

USER MANUAL

TEMPLATE TAXONOMYIMPORT2DARWIN: ENCODING TAXONOMICAL DATA IN XML-FILE

Version		Author(s)	Date	Description
1.0	TaxonomyImport2DaRWIn_v1.xlsm	MAdam	December 2014	Taxonomical data export to xml

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USER INFORMATION

Template tested with Excel 2007.

1. Open the template document and save it with a custom name “[CUSTOMNAME].xlsm”.

If a Security Warning appears, then Enable macros (click options... and select “Enable this content”).

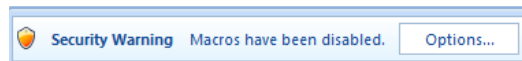


Figure 1 - Security Warning for macros

You can also access these options through the Excel Options > Trust Center **1**. Then, click on “Trust Center Settings” **2**. In the new window, in “Macro Settings” **3**, check “Enable all macros” **4**.

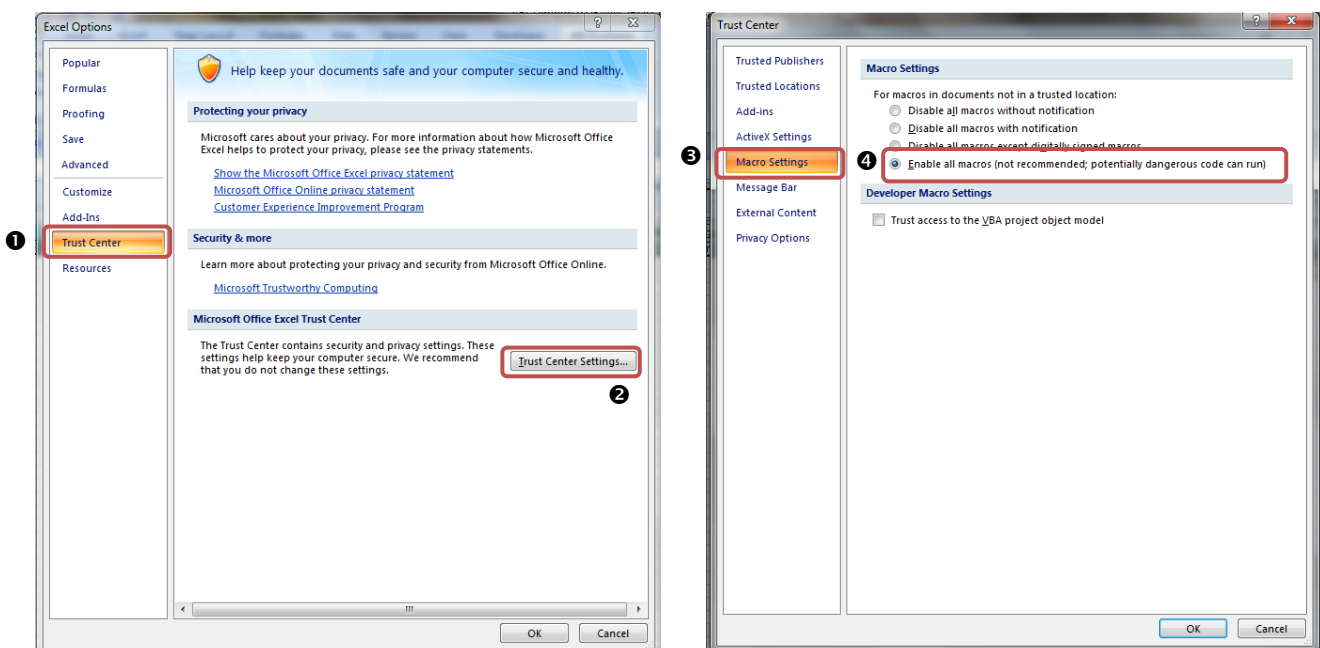


Figure 2 - Excel options: enable macros

2. Fill in the worksheet TAXONOMY and check column headings

All taxonomical trees/taxons you wish to import have to be stored in a worksheet named TAXONOMY.

You can check if you use to correct column heading names by clicking on “Columns mapping” in the “Taxonomy2XML” ribbon.

3. Click on “Export” to export the data

When running the Export code, an XML-file is produced and this XML-file can be saved in a folder defined by the user. During the export, Excel is unavailable (the worksheet could disappear or turn into blue during the process). This may take several minutes, depending on the number of lines and the quantity of information.

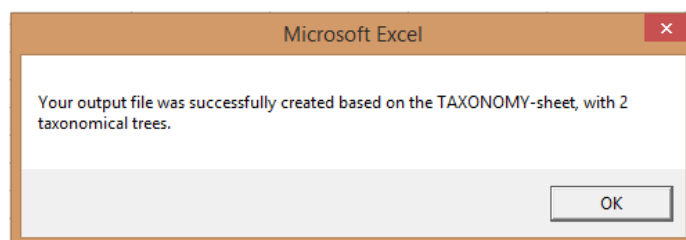


Figure 3 - Summary of your export

TEMPLATE STRUCTURE

The template for encoding consists of the worksheet TAXONOMY, containing taxonomical trees you wish to add in DaRWIn.

The requirements are extremely limited... Only the presence of a worksheet named “TAXONOMY” containing data stored in columns with predefined heading names in the first row is obligatory.

The following levels are available: domain, kingdom, super_phylum, phylum, sub_phylum, super_class, class, sub_class, infra_class, super_order, order, sub_order, infra_order, section, sub_section, super_family, family, sub_family, super_tribe, tribe, sub_tribe, infra_tribe, genus, sub_genus, species, sub_species, variety, sub_variety, form, sub_form, abberans.

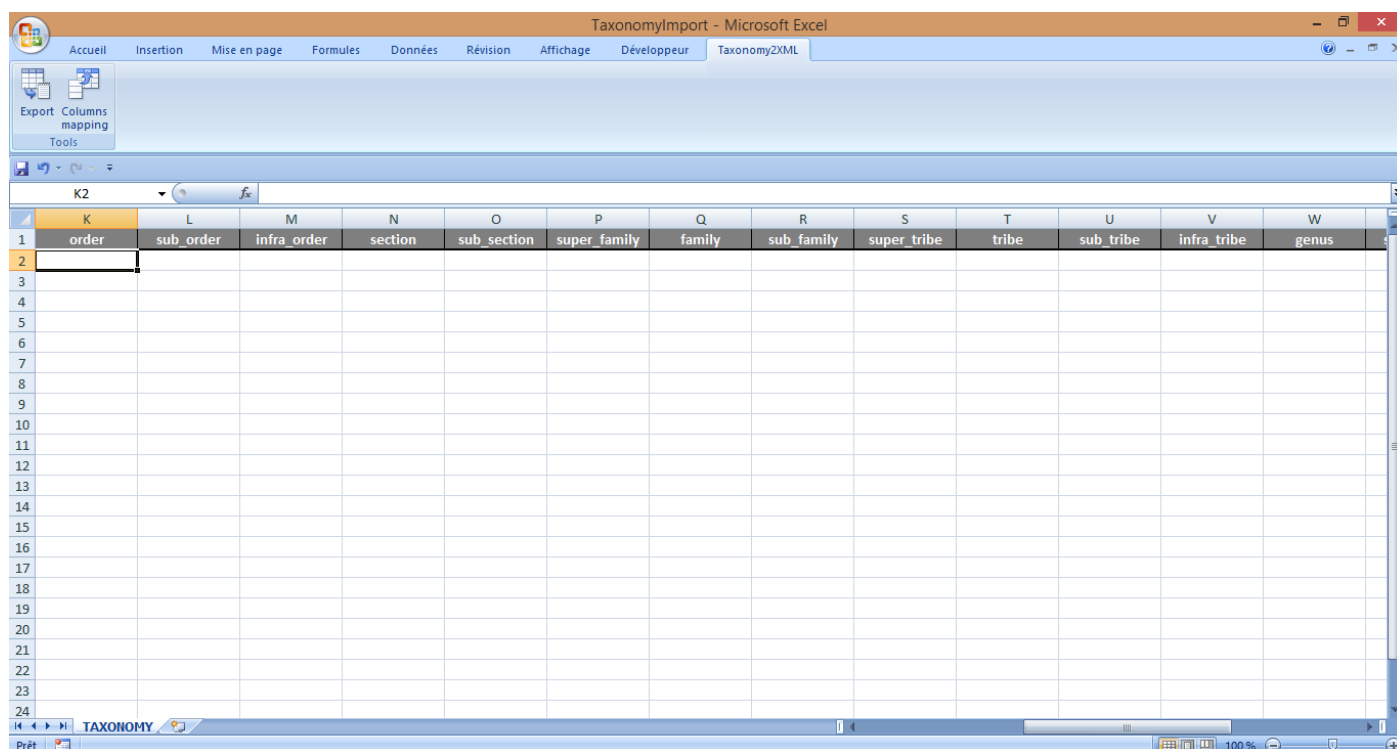


Figure 4 - Taxonomy Import template

One row is one taxonomical tree. For each new taxonomical level to create, the direct parent has to be completed and has to be present in DaRWIn. It is exactly the same principle than when you create an entry in the Taxonomy Catalogue in DaRWIn: you're asked to precise the parent to which this taxonomical unit has to be linked.

Example: if you wish to create new genus, sub genus, species, sub species, etc. that are linked to a family already present in DaRWIn, you need to complete the family column for each row, so that the system knows where to link each new taxonomical level and is able to create a correct taxonomical tree.

When completing the template, keep in mind that the parent of each row has to be recognized in DaRWIn. If the higher parent for a row doesn't exist yet in DaRWIn, the import is cancelled and no taxon name will be imported into DaRWIn.

Only data stored in columns where the title was recognized will be exported. The presence or absence of columns is completely customizable. It is your responsibility to prepare a template with correct taxonomical trees. You can also add as many columns as you wish, keeping in mind that they will not be recognized and thus the information they contain will not be exported to the XML file.

A tool was added to verify the correct mapping of columns in the template before export. It will tell you which columns are not recognized and if the TAXONOMY-sheet is well found.

A warning message will also pop up if a column is not recognized, telling you which headers are concerned. You can decide to go on with the export, by clicking "Yes": the program export your data without taking unrecognized columns into account. You can abort the export, by clicking on "Cancel" in case of misspelling...

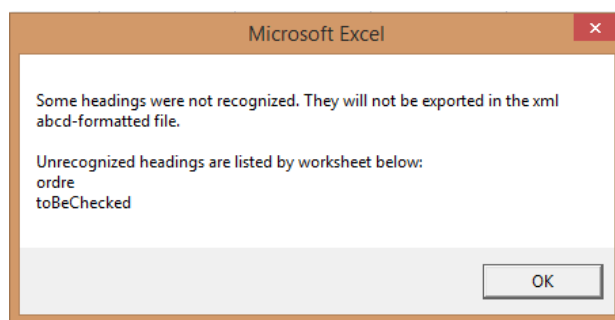


Figure 5 - Result of columns mapping

In this example (Figure 5):

- toBeChecked could be additional information, for internal purpose
- ordre is obviously misspelled and should be corrected to order

HOW TO USE THE TEMPLATE?

Each column should be completed with:

- For higher level, if you wish to link the imported taxon to an existing level in DaRWIn : the exact same name that the one encoded in DaRWIn. Remember that matching will only occur for exact match between the names in the template and the name in DaRWIn. When you wish to link your taxon name to an existing level in DaRWIn, you have to use the exact same name in the template than what was written in DaRWIn. If a parent is recognized, each subsequent level will be created if the system doesn't find it in DaRWIn. That is, if you forget to precise the authorship in the template and if the authorship for the level is present in DaRWIn, a new level without authorship will be created.

Consequently, you need to be extremely careful when you prepare a template for importing taxonomy: check carefully if the level you're about to create doesn't already exist in DaRWIn, maybe with a slightly different name, and be vigilant with the spelling of taxonomical names.

Examples:

- If you wish to create new taxons linked to the Gastropoda, you have to use “Gastropoda Cuvier, 1797” in the “class” column. “Gastropoda” won’t work, and without higher level referenced in the template, the import will abort.
- If you wish to create new taxons linked to the family of Canidae, you have to use “*Canidae Fischer von Waldhei*”. If you use “*Canidae*” and you’ve written the correct order name, that is “*Carnivora Bowdich*” in DaRWIn, the system will create a family “*Canidae*” and link all new taxa to this new family. The consequence is a duplicated tree in DaRWIn: “*Canidae*” and “*Canidae Fischer von Waldhei*”.
- For creating new taxon entry, use the complete name (authorship included when possible), since this is what will be stored as “name” when creating the taxonomical level.

If you try to create a taxon that already exist in DaRWIn, it won’t work: duplicates are not allowed in the Taxonomy Catalogue in DaRWIn. Nevertheless, it is possible to import a taxon that already exists but with a different taxonomical tree than what is referenced in DaRWIn. This won’t be considered as a duplicate, since its parents aren’t identical...

Example :

DaRWIn	Import 1	Import 2
Class_1	Class_1	Class_1
Order_1	Order_1	Order_1
Family_1	Family_1	Family_2
Genus_1	Genus_1	Genus_1
Species_1	Species_1	Species_1
Result:	No import: no duplicates allowed	Import OK: same name but different taxonomical tree

The taxonomy in DaRWIn follows a strictly defined structured and does not allow a follow-up of taxonomy. There is a high risk of errors when using expressions like « Various amphipods » or « sp1 » and thus the result of import cannot be guaranteed. In the case of an uncertain/incomplete determination, the good DaRWIn practice is to fill in only the taxonomy levels you are sure of and to leave the rest blank. For example, if the genus/species for a specimen is unknown/undescribed, you would have to fill in the taxonomical tree up to the family level, and leave genus and species blank. Expressions like « [family name] gen. n. det. » are not to be used in the database. You can add a comment to precise the determination status. Alternatively, it is possible to add a suggestion or report a problem in the ‘suggestions/report problem’ widget, directly in the DaRWIn interface. By doing so, the specimen is flagged, can be easily monitored, and when possible, updated or corrected.