Draft of taxonomy API standard
DINA TC workshop 2017-05-18
Editable version: https://docs.google.com/spre

Note1: Most of the API calls listed below can be extended with {id} to get an individu
Note 2: We have favored a small number of configurable API calls, instead of provid
Note 3: The DINA API standard enforces pagination. It is important that pagination is
Note 4: A classification needs to store and allow manipulation of the order of siblings
Note 5: These API calls do not support specific operations for hybrid taxa. For the su
Note 6: For use cases, SH = Specimen Handling; TH = Taxonomy Handling (see se

DINA-Web call (suggested)	Parameters
/api/taxonomy/	-
/api/taxonomy/classification/	-
/api/taxonomy/classification/	-
/api/taxonomy/vernacular_language/	classification
/api/taxonomy/vernacular_language/	
/api/taxonomy/mandatory_language/	classification
/api/taxonomy/mandatory_language/	classification
/api/taxonomy/taxon/	classification, rank, scientific_name, author, year, vernacular_name, language, ancestor[={taxon_id} # root taxon for search],
/api/taxonomy/taxon/	
/api/taxonomy/subtree/	taxon
/api/taxonomy/rank/	classification
/api/taxonomy/rank/	classification
/api/taxonomy/vernacular_name/	classification, taxon, language
/api/taxonomy/vernacular_name/	
/api/taxonomy/act/	classification, taxon, date_from, date_to, user
/api/taxonomy/batch/	classification, file_type
/api/taxonomy/batch/	classification, file_type
/api/taxonomy/batch/{id}/	

Possible extensions

DINA-Web call (suggested)	Parameters
/api/taxonomy/common_ancestor/	taxon_list
/api/taxonomy/filter	
/api/taxonomy/filter	

ual object. PUT and DELETE will require
ling specialized instances for searching
s supported, for instance to communica
s (essential for some use cases). On th
ubtree operation, a clear understanding
parate document describing use cases)

PlutoF equivalent
/api/taxonomy/
/api/taxonomy/tree/
/api/taxonomy/tree/
/api/taxonomy/language/
/api/taxonomy/language/
NA
NA
/api/taxonomy/taxon
/api/taxonomy/taxon
/api/taxonomy/taxon/<id>/subtree
/api/taxonomy/rank/
/api/taxonomy/rank/
/api/taxonomy/vernacular_name
/api/taxonomy/vernacular_name
/api/taxonomy/act/
NA
NA
NA

PlutoF equivalent
/api/taxonomy/taxon/<id>/higher_taxa_intersection?given_ids=<included_id>,<included_id>,<included_id>...
/api/taxonomy/filter/
/api/taxonomy/filter/

e one or more {id} to identify the record(s) that will be modified or deleted. POST does
, matching, cloning of subtrees into new classifications etc. This means that the /api/ta
ite order of siblings. This allows calls for next sibling and previous sibling to be compo
e implementation side, the easiest solution might be to introduce an integer field givin
| of how hybrid taxa will be treated is important for understanding the API functionality.
)

Comment/explanation (for GET method)

Documentation of the API, returns all the endpoints
Returns the classification(s)
Creates/modifies/deletes a classification
Returns the language(s) of vernacular names
Creates/modifies/deletes a language of vernacular names
Returns the mandatory language(s) for vernacular names
Creates/modifies/deletes the mandatory language(s) for vernacular names

matching, searches etc by setting appropriate parameters. We suggest that
search_type adheres to standardized terms used in e.g. Apache Lucene.
Examples:
?filter[classification]=168 # all taxa for one classification
?filter[classification]=168&filter[scientific_name]=alt&search_type=begins_

Creates/modifies/deletes taxon record(s)

Returns the entire subtree rooted at the specified taxon. Is this the same as
/api/taxonomy/taxon/?filter[ancestor]={taxon_id}? Does it return both taxa and
related objects?
Returns the rank(s) that are used
Creates/modifies/deletes ranks

Returns vernacular name(s)

Create/modify/delete vernacular name(s)

Returns all acts (creation, updates and deletes) on taxon records

Allows you to download an entire classification using Darwin Core Archives or
similar formats. Receipt will be the ID of the download operation.
Allows you to upload an entire classification using Darwin Core Archives or similar
formats. Receipt will be the ID of the upload operation.
Gives you progress information on the batch operation {id}. On completion of a
download you will get the URL of the result file and an expiry time stamp.

Comment/explanation (for GET method)

Returns the most recent common ancestor of the specified taxa (if they are in the
same classification)

Returns defined filter(s)
Create/delete defined filter(s)

s not allow an {id}, since the id is assigned upon the
axonomy/taxon call will require a fair amount of
sed using the call "siblings" and based on the pagination
g the sort order of the siblings. PlutoF stores one traversal
. A common solution is to distinguish one hybrid parent as

Methods	Use Case(s)
GET	
GET	
POST/PUT/DELETE	
GET	
POST/PUT/DELETE	
GET	
POST/PUT/DELETE	
GET	SH-A, SH-C
	SH-B, TH-A, TH-
POST/PUT/DELETE	B, TH-C
GET	
GET/POST/PUT/DELETE	
POST/PUT/DELETE	
GET	
POST/PUT/DELETE	
GET	
GET	
POST	All use cases
GET	All use cases

Methods	Use Case(s)
GET	
GET	
POST/DELETE	