

# Package ‘solvebio’

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**Type** Package

**Title** The Official SolveBio API Client

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**Description** R language bindings for SolveBio's API.

SolveBio is a biomedical knowledge hub that enables life science organizations to collect and harmonize the complex, disparate “multi-omic” data essential for today's R&D and BI needs.

For more information, visit <<https://www.solvebio.com>>.

**URL** <https://github.com/solvebio/solvebio-r>

**Imports** httr, jsonlite, dplyr (>= 0.5.0), mime

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**Collate** solvebio.R annotation.R application.R beacon.R beacon\_set.R dataset.R dataset\_commit.R dataset\_export.R dataset\_field.R dataset\_import.R dataset\_migration.R object.R shiny.R user.R utils.R vault.R zzz.R

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---

Annotator.annotate      *Annotator.annotate*

---

## Description

Annotate a data table/frame with additional fields.

## Usage

```
Annotator.annotate(records, fields, include_errors = FALSE, raw = FALSE,
  env = solvebio:::solveEnv)
```

**Arguments**

records	The data table or data frame to annotate.
fields	The fields to add.
include_errors	Set to TRUE to include errors in the output (default: FALSE).
raw	Set to TRUE to return the raw response (default: FALSE).
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Annotator.annotate(records=tbl, fields=fields)  
  
## End(Not run)
```

---

Application.all

*Application.all*

---

**Description**

Retrieves the metadata about all application on SolveBio available to the current user.

**Usage**

```
Application.all(env = solvebio:::solveEnv, ...)
```

**Arguments**

env	(optional) Custom client environment.
...	(optional) Additional query parameters.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Application.all()  
  
## End(Not run)
```

---

Application.create     *Application.create*

---

### Description

Create a new SolveBio application.

### Usage

```
Application.create(name, redirect_uris, env = solvebio:::.solveEnv, ...)
```

### Arguments

name	The name of the application.
redirect_uris	A list of space-separated OAuth2 redirect URIs.
env	(optional) Custom client environment.
...	(optional) Additional application attributes.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
Application.create(  
  name="My new application",  
  redirect_uris="http://localhost:3838/"  
)  
  
## End(Not run)
```

---

Application.delete     *Application.delete*

---

### Description

Delete a specific application from SolveBio.

### Usage

```
Application.delete(client_id, env = solvebio:::.solveEnv)
```

**Arguments**

client\_id      The client ID for the application.  
env            (optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Application.delete("abcd1234")  
  
## End(Not run)
```

---

Application.retrieve    *Application.retrieve*

---

**Description**

Retrieves the metadata about a specific application SolveBio.

**Usage**

```
Application.retrieve(client_id, env = solvebio:::solveEnv)
```

**Arguments**

client\_id      The client ID for the application.  
env            (optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Application.retrieve("abcd1234")  
  
## End(Not run)
```

---

Application.update      *Application.update*

---

**Description**

Updates the attributes of an existing application.

**Usage**

```
Application.update(client_id, env = solvebio:::.solveEnv, ...)
```

**Arguments**

client_id	The client ID for the application.
env	(optional) Custom client environment.
...	Application attributes to change.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:
Application.update(
  "abcd1234",
  name="New app name"
)

## End(Not run)
```

---

Beacon.all      *Beacon.all*

---

**Description**

Retrieves the metadata about all beacons on SolveBio accessible to the current user.

**Usage**

```
Beacon.all(env = solvebio:::.solveEnv, ...)
```

**Arguments**

env	(optional) Custom client environment.
...	(optional) Additional query parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Beacon.all()  
  
## End(Not run)
```

---

Beacon.create

*Beacon.create*

---

## Description

Add a new beacon to an existing beacon set. The beacon set must already exist in order to add beacons.

## Usage

```
Beacon.create(beacon_set_id, vault_object_id, title,  
              env = solvebio:::.solveEnv, ...)
```

## Arguments

beacon_set_id	The ID of the parent beacon set.
vault_object_id	The ID of the vault object (i.e. dataset) queried by the beacon.
title	The title displayed for the beacon.
env	(optional) Custom client environment.
...	(optional) Additional beacon attributes (such as description and params).

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Beacon.create(  
  beacon_set_id="1234",  
  vault_object_id="1234567890",  
  title="My new beacon"  
)  
  
## End(Not run)
```



---

Beacon.delete	<i>Beacon.delete</i>
---------------	----------------------

---

### Description

Delete a specific beacon from SolveBio.

### Usage

```
Beacon.delete(id, env = solvebio:::solveEnv)
```

### Arguments

id	The ID of the beacon.
env	(optional) Custom client environment.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
Beacon.delete("1234567890")  
  
## End(Not run)
```

---

Beacon.query	<i>Beacon.query</i>
--------------	---------------------

---

### Description

Query an individual beacon.

### Usage

```
Beacon.query(id, query, entity_type, env = solvebio:::solveEnv, ...)
```

### Arguments

id	The ID of the beacon.
query	The entity ID or query string.
entity_type	(optional) A valid SolveBio entity type.
env	(optional) Custom client environment.
...	(optional) Additional query parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
Beacon.query(
  id="1234",
  query="BRCA2",
  entity_type="gene"
)

## End(Not run)
```

---

Beacon.retrieve	<i>Beacon.retrieve</i>
-----------------	------------------------

---

## Description

Retrieves the metadata about a specific beacon on SolveBio.

## Usage

```
Beacon.retrieve(id, env = solvebio:::solveEnv)
```

## Arguments

id	The ID of the beacon.
env	(optional) Custom client environment.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
Beacon.retrieve("1234")

## End(Not run)
```

---

Beacon.update	<i>Beacon.update</i>
---------------	----------------------

---

### Description

Updates the attributes of an existing beacon.

### Usage

```
Beacon.update(id, env = solvebio:::.solveEnv, ...)
```

### Arguments

id	The ID of the beacon to update.
env	(optional) Custom client environment.
...	Beacon attributes to change.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
Beacon.update(  
  id="1234",  
  title="New Beacon Title"  
)  
  
## End(Not run)
```

---

BeaconSet.all	<i>BeaconSet.all</i>
---------------	----------------------

---

### Description

Retrieves the metadata about all beacon sets on SolveBio accessible to the current user.

### Usage

```
BeaconSet.all(env = solvebio:::.solveEnv, ...)
```

### Arguments

env	(optional) Custom client environment.
...	(optional) Additional query parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
BeaconSet.all()  
  
## End(Not run)
```

---

BeaconSet.create	<i>BeaconSet.create</i>
------------------	-------------------------

---

## Description

Create a new beacon set.

## Usage

```
BeaconSet.create(title, description, is_shared = FALSE,  
  env = solvebio:::solveEnv, ...)
```

## Arguments

title	The title displayed for the beacon set.
description	(optional) An optional description for the new beacon set.
is_shared	If TRUE, everyone else in your account will be able to see and query the beacon set, but will not be able to edit it. (Default: FALSE)
env	(optional) Custom client environment.
...	(optional) Additional beacon set attributes.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
BeaconSet.create(  
  title="My new beacon set",  
)  
  
## End(Not run)
```

---

BeaconSet.delete	<i>BeaconSet.delete</i>
------------------	-------------------------

---

### Description

Delete a specific beacon set (including all its beacons) from SolveBio.

### Usage

```
BeaconSet.delete(id, env = solvebio:::.solveEnv)
```

### Arguments

id	The ID of the beacon set.
env	(optional) Custom client environment.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
BeaconSet.delete("1234")  
  
## End(Not run)
```

---

BeaconSet.query	<i>BeaconSet.query</i>
-----------------	------------------------

---

### Description

Query a beacon set (i.e. all the beacons within a beacon set).

### Usage

```
BeaconSet.query(id, query, entity_type, env = solvebio:::.solveEnv, ...)
```

### Arguments

id	The ID of the beacon set.
query	The entity ID or query string.
entity_type	(optional) A valid SolveBio entity type.
env	(optional) Custom client environment.
...	(optional) Additional query parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
BeaconSet.query(
  id="1234",
  query="BRCA2",
  entity_type="gene"
)

## End(Not run)
```

---

BeaconSet.retrieve      *BeaconSet.retrieve*

---

## Description

Retrieves the metadata about a specific beacon set on SolveBio.

## Usage

```
BeaconSet.retrieve(id, env = solvebio:::solveEnv)
```

## Arguments

id	The ID of the beacon set.
env	(optional) Custom client environment.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
BeaconSet.retrieve("1234")

## End(Not run)
```

---

BeaconSet.update	<i>BeaconSet.update</i>
------------------	-------------------------

---

### Description

Updates the attributes of an existing beacon set.

### Usage

```
BeaconSet.update(id, env = solvebio:::.solveEnv, ...)
```

### Arguments

id	The ID of the beacon set to update.
env	(optional) Custom client environment.
...	Beacon set attributes to change.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
BeaconSet.update(  
  id="1234",  
  title="New Beacon Set Title"  
)  
  
## End(Not run)
```

---

createEnv	<i>createEnv</i>
-----------	------------------

---

### Description

Create a new SolveBio environment.

### Usage

```
createEnv(token, token_type = "Token", host = "https://api.solvebio.com")
```

**Arguments**

token            A SolveBio API key or OAuth2 token  
token\_type      SolveBio token type (default: Token)  
host            (optional) The SolveBio API host (default: <https://api.solvebio.com>)

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
env <- createEnv("MyAPIkey")  
User.retrieve(env = myEnv)  
  
## End(Not run)
```

---

Dataset.all

*Dataset.all*

---

**Description**

Retrieves the metadata about datasets on SolveBio.

**Usage**

```
Dataset.all(env = solvebio:::.solveEnv, ...)
```

**Arguments**

env            (optional) Custom client environment.  
...            (optional) Additional query parameters (e.g. page).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Dataset.all()  
  
## End(Not run)
```



---

Dataset.count	<i>Dataset.count</i>
---------------	----------------------

---

### Description

Returns the total number of records for a given SolveBio dataset.

### Usage

```
Dataset.count(id, env = solvebio:::.solveEnv, ...)
```

### Arguments

id	The ID of a SolveBio dataset, or a Dataset object.
env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. filters, limit, offset).

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:
dataset <- Dataset.get_by_full_path("solvebio:public:/ClinVar/3.7.4-2017-01-30/Variants-GRCh37")
Dataset.count(dataset)
Dataset.count(dataset, filters='[["gene_symbol", "BRCA2"]]' )

## End(Not run)
```

---

Dataset.create	<i>Dataset.create</i>
----------------	-----------------------

---

### Description

Create an empty SolveBio dataset.

### Usage

```
Dataset.create(vault_id, vault_parent_object_id, name,
  env = solvebio:::.solveEnv, ...)
```

**Arguments**

vault\_id            The ID of the vault.  
 vault\_parent\_object\_id            The parent object (folder) ID in the vault.  
 name                The name of the dataset in the parent folder.  
 env                 (optional) Custom client environment.  
 ...                 (optional) Additional dataset attributes.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:
Dataset.create(vault_id=vault$id, vault_parent_object_id=NULL, name="My Dataset")

## End(Not run)
```

---

Dataset.data

*Dataset.data*

---

**Description**

Returns one page of documents from a SolveBio dataset and processes the response.

**Usage**

```
Dataset.data(id, filters, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id                 The ID of a SolveBio dataset, or a Dataset object.  
 filters            (optional) Query filters.  
 env                (optional) Custom client environment.  
 ...                (optional) Additional query parameters (e.g. limit, offset).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:
Dataset.data("1234567890")

## End(Not run)
```

---

Dataset.delete	<i>Dataset.delete</i>
----------------	-----------------------

---

**Description**

Delete a specific dataset from SolveBio.

**Usage**

```
Dataset.delete(id, env = solvebio:::.solveEnv)
```

**Arguments**

id	String The ID of a SolveBio dataset
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Dataset.delete("1234567890")  
  
## End(Not run)
```

---

Dataset.facets	<i>Dataset.facets</i>
----------------	-----------------------

---

**Description**

Retrieves aggregated statistics or term counts for one or more fields in a SolveBio dataset. Returns a list of data frames, one for each requested facet.

**Usage**

```
Dataset.facets(id, facets, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id	The ID of a SolveBio dataset, or a Dataset object.
facets	A list of one or more field facets.
env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. filters, limit, offset).

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Dataset.facets("1234567890", list("clinical_significance", "gene_symbol"))  
  
## End(Not run)
```

---

Dataset.get\_by\_full\_path

*Dataset.get\_by\_full\_path*

---

## Description

A helper function to get a dataset by its full path.

## Usage

```
Dataset.get_by_full_path(full_path, env = solvebio::.solveEnv)
```

## Arguments

full_path	A valid full path to a dataset.
env	(optional) Custom client environment.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Dataset.get_by_full_path("solvebio:public:/ClinVar/3.7.4-2017-01-30/Variants-GRCh37")  
  
## End(Not run)
```

---

Dataset.get\_or\_create\_by\_full\_path  
*Dataset.get\_or\_create\_by\_full\_path*

---

### Description

A helper function to get or create a dataset by its full path.

### Usage

```
Dataset.get_or_create_by_full_path(full_path, env = solvebio:::.solveEnv, ...)
```

### Arguments

`full_path`      A valid full path to a dataset.  
`env`              (optional) Custom client environment.  
`...`             Additional dataset creation parameters.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
Dataset.get_or_create_by_full_path("MyVault:/folder/sub-folder/dataset")  
  
## End(Not run)
```

---

Dataset.query      *Dataset.query*

---

### Description

Queries a SolveBio dataset and returns an R data frame containing all records (up to 500,000). Returns a single page of results otherwise (default).

### Usage

```
Dataset.query(id, paginate = FALSE, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id	The ID of a SolveBio dataset, or a Dataset object.
paginate	When set to TRUE, retrieves up to 500,000 records.
env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. filters, limit, offset).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Dataset.query("12345678790", paginate=TRUE)  
  
## End(Not run)
```

---

Dataset.retrieve	<i>Dataset.retrieve</i>
------------------	-------------------------

---

**Description**

Retrieves the metadata about a specific dataset from SolveBio.

**Usage**

```
Dataset.retrieve(id, env = solvebio:::.solveEnv)
```

**Arguments**

id	String The ID of a SolveBio dataset
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Dataset.retrieve("1234567890")  
  
## End(Not run)
```

---

Dataset.template	<i>Dataset.template</i>
------------------	-------------------------

---

**Description**

Retrieves the template for a dataset.

**Usage**

```
Dataset.template(id, env = solvebio:::.solveEnv)
```

**Arguments**

id	String The ID of a SolveBio dataset
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Dataset.template("1234567890")  
  
## End(Not run)
```

---

Dataset.update	<i>Dataset.update</i>
----------------	-----------------------

---

**Description**

Updates the attributes of an existing dataset.

**Usage**

```
Dataset.update(id, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id	The ID of the dataset to update.
env	(optional) Custom client environment.
...	Dataset attributes to change.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
Dataset.update(
  id="1234",
  name="New Dataset Name",
)

## End(Not run)
```

---

DatasetCommit.all      *DatasetCommit.all*

---

## Description

Retrieves the metadata about all dataset commits on SolveBio.

## Usage

```
DatasetCommit.all(env = solvebio:::solveEnv, ...)
```

## Arguments

env                    (optional) Custom client environment.  
...                    (optional) Additional query parameters (e.g. page).

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
DatasetCommit.all()

## End(Not run)
```



---

DatasetCommit.delete    *DatasetCommit.delete*

---

### Description

Deletes a specific dataset commit on SolveBio.

### Usage

```
DatasetCommit.delete(id, env = solvebio:::.solveEnv)
```

### Arguments

id	String The ID or full name of a SolveBio dataset commit.
env	(optional) Custom client environment.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
DatasetCommit.delete(<ID>)  
  
## End(Not run)
```

---

DatasetCommit.retrieve  
*DatasetCommit.retrieve*

---

### Description

Retrieves the metadata about a specific dataset commit on SolveBio.

### Usage

```
DatasetCommit.retrieve(id, env = solvebio:::.solveEnv)
```

### Arguments

id	String The ID of a SolveBio dataset commit.
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetCommit.retrieve(<ID>)  
  
## End(Not run)
```

---

DatasetExport.all	<i>DatasetExport.all</i>
-------------------	--------------------------

---

**Description**

Retrieves the metadata about all dataset exports on SolveBio.

**Usage**

```
DatasetExport.all(env = solvebio:::solveEnv, ...)
```

**Arguments**

env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. page).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetExport.all()  
  
## End(Not run)
```

---

DatasetExport.create    *DatasetExport.create*

---

### Description

Create a new dataset export.

### Usage

```
DatasetExport.create(dataset_id, format = "json", params = list(),
  env = solvebio:::solveEnv, ...)
```

### Arguments

dataset_id	The target dataset ID.
format	(optional) The export format (default: json).
params	(optional) Query parameters for the export.
env	(optional) Custom client environment.
...	(optional) Additional dataset export parameters.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:
DatasetExport.create(dataset_id=<ID>, format='json', params=list(fields=c("field_1"), limit=100))
## End(Not run)
```

---

DatasetExport.delete    *DatasetExport.delete*

---

### Description

Deletes a specific dataset export on SolveBio.

### Usage

```
DatasetExport.delete(id, env = solvebio:::solveEnv)
```

**Arguments**

id                   String The ID of a SolveBio dataset export.  
env                   (optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetExport.delete(<ID>)  
  
## End(Not run)
```

---

DatasetExport.retrieve

*DatasetExport.retrieve*

---

**Description**

Retrieves the metadata about a specific dataset export on SolveBio.

**Usage**

```
DatasetExport.retrieve(id, env = solvebio:::.solveEnv)
```

**Arguments**

id                   String The ID of a SolveBio dataset export.  
env                   (optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetExport.retrieve(<ID>)  
  
## End(Not run)
```

---

DatasetField.all      *DatasetField.all*

---

**Description**

Retrieves the metadata about all dataset fields on SolveBio.

**Usage**

```
DatasetField.all(env = solvebio:::.solveEnv, ...)
```

**Arguments**

env                    (optional) Custom client environment.  
...                    (optional) Additional query parameters (e.g. page).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetField.all()  
  
## End(Not run)
```

---

DatasetField.create      *DatasetField.create*

---

**Description**

Create a new dataset field.

**Usage**

```
DatasetField.create(dataset_id, name, data_type = "auto",  
  env = solvebio:::.solveEnv, ...)
```

**Arguments**

dataset\_id            The dataset ID.  
name                   The name of the dataset field.  
data\_type             (optional) The data type for the field (default: auto).  
env                    (optional) Custom client environment.  
...                    (optional) Additional dataset import attributes.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
DatasetField.create(dataset_id=<ID>, name="my_field", title="My Field", data_type="string")  
  
## End(Not run)
```

---

DatasetField.facets     *DatasetField.facets*

---

## Description

Returns the facets for a given dataset field.

## Usage

```
DatasetField.facets(id, env = solvebio:::.solveEnv, ...)
```

## Arguments

id	String The ID of a dataset field.
env	(optional) Custom client environment.
...	(optional) Additional query parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
DatasetField.facets(691)  
  
## End(Not run)
```

---

DatasetField.retrieve *DatasetField.retrieve*

---

**Description**

Retrieves the metadata about a specific dataset field.

**Usage**

```
DatasetField.retrieve(id, env = solvebio:::.solveEnv)
```

**Arguments**

id	String The ID of a dataset field.
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetField.retrieve(691)  
  
## End(Not run)
```

---

DatasetField.update *DatasetField.update*

---

**Description**

Updates the attributes of an existing dataset field. NOTE: The data\_type of a field cannot be changed.

**Usage**

```
DatasetField.update(id, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id	The ID of the dataset field to update.
env	(optional) Custom client environment.
...	Dataset field attributes to change.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
DatasetField.update(
  id="1234",
  title="New Field Title"
)

## End(Not run)
```

---

DatasetImport.all      *DatasetImport.all*

---

## Description

Retrieves the metadata about all dataset imports on SolveBio.

## Usage

```
DatasetImport.all(env = solvebio:::.solveEnv, ...)
```

## Arguments

env                    (optional) Custom client environment.  
...                    (optional) Additional query parameters (e.g. page).

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
DatasetImport.all()

## End(Not run)
```



---

DatasetImport.create *DatasetImport.create*

---

### Description

Create a new dataset import. Either an object\_id, manifest, or data\_records is required.

### Usage

```
DatasetImport.create(dataset_id, commit_mode = "append",  
  env = solvebio:::.solveEnv, ...)
```

### Arguments

dataset_id	The target dataset ID.
commit_mode	(optional) The commit mode (default: append).
env	(optional) Custom client environment.
...	(optional) Additional dataset import attributes.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
DatasetImport.create(dataset_id=<ID>, upload_id=<ID>)  
  
## End(Not run)
```

---

DatasetImport.delete *DatasetImport.delete*

---

### Description

Deletes a specific dataset import on SolveBio.

### Usage

```
DatasetImport.delete(id, env = solvebio:::.solveEnv)
```

### Arguments

id	String The ID of a SolveBio dataset import.
env	(optional) Custom client environment.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
DatasetImport.delete(<ID>)  
  
## End(Not run)
```

---

DatasetImport.retrieve

*DatasetImport.retrieve*

---

## Description

Retrieves the metadata about a specific dataset import on SolveBio.

## Usage

```
DatasetImport.retrieve(id, env = solvebio:::.solveEnv)
```

## Arguments

id	String The ID of a SolveBio dataset import.
env	(optional) Custom client environment.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
DatasetImport.retrieve(<ID>)  
  
## End(Not run)
```



**Arguments**

source_id	The source dataset ID.
target_id	The target dataset ID.
commit_mode	(optional) The commit mode (default: append).
source_params	(optional) The query parameters used on the source dataset.
target_fields	(optional) A list of valid dataset fields to add or override in the target dataset.
include_errors	(optional) If TRUE, a new field (_errors) will be added to each record containing expression evaluation errors (default: FALSE).
env	(optional) Custom client environment.
...	(optional) Additional dataset migration attributes.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetMigration.create(dataset_id=<ID>, upload_id=<ID>)  
  
## End(Not run)
```

---

DatasetMigration.delete  
*DatasetMigration.delete*

---

**Description**

Deletes specific dataset migration on SolveBio.

**Usage**

```
DatasetMigration.delete(id, env = solvebio:::solveEnv)
```

**Arguments**

id	String The ID of a SolveBio dataset migration.
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetMigration.delete(<ID>)  
  
## End(Not run)
```

---

```
DatasetMigration.retrieve  
  DatasetMigration.retrieve
```

---

**Description**

Retrieves the metadata about a specific dataset migration on SolveBio.

**Usage**

```
DatasetMigration.retrieve(id, env = solvebio:::solveEnv)
```

**Arguments**

id	String The ID of a SolveBio dataset migration.
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
DatasetMigration.retrieve(<ID>)  
  
## End(Not run)
```

---

Expression.evaluate    *Expression.evaluate*

---

### Description

Evaluate a SolveBio expression.

### Usage

```
Expression.evaluate(expression, data_type = "string", is_list = FALSE,  
  data = NULL, raw = FALSE, env = solvebio::.solveEnv)
```

### Arguments

expression	The SolveBio expression string.
data_type	The data type to cast the expression result (default: string).
is_list	Set to TRUE if the result is expected to be a list (default: FALSE).
data	Variables used in the expression (default: NULL).
raw	Set to TRUE to return the raw response (default: FALSE).
env	(optional) Custom client environment.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
Expression.evaluate("1 + 1", data_type="integer", is_list=FALSE)  
  
## End(Not run)
```

---

login                    *login*

---

### Description

Store and verify your SolveBio credentials.

### Usage

```
login(api_key, api_host, env = solvebio::.solveEnv)
```

**Arguments**

api\_key            Your SolveBio API key  
api\_host           SolveBio API host (default: <https://api.solvebio.com>)  
env                (optional) The R environment used to store API credentials.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
login()  
  
## End(Not run)
```

---

Object.all

*Object.all*

---

**Description**

Retrieves the metadata about all objects on SolveBio accessible to the current user.

**Usage**

```
Object.all(env = solvebio:::solveEnv, ...)
```

**Arguments**

env                (optional) Custom client environment.  
...                (optional) Additional query parameters.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Object.all()  
  
## End(Not run)
```

---

Object.create	<i>Object.create</i>
---------------	----------------------

---

### Description

Create a SolveBio object.

### Usage

```
Object.create(vault_id, parent_object_id, object_type, filename,  
             env = solvebio:::solveEnv, ...)
```

### Arguments

<code>vault_id</code>	The target vault ID.
<code>parent_object_id</code>	The ID of the parent object (folder) or NULL for the vault root.
<code>object_type</code>	The type of object (i.e. "folder").
<code>filename</code>	The filename (i.e. the name) of the object.
<code>env</code>	(optional) Custom client environment.
<code>...</code>	(optional) Additional object attributes.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
Object.create(  
  vault_id="1234567890",  
  parent_object_id=NULL,  
  object_type="folder",  
  filename="My Folder"  
)  
  
## End(Not run)
```



---

Object.delete	<i>Object.delete</i>
---------------	----------------------

---

**Description**

Delete a specific object from SolveBio.

**Usage**

```
Object.delete(id, env = solvebio:::.solveEnv)
```

**Arguments**

id	The ID of the object.
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Object.delete("1234567890")  
  
## End(Not run)
```

---

Object.get_by_full_path	<i>Object.get_by_full_path</i>
-------------------------	--------------------------------

---

**Description**

A helper function to get an object on SolveBio by its full path.

**Usage**

```
Object.get_by_full_path(full_path, env = solvebio:::.solveEnv, ...)
```

**Arguments**

full_path	The full path to the object.
env	(optional) Custom client environment.
...	(optional) Additional query parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Object.get_by_full_path("solvebio:public:/ClinVar")  
  
## End(Not run)
```

---

Object.get\_by\_path      *Object.get\_by\_path*

---

## Description

A helper function to get an object on SolveBio by its path. Used as a pass-through function from some Vault methods.

## Usage

```
Object.get_by_path(path, env = solvebio:::solveEnv, ...)
```

## Arguments

path	The path to the object, relative to a vault.
env	(optional) Custom client environment.
...	(optional) Additional query parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Object.get_by_path("/ClinVar")  
  
## End(Not run)
```

---

```
Object.get_download_url  
    Object.get_download_url
```

---

### Description

Helper method to get the download URL for a file object.

### Usage

```
Object.get_download_url(id, env = solvebio:::.solveEnv)
```

### Arguments

id	The ID of the object.
env	(optional) Custom client environment.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
Object.get_download_url("1234567890")  
  
## End(Not run)
```

---

```
Object.retrieve    Object.retrieve
```

---

### Description

Retrieves the metadata about a specific object on SolveBio.

### Usage

```
Object.retrieve(id, env = solvebio:::.solveEnv)
```

### Arguments

id	The ID of the object.
env	(optional) Custom client environment.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Object.retrieve("1234567890")  
  
## End(Not run)
```

---

Object.update	<i>Object.update</i>
---------------	----------------------

---

## Description

Updates the attributes of an existing vault object.

## Usage

```
Object.update(id, env = solvebio:::solveEnv, ...)
```

## Arguments

id	The ID of the vault to update.
env	(optional) Custom client environment.
...	Object attributes to change.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Object.update(  
  id="1234",  
  filename="New Name",  
)  
  
## End(Not run)
```

---

Object.upload\_file      *Object.upload\_file*

---

**Description**

Upload a local file to a vault on SolveBio. The vault path provided is the parent directory for uploaded file.

**Usage**

```
Object.upload_file(local_path, vault_id, vault_path, filename,
  env = solvebio:::solveEnv)
```

**Arguments**

local_path	The path to the local file
vault_id	The SolveBio vault ID
vault_path	The remote path in the vault
filename	(optional) The filename for the uploaded file in the vault (default: the basename of the local_path)
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:
Object.upload_file("my_file.json.gz", vault$id, "/parent/directory/")

## End(Not run)
```

---

protectedServer      *protectedServer*

---

**Description**

Wraps an existing Shiny server in an OAuth2 flow.

**Usage**

```
protectedServer(server, client_id, client_secret,
  base_url = "https://my.solvebio.com")
```

**Arguments**

server	Your original Shiny server function.
client_id	Your application's client ID.
client_secret	(optional) Your application's client secret.
base_url	(optional) Override the default login host (default: <a href="https://my.solvebio.com">https://my.solvebio.com</a> ).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:
protectedServer(
  server=server,
  client_id="abcd1234"
)

## End(Not run)
```

---

User.retrieve

*User.retrieve*

---

**Description**

Retrieves information about the current user.

**Usage**

```
User.retrieve(env = solvebio:::.solveEnv)
```

**Arguments**

env (optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:
User.retrieve()

## End(Not run)
```

---

`Vault.all`*Vault.all*

---

**Description**

Retrieves the metadata about all accessible vaults.

**Usage**

```
Vault.all(..., env = solvebio:::.solveEnv)
```

**Arguments**

... (optional) Additional query parameters (e.g. limit, offset).  
env (optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Vault.all()  
  
## End(Not run)
```

---

`Vault.create`*Vault.create*

---

**Description**

Create a new SolveBio vault.

**Usage**

```
Vault.create(name, env = solvebio:::.solveEnv, ...)
```

**Arguments**

name The unique name of the vault.  
env (optional) Custom client environment.  
... (optional) Additional vault attributes.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Vault.create(name="my-domain:MyVault")  
  
## End(Not run)
```

---

Vault.create\_dataset    *Vault.create\_dataset*

---

## Description

Create a new dataset in a vault.

## Usage

```
Vault.create_dataset(id, path, name, env = solvebio:::solveEnv, ...)
```

## Arguments

id	The ID of the vault.
path	The path to the dataset, within the vault.
name	The name (filename) for the dataset.
env	(optional) Custom client environment.
...	(optional) Additional dataset creation parameters.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
vault = Vault.get_personal_vault()  
Vault.create_dataset(vault$id, path="/", name="My Dataset")  
  
## End(Not run)
```



---

Vault.create\_folder     *Vault.create\_folder*

---

### Description

Create a new folder in a vault.

### Usage

```
Vault.create_folder(id, path, recursive = FALSE, env = solvebio:::solveEnv, ...)
```

### Arguments

id	The ID of the vault.
path	The path to the folder, within the vault.
recursive	Create all parent directories that do not yet exist (default: FALSE).
env	(optional) Custom client environment.
...	(optional) Additional folder creation parameters.

### References

<https://docs.solvebio.com/>

### Examples

```
## Not run:  
vault = Vault.get_personal_vault()  
Vault.create_folder(vault$id, "/My Folder")  
  
## End(Not run)
```

---

Vault.datasets     *Vault.datasets*

---

### Description

Retrieves all datasets in a specific vault.

### Usage

```
Vault.datasets(id, env = solvebio:::solveEnv, ...)
```

**Arguments**

id                    The ID of the vault.  
env                    (optional) Custom client environment.  
...                    (optional) Additional query parameters (e.g. limit, offset).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
vault = Vault.get_personal_vault()  
Vault.datasets(vault$id)  
  
## End(Not run)
```

---

Vault.delete

*Vault.delete*

---

**Description**

Delete a specific vault from SolveBio. This operation cannot be undone.

**Usage**

```
Vault.delete(id, env = solvebio:::.solveEnv)
```

**Arguments**

id                    String The ID of a SolveBio vault.  
env                    (optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Vault.delete("1")  
  
## End(Not run)
```

---

Vault.files	<i>Vault.files</i>
-------------	--------------------

---

**Description**

Retrieves all files in a specific vault.

**Usage**

```
Vault.files(id, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id	The ID of the vault.
env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. limit, offset).

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
vault = Vault.get_personal_vault()  
Vault.files(vault$id)  
  
## End(Not run)
```

---

Vault.folders	<i>Vault.folders</i>
---------------	----------------------

---

**Description**

Retrieves all folders in a specific vault.

**Usage**

```
Vault.folders(id, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id	The ID of the vault.
env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. limit, offset).

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
vault = Vault.get_personal_vault()  
Vault.folders(vault$id)  
  
## End(Not run)
```

---

```
Vault.get_by_full_path  
Vault.get_by_full_path
```

---

## Description

Retrieves a specific vault by its full path (domain:vault).

## Usage

```
Vault.get_by_full_path(full_path, verbose = TRUE,  
  env = solvebio::.solveEnv)
```

## Arguments

full_path	The full path of a SolveBio vault.
verbose	Print warning/error messages (default: TRUE).
env	(optional) Custom client environment.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Vault.get_by_full_path("SolveBio:Public")  
  
## End(Not run)
```

---

```
Vault.get_or_create_by_full_path  
    Vault.get_or_create_by_full_path
```

---

**Description**

Retrieves or creates a specific vault by its full path (domain:vault).

**Usage**

```
Vault.get_or_create_by_full_path(full_path, env = solvebio:::.solveEnv, ...)
```

**Arguments**

full_path	The full path of a SolveBio vault.
env	(optional) Custom client environment.
...	(optional) Additional parameters.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Vault.get_or_create_by_full_path("My New Vault")  
  
## End(Not run)
```

---

```
Vault.get_personal_vault  
    Vault.get_personal_vault
```

---

**Description**

Retrieves the current users"s personal, private vault.

**Usage**

```
Vault.get_personal_vault(env = solvebio:::.solveEnv)
```

**Arguments**

env	(optional) Custom client environment.
-----	---------------------------------------

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
Vault.get_personal_vault()  
  
## End(Not run)
```

---

Vault.objects	<i>Vault.objects</i>
---------------	----------------------

---

## Description

Retrieves all objects in a specific vault.

## Usage

```
Vault.objects(id, env = solvebio:::solveEnv, ...)
```

## Arguments

id	The ID of the vault.
env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. limit, offset).

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:  
vault = Vault.get_personal_vault()  
Vault.objects(vault$id)  
  
## End(Not run)
```

---

Vault.retrieve	<i>Vault.retrieve</i>
----------------	-----------------------

---

**Description**

Retrieves the metadata about a specific SolveBio vault.

**Usage**

```
Vault.retrieve(id, env = solvebio:::.solveEnv)
```

**Arguments**

id	String The ID of a SolveBio vault
env	(optional) Custom client environment.

**References**

<https://docs.solvebio.com/>

**Examples**

```
## Not run:  
Vault.retrieve("1234567890")  
  
## End(Not run)
```

---

Vault.search	<i>Vault.search</i>
--------------	---------------------

---

**Description**

Search for objects in a specific vault.

**Usage**

```
Vault.search(id, query, env = solvebio:::.solveEnv, ...)
```

**Arguments**

id	The ID of the vault.
query	The search query.
env	(optional) Custom client environment.
...	(optional) Additional query parameters (e.g. limit, offset).

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
vault = Vault.get_personal_vault()
Vault.search('test')

## End(Not run)
```

---

Vault.update

*Vault.update*

---

## Description

Updates the attributes of an existing vault.

## Usage

```
Vault.update(id, env = solvebio:::solveEnv, ...)
```

## Arguments

id	The ID of the vault to update.
env	(optional) Custom client environment.
...	Vault attributes to change.

## References

<https://docs.solvebio.com/>

## Examples

```
## Not run:
Vault.update(
  id="1234",
  name="New Vault Name",
)

## End(Not run)
```



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