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`bayes_cluster` *Bayesian Cluster Detection Method*

Description

Implementation of the Bayesian Cluster detection model of Wakefield and Kim (2013) for a study region with `n` areas. The prior and posterior probabilities of each of the `n.zones` single zones being a cluster/anti-cluster are estimated using Markov chain Monte Carlo. Furthermore, the posterior probability of k clusters/anti-clusters is computed.

Usage

```
bayes_cluster(
  y,
  E,
  population,
  sp.obj,
```

```
  centroids,
  max.prop,
  shape,
  rate,
  J,
  pi0,
  n.sim.lambda,
  n.sim.prior,
  n.sim.post,
  burnin.prop = 0.1,
  theta.init = vector(mode = "numeric", length = 0)
)
```

Arguments

y	vector of length n of the observed number of disease in each area
E	vector of length n of the expected number of disease in each area
population	vector of length n of the population in each area
sp.obj	an object of class SpatialPolygons
centroids	n x 2 table of the (x,y)-coordinates of the area centroids. The coordinate system must be grid-based
max.prop	maximum proportion of the study region's population each single zone can contain
shape	vector of length 2 of narrow/wide shape parameter for gamma prior on relative risk
rate	vector of length 2 of narrow/wide rate parameter for gamma prior on relative risk
J	maximum number of clusters/anti-clusters
pi0	prior probability of no clusters/anti-clusters
n.sim.lambda	number of importance sampling iterations to estimate lambda
n.sim.prior	number of MCMC iterations to estimate prior probabilities associated with each single zone
n.sim.post	number of MCMC iterations to estimate posterior probabilities associated with each single zone
burnin.prop	proportion of MCMC samples to use as burn-in
theta.init	Initial configuration used for MCMC sampling

Value

List containing return(list(prior.map=prior.map, post.map=post.map, pk.y=pk.y))

prior.map	A list containing, for each area: 1) high.area the prior probability of cluster membership, 2) low.area anti-cluster membership, and 3) RR.est.area smoothed prior estimates of relative risk

post.map	A list containing, for each area: 1) high.area the posterior probability of cluster membership, 2) low.area anti-cluster membership, and 3) RR.est.area smoothed posterior estimates of the relative risk
pk.y	posterior probability of k clusters/anti-clusters given y for k=0,...,J

Author(s)

Albert Y. Kim

References

Wakefield J. and Kim A.Y. (2013) A Bayesian model for cluster detection.

Examples

```
## Note for the NYleukemia example, 4 census tracts were completely surrounded
## by another unique census tract; when applying the Bayesian cluster detection
## model in [bayes_cluster()], we merge them with the surrounding
## census tracts yielding `n=277` areas.

## Load data and convert coordinate system from latitude/longitude to grid
data(NYleukemia)
sp.obj <- NYleukemia$spatial.polygon
population <- NYleukemia$data$population
cases <- NYleukemia$data$cases
centroids <- latlong2grid(NYleukemia$geo[, 2:3])

## Identify the 4 census tract to be merged into their surrounding census tracts
remove <- NYleukemia$surrounded
add <- NYleukemia$surrounding

## Merge population and case counts and geographical objects accordingly
population[add] <- population[add] + population[remove]
population <- population[-remove]
cases[add] <- cases[add] + cases[remove]
cases <- cases[-remove]
sp.obj <-
 SpatialPolygons(sp.obj@polygons[-remove], proj4string=CRS("+proj=longlat +ellps=WGS84"))
centroids <- centroids[-remove, ]

## Set parameters
y <- cases
E <- expected(population, cases, 1)
max.prop <- 0.15
shape <- c(2976.3, 2.31)
rate <- c(2977.3, 1.31)
J <- 7
pi0 <- 0.95
n.sim.lambda <- 10^4
n.sim.prior <- 10^5
n.sim.post <- 10^5
```

```
## (Uncomment first) Compute output
#output <- bayes_cluster(y, E, population, sp.obj, centroids, max.prop,
#  shape, rate, J, pi0, n.sim.lambda, n.sim.prior, n.sim.post)
#plotmap(output$prior.map$high.area, sp.obj)
#plotmap(output$post.map$high.area, sp.obj)
#plotmap(output$post.map$RR.est.area, sp.obj, log=TRUE)
#barplot(output$pk.y, names.arg=0:J, xlab="k", ylab="P(k|y)")
```

`besag_newell` *Besag-Newell Cluster Detection Method*

Description

Besag-Newell cluster detection method. There are differences with the original paper and our implementation:

- we base our analysis on k cases, rather than k *other* cases as prescribed in the paper.
- we do not subtract 1 from the *accumulated numbers of other cases* and *accumulated numbers of others at risk*, as was prescribed in the paper to discount selection bias
- M is the total number of areas included, not the number of additional areas included. i.e. M starts at 1, not 0.
- p-values are not based on the original value of k, rather the actual number of cases observed until we view k or more cases. Ex: if $k = 10$, but as we consider neighbors we encounter 1, 2, 9 then 12 cases, we base our p-values on $k = 12$
- we do not provide a Monte-Carlo simulated R: the number of tests that attain significance at a fixed level α

The first two and last differences are because we view the testing on an area-by-area level, rather than a case-by-case level.

Usage

```
besag_newell(geo, population, cases, expected.cases = NULL, k, alpha.level)
```

Arguments

`geo`	an `n x 2` table of the (x,y)-coordinates of the area centroids
`population`	aggregated population counts for all `n` areas
`cases`	aggregated case counts for all `n` areas
`expected.cases`	expected numbers of disease for all `n` areas
`k`	number of cases to consider
`alpha.level`	alpha-level threshold used to declare significance

Details

For the `population` and `cases` tables, the rows are bunched by areas first, and then for each area, the counts for each strata are listed. It is important that the tables are balanced: the strata information are in the same order for each area, and counts for each area/strata combination appear exactly once (even if zero).

Value

List containing

`clusters`	information on all clusters that are α-level significant, in decreasing order of the p-value
`p.values`	for each of the n areas, p-values of each cluster of size at least k
`m.values`	for each of the n areas, the number of areas need to observe at least k cases
`observed.k.values`	based on `m.values`, the actual number of cases used to compute the p-values

Note

The `clusters` list elements are themselves lists reporting:

`location.IDs.included`	ID's of areas in cluster, in order of distance
`population`	population of cluster
`number.of.cases`	number of cases in cluster
`expected.cases`	expected number of cases in cluster
`SMR`	estimated SMR of cluster
`p.value`	p-value

Author(s)

Albert Y. Kim

References

Besag J. and Newell J. (1991) The Detection of Clusters in Rare Diseases *Journal of the Royal Statistical Society. Series A (Statistics in Society)*, **154**, 143–155

Examples

```
## Load Pennsylvania Lung Cancer Data
data(pennLC)
data <- pennLC$data

## Process geographical information and convert to grid
geo <- pennLC$geo[,2:3]
geo <- latlong2grid(geo)
```

```
## Get aggregated counts of population and cases for each county
population <- tapply(data$population,data$county,sum)
cases <- tapply(data$cases,data$county,sum)

## Based on the 16 strata levels, computed expected numbers of disease
n.strata <- 16
expected.cases <- expected(data$population, data$cases, n.strata)

## Set Parameters
k <- 1250
alpha.level <- 0.05

# not controlling for stratas
results <- besag_newell(geo, population, cases, expected.cases=NULL, k,
                        alpha.level)

# controlling for stratas
results <- besag_newell(geo, population, cases, expected.cases, k, alpha.level)
```

`circle` *Compute cartesian coordinates of a cluster center and radius*

Description

This function is used for plotting purposes

Usage

```
circle(geo, cluster.center, cluster.end)
```

Arguments

`geo`	A `n x 2` table of the x-coordinate and y-coordinates of the centroids of each area
`cluster.center`	The area index (an integer between 1 and n) indicating the center of the circle
`cluster.end`	The area index (an integer between 1 and n) indicating the area at the end of the circle

Value

`cluster.radius`	A data frame that you can plot

Author(s)

Albert Y. Kim

Examples

```
data(pennLC)
geo <- pennLC$geo[,2:3]
plot(geo,type='n')
text(geo,labels=1:nrow(geo))
lines( circle(geo, 23, 46), col = "red" )
```

`create_geo_objects` *Create geographical objects to be used in Bayesian Cluster Detection Method*

Description

This internal function creates the geographical objects needed to run the Bayesian cluster detection method in `bayes_cluster()`. Specifically it creates all single zones based data objects, where single zones are the *zones* defined by Kulldorff (1997).

Usage

```
create_geo_objects(max.prop, population, centroids, sp.obj)
```

Arguments

`max.prop`	maximum proportion of study region's population each single zone can contain
`population`	vector of length `n` of the population of each area
`centroids`	`n x 2` table of the (x,y)-coordinates of the area centroids. The coordinate system must be grid-based
`sp.obj`	object of class SpatialPolygons (See SpatialPolygons-class) representing the study region

Value

`overlap`	list with two elements: `1. presence` which lists for each area all the single zones it is present in and `2. cluster.list` for each single zone its component areas
`cluster.coords`	`n.zones x 2` matrix of the center and radial area of each single zone

Author(s)

Albert Y. Kim

References

Wakefield J. and Kim A.Y. (2013) A Bayesian model for cluster detection.*Biostatistics*, **14**, 752–765.

Examples

```
data(pennLC)
max.prop <- 0.15
population <- tapply(pennLC$data$population, pennLC$data$county, sum)
centroids <- latlong2grid(pennLC$geo[, 2:3])
sp.obj <- pennLC$spatial.polygon
output <- create_geo_objects(max.prop, population, centroids, sp.obj)
## number of single zones
nrow(output$cluster.coords)
```

---

eBayes *Empirical Bayes Estimates of Relative Risk*

Description

The computes empirical Bayes estimates of relative risk of study region with n areas, given observed and expected numbers of counts of disease and covariate information.

Usage

```
eBayes(Y, E, Xmat = NULL)
```

Arguments

Y	a length n vector of observed cases
E	a length n vector of expected number of cases
Xmat	n x p dimension matrix of covariates

Value

A list with 5 elements:

RR	the ecological relative risk posterior mean estimates
RRmed	the ecological relative risk posterior median estimates
beta	the MLE's of the regression coefficients
alpha	the MLE of negative binomial dispersion parameter
SMR	the standardized mortality/morbidity ratio Y/E

References

Clayton D. and Kaldor J. (1987) Empirical Bayes estimates of age-standardized relative risks for use in disease mapping. *Biometrics*, **43**, 671–681

Examples

```
data(scotland)
data <- scotland$data
x <- data$AFF
Xmat <- cbind(x,x^2)
results <- eBayes(data$cases,data$expected,Xmat)
scotland.map <- scotland$spatial.polygon
mapvariable(results$RR, scotland.map)
```

EBpostdens — *Produce plots of empirical Bayes posterior densities when the data Y are Poisson with expected number E and relative risk theta, with the latter having a gamma distribution with known values alpha and beta, which are estimated using empirical Bayes.*

Description

This function produces plots of empirical Bayes posterior densities which are gamma distributions with parameters (alpha+Y, (alpha+E*mu)/mu) where mu = exp(x beta). The SMRs are drawn on for comparison.

Usage

```
EBpostdens(
  Y,
  E,
  alpha,
  beta,
  Xrow = NULL,
  lower = NULL,
  upper = NULL,
  main = ""
)
```

Arguments

Y	observed disease counts
E	expected disease counts
alpha	x
beta	x
Xrow	x
lower	x
upper	x
main	x

Value

A plot containing the gamma posterior distribution

Author(s)

Jon Wakefield

Examples

```
data(scotland)
Y <- scotland$data$cases
E <- scotland$data$expected
ebresults <- eBayes(Y,E)
EBpostdens(Y[1], E[1], ebresults$alpha, ebresults$beta, lower=0, upper=15,
          main="Area 1")
```

`EBpostthresh` *Produce the probabilities of exceeding a threshold given a posterior gamma distribution.*

Description

This function produces the posterior probabilities of exceeding a threshold given a gamma distributions with parameters (alpha+Y, (alpha+E*mu)/mu) where mu = exp(x beta). This model arises from Y being Poisson with mean theta times E where theta is the relative risk and E are the expected numbers. The prior on theta is gamma with parameters alpha and beta. The parameters alpha and beta may be estimated using empirical Bayes.

Usage

```
EBpostthresh(Y, E, alpha, beta, Xrow = NULL, rrthresh)
```

Arguments

`Y`	observed disease counts
`E`	expected disease counts
`alpha`	x
`beta`	x
`Xrow`	x
`rrthresh`	x

Value

Posterior probabilities of exceedence are returned.

Author(s)

Jon Wakefield

See Also

eBayes()

Examples

```
data(scotland)
Y <- scotland$data$cases
E <- scotland$data$expected
ebresults <- eBayes(Y,E)
#Find probabilities of exceedence of 3
thresh3 <- EBpostthresh(Y, E, alpha=ebresults$alpha, beta=ebresults$beta, rrthresh=3)
mapvariable(thresh3, scotland$spatial.polygon)
```

---

estimate_lambda *Estimate lambda values*

Description

Internal function to estimate values of lambda needed for MCMC_simulation and prior probability of k clusters/anti-clusters for k=0,...,J

Usage

```
estimate_lambda(n.sim, J, prior.z, overlap, pi0)
```

Arguments

n.sim	number of importance sampling iterations
J	maximum number of clusters/anti-clusters to consider
prior.z	prior probability of each single zone
overlap	output of create_geo_objects(): list with two elements: presence which lists for each area all the single zones it is present in and and cluster_list for each single zone its component areas
pi0	prior probability of no clusters

Value

estimates of lambda and prior.j

References

Wakefield J. and Kim A.Y. (2013) A Bayesian model for cluster detection. *Biostatistics*, **14**, 752–765.

`expected` *Compute Expected Numbers of Disease*

Description

Compute the internally indirect standardized expected numbers of disease.

Usage

```
expected(population, cases, n.strata)
```

Arguments

`population`	a vector of population counts for each strata in each area
`cases`	a vector of the corresponding number of cases
`n.strata`	number of strata considered

Details

The `population` and `cases` vectors must be *balanced*: all counts are sorted by area first, and then within each area the counts for all strata are listed (even if 0 count) in the same order.

Value

`expected.cases`	a vector of the expected numbers of disease for each area

Author(s)

Albert Y. Kim

References

Elliot, P. et al. (2000) *Spatial Epidemiology: Methods and Applications*. Oxford Medical Publications.

Examples

```
data(pennLC)
population <- pennLC$data$population
cases <- pennLC$data$cases
## In each county in Pennsylvania, there are 2 races, gender and 4 age bands
## considered = 16 strata levels
pennLC$data[1:16,]
expected(population, cases, 16)
```

GammaPriorCh *Compute Parameters to Calibrate a Gamma Distribution*

Description

Compute parameters to calibrate the prior distribution of a relative risk that has a gamma distribution.

Usage

```
GammaPriorCh(theta, prob, d)
```

Arguments

theta	upper quantile
prob	upper quantile
d	degrees of freedom

Value

List containing

a	shape parameter
b	rate parameter

Author(s)

Jon Wakefield

See Also

LogNormalPriorCh

Examples

```
param <- GammaPriorCh(5, 0.975,1)
curve(dgamma(x,shape=param$a,rate=param$b),from=0,to=6,n=1000,ylab="density")
```

grid2latlong *Convert Coordinates from Grid to Latitude/Longitude*

Description

Convert geographic coordinates from Universal Transverse Mercator system to Latitude/Longitude.

Usage

```
grid2latlong(input)
```

Arguments

input	A data frame with columns named x and y of the UTM coordinates to convert or an n x 2 matrix of grid coordinates or an object of class SpatialPolygons (See SpatialPolygons-class)

Details

Longitude/latitudes are not a grid-based coordinate system: latitudes are equidistant but the distance between longitudes varies.

Value

Either a data frame with the corresponding longitude and latitude, or a SpatialPolygons object with the coordinates changed.

Note

Rough conversion of US lat/long to km (used by GeoBUGS): (see also forum.swarthmore.edu/dr.math/problems/longandlat.ht
Radius of earth: r = 3963.34 (equatorial) or 3949.99 (polar) mi = 6378.2 or 6356.7 km, which implies: km per mile = 1.609299 or 1.609295 a change of 1 degree of latitude corresponds to the same number of km, regardless of longitude. arclength=r*theta, so the multiplier for coord y should probably be just the radius of earth. On the other hand, a change of 1 degree in longitude corresponds to a different distance, depending on latitude. (at N pole, the change is essentially 0. at the equator, use equatorial radius. Perhaps for U.S., might use an "average" latitude, 30 deg is roughly Houston, 49deg is most of N bdry of continental 48 states. 0.5(30+49)=39.5 deg. so use r approx 6378.2*sin(51.5)

Author(s)

Lance A. Waller

Examples

```
coord <- data.frame(rbind(
# Montreal, QC
c(-6414.30, 5052.849),
# Vancouver, BC
c(-122.6042, 45.6605)
))

grid2latlong(coord)
```

`kulldorff` *Kulldorff Cluster Detection Method*

Description

Kulldorff spatial cluster detection method for a study region with `n` areas. The method constructs *zones* by consecutively aggregating nearest-neighboring areas until a proportion of the total study population is included. Given the observed number of cases, the likelihood of each zone is computed using either binomial or poisson likelihoods. The procedure reports the zone that is the *most likely cluster* and generates significance measures via Monte Carlo sampling. Further, *secondary clusters*, whose Monte Carlo p-values are below the α-threshold, are reported as well.

Usage

```
kulldorff(
  geo,
  cases,
  population,
  expected.cases = NULL,
  pop.upper.bound,
  n.simulations,
  alpha.level,
  plot = TRUE
)
```

Arguments

`geo`	an `n x 2` table of the (x,y)-coordinates of the area centroids
`cases`	aggregated case counts for all `n` areas
`population`	aggregated population counts for all `n` areas
`expected.cases`	expected numbers of disease for all `n` areas
`pop.upper.bound`	the upper bound on the proportion of the total population each zone can include
`n.simulations`	number of Monte Carlo samples used for significance measures
`alpha.level`	alpha-level threshold used to declare significance
`plot`	flag for whether to plot histogram of Monte Carlo samples of the log-likelihood of the most likely cluster

Details

If `expected.cases` is specified to be `NULL`, then the binomial likelihood is used. Otherwise, a Poisson model is assumed. Typical values of `n.simulations` are `99`, `999`, `9999`

Value

List containing:

`most.likely.cluster`
: information on the most likely cluster

`secondary.clusters`
: information on secondary clusters, if none `NULL` is returned

`type`
: type of likelihood

`log.lkhd`
: log-likelihood of each zone considered

`simulated.log.lkhd`
: `n.simulations` Monte Carlo samples of the log-likelihood of the most likely cluster

Note

The `most.likely.cluster` and `secondary.clusters` list elements are themselves lists reporting:

`location.IDs.included`	ID's of areas in cluster, in order of distance
`population`	population of cluster
`number.of.cases`	number of cases in cluster
`expected.cases`	expected number of cases in cluster
`SMR`	estimated SMR of cluster
`log.likelihood.ratio`	log-likelihood of cluster
`monte.carlo.rank`	rank of lkhd of cluster within Monte Carlo simulated values
`p.value`	Monte Carlo p-value

Author(s)

Albert Y. Kim

References

SatScan: Software for the spatial, temporal, and space-time scan statistics https://www.satscan.org/ Kulldorff, M. (1997) A spatial scan statistic. *Communications in Statistics: Theory and Methods*, **26**, 1481–1496. Kulldorff M. and Nagarwalla N. (1995) Spatial disease clusters: Detection and Inference. *Statistics in Medicine*, **14**, 799–810.

Examples

```
## Load Pennsylvania Lung Cancer Data
data(pennLC)
data <- pennLC$data

## Process geographical information and convert to grid
geo <- pennLC$geo[,2:3]
geo <- latlong2grid(geo)

## Get aggregated counts of population and cases for each county
population <- tapply(data$population,data$county,sum)
cases <- tapply(data$cases,data$county,sum)

## Based on the 16 strata levels, computed expected numbers of disease
n.strata <- 16
expected.cases <- expected(data$population, data$cases, n.strata)

## Set Parameters
pop.upper.bound <- 0.5
n.simulations <- 999
alpha.level <- 0.05
plot <- TRUE

## Kulldorff using Binomial likelihoods
binomial <- kulldorff(geo, cases, population, NULL, pop.upper.bound, n.simulations,
                      alpha.level, plot)
cluster <- binomial$most.likely.cluster$location.IDs.included

## plot
plot(pennLC$spatial.polygon,axes=TRUE)
plot(pennLC$spatial.polygon[cluster],add=TRUE,col="red")
title("Most Likely Cluster")

## Kulldorff using Poisson likelihoods
poisson <- kulldorff(geo, cases, population, expected.cases, pop.upper.bound,
                     n.simulations, alpha.level, plot)
cluster <- poisson$most.likely.cluster$location.IDs.included

## plot
plot(pennLC$spatial.polygon,axes=TRUE)
plot(pennLC$spatial.polygon[cluster],add=TRUE,col="red")
title("Most Likely Cluster Controlling for Strata")
```

---

latlong2grid *Convert Coordinates from Latitude/Longitude to Grid*

Description

Convert geographic latitude/longitude coordinates to kilometer-based grid coordinates.

Usage

```
latlong2grid(input)
```

Arguments

input	either an n x 2 matrix of longitude and latitude coordinates in decimal format or an object of class SpatialPolygons

Details

Longitude/latitudes are not a grid-based coordinate system: latitudes are equidistant but the distance between longitudes varies.

Value

Either a data frame with the corresponding (x,y) kilometer-based grid coordinates, or a SpatialPolygons object with the coordinates changed.

Note

Rough conversion of US lat/long to km (used by GeoBUGS): (see also forum.swarthmore.edu/dr.math/problems/longandlat.ht
Radius of earth: r = 3963.34 (equatorial) or 3949.99 (polar) mi = 6378.2 or 6356.7 km, which implies: km per mile = 1.609299 or 1.609295 a change of 1 degree of latitude corresponds to the same number of km, regardless of longitude. arclength=r*theta, so the multiplier for coord y should probably be just the radius of earth. On the other hand, a change of 1 degree in longitude corresponds to a different distance, depending on latitude. (at N pole, the change is essentially 0. at the equator, use equatorial radius.

Author(s)

Lance A. Waller

Examples

```
## Convert coordinates
coord <- data.frame(rbind(
 # Montreal, QC:  Latitude: 45deg 28' 0" N (deg min sec), Longitude: 73deg 45' 0" W
 c(-73.7500, 45.4667),
 # Vancouver, BC:  Latitude: 45deg 39' 38" N (deg min sec), Longitude: 122deg 36' 15" W
 c(-122.6042, 45.6605)
))
latlong2grid(coord)
## Convert SpatialPolygon
data(pennLC)
new <- latlong2grid(pennLC$spatial.polygon)
par(mfrow=c(1,2))
plot(pennLC$spatial.polygon,axes=TRUE)
title("Lat/Long")
plot(new,axes=TRUE)
title("Grid (in km)")
```

leglabs *Make legend labels*

Description

leglabs makes character strings from the same break points. This function was copied from the soon-to-be deprecated maptools package with permission from author Roger Bivand

Usage

```
leglabs(vec, under = "under", over = "over", between = "-", reverse = FALSE)
```

Arguments

vec	vector of break values
under	character value for under
over	character value for over
between	character value for between
reverse	flag to reverse order of values, you will also need to reorder colours, see example

Author(s)

Roger Bivand, Nick Bearman, Nicholas Lewin-Koh

LogNormalPriorCh *Compute Parameters to Calibrate a Log-normal Distribution*

Description

Compute parameters to calibrate the prior distribution of a relative risk that has a log-normal distribu

Usage

```
LogNormalPriorCh(theta1, theta2, prob1, prob2)
```

Arguments

theta1	lower quantile
theta2	upper quantile
prob1	lower probability
prob2	upper probability

Value

A list containing

mu	mean of log-normal distribution
sigma	variance of log-normal distribution

Author(s)

Jon Wakefield

Examples

```
# Calibrate the log-normal distribution s.t. the 95% confidence interval is [0.2, 5]
param <- LogNormalPriorCh(0.2, 5, 0.025, 0.975)
curve(dlnorm(x,param$mu,param$sigma), from=0, to=6, ylab="density")
```

---

mapvariable *Plot Levels of a Variable in a Colour-Coded Map*

Description

Plot levels of a variable in a colour-coded map along with a legend.

Usage

```
mapvariable(
  y,
  spatial.polygon,
  ncut = 1000,
  nlevels = 10,
  lower = NULL,
  upper = NULL,
  main = NULL,
  xlab = NULL,
  ylab = NULL
)
```

Arguments

y	variable to plot
spatial.polygon	an object of class SpatialPolygons (See SpatialPolygons-class)
ncut	number of cuts in colour levels to plot
nlevels	number of levels to include in legend
lower	lower bound of levels
upper	upper bound of levels

main	an overall title for the plot
xlab	a title for the x axis
ylab	a title for the y axis

Value

A map colour-coded to indicate the different levels of y

Author(s)

Jon Wakefield, Nicky Best, Sebastien Haneuse, and Albert Y. Kim

References

Bivand, R. S., Pebesma E. J., and Gomez-Rubio V. (2008) *Applied Spatial Data Analysis with R*. Springer Series in Statistics. E. J. Pebesma and R. S. Bivand. (2005) Classes and methods for spatial data in R. *R News*, **5**, 9–13.

Examples

```
data(scotland)
map <- scotland$spatial.polygon
y <- scotland$data$cases
E <- scotland$data$expected
SMR <- y/E
mapvariable(SMR,map,main="Scotland",xlab="Eastings (km)",ylab="Northings (km)")
```

NYleukemia *Upstate New York Leukemia Data*

Description

Census tract level (n=281) leukemia data for the 8 counties in upstate New York from 1978-1982, paired with population data from the 1980 census. Note that 4 census tracts were completely surrounded by another unique census tract; when applying the Bayesian cluster detection model in bayes_cluster(), we merge them with the surrounding census tracts yielding n=277 areas.

Usage

```
NYleukemia
```

Format

List with 5 items:

geo table of the FIPS code, longitude, and latitude of the geographic centroid of each census tract

data table of the FIPS code, number of cases, and population of each census tract

spatial.polygon bject of class SpatialPolygons

surrounded row IDs of the 4 census tracts that are completely surrounded by the

surrounding census tracts

References

Turnbull, B. W. et al (1990) Monitoring for clusters of disease: application to leukemia incidence in upstate New York *American Journal of Epidemiology*, **132**, 136–143

Examples

```
## Load data and convert coordinate system from latitude/longitude to grid
data(NYleukemia)
map <- NYleukemia$spatial.polygon
population <- NYleukemia$data$population
cases <- NYleukemia$data$cases
centroids <- latlong2grid(NYleukemia$geo[, 2:3])

## Identify the 4 census tract to be merged into their surrounding census tracts.
remove <- NYleukemia$surrounded
add <- NYleukemia$surrounding

## Merge population and case counts
population[add] <- population[add] + population[remove]
population <- population[-remove]
cases[add] <- cases[add] + cases[remove]
cases <- cases[-remove]

## Modify geographical objects accordingly
map <- SpatialPolygons(map@polygons[-remove], proj4string=CRS("+proj=longlat +ellps=WGS84"))
centroids <- centroids[-remove, ]

## Plot incidence in latitude/longitude
plotmap(cases/population, map, log=TRUE, nclr=5)
points(grid2latlong(centroids), pch=4)
```

NYleukemia_sf *Upstate New York Leukemia*

Description

Census tract level (n=281) leukemia data for the 8 counties in upstate New York from 1978-1982, paired with population data from the 1980 census. Note that 4 census tracts were completely surrounded by another unique census tract; when applying the Bayesian cluster detection model in `bayes_cluster()`, we merge them with the surrounding census tracts yielding n=277 areas.

Usage

```
NYleukemia_sf
```

Format

An sf 'POLYGON' data frame with 281 rows and 4 variables:

geometry Geometric representation of 8 counties in upstate New York

cases Number of cases per county

population Population of each census tract

censustract.FIPS 11-digit Federal Information Processing System identification number for each county

Source

Turnbull, B. W. et al (1990) Monitoring for clusters of disease: application to leukemia incidence in upstate New York *American Journal of Epidemiology*, **132**, 136–143

Examples

```
# Static map of NY Leukemia rate per county
library(ggplot2)
## Not run:
ggplot(NYleukemia_sf) +
  geom_sf(aes(fill= cases/population)) +
  scale_fill_gradient(low = "white", high = "red")

## End(Not run)
```

---

pennLC *Pennsylvania Lung Cancer*

Description

County-level (n=67) population/case data for lung cancer in Pennsylvania in 2002, stratified on race (white vs non-white), gender and age (Under 40, 40-59, 60-69 and 70+). Additionally, county-specific smoking rates.

Usage

```
pennLC
```

Format

List of 3 items

geo a table of county IDs, longitude/latitude of the geographic centroid of each county

data a table of county IDs, number of cases, population and strata information

smoking a table of county IDs and proportion of smokers

spatial.polygon an object of class SpatialPolygons

Source

Population data was obtained from the 2000 decennial census, lung cancer and smoking data were obtained from the Pennsylvania Department of Health website: https://www.health.pa.gov/Pages/default.aspx

Examples

```
data(pennLC)
pennLC$geo
pennLC$data
pennLC$smoking
# Map smoking rates in Pennsylvania
mapvariable(pennLC$smoking[,2], pennLC$spatial.polygon)
```

---

pennLC_sf *Pennsylvania Lung Cancer*

Description

County-level (n=67) population/case data for lung cancer in Pennsylvania in 2002, stratified on race (white vs non-white), gender and age (Under 40, 40-59, 60-69 and 70+). Additionally, county-specific smoking rates.

Usage

```
pennLC_sf
```

Format

An sf POLYGON data frame with 1072 rows = 67 counties x 2 race x 2 gender x 4 age bands

county Pennsylvania county

cases Number of cases per county split by strata

population Population per county split by strata

race Race (w = white and o = non-white)

gender Gender (f = female and m = male)

age Age (4 bands)

smoking Overall county smoking rate (not broken down by strata)

geometry Geometric representation of counties in Pennsylvania

Source

Population data was obtained from the 2000 decennial census, lung cancer and smoking data were obtained from the Pennsylvania Department of Health website:https://www.health.pa.gov/Pages/default.aspx.

Examples

```
library(ggplot2)
library(dplyr)
# Sum cases & population for each county
lung_cancer_rate <- pennLC_sf %>%
  group_by(county) %>%
  summarize(cases = sum(cases), population = sum(population)) %>%
  mutate(rate = cases/population)

# Static map of Pennsylvania lung cancer rates for each county
## Not run:
ggplot() +
  geom_sf(data = lung_cancer_rate, aes(fill = rate))

## End(Not run)
```

---

plotmap *Plot Levels of a Variable in a Colour-Coded Map*

Description

Plot levels of a variable in a colour-coded map.

Usage

```
plotmap(
  values,
  map,
  log = FALSE,
  nclr = 7,
  include.legend = TRUE,
  lwd = 0.5,
  round = 3,
  brks = NULL,
  legend = NULL,
  location = "topright",
  rev = FALSE
)
```

Arguments

values	variable to plot
map	an object of class SpatialPolygons (See SpatialPolygons-class)
log	boolean of whether to plot values on log scale
nclr	number of colour-levels to use
include.legend	boolean of whether to include legend
lwd	line width of borders of areas
round	number of digits to round to in legend
brks	if desired, pre-specified breaks for legend
legend	if desired, a pre-specified legend
location	location of legend
rev	boolean of whether to reverse colour scheme (darker colours for smaller values)

Value

A map colour-coded to indicate the different levels of values.

Author(s)

Albert Y. Kim

Examples

```
## Load data
data(scotland)
map <- scotland$spatial.polygon
y <- scotland$data$cases
E <- scotland$data$expected
SMR <- y/E
## Plot SMR
plotmap(SMR, map, nclr=9, location="topleft")
```

---

polygon2spatial_polygon

Convert a Polygon to a Spatial Polygons Object

Description

Converts a polygon (a matrix of coordinates with NA values to separate subpolygons) into a Spatial Polygons object.

Usage

```
polygon2spatial_polygon(
  poly,
  coordinate.system,
  area.names = NULL,
  nrepeats = NULL
)
```

Arguments

poly	a 2-column matrix of coordinates, where each complete subpolygon is separated by NA's
coordinate.system	the coordinate system to use
area.names	names of all areas
nrepeats	number of sub polygons for each area

Details

Just as when plotting with the graphics::polygon() function, it is assumed that each subpolygon is to be closed by joining the last point to the first point. In the matrix poly, NA values separate complete subpolygons. In the case with an area consists of more than one separate closed polygon, nrepeats specifies the number of closed polygons associated with each area.

Value

An object of class SpatialPolygons (See SpatialPolygons-class from the **sp** package).

Author(s)

Albert Y. Kim

References

Bivand, R. S., Pebesma E. J., and Gomez-Rubio V. (2008) *Applied Spatial Data Analysis with R*. Springer Series in Statistics. E. J. Pebesma and R. S. Bivand. (2005) Classes and methods for spatial data in R. *R News*, **5**, 9–13.

Examples

```
data(scotland)

polygon <- scotland$polygon$polygon
coord.system <- "+proj=eqc +lat_ts=0 +lat_0=0 +lon_0=0 +x_0=0 +y_0=0 "
coord.system <- paste(coord.system, "+ellps=WGS84 +datum=WGS84 +units=m +no_defs", sep = "")
names <- scotland$data$county.names
nrepeats <- scotland$polygon$nrepeats

spatial.polygon <- polygon2spatial_polygon(polygon,coord.system,names,nrepeats)
```

```
par(mfrow=c(1,2))
# plot using polygon function
plot(polygon,type='n',xlab="Eastings (km)",ylab="Northings (km)",main="Polygon File")
polygon(polygon)

# plot as spatial polygon object
plot(spatial.polygon,axes=TRUE)
title(xlab="Eastings (km)",ylab="Northings (km)",main="Spatial Polygon")

# Note that area 23 (argyll-bute) consists of 8 separate polygons
nrepeats[23]
plot(spatial.polygon[23],add=TRUE,col="red")
```

`process_MCMC_sample` *Process MCMC Sample*

Description

Take the output of sampled configurations from `MCMC_simulation` and produce area-by-area summaries

Usage

```
process_MCMC_sample(sample, param, RR.area, cluster.list, cutoffs)
```

Arguments

`sample`	list objects of sampled configurations
`param`	mean relative risk associted with each of the `n.zones` single zones considering the wide prior
`RR.area`	mean relative risk associated with each of the `n` areas considering the narrow prior
`cluster.list`	list of length `n.zones` listing, for each single zone, its component areas
`cutoffs`	cutoffs used to declare highs (clusters) and lows (anti-clusters)

Value

`high.area`	Probability of cluster membership for each area
`low.area`	Probability of anti-cluster membership for each area
`RR.est.area`	Smoothed relative risk estimates for each area

References

Wakefield J. and Kim A.Y. (2013) A Bayesian model for cluster detection. *Biostatistics*, **14**, 752–765.

scotland *Lip Cancer in Scotland*

Description

County-level (n=56) data for lip cancer among males in Scotland between 1975-1980

Usage

```
scotland
```

Format

List containing:

geo a table of county IDs, x-coordinates (eastings) and y-coordinates (northings) of the geographic centroid of each county.

data a table of county IDs, number of cases, population and strata information

spatial.polygon a Spatial Polygons class (See SpatialPolygons-class) map of Scotland

polygon a polygon map of Scotland (See `polygon2spatial_polygon()`

Source

Kemp I., Boyle P., Smans M. and Muir C. (1985) Atlas of cancer in Scotland, 1975-1980, incidence and epidemiologic perspective *International Agency for Research on Cancer* **72**.

References

Clayton D. and Kaldor J. (1987) Empirical Bayes estimates of age-standardized relative risks for use in disease mapping. *Biometrics*, **43**, 671–681.

Examples

```
data(scotland)
data <- scotland$data
scotland.map <- scotland$spatial.polygon
SMR <- data$cases/data$expected
mapvariable(SMR,scotland.map)
```

scotland_sf *Lip Cancer in Scotland*

Description

County-level (n=56) data for lip cancer among males in Scotland between 1975-1980

Usage

```
scotland_sf
```

Format

A data frame with 56 rows representing counties and 5 variables:

geometry Geometric representation of counties in Scotland

cases Number of Lip Cancer cases per county

county.names Scotland County name

AFF Proportion of the population who work in agricultural fishing and farming

expected Expected number of lip cancer cases

Source

Kemp I., Boyle P., Smans M. and Muir C. (1985) Atlas of cancer in Scotland, 1975-1980, incidence and epidemiologic perspective *International Agency for Research on Cancer* **72**.

References

Clayton D. and Kaldor J. (1987) Empirical Bayes estimates of age-standardized relative risks for use in disease mapping. *Biometrics*, **43**, 671–681.

Examples

```
library(ggplot2)
## Not run:
ggplot() +
geom_sf(data = scotland_sf, aes(fill= cases))

## End(Not run)
```

zones *Create set of all single zones and output geographical information*

Description

Based on the population counts and centroid coordinates of each of n areas, output the set of n.zones single zones as defined by Kulldorff and other geographical information.

Usage

```
zones(geo, population, pop.upper.bound)
```

Arguments

geo	n x 2 table of the (x,y)-coordinates of the area centroids
population	a vector of population counts of each area
pop.upper.bound	maximum proportion of study region each zone can contain

Value

A list containing

nearest.neighbors	list of n elements, where each element is a vector of the nearest neighbors in order of distance up until pop.upper.bound of the total population is attained
cluster.coords	n.zones x 2 table of the center and the radial area for each zone
dist	n x n inter-point distance matrix of the centroids

Author(s)

Albert Y. Kim

References

Kulldorff, M. (1997) A spatial scan statistic. *Communications in Statistics: Theory and Methods*, **26**, 1481–1496. Kulldorff M. and Nagarwalla N. (1995) Spatial disease clusters: Detection and Inference. *Statistics in Medicine*, **14**, 799–810.

Examples

```
data(pennLC)
geo <- pennLC$geo[,2:3]
geo <- latlong2grid(geo)
population <- tapply(pennLC$data$population, pennLC$data$county, sum)
pop.upper.bound <- 0.5
geo.info <- zones(geo, population, pop.upper.bound)
```

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