

# Package ‘tsriadditive’

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**Title** Two Stage Residual Inclusion Additive Hazards Estimator

**Version** 1.0.0

**Description** Additive hazards models with two stage residual inclusion method are fitted under either survival data or competing risks data. The estimator incorporates an instrumental variable and therefore can recover causal estimand in the presence of unmeasured confounding under some assumptions. A.Ying, R. Xu and J. Murphy. (2019) <[doi:10.1002/sim.8071](https://doi.org/10.1002/sim.8071)>.

**Depends** R (>= 3.5.0)

**Imports** survival

**License** LGPL (>= 2)

**Encoding** UTF-8

**URL** <https://onlinelibrary.wiley.com/doi/abs/10.1002/sim.8071>

**LazyData** true

**RoxygenNote** 6.1.1

**NeedsCompilation** no

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**Repository** CRAN

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## R topics documented:

plot.tsriadditive . . . . .	2
predict.tsriadditive . . . . .	3
summary.tsriadditive . . . . .	4
tsriadditive . . . . .	5
<b>Index</b>	<b>6</b>

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plot.tsriadditive	<i>Plotting Predicted Survival Function or Cumulative Incidence Function with Pointwise Confidence Intervals</i>
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### Description

The function will plot the predicted survival function when fitting a survival model and the predicted cumulative incidence function when fitting a competing risks model. Corresponding pointwise confidence intervals at level alpha are also included.

### Usage

```
## S3 method for class 'tsriadditive'  
plot(x, newtreatment = NULL, newIV = NULL,  
      newcovariates = NULL, alpha = 0.05, unit = "", ...)
```

### Arguments

x	the fitting object after fitting our model
newtreatment	a new treatment value
newIV	a new instrumental variable value
newcovariates	a new observed covariates
alpha	the confidence level $1 - \alpha$ for confidence interval
unit	the time unit we focus
...	the other arguments you want to put in the built-in plot function

### Value

No return value, called for side effects

### Examples

```
survtime <- rexp(100)  
cause <- rbinom(100, 1, 0.7)  
treatment <- rbinom(100, 1, 0.5)  
IV <- rnorm(100)  
covariates <- rnorm(100)  
fit <- tsriadditive(survtime, cause, treatment, IV, covariates)  
plot(fit, 1, 0, 0)
```

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predict.tsriadditive *Predict method for Additive Hazards Model with Two Stage Residual Inclusion Method Fits*

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### Description

Predicted values based on tsriadditive object.

### Usage

```
## S3 method for class 'tsriadditive'
predict(object, newtreatment = NULL,
        newIV = NULL, newcovariates = NULL, ...)
```

### Arguments

object	an object of class "tsriadditive", usually, a result of a call to tsriadditive.
newtreatment	a new treatment value.
newIV	a new instrumental variable value.
newcovariates	a new observed covariates.
...	further arguments passed to or from other methods.

### Value

predict.tsriadditive produces a vector of predictions based on new values. A list with the following components is returned:

newobsz	the vector grouping newtreatment, new IV and newcovariates
score_pred	the predicted scores
hazard_pred	the predicted baseline hazards function
surival_pred	the predicted survival function

### Examples

```
survtime <- rexp(100)
cause <- rbinom(100, 1, 0.7)
treatment <- rbinom(100, 1, 0.5)
IV <- rnorm(100)
covariates <- rnorm(100)
fit <- tsriadditive(survtime, cause, treatment, IV, covariates)
predict(fit, 1, 0, 0)
```

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summary.tsriadditive *Summarizing Additive Hazards Model with Two Stage Residual Inclusion Method Fits*

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## Description

summary method for class "tsriadditive".

## Usage

```
## S3 method for class 'tsriadditive'  
summary(object, ...)  
  
## S3 method for class 'summary.tsriadditive'  
print(x, ...)
```

## Arguments

object	an object of class "tsriadditive", usually, a result of a call to tsriadditive.
...	further arguments passed to or from other methods.
x	an object of class "summary.tsriadditive", usually, a result of a call to summary.tsriadditive.

## Value

print.summary.lm tries to be smart about formatting coefficients, an estimated variance covariance matrix of the coefficients, Z-values and the corresponding P-values

## Examples

```
survtime <- rexp(100)  
cause <- rbinom(100, 1, 0.7)  
treatment <- rbinom(100, 1, 0.5)  
IV <- rnorm(100)  
covariates <- rnorm(100)  
fit <- tsriadditive(survtime, cause, treatment, IV, covariates)  
summary(fit)
```

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tsriadditive	<i>Fitting Additive Hazards Models with Two Stage Residual Inclusion Method</i>
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### Description

tsriadditive is used to fit additive hazards models with two stage residual inclusion method.

### Usage

```
tsriadditive(survtime, cause = NULL, treatment = NULL, IV = NULL,  
             covariates = NULL)
```

### Arguments

survtime	the event time
cause	the indicator records the cause. Default to all one. Zero means right censoring. Greater than or equal to two means other cause.
treatment	the treatment variable, can be null
IV	the instrumental variable
covariates	all the observed confounders

### Value

tsriadditive returns an object of class "tsriadditive". An object of class "tsriadditive" is a list containing the following components:

coef	an estimate of the coefficients
baseline	an estimate of the baseline hazards function
vcov	an estimate of the variance covariance matrix of coef
byprod	a byproduct, that will used by other functions

### References

Ying, A., Xu, R. and Murphy, J. Two-Stage Residual Inclusion for Survival Data and Competing Risks - An Instrumental Variable Approach with Application to SEER- Medicare Linked Data. *Statistics in Medicine*, 38(10): 1775-1801, 2019.

### Examples

```
survtime <- rexp(100)  
cause <- rbinom(100, 1, 0.7)  
treatment <- rbinom(100, 1, 0.5)  
IV <- rnorm(100)  
covariates <- rnorm(100)  
fit <- tsriadditive(survtime, cause, treatment, IV, covariates)
```

# Index

`plot.tsriadditive`, [2](#)  
`predict.tsriadditive`, [3](#)  
`print.summary.tsriadditive`  
    (`summary.tsriadditive`), [4](#)  
  
`summary.tsriadditive`, [4](#)  
  
`tsriadditive`, [5](#)