trend`. For CAR models and for SAR models of type SEM, the implicit spatial trend is `Trend = rho * C %*% (Y - Mu)` (see stan_car or stan_sar). For SAR models of type SLM, the spatial trend is `rho * C * y`.
`...`	Not used
`trend`	For auto-normal models (CAR and SAR models with Gaussian likelihood only); if `trend = FALSE`, the fitted values will not include the implicit spatial trend term. Rather, the fitted values will equal `Mu`: the intercept plus any other terms explicitly included in the model formula and the `re` argument ('random effects'). If `trend = TRUE` (the default), `fitted = Mu + Trend`. For CAR models and SAR models of type SEM, the spatial trend is `rho * C (y - Mu)`. For SAR models of type SLM, the spatial trend is `rho * C * y`.

Details

When `rates = FALSE` and the model is Poisson or Binomial, the fitted values returned by the `fitted` method are the expected value of the response variable. The `rates` argument is used to translate count outcomes to rates by dividing by the appropriate denominator. The behavior of the `rates` argument depends on the model specification. Consider a Poisson model of disease incidence, such as the following intercept-only case:

```
fit <- stan_glm(y ~ offset(log(E)),
                data = data,
                family = poisson())
```

If the fitted values are extracted using `rates = FALSE`, then `fitted(fit)` will return the expectation of y. If `rates = TRUE` (the default), then `fitted(fit)` will return the expected value of the rate $\frac{y}{E}$.

If a binomial model is used instead of the Poisson, then using `rates = TRUE` with the `fitted` method will return the expectation of $\frac{y}{N}$ where y is the number of 'successes' and N is the sum of the number of 'successes' and 'failures', as in:

```
fit <- stan_glm(cbind(successes, failures) ~ 1,
                data = data,
                family = binomial())
```

Value

By default, these methods return a `data.frame`. The column named `mean` is what most users will be looking for. These contain the fitted values (for the `fitted` method), the residuals (fitted values minus observed values, for the `resid` method), or the spatial trend (for the `spatial` method). The `mean` column is the posterior mean of each value, and the column `sd` contains the posterior standard deviation for each value. The posterior distributions are also summarized by select quantiles.

If `summary = FALSE` then the method returns an S-by-N matrix of MCMC samples, where S is the number of MCMC samples and N is the number of observations in the data.

For spatial GLMs, the `spatial` method returns values on the scale of the linear predictor. Hence, for a Poisson with log link function, the spatial trend is on the log scale (in the same way that the intercept and coefficients are on the log scale).

Examples

```
sar_list <- prep_sar_data2(row = 10, col = 10, quiet = TRUE)
W <- sar_list$W
x <- sim_sar(w = W, rho = 0.8)
y <- sim_sar(w = W, rho = 0.7, mu = 1 + 0.5 * x)
dat <- data.frame(x = x, y = y)

fit <- stan_sar(y ~ x, data = dat, sar = sar_list,
                  chains = 1, iter = 800)

# Residuals
r = resid(fit)
head(r)
```

```
moran_plot(r$mean, W)

# when residuals are not detrended, they exhibit spatial autocorrelation
r2 = resid(fit, detrend = FALSE)
mc(r$mean, W)
mc(r2$mean, W)

r_mat <- resid(fit, summary = FALSE)
r_mean <- apply(r_mat, 2, mean)
head(r_mean)
mean(r_mean)

# Fitted values
f <- fitted(fit)
head(f)

# Spatial trend
sp_trend  <- spatial(fit)
head(sp_trend)

# another way to obtain detrended residuals
sp <- spatial(fit, summary = FALSE)
r <- resid(fit, detrend = FALSE, summary = FALSE)
# detrended residuals (matrix of samples):
r_det <- r - sp
# summarize (take posterior means):
r_det <- apply(r_det, 2, mean)
r <- apply(r, 2, mean)
# Moran coefficients:
mc(r_det, W)
mc(r, W)
```

`row_standardize` *Row-standardize a matrix; safe for zero row-sums.*

Description

Row-standardize a matrix; safe for zero row-sums.

Usage

```
row_standardize(C, warn = FALSE, msg = "Row standardizing connectivity matrix")
```

Arguments

`C`	A matrix
`warn`	Print message `msg` if `warn = TRUE`.
`msg`	A warning message; used internally by geostan.

Value

A row-standardized matrix, W (i.e., all row sums equal 1, or zero).

Examples

```
A <- shape2mat(georgia)
head(Matrix::summary(A))
Matrix::rowSums(A)

W <- row_standardize(A)
head(Matrix::summary(W))
Matrix::rowSums(W)
```

---

sentencing *Florida state prison sentencing counts by county, 1905-1910*

Description

Simple features (`sf`) with historic (1910) county boundaries of Florida with aggregated state prison sentencing counts and census data. Sentencing and population counts are aggregates over the period 1905-1910, where populations were interpolated linearly between decennial censuses of 1900 and 1910.

Usage

```
sentencing
```

Format

Simple features (`sf`)/`data.frame` with the following attributes:

name County name

wpop White population total for years 1905-1910

bpop Black population total for years 1905-1910

sents Number of state prison sentences, 1905-1910

plantation_belt Binary indicator for inclusion in the plantation belt

pct_ag_1910 Percent of land area in agriculture, 1910

expected_sents Expected sentences given demographic information and state level sentencing rates by race

sir_raw Standardized incident ratio (observed/expected sentences)

Source

Donegan, Connor. "The Making of Florida's 'Criminal Class': Race, Modernity and the Convict Leasing Program." Florida Historical Quarterly 97.4 (2019): 408-434. https://osf.io/2wj7s/.

Mullen, Lincoln A. and Bratt, Jordon. "USABoundaries: Historical and Contemporary Boundaries of the United States of America," Journal of Open Source Software 3, no. 23 (2018): 314, doi:10.21105/joss.00314.

Examples

```
data(sentencing)
print(sentencing)
```

---

se_log *Standard error of log(x)*

Description

Transform the standard error of `x` to standard error of `log(x)`.

Usage

```
se_log(x, se, method = c("mc", "delta"), nsim = 5000, bounds = c(0, Inf))
```

Arguments

`x`	An estimate
`se`	Standard error of `x`
`method`	The `"delta"` method uses a Taylor series approximation; the default method, `"mc"`, uses a simple monte carlo method.
`nsim`	Number of draws to take if `method = "mc"`.
`bounds`	Lower and upper bounds for the variable, used in the monte carlo method. Must be a length-two numeric vector with lower bound greater than or equal to zero (i.e. `c(lower, upper)` as in default `bounds = c(0, Inf)`.

Details

The delta method returns `x^(-1) * se`. The monte carlo method is detailed in the examples section.

Value

Numeric vector of standard errors

Examples

```
data(georgia)
x = georgia$college
se = georgia$college.se

lse1 = se_log(x, se)
lse2 = se_log(x, se, method = "delta")
plot(lse1, lse2); abline(0, 1)

# the monte carlo method
x = 10
se = 2
z = rnorm(n = 20e3, mean = x,  sd = se)
l.z = log(z)
sd(l.z)
se_log(x, se, method = "mc")
se_log(x, se, method = "delta")
```

---

shape2mat *Create spatial and space-time connectivity matrices*

Description

Creates sparse matrix representations of spatial connectivity structures

Usage

```
shape2mat(
  shape,
  style = c("B", "W"),
  queen,
  method = c("queen", "rook", "knn"),
  k = 1,
  longlat = NULL,
  snap = sqrt(.Machine$double.eps),
  t = 1,
  st.style = c("contemp", "lag"),
  quiet = FALSE
)
```

Arguments

shape	An object of class sf, SpatialPolygons or SpatialPolygonsDataFrame.
style	What kind of coding scheme should be used to create the spatial connectivity matrix? Defaults to "B" for binary; use "W" for row-standardized weights.

queen	Deprecated: use the 'method' argument instead. This option is passed to poly2nb to set the contiguity condition. Defaults to TRUE so that a single shared boundary point (rather than a shared border/line) between polygons is sufficient for them to be considered neighbors.
method	Method for determining neighbors: queen, rook, or k-nearest neighbors. See Details for more information.
k	Number of neighbors to select for k-nearest neighbor method. Passed to spdep::knearneigh.
longlat	If longlat = TRUE, Great Circle (rather than Euclidean) distances are used; great circle circle distances account for curvature of the Earth.
snap	Passed to spdep::poly2nb; "boundary points less than 'snap' distance apart are considered to indicate contiguity."
t	Number of time periods. Only the binary coding scheme is available for space-time connectivity matrices.
st.style	For space-time data, what type of space-time connectivity structure should be used? Options are "lag" for the lagged specification and "contemp" (the default) for contemporaneous specification (see Details).
quiet	If TRUE, messages will be silenced.

Details

The method argument currently has three options. The queen contiguity condition defines neighbors as polygons that share at least one point with one another. The rook condition requires that they share a line or border with one another. K-nearest neighbors is based on distance between centroids. All methods are implemented using the spdep package and then converted to sparse matrix format.

Alternatively, one can use spdep directly to create a `listw` object and then convert that to a sparse matrix using `as(listw, 'CsparseMatrix')` for use with geostan.

Haining and Li (Ch. 4) provide a helpful discussion of spatial connectivity matrices (Ch. 4).

The space-time connectivity matrix can be used for eigenvector space-time filtering (stan_esf. The 'lagged' space-time structure connects each observation to its own past (one period lagged) value and the past value of its neighbors. The 'contemporaneous' specification links each observation to its neighbors and to its own in situ past (one period lagged) value (Griffith 2012, p. 23).

Value

A spatial connectivity matrix in sparse matrix format. Binary matrices are of class ngCMatrix, row-standardized are of class dgCMatrix, created by sparseMatrix.

Source

Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio, Virgilio (2013). Applied spatial data analysis with R, Second edition. Springer, NY. https://asdar-book.org/

Griffith, Daniel A. (2012). Space, time, and space-time eigenvector filter specifications that account for autocorrelation. Estadística Espanola, 54(177), 7-34.

Haining, Robert P. and Li, Guangquan (2020). Modelling Spatial and Spatial-Temporal Data: A Bayesian Approach. CRC Press.

See Also

edges row_standardize n_nbs

Examples

```
data(georgia)

## binary adjacency matrix
C <- shape2mat(georgia, "B", method = 'rook')

## number of neighbors per observation
summary( n_nbs(C) )
head(Matrix::summary(C))

## row-standardized matrix
W <- shape2mat(georgia, "W", method = 'rook')

## summary of weights
E <- edges(W, unique_pairs_only = FALSE)
summary(E$weight)

## space-time matricies
## for eigenvector space-time filtering
## if you have multiple years with same geometry/geography,
## provide the geometry (for a single year!) and number of years \code{t}
Cst <- shape2mat(georgia, t = 5)
dim(Cst)
EVst <- make_EV(Cst)
dim(EVst)
```

---

sim_sar *Simulate spatially autocorrelated data*

Description

Given a spatial weights matrix and degree of autocorrelation, returns autocorrelated data.

Usage

```
sim_sar(
  m = 1,
  mu = rep(0, nrow(w)),
  rho,
  sigma = 1,
  w,
  type = c("SEM", "SLM"),
  approx = FALSE,
  K = 20,
```

```
  ...
)
```

Arguments

m	The number of samples required. Defaults to m=1 to return an n-length vector; if m>1, an m x n matrix is returned (i.e. each row will contain a sample of auto-correlated values).
mu	An n-length vector of mean values. Defaults to a vector of zeros with length equal to nrow(w).
rho	Spatial autocorrelation parameter in the range (-1, 1). A single numeric value.
sigma	Scale parameter (standard deviation). Defaults to sigma = 1. A single numeric value.
w	n x n spatial weights matrix; typically row-standardized.
type	Type of SAR model: spatial error model ("SEM") or spatial lag model ("SLM").
approx	Use power of matrix W to approximate the inverse term?
K	Number of matrix powers to use if approx = TRUE.
...	further arguments passed to MASS::mvrnorm.

Details

This function takes n = nrow(w) draws from the normal distribution using rnorm to obtain vector x; if type = 'SEM', it then pre-multiplies xby the inverse of the matrix(I - rho * W)to obtain spatially autocorrelated values. Fortype = 'SLM', the multiplier matrix is applied to x + mu to produce the desired values.

The approx method approximates the matrix inversion using the method described by LeSage and Pace (2009, p. 40). For high values of rho, larger values of K are required for the approximation to suffice; you want rho^K to be near zero.

Value

If m = 1 then sim_sar returns a vector of the same length as mu, otherwise an m x length(mu) matrix with one sample in each row.

Source

LeSage, J. and Pace, R. K. (2009). *An Introduction to Spatial Econometrics*. CRC Press.

See Also

aple, mc, moran_plot, lisa, shape2mat

Examples

```
# spatially autocorrelated data on a regular grid
library(sf)
row = 10
col = 10
sar_parts <- prep_sar_data2(row = row, col = col)
w <- sar_parts$W
x <- sim_sar(rho = 0.65, w = w)
dat <- data.frame(x = x)

# create grid
sfc = st_sfc(st_polygon(list(rbind(c(0,0), c(col,0), c(col,row), c(0,0)))))
grid <- st_make_grid(sfc, cellsize = 1, square = TRUE)
st_geometry(dat) <- grid
plot(dat)

# draw form SAR (SEM) model
z <- sim_sar(rho = 0.9, w = w)
moran_plot(z, w)
grid$z <- z

# multiple sets of observations
# each row is one N-length draw from the SAR model
x <- sim_sar(rho = 0.7, w = w, m = 4)
nrow(w)
dim(x)
apply(x, 1, aple, w = w)
apply(x, 1, mc, w = w)

# Spatial lag model (SLM): y = rho*Wy + beta*x + epsilon
x <- sim_sar(rho = 0.5, w = w)
y <- sim_sar(mu = x, rho = 0.7, w = w, type = "SLM")

# Spatial Durbin lag model (SLM with spatial lag of x)
# SDLM: y = rho*Wy + beta*x + gamma*Wx + epsilon
x = sim_sar(w = w, rho = 0.5)
mu <- -0.5*x + 0.5*(w %*% x)[,1]
y <- sim_sar(mu = mu, w = w, rho = 0.6, type = "SLM")
```

`spill` *Spillover/diffusion effects for spatial lag models*

Description

Spillover/diffusion effects for spatial lag models

Usage

```
spill(beta, gamma = 0, rho, W, approx = TRUE, K = 15)

impacts(object, approx = TRUE, K = 15)

## S3 method for class 'impacts_slm'
print(x, digits = 2, ...)
```

Arguments

beta	Coefficient for covariates (numeric vector)
gamma	Coefficient for spatial lag of covariates
rho	Spatial dependence parameter (single numeric value)
W	Spatial weights matrix
approx	For a computationally efficient approximation to the required matrix inverse (after LeSage and Pace 2009, pp. 114–115); if FALSE, then a proper matrix inverse will be computed using Matrix::solve.
K	Degree of polynomial in the expansion to use when 'approx = TRUE'.
object	A fitted spatial lag model (from stan_sar)
x	An object of class 'impacts_slm', as returned by geostan::impacts
digits	Round results to this many digits
...	Additional arguments will be passed to base::print

Details

These methods apply only to the spatial lag and spatial Durbin lag models (SLM and SDLM) as fit by geostan::stan_sar.

The equation for these SAR models specifies simultaneous feedback between all units, such that changing the outcome in one location has a spill-over effect that may extend to all other locations (a ripple or diffusion effect); the induced changes will also react back onto the first unit. (This presumably takes time, even if the observations are cross-sectional.)

These spill-overs have to be incorporated into the interpretation and reporting of the regression coefficients of SLM and SDLM models. A unit change in the value of X in one location will impact y in that same place ('direct' impact) and will also impact y elsewhere through the diffusion process ('indirect' impact). The 'total' expected impact of a unit change in X is the sum of the direct and indirect effects (LeSage and Pace 2009).

The spill function is for quickly calculating average spillover effects given point estimates of parameters.

The impacts function calculates the (average) direct, indirect, and total effects once for every MCMC sample to produce samples from the posterior distribution for the impacts; the samples are returned together with a summary of the posterior distribution (mean, median, and select quantiles).

Source

LeSage, James and Pace, R. Kelley (2009). *Introduction to Spatial Econometrics*. CRC Press.

LeSage, James (2014). What Regional Scientists Need to Know about Spatial Econometrics. *The Review of Regional Science* 44: 13-32 (2014 Southern Regional Science Association Fellows Address).

Examples

```
##
## SDLM data
##

parts <- prep_sar_data2(row = 9, col = 9, quiet = TRUE)
W <- parts$W
x <- sim_sar(w=W, rho=.6)
Wx <- (W %*% x)[,1]
mu <- .5 * x + .25 * Wx
y <- sim_sar(w=W, rho=0.6, mu = mu, type = "SLM")
dat <- cbind(y, x)

# impacts per the above parameters
spill(0.5, 0.25, 0.6, W)

##
## impacts for SDLM
##

fit <- stan_sar(y ~ x, data = dat, sar = parts,
                type = "SDLM", iter = 500,
                slim = TRUE, quiet = TRUE)

# impacts (posterior distribution)
impax <- impacts(fit)
print(impax)

# plot posterior distributions
og = par(mfrow = c(1, 3),
         mar = c(3, 3, 1, 1))
S <- impax$samples[[1]]
hist(S[,1], main = 'Direct')
hist(S[,2], main = 'Indirect')
hist(S[,3], main = 'Total')
par(og)

##
## The approximate method
##

# High rho value requires more K; rho^K must be near zero
Ks <- c(10, 15, 20, 30, 35, 40)
print(cbind(Ks, 0.9^Ks))
```

```
# understand sensitivity of results to K when rho is high
spill(0.5, -0.25, 0.9, W, approx = TRUE, K = 10)
spill(0.5, -0.25, 0.9, W, approx = TRUE, K = 20)
spill(0.5, -0.25, 0.9, W, approx = TRUE, K = 30)
spill(0.5, -0.25, 0.9, W, approx = TRUE, K = 50)

# the correct results
spill(0.5, -0.25, 0.9, W, approx = FALSE)

# moderate and low rho values are fine with smaller K
spill(0.5, -0.25, 0.7, W, approx = TRUE, K = 15)
spill(0.5, -0.25, 0.7, W, approx = FALSE)
```

---

sp_diag *Visual displays of spatial data and spatial models*

Description

Visual diagnostics for areal data and model residuals

Usage

```
sp_diag(y, shape, ...)

## S3 method for class 'geostan_fit'
sp_diag(
  y,
  shape,
  name = "Residual",
  plot = TRUE,
  mc_style = c("scatter", "hist"),
  style = c("W", "B"),
  w = y$C,
  rates = TRUE,
  binwidth = function(x) 0.5 * stats::sd(x, na.rm = TRUE),
  size = 0.1,
  ...
)

## S3 method for class 'numeric'
sp_diag(
  y,
  shape,
  name = "y",
  plot = TRUE,
  mc_style = c("scatter", "hist"),
```

```
  style = c("W", "B"),
  w = shape2mat(shape, match.arg(style)),
  binwidth = function(x) 0.5 * stats::sd(x, na.rm = TRUE),
  ...
)
```

Arguments

y	A numeric vector, or a fitted geostan model (class geostan_fit).
shape	An object of class sf or another spatial object coercible to sf with sf::st_as_sf such as SpatialPolygonsDataFrame.
...	Additional arguments passed to residuals.geostan_fit.
name	The name to use on the plot labels; default to "y" or, if y is a geostan_fit object, to "Residuals".
plot	If FALSE, return a list of gg plots.
mc_style	Character string indicating how to plot the residual Moran coefficient (only used if y is a fitted model): if mc = "scatter", then moran_plot will be used with the marginal residuals; if mc = "hist", then a histogram of Moran coefficient values will be returned, where each plotted value represents the degree of residual autocorrelation in a draw from the join posterior distribution of model parameters.
style	Style of connectivity matrix; if w is not provided, style is passed to shape2mat and defaults to "W" for row-standardized.
w	An optional spatial connectivity matrix; if not provided and y is a numeric vector, one will be created using shape2mat. If w is not provided and y is a fitted geostan model, then the spatial connectivity matrix that is stored with the fitted model (y$C) will be used.
rates	For Poisson and binomial models, convert the outcome variable to a rate before plotting fitted values and residuals. Defaults to rates = TRUE.
binwidth	A function with a single argument that will be passed to the binwidth argument in geom_histogram. The default is to set the width of bins to 0.5 * sd(x).
size	Point size and linewidth for point-interval plot of observed vs. fitted values (passed to geom_pointrange).

Details

When provided with a numeric vector, this function plots a histogram, Moran scatter plot, and map.

When provided with a fitted geostan model, the function returns a point-interval plot of observed values against fitted values (mean and 95 percent credible interval), a Moran scatter plot for the model residuals, and a map of the mean posterior residuals (means of the marginal distributions). If if mc_style = 'hist', the Moran scatter plot is replaced by a histogram of Moran coefficient values calculated from the joint posterior distribution of the residuals.

Value

A grid of spatial diagnostic plots. If plot = TRUE, the ggplots are drawn using grid.arrange; otherwise, they are returned in a list. For the geostan_fit method, the underlying data for the Moran coefficient (as required for mc_style = "hist") will also be returned if plot = FALSE.

See Also

me_diag, mc, moran_plot, aple

Examples

```
data(georgia)
sp_diag(georgia$college, georgia)

bin_fn <- function(y) mad(y, na.rm = TRUE)
sp_diag(georgia$college, georgia, binwidth = bin_fn)


fit <- stan_glm(log(rate.male) ~ log(income),
                data = georgia,
                centerx = TRUE,
                chains = 1, iter = 1e3) # for speed only
sp_diag(fit, georgia)
```

---

stan_car *Conditional autoregressive (CAR) models*

Description

Use the CAR model as a prior on parameters, or fit data to a spatial Gaussian CAR model.

Usage

```
stan_car(
  formula,
  slx,
  re,
  data,
  C,
  car_parts = prep_car_data(C, "WCAR"),
  family = gaussian(),
  prior = NULL,
  ME = NULL,
  centerx = FALSE,
  prior_only = FALSE,
  censor_point,
  zmp,
  chains = 4,
  iter = 2000,
  refresh = 500,
  keep_all = FALSE,
  slim = FALSE,
  drop = NULL,
```

```
  pars = NULL,
  control = NULL,
  quiet = FALSE,
  ...
)
```

Arguments

formula	A model formula, following the R formula syntax. Binomial models can be specified by setting the left hand side of the equation to a data frame of successes and failures, as in `cbind(successes, failures) ~ x`.
slx	Formula to specify any spatially-lagged covariates. As in, `~ x1 + x2` (the intercept term will be removed internally). When setting priors for `beta`, remember to include priors for any SLX terms.

re	To include a varying intercept (or "random effects") term, `alpha_re`, specify the grouping variable here using formula syntax, as in `~ ID`. Then, `alpha_re` is a vector of parameters added to the linear predictor of the model, and:
	`alpha_re ~ N(0, alpha_tau)`
	`alpha_tau ~ Student_t(d.f., location, scale).`
	With the CAR model, any `alpha_re` term should be at a *different* level or scale than the observations; that is, at a different scale than the autocorrelation structure of the CAR model itself.

data	A `data.frame` or an object coercible to a data frame by `as.data.frame` containing the model data.
C	Spatial connectivity matrix which will be used internally to create `car_parts` (if `car_parts` is missing); if the user provides an `slx` formula for the model, the required connectivity matrix will be taken from the `car_parts` list. See shape2mat.
car_parts	A list of data for the CAR model, as returned by prep_car_data. If not provided by the user, then `C` will automatically be passed to `prep_car_data` to create it.
family	The likelihood function for the outcome variable. Current options are `auto_gaussian()`, `binomial(link = "logit")`, and `poisson(link = "log")`; if `family = gaussian()` is provided, it will automatically be converted to `auto_gaussian()`.
prior	A named list of parameters for prior distributions (see priors): **intercept** The intercept is assigned a Gaussian prior distribution (see normal. **beta** Regression coefficients are assigned Gaussian prior distributions. Variables must follow their order of appearance in the model `formula`. Note that if you also use `slx` terms (spatially lagged covariates), and you use custom priors for `beta`, then you have to provide priors for the slx terms. Since slx terms are *prepended* to the design matrix, the prior for the slx term will be listed first. **car_scale** Scale parameter for the CAR model, `car_scale`. The scale is assigned a Student's t prior model (constrained to be positive).

car_rho The spatial autocorrelation parameter in the CAR model, rho, is assigned a uniform prior distribution. By default, the prior will be uniform over all permissible values as determined by the eigenvalues of the connectivity matrix, C. The range of permissible values for rho is automatically printed to the console by prep_car_data.

tau The scale parameter for any varying intercepts (a.k.a exchangeable random effects, or partial pooling) terms. This scale parameter, tau, is assigned a Student's t prior (constrained to be positive).

ME — To model observational uncertainty (i.e. measurement or sampling error) in any or all of the covariates, provide a list of data as constructed by the prep_me_data function.

centerx — To center predictors on their mean values, use centerx = TRUE. If the ME argument is used, the modeled covariate (i.e., latent variable), rather than the raw observations, will be centered. When using the ME argument, this is the recommended method for centering the covariates.

prior_only — Logical value; if TRUE, draw samples only from the prior distributions of parameters.

censor_point — Integer value indicating the maximum censored value; this argument is for modeling censored (suppressed) outcome data, typically disease case counts or deaths.

zmp — Use zero-mean parameterization for the CAR model? Only relevant for Poisson and binomial outcome models (i.e., hierarchical models). See details below; this can sometimes improve MCMC sampling when the data is sparse, but does not alter the model specification.

chains — Number of MCMC chains to use.

iter — Number of samples per chain.

refresh — Stan will print the progress of the sampler every refresh number of samples. Set refresh=0 to silence this.

keep_all — If keep_all = TRUE then samples for all parameters in the Stan model will be kept; this is necessary if you want to do model comparison with Bayes factors and the bridgesampling package.

slim — If slim = TRUE, then the Stan model will not collect the most memory-intensive parameters (including n-length vectors of fitted values, log-likelihoods, and ME-modeled covariate values). This will disable many convenience functions that are otherwise available for fitted geostan models, such as the extraction of residuals, fitted values, and spatial trends, WAIC, and spatial diagnostics, and ME diagnostics; many quantities of interest, such as fitted values and spatial trends, can still be calculated manually using given parameter estimates. The "slim" option is designed for data-intensive routines, such as regression with raster data, Monte Carlo studies, and measurement error models. For more control over which parameters are kept or dropped, use the drop argument instead of slim.

drop — Provide a vector of character strings to specify the names of any parameters that you do not want MCMC samples for. Dropping parameters in this way can improve sampling speed and reduce memory usage. The following parameter vectors can potentially be dropped from CAR models:

fitted The N-length vector of fitted values

log_lambda_mu Linear predictor inside the CAR model (for Poisson and binomial models)

alpha_re Vector of 'random effects'/varying intercepts.

x_true N-length vector of 'latent'/modeled covariate values created for measurement error (ME) models.

If `slim = TRUE`, then `drop` will be ignored.

`pars` Optional; specify any additional parameters you'd like stored from the Stan model.

`control` A named list of parameters to control the sampler's behavior. See `stan` for details.

`quiet` Controls (most) automatic printing to the console. By default, any prior distributions that have not been assigned by the user are printed to the console. If `quiet = TRUE`, these will not be printed. Using `quiet = TRUE` will also force `refresh = 0`.

`...` Other arguments passed to `sampling`.

Details

CAR models are discussed in Cressie and Wikle (2011, p. 184-88), Cressie (2015, Ch. 6-7), and Haining and Li (2020, p. 249-51). It is often used for areal or lattice data.

Details for the Stan code for this implementation of the CAR model can be found in Donegan (2021) and the geostan vignette 'Custom spatial models with Rstan and geostan'.

For outcome variable y and N-by-N connectivity matrix C, a standard spatial CAR model may be written as

$$y = \mu + \rho C(y - \mu) + \epsilon$$

where ρ is a spatial dependence or autocorrelation parameter. The models accounts for autocorrelated errors in the regression.

The model is defined by its covariance matrix. The general scheme for the CAR model is as follows:

$$y \sim Gauss(\mu, (I - \rho C)^{-1} M),$$

where I is the identity matrix, ρ is a spatial dependence parameter, C is a spatial connectivity matrix, and M is a diagonal matrix of variance terms. The diagonal of M contains a scale parameter τ multiplied by a vector of weights (often set to be proportional to the inverse of the number of neighbors assigned to each site).

The covariance matrix of the CAR model contains two parameters: ρ (`car_rho`) which controls the kind (positive or negative) and degree of spatial autocorrelation, and the scale parameter τ. The range of permissible values for ρ depends on the specification of $\boldsymbol{C}$ and $\boldsymbol{M}$; for specification options, see prep_car_data and Cressie and Wikle (2011, pp. 184-188) or Donegan (2021).

Further details of the models and results depend on the `family` argument, as well as on the particular CAR specification chosen (from prep_car_data).

Auto-Normal:

When `family = auto_gaussian()` (the default), the CAR model is applied directly to the data as follows:

$$y \sim Gauss(\mu, (I - \rho C)^{-1} M),$$

where μ is the mean vector (with intercept, covariates, etc.), C is a spatial connectivity matrix, and M is a known diagonal matrix containing the conditional variances τ_i^2. C and M are provided by prep_car_data.

The auto-Gaussian model contains an implicit spatial trend (i.e. autocorrelation) component ϕ which can be calculated as follows (Cressie 2015, p. 564):

$$\phi = \rho C(y - \mu).$$

This term can be extracted from a fitted auto-Gaussian model using the spatial method.

When applied to a fitted auto-Gaussian model, the residuals.geostan_fit method returns 'de-trended' residuals R by default. That is,

$$R = y - \mu - \rho C(y - \mu).$$

To obtain "raw" residuals ($y - \mu$), use `residuals(fit, detrend = FALSE)`. Similarly, the fitted values obtained from the fitted.geostan_fit will include the spatial trend term by default.

Poisson:

For `family = poisson()`, the model is specified as:

$$y \sim Poisson(e^{O+\lambda})$$

$$\lambda \sim Gauss(\mu, (I - \rho C)^{-1} \boldsymbol{M}).$$

If the raw outcome consists of a rate $\frac{y}{p}$ with observed counts y and denominator p (often this will be the size of the population at risk), then the offset term $O = log(p)$ is the log of the denominator.

The same model can also be described or specified such that ϕ has a mean of zero:

$$y \sim Poisson(e^{O+\mu+\phi})$$

$$\phi \sim Gauss(0, (I - \rho C)^{-1} \boldsymbol{M}).$$

This is the zero-mean parameterization (ZMP) of the CAR model; although the non-ZMP is typically better for MCMC sampling, use of the ZMP can greatly improve MCMC sampling *when the data is sparse*. Use `zmp = TRUE` in `stan_car` to apply this specification. (See the geostan vignette on 'custom spatial models' for full details on implementation of the ZMP.)

For all CAR Poisson models, the spatial method returns the (zero-mean) parameter vector ϕ. When `zmp = FALSE` (the default), phi is obtained by subtraction: $\phi = \lambda - \mu$.

In the Poisson CAR model, ϕ contains a latent spatial trend as well as additional variation around it: $\phi_i = \rho \sum_{i=1}^{n} c_{ij}\phi_j + \epsilon_i$, where $\epsilon_i \sim Gauss(0, \tau_i^2)$. If for some reason you would like to extract the smoother latent/implicit spatial trend from ϕ, you can do so by calculating (following Cressie 2015, p. 564):

$$\rho C \phi.$$

Binomial:

For `family = binomial()`, the model is specified as:

$$y \sim Binomial(N, \lambda)$$

$$logit(\lambda) \sim Gauss(\mu, (I - \rho C)^{-1}\boldsymbol{M}).$$

where outcome data y are counts, N is the number of trials, λ is the 'success' rate, and μ contains the intercept and possibly covariates. Note that the model formula should be structured as: `cbind(sucesses, failures) ~ x`, such that `trials = successes + failures`.

As is also the case for the Poisson model, ϕ contains a latent spatial trend as well as additional variation around it. If you would like to extract the latent/implicit spatial trend from ϕ, you can do so by calculating:

$$\rho C \phi.$$

The zero-mean parameterization (ZMP) of the CAR model can also be applied here (see the Poisson model for details); ZMP provides an equivalent model specification that can improve MCMC sampling when data is sparse.

Additional functionality:

The CAR models can also incorporate spatially-lagged covariates, measurement/sampling error in covariates (particularly when using small area survey estimates as covariates), missing outcome data, and censored outcomes (such as arise when a disease surveillance system suppresses data for privacy reasons). For details on these options, please see the Details section in the documentation for stan_glm.

Value

An object of class class `geostan_fit` (a list) containing:

summary Summaries of the main parameters of interest; a data frame.

diagnostic Residual spatial autocorrelation as measured by the Moran coefficient.

stanfit an object of class `stanfit` returned by `rstan::stan`

data a data frame containing the model data

family the user-provided or default `family` argument used to fit the model

formula The model formula provided by the user (not including CAR component)

slx The `slx` formula

re A list containing `re`, the varying intercepts (`re`) formula if provided, and `Data` a data frame with columns `id`, the grouping variable, and `idx`, the index values assigned to each group.

priors Prior specifications.

x_center If covariates are centered internally (`centerx = TRUE`), then `x_center` is a numeric vector of the values on which covariates were centered.

spatial A data frame with the name of the spatial component parameter (either "phi" or, for auto Gaussian models, "trend") and method ("CAR")

ME A list indicating if the object contains an ME model; if so, the user-provided ME list is also stored here.

C Spatial connectivity matrix (in sparse matrix format).

Author(s)

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Source

Besag, Julian (1974). Spatial interaction and the statistical analysis of lattice systems. *Journal of the Royal Statistical Society* B36.2: 192–225.

Cressie, Noel (2015 (1993)). *Statistics for Spatial Data*. Wiley Classics, Revised Edition.

Cressie, Noel and Wikle, Christopher (2011). *Statistics for Spatio-Temporal Data*. Wiley.

Donegan, Connor (2021). Building spatial conditional autoregressive (CAR) models in the Stan programming language. *OSF Preprints*. doi:10.31219/osf.io/3ey65.

Haining, Robert and Li, Guangquan (2020). *Modelling Spatial and Spatial-Temporal Data: A Bayesian Approach*. CRC Press.

Examples

```
##
## model mortality risk
##

# simple spatial model for log rates

data(georgia)
C <- shape2mat(georgia, style = "B")
cars <- prep_car_data(C)

# MCMC specs: set for purpose of demo speed
iter = 500
chains = 2

fit <- stan_car(log(rate.male) ~ 1, data = georgia,
          car_parts = cars, iter = iter, chains = chains)

# model diagnostics
sp_diag(fit, georgia)

# A more appropriate model for mortality rates:
# hierarchical spatial Poisson model
fit <- stan_car(deaths.male ~ offset(log(pop.at.risk.male)),
                car_parts = cars,
                data = georgia,
                family = poisson(),
                iter = iter,
                chains = chains)

# model diagnostics
sp_diag(fit, georgia)

# county mortality rates (estimates)
eta = fitted(fit)

# spatial trend component
phi = spatial(fit)
```

```
##
## Distance-based weights matrix:
##   the 'DCAR' model
##

library(sf)
A <- shape2mat(georgia, "B")
D <- sf::st_distance(sf::st_centroid(georgia))
D <- D * A
dcars <- prep_car_data(D, "DCAR", k = 1)

Dfit <- stan_car(deaths.male ~ offset(log(pop.at.risk.male)),
                 data = georgia,
                 car = dcars,
                 family = poisson(),
                 iter = iter,
                 chains = chains)

waic(Dfit); waic(fit)
```

---

stan_esf *Spatial filtering*

Description

Fit a spatial regression model using eigenvector spatial filtering (ESF).

Usage

```
stan_esf(
  formula,
  slx,
  re,
  data,
  C,
  EV = make_EV(C, nsa = nsa, threshold = threshold),
  nsa = FALSE,
  threshold = 0.25,
  family = gaussian(),
  prior = NULL,
  ME = NULL,
  centerx = FALSE,
  censor_point,
  prior_only = FALSE,
  chains = 4,
  iter = 2000,
```

```
  refresh = 500,
  keep_all = FALSE,
  slim = FALSE,
  drop = NULL,
  pars = NULL,
  control = NULL,
  quiet = FALSE,
  ...
)
```

Arguments

formula	A model formula, following the R formula syntax. Binomial models are specified by setting the left hand side of the equation to a data frame of successes and failures, as in cbind(successes, failures) ~ x.
slx	Formula to specify any spatially-lagged covariates. As in, ~ x1 + x2 (the intercept term will be removed internally). When setting priors for beta, remember to include priors for any SLX terms.
re	To include a varying intercept (or "random effects") term, alpha_re, specify the grouping variable here using formula syntax, as in ~ ID. Then, alpha_re is a vector of parameters added to the linear predictor of the model, and: alpha_re ~ N(0, alpha_tau) alpha_tau ~ Student_t(d.f., location, scale).
data	A data.frame or an object coercible to a data frame by as.data.frame containing the model data.
C	Spatial connectivity matrix. This will be used to calculate eigenvectors if EV is not provided by the user. See shape2mat. Use of row-normalization (as in 'shape2mat(shape, 'W') is not recommended for creating EV. Matrix C will also be used ('as is') to create any user-specified slx terms.
EV	A matrix of eigenvectors from any (transformed) connectivity matrix, presumably spatial or network-based (see make_EV). If EV is provided, still also provide a spatial weights matrix C for other purposes; threshold and nsa are ignored for user provided EV.
nsa	Include eigenvectors representing negative spatial autocorrelation? Defaults to nsa = FALSE. This is ignored if EV is provided.
threshold	Eigenvectors with standardized Moran coefficient values below this threshold value will be excluded from the candidate set of eigenvectors, EV. This defaults to threshold = 0.25, and is ignored if EV is provided.
family	The likelihood function for the outcome variable. Current options are family = gaussian(), student_t() and poisson(link = "log"), and binomial(link = "logit").
prior	A named list of parameters for prior distributions (see priors): **intercept** The intercept is assigned a Gaussian prior distribution (see normal.

beta Regression coefficients are assigned Gaussian prior distributions. Variables must follow their order of appearance in the model `formula`. Note that if you also use `slx` terms (spatially lagged covariates), and you use custom priors for `beta`, then you have to provide priors for the slx terms. Since slx terms are *prepended* to the design matrix, the prior for the slx term will be listed first.

sigma For `family = gaussian()` and `family = student_t()` models, the scale parameter, `sigma`, is assigned a (half-) Student's t prior distribution. The half-Student's t prior for `sigma` is constrained to be positive.

nu `nu` is the degrees of freedom parameter in the Student's t likelihood (only used when `family = student_t()`). `nu` is assigned a gamma prior distribution. The default prior is `prior = list(nu = gamma2(alpha = 3, beta = 0.2))`.

tau The scale parameter for random effects, or varying intercepts, terms. This scale parameter, `tau`, is assigned a half-Student's t prior. To set this, use, e.g., `prior = list(tau = student_t(df = 20, location = 0, scale = 20))`.

beta_ev The eigenvector coefficients are assigned the horseshoe prior (Piironen and Vehtari, 2017), parameterized by `global_scale` (to control overall prior sparsity), plus the degrees of freedom and scale of a Student's t model for any large coefficients (see `priors`). To allow the spatial filter to account for a greater amount of spatial autocorrelation (i.e., if you find the residuals contain spatial autocorrelation), increase the global scale parameter (to a maximum of `global_scale = 1`).

`ME` To model observational uncertainty (i.e. measurement or sampling error) in any or all of the covariates, provide a list of data as constructed by the `prep_me_data` function.

`centerx` To center predictors on their mean values, use `centerx = TRUE`. If the ME argument is used, the modeled covariate (i.e., latent variable), rather than the raw observations, will be centered. When using the ME argument, this is the recommended method for centering the covariates.

`censor_point` Integer value indicating the maximum censored value; this argument is for modeling censored (suppressed) outcome data, typically disease case counts or deaths. For example, the US Centers for Disease Control and Prevention censors (does not report) death counts that are nine or fewer, so if you're using CDC WONDER mortality data you could provide `censor_point = 9`.

`prior_only` Draw samples from the prior distributions of parameters only.

`chains` Number of MCMC chains to estimate. Default `chains = 4`.

`iter` Number of samples per chain. Default `iter = 2000`.

`refresh` Stan will print the progress of the sampler every `refresh` number of samples. Defaults to `500`; set `refresh=0` to silence this.

`keep_all` If `keep_all = TRUE` then samples for all parameters in the Stan model will be kept; this is necessary if you want to do model comparison with Bayes factors and the `bridgesampling` package.

`slim` If `slim = TRUE`, then the Stan model will not collect the most memory-intensive parameters (including n-length vectors of fitted values, log-likelihoods, and ME-modeled covariate values). This will disable many convenience functions that

are otherwise available for fitted geostan models, such as the extraction of residuals, fitted values, and spatial trends, WAIC, and spatial diagnostics, and ME diagnostics; many quantities of interest, such as fitted values and spatial trends, can still be calculated manually using given parameter estimates. The "slim" option is useful for data-intensive routines, such as regression with raster data, Monte Carlo studies, and measurement error models. For more control over which parameters are kept or dropped, use the drop argument instead of slim.

drop — Provide a vector of character strings to specify the names of any parameters that you do not want MCMC samples for. Dropping parameters in this way can improve sampling speed and reduce memory usage. The following parameter vectors can potentially be dropped from ESF models:

fitted The N-length vector of fitted values

alpha_re Vector of 'random effects'/varying intercepts.

x_true N-length vector of 'latent'/modeled covariate values created for measurement error (ME) models.

esf The N-length eigenvector spatial filter.

beta_ev The vector of coefficients for the eigenvectors.

If slim = TRUE, then drop will be ignored.

pars — Optional; specify any additional parameters you'd like stored from the Stan model.

control — A named list of parameters to control the sampler's behavior. See stan for details.

quiet — By default, any prior distributions that have not been assigned by the user are printed to the console. If quiet = TRUE, these will not be printed.

... — Other arguments passed to sampling.

Details

Eigenvector spatial filtering (ESF) is a method for spatial regression analysis. ESF is extensively covered in Griffith et al. (2019). This function implements the methodology introduced in Donegan et al. (2020), which uses Piironen and Vehtari's (2017) regularized horseshoe prior.

By adding a spatial filter to a regression model, spatial autocorrelation patterns are shifted from the residuals to the spatial filter. ESF models take the spectral decomposition of a transformed spatial connectivity matrix, C. The resulting eigenvectors, E, are mutually orthogonal and uncorrelated map patterns (at various scales, 'local' to 'regional' to 'global'). The spatial filter equals $E\beta_E$ where β_E is a vector of coefficients.

ESF decomposes the data into a global mean, α, global patterns contributed by covariates $X\beta$, spatial trends $E\beta_E$, and residual variation. Thus, for family=gaussian(),

$$y \sim Gauss(\alpha + X * \beta + E\beta_E, \sigma).$$

An ESF component can be incorporated into the linear predictor of any generalized linear model. For example, using stan_esf with family = poisson() and adding a 'random effects' term for each spatial unit (via the re argument) will produce a model that resembles the BYM model (combining spatially structured and spatially-unstructured components).

The spatial.geostan_fit method will return $E\beta_E$.

The model can also be extended to the space-time domain; see shape2mat to specify a space-time connectivity matrix.

The coefficients β_E are assigned the regularized horseshoe prior (Piironen and Vehtari, 2017), resulting in a relatively sparse model specification. In addition, numerous eigenvectors are automatically dropped because they represent trace amounts of spatial autocorrelation (this is controlled by the `threshold` argument). By default, `stan_esf` will drop all eigenvectors representing negative spatial autocorrelation patterns. You can change this behavior using the `nsa` argument.

Additional functionality:

The ESF models can also incorporate spatially-lagged covariates, measurement/sampling error in covariates (particularly when using small area survey estimates as covariates), missing outcome data, and censored outcomes (such as arise when a disease surveillance system suppresses data for privacy reasons). For details on these options, please see the Details section in the documentation for stan_glm.

Value

An object of class class `geostan_fit` (a list) containing:

summary Summaries of the main parameters of interest; a data frame

diagnostic Residual spatial autocorrelation as measured by the Moran coefficient.

data a data frame containing the model data

EV A matrix of eigenvectors created with `w` and `geostan::make_EV`

C The spatial weights matrix used to construct EV

family the user-provided or default `family` argument used to fit the model

formula The model formula provided by the user (not including ESF component)

slx The `slx` formula

re A list containing `re`, the random effects (varying intercepts) formula if provided, and `data` a data frame with columns `id`, the grouping variable, and `idx`, the index values assigned to each group.

priors Prior specifications.

x_center If covariates are centered internally (`centerx = TRUE`), then `x_center` is a numeric vector of the values on which covariates were centered.

ME The `ME` data list, if one was provided by the user for measurement error models.

spatial A data frame with the name of the spatial component parameter ("esf") and method ("ESF")

stanfit an object of class `stanfit` returned by `rstan::stan`

Author(s)

Connor Donegan, <connor.donegan@gmail.com>

Source

Chun, Y., D. A. Griffith, M. Lee and P. Sinha (2016). Eigenvector selection with stepwise regression techniques to construct eigenvector spatial filters. *Journal of Geographical Systems*, 18(1), 67-85. doi:10.1007/s1010901502253.

Dray, S., P. Legendre & P. R. Peres-Neto (2006). Spatial modelling: a comprehensive framework for principal coordinate analysis of neighbour matrices (PCNM). *Ecological Modeling*, 196(3-4), 483-493.

Donegan, C., Y. Chun and A. E. Hughes (2020). Bayesian estimation of spatial filters with Moran's Eigenvectors and hierarchical shrinkage priors. *Spatial Statistics*. doi:10.1016/j.spasta.2020.100450 (open access: doi:10.31219/osf.io/fah3z).

Griffith, Daniel A., and P. R. Peres-Neto (2006). Spatial modeling in ecology: the flexibility of eigenfunction spatial analyses. *Ecology* 87(10), 2603-2613.

Griffith, D., and Y. Chun (2014). Spatial autocorrelation and spatial filtering, Handbook of Regional Science. Fischer, MM and Nijkamp, P. eds.

Griffith, D., Chun, Y. and Li, B. (2019). *Spatial Regression Analysis Using Eigenvector Spatial Filtering*. Elsevier.

Piironen, J and A. Vehtari (2017). Sparsity information and regularization in the horseshoe and other shrinkage priors. In *Electronic Journal of Statistics*, 11(2):5018-5051.

Examples

```
data(sentencing)
# spatial weights matrix with binary coding scheme
C <- shape2mat(sentencing, style = "B", quiet = TRUE)

# expected number of sentences
log_e <- log(sentencing$expected_sents)

# fit spatial Poisson model with ESF + unstructured 'random effects'
fit.esf <- stan_esf(sents ~ offset(log_e),
                    re = ~ name,
                    family = poisson(),
                    data = sentencing,
                    C = C,
                    chains = 2, iter = 800) # for speed only

# spatial diagnostics
sp_diag(fit.esf, sentencing)

# plot marginal posterior distributions of beta_ev (eigenvector coefficients)
plot(fit.esf, pars = "beta_ev")

# calculate log-standardized incidence ratios (SIR)
#  # SIR = observed/exected number of cases
# in this case, prison sentences
library(ggplot2)
library(sf)
f <- fitted(fit.esf, rates = FALSE)$mean
SSR <-  f / sentencing$expected_sents
```

```
log.SSR <- log( SSR, base = 2 )

# map the log-SSRs
 ggplot(sentencing) +
   geom_sf(aes(fill = log.SSR)) +
   scale_fill_gradient2(
    midpoint = 0,
    name = NULL,
    breaks = seq(-3, 3, by = 0.5)
  ) +
   labs(title = "Log-Standardized Sentencing Ratios",
    subtitle = "log( Fitted/Expected ), base 2"
 ) +
   theme_void()
```

---

stan_glm *Generalized linear models*

Description

Fit a generalized linear model.

Usage

```
stan_glm(
  formula,
  slx,
  re,
  data,
  C,
  family = gaussian(),
  prior = NULL,
  ME = NULL,
  centerx = FALSE,
  prior_only = FALSE,
  censor_point,
  chains = 4,
  iter = 2000,
  refresh = 1000,
  keep_all = FALSE,
  slim = FALSE,
  drop = NULL,
  pars = NULL,
  control = NULL,
  quiet = FALSE,
  ...
)
```

Arguments

formula	A model formula, following the R formula syntax. Binomial models are specified by setting the left hand side of the equation to a data frame of successes and failures, as in `cbind(successes, failures) ~ x`.
slx	Formula to specify any spatially-lagged covariates. As in, `~ x1 + x2` (the intercept term will be removed internally). When setting priors for `beta`, remember to include priors for any SLX terms.

re	To include a varying intercept (or "random effects") term, `alpha_re`, specify the grouping variable here using formula syntax, as in `~ ID`. Then, `alpha_re` is a vector of parameters added to the linear predictor of the model, and:
	
	`alpha_re ~ N(0, alpha_tau)`
	`alpha_tau ~ Student_t(d.f., location, scale).`

data	A `data.frame` or an object coercible to a data frame by `as.data.frame` containing the model data.
C	Spatial connectivity matrix which will be used to calculate residual spatial autocorrelation as well as any user specified `slx` terms. See `shape2mat`.
family	The likelihood function for the outcome variable. Current options are `poisson(link = "log")`, `binomial(link = "logit")`, `student_t()`, and the default `gaussian()`.
prior	A named list of parameters for prior distributions (see `priors`): **intercept** The intercept is assigned a Gaussian prior distribution (see `normal`. **beta** Regression coefficients are assigned Gaussian prior distributions. Variables must follow their order of appearance in the model `formula`. Note that if you also use `slx` terms (spatially lagged covariates), and you use custom priors for `beta`, then you have to provide priors for the slx terms. Since slx terms are *prepended* to the design matrix, the prior for the slx term will be listed first. **sigma** For `family = gaussian()` and `family = student_t()` models, the scale parameter, `sigma`, is assigned a (half-) Student's t prior distribution. The half-Student's t prior for `sigma` is constrained to be positive. **nu** `nu` is the degrees of freedom parameter in the Student's t likelihood (only used when `family = student_t()`). `nu` is assigned a gamma prior distribution. The default prior is `prior = list(nu = gamma2(alpha = 3, beta = 0.2))`. **tau** The scale parameter for random effects, or varying intercepts, terms. This scale parameter, `tau`, is assigned a half-Student's t prior. To set this, use, e.g., `prior = list(tau = student_t(df = 20, location = 0, scale = 20))`.
ME	To model observational uncertainty (i.e. measurement or sampling error) in any or all of the covariates, provide a list of data as constructed by the `prep_me_data` function.
centerx	To center predictors on their mean values, use `centerx = TRUE`. If the ME argument is used, the modeled covariate (i.e., latent variable), rather than the raw observations, will be centered. When using the ME argument, this is the recommended method for centering the covariates.

`prior_only` Draw samples from the prior distributions of parameters only.

`censor_point` Integer value indicating the maximum censored value; this argument is for modeling censored (suppressed) outcome data, typically disease case counts or deaths. For example, the US Centers for Disease Control and Prevention censors (does not report) death counts that are nine or fewer, so if you're using CDC WONDER mortality data you could provide `censor_point = 9`.

`chains` Number of MCMC chains to estimate.

`iter` Number of samples per chain.

`refresh` Stan will print the progress of the sampler every `refresh` number of samples; set `refresh=0` to silence this.

`keep_all` If `keep_all = TRUE` then samples for all parameters in the Stan model will be kept; this is required if you want to do model comparison with Bayes factors and the `bridgesampling` package.

`slim` If `slim = TRUE`, then the Stan model will not collect the most memory-intensive parameters (including n-length vectors of fitted values, log-likelihoods, and ME-modeled covariate values). This will disable many convenience functions that are otherwise available for fitted `geostan` models, such as the extraction of residuals, fitted values, and spatial trends, WAIC, and spatial diagnostics, and ME diagnostics; many quantities of interest, such as fitted values and spatial trends, can still be calculated manually using given parameter estimates. The "slim" option is designed for data-intensive routines, such as regression with raster data, Monte Carlo studies, and measurement error models. For more control over which parameters are kept or dropped, use the `drop` argument instead of `slim`.

`drop` Provide a vector of character strings to specify the names of any parameters that you do not want MCMC samples for. Dropping parameters in this way can improve sampling speed and reduce memory usage. The following parameter vectors can potentially be dropped from GLM models:

'fitted' The N-length vector of fitted values

'alpha_re' Vector of 'random effects'/varying intercepts.

'x_true' N-length vector of 'latent'/modeled covariate values created for measurement error (ME) models.

Using `drop = c('fitted', 'alpha_re', 'x_true')` is equivalent to `slim = TRUE`. If `slim = TRUE`, then `drop` will be ignored.

`pars` Specify any additional parameters you'd like stored from the Stan model.

`control` A named list of parameters to control the sampler's behavior. See stan for details.

`quiet` Controls (most) automatic printing to the console. By default, any prior distributions that have not been assigned by the user are printed to the console. If `quiet = TRUE`, these will not be printed. Using `quiet = TRUE` will also force `refresh = 0`.

`...` Other arguments passed to sampling.

Details

Fit a generalized linear model using the R formula interface. Default prior distributions are designed to be weakly informative relative to the data. Much of the functionality intended for spatial models, such as the ability to add spatially lagged covariates and observational error models, are also available in `stan_glm`. All of `geostan`'s spatial models build on top of the same Stan code used in `stan_glm`.

Spatially lagged covariates (SLX):

The `slx` argument is a convenience function for including SLX terms. For example,

$$y = WX\gamma + X\beta + \epsilon$$

where W is a row-standardized spatial weights matrix (see `shape2mat`), WX is the mean neighboring value of X, and γ is a coefficient vector. This specifies a regression with spatially lagged covariates. SLX terms can specified by providing a formula to the `slx` argument:

```
stan_glm(y ~ x1 + x2, slx = ~ x1 + x2, \...),
```

which is a shortcut for

```
stan_glm(y ~ I(W \%*\% x1) + I(W \%*\% x2) + x1 + x2, \...)
```

SLX terms will always be *prepended* to the design matrix, as above, which is important to know when setting prior distributions for regression coefficients.

For measurement error (ME) models, the SLX argument is the only way to include spatially lagged covariates since the SLX term needs to be re-calculated on each iteration of the MCMC algorithm.

Measurement error (ME) models:

The ME models are designed for surveys with spatial sampling designs, such as the American Community Survey (ACS) estimates. For a tutorial, see `vignette("spatial-me-models", package = "geostan")`.

Given estimates x, their standard errors s, and the target quantity of interest (i.e., the unknown true value) z, the ME models have one of the the following two specifications, depending on the user input. If a spatial CAR model is specified, then:

$$x \sim Gauss(z, s^2)$$
$$z \sim Gauss(\mu_z, \Sigma_z)$$
$$\Sigma_z = (I - \rho C)^{-1} M$$
$$\mu_z \sim Gauss(0, 100)$$
$$\tau_z \sim Student(10, 0, 40), \tau > 0$$
$$\rho_z \sim uniform(l, u)$$

where Σ specifies the covariance matrix of a spatial conditional autoregressive (CAR) model with scale parameter τ (on the diagonal of M), autocorrelation parameter ρ, and l, u are the lower and upper bounds that ρ is permitted to take (which is determined by the extreme eigenvalues of the spatial connectivity matrix C). M contains the inverse of the row sums of C on its diagonal multiplied by τ (following the "WCAR" specification).

For non-spatial ME models, the following is used instead:

$$x \sim Gauss(z, s^2)$$

$$z \sim student_t(\nu_z, \mu_z, \sigma_z)$$

$$\nu_z \sim gamma(3, 0.2)$$

$$\mu_z \sim Gauss(0, 100)$$

$$\sigma_z \sim student(10, 0, 40)$$

For strongly skewed variables, such as census tract poverty rates, it can be advantageous to apply a logit transformation to z before applying the CAR or Student-t prior model. When the `logit` argument is used, the first two lines of the model specification become:

$$x \sim Gauss(z, s^2)$$

$$logit(z) \sim Gauss(\mu_z, \Sigma_z)$$

and similarly for the Student t model:

$$x \sim Gauss(z, s^2)$$

$$logit(z) \sim student(\nu_z, \mu_z, \sigma_z)$$

Missing data:

For most geostan models, missing (NA) observations are allowed in the outcome variable. However, there cannot be any missing covariate data. Models that can handle missing data are: any Poisson or binomial model (GLM, SAR, CAR, ESF, ICAR), all GLMs and ESF models. The only models that cannot handle missing outcome data are the CAR and SAR models when the outcome is a continuous variable (auto-normal/Gaussian models).

When observations are missing, they will simply be ignored when calculating the likelihood in the MCMC sampling process (reflecting the absence of information). The estimated model parameters (including any covariates and spatial trend) will then be used to produce estimates or fitted values for the missing observations. The `fitted` and `posterior_predict` functions will work as normal in this case, and return values for all rows in your data.

Censored counts:

Vital statistics systems and disease surveillance programs typically suppress case counts when they are smaller than a specific threshold value. In such cases, the observation of a censored count is not the same as a missing value; instead, you are informed that the value is an integer somewhere between zero and the threshold value. For Poisson models (`family = poisson()`), you can use the `censor_point` argument to encode this information into your model.

Internally, `geostan` will keep the index values of each censored observation, and the index value of each of the fully observed outcome values. For all observed counts, the likelihood statement will be:

$$p(y_i|data, model) = poisson(y_i|\mu_i),$$

as usual, where μ_i may include whatever spatial terms are present in the model.

For each censored count, the likelihood statement will equal the cumulative Poisson distribution function for values zero through the censor point:

$$p(y_i|data, model) = \sum_{m=0}^{M} Poisson(m|\mu_i),$$

where M is the censor point and μ_i again is the fitted value for the i^{th} observation.

For example, the US Centers for Disease Control and Prevention's CDC WONDER database censors all death counts between 0 and 9. To model CDC WONDER mortality data, you could provide `censor_point = 9` and then the likelihood statement for censored counts would equal the summation of the Poisson probability mass function over each integer ranging from zero through 9 (inclusive), conditional on the fitted values (i.e., all model parameters). See Donegan (2021) for additional discussion, references, and Stan code.

Value

An object of class class `geostan_fit` (a list) containing:

summary Summaries of the main parameters of interest; a data frame

diagnostic Residual spatial autocorrelation as measured by the Moran coefficient.

stanfit an object of class `stanfit` returned by `rstan::stan`

data a data frame containing the model data

family the user-provided or default `family` argument used to fit the model

formula The model formula provided by the user (not including ESF component)

slx The `slx` formula

C The spatial weights matrix, if one was provided by the user.

re A list containing `re`, the random effects (varying intercepts) formula if provided, and `Data` a data frame with columns `id`, the grouping variable, and `idx`, the index values assigned to each group.

priors Prior specifications.

x_center If covariates are centered internally (`centerx = TRUE`), then `x_center` is a numeric vector of the values on which covariates were centered.

ME The `ME` data list, if one was provided by the user for measurement error models.

spatial NA, slot is maintained for use in `geostan_fit` methods.

Author(s)

Connor Donegan, <connor.donegan@gmail.com>

Source

Donegan, Connor and Chun, Yongwan and Griffith, Daniel A. (2021). Modeling community health with areal data: Bayesian inference with survey standard errors and spatial structure. *Int. J. Env. Res. and Public Health* 18 (13): 6856. DOI: 10.3390/ijerph18136856 Data and code: https://github.com/ConnorDonegan/survey-HBM.

Donegan, Connor (2021). Building spatial conditional autoregressive (CAR) models in the Stan programming language. *OSF Preprints*. doi:10.31219/osf.io/3ey65.

Examples

```
##
## Linear regression model
##

N = 100
x <- rnorm(N)
y <- .5 * x + rnorm(N)
dat <- cbind(y, x)

# no. of MCMC samples
iter = 700

# no. of MCMC chains
chains = 2

# fit model
#  (warnings for low ESS are expected in this example;
#   for analysis, use chains=4, and higher iter)
fit <- stan_glm(y ~ x, data = dat, iter = iter, chains = chains, quiet = TRUE)

# see results with MCMC diagnostics
print(fit)

##
## Custom prior distributions
##

prior_list <- list(
      intercept = normal(0, 1),
      beta = normal(0, 1),
      sigma = student_t(10, 0, 2)
)

fit2 <- stan_glm(y ~ x, data = dat, prior = prior_list, iter = iter,
                quiet = TRUE)

print(fit2)

# example prior for two covariates
pl <- list(beta = normal(c(0, 0),
                         c(1, 1))
           )

##
## Poisson model for count data
## with county 'random effects'
##

data(sentencing)

# denominator in standardized rate Y/E
```

```
# (observed count Y over expected count E)
# (use the log-denominator as the offest term)
sentencing$log_e <- log(sentencing$expected_sents)

# fit model
fit.pois <- stan_glm(sents ~ offset(log_e),
                     re = ~ name,
                     family = poisson(),
                     data = sentencing,
                     iter = 700,
                     chains = 2,
                     quiet = TRUE)

# Spatial autocorrelation/residual diagnostics
sp_diag(fit.pois, sentencing)

# summary of results with MCMC diagnostics
print(fit.pois)

# MCMC diagnostics from rstan methods
# MCMC diagnostics plot: Rhat values should all by very near 1
# rstan::stan_rhat(fit.pois$stanfit)
# effective sample size for all parameters and generated quantities
# (including residuals, predicted values, etc.)
# rstan::stan_ess(fit.pois$stanfit)
# or for a particular parameter
# rstan::stan_ess(fit.pois$stanfit, "alpha_re")

##
## Visualize the posterior predictive distribution
##

# plot observed values and model replicate values
yrep <- posterior_predict(fit.pois, S = 65)
y <- sentencing$sents
ltgray <- rgb(0.3, 0.3, 0.3, 0.5)

plot(density(yrep[1,]), col = ltgray,
     ylim = c(0, 0.014), xlim = c(0, 700),
     bty = 'L', xlab = NA, main = NA)

for (i in 2:nrow(yrep)) lines(density(yrep[i,]), col = ltgray)

lines(density(sentencing$sents), col = "darkred", lwd = 2)

legend("topright", legend = c('Y-observed', 'Y-replicate'),
       col = c('darkred', ltgray), lwd = c(1.5, 1.5))

# plot replicates of Y/E
E <- sentencing$expected_sents

# set plot margins
old_pars <- par(mar=c(2.5, 3.5, 1, 1))
```

```
# plot yrep
plot(density(yrep[1,] / E), col = ltgray,
    ylim = c(0, 0.9), xlim = c(0, 7),
    bty = 'L', xlab = NA, ylab = NA, main = NA)

for (i in 2:nrow(yrep)) lines(density(yrep[i,] / E), col = ltgray)

# overlay y
lines(density(sentencing$sents / E), col = "darkred", lwd = 2)

# legend, y-axis label
legend("topright", legend = c('Y-observed', 'Y-replicate'),
      col = c('darkred', ltgray), lwd = c(1.5, 1.5))

mtext(side = 2, text = "Density", line = 2.5)

# return margins to previous settings
par(old_pars)
```

---

stan_icar *Intrinsic autoregressive models*

Description

The intrinsic conditional auto-regressive (ICAR) model for spatial count data. Options include the BYM model, the BYM2 model, and a solo ICAR term.

Usage

```
stan_icar(
  formula,
  slx,
  re,
  data,
  C,
  family = poisson(),
  type = c("icar", "bym", "bym2"),
  scale_factor = NULL,
  prior = NULL,
  ME = NULL,
  centerx = FALSE,
  censor_point,
  prior_only = FALSE,
  chains = 4,
  iter = 2000,
  refresh = 500,
  keep_all = FALSE,
```

```
  slim = FALSE,
  drop = NULL,
  pars = NULL,
  control = NULL,
  quiet = FALSE,
  ...
)
```

Arguments

formula	A model formula, following the R formula syntax. Binomial models can be specified by setting the left hand side of the equation to a data frame of successes and failures, as in `cbind(successes, failures) ~ x`.
slx	Formula to specify any spatially-lagged covariates. As in, `~ x1 + x2` (the intercept term will be removed internally). When setting priors for `beta`, remember to include priors for any SLX terms.

re	To include a varying intercept (or "random effects") term, `alpha_re`, specify the grouping variable here using formula syntax, as in `~ ID`. Then, `alpha_re` is a vector of parameters added to the linear predictor of the model, and:
	`alpha_re ~ N(0, alpha_tau)`
	`alpha_tau ~ Student_t(d.f., location, scale).`
	Before using this term, read the `Details` section and the `type` argument. Specifically, if you use `type = bym`, then an observational-level `re` term is already included in the model. (Similar for `type = bym2`.)

data	A `data.frame` or an object coercible to a data frame by `as.data.frame` containing the model data.
C	Spatial connectivity matrix which will be used to construct an edge list for the ICAR model, and to calculate residual spatial autocorrelation as well as any user specified `slx` terms. It will automatically be row-standardized before calculating `slx` terms (matching the ICAR model). `C` must be a binary symmetric `n x n` matrix.
family	The likelihood function for the outcome variable. Current options are `binomial(link = "logit")` and `poisson(link = "log")`.
type	Defaults to "icar" (partial pooling of neighboring observations through parameter `phi`); specify "bym" to add a second parameter vector `theta` to perform partial pooling across all observations; specify "bym2" for the innovation introduced by Riebler et al. (2016). See `Details` for more information.
scale_factor	For the BYM2 model, optional. If missing, this will be set to a vector of ones. See `Details`.
prior	A named list of parameters for prior distributions (see `priors`): **intercept** The intercept is assigned a Gaussian prior distribution (see `normal`. **beta** Regression coefficients are assigned Gaussian prior distributions. Variables must follow their order of appearance in the model `formula`. Note that if you also use `slx` terms (spatially lagged covariates), and you use custom priors for `beta`, then you have to provide priors for the slx terms.

Since slx terms are *prepended* to the design matrix, the prior for the slx term will be listed first.

sigma For `family = gaussian()` and `family = student_t()` models, the scale parameter, `sigma`, is assigned a (half-) Student's t prior distribution. The half-Student's t prior for `sigma` is constrained to be positive.

nu `nu` is the degrees of freedom parameter in the Student's t likelihood (only used when `family = student_t()`). `nu` is assigned a gamma prior distribution. The default prior is `prior = list(nu = gamma2(alpha = 3, beta = 0.2))`.

tau The scale parameter for random effects, or varying intercepts, terms. This scale parameter, `tau`, is assigned a half-Student's t prior. To set this, use, e.g., `prior = list(tau = student_t(df = 20, location = 0, scale = 20))`.

`ME` To model observational uncertainty (i.e. measurement or sampling error) in any or all of the covariates, provide a list of data as constructed by the `prep_me_data` function.

`centerx` To center predictors on their mean values, use `centerx = TRUE`. If the ME argument is used, the modeled covariate (i.e., latent variable), rather than the raw observations, will be centered. When using the ME argument, this is the recommended method for centering the covariates.

`censor_point` Integer value indicating the maximum censored value; this argument is for modeling censored (suppressed) outcome data, typically disease case counts or deaths. For example, the US Centers for Disease Control and Prevention censors (does not report) death counts that are nine or fewer, so if you're using CDC WONDER mortality data you could provide `censor_point = 9`.

`prior_only` Draw samples from the prior distributions of parameters only.

`chains` Number of MCMC chains to estimate.

`iter` Number of samples per chain. .

`refresh` Stan will print the progress of the sampler every `refresh` number of samples; set `refresh=0` to silence this.

`keep_all` If `keep_all = TRUE` then samples for all parameters in the Stan model will be kept; this is necessary if you want to do model comparison with Bayes factors and the `bridgesampling` package.

`slim` If `slim = TRUE`, then the Stan model will not collect the most memory-intensive parameters (including n-length vectors of fitted values, log-likelihoods, and ME-modeled covariate values). This will disable many convenience functions that are otherwise available for fitted `geostan` models, such as the extraction of residuals, fitted values, and spatial trends, WAIC, and spatial diagnostics, and ME diagnostics; many quantities of interest, such as fitted values and spatial trends, can still be calculated manually using given parameter estimates. The "slim" option is designed for data-intensive routines, such as regression with raster data, Monte Carlo studies, and measurement error models. For more control over which parameters are kept or dropped, use the `drop` argument instead of `slim`.

`drop` Provide a vector of character strings to specify the names of any parameters that you do not want MCMC samples for. Dropping parameters in this way can

improve sampling speed and reduce memory usage. The following parameter vectors can potentially be dropped from ICAR models:

fitted The N-length vector of fitted values

alpha_re Vector of 'random effects'/varying intercepts.

x_true N-length vector of 'latent'/modeled covariate values created for measurement error (ME) models.

phi The N-length vector of spatially-autocorrelated parameters (with the ICAR prior).

theta The N-length vector of spatially unstructured parameters ('random effects'), for the BYM and BYM2 models.

If `slim = TRUE`, then `drop` will be ignored.

`pars` Optional; specify any additional parameters you'd like stored from the Stan model.

`control` A named list of parameters to control the sampler's behavior. See `stan` for details.

`quiet` Controls (most) automatic printing to the console. By default, any prior distributions that have not been assigned by the user are printed to the console. If `quiet = TRUE`, these will not be printed. Using `quiet = TRUE` will also force `refresh = 0`.

`...` Other arguments passed to sampling.

Details

The intrinsic conditional autoregressive (ICAR) model for spatial data was introduced by Besag et al. (1991). The Stan code for the ICAR component of the model and the BYM2 option is from Morris et al. (2019) with adjustments to enable non-binary weights and disconnected graph structures (see Freni-Sterrantino (2018) and Donegan (2021)).

The exact specification depends on the `type` argument.

ICAR:

For Poisson models for count data, y, the basic model specification (`type = "icar"`) is:

$$y\ Poisson(e^{O+\mu+\phi})$$

$$\phi \sim ICAR(\tau_s)$$

$$\tau_s \sim Gauss(0, 1)$$

where μ contains an intercept and potentially covariates. The spatial trend phi has a mean of zero and a single scale parameter τ_s (which user's will see printed as the parameter named `spatial_scale`).

The ICAR prior model is a CAR model that has a spatial autocorrelation parameter ρ equal to 1 (see stan_car). Thus the ICAR prior places high probability on a very smooth spatially (or temporally) varying mean. This is rarely sufficient to model the amount of variation present in social and health data. For this reason, the BYM model is typically employed.

BYM:

Often, an observational-level random effect term, `theta`, is added to capture (heterogeneous or unstructured) deviations from $\mu + \phi$. The combined term is referred to as a convolution term: $convolution = \phi + \theta$.

This is known as the BYM model (Besag et al. 1991), and can be specified using `type = "bym"`: $y \sim Poisson(e^{O+\mu+\phi+\theta})$

$$\phi \sim ICAR(\tau_s)$$

$$\theta \sim Gaussian(0, \tau_{ns})$$

$$\tau_s \sim Gaussian(0, 1)$$

$$\tau_{ns} \sim Gaussian(0, 1)$$

The model is named after Besag, York, and Mollié (1991).

BYM2:

Riebler et al. (2016) introduce a variation on the BYM model (`type = "bym2"`). This specification combines ϕ and θ using a mixing parameter ρ that controls the proportion of the variation that is attributable to the spatially autocorrelated term ϕ rather than the spatially unstructured term θ. The terms share a single scale parameter τ:

$$convolution = [sqrt(\rho * S) * \tilde{\phi} + sqrt(1 - \rho)\tilde{\theta}] * \tau$$

$$\tilde{\phi} \sim Gaussian(0, 1)$$

$$\tilde{\theta} \sim Gaussian(0, 1)$$

$$\tau \sim Gaussian(0, 1)$$

The terms $\tilde{\phi}$, $\tilde{\theta}$ are standard normal deviates, ρ is restricted to values between zero and one, and S is the 'scale_factor' (a constant term provided by the user). By default, the 'scale_factor' is equal to one, so that it does nothing. Riebler et al. (2016) argue that the interpretation or meaning of the scale of the ICAR model depends on the graph structure of the connectivity matrix C. This implies that the same prior distribution assigned to τ_s will differ in its implications if C is changed; in other words, the priors are not transportable across models, and models that use the same nominal prior actually have different priors assigned to τ_s.

Borrowing `R` code from Morris (2017) and following Freni-Sterrantino et al. (2018), the following `R` code can be used to create the 'scale_factor' S for the BYM2 model (note, this requires the INLA R package), given a spatial adjacency matrix, C:

```
## create a list of data for stan_icar
icar.data <- geostan::prep_icar_data(C)
## calculate scale_factor for each of k connected group of nodes
k <- icar.data$k
scale_factor <- vector(mode = "numeric", length = k)
for (j in 1:k) {
  g.idx <- which(icar.data$comp_id == j)
  if (length(g.idx) == 1) {
       scale_factor[j] <- 1
       next
    }
```

```
  Cg <- C[g.idx, g.idx]
  scale_factor[j] <- scale_c(Cg)
}
```

This code adjusts for 'islands' or areas with zero neighbors, and it also handles disconnected graph structures (see Donegan and Morris 2021). Following Freni-Sterrantino (2018), disconnected components of the graph structure are given their own intercept term; however, this value is added to ϕ automatically inside the Stan model. Therefore, the user never needs to make any adjustments for this term. (To avoid complications from using a disconnected graph structure, you can apply a proper CAR model instead of the ICAR: stan_car).

Note, the code above requires the `scale_c` function; it has package dependencies that are not included in `geostan`. To use `scale_c`, you have to load the following `R` function:

```
#' compute scaling factor for adjacency matrix, accounting for differences in spatial connectivity
#'
#' @param C connectivity matrix
#'
#' @details
#'
#' Requires the following packages:
#'
#' library(Matrix)
#' library(INLA);
#' library(spdep)
#' library(igraph)
#'
#' @source  Morris (2017)
#'
scale_c <- function(C) {
 geometric_mean <- function(x) exp(mean(log(x)))
 N = dim(C)[1]
 Q =  Diagonal(N, rowSums(C)) - C
 Q_pert = Q + Diagonal(N) * max(diag(Q)) * sqrt(.Machine$double.eps)
 Q_inv = inla.qinv(Q_pert, constr=list(A = matrix(1,1,N),e=0))
 scaling_factor <- geometric_mean(Matrix::diag(Q_inv))
 return(scaling_factor)
}
```

Additional functionality:

The ICAR models can also incorporate spatially-lagged covariates, measurement/sampling error in covariates (particularly when using small area survey estimates as covariates), missing outcome data, and censored outcomes (such as arise when a disease surveillance system suppresses data for privacy reasons). For details on these options, please see the Details section in the documentation for stan_glm.

Value

An object of class class `geostan_fit` (a list) containing:

summary Summaries of the main parameters of interest; a data frame

diagnostic Residual spatial autocorrelation as measured by the Moran coefficient.

stanfit an object of class `stanfit` returned by `rstan::stan`

data a data frame containing the model data

edges The edge list representing all unique sets of neighbors and the weight attached to each pair (i.e., their corresponding element in the connectivity matrix C

C Spatial connectivity matrix

family the user-provided or default `family` argument used to fit the model

formula The model formula provided by the user (not including ICAR component)

slx The `slx` formula

re A list with two name elements, `formula` and `Data`, containing the formula `re` and a data frame with columns `id` (the grouping variable) and `idx` (the index values assigned to each group).

priors Prior specifications.

x_center If covariates are centered internally (`centerx = TRUE`), then `x_center` is a numeric vector of the values on which covariates were centered.

spatial A data frame with the name of the spatial parameter (`"phi"` if `type = "icar"` else `"convolution"`) and method (`toupper(type)`).

Author(s)

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Source

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Morris, M., Wheeler-Martin, K., Simpson, D., Mooney, S. J., Gelman, A., & DiMaggio, C. (2019). Bayesian hierarchical spatial models: Implementing the Besag York Mollié model in stan. *Spatial and spatio-temporal epidemiology*, 31, 100301.

Riebler, A., Sorbye, S. H., Simpson, D., & Rue, H. (2016). An intuitive Bayesian spatial model for disease mapping that accounts for scaling. *Statistical Methods in Medical Research*, 25(4), 1145-1165.

See Also

shape2mat, stan_car, stan_esf, stan_glm, prep_icar_data

Examples

```
data(sentencing)
C <- shape2mat(sentencing, "B")
log_e <- log(sentencing$expected_sents)
fit.bym <- stan_icar(sents ~ offset(log_e),
                     family = poisson(),
                     data = sentencing,
                     type = "bym",
                     C = C,
                     chains = 2, iter = 800) # for speed only

# spatial diagnostics
sp_diag(fit.bym, sentencing)

# check effective sample size and convergence
library(rstan)
rstan::stan_ess(fit.bym$stanfit)
rstan::stan_rhat(fit.bym$stanfit)
```

---

stan_sar *Simultaneous autoregressive (SAR) models*

Description

Fit data to a simultaneous spatial autoregressive (SAR) model, or use the SAR model as the prior model for a parameter vector in a hierarchical model.

Usage

```
stan_sar(
  formula,
  slx,
  re,
  data,
  C,
  sar_parts = prep_sar_data(C, quiet = TRUE),
  family = auto_gaussian(),
  type = c("SEM", "SDEM", "SDLM", "SLM"),
  prior = NULL,
  ME = NULL,
  centerx = FALSE,
  prior_only = FALSE,
  censor_point,
```

```
  zmp,
  chains = 4,
  iter = 2000,
  refresh = 500,
  keep_all = FALSE,
  pars = NULL,
  slim = FALSE,
  drop = NULL,
  control = NULL,
  quiet = FALSE,
  ...
)
```

Arguments

formula	A model formula, following the R formula syntax. Binomial models can be specified by setting the left hand side of the equation to a data frame of successes and failures, as in cbind(successes, failures) ~ x.
slx	Formula to specify any spatially-lagged covariates. As in, ~ x1 + x2 (the intercept term will be removed internally). When setting priors for beta, remember to include priors for any SLX terms.
re	To include a varying intercept (or "random effects") term, alpha_re, specify the grouping variable here using formula syntax, as in ~ ID. Then, alpha_re is a vector of parameters added to the linear predictor of the model, and: alpha_re ~ N(0, alpha_tau) alpha_tau ~ Student_t(d.f., location, scale). With the SAR model, any alpha_re term should be at a *different* level or scale than the observations; that is, at a different scale than the autocorrelation structure of the SAR model itself.
data	A data.frame or an object coercible to a data frame by as.data.frame containing the model data.
C	Spatial connectivity matrix which will be used internally to create sar_parts (if sar_parts is missing); if the user provides an slx formula for the model, the required connectivity matrix will be taken from the sar_parts list. See shape2mat.
sar_parts	List of data constructed by prep_sar_data. If not provided, then C will automatically be passed to prep_sar_data to create sar_parts.
family	The likelihood function for the outcome variable. Current options are auto_gaussian(), binomial() (with logit link function) and poisson() (with log link function); if family = gaussian() is provided, it will automatically be converted to auto_gaussian().
type	Type of SAR model (character string): spatial error model ('SEM'), spatial Durbin error model ('SDEM'), spatial Durbin lag model ('SDLM'), or spatial lag model ('SLM'). see Details below.
prior	A named list of parameters for prior distributions (see priors): **intercept** The intercept is assigned a Gaussian prior distribution (see normal.

beta Regression coefficients are assigned Gaussian prior distributions. Variables must follow their order of appearance in the model `formula`. Note that if you also use `slx` terms (spatially lagged covariates), and you use custom priors for `beta`, then you have to provide priors for the slx terms. Since slx terms are *prepended* to the design matrix, the prior for the slx term will be listed first.

sar_scale Scale parameter for the SAR model, `sar_scale`. The scale is assigned a Student's t prior model (constrained to be positive).

sar_rho The spatial autocorrelation parameter in the SAR model, `rho`, is assigned a uniform prior distribution. By default, the prior will be uniform over all permissible values as determined by the eigenvalues of the spatial weights matrix. The range of permissible values for `rho` is printed to the console by `prep_sar_data`.

tau The scale parameter for any varying intercepts (a.k.a exchangeable random effects, or partial pooling) terms. This scale parameter, `tau`, is assigned a Student's t prior (constrained to be positive).

`ME` To model observational uncertainty in any or all of the covariates (i.e. measurement or sampling error), provide a list of data constructed by the `prep_me_data` function.

`centerx` To center predictors on their mean values, use `centerx = TRUE`. This increases sampling speed. If the ME argument is used, the modeled covariate (i.e., the latent variable), rather than the raw observations, will be centered.

`prior_only` Logical value; if `TRUE`, draw samples only from the prior distributions of parameters.

`censor_point` Integer value indicating the maximum censored value; this argument is for modeling censored (suppressed) outcome data, typically disease case counts or deaths which are left-censored to protect confidentiality when case counts are very low.

`zmp` Use zero-mean parameterization for the SAR model? Only relevant for Poisson and binomial outcome models (i.e., hierarchical models). See details below; this can sometimes improve MCMC sampling when the data is sparse, but does not alter the model specification.

`chains` Number of MCMC chains to use.

`iter` Number of MCMC samples per chain.

`refresh` Stan will print the progress of the sampler every `refresh` number of samples. Set `refresh=0` to silence this.

`keep_all` If `keep_all = TRUE` then samples for all parameters in the Stan model will be kept; this is necessary if you want to do model comparison with Bayes factors using the `bridgesampling` package.

`pars` Specify any additional parameters you'd like stored from the Stan model.

`slim` If `slim = TRUE`, then the Stan model will not save the most memory-intensive parameters (including n-length vectors of fitted values, other 'random effects', and ME-modeled covariate values). This will disable some convenience functions that are otherwise available for fitted `geostan` models, such as the extraction of residuals, fitted values, and spatial trends, spatial diagnostics, and ME diagnostics. The "slim" option is designed for data-intensive routines, such as regression with raster data, Monte Carlo studies, and measurement error models.

`drop` Provide a vector of character strings to specify the names of any parameters that you do not want MCMC samples for. Dropping parameters in this way can improve sampling speed and reduce memory usage. The following parameter vectors can potentially be dropped from SAR models:

fitted The N-length vector of fitted values

alpha_re Vector of 'random effects'/varying intercepts.

log_lambda_mu Linear predictor inside the SAR model (for Poisson and binomial models)

x_true N-length vector of 'latent'/modeled covariate values created for measurement error (ME) models.

Using `drop = c('fitted', 'alpha_re', 'x_true', 'log_lambda_mu')` is equivalent to `slim = TRUE`. Note that if `slim = TRUE`, then `drop` will be ignored—so only use one or the other.

`control` A named list of parameters to control the sampler's behavior. See `stan` for details.

`quiet` Controls (most) automatic printing to the console. By default, any prior distributions that have not been assigned by the user are printed to the console; if `quiet = TRUE`, these will not be printed. Using `quiet = TRUE` will also force `refresh = 0`.

`...` Other arguments passed to `sampling`.

Details

Discussions of SAR models may be found in Cliff and Ord (1981), Cressie (2015, Ch. 6), LeSage and Pace (2009), and LeSage (2014). The Stan implementation draws from Donegan (2021). It is a multivariate normal distribution with covariance matrix of $\Sigma = \sigma^2(I - \rho C)^{-1}(I - \rho C')^{-1}$..

There are two SAR specification options which are commonly known as the spatial error ('SEM') and the spatial lag ('SLM') models. When the spatial-lags of all covariates are included in the linear predictor (as in $\mu = \alpha + X\beta + WX\gamma$), then the model is referred to as a spatial Durbin model; depending on the model type, it becomes a spatial Durbin error model ('SDEM') or a spatial Durbin lag model ('SDLM'). To control which covariates are introduced in spatial-lag form, use the `slx` argument together with 'type = SEM' or 'type = SLM'.

Auto-normal: spatial error:

The spatial error specification ('SEM') is

$$y = \mu + (I - \rho C)^{-1}\epsilon$$

$$\epsilon \sim Gauss(0, \sigma^2)$$

where C is the spatial connectivity matrix, I is the n-by-n identity matrix, and ρ is a spatial autocorrelation parameter. In words, the errors of the regression equation are spatially autocorrelated. The expected value for the SEM is the usual μ: the intercept plus `X*beta` and any other terms added to the linear predictor.

Re-arranging terms, the model can also be written as follows:

$$y = \mu + \rho C(y - \mu) + \epsilon$$

which shows more intuitively the implicit spatial trend component, $\phi = \rho C(y - \mu)$. This term ϕ can be extracted from a fitted auto-Gaussian/auto-normal model using the spatial method.

When applied to a fitted auto-Gaussian model, the residuals.geostan_fit method returns 'de-trended' residuals R by default. That is,

$$R = y - \mu - \rho C(y - \mu).$$

To obtain "raw" residuals ($y - \mu$), use `residuals(fit, detrend = FALSE)`. Similarly, the fitted values obtained from the fitted.geostan_fit will include the spatial trend term by default.

Auto-normal: spatial lag:

The second SAR specification type is the 'spatial lag of y' ('SLM'). This model describes a diffusion or contagion process:

$$y = \rho C y + \mu + \epsilon$$
$$\epsilon \sim Gauss(0, \sigma^2)$$

This is very attractive for modeling actual contagion or diffusion processes (or static snapshots of such processes). The model does not allow for the usual interpretation of regression coefficients as marginal effects. To interpret SLM results, use impacts.

Note that the expected value of the SLM is equal to $(I - \rho C)^{-1}\mu$.

The spatial method returns the vector

$$\phi = \rho C y,$$

the spatial lag of y.

The residuals.geostan_fit method returns 'de-trended' residuals R by default:

$$R = y - \rho C y - \mu,$$

where μ contains the intercept and any covariates (and possibly other terms).

Similarly, the fitted values obtained from the fitted.geostan_fit will include the spatial trend $\rho C y$ by default to equal

$$\rho C y + \mu.$$

For now at least, the SLM/SDLM option is only supported for auto-normal models (as opposed to hierarchical Poisson and binomial models).

Poisson:

For `family = poisson()`, the model is specified as:

$$y \sim Poisson(e^{O+\lambda})$$
$$\lambda \sim Gauss(\mu, \Sigma)$$
$$\Sigma = \sigma^2(I - \rho C)^{-1}(I - \rho C')^{-1}$$

where O is a constant/offset term and e^{λ} is a rate parameter.

If the raw outcome consists of a rate $\frac{y}{p}$ with observed counts y and denominator p (often this will be the size of the population at risk), then the offset term should be the log of the denominator: $O = log(p)$.

This same model can be written (equivalently) as:

$$y \sim Poisson(e^{O+\mu+\phi})$$

$$\phi \sim Gauss(0, \Sigma)$$

This second version is referred to here as the zero-mean parameterization (ZMP), since the SAR model is forced to have mean of zero. Although the non-ZMP is typically better for MCMC sampling, use of the ZMP can greatly improve MCMC sampling *when the data is sparse*. Use `zmp = TRUE` in `stan_sar` to apply this specification. (See the geostan vignette on 'custom spatial models' for full details on implementation of the ZMP.)

For Poisson models, the spatial method returns the (zero-mean) parameter vector ϕ. When `zmp = FALSE` (the default), ϕ is obtained by subtraction: $\phi = \lambda - \mu$.

In the Poisson SAR model, ϕ contains a latent (smooth) spatial trend as well as additional variation around it (this is merely a verbal description of the CAR model). If you would like to extract the latent/implicit spatial trend from ϕ, you can do so by calculating:

$$\rho C \phi.$$

Binomial:

For `family = binomial()`, the model is specified as:

$$y \sim Binomial(N, \lambda)$$

$$logit(\lambda) \sim Gauss(\mu, \Sigma)$$

$$\Sigma = \sigma^2 (I - \rho C)^{-1} (I - \rho C')^{-1},$$

where outcome data y are counts, N is the number of trials, and λ is the rate of 'success'. Note that the model formula should be structured as: `cbind(sucesses, failures) ~ 1` (for an intercept-only model), such that `trials = successes + failures`.

For fitted Binomial models, the `spatial` method will return the parameter vector `phi`, equivalent to:

$$\phi = logit(\lambda) - \mu.$$

The zero-mean parameterization (ZMP) of the SAR model can also be applied here (see the Poisson model for details); ZMP provides an equivalent model specification that can improve MCMC sampling when data is sparse.

As is also the case for the Poisson model, ϕ contains a latent spatial trend as well as additional variation around it. If you would like to extract the latent/implicit spatial trend from ϕ, you can do so by calculating:

$$\rho C \phi.$$

Additional functionality:

The SAR models can also incorporate spatially-lagged covariates, measurement/sampling error in covariates (particularly when using small area survey estimates as covariates), missing outcome data (for Poisson and binomial models), and censored outcomes (such as arise when a disease surveillance system suppresses data for privacy reasons). For details on these options, please see the Details section in the documentation for stan_glm.

Value

An object of class class `geostan_fit` (a list) containing:

summary Summaries of the main parameters of interest; a data frame.

diagnostic Residual spatial autocorrelation as measured by the Moran coefficient.

stanfit an object of class `stanfit` returned by `rstan::stan`

data a data frame containing the model data

family the user-provided or default `family` argument used to fit the model

formula The model formula provided by the user (not including CAR component)

slx The `slx` formula

re A list containing `re`, the varying intercepts (`re`) formula if provided, and `Data` a data frame with columns `id`, the grouping variable, and `idx`, the index values assigned to each group.

priors Prior specifications.

x_center If covariates are centered internally (`centerx = TRUE`), then `x_center` is a numeric vector of the values on which covariates were centered.

spatial A data frame with the name of the spatial component parameter (either "phi" or, for auto Gaussian models, "trend") and method ("SAR")

ME A list indicating if the object contains an ME model; if so, the user-provided ME list is also stored here.

C Spatial weights matrix (in sparse matrix format).

sar_type Type of SAR model: 'SEM', 'SDEM', 'SDLM', or 'SLM'.

Author(s)

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Source

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LeSage, James, & Pace, Robert Kelley (2009). *Introduction to Spatial Econometrics*. Chapman and Hall/CRC.

Examples

```
##
## simulate SAR data on a regular grid
##

sars <- prep_sar_data2(row = 10, col = 10, quiet = TRUE)
w <- sars$W

# draw x
x <- sim_sar(w = w, rho = 0.5)

# draw y = mu + rho*W*(y - mu) + epsilon
# beta = 0.5, rho = 0.5
y <- sim_sar(w = w, rho = .5, mu = 0.5 * x)
dat <- data.frame(y = y, x = x)

##
## fit SEM
##

fit_sem <- stan_sar(y ~ x, data = dat, sar = sars,
                    chains = 1, iter = 800)
print(fit_sem)

##
## data for SDEM
##

# mu = x*beta + wx*gamma; beta=1, gamma=-0.25
x <- sim_sar(w = w, rho = 0.5)
mu <- 1 * x - 0.25 * (w %*% x)[,1]
y <- sim_sar(w = w, rho = .5, mu = mu)
# or for SDLM:
# y <- sim_sar(w = w, rho = 0.5, mu = mu, type = "SLM")
dat <- data.frame(y=y, x=x)

#
## fit models
##

# SDEM
# y = mu + rho*W*(y - mu) + epsilon
# mu = beta*x + gamma*Wx
fit_sdem <- stan_sar(y ~ x, data = dat,
                    sar_parts = sars, type = "SDEM",
                    iter = 800, chains = 1,
                    quiet = TRUE)

# SDLM
# y = rho*Wy + beta*x + gamma*Wx + epsilon
fit_sdlm <- stan_sar(y ~ x, data = dat,
                    sar_parts = sars,
```

```
                    type = "SDLM",
                    iter = 800,
                    chains = 1,
                    quiet = TRUE)

# compare by DIC
dic(fit_sdem)
dic(fit_sdlm)


##
## Modeling mortality rates
##

# simple spatial regression
data(georgia)
W <- shape2mat(georgia, style = "W")

fit <- stan_sar(log(rate.male) ~ 1,
                C = W,
                data = georgia,
                iter = 900
                )

# view fitted vs. observed, etc.
sp_diag(fit, georgia)

# A more appropriate model for count data:
# hierarchical spatial poisson model
fit2 <- stan_sar(deaths.male ~ offset(log(pop.at.risk.male)),
                C = W,
                data = georgia,
                family = poisson(),
                chains = 1, # for ex. speed only
                iter = 900,
                quiet = TRUE
                 )

# view fitted vs. observed, etc.
sp_diag(fit2, georgia)
```

`waic` *Model comparison*

Description

Deviance Information Criteria (DIC) and Widely Application Information Criteria (WAIC) for model comparison.

Usage

```
waic(object, pointwise = FALSE, digits = 2)

dic(object, digits = 1)
```

Arguments

object	A fitted geostan model
pointwise	Logical (defaults to FALSE), should a vector of values for each observation be returned?
digits	Round results to this many digits.

Details

WAIC (widely applicable information criteria) and DIC (deviance information criteria) are used for model comparison. They are based on theories of out-of-sample predictive accuracy. The DIC is implemented with penalty term defined as 1/2 times the posterior variance of the deviance (Spiegelhatler et al. 2014).

The limitations of these methods include that DIC is less robust than WAIC and that WAIC is not strictly valid for autocorrelated data (viz. geostan's spatial models).

For both DIC and WAIC, lower values indicate better models.

Value

WAIC returns a vector of length 3 with the WAIC value, a penalty term which measures the effective number of parameters estimated by the model Eff_pars, and log predictive density Lpd. If pointwise = TRUE, results are returned in a data.frame.

DIC returns a vector of length 2: the DIC value and the penalty term (which is part of the DIC calculation).

Source

D. Spiegelhatler, N. G. Best, B. P. Carlin and G. Linde (2014) The Deviance Information Criterion: 12 Years on. J. Royal Statistical Society Series B: Stat Methodology. 76(3): 485-493.

Watanabe, S. (2010). Asymptotic equivalence of Bayes cross validation and widely application information criterion in singular learning theory. Journal of Machine Learning Research 11, 3571-3594.

Examples

```
data(georgia)

fit <- stan_glm(log(rate.male) ~ 1, data = georgia,
                iter=600, chains = 2, quiet = TRUE)
fit2 <- stan_glm(log(rate.male) ~ log(income), data = georgia,
                centerx = TRUE, iter=600, chains = 2, quiet = TRUE)

dic(fit)
```

```
dic(fit2)

waic(fit)
waic(fit2)
```

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