

GOBii

Sequence 1: Full dataset

- Login and get token
- Get the list of datasets
 - Call : /allelematrices
 - Params: Auth token
 - Type: Get
 - Note:
- Submit request for a dataset extraction
 - Call: /allelematrix-search
 - Params: Auth token, MatrixDbId
 - Type: Get
- Check the status of Job
 - Call: /allelematrix-search /status/
 - Params: Auth token, JobId
 - Type: Get
- Download the dataset
 - Call: URL from previous call
 - Params: Auth token, url
 - Type: Get

Sequence 2: Based on external code(sampleId)

- Login and get token
- Submit request for a dataset extraction
 - Call: /allelematrix-search
 - Params: Auth token, markerprofileDbId
 - Type: Get
 - Note:
 - Currently we can get the data for list of Id's.
 - If both the samples have different markers they are joined together and 'N' is filled in that position.
 - If at least one of the externalCode exists, data is returned for it and no error is thrown for the missing.
 - There is no order in the file (not as sampleId's)
 - External code is not returned in the request.
 - Also, from extractor UI when submitting an extract request they are not going to the same endpoint. GOBii end point required us to pass a dataset type where as brapi endpoint doesnot require one. It is assumed that it is codominant-nonnucleotide type always.
- Check the status of Job
 - Call: /allelematrix-search /status/
 - Params: Auth token, JobId
 - Type: Get

- Download the dataset
 - Call: URL from previous call
 - Params: Auth token, url
 - Type: Get

BMS

Sequence 1: Full Trial

- Login and get a token
- Get the list of crops
 - Call: / crops
 - Params: Auth token
 - Type: Get
- Get studies list
 - Call: / trials
 - Params: Auth token, crop, pageNumber
 - Type: Get
- Get Study Data
 - Call: / studies/{studyDbId}/table
 - Params: Auth token, crop, studyDbId
 - Type: Get

(Not a brapi call might get deprecated)

 - Call: /phenotypes-search/{studyDbId}/
 - Params: Auth token, crop, studyDbId
 - Type: Post

Return:

 - observationUnitDbId -- plot -id
 - germplasmDbId ---
 - Note:

If there is a metadata field with gobii-dataset id in the trial/study we can fetch it directly.
- Get the external code
 - Call: / samples-search
 - Params: studyDbId
 - Type: POST

Sequence 2: Based on external code(sampleId)

- Login and get a token
- Get the list of crops
 - Call: / crops
 - Params: Auth token
 - Type: Get
- Get the information based on sampleId's

- Call: /phenotypes-search
- Params: studyDbId
- Type: POST

Information for dashboard

- Crops
 - Trials
 - Per year
 - Per location
 -