



Xper²

Software for structured descriptive data and identification keys

User manual

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1 Introduction

The Xper² software¹ as we use it in the workshop is a standalone program which can be used independently (i.e. you can close the TaxEditor now). The database of the stand-alone version is compatible with the EDIT Platform and full integration of Xper² as the descriptive data editor for the platform is the plan for the future (at the same time maintaining the possibility to use the stand-alone version).



With its intuitive interface, Xper² is aimed at professional taxonomists as well as naturalists who want to identify specimens using a readymade application.

The software, terminology and workshop materials

Xper² is free of charge; download: <http://lisupmc.snv.jussieu.fr/lis/?q=en/resources/software/xper2>

Written in Java, it is available on Windows™, Mac™, and Linux in French, English, Spanish and Chinese versions. Xper² consists of three components: two java desktop applications (one used to manage the descriptive data contained in knowledge bases, and one used to perform interactive identification of the taxa described in these knowledge bases) and a java applet which allows users to perform interactive identifications online.

Descriptive data are structured. In Xper² we use the following terminology :

- The **described entities**: taxa, specimens (“items”)
- The **descriptors**: properties used to describe the items (“characters”)
- The **states** or **descriptorstates**: possible values for each one of the descriptors (“character states”)
- The **description**: all states attributed to an item for each descriptor
- **Groups**: used to structure and to filter lists

In the Xper folder you will find a number of files and subdirectories:

- Xper2-Editor-2.3.2.exe: The Xper² program.
- Guideline_Xper2.pdf: A graphic illustration of the program’s capabilities
- Folders Example and Cichorieae_full contain example knowledge-bases.
- Cichorieae_fullsdd.xml is an sdd-formatted export file used below as a complex example for key generation which was created for the Cichorieae exemplar group² of the EDIT project.
- Leaves: Some leaves images that can be used as examples (for copyright please refer to http://offene-naturfuehrer.de/web/H%C3%A4ufige_Laubb%C3%A4ume_nach_Bl%C3%A4ttern_bestimmen)

¹ Xper² is a long-standing development by our partners at the University Paris 6, Laboratoire Informatique et Systématique, UMR 7205 Institut de Systématique, Evolution, Biodiversité - Prof. Régine Vignes Lebbe and her group. The following text was slightly adapted from scripts used by Régine Lebbe during an EDIT Platform workshop at the Caryophyllales 2015 conference in Berlin.

² Kilian N. Hand R. & Raab-Straube E. von; general editors) 2009+ (continuously updated): *Cichorieae* Systematics Portal. Published at <http://cichorieae.e-taxonomy.net/portal/>



2 Tutorial: creating a first application

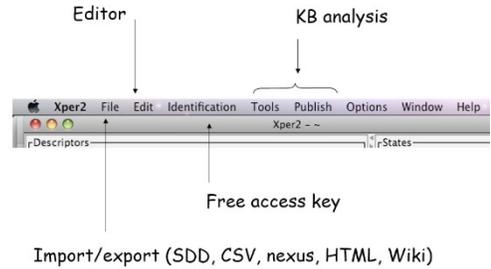
Open the Xper² programme by double-clicking on the Xper2-Editor-2.3.2.exe file.

The menu gives access to the main functionalities of the program.

This section proposes 10 simple steps to create your first application using Xper².

(i) Start by creating a new knowledge base.

In the menu, go to *File -> New base*.



(ii) Give a name to your new knowledge base



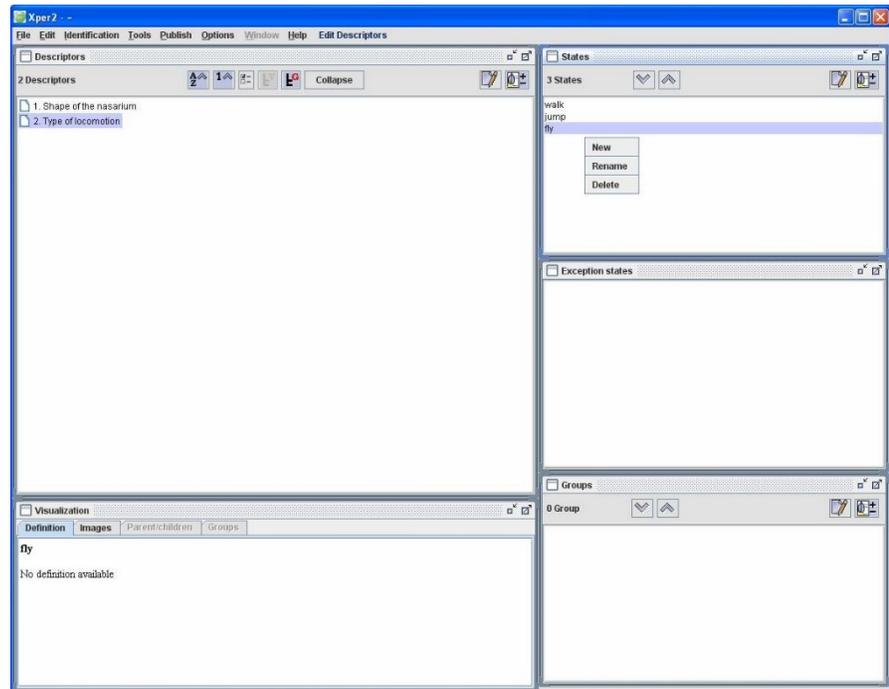
(iii) Edit *Descriptors* and *States*

To make the descriptions comparable, the data must be expressed in a structured format, using the same terminology. So you have to define the list of descriptors (or characters like “Leaf [shape]” and the values accepted (states ; i.e. “ovate”, “obovate”, “linear”, etc.) for each one.

You can use the images of leaves in your Xper folder to create a key, or use your own group to define a character matrix for a few species and construct the key (download and link illustrating images from the web)..



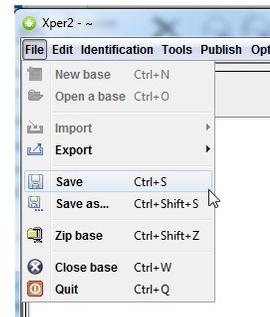
Click in a window with the right mouse button and choose *New* or *Rename* to label descriptors and states for each descriptor.



(iv) Save the knowledge base

In the menu, select *File -> Save* to save under the current name, with *File -> Save as...* you can store it under a different name.

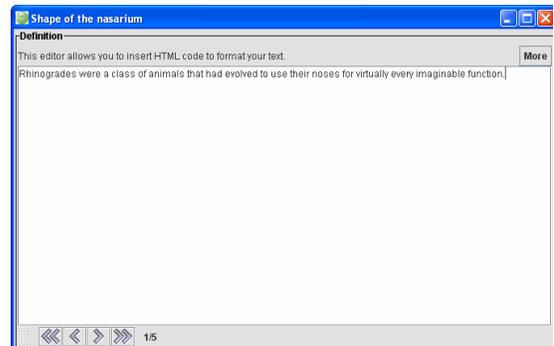
Note: a knowledge base is stored in several files ; you can use *File -> Zip base* to store all the files in a single compressed file (.zip format).



(v) Adding text to define or comment on description elements

Click on the pencil button  to add text on a selected element ((descriptor, state, group, or taxon). For example, add a comment on the descriptor “Shape of the nasarium”.

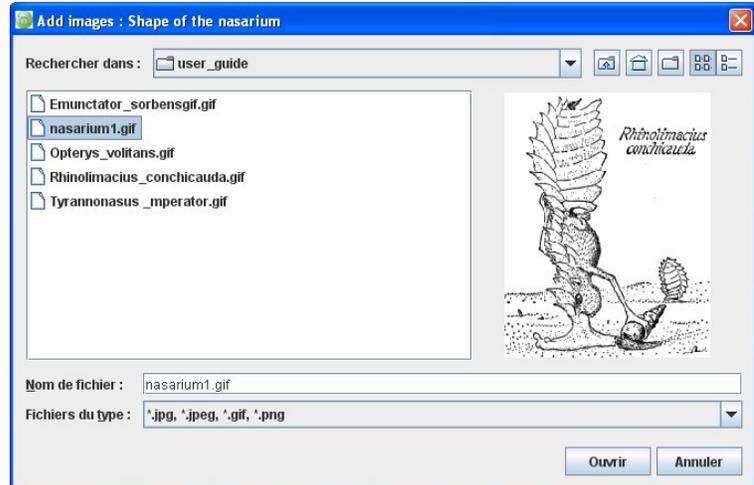
Note that you can include HTML tags to format the text or to add hyperlinks.





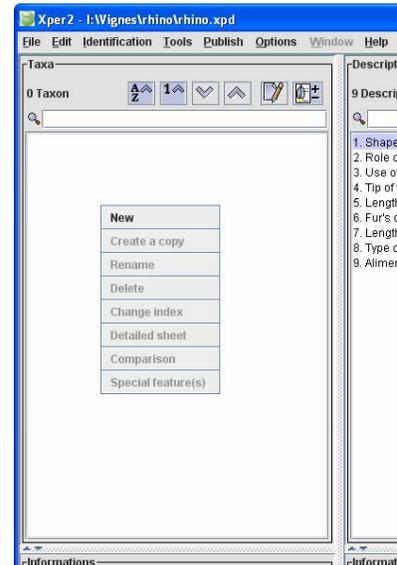
(vi) Adding illustrations

Click on the button  and select one or several pictures to illustrate the selected element (descriptor, state, group, or taxon).



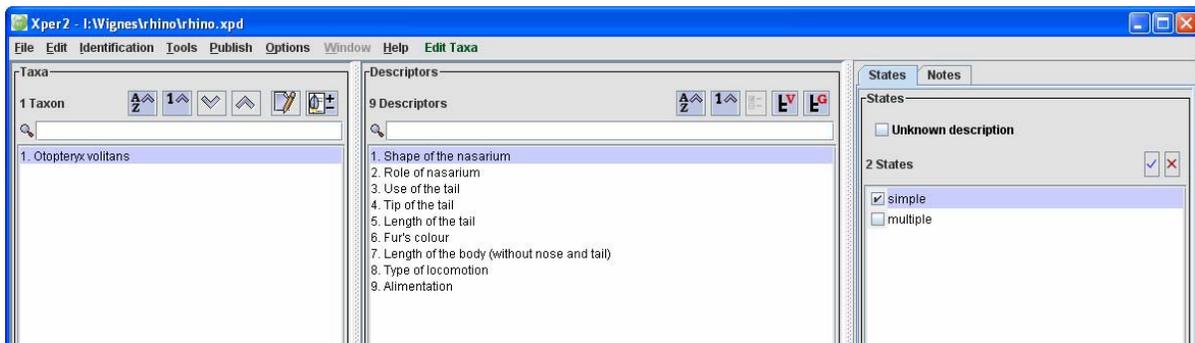
(vii) Edit taxon list

In the menu, select *Edit* -> *Edit taxa*. Click on the *Taxa* window to add taxon names



(viii) Edit the description of a taxon

Select a taxon in the list. Select a descriptor. Check the respective state(s).
If you don't know, check *Unknown description*.







(ix) Metadata

In the menu, select *Edit* -> *Properties*.

Fill the different forms to describe the metadata (context, authors etc.)

(x) Check the descriptions

In the menu, select *Tools* -> *Check the base*.

The window displays information specially about the consistency of the descriptions (*Data checking*) and about the possibility or not to distinguish the different taxa (*Taxa checking*). If necessary, correct the descriptions or add new descriptors to separate the taxonomic descriptions.

Save your sample knowledge base and close it.



3 A real-world example: *Hymenophyllaceae* of the Comores

Open the example knowledge base. Wait a moment for image processing.

- Gain an overview of the taxa, descriptors and states present.
- Try out the interactive identification.
- Note that (in the stand-alone version) the nomenclature, taxonomy and factual data about the taxon are stored as free text.
- Check the database - What's wrong with the descriptor "Front dimorphism in shape"?
- Look at the analytical functions (in the menu under *Publish*)
- Try the export functions – use "Test" as a filename (you can overwrite thumbnails and ignore the nexus error message; open the index.html in the web folder with Internet Explorer).

Key generation

Apart from the interactive key provided by the Xper² application itself, you can also generate a polytomous key from Xper², using the LIS iKey+ webservice³.

Make sure you have exported your test.sdd.xml export file from the example knowledge base.

In your web-browser, open

<http://www.identificationkey.fr/ikeyplus/>

Click on *Upload your SDD file*

Before you actually upload the file, look at the help links in the interface where the different options are described in an exemplary way.

Upload your test.sdd.xml export file and/or use the *Cichorieae* example (Cichorieae.fullsdd.xml) for a more complex example.

You could cut and paste the resulting txt- or html- formatted key into the TaxEditor, or use the *Polytomous Key Editor* to create a semi-structured key for your taxonomic treatment in the EDIT Platform for Cybertaxonomy.

The screenshot displays the iKey+ web service interface. At the top, it features the LIS logo and the VIBRANT logo. The main heading is "iKey+ Identification Key generation web service". Below this, a three-step process is outlined: 1) Generate your SDD file, 2) Upload your SDD file, and 3) Create your Identification Key. A sidebar on the left provides links for "Create an Identification Key", "How to generate a SDD file?", and "About the webservice". A section titled "This webservice can have several uses:" lists three scenarios: being a biologist, belonging to an institute, or belonging to an institute. The bottom section, "Create an Identification Key", includes options for prioritizing descriptors, merging descriptor states, and various verbosity settings. It also features a file upload area with a "Browse" button and a "Save" button.

³ Burguiere T., Causse F., Ung V. & Vignes-Lebbe R. 2013: IKey+: a new single-access key generation web service. *Systematic Biology* 62(1): 157-161. doi: 10.1093/sysbio/sys069. <http://sysbio.oxfordjournals.org/content/62/1/157>