

Package ‘AnimalAPD’

March 18, 2021

Title Compare Activity Patterns with Activity Probability Density (APD)

Version 1.0.0

Description Calculation and analyses of Activity Probability Density (APD) for comparing animal activity patterns with automated Bayesian model selection using 'STAN'. See Campbell et al. (in press) "A new approach to comparing animal temporal activity: a more informative, robust, and flexible method that controls for nested data, quantifies relationship asymmetries, and allows linear modelling of temporal behaviour."

Imports brms, circular, overlap, graphics, stats, loo, ggplot2, gridExtra, activityGCMM

Depends R (>= 3.5.0)

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

NeedsCompilation no

Author Liz AD Campbell [aut, cre] (<<https://orcid.org/0000-0002-8302-7430>>)

Maintainer Liz AD Campbell <liz.campbell@zoo.ox.ac.uk>

Repository CRAN

Date/Publication 2021-03-18 09:30:02 UTC

R topics documented:

APDraw	2
APDRE	3
APDREcorr	6
boarexample	8
exampleAPDRE	9
exampleAPDREcorr	9

plotAPDavg	10
plotAPDcorr	10
plotAPDev	12
wolfexample	12

Index	14
--------------	-----------

APDraw	<i>Calculate Raw APD Values</i>
--------	---------------------------------

Description

Calculates raw APD values, uncorrected for hierarchical data structure

Usage

```
APDraw(focal, contingent, adjust = 1)
```

Arguments

focal	Vector of observations in radians of one species/group/individual/etc. for which predictions on another will be made
contingent	Vector of observations in radians of a species/group/individual/etc. from which predictions will be made
adjust	Smoothing of predicted line; recommended to use default value for observed values and higher value for estimations from circular models; default=1

Value

Numeric vector of raw APD values, without correction for nested data structure

Examples

```
data(wolfexample)
data(boarexample)
APDraw(focal=wolfexample$Radians, contingent=boarexample$Radians)
```

Description

Calculation of animal activity probability density controlling for nested data with random intercepts using Bayesian GLMMs with 'STAN' and `brm`. The function can automatically select the statistical distribution that is most appropriate for the dataset (weibull, frechet, gamma, lognormal, inverse gaussian) using `loo` and automatically ensures that MCMC chains converge and that a specified minimum effective sample size from the posterior distribution is achieved. An APD activity curve plot is provided.

Package: AnimalAPD Version: 1.0.0 Date: 2020-11-08

Usage

```
APDRE(  
  focal,  
  contingent,  
  RE1,  
  RE2 = NULL,  
  weibullGLMM = TRUE,  
  frechetGLMM = TRUE,  
  gammaGLMM = TRUE,  
  lognormalGLMM = FALSE,  
  invgaussianGLMM = TRUE,  
  cores = 1,  
  iter = 5000,  
  burnin = iter/2,  
  center = "pi",  
  Reloo = TRUE,  
  adapt_delta = 0.95,  
  adjust = 1,  
  minESS = 1000,  
  col = "deeppink3",  
  histcol = "deeppink",  
  linecol = "black",  
  xlimCV = NULL,  
  min = TRUE,  
  max = TRUE,  
  points = TRUE,  
  mean = TRUE,  
  HDI = TRUE,  
  rawmean = FALSE,  
  ...  
)
```

Arguments

<code>focal</code>	Vector of observations in radians of one species/group/individual/etc. for which predictions on another will be made
<code>contingent</code>	Vector of observations in radians or output from generalized circular mixture model of activity curves from <code>link[activityGCMM]{GCMM}</code> of a species/group/individual/etc. from which predictions will be made
<code>RE1</code>	Vector identifying a random intercept for observations of the focal to control for hierarchical data (e.g. camera trap IDs)
<code>RE2</code>	Optional vector identifying levels of a second random effect, for data with additional hierarchical levels (e.g. study sites, sampling periods, data collection seasons); default is NULL
<code>weibullGLMM</code>	Specifies whether to run a weibull GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
<code>frechetGLMM</code>	Specifies whether to run a frechet GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
<code>gammaGLMM</code>	Specifies whether to run a Gamma GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
<code>lognormalGLMM</code>	Specifies whether to run a lognormal GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
<code>invgaussianGLMM</code>	Specifies whether to run a inverse.gaussian GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
<code>cores</code>	Number of cores to use when running MCMC chains in parallel; default=1
<code>iter</code>	Number of MCMC interactions per chain; default=5000
<code>burnin</code>	Number of MCMC interactions discarded as burnin; default=iter/2
<code>center</code>	Value to use as center of graph; default=pi
<code>Reloo</code>	Whether to use reloo when running leave-one-out cross-validation of models (loo)
<code>adapt_delta</code>	Value to use for adapt_delta with brms; default=0.95
<code>adjust</code>	Smoothing of predicted line; recommended to use default value for observed values and higher value for estimations from circular models
<code>minESS</code>	Desired minimum effective sample size; default=1000
<code>col</code>	Specifies colour of points for the focal in the graph
<code>histcol</code>	Specifies colour of the histogram plot of the posterior distribution
<code>linecol</code>	Specifies colour of HDI line in histogram plot of the posterior distribution
<code>xlimCV</code>	A vector of two values indicating the x axis limits for the histCV graph
<code>min</code>	Whether to include minimum APD on the graph; default=TRUE; default=TRUE
<code>max</code>	Whether to include maximum APD on the graph; default=TRUE; default=TRUE
<code>points</code>	Whether to include datapoints for observations of the focal on the graph; default=TRUE

mean	Whether to include the estimated mean APD from the GLMM on the graph; default=TRUE
HDI	Whether to include the estimated 95% highest density interval of mean APD from the GLMM on the graph; default=TRUE
rawmean	Whether to include the raw mean, not correcting for random effects, on the graph; default=FALSE
...	Additional parameters

Value

Prints graph of activity curve and APD estimates from best-fitting GLMM and prints summary of analysis. Returns object of class APD is returned, containing a list of analysis results and details:

data List of data used in analysis

output Matrix with summary output from selected model

distribution Name of distribution of selected model

model An object of class `brmsfit` containing output from the selected model, including the posterior samples and other information. See [brm](#)

CVposterior Numeric vector of posterior samples for the calculated family-specific population coefficient of variation (CV)

allmodels List of objects of class `brmsfit` containing output from all models from the analysis.

rawvalues Numeric vector of the raw, uncorrected APD values

rawsummary List of summary stats of raw APD values

Author(s)

Liz AD Campbell

See Also

[GCMM brm loo](#)

Examples

```
data(wolfexample)
data(boarexample)
APDRE(focal=wolfexample$Radians, contingent=boarexample$Radians,
      RE1=wolfexample$SamplingPeriod, weibullGLMM=TRUE, frechetGLMM=FALSE,
      gammaGLMM=FALSE, lognormalGLMM=FALSE, invgaussianGLMM=FALSE,
      min=TRUE, max=TRUE, points=TRUE, mean=TRUE, HDI=TRUE, rawmean=FALSE)
```

APDREcorr	<i>APDREcorr Correlations between Activity Patterns using APD GLMMs</i>
-----------	---

Description

Calculates estimated relationships between activity probability density (APD) of the focal and contingent(s) using Bayesian GLMMs with 'STAN' using [brm](#), with the option to automatically select the statistical distribution that best fits the dataset (weibull, frechet, gamma, lognormal, inverse gaussian) by [loo](#). The function automatically ensures that MCMC chains reach convergence and that the specified minimum effective sample size from the posterior distribution is achieved.

Package: AnimalAPD Version: 1.0.0 Date: 2020-11-10

Usage

```
APDREcorr(
  focal,
  cont1,
  cont2 = NULL,
  cont3 = NULL,
  cont4 = NULL,
  RE1,
  RE2 = NULL,
  weibullGLMM = TRUE,
  frechetGLMM = TRUE,
  gammaGLMM = TRUE,
  lognormalGLMM = FALSE,
  invgaussianGLMM = TRUE,
  cores = 1,
  iter = 5000,
  minESS = 1000,
  burnin = iter/2,
  thin = 1,
  adapt_delta = 0.95,
  center = "pi",
  adjust = 1,
  Reloo = TRUE,
  plothist = TRUE,
  ploteffects = TRUE,
  histcol = "cyan4",
  effectcol = "cyan4",
  linecol = "red"
)
```

Arguments

focal	Vector of observations in radians of one species/group/individual/etc. for which predictions on another will be made.
cont1	Vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM , of a species/group/individual/etc. from which predictions will be made
cont2	Optional vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM , of additional species/group/individual/etc. from which predictions will be made
cont3	Optional vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM , of additional species/group/individual/etc. from which predictions will be made
cont4	Optional vector of observations in radians, or output from generalized circular mixture model of activity curves from GCMM , of additional species/group/individual/etc. from which predictions will be made
RE1	Vector identifying a random intercept for observations of the focal to control for hierarchical data (e.g. camera trap IDs)
RE2	Optional vector identifying levels of a second random effect, for data with additional hierarchical levels (e.g. study sites, sampling periods, data collection seasons); default is NULL
weibullGLMM	Specifies whether to run a weibull GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
frechetGLMM	Specifies whether to run a frechet GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
gammaGLMM	Specifies whether to run a Gamma GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
lognormalGLMM	Specifies whether to run a lognormal GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
invgaussianGLMM	Specifies whether to run a inverse.gaussian GLMM, using the brms package; default is TRUE for all and results from the best-fitting model are returned
cores	Number of cores to use when running MCMC chains in parallel; default=1
iter	Number of MCMC interactions per chain; burnin is iter/2; default=5000
minESS	Desired minimum effective sample size; default=1000
burnin	Number of MCMC iterations to be discarded as the burn-in; default=iter/2
thin	Thinning rate for saving MCMC draws; default=1
adapt_delta	Value to use for adapt_delta with brms; default=0.95; see also brms
center	Value to use as center of graph; default=pi
adjust	Smoothing of predicted line; recommended to use default value for observed values and higher value for estimations from circular models
Reloo	Whether to use reloo when running leave-one-out cross-validation of models (loo); see also brms and loo

plothist	Whether to plot histograms of samples from the posterior distribution for the correlation parameters; default=TRUE
ploteffects	Whether to plot predicted effects; default=TRUE
histcol	Colour for histogram bars
effectcol	Colour for predicted effect plot 95% HDI
linecol	Colour for histogram lines for the 95% HDI and 0

Value

Prints results of best-fitting model and posterior samples and/or predicted effects of parameter estimates if `plothist=TRUE` and `ploteffects=TRUE`, and returns object of class `APD` with list of analysis results and information.

`data` List of data used in analysis

`model` Object of class `brmsfit` containing results and information for best-fitting model.

`distribution` Character vector of statistical distribution of best-fitting model

`allmodels` List of output for all tested models; object of class `brmsfit`

Author(s)

Liz AD Campbell

See Also

[GCMM brm loo](#)

Examples

```
data(wolfexample)
data(boarexample)
APDREcorr(focal=wolfexample$Radians,cont1=boarexample$Radians,
          RE1=wolfexample$SamplingPeriod)
```

boarexample

Camera Trap Observations of wild boar

Description

Example dataset with boar observation times in radians and the sampling period during which each observation was recorded

Usage

boarexample

Format

Dataframe with 2 columns and 35 rows Radians Time of observations, in radians from 0 to 2pi
 SamplingPeriod Variable identifying camera trap sampling period

Source

\ Campbell L.A.D. 2017

Examples

```
## Not run: APDRE(focal=wolfexample$Radians, contingent=boarexample$Radians, RE1=wolfexample$SamplingPeriod,
  weibullGLMM=FALSE, frechetGLMM=FALSE, gammaGLMM=FALSE,
  lognormalGLMM=FALSE, invgaussianGLMM=FALSE,
  mean=FALSE, HDI=FALSE, rawmean=TRUE)
## End(Not run)
```

exampleAPDRE

Executable Example of APDRE Function

Description

Example of APDRE function using data included in the package

Usage

```
exampleAPDRE()
```

Value

Provides message with example code for using the APDRE function with data included in the package

exampleAPDREcorr

Executable Example of APDREcorr Function

Description

Example of APDREcorr function using data included in the package

Usage

```
exampleAPDREcorr()
```

Value

Prints message with example code for using the APDRE function using data included in the package

plotAPDavg *Plot APDavg Posterior Samples*

Description

Plot histogram of samples from posterior distribution for estimated APDavg from [APDRE](#) function

Usage

```
plotAPDavg(model, histcol = "deeppink", linecol = "black")
```

Arguments

model	Output from APDRE function, an object of class APD
histcol	Colour for histogram
linecol	Colour for 95% HDI line

Value

Histogram plot of samples from posterior distribution for estimated APDavg

Examples

```
data(wolfexample)
data(boarexample)
WolfBoarAPD<-APDRE(focal=wolfexample$Radians, contingent=boarexample$Radians,
  RE1=wolfexample$SamplingPeriod)
plotAPDavg(WolfBoarAPD)
```

plotAPDcorr *Plot APDcorr Posterior Samples and Predicted Effects*

Description

Plot histogram of posterior distribution samples and/or predicted effects of parameter estimated from [APDREcorr](#) function

Usage

```
plotAPDcorr(
  model,
  hist = TRUE,
  effects = TRUE,
  histcol = c("cyan4", "cyan4", "cyan4", "cyan4"),
  linecol = "red",
  effectcol = c("cyan4", "cyan4", "cyan4", "cyan4"),
  yname = "Focal",
  xname = c("C1", "C2", "C3", "C4")
)
```

Arguments

model	Object of class APD of model output from APDREcorr function
hist	Logical argument for whether to plot histogram of posterior distribution samples; default=TRUE
effects	Logical argument for whether to plot predicted effects; default=TRUE
histcol	Colour for posterior distribution histogram
linecol	Colour for 95% HDI line on posterior distribution histogram
effectcol	Colour for 95% HDI ribbon in line plot of predicted effects
yname	Character vector of name of focal, to be used in the y axis labels
xname	Character vector of name(s) of contingent(s), to be used in the x axis labels

Value

Histogram plot(s) of samples from posterior distribution for estimated relationship between focal and contingent(s), if `plothist=TRUE`

Plot of predicted effects (mean and 95% highest density interval) for relationship between focal APD and contingent(s) APD, if `ploteffects=TRUE`

Examples

```
data(wolfexample)
data(boarexample)
WolfBoarAPDc<-APDREcorr(focal=wolfexample$Radians, cont1=boarexample$Radians,
  RE1=wolfexample$SamplingPeriod)
plotAPDcorr(WolfBoarAPDc, yname="Wolf", xname="Boar")
```

plotAPDcv *Plot APDcv Posterior Samples*

Description

Plot histogram of samples from posterior distribution for estimated APD family-specific population coefficient of variation (CV) from [APDRE](#) function

Usage

```
plotAPDcv(model, histcol = "deeppink", linecol = "black")
```

Arguments

model	Output from APDRE function, an object of class APD
histcol	Colour for histogram
linecol	Colour for 95% HDI line

Value

Histogram plot of samples from posterior distribution for estimated APDavg

Examples

```
data(wolfexample)
data(boarexample)
WolfBoarAPD<-APDRE(focal=wolfexample$Radians, contingent=boarexample$Radians,
  RE1=wolfexample$SamplingPeriod)
plotAPDcv(WolfBoarAPD)
```

wolfexample *Camera Trap Observations of African golden wolves*

Description

Example dataset with wolf observation times in radians and the sampling period during which each observation was recorded

Usage

```
wolfexample
```

Format

Dataframe with 2 columns and 30 rows Radians Time of observations, in radians from 0 to 2pi
SamplingPeriod variable identifying camera trap sampling period

Source

\ Campbell L.A.D. 2017

Index

- * **Bayesian**

 - APDRE, 3

 - APDREcorr, 6

- * **activity;**

 - APDRE, 3

 - APDREcorr, 6

- * **cameratrap;**

 - APDRE, 3

 - APDREcorr, 6

- * **datasets**

 - boarexample, 8

 - wolfexample, 12

- * **temporal;**

 - APDRE, 3

 - APDREcorr, 6

APDraw, 2

APDRE, 3, 10, 12

APDREcorr, 6, 10, 11

boarexample, 8

brm, 3, 5, 6, 8

brms, 7

exampleAPDRE, 9

exampleAPDREcorr, 9

GCMM, 5, 7, 8

loo, 3, 5–8

plotAPDavg, 10

plotAPDcorr, 10

plotAPDcv, 12

wolfexample, 12