

# Draft of taxonomy API standard

DINA TC workshop 2017-05-18

Editable version:

<https://docs.google.com/spreadsheets/d/1uaJh1qt6mvY0ZCEB6uBKdnUnyGdpQnZcnFqTMHTS5pA/edit#gid=0>

**Note 1:** Most of the API calls listed below can be extended with {id} to get an individual object. PUT and DELETE will require one or more {id} to identify the record(s) that will be modified or deleted. POST does not allow an {id}, since the id is assigned upon the

**Note 2:** We have favored a small number of configurable API calls, instead of providing specialized instances for searching, matching, cloning of subtrees into new classifications etc. This means that the /api/taxonomy/taxon call will require a fair amount of

**Note 3:** The DINA API standard enforces pagination. It is important that pagination is supported, for instance to communicate order of siblings. This allows calls for next sibling and previous sibling to be composed using the call "siblings" and based on the pagination

**Note 4:** A classification needs to store and allow manipulation of the order of siblings (essential for some use cases). On the implementation side, the easiest solution might be to introduce an integer field giving the sort order of the siblings. PlutoF stores one traversal

**Note 5:** These API calls do not support specific operations for hybrid taxa. For the subtree operation, a clear understanding of how hybrid taxa will be treated is important for understanding the API functionality. A common solution is to distinguish one hybrid parent as

**Note 6:** For use cases, SH = Specimen Handling; TH = Taxonomy Handling (see separate document describing use cases)

DINA-Web call (suggested)	Parameters	PlutoF equivalent	Comment/explanation (for GET method)	Methods	Use Case(s)
/api/taxonomy/	-	/api/taxonomy/	Documentation of the API, returns all the endpoints	GET	
/api/taxonomy/classification/	-	/api/taxonomy/tree/	Returns the classification(s)	GET	
/api/taxonomy/classification/	-	/api/taxonomy/tree/	Creates/modifies/deletes a classification	POST/PUT/DELETE	
/api/taxonomy/vernacular_language/	classification	/api/taxonomy/language/	Returns the language(s) of vernacular names	GET	
/api/taxonomy/vernacular_language/		/api/taxonomy/language/	Creates/modifies/deletes a language of vernacular names	POST/PUT/DELETE	
/api/taxonomy/mandatory_language/	classification	NA	Returns the mandatory language(s) for vernacular names	GET	
/api/taxonomy/mandatory_language/	classification	NA	Creates/modifies/deletes the mandatory language(s) for vernacular names	POST/PUT/DELETE	
	classification, rank, scientific_name, author, year, vernacular_name, language, ancestor[=(taxon_id) # root taxon for search],		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=begin_		
/api/taxonomy/taxon/		/api/taxonomy/taxon	Creates/modifies/deletes taxon record(s)	POST/PUT/DELETE	SH-A, SH-C SH-B, TH-A, TH-B, TH-C
/api/taxonomy/taxon/		/api/taxonomy/taxon	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?	GET	
/api/taxonomy/subtree/	taxon	/api/taxonomy/taxon/<id>/subtree	Returns the rank(s) that are used	GET/POST/PUT/DELETE	
/api/taxonomy/rank/	classification	/api/taxonomy/rank/	Creates/modifies/deletes ranks	POST/PUT/DELETE	
/api/taxonomy/rank/	classification, taxon, language	/api/taxonomy/vernacular_name	Returns vernacular name(s)	GET	
/api/taxonomy/vernacular_name/		/api/taxonomy/vernacular_name	Create/modify/delete vernacular name(s)	POST/PUT/DELETE	
/api/taxonomy/vernacular_name/	classification, taxon, date_from, date_to, user	/api/taxonomy/act/	Returns all acts (creation, updates and deletes) on taxon records	GET	
/api/taxonomy/act/	classification, file_type	NA	Allows you to download an entire classification using Darwin Core Archives or similar formats. Receipt will be the ID of the download operation.	GET	
/api/taxonomy/batch/	classification, file_type	NA	Allows you to upload an entire classification using Darwin Core Archives or similar formats. Receipt will be the ID of the upload operation.	POST	All use cases
/api/taxonomy/batch/		NA	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.	GET	All use cases

## Possible extensions

DINA-Web call (suggested)	Parameters	PlutoF equivalent	Comment/explanation (for GET method)	Methods	Use Case(s)
/api/taxonomy/common_ancestor/	taxon_list	/api/taxonomy/taxon/<id>/higher_taxa_intersection?given_ids=<included_id> >,<included_id>,<included_id>...	Returns the most recent common ancestor of the specified taxa (if they are in the same classification)	GET	
/api/taxonomy/filter		/api/taxonomy/filter/	Returns defined filter(s)	GET	
/api/taxonomy/filter		/api/taxonomy/filter/	Create/delete defined filter(s)	POST/DELETE	