Package: rstanbdp (via r-universe)

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Title Bayesian Deming Regression for Method Comparison

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Description Regression methods to quantify the relation between two measurement methods are provided by this package. The focus is on a Bayesian Deming regressions family. With a Bayesian method the Deming regression can be run in a traditional fashion or can be run in a robust way just decreasing the degree of freedom d.f. of the sampling distribution. With d.f. = 1 an extremely robust Cauchy distribution can be sampled. Moreover, models for dealing with heteroscedastic data are also provided. For reference see G. Pioda (2024) <https://piodag.github.io/bd1/>.

License GPL (>= 3)

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Biarch true

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`rstanbdp-package` *The 'rstanbdp' package.*

Description

Bayesian Deming regression for Method Comparison

References

Stan Development Team (NA). RStan: the R interface to Stan. R package version 2.32.5. https://mc-stan.org _PATH

`bdpCalcResponse` *Plot the calculated Y response with CI from the full Bayesian posterior distribution*

Description

Plot the calculated Y response with CI from the full Bayesian posterior distribution

Usage

```
bdpCalcResponse(bdpreg, Xval, ci = 0.95, ...)
```

Arguments

bdpreg	bdpreg object
Xval	Reference method data
ci	Probability for the HDI credibility interval. Default 0.95.
...	Arguments passed to hist (e.g. breaks, xlim, ...).

Value

no return

---

bdpExtract *Extract relevant data from the Bayesian Deming regression*

Description

Extract relevant data from the Bayesian Deming regression

Usage

```
bdpExtract(bdpreg)
```

Arguments

bdpreg	bdpreg object created with bdpreg

Value

A data frame with extracted data

---

bdpPairs *Pairs plot of the full posterior predictors*

Description

Pairs plot of the full posterior predictors

Usage

```
bdpPairs(bdpreg, ...)
```

Arguments

bdpreg	bdpreg object created with bdpreg
...	Arguments passed to rstan::pairs.

Value

Pairs plot of the stanfit object

bdpPlot — *Plot Bayesian Deming regression and the confidence intervals from the full posterior distribution*

Description

Plot Bayesian Deming regression and the confidence intervals from the full posterior distribution

Usage

```
bdpPlot(bdpreg, ci = 0.95, ...)
```

Arguments

bdpreg	bdpreg object created with bdpreg
ci	Probability for the HDI credibility interval. Default 0.95
...	Arguments passed to plot (e.g. xlim, xlab, main)

Value

no return

bdpPlotBE — *Plot regression posterior pairs with CI Box and MD ellipses*

Description

Plot regression posterior pairs with CI Box and MD ellipses

Usage

```
bdpPlotBE(bdpreg, cov.method = "MCD", ci = 0.95, ...)
```

Arguments

bdpreg	bdpreg object created with bdpreg
cov.method	rrcov covariance method ("SDe", "MCD", or "Classical"). Default MCD.
ci	Probability for the HDI credibility interval. Default 0.95.
...	Arguments passed to plot (e.g. xlim, xlab, main)

Value

no return

bdpPlotResiduals *Plot studentized residuals from the Bayesian Deming regression*

Description

Plot studentized residuals from the Bayesian Deming regression

Usage

```
bdpPlotResiduals(bdpreg, legend.pos = "bottomleft", legend.horizon = TRUE, ...)
```

Arguments

bdpreg	bdpreg object created with bdpreg
legend.pos	Legend position (e.g. bottomleft, bottomright, topright). Default bottomleft
legend.horizon	Legend horiz boolean parameter. Default TRUE.
...	Arguments passed to plot (e.g. xlim, xlab, main)

Value

no return

bdpPrint *Print summary of sampled data*

Description

Print summary of sampled data

Usage

```
bdpPrint(bdpreg, digits_summary = 4, ...)
```

Arguments

bdpreg	bdpreg object created with bdpreg
digits_summary	number of digits for the results
...	Arguments passed to rstan::print

Value

Print of the stanfit object

bdpreg *Bayesian Deming Pioda Regression for two method comparison with Rstan*

Description

bdpreg is used to compare two measurement methods by means of a Bayesian regression analysis.

Usage

```
bdpreg(
  X,
  Y,
  ErrorRatio = 1,
  df = NULL,
  trunc = TRUE,
  heteroscedastic = c("homo", "linear"),
  slopeMu = 1,
  slopeSigma = 0.3,
  slopeTruncMin = 0.3333,
  slopeTruncMax = 10,
  interceptMu = 0,
  interceptSigma = 30,
  sigmaLambda = 0.3,
  AlphaMu = 1,
  AlphaSigma = 10,
  BetaMu = 0.1,
  BetaSigma = 0.5,
  BetaTruncMin = -1,
  BetaTruncMax = 1,
  ...
)
```

Arguments

X	Numeric vector of input values.
Y	Numeric vector of output values.
ErrorRatio	Deming variance ratio between reference and test method. Default = 1.
df	Degree of freedom. Must be df >= 1 (robust Cauchy regression). Default is $N - 2$, For robust regression set it to $df < N - 2$
trunc	Boolean. Default TRUE. Use truncated slope prior for stability with extreme ErrorRatios. See slopeTruncMin.
heteroscedastic	Bayesian Deming model choice. Alternatives are: "homo" - Homoscedastic model. Default.

	"linear" - Heteroscedastic with linear growth of the variance. Highly experimental model. "exponential" - Heteroscedastic with exponential growth of the variance. Highly experimental model.
slopeMu	Slope normal Mu prior value. Default 1.
slopeSigma	Slope normal Sigma prior value. Default 0.3.
slopeTruncMin	slope normal lower truncation limit. Default 0.3333.
slopeTruncMax	slope normal higher truncation limit. Default 10.
interceptMu	Intercept normal Mu prior value. Default 0.
interceptSigma	Intercept normal Sigma prior value. Default 30.
sigmaLambda	sigma exponential prior lambda. Default 0.3.
AlphaMu	Lin. heterosc. intercept normal mu prior. Must be > 0. Default 1.
AlphaSigma	Lin. heterosc. intercept normal sigma prior. Default 10.
BetaMu	Lin. heterosc. slope normal prior. Default 0.1.
BetaSigma	Lin. heterosc. slope normal prior. Default 0.5.
BetaTruncMin	Lin. heterosc. slope normal prior truncation min. Default -1.
BetaTruncMax	Lin. heterosc. slope normal prior truncation min. Default 1.
...	Arguments passed to rstan::sampling (e.g. iter, chains)

Details

The Bayesian Deming regression can be run in a traditional fashion. In this case the error term is sampled from a T distribution with $N - 2$ degree of freedom (N sample size).

The Bayesian Deming regression can be run as a robust regression specifying a decreased df parameter. It is possible to set $df = 1$ and perform the sampling from an extremely robust Cauchy distribution to suppress leveraged outliers. For moderate robustness a reasonably low value of df in the interval $[6; 10]$ can be an appropriated choice.

ErrorRatio can be set as usual for classical Deming regression. Default is 1. Strong ErrorRatio can lead to instability in the chains that may not converge after the burn in. For this purpose the trunc parameter can be used. In this way the normal distribution for the slope gets truncated at a minimum of 0.3333 (default). The parameter slopeTruncMin can override this value.

With the parameter heteroschedastic it is possible to use an alternative regression which models the heteroscedasticity with a linear growing variance. Alpha and Beta are the intercept and the slope for the variance variation. Alpha must be > 0. Beta is usually zero if no real heteroscedasticity is detected. Alternatively Beta shows low positive values, typically below 0.5 if heteroscedasticity is successfully modeled. The CI of Beta could indeed act as a test for heteroscedasticity. According to these empiric observations, Beta is also truncated to avoid erratic behavior of the Hamiltonian sampler.

The Bayesian Deming regression is recommended in many cases where traditional and non parametric method fail. It is particularly convenient with very small data set and/or with data set with low digit precision. In fact Bayesian Deming regression has no problem with ties.

The method with linear heteroscedastic fitting can be a meaningful answer to heteroscedastic data set. The CI are much narrower and the trade off between robustness and power can find a natural solution. It must be considered as highly experimental but also highly promising method. Users are advised to carefully check the sampled output for undesirable correlation between Alpha and/or Beta vs the slope and/or intercept. A plot with `pairs()` highly recommended.

Stan is usually good enough that init values for the chains must not be specified. In extreme cases it is anyway possible to set init values as a list of list.

Value

An object of class `bdpreg` which contains `out` a `stanfit` object returned by `rstan::sampling` and `standata` as list of input parameters.

References

G. Pioda (2014) https://piodag.github.io/bd1/

Examples

```
library(rstanbdp)
data(glycHem)

# Bayesian Deming Regression, for example with  df=10
fit.1 <-bdpreg(glycHem$Method1,glycHem$Method2,heteroscedastic="homo",
              df=10,chain=1,iter=1000)

# Print results
bdpPrint(fit.1,digits_summary = 4)

# Plot 2D intercepts /slopes pairs with CI and MD distance
bdpPlotBE(fit.1,cov.method="MCD",ci=0.95)

# Plot regression with CI
bdpPlot(fit.1,ci=0.95)

# Calculate response, plot histogram and CI
bdpCalcResponse(fit.1,Xval = 6)

# Extract Xhat, Yhat and Residuals
bdpExtract(fit.1)

# Plot a traceplot of the sampled chains
bdpTraceplot(fit.1)

# Plot standardized residuals
bdpPlotResiduals(fit.1)

# Plot posterior samples pairwise
bdpPairs(fit.1)
```

bdpSummary *Print summary of sampled data*

Description

Print summary of sampled data

Usage

```
bdpSummary(bdpreg, ...)
```

Arguments

bdpreg	bdpreg object created with bdpreg
...	Arguments passed to `rstan::summary`

Value

Summary list of the `stanfit` object

bdpTraceplot *Plot a traceplot of the sampled chains*

Description

Plot a traceplot of the sampled chains

Usage

```
bdpTraceplot(bdpreg, ...)
```

Arguments

bdpreg	bdpreg object created with bdpreg
...	Arguments passed to `rstan::traceplot` (e.g. iter, chains).

Value

Traceplot of the `stanfit` object

bmpMD *Mahalanobis distance for the posterior pairs*

Description

Mahalanobis distance for the posterior pairs

Usage

```
bmpMD(stanRegr, cov.method)
```

Arguments

stanRegr	Rstan rstanbdp object
cov.method	rrcov covariance method ("SDe", "MCD", or "Classical"). Default MCD.

Value

Chi squared probability of the MD

glycHem *Method comparison of glycated hemoglobin measurement*

Description

This data gives the glycated hemoglobin measured in 20 patients.

Usage

```
data(glycHem)
```

Format

A data frame with 20 observations on the following 2 variables.

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