

Package ‘transmdl’

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Type Package

Title Semiparametric Transformation Models

Version 0.1.0

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Description To make the semiparametric transformation models easier to apply in real studies, we introduce this R package, in which the MLE in transformation models via an EM algorithm proposed by Zeng D, Lin DY(2007) <[doi:10.1111/j.1369-7412.2007.00606.x](https://doi.org/10.1111/j.1369-7412.2007.00606.x)> and adaptive lasso method in transformation models proposed by Liu XX, Zeng D(2013) <[doi:10.1093/biomet/ast029](https://doi.org/10.1093/biomet/ast029)> are implemented. C++ functions are used to compute complex loops. The coefficient vector and cumulative baseline hazard function can be estimated, along with the corresponding standard errors and P values.

License GPL (>= 2)

Encoding UTF-8

RoxxygenNote 7.1.2

Imports graphics, Rcpp, statmod, stats, survival

LinkingTo Rcpp, RcppEigen

Suggests MASS

NeedsCompilation yes

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EM_est*Estimate parameters and hazard function via EM algorithm.***Description**

Estimate the vector of parameters for baseline covariates β and baseline cumulative hazard function $\Lambda(\cdot)$ using the expectation-maximization algorithm. $\Lambda(t)$ is estimated as a step function with jumps only at the observed failure times. Typically, it would only be used in a call to `trans.m` or `Simu`.

Usage

```
EM_est(Y, X, delta, alpha, Q = 60, EM_itmax = 250)
```

Arguments

<code>Y</code>	observed event times
<code>X</code>	design matrix
<code>delta</code>	censoring indicator. If Y_i is censored, <code>delta=0</code> . If not, <code>delta=1</code> .
<code>alpha</code>	parameter in transformation function
<code>Q</code>	number of nodes and weights in Gaussian quadrature. Defaults to 60.
<code>EM_itmax</code>	maximum iteration of EM algorithm. Defaults to 250.

Value

a list containing

<code>beta_new</code>	estimator of β
<code>Lamb_Y</code>	estimator of $\Lambda(Y)$
<code>lamb_Y</code>	estimator of $\lambda(Y)$
<code>lamb_Ydot</code>	estimator of $\lambda(Y')$
<code>Y_eq_Yhat</code>	a matrix used in <code>trans.m</code> and <code>Simu</code>
<code>Y_geq_Yhat</code>	a matrix used in <code>trans.m</code> and <code>Simu</code>

References

- Abramowitz, M., and Stegun, I.A. (1972). Handbook of Mathematical Functions (9th ed.). Dover Publications, New York.
- Evans, M. and Swartz, T. (2000). Approximating Integrals via Monte Carlo and Deterministic Methods. Oxford University Press.
- Liu, Q. and Pierce, D.A. (1994). A note on Gauss-Hermite quadrature. *Biometrika* 81: 624-629.

Examples

```
gen_data = generate_data(200, 1, 0.5, c(-0.5, 1))
delta = gen_data$delta
Y = gen_data$Y
X = gen_data$X
EM_est(Y, X, delta, alpha = 1)$beta_new - c(-0.5, 1)
```

`generate_data` *Generate data for simulation.*

Description

Generate observed event times, covariates and other data used for simulations in the paper.

Usage

```
generate_data(n, alpha, rho, beta_true, now_repeat = 1)
```

Arguments

<code>n</code>	number of subjects
<code>alpha</code>	parameter in transformation function
<code>rho</code>	parameter in baseline cumulative hazard function $\Lambda(t) = \rho \log(1 + t)$ assumed in simulation
<code>beta_true</code>	parameter β
<code>now_repeat</code>	number of duplication of simulation

Details

The survival function for t of the i th observation takes the form

$$S_i(t|X_i) = \exp \left\{ -H\{\Lambda(t) \exp(\beta^T X_i)\} \right\}.$$

The failure time T_i can be generated by

$$T_i = \begin{cases} \exp\left\{\frac{U^{-\alpha}-1}{\alpha\rho\exp\{\beta^T X_i\}}\right\} - 1 & \alpha > 0, \\ \exp\left\{\frac{-\log(U)}{\rho\exp\{\beta^T X_i\}}\right\} - 1, & \alpha = 0. \end{cases}$$

Value

a list containing

X	design matrix
beta_X	$X \cdot \beta^T$
Y	observed event time

References

Abramowitz, M., and Stegun, I.A. (1972). Handbook of Mathematical Functions (9th ed.). Dover Publications, New York. +- Evans, M. and Swartz, T. (2000). Approximating Integrals via Monte Carlo and Deterministic Methods. Oxford University Press.

Liu, Q. and Pierce, D.A. (1994). A note on Gauss-Hermite quadrature. Biometrika 81: 624-629.

Examples

```
generate_data(200, 0.5, 1, c(0.5, -1))
```

trans_lasso

Adaptive LASSO for Semiparametric Transformation Models.

Description

Select the important variables in semiparametric transformation models for right censored data using adaptive lasso.

Usage

```
trans_lasso(Z, Y, delta_i, r, lamb_vec, solu = TRUE)
```

Arguments

Z	the baseline covariates
Y	observed event times
delta_i	censoring indicator. If Y is censored, $\text{delta}_i=0$. If not, $\text{delta}_i=1$.
r	parameter in transformation function
lamb_vec	the grad of the tuning parameter λ
solu	determines whether the solution path will be plotted. The default is TRUE.

Details

The initial value of the coefficient β used as the adapting weights is EM estimator, which is computed by the function `EM_est`. The tuning parameter λ is data-dependent and we select it using generalized crossvalidation. There may be some errors for small λ , in which case the λ and the number of adaptive lasso iteration are recorded in the `skip_para`.

Value

a list containing

<code>beta_res</code>	the estimated β with the selected tuning parameter λ
<code>GCV_res</code>	the value of GCV with the selected tuning parameter λ
<code>lamb_res</code>	the selected tuning parameter λ
<code>beta_all</code>	estimated β with all tuning parameters
<code>CSV_all</code>	value of GCV with all tuning parameters
<code>skip_para</code>	a list containing the λ and the number of adaptive lasso iteration when adaptive lasso doesn't work.

References

Xiaoxi, L. , & Donglin, Z. . (2013). Variable selection in semiparametric transformation models for right-censored data. *Biometrika*(4), 859-876.

Examples

```

if(!requireNamespace("MASS", quietly = TRUE))
{stop("package MASS needed for this example. Please install it.")}

gen_lasdat = function(n,r,rho,beta_true,a,b,seed=66,std = FALSE)
{
  set.seed(seed)
  beta_len = length(beta_true)
  beta_len = beta_len
  sigm = matrix(0, nrow = beta_len, ncol = beta_len)
  for(i in 1:(beta_len-1))
  {
    diag(sigm[1:(beta_len+1-i),i:beta_len]) = rho^(i-1)
  }
  sigm[1,beta_len] = rho^(beta_len-1)
  sigm[lower.tri(sigm)] = t(sigm)[lower.tri(sigm)]

  Z = MASS::mvrnorm(n, mu = rep(0, beta_len), Sigma = sigm)
  beta_Z.true = c(Z %*% beta_true)
  U = runif(n)
  if(r>0)
  {
    t = ((U^(-r)-1)/(a*r*exp(beta_Z.true)))^(1/b)
  }else if(r == 0)
  {
  }
}

```

```

t = (-log(U)/(a*exp(beta_Z.true)))^(1/b)
#t = (exp(-log(U)/(0.5 * exp(beta_Z.true)))) - 1
}
C = runif(n,0,8)
Y = pmin(C,t)
delta_i = ifelse( C >= t, 1, 0)
if(std)
{
  Z = apply(Z,2,normalize)
}
return(list(Z = Z, Y = Y, delta_i = delta_i,censor = mean(1-delta_i)))
}

now_rep=1
dat = gen_lasdat(100,1,0.5,c(0.3,0.5,0.7,0,0,0,0,0,0),2,5,seed= 6+60*now_rep, std = FALSE)
Z = dat$Z
Y = dat$Y
delta_i = dat$delta_i

tra_ala = trans_lasso(Z,Y,delta_i,lamb_vec = c(5,7),r=1)
tra_ala$GCV_res
tra_ala$beta_res
tra_ala$lamb_res

```

trans_m

Regression Analysis of Right-censored Data using Semiparametric Transformation Models.

Description

This function is used to conduct the regression analysis of right-censored data using semiparametric transformation models. It calculates the estimators, standard errors and p values. A plot of estimated baseline cumulative hazard function and confidence intervals can be produced.

Usage

```

trans_m(
  X,
  delta,
  Y,
  plot.Lamb = TRUE,
  alpha = seq(0.1, 1.1, by = 0.1),
  trsmodel = TRUE,
  EM_itmax = 250,
  show_res = TRUE
)

```

Arguments

X	design matrix
delta	censoring indicator. If Y_i is censored, delta=0. If not, delta=1.
Y	observed event times
plot.Lamb	If TRUE, plot the estimated baseline cumulative hazard function and confidence intervals. The default is TRUE.
alpha	parameter in transformation function. Generally, α can not be observed in medical applications. In that situation, alpha indicates the scale of choosing α . The default is (0.1, 0.2, ..., 1.1). If α is known, alpha indicates the true value of α .
trsmodel	logical value indicating whether to implement transformation models. The default is TRUE.
EM_itmax	maximum iteration of EM algorithm. Defaults to 250.
show_res	show results after trans_m.

Details

If α is unknown, we first set $\alpha = \text{alpha}$. Then, for each α , we estimate the parameters and record the value of observed log-likelihood function. The α that maximizes the observed log-likelihood function and the corresponding $\hat{\beta}$ and $\hat{\Lambda}(\cdot)$ are chosen as the best estimators. Nonparametric maximum likelihood estimators are developed for the regression parameters and cumulative intensity functions of these models based on censored data.

Value

a list containing

beta.est	estimators of β
SE.beta	standard errors of the estimated β
SE.Ydot	standard errors of the estimated $\Lambda(Y')$
Ydot	vector of sorted event times with duplicate values removed
Lamb.est	estimated baseline cumulative hazard
lamb.est	estimated jump sizes of baseline cumulative hazard function
choose.alpha	the chosen α
Lamb.upper	upper confidence limits for the estimated baseline cumulative hazard function
Lamb.lower	lower confidence limits for the estimated baseline cumulative hazard function
p.beta	P values of estimated β
p.Lamb	P values of estimated baseline cumulative hazard
p.beta	

References

Cheng, S.C., Wei, L.J., and Ying, Z. (1995). Analysis of transformation models with censored data.

Biometrika 82, 835-845.

Zeng, D. and Lin, D.Y. (2007). Maximum likelihood estimation in semiparametric regression models with censored data. J. R. Statist. Soc. B 69, 507-564.

- Abramowitz, M., and Stegun, I.A. (1972). Handbook of Mathematical Functions (9th ed.). Dover Publications, New York.
- Evans, M. and Swartz, T. (2000). Approximating Integrals via Monte Carlo and Deterministic Methods. Oxford University Press.
- Liu, Q. and Pierce, D.A. (1994). A note on Gauss-Hermite quadrature. *Biometrika* 81, 624-629.
- Louis, T. (1982). Finding the Observed Information Matrix when Using the EM Algorithm. *Journal of the Royal Statistical Society. Series B (Methodological)*, 44(2), 226-233.

See Also

[EM_est](#)

Examples

```
gen_data = generate_data(200, 1, 0.5, c(-0.5,1))
delta = gen_data$delta
Y = gen_data$Y
X = gen_data$X
res.trans = trans_m(X, delta, Y, plot.Lamb = TRUE, show_res = FALSE)
```

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