
BaseSpacePy Documentation

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Morten Kallberg

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AVAILABLE MODULES

1.1 API

class BaseSpacePy.api.BaseSpaceAPI.**BaseSpaceAPI** (*clientKey, clientSecret, apiServer, version, appSessionId, AccessToken=''*)

The main API class used for all communication with the REST server

appResultFileUpload (*Id, localPath, fileName, directory, contentType, multipart=0*)

Uploads a file associated with an AppResult to BaseSpace and returns the corresponding file object

Parameters

- **Id** – AppResult id.
- **localPath** – The local path to the file to be uploaded.
- **fileName** – The desired filename in the AppResult folder on the BaseSpace server.
- **directory** – The directory the file should be placed in.
- **contentType** – The content-type of the file.

createAppResult (*Id, name, desc, appSessionId=None*)

Create an AppResult object

Parameters

- **Id** – The id for the project in which the AppResult is to be added
- **name** – The name of the AppResult
- **desc** – A description of the AppResult
- **appSessionId** – (Optional) If not appSessionId is used the one used to initialize the BaseSpaceAPI instance

will be used. If appSessionId is set equal an empty string, a new appsession we be created for the

fileDownload (*Id, localDir, name, range=[]*)

Downloads a BaseSpace file to a local directory

Parameters

- **Id** – The file id
- **localDir** – The local directory to place the file in
- **name** – The name of the local file
- **range** – (Optional) The byte range of the file to retrieve (not yet implemented)

filterVariantSet (*Id, Chrom, StartPos, EndPos, Format, queryPars*={'Limit': '100', 'SortBy': 'Position', 'SortDir': 'Asc', 'Offset': '0'})

List the variants in a set of variants. Maximum returned records is 1000

Parameters

- **Id** – The id of the variant file
- **Chrom** – The chromosome of interest
- **StartPos** – The start position of the sequence of interest
- **EndPos** – The start position of the sequence of interest
- **Format** – Set to 'vcf' to get the results as lines in VCF format
- **queryPars** – An (optional) object of type QueryParameters for custom sorting and filtering

getAccess (*obj, accessType*='write', *web*=0, *redirectURL*='', *state*='')

Parameters

- **obj** – The data object we wish to get access to
- **accessType** – (Optional) the type of access (read/write), default is write
- **web** – (Optional) true if the App is web-based, default is false meaning a device based app
- **redirectURL** – (Optional) For the web-based case, a
- **state** – (Optional)

getAccessToken ()

Returns the access-token that was used to initialize the BaseSpaceAPI object.

getAccessibleRunsByUser (*Id, queryPars*={'Limit': '100', 'SortBy': 'Id', 'SortDir': 'Asc', 'Offset': '0'})

Returns a list of accessible runs for the User with id=Id

Parameters

- **Id** – An user id
- **queryPars** – An (optional) object of type QueryParameters for custom sorting and filtering

getAppResultById (*Id*)

Returns an AppResult object corresponding to Id

Parameters **Id** – The Id of the AppResult

getAppResultFiles (*Id, queryPars*={'Limit': '100', 'SortBy': 'Id', 'SortDir': 'Asc', 'Offset': '0'})

Returns a list of File object for the AppResult with id = Id

Parameters

- **Id** – The id of the appresult.
- **queryPars** – An (optional) object of type QueryParameters for custom sorting and filtering

getAppResultsByProject (*Id, queryPars*={'Limit': '100', 'SortBy': 'Id', 'SortDir': 'Asc', 'Offset': '0'}, *statuses*=[])

Returns a list of AppResult object associated with the project with Id

Parameters

- **Id** – The project id
- **queryPars** – An (optional) object of type QueryParameters for custom sorting and filtering

- **statuses** – An (optional) list of AppResult statuses to filter by

getAppSession (*Id*='')

Returns an AppSession instance containing user and data-type the app was triggered by/on :param Id: (Optional) The AppSessionId, id not supplied the AppSessionId used for instantiating the BaseSpaceAPI instance.

Parameters **Id** – (Optional) AppSession id, if not supplied the AppSession id used to initialize the

getAvailableGenomes (*queryParams*={'Limit': '100', 'SortBy': 'Id', 'SortDir': 'Asc', 'Offset': '0'})

Returns a list of all available genomes

Parameters **queryParams** – An (optional) object of type QueryParameters for custom sorting and filtering

getCoverageMetaInfo (*Id*, *Chrom*)

Returns Metadata about coverage as a CoverageMetadata instance

Parameters

- **Id** – he Id of the Bam file
- **Chrom** – Chromosome to query

getFileById (*Id*)

Returns a file object by Id

Parameters **Id** – The id of the file

getFilesBySample (*Id*, *queryParams*={'Limit': '100', 'SortBy': 'Id', 'SortDir': 'Asc', 'Offset': '0'})

Returns a list of File objects associated with sample with Id

Parameters

- **Id** – A Sample id
- **queryParams** – An (optional) object of type QueryParameters for custom sorting and filtering

getGenomeById (*Id*)

Returns an instance of Genome with the specified Id

Parameters **Id** – The genome id

getIntervalCoverage (*Id*, *Chrom*, *StartPos*=None, *EndPos*=None)

Mean coverage levels over a sequence interval

Parameters

- **Id** – Chromosome to query
- **Chrom** – The Id of the resource
- **StartPos** – Get coverage starting at this position. Default is 1
- **EndPos** – Get coverage up to and including this position. Default is StartPos + 1280

:return:CoverageResponse – an instance of CoverageResponse

getProjectById (*Id*)

Request a project object by Id

Parameters **Id** – The Id of the project

getProjectByUser (*Id*, *queryParams*={'Limit': '100', 'SortBy': 'Id', 'SortDir': 'Asc', 'Offset': '0'})

Returns a list available projects for a User with the specified Id

Parameters

- **Id** – The id of the user
- **qp** – An (optional) object of type QueryParameters for custom sorting and filtering

getSampleById (*Id*)

Returns a Sample object

Parameters **Id** – The id of the sample**getSamplesByProject** (*Id, queryParams={ 'Limit': '100', 'SortBy': 'Id', 'SortDir': 'Asc', 'Offset': '0' }*)

Returns a list of samples associated with a project with Id

Parameters

- **Id** – The id of the project
- **queryParams** – An (optional) object of type QueryParameters for custom sorting and filtering

getServerUri ()

Returns the server uri used by this instance

getUserById (*Id*)

Returns the User object corresponding to Id

Parameters **Id** – The Id of the user**getVariantMetadata** (*Id, Format*)

Returns a VariantMetadata object for the variant file

Parameters

- **Id** – The Id of the VCF file
- **Format** – Set to 'vcf' to get the results as lines in VCF format

getVerificationCode (*scope*)

Returns the BaseSpace dictionary containing the verification code and verification url for the user to approve access to a specific data scope.

Corresponding curl call: curlCall = 'curl -d "response_type=device_code" -d "client_id=' + client_key + "' -d "scope=' + scope + "' ' + deviceURL

For details see: <https://developer.basespace.illumina.com/docs/content/documentation/authentication/obtaining-access-tokens>**Parameters** **scope** – The scope that access is requested for**getWebVerificationCode** (*scope, redirectURL, state=''*)

Generates the URL the user should be redirected to for web-based authentication

Parameters

- **scope** – The scope that access is requested for
- **redirectURL** – The redirect URL

State An optional state parameter that will be passed through to the redirect response**obtainAccessToken** (*deviceCode*)

Returns a user specific access token.

Parameters **deviceCode** – The device code returned by the verification code method**setAppSessionState** (*Id, Status, Summary*)

Set the status of an AppResult object

Parameters

- **Id** – The id of the AppResult
- **Status** – The status assignment string must
- **Summary** – The summary string

1.2 Models

1.2.1 Project

class BaseSpacePy.model.Project.**Project**

Represents a BaseSpace Project object.

createAppResult (*api, name, desc, appSessionId=None*)

Return a newly created app result object

Parameters

- **api** – An instance of BaseSpaceAPI
- **name** – The name of the app result
- **desc** – A description of the app result

getAccessStr (*scope='write'*)

Returns the scope-string to used for requesting BaseSpace access to the object

Parameters **scope** – The scope-type that is request (writelread)

getAppResults (*api, statuses=[]*)

Returns a list of AppResult objects.

Parameters

- **api** – An instance of BaseSpaceAPI
- **statuses** – An optional list of statuses

getSamples (*api*)

Returns a list of Sample objects.

Parameters **api** – An instance of BaseSpaceAPI

isInit ()

Is called to test if the Project instance has been initialized.

Throws: ModelNotInitializedException - Indicates the object has not been populated yet.

1.2.2 AppSession and AppResult

class BaseSpacePy.model.AppSession.**AppSession**

AppLaunch contains the data returned

setStatus (*api, Status, Summary*)

Sets the status of the AppSession (note: once set to ‘completed’ or ‘aborted’ no more work can be done to the instance)

Parameters

- **api** – An instance of BaseSpaceAPI

- **Status** – The status value, must be completed, aborted, working, or suspended
- **Summary** – The status summary

class BaseSpacePy.model.AppResult.**AppResult**

getAccessStr (*scope='write'*)

Returns the scope-string to be used for requesting BaseSpace access to the object

Parameters **scope** – The scope-type that is request (writelread)

getFiles (*api, myQp={}*)

Returns a list of file objects

Parameters

- **api** – An instance of BaseSpaceAPI
- **myQp** – (Optional) QueryParameters for sorting and filtering the file list

isInit ()

Is called to test if the Project instance has been initialized

Throws: ModelNotInitializedException - if the instance has not been populated.

uploadFile (*api, localPath, fileName, directory, contentType*)

Uploads a local file to the BaseSpace AppResult

Parameters

- **api** – An instance of BaseSpaceAPI
- **localPath** – The local path of the file
- **fileName** – The filename
- **directory** – The remote directory to upload to
- **contentType** – The content-type of the file

1.2.3 Sample

class BaseSpacePy.model.Sample.**Sample**

Representation of a BaseSpace Sample object.

getAccessStr (*scope='write'*)

Returns the scope-string to used for requesting BaseSpace access to the sample.

Parameters **scope** – The scope type that is request (writelread).

getFiles (*api, myQp={}*)

Returns a list of File objects

Parameters

- **api** – A BaseSpaceAPI instance
- **myQp** – Query parameters to sort and filter the file list by.

isInit ()

Is called to test if the sample instance has been initialized.

Throws: ModelNotInitializedException - Indicated the Id variable is not set.

1.2.4 File

class BaseSpacePy.model.File.**File**

Represents a BaseSpace file object.

downloadFile (*api, localDir, range=[]*)

Download the file object to the specified localDir or a byte range of the file, by specifying the start and stop byte in the range.

Parameters

- **api** – A BaseSpaceAPI with read access on the scope including the file object.
- **loadlDir** – The local directory to place the file in.
- **range** – Specify the start and stop byte of the file chunk that needs retrieved.

filterVariant (*api, Chrom, StartPos, EndPos, q=None*)

Returns a list of Variant objects available in the specified region

Parameters

- **api** – An instance of BaseSpaceAPI
- **Chrom** – Chromosome as a string - for example 'chr2'
- **StartPos** – The start position of region of interest as a string
- **EndPos** – The end position of region of interest as a string
- **q** – An instance of

getCoverageMeta (*api, Chrom*)

Return an object of CoverageMetadata for the selected region

Parameters

- **api** – An instance of BaseSpaceAPI.
- **Chrom** – The chromosome of interest.

getIntervalCoverage (*api, Chrom, StartPos, EndPos*)

Return a coverage object for the specified region and chromosome.

Parameters

- **api** – An instance of BaseSpaceAPI
- **Chrom** – Chromosome as a string - for example 'chr2'
- **StartPos** – The start position of region of interest as a string
- **EndPos** – The end position of region of interest as a string

getVariantMeta (*api*)

Return the the meta info for a VCF file as a VariantInfo object

Parameters **api** – An instance of BaseSpaceAPI

isInit ()

Is called to test if the File instance has been initialized.

Throws: ModelNotInitializedException if the instance has not been populated yet.

isValidFileOption (*filetype*)

Is called to test if the File instance is matches the filetype parameter

Parameters **filetype** – The filetype for coverage or variant requests

1.2.5 QueryParameters

```
class BaseSpacePy.model.QueryParameters.QueryParameters (pars={}, required=['SortBy',  
                                     'Offset', 'Limit', 'SortDir'])
```

The QueryParameters class can be passed as an optional arguments for a specific sorting of list-responses (such as lists of sample, AppResult, or variants)

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