

Package ‘pda’

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Type Package

Title Privacy-Preserving Distributed Algorithms

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Description A collection of privacy-preserving distributed algorithms for conducting multi-site data analyses. The regression analyses can be linear regression for continuous outcome, logistic regression for binary outcome, Cox proportional hazard regression for time-to event outcome, Poisson regression for count outcome, or multi-categorical regression for nominal or ordinal outcome. The PDA algorithm runs on a lead site and only requires summary statistics from collaborating sites, with one or few iterations. The package can be used together with the online system ([<https://pda-ota.pdamethods.org/>](https://pda-ota.pdamethods.org/)) for safe and convenient collaboration. For more information, please visit our software websites: [<https://github.com/Pencil/pda>](https://github.com/Pencil/pda), and [<https://pdamethods.org/>](https://pdamethods.org/).

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Contents

| | |
|--------------------------|-----------|
| ADAP_data | 2 |
| covid | 3 |
| cs | 3 |
| getCloudConfig | 4 |
| LOS | 4 |
| lung2 | 5 |
| ODACAT_nominal | 5 |
| ODACAT_ordinal | 6 |
| pda | 6 |
| pdaGet | 9 |
| pdaList | 10 |
| pdaPut | 10 |
| pdaSync | 11 |
| Index | 12 |

| | |
|-----------|----------------------------|
| ADAP_data | <i>ADAP simulated data</i> |
|-----------|----------------------------|

Description

A simulated data set for ADAP demonstration

Usage

ADAP_data

Format

A list containing the following elements:

sites site id, 300 'site1', 300 'site2', 300 'site3'

status binary outcome of length 900

x 900 by 49 matrix generated by standard normal distribution, representing the covariates

| | |
|-------|--|
| covid | <i>COVID-19 LOS and mortality data</i> |
|-------|--|

Description

A simulated data set of hospitalization Length of Stay (LOS) and mortality from 6 sites

Usage

covid

Format

A data frame with 2100 rows and 6 variables:

site site id, 600 'site1', 500 'site2', 400 'site3', 300 'site4', 200 'site5', 100 'site6'

age continuous age in year, min 3 max 97

sex 2 categories, '1' for male and '0' for female

lab lab test results, continuous value ranging from 2.3 to 97.4

los LOS in days, ranging from 1 to 29

death mortality status, '1' for death and '0' for alive.

| | |
|----|----------------------------|
| cs | <i>CrabSatellites data</i> |
|----|----------------------------|

Description

A data set modified from the CrabSatellites data in countreg package (see demo(ODAH)).

Usage

cs

Format

A data frame containing 173 observations on 4 variables.

site Simulated site id, 85 'site1' and 88 'site2'.

satellites Number of satellites. Treated as (zero-inflated) count outcome in ODAH

width Carapace width (cm).

weight Weight (kg).

Source

<https://rdrr.io/rforge/countreg/man/CrabSatellites.html>

| | |
|----------------|--|
| getCloudConfig | <i>gather cloud settings into a list</i> |
|----------------|--|

Description

gather cloud settings into a list

Usage

```
getCloudConfig(site_id,dir,uri,secret)
```

Arguments

| | |
|---------|-------------------------------------|
| site_id | site identifier |
| dir | shared directory path if flat files |
| uri | web uri if web service |
| secret | web token if web service |

Value

A list of cloud parameters: site_id, secret and uri

See Also

pda

| | |
|-----|----------------------------|
| LOS | <i>Length of Stay data</i> |
|-----|----------------------------|

Description

A simulated data set of hospitalization Length of Stay (LOS) from 3 sites

Usage

LOS

Format

A data frame with 1000 rows and 5 variables:

site site id, 500 'site1', 400 'site2' and 100 'site3'

age 3 categories, 'young', 'middle', and 'old'

sex 2 categories, 'M' for male and 'F' for female

lab lab test results, continuous value ranging from 0 to 100

los LOS in days, ranging from 1 to 28. Treated as continuous outcome in DLM

| | |
|-------|---------------------------------------|
| lung2 | <i>Lung cancer survival time data</i> |
|-------|---------------------------------------|

Description

A data set modified from the lung data in survival package (see demo(ODAC)).

Usage

```
lung2
```

Format

A data frame with 228 rows and 5 variables:

site simulated site id, 86 'site1', 83 'site2' and 59 'site3'

time survival time in days

status censoring status 0=censored, 1=dead

age age in years

sex 1 for female and 0 for male

Source

<https://CRAN.R-project.org/package=survival>

| | |
|----------------|------------------------------|
| ODACAT_nominal | <i>ODACAT simulated data</i> |
|----------------|------------------------------|

Description

A simulated data set for ODACAT demonstration

Usage

```
ODACAT_nominal
```

Format

A data frame with 300 rows and 5 variables:

id.site site id, 102 'site1', 100 'site2', 98 'site3'

outcome 3-category outcome, possible values are 1,2,3. Category 3 will be used as reference

X1 the first covariate, continuous

X2 the second covariate, binary

X3 the third covariate, binary

| | |
|----------------|------------------------------|
| ODACAT_ordinal | <i>ODACAT simulated data</i> |
|----------------|------------------------------|

Description

A simulated data set for ODACAT demonstration

Usage

ODACAT_ordinal

Format

A data frame with 300 rows and 5 variables:

id.site site id, 105 'site1', 105 'site2', 90 'site3'

outcome 3-category outcome, possible values are 1,2,3. Category 3 will be used as reference

X1 the first covariate, continuous

X2 the second covariate, binary

X3 the third covariate, binary

| | |
|-----|--|
| pda | <i>PDA: Privacy-preserving Distributed Algorithm</i> |
|-----|--|

Description

Fit Privacy-preserving Distributed Algorithms for linear, logistic, Poisson and Cox PH regression with possible heterogeneous data across sites.

Usage

pda(ipdata,site_id,control,dir,uri,secret,hosdata)

Arguments

| | |
|---------|--|
| ipdata | Local IPD data in data frame, should include at least one column for the outcome and one column for the covariates |
| site_id | Character site name |
| control | pda control data |
| dir | directory for shared flat file cloud |
| uri | Universal Resource Identifier for this run |
| secret | password to authenticate as site_id on uri |
| hosdata | hospital-level data, should include the same name as defined in the control file |

Value

control

control

References

Michael I. Jordan, Jason D. Lee & Yun Yang (2019) Communication-Efficient Distributed Statistical Inference,

Journal of the American Statistical Association, 114:526, 668-681

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Journal of the American Medical Informatics Association, 27.3:376–385,

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Journal of the American Medical Informatics Association, 27.7:1028–1036,

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(ODAH) Mackenzie J. Edmondson, et al. (2021) An Efficient and Accurate Distributed Learning Algorithm for Modeling Multi-Site Zero-Inflated Count Outcomes. medRxiv, pp.2020-12.

doi:[10.1101/2020.12.17.20248194](https://doi.org/10.1101/2020.12.17.20248194).

(ADAP) Xiaokang Liu, et al. (2021) ADAP: multisite learning with high-dimensional heterogeneous data via A Distributed Algorithm for Penalized regression.

(dGEM) Jiayi Tong, et al. (2022) dGEM: Decentralized Generalized Linear Mixed Effects Model

See Also

pdaPut, pdaList, pdaGet, getCloudConfig and pdaSync.

Examples

```
require(survival)
require(data.table)
require(pda)
data(lung)
```

```
## In the toy example below we aim to analyze the association of lung status with
## age and sex using logistic regression, data(lung) from 'survival', we randomly
```

```

## assign to 3 sites: 'site1', 'site2', 'site3'. we demonstrate using PDA ODAL can
## obtain a surrogate estimator that is close to the pooled estimate. We run the
## example in local directory. In actual collaboration, account/password for pda server
## will be assigned to the sites at the server https://pda.one.
## Each site can access via web browser to check the communication of the summary stats.

## for more examples, see demo(ODAC) and demo(ODAP)

# Create 3 sites, split the lung data amongst them
sites = c('site1', 'site2', 'site3')
set.seed(42)
lung2 <- lung[,c('status', 'age', 'sex')]
lung2$sex <- lung2$sex - 1
lung2$status <- ifelse(lung2$status == 2, 1, 0)
lung_split <- split(lung2, sample(1:length(sites), nrow(lung), replace=TRUE))
## fit logistic reg using pooled data
fit.pool <- glm(status ~ age + sex, family = 'binomial', data = lung2)

# ##### STEP 1: initialize #####
control <- list(project_name = 'Lung cancer study',
               step = 'initialize',
               sites = sites,
               heterogeneity = FALSE,
               model = 'ODAL',
               family = 'binomial',
               outcome = "status",
               variables = c('age', 'sex'),
               optim_maxit = 100,
               lead_site = 'site1',
               upload_date = as.character(Sys.time()) )

## run the example in local directory:
## specify your working directory, default is the tempdir
mydir <- tempdir()
## assume lead site1: enter "1" to allow transferring the control file
pda(site_id = 'site1', control = control, dir = mydir)
## in actual collaboration, account/password for pda server will be assigned, thus:
## Not run: pda(site_id = 'site1', control = control, uri = 'https://pda.one', secret='abc123')
## you can also set your environment variables, and no need to specify them in pda:
## Not run: Sys.setenv(PDA_USER = 'site1', PDA_SECRET = 'abc123', PDA_URI = 'https://pda.one')
## Not run: pda(site_id = 'site1', control = control)

##' assume remote site3: enter "1" to allow tranferring your local estimate
pda(site_id = 'site3', ipdata = lung_split[[3]], dir=mydir)

##' assume remote site2: enter "1" to allow tranferring your local estimate
pda(site_id = 'site2', ipdata = lung_split[[2]], dir=mydir)

##' assume lead site1: enter "1" to allow tranferring your local estimate
##' control.json is also automatically updated
pda(site_id = 'site1', ipdata = lung_split[[1]], dir=mydir)

```



```

##' if lead site1 initialized before other sites,
##' lead site1: uncomment to sync the control before STEP 2
## Not run: pda(site_id = 'site1', control = control)
## Not run: config <- getCloudConfig(site_id = 'site1')
## Not run: pdaSync(config)

#' ##### STEP 2: derivative #####
##' assume remote site3: enter "1" to allow tranferring your derivatives
pda(site_id = 'site3', ipdata = lung_split[[3]], dir=mydir)

##' assume remote site2: enter "1" to allow tranferring your derivatives
pda(site_id = 'site2', ipdata = lung_split[[2]], dir=mydir)

##' assume lead site1: enter "1" to allow tranferring your derivatives
pda(site_id = 'site1', ipdata = lung_split[[1]], dir=mydir)

#' ##### STEP 3: estimate #####
##' assume lead site1: enter "1" to allow tranferring the surrogate estimate
pda(site_id = 'site1', ipdata = lung_split[[1]], dir=mydir)

##' the PDA ODAL is now completed!
##' All the sites can still run their own surrogate estimates and broadcast them.

##' compare the surrogate estimate with the pooled estimate
config <- getCloudConfig(site_id = 'site1', dir=mydir)
fit.odal <- pdaGet(name = 'site1_estimate', config = config)
cbind(b.pool=fit.pool$coef,
      b.odal=fit.odal$btilde,
      sd.pool=summary(fit.pool)$coef[,2],
      sd.odal=sqrt(diag(solve(fit.odal$Htilde)/nrow(lung2))))

## see demo(ODAL) for more optional steps

```

pdaGet

Function to download json and return as object

Description

Function to download json and return as object

Usage

```
pdaGet(name,config)
```

Arguments

| | |
|--------|---------------------|
| name | of file |
| config | cloud configuration |

Value

A list of data objects from the json file on the cloud

See Also

pda

pdaList *Function to list available objects*

Description

Function to list available objects

Usage

```
pdaList(config)
```

Arguments

config a list of variables for cloud configuration

Value

A list of (json) files on the cloud

See Also

pda

pdaPut *Function to upload object to cloud as json*

Description

Function to upload object to cloud as json

Usage

```
pdaPut(obj, name, config)
```

Arguments

obj R object to encode as json and uploaded to cloud
name of file
config a list of variables for cloud configuration

Value

NONE

See Also

pda

pdaSync

pda control synchronize

Description

update pda control if ready (run by lead)

Usage

pdaSync(config)

Arguments

config cloud configuration

Value

control

See Also

pda

Index

* datasets

ADAP_data, 2

covid, 3

cs, 3

LOS, 4

lung2, 5

ODACAT_nominal, 5

ODACAT_ordinal, 6

ADAP_data, 2

covid, 3

cs, 3

getCloudConfig, 4

LOS, 4

lung2, 5

ODACAT_nominal, 5

ODACAT_ordinal, 6

pda, 6

pdaGet, 9

pdaList, 10

pdaPut, 10

pdaSync, 11