Package: TruncatedPCQM (via r-universe)

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Title Density Estimation for Point-Centered Quarter Method with Truncated Sampling

Version 0.1.2

Maintainer Wenzhe Huang <51280155097@stu.ecnu.edu.cn>

Description Implements a systematic methodology for estimating population density from point-centered quarter method (PCQM) surveys when distance measurements are truncated by a maximum search radius (right-censored). The package provides a unified framework for analyzing such incomplete data, addressing both completely randomly distributed (Poisson) and spatially aggregated (Negative Binomial) populations. Key features include: (1) Adjusted moment-based density estimators for censored distances; (2) Maximum likelihood estimation (MLE) of density under the Poisson (CSR) model; and (3) Simultaneous MLE of density and an aggregation parameter under the Negative Binomial model. For more details, see Huang, Shen, Xing, and Zhao (2026) <doi:10.48550/arXiv.2603.08276>.

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BugReports https://github.com/rcjhrpyt-droid/TruncatedPCQM/issues

Repository https://rcjhrpyt-droid.r-universe.dev

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Contents

`adjusted_moments` *Adjusted Moment-based Estimators for Right-censored PCQM Data*

Description

Computes various density estimators (DK, Cottam, Pollard, Shen, Morisita) using adjusted moments to account for right-censoring in PCQM data.

Usage

```
adjusted_moments(
  distances,
  C = 20,
  q = 4,
  l = 1,
  init_method = "Pollard_censored"
)
```

Arguments

`distances`	A numeric vector, matrix, data.frame, or list of point-to-tree distances. For matrix/data.frame inputs, each row represents a sampling point and each column a sector.
`C`	Maximum search radius (censoring threshold). Distances exceeding C are treated as right-censored observations. Default is 20.
`q`	Number of sectors per sampling point. Default is 4.
`l`	Neighbor order. Default is 1.
`init_method`	Method for obtaining initial λ estimate used in NBD-based estimators. One of: "Pollard_censored" (default), "Cottam_censored", or "DK_censored" (only for l = 1).

Value

An object of class `"pcqm_moments"` containing:

- `DK_censored`: Diggle-Koedam estimator value (NA if l is not 1)
- `Cottam_censored`: Cottam-type estimator value

- `Pollard_censored`: Pollard-type estimator value
- `Shen_censored`: Shen's NBD-based estimator value (NA if estimated k < 1)
- `Morisita_censored`: Morisita's first estimator value (NA if l = 1)
- `k_hat`: Estimated aggregation parameter k from Shen's estimator
- `censored_rate`: Proportion of censored sectors
- `n_points`: Number of sampling points
- `n_sectors`: Total number of sectors analyzed
- `n_censored`: Number of censored observations (R > C)
- `call`: Original function call

Examples

```
distances_matrix <- matrix(c(
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000,    7.655136,   13.815876,   10.423496,
     6.094721,    4.135461,    7.732912,    5.454545,
  9999.000000, 9999.000000,   14.787289,   15.670821,
  9999.000000,    9.825537,   11.611850,   15.757861,
  9999.000000,    9.670381,   14.055394,   17.075678,
    11.529219,    4.464136,    7.793114,   11.309553,
    13.307828,    5.864490,   13.309636,    5.897720,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000,   18.201084, 9999.000000,
  9999.000000,    7.809056,   12.612496,    5.601366,
     9.201294, 9999.000000,    8.353524,    9.683701,
     6.592604,   19.117869,   19.758384,   12.923507,
    15.574824,   10.643719,    9.494539,    7.382031,
     9.143077, 9999.000000,   15.551414,    5.266916,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
    18.604278,    7.279454,    9.385355,    5.573127,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
    11.980811, 9999.000000,   11.853695,   14.405252
), nrow = 20, ncol = 4, byrow = TRUE)


moment_result <- adjusted_moments(
  distances = distances_matrix,
  C = 20,
  q = 4,
  l = 2,
  init_method = "Pollard_censored"
)

moment_result
```

csr_mle *CSR-based Maximum Likelihood Estimator for Right-censored PCQM Data*

Description

Computes the maximum likelihood estimate (MLE) of population density under complete spatial randomness (CSR), accounting for right-censored point-centered quarter method (PCQM) distances.

Usage

```
csr_mle(
  distances,
  C = 20,
  q = 4,
  l = 1,
  lambda_lower = 1e-04,
  lambda_upper = 1
)
```

Arguments

distances	A numeric vector, matrix, data.frame, or list of point-to-tree distances. For matrix/data.frame inputs, each row represents a sampling point and each column a sector.
C	Maximum search radius (censoring threshold). Distances exceeding C are treated as right-censored observations. Default is 20.
q	Number of sectors per sampling point. Default is 4.
l	Neighbor order. Default is 1.
lambda_lower	Lower bound for λ in numerical optimization. Must be positive. Default is 1e-4.
lambda_upper	Upper bound for λ in numerical optimization. Must be positive. Default is 1.

Value

An object of class "pcqm_csr_mle" containing:

- lambda: MLE of population density (individuals per unit area)
- logLik: Maximized log-likelihood value
- n_obs: Number of fully observed (non-censored) distances
- n_censored: Number of censored observations (R > C)
- n_sectors: Total number of sectors analyzed
- n_points: Inferred number of sampling points
- censored_rate: Proportion of censored sectors
- call: Original function call

Examples

```
distances_matrix <- matrix(c(
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000,    7.655136,   13.815876,   10.423496,
     6.094721,    4.135461,    7.732912,    5.454545,
  9999.000000, 9999.000000,   14.787289,   15.670821,
  9999.000000,    9.825537,   11.611850,   15.757861,
  9999.000000,    9.670381,   14.055394,   17.075678,
    11.529219,    4.464136,    7.793114,   11.309553,
    13.307828,    5.864490,   13.309636,    5.897720,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000,   18.201084, 9999.000000,
  9999.000000,    7.809056,   12.612496,    5.601366,
     9.201294, 9999.000000,    8.353524,    9.683701,
     6.592604,   19.117869,   19.758384,   12.923507,
    15.574824,   10.643719,    9.494539,    7.382031,
     9.143077, 9999.000000,   15.551414,    5.266916,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
    18.604278,    7.279454,    9.385355,    5.573127,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
    11.980811, 9999.000000,   11.853695,   14.405252
), nrow = 20, ncol = 4, byrow = TRUE)

csr_result <- csr_mle(
  distances = distances_matrix,
  C = 20,
  q = 4,
  l = 2,
  lambda_lower = 1e-4,
  lambda_upper = 1
)

csr_result
```

`nbd_mle` *NBD-based Maximum Likelihood Estimator for Right-censored PCQM Data*

Description

Computes the maximum likelihood estimate (MLE) of population density under Negative Binomial model, accounting for right-censored point-centered quarter method (PCQM) distances.

Usage

```
nbd_mle(
  distances,
  C = 20,
  q = 4,
  l = 1,
  init_method = "Shen_censored",
  lambda_lower = 1e-04,
  lambda_upper = 1
)
```

Arguments

distances	A numeric vector, matrix, data.frame, or list of point-to-tree distances. For matrix/data.frame inputs, each row represents a sampling point and each column a sector.
C	Maximum search radius (censoring threshold). Distances exceeding C are treated as right-censored observations. Default is 20.
q	Number of sectors per sampling point. Default is 4.
l	Neighbor order. Default is 1.
init_method	Method for obtaining initial parameter values. One of: "Shen_censored" (default), "Pollard_censored", "Cottam_censored", or "DK_censored" (l=1 only).
lambda_lower	Lower bound for λ in numerical optimization. Must be positive. Default is 1e-4.
lambda_upper	Upper bound for λ in numerical optimization. Must be positive. Default is 1.

Value

An object of class "pcqm_nbd_mle" containing:

- lambda: MLE of population density (individuals per unit area)
- k: MLE of aggregation parameter (smaller values indicate stronger aggregation)
- logLik: Maximized log-likelihood value
- n_obs: Number of fully observed (non-censored) distances
- n_censored: Number of censored observations (R > C)
- n_sectors: Total number of sectors analyzed
- n_points: Inferred number of sampling points
- censored_rate: Proportion of censored sectors
- call: Original function call

Examples

```
distances_matrix <- matrix(c(
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000,    7.655136,   13.815876,   10.423496,
     6.094721,    4.135461,    7.732912,    5.454545,
```

```
  9999.000000, 9999.000000,   14.787289,   15.670821,
  9999.000000,    9.825537,   11.611850,   15.757861,
  9999.000000,    9.670381,   14.055394,   17.075678,
    11.529219,    4.464136,    7.793114,   11.309553,
    13.307828,    5.864490,   13.309636,    5.897720,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000,   18.201084, 9999.000000,
  9999.000000,    7.809056,   12.612496,    5.601366,
     9.201294, 9999.000000,    8.353524,    9.683701,
     6.592604,   19.117869,   19.758384,   12.923507,
    15.574824,   10.643719,    9.494539,    7.382031,
     9.143077, 9999.000000,   15.551414,    5.266916,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
    18.604278,    7.279454,    9.385355,    5.573127,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
    11.980811, 9999.000000,   11.853695,   14.405252
), nrow = 20, ncol = 4, byrow = TRUE)

nbd_result <- nbd_mle(
  distances = distances_matrix,
  C = 20,
  q = 4,
  l = 2,
  init_method = "Pollard_censored",
  lambda_lower = 1e-4,
  lambda_upper = 10
)

nbd_result
```

---

print *Print Methods for PCQM Density Estimation Objects*

Description

Provides formatted console output for fitted PCQM (Point-Centered Quarter Method) density estimation results under different model assumptions. The following specialized print methods for S3 classes are supported:

- `print.pcqm_csr_mle` – display CSR-based PCQM maximum likelihood estimation results.
- `print.pcqm_moments` – display adjusted moment-based PCQM density estimators.
- `print.pcqm_nbd_mle` – display NBD-based PCQM maximum likelihood estimation results.

Usage

```
## S3 method for class 'pcqm_csr_mle'
print(x, digits = 6, ...)

## S3 method for class 'pcqm_moments'
print(x, digits = 6, ...)

## S3 method for class 'pcqm_nbd_mle'
print(x, digits = 6, ...)
```

Arguments

x	An object of class "pcqm_csr_mle", "pcqm_moments", or "pcqm_nbd_mle", returned by csr_mle, adjusted_moments, or nbd_mle, respectively.
digits	Number of decimal places to display for numeric estimates. Default is 6.
...	Additional arguments passed to the generic print method (currently unused; included for S3 consistency).

Value

The input model object x, invisibly. These functions are called primarily for their side effect of printing a formatted summary of the PCQM density estimation results to the R console.

See Also

csr_mle for CSR-based MLE estimation; adjusted_moments for adjusted moment estimators; nbd_mle for NBD-based MLE estimation.

Examples

```
distances_matrix <- matrix(c(
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000,    7.655136,   13.815876,   10.423496,
     6.094721,    4.135461,    7.732912,    5.454545,
  9999.000000, 9999.000000,   14.787289,   15.670821,
  9999.000000,    9.825537,   11.611850,   15.757861,
  9999.000000,    9.670381,   14.055394,   17.075678,
    11.529219,    4.464136,    7.793114,   11.309553,
    13.307828,    5.864490,   13.309636,    5.897720,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000,   18.201084, 9999.000000,
  9999.000000,    7.809056,   12.612496,    5.601366,
     9.201294, 9999.000000,    8.353524,    9.683701,
     6.592604,   19.117869,   19.758384,   12.923507,
    15.574824,   10.643719,    9.494539,    7.382031,
     9.143077, 9999.000000,   15.551414,    5.266916,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
    18.604278,    7.279454,    9.385355,    5.573127,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
  9999.000000, 9999.000000, 9999.000000, 9999.000000,
```

```
    11.980811, 9999.000000,   11.853695,   14.405252
), nrow = 20, ncol = 4, byrow = TRUE)

# CSR-based MLE
csr_result <- csr_mle(
  distances = distances_matrix,
  C = 20,
  q = 4,
  l = 2,
  lambda_lower = 1e-4,
  lambda_upper = 1
)
print(csr_result)

# Adjusted Moment Estimators
moment_result <- adjusted_moments(
  distances = distances_matrix,
  C = 20,
  q = 4,
  l = 2,
  init_method = "Pollard_censored"
)
print(moment_result)

# NBD-based MLE
nbd_result <- nbd_mle(
  distances = distances_matrix,
  C = 20,
  q = 4,
  l = 2,
  init_method = "Pollard_censored",
  lambda_lower = 1e-4,
  lambda_upper = 10
)
print(nbd_result)
```

`summary` *Summary Methods for PCQM Density Estimation Objects*

Description

Generate structured summary objects and formatted console output for PCQM (Point-Centered Quarter Method) density estimation results under different model assumptions.

Supported S3 methods:

- `summary.pcqm_csr_mle`
- `summary.pcqm_moments`
- `summary.pcqm_nbd_mle`
- `print.summary.pcqm_*`

Usage

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

## S3 method for class 'summary.pcqm_csr_mle'
print(x, digits = 6, ...)

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

## S3 method for class 'summary.pcqm_moments'
print(x, digits = 6, ...)

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

## S3 method for class 'summary.pcqm_nbd_mle'
print(x, digits = 6, ...)
```

Arguments

`object`	Model object returned by `csr_mle`, `adjusted_moments`, or `nbd_mle`.
`...`	Additional arguments (unused).
`x`	Summary object returned by corresponding `summary()` method.
`digits`	Number of digits to display.

Value

An object of class `"summary.pcqm_csr_mle"`, a named list with components:

model Character string: `"csr_mle"`.

lambda Estimated population density (intensity parameter λ). `NA` if estimation failed.

logLik Maximized log-likelihood evaluated at $\hat{\lambda}$.

n_points Number of focal sampling points.

n_sectors Total number of sectors.

n_censored Number of censored sectors.

censored_rate Proportion of censored sectors.

An object of class `"summary.pcqm_moments"`, a named list with components:

model Character string: `"moments"`.

estimators Named numeric vector of valid adjusted moment estimators (NA removed).

k_hat Estimated aggregation (dispersion) parameter $\hat{k}$.

n_points Number of focal sampling points.

n_sectors Total number of sectors.

n_censored Number of censored sectors.

censored_rate Proportion of censored sectors.

An object of class `"summary.pcqm_nbd_mle"`, a named list with components:

model Character string: `"nbd_mle"`.

lambda Estimated population density (intensity parameter λ). `NA` if estimation failed.

k Estimated aggregation (dispersion) parameter of the Negative Binomial distribution. `NA` if estimation failed.

logLik Maximized log-likelihood evaluated at $(\hat{\lambda}, \hat{k})$.

n_points Number of focal sampling points.

n_sectors Total number of sectors.

n_censored Number of censored sectors.

censored_rate Proportion of censored sectors.

Index