Package ‘SBSA’

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R topics documented:

SBSA-package ................................................................. 2
fitSBSA ................................................................. 2

Index 6
SBSA-package

**Simplified Bayesian Sensitivity Analysis**

**Description**

Simplified Bayesian sensitivity analysis of models with partially observed confounders.

**Details**

The SBSA package is an implementation of algorithms for simplified Bayesian sensitivity analysis described in Gustafson *et al* (2010). It has one entry function, `fitSBSA`. For more details refer to the relevant help files.

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**References**


**See Also**

`fitSBSA`

**Examples**

```r
## see examples for fitSBSA
```

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**fitSBSA**

*Fitting Simplified Bayesian Sensitivity Models*

**Description**

Conducts sensitivity analysis over a model involving unobserved and poorly measured covariates.

**Usage**

```r
fitSBSA(y, x, w, a, b, k2=NULL, e12=NULL, cor.alpha=0, sd.alpha=1e+06, nrep=5000, sampler.jump=c(alpha=.15, beta.z=.1, sigma.sq=.5, tau.sq=.05, beta.u.gamma.x=.3, gamma.z=.15), q.steps=25, family=c("continuous", "binary"))
```
Arguments

\( y \)  
- a vector of outcomes

\( x \)  
- a (standardized) vector of exposures

\( w \)  
- a (standardized) matrix of noisy measurements

\( a \)  
- parameter of the prior for magnitude of measurement error on confounder \( Z_j \)

\( b \)  
- parameter of the prior for magnitude of measurement error on confounder \( Z_j \)

\( k2 \)  
- (optional) magnitude of prior uncertainty about \( (U|X, Z) \) regression coefficients

\( e12 \)  
- (optional) residual variance for \( (U|X, Z) \)

\( \text{cor}.\alpha \)  
- (optional) value of the \( \rho \) parameter of the bivariate normal prior for \( \alpha \)

\( \text{sd}.\alpha \)  
- (optional) value of the \( \sigma \) parameter of the bivariate normal prior for \( \alpha \)

\( \text{nrep} \)  
- number of MCMC steps

\( \text{sampler}.\text{jump} \)  
- named vector of standard deviation of
  - \( \text{alpha} \) jump for block reparametrizing \( \alpha \)
  - \( \text{beta}.z \) jump for block reparametrizing \( \beta_z \)
  - \( \text{sigma}.sq \) (continuous case only) jump for block reparametrizing \( \sigma^2 \)
  - \( \text{tau}.sq \) jump for block reparametrizing \( \tau^2 \)
  - \( \text{beta}.u\.gamma.x \) jump for block reparametrizing \( \beta_u \) and \( \gamma_z \)
  - \( \text{gamma}.z \) jump for block reparametrizing \( \gamma_z \)

\( \text{q.steps} \)  
- number of steps in numeric integration of likelihood (only used for binary outcome variables)

\( \text{family} \)  
- a character string indicating the assumed distribution of the outcome. Valid values are "continuous", the default, or "binary".

Details

The function uses a simplified Bayesian sensitivity analysis algorithm that models the outcome variable \( Y \) in terms of exposure \( X \) and confounders \( Z = (Z_1, \ldots, Z_p) \) and \( U = (U_1, \ldots, U_q) \), where \( U \)s are unobserved, and \( Z \)s are measured imprecisely as \( W \)s. (I.e., the observed data is \( (Y, X, W) \).) Parameters of the model are then estimated using MCMC with reparametrizing block-sampling. The estimated parameters are as follows:

\[
\begin{align*}
  \tau & \sim N_p(Z, \text{diag} \tau^2) \\
  \gamma_x, \gamma_z & \sim N(\gamma_x X + \gamma'_z Z) \\
  \alpha, \beta_u, \beta_z, \sigma & \sim N(\alpha_0 + \alpha_x X + \beta_u U + \beta'_z Z, \sigma^2)
\end{align*}
\]

Value

a list with the following elements:

\( \text{acc} \)  
- a vector of counts of how many times each block sampler successfully made a jump. Vector elements are named by their block, as in the \( \text{sampler}.\text{jump} \) argument.

\( \text{alpha} \)  
- a \( \text{nrep} \times 2 \) matrix of the value of \( \alpha \) parameter at each MCMC step
fitSBSA

beta.z  a nrep × p matrix of the value of βz parameter at each MCMC step
gamma.z  a nrep × p matrix of the value of γz parameter at each MCMC step
tau.sq  a nrep × p matrix of the value of τ2 parameter at each MCMC step
gamma.x  a vector of the value of γx parameter at each MCMC step
beta.u  a vector of the value of βu parameter at each MCMC step
sigma.sq  a vector of the value of σ2 parameter at each MCMC step

References

Examples
### simulated data example
n <- 1000

### exposure and true confounders equi-correlated with corr=.6
tmp <- sqrt(.6)*matrix(rnorm(n),n,5) +
      sqrt(1-.6)*matrix(rnorm(n*5),n,5)
x <- tmp[,1]
z <- tmp[,2:5]

### true outcome relationship
y <- rnorm(n, x + z%*%rep(.4, 4))

### first two confounders are poorly measured, ICC=.7, .85
### third is correctly measured, fourth is unobserved
w <- z[,1:3]
w[,1] <- w[,1] + rnorm(n, sd=sqrt(1/.7-1))
w[,2] <- w[,2] + rnorm(n, sd=sqrt(1/.85-1))

### fitSBSA expects standardized exposure, noisy confounders
x.sdz <- (x-mean(x))/sqrt(var(x))
w.sdz <- apply(w, 2, function(x) {(x-mean(x))/sqrt(var(x))})

### prior information: ICC very likely above .6, mode at .8
### via Beta(5.21) distribution
fit <- fitSBSA(y, x.sdz, w.sdz, a=5, b=21, nrep=10000,
sampler.jump=c(alpha=.02, beta.z=.03,
sigma.sq=.05, tau.sq=.004,
beta.u.gamma.x=.4, gamma.z=.5))

### check MCMC behaviour
print(fit$acc)
plot(fit$alpha[,2], pch=20)

### inference on target parameter in original scale
trgt <- fit$alpha[1001:10000,2]/sqrt(var(x))
print(c(mean(trgt), sqrt(var(trgt))))
Index

*Topic **Bayesian inference**
  SBSA-package, 2

*Topic **Measurement error**
  SBSA-package, 2

*Topic **Sensitivity analysis**
  SBSA-package, 2

*Topic **TODO**
  fitSBSA, 2

*Topic **Unobserved confounder**
  SBSA-package, 2

fitSBSA, 2, 2

SBSA (SBSA-package), 2
SBSA-package, 2