Package 'phensim.R'

November 30, 2022

Type Package

Title PHENSIM wrapper R package

Version 0.1.0

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Description phensim.R is a command line wrapper package for PHENSIM service.
For more details check the guidelines.

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Encoding UTF-8

Imports httr, jsonlite, rlang, data.table

RoxygenNote 7.1.2

NeedsCompilation no

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`getResults` *Get simulation job results.*

Description

Let the user retrieve all results from a specified simulation job.

Usage

```
getResults(job_id, type = "output")
```

Arguments

job_id	Simulation's id whose results the user wants to retrieve (as Integer)
type	Type of results the user is interested in (String value, one of: "output", "pathway_output", "nodes_output"; Default: "output")

Details

The user can choose from 3 different results, specified by the function parameter *type*.

- *output* : results will be given in "raw" format, an "all-in-one" solution that shows every evaluation from PHENSIM (Activity-Score, P-value, ...) for each node (biological element) from every pathway;
- *pathway_output* : matrix-form auxilary details showing all random values generated during the simulation process, given by pathway;
- *nodes_output* : matrix-form auxilary details showing all random values generated during the simulation process, given by nodes (biological elements);

Value

The function returns the requested results as data frame.

Examples

```
df <- getResults(3777, type="pathway_output")
```

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infoJob *Prints more details for queried job*

Description

Gives all details about the requested job id. Typical work-flow would be calling listJobs (check "?listJobs") and calling infoJob passing the job_id.
The method gives information about creation data, job's status, id, name, organism, and simulation parameters.
For more details check PHENSIM docs at `https://phensim.tech/docs/api`

Usage

```
infoJob(job_id)
```

Arguments

job_id	Simulation's id (as Integer)

Value

Details for queried job

Examples

```
infoJob(691)
```

jobParameters *Get job simulation parameters*

Description

Retrieve parameters for specific job simulation.

Usage

```
jobParameters(job_id, save = 0, view = 1)
```

Arguments

job_id	Simulation's id whose parameters will be retrieved (as Integer);
save	Set this flag to 1 to save job parameters as local file (default 0);
view	This flag is set to 1 by default and will always print data (can be set to 0 otherwise);

Details

Requests and prints the parameters file for a specific job, as inputted during submission. This file should contain only the nodes' expression indication.
This method requires the simulation's id, accessible from listJobs() details.
Note: this method also gives the possibility to save locally the file.

For more details check PHENSIM docs at https://phensim.tech/docs/api

Value

This function prints the requested info and also returns the data as String (is var assignable).

Examples

```
jobParameters(691)
```

listJobs *Lists all jobs available to the current user*

Description

Lists all jobs available to the user at that moment, printing the jobs' IDs, names and current states
For more details check PHENSIM docs at https://phensim.tech/docs/api

Usage

```
listJobs()
```

Value

Printed info

serviceInfo *Test APIs service status*

Description

Checks if APIs token is correctly set up. Furthermore, prints all info about the user account registered for that token.
For more details check PHENSIM docs at `https://phensim.tech/docs/api`

Usage

```
serviceInfo()
```

Value

If the token is correctly set up, prints the user account info

setToken *APIs token setup procedure*

Description

Starts an interactive procedure to set up your APIs token (required to use other services)

Usage

```
setToken()
```

submitJob *Interactive procedure to submit a new simulation*

Description

Starts an interactive procedure to submit a new simulation job in PHENSIM

Usage

```
submitJob()
```

Details

The procedure guides the user through the steps required to fill all simulation fields.
In each step the user is asked to insert a value or select a file to set that specific simulation parameter
There are 17 parameters the user can set during the procedure:

- *name* : the name that wil be given to the simulation;
- *organism* : the organism on which perform the simulation (using KEGG accession number);
- *epsilon* : a numeric value to determine non-expressed node;
- *seed* : seed value for RNG to allow reproducibility;
- *fdr* : string value for FDR alrithm, one of: BH, QV, LOC (default: BH);
- *reactome* : boolean value to use reactome with KEGG;
- *fast* : boolean value to use the fast method for the perturbation computation (default: true);
- *miRNAs* : boolean value to enable MITHrIL miRNA enrichment feature;
- *miRNAEvidence* : string value to select miRNA-target interactions (One of: STRONG, WEAK, PREDICTION; Default: STRONG);
- *simulationParametersFile* : file of simulation parameters, formatted as a list of entity-regulationtype;
- *enrichmentDatabaseFile* : file of enrichment database;
- *filter* : filter for the enrichment database;
- *nonExpressedNodesFile* : file of non-expressed nodes file;
- *knockoutNodesFile* : file of knocked-out nodes;
- *customNodeTypesFile* : file of custom node types;
- *customEdgeTypesFile* : file of custom edge types;
- *customEdgeSubtypesFile* : file of custom edge subtypes;

NOTE: all parameters are OPTIONAL (default value will be used eventually) except for *name*, *organism* and *simulationParametersFile*, they have to be set otherwise the procedure will fail.
Furthermore, the *submit* parameter is automatically set to 1, so the simulation will be automatically submitted once the procedure in done.

For more details check PHENSIM docs at `https://phensim.tech/docs/api`

Value

Submitting a new simulation job returns the APIs call response with all details.