0.1 ei.hier: Hierarchical Ecological Inference Model for 2×2 Tables

Given contingency tables with observed marginals, ecological inference (EI) models estimate each internal cell value for each table. The hierarchical EI model estimates a Bayesian model for 2×2 tables. The model is implemented using a Markov Chain Monte Carlo algorithm (via a combination of slice and Gibbs sampling). For a Bayesian implementation of EI that accounts for temporal dependence, see Quinn's dynamic EI model (Section **??**). For contingency tables larger than 2 rows by 2 columns, see R×C EI (Section **??**).

Syntax

```
> z.out <- zelig(cbind(t0, t1) ~ x0 + x1, N = NULL,
                 model = "MCMCei.hier", data = mydata)
> x.out <- setx(z.out, fn = NULL, cond = TRUE)
> s.out <- sim(z.out, x = x.out)
```

Inputs

- `t0`, `t1`: numeric vectors (either counts or proportions) containing the column margins of the units to be analyzed.
- `x0`, `x1`: numeric vectors (either counts or proportions) containing the row margins of the units to be analyzed.
- `N`: total counts per contingency table (unit). If `t0`,`t1`, `x0` and `x1` are proportions, you must specify `N`.

Additional Inputs

In addition, `zelig()` accepts the following additional inputs for `ei.hier` to monitor the convergence of the Markov chain:

- `burnin`: number of the initial MCMC iterations to be discarded (defaults to 5,000).
- `mcmc`: number of the MCMC iterations after burnin (defaults to 50,000).
- `thin`: thinning interval for the Markov chain. Only every `thin`-th draw from the Markov chain is kept. The value of `mcmc` must be divisible by this value. The default value is 1.
- `verbose`: defaults to `FALSE`. If `TRUE`, the progress of the sampler (every 10%) is printed to the screen.
- `seed`: seed for the random number generator. The default is `NA` which corresponds to a random seed of 12345.

The model also accepts the following additional arguments to specify prior parameters used in the model:

- `m0`: prior mean of μ_0 (defaults to 0).
- `M0`: prior variance of μ_0 (defaults to 2.287656).
- `m1`: prior mean of μ_1 (defaults to 0).
- `M1`: prior variance of μ_1 (defaults to 2.287656).
- `a0`: $a_0/2$ is the shape parameter for the Inverse Gamma prior on σ_0^2 (defaults to 0.825).
- `b0`: $b_0/2$ is the scale parameter for the Inverse Gamma prior on σ_0^2 (defaults to 0.0105).
- `a1`: $a_1/2$ is the shape parameter for the Inverse Gamma prior on σ_1^2 (defaults to 0.825).
- `b1`: $b_1/2$ is the scale parameter for the Inverse Gamma prior on σ_1^2 (defaults to 0.0105).

Users may wish to refer to `help(MCMChierEI)` for more information.

Convergence

Users should verify that the Markov Chain converges to its stationary distribution. After running the `zelig()` function but before performing `setx()`, users may conduct the following convergence diagnostics tests:

- `geweke.diag(z.out$coefficients)`: The Geweke diagnostic tests the null hypothesis that the Markov chain is in the stationary distribution and produces z-statistics for each estimated parameter.

- `heidel.diag(z.out$coefficients)`: The Heidelberger-Welch diagnostic first tests the null hypothesis that the Markov Chain is in the stationary distribution and produces p-values for each estimated parameter. Calling `heidel.diag()` also produces output that indicates whether the mean of a marginal posterior distribution can be estimated with sufficient precision, assuming that the Markov Chain is in the stationary distribution.

- `raftery.diag(z.out$coefficients)`: The Raftery diagnostic indicates how long the Markov Chain should run before considering draws from the marginal posterior distributions sufficiently representative of the stationary distribution.

If there is evidence of non-convergence, adjust the values for `burnin` and `mcmc` and rerun `zelig()`.

Advanced users may wish to refer to `help(geweke.diag)`, `help(heidel.diag)`, and `help(raftery.diag)` for more information about these diagnostics.

Examples

1. Basic examples

   Attaching the example dataset:

   ```
   > data(eidat)
   > eidat
   ```

   Estimating the model using `ei.hier`:

   ```
   > z.out <- zelig(cbind(t0, t1) ~ x0 + x1, model = "ei.hier", data = eidat,
   +     mcmc = 40000, thin = 10, burnin = 10000, verbose = TRUE)
   > summary(z.out)
   ```

   Setting values for in-sample simulations given marginal values of `x0`, `x1`, `t0`, and `t1`:

   ```
   > x.out <- setx(z.out, fn = NULL, cond = TRUE)
   ```

   In-sample simulations from the posterior distribution:

   ```
   > s.out <- sim(z.out, x = x.out)
   ```

   Summarizing in-sample simulations at aggregate level weighted by the count in each unit:

   ```
   > summary(s.out)
   ```

   Summarizing in-sample simulations at unit level for the first 5 units:

   ```
   > summary(s.out, subset = 1:5)
   ```

Model

Consider the following 2×2 contingency table for the racial voting example. For each geographical unit $i = 1, \ldots, p$, the marginals t_i^0, t_i^1, x_i^0, and x_i^1 are known, and we would like to estimate n_i^{00}, n_i^{01}, n_i^{10}, and n_i^{11}.

	No Vote	Vote	
Black	n_i^{00}	n_i^{01}	x_i^0
White	n_i^{10}	n_i^{11}	x_i^1
	t_i^0	t_i^1	N_i

The marginal values x_i^0, x_i^1, t_i^0, t_i^1 are observed as either counts or fractions. If fractions, the counts can be obtained by multiplying by the total counts per table $N_i = n_i^{00} + n_i^{01} + n_i^{10} + n_i^{11}$ and rounding to the nearest integer. Although there are four internal cells, only two unknowns are modeled since $n_i^{01} = x_i^0 - n_i^{00}$ and $n_i^{11} = s_i^1 - n_i^{10}$.

The hierarchical Bayesian model for ecological inference in 2×2 is illustrated as following:

- The *stochastic component* of the model assumes that

$$\begin{aligned} n_i^{00} \mid x_i^0, \beta_i^b &\sim \text{Binomial}\left(x_i^0, \beta_i^b\right), \\ n_i^{10} \mid x_i^1, \beta_i^w &\sim \text{Binomial}\left(x_i^1, \beta_i^w\right) \end{aligned}$$

  where β_i^b is the fraction of the black voters who vote and β_i^w is the fraction of the white voters who vote. β_i^b and β_i^w as well as their aggregate level summaries are the focus of inference.

- The *systematic component* is

$$\begin{aligned} \beta_i^b &= \frac{\exp \theta_i^0}{1 - \exp \theta_i^0} \\ \beta_i^w &= \frac{\exp \theta_i^1}{1 - \exp \theta_i^1} \end{aligned}$$

  The logit transformations of β_i^b and β_i^w, θ_i^0, and θ_i^1 now take value on the real line. (Future versions may allow β_i^b and β_i^w to be functions of observed covariates.)

- The *priors* for θ_i^0 and θ_i^1 are given by

$$\begin{aligned} \theta_i^0 \mid \mu_0, \sigma_0^2 &\sim \text{Normal}\left(\mu_0, \sigma_0^2\right), \\ \theta_i^1 \mid \mu_1, \sigma_1^2 &\sim \text{Normal}\left(\mu_1, \sigma_1^2\right) \end{aligned}$$

  where μ_0 and μ_1 are the means, and σ_0^2 and σ_1^2 are the variances of the two corresponding (independent) normal distributions.

- The *hyperpriors* for μ_0 and μ_1 are given by

$$\begin{aligned}
\mu_0 &\sim \text{Normal}\left(m_0, M_0\right), \\
\mu_1 &\sim \text{Normal}\left(m_1, M_1\right),
\end{aligned}$$

  where m_0 and m_1 are the means of the (independent) normal distributions while M_0 and M_1 are the variances.

- The *hyperpriors* for σ_0^2 and σ_1^2 are given by

$$\begin{aligned}
\sigma_0^2 &\sim \text{Inverse Gamma}\left(\frac{a_0}{2}, \frac{b_0}{2}\right), \\
\sigma_1^2 &\sim \text{Inverse Gamma}\left(\frac{a_1}{2}, \frac{b_1}{2}\right),
\end{aligned}$$

  where $a_0/2$ and $a_1/2$ are the shape parameters of the (independent) Gamma distributions while $b_0/2$ and $b_1/2$ are the scale parameters.

  The default hyperpriors for μ_0, μ_1, σ_0^2, and σ_1^2 are chosen such that the prior distributions of β^b and β^w are flat.

Output Values

The output of each Zelig command contains useful information which you may view. For example, if you run

```
> z.out <- (cbind(t0, t1) ~ x0 + x1, N = NULL,
          model = "ei.hier", data = mydata)
```

then you may examine the available information in `z.out` by using `names(z.out)`, see the draws from the posterior distribution of the quantities of interest by using `z.out$coefficients`, and a default summary of information through `summary(z.out)`. Other elements available through the `$` operator are listed below.

- From the `zelig()` output object `z.out`, you may extract:
  - `coefficients`: draws from the posterior distributions of the parameters.
  - `zelig.data`: the input data frame if `save.data = TRUE`.
  - `N`: the total counts when the inputs are fractions.
  - `seed`: the random seed used in the model.
- From `summary(z.out)`, you may extract:

- `summary`: a matrix containing the summary information of the posterior estimation of β_i^b andβ_i^w for each unit and the parameters μ_0, μ_1, σ_1 and σ_2 based on the posterior distribution. The first p rows correspond to β_i^b, $i = 1, \ldots p$, the row names are in the form of `p0table`i. The $(p+1)$-th to the $2p$-th rows correspond to β_i^w, $i = 1, \ldots, p$. The row names are in the form of `p1table`i. The last four rows contain information about μ_0, μ_1, σ_0^2 and σ_1^2, the prior means and variances of θ_0 and θ_1.

- From the `sim()` output object `s.out`, you may extract quantities of interest arranged as arrays indexed by simulation $\times$ column $\times$ row $\times$ observation, where column and row refer to the column dimension and the row dimension of the contingency table, respectively. In this model, only 2×2 contingency tables are analyzed, hence column$=2$ and row$=2$ in all cases. Available quantities are:
  - `qi$ev`: the simulated expected values of each internal cell given the observed marginals.
  - `qi$pr`: the simulated expected values of each internal cell given the observed marginals.

How to Cite

To cite the *ei.hier* Zelig model use:

> Ben Goodrich and Ying Lu. 2007. "ei.hier: Hierarchical Ecological Inference Model for 2x2 tables" in Kosuke Imai,Gary King, and Olivia Lau, "Zelig: Everyone's Statistical Software," `http://gking.harvard.edu/zelig`.

To cite Zelig as a whole, please reference these two sources:

> Kosuke Imai, Gary King, and Olivia Lau. 2007. "Zelig: Everyone's Statistical Software," `http://GKing.harvard.edu/zelig`.

> Kosuke Imai, Gary King, and Olivia Lau. 2007. "Toward A Common Framework for Statistical Analysis and Development," `http://gking.harvard.edu/files/abs/z-abs.shtml`.

See also

ei.hier function is part of the MCMCpack library by Andrew D. Martin and Kevin M. Quinn (Martin and Quinn 2005). The convergence diagnostics are part of the CODA library by Martyn Plummer, Nicky Best, Kate Cowles, and Karen Vines (Plummer et al. 2005). Sample date are adapted from Martin and Quinn (2005).

Bibliography

Martin, A. D. and Quinn, K. M. (2005), *MCMCpack: Markov chain Monte Carlo (MCMC) Package.*

Plummer, M., Best, N., Cowles, K., and Vines, K. (2005), *coda: Output analysis and diagnostics for MCMC.*