# Package 'logconPH'

December 13, 2014

**Type** Package

**Title** CoxPH Model with Log Concave Baseline Distribution

**Version** 1.4

**Date** 2014-10-27

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**Description** Computes a cox PH model with a log concave baseline distribution. If no covariates are provided, estimates the log concave NPMLE. Built specifically for interval censored data, where data is a n by 2 matrix with [i, 1] as the left side of the interval for subject i and [i,2] as right side. Uncensored data can be entered by setting [i,1] = [i,2]. Alternatively, this can also handle uncensored data. If all the data is uncensored, you may enter data as a length(n) vector.

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## R topics documented:

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logconPH-package            *Computing a Cox PH Model with a Log Concave Baseline*

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### Description

Fits the log concave NPMLE with logconcave(), either as univaraite data or as a Cox-PH model with the a logconcave baseline distribution. Estimated densities, probabilities and quantiles can be found for a given fit via dLC, pLC and qLC.

**Details**

| Package: | logconPH |
|----------|----------|
| Type: | Package |
| Version: | 1.0 |
| Date: | 2014-10-16 |
| License: | NA |

Computes the univariate log concave estimator. Built specifically for interval censored data. The times should follow standard interval censored notation, i.e. an n by 2 matrix where [i, 1] is the left side of the interval for subject i and [i,2] is right side. Left censoring is handled by setting the left side to 0, right censoring is handled by setting the right side to inf. Uncensored observations are handled by setting the left side equal to the right side. Alternatively, this package can also handle purely uncensored data. If all the data is uncensored, you may enter data as a length(n) vector (as apposed to using the current status form of the data, cbind(uncensored_data, uncensrored_data) ). Entering uncensored data in this format leads to significantly faster computation.

In the case of uncensored data, the motivation for the logconcave shape constraint is to obtain valid density estimates without specificying either a parametric family or a smoothing parameter. For interval censored data, while the density estimates should be consistent, they are fairly unstable. However, survival estimates empirically show a better rate of convergence than the unconstrained NPMLE without having to select a parametric family, making for a much more efficient estimator than the NPMLE, while being more flexible than a parametric esitmator.

**Author(s)**

Clifford Anderson-Bergman

Maintainer: Clifford Anderson-Bergman <cianders@uci.edu>

**References**

Semi- and Non-parametric Methods for Interval Censored Data with Shape Constraints (Anderson-Bergman 2014)

**Examples**

```
fit = logconcave(rnorm(500) )
# Fits a log concave estimator to an uncensored sample

qLC(0.5, fit)
# Estimates the median

simData <- sim_Censored(n = 400)
# Simulates current status data

fit = logconcave(simData)
# Fits a log concave estimator to an interval censored sample

pLC(0.5, fit)
# Estimates the cdf at t = 0.5

plotLC(fit,  surv)
# Plots the estimated survival function.
# Options for second argument are pdf, cdf and surv

simData <- simPH_Censored()
```

```
# Simulates current status data from a Cox-PH model

fit <- logconcave(times = simData$times, covariates = simData$x)
# Fits a Cox-PH model with a logconcave baseline distribution

plotLC(fit, covars = c(0,0) )
# Plots the estimated baseline survival function

linesLC(fit, covars = c(1,1), col = red)
# Plots the estimated survival function with x1 = 1, x2 = 1
```

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dLC                              *Density estimates from a log concave fit*

---

### Description

Returns the the estimated density from a log concave fit

### Usage

```
dLC(x, fit, covars)
```

### Arguments

| | |
|---|---|
| x | A vector of numeric values for which the estimated density will be calculated |
| fit | Log concave fit (from the logconcave() function) |
| covars | A matrix of covariate values. Number of columns must match number in original fit |

### Author(s)

Clifford Anderson-Bergman

### Examples

```
fit = logconcave(rnorm(500) )
# Fits a log concave estimator to an uncensored sample

dLC(0, fit)
# Estimates the density at the true mode

simData <- simPH_Censored()
# Simulates current status data from a CoxPH model

fit <- logconcave(simData$times, simData$x)
# Fits coxPH model

dLC(1, fit, covars = c(0,0))
# Estimates the baseline density at t = 1
```

---

linesLC                    *Draws Lines for Logconcave Fit*

---

**Description**

Plots the fit of a log concave object

**Usage**

```
linesLC(fit, funtype = surv, covars = NA, ...)
```

**Arguments**

| | |
|---|---|
| fit | A fit object returned from a call to logconcave |
| funtype | Type of function plotted. Choices are 'surv', 'pdf' or 'cdf'. If missing, 'surv' in default |
| covars | CoxPH covariates |
| ... | Additional arguments to be passed to lines |

**Author(s)**

Clifford Anderson-Bergman

**Examples**

```
fit = logconcave(rnorm(500) )
# Fits a log concave estimator to an uncensored sample

plotLC(fit)
# Plots the estimated survival distribution

simData <- simPH_Censored()
# Simulates current status data from a CoxPH model

fit <- logconcave(simData$times, simData$x)
# Fits coxPH model

plotLC(fit, covars = c(0,0), funtype = cdf)
# Plots the estimated baseline cdf

linesLC(fit, covars = c(1,1), funtype = cdf, col = red)
# Plots the estimates cdf with covariates c(1,1)
```

---

logconcave                    *Cox PH model with Log Concave Baseline*

---

**Description**

Fits a semi-parametric Cox PH model with a log-concave baseline distribution for interval censored or uncensored data. If no covariates are supplied, logconcave() will fit the log concave NPMLE.

For interval censoring, the data should follow standard interval censored notation, i.e. times are entered as an n by 2 matrix where [i, 1] is the left side of the interval for subject i and [i,2] is right side. Left censoring is handled by setting the left side to 0, right censoring is handled by setting the right side to inf. Uncensored observations are handled by setting the left side equal to the right side. Alternatively, this package can also handle purely uncensored data. If all the data is uncensored, you may enter data as a length(n) vector (as apposed to using the current status form of the data, cbind(uncensored_data, uncensrored_data) ). Entering uncensored data in this format leads to significantly faster computation.

In the case of uncensored data, the motivation for the logconcave shape constraint is to obtain valid density estimates without specificying either a parametric family or a smoothing parameter. For interval censored data, while the density estimates should be consistent, they are fairly unstable. However, survival estimates empirically show a better rate of convergence than the unconstrained NPMLE without having to select a parametric family, making for a much more efficient estimator than the NPMLE, while being more flexible than a parametric esitmator.

**Usage**

```
logconcave(times, covariates, aug = TRUE)
```

**Arguments**

| | |
|---|---|
| times | Time of event for survival data. If all times are uncensored, can be entered a vector. If times are censored, should be a nx2 matrix of interval censored data |
| covariates | Optional covariates argument to be fit a Cox-PH model with a logconcave baseline |
| aug | Should the baseline logconcave density be augmented? If aug = FALSE, algorithm may fail in certain situations |

**Details**

Uses a sequential quadratic programming algorithm, paired with a univariate optimization step. For more details, see Semi- and Non- Parametric Methods for Interval Censored Data with Shape Constraints (Anderson-Bergman 2014)

**Author(s)**

Clifford Anderson-Bergman <cianders@uci.edu>

## Examples

```
fit = logconcave(rnorm(500) )
# Fits a log concave estimator to an uncensored sample

qLC(0.5, fit)
# Estimates the median

simData <- sim_Censored(n = 400)
# Simulates current status data

fit = logconcave(simData)
# Fits a log concave estimator to an interval censored sample

pLC(0.5, fit)
# Estimates the cdf at t = 0.5

plotLC(fit,  surv)
# Plots the estimated survival function.
# Options for second argument are pdf, cdf and surv

simData <- simPH_Censored()
# Simulates current status data from a Cox-PH model

fit <- logconcave(times = simData$times, covariates = simData$x)
# Fits a Cox-PH model with a logconcave baseline distribution

plotLC(fit, covars = c(0,0) )
# Plots the estimated baseline survival function

linesLC(fit, covars = c(1,1), col = red)
# Plots the estimated survival function with x1 = 1, x2 = 1
```

---

pLC                     *Probability estimates from a log concave fit*

---

## Description

Returns the the estimated probability from a log concave fit

## Usage

```
pLC(x, fit, covars)
```

## Arguments

| | |
|---|---|
| x | A vector of numeric values for which the estimated probabilities will be calculated |
| fit | Log concave fit (from the logconcave() function) |
| covars | A matrix of covariate values. Number of columns must match number in original fit |

## Author(s)

Clifford Anderson-Bergman

## Examples

```
fit = logconcave(rnorm(500) )
# Fits a log concave estimator to an uncensored sample

pLC(0, fit)
# Estimates the cdf at the true mode

simData <- simPH_Censored()
# Simulates current status data from a CoxPH model

fit <- logconcave(simData$times, simData$x)
# Fits coxPH model

pLC(1, fit, covars = c(0,0))
# Estimates the baseline probability at t = 1
```

---

plotLC                        *Plots Logconcave Fit*

---

## Description

Plots the fit of a log concave object

## Usage

```
plotLC(fit, funtype = surv, covars = NA, ...)
```

## Arguments

| | |
|---|---|
| fit | A fit object returned from a call to logconcave |
| funtype | Type of function plotted. Choices are 'surv', 'pdf' or 'cdf'. If missing, 'surv' in default |
| covars | CoxPH covariates |
| ... | Additional arguments to be passed to plot |

## Author(s)

Clifford Anderson-Bergman

## Examples

```
fit = logconcave(rnorm(500) )
# Fits a log concave estimator to an uncensored sample

plotLC(fit)
# Plots the estimated survival distribution

simData <- simPH_Censored()
```

```
# Simulates current status data from a CoxPH model

fit <- logconcave(simData$times, simData$x)
# Fits coxPH model

plotLC(fit, covars = c(0,0), funtype = cdf)
# Plots the estimated baseline cdf

linesLC(fit, covars = c(1,1), funtype = cdf, col = red)
# Plots the estimates cdf with covariates c(1,1)
```

---

qLC                          *Quantiles estimates from a log concave fit*

---

### Description

Returns the the estimated probability from a log concave fit

### Usage

```
qLC(p, fit, covars)
```

### Arguments

| | |
|---|---|
| p | A vector of numeric values for which the estimated quantiles will be calculated |
| fit | Log concave fit (from the logconcave() function) |
| covars | A matrix of covariate values. Number of columns must match number in original fit |

### Author(s)

Clifford Anderson-Bergman

### Examples

```
fit = logconcave(rnorm(500) )
# Fits a log concave estimator to an uncensored sample

qLC(0.5, fit)
# Estimates the median

simData <- simPH_Censored()
# Simulates current status data from a CoxPH model

fit <- logconcave(simData$times, simData$x)
# Fits coxPH model

qLC(0.5, fit, covars = c(0,0))
# Estimates the baseline median
```

---

simPH_Censored            *Simulate current status data from Cox-PH model*

---

### Description

Simulates current status data from a Cox-PH model with a gamma baseline distribution. Used for demonstration of use of logconcave function.

### Usage

```
simPH_Censored(n = 100, b1 = 0.5, b2 = -0.5, shape = 2)
```

### Arguments

| | |
|---|---|
| n | Number of samples simulated |
| b1 | Value of first regression coefficient |
| b2 | Value of second regression coefficient |
| shape | Shape parameter of baseline gamma distribution |

### Author(s)

Clifford Anderson-Bergman

### Examples

```
simData <- simPH_Censored()
# Simulates censored data from a Cox-PH model

fit <- logconcave(times = simData$times, covariates = simData$x)
# Fits a Cox-PH model with a logconcave baseline distribution
```

---

sim_Censored            *Simulate current status data from a beta(2,2) distribution*

---

### Description

Simulates current status data from a beta(2,2) distribution. Inspection times follow a uniform(0,1) distribution.

### Usage

```
sim_Censored(n = 100)
```

### Arguments

| | |
|---|---|
| n | Number of samples simulated |

### Author(s)

Clifford Anderson-Bergman

## Examples

```
simData <- sim_Censored()
# Simulates current status data

fit <- logconcave(simData)
# Fits a log concave fit
```

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