BRAHMS 7 UPGRADE NOTES

July 2012

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A powerful and flexible online service

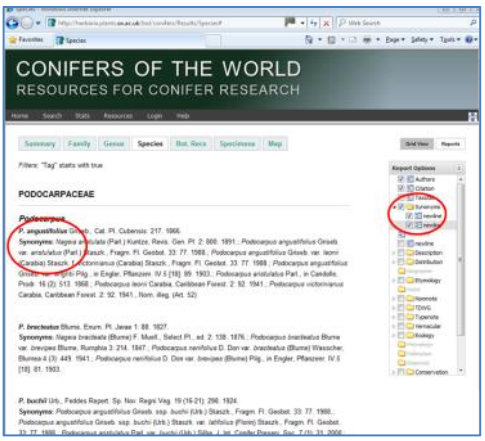
BRAHMS online (BOL) has been heavily upgraded to a new system with flexible analysis and reporting features for family, genus, species, botanical record, specimen, seed, living collection, map and image data.

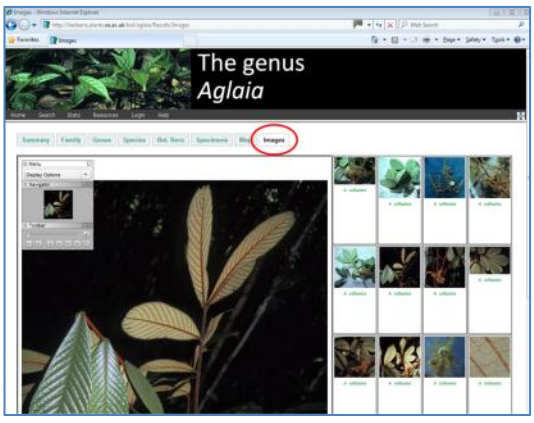
BRAHMS online is programmed using the latest Microsoft .net framework in C#. The web components use the MVC framework.

As well as using the BOL service on the secure BRAHMS server, BRAHMS online can be installed on your own server or indeed, any computer running windows. The largest online system (June 2012) is the National Herbarium Netherlands database with some 2 million specimens. Amongst its many features, the new BOL version includes:

- Stats overview of data linked to a website.
- Zoomify for online image viewing.
- Image based online loans management and determination returns.
- Support for e-floras and online monographs.
- Map clustering and a map data browser with Zoom tools.
- Support to publish seed banks and botanic gardens online.
- Substantial search speed increase for large (> 1m specimens) databases.
- BOL now operates on 32 and 64 bit servers.

Many of the new features are described in the Millennium Seed Bank Data Warehouse guide on http://herbaria.plants.ox.ac.uk/bol/content/documentation/MSBP_Data_Warehouse_help_document.pdf . Most of the examples in this document refer to seed data but apply equally to other BOL data categories.





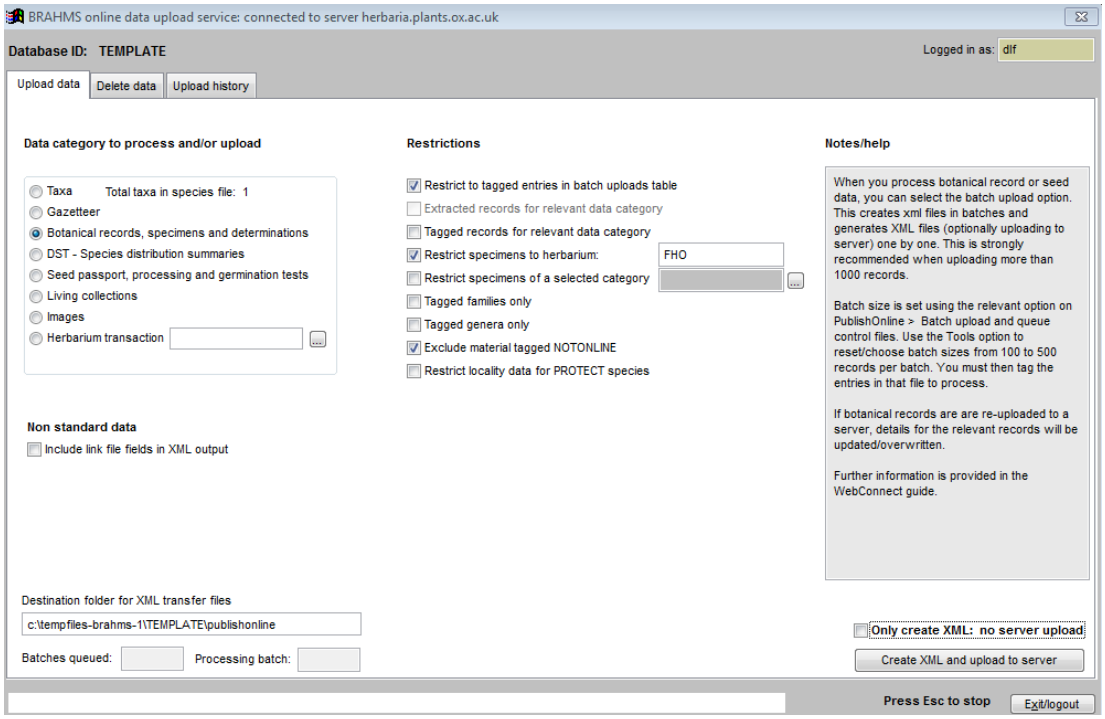
Some sample screens grabbed from various BRAHMS online sites.

BRAHMS WebConnect

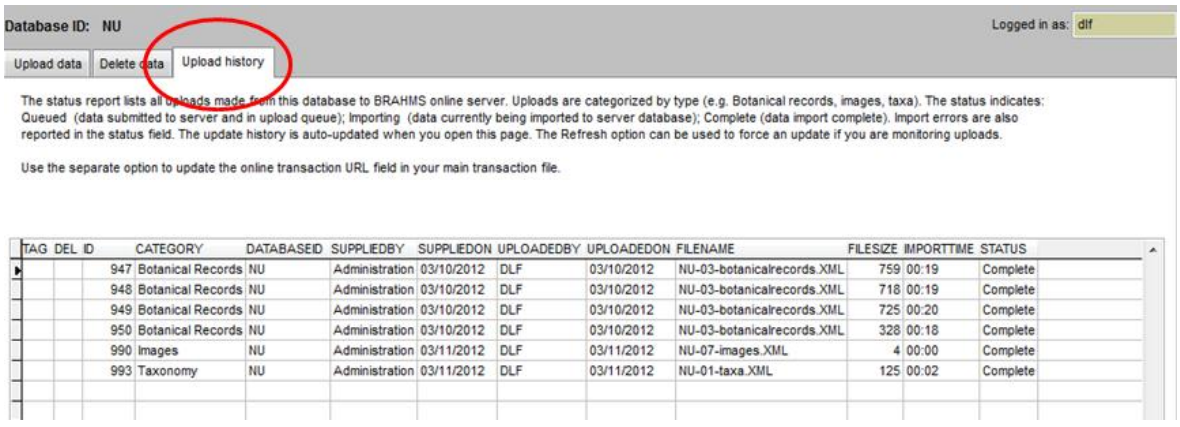
An updated WebConnect system in BRAHMS provides a seamless link to BRAHMS online for website design and data uploading. Some features of the revised WebConnect component:

- A new PublishOnline menu in BRAHMS.
- Improved web page design HTML controls for HTML dummies (i.e. most of us…).
- Taxonomic data uploading implemented, for example descriptions and synonymy.
- Botanical records, specimens and determinations uploaded together.
- All data are now transferred using XML files.
- A great number of upload restrictions may be applied.
- A system of batch queuing data to the server, ideal for larger data uploads.
- Monitor your uploads history.
- A new flexible system for implementing image slide shows http://nivo.dev7studios.com/.

For full details, refer to the revised WebConnect guide on
http://herbaria.plants.ox.ac.uk/bol/content/documentation/BRAHMSWebConnect.pdf



The WebConnect data uploads screen

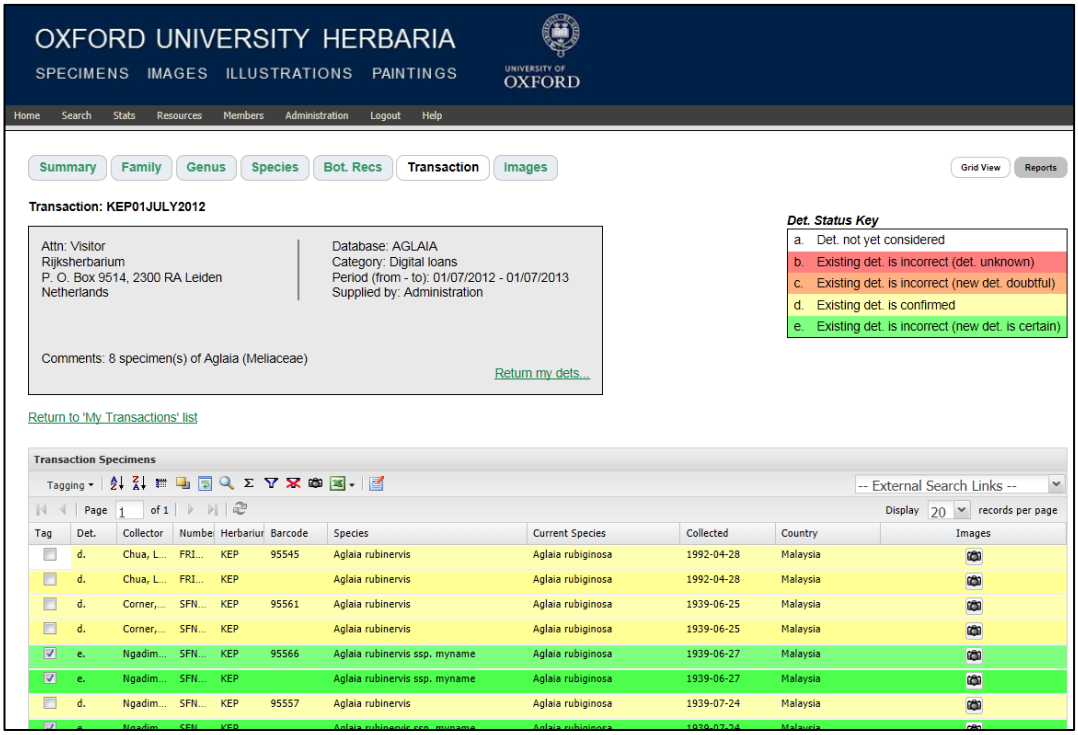


TAG	DEL	ID	CATEGORY	DATABASEID	SUPPLIEDBY	SUPPLIEDON	UPLOADEDBY	UPLOADEDON	FILENAME	FILESIZE	IMPORTTIME	STATUS
		947	Botanical Records	NU	Administration	03/10/2012	DLF	03/10/2012	NU-03-botanicalrecords.XML	759	00:19	Complete
		948	Botanical Records	NU	Administration	03/10/2012	DLF	03/10/2012	NU-03-botanicalrecords.XML	718	00:19	Complete
		949	Botanical Records	NU	Administration	03/10/2012	DLF	03/10/2012	NU-03-botanicalrecords.XML	725	00:20	Complete
		950	Botanical Records	NU	Administration	03/10/2012	DLF	03/10/2012	NU-03-botanicalrecords.XML	328	00:18	Complete
		990	Images	NU	Administration	03/11/2012	DLF	03/11/2012	NU-07-images.XML	4	00:00	Complete
		993	Taxonomy	NU	Administration	03/11/2012	DLF	03/11/2012	NU-01-taxa.XML	125	00:02	Complete

A sample WebConnect uploads history screen

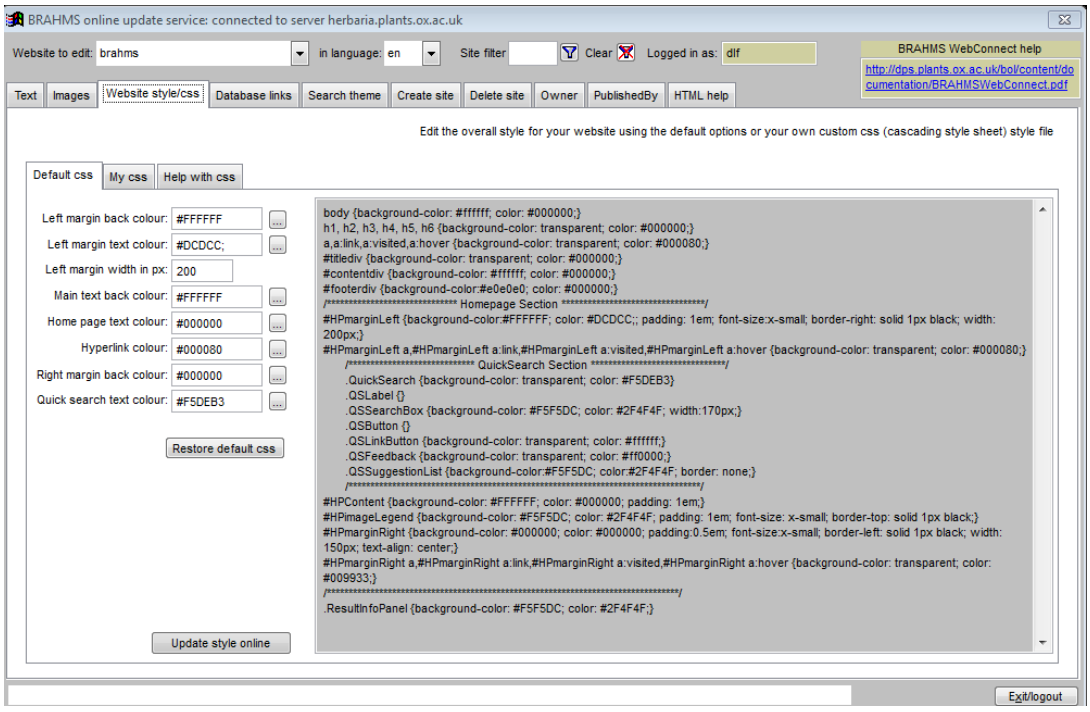
Online herbarium transactions: image based loans

BRAHMS and BRAHMS online (BOL) provide facilities to generate and manage online, image based loans. For full details, refer to:
http://herbaria.plants.ox.ac.uk/bol/content/documentation/onlineloans.pdf



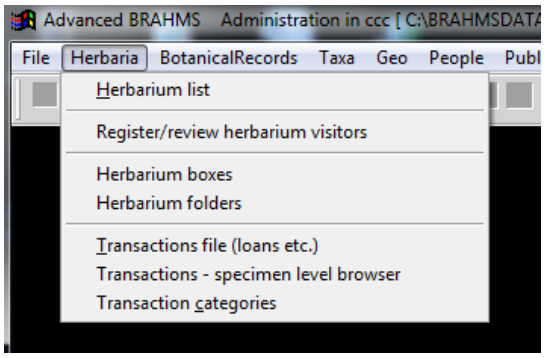
Website style and css file editing

Amongst the changes with WebConnect, more control over website layout is provided through editing access to your css (Cascading Style Sheet) file. Those interested can create/upload a custom css to help standardise fonts, colors, background, borders, text formatting and link effects on your BOL websites.



Herbarium options – a new menu

A reorganisation of herbarium related functions under a new principal 'Herbaria' menu as shown below. If needed, ensure the menu option is enabled from **Utilities > My setup > Active modules**.



Herbarium boxes and folders

Curation features have been added to manage herbarium boxes and specimen folders. Items are identified by barcodes. Herbarium specimens can now be linked to individual boxes and folders and the number of herbarium sheets per folder and folders per box auto-calculated. Folders are linked into boxes and can be assigned a taxa group (down to species level) and a geographic text, often a 'region'. These features have been added in part to support high volume, high resolution herbarium scanning initiatives such as that currently being implemented by Naturalis in the Netherlands.

Rapid specimen scanning

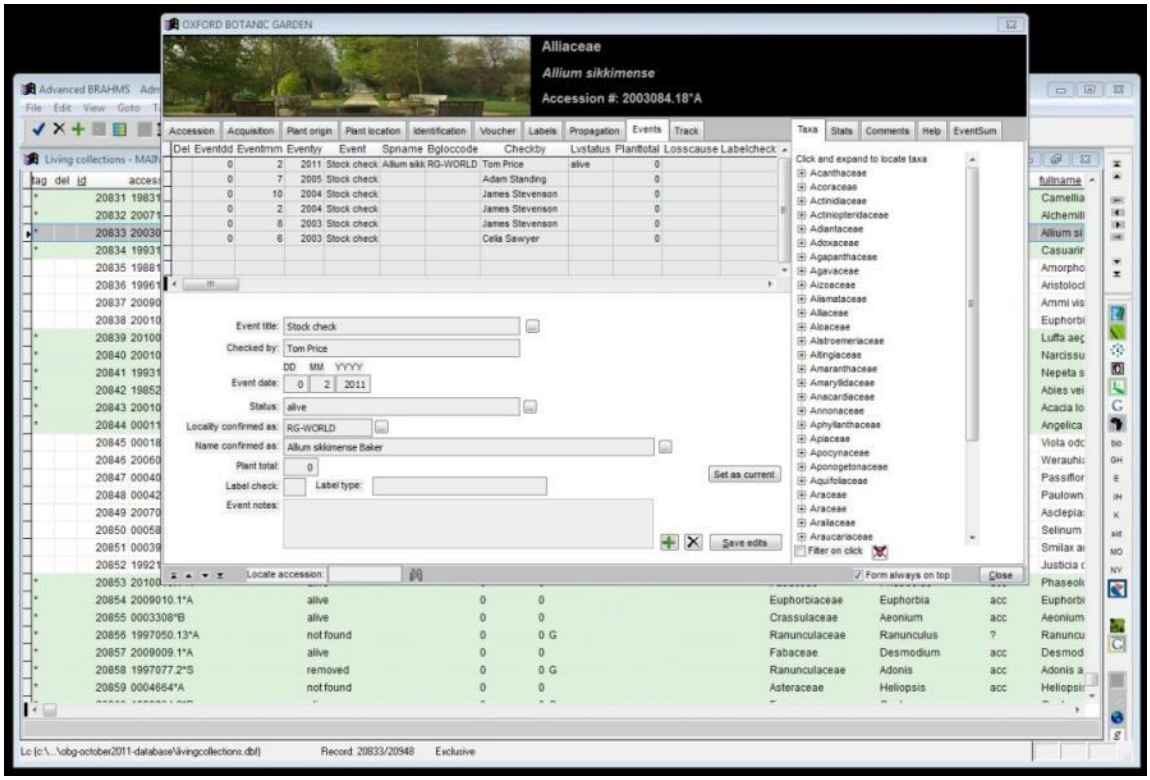
High volume, high resolution rapid specimen imaging tools developed in collaboration with Naturalis, Netherlands. For each herbarium box, images are scanned for the box (barcode), each folder cover within a box and each sheet within each folder. Barcodes (matrix) are included in the data returned from the scanner and all data are saved to a .csv file using post scan

software developed by Naturalis.

The CSV file is imported to RDE using a new **Tools** import option. Data and image file names are added, based on the correctly sorted, scanned images for each box, folder (taxa + region) and auto-propagated to all sheets within the folder, these having the same taxa and geo-region coding. Data from specimen images can then be added on a limited basis depending on resources (*e.g.* collector name, number, date, country). This process is currently being further developed and tested at the Naturalis herbaria in Wageningen and Leiden. The image shows the new scanning process underway at Wageningen.

Botanic Gardens

The Living Collections module for botanic gardens has been extended and refined after a year of use at the Oxford Botanic Garden.



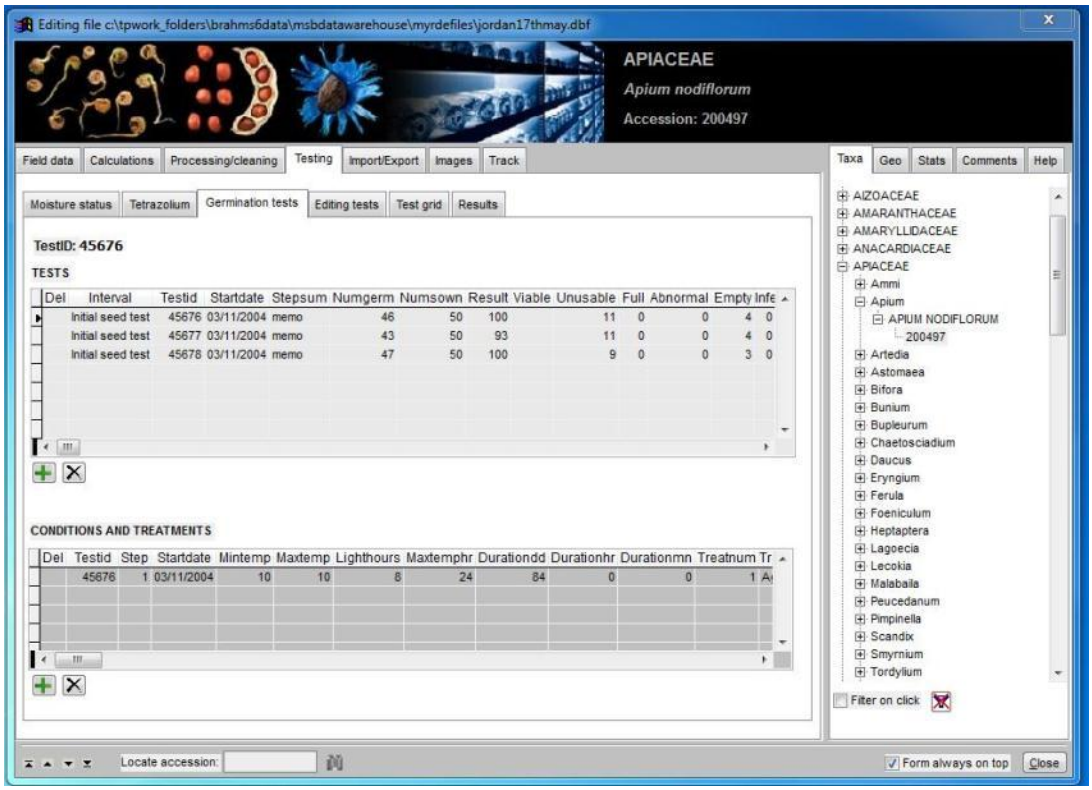
See short 2012 Oxford Plant Systematics article on:
http://herbaria.plants.ox.ac.uk/bol/content/documentation/OPS2012_OBG.pdf

Further details are provided in:
http://herbaria.plants.ox.ac.uk/bol/content/documentation/BRAHMSLivingCollections.pdf

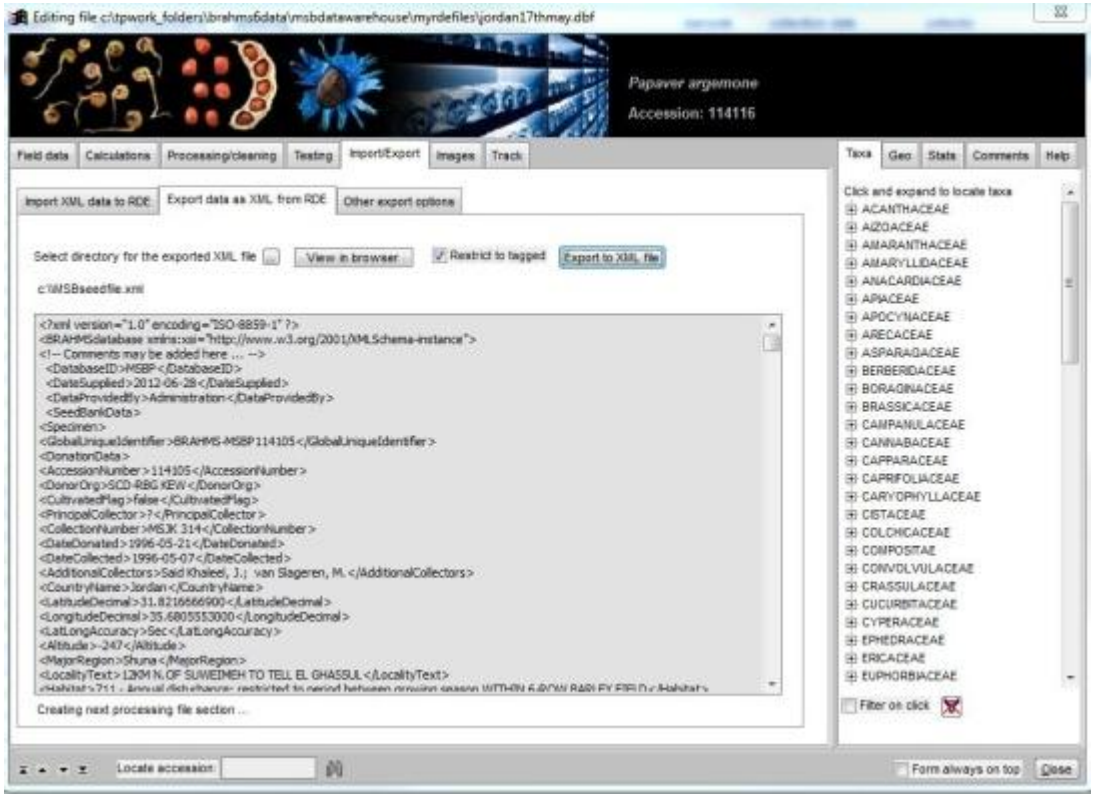
A number of new fields provided to record propagation details. These now include propagation type, date, done by who, propagation result, seed treatment, parent/crossing details where relevant and general notes.

Seed management

The BRAHMS Seed Management module has been developed collaboratively with the Millennium Seed Bank (MSB) Partnership at RBG Kew. Our focus has been on the development of the RDE template for seed collections allowing users to compile field, processing, germination, seed weight and tetrazolium test data in one simple data entry form. Partners duplicating material to the MSB for conservation storage are able to generate xml files directly from RDE, the resulting files being importable into the data management system at MSB. This transfer can also work in the reverse direction enabling data repatriation to Partners across the global MSB Partnership. The template also maps across to the online MSB Data Warehouse (http://herbaria.plants.ox.ac.uk/bol/msbp). Plans are being developed to extend functionality of the BOL online seed bank pages to facilitate seed exchange and purchase direct from the website; a service required by the many Tree Seed Centres within the MSBP.



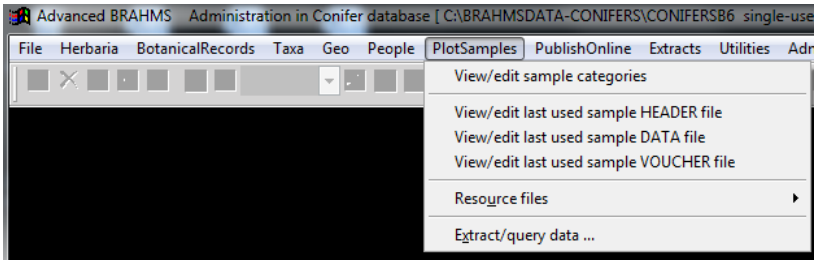
The Seed Manager data capture form in use for germination tests in an RDE file.



Generating an XML transfer file from the seed RDE file.

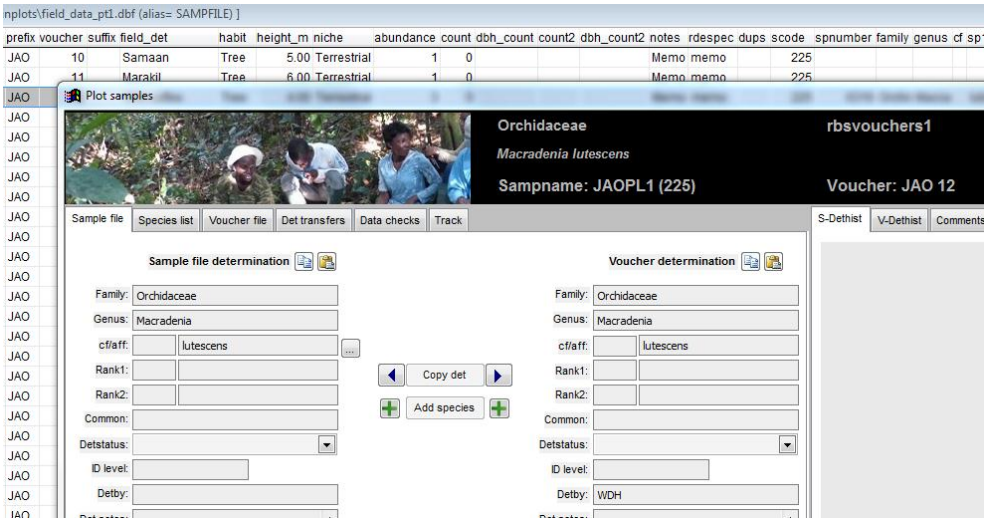
Plot sample module

A heavily revised sample plot module with a new menu interface has been implemented, in collaboration with William Hawthorne and very much geared towards Rapid Botanical Survey work as described in the Hawthorne guide now linked on the BRAHMS home page.



Aside from re-structuring the plot-sample menus, new tools have been added for plot header and data files. A new system to store plot vouchers added and integrated with the plot data file. Plot vouchering is a vital part of botanical survey.

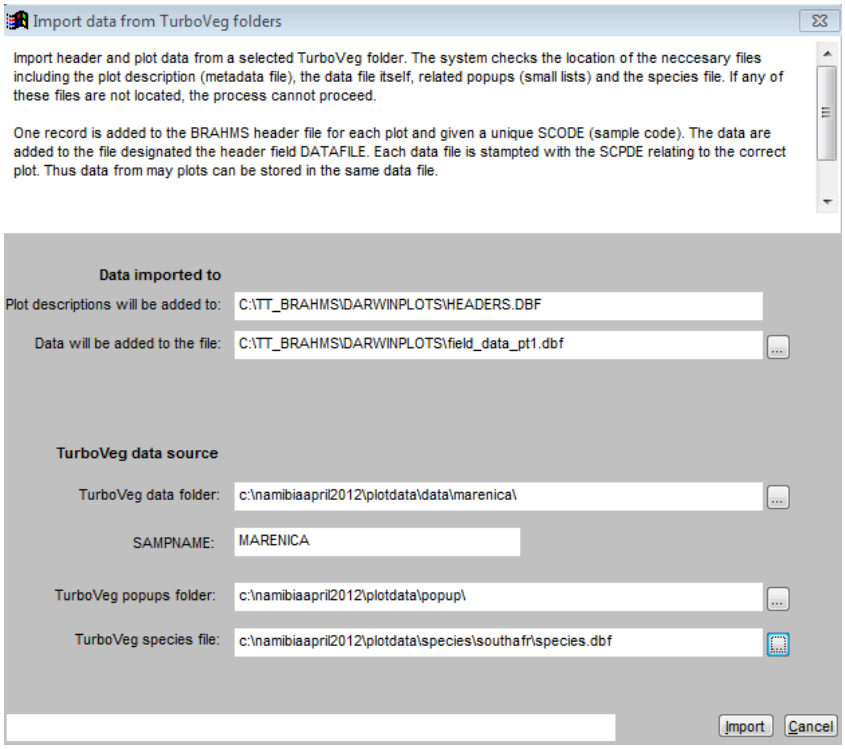
Vouchers from a plot survey in Liberia, often sterile, are identified and the data added to the plot voucher file. Each voucher is assigned a voucher code and this is also added to the plot sample record. Photo credits William Hawthorne.



Plot and voucher data can be viewed together to facilitate det updates. Data can be copied from voucher to plot file, vice versa. Further tools are provided on the form when browsing a sample data file.

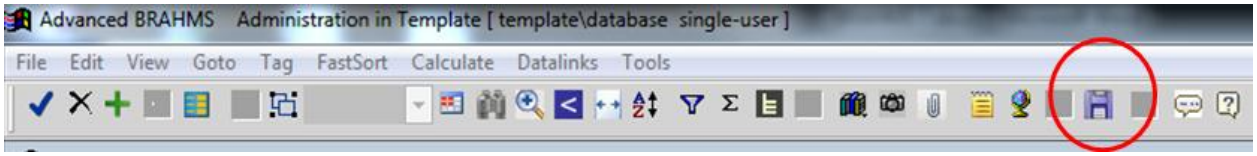
TurboVeg data importer

Plot data stored in standard TurboVeg files (habitat + abundance + species + various popup lists) can be imported to the BRAHMS plot sample module using the Tools option provided in an opened plot header file.



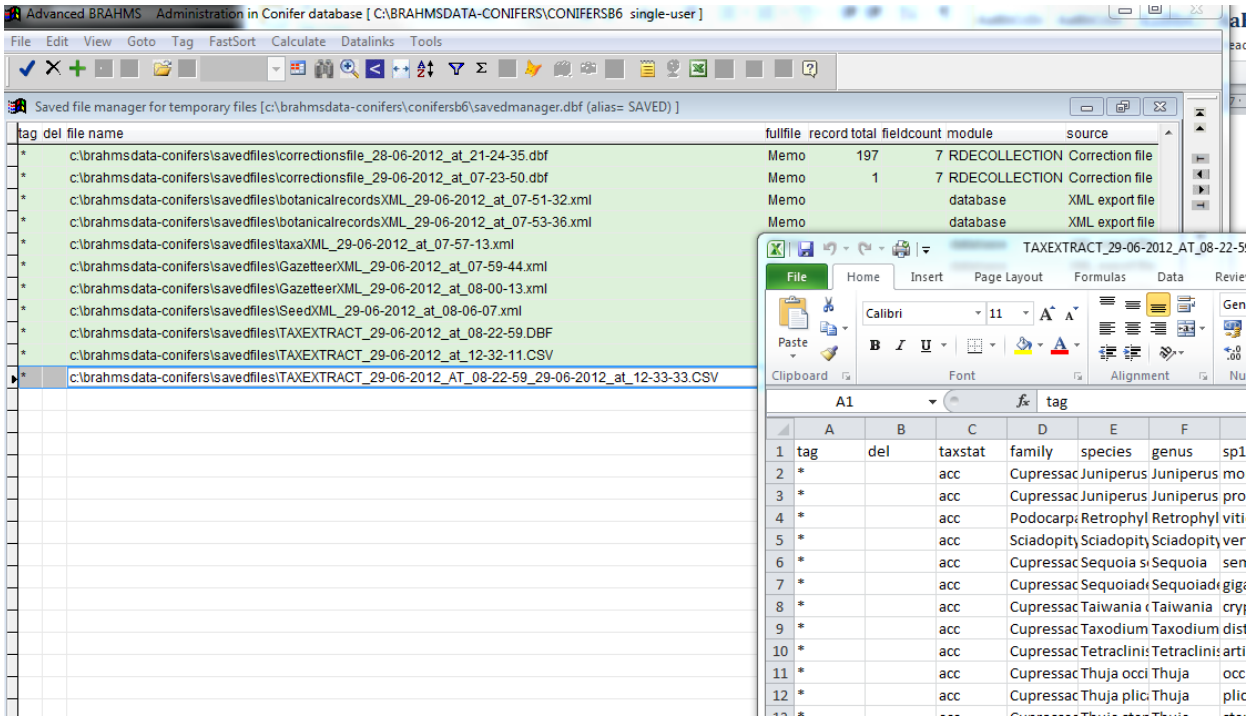
This option asks the user to locate the various folders where the TV habitat and abundance file are stored; some smaller dictionaries (popups) and the species reference list. Data for each plot is added to a BRAHMS plot header file and the data are added to a data file. Species names are added to the data file. The species names can subsequently be coded against an existing BRAHMS species list, and this process exposes new and potentially incorrect species names.

Saved File Manager



The 'Copy/Save as' function has been upgraded together with a new saved file manager.

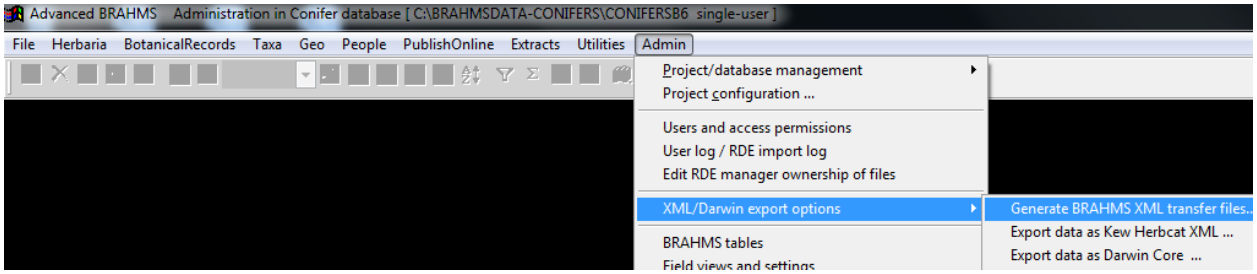
- All saved files are named with date and time, thus not overwriting earlier saved files.
- Saved files can be registered in the manager which is now accessed from the main File menu.
- Any file category (DBF,CSV, XML, XLS, MDB, etc.) can be opened directly from the file manager using the relevant software by dbl-clicking on the file name.
- The saved files manager is more easily accessible on the main **File** menu.



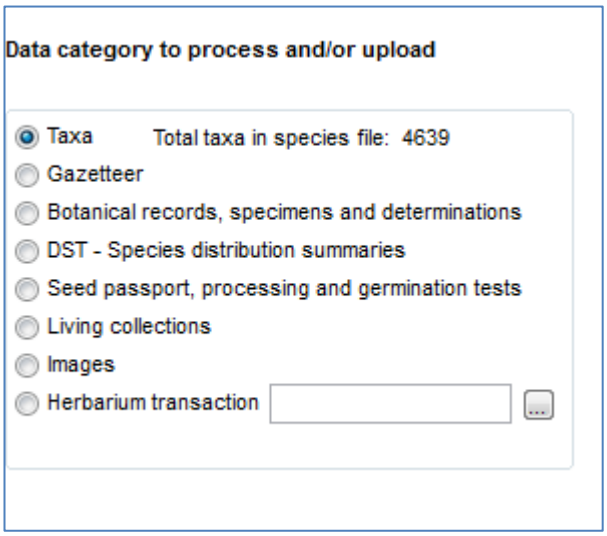
The Saved File Manager provides a central mechanism to open files of different types. Here shown open a saved .csv file.

XML exporting

The XML exporter (**Admin > XML/Darwin export options**) uses the same function as WebConnect. XML provides the most comprehensive way to export data from BRAHMS.



All XML files generated are saved to and can be opened from the saved file manager.

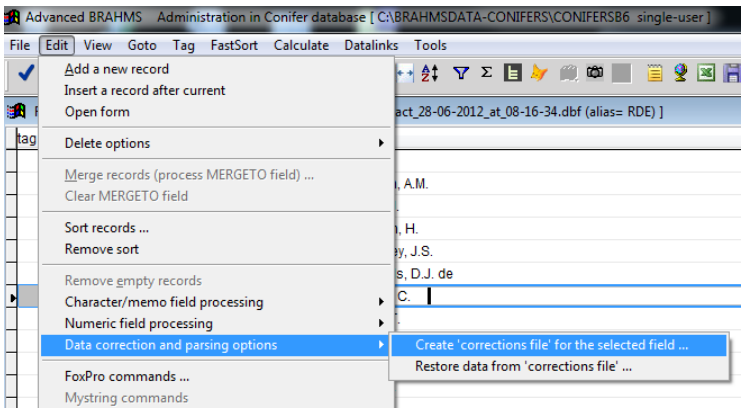


XML files can be created for the following data categories

An example XML output

Data correction files

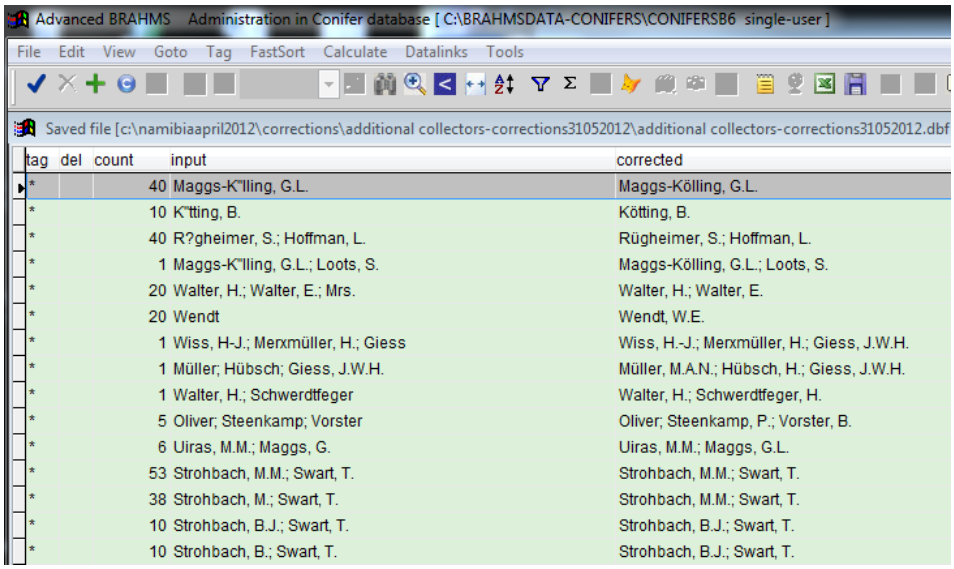
This function helps to clean up data in a selected field which includes misspellings and other errors. The contents of any non-read only field (*e.g.* any RDE field) can be uniquely copied to a 'correction file', edited, and then returned to the relevant data field in the donor file to update the data. Correction files can usefully be shared between projects.



Step 1: Choose a field that contains data to be edited. Typical examples are the fields such as COLLECTOR, ADDCOLL and DETBY in RDE files. But it could be any non-read only field in any BRAHMS file.

Step 2: Select **Edit > Data correction and parsing options > Create a corrections file for the selected field**. This will create a data file with one record for each different entry on the selected field. The file will be auto-registered in your saved file manager. It includes the fields INPUT (the list of names from the donor file) and CORRECTED (the field you can edit). By default INOUT fields are copied to CORRECTED as a) many entries will be correct and b) wrong entries are usually quite similar to the input field. may be similar.

Step 3: Edit the data in the field CORRECTED. After editing, entries that were already correct will have the same value as the original INPUT field.



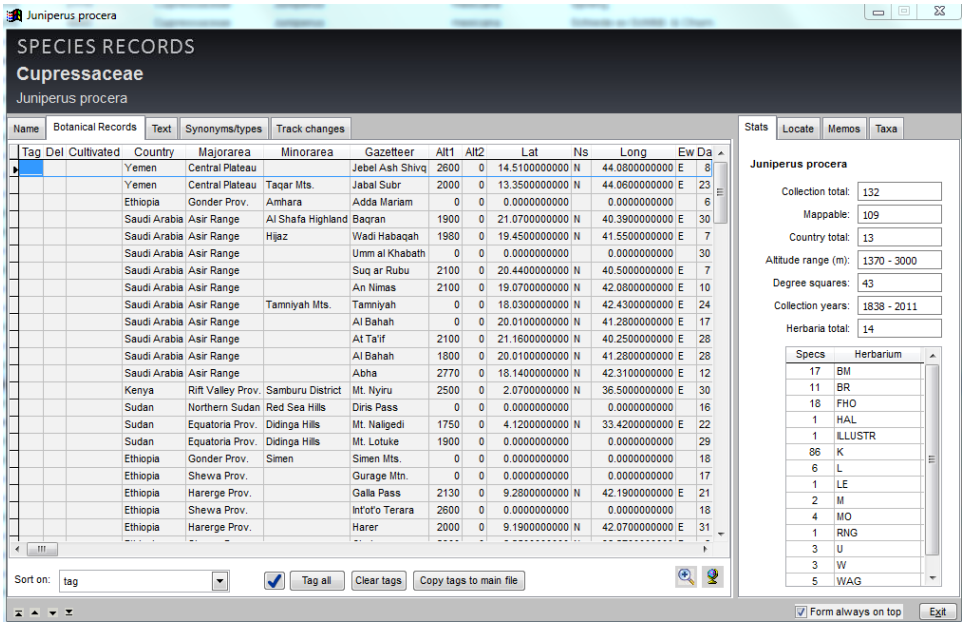
tag	del	count	input	corrected
*		40	Maggs-K"lling, G.L.	Maggs-Kölling, G.L.
*		10	K"tting, B.	Kötting, B.
*		40	R?gheimer, S.; Hoffman, L.	Rügheimer, S.; Hoffman, L.
*		1	Maggs-K"lling, G.L.; Loots, S.	Maggs-Kölling, G.L.; Loots, S.
*		20	Walter, H.; Walter, E.; Mrs.	Walter, H.; Walter, E.
*		20	Wendt	Wendt, W.E.
*		1	Wiss, H-J.; Merxmüller, H.; Giess	Wiss, H.-J.; Merxmüller, H.; Giess, J.W.H.
*		1	Müller; Hübsch; Giess, J.W.H.	Müller, M.A.N.; Hübsch, H.; Giess, J.W.H.
*		1	Walter, H.; Schwerdtfeger	Walter, H.; Schwerdtfeger, H.
*		5	Oliver; Steenkamp; Vorster	Oliver; Steenkamp, P.; Vorster, B.
*		6	Uiras, M.M.; Maggs, G.	Uiras, M.M.; Maggs, G.L.
*		53	Strohbach, M.M.; Swart, T.	Strohbach, M.M.; Swart, T.
*		38	Strohbach, M.; Swart, T.	Strohbach, M.M.; Swart, T.
*		10	Strohbach, B.J.; Swart, T.	Strohbach, B.J.; Swart, T.
*		10	Strohbach, B.; Swart, T.	Strohbach, B.J.; Swart, T.

The above correct file was created from a large RDE file with plenty of problem spellings with collector names (mostly missing initials and accent problems). The INPUT field contains a unique list of entries generated from the RDE file and these have been edited and corrected where necessary. The COUNT field indicates the number of records with the entry.

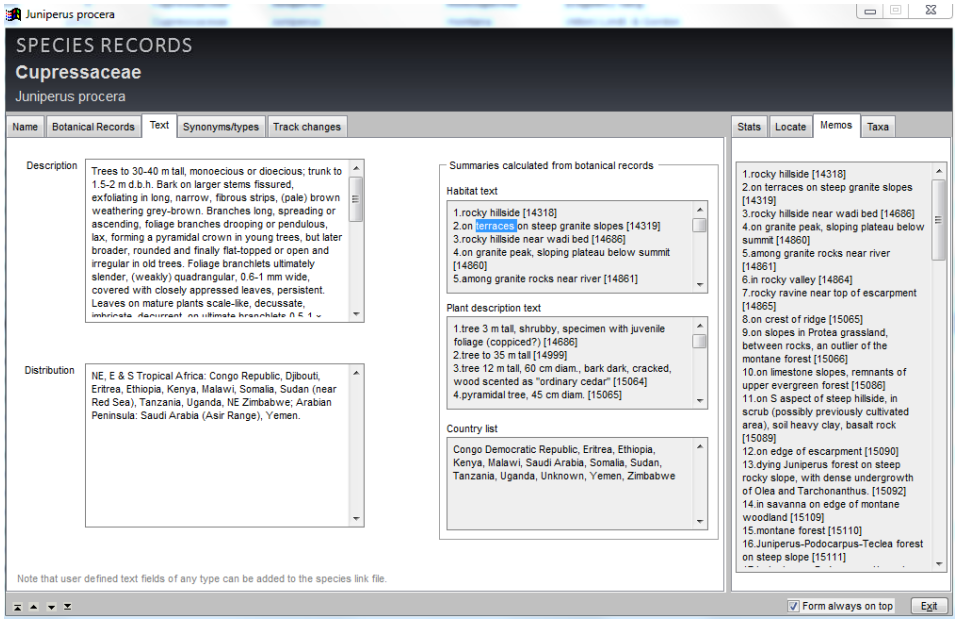
Step 4: Once the file has been edited, it can be fed back into the relevant file using Select **Edit > Data correction and parsing options > Restore data from corrections file.** In the above example, any field with the entry W. Giess would be corrected to Giess, J.W.H.

Species form

The main species file has an entirely new form providing improved editing controls, access to botanical record data and various useful stats. The form can be used together with the data grid and can be dragged over to a separate monitor.



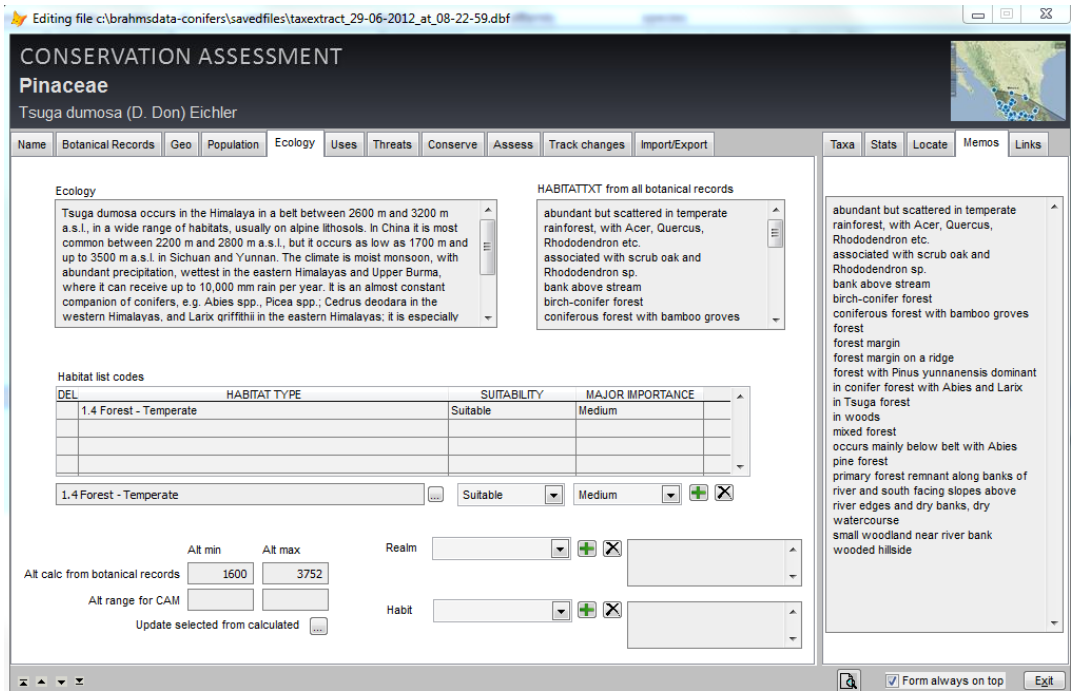
Here showing botanical records for the current species and the stats screen with a summary of the botanical records including a summary of the herbaria the specimen data are derived from.

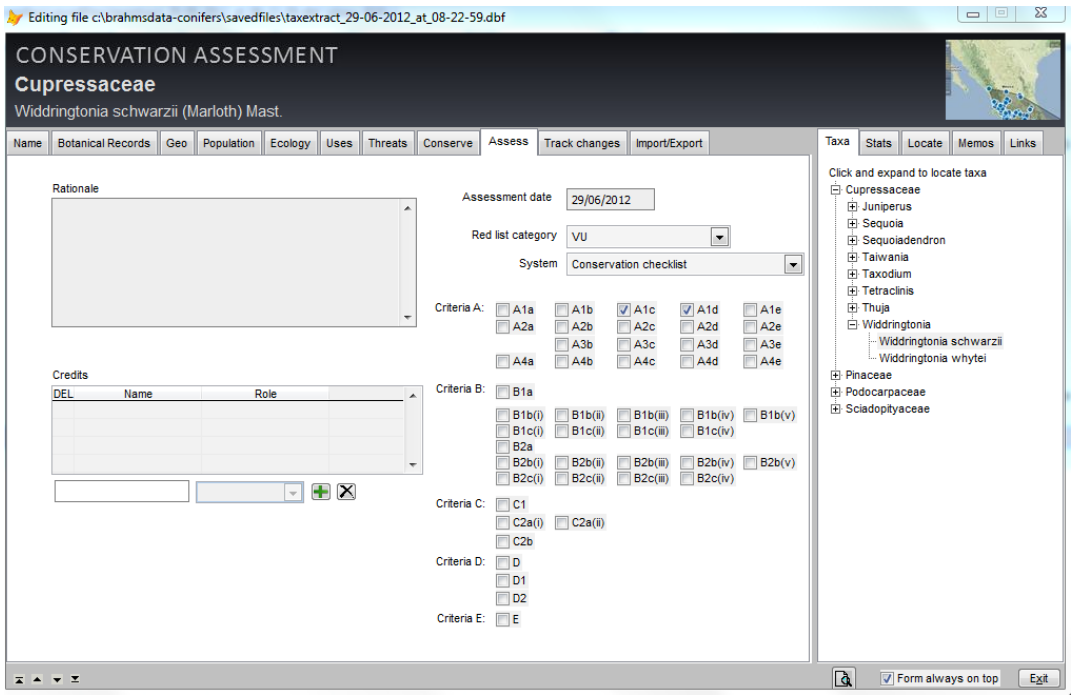


The species form Text page includes an assembled summary of all HABITATTXT and PLANTDESC memos for all botanical records of the current species. Dbl-clicking on any memo text area opens the text in a larger editing area on the right pane. The summaries are useful when preparing species descriptions.

Conservation Assessment Module (CAM) beta

A new module (currently beta) to store data for conservation assessments has been added in collaboration with the Red Listing and conservation assessment projects at RBG Kew. Data are entered via Taxa RDE files using the CAM form, opened in taxa RDE files. Lookup values for all options can be pre-loaded into your custom lookup dictionary using Admin > Custom lookups > Tools. The custom look file is currently in development but a first draft is in the setupdata/cam folder.

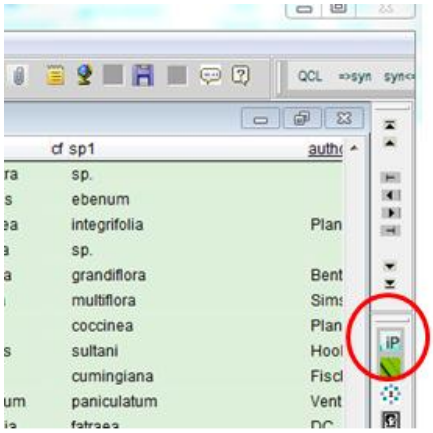


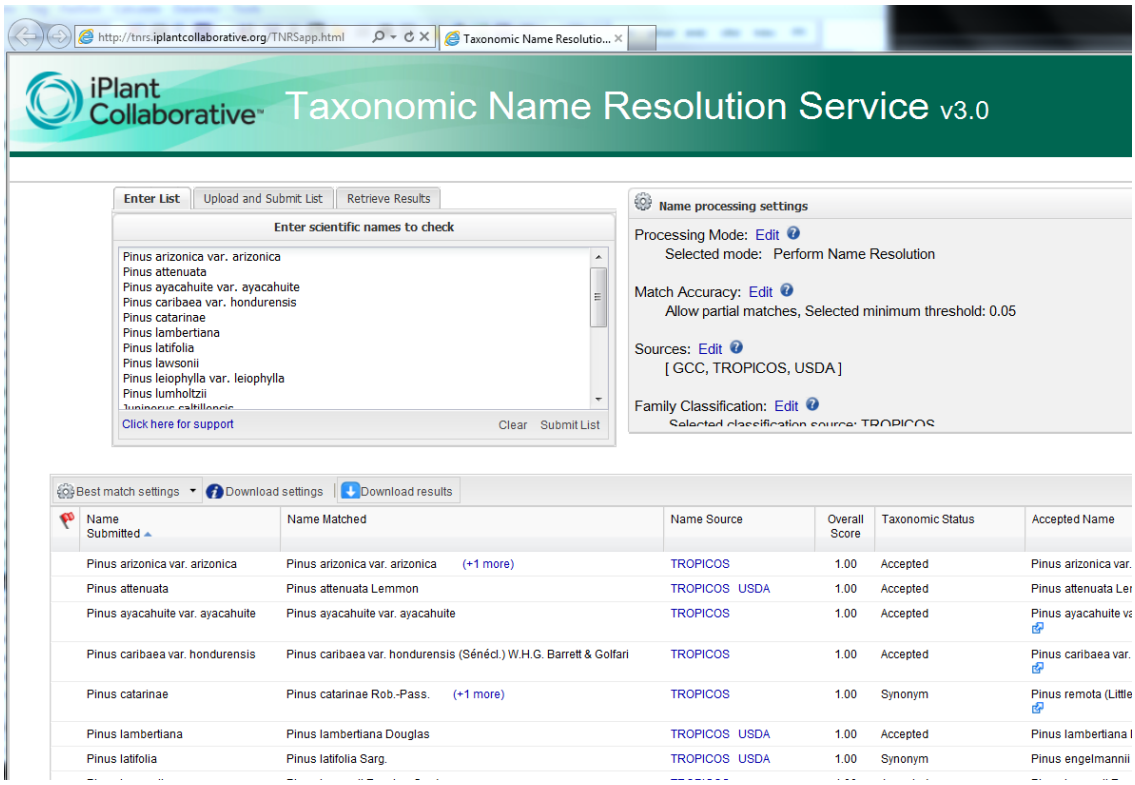


Assessment data are stored in a single RDE file. Botanical records stored in your database are used to help calculate country occurrence, altitude range and AOO /EOO, the latter through a direct link to GeoCAT. Selected botanical records (*e.g.* cultivated or inaccurate records) can be excluded from calculations. The CAM module is currently being extended to generate XML that can be uploaded to IUCN.

Taxonomic Name Resolution Service

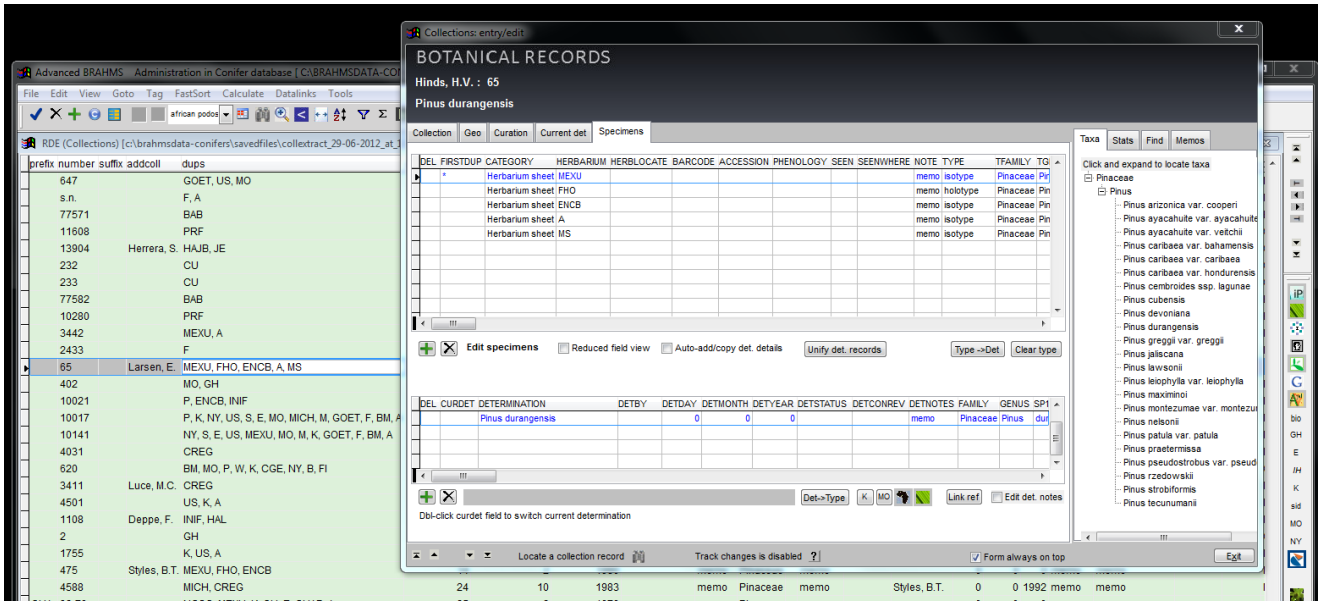
Links to the Taxonomic Name Resolution online service (http://tnrs.iplantcollaborative.org/TNRSapp.html) have been implemented with a new internet toolbar option. The toolbar option assembled tagged taxa names in the current file onto a clipboard – allowing to copy/paste the names to the TNRS 'submit' text area.



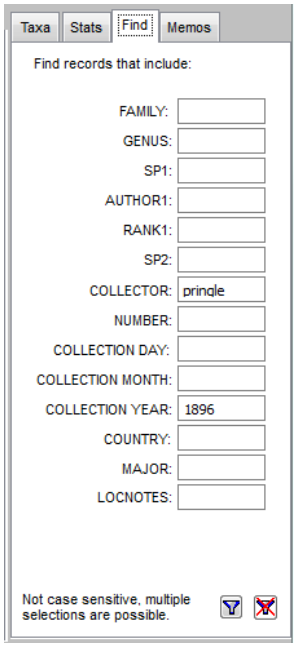


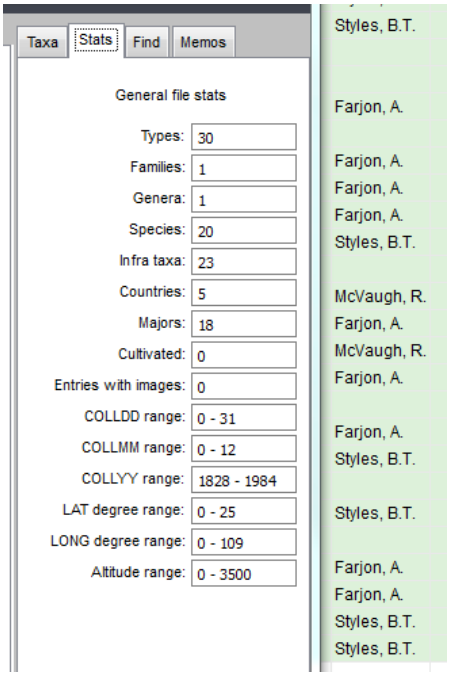
Up to 5000 names can be submitted at once. Each name is checked against the sources you select on the TNRS setup option.

A new form for RDE and botanical records



The data capture form for RDE and the main botanical records file has been heavily revised. The form can be used at the same time as the data grid on the same or a separate monitor.





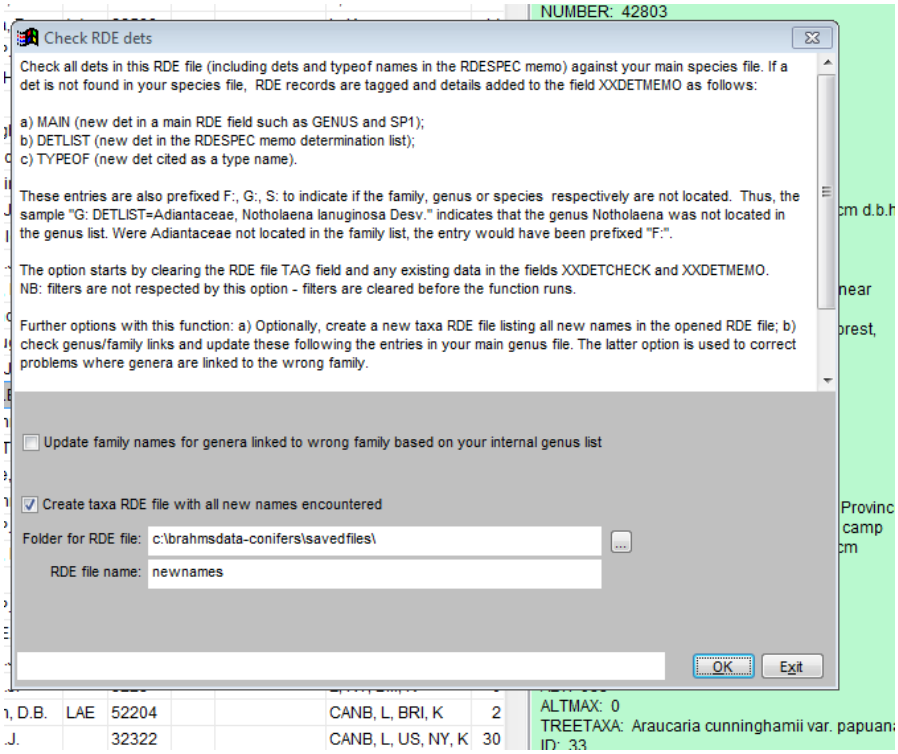
The Find tab provides handy search options for RDE records. The Stats pane provides a general summary about the data in an open RDE file. Erroneous ranges are highlighted in bold.

RDE botanical records species name checker

This handy new tool helps you check through any botanical records RDE file – looking for names that are not already registered in your main species list. This is not always an easy task as determinations and names used for types are often 'hidden' in the RDESPEC memo. Problems in larger and older RDE files build up especially when the main species list has been extensively edited - leaving redundant names in the RDE file. And these names can be difficult to locate. When such RDE files are transferred to BRAHMS, this may result in many new names being inappropriately added to your taxa files. The function is found in botanical record RDE files using **Tools > Data checks >Taxa > Check all dets including names in RDESPEC memo.**

Optionally, any new names encountered can be used to create a Taxa RDE file. Also, any many new names are often due to simple family name re-designations, you can auto-update the family names in the RDE file based on your database family – genus arrangements.

For a full description: http://herbaria.plants.ox.ac.uk/bol/content/documentation/RDEdetchecking.pdf



RDE name checking form

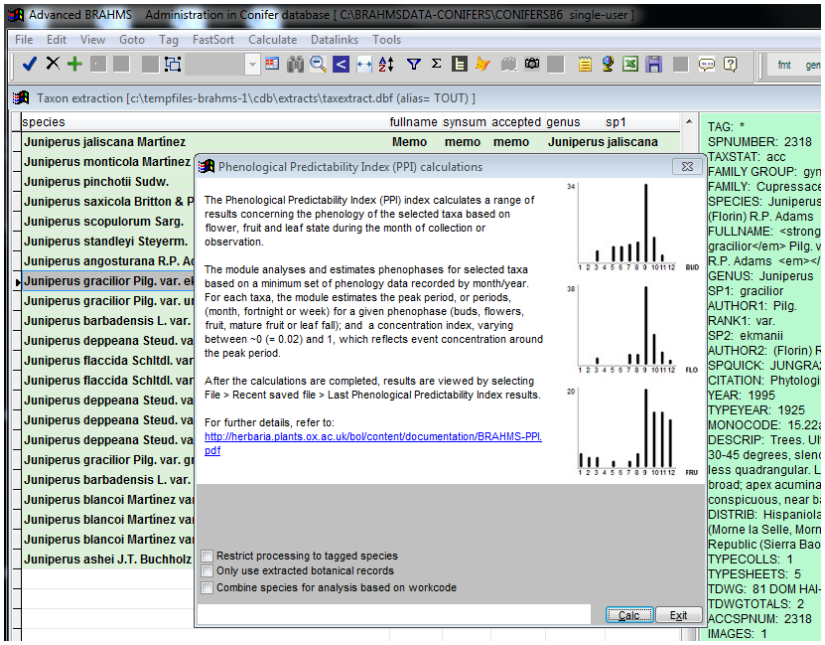
Phenology and phenophase analysis

Results from the PPI tool allow you to analyse and estimate phenophases for selected taxa based on a minimum set of phenology data recorded by month. PPI produces three taxon-specific results:

- Maximum probability period (currently month) for the phenophase;
- A predictability index, varying between ~0 (= 0.02) and 1;
- Chart of the predictability indexes for the periods (currently 12 months of the year).

Phenological Predictability Index in BRAHMS: a tool for herbarium-based phenological studies. Ecography Volume 35, Issue 4, pages 289-293, April 2012. (http://onlinelibrary.wiley.com/doi/10.1111/j.1600-0587.2011.07329.x/abstract).

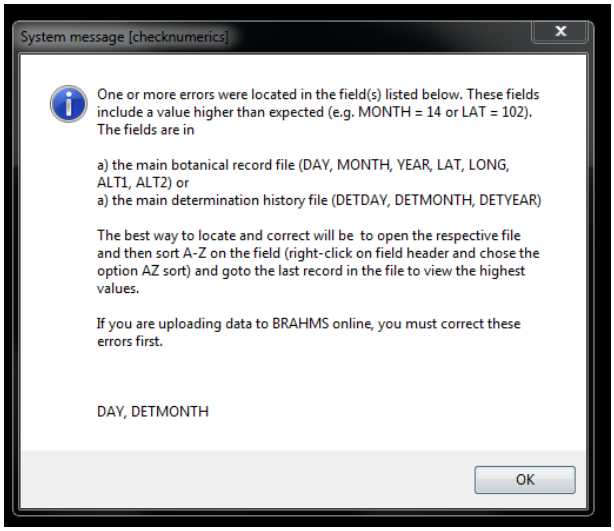
For implementation within BRAHMS, see http://herbaria.plants.ox.ac.uk/bol/content/documentation/BRAHMS-PPI.pdf



The Phenological Predictability Index (PPI) processing screen in a taxa extract.

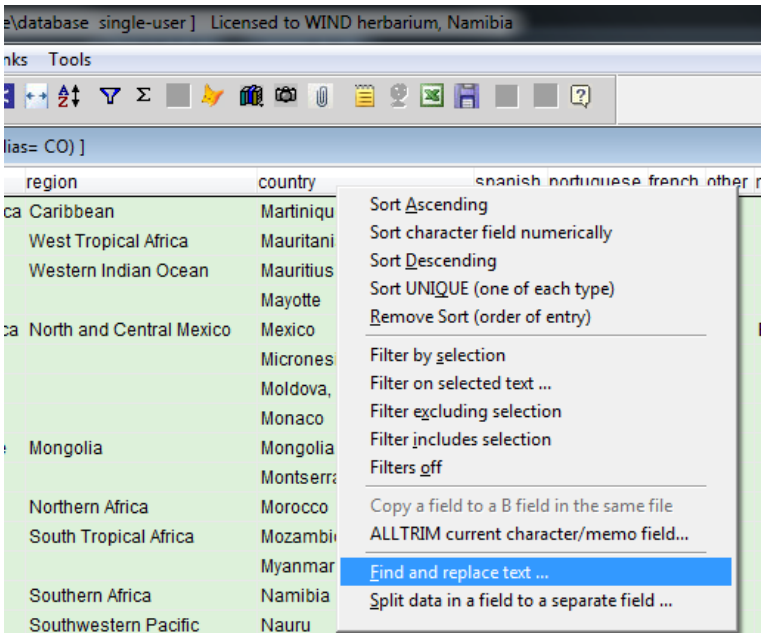
Improved error checking on re-indexing

Re-indexing now checks for obvious errors in altitude, collection date, detby date and lat/long fields.



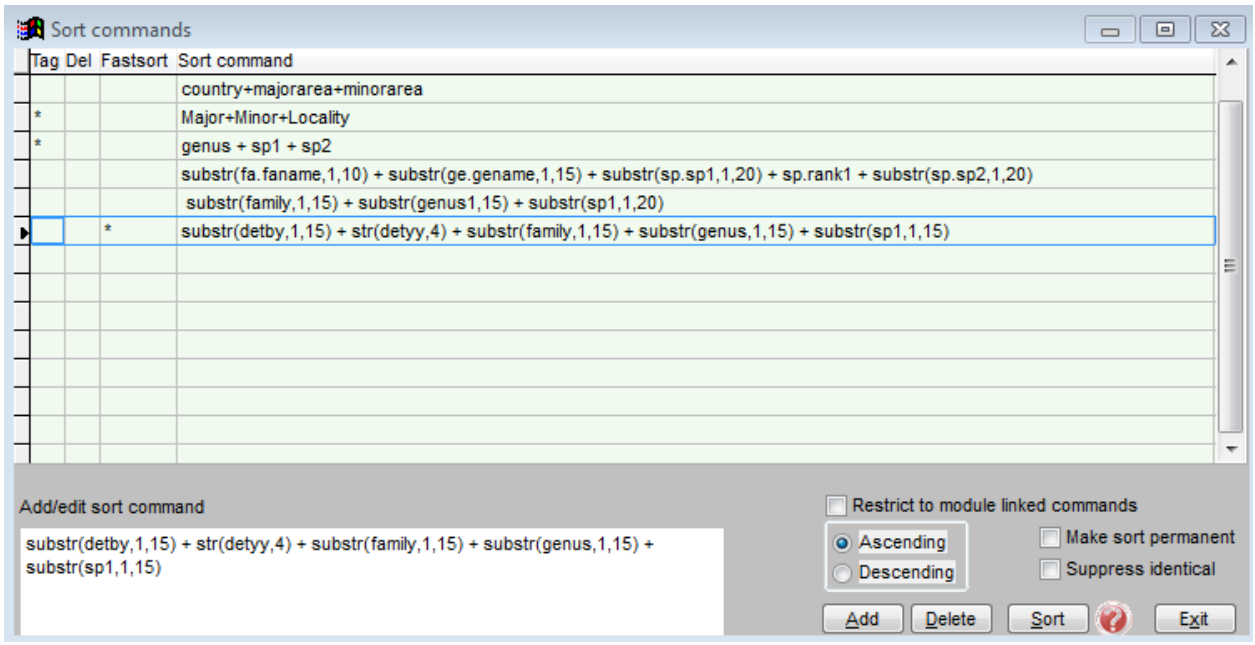
Short cut menus extended

New shortcut menus on data grid header right-clicks include find/replace, split data, an alltrim function for character/memo fields and a field duplication option for column duplication to a '_b' field.



Advanced sort and saved FastSort

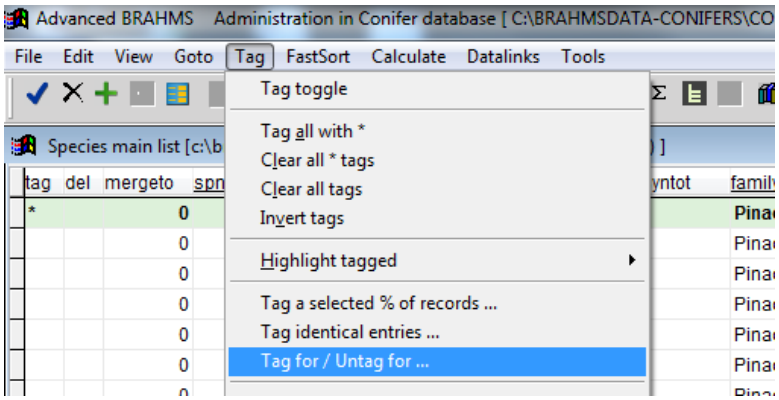
New Advanced Sort module with improved control over sort commands. A favourite command can be marked for addition to the FastSort menu.



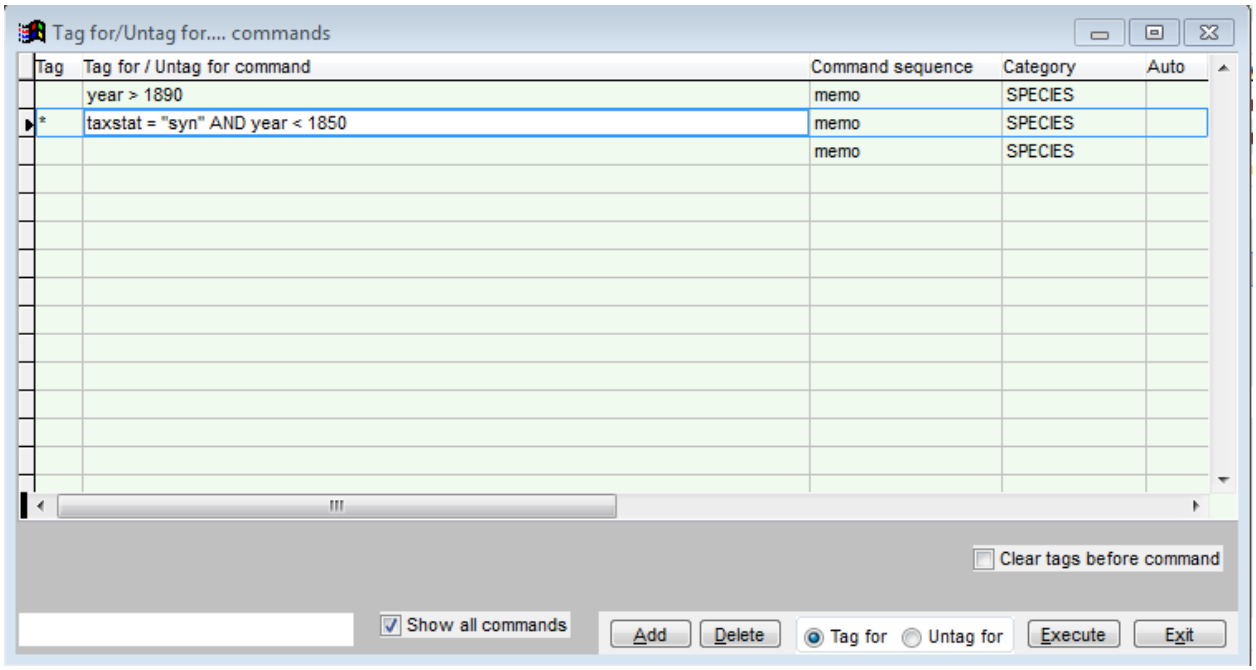
Advanced sort commands are easier to add, edit and select. You can add a common used advanced sort to your FastSort menu.

Tag for commands

New 'Tag for' commands module with improved control over commands. Commands are saved in a project file and thus can be reused.



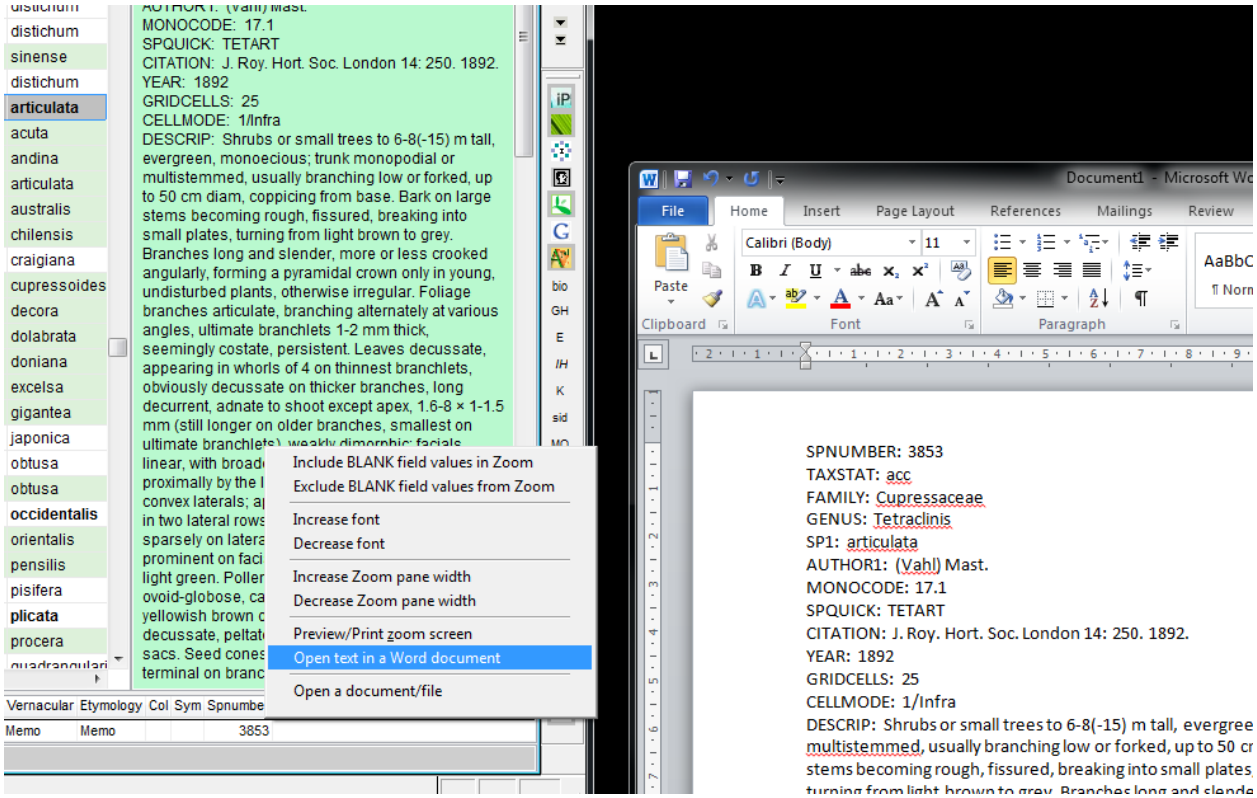
The Tag for menu option



The Tag for command screen

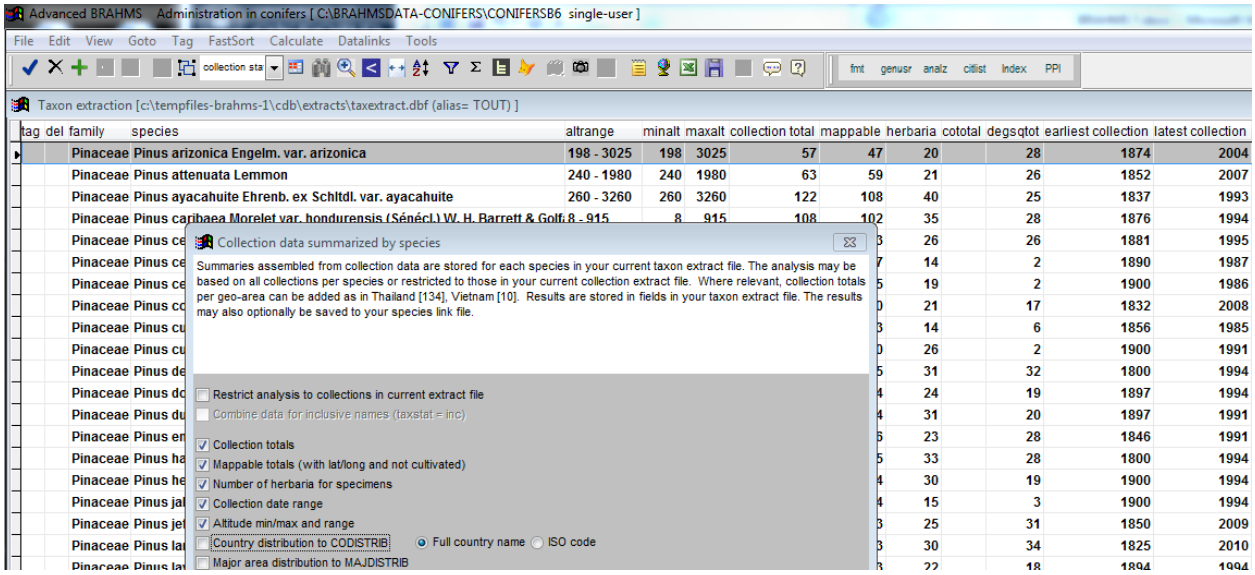
Zoom window enhancements

The Zoom window has a new option to open Zoom content as a Word document. Handy for spell checking.



Taxa extract collection analysis

Some additional calculations added to the taxa extract under **Tools > Collection data analysis**



New calculations per taxa include total number of mappable records and the total number of different herbaria for specimens.