Package ‘SurrogateBMA’

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Type Package

Title Flexible Evaluation of Surrogate Markers with Bayesian Model Averaging

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Author Yunshan Duan

Maintainer Yunshan Duan `<yunshan@utexas.edu>`

Description Provides functions to estimate the proportion of treatment effect explained by the surrogate marker using Bayesian Model Averaging approach.

License GPL (>= 2)

Imports Rcpp (>= 1.0.9), MCMCpack, mvtnorm

LinkingTo Rcpp, RcppEigen, RcppNumerical

Depends R (>= 3.5.0)

LazyData true

R topics documented:

`exampleData` *Example data*

Description

Example data

Usage

```
data("exampleData")
```

Format

A data frame with 400 rows and 3 variables:

`Y` the primary outcome

`S` the surrogate marker

`A` the treatmentt arm

Examples

```
data(exampleData)
names(exampleData)
```

`gen.prior` *Generates the default prior hyperparameters*

Description

Generates a list of hyper-parameters we use by default in the inverse-Gamma-Normal prior for the variance and coefficients, including a0_list, b0_list, mu0_list, Gamma0_list, Gamma0_inv_list , each being a list of 5 with 5 parameters under the 5 different candidate models. An Inv-Gamma(a0, b0) - Normal(mu0, σ^2 Gamma0) prior is assumed.

Usage

```
gen.prior()
```

Value

A list of hyper-parameters, including a0_list, b0_list, mu0_list, Gamma0_list, Gamma0_inv_list , each being a list of 5 with 5 parameters under the 5 different candidate models.

Author(s)

Yunshan Duan

References

Duan and Parast (2023+). Flexible Evaluation of Surrogate Markers with Bayesian Model Averaging.

Examples

```
gen.prior()

# if we want to change the prior parameter a0 in model 1
prior.para <- gen.prior()
prior.para$a0_list[[1]] <- 1
```

post.model — *Calculates the posterior probability of the candidate models*

Description

Gives the posterior probability of each candidate model being true.

Usage

```
post.model(Y, S, A, prior.para = NULL)
```

Arguments

Y	numeric vector; primary outcome, assumed to be continuous.
S	numeric vector; surrogate marker, assumed to be continuous.
A	numeric vector; treatment arm, assumed to be binary. The treatment arm = 1 when the patient is enrolled in the treatment group, treatment arm = 0 when in the control group.
prior.para	a list of hyper-parameters in the inverse-Gamma-Normal prior for the variance and coefficients, including a0_list, b0_list, mu0_list, Gamma0_list, Gamma0_inv_list , each being a list of 5 with 5 parameters under the 5 different candidate models. An Inv-Gamma(a0, b0) - Normal(mu0, σ^2 Gamma0) prior is assumed.

Value

a numeric vector; the posterior probabilities of the candidate models.

Author(s)

Yunshan Duan

References

Duan and Parast (2023+). Flexible Evaluation of Surrogate Markers with Bayesian Model Averaging.

Examples

```
data(exampleData)
post.model(Y = exampleData$Y, S = exampleData$S, A = exampleData$A)
```

R.BMA.est *Calculates the proportion of treatment effect explained*

Description

Calculates the proportion of treatment effect on the primary outcome explained by the treatment effect on the surrogate marker using Bayesian Model Averaging. This function is intended to be used for a fully observed continuous outcome and one single continuous surrogate marker. The user can also request to calculate a 95% credible interval, evaluated by Bayesian bootstrapping.

Usage

```
R.BMA.est(Y, S, A, nmc = 500, nBB = 100, conf.int = TRUE, alpha = 0.05, prior.para = NULL)
```

Arguments

`Y`	numeric vector; primary outcome, assumed to be continuous.
`S`	numeric vector; surrogate marker, assumed to be continuous.
`A`	numeric vector; treatment arm, assumed to be binary. The treatment arm = 1 when the patient is enrolled in the treatment group, treatment arm = 0 when in the control group.
`nmc`	number of MCMC samples in posterior inference, default is 500.
`nBB`	number of replicates in Bayesian bootstrap, default is 100. Igored if conf.int = FALSE.
`conf.int`	TRUE or FALSE; indicates whether a 95% credible interval for the proportion explained is requested, default is TRUE.
`alpha`	the confidence level for the credible interval, the 100(1 - α)% credible interval is calculated. Default is 0.05, ignored if conf.int = FALSE.
`prior.para`	a list of hyper-parameters in the inverse-Gamma-Normal prior for the variance and coefficients, including a0_list, b0_list, mu0_list, Gamma0_list, Gamma0_inv_list , each being a list of 5 with 5 parameters under the 5 different candidate models. An Inv-Gamma(a0, b0) - Normal(mu0, σ^2 Gamma0) prior is assumed.

Value

`R.BMA`	the estimate of the proportion explained by the surrogate marker.
`p.model`	the posterior probability of the candidate models being true.
`ci`	the credible interval for the proportion explained by the surrogate marker.

Author(s)

Yunshan Duan

References

Duan and Parast (2023+). Flexible Evaluation of Surrogate Markers with Bayesian Model Averaging.

Examples

```
data(exampleData)
R.BMA.est(Y = exampleData$Y, S = exampleData$S, A = exampleData$A)
```

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