

A simple run of SLIDE

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Installing slide

use the following command to install slide

```
#library(devtools)
#install_github("jishnu-lab/SLIDE")
```

Reading Sample data

To obtain the the latent factor Z first run the LFD to obtain Z For this vignette the sample is located in the data folder of the github repository

```
y <- readRDS(file="./Data/y.rds")
z <- readRDS(file="./Data/z.rds")
```

Running SLIDE

In this section, we are running slide to capture standalone and interaction terms.

```
library(SLIDE)
library(doParallel)
```

```
## Loading required package: foreach
```

```
## Loading required package: iterators
```

```
## Loading required package: parallel
```

```
res <- SLIDE(z,y,do_interacts = T,spec=0.5)
```

```
## Loading required package: dplyr
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
## filter, lag
```

```

## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union

## selecting marginal variables using method 4 . . .
## no splitting . . . skipping aggregation
## final marginal spec: 0.5
## starting interaction selection . . .
## [1] "Before doing interaction SLIDE"
## [1] "z4" "z10"
## starting interactions.....
## interaction terms with 4
## no splitting . . . skipping aggregation
## interaction terms with 10
## no splitting . . . skipping aggregation
## no interaction vars . . . upsilon is marginal variable
## [1] "printig the yhat of each maginals:"
## NULL
## running knockoffs on marginal/interaction submodels . . .
## no splitting . . . skipping aggregation
## [1] "upsilon colnames:"

print("The significant stand alone latent factors:")

## [1] "The significant stand alone latent factors:"

print(res$marginal_vars)

## [1] 4 10

print("The significant interacting latent factors:")

## [1] "The significant interacting latent factors:"

print(res$interaction_vars)

## [1] "Z4.Z27"

```