Package 'failCompare'

January 14, 2022

Title Fitting, Ranking, and Testing Failure Time Models

Version 1.0.0

Description Tools for fitting and comparing the performance of failure-time models from the F distribution family, Vitality family, and others.

License GPL (>= 3)

Encoding UTF-8

URL https://github.com/Columbia-Basin-Research-West/failCompare

BugReports https://github.com/Columbia-Basin-Research-West/failCompare/issues

LazyData true

Roxygen list(markdown = TRUE)

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Depends R (>= 2.10)

Suggests rmarkdown,
knitr,
testthat (>= 3.0.0)

VignetteBuilder knitr

Imports survival,
flexsurv,
vitality

Config/testthat/edition 3

R topics documented:

`chinook` *Lifespans of microacoustic tags used as part of a juvenile salmon survival study conducted during two seasons.*

Description

Lifespans of microacoustic tags used as part of a juvenile salmon survival study conducted during two seasons.

Usage

```
chinook
```

Format

A data frame with 150 rows and 2 variables:

days life span of acoustic tag, in days

season spring or summer study ...

fc_boot *Nonparametric bootstrap of failure time model object*

Description

Nonparametric bootstrap of failure time model object

Usage

```
fc_boot(mod_obj, nrep, type = "pred", times = NULL, tol = 0.9, ...)
```

Arguments

mod_obj	failure time model object of class "fc_obj"
nrep	number of resampling replicates
type	character describing whether bootstrap samples of predicted survivals ("pred") or parameters ("par") should be returned.
times	times at which survival fraction will be estimated, if type="pred".
tol	optional tolerance setting for the estimated proportion of bootstrap data sets that cannot be fit, default = 0.9
...	arguments passed to the optimizer

Details

Random sampling of the failure time data with replacement as a means for propagating uncertainty in predictions of survival probability and estimates of parameter sampling distributions (Tibshirani and Efron 1993).

Value

if `type="pred"` survival fraction or proportion of failed subjects (nrep x times) is returned, and if `type="par"` a matrix of bootstrap parameter estimates dimensions (nrep x number of parameters).

References

Efron, B. and Tibshirani, R. 1993 An Introduction to the Bootstrap. Chapman and Hall, New York.

Townsend R., L., J. R. Skalski, P. Dillingham, T. W. Steig. 2006 Correcting bias in survival estimation resulting from tag failure in acoustic and radiotelemetry studies. Journal of Agricultural Biological and Environmental Statistics.11:183-196.

See Also

fc_fit

Examples

```
data(sockeye)
taglife=sockeye[,"days"]
weib_mod=fc_fit(taglife,model="weibull")
fc_boot(weib_mod,nrep=60,times = 10:20)
```

fc_combine *Combination of multiple failure time model objects into a list of models*

Description

A combination of multiple failure time model objects into a list of models.

Usage

```
fc_combine(mod_ls)
```

Arguments

mod_ls	list of fc_mods

Details

A convenience function for combining model failure time model objecs `fc_obj` into a failure model list object `fc_list`. Lists that include the "Kaplan-Meier" model or duplicates are not allowed. Model lists with different censoring selections are also not allowed.

Value

fc_list object

References

Li, T., and Anderson, J.J. 2009. The vitality model: a way to understand population survival and demographic heterogeneity. Theoretical Population Biology 76(2):118-131.

Li, T., and Anderson, J.J. 2013. Shaping human mortality patterns through intrinsic and extrinsic vitality processes. Demographic Research 28:341-372.

See Also

`fc_select` and `fc_fit`

Examples

```
### Load example dataframe
data(sockeye)
taglife=sockeye[,"days"] #define vector of times

### Fit a 2-parameter Weibull model
weib_mod=fc_fit(time=taglife,model="weibull")

### Fit a 4-parameter Vitality 2013 model
vit_mod=fc_fit(time=taglife,model="vitality.4p")

# Combine two "fc_obj" objects into a model list of class "fc_list"
fc_combine(mod_ls = list(weib_mod,vit_mod))
```

fc_diff *Log-rank test of two data sets*

Description

A log-rank test of two data sets using the "survival" package

Usage

```
fc_diff(data, time, group, censorID = NULL)
```

Arguments

data	dataframe containing all variables
time	numeric failure times
group	character or factor grouping variable
censorID	logical vector the same length as "time" indicating censored observations

Value

Returns the results of a log-rank test for comparing two survival distributions.

fc_fit *Fitting one or a set of failure time models*

Description

Routines for fitting a common failure time model or models

Usage

```
fc_fit(time, model, SEs = TRUE, censorID = NULL, rc.value = NULL, ...)
```

Arguments

time	numeric vector of failure times
model	character string specifiifying the model(s) to be fit
SEs	logical for whether standard errors should be estimated
censorID	binary or logical variable the same length as time indicating censored observations, with zeros or FALSE indicating a cenosored observation
rc.value	rc.value right-censoring cutoff value (i.e.,only observations with times > rc.value are censored due to termination of the experiment or study)
...	additional arguments passed to optimizer

Details

This is a model fitting routine used to fit one or a set of failure time models:

- "weibull" = 2-parameter Weibull
- "weibull3" = 3-parameter Weibull
- "gompertz" = Gompertz Model
- "gamma" = Gamma distribution (2-parameter)
- "lognormal" = Log-Normal distribution
- "llogis" = Log-Logistic distribution
- "gengamma" = Generalized Gamma Distribution (3-parameter; Prentice 1974 parameterization)
- "vitality.ku" = 4-parameter vitality model from Li and Anderson (2009)
- "vitality.4p" = 4-parameter vitality model from Li and Anderson (2013)
- "kaplan-meier" = Kaplan-Meier nonparametric estimate (NOTE: this model cannot be specified in a list with any other model

Details on the parameterization of these distributions can be found in the appendix of the failCompare user manual . If a single model is specified, a "fc_obj" is created, which can be used to adjust a CJS model in the "cbrATLAS" package.

If multiple models are specified, a "fc_list" is created containing output from all models that could be fit with default optimizer settings. A warning will appear if any of the models could not be fit, in which case the user should either remove the model from consideration or specifiy initial parameter values.

Objects of class fc_list may serve as an input in the fc_rank() function, which ranks the performance of the model using the Skalski and Whitlock (2020) GOF measure.

Printing a fc_obJ will display parameter estimates and accompanying standard errors, if available.

Each fc_obJ is a list of the following extractable objects:

- "mod_choice" = model name
- "times" = dataframe of failure time, survival fraction, and censoring binary var
- "fit_vals" = failure times and predicted survival under the model, 95% LCL an UCL if available
- "mod_objs" = actual model object created by "flexsurvdist" or "vitality package"– much more to extract from "flexsurvdist
- "par_tab" = table of parameter estimates and SE in failCompare recognized order
- "KM_DF" = table of product limit (Kaplan-Meier) estimates for plotting (Kaplan and Meier 1954)
- "KM_mod" = survival package K-M model estimates
- 'censored' = binary/logical variable the length of the data describing individual observations that are censored

Value

Returns failure model object of class "fc_obj" if one model specified OR a failure model list object of class "fc_list" if multiple models are specified.

References

Kaplan, E.L., and Meier, P. 1958. Nonparametric estimation from incomplete observations. Journal of the American Statistical Association 53(282):457-481.

Li, T., and Anderson, J.J. 2009. The vitality model: a way to understand population survival and demographic heterogeneity. Theoretical Population Biology 76(2):118-131.

Li, T., and Anderson, J.J. 2013. Shaping human mortality patterns through intrinsic and extrinsic vitality processes. Demographic Research 28:341-372.

Prentice, R. L. 1974. A Log Gamma Model and Its Maximum Likelihood Estimation. Biometrika: 61(3):539-544.

Skalski, J. R., and S. L. Whitlock. 2020. Vitality models found useful in modeling tag-failure times in acoustic-tag survival studies. Animal Biotelemetry 8(1):1-10.DOI:10.1186/s40317-020-00213-z.

`fc_fit_single` *Fitting a single failure time model*

Description

Fitting a single failure time model

Usage

```
fc_fit_single(y, y_sfrac, model, Hess, non_cen, KM_DF, KM_mod)
```

Arguments

`y`	failure time
`y_sfrac`	survival fraction
`model`	failure time model
`Hess`	calculating standard errors
`non_cen`	logical of length(y)
`KM_DF`	K-M model predictions
`KM_mod`	K-M model object

Details

function for fitting an indiviudal failure time model assuming inputs have been vetted by user-facing function fc_fit().

Value

"fc_obj" if successful NULL if otherwise

fc_mod_ls *List of supported models and parameter names.*

Description

List of supported models and parameter names.

Usage

```
fc_mod_ls
```

Format

named list of default failCompare models

fc_plot *Plotting failure time and sample survival function*

Description

Plotting failure time and sample survival function

Usage

```
fc_plot(
  time,
  surv,
  censorID,
  group = NULL,
  hist = T,
  surv_curv = T,
  main,
  ylim,
  xlim,
  ylab,
  xlab,
  ...
)
```

Arguments

time	failure time (x axis)
surv	survival function (y axis)
censorID	binary or logical variable the same length as time indicating censored observations, with zeros or FALSE indicating a cenosored observation
group	grouping variable, limit of 3
hist	logical show histogram of failure times
surv_curv	logical show histogram of failure times

main	title for scatterplot
ylim	y axis limits for survival plot, used to override default of c(0,1)
xlim	x axis limits for survival plot
ylab	y axis limits for survival plot, used to override default of c(0,1)
xlab	x axis limits for survival plot
...	additional argument passed to plot()

Details

plot of type "data" shown by default. For "residual" type plot showing (Kaplan-Meier estimates - parametric model fit), plot a singular model of class=fc_obj.

Value

histogram of failure times and/or scatter plot of sample survival function.

`fc_pred` *Failure time predictions*

Description

generates predictions from failure time model objects.

Usage

```
fc_pred(mod_obj = NULL, times, pars = NULL, model = NULL)
```

Arguments

mod_obj	model object (class = fc_obj)
times	time vector
pars	parameter estimates, if mod_obj absent
model	survival model name, if mod_obj absent

Value

numeric vector failure/survival probability

fc_rank *Ranking failure time models*

Description

This provides a ranking of failure time models.

Usage

```
fc_rank(x)
```

Arguments

x	an object of class "fc_list"

Details

This uses the Skalski and Whitlock (2020) goodness-of-fit measure to rank parametric failure time models. The statistic is based on the squared difference between a given parametric model and the product-limit estimate of the survival estimate described by Kaplan and Meier (1954).

Value

Creates a table of models ranked in ascending order according to a goodness-of-fit measure.

References

Kaplan, E.L., and Meier, P. 1958. Nonparametric estimation from incomplete observations. Journal of the American Statistical Association 53(282):457-481.

Skalski, J. R., and S. L. Whitlock. 2020. Vitality models found useful in modeling tag-failure times in acoustic-tag survival studies. Animal Biotelemetry 8(1):1-10. doi:10.1186/s40317-020-00213-z#'

fc_select *Selecting a failure time model from a list*

Description

select failure time model from predefined list of candidate models produced by the function `fc_fit()`. Kaplan-Meier nonparametric model is selectable from any list.

Usage

```
fc_select(mod_ls, model)
```

Arguments

mod_ls	failure model list object (i.e., class fc_list)
model	model selected from list of those available. Options include:

- "weibull" = 2-parameter Weibull
- "weibull3" = 3-parameter Weibull
- "gompertz" = Gompertz Model
- "gamma" = Gamma distribution (2-parameter)
- "lognormal" = Log-Normal distribution
- "llogis" = Log-Logistic distribution
- "gengamma" = Generalized Gamma Distribution
- "vitality.ku" = 4-parameter vitality model
- "vitality.4p" = 4-parameter vitality model
- "kaplan-meier" = Kaplan-Meier nonparametric estimate (always selectable)

Value

Returns a failure time model object of class fc_obj .

See Also

fc_fit

---

fc_surv *Compute sample survival function*

Description

Computes a sample survival function.

Usage

```
fc_surv(time, censorID = NULL, rc.value = NULL)
```

Arguments

time	failure or censoring time
censorID	binary or logical variable the same length as time indicating censored observations, with zeros or FALSE indicating a cenosored observation
rc.value	time after which all values are censored

Details

Calculates a sample survival function accounting for right censoring. In the absence of censoring, it uses the basic survival function estimator, or otherwise uses the Kaplan-Meier product limit estimate.

Value

a numeric vector of survival fraction estimates sample survival function

fc_test *Simulated Kolmogorov-Smirnov Test*

Description

Simulated Kolmogorov-Smirnov Test

Usage

```
fc_test(times, iters = 50000, model = "gompertz", label = "", plot = FALSE)
```

Arguments

times	numeric vector of failure times
iters	replicates for bootstrap (default to 50k)
model	distribution
label	optional argument for labeling plots
plot	optional argument for creating histogram

Details

performs a a simulation-based Kolmogorov-Smirnov test.

Value

p-value and optionallyhistogram of based on a Monte Carlo estimate of the sampling distribution of the D statistic.

See Also

ks.test. rweibull.

fc_tryfit *Error handling for fitting failCompare models*

Description

Error handling for fitting failCompare models

Usage

```
fc_tryfit(
  y = y,
  y_sfrac = NULL,
  fit_call,
  model = "weibull3",
  non_cen = NULL,
  Hess = NULL
)
```

Arguments

y	numeric time argument of failure times carried through
y_sfrac	survival fraction
fit_call	call to dependent model fitting functions.
model	model argument passed from fc_fit()
non_cen	logical indicating censored variables for use by flexsurv and vitality models
Hess	logical arguement to fc_fit() carried through

Details

Prevents errors from interupting single- and multi-model runs using fc_fit

Value

model fitting output for internal use by fc_fit

---

ks.test_fc *ks.test with suppressed warnings*

Description

ks.test with suppressed warnings

Usage

```
ks.test_fc(...)
```

Arguments

...	inputs to stats::ks.test() function

Value

expected output from ks.test

---

logweib3.lik *3-parameter weibull likelihood*

Description

3-parameter weibull likelihood

Usage

```
logweib3.lik(x, tags.in)
```

Arguments

x	estimated parameters (beta, gamma, eta) or (shape,thrsh,scale)
tags.in	observed time to failure

Value

log likelihood

---

pike *Lifespans of rats in an example described in Lee and Wang 2003.*

Description

Lifespans of rats in an example described in Lee and Wang 2003.

Usage

```
pike
```

Format

A data frame with 35 rows and 2 variables:

days time until death of fish

death 1s indicate observed failures ...

---

plot.fc_list *Plotting fitted values when object of class "fc_list" is called*

Description

Plotting fitted values when object of class "fc_list" is called

Usage

```
## S3 method for class 'fc_list'
plot(x, model = NULL, km = F, res = 100, xlim, ...)
```

Arguments

x	fc_list object (ranked or not). See fc_rank for information on ranking.
model	vector of up 1-3 models contained within the "fc_list" object
km	logical for showing step function of kaplan-meier estimates alongside model
res	fineness of survival function preds (i.e., increments between which the line of the function is drawn).
xlim	numeric vector of length 2 describing x axis limits, used to override default of +/- 5% of min and max
...	additional arguments passed to plot()

Details

Plot type "data" shown by default. For "residual" type plot showing (kaplan-meier estimates - parametric model fit) plot a singual model of class=fc_obj. Consider decreasing res if failure time range <10 and increasing if above 100.

Value

plot and a message

See Also

`plot.fc_obj`

`plot.fc_obj` *generic function that plots fitted values when a object of class "fc_obj" is called*

Description

generic function that plots fitted values when a object of class "fc_obj" is called

Usage

```
## S3 method for class 'fc_obj'
plot(x, km = FALSE, km.ci = FALSE, res = 100, type = "data", ...)
```

Arguments

`x`	of class "fc_obj", created using
`km`	Show kaplan-meier estimates
`km.ci`	Show 95% confidence limits surrounding kaplan-meier estimates
`res`	Number of evenly space points within the range of the data for plotting
`type`	Plotting survival curve of data ("data") versus difference between Kaplan-Meier estimates and predictions from a parametric model ("resid")
`...`	arguements passed to plot `plot`

Value

plot and potentially a message about unplotted models in the set

print.fc_list *Generic function that limits the amount of output displayed when an fc_list is called*

Description

Printed output for class "fc_list"

Usage

```
## S3 method for class 'fc_list'
print(x, ...)
```

Arguments

x	an object of class "fc_list"
...	additional arguments to print()

Value

description of list of models

print.fc_obj *Generic function that limits the amount of output displayed when an fc_obj is called*

Description

Generic function that limits the amount of output displayed when an fc_obj is called

Usage

```
## S3 method for class 'fc_obj'
print(x, ...)
```

Arguments

x	an object of class "fc_obj"
...	additional arguments to print()

pvit09 *Cumulative distribution function of Vitality 2009 model*

Description

Cumulative distribution function of Vitality 2009 model

Usage

```
pvit09(x, par1, par2, par3, par4)
```

Arguments

x	time
par1	r
par2	s
par3	k
par4	u

Value

cumulative probability

pvit13 *Cumulative distribution function of Vitality 2013 model*

Description

Cumulative distribution function of Vitality 2013 model

Usage

```
pvit13(x, par1, par2, par3, par4)
```

Arguments

x	time
par1	r
par2	s
par3	lambda
par4	beta

Value

cumulative probability

rvitality *Generating samples from 2009 and 2013 Vitality models*

Description

Generating samples from 2009 and 2013 Vitality models

Usage

```
rvitality(
  parms,
  times_dat,
  t_seq_fineness = 0.005,
  quant_seq = seq(0, 1, 0.005),
  model = "Vitality09"
)
```

Arguments

parms	vector of parameters, Vitality 2009 (r,s,k,u), Vitality 2013 (r,s,lambda,beta)
times_dat	survival times used for determining # samples to generate and range of slices
t_seq_fineness	time increments to with which to slice up the survival curve
quant_seq	bins in which to place simulated times
model	either "Vitality09" ot "Vitality13"

Value

random values

rweibull3 *random number generation for 3-parameter weibull*

Description

random number generation for 3-parameter weibull

Usage

```
rweibull3(n, shape, scale = 1, thres = 0)
```

Arguments

n	sample size
shape	beta
scale	lambda
thres	gamma

Value

vector of random values from the 3-parameter weibull model

`sockeye` *Lifespans of microacoustic tags used as part of a juvenile salmon survival study conducted during two seasons.*

Description

Lifespans of microacoustic tags used as part of a juvenile salmon survival study conducted during two seasons.

Usage

```
sockeye
```

Format

A data frame with 50 rows and 1 variable:

days life span of acoustic tag, in days ...

`steelhead` *Lifespans of microacoustic tags used as part of a juvenile steelhead survival study with premature tag failures that require censoring at 79 days.*

Description

Lifespans of microacoustic tags used as part of a juvenile steelhead survival study with premature tag failures that require censoring at 79 days.

Usage

```
steelhead
```

Format

A data frame with 82 rows and 1 variables:

Day life span of acoustic tag, in days

...

summary.fc_list *Generic function for summarizing an object of class "fc_list"*

Description

Generic function for summarizing an object of class "fc_list"

Usage

```
## S3 method for class 'fc_list'
summary(object, ...)
```

Arguments

object	object of class fc_list
...	additional arguments to summary

Value

Summary of model fitting calls and GOF rankings (if available)

summary.fc_obj *Generic function for summarizing an object of class "fc_obj"*

Description

Generic function for summarizing an object of class "fc_obj"

Usage

```
## S3 method for class 'fc_obj'
summary(object, ...)
```

Arguments

object	object of class fc_obj
...	additional arguments to summary

Value

Summary of fc_obj model of calls to model fitting functions.

`taglife.fn_weib3` *Fitting 3-parameter Weibull model to failure time data (adapted from R. Townsend's code)*

Description

Fitting 3-parameter Weibull model to failure time data (adapted from R. Townsend's code)

Usage

```
taglife.fn_weib3(tags.in, model.in = "weibull", tag.se = T)
```

Arguments

`tags.in`	vector of observed time to failure (days)
`model.in`	name of model to use. Current option is "Weibull" for 3-parameter Weibull
`tag.se`	logical for whether to compute SEs

Value

Returns a list with model objects (mod_obj), fitted values (fit_vals) and table of parameter estimates (par_tab).

`trout` *Lifespans of rainbow trout exposed to gas supersaturation. Based on example given in Salinger et al. 2003.*

Description

Lifespans of rainbow trout exposed to gas supersaturation. Based on example given in Salinger et al. 2003.

Usage

```
trout
```

Format

A data frame with 35 rows and 2 variables:

days time until death of fish

censored Observation was censored ...

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