

Package: pcatsAPIclientR (via r-universe)

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Type Package

Title 'PCATS' API Client

Version 1.1.0

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Description Provides an R interface to the 'PCATS' API
<https://pcats.research.cchmc.org/api/__docs__/>, allowing R
users to submit tasks and retrieve results.

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Encoding UTF-8

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Suggests testthat

NeedsCompilation no

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dynamicGP	<i>Performs a data analysis for data with adaptive treatments.</i>
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Description

Performs Bayesian's Gaussian process regression or Bayesian additive regression tree for data with adaptive treatment(s).

Usage

```
dynamicGP(
  datafile = NULL,
  dataref = NULL,
  method = "BART",
  stg1.outcome,
  stg1.treatment,
  stg1.x.explanatory = NULL,
  stg1.x.confounding = NULL,
  stg1.tr.hte = NULL,
  stg1.tr.values = NULL,
  stg1.tr.type = "Discrete",
  stg1.time,
  stg1.time.value = NULL,
  stg1.outcome.type = "Continuous",
  stg1.outcome.bound_censor = "neither",
  stg1.outcome.lb = NULL,
  stg1.outcome.ub = NULL,
  stg1.outcome.censor.lv = NULL,
  stg1.outcome.censor.uv = NULL,
  stg1.outcome.censor.yn = NULL,
  stg1.outcome.link = "identity",
  stg1.c.margin = NULL,
  stg2.outcome,
  stg2.treatment,
  stg2.x.explanatory = NULL,
  stg2.x.confounding = NULL,
  stg2.tr1.hte = NULL,
  stg2.tr2.hte = NULL,
  stg2.tr.values = NULL,
  stg2.tr.type = "Discrete",
  stg2.time,
  stg2.time.value = NULL,
```

```

stg2.outcome.type = "Continuous",
stg2.outcome.bound_censor = "neither",
stg2.outcome.lb = NULL,
stg2.outcome.ub = NULL,
stg2.outcome.censor.lv = NULL,
stg2.outcome.censor.uv = NULL,
stg2.outcome.censor.yn = NULL,
stg2.outcome.link = "identity",
stg2.c.margin = NULL,
burn.num = 500,
mcmc.num = 500,
x.categorical = NULL,
mi.datafile = NULL,
mi.dataref = NULL,
sheet = NULL,
mi.sheet = NULL,
seed = 5000,
token = NULL,
use.cache = NULL
)

```

Arguments

datafile	File to upload (.csv or .xls)
dataref	Reference to already uploaded file.
method	The method to be used. "GP" for GP method and "BART" for BART method. The default value is "BART".
stg1.outcome	The name of the intermediate outcome variable for stage 1.
stg1.treatment	The name of the treatment variable for stage 1.
stg1.x.explanatory	A vector of the name of the explanatory variables for stage 1.
stg1.x.confounding	A vector of the name of the confounding variables for stage 1.
stg1.tr.hte	An optional vector specifying categorical variables which may have heterogeneous treatment effect with the treatment variable for stage 1.
stg1.tr.values	User-defined values for the calculation of ATE if the treatment variable is continuous for stage 1.
stg1.tr.type	The type of treatment at stage 1. "Continuous" for continuous treatment and "Discrete" for categorical treatment. The default value is "Discrete".
stg1.time	Time variable.
stg1.time.value	Pre-specified time exposure.
stg1.outcome.type	Intermediate outcome type ("Continuous" or "Discrete") for stage 1.

`stg1.outcome.bound_censor`
 The default value is "neither". "neither" if the intermediate outcome is not bounded or censored. "bounded" if the intermediate outcome is bounded. "censored" if the intermediate outcome is censored.

`stg1.outcome.lb`
 Stage 1 lower bound if the intermediate outcome is bounded.

`stg1.outcome.ub`
 Stage 1 upper bound if the intermediate outcome is bounded.

`stg1.outcome.censor.lv`
 lower variable of censored interval if the intermediate outcome is censored.

`stg1.outcome.censor.uv`
 upper variable of censored interval if the intermediate outcome is censored.

`stg1.outcome.censor.yn`
 Censoring variable if the intermediate outcome is censored.

`stg1.outcome.link`
 function for the intermediate outcome; the default value is "identity". "identity" if no transformation needed. "log" for log transformation. "logit" for logit transformation.

`stg1.c.margin` An optional vector of user-defined values of c for PrTE at stage 1.

`stg2.outcome` The name of the outcome variable for stage 2.

`stg2.treatment` The name of the treatment variable for stage 2.

`stg2.x.explanatory`
 A vector of the name of the explanatory variables for stage 2.

`stg2.x.confounding`
 A vector of the name of the confounding variables for stage 2.

`stg2.tr1.hte` At stage 2, an optional vector specifying categorical variables which may have heterogeneous treatment effect with the stage 1 treatment variable

`stg2.tr2.hte` At stage 2, an optional vector specifying categorical variables which may have heterogeneous treatment effect with the stage 2 treatment variable

`stg2.tr.values` User-defined values for the calculation of ATE if the treatment variable is continuous for stage 2.

`stg2.tr.type` The type of treatment at stage 2. "Continuous" for continuous treatment and "Discrete" for categorical treatment. The default value is "Discrete".

`stg2.time` Time variable.

`stg2.time.value`
 Pre-specified time exposure.

`stg2.outcome.type`
 Outcome type ("Continuous" or "Discrete") for stage 2.

`stg2.outcome.bound_censor`
 The default value is "neither". "neither" if the intermediate outcome is not bounded or censored. "bounded" if the intermediate outcome is bounded. "censored" if the intermediate outcome is censored.

`stg2.outcome.lb`
 Stage 2 lower bound if the outcome is bounded.

stg2.outcome.ub	Stage 2 upper bound if the outcome is bounded.
stg2.outcome.censor.lv	lower variable of censored interval if the outcome is censored.
stg2.outcome.censor.uv	upper variable of censored interval if the outcome is censored.
stg2.outcome.censor.yn	Censoring variable if the outcome is censored.
stg2.outcome.link	function for the outcome; the default value is "identity". "identity" if no transformation needed. "log" for log transformation. "logit" for logit transformation.
stg2.c.margin	An optional vector of user-defined values of c for PrTE at stage 2.
burn.num	numeric; the number of MCMC 'burn-in' samples, i.e. number of MCMC to be discarded. The default value is 500.
mcmc.num	numeric; the number of MCMC samples after 'burn-in'. The default value is 500.
x.categorical	A vector of the name of categorical variables in data.
mi.datafile	File to upload (.csv or .xls) that contains the imputed data in the model.
mi.dataref	Reference to already uploaded file that contains the imputed data in the model.
sheet	If datafile or dataref points to an Excel file this variable specifies which sheet to load.
mi.sheet	If mi.datafile or mi.dataurl points to an Excel file this variable specifies which sheet to load.
seed	Sets the seed. The default value is 5000.
token	Authentication token.
use.cache	Use cached results (default True).

Value

jobid

dynamicGP.cate	<i>Get conditional average treatment effect for data with two time points.</i>
----------------	--

Description

Estimate the conditional average treatment effect of user-specified treatment groups.

Usage

```
dynamicGP.cate(  
  jobid,  
  x,  
  control.tr,  
  treat.tr,  
  c.margin = NULL,  
  token = NULL,  
  use.cache = NULL  
)
```

Arguments

jobid	job id of the "dynamicGP".
x	The name of variable which may have the heterogeneous treatment effect. x should be a categorical variable.
control.tr	A vector of the values of the treatment variables at all stages as the reference group.
treat.tr	A vector of the values of the treatment variables at all stages compared to the reference group.
c.margin	An optional vector of user-defined values of c for PrCTE.
token	Authentication token.
use.cache	Use cached results (default True).

Details

The contrast of potential outcomes for the reference group and the treatment group is estimated at a list of x values if x is not a factor. If x is a factor, the conditional average treatment effect is estimated at each value of levels of x.

Value

jobid

Note

The conditional average treatment effect is estimated based on the sample data. The observations with missing covariates in the model are excluded. For the unspecified variables in the model, the observed data is used to estimate the conditional average treatment effect.

job_status	<i>Return job status</i>
------------	--------------------------

Description

Return status of the previously submitted job

Usage

```
job_status(jobid, token = NULL)
```

Arguments

jobid	Job ID of the previously submitted job
token	Authentication token.

Value

status

ploturl	<i>Return plot URL</i>
---------	------------------------

Description

Return plot URL

Usage

```
ploturl(jobid, plottype = "", token = NULL)
```

Arguments

jobid	Job ID of the previously submitted job
plottype	Plot type
token	Authentication token.

Value

url

printgp	<i>Print job results</i>
---------	--------------------------

Description

Return formatted string with job results

Usage

```
printgp(jobid, token = NULL)
```

Arguments

jobid	Job ID of the previously submitted job
token	Authentication token.

Value

formatted text

results	<i>Return job results</i>
---------	---------------------------

Description

Return job results

Usage

```
results(jobid, token = NULL)
```

Arguments

jobid	Job ID of the previously submitted job
token	Authentication token.

Value

results

staticGP	<i>Performs a data analysis for data with non-adaptive treatment(s).</i>
----------	--

Description

Performs Bayesian's Gaussian process regression or Bayesian additive regression tree for data with non-adaptive treatment(s).

Usage

```
staticGP(  
  datafile = NULL,  
  dataref = NULL,  
  method = "BART",  
  outcome,  
  outcome.type = "Continuous",  
  outcome.bound_censor = "neither",  
  outcome.lb = NULL,  
  outcome.ub = NULL,  
  outcome.censor.yn = NULL,  
  outcome.censor.lv = NULL,  
  outcome.censor.uv = NULL,  
  outcome.link = "identity",  
  treatment,  
  x.explanatory = NULL,  
  x.confounding = NULL,  
  tr.type = "Discrete",  
  tr.values = NULL,  
  c.margin = NULL,  
  tr.hte = NULL,  
  time,  
  time.value = NULL,  
  burn.num = 500,  
  mcmc.num = 500,  
  x.categorical = NULL,  
  mi.datafile = NULL,  
  mi.dataref = NULL,  
  sheet = NULL,  
  mi.sheet = NULL,  
  seed = 5000,  
  token = NULL,  
  use.cache = NULL  
)
```

Arguments

datafile File to upload (.csv or .xls)

<code>dataref</code>	Reference to already uploaded file.
<code>method</code>	The method to be used. "GP" for GP method and "BART" for BART method. The default value is "BART".
<code>outcome</code>	The name of the outcome variable.
<code>outcome.type</code>	Outcome type ("Continuous" or "Discrete"). The default value is "Continuous".
<code>outcome.bound_censor</code>	The default value is "neither". "neither" if the outcome is not bounded or censored. "bounded" if the outcome is bounded. "censored" if the outcome is censored.
<code>outcome.lb</code>	Putting a lower bound if the outcome is bounded.
<code>outcome.ub</code>	Putting a upper bound if the outcome is bounded.
<code>outcome.censor.yn</code>	Censoring variable if outcome is censored.
<code>outcome.censor.lv</code>	lower variable of censored interval if outcome is censored.
<code>outcome.censor.uv</code>	upper variable of censored interval if outcome is censored.
<code>outcome.link</code>	function for outcome; the default value is "identity". "identity" if no transformation needed. "log" for log transformation. "logit" for logit transformation.
<code>treatment</code>	The vector of the name of the treatment variables. Users can input at most two treatment variables.
<code>x.explanatory</code>	The vector of the name of the explanatory variables.
<code>x.confounding</code>	The vector of the name of the confounding variables.
<code>tr.type</code>	The type of the first treatment. "Continuous" for continuous treatment and "Discrete" for categorical treatment. The default value is "Discrete".
<code>tr.values</code>	user-defined values for the calculation of ATE if the first treatment variable is continuous
<code>c.margin</code>	An optional vector of user-defined values of c for PrTE.
<code>tr.hte</code>	An optional vector specifying variables which may have heterogeneous treatment effect with the first treatment variable
<code>time</code>	Time variable.
<code>time.value</code>	Pre-specified time exposure.
<code>burn.num</code>	numeric; the number of MCMC 'burn-in' samples, i.e. number of MCMC to be discarded. The default value is 500.
<code>mcmc.num</code>	numeric; the number of MCMC samples after 'burn-in'. The default value is 500.
<code>x.categorical</code>	A vector of the name of categorical variables in data.
<code>mi.datafile</code>	File to upload (.csv or .xls) that contains the imputed data in the model.
<code>mi.dataref</code>	Reference to already uploaded file that contains the imputed data in the model.
<code>sheet</code>	If datafile or dataref points to an Excel file this variable specifies which sheet to load.

mi.sheet	If mi.datafile or mi.dataurl points to an Excel file this variable specifies which sheet to load.
seed	Sets the seed. The default value is 5000.
token	Authentication token.
use.cache	Use cached results (default True).

Value

jobid

staticGP.cate	<i>Get conditional average treatment effect</i>
---------------	---

Description

Estimate the conditional average treatment effect of user-specified treatment groups.

Usage

```
staticGP.cate(
  jobid,
  x,
  control.tr,
  treat.tr,
  c.margin = NULL,
  token = NULL,
  use.cache = NULL
)
```

Arguments

jobid	job id of the "staticGP".
x	The name of a categorical variable which may have the heterogeneous treatment effect.
control.tr	The value of the treatment variable as the reference group.
treat.tr	The value of the treatment variable compared to the reference group.
c.margin	An optional vector of user-defined values of c for PrCTE.
token	Authentication token.
use.cache	Use cached results (default True).

Details

The contrast of potential outcomes for the reference group and the treatment group is estimated at each value of x.

Value

Return jobid

Note

The conditional average treatment effect is estimated based on the sample data. The observations with missing covariates in the model are excluded. For the unspecified variables in the model, the original data is used to estimate the conditional average treatment effect.

uploadfile	<i>Upload a file</i>
------------	----------------------

Description

Upload a file

Usage

```
uploadfile(filename, token = NULL)
```

Arguments

filename	Filename of a file to upload
token	Authentication token.

Value

Backend filename reference

wait_for_result	<i>Wait while the job status is pending</i>
-----------------	---

Description

Return when the job status is finished (either successfully or otherwise)

Usage

```
wait_for_result(jobid, token = NULL)
```

Arguments

jobid	Job ID of the previously submitted job
token	Authentication token.

Value

status

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