

# Package: PEcAn.priors (via r-universe)

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**Type** Package

**Title** PEcAn Functions Used to Estimate Priors from Data

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**Description** Functions to estimate priors from data.

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**LazyLoad** yes

**LazyData** FALSE

**Imports** PEcAn.logger, PEcAn.MA, ggplot2, MASS

**Suggests** PEcAn.visualization, testthat

**Encoding** UTF-8

**RoxygenNote** 7.3.1

**Repository** <https://pecanproject.r-universe.dev>

**RemoteUrl** <https://github.com/PecanProject/pecan>

**RemoteRef** HEAD

**RemoteSha** d5c7bffdf233077968945a182c11240b5d76e42d

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create.density.df	<i>Create Density Data Frame from Sample</i>
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## Description

Returns a data frame from [stats::density](#) function

## Usage

```
create.density.df(
  samps = NULL,
  zero.bounded = FALSE,
  distribution = NULL,
  n = 1000,
  ...
)
```

## Arguments

samps            a vector of samples from a distribution

zero.bounded

distribution    list with elements distn, parama, paramb, e.g. `list('norm', 0, 1)`

## Value

data frame with x and y = dens(x)

## Author(s)

David LeBauer

## Examples

```
prior.df <- create.density.df(distribution = list('norm',0,1))
plot(prior.df)
samp.df <- create.density.df(samps = rnorm(100))
lines(samp.df)
```

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fit.dist	<i>Fit distribution to data</i>
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**Description**

Fit a distribution to data

**Usage**

```
fit.dist(  
  trait.data,  
  trait = colnames(trait.data),  
  dists = c("weibull", "lognormal", "gamma"),  
  n = NULL  
)
```

**Arguments**

trait.data	data for distribution
dists	list of distribution names

**Value**

best fit distribution

**Author(s)**

David LeBauer

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get.quantiles.from.density	<i>Get the quantiles from prior density</i>
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**Description**

Find quantiles on a density data frame

**Usage**

```
get.quantiles.from.density(density.df, quantiles = c(0.025, 0.5, 0.975))
```

**Arguments**

quantiles	default is the median and 95% CI;
priordensity	density dataframe generated by <a href="#">create.density.df</a>

**Author(s)**

David LeBauer

**Examples**

```
prior.df <- create.density.df(distribution = list('norm',0,1))
get.quantiles.from.density(prior.df)
samp.df <- create.density.df(samps = rnorm(100))
get.quantiles.from.density(samp.df)
```

---

get.sample

*Get Samples*

---

**Description**

Take n random samples from prior

**Usage**

```
get.sample(prior, n = NULL, p = NULL)
```

**Arguments**

prior	data.frame with distn, parama, and optionally paramb.
n	number of samples to return from a random sample of the rdistrn family of functions (e.g. rnorm)
p	vector of quantiles from which to sample the distribution; typically pre-generated upstream in the workflow to be used by the qdistrn family of functions (e.g. qnorm)

**Details**

Similar to the prior sample function [pr.samp](#), except 1) it takes the prior as a named dataframe or list and it can return either a random sample of length n OR a sample from a quantile specified as p

**Value**

vector with n random samples from prior

**See Also**

[pr.samp](#)

**Examples**

```
## Not run:  
# return 1st through 99th quantile of standard normal distribution:  
PEcAn.priors::get.sample(  
  prior = data.frame(distn = 'norm', parama = 0, paramb = 1),  
  p = 1:99/100)  
# return 100 random samples from standard normal distribution:  
PEcAn.priors::get.sample(  
  prior = data.frame(distn = 'norm', parama = 0, paramb = 1),  
  n = 100)  
  
## End(Not run)
```

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plot_densities	<i>Plot probability density and data</i>
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**Description**

Plot probability density and data

**Usage**

```
plot_densities(density.plot_inputs, outdir, ...)
```

**Arguments**

density.plot_inputs	list containing trait.samples and trait.df
outdir	directory in which to generate figure as pdf
...	passed on to plot_density

**Value**

outputs plots in outdir/sensitivity.analysis.pdf file

**Author(s)**

David LeBauer

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plot\_posterior.density      *Add posterior density to a plot*

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**Description**

Add posterior density to a plot

**Usage**

```
plot_posterior.density(posterior.density, base.plot = NULL)
```

**Arguments**

posterior.density      data frame containing columns x and y  
base.plot              a ggplot object (grob), created if none provided

**Value**

plot with posterior density line added

**Author(s)**

David LeBauer

---

plot\_prior.density      *Plots a prior density from a parameterized probability distribution*

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**Description**

Plots a prior density from a parameterized probability distribution

**Usage**

```
plot_prior.density(prior.density, base.plot = NULL, prior.color = "black")
```

**Arguments**

prior.density      data frame containing columns x and y  
base.plot              a ggplot object (grob), created if none provided  
prior.color          color of line to be plotted

**Value**

plot with prior density added

**Author(s)**

David LeBauer

**See Also**[pr.dens](#)**Examples**

```
## Not run:  
plot_prior.density(pr.dens('norm', 0, 1))  
  
## End(Not run)
```

---

`plot_trait`*Plot trait density and data*

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**Description**

Plot trait density and data

**Usage**

```
plot_trait(  
  trait,  
  prior = NULL,  
  posterior.sample = NULL,  
  trait.df = NULL,  
  fontsize = list(title = 18, axis = 14),  
  x.lim = NULL,  
  y.lim = NULL,  
  logx = FALSE  
)
```

**Arguments**

<code>trait</code>	dataframe with id, figid and units of the trait to be plotted
<code>prior</code>	named distribution with parameters
<code>posterior.sample</code>	samples from posterior distribution whose density should be plotted
<code>trait.df</code>	data to be plotted, in a format accepted by <a href="#">jagify</a>
<code>fontsize, x.lim, y.lim, logx</code>	passed on to <code>ggplot</code>

**Value**

plot (grob) object

**Author(s)**

David LeBauer

**Examples**

```
## Not run:
prior1 <- data.frame(distn = 'norm',
                     parama = 20,
                     paramb = 5)
data1 <- data.frame(Y = c(19, 21), se = c(1,1))
trait1 <- data.frame(id = 'Vcmax', figid = 'Vcmax', units = 'umol CO2 m-2 s-1')
plot_trait(trait = trait1,
           prior = prior1,
           trait.df = data1)

## End(Not run)
```

pr.dens

*Calculate densities***Description**

Calculates density at n points across the range of a parameter

**Usage**

```
pr.dens(distn, parama, paramb, n = 1000, alpha = 0.001)
```

**Arguments**

distn	distribution
parama	parameter
paramb	parameter
n	length of vector to be returned
alpha	sets range at which the distribution will be evaluated (e.g. from alpha to 1-alpha)

**Details**

For a distribution and parameters, return the density for values ranging from alpha to 1-alpha

**Value**

dataframe with equally spaced x values and the corresponding densities

**Author(s)**

David LeBauer



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pr.samp	<i>Sample from prior</i>
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**Description**

Take n random samples from prior

**Usage**

```
pr.samp(distn, parama, paramb, n)
```

**Arguments**

distn	
parama	
paramb	
n	number of samples to return

**Value**

vector with n random samples from prior

**See Also**

{code}get.sample

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prior.fn	<i>prior.fn</i>
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**Description**

Prior fitting function for optimization

**Usage**

```
prior.fn(parms, x, alpha, distn, central.tendency = NULL, trait = NULL)
```

**Arguments**

parms	target for optimization
x	vector with c(lcl, ucl, ct) lcl / ucl = confidence limits, ct = entral tendency
alpha	quantile at which lcl/ucl are estimated (e.g. for a 95% CI, alpha = 0.5)
distn	named distribution, one of 'lnorm', 'gamma', 'weibull', 'beta'; support for other distributions not currently implemented
central.tendency	one of 'mode', 'median', and 'mean'
trait	name of trait, can be used for exceptions (currently used for trait == 'q')

**Details**

This function is used within [DEoptim](#) to parameterize a distribution to the central tendency and confidence interval of a parameter. This function is not very robust; currently it needs to be tweaked when distributions require starting values (e.g. beta, f)

**Value**

parms

**Author(s)**

David LeBauer

**Examples**

```
## Not run:
  DEoptim(fn = prior.fn,
        lower = c(0, 0),
        upper = c(1000, 1000),
        x=c(2, 6, 3.3),
        alpha = 0.05,
        distn = 'lnorm')$optim$bestmem

## End(Not run)
```

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priorfig

*Prior Figure*

---

**Description**

Plot prior density and data

**Usage**

```
priorfig(
  priordata = NA,
  priordensity = NA,
  trait = NA,
  xlim = "auto",
  fontsize = 18
)
```

**Arguments**

priordata	observations to be plotted as points
priordensity	density of prior distribution, calculated by <a href="#">prior.density</a>
trait	dataframe with id, figid and units of the trait
xlim	limits for x axis

*priorfig*

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**Value**

plot / grob of prior distribution with data used to inform the distribution

**Author(s)**

David LeBauer

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