Package: SizeEstimation (via r-universe)

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Type Package

Title Estimating the Sizes of Populations at Risk of HIV Infection from Multiple Data Sources Using a Bayesian Hierarchical Model

Version 1.1.1

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Description This function develops an algorithm for presenting a Bayesian hierarchical model for estimating the sizes of local and national drug injected populations in Bangladesh. The model incorporates multiple commonly used data sources including mapping data, surveys, interventions, capture-recapture data, estimates or guesstimates from organizations, and expert opinion.

Imports MCMCpack, msm

License GPL-3

LazyData TRUE

RoxygenNote 5.0.1

NeedsCompilation no

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Additional_repositories `https://cranhaven.r-universe.dev`

Repository https://cranhaven.r-universe.dev

RemoteUrl https://github.com/cranhaven/cranhaven.r-universe.dev

RemoteRef package/SizeEstimation

RemoteSha b626180740521939d5ccd5b5e997f6b2403e978e

RemoteSubdir SizeEstimation

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`DATA` *The number of people who inject drugs in Bangladesh in 2004.*

Description

The data is on the number of people who inject drugs(PWID) in Bangladesh in 2004 from several sources and sampling methods. PWID were defined as male drug users who had taken drugs primarily intraveneously in the previous three to six months.

Usage

```
DATA
```

Format

A data frame with 64 obsevations on 9 variables.

First column is district. Second column is area. Third column is size of the population in that area. Fourth column is National Assessment of the situation and Response to Opioid/Opiate Use in Bangladesh(NASROB). Fifth column is the the data from Behavioral Surveillance Surveys in four cities(BSS). Sixth column is the data from Needle Exchange Program(NEP). Seventh column is the number of people who are captured by boyh BSS and NEP. Eighth column is the data from CARE Bangladesh Rapid Situation Assessment(RSA). Ninth column is division.

Source

Bao L, Raftery A, Reddy A. (2015) Estimating the Sizez of Populations At Risk of HIV Infection From Multiple Data Sources Using a Bayesian Hierarchical Model, Statistics and Its Interface.

References

Bao L, Raftery A, Reddy A. (2015) Estimating the Sizez of Populations At Risk of HIV Infection From Multiple Data Sources Using a Bayesian Hierarchical Model, Statistics and Its Interface.

`sizeestima` *Estimating the sizes of populations who inject drugs from multiple data sources using a Bayesian hierarchical model.*

Description

This R package is for reproducing Bao L, Raftery A, Reddy A. (2015) Estimating the Sizes of Populations At Risk of HIV Infection From Multiple Data Sources Using a Bayesian Hierarchical Model, Statistics and Its Interface. This function develops an algorithm for presenting a Bayesian hierarchical model for estimating the sizes of drug injected populations in Bangladesh. The model incorporates multiple commonly used data sources including mapping data, surveys, interventions, capture-recapture data, estimates or guesstimates from organizations, and expert opinion. This function provides the posterior samples of burnin thin at-risk population sizes at the subnational level.

Usage

```
sizeestima(DATA, size, burnin, thin)
```

Arguments

`DATA`	dataset from Bangladesh which used in Bao L, Raftery A, Reddy A. (2015) Estimating the Sizez of Populations At Risk of HIV Infection From Multiple Data Sources Using a Bayesian Hierarchical Model, Statistics and Its Interface.
`size`	the number of iteration in MCMC algorithm.
`burnin`	the number of Burn-In in MCMC algorithm.
`thin`	keep every thin-th scan.

Details

This function runs MCMC algorithm for reproducing Bao L, Raftery A, Reddy A. (2015) Estimating the Sizez of Populations At Risk of HIV Infection From Multiple Data Sources Using a Bayesian Hierarchical Model, Statistics and Its Interface.

Value

A matrix of posterior samples of at-risk population sizes at the sub-national level, where the rows correspond to sub-national areas and the columns correspond to MCMC iterations.

Author(s)

Le Bao, Adrian E. Raftery, Kyongwon Kim

References

Bao L, Raftery A, Reddy A. (2015) Estimating the Sizes of Populations At Risk of HIV Infection From Multiple Data Sources Using a Bayesian Hierarchical Model, Statistics and Its Interface.

See Also

`rtnorm` `rinvgamma` `dtnorm`

Examples

```
#n.total=sizeestima(DATA,500000,501,100)
```

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