

Package ‘lpl’

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Type Package

Title Local Partial Likelihood Estimation and Simultaneous Confidence Band

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Depends R (>= 3.5.0), MASS, parallel, survival

Description Local partial likelihood estimation by Fan, Lin and Zhou(2006)<[doi:10.1214/009053605000000796](https://doi.org/10.1214/009053605000000796)> and simultaneous confidence band is a set of tools to test the covariates-biomarker interaction for survival data. Test for the covariates-biomarker interaction using the bootstrap method and the asymptotic method with simultaneous confidence band (Liu, Jiang and Chen (2015)<[doi:10.1002/sim.6563](https://doi.org/10.1002/sim.6563)>).

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Description

This package fits a multivariable local partial likelihood model for covariate-biomarker interaction with survival data.

Details

"lpl" is a R package for multivariate covariate-biomarker interaction using local partial likelihood method.

Please use the following steps to install 'lpl' package:

1. First, you need to install the 'devtools' package. You can skip this step if you have 'devtools' installed in your R. Invoke R and then type

```
install.packages("devtools")
```

2. Load the devtools package.

```
library(devtools)
```

3. Install "lpl" package with R command

```
install_github("statapps/lpl")
```

"lpl" uses local partial likelihood to estimate covariate-biomarker interactions and bootstrap method to test the significance of the interactions.

Author(s)

Siwei Zhang and Bingshu E. Chen

Maintainer: Bingshu E. Chen <bingshu.chen@queensu.ca>

References

1. Fan, J., Lin, H., Zhou, Y. (2006). Local partial-likelihood estimation for lifetime data. *The Annals of Statistics*. 34, 290-325.
2. Liu, Y., Jiang, W. and Chen, B. E. (2015). Testing for treatment-biomarker interaction based on local partial-likelihood. *Statistics in Medicine*. 34, 3516-3530.
3. Zhang, S., Jiang, W. and Chen, B. E. (2016). Estimate and test of multivariate covariates and biomarker interactions for survival data based on local partial likelihood. Manuscript in preparation.

See Also

coxph, survival

Examples

```
# fit = lpl(y~trt+age+biomarker)
```

`control`*Auxiliary function for lpl fitting*

Description

Auxiliary function for `lple` fitting. Typically only used internally by `'lpl'`, but may be used to construct a control argument to either function.

Usage

```
# lpl.control(h, kernel = 'gaussian', B, w0, p1, pctl)
```

Arguments

<code>h</code>	bandwidth of kernel function. The default value is <code>h = 0.2</code>
<code>kernel</code>	kernel function types, including "gaussian", "epanechnikov", "rectangular", "triangular", "biweight", "cosine", "optcosine". The default value is 'gaussian'
<code>B</code>	number of bootstrap times. The default value is 200
<code>w0</code>	the estimated points in the interval of (0,1), select arbitrarily. The default value is <code>seq(0.05, 0.95, 0.025)</code>
<code>p1</code>	the number of dependend variables that make interactions with the biomarker <code>w</code> . The default value is 1
<code>pctl</code>	the estimated points that want to be shown in the output. The default value is <code>seq(0.2, 0.8, 0.1)</code>

Details

Control is used in model fitting of `lpl`.

Value

This function checks the internal consistency and returns a list of value as inputed to control model fit of `lpl`.

Author(s)

Siwei Zhang and Bingshu E. Chen

See Also

[lplb](#), [lple](#)

Examples

```
## The default control values are: h = 0.2, kernel = 'gaussian', B = 200,
## w0 = seq(0.05, 0.95, 0.025), p1 = 1, pct1 = seq(0.2, 0.8, 0.1)
##
## To fit the lpl model with some control variables changed,

w0=seq(0.05, 0.95, by=0.05)
ctl = lpl.control(w0=w0, h=0.3, p1=2, B=100)

## then fit the lple model
```

lplb	<i>Local partial likelihood bootstrap (LPLB) method to fit biomarker Models</i>
------	---

Description

{lplb} is a R package for local partial likelihood estimation (LPLE) (Fan et al., 2006) of the coefficients of covariates with interactions of the biomarker W , and hypothesis test of whether the relationships between covariates and W are significant, by using bootstrap method.

Usage

```
## Default S3 method:
lplb(x, y, control, ...)
## S3 method for class 'formula'
lplb(formula, data=list(...), control = list(...), ...)

# use
#       lplb(y ~ X1+X2+...+Xp+w, data=data, control)
#
# to fit a model with interactions between biomarker (w) with the first p1
# terms of dependent variables.
# p1 is included in 'control'. p1<p. See 'lplb.control' for details
#
# use
#       lplb(x, y, control)
#
# to fit a model without the formula
#
# Biomarker w should be the 'LAST' dependend variable
```

Arguments

formula	an object of class "formula"(or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
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data	an optional data frame, list or environment (or object coercible by 'as.data.frame' to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
x, y	For 'lplb.default', x is a design matrix of dimension $n * (p+1)$ and y is a vector of observations of length n for a "Surv" object for "coxph".
control	a list of parameters for controlling the fitting process. See 'lplb.control' for details
...	additional arguments to be passed to the low level regression fitting functions (see below).

Details

Here 'w' is a Biomarker variable. This variable is required and shall be the last dependent variable in the formula.

'x.cdf' is a function that maps biomarker values to interval (0, 1) using its empirical cumulative distribution function.

Value

lplb returns an object of class inheriting from "lplb" which inherits from the class 'coxph'. See later in this section.

The function "print" (i.e., "print.lplb") can be used to obtain or print a summary of the results.

An object of class "lplb" is a list containing at least the following components:

beta_w	a matrix of $m * p1$, the estimated coefficients at each of the m estimated points, for the first p1 dependent variables with interactions of the biomarker w
Q1	the test statistic of the data
mTstar	a vector of the test statistics from B times' bootstrap
pvalue	the p-value of the hypothesis that beta_w is a constant

Note

This package was build on code developed by Yicong Liu for simple treatment-biomaker interaction model.

Author(s)

Siwei Zhang and Bingshu E. Chen (bingshu.chen@queensu.ca)

References

Zhang, S., Jiang, W. and Chen, B. E. (2016). Estimate and test of multivariate covariates and biomarker interactions for survival data based on local partial likelihood. Manuscript in preparation.

See Also

[coxph](#), [lpl.control](#) [print.lple](#) [plot.lple](#)

Examples

```
dat = lp1DemoData(50)
fit = lplb(Surv(time, status)~z1 + z2 + w, data = dat, B = 3, p1 = 2)
print(fit)
```

lple	<i>Local partial likelihood estimate (LPLE) method to fit biomarker Models</i>
------	--

Description

{lple} is a R package for local partial likelihood estimation (LPLE) (Fan et al., 2006) of the coefficients of covariates with interactions of the biomarker W , and hypothesis test of whether the relationships between covariates and W are significant, by using bootstrap method.

Usage

```
## Default S3 method:
lple(x, y, control, ...)
## S3 method for class 'formula'
lple(formula, data=list(...), control = list(...), ...)

# use
#       lple(y ~ X1+X2+...+Xp+w, data=data, control)
#
# to fit a model with interactions between biomarker (w) with the first p1
# terms of dependent variables.
# p1 is included in 'control'. p1<p. See 'lplb.control' for details
#
# use
#       lple(x, y, control)
#
# to fit a model without the formula
#
# Biomarker w should be the 'LAST' dependend variable
```

Arguments

formula	an object of class "formula"(or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
data	an optional data frame, list or environment (or object coercible by 'as.data.frame' to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
x, y	For 'lple.default', x is a design matrix of dimension $n * (p+1)$ and y is a vector of observations of length n for a "Surv" object for "coxph".

control	a list of parameters for controlling the fitting process. See 'lplb.control' for details
...	additional arguments to be passed to the low level regression fitting functions (see below).

Details

Here 'w' is a Biomarker variable. This variable is required and shall be the last dependent variable in the formula.

'x.cdf' is a function that maps biomarker values to interval (0, 1) using its empirical cumulative distribution function.

Value

lple returns an object of class inheriting from "lple" which inherits from the class 'coxph'. See later in this section.

The function "print" (i.e., "print.lple") can be used to obtain or print a summary of the results.

An object of class "lple" is a list containing at least the following components:

beta_w	a matrix of $m * p1$, the estimated coefficients at each of the m estimated points, for the first $p1$ dependent variables with interactions of the biomarker w
Q1	the test statistic of the data
mTstar	a vector of the test statistics from B times' bootstrap
pvalue	the p-value of the hypothesis that β_w is a constant

Note

This package was build on code developed by Yicong Liu for simple treatment-biomaker interaction model.

Author(s)

Siwei Zhang and Bingshu E. Chen (bingshu.chen@queensu.ca)

References

Zhang, S., Jiang, W. and Chen, B. E. (2016). Estimate and test of multivariate covariates and biomarker interactions for survival data based on local partial likelihood. Manuscript in preparation.

See Also

[coxph](#), [lpl.control](#) [print.lple](#) [plot.lple](#)

Examples

```
dat = lplDemoData(50)
fit = lple(Surv(time, status)~z1 + w, data = dat, p1 = 1)
print(fit)
predict(fit)
survfit(fit, se.fit = FALSE)
```

plot.lple

The Plot Function of lple

Description

Draw a series of plots of `beta_w` vs. `w_est` for each dependent variable with interactions with the biomarker `w`. See also: [lple](#), [lpl.control](#)

Usage

```
## S3 method for class 'lple'
plot(x, ..., scale = c('original', 'transformed'))
```

Arguments

<code>x</code>	a <code>lple</code> class returned from <code>lple</code> fit.
<code>scale</code>	choose the scale of biomarker variable, 'original' or 'o' for the original biomarker scale. 'transformed' or 't' for transformed scale that maps biomarker to interval (0, 1). The default is to plot in the original scale.
<code>...</code>	other options used in <code>plot()</code> .

Details

`plot.lple` is called to plot the relationships between `beta_w` and `w_est` for each dependent variable with interactions with the biomarker `w`, from the [lple](#) fit model.

The number of interaction terms can be set in [lpl.control](#).

The default method, `print.default` has its own help page. Use `methods("print")` to get all the methods for the `print` generic.

Value

No return value, called for plot model fit

Author(s)

Bingshu E. Chen and Siwei Zhang

See Also

[lplb](#), [lple](#), [lpl.control](#), [print.lple](#)

Examples

```
dat = lplDemoData(50)
fit = lple(Surv(time, status)~z1 + w, data = dat, p1 = 1)
plot(fit)
```

predict.lple	<i>predict a lple object</i>
--------------	------------------------------

Description

Compute fitted values and prediction error for a model fitted by lple

Usage

```
## S3 method for class 'lple'
## S3 method for class 'lple'
predict(object, newdata, newy=NULL, ...)
## S3 method for class 'lple'
residuals(object, type=c("martingale", "deviance"), ...)
```

Arguments

object	a model object from the lple fit
newdata	optional new data at which to do predictions. If absent, predictions are for the dataframe used in the original fit
newy	optional new response data. Default is NULL
type	type of residuals, the default is a martingale residual
...	additional arguments affecting the predictions produced

Details

predict.lple is called to predict object from the lple model [lple](#).

The default method, predict has its own help page. Use methods("predict") to get all the methods for the predict generic.

Value

predict.lple returns a list of predicted values, prediction error and residuals.

lp	linear predictor of $\beta(w)*Z$, where $\beta(w)$ is the fitted regression coefficient and Z is covariance matrix.
risk	risk score, $\exp(lp)$. When new y is provided, both lp and risk will be ordered by survival time of the new y.

residuals	martingale residuals of the prediction, if available.
pe.mres	prediction error based on martingale residual, if both new data and new y is provided.
cumhaz	cumulative hazard function.
time	time for cumulative hazard function. Time from new y will be used is provided

Author(s)

Bingshu E. Chen

See Also

The default method for predict [predict](#),

For the Cox model prediction: [predict.coxph](#). [#survfit.lple](#)

<code>print.lplb</code>	<i>print a lplb object</i>
-------------------------	----------------------------

Description

`print` are used to provide a short summary of `lplb` outputs.

Usage

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

Arguments

<code>x</code>	a <code>lplb</code> class returned from <code>lplb</code> fit
<code>...</code>	other options used in <code>print()</code>

Details

`print.lplb` is called to print object or summary of object from the `lplb` model [lplb](#).

The default method, `print.default` has its own help page. Use `methods("print")` to get all the methods for the `print` generic.

Value

No return value, called for printing model fit

Author(s)

Siwei Zhand and Bingshu E. Chen

See Also

The default method for print [print.default](#), [lplb](#)

Examples

```
#
# See examples in lplb and lple
#
```

```
print.lple          print a lple object
```

Description

print are used to provide a short summary of lple outputs.

Usage

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

Arguments

```
x                the results of a lple fit
...              other options used in print()
```

Details

print.lple is called to print object or summary of object from the lple model [lple](#).

The default method, print.default has its own help page. Use methods("print") to get all the methods for the print generic.

Value

No return value, called for printing model fit

Author(s)

Siwei Zhand and Bingshu E. Chen

See Also

The default method for print [print.default](#), [lple](#)

Examples

```
#
# see example in lple
#
```

survfit.lple	<i>Compute a Survival Curve from a Local Linear Partial Likelihood Estimate.</i>
--------------	--

Description

Computes the predicted survival function for a model fitted by (lple).

Usage

```
## S3 method for class 'lple'
## S3 method for class 'lple'
survfit(formula, se.fit=TRUE, conf.int=.95, ...)
```

Arguments

formula	a fitted model from (lple) fit
se.fit	a logical value indicating whether standard errors shall be computed. Default is TRUE
conf.int	The level for a two-sided confidence interval on the survival curve. Default is 0.95
...	other arguments to the specific method

Details

survfit.lple is called to compute baseline survival function from the lple model [lple](#).

The default method, survfit has its own help page. Use methods("survfit") to get all the methods for the survfit generic.

Value

survfit.lple returns a list of predicted baseline survival function, cumulative hazard function and residuals.

surv	Predicted baseline survival function when $\beta(w) = 0$.
cumhaz	Baseline cumulative hazard function, $-\log(\text{surv})$.
hazard	Baseline hazard function.
varhaz	Variance of the baseline hazard.
residuals	Martingale residuals of the (lple) model.
std.err	Standard error for the cumulative hazard function, if se.fit = TRUE.

See [survfit](#) for more detail about other output values such as upper, lower, conf.type. Confidence interval is based on log-transformation of survival function.

Author(s)

Bingshu E. Chen

See Also

The default method for survfit [survfit](#), [#survfit.lple](#)

Examples

```
#  
# See example in lple  
#
```

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