

Package ‘CRTspat’

October 15, 2023

Title Workflow for Cluster Randomised Trials with Spillover

Version 1.0.0

Maintainer Thomas Smith <Thomas-a.Smith@unibas.ch>

Description Design, workflow and statistical analysis of Cluster Randomised Trials of (health) interventions where there may be geographical contamination between the arms (see <<https://thomasasmith.github.io/articles/CRTspat.html>>).

License MIT + file LICENSE

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

VignetteBuilder knitr

Additional_repositories <https://inla.r-inla-download.org/R/stable/>

Imports ggplot2,
stats,
utils,
geepack,
MASS,
tidyr,
magrittr,
dplyr,
OOR,
lme4,
sf,
Matrix,
spatstat.geom,
spatstat.random,
jagsUI,
TSP

Suggests knitr, rmarkdown, INLA,
testthat (>= 2.0.0)

Config/testthat/edition 2

Depends R (>= 3.5.0)

R topics documented:

aggregateCRT	2
anonymize_site	3
coef.CRTanalysis	4
compute_distance	4
compute_mesh	6
CRTanalysis	7
CRTpower	10
CRTsp	11
CRTwrite	13
fitted.CRTanalysis	14
latlong_as_xy	15
plotCRT	16
predict.CRTanalysis	18
randomizeCRT	19
readdata	20
residuals.CRTanalysis	20
simulateCRT	21
specify_buffer	24
specify_clusters	24
summary.CRTanalysis	26
summary.CRTsp	26
Index	28

aggregateCRT	<i>Aggregate data across records with duplicated locations</i>
--------------	--

Description

aggregateCRT aggregates data from a "CRTsp" object or trial data frame containing multiple records with the same location, and outputs a list of class "CRTsp" containing single values for each location, for both the coordinates and the auxiliary variables.

Usage

```
aggregateCRT(trial, auxiliaries = NULL)
```

Arguments

trial	An object of class "CRTsp" containing locations (x,y) and variables to be summed
auxiliaries	vector of names of auxiliary variables to be summed across each location

Details

Variables that in the trial dataframe that are not included in auxiliaries are retained in the output algorithm "CRTsp" object, with the value corresponding to that of the first record for the location in the input data frame

Value

A list of class "CRTsp"

Examples

```
{
  trial <- readdata('example_site.csv')
  trial$base_denom <- 1
  aggregated <- aggregateCRT(trial, auxiliaries = c("RDT_test_result", "base_denom"))
}
```

anonymize_site

*Anonymize locations of a trial site***Description**

anonymize_site transforms coordinates to remove potential identification information.

Usage

```
anonymize_site(trial, ID = NULL, latvar = "lat", longvar = "long")
```

Arguments

trial	"CRTsp" object or trial data frame with co-ordinates of households
ID	name of column used as an identifier for the points
latvar	name of column containing latitudes in decimal degrees
longvar	name of column containing longitudes in decimal degrees

Details

The coordinates are transformed to support confidentiality of information linked to households by replacing precise geo-locations with transformed co-ordinates which preserve distances but not positions. The input may have either lat long or x,y coordinates. The function first searches for any lat long co-ordinates and converts these to x,y Cartesian coordinates. These are then rotated by a random angle about a random origin. The returned object has transformed co-ordinates re-centred at the origin. Centroids stored in the "CRTsp" object are removed. Other data are unchanged.

Value

A list of class "CRTsp".

Examples

```
#Rotate and reflect test site locations
transformedTestlocations <- anonymize_site(trial = readdata("exampleCRT.txt"))
```

coef.CRTanalysis	<i>Extract model coefficients</i>
------------------	-----------------------------------

Description

coef.CRTanalysis method for extracting model fitted values

Usage

```
## S3 method for class 'CRTanalysis'
coef(object, ...)
```

Arguments

object	CRTanalysis object
...	other arguments

Value

the model coefficients returned by the statistical model run within the CRTanalysis function

Examples

```
{example <- readdata('exampleCRT.txt')
exampleGEE <- CRTanalysis(example, method = "GEE")
coef(exampleGEE)
}
```

compute_distance	<i>Compute distance or surround values for a cluster randomized trial</i>
------------------	---

Description

compute_distance computes distance or surround values for a cluster randomized trial (CRT)

Usage

```
compute_distance(trial, distance = "nearestDiscord", scale_par = NULL)
```

Arguments

trial	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), and arm assignments (factor arm).	
distance	the quantity(s) to be computed. Options are:	
	"nearestDiscord"	distance to nearest discordant location (km)
	"disc"	disc
	"kern"	kernel-based measure
	"hdep"	Tukey half space depth

"sdep"	simplicial depth
scale_par	scale parameter equal to the disc radius in km if distance = "disc" or to the standard deviance of the kernels if distance = "kern"

Details

For each selected distance measure, the function first checks whether the variable is already present, and carries out the calculations only if the corresponding field is absent from the `trial` data frame.

If distance = "nearestDiscord" is selected the computed values are Euclidean distances assigned a positive sign for the intervention arm of the trial, and a negative sign for the control arm.

If distance = "disc" is specified, the disc statistic is computed for each location as the number of locations within the specified radius that are in the intervention arm ([Anaya-Izquierdo & Alexander\(2020\)](#)). The input value of `scale_par` is stored in the design list of the output "CRTsp" object. Recalculation is carried out if the input value of `scale_par` differs from the one in the input design list. The value of the the surround calculated based on intervened locations is divided by the value of the surround calculated on the basis of all locations, so the value returned is a proportion.

If distance = "kern" is specified, the Normal curve with standard deviation `scale_par` is used to simulate diffusion of the intervention effect by Euclidean distance. For each location in the trial, the contributions of all intervened locations are summed. As with distance = "disc", when distance = "kern" the surround calculated based on intervened locations is divided by the value of the surround calculated on the basis of all locations, so the value returned is a proportion.

If either distance = "hdep" or distance = "sdep" is specified then both the simplicial depth and Tukey half space depth are calculated using the algorithm of [Rousseeuw & Ruts\(1996\)](#). The half-depth probability within the intervention cloud (d_i) is computed with respect to other locations in the intervention arm ([Anaya-Izquierdo & Alexander\(2020\)](#)). The half-depth within the half-depth within the control cloud (d_c) is also computed. CRTspat returns the proportion $d_i/(d_c + d_i)$.

Value

The input "CRTsp" object with additional column(s) added to the `trial` data frame with variable name corresponding to the input value of distance.

Examples

```
{
# Calculate the disc with a radius of 0.5 km
exampletrial <- compute_distance(trial = readdata('exampleCRT.txt'),
distance = 'disc', scale_par = 0.5)
}
```

compute_mesh	compute_mesh <i>create objects required for INLA analysis of an object of class "CRTsp"</i> .
--------------	---

Description

compute_mesh create objects required for INLA analysis of an object of class "CRTsp".

Usage

```
compute_mesh(
  trial = trial,
  offset = -0.1,
  max.edge = 0.25,
  inla.alpha = 2,
  maskbuffer = 0.5,
  pixel = 0.5
)
```

Arguments

trial	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), and arm assignments (factor arm) and outcome.
offset	see inla.mesh.2d documentation
max.edge	see inla.mesh.2d documentation
inla.alpha	parameter related to the smoothness (see inla documentation)
maskbuffer	numeric: width of buffer around points (km)
pixel	numeric: size of pixel (km)

Details

compute_mesh carries out the computationally intensive steps required for setting-up an INLA analysis of an object of class "CRTsp", creating the prediction mesh and the projection matrices. The mesh can be reused for different models fitted to the same geography. The computational resources required depend largely on the resolution of the prediction mesh. The prediction mesh is thinned to include only pixels centred at a distance less than maskbuffer from the nearest point.

A warning may be generated if the Matrix library is not loaded.

Value

list

- prediction Data frame containing the prediction points and covariate values
- A projection matrix from the observations to the mesh nodes.
- Ap projection matrix from the prediction points to the mesh nodes.
- indexs index set for the SPDE model
- spde SPDE model
- pixel pixel size (km)

Examples

```
{
# low resolution mesh for test dataset
library(Matrix)
example <- readdata('exampleCRT.txt')
exampleMesh=compute_mesh(example, pixel = 0.5)
}
```

CRTanalysis

Analysis of cluster randomized trial with contamination

Description

CRTanalysis carries out a statistical analysis of a cluster randomized trial (CRT).

Usage

```
CRTanalysis(
  trial,
  method = "GEE",
  distance = "nearestDiscord",
  scale_par = NULL,
  cfunc = "L",
  link = "logit",
  numerator = "num",
  denominator = "denom",
  excludeBuffer = FALSE,
  alpha = 0.05,
  baselineOnly = FALSE,
  baselineNumerator = "base_num",
  baselineDenominator = "base_denom",
  personalProtection = FALSE,
  clusterEffects = TRUE,
  spatialEffects = FALSE,
  requireMesh = FALSE,
  inla_mesh = NULL
)
```

Arguments

trial	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), and arm assignments (factor arm) and outcome data (see details).												
method	statistical method with options: <table> <tbody> <tr> <td>"EMP"</td> <td>simple averages of the data</td> </tr> <tr> <td>"T"</td> <td>comparison of cluster means by t-test</td> </tr> <tr> <td>"GEE"</td> <td>Generalised Estimating Equations</td> </tr> <tr> <td>"LME4"</td> <td>Generalized Linear Mixed-Effects Models</td> </tr> <tr> <td>"INLA"</td> <td>Integrated Nested Laplace Approximation (INLA)</td> </tr> <tr> <td>"MCMC"</td> <td>Markov chain Monte Carlo using "JAGS"</td> </tr> </tbody> </table>	"EMP"	simple averages of the data	"T"	comparison of cluster means by t-test	"GEE"	Generalised Estimating Equations	"LME4"	Generalized Linear Mixed-Effects Models	"INLA"	Integrated Nested Laplace Approximation (INLA)	"MCMC"	Markov chain Monte Carlo using "JAGS"
"EMP"	simple averages of the data												
"T"	comparison of cluster means by t-test												
"GEE"	Generalised Estimating Equations												
"LME4"	Generalized Linear Mixed-Effects Models												
"INLA"	Integrated Nested Laplace Approximation (INLA)												
"MCMC"	Markov chain Monte Carlo using "JAGS"												

"WCA" Within cluster analysis

distance Measure of distance or surround with options:

"nearestDiscord"	distance to nearest discordant location (km)
"disc"	disc
"kern"	surround based on sum of normal kernels
"hdep"	Tukey half space depth
"sdep"	simplicial depth

scale_par numeric: pre-specified value of contamination parameter or disc radius

cfunc transformation defining the contamination function with options:

"Z"	arm effects not considered	reference model
"X"	contamination not modelled	the only valid value of cfunc for methods "EMP", "T" and "GEE"
"L"	inverse logistic (sigmoid)	the default for "INLA" and "MCMC" methods
"P"	inverse probit (error function)	available with "INLA" and "MCMC" methods
"S"	piecewise linear	only available with the "MCMC" method
"E"	estimation of scale factor	only available with distance = "disc" or distance = "kern"
"R"	rescaled linear	

link link function with options:

"logit"	(the default). numerator has a binomial distribution with denominator denominator.
"log"	numerator is Poisson distributed with an offset of log(denominator).
"cloglog"	numerator is Bernoulli distributed with an offset of log(denominator).
"identity"	The outcome is numerator/denominator with a normally distributed error function.

numerator string: name of numerator variable for outcome

denominator string: name of denominator variable for outcome data (if present)

excludeBuffer logical: indicator of whether any buffer zone (records with buffer=TRUE) should be excluded from analysis

alpha numeric: confidence level for confidence intervals and credible intervals

baselineOnly logical: indicator of whether required analysis is of effect size or of baseline only

baselineNumerator string: name of numerator variable for baseline data (if present)

baselineDenominator string: name of denominator variable for baseline data (if present)

personalProtection logical: indicator of whether the model includes local effects with no contamination

clusterEffects logical: indicator of whether the model includes cluster random effects

spatialEffects logical: indicator of whether the model includes spatial random effects

requireMesh logical: indicator of whether spatial predictions are required

inla_mesh string: name of pre-existing INLA input object created by compute_mesh()

Details

CRTanalysis is a wrapper for the statistical analysis packages: **geepack**, **INLA**, **jagsUI**, and the **t.test** function of package **stats**.

The wrapper does not provide an interface to the full functionality of these packages. It is specific for typical analyses of cluster randomized trials with geographical clustering. Further details are provided in the **vignette**.

The key results of the analyses can be extracted using a `summary()` of the output list. The `model_object` in the output list is the usual output from the statistical analysis routine, and can be also be inspected with `summary()`, or analysed using `stats::fitted()` for purposes of evaluation of model fit etc..

`link = "cloglog"` specifies a complementary log-log link function for which the numerator must be coded as 0 or 1. Technically the binomial denominator is then 1. The value of denominator is used as a rate multiplier.

With the "INLA" and "MCMC" methods 'iid' random effects are used to model extra-Poisson variation.

`scale_par` specifies the contamination parameter for models where this is fixed (`cfunc = "R"`).

Value

list of class `CRTanalysis` containing the following results of the analysis:

- `description` : description of the dataset
- `method` : statistical method
- `pt_est` : point estimates
- `int_est` : interval estimates
- `model_object` : object returned by the fitting routine
- `contamination` : function values and statistics describing the estimated contamination

Examples

```
example <- readdata('exampleCRT.txt')
# Analysis of test dataset by t-test
exampleT <- CRTanalysis(example, method = "T")
summary(exampleT)
# Standard GEE analysis of test dataset ignoring contamination
exampleGEE <- CRTanalysis(example, method = "GEE")
summary(exampleGEE)
# LME4 analysis with error function contamination function
exampleLME4 <- CRTanalysis(example, method = "LME4", cfunc = "P")
summary(exampleLME4)
```

Description

CRTpower carries out power and sample size calculations for CRTs.

Usage

```
CRTpower(
  trial = NULL,
  locations = NULL,
  alpha = 0.05,
  desiredPower = 0.8,
  effect = NULL,
  yC = NULL,
  outcome_type = "d",
  sigma2 = NULL,
  phi = 1,
  N = 1,
  ICC = NULL,
  k = NULL,
  sd_h = 0
)
```

Arguments

trial	dataframe or 'CRTsp' object containing Cartesian coordinates of locations in columns 'x' and 'y'.
locations	numeric: total number of units available for randomization (required if trial is not specified)
alpha	numeric: confidence level
desiredPower	numeric: desired power
effect	numeric: required effect size
yC	numeric: baseline value of outcome
outcome_type	character with options - 'y': continuous; 'n': count; 'e': event rate; 'p': proportion; 'd': dichotomous.
sigma2	numeric: variance of the outcome (required for outcome_type = 'y')
phi	numeric: overdispersion parameter (for outcome_type = 'n' or outcome_type = 'e')
N	numeric: mean of the denominator for proportions (for outcome_type = 'p')
ICC	numeric: Intra-Cluster Correlation
k	integer: number of clusters in each arm (required if trial is not specified)
sd_h	standard deviation of number of units per cluster (required if trial is not specified)

Details

Power and sample size calculations are for a two-arm trial using the formulae of [Hemming et al, 2011](#) which use a normal approximation for the inter-cluster variation. For counts or event rate data a quasi-Poisson model is assumed. The functions do not consider any loss in power due to contamination, loss to follow-up etc. If geolocations are not input power and sample size calculations are based on the scalar input parameters.

If a trial dataframe or 'CRTsp' object containing a pre-existing randomization is input then the numbers and sizes of clusters are in the input data are used to estimate the power. If buffer zones have been specified then separate calculations are made for the core area and for the full site. The output is an object of class 'CRTsp' containing any input trial data.frame and values for:

- The required numbers of clusters to achieve the specified power.
- The design effect based on the input ICC.
- Calculations of the nominal power (ignoring any bias caused by contamination effects)

Value

A list of class 'CRTsp' object comprising the input data, cluster and arm assignments, trial description and results of power calculations

Examples

```
{# Example without input geolocations
examplePower1 = CRTpower(locations = 3000, ICC=0.10, effect=0.4, alpha = 0.05,
  outcome_type = 'd', desiredPower = 0.8, yC=0.35, k = 20, sd_h=5)
summary(examplePower1)
# Example with input geolocations and randomisation
examplePower2 = CRTpower(trial = readdata('example_site.csv'), desiredPower = 0.8,
  effect=0.4, yC=0.35, outcome_type = 'd', ICC = 0.05, k = 20)
summary(examplePower2)
}
```

CRTsp

Create or update a "CRTsp" object

Description

CRTsp coerces data frames containing co-ordinates and location attributes into objects of class "CRTsp" or creates a new "CRTsp" object by simulating a set of Cartesian co-ordinates for use as the locations in a simulated trial site

Usage

```
CRTsp(
  x = NULL,
  design = NULL,
  geoscale = NULL,
  locations = NULL,
  kappa = NULL,
  mu = NULL
)
```

Arguments

x	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), and arm assignments (factor arm). Optionally specification of a buffer zone (logical buffer); any other variables required for subsequent analysis.
design	list: an optional list containing the requirements for the power of the trial
geoscale	standard deviation of random displacement from each settlement cluster center (for new objects)
locations	number of locations in population (for new objects)
kappa	intensity of Poisson process of settlement cluster centers (for new objects)
mu	mean number of points per settlement cluster (for new objects)

Details

If a data frame or "CRTsp" object is input then the output "CRTsp" object is validated, a description of the geography is computed and power calculations are carried out.

If geoscale, locations, kappa and mu are specified then a new trial dataframe is constructed corresponding to a novel simulated human settlement pattern. This is generated using the Thomas algorithm (rThomas) in `spatstat.random` allowing the user to defined the density of locations and degree of spatial clustering. The resulting trial data frame comprises a set of Cartesian coordinates centred at the origin.

Value

A list of class "CRTsp" containing the following components:

design	list:	parameters required for power calculations
geom_full	list:	summary statistics describing the site
geom_core	list:	summary statistics describing the core area (when a buffer is specified)
trial	data frame:	rows correspond to geolocated points, as follows:
	x	numeric vector: x-coordinates of locations
	y	numeric vector: y-coordinates of locations
	cluster	factor: assignments to cluster of each location
	arm	factor: assignments to "control" or "intervention" for each location
	nearestDiscord	numeric vector: Euclidean distance to nearest discordant location (km)
	buffer	logical: indicator of whether the point is within the buffer
	...	other objects included in the input "CRTsp" object or data frame

Examples

```
{# Generate a simulated area with 10,000 locations
example_area = CRTsp(geoscale = 1, locations=10000, kappa=3, mu=40)
summary(example_area)
}
```

CRTwrite

Export of GIS layer from 'CRTsp'

Description

CRTwrite exports a simple features object in a GIS format

Usage

```
CRTwrite(
  object,
  dsn,
  feature = "clusters",
  buffer_width,
  maskbuffer = 0.2,
  ...
)
```

Arguments

object	object of class 'CRTsp'								
dsn	dataset name (relative path) for output objects								
feature	feature to be exported, options are: <table> <tbody> <tr> <td>'cluster'</td> <td>cluster assignments</td> </tr> <tr> <td>'arms'</td> <td>arm assignments</td> </tr> <tr> <td>'buffer'</td> <td>buffer zone or contamination zone</td> </tr> <tr> <td>'mask'</td> <td>mask for areas that are distant from habitations</td> </tr> </tbody> </table>	'cluster'	cluster assignments	'arms'	arm assignments	'buffer'	buffer zone or contamination zone	'mask'	mask for areas that are distant from habitations
'cluster'	cluster assignments								
'arms'	arm assignments								
'buffer'	buffer zone or contamination zone								
'mask'	mask for areas that are distant from habitations								
buffer_width	width of buffer between discordant locations (km)								
maskbuffer	radius of buffer drawn around inhabited areas (km)								
...	other arguments passed to 'sf::write_sf'								

Details

'sf::write_sf' is used to format the output. The function returns TRUE on success, FALSE on failure, invisibly.

If the input object contains a 'centroid' then this is used to compute lat long coordinates, which are assigned the "WGS84" coordinate reference system. Otherwise the objects have equirectangular co-ordinates with centroid (0,0).

If feature = 'buffer' then buffer width determination is as described under plotCRT().

The output vector objects are constructed by forming a Voronoi tessellation of polygons around each of the locations and combining these polygons. The polygons on the outside of the study area extend outwards to an external rectangle. The 'mask' is used to mask out the areas of these polygons that are at a distance > maskbuffer from the nearest location.

Value

obj, invisibly

Examples

```
tmpdir = tempdir()
dsn <- paste0(tmpdir, '/arms')
CRTwrite(readdata('exampleCRT.txt'), dsn = dsn, feature = 'arms',
driver = 'ESRI Shapefile', maskbuffer = 0.2)
```

<code>fitted.CRTanalysis</code>	<i>Extract model fitted values</i>
---------------------------------	------------------------------------

Description

`fitted.CRTanalysis` method for extracting model fitted values

Usage

```
## S3 method for class 'CRTanalysis'
fitted(object, ...)
```

Arguments

<code>object</code>	CRTanalysis object
<code>...</code>	other arguments

Value

the fitted values returned by the statistical model run within the `CRTanalysis` function

Examples

```
{example <- readdata('exampleCRT.txt')
exampleGEE <- CRTanalysis(example, method = "GEE")
fitted_values <- fitted(exampleGEE)
}
```

latlong_as_xy	<i>Convert lat long co-ordinates to x,y</i>
---------------	---

Description

latlong_as_xy converts co-ordinates expressed as decimal degrees into x,y

Usage

```
latlong_as_xy(trial, latvar = "lat", longvar = "long")
```

Arguments

trial	A trial dataframe or list of class "CRTsp" containing latitudes and longitudes in decimal degrees
latvar	name of column containing latitudes in decimal degrees
longvar	name of column containing longitudes in decimal degrees

Details

The output object contains the input locations replaced with Cartesian coordinates in units of km, centred on (0,0), corresponding to using the equirectangular projection (valid for small areas). Other data are unchanged.

Value

A list of class "CRTsp" containing the following components:

geom_full	list:	summary statistics describing the site
trial	data frame:	rows correspond to geolocated points, as follows:
	x	numeric vector: x-coordinates of locations
	y	numeric vector: y-coordinates of locations
	...	other objects included in the input "CRTsp" object or data frame

Examples

```
examplexy <- latlong_as_xy(readdata("example_latlong.csv"))
```

plotCRT

*Graphical displays of the geography of a CRT***Description**

plotCRT returns graphical displays of the geography of a CRT or of the results of statistical analyses of a CRT

Usage

```
plotCRT(
  object,
  map = FALSE,
  distance = "nearestDiscord",
  fill = "arms",
  showLocations = FALSE,
  showClusterBoundaries = TRUE,
  showClusterLabels = FALSE,
  showBuffer = FALSE,
  cpalette = NULL,
  buffer_width = NULL,
  maskbuffer = 0.2,
  labelsizes = 4,
  legend.position = NULL
)
```

Arguments

object	object of class 'CRTanalysis' produced by CRTanalysis()
map	logical: indicator of whether a map is required
distance	measure of distance or surround with options:

"nearestDiscord"	distance to nearest discordant location (km)
"disc"	disc
"hdep"	Tukey's half space depth
"sdep"	simplicial depth

fill	fill layer of map with options:
------	---------------------------------

'cluster'	cluster assignment
'arms'	arm assignment
'nearestDiscord'	distance to the nearest discordant location
'disc'	disc measure of surround
'hdep'	Tukey's half space depth
'sdep'	simplicial depth
'prediction'	model prediction of the outcome
'none'	No fill

showLocations	logical: determining whether locations are shown
showClusterBoundaries	logical: determining whether cluster boundaries are shown
showClusterLabels	logical: determining whether the cluster numbers are shown
showBuffer	logical: whether a buffer zone should be overlayed
cpalette	colour palette (to use different colours for clusters this must be at least as long as the number of clusters.
buffer_width	width of buffer zone to be overlayed (km)
maskbuffer	radius of buffer around inhabited areas (km)
labelsize	size of cluster number labels
legend.position	(using ggplot2::themes syntax)

Details

If `map = FALSE` and the input is a trial data frame or a `CRTsp` object, containing a randomisation to arms, a stacked bar chart of the outcome grouped by the specified distance is produced. If the specified distance has not yet been calculated an error is returned.

If `map = FALSE` and the input is a `CRTanalysis` object a plot of the estimated contamination function is generated. The fitted contamination function is plotted as a continuous blue line against the measure the surround or of the distance to the nearest discordant location. Using the same axes, data summaries are plotted for ten categories of distance from the boundary. Both the average of the outcome and confidence intervals are plotted.

- For analyses with logit link function the outcome is plotted as a proportion.
- For analyses with log or cloglog link function the outcome is plotted on a scale of the Williams mean ($\text{mean of } \exp(\log(x + 1)) - 1$)

If `map = TRUE` a thematic map corresponding to the value of `fill` is generated.

- `fill = 'clusters'` or leads to thematic map showing the locations of the clusters
- `fill = 'arms'` leads to a thematic map showing the geography of the randomization
- `fill = 'distance'` leads to a raster plot of the distance to the nearest discordant location.
- `fill = 'prediction'` leads to a raster plot of predictions from an 'INLA' model.

If `showBuffer = TRUE` the map is overlaid with a grey transparent layer showing which areas are within a defined distance of the boundary between the arms. Possibilities are:

- If the trial has not been randomised or if `showBuffer = FALSE` no buffer is displayed
- If `buffer_width` takes a positive value then buffers of this width are displayed irrespective of any pre-specified or contamination limits.
- If the input is a 'CRTanalysis' and contamination limits have been estimated by an 'LME4' or 'INLA' model then these limits are used to define the displayed buffer.
- If `buffer_width` is not specified and no contamination limits are available, then any pre-specified buffer (e.g. one generated by `specify_buffer()`) is displayed.

A message is output indicating which of these possibilities applies.

Value

graphics object produced by the ggplot2 package

Examples

```
{example <- readdata('exampleCRT.txt')
#Plot of data by distance
plotCRT(example)
#Map of locations only
plotCRT(example, map = TRUE, fill = 'none', showLocations = TRUE,
         showClusterBoundaries=FALSE, maskbuffer=0.2)
#show cluster boundaries and number clusters
plotCRT(example, map = TRUE, fill ='none', showClusterBoundaries=TRUE,
         showClusterLabels=TRUE, maskbuffer=0.2, labelsize = 2)
#show clusters in colour
plotCRT(example, map = TRUE, fill = 'clusters', showClusterLabels = TRUE,
         labelsize=2, maskbuffer=0.2)
#show arms
plotCRT(example, map = TRUE,
         fill = 'arms', maskbuffer=0.2, legend.position=c(0.8,0.8))
#contamination plot
analysis <- CRTanalysis(example)
plotCRT(analysis, map = FALSE)
}
```

predict.CRTanalysis *Model predictions*

Description

predict.CRTanalysis method for extracting model predictions

Usage

```
## S3 method for class 'CRTanalysis'
predict(object, ...)
```

Arguments

object	CRTanalysis object
...	other arguments

Value

the model predictions returned by the statistical model run within the CRTanalysis function

Examples

```
{example <- readdata('exampleCRT.txt')
exampleGEE <- CRTanalysis(example, method = "GEE")
predictions <- predict(exampleGEE)
}#'
```

randomizeCRT

*Randomize a two-armed cluster randomized trial***Description**

randomizeCRT carries out randomization of clusters for a CRT and augments the trial dataframe with assignments to arms

Usage

```
randomizeCRT(
  trial,
  matchedPair = FALSE,
  baselineNumerator = "base_num",
  baselineDenominator = "base_denom"
)
```

Arguments

trial	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), and arm assignments (factor arm). Optionally: specification of a buffer zone (logical buffer); any other variables required for subsequent analysis.
matchedPair	logical: indicator of whether pair-matching on the baseline data should be used in randomization
baselineNumerator	name of numerator variable for baseline data (required for matched-pair randomization)
baselineDenominator	name of denominator variable for baseline data (required for matched-pair randomization)

Value

A list of class "CRTsp" containing the following components:

design	list:	parameters required for power calculations
geom_full	list:	summary statistics describing the site
geom_core	list:	summary statistics describing the core area (when a buffer is specified)
trial	data frame:	rows correspond to geolocated points, as follows:
	x	numeric vector: x-coordinates of locations
	y	numeric vector: y-coordinates of locations
	cluster	factor: assignments to cluster of each location
	pair	factor: assigned matched pair of each location (for matchedPair randomisations)
	arm	factor: assignments to "control" or "intervention" for each location
	...	other objects included in the input "CRTsp" object or data frame

Examples

```
# Randomize the clusters in an example trial
exampleCRT <- randomizeCRT(trial = readdata('exampleCRT.txt'), matchedPair = TRUE)
```

readdata	<i>Read example dataset</i>
----------	-----------------------------

Description

readdata reads a file from the package library of example datasets

Usage

```
readdata(filename)
```

Arguments

filename	name of text file stored within the package
----------	---

Details

The input file name should include the extension (either .csv or .txt). The resulting object is a data frame if the extension is .csv.

Value

R object corresponding to the text file

Examples

```
exampleCRT <- readdata('exampleCRT.txt')
```

residuals.CRTanalysis	<i>Extract model residuals</i>
-----------------------	--------------------------------

Description

residuals.CRTanalysis method for extracting model residuals

Usage

```
## S3 method for class 'CRTanalysis'
residuals(object, ...)
```

Arguments

object	CRTanalysis object
...	other arguments

Value

the residuals from the statistical model run within the CRTanalysis function

Examples

```
{example <- readdata('exampleCRT.txt')
exampleGEE <- CRTanalysis(example, method = "GEE")
residuals <- residuals(exampleGEE)
}
```

simulateCRT

*Simulation of cluster randomized trial with contamination***Description**

simulateCRT generates simulated data for a cluster randomized trial (CRT) with geographic contamination between arms.

Usage

```
simulateCRT(
  trial = NULL,
  effect = 0,
  outcome0 = NULL,
  generateBaseline = TRUE,
  matchedPair = TRUE,
  scale = "proportion",
  baselineNumerator = "base_num",
  baselineDenominator = "base_denom",
  denominator = NULL,
  ICC_inp = NULL,
  kernels = 200,
  sd = NULL,
  theta_inp = NULL,
  tol = 0.005
)
```

Arguments

trial	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), and arm assignments (factor arm). Each location may also be assigned a propensity (see details).
effect	numeric. The simulated effect size (defaults to 0)
outcome0	numeric. The anticipated value of the outcome in the absence of intervention
generateBaseline	logical. If TRUE then baseline data and the propensity will be simulated
matchedPair	logical. If TRUE then the function tries to carry out randomization using pair-matching on the baseline data (see details)
scale	measurement scale of the outcome. Options are: 'proportion' (the default); 'count'; 'continuous'.

baselineNumerator	optional name of numerator variable for pre-existing baseline data
baselineDenominator	optional name of denominator variable for pre-existing baseline data
denominator	optional name of denominator variable for the outcome
ICC_inp	numeric. Target intra cluster correlation, provided as input when baseline data are to be simulated
kernels	number of kernels used to generate a de novo propensity
sd	numeric. standard deviation of the normal kernel measuring spatial smoothing leading to contamination
theta_inp	numeric. input contamination range
tol	numeric. tolerance of output ICC

Details

Synthetic data are generated by sampling around the values of variable propensity, which is a numerical vector (taking positive values) of length equal to the number of locations. There are three ways in which propensity can arise:

1. propensity can be provided as part of the input trial object.
2. Baseline numerators and denominators (values of baselineNumerator and baselineDenominator may be provided. propensity is then generated as the numerator:denominator ratio for each location in the input object
3. Otherwise propensity is generated using a 2D Normal kernel density. The `OOR::StoS00` is used to achieve an intra-cluster correlation coefficient (ICC) that approximates the value of 'ICC_inp' by searching for an appropriate value of the kernel bandwidth.

$num[i]$, the synthetic outcome for location i is simulated with expectation:

$$E(num[i]) = outcome0[i] * propensity[i] * denom[i] * (1 - effect * I[i]) / mean(outcome0[] * propensity[])$$

The sampling distribution of $num[i]$ depends on the value of scale as follows:

- `scale='continuous'`: Values of num are sampled from a Normal distributions with means $E(num[i])$ and variance determined by the fitting to `ICC_inp`.
- `scale='count'`: Simulated events are allocated to locations via multivariate hypergeometric distributions parameterised with $E(num[i])$.
- `scale='proportion'`: Simulated events are allocated to locations via multinomial distributions parameterised with $E(num[i])$.

`denominator` may specify a vector of numeric (non-zero) values in the input "CRTsp" or `data.frame` which is returned as variable `denom`. It acts as a scale-factor for continuous outcomes, rate-multiplier for counts, or denominator for proportions. For discrete data all values of `denom` must be > 0.5 and are rounded to the nearest integer in calculations of num .

By default, `denom` is generated as a vector of ones, leading to simulation of dichotomous outcomes

if scale='proportion'.

If baseline numerators and denominators are provided then the output vectors `base_denom` and `base_num` are set to the input values. If baseline numerators and denominators are not provided then the synthetic baseline data are generated by sampling around propensity in the same way as the outcome data, but with the effect size set to zero.

If `matchedPair` is TRUE then pair-matching on the baseline data will be used in randomization providing there are an even number of clusters. If there are an odd number of clusters then matched pairs are not generated and an unmatched randomization is output.

Either `sd` or `theta_inp` must be provided. If both are provided then the value of `sd` is overwritten by the standard deviation implicit in the value of `theta_inp`. Contamination is simulated as arising from a diffusion-like process.

For further details see [Multerer \(2021\)](#)

Value

A list of class "CRTsp" containing the following components:

<code>geom_full</code>	list:	summary statistics describing the site cluster assignments, and randomization
<code>design</code>	list:	values of input parameters to the design
<code>trial</code>	data frame:	rows correspond to geolocated points, as follows:
	<code>x</code>	numeric vector: x-coordinates of locations
	<code>y</code>	numeric vector: y-coordinates of locations
	<code>cluster</code>	factor: assignments to cluster of each location
	<code>arm</code>	factor: assignments to control or intervention for each location
	<code>nearestDiscord</code>	numeric vector: signed Euclidean distance to nearest discordant location (km)
	<code>propensity</code>	numeric vector: propensity for each location
	<code>base_denom</code>	numeric vector: denominator for baseline
	<code>base_num</code>	numeric vector: numerator for baseline
	<code>denom</code>	numeric vector: denominator for the outcome
	<code>num</code>	numeric vector: numerator for the outcome
	<code>...</code>	other objects included in the input "CRTsp" object or data.frame

Examples

```
{smalltrial <- readdata('smalltrial.csv')
simulation <- simulateCRT(smalltrial,
  effect = 0.25,
  ICC_inp = 0.05,
  outcome0 = 0.5,
  matchedPair = FALSE,
  scale = 'proportion',
  sd = 0.6,
  tol = 0.05)
summary(simulation)
}
```

specify_buffer	<i>Specification of buffer zone in a cluster randomized trial</i>
----------------	---

Description

specify_buffer specifies a buffer zone in a cluster randomized trial (CRT) by flagging those locations that are within a defined distance of those in the opposite arm.

Usage

```
specify_buffer(trial, buffer_width = 0)
```

Arguments

trial	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), and arm assignments (factor arm).
buffer_width	minimum distance between locations in opposing arms for them to qualify to be included in the core area (km)

Value

A list of class "CRTsp" containing the following components:

geom_full	list:	summary statistics describing the site, cluster assignments, and randomization.
geom_core	list:	summary statistics describing the core area
trial	data frame:	rows correspond to geolocated points, as follows:
	x	numeric vector: x-coordinates of locations
	y	numeric vector: y-coordinates of locations
	cluster	factor: assignments to cluster of each location
	arm	factor: assignments to "control" or "intervention" for each location
	nearestDiscord	numeric vector: signed Euclidean distance to nearest discordant location (km)
	buffer	logical: indicator of whether the point is within the buffer
	...	other objects included in the input "CRTsp" object or data frame

Examples

```
#Specify a buffer of 200m
exampletrial <- specify_buffer(trial = readdata('exampleCRT.txt'), buffer_width = 0.2)
```

specify_clusters	<i>Algorithmically assign locations to clusters in a CRT</i>
------------------	--

Description

specify_clusters algorithmically assigns locations to clusters by grouping them geographically

Usage

```
specify_clusters(
  trial = trial,
  k = NULL,
  h = NULL,
  algorithm = "NN",
  reuseTSP = FALSE
)
```

Arguments

trial	A CRT object or data frame containing (x,y) coordinates of households
k	integer: number of clusters in each arm
h	integer: number of locations per cluster
algorithm	algorithm for cluster boundaries, with options:
NN	Nearest neighbour: assigns equal numbers of locations to each cluster
kmeans	kmeans clustering: aims to partition locations so that each belongs to the cluster with the nearest centroid.
TSP	travelling salesman problem heuristic: Assigns locations sequentially along a travelling salesman path.
reuseTSP	logical: indicator of whether a pre-existing path should be used by the TSP algorithm

Details

The reuseTSP parameter is used to allow the path to be reused for creating alternative allocations with different cluster sizes.

Either k or h must be specified. If both are specified the input value of k is ignored.

Value

A list of class "CRTsp" containing the following components:

geom_full	list:	summary statistics describing the site, and cluster assignments.
trial	data frame:	rows correspond to geolocated points, as follows:
	x	numeric vector: x-coordinates of locations
	y	numeric vector: y-coordinates of locations
	cluster	factor: assignments to cluster of each location
	...	other objects included in the input "CRTsp" object or data frame

Examples

```
#Assign clusters of average size h = 40 to a test set of co-ordinates, using the kmeans algorithm
exampletrial <- specify_clusters(trial = readdata('exampleCRT.txt'),
                                h = 40, algorithm = 'kmeans', reuseTSP = FALSE)
```

summary.CRTanalysis	<i>Summary of the results of a statistical analysis of a CRT</i>
---------------------	--

Description

summary.CRTanalysis generates a summary of a CRTanalysis including the main results

Usage

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

Arguments

object	an object of class "CRTanalysis"
...	other arguments used by summary

Value

No return value, writes text to the console.

Examples

```
{example <- readdata('exampleCRT.txt')
exampleT <- CRTanalysis(example, method = "T")
summary(exampleT)
}
```

summary.CRTsp	<i>Summary description of a "CRTsp" object</i>
---------------	--

Description

summary.CRTsp provides a description of a "CRTsp" object

Usage

```
## S3 method for class 'CRTsp'
summary(object, maskbuffer = 0.2, ...)
```

Arguments

object	an object of class "CRTsp" or a data frame containing locations in (x,y) coordinates, cluster assignments (factor cluster), arm assignments (factor arm) and buffer zones (logical buffer), together with any other variables required for subsequent analysis.
maskbuffer	radius of area around a location to include in calculation of areas
...	other arguments used by summary

Value

No return value, write text to the console.

Examples

```
summary(CRTsp(readdata('exampleCRT.txt')))
```

Index

aggregateCRT, [2](#)
anonymize_site, [3](#)

coef.CRTanalysis, [4](#)
compute_distance, [4](#)
compute_mesh, [6](#)
CRTanalysis, [7](#)
CRTpower, [10](#)
CRTsp, [11](#)
CRTwrite, [13](#)

fitted.CRTanalysis, [14](#)

latlong_as_xy, [15](#)

plotCRT, [16](#)
predict.CRTanalysis, [18](#)

randomizeCRT, [19](#)
readdata, [20](#)
residuals.CRTanalysis, [20](#)

simulateCRT, [21](#)
specify_buffer, [24](#)
specify_clusters, [24](#)
summary.CRTanalysis, [26](#)
summary.CRTsp, [26](#)