

Package: DHARMa.helpers (via r-universe)

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Title Helper functions to check models not (yet) directly supported by DHARMa

Version 0.0.2

Description Helper functions to check models not (yet) directly supported by the DHARMa package, such as Bayesian models fitted with brms, or exponential random graph models (ERGMs).

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Encoding UTF-8

LazyData true

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URL <https://github.com/Pakillo/DHARMa.helpers>,
<https://pakillo.github.io/DHARMa.helpers/>

BugReports <https://github.com/Pakillo/DHARMa.helpers/issues>

Imports DHARMa, brms

Suggests MCMCglimm

Repository <https://pakillo.r-universe.dev>

RemoteUrl <https://github.com/Pakillo/DHARMa.helpers>

RemoteRef HEAD

RemoteSha 231335da3349c719b27606bc78d4236b09895585

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dh_check_brms

*Check Bayesian models fitted with brms***Description**

Check Bayesian models fitted with brms

Usage

```
dh_check_brms(
  model,
  resp = NULL,
  integer = FALSE,
  plot = TRUE,
  nsamples = 1000,
  ntrys = 5,
  ...
)
```

Arguments

model	A fitted model <code>brms::brmsfit-class()</code> . Categorical and ordinal models not supported by now.
resp	Optional name of response variable (for multivariate models).
integer	Logical (TRUE/FALSE), indicating if response is an integer, as in Poisson and binomial models
plot	Logical. Plot residual checks? Default is TRUE.
nsamples	Integer. Number of samples to draw from the posterior.
ntrys	Integer. Number of tries to use for truncated distributions. See <code>brms::posterior_predict()</code> .
...	Further arguments for <code>DHARMA::plotResiduals()</code>

Value

An object of type DHARMA. See `DHARMA::createDHARMA()` for more details.

See Also

<https://frodriquezsanchez.net/post/using-dharma-to-check-bayesian-models-fitted-with-brms/>

Examples

```
#' # Example models taken from brms::brm()

# Poisson regression for the number of seizures in epileptic patients
fit1 <- brm(count ~ zAge + zBase * Trt + (1|patient),
```

```
      data = epilepsy, family = poisson())
simres <- dh_check_brms(fit1, integer = TRUE)
plot(simres, form = epilepsy$zAge)
testDispersion(simres)

# Probit regression using the binomial family
ntrials <- sample(1:10, 100, TRUE)
success <- rbinom(100, size = ntrials, prob = 0.4)
x <- rnorm(100)
data4 <- data.frame(ntrials, success, x)
fit4 <- brm(success | trials(ntrials) ~ x, data = data4,
            family = binomial("probit"))
summary(fit4)
simres <- dh_check_brms(fit4, integer = TRUE)
plot(simres, form = data4$x)

# Multivariate (multiresponse) model
data("BTdata", package = "MCMCglmm")
bf_tarsus <- bf(tarsus ~ sex + (1|p|fosternest) + (1|q|dam))
bf_back <- bf(back ~ hatchdate + (1|p|fosternest) + (1|q|dam))
fit <- brm(bf_tarsus + bf_back + set_rescor(TRUE),
          data = BTdata, chains = 2, cores = 2)
dh_check_brms(fit, resp = "tarsus")
brms::pp_check(fit, resp = "tarsus")
dh_check_brms(fit, resp = "back")
brms::pp_check(fit, resp = "back")
```

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