

Package: stansum (via r-universe)

October 10, 2026

Title Bayesian Models for Aggregated Relational Data and Network Scale-Up Method

Version 1.0.1

Description Interface to various precompiled Stan models for Aggregated Relational Data that estimate, among other things, network degrees. Includes models by Zheng et al (2006) [<doi:10.1198/016214505000001168>](https://doi.org/10.1198/016214505000001168), Maltiel et al (2015) [<doi:10.1214/15-AOAS827>](https://doi.org/10.1214/15-AOAS827), Baum & Marsden (2023) [<doi:10.1016/j.socnet.2023.02.001>](https://doi.org/10.1016/j.socnet.2023.02.001).

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Encoding UTF-8

Roxygen list(markdown = TRUE)

Depends R (>= 3.4.0)

Imports instantiate (>= 0.2.3)

Additional_repositories <https://mc-stan.org/r-packages/>

SystemRequirements CmdStan
(<https://mc-stan.org/users/interfaces/cmdstan>)

Suggests cmdstanr (>= 0.5.2), knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

LazyData true

URL <https://coalesce-lab.github.io/stansum/>

Config/roxygen2/version 8.1.0

Config/pak/sysreqs cmake make libuv1-dev

Repository <https://coalesce-lab.r-universe.dev>

Date/Publication 2026-09-22 14:01:19 UTC

RemoteUrl <https://github.com/coalesce-lab/stansum>

RemoteRef HEAD

RemoteSha 8975af2a86b72a2f29a3cbec88c9f1775d807824

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Fake	<i>Datasets generated from ARD models</i>
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Description

Some artificial datasets simulated from various ARD models.

Usage

Fake_maltiel_RD

Format

Unless stated otherwise below all datasets are data frames with respondents in rows and subpopulations in columns.

Details

- Fake_maltiel_RD is sampled from Maltiel et al (2015) Random Degree model assuming 1000 respondents and 3 subpopulations.

References

Maltiel, R., Raftery, A. E., McCormick, T. H., & Baraff, A. J. (2015). Estimating Population Size Using the Network Scale Up Method. The Annals of Applied Statistics, 9(3), 1247–1277. <https://doi.org/10.1214/15-A0AS827>

get_model	<i>List or get Stan model objects</i>
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Description

List Stan models available in this package or load them in the form of CmdStanModel objects as implemented in the **cmdstanr** package.

Usage

```
get_model(name, ...)
```

```
list_models()
```

Arguments

name	character; name of the model to load
...	arguments passed to instantiate::stan_package_model

Value

get_model returns an "CmdStanModel" object.

list_models returns a character vector of model names provided with the package.

maltiel_bem	<i>Maltiel et al (2015) Barrier Effects Model</i>
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Description

Bayesian model for ARD including parameters capturing barrier effects.

- maltiel_bem_count – model for count responses
- maltiel_bem_dichotomous – model for dichotomous responses proposed by Baum & Marsden (2023).
- maltiel_bem_trichotomous – model for trichotomous responses proposed by Baum & Marsden (2023).

Usage

```
maltiel_bem_count(N, K, y, m, L, ...)
```

```
maltiel_bem_dichotomous(N, K, y, m, L, ...)
```

```
maltiel_bem_trichotomous(N, K, y, m, L, ...)
```

Arguments

N	integer; population size
K	integer; number of sub-populations
y	integer matrix; ARD
m	numeric; vector of fractional sizes of sub-populations
L	numeric; lower bound on degree
...	other arguments passed to <code>cmdstanr::sample()</code>

Details

Calling this function(s) will load the model object using `get_model()` and sample from the posterior using the `cmdstanr::sample()` method.

Value

Object of class `cmdstanr::CmdStanMCMC` containing the samples.

References

Baum, D. S., & Marsden, P. V. (2023). Uses and limitations of dichotomous aggregate relational data. *Social Networks*, 74, 42–61. doi:10.1016/j.socnet.2023.02.001

Maltiel, R., Raftery, A. E., McCormick, T. H., & Baraff, A. J. (2015). Estimating Population Size Using the Network Scale Up Method. *The Annals of Applied Statistics*, 9(3), 1247–1277. doi:10.1214/15AOAS827

See Also

Use `get_model()` to return Stan model object of class `cmdstanr::CmdStanModel` without fitting it.

Other models in this package: `maltiel_cm`, `maltiel_rdm`, `maltiel_tbm`, `test_model()`, `zheng_bem`, `zheng_gp`

Other models of Maltiel et al (2015): `maltiel_cm`, `maltiel_rdm`, `maltiel_tbm`

`maltiel_cm`

Maltiel et al (2015) Combined Model

Description

Bayesian model for ARD with both barrier effect and transmission bias parameters.

- `maltiel_cm_count` – combined model for count responses, as described in section 2.4 of Maltiel et al (2015). It carries both the per-sub-population overdispersion ρ_k of the barrier effects model and the transmission bias τ_k of the transmission bias model: $y_{ik} \sim \text{Binomial}(d_i, \tau_k * q_{ik})$ with $d_i \sim \text{LogNormal}(\mu, \sigma^2)$ and $q_{ik} \sim \text{Beta}(m_k, \rho_k)$. Multiplying q_{ik} by τ_k breaks the Beta-Binomial conjugacy, so – unlike `maltiel_bem_count()` – the latent q_{ik} cannot be integrated out and are sampled together with the remaining parameters. This adds $N * K$ parameters, so fits are substantially slower than for the component models.

Usage

```
maltiel_cm_count(N, K, y, m, L, eta, v, ...)
```

Arguments

N	integer; population size
K	integer; number of sub-populations
y	numeric matrix; ARD counts (N x K)
m	numeric vector; fractional sub-population sizes (length K)
L	numeric vector; lower bounds on individual degrees (length N). Must satisfy $L[i] \geq \max(y[i, :])$ for each respondent i so that the degree is always at least as large as the maximum observed count.
eta	numeric vector; Beta prior shape 1 for each transmission bias (length K)
v	numeric vector; Beta prior shape 2 for each transmission bias (length K)
...	other arguments passed to <code>cmdstanr::sample()</code>

Details

Calling this function(s) will load the model object using `get_model()` and sample from the posterior using the `cmdstanr::sample()` method.

The transmission biases `tau_k` and the degrees `d_i` are only weakly identified from ARD alone: scaling `tau_k` down and the degrees up leaves the reported counts largely unchanged. The `eta / v` prior on `tau` is what resolves this, so an uninformative `eta = v = 1` will typically pull the posterior for `tau` below 1 and inflate the estimated degrees. Supply an informative prior reflecting what is known about transmission for each sub-population.

Value

Object of class `cmdstanr::CmdStanMCMC` containing the samples.

References

Maltiel, R., Raftery, A. E., McCormick, T. H., & Baraff, A. J. (2015). Estimating Population Size Using the Network Scale Up Method. *The Annals of Applied Statistics*, 9(3), 1247–1277. doi:10.1214/15AOAS827

See Also

Use `get_model()` to return Stan model object of class `cmdstanr::CmdStanModel` without fitting it.

Other models in this package: `maltiel_bem`, `maltiel_rdm`, `maltiel_tbm`, `test_model()`, `zheng_bem`, `zheng_gp`

Other models of Maltiel et al (2015): `maltiel_bem`, `maltiel_rdm`, `maltiel_tbm`

Examples

```
data("Fake_maltiel_RD", package = "stansum")
y <- data.matrix(Fake_maltiel_RD)[1:50, ]
K <- ncol(y)
r <- maltiel_cm_count(
  N = nrow(y),
  K = K,
  y = y,
  m = rep(0.01, K),
  L = apply(y, 1, max),
  eta = rep(1, K),
  v = rep(1, K),
  chains = 1,
  iter_warmup = 200,
  iter_sampling = 10
)
```

maltiel_rdm

Maltiel et al (2015) Random Degree Model

Description

Bayesian model for ARD with random degree parameters.

- maltiel_rdm_count – model for count responses
- maltiel_rdm_dichotomous – model for dichotomous responses proposed by Baum & Marsden (2023).

Usage

```
maltiel_rdm_count(N, K, y, m, L, ...)
```

```
maltiel_rdm_dichotomous(N, K, y, m, L, ...)
```

Arguments

N	integer; population size
K	integer; number of sub-populations
y	integer matrix; ARD
m	numeric; vector of fractional sizes of sub-populations
L	numeric; lower bound on degree
...	other arguments passed to <code>cmdstanr::sample()</code>

Details

Calling this function(s) will load the model object using `get_model()` and sample from the posterior using the `cmdstanr::sample()` method.

Value

Object of class `cmdstanr::CmdStanMCMC` containing the samples.

References

Baum, D. S., & Marsden, P. V. (2023). Uses and limitations of dichotomous aggregate relational data. *Social Networks*, 74, 42–61. doi:10.1016/j.socnet.2023.02.001

Maltiel, R., Raftery, A. E., McCormick, T. H., & Baraff, A. J. (2015). Estimating Population Size Using the Network Scale Up Method. *The Annals of Applied Statistics*, 9(3), 1247–1277. doi:10.1214/15AOAS827

See Also

Use `get_model()` to return Stan model object of class `cmdstanr::CmdStanModel` without fitting it.

Other models in this package: `maltiel_bem`, `maltiel_cm`, `maltiel_tbm`, `test_model()`, `zheng_bem`, `zheng_gp`

Other models of Maltiel et al (2015): `maltiel_bem`, `maltiel_cm`, `maltiel_tbm`

maltiel_tbm

Maltiel et al Transmission Bias Model

Description

Bayesian model for ARD with transmission bias parameters.

- `maltiel_tbm_count` – transmission bias model for count responses. All `tau_k` are estimated from the data.

Usage

```
maltiel_tbm_count(N, K, y, m, L, eta, v, ...)
```

Arguments

N	integer; population size
K	integer; number of sub-populations
y	numeric matrix; ARD counts (N x K)
m	numeric vector; fractional sub-population sizes (length K)
L	numeric vector; lower bounds on individual degrees (length N). Must satisfy $L[i] \geq \max(y[i, :])$ for each respondent i so that the degree is always at least as large as the maximum observed count.

<code>eta</code>	numeric vector; Beta prior shape 1 for each transmission bias (length K)
<code>v</code>	numeric vector; Beta prior shape 2 for each transmission bias (length K)
<code>...</code>	other arguments passed to <code>cmdstanr::sample()</code>

Details

Calling this function(s) will load the model object using `get_model()` and sample from the posterior using the `cmdstanr::sample()` method.

Value

Object of class `cmdstanr::CmdStanMCMC` containing the samples.

References

Maltiel, R., Raftery, A. E., McCormick, T. H., & Baraff, A. J. (2015). Estimating Population Size Using the Network Scale Up Method. *The Annals of Applied Statistics*, 9(3), 1247–1277. doi:10.1214/15AOAS827

See Also

Use `get_model()` to return Stan model object of class `cmdstanr::CmdStanModel` without fitting it.

Other models in this package: `maltiel_bem`, `maltiel_cm`, `maltiel_rdm`, `test_model()`, `zheng_bem`, `zheng_gp`

Other models of Maltiel et al (2015): `maltiel_bem`, `maltiel_cm`, `maltiel_rdm`

Examples

```
data("Fake_maltiel_RD", package = "stansum")
K <- ncol(Fake_maltiel_RD)
r <- maltiel_tbm_count(
  N = nrow(Fake_maltiel_RD),
  K = K,
  y = data.matrix(Fake_maltiel_RD),
  m = rep(0.01, K),
  L = apply(data.matrix(Fake_maltiel_RD), 1, max),
  eta = rep(1, K),
  v = rep(1, K),
  chains = 1,
  iter_warmup = 200,
  iter_sampling = 10
)
```

test_model	<i>A simple Bernoulli model for testing purposes</i>
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Description

A test Bernoulli model taken from Stan documentation.

Usage

```
test_model(N, y, ...)
```

Arguments

N	integer; number of trials
y	integer; vector of Bernoulli outcomes
...	other arguments passed to cmdstanr::sample()

Details

Calling this function(s) will load the model object using [get_model\(\)](#) and sample from the posterior using the [cmdstanr::sample\(\)](#) method.

Value

Object of class [cmdstanr::CmdStanMCMC](#) containing the samples.

See Also

Use [get_model\(\)](#) to return Stan model object of class [cmdstanr::CmdStanModel](#) without fitting it. Other models in this package: [maltiel_bem](#), [maltiel_cm](#), [maltiel_rdm](#), [maltiel_tbm](#), [zheng_bem](#), [zheng_gp](#)

zheng_bem	<i>Zheng et al (2006) Barrier Effects Model</i>
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Description

Bayesian model for ARD...

- `zheng_bem_count` – model for count responses
- `zheng_bem_count2` – model for count responses with different parametrization for omega and different priors
- `zheng_bem_dichotomous` – model for dichotomous responses proposed by Baum & Marsden (2023).
- `zheng_bem_trichotomous` – model for trichotomous responses proposed by Baum & Marsden (2023).

Usage

```
zheng_bem_count(N, K, y, ...)

zheng_bem_count2(N, K, y, ...)

zheng_bem_dichotomous(N, K, y, ...)

zheng_bem_trichotomous(N, K, y, ...)
```

Arguments

N	integer; sample size
K	integer; number of sub-populations
y	integer matrix; ARD
...	other arguments passed to <code>cmdstanr::sample()</code>

Details

Calling this function(s) will load the model object using `get_model()` and sample from the posterior using the `cmdstanr::sample()` method.

Value

Object of class `cmdstanr::CmdStanMCMC` containing the samples.

References

Baum, D. S., & Marsden, P. V. (2023). Uses and limitations of dichotomous aggregate relational data. *Social Networks*, 74, 42–61. doi:10.1016/j.socnet.2023.02.001

Zheng, T., Salganik, M. J., & Gelman, A. (2006). How Many People Do You Know in Prison? Using Overdispersion in Count Data to Estimate Social Structure in Networks. *Journal of the American Statistical Association*, 101(474), 409–423. doi:10.1198/016214505000001168

See Also

Use `get_model()` to return Stan model object of class `cmdstanr::CmdStanModel` without fitting it.

Other models in this package: `maltiel_bem`, `maltiel_cm`, `maltiel_rdm`, `maltiel_tbm`, `test_model()`, `zheng_gp`

Other models of Zheng et al (2006): `zheng_gp`

zheng_gp

*Zheng et al (2006) Group Prevalence Model***Description**

Bayesian model for ARD...

- `zheng_gp_count` – model for count responses
- `zheng_gp_dichotomous` – model for dichotomous responses proposed by Baum & Marsden (2023).

Usage

```
zheng_gp_count(N, K, y, ...)
```

```
zheng_gp_dichotomous(N, K, y, ...)
```

Arguments

N	integer; population size
K	integer; number of sub-populations
y	integer matrix; ARD
...	other arguments passed to <code>cmdstanr::sample()</code>

Details

Calling this function(s) will load the model object using `get_model()` and sample from the posterior using the `cmdstanr::sample()` method.

Value

Object of class `cmdstanr::CmdStanMCMC` containing the samples.

References

Baum, D. S., & Marsden, P. V. (2023). Uses and limitations of dichotomous aggregate relational data. *Social Networks*, 74, 42–61. doi:10.1016/j.socnet.2023.02.001

Zheng, T., Salganik, M. J., & Gelman, A. (2006). How Many People Do You Know in Prison? Using Overdispersion in Count Data to Estimate Social Structure in Networks. *Journal of the American Statistical Association*, 101(474), 409–423. doi:10.1198/016214505000001168

See Also

Use `get_model()` to return Stan model object of class `cmdstanr::CmdStanModel` without fitting it.

Other models in this package: `maltiel_bem`, `maltiel_cm`, `maltiel_rdm`, `maltiel_tbm`, `test_model()`, `zheng_bem`

Other models of Zheng et al (2006): `zheng_bem`

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