Package ‘bayesplay’

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Type Package
Title The Bayes Factor Playground
Version 0.9.3
Description A lightweight modelling syntax for defining likelihoods and priors and for computing Bayes factors for simple one parameter models. It includes functionality for computing and plotting priors, likelihoods, and model predictions. Additional functionality is included for computing and plotting posteriors.
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extract_posterior Extract the posterior

Description
Extract the posterior object from a product object

Usage
extract_posterior(x)

Arguments
x a product object

Value
a posterior object

extract_predictions Extract predictions

Description
Extract the marginal predictions over the prior

Usage
extract_predictions(x)

Arguments
x a product object

Value
a prediction object
integral  

**Compute integral**

**Description**

Computes the definite integral of a product object over the range of the parameter.

**Usage**

`integral(obj)`

**Arguments**

- **obj**  
  a product object

**Value**

A numeric of the marginal likelihood.

**Examples**

```r
# define a likelihood
data_model <- likelihood(family = "normal", mean = 5.5, sd = 32.35)

# define a prior
prior_model <- prior(family = "normal", mean = 5.5, sd = 13.3)

# multiply the likelihood by the prior
model <- data_model * prior_model

# take the integral
integral(model)
```

---

likelihood  

**Specify a likelihood**

**Description**

Define likelihoods using different distribution families.

**Usage**

`likelihood(family, ...)`

**Arguments**

- **family**  
  the likelihood distribution (see details)
- **...**  
  see details
Details

Available distribution families:
The following distribution families can be used for the likelihood
- normal a normal distribution
- student_t a scaled and shifted t-distribution
- noncentral_t a noncentral t (for t statistic)
- noncentral_d a noncentral t (for one sample d)
- noncentral_d2 a noncentral t (for independent samples d)
- binomial a binomial distribution

The parameters that need to be specified will be dependent on the family

normal distribution:
When family is set to normal then the following parameters must be set
- mean mean of the normal likelihood
- sd standard deviation of the normal likelihood

student_t distribution:
When family is set to student_t then the following parameters may be set
- mean mean of the scaled and shifted t likelihood
- sd standard deviation of the scaled and shifted t likelihood
- df degrees of freedom

noncentral_t distribution:
When family is set to noncentral_t then the following parameters may be set
- t the t value of the data
- df degrees of freedom

noncentral_d distribution:
When family is set to noncentral_d then the following parameters may be set
- d the d (mean / sd) value of the data
- n the sample size

noncentral_d2 distribution:
When family is set to noncentral_d2 then the following parameters may be set
- d the d (mean / s_pooled) value of the data
- n1 the sample size of group 1
- n2 the sample size of group 2

\[ s_{\text{pooled}} = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}} \]

binomial distribution:
When the family is set to binomial then the following parameters may be set
- successes the number of successes
- trials the number of trials
names.bayesplay-method

Value

an object of class likelihood

Examples

# specify a normal likelihood
likelihood(family = "normal", mean = 5.5, sd = 32.35)

# specify a scaled and shifted t likelihood
likelihood(family = "student_t", mean = 5.5, sd = 32.35, df = 10)

# specify non-central t likelihood (t scaled)
likelihood(family = "noncentral_t", t = 10, df = 10)

# specify non-central t likelihood (d scaled)
likelihood(family = "noncentral_d", d = 10, n = 10)

# specify non-central t likelihood (independent samples d scaled)
likelihood(family = "noncentral_d2", d = 10, n1 = 10, n2 = 12)

# specify a binomial likelihood
likelihood(family = "binomial", successes = 2, trials = 10)

---

names.bayesplay-method

Get names from data slot

Description

Get names from data slot

Usage

## S4 method for signature 'bayesplay'

names(x)

Arguments

x a bayesplay object

Value

the field names from the data slot
**prior**

**Description**

Plots an object created by bayesplay.

**Usage**

```r
## S3 method for class 'prior'
plot(x, ...)

## S3 method for class 'posterior'
plot(x, add_prior = FALSE, ...)

## S3 method for class 'likelihood'
plot(x, ...)

## S3 method for class 'product'
plot(x, ...)

## S3 method for class 'prediction'
plot(x, model_name = "model", ...)
```

**Arguments**

- `x`: a prediction object
- `...`: arguments passed to methods
- `add_prior`: set to TRUE to add prior to the posterior plot
- `model_name`: name of the model

**Value**

a ggplot2 object

---

**prior**

**Description**

Define priors using different different distribution families.

**Usage**

```r
prior(family, ...)
```
Arguments

family the prior distribution (see details)
...
see details

Details

Available distribution families:
The following distributions families can be used for the prior
• normal a normal distribution
• student_t a scaled and shifted t-distribution
• cauchy a Cauchy distribution
• uniform a uniform distribution
• point a point
• beta a beta distribution The parameters that need to be specified will be dependent on the
  family

Normal distribution:
When family is set to normal then the following parameters may be be set
• mean mean of the normal prior
• sd standard deviation of the normal prior
• range (optional) a vector specifying the parameter range

Student t distribution:
When family is set to student_t then the following parameters may be set
• mean mean of the scaled and shifted t prior
• sd standard deviation of the scaled and shifted t prior
• df degrees of freedom of the scaled and shifted t prior
• range (optional) a vector specifying the parameter range

Cauchy distribution:
When family is set to cauchy then the following parameters may be set
• location the centre of the Cauchy distribution (default: 0)
• scale the scale of the Cauchy distribution
• range (optional) a vector specifying the parameter range

Uniform distribution:
When family is set to uniform then the following parameters must be set
• min the lower bound
• max the upper bound

Point:
When family is set to point then the following parameters may be set
• point the location of the point prior (default: 0)

Beta:
When family is set to beta then the following parameters may be set
• alpha the first shape parameter
• beta the second shape parameter
sd_ratio

Value

an object of class prior

Examples

    # specify a normal prior
    prior(family = "normal", mean = 0, sd = 13.3)

    # specify a half-normal (range 0 to Infinity) prior
    prior(family = "normal", mean = 0, sd = 13.3, range = c(0, Inf))

    # specify a student t prior
    prior(family = "student_t", mean = 0, sd = 13.3, df = 79)

    # specify a truncated t prior
    prior(family = "student_t", mean = 0, sd = 13.3, df = 79, range = c(-40, 40))

    # specify a cauchy prior
    prior(family = "cauchy", location = 0, scale = .707)

    # specify a half cauchy prior
    prior(family = "cauchy", location = 0, scale = 1, range = c(-Inf, 0))

    # specify a uniform prior
    prior(family = "uniform", min = 0, max = 20)

    # specify a point prior
    prior(family = "point", point = 0)

    # specify a beta prior
    prior(family = "beta", alpha = 2.5, beta = 3.8)

sd_ratio

Compute the Savage-Dickey density ratio

Description

Computes the Savage-Dickey density ratio from a posterior object at a specified point

Usage

sd_ratio(x, point)

Arguments

  x a posterior object

  point the point at which to evaluate the Savage-Dickey ratio
Value

A numeric of the Savage-Dickey density ratio

Examples

```r
# define a likelihood
data_model <- likelihood(family = "normal", mean = 5.5, sd = 32.35)

# define a prior
prior_model <- prior(family = "normal", mean = 5.5, sd = 13.3)

model <- extract_posterior(data_model * prior_model)

# compute the Savage-Dickey density ratio at 0
sd_ratio(model, 0)
```

summary.bf-method  

Summarise a Bayes factor

Description

Provide a verbal summary of a Bayes factor and the level of evidence

Usage

```r
## S4 method for signature 'bf'
summary(object)
```

Arguments

- `object`  
a `bf` object

Value

No return, called for side effects

visual_compare  

Visually compare two models

Description

Visually compare two models

Usage

```r
visual_compare(model1, model2, ratio = FALSE)
```
Arguments

model1 a predictive object
model2 a predictive object
ratio show ratio rather than comparison (default: FALSE)

Value

A ggplot2 object

Examples

# define two models
data_model <- likelihood(family = "normal", .5, 1)
h0_mod <- prior(family = "point", point = 0)
h1_mod <- prior(family = "normal", mean = 0, sd = 10)
m0 <- extract_predictions(data_model * h0_mod)
m1 <- extract_predictions(data_model * h1_mod)

# visually compare the model
visual_compare(m0, m1)
# plot the ratio of the two model predictions
visual_compare(m0, m1, ratio = TRUE)
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