

# Package ‘spatialAtomizeR’

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**Type** Package

**Title** Spatial Analysis with Misaligned Data Using Atom-Based Regression Models

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**Description** Implements atom-based regression models (ABRM) for analyzing spatially misaligned data. Provides functions for simulating misaligned spatial data, preparing NIMBLE model inputs, running MCMC diagnostics, and comparing different spatial analysis methods including dasymetric mapping. All main functions return S3 objects with print(), summary(), and plot() methods for intuitive result exploration. Methods are described in Nethery et al. (2023) <doi:10.1101/2023.01.10.23284410>. Further methodological details and software implementation are described in Qian et al. (in review).

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**Encoding** UTF-8

**Depends** R (>= 4.0.0), nimble

**Imports** sp, sf, spdep, MASS, raster, dplyr, tidyr, ggplot2, reshape2, coda, BiasedUrn, stats, utils, grDevices, methods

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown

**VignetteBuilder** knitr

**URL** <https://github.com/bellayqian/spatialAtomizeR>

**BugReports** <https://github.com/bellayqian/spatialAtomizeR/issues>

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|                 |                                                  |
|-----------------|--------------------------------------------------|
| biasedUrn_rmfnc | <i>R Wrapper Function for BiasedUrn Sampling</i> |
|-----------------|--------------------------------------------------|

---

**Description**

Wraps the BiasedUrn::rMFNCHypergeo function for use in NIMBLE models

**Usage**

```
biasedUrn_rmfnc(total, odds, ni)
```

**Arguments**

|       |                                          |
|-------|------------------------------------------|
| total | Integer, total number of items to sample |
| odds  | Numeric vector of odds for each category |
| ni    | Integer vector of population sizes       |

**Value**

Numeric vector of sampled counts

---

|                        |                               |
|------------------------|-------------------------------|
| check_mcmc_diagnostics | <i>Check MCMC Diagnostics</i> |
|------------------------|-------------------------------|

---

**Description**

Calculates convergence diagnostics including Gelman-Rubin statistics and effective sample sizes for MCMC output

**Usage**

```
check_mcmc_diagnostics(mcmc_output, sim_metadata = NULL)
```

**Arguments**

|              |                                            |
|--------------|--------------------------------------------|
| mcmc_output  | Output from NIMBLE MCMC containing samples |
| sim_metadata | Optional list with simulation metadata     |

**Value**

List with diagnostic results including convergence statistics and plots

---

`create_comparison_plots`*Create Comparison Plots*

---

**Description**

Create Comparison Plots

**Usage**

```
create_comparison_plots(comparison_data, output_dir, true_params = NULL)
```

**Arguments**

|                              |                                    |
|------------------------------|------------------------------------|
| <code>comparison_data</code> | Data frame with comparison results |
| <code>output_dir</code>      | Output directory for plots         |
| <code>true_params</code>     | True parameter values (optional)   |

**Value**

No return value, called for side effects. Creates and displays/saves comparison plots of coefficient estimates, bias, and coverage rates across different methods. If `output_dir` is provided, plots are saved to a PDF file.

---

`create_diagnostic_plots`*Create Diagnostic Plots*

---

**Description**

Create Diagnostic Plots

**Usage**

```
create_diagnostic_plots(chains_list, sim_metadata)
```

**Arguments**

|                           |                     |
|---------------------------|---------------------|
| <code>chains_list</code>  | List of MCMC chains |
| <code>sim_metadata</code> | Simulation metadata |

**Value**

List with trace and density plots

---

```
create_sensitivity_summary_plots
```

*Create Sensitivity Summary Plots*

---

**Description**

Create Sensitivity Summary Plots

**Usage**

```
create_sensitivity_summary_plots(combined_results, output_dir)
```

**Arguments**

|                  |                             |
|------------------|-----------------------------|
| combined_results |                             |
|                  | Combined results data frame |
| output_dir       | Output directory            |

**Value**

No return value, called for side effects. Creates and displays/saves summary plots for sensitivity analysis including correlation effects, bias patterns, and coverage rates. If output\_dir is provided, plots are saved to a PDF file.

---

```
create_summary_statistics
```

*Create Summary Statistics*

---

**Description**

Create Summary Statistics

**Usage**

```
create_summary_statistics(all_results, output_dir)
```

**Arguments**

|             |                             |
|-------------|-----------------------------|
| all_results | Combined results data frame |
| output_dir  | Output directory            |

**Value**

A list with two components: method\_summary (data frame containing overall summary statistics for each method, including mean bias, relative bias, and coverage rates) and param\_summary (data frame containing parameter-specific comparisons across methods). The function also saves these summaries to CSV files in the output directory.

---

|                    |                           |
|--------------------|---------------------------|
| dasymetric_mapping | <i>Dasymetric Mapping</i> |
|--------------------|---------------------------|

---

**Description**

Maps X-grid covariates to Y-grid using centroid-based spatial join

**Usage**

```
dasymetric_mapping(misaligned_data)
```

**Arguments**

|                 |                                                         |
|-----------------|---------------------------------------------------------|
| misaligned_data | List with gridx and gridy from simulate_misaligned_data |
|-----------------|---------------------------------------------------------|

**Value**

sf object with Y grid containing mapped X covariates

---

|           |                                                                     |
|-----------|---------------------------------------------------------------------|
| dmfnchypg | <i>Density function for multivariate non-central hypergeometric</i> |
|-----------|---------------------------------------------------------------------|

---

**Description**

Density function for multivariate non-central hypergeometric

**Usage**

```
dmfnchypg(x, total, odds, ni, log = 0)
```

**Arguments**

|       |                                 |
|-------|---------------------------------|
| x     | Vector of counts                |
| total | Total number of items           |
| odds  | Vector of odds                  |
| ni    | Vector of category sizes        |
| log   | Logical, return log probability |

**Value**

The log-probability (if log=1) or probability (if log=0)

---

|                      |                             |
|----------------------|-----------------------------|
| fit_dasymetric_model | <i>Fit Dasymetric Model</i> |
|----------------------|-----------------------------|

---

**Description**

Fits regression model to dasymetrically mapped data

**Usage**

```
fit_dasymetric_model(mapped_data, outcome_type)
```

**Arguments**

|              |                                                       |
|--------------|-------------------------------------------------------|
| mapped_data  | Output from dasymetric_mapping                        |
| outcome_type | Distribution type: 'normal', 'poisson', or 'binomial' |

**Value**

Data frame with parameter estimates and confidence intervals

---

|                     |                                            |
|---------------------|--------------------------------------------|
| gen_correlated_spat | <i>Generate Correlated Spatial Effects</i> |
|---------------------|--------------------------------------------|

---

**Description**

Generate Correlated Spatial Effects

**Usage**

```
gen_correlated_spat(
  W,
  n_vars,
  rho = 0.6,
  var_spat = 1,
  correlation = 0.5,
  verify = FALSE
)
```

**Arguments**

|             |                                               |
|-------------|-----------------------------------------------|
| W           | Spatial adjacency matrix                      |
| n_vars      | Number of variables                           |
| rho         | Spatial correlation parameter (default = 0.6) |
| var_spat    | Spatial variance (default = 1)                |
| correlation | Correlation between variables (default = 0.5) |
| verify      | Logical for verification (default = FALSE)    |

**Value**

Matrix of spatial effects

---

```
get_abrm_model
```

*Get ABRM Model Code for NIMBLE*

---

**Description**

Returns the NIMBLE code for the Atom-Based Regression Model with mixed-type variables. Automatically registers custom distributions if not already registered.

**Usage**

```
get_abrm_model()
```

**Value**

A nimbleCode object containing the model specification

---

```
plot.abrm
```

*Plot method for abrm objects*

---

**Description**

Plot method for abrm objects

**Usage**

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

**Arguments**

|     |                                |
|-----|--------------------------------|
| x   | An object of class "abrm"      |
| ... | Additional arguments (ignored) |

**Value**

Invisibly returns the input object x. The function is called for its side effect of displaying MCMC diagnostic plots (trace plots and density plots) if they are available in the abrm object.



---

plot.abrm\_comparison    *Plot method for abrm\_comparison objects*

---

**Description**

Plot method for abrm\_comparison objects

**Usage**

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

**Arguments**

|     |                                      |
|-----|--------------------------------------|
| x   | An object of class "abrm_comparison" |
| ... | Additional arguments (ignored)       |

**Value**

Invisibly returns the input object x. The function is called for its side effect of displaying comparison plots between methods if true parameters are available in the comparison object.

---

prepare\_adjacency\_matrices  
                          *Prepare Adjacency Matrices*

---

**Description**

Prepare Adjacency Matrices

**Usage**

```
prepare_adjacency_matrices(gridy_yorder, gridx_xorder)
```

**Arguments**

|              |                  |
|--------------|------------------|
| gridy_yorder | Reordered Y grid |
| gridx_xorder | Reordered X grid |

**Value**

List containing W\_x and W\_y adjacency matrices

---

```
prepare_nimble_inputs
```

---

*Prepare NIMBLE Model Inputs*

---

**Description**

Prepare NIMBLE Model Inputs

**Usage**

```
prepare_nimble_inputs(
  bookkeeping,
  adjacency,
  data,
  norm_idx_x = NULL,
  pois_idx_x = NULL,
  binom_idx_x = NULL,
  norm_idx_y = NULL,
  pois_idx_y = NULL,
  binom_idx_y = NULL,
  dist_y = 2
)
```

**Arguments**

|             |                                                                 |
|-------------|-----------------------------------------------------------------|
| bookkeeping | Output from prepare_spatial_bookkeeping                         |
| adjacency   | Output from prepare_adjacency_matrices                          |
| data        | Original simulated data                                         |
| norm_idx_x  | Indices of normal-distributed X covariates                      |
| pois_idx_x  | Indices of Poisson-distributed X covariates                     |
| binom_idx_x | Indices of binomial-distributed X covariates                    |
| norm_idx_y  | Indices of normal-distributed Y covariates                      |
| pois_idx_y  | Indices of Poisson-distributed Y covariates                     |
| binom_idx_y | Indices of binomial-distributed Y covariates                    |
| dist_y      | Distribution type for outcome (1=normal, 2=poisson, 3=binomial) |

**Value**

List containing constants, data, and inits for NIMBLE

---

```
prepare_spatial_bookkeeping
```

*Prepare Spatial Bookkeeping*

---

**Description**

Prepare Spatial Bookkeeping

**Usage**

```
prepare_spatial_bookkeeping(data)
```

**Arguments**

data                      List containing gridy, gridx, and atoms from simulate\_misaligned\_data

**Value**

List of bookkeeping objects for NIMBLE model

---

```
print.abrm
```

*Print method for abrm objects*

---

**Description**

Print method for abrm objects

**Usage**

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

**Arguments**

x                          An abrm object  
 ...                        Additional arguments (unused)

**Value**

Invisibly returns the input object x. The function is called for its side effect of printing a summary of the ABRM model results including convergence status, number of parameters estimated, and key fit statistics.

---

```
print.abrm_comparison Print method for abrm_comparison objects
```

---

**Description**

Print method for abrm\_comparison objects

**Usage**

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

**Arguments**

|     |                               |
|-----|-------------------------------|
| x   | A abrm_comparison object      |
| ... | Additional arguments (unused) |

**Value**

Invisibly returns the input object x. The function is called for its side effect of printing a summary of method comparison results including the number of simulations and methods compared.

---

```
print.misaligned_data Print method for misaligned_data objects
```

---

**Description**

Print method for misaligned\_data objects

**Usage**

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

**Arguments**

|     |                               |
|-----|-------------------------------|
| x   | A misaligned_data object      |
| ... | Additional arguments (unused) |

**Value**

Invisibly returns the input object x. The function is called for its side effect of printing a summary of the simulated misaligned spatial data including grid dimensions and number of atoms.

---

```
print.sensitivity_analysis
```

*Print method for sensitivity\_analysis objects*

---

**Description**

Print method for sensitivity\_analysis objects

**Usage**

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

**Arguments**

|     |                               |
|-----|-------------------------------|
| x   | A sensitivity_analysis object |
| ... | Additional arguments (unused) |

**Value**

Invisibly returns the input object x. The function is called for its side effect of printing a summary of the sensitivity analysis results including the number of simulations and scenarios tested.

---

```
print_convergence_summary
```

*Print Convergence Summary*

---

**Description**

Print Convergence Summary

**Usage**

```
print_convergence_summary(convergence_results)
```

**Arguments**

|                     |                                     |
|---------------------|-------------------------------------|
| convergence_results | Results from check_mcmc_diagnostics |
|---------------------|-------------------------------------|

**Value**

No return value, called for side effects. Prints convergence diagnostics including overall convergence status, minimum effective sample size, median ESS, maximum Rhat statistic, and identifies parameters with high relative variance.

---

```
register_nimble_distributions
```

*Register Custom NIMBLE Distributions*

---

### Description

Registers the custom distributions for use in NIMBLE models.

### Usage

```
register_nimble_distributions()
```

### Value

Invisible TRUE

---

```
Rmfnchypg
```

*Nimble R Call Wrapper for BiasedUrn*

---

### Description

Internal wrapper to call R function from compiled Nimble code.

### Usage

```
Rmfnchypg(total, odds, ni)
```

### Arguments

|       |                          |
|-------|--------------------------|
| total | Total number of items    |
| odds  | Vector of odds           |
| ni    | Vector of category sizes |

### Value

Vector of sampled counts

---

rmfnchypg

*Random generation for multivariate non-central hypergeometric*


---

**Description**

Random generation for multivariate non-central hypergeometric

**Usage**

```
rmfnchypg(n, total, odds, ni)
```

**Arguments**

|       |                                           |
|-------|-------------------------------------------|
| n     | number of observations (only n=1 is used) |
| total | Total number of items                     |
| odds  | Vector of odds                            |
| ni    | Vector of category sizes                  |

**Value**

Vector of sampled counts

---

run\_abrm

*Run ABRM Analysis*


---

**Description**

Runs the Atom-Based Regression Model on simulated data

**Usage**

```
run_abrm(
  gridx,
  gridy,
  atoms,
  model_code,
  true_params = NULL,
  norm_idx_x = NULL,
  pois_idx_x = NULL,
  binom_idx_x = NULL,
  norm_idx_y = NULL,
  pois_idx_y = NULL,
  binom_idx_y = NULL,
  dist_y = 2,
  niter = 50000,
```

```

    nburnin = 30000,
    nchains = 2,
    thin = 10,
    sim_metadata = NULL,
    save_plots = TRUE,
    output_dir = NULL
  )

```

## Arguments

|              |                                                                                                                                                                                                           |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| gridx        | The X-grid sf dataframe, containing a numeric area ID variable named 'ID' and covariates named 'covariate_x_1','covariate_x_2',...                                                                        |
| gridy        | The Y-grid sf dataframe, containing a numeric area ID variable named 'ID', covariates named 'covariate_y_1','covariate_y_2',..., and an outcome named 'y'.                                                |
| atoms        | The atom sf dataframe, which should contain numeric variables named 'ID_x' and 'ID_y' holding the X-grid and Y-grid cell IDs for each atom, as well as an atom-level population count named 'population'. |
| model_code   | NIMBLE model code from get_abrm_model()                                                                                                                                                                   |
| true_params  | The true outcome model regression coefficient parameters, if known (e.g., from simulate_misaligned_data())                                                                                                |
| norm_idx_x   | Vector of numeric indices of X-grid covariates (ordered as 'covariate_x_1','covariate_x_2',...) that should be treated as normally-distributed                                                            |
| pois_idx_x   | Vector of numeric indices of X-grid covariates (ordered as 'covariate_x_1','covariate_x_2',...) that should be treated as Poisson-distributed                                                             |
| binom_idx_x  | Vector of numeric indices of X-grid covariates (ordered as 'covariate_x_1','covariate_x_2',...) that should be treated as binomial-distributed                                                            |
| norm_idx_y   | Vector of numeric indices of Y-grid covariates (ordered as 'covariate_y_1','covariate_y_2',...) that should be treated as normally-distributed                                                            |
| pois_idx_y   | Vector of numeric indices of Y-grid covariates (ordered as 'covariate_y_1','covariate_y_2',...) that should be treated as Poisson-distributed                                                             |
| binom_idx_y  | Vector of numeric indices of Y-grid covariates (ordered as 'covariate_y_1','covariate_y_2',...) that should be treated as binomial-distributed                                                            |
| dist_y       | Distribution type for outcome (1=normal, 2=poisson, 3=binomial)                                                                                                                                           |
| niter        | Number of MCMC iterations (default: 50000)                                                                                                                                                                |
| nburnin      | Number of burn-in iterations (default: 30000)                                                                                                                                                             |
| nchains      | Number of MCMC chains (default: 2)                                                                                                                                                                        |
| thin         | Thinning interval (default: 10)                                                                                                                                                                           |
| sim_metadata | Optional simulation metadata list                                                                                                                                                                         |
| save_plots   | Logical, whether to save diagnostic plots (default: TRUE)                                                                                                                                                 |
| output_dir   | Directory for saving outputs (default: NULL)                                                                                                                                                              |

## Value

List containing MCMC results and parameter estimates



---

|                  |                                     |
|------------------|-------------------------------------|
| run_both_methods | <i>Run Both Methods and Compare</i> |
|------------------|-------------------------------------|

---

## Description

Runs both ABRM and dasymetric mapping methods and compares results

## Usage

```
run_both_methods(
  sim_data,
  sim_metadata,
  model_code,
  nimble_params,
  output_dir,
  norm_idx_x,
  pois_idx_x,
  binom_idx_x,
  norm_idx_y,
  pois_idx_y,
  binom_idx_y,
  dist_y,
  outcome_type
)
```

## Arguments

|               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|---------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| sim_data      | List of data elements to be used in the ABRM, structured like the output from the simulate_misaligned_data() function. The first element of this list is the Y-grid sf dataframe (named 'gridy'), containing a numeric area ID variable named 'ID_y', covariates named 'covariate_y_1','covariate_y_2',..., and an outcome named 'y'. The second element of this list is the X-grid sf dataframe (named 'gridx'), containing a numeric area ID variable named 'ID_x' and covariates named 'covariate_x_1','covariate_x_2',... The third element of the list is the atom sf dataframe (named 'atoms'), which should contain variables named 'ID_x' and 'ID_y' holding the X-grid and Y-grid cell IDs for each atom, as well as an atom-level population count named 'population'. |
| sim_metadata  | Simulation metadata                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| model_code    | NIMBLE model code                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| nimble_params | List of NIMBLE parameters (niter, nburnin, thin, nchains)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| output_dir    | Output directory                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| norm_idx_x    | Indices of normal X covariates                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| pois_idx_x    | Indices of Poisson X covariates                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| binom_idx_x   | Indices of binomial X covariates                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| norm_idx_y    | Indices of normal Y covariates                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

|              |                                                                 |
|--------------|-----------------------------------------------------------------|
| pois_idx_y   | Indices of Poisson Y covariates                                 |
| binom_idx_y  | Indices of binomial Y covariates                                |
| dist_y       | Distribution type for outcome (1=normal, 2=poisson, 3=binomial) |
| outcome_type | Outcome distribution name                                       |

**Value**

List with combined comparison, ABRM results, and dasymetric results

---

|                  |                                          |
|------------------|------------------------------------------|
| run_nimble_model | <i>Run NIMBLE Model with Diagnostics</i> |
|------------------|------------------------------------------|

---

**Description**

Run NIMBLE Model with Diagnostics

**Usage**

```
run_nimble_model(
  constants,
  data,
  inits,
  sim_metadata = NULL,
  model_code,
  niter = 50000,
  nburnin = 30000,
  nchains = 2,
  thin = 10,
  save_plots = TRUE,
  output_dir = NULL
)
```

**Arguments**

|              |                                                           |
|--------------|-----------------------------------------------------------|
| constants    | List of model constants                                   |
| data         | List of data                                              |
| inits        | List of initial values                                    |
| sim_metadata | List with simulation metadata (optional)                  |
| model_code   | NIMBLE code object                                        |
| niter        | Number of MCMC iterations (default: 50000)                |
| nburnin      | Number of burn-in iterations (default: 30000)             |
| nchains      | Number of MCMC chains (default: 2)                        |
| thin         | Thinning interval (default: 10)                           |
| save_plots   | Logical, whether to save diagnostic plots (default: TRUE) |
| output_dir   | Directory for saving plots (default: NULL)                |

**Value**

List containing MCMC samples, summary, and convergence diagnostics

---

run\_sensitivity\_analysis

*Run Sensitivity Analysis*

---

**Description**

Performs sensitivity analysis across different correlation structures

**Usage**

```
run_sensitivity_analysis(
  correlation_grid = c(0.2, 0.6),
  n_sims_per_setting = 3,
  base_params = list(dist_covariates_x = c("normal", "poisson", "binomial"),
    dist_covariates_y = c("normal", "poisson", "binomial"), dist_y = "poisson",
    x_intercepts = c(4, -1, -1), y_intercepts = c(4, -1, -1), beta0_y = -1, beta_x =
    c(-0.03, 0.1, -0.2), beta_y = c(0.03, -0.1, 0.2)),
  mcmc_params = list(niter = 50000, nburnin = 30000, thin = 10, nchains = 2),
  model_code,
  base_seed = 123,
  output_dir = NULL
)
```

**Arguments**

|                    |                                                              |
|--------------------|--------------------------------------------------------------|
| correlation_grid   | Vector of correlation values to test                         |
| n_sims_per_setting | Number of simulations per correlation setting                |
| base_params        | List of base simulation parameters                           |
| mcmc_params        | List of MCMC parameters                                      |
| model_code         | NIMBLE model code                                            |
| base_seed          | Base random seed                                             |
| output_dir         | Output directory for results (default: NULL, uses tempdir()) |

**Value**

List with combined results, summary statistics, and output directory

---

simulate\_misaligned\_data

*Simulate Misaligned Spatial Data*


---

## Description

Simulate Misaligned Spatial Data

## Usage

```
simulate_misaligned_data(
  seed = 2,
  dist_covariates_x = c("normal", "poisson", "binomial"),
  dist_covariates_y = c("normal", "poisson", "binomial"),
  dist_y = "poisson",
  x_intercepts = rep(0, 3),
  y_intercepts = rep(0, 3),
  rho_x = 0.6,
  rho_y = 0.6,
  x_correlation = 0.5,
  y_correlation = 0.5,
  beta0_y = NULL,
  beta_x = NULL,
  beta_y = NULL,
  diff_pops = TRUE,
  xy_cov_cor = FALSE
)
```

## Arguments

|                   |                                                                                                                                              |
|-------------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| seed              | Random seed (default = 2)                                                                                                                    |
| dist_covariates_x | Vector specifying distribution type for each synthetic X-grid covariate ('poisson', 'binomial', or 'normal')                                 |
| dist_covariates_y | Vector specifying distribution type for each synthetic Y-grid covariate ('poisson', 'binomial', or 'normal')                                 |
| dist_y            | Distribution type for synthetic outcome variable (one of 'poisson', 'binomial', or 'normal')                                                 |
| x_intercepts      | Intercepts for X covariates                                                                                                                  |
| y_intercepts      | Intercepts for Y covariates                                                                                                                  |
| rho_x             | Spatial correlation parameter for X-grid covariates (0 to 1 with higher values yielding more spatial correlation, default = 0.6)             |
| rho_y             | Spatial correlation parameter for Y-grid covariates and outcome (0 to 1 with higher values yielding more spatial correlation, default = 0.6) |

|               |                                                                                                                                                                                                                                                                                                                                      |
|---------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x_correlation | Between-variable correlation for all pairs of X-grid covariates (default = 0.5)                                                                                                                                                                                                                                                      |
| y_correlation | Between-variable correlation for all pairs of Y-grid covariates (default = 0.5)                                                                                                                                                                                                                                                      |
| beta0_y       | Intercept for outcome model                                                                                                                                                                                                                                                                                                          |
| beta_x        | Outcome model coefficients for X-grid covariates                                                                                                                                                                                                                                                                                     |
| beta_y        | Outcome model coefficients for Y-grid covariates                                                                                                                                                                                                                                                                                     |
| diff_pops     | Logical, indicating whether the atoms should be generated with different population sizes (diff_pops = TRUE) or a common population size (diff_pops = FALSE)                                                                                                                                                                         |
| xy_cov_cor    | Logical, indicating whether the atom-level spatial random effects for X-grid and Y-grid covariates should be correlated (xy_cov_cor = TRUE) or not. When set to TRUE, the x_correlation and rho_x parameters are used to generate all covariates (separate correlation parameters are not allowed for X-grid and Y-grid covariates). |

**Value**

List containing gridy, gridx, atoms, and true\_params

---

summary.abrm

---

*Summary method for abrm objects*


---

**Description**

Summary method for abrm objects

**Usage**

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

**Arguments**

|        |                               |
|--------|-------------------------------|
| object | An abrm object                |
| ...    | Additional arguments (unused) |

**Value**

Invisibly returns the input object object. The function is called for its side effect of printing the ABRM model summary including detailed parameter estimates.

---

```
summary.abrm_comparison
```

*Summary method for abrm\_comparison objects*

---

### Description

Summary method for abrm\_comparison objects

### Usage

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

### Arguments

|        |                                      |
|--------|--------------------------------------|
| object | An object of class "abrm_comparison" |
| ...    | Additional arguments (ignored)       |

### Value

Invisibly returns the input object object. The function is called for its side effect of printing the method comparison summary including combined comparison results across all simulations.

---

```
summary.misaligned_data
```

*Summary method for misaligned\_data objects*

---

### Description

Summary method for misaligned\_data objects

### Usage

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

### Arguments

|        |                               |
|--------|-------------------------------|
| object | A misaligned_data object      |
| ...    | Additional arguments (unused) |

### Value

Invisibly returns the input object object. The function is called for its side effect of printing the misaligned data summary including grid information and true parameter values (beta\_x and beta\_y).

---

`summary.sensitivity_analysis`*Summary method for sensitivity\_analysis objects*

---

**Description**

Summary method for sensitivity\_analysis objects

**Usage**

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

**Arguments**

|                     |                               |
|---------------------|-------------------------------|
| <code>object</code> | A sensitivity_analysis object |
| <code>...</code>    | Additional arguments (unused) |

**Value**

Invisibly returns the input object `object`. The function is called for its side effect of printing the sensitivity analysis summary including comprehensive results across all simulation scenarios.

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