



 **WouterKoch** Subsets and morphs behave correctly. Fixes #5. 8a1a3ef on 13 Mar

1 contributor

34 lines (28 sloc) 4.37 KB

Raw

Blame

History



Taxon identification widget

Javascript-based widget implementing a hybrid multiple access key approach for taxon identification, by the [Norwegian Biodiversity Information Centre \(NBIC/Artsdatabanken\)](#).

Based on what is currently known about a taxon, the user is presented with one or more relevant questions in an optimized order, until one taxon remains. This approach can represent all preexisting keys, whether they are purely dichotomous, matrix-based, or anything in between. It also allows for easily expanding/linking data sets with more information, more species and/or additional properties.

Key features

- Keys (content) are read directly from a standardized spreadsheet format as CSV-files. While other formats exist, these are further removed from the daily, spreadsheet oriented reality of the biologists whose input we rely on. See the [data format guide](#) for more information.
- Required parameters are kept to a bare minimum.
- Code is linked to (but not depending on) other NBIC systems, such as the taxonomic backbone, map service and content management system (CMS).
- The interface is mobile ready and can be used stand-alone or as an iframe widget.
- Accepts a list of taxa that possible outcomes will be filtered by, allowing to run a key for only a particular subset of all of the taxa it distinguishes between.
- Users can choose to see one question at a time and swipe/navigate through these (simple, low threshold), or view a list of questions (more detailed overview of relevant domain knowledge).
- Using durandal, bootstrap, lodash and a bit of jquery.
- MIT licensed.

Url parameters

The following parameters can be passed to the widget

- **csv=[url]**: url to the csv containing the dataset. Note that this has to be hosted on either the same domain or one that supports Cross-origin resource sharing.
- **taxon=[x,y]**: a comma-separated list of taxa id's one wishes to distinguish between and within. See data format guide for more information.
- **minimal**: results in a more sober output with fewer headers and colored blocks, for better integration when used as an in-line widget.
- **height=[css height]**: specify a height for the widget, e.g. "500px" (include the "px"). Default is 100%.
- **fg=[html color]**: specify the dark color for custom styling of colored elements. E.g. "006585" (omit the #). Default NBIC's orange.
- **bg=[html color]**: specify the light color for custom styling of colored elements. E.g. EEF. Default white.

Data model overview

The key concepts in the data format and their effect on user experience:

- **Key:** a dataset describing a set of taxa and their diagnostic properties. A key title, its geographic range, intro text, a link to a description in the NBIC CMS and its language can be specified.
- **Taxon:** a possible outcome of the identification. Refers to an entity in the NBIC taxonomic backbone and can have links to a an image file, description in the NBIC CMS, and a follow-up key to further determine a specimen in another key. Can be given a sort order (default sort order is the number of hits in the [NBIC Species Map Service](#))
- **Characters and states:** questions and answers. Can have links to an image file, a description in the NBIC CMS, a logical dependency on previous answers, and a mulit-state property (when several states of one character can be true simultaneously). Can be given a sort order (default sort order is the standard deviation from the 'perfect' question, whose states evenly dismiss a maximum number of the remaining taxa).
- **Taxon-state relationships:** a matrix of numerical values linking taxa to relevant states.
- **Subsets and morphs:** custom subsets of taxa that are not formal taxonomic levels themselves, such as sex, color variations, etc. Subsets will be visible to the user as different outcomes, and questions to distinguish between subsets will be asked even when the taxon containing them is determined. Morphs will only be visible to the user when it "happens" to have a particular outcome, but no questions will be asked to distinguish between morphs within a taxon. It does allow for a more appropriate image file to be displayed and a different set of taxon-determining questions to be asked.

A data format guide for domain experts (biologists) is available in [English](#) and [Norwegian](#) .