# Package 'transform.hazards'

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Type Package
<b>Title</b> Transforms Cumulative Hazards to Parameter Specified by ODE System
Version 0.1.1
Equations (ODEs) driven by a vector of cumulative hazard functions.  The package provides a method for estimating these parameters using an estimator defined by a corresponding Stochastic Differential Equation (SDE) system driven by cumulative hazard estimates. By providing cumulative hazard estimates as input, the package gives estimates of the parameter as output, along with pointwise (co)variances derived from an asymptotic expression. Examples of parameters that can be targeted in this way include the survival function, the restricted mean survival function, cumulative incidence functions, among others; see Ryalen, Stensrud, and Røysland (2018) <doi:10.1093 asy035="" biomet="">, and further applications in Stensrud, Røysland, and Ryalen (2019) <doi:10.1111 biom.13102=""> and Ryalen et al. (2021) <doi:10.1093 biostatistics="" kxab009="">.</doi:10.1093></doi:10.1111></doi:10.1093>
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pluginEstimate SDE plugin estimator solver
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#### **Description**

Calculates recursive estimator for given hazard estimates, integrand function and gradients.

#### Usage

```
pluginEstimate(n, hazMatrix, F_fun, JacobianList, X0, V0, isLebesgue = NULL)
```

#### **Arguments**

n	Total number of indiivduals
hazMatrix	Matrix consisting of hazards(rows) and their increments(columns) along the same time scale
F_fun	Integrand function $F = (F_1, F_2,)$ for the differential equation system
JacobianList	The Jacobian matrices of F_1, F_2, organized in a list
X0	Matrix containing initial values for the parameter
V0	Matrix containing initial values for the variance
isLebesgue	(Optional, to improve efficientcy) Provide the index of A (e.g. 2) that is a regular dt integral, i.e. not a cumulative hazard.

#### Value

list containing the parameter estimate X, and its covariance estimates V/n

#### Author(s)

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#### References

Ryalen, P.C., Stensrud, M.J., Røysland, K.: *Transforming cumulative hazards*, arXiv, to appear in Biometrika 2018.

### Examples

```
fit <- survfit(Surv(from, to, event==1)~1, data=dfr)</pre>
times <- fit$time
dN <- fit$n.event
Y <- fit$n.risk
Y[1] <- n
dA <- matrix(dN/Y,nrow=1,ncol=length(dN))</pre>
# Function specification
F_fun_Survival <- function(x)-matrix(x,1,1)
JacobianListSurvival <- list(function(x)-matrix(1,1,1))</pre>
X0_Survival <- matrix(1,1,1)</pre>
V0_Survival <- matrix(0,1,1)</pre>
paramEst_survival <- pluginEstimate(</pre>
 n,dA,F_fun_Survival,JacobianListSurvival,X0_Survival,V0_Survival
KM \leftarrow cumprod(1 - dA)
Greenwood <- KM^2 * cumsum(dA^2)</pre>
plot(
 times,paramEst_survival$X,type="s",main="SDE plugin survival estimates",
 ylab="",xlab="time"
lines(times,paramEst_survival$X + 1.96*sqrt(paramEst_survival$covariance[1,1,]),type="s")
lines(times,paramEst\_survival\$X - 1.96*sqrt(paramEst\_survival\$covariance[1,1,]), type="s")
lines(seq(0,10,length.out=100),exp(-seq(0,10,length.out=100)),col=2)
legend("topright",c("SDE plugin estimates","Exact"),lty=1,col=c(1,2),bty="n")
plot(
 times,paramEst_survival$covariance,type="s",
 main="SDE plugin variance vs Greenwood variance",ylab="",xlab="time"
lines(times,Greenwood,type="s",col=4,lty=1)
legend("topright",c("SDE plugin estimates","Greenwood"),lty=1,col=c(1,4),bty="n")
######### Competing risks and Cumulative incidence(two states) ################
n <- 200
x1 \leftarrow rexp(n,1)
x2 <- rexp(n, 1.3)
to.states <- ifelse(x1 < x2, 0, 1)
dfr <- data.frame(from=0,to=c(x1[to.states==0],x2[to.states==1]),to.state=to.states)</pre>
dfr <- dfr[order(dfr$to),]</pre>
nrisk <- c(n,n:1)
dA1 <- c(0,1*(dfr$to.state==0))/nrisk
dA2 \leftarrow c(0,1*(dfr$to.state==1))/nrisk
```

```
hazMatrix <- rbind(dA1,dA2)</pre>
F_{\text{fun\_cuminc}} \leftarrow \text{function}(X) \text{rbind}(c(X[2],0),c(-X[2],-X[2]))
JacobianList_cuminc <- list( function(X)matrix(c(0,0,1,-1),nrow=2),
                            function(X)matrix(c(0,0,0,-1),nrow=2))
X0_cuminc <- matrix(c(0,1),nrow=2,ncol=1)
V0_cuminc <- matrix(0,nrow=2,ncol=2)</pre>
paramEst_cuminc <- pluginEstimate(n,hazMatrix,F_fun_cuminc,JacobianList_cuminc,X0_cuminc,V0_cuminc)</pre>
times <- c(0,dfr$to)
plot(
 times,paramEst_cuminc$X[1,],type="s",ylab="",xlab="time",
 main="SDE plugin cumulative incidence estimate", ylim=c(0,0.7)
)
lines(times,paramEst_cuminc$X[1,] + 1.96*sqrt(paramEst_cuminc$covariance[1,1,]),type="s")
lines(times,paramEst_cuminc$X[1,] - 1.96*sqrt(paramEst_cuminc$covariance[1,1,]),type="s")
lines(seq(0,10,length.out = 1000),10/1000*cumsum(exp(-seq(0,10,length.out = 1000)*(1 + 1.3))),col=2)
legend("topright",c("SDE plugin estimates","Exact"),lty=1,col=c(1,2),bty="n")
####################### Relative survival(two different populations) ##############################
n <- 300
t1 <- sort(rexp(n,1))</pre>
t2 <- sort(rexp(n,1.3))
times \leftarrow sort(c(0,t1,t2))
nrisk <- 300:1
dA1 <- 1*(t1 %in% times)/nrisk
dA2 <- 1*(t2 %in% times)/nrisk
tmatch1 <- match(t1,times)</pre>
tmatch2 <- match(t2,times)</pre>
hazMatrix <- matrix(0,nrow=2,ncol=length(times))</pre>
hazMatrix[1,tmatch1] <- dA1</pre>
hazMatrix[2,tmatch2] <- dA2</pre>
F_fun_RelSurv <- function(X)matrix(c(-X,X),ncol=2)</pre>
JacobianList_RelSurv <- list(function(X)matrix(-1,nrow=1,ncol=1),</pre>
                            function(X)matrix(1,nrow=1,ncol=1))
X0_RelSurv <- matrix(1,nrow=1,ncol=1)</pre>
V0_RelSurv <- matrix(0,nrow=1,ncol=1)</pre>
paramEst_relsurv <- pluginEstimate(</pre>
 n, hazMatrix, F_fun_RelSurv, JacobianList_RelSurv, X0_RelSurv, V0_RelSurv
```

```
plot(
    times,paramEst_relsurv$X[1,],type="s",ylab="",xlab="time",
    main="SDE plugin relative survival estimate",ylim=c(-1,5.8),xlim=c(0,4)
)
lines(times,paramEst_relsurv$X[1,] + 1.96*sqrt(paramEst_relsurv$covariance[1,,]),type="s")
lines(times,paramEst_relsurv$X[1,] - 1.96*sqrt(paramEst_relsurv$covariance[1,,]),type="s")
lines(seq(0,10,length.out = 100),exp(seq(0,10,length.out = 100)*(1.3-1)),col=2)
legend("topleft",c("SDE plugin estimates","Exact"),lty=1,col=c(1,2),bty="n")
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