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# **python-genomespaceclient documentation**

*Release 0.1.0*

**GVL Project**

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This is a python client for the GenomeSpace API. There's a Python API (the `genomespaceclient` module), and a command-line script (`genomespace`).



# CHAPTER 1

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## Installation

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Install the latest release from PyPi:

```
pip install python-genomespaceclient
```





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### Commandline usage example

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```
# Create remote folder, including all intermediate paths
genomospace -u <username> -p <password> mkdir -p https://dm.genomospace.org/
↳datamanager/v1.0/file/Home/MyBucket/f1/f2/

# copy local files recursively to remote location
genomospace -u <username> -p <password> cp -R /tmp/ https://dm.genomospace.org/
↳datamanager/v1.0/file/Home/MyBucket/

# copy local files matching pattern to remote location - note that paths with \_
↳wildcards must be enclosed in quotes
genomospace -u <username> -p <password> cp '/tmp/*.txt' https://dm.genomospace.org/
↳datamanager/v1.0/file/Home/MyBucket/

# list remote files
genomospace -u <username> -p <password> ls https://dm.genomospace.org/datamanager/v1.
↳0/file/Home/MyBucket/

# move remote file to new location
genomospace -u <username> -p <password> mv https://dm.genomospace.org/datamanager/v1.
↳0/file/Home/MyBucket/hello.txt https://dm.genomospace.org/datamanager/v1.0/file/
↳Home/MyBucket/world.txt

# download remote files matching pattern, with verbose output
genomospace -vvv -u <username> -p <password> mv https://dm.genomospace.org/
↳datamanager/v1.0/file/Home/MyBucket/*.txt /tmp/

# delete remote file
genomospace -u <username> -p <password> rm https://dm.genomospace.org/datamanager/v1.
↳0/file/Home/MyBucket/world.txt
```



## CHAPTER 3

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### Python usage example

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```
from genomespaceclient import GenomeSpaceClient

client = GenomeSpaceClient(username="<username>", password="<password>")
client.mkdir("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/f1/f2".  
↳ create_path=True)
client.copy("/tmp/", "https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/  
↳", recurse=True)
client.list("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/")
client.move("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/hello.txt  
↳", "https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/world.txt")
client.copy("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/*.txt", "  
↳ tmp/")
client.delete("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/*.txt")
```



Wildcard copying syntax is the same as unix path globbing, except that the ‘?’ symbol is not supported (This is because the ‘?’ is a reserved character in a URL)

## 4.1 Documentation

### 4.1.1 API reference

This section contains the API documentation for the GenomeSpace client.

#### genomespaceclient package

#### genomespaceclient module

**class** genomespaceclient.client.GSAceObject (*permission, sid, ace\_id=None*)

Bases: object

See: <http://www.genomespace.org/support/api/restful-access-to-dm#ace>

**\_\_init\_\_** (*permission, sid, ace\_id=None*)

Initialize self. See help(type(self)) for accurate signature.

**class** genomespaceclient.client.GSAclObject (*object\_id, object\_type*)

Bases: object

See: <http://www.genomespace.org/support/api/restful-access-to-dm#acl>

**\_\_init\_\_** (*object\_id, object\_type*)

Initialize self. See help(type(self)) for accurate signature.

**class** genomespaceclient.client.GSDataFormat (*name, url, file\_extension, description*)

Bases: object

See: [http://www.genomespace.org/support/api/restful-access-to-dm#appendix\\_c](http://www.genomespace.org/support/api/restful-access-to-dm#appendix_c)

`__init__` (*name, url, file\_extension, description*)  
Initialize self. See `help(type(self))` for accurate signature.

**class** `genomesspaceclient.client.GSDirectoryListing` (*contents, directory*)

Bases: `object`

See: [http://www.genomesspace.org/support/api/restful-access-to-dm#appendix\\_b](http://www.genomesspace.org/support/api/restful-access-to-dm#appendix_b)

`__init__` (*contents, directory*)  
Initialize self. See `help(type(self))` for accurate signature.

**class** `genomesspaceclient.client.GSEffectiveAcl` (*access\_control\_entries, effective\_acl\_object, effective\_acl\_id=None*)

Bases: `object`

See: [http://www.genomesspace.org/support/api/restful-access-to-dm#appendix\\_f](http://www.genomesspace.org/support/api/restful-access-to-dm#appendix_f)

`__init__` (*access\_control\_entries, effective\_acl\_object, effective\_acl\_id=None*)  
Initialize self. See `help(type(self))` for accurate signature.

**class** `genomesspaceclient.client.GSFileMetadata` (*name, path, url, parentUrl, size, owner, is\_directory, is\_link, target\_path, last\_modified, data\_format, available\_data\_formats, effective\_acl*)

Bases: `object`

See: [http://www.genomesspace.org/support/api/restful-access-to-dm#appendix\\_a](http://www.genomesspace.org/support/api/restful-access-to-dm#appendix_a)

`__init__` (*name, path, url, parentUrl, size, owner, is\_directory, is\_link, target\_path, last\_modified, data\_format, available\_data\_formats, effective\_acl*)  
Initialize self. See `help(type(self))` for accurate signature.

**class** `genomesspaceclient.client.GSSidObject` (*name, sid\_type, sid\_id=None*)

Bases: `object`

See: <http://www.genomesspace.org/support/api/restful-access-to-dm#sid>

`__init__` (*name, sid\_type, sid\_id=None*)  
Initialize self. See `help(type(self))` for accurate signature.

**class** `genomesspaceclient.client.GenomeSpaceClient` (*username=None, password=None, token=None*)

Bases: `object`

A simple GenomeSpace client

`__init__` (*username=None, password=None, token=None*)  
Constructs a new GenomeSpace client. A username/password combination or a token must be supplied.

#### Parameters

- **username** (`str`) – GenomeSpace username
- **password** (`str`) – GenomeSpace password
- **token** (`str`) – A GenomeSpace auth token. If supplied, the token will be used instead of the username/password.

**copy** (*source, destination, recurse=False*)  
Copies a file to/from/within GenomeSpace.

E.g. .. code-block:: python

```
client.copy("/tmp/local_file.txt", "https://dm.genomesspace.org/datamanager/v1.0/file/Home/MyBucket/hello.txt")
```

**Parameters**

- **source** (*str*) – Local filename or GenomeSpace URL of source file.
- **destination** (*str*) – Local filename or GenomeSpace URL of destination file.

**delete** (*genomespace\_url*, *recurse=False*)

Deletes a file within a GenomeSpace folder.

E.g. .. code-block:: python

```
client.delete("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/world.txt")
```

**Parameters** **genomespace\_url** (*str*) – GenomeSpace URL of file to delete.

**get\_metadata** (*genomespace\_url*)

Gets metadata information of a genomespace file/folder. See: [http://www.genomespace.org/support/api/restful-access-to-dm#file\\_metadata](http://www.genomespace.org/support/api/restful-access-to-dm#file_metadata)

E.g.

```
client.get_metadata("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket/world.txt")
```

**Parameters** **genomespace\_url** (*str*) – GenomeSpace URL of file to delete.

**Return type** dict

**Returns** a JSON dict in the format documented here: [http://www.genomespace.org/support/api/restful-access-to-dm#appendix\\_b](http://www.genomespace.org/support/api/restful-access-to-dm#appendix_b)

**get\_remaining\_token\_time** (*genomespace\_url*)

Gets the time to live for the gs-token if you have one. If you don't have one, will return 0, as the non-existent token has no time left to live. See: [http://www.genomespace.org/support/api/restful-access-to-identity-server#get\\_token\\_time](http://www.genomespace.org/support/api/restful-access-to-identity-server#get_token_time)

E.g.

```
client.get_remaining_token_time('https://genomespace.genome.edu.au/')
```

**Parameters** **genomespace\_url** (*str*) – GenomeSpace URL.

**Return type** int

**Returns** the time the token has left to live in milliseconds.

**isdir** (*genomespace\_url*)

Returns True if a given genomespace\_url is a directory

**Parameters** **genomespace\_url** (*str*) – GenomeSpace URL of file to delete.

**Return type** bool

**Returns** True if the url is a directory. False otherwise.

**list** (*genomespace\_url*)

Returns a list of files within a GenomeSpace folder.

E.g. .. code-block:: python

```
client.list("https://dm.genomespace.org/datamanager/v1.0/file/Home/MyBucket")
```

**Parameters** `genomesspace_url` (`str`) – GenomeSpace URL of folder to list.

**Return type** `dict`

**Returns** a JSON dict in the format documented here: [http://www.genomesspace.org/support/api/restful-access-to-dm#appendix\\_b](http://www.genomesspace.org/support/api/restful-access-to-dm#appendix_b)

**mkdir** (`genomesspace_url`, `create_path=True`)

Creates a folder at a given location.

E.g. .. code-block:: python

```
client.mkdir("https://dm.genomesspace.org/datamanager/v1.0/file/Home/MyBucket/Folder1")
```

**Parameters**

- **genomesspace\_url** (`str`) – GenomeSpace URL of file to delete.
- **create\_path** (`boolean`) – Create intermediate directories as required.

**move** (`source`, `destination`)

Moves a file within GenomeSpace.

E.g. .. code-block:: python

```
client.move("https://dm.genomesspace.org/datamanager/v1.0/file/Home/MyBucket/hello.txt",  
           "https://dm.genomesspace.org/datamanager/v1.0/file/Home/MyBucket/world.txt")
```

**Parameters**

- **source** – GenomeSpace URL of source file. Cannot be a local file.
- **destination** – Local filename or GenomeSpace URL of destination file. If destination is a local file, the file will be copied to the destination and the source file deleted.

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