

# Package ‘longsurr’

October 13, 2022

**Type** Package

**Title** Longitudinal Surrogate Marker Analysis

**Version** 1.0

**Description** Assess the proportion of treatment effect explained by a longitudinal surrogate marker as described in Agniel D and Parast L (2021) <[doi:10.1111/biom.13310](https://doi.org/10.1111/biom.13310)>.

**License** GPL

**Imports** stringr, splines, mgcv, Rsurrogate, dplyr, here, tidyr, fs, KernSmooth, stats, fdapace, grf, lme4, mvnfast, plyr, tibble, magrittr, glue, purrr, readr, refund, fda, fda.usc

**NeedsCompilation** no

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**Depends** R (>= 3.5.0)

**Repository** CRAN

**Date/Publication** 2022-09-29 10:00:02 UTC

## R topics documented:

estimate_surrogate_value . . . . .	2
full_data . . . . .	3
presmooth_data . . . . .	4

<b>Index</b>	<b>5</b>
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 estimate\_surrogate\_value

*Estimate the surrogate value of a longitudinal marker*


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### Description

Estimate the surrogate value of a longitudinal marker

### Usage

```
estimate_surrogate_value(y_t, y_c, X_t, X_c, method = c("gam", "linear",
  "kernel"), k = 3, var = FALSE, bootstrap_samples = 50, alpha = 0.05)
```

### Arguments

y_t	vector of n1 outcome measurements for treatment group
y_c	vector of n0 outcome measurements for control or reference group
X_t	n1 x T matrix of longitudinal surrogate measurements for treatment group, where T is the number of time points
X_c	n0 x T matrix of longitudinal surrogate measurements for control or reference group, where T is the number of time points
method	method for dimension-reduction of longitudinal surrogate, either 'gam', 'linear', or 'kernel'
k	number of eigenfunctions to use in semimetric
var	logical, if TRUE then standard error estimates and confidence intervals are provided
bootstrap_samples	number of bootstrap samples to use for standard error estimation, used if var = TRUE, default is 50
alpha	alpha level, default is 0.05

### Value

a tibble containing estimates of the treatment effect (Deltahat), the residual treatment effect (Deltahat\_S), and the proportion of treatment effect explained (R); if var = TRUE, then standard errors of Deltahat\_S and R are also provided (Deltahat\_S\_se and R\_se), and quantile-based 95% confidence intervals for Deltahat\_S and R are provided (Deltahat\_S\_ci\_l [lower], Deltahat\_S\_ci\_h [upper], R\_ci\_l [lower], R\_ci\_u [upper])

### References

Agniel D and Parast L (2021). Evaluation of Longitudinal Surrogate Markers. *Biometrics*, 77(2): 477-489.

**Examples**

```
library(dplyr)
data(full_data)

wide_ds <- full_data %>%
  dplyr::select(id, a, tt, x, y) %>%
  tidyr::spread(tt, x)

wide_ds_0 <- wide_ds %>% filter(a == 0)
wide_ds_1 <- wide_ds %>% filter(a == 1)
X_t <- wide_ds_1 %>% dplyr::select(`-1`:`1`) %>% as.matrix
y_t <- wide_ds_1 %>% pull(y)
X_c <- wide_ds_0 %>% dplyr::select(`-1`:`1`) %>% as.matrix
y_c <- wide_ds_0 %>% pull(y)

estimate_surrogate_value(y_t = y_t, y_c = y_c, X_t = X_t, X_c = X_c,
  method = 'gam', var = FALSE)
estimate_surrogate_value(y_t = y_t, y_c = y_c, X_t = X_t, X_c = X_c,
  method = 'linear', var = TRUE, bootstrap_sample = 50)
```

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full\_data

*Example data to illustrate functions*

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**Description**

Simulated nonsmooth data to illustrate functions

**Usage**

```
data("full_data")
```

**Format**

A data frame with 10100 observations on the following 5 variables.

id a unique person ID  
a treatment group, 0 or 1  
tt time  
x surrogate marker value  
y primary outcome

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presmooth_data	<i>Pre-smooth sparse longitudinal data</i>
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**Description**

Pre-smooth sparse longitudinal data

**Usage**

```
presmooth_data(obs_data, ...)
```

**Arguments**

obs_data	data.frame or tibble containing the observed data, with columns <code>id</code> identifying the individual measured, <code>tt</code> identifying the time of the observation, <code>x</code> the value of the surrogate at time <code>tt</code> , and <code>a</code> indicating 1 for treatment arm and 0 for control arm.
...	additional arguments passed on to <code>fpca</code>

**Value**

list containing matrices  $X_t$  and  $X_c$ , which are the smoothed surrogate values for the treated and control groups, respectively, for use in downstream analyses

**Examples**

```
library(dplyr)
data(full_data)
obs_ds <- group_by(full_data, id)
obs_data <- sample_n(obs_ds, 5)
obs_data <- ungroup(obs_data)

head(obs_data)
presmooth_X <- presmooth_data(obs_data)
```

# Index

\* **datasets**

full\_data, [3](#)

estimate\_surrogate\_value, [2](#)

full\_data, [3](#)

presmooth\_data, [4](#)