Package: SDALGCP2 (via r-universe)

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Title Discrete Log-Gaussian Cox Processes for Aggregated Disease Counts

Version 0.1.1

Description Fits a spatially discrete approximation to a log-Gaussian Cox process model for spatially aggregated disease count data, estimated by Monte Carlo Maximum Likelihood as in Christensen (2004) <doi:10.1198/106186004X2525> and Johnson, Diggle and Giorgi (2019) <doi:10.1002/sim.8339>. Performance-critical steps (aggregated correlation assembly, Metropolis-adjusted Langevin algorithm (MALA) sampling, the Monte Carlo likelihood, and the Kronecker-structured space-time likelihood) are implemented in C++ via 'RcppArmadillo'. Provides a one-line, 'glm'-like interface and statistical extensions including a nugget term, general 'Matern' smoothness, raster and misaligned covariates, restricted spatial regression, importance-sampling diagnostics and re-anchored Monte Carlo maximum likelihood (MCML).

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coef_plot *Coefficient plot of fixed effects (and sigma^2) with confidence intervals*

Description

Coefficient plot of fixed effects (and sigma^2) with confidence intervals

Usage

```
coef_plot(object, level = 0.95, intercept = FALSE)
```

Arguments

object	a fitted "SDALGCP2" object.
level	confidence level.
intercept	logical; include the intercept.

Value

a ggplot object.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
coef_plot(fit)
```

confint.SDALGCP2 *Wald confidence intervals for an SDALGCP2 fit*

Description

Wald confidence intervals for an SDALGCP2 fit

Usage

```
## S3 method for class 'SDALGCP2'
confint(object, parm, level = 0.95, ...)
```

Arguments

object	an object of class "SDALGCP2".
parm	parameters to report (names or indices); default all.
level	confidence level.
...	unused.

Value

a matrix of lower/upper confidence limits.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
confint(fit)
```

---

control_mcmc *MCMC control settings for the MALA sampler*

Description

MCMC control settings for the MALA sampler

Usage

```
control_mcmc(
  n.sim = 10000,
  burnin = 2000,
  thin = 8,
  h = NULL,
  c1.h = 0.01,
  c2.h = 1e-04
)
```

Arguments

n.sim	total number of iterations.
burnin	burn-in iterations to discard.
thin	thinning interval; (n.sim - burnin) must be a multiple.
h	initial Langevin step size; if missing, 1.65 / d^(1/6) is used.
c1.h, c2.h	step-size adaptation constants.

Value

a named list consumed by `laplace_sampling` / the fit.

Examples

```
## 1000 retained draws (5000 iterations, 2000 burn-in, thin every 3)
ctrl <- control_mcmc(n.sim = 5000, burnin = 2000, thin = 3)
str(ctrl)
```

`exceedance` *Exceedance probabilities P(risk > threshold)*

Description

Exceedance probabilities P(risk > threshold)

Usage

```
exceedance(object, thresholds, which = c("adjusted_rr", "relative_risk"))
```

Arguments

`object`	an `"SDALGCP2_pred"` object from `predict.SDALGCP2`.
`thresholds`	numeric vector of thresholds.
`which`	which quantity: `"adjusted_rr"` (the covariate-adjusted relative risk $\exp(S)$, default) or `"relative_risk"` (the relative risk $\exp(d'\beta + S)$).

Value

a matrix of exceedance probabilities (locations x thresholds).

See Also

`map_exceedance` to map them.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
pr <- predict(fit, type = "discrete")
## P(adjusted relative risk > 1) and > 1.5 for every region
ex <- exceedance(pr, thresholds = c(1, 1.5), which = "adjusted_rr")
head(ex)
```

`laplace_sampling` *Sample the latent field [S | Y] (Poisson, non-nested) via C++ MALA*

Description

Draws posterior samples of the latent Gaussian field for the Poisson, non-nested case. The Laplace mode (Newton step) and the adaptive Metropolis- adjusted Langevin (MALA) loop both run in C++ for speed, with a fixed-seed path for reproducibility.

Usage

```
laplace_sampling(mu, Sigma, y, units.m, control.mcmc)
```

Arguments

`mu`	prior mean vector.
`Sigma`	prior covariance matrix.
`y`	count vector.
`units.m`	offset vector.
`control.mcmc`	list from `control_mcmc`.

Value

list with `samples` (kept x n matrix) and `h` (step sizes).

Examples

```
## sample [S | Y] for a tiny 10-unit Poisson example
set.seed(1)
n <- 10
D <- as.matrix(dist(cbind(runif(n), runif(n))))
Sigma <- 0.4 * exp(-D / 0.3)
mu <- rep(log(2), n); m <- rep(100, n)
y <- rpois(n, m * exp(mu + as.numeric(t(chol(Sigma)) %*% rnorm(n))))
out <- laplace_sampling(mu, Sigma, y, m, control_mcmc(n.sim = 2000, burnin = 500, thin = 3))
dim(out$samples)     # (retained draws) x n
```

`liver` *Primary biliary cirrhosis incidence in North East England*

Description

A real aggregated disease-count dataset: incident primary biliary cirrhosis (a chronic liver disease) cases by Lower-layer Super Output Area (LSOA) in the Newcastle and Gateshead area of North East England, with population and area deprivation covariates. This is the case study of Johnson et al. (2019) and a realistic test bed for the spatial model: `cases ~ deprivation + offset(log(pop))`.

Usage

```
liver
```

Format

An `sf` object of 545 LSOA polygons (British National Grid, EPSG:27700) with columns:

lsoa LSOA 2004 census code.

cases observed incident case count in the LSOA.

pop population at risk (the offset; use `offset(log(pop))`).

IMD Index of Multiple Deprivation score (higher = more deprived).

Income income-deprivation score.

Employment employment-deprivation score.

geometry the LSOA polygon.

Source

Johnson, O., Diggle, P. and Giorgi, E. (2019), "A spatially discrete approximation to log-Gaussian Cox processes for modelling aggregated disease count data", *Statistics in Medicine*, 38(24), 4871-4884. doi:10.1002/sim.8339. Population and area-deprivation covariates are from the 2004 English indices of deprivation (Lower-layer Super Output Area level). See `data-raw/liver.R` in the package sources.

See Also

`sdalgcp_data` for a small simulated example.

Examples

```
data(liver)
summary(liver$cases)
plot(liver["IMD"])
```

`map_exceedance` *Map exceedance probabilities P(risk > threshold)*

Description

Map exceedance probabilities P(risk > threshold)

Usage

```
map_exceedance(
  x,
  threshold = 1,
  which = c("adjusted_rr", "relative_risk"),
  bound = NULL,
  ...
)
```

Arguments

`x`	an `"SDALGCP2_pred"` object.
`threshold`	a single relative-risk threshold.
`which`	`"adjusted_rr"` (covariate-adjusted, default) or `"relative_risk"`.
`bound`	optional `sf` boundary (continuous only).
`...`	unused.

Value

a `ggplot` object.

See Also

`exceedance` for the underlying probabilities.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
pr <- predict(fit, type = "discrete")
map_exceedance(pr, threshold = 1.5)           # P(adjusted RR > 1.5)
```

mc_diagnostics *Importance-sampling diagnostics for an MCML fit*

Description

The MCML estimate reweights latent samples drawn at the anchor towards the optimum. When the optimum is far from the anchor the weights become uneven and the estimate unreliable. This reports the effective sample size of the importance weights at the maximiser and a Monte Carlo standard error for the maximised log-likelihood, $\mathrm{SE} \approx \sqrt{1/\mathrm{ESS} - 1/B}$.

Usage

```
mc_diagnostics(object, warn_frac = 0.1)
```

Arguments

object	a fitted "SDALGCP2" object.
warn_frac	warn if the ESS falls below this fraction of B.

Value

invisibly, a list with B, ESS, ESS_frac and se_loglik.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
d <- mc_diagnostics(fit)
d$ESS_frac          # importance-sampling ESS as a fraction of the draws
```

mcml_fit *Monte Carlo maximum likelihood estimation for the spatial SDALGCP*

Description

Vectorised, Cholesky-based MCML estimation. Simulates the latent field at an anchor, then profiles the importance-sampling MCML objective over the supplied phi grid.

Usage

```
mcml_fit(
  formula,
  data,
  corr,
  par0 = NULL,
  control.mcmc = NULL,
  phi_method = c("grid", "direct"),
  nugget = FALSE,
  reanchor = 0L,
  reanchor_tol = 0.01,
  messages = FALSE
)
```

Arguments

formula	model formula, optionally with an `offset()` term.
data	data frame holding the model variables.
corr	list with R (N x N x n_phi correlation array) and phi, e.g. from `precompute_corr`.
par0	optional starting values `c(beta, sigma2, phi)`; if NULL they are derived from a Poisson GLM.
control.mcmc	list from `control_mcmc` (defaults if NULL).
phi_method	`"grid"` (profile over the corr phi grid, default) or `"direct"` (optimise phi continuously; exponential/Matern kernel).
nugget	logical; if TRUE (requires `phi_method = "direct"`) add a relative nugget, fitting covariance $\sigma^2(R(\phi) + \nu I)$.
reanchor	number of re-anchoring passes (re-simulate the latent field at the current optimum and refit) to raise the importance-sampling ESS.
reanchor_tol	relative-change tolerance for stopping the re-anchoring loop.
messages	logical; print optimiser progress.

Value

an object of class `"SDALGCP2"` (estimates, covariance, profile, latent samples and metadata).

See Also

`SDALGCP2` (the end-to-end wrapper), `precompute_corr`

Examples

```
data(sdalgcp_data)
df  <- sf::st_drop_geometry(sdalgcp_data)
pts <- sda_points(sdalgcp_data, delta = 1.2, method = 3)
cc  <- precompute_corr(pts, phi = seq(2, 8, length.out = 6))
fit <- mcml_fit(cases ~ x1 + offset(log(pop)), df, cc,
```

```
                control.mcmc = control_mcmc(n.sim = 2000, burnin = 500, thin = 5))
summary(fit)
```

`model_check` *Posterior-predictive model checking for an SDALGCP2 fit*

Description

Compares observed counts with fitted Poisson means, returns Pearson residuals, and tests them for residual spatial autocorrelation with Moran's I. A non-significant Moran's I indicates the spatial random effect has absorbed the spatial structure.

Usage

```
model_check(object, pred = NULL, nsim = 999, plot = TRUE)
```

Arguments

`object`	a fitted `"SDALGCP2"` object.
`pred`	a discrete prediction from `predict(object, "discrete")`; if `NULL` one is computed with the fitting MCMC controls.
`nsim`	permutations for the Moran's I p-value.
`plot`	logical; draw the observed-vs-fitted scatter.

Value

invisibly, a list with `fitted`, `residuals` and `moran`.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
chk <- model_check(fit, plot = FALSE)
chk$moran            # residual Moran's I and its permutation p-value
```

phi_profile *Profile likelihood and confidence interval for the spatial scale phi*

Description

Spline-smoothed profile deviance for `phi`, with the `coverage`-level confidence interval where the deviance crosses the chi-squared cutoff.

Usage

```
phi_profile(object, coverage = 0.95, plot = TRUE)
```

Arguments

`object`	a fitted `"SDALGCP2"` object.
`coverage`	confidence level.
`plot`	logical; draw the deviance curve.

Value

invisibly, a list with the interval and the smoothed profile; a `ggplot` is drawn when `plot = TRUE`.

Examples

```
data(sdalgcp_data)
## profile phi on a grid (scale = "grid") so there is a deviance curve to draw
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(scale = "grid", n_sim = 2000,
                                         burnin = 500, thin = 5, reanchor = 0))
phi_profile(fit)
```

plot.sdalgcp *Map an sdalgcp fit*

Description

Predicts and maps a chosen quantity. Works for spatial fits (discrete or continuous) and spatio-temporal fits (select a `time`).

Usage

```
## S3 method for class 'sdalgcp'
plot(
  x,
  what = c("relative_risk", "adjusted_rr", "relative_risk_se", "adjusted_rr_se",
    "exceedance"),
  type = c("discrete", "continuous"),
  time = NULL,
  threshold = 1,
  which = c("adjusted_rr", "relative_risk"),
  cellsize = NULL,
  sampler = c("mcmc", "laplace"),
  ...
)
```

Arguments

x	an "sdalgcp" fit.
what	one of "relative_risk" (relative risk, default), "adjusted_rr" (covariate-adjusted relative risk), "relative_risk_se", "adjusted_rr_se" or "exceedance".
type	"discrete" (default) or "continuous" (spatial fits).
time	for spatio-temporal fits, the time to map (default: first; use NULL to facet all times).
threshold	threshold for what = "exceedance".
which	for exceedance: "adjusted_rr" (default) or "relative_risk".
cellsize	grid spacing for type = "continuous".
sampler	"mcmc" (default) or "laplace".
...	passed to the mapping layer.

Value

a ggplot object.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
plot(fit)                               # relative-risk map (predicts internally)
plot(fit, what = "exceedance", threshold = 1.5)
```

plot.SDALGCP2 *Plot an SDALGCP2 fit (the phi profile deviance)*

Description

Plot an SDALGCP2 fit (the phi profile deviance)

Usage

```
## S3 method for class 'SDALGCP2'
plot(x, ...)
```

Arguments

x	an "SDALGCP2" object.
...	passed to phi_profile.

Value

invisibly, the profile (see phi_profile).

Examples

```
data(sdalgcp_data)
fit <- SDALGCP2(cases ~ x1 + offset(log(pop)),
                sf::st_drop_geometry(sdalgcp_data), sdalgcp_data, delta = 1.2,
                control.mcmc = control_mcmc(n.sim = 2000, burnin = 500, thin = 5))
plot(fit)   # profile deviance for the spatial scale phi
```

plot.SDALGCP2_pred *Map a fitted SDALGCP2 prediction*

Description

Maps any of the four predicted quantities from predict.SDALGCP2 – the relative risk "relative_risk", the covariate-adjusted relative risk "adjusted_rr", or their standard errors "relative_risk_se"/"adjusted_rr_se" – for either discrete (choropleth) or continuous (raster) predictions.

Usage

```
## S3 method for class 'SDALGCP2_pred'
plot(
  x,
 variable = c("relative_risk", "adjusted_rr", "relative_risk_se", "adjusted_rr_se"),
  bound = NULL,
  midpoint = NULL,
  title = NULL,
  ...
)
```

Arguments

x	an object of class "SDALGCP2_pred".
variable	one of "relative_risk", "adjusted_rr", "relative_risk_se", "adjusted_rr_se".
bound	optional sf boundary; continuous surfaces are masked to it and its outline overlaid.
midpoint	optional value to centre a diverging colour scale (defaults to 1 for the relative-risk columns, none for the standard errors).
title	optional plot title.
...	unused.

Value

a ggplot object.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
pr <- predict(fit, type = "discrete")
plot(pr, variable = "relative_risk")          # choropleth of relative risk
plot(pr, variable = "adjusted_rr_se")         # its uncertainty
```

---

plot.SDALGCP2_ST_pred *Map a spatio-temporal prediction for one time*

Description

Maps a chosen quantity ("relative_risk", "adjusted_rr", "relative_risk_se", "adjusted_rr_se" or "exceedance") for a selected time slice of a spatio-temporal prediction.

Usage

```
## S3 method for class 'SDALGCP2_ST_pred'
plot(
  x,
  time = attr(x, "times")[1],
  what = c("relative_risk", "adjusted_rr", "relative_risk_se", "adjusted_rr_se",
    "exceedance"),
  threshold = 1,
  which = c("adjusted_rr", "relative_risk"),
  ...
)
```

Arguments

x	an "SDALGCP2_ST_pred" object from predict() on an "SDALGCP2_ST" fit.
time	the time to map (one of the fitted times); defaults to the first. Use NULL to facet all times.
what	one of "relative_risk", "adjusted_rr", "relative_risk_se", "adjusted_rr_se", "exceedance".
threshold	threshold for what = "exceedance".
which	for exceedance: "adjusted_rr" (default) or "relative_risk".
...	unused.

Value

a ggplot object.

Examples

```
data(sdalgcp_data)
times <- 1:3
panel <- do.call(rbind, lapply(times, function(t) {
  d <- sdalgcp_data; d$time <- t
  d$cases <- rpois(nrow(d), d$pop * exp(-6 + 0.6 * d$x1 + 0.1 * (t - 2)))
  d
}))
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = panel, time = "time",
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
pr <- predict(fit)
plot(pr, time = 2)                # one time slice
plot(pr, time = NULL)             # facet all times
plot(pr, what = "exceedance", threshold = 1.2, time = 3)
```

precompute_corr *Precompute aggregated region-level correlation matrices*

Description

Builds the $N \times N \times$ `length(phi)` array of region-level correlations used by the SDA-LGCP model, where

$$R(\phi)_{ij} = \sum_{k,l} w_{ik} w_{jl}\, C(\|x_{ik} - x_{jl}\|; \phi, \kappa)$$

(population-weighted) or the unweighted mean over candidate-point pairs. The heavy reduction runs in C++ (OpenMP-parallel over region pairs).

Usage

```
precompute_corr(points, phi, kappa = 0.5, weighted = NULL, nthreads = 0L)
```

Arguments

`points`	a list of length N; each element holds `$xy` (an $n_i \times 2$ matrix of candidate-point coordinates) and, when weighted, `$weight` (a length-n_i vector summing to 1). The `"weighted"` and `"my_shp"` attributes produced by the point-generation step are honoured and carried through.
`phi`	numeric vector of spatial scale parameters.
`kappa`	Matern smoothness; `0.5` (exponential, default), `1.5` or `2.5` use closed forms in C++.
`weighted`	logical; if `NULL` (default) it is taken from `attr(points, "weighted")`.
`nthreads`	number of OpenMP threads; `0` (default) uses the OpenMP runtime default.

Value

a list with `R` (the correlation array) and `phi`, carrying `weighted`, `my_shp` and `S_coord` attributes on `R`.

See Also

`sda_points`, `mcml_fit`

Examples

```
data(sdalgcp_data)
pts <- sda_points(sdalgcp_data, delta = 1.2, method = 3)
cc  <- precompute_corr(pts, phi = c(2, 4, 6))
dim(cc$R)            # N x N x length(phi)
```

`predict.sdalgcp` *Predict relative risk from an sdalgcp fit*

Description

Returns a prediction object carrying, for every location, the posterior mean and standard error of the relative risk `relative_risk` ($\exp(\eta) = \exp(d'\beta + S)$) and the covariate-adjusted relative risk `adjusted_rr` ($\exp(S)$). Map it with `plot()` and get hotspot probabilities with `exceedance`.

Usage

```
## S3 method for class 'sdalgcp'
predict(
  object,
  type = c("discrete", "continuous"),
  sampler = c("mcmc", "laplace"),
  cellsize = NULL,
  ...
)
```

Arguments

`object`	an `"sdalgcp"` fit.
`type`	`"discrete"` (region level, default) or `"continuous"` (a grid surface). Ignored for spatio-temporal fits.
`sampler`	`"mcmc"` (default) or `"laplace"`.
`cellsize`	grid spacing for `type = "continuous"`.
`...`	passed to the underlying predictor.

Value

for a spatial fit, an `sf` of class `"SDALGCP2_pred"` with `relative_risk`, `relative_risk_se`, `adjusted_rr` and `adjusted_rr_se` columns (polygons for `type = "discrete"`, grid points for `"continuous"`); for a spatio-temporal fit, an `"SDALGCP2_ST_pred"` object (see `predict.SDALGCP2_ST`).

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
pr <- predict(fit)            # discrete by default; an sf of relative risks
head(pr)
```

`predict.SDALGCP2` *Predict relative risk from a fitted SDALGCP2 model*

Description

Predict relative risk from a fitted SDALGCP2 model

Usage

```
## S3 method for class 'SDALGCP2'
predict(
  object,
  type = c("discrete", "continuous"),
  sampler = c("mcmc", "laplace"),
  cellsize = NULL,
  pred.loc = NULL,
  control.mcmc = NULL,
  ...
)
```

Arguments

`object`	an object of class `"SDALGCP2"` from `SDALGCP2` or `mcml_fit`.
`type`	`"discrete"` for region-level inference or `"continuous"` for a spatially continuous surface.
`sampler`	`"mcmc"` (MALA, default) or `"laplace"` (fast Gaussian approximation, no MCMC).
`cellsize`	grid spacing for continuous prediction (ignored if `pred.loc` supplied).
`pred.loc`	optional data frame of prediction coordinates (`x`, `y`) for continuous prediction.
`control.mcmc`	optional MCMC controls; defaults to those used at fitting.
`...`	unused.

Value

an `sf` (class `c("SDALGCP2_pred", "sf", "data.frame")`) with one row per location – polygons for `type = "discrete"`, grid-cell points for `type = "continuous"` – carrying the posterior mean and standard error of two relative-risk quantities:

`relative_risk`, `relative_risk_se` the relative risk $\exp(d'\beta + S)$ – the fitted risk relative to the offset baseline, combining the covariate effect and the residual spatial variation. This is the headline disease-mapping quantity.

`adjusted_rr`, `adjusted_rr_se` the covariate-adjusted relative risk $\exp(S)$ – the purely spatial relative risk that remains after holding the covariates fixed (the spatial signal the covariates do not explain).

The full posterior draws are retained as object attributes so that `exceedance` and `map_exceedance` can be computed for either quantity. Map a column with `plot.SDALGCP2_pred`.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))

## region-level (discrete) prediction: an sf you can map or st_write()
pr <- predict(fit, type = "discrete")
head(pr)                       # relative_risk / adjusted_rr (+ standard errors)
plot(pr, variable = "relative_risk")

## continuous surface on a grid
pr_c <- predict(fit, type = "continuous", cellsize = 1)
```

`predict.SDALGCP2_ST` *Discrete (region x time) prediction for a spatio-temporal fit*

Description

Draws the latent field at the fitted optimum and returns posterior mean and SD of the incidence relative risk $\exp(\mu + S)$ and covariate-adjusted relative risk $\exp(S)$ for every region and time.

Usage

```
## S3 method for class 'SDALGCP2_ST'
predict(object, control.mcmc = NULL, ...)
```

Arguments

`object`	an `"SDALGCP2_ST"` fit.
`control.mcmc`	optional MCMC controls (defaults to the fitting ones).
`...`	unused.

Value

a long `sf` of class `c("SDALGCP2_ST_pred", "sf", "data.frame")` with one row per region and time (ordered region-fastest within each time block) and columns `region`, `time`, `relative_risk`, `relative_risk_se` ($\exp(\mu+S)$), `adjusted_rr` and `adjusted_rr_se` ($\exp(S)$) – the same column names as the spatial `predict.SDALGCP2`. The posterior draws are kept in object attributes (for exceedance); map a time slice with `plot.SDALGCP2_ST_pred`.

Examples

```
data(sdalgcp_data)
## stack the spatial example into a 3-time panel with a mild temporal trend
times <- 1:3
panel <- do.call(rbind, lapply(times, function(t) {
  d <- sdalgcp_data; d$time <- t
  d$cases <- rpois(nrow(d), d$pop * exp(-6 + 0.6 * d$x1 + 0.1 * (t - 2)))
  d
}))
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = panel, time = "time",
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
pr <- predict(fit)        # a long sf: region x time
head(pr)
plot(pr, time = 2)        # map the relative risk at time 2
```

`print.SDALGCP2` *Print an SDALGCP2 fit*

Description

Print an SDALGCP2 fit

Usage

```
## S3 method for class 'SDALGCP2'
print(x, ...)
```

Arguments

`x`	an "SDALGCP2" object.
`...`	unused.

Value

`x`, invisibly.

print.summary.SDALGCP2 *Print a summary of an SDALGCP2 fit*

Description

Print a summary of an SDALGCP2 fit

Usage

```
## S3 method for class 'summary.SDALGCP2'
print(x, ...)
```

Arguments

x	a "summary.SDALGCP2" object.
...	unused.

Value

x, invisibly.

report *One-call panel of post-fit graphics*

Description

Returns the maps and summaries an analyst usually wants after fitting: relative-risk and uncertainty maps, an exceedance map, the coefficient plot and the phi profile. The pieces are returned as a named list of ggplot objects so they can be arranged or printed individually.

Usage

```
report(object, pred = NULL, threshold = 1.5, ...)
```

Arguments

object	a fitted "SDALGCP2" object.
pred	optional discrete prediction; computed if NULL.
threshold	relative-risk threshold for the exceedance map.
...	passed to predict.SDALGCP2 when pred is computed.

Value

a named list of ggplot objects.

Examples

```
data(sdalgcp_data)
fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = sdalgcp_data,
               control = sdalgcp_control(n_sim = 2000, burnin = 500, thin = 5,
                                         reanchor = 0))
figs <- report(fit, threshold = 1.5)
names(figs)          # relative_risk, uncertainty, exceedance, coefficients, ...
figs$relative_risk   # print one of the maps
```

`sda_points` *Generate candidate sampling points inside each region*

Description

For every polygon feature in `my_shp` it produces candidate points and aggregation weights, in the list format consumed by `precompute_corr`.

Usage

```
sda_points(
  my_shp,
  delta,
  method = 1L,
  weighted = FALSE,
  pop_shp = NULL,
  rho = 0.55,
  giveup = 1000L
)
```

Arguments

`my_shp`	an `sf` object of `POLYGON/MULTIPOLYGON` features.
`delta`	point spacing (grid step / SSI inhibition distance).
`method`	1 = SSI (default), 2 = uniform random, 3 = regular grid.
`weighted`	logical; if `TRUE`, weights are population density read from `pop_shp`, otherwise equal weights.
`pop_shp`	a `terra::SpatRaster` of population density (required when `weighted = TRUE`).
`rho`	packing density used to choose the number of points.
`giveup`	SSI rejection limit.

Value

a list of length `nrow(my_shp)`; each element has `xy` and `weight`. Carries `"weighted"` and `"my_shp"` attributes.

See Also

precompute_corr, which consumes this output.

Examples

```
data(sdalgcp_data)
pts <- sda_points(sdalgcp_data, delta = 1.2, method = 3)   # regular grid points
length(pts)          # one entry per region
str(pts[[1]])        # $xy candidate coordinates and $weight
```

---

sdalgcp *Fit a spatially discrete LGCP model for aggregated counts*

Description

The main user interface, designed to feel like glm: give a formula and an sf data object and it does the rest. The same call covers three settings, chosen from the arguments you supply:

- **spatial** (default): sdalgcp(y ~ x + offset(log(pop)), data);
- **raster covariates**: add rasters = a SpatRaster whose layers are named in the formula – these enter on the intensity scale (see SDALGCP2_raster);
- **spatio-temporal**: add time = the name of a time column.

Usage

```
sdalgcp(
  formula,
  data,
  time = NULL,
  rasters = NULL,
  covariates = NULL,
  popden = NULL,
  control = sdalgcp_control(),
  verbose = FALSE
)
```

Arguments

formula	a model formula, e.g. cases ~ x1 + offset(log(pop)).
data	an sf object of polygons whose columns hold the response, covariates and offset (one row per region, or per region-time for spatio-temporal fits).
time	optional name of a time column in data; if given, a spatio-temporal model is fitted (data must have one row per region and time).
rasters	optional terra::SpatRaster of spatially continuous covariates (layers named in formula).

covariates	optional named list of sf **point** layers giving covariates observed on a different support (e.g. monitors); each is kriged to the candidate points and enters with a Berkson correction (see SDALGCP2_misaligned).
popden	optional population-density SpatRaster; if supplied, the region aggregation is population-weighted.
control	a sdalgcp_control list of settings (smart defaults).
verbose	logical; print progress.

Value

a fitted model object of class c("sdalgcp", ...) with print, summary, confint, predict and plot methods.

See Also

predict.sdalgcp, sdalgcp_control, SDALGCP2, SDALGCP2_raster, SDALGCP2_ST

Examples

```
library(sf)
set.seed(1)
grid <- st_make_grid(st_as_sfc(st_bbox(c(xmin = 0, ymin = 0, xmax = 20, ymax = 20))),
                     n = c(8, 8))
regions <- st_sf(geometry = grid)
regions$x1  <- as.numeric(scale(st_coordinates(st_centroid(regions))[, 1]))
regions$pop <- round(runif(nrow(regions), 500, 3000))
regions$cases <- rpois(nrow(regions), regions$pop * exp(-6 + 0.5 * regions$x1))

fit <- sdalgcp(cases ~ x1 + offset(log(pop)), data = regions)  # that's it
summary(fit)
rr <- predict(fit)          # an sf you can plot() directly
plot(fit)                   # default relative-risk map
```

---

sdalgcp_control *Control settings for* sdalgcp

Description

Bundles the technical knobs so that a default fit needs none of them.

Usage

```
sdalgcp_control(
  delta = NULL,
  points_per_region = 16,
  point_method = c("regular", "uniform", "ssi"),
  scale = c("continuous", "grid"),
```

```
  phi = NULL,
  kappa = 0.5,
  kappa_t = 0.5,
  nugget = FALSE,
  confounding = c("none", "restricted"),
  reanchor = 2L,
  n_sim = 10000L,
  burnin = 2000L,
  thin = 8L,
  tilt_spatial = FALSE,
  nthreads = 0L
)
```

Arguments

`delta`	candidate-point spacing. If `NULL` (default) it is chosen automatically to place roughly `points_per_region` points in a typical region.
`points_per_region`	target number of candidate points per region used to pick `delta` automatically.
`point_method`	how candidate points are laid out: `"regular"` (deterministic grid, default), `"uniform"` or `"ssi"`.
`scale`	how the spatial scale ϕ is estimated: `"continuous"` (optimised directly, no grid – the default) or `"grid"` (profiled over `phi`). Spatio-temporal fits always profile ϕ on a grid.
`phi`	optional ϕ grid (only used when `scale = "grid"` or for spatio-temporal fits); chosen from the geometry if `NULL`.
`kappa`	spatial Matern smoothness (`0.5`, `1.5` or `2.5`).
`kappa_t`	temporal Matern smoothness (spatio-temporal fits).
`nugget`	logical; add an unstructured region-level term (overdispersion). Requires `scale = "continuous"`.
`confounding`	`"none"` (default) or `"restricted"`. With `"restricted"`, restricted spatial regression is used: the spatial random effect is constrained to the orthogonal complement of the fixed-effect design so it cannot absorb a spatially structured covariate (avoids spatial confounding / attenuation of `beta`). Spatial models only.
`reanchor`	number of re-anchoring passes (re-simulate the latent field at the optimum and refit) for reliable variance estimates. Default `2`.
`n_sim, burnin, thin`	MCMC length controls for the latent-field sampler.
`tilt_spatial`	logical; for raster covariates, use the fully covariate-tilted correlation (see `SDALGCP2_raster`).
`nthreads`	OpenMP threads for the correlation assembly (0 = default).

Value

a list of control settings.

See Also

sdalgcp

Examples

```
## defaults, then a faster grid-based fit with a nugget term
str(sdalgcp_control())
ctrl <- sdalgcp_control(scale = "grid", nugget = FALSE, n_sim = 4000,
                        burnin = 1000, thin = 6)
```

---

sdalgcp_data *Simulated aggregated disease-count data*

Description

A small, self-contained example dataset used throughout the help pages and vignettes. It is simulated from the model the package fits: an 8x8 lattice of regions, a spatially structured covariate, a latent Gaussian spatial field with exponential covariance, and Poisson counts with a population offset. The true fixed effects are `(Intercept)` = `-6` and `x1` = `0.6`; the latent field has variance $\sigma^2 = 0.3$ and exponential scale $\phi = 4$.

Usage

```
sdalgcp_data
```

Format

An sf object of 64 `POLYGON` regions with columns:

region integer region identifier (1-64).

cases observed disease count in the region.

x1 a standardised, spatially structured covariate.

pop population at risk (the offset; use `offset(log(pop))`).

geometry the region polygon.

Source

Simulated; see `data-raw/sdalgcp_data.R` in the package sources.

See Also

liver for a real disease-count example.

Examples

```
data(sdalgcp_data)
summary(sdalgcp_data$cases)
plot(sdalgcp_data["cases"])
```

SDALGCP2 *Fit a spatial SDA-LGCP model*

Description

End-to-end user entry point: generates candidate points inside each region, assembles the aggregated region-level correlation array (C++), and estimates parameters by Monte Carlo maximum likelihood.

Usage

```
SDALGCP2(
  formula,
  data,
  my_shp,
  delta,
  phi = NULL,
  method = 1L,
  weighted = FALSE,
  pop_shp = NULL,
  kappa = 0.5,
  par0 = NULL,
  control.mcmc = NULL,
  phi_method = c("grid", "direct"),
  nugget = FALSE,
  confounding = c("none", "restricted"),
  reanchor = 0L,
  rho = 0.55,
  giveup = 1000L,
  nthreads = 0L,
  messages = FALSE
)
```

Arguments

formula	model formula, e.g. cases ~ x1 + offset(log(pop)).
data	data frame with the model variables (one row per region).
my_shp	sf polygons (or anything coercible via st_as_sf).
delta	candidate-point spacing.
phi	numeric vector of spatial scale parameters to profile; if NULL, a default grid from sqrt(min area) to extent/10.
method	point method: 1 = SSI, 2 = uniform, 3 = regular grid.
weighted	logical; population-weighted aggregation using pop_shp.
pop_shp	population-density SpatRaster (needed if weighted).
kappa	Matern smoothness for the spatial kernel (0.5 default).

par0	optional starting values c(beta, sigma2, phi).
control.mcmc	list from control_mcmc.
phi_method	how the spatial scale is estimated: "grid" (profile over the supplied phi grid, the robust default) or "direct" (optimise phi continuously inside the MCML objective; exponential kernel only). See the package vignette/PDF on the double-integral derivation.
nugget	logical; if TRUE (requires phi_method = "direct") add an unstructured region-level term, fitting covariance $\sigma^2(R(\phi) + \nu I)$ and estimating the relative nugget $\nu = \tau^2/\sigma^2$ with a standard error. Absorbs overdispersion not explained by the spatial structure.
confounding	"none" (default) or "restricted" for restricted spatial regression (constrains the spatial random effect orthogonal to the fixed-effect design; fitted by a Laplace-approximate marginal likelihood).
reanchor	number of re-anchoring passes: after fitting, the latent field is re-simulated at the current optimum and the model refit, which keeps the importance weights near-uniform (raises the MC effective sample size). 0 (default) fits once; 2-3 is usually ample.
rho, giveup	point-generation controls.
nthreads	OpenMP threads for the correlation build.
messages	logical; print optimiser progress.

Value

an object of class "SDALGCP2".

See Also

mcml_fit, precompute_corr, sda_points

Examples

```
library(sf)
## ---- simulate a lattice of regions and aggregated counts ----
set.seed(1)
bound <- st_as_sfc(st_bbox(c(xmin = 0, ymin = 0, xmax = 20, ymax = 20)))
shp   <- st_sf(geometry = st_make_grid(bound, n = c(8, 8)))
N     <- nrow(shp)

pts   <- sda_points(shp, delta = 1.2, method = 3)      # regular grid points
phi_grid <- seq(1, 5, length.out = 8)
corr  <- precompute_corr(pts, phi_grid)
Sig   <- 0.5 * corr$R[, , which.min(abs(phi_grid - 2.5))]
x1    <- as.numeric(scale(st_coordinates(st_centroid(shp))[, 1]))
pop   <- round(runif(N, 500, 3000))
y     <- rpois(N, pop * exp(cbind(1, x1) %*% c(-6, 0.5) +
                            as.numeric(t(chol(Sig)) %*% rnorm(N))))
dat   <- data.frame(y = y, x1 = x1, pop = pop)
```

```
## ---- fit ----
ctrl <- control_mcmc(n.sim = 6000, burnin = 1500, thin = 6, h = 1.65 / N^(1/6))
fit  <- SDALGCP2(y ~ x1 + offset(log(pop)), dat, shp, delta = 1.2,
                 phi = phi_grid, method = 3, control.mcmc = ctrl)
summary(fit)

## ---- predict ----
pred_d <- predict(fit, type = "discrete",   sampler = "mcmc",    control.mcmc = ctrl)
pred_c <- predict(fit, type = "continuous", sampler = "laplace", cellsize = 1,
                  control.mcmc = ctrl)
```

`SDALGCP2_misaligned` *Fit an SDA-LGCP with covariates measured on a different support*

Description

Covariates observed on a *different support* from the outcome (e.g. air- quality monitors at point locations) are kriged to the candidate points and enter the model on the intensity scale with a Berkson correction that propagates the prediction uncertainty (see `math/confounding-and-misalignment.pdf`).

Usage

```
SDALGCP2_misaligned(
  formula,
  data,
  delta,
  covariates,
  phi = NULL,
  method = 3L,
  weighted = FALSE,
  pop_shp = NULL,
  berkson = TRUE,
  control.mcmc = NULL,
  max_iter = 10L,
  tol = 0.001,
  messages = FALSE
)
```

Arguments

`formula`	model formula; the covariate names appear on the right-hand side.
`data`	`sf` polygons holding the response and offset (one row/region).
`delta`	candidate-point spacing.
`covariates`	a named list; each element is an `sf` carrying a column of the same name – the covariate's observed values on its own support, either **points** (e.g. monitors; plain kriging) or **polygons** (areal averages on a different partition; aggregated areal kriging).

phi	spatial-scale grid for the outcome model (default from geometry).
method, weighted, pop_shp	point-generation controls.
berkson	logical; include the Berkson uncertainty correction (default TRUE). FALSE gives the naive kriged-mean plug-in.
control.mcmc	list from control_mcmc.
max_iter, tol	outer Gauss-Newton controls.
messages	logical; print progress.

Value

an object of class "SDALGCP2" with misaligned = TRUE.

See Also

SDALGCP2_raster, sdalgcp

Examples

```
data(sdalgcp_data)
set.seed(1)
## a covariate z observed only at 40 scattered monitor points (a different support)
mon <- sf::st_as_sf(data.frame(x = runif(40, 0, 20), y = runif(40, 0, 20)),
                    coords = c("x", "y"))
mon$z <- scale(sf::st_coordinates(mon)[, 1])[, 1]
fit <- SDALGCP2_misaligned(cases ~ z + offset(log(pop)), sdalgcp_data, delta = 1.5,
                           covariates = list(z = mon),
                       control.mcmc = control_mcmc(n.sim = 2000, burnin = 500, thin = 5))
summary(fit)
```

SDALGCP2_raster *Fit an SDA-LGCP with spatially continuous (raster) covariates*

Description

Covariates supplied as rasters enter the model at the candidate-point level and are aggregated on the intensity (exp) scale via a log-sum-exp offset $b_i(\beta) = \log \sum_k w_{ik} \exp(z(x_{ik})^\top \beta)$ – the statistically correct alternative to averaging the predictor over each polygon. Estimation is a Gauss-Newton fixed point that reuses mcml_fit with the intensity-tilted effective design.

Usage

```
SDALGCP2_raster(
  formula,
  data,
  my_shp,
  delta,
  rasters,
  phi = NULL,
  method = 3L,
  weighted = FALSE,
  pop_shp = NULL,
  kappa = 0.5,
  tilt_spatial = FALSE,
  control.mcmc = NULL,
  max_iter = 10L,
  tol = 0.001,
  messages = FALSE
)
```

Arguments

formula	model formula; right-hand-side names must match raster layer names. The response and an offset(log(pop)) come from data.
data	data frame with the response and offset (one row per region).
my_shp	sf polygons.
delta	candidate-point spacing.
rasters	a terra::SpatRaster (or object coercible by terra::rast) whose layers are the spatially varying covariates named in formula.
phi	spatial-scale grid (default chosen from the geometry).
method, weighted, pop_shp	point-generation controls (see sda_points).
kappa	Matern smoothness for the spatial correlation.
tilt_spatial	logical; if FALSE (default) the spatial correlation uses the population weights and is precomputed once (covariates enter only through the log-sum-exp offset). If TRUE, the correlation $R^c(\beta)$ is rebuilt each iteration from the intensity-tilted weights $c_{ik}(\beta)$ and a log-normal aggregation correction $\frac{1}{2}\sigma^2(1 - R^c_{ii})$ is added – the fully tilted model (more accurate, more costly).
control.mcmc	list from control_mcmc.
max_iter, tol	outer Gauss-Newton iteration controls.
messages	logical; print progress.

Value

an object of class "SDALGCP2" (as mcml_fit) with extra fields raster = TRUE and n_iter.

See Also

SDALGCP2, mcml_fit

Examples

```
data(sdalgcp_data)
## a spatially continuous covariate supplied as a raster layer named "z"
r <- terra::rast(terra::ext(0, 20, 0, 20), resolution = 0.5)
terra::values(r) <- as.numeric(scale(terra::crds(r)[, 1]))   # west-east gradient
names(r) <- "z"
df <- sf::st_drop_geometry(sdalgcp_data)
fit <- SDALGCP2_raster(cases ~ z + offset(log(pop)), df, sdalgcp_data,
                       delta = 1.5, rasters = r,
                      control.mcmc = control_mcmc(n.sim = 2000, burnin = 500, thin = 5))
summary(fit)
```

SDALGCP2_ST *Fit a spatio-temporal SDA-LGCP model (Kronecker-free)*

Description

Separable space-time SDA-LGCP for aggregated counts observed over the same N regions at T times. The spatial scale phi is profiled on a grid; the temporal Matern range nu is estimated continuously. The likelihood never forms the $(NT) \times (NT)$ covariance.

Usage

```
SDALGCP2_ST(
  formula,
  data,
  my_shp,
  times,
  delta,
  phi = NULL,
  kappa = 0.5,
  kappa_t = 0.5,
  method = 3L,
  weighted = FALSE,
  pop_shp = NULL,
  control.mcmc = NULL,
  reanchor = 0L,
  rasters = NULL,
  covariates = NULL,
  confounding = c("none", "restricted"),
  berkson = TRUE,
  max_iter = 10L,
  tol = 0.001,
```

```
  messages = FALSE
)
```

Arguments

formula	model formula (with optional offset(log(pop))).
data	data frame of N*T rows ordered by time then region (rows (t-1)*N + 1:N are time t).
my_shp	sf polygons for the N regions.
times	numeric vector of length T of observation times.
delta	candidate-point spacing.
phi	spatial-scale grid (default from geometry).
kappa	spatial Matern smoothness.
kappa_t	temporal Matern smoothness.
method, weighted, pop_shp	point-generation controls.
control.mcmc	list from control_mcmc.
reanchor	number of re-anchoring passes (re-simulate the latent field at the current optimum and refit); improves the variance-parameter estimates.
rasters	optional terra::SpatRaster of spatially continuous, time-invariant covariates (layers named in formula); they enter on the intensity scale as in SDALGCP2_raster, fitted by a Gauss-Newton tilting loop around the space-time likelihood.
covariates	optional named list of sf covariate layers measured on a different (time-invariant) support; each is kriged to the candidate points with a Berkson correction as in SDALGCP2_misaligned.
confounding	"none" (default) or "restricted" for restricted spatial regression against space-time confounding (see Details).
berkson	logical; include the Berkson uncertainty correction for covariates (default TRUE).
max_iter, tol	Gauss-Newton controls for the rasters/covariates tilting loop.
messages	logical; print progress.

Details

With rasters or covariates the covariate surface is taken to be constant over time (time-varying covariates can still be supplied as ordinary columns of data). confounding = "restricted" constrains the space-time random effect to the orthogonal complement of the fixed-effect design and is fitted by an analytic Laplace-marginal likelihood; it reduces to the spatial restricted fit when T = 1 and is not currently combined with rasters/covariates.

Value

an object of class c("SDALGCP2_ST","SDALGCP2") with phi_opt, nu_opt, coefficient table and covariance.

See Also

sdalgcp (friendly wrapper), predict.SDALGCP2_ST

Examples

```
data(sdalgcp_data)
shp <- sdalgcp_data
## build a 3-time panel (data frame, N*T rows ordered by time then region)
times <- 1:3
dat <- do.call(rbind, lapply(times, function(t) {
  d <- sf::st_drop_geometry(shp); d$time <- t
  d$cases <- rpois(nrow(d), d$pop * exp(-6 + 0.6 * d$x1 + 0.1 * (t - 2)))
  d
}))
fit <- SDALGCP2_ST(cases ~ x1 + offset(log(pop)), dat, shp, times = times,
                   delta = 1.5,
                   control.mcmc = control_mcmc(n.sim = 2000, burnin = 500, thin = 5))
fit$phi_opt; fit$nu_opt

## restricted spatial regression against space-time confounding
fit_c <- SDALGCP2_ST(cases ~ x1 + offset(log(pop)), dat, shp, times = times,
                     delta = 1.5, phi = c(2, 4, 6), confounding = "restricted")
fit_c$beta_opt

## a spatially continuous (raster) covariate, aggregated on the intensity scale
r <- terra::rast(terra::ext(0, 20, 0, 20), resolution = 0.5)
terra::values(r) <- as.numeric(scale(terra::crds(r)[, 1])); names(r) <- "z"
fit_r <- SDALGCP2_ST(cases ~ z + offset(log(pop)), dat, shp, times = times,
                     delta = 1.5, phi = c(2, 4, 6), rasters = r, max_iter = 4,
                     control.mcmc = control_mcmc(n.sim = 2000, burnin = 500, thin = 5))
fit_r$beta_opt
```

---

summary.SDALGCP2 *Summary of an SDALGCP2 fit*

Description

Summary of an SDALGCP2 fit

Usage

```
## S3 method for class 'SDALGCP2'
summary(object, ...)
```

Arguments

object	an object of class "SDALGCP2" from mcml_fit.
...	unused.

Value

an object of class `"summary.SDALGCP2"` with a coefficient table.

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