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SYNOPTKEY – a PHP program for online presentation of synoptic determination keys

Alexander N. SCHMIDT-LEBUHN & Michael KESSLER

Abstract: SCHMIDT-LEBUHN, A.N. & KESSLER, M. 2007: SYNOPTKEY – a PHP program for online presentation of synoptic determination keys. Schlechtendalia **16**: 101–105.

Synoptic keys have several advantages over analytic keys, but for a long time were rarely used due to their unwieldy size in print. With the advent of electronic data storage and online floras, their implementation has become more practical. SYNOPTKEY is a short PHP program that can be integrated into websites to provide online synoptic determination keys. It is available for download under http://www.minthostachys.com/files/synoptkey.zip. Data files to be used by the program can be prepared with standard spreadsheet calculation software, e.g. MS Excel, StarCalc, etc.

Zusammenfassung: SCHMIDT-LEBUHN, A.N. & KESSLER, M. 2007: SYNOPTKEY – ein PHP-Programm für Online-Präsentation synoptischer Bestimmungsschlüssel. Schlechtendalia **16**: 101–105.

Synoptische Schlüssel haben gegenüber analytischen Schlüsseln einige Vorteile, werden aber seit langer Zeit wegen ihrer schwer handhabbaren Größe kaum genutzt. Mit dem Aufkommen elektronischer Datenspeicherung und von Online-Floren wurde jedoch deren Nutzung immer praktikabler. SYNOPTKEY ist ein kurzes PHP-Programm, welches in Web-Seiten integriert werden kann, um synoptische Online-Bestimmungsschlüssel verfügbar zu machen. Es kann unter folgender Webadresse heruntergeladen werden: http://www.minthostachys.com/files/synoptkey.zip.

Datensätze, die für das Programm nutzbar sind, können mit üblicher Tabellenkalkulationssoftware erstellt werden, z.B. MS Excel, StarCalc, etc.

Keywords: Determination, identification, keys, online, PHP.

Introduction

Keys for the identification of taxa or determination of specimens are an indispensable tool for all researchers in organismal biology, from taxonomy and systematics to floristics, biogeography and the investigation of biodiversity patterns. As such, keys have a long history of experiments and attempts at finding the "best" way to provide a determination aid (e.g., VOSS 1952; LEENHOUTS 1966). There are two main types of keys, both of which exist in several variations: analytic keys, used by following predetermined sequences of questions, and synoptic keys, basically tables of taxa vs. characters.

Synoptic keys are in at least two ways superior to analytic keys: they allow for arbitrary entry, i.e., the user can decide himself with what characters he wants to start the determination process, and can exclude a number of taxa even if some characters usually considered crucial are unavailable; and they provide a much larger amount of data

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on each taxon that is thus available for other purposes. Their greatest drawback and the reason why they have traditionally been much overshadowed by analytic keys, is that they are extremely unwieldy in print, especially for large numbers of taxa. For printed monographs, field guides and floras, this will continue to be a problem, but for electronic floras such limitations do not exist. Not surprisingly therefore, the computer age has seen a renaissance of synoptic keys (BRACH & SONG 2005; DALLWITZ et al. 2006; FARR 2006).

In 2006, the work on an online supplement to a field guide to the ferns of Bolivia was begun (KESSLER et al., unpubl. data; http://www.fernsofbolivia.uni-goettingen.de). One of the functions that were to be provided was an interactive online synoptic key to all taxa. It was implemented as a dynamic web page containing PHP code, with the character tables as separate data files to be loaded as needed. Apart from the "Ferns of Bolivia" project, this small and easy to use PHP program can of course be integrated into other websites, and it is here presented to the public in the hope that it will facilitate making more online determination aids available.

Individual synoptic keys to be processed by the program can be easily prepared using standard spreadsheet calculation software. The most important precondition for successful use of the program is an understanding of how to integrate it into an existing website.

How to "install" SYNOPTKEY

SYNOPTKEY is a PHP program (The PHP group, http://php.net) that generates a dynamic web page. Therefore, it is not a separate program file like other applications, but must be integrated into an HTML file. The program code is available for download at http://www.minthostachys.com/files/synoptkey.zip.

The server hosting the website must have the language PHP installed. Most should; if uncertain, the system's administrator or provider has to be contacted. An HTML page must be prepared for the website and the complete program code be pasted into an appropriate position, e.g., below a general heading or explanation. The page has to be saved with a ".php" extension instead of the usual ".html" or ".htm" so that the server knows to expect a dynamic website. Now data files containing the actual keys have to be provided, and the new ".php" page must be linked from another page using at least one hyperlink with the following structure: [website and/or folder]/[file containing the program].php?key=[folder]/[filename].csv&status=new. Example: if the ".php" file is simply named "synoptkey.php", it is placed in the same folder as the linking page, and the program is meant to start with a key called "Botrychium.csv" placed in a subfolder named "synopt", the link should read as follows: synoptkey.php?key=synopt/Botrychium.csv&status=new.

How to prepare synoptic keys for use in SYNOPTKEY

The data for synoptic keys is best prepared using spreadsheet calculation programs like MS Excel, StarCalc, or similar. They must conform to the format shown in table 1.

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Table 1: Format of data files to be processed by the SYNOPTKEY program.

	Taxon Treatment	**Leaflet length**	**Scale color**	**[…ad infinitum]**
Weight		5	10	
State0		**2-3 cm**	**reddish#redscale.jpg**	[...]
State1		**3-5 cm**	**brown#brownscale.jpg**	[...]
State2		**>5 cm**		
[...]				
State9				
Planta extincta	plantella.html#extincta	0	0	[...]
Plantella	#keydata/plantella.csv	1, 2	1	[...]
[...ad infinitum]	[...]	[...]	[...]	[...]

The information in bold fields will be shown to the user. The entries here shown in italics will be ignored by the program, but they are useful as a legend for the author of the table. The data shown as plain text is what the program really works with, but it will not directly be shown to the user.

Taxa are listed in lines (beginning with line 13), characters in rows (beginning with row 3). The first line contains the character descriptions, i.e., the questions that will be presented to the user. Their weights are entered into the second line; these should be numbers higher than zero. Questions with higher weights will be selected first, as long as they have not been skipped and answering them will still serve to exclude taxa. Lines 3 to 12 contain up to 10 different character states for each character. They must always begin with state 0 (in line 3), and it is up to the person preparing the data file to make sure that all possible character states are described. It is possible to have the program showing one image as an illustration for each character state. If a character state entry contains a "#", the letters following it will be interpreted as the address and filename of the image file, which will then be shown as a thumbnail. Starting with line 13, the taxa are listed. The first row contains the taxon names, the third to final rows give the specific character states found in the respective taxa, which must be given as numbers ranging from 0 to 9. Variability is indicated by listing all possible states in the same field (not "0-2"!). Apart from the numbers, only a dash ("-") and a question mark ("?") should be used as entries. They usually indicate inapplicability or missing data, respectively, but the program treats them in the same way. The second row contains information regarding how the website should react to clicking the taxa. No entry will lead to plain text taxa that cannot be clicked. Entries starting with "#" will be interpreted as the addresses of data files containing subkeys, so that "#keydata/plantella.csv" will prompt the program to generate a link to itself and load the file "plantella.

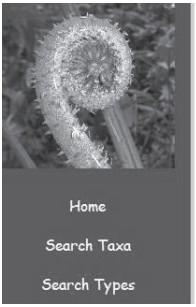
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csv" in the website's "keydata" folder once activated. All other entries will be interpreted as URLs, so that the synoptic key can be linked to other online resources.

Once a data table is finished, it has to be saved in the comma separated value (csv) format using semicolons (";") as separators, which is the default in MS Excel. Other occurrences of semicolons in the file have to be avoided, so it is best to use the search and replace function before saving to replace them all with commas. The resulting csv file must now be placed on the website, and it can be used by either linking to if from another data table (if it represents a subkey of the latter), or by using the starting link described above.

How to use the synoptic keys

If the program and data have been properly prepared, the user will be presented with two rows of information (fig. 1). To the left, he will find a list of the taxa that are still available, i.e., matching the information entered so far. To the right, one of the characters with the highest weight still available will be shown along with a list of all possible character states. A link labelled "skip question" will also be shown, as will another labelled "back to last question" if applicable. Once the user clicks one of the possible character states, the SYNOPTKEY program is called again. It excludes all taxa not matching the newly received information and marks the question for the last character as already answered. Skipping a character will reduce its weight to zero, and the program is called again to select the next best possibility. If all remaining characters have been skipped, they will be presented again one after the other. Characters will be selected until there are none left that can be used to differentiate between the taxa - usually this should be once only one taxon is available. Whether the taxon names can be clicked, and to what effect, depends on the data files that are currently being processed.



Ferns of Bolivia Synoptic Keys

Remaining Taxa:

Ophioglossum palmatum
Ophioglossum crotalophoroides
Ophioglossum scariosum
Ophioglossum nudicaule
Ophioglossum reticulatum

Shape of sterile blades

deeply palmately lobed

entire, narrowly to broadly elliptic to oblong, mostly 0.5-1.5 cm wide, bases cuneate, often narrowly so

entire, cordiform, mostly (2)3-6 cm wide, bases cordate

Skip this question

Fig. 1: Example of a website using SYNOPTKEY.

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Addresses of the authors

Alexander N. Schmidt-Lebuhn, Martin-Luther-Universität Halle-Wittenberg, Institut für Biologie, Institutsbereich Geobotanik und Botanischer Garten, Abteilung Pflanzenökologie, Am Kirchtor 1, D-06099 Halle (Saale), Germany.
(E-mail: schmidtleb@yahoo.de)

Michael Kessler, Georg-August-Universität Göttingen, Albrecht-von-Haller-Institut für Pflanzenwissenschaften, Abteilung Systematische Botanik, Untere Karspüle 2, D-37073 Göttingen, Germany. (E-mail: mkessle2@gwdg.de)

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Autor(en)/Author(s): Schmidt-Lebuhn Alexander N., Kessler Michael

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