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# **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, samples=[], appSessionId=None*)

Create an AppResult object

### Parameters

- **Id** – The id of the project in which the AppResult is to be added
- **name** – The name of the AppResult
- **desc** – A description of the AppResult
- **samples** – (Optional) The samples
- **appSessionId** – (Optional) If no appSessionId is given, the id used to initialize the BaseSpaceAPI instance

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

**createProject** (*Name*)

Creates a project with the specified name and returns the project object. If a project with this name already exists, the existing project is returned.

**Parameters** **Name** – Name of the project

**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, queryParams={‘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
- **queryParams** – 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, queryParams={‘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
- **queryParams** – 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, queryParams={‘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.
- **queryParams** – An (optional) object of type QueryParameters for custom sorting and filtering

**getAppResultsByProject** (*Id*, *queryParams*={'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
- **queryParams** – An (optional) object of type QueryParameters for custom sorting and filtering
- **statuses** – An (optional) list of AppResult statuses to filter by

**getSession** (*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

**getSessionById** (*id*)

Returns the appSession identified by id

**Parameters** **id** – The id of the appSession

**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

**setTimeout** (*time*)

Specify the timeout in seconds for each request made

**Parameters** **time** – timeout in second

## 1.2 Models

### 1.2.1 Project

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

Represents a BaseSpace Project object.

**createAppResult** (*api, name, desc, appSessionId=None, samples=[]*)

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 be used for requesting BaseSpace access to the object

**Parameters** **scope** – The scope-type that is requested (write/read)

**getAppResults** (*api, myQp={}, 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

**getReferencedSamples** (*api*)

Returns a list of sample objects references by the AppResult. NOTE this method makes one request to REST server per sample

**getReferencedSamplesIds** ()

Return a list of sample ids for the samples referenced.

**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.

**getReferencedAppResults** (*api*)

Return the AppResults referenced by this sample. Note the returned AppResult objects do not have their “References” field set, to get a fully populate AppResult object you must use getAppResultById in BaseSpaceAPI.

**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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