BRAHMS

BOTANICAL RESEARCH AND HERBARIUM MANAGEMENT SYSTEM

TRAINING GUIDE AND INTRODUCTORY COURSE

Updated June 2013
Applies to v. 7.3 onwards

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ABOUT THIS GUIDE

This guide is a training guide, not a manual. More comprehensive documentation is available on http://dps.plants.ox.ac.uk/bol/BRAHMS/Documentation/Index. The guide is suitable for beginner and intermediate levels, addressing collection management and research topics.

The correct way to quote this guide is ‘Filer, D.L. (2013). Botanical Research And Herbarium Management System training guide. Department of Plant Sciences, University of Oxford.’

Unless carefully managed, courses can bewilder the first time user.
This guide helps to introduce the system in gradual steps.

Syntax used

The text **Admin > Users and access permissions** means:

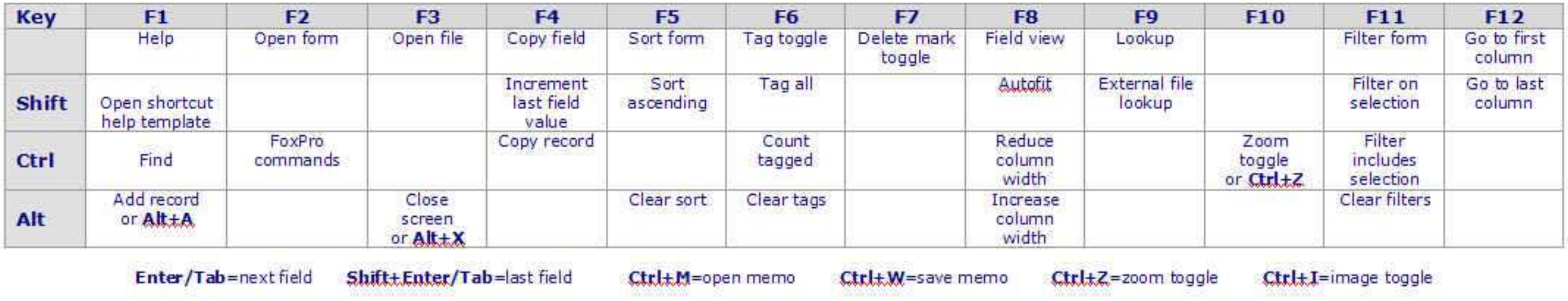
Select the menu option **Admin** followed by the menu option **Users and access permissions**.

Function key template

You can cut out the function key template from the guide, fold the page appropriately and keep it near your keyboard. Using function keys speeds things up.

FUNCTION KEY TEMPLATE

(you can fold this page and put near your keyboard)



Key	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12
	Help	Open form	Open file	Copy field	Sort form	Tag toggle	Delete mark toggle	Field view	Lookup		Filter form	Go to first column
Shift	Open shortcut help template			Increment last field value	Sort ascending	Tag all		Autofit	External file lookup		Filter on selection	Go to last column
Ctrl	Find	FoxPro commands		Copy record		Count tagged		Reduce column width		Zoom toggle or **Ctrl+Z**	Filter includes selection	
Alt	Add record or **Alt+A**		Close screen or **Alt+X**		Clear sort	Clear tags		Increase column width			Clear filters	

Enter/Tab=next field **Shift+Enter/Tab**=last field **Ctrl+M**=open memo **Ctrl+W**=save memo **Ctrl+Z**=zoom toggle **Ctrl+I**=image toggle

INSTALLATION

Training course folder

On courses, you may be given a zip file which will open to create a folder called **BRAHMS Training Course**. This folder includes all the resources you need.

If you do not have this folder, you can separately download components as follows:

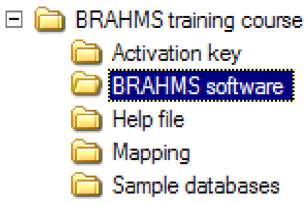
BRAHMS: http://dps.plants.ox.ac.uk/bol/BRAHMS/Software/Index
Conifer database: http://dps.plants.ox.ac.uk/bol/BRAHMS/Sample/Conifers
DIVA GIS: http://www.diva-gis.org/
Sample base maps data: http://dps.plants.ox.ac.uk/bol/BRAHMS/GroupResources/Index

If BRAHMS is already installed on your PC

If you previously installed BRAHMS for testing, delete your existing BRAHMS folder. Also, delete all \tempfiles-brahms folders. Then proceed to install the new system. If you have one or more active BRAHMS databases, follow the link for installation help on http://dps.plants.ox.ac.uk/bol/BRAHMS/Software/Index

System installation

- Locate the brahms.zip file in the software folder - or locate your software download file.



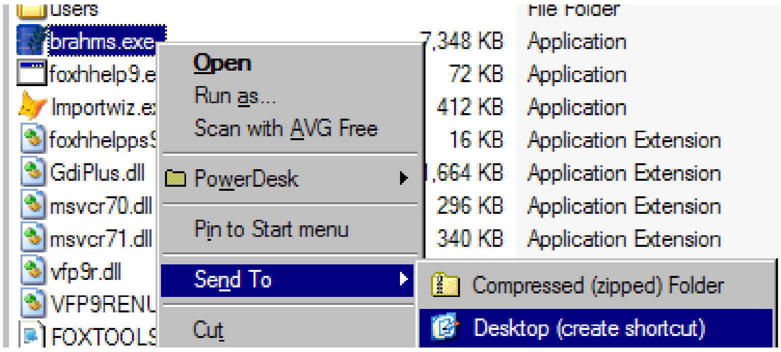
- **Extract** the software zip file to the top level of your C: drive (usually referred to as ‘Local Disk (C:)’ or ‘DRIVE_C (C:)’. This will create a folder called C:\BRAHMS7. You can extract the software zip elsewhere if you wish. The software folder will always be created relative to the folder you choose.

Activation key

- If you do not have a key in your Activation key folder, login to the BRAHMS website and download your key from http://dps.plants.ox.ac.uk/bol/BRAHMS/Members. If you cannot login, please register using the menu option provided on the home page. Copy the file BRAHMSKEY.MEM (unzipped) to the BRAHMS7 folder.

Creating a desktop shortcut to BRAHMS

- **Locate** the file BRAHMS.EXE (represented by a blue drum) in the BRAHMS7 folder. The ‘.exe’ file extension may be hidden.
- **Right-click** on this file and choose **Send to > Desktop (create shortcut)**.



- Optionally, **right-click** on the new shortcut, choose the **Rename** option and type in “BRAHMS”.

THE CONIFER DATABASE

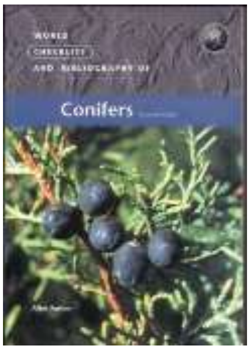
About the conifer database

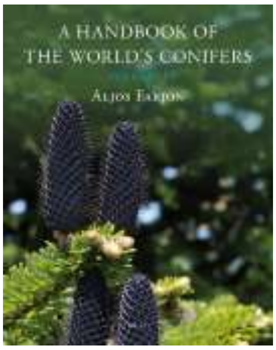
The conifer database has been provided by Aljos Farjon, RBG Kew - a taxonomist of gymnosperms and chair of the IUCN Conifer Specialist Group. If you wish to use the data for a research publication or any other purpose beyond training, kindly consult first with A.Farjon@kew.org.

The conifer database includes all published conifer names with nomenclatural details, IUCN conservation codes, TDWG geographic distribution codes, species descriptions and more. It also includes specimen data across the group, almost all referenced for mapping. Species texts (*e.g.* description) have been truncated to a maximum of 500 characters.

The conifer database has been used to help publish a number of publications including:

- A taxonomic monograph on *Pinus* for Latin America (Farjon, A. & Styles, B. T., 1997. Flora Neotropica Monograph 75, The New York Botanical Garden
- A World Checklist And Bibliography of Conifers, Aljos Farjon, 1998
- A Monograph of Cupressaceae and Sciadopitys, Aljos Farjon, 2005
- A Handbook of the World's Conifers. Publication: 2010
- An Atlas of the World's Conifers, an Analysis of their Distribution, Biogeography, Diversity and Conservation Status, Aljos Farjon and Denis Filer: 2013



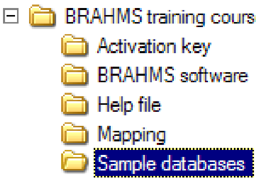


Download database from BRAHMS website

If you do not have the conifer database, it can be downloaded from http://dps.plants.ox.ac.uk/bol/BRAHMS/Sample/Conifers.

Installing the conifer database

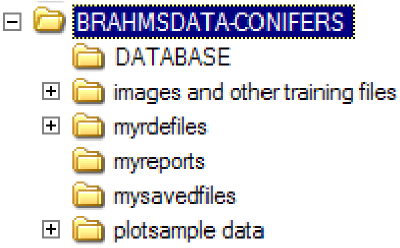
- Locate the conifer database.zip file in the samples folder as shown below or locate your sample database download file.



BRAHMS training course
Activation key
BRAHMS software
Help file
Mapping
Sample databases

- **Extract** the zip file to the top level of your C: drive (usually referred to as 'Local Disk (C:)' or 'DRIVE_C (C:)'. This will create C:\ BRAHMSDATA-CONIFERS.

If you have installed to another folder, you will have problems later on with this guide. In this case, move the folder to C: to create c:\brahmsdata-conifers.



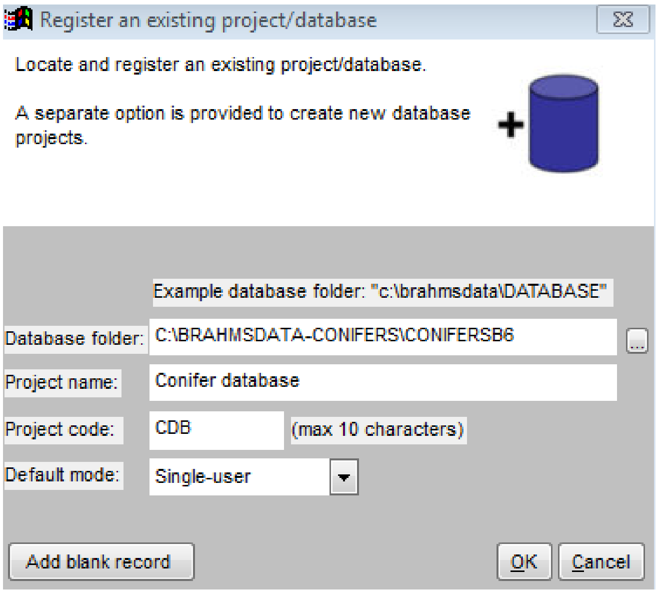
BRAHMSDATA-CONIFERS
DATABASE
images and other training files
myrdefiles
myreports
mysavedfiles
plotsample data

The installed database folder includes several subfolders similar to the above. Of these the most important is DATABASE. The **myrdefiles**, **myreports** and **mysavedfiles** folders are empty folder provided as suggested locations for various files..

Register the conifer database in BRAHMS

- Log into the **TEMPLATE** database using user name Administrator and password A.
- Select **File > Database manager**.

Assuming the conifer database is not yet registered, click the + toolbar. Add an entry for the Conifer database as shown in the following screen.



Register an existing project/database

Locate and register an existing project/database.

A separate option is provided to create new database projects.

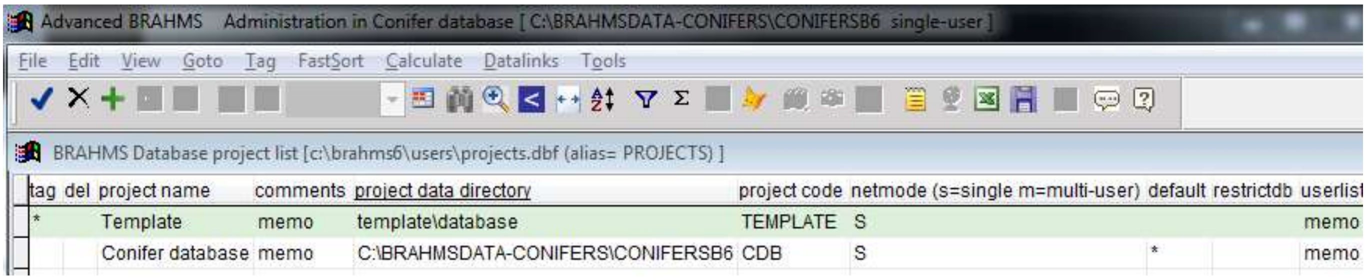
Example database folder: "c:\brahmsdata\DATABASE"

Database folder: C:\BRAHMSDATA-CONIFERS\CONIFERSB6

Project name: Conifer database

Project code: CDB (max 10 characters)

Default mode: Single-user



Advanced BRAHMS Administration in Conifer database [C:\BRAHMSDATA-CONIFERS\CONIFERSB6 single-user]

BRAHMS Database project list [c:\brahms6\users\projects.dbf (alias= PROJECTS)]

tag	del	project name	comments	project data directory	project code	netmode (s=single m=multi-user)	default	restrictdb	userlist
*		Template	memo	template\database	TEMPLATE	S			memo
		Conifer database	memo	C:\BRAHMSDATA-CONIFERS\CONIFERSB6	CDB	S	*		memo

Note that the database folder is pointing to the DATABASE subfolder.

PREPARE FOR MAPPING

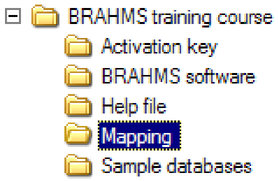
This step may be done now or later on.

Installation steps

If you do not have a special training course folder and wish to install DIVA, you can visit:

DIVA GIS: http://www.diva-gis.org/
Sample base maps data: http://dps.plants.ox.ac.uk/bol/BRAHMS/GroupResources/Index

- **Locate** the folder 'C:\ BRAHMS training course \ Mapping'.



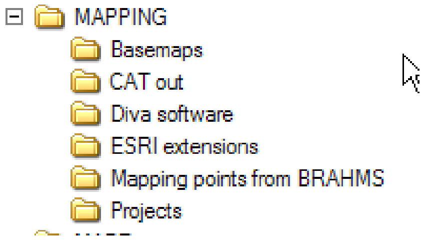
- **Extract** the mapping. zip file to the top level of your C: drive (usually referred to as 'Local Disk (C:)' or 'DRIVE_C (C:)'. This will create C:\ MAPPING.

Installation of DIVA GIS

If you wish to install DIVA (you may already have ArcView or another GIS):

- Locate the file SETUP.EXE in the folder Mapping \ Diva software OR from your download
- **Run this setup**. This will install DIVA GIS on your PC.

Mapping folder explained



! It is convenient to keep all your mapping resources and files under one main folder (here \MAPPING). In particular, it is useful to have the 'basemaps' folder adjacent to the 'mapping points from BRAHMS' folder

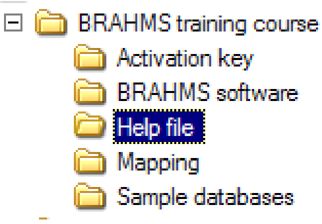
Basemaps	Country and internal admin boundary .SHP for use with DIVA and/or ArcView.
CAT out	A folder for Conservation Assessment results generated by the CATS tool (ArcView users only).
Diva software	Diva setup files – ready to install. Just run the SETUP.EXE file.
ESRI extensions	CATS.AVX file and PDF file documenting the Conservation Assessment Tools.
Mapping points from BRAHMS	Empty folder for your BRAHMS generated map files.
Projects	Empty folder for you to save APR and DIV projects to.

THE BRAHMS HELP FILE

Move or copy the help file to your desktop

If you do not have a special training course folder, the help file is available on http://dps.plants.ox.ac.uk/bol/BRAHMS/Documentation/Download/

- **Locate** the folder 'C:\ BRAHMS training course \ Help file'.
- **Drag** the file BRAHMS.CHM onto your desktop. This will be useful to have quick access.

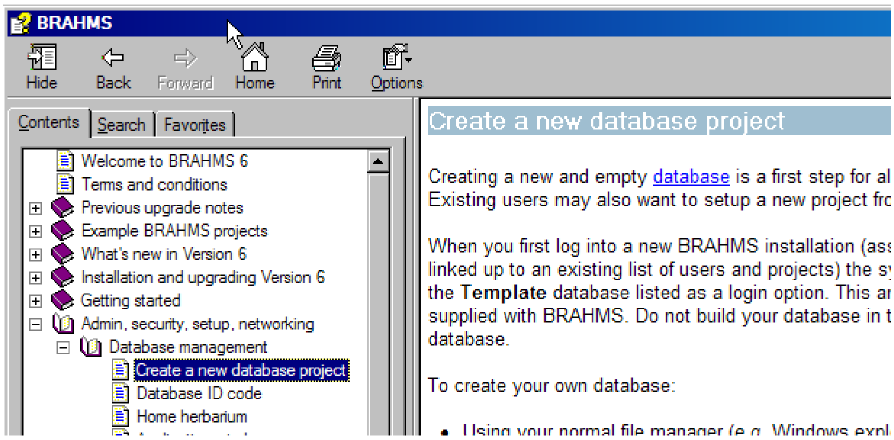


BRAHMS training course
- Activation key
- BRAHMS software
- Help file
- Mapping
- Sample databases

! The CHM help file will not work correctly if stored on a network drive. Locate it on your local drive.

Opening the help file and reading a topic

- Using your file manager (*e.g.* Windows Explorer), locate and **dbl-click** the help file icon to open. Note there are **Contents**, **Search** and **Favorites** tabs.
- Click on the **Contents** tab.
- To open a section (purple book icon),click on the left hand side **+**.
- To display a topic, click on the page you want to open.



- Welcome to BRAHMS 6
- Terms and conditions
- Previous upgrade notes
- Example BRAHMS projects
- What's new in Version 6
- Installation and upgrading Version 6
- Getting started
- Admin, security, setup, networking
  - Database management
    - Create a new database project
    - Database ID code
    - Home herbarium

Create a new database project

Creating a new and empty database is a first step for al
Existing users may also want to setup a new project frc

When you first log into a new BRAHMS installation (ass
linked up to an existing list of users and projects) the sy
the **Template** database listed as a login option. This ai
supplied with BRAHMS. Do not build your database in t
database.

To create your own database:

- Using your normal file manager (e.g. Windows expl

A screen shot of the help file with the Contents tab selected and a topic selected.

Contents tab

Using the help file Contents tab, locate the following topics:

- System fundamentals > Logging in and out
- Mapping > Producing maps > Google Earth mapping
- Rapid Data Entry (RDE) > RDE file manager > Creating and registering files
- Troubleshooting > Index problems

Search tab

Using the Search tab, search for the following topics. Remember to **Dbl-click** a page to open a search result.

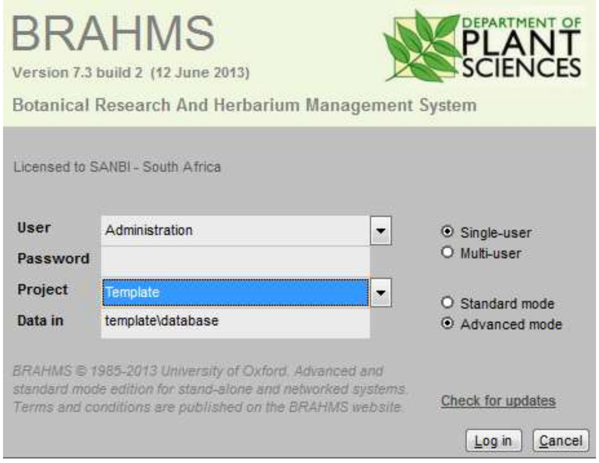
- 'Activation key'
- 'Function keys'
- 'Navigation'
- 'Add synonym'
- 'Backing up'

LOG IN/OUT AND EDIT THE USER FILE

Logging in

Initially, the project to open is the **Template** project stored in the template\database folder. This is an empty database provided with BRAHMS.

- To log into a newly installed system, enter password '**A**' followed by <Enter>.
- Choose Advanced mode, and Single user (the default options).



BRAHMS

Version 7.3 build 2 (12 June 2013)

Botanical Research And Herbarium Management System

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User Administration

Password

Project Template

Data in template\database

● Single-user
○ Multi-user

○ Standard mode
● Advanced mode

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A typical login screen with a user entering in single-user mode.

Adding your username

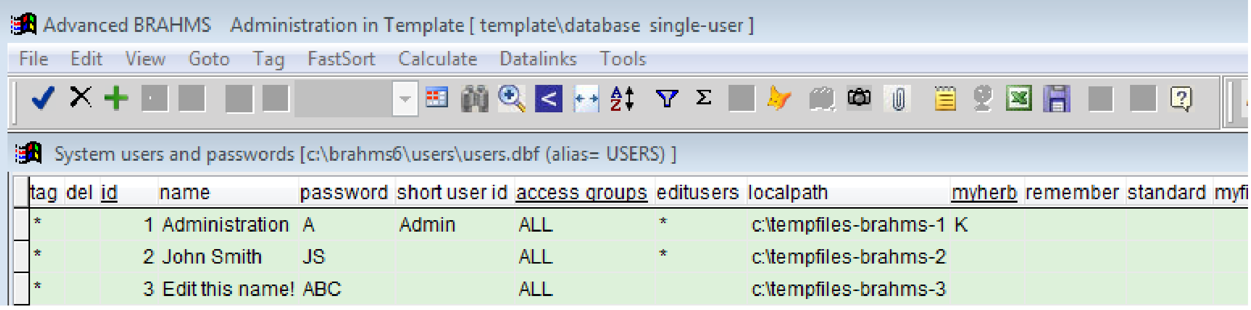
- On the main menu, select **Admin > Users and access permissions**.

Advanced BRAHMS Administration in Template [template\database single-user]

Selecting an option on the main menu

- Click + on the main toolbar to add a new record.
- Add your first and last name (maximum of 2 names) and a password.
- All the other fields in this file can be left with their default values.
- Note that the field ACCESS GROUPS defaults to 'ALL'. This means that the user has full administrative access to the database.

! On networks, system administrators can set access permissions for each user.



Advanced BRAHMS Administration in Template [template\database single-user]

System users and passwords [c:\brahms6\users\users.dbf (alias= USERS)]

tag	del	id	name	password	short user id	access groups	editusers	localpath	myherb	remember	standard	myfi
*		1	Administration	A	Admin	ALL	*	c:\tempfiles-brahms-1	K			
*		2	John Smith	JS		ALL	*	c:\tempfiles-brahms-2				
*		3	Edit this name!	ABC		ALL		c:\tempfiles-brahms-3				

*The field EDITUSERS is important. If marked *, that user can edit the users and projects files. Other users, even if they have Admin status (ALL), cannot.*

Logging out

- Log out of BRAHMS using **File > Exit BRAHMS**. This closes down open database files.

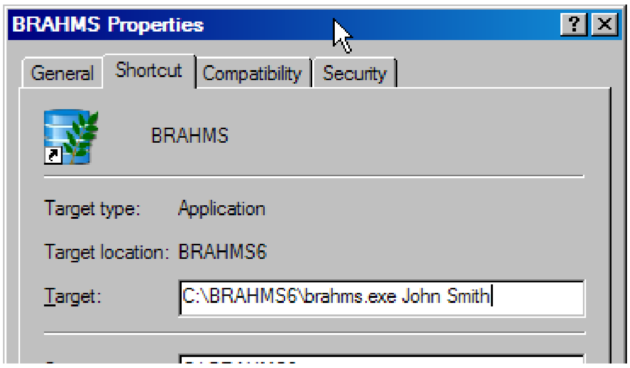
Logging in with your own user name

- Now log in again but this time choose your own user name. A new folder will be created for temp files – these files are explained in the next section.

! You should always log into BRAHMS using your personal log in name rather than Administrator. On networks, system administrators can set access permissions for each user.

Add your username to your desktop shortcut

- **Right-click** on your BRAHMS desktop shortcut, select **Properties** and add your name as shown below. This speeds up login, especially when the user file has many entries.



Target type: Application

Target location: BRAHMS6

Target: C:\BRAHMS6\brahms.exe John Smith

A maximum of 2 words (first and last name) is permitted when editing this option.

TEMPFILES-BRAHMS FOLDERS

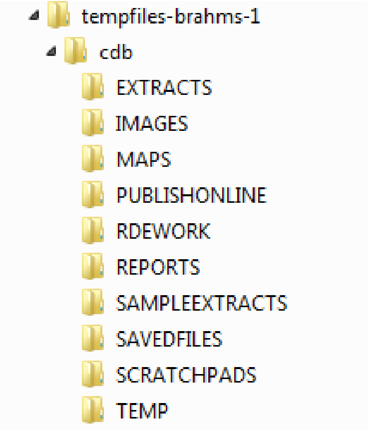
What are tempfiles folders?

Tempfiles-brahms folders are used by BRAHMS for various temporary files. For example, when you make a query, the results are sent to this folder.

Folder creation

When you log into BRAHMS, the system checks if you have a tempfiles folder. If not, one will be created automatically and called '\tempfiles-brahms'. The exact name and location of this folder depends on your username and project code settings. A typical example is 'C:\tempfiles-brahms1'.

Each user on a given workstation has a separate work folder. If a user has more than one project, several sub-folders will be created, one per project.



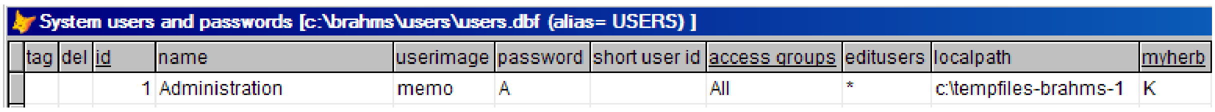
- tempfiles-brahms-1
  - cdb
    - EXTRACTS
    - IMAGES
    - MAPS
    - PUBLISHONLINE
    - RDEWORK
    - REPORTS
    - SAMPLEEXTRACTS
    - SAVEDFILES
    - SCRATCHPADS
    - TEMP

A typical tempfiles folder

Folder deletion

Normally, you do not need to delete these folders unless there is a specific problem. If you delete work folders, BRAHMS re-creates the folders when you next log in. No data are lost. To delete your tempfiles folders(s):

- Log out of BRAHMS
- Locate the folder(s) **c:\tempfiles-brahmsa** (the name may vary slightly).
- Delete the folder(s).
- Log in again - the work folder is re-created.



System users and passwords [c:\brahms\users\users.dbf (alias= USERS)]

tag	del	id	name	userimage	password	short user id	access groups	editusers	localpath	myherb
		1	Administration	memo	A		All	*	c:\tempfiles-brahms-1	K

Work folder paths are auto added to the user file LOCALPATH field. Where necessary (on some network or Terminal Server systems), path drives and names can be edited. The default is always local disk C:.

When to delete tempfiles folders

When you upgrade BRAHMS, you will be asked to delete your tempfiles folders. If you experience a system crash or see any messages about bad index files, it is recommended that you delete your temporary work folder(s).

PERSONAL AND SYSTEM-WIDE CONFIGURATION

Some configuration settings are system-wide and apply to all users of the current database. Others are personal and are associated with individual users. If using BRAHMS as a single user system, these categories can be treated equally.

Personal settings are stored in the user file and preferences added here will apply to that user in any database. System-wide settings are stored as part of a given database and apply only to that database.

Personal settings examples

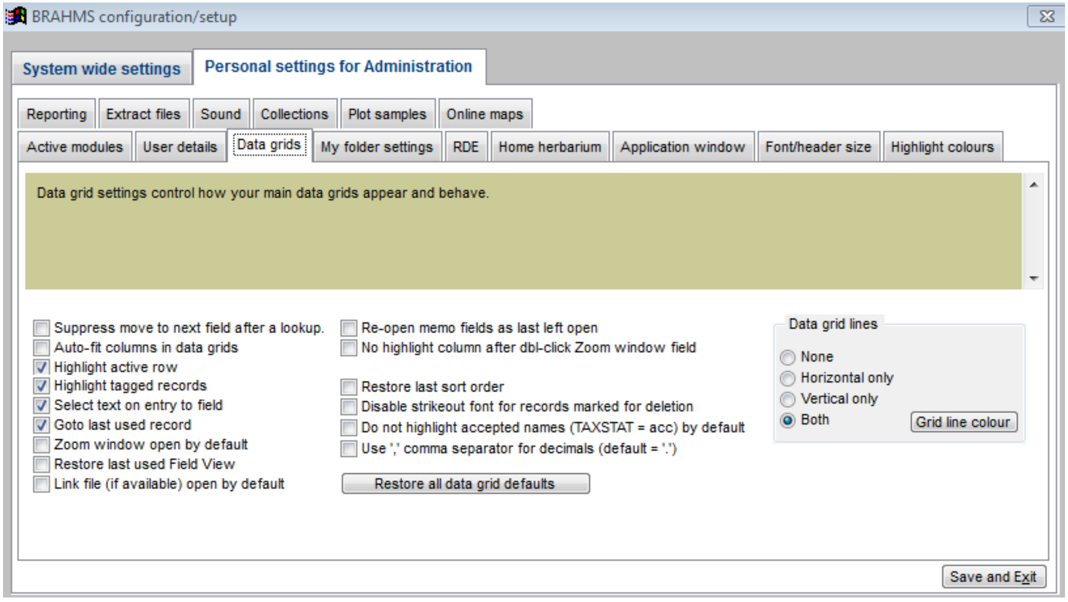
If running BRAHMS on a network with multiple users, normally, only the system administrator will have access to the **Admin** menu and thus system-wide settings. In this case, you can edit your personal settings by selecting **Utilities > My setup/profile**. There are many configuration options – here are a few examples:

Active modules

- Select **Utilities > My setup/Profile** > **Active modules**. Here, you can include/exclude main menu options.

Data grid options

- Select **Utilities > My setup/Profile** > **Data grids**. Here, you can experiment with different data grid settings, for example, whether to select text on entry to a field.



Data grid settings control how your main data grids appear and behave.

☐ Suppress move to next field after a lookup.
☐ Auto-fit columns in data grids
☑ Highlight active row
☑ Highlight tagged records
☑ Select text on entry to field
☑ Goto last used record
☐ Zoom window open by default
☐ Restore last used Field View
☐ Link file (if available) open by default

☐ Re-open memo fields as last left open
☐ No highlight column after dbl-click Zoom window field
☐ Restore last sort order
☐ Disable strikeout font for records marked for deletion
☐ Do not highlight accepted names (TAXSTAT = acc) by default
☐ Use ',' comma separator for decimals (default = '.')

Data grid lines
○ None
○ Horizontal only
○ Vertical only
● Both

Many useful features can be found under the Data grids tab. Settings are remembered for each user.

Highlight colours

Select Select **Utilities > My setup/Profile** > **Highlight colours**. Here, you can set colour preferences for tags, column clicks, the zoom window and a few other things.

Home herbarium

Select Select **Utilities > My setup/Profile** > Home Herbarium to add your own herbarium code (if relevant). BRAHMS uses this to give preference to your herbarium when displaying barcodes and/or accession numbers – and also for certain functions linked to loans management,

System-wide setting examples

Mapping configuration options

- Select **Admin > Project configuration > Maps.** Choose the software you are likely to use the most.

- On the same tab, choose the map units you use most commonly. The choices are Degrees/Minutes/Seconds (DMS), Decimal degrees (DD) and Degrees and decimal minutes (DM).

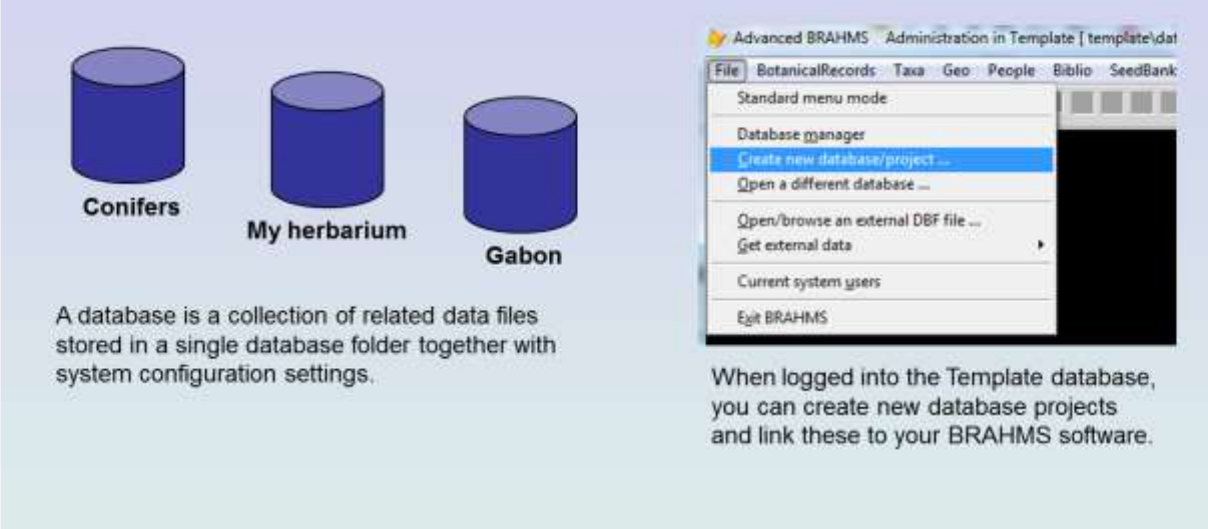
Date format

- Select **Admin > Project configuration > Dates** and choose your date language/format. The month names for the 5 styles can be edited using **Admin > Month names**.

DATABASES AND DATA FILES

Databases

When you log into BRAHMS, you need to select a database/project to open. The BRAHMS system is delivered with one empty database called **Template**. This can be copied to make entirely new database projects.

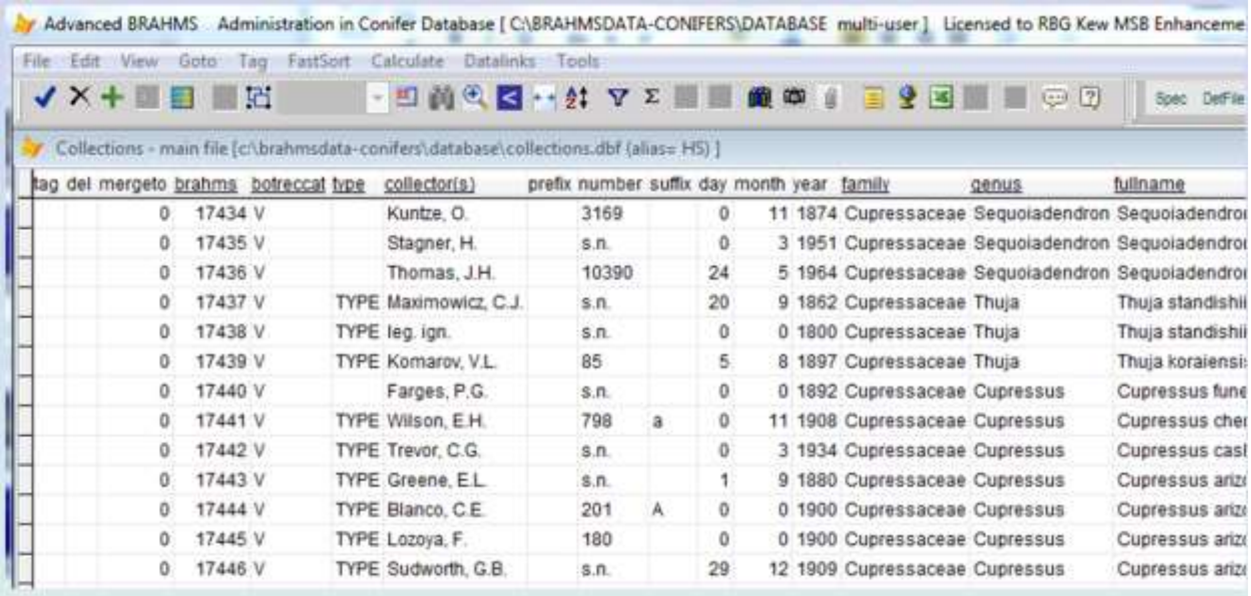


A database is a collection of related data files stored in a single database folder together with system configuration settings.

When logged into the Template database, you can create new database projects and link these to your BRAHMS software.

Data files

Most BRAHMS menu options open up data files as shown here with botanical records. Data files consists of records and columns.



Advanced BRAHMS Administration in Conifer Database [C:\BRAHMSDATA-CONIFERS\DATABASE multi-user] Licensed to RBG Kew MSB Enhanceme

Collections - main file [c:\brahmsdata-conifers\database\collections.dbf (alias= HS)]

tag	del	mergeto	brahms	botreccat	type	collector(s)	prefix	number	suffix	day	month	year	family	genus	fullname
		0	17434	V		Kuntze, O.		3169		0	11	1874	Cupressaceae	Sequoiadendron	Sequoiadendro
		0	17435	V		Stagner, H.		s.n.		0	3	1951	Cupressaceae	Sequoiadendron	Sequoiadendro
		0	17436	V		Thomas, J.H.		10390		24	5	1964	Cupressaceae	Sequoiadendron	Sequoiadendro
		0	17437	V	TYPE	Maximowicz, C.J.		s.n.		20	9	1862	Cupressaceae	Thuja	Thuja standishii
		0	17438	V	TYPE	leg. ign.		s.n.		0	0	1800	Cupressaceae	Thuja	Thuja standishii
		0	17439	V	TYPE	Komarov, V.L.		85		5	8	1897	Cupressaceae	Thuja	Thuja koraiensi
		0	17440	V		Farges, P.G.		s.n.		0	0	1892	Cupressaceae	Cupressus	Cupressus fune
		0	17441	V	TYPE	Wilson, E.H.		798	a	0	11	1908	Cupressaceae	Cupressus	Cupressus che
		0	17442	V	TYPE	Trevor, C.G.		s.n.		0	3	1934	Cupressaceae	Cupressus	Cupressus cas
		0	17443	V	TYPE	Greene, E.L.		s.n.		1	9	1880	Cupressaceae	Cupressus	Cupressus ariz
		0	17444	V	TYPE	Blanco, C.E.		201	A	0	0	1900	Cupressaceae	Cupressus	Cupressus ariz
		0	17445	V	TYPE	Lozoya, F.		180		0	0	1900	Cupressaceae	Cupressus	Cupressus ariz
		0	17446	V	TYPE	Sudworth, G.B.		s.n.		29	12	1909	Cupressaceae	Cupressus	Cupressus ariz

BRAHMS is a relational database. Several of the columns you see in the above screen, for example the family name, are held in separate tables but are displayed together with botanical record data.

When you open any file, the menu options change to the data editing menu.

OPENING AND CLOSING FILES

The purpose of this exercise section is to provide some basic orientation on where some of the more commonly used options are on the menu system.

Log into the Conifer database

BRAHMS

Version 6.7 (10 May 2010)

Botanical Research And Herbarium Management System

Licensed to RBG Kew MSB Enhancement Project

User Administration

Password ****

Project Conifer Database

Data in c:\brahmsdata-conifers\database

● Single-user
○ Multi-user

○ Standard mode
● Advanced mode

BRAHMS © 1985-2010 University of Oxford. Advanced and standard mode edition for stand-alone and networked systems. Terms and conditions are published on the BRAHMS website. Check for updates

When you log in, select the Conifer database, not the Template database.

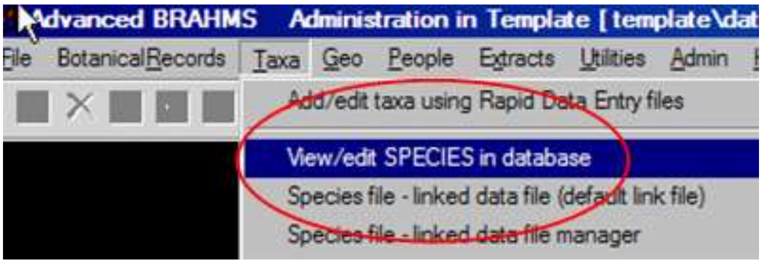
Missing menu options?

If you do not see a menu option required for the exercises below, for example **Maps**, select **Utilities > My setup/Profile > Active modules …** to switch the missing menu option on

For example, is the menu option **PublishOnline** visible? If not, select **Utilities > My setup/Profile > Active modules …** and enabled it now.

Locate, open and close a selection of database files

After opening each file, close the file by clicking on the top right close window **X**. Or you can use the keys **Alt+X**.



Advanced BRAHMS Administration in Template [template\dat

Opening the main species file

- Main species file: **Taxa > View/edit SPECIES in database**
- Main genus file: **Taxa > View/edit GENERA in database**
- Main family file: **Taxa > View/edit FAMILIES in database**
- Taxonomic status categories: **Taxa > Resource files > Taxonomic status**
- Main botanical records file: **BotanicalRecords > View/edit botanical records in database**
- Main specimen file: **BotanicalRecords > View/edit specimens in database**
- Herbarium list: **BotanicalRecords > Herbarium list**
- Type categories: **BotanicalRecords > Resources files > Type categories**
- Specimen categories **BotanicalRecords > Resources files > Specimen categories**
- Country list: **Geo > View/edit countries in database**
- Main gazetteer: **Geo > View/edit gazetteer in database**

People:	**People > View/edit people in database**
Map projects:	**Maps > Saved ArcView (APR) and DIVA (DIV) projects**
Map colours:	**Maps > Colours and opacity**
Image library:	**Images > View/edit images registered in database**
Month names	**Admin > Month names**
Custom lookup values	**Admin > Custom lookups**
Database manager	**File > Database manager**

Can you now locate and open …

The file that lists BRAHMS online servers registered in your database.

The file that stores zones and locations in Botanic Gardens.

The file that stores default function key assignments.

Demonstration of relation database

In a relation database, data are stored efficiently in separate files in a way that reduces the need to store the same element of data more than once. For example, you may have 1000 specimens in the family Cupressaceae or from the country Mexico. But the words 'Cupressaceae' and 'Mexico' should only be stored once, not 1000 times. Also, imagine you want to store a description of the Cupressaceae. Clearly, that description should only be stored once. The same idea applies to collector, species, locality and herbarium and other names.

Let's look more closely at the family name 'Cupressaceae'. Aside from any other considerations, if it is stored once only in a file of family names, it will be much easier to make changes to the description or any other facts about this family - or even the name itself.

In the conifer database:

- Select **Taxa > View/edit families in database**
- Locate the family Cupressaceae and edit the name to 'Cupressaceaexxx'
- Now close the family file
- Select **Taxa > View/edit species** in database and browse down to locate some names in this family

You can see that the single edit you made in the family file is 'inherited' by all records in the species file. This is because the species file is related to the family file using a numeric code (in this case via the genus file).

- Now select **BotanicalRecords > View/edit botanical records in database**

Again, you can see the related family name appearing as you edit it in the family file.

- Select **Taxa > View/edit families in database** to locate and edit the name back to the correct name.

If you want to test this further, you can try editing the name of a country and then locate botanical records from that country.

! Note that RDE files are, by design, not relational. The data in RDE files only becomes relational when the files are transferred into BRAHMS.

THE MAIN SYSTEM TOOLBAR OPTIONS

✓	Tag toggle. Adds or removes * to the **TAG** field. Tagging used throughout BRAHMS. A right-click on this toolbar set a filter to show only tagged records.
✕	Delete toggle. Adds or removes * to the **DEL** field. To remove records marked in this way, select **Edit > Delete options > Remove records marked for deletion**. Deletion throughout BRAHMS is a two-stage process.
+	Add a record. In selected modules including RDE, the add function can be configured using the C toolbar.
	Access custom designed forms, if available.
	Opens a data file.
	Open/close a linked data file.
All fields	Field view selector drop-down menu. Enabled when one or more field views available.
	Define and/or select a field view.
	Find a record using custom find form.
	Open Zoom pane - display fields for the current record in the right window pane. Right-click the zoom window for more options.
	Reduces field widths by a %. Right-click to increase field widths.
↔	Auto fit data columns.
A Z ↕	Open the sort form to carry out compound sorts. For simple field sorts, right-click the column header name. A list of convenient sorts usually available on the **Fastsort** menu option.
	Set a filter on current field or another field as selected. Multiple filters can be set. To clear all filters, right-click filter button or use the Clear filters option on the Filter form.
Σ	Analyse data in selected column.
	Display taxa in tree view with options to navigate/filter on taxa.
	Open the FoxPro command library.
	Link the current record to any reference stored in your reference lists.
	Open image viewer + image toolbar
	Link documents such as PDFs, Excel, Videos, whatever to any record.
	Copy/Save as options.
	Check and transfer the contents on an RDE file to BRAHMS.
	Design and generate visual reports from any BRAHMS module.
	Design and generate text reports from any BRAHMS module.
	Create maps using your preferred GIS.
	Open current file in Excel. Respects current filters, sort order and field selection.
	Edit comments for records. Activate if the COMMENTS field is available in the current file. Right-click to restrict the view to records with comments.
?	Field level documentation and local data rules for current file.

DATABASE FUNDAMENTALS

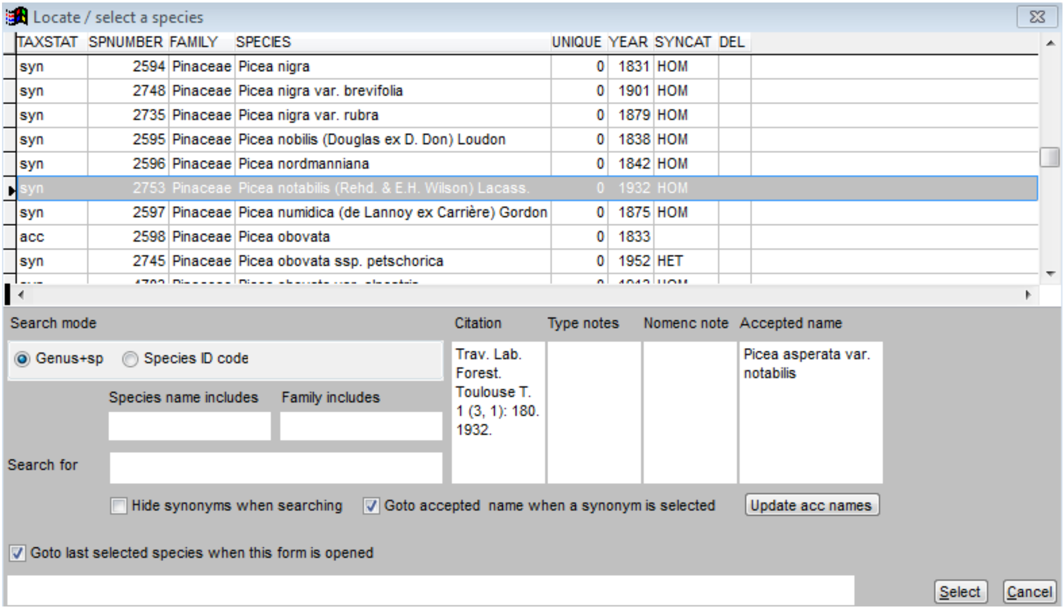
Basic record and field navigation

- Select **Taxa > View/edit species in database** to open the main species file.
- Press **ENTER** (or TAB) several times to move forwards to the next fields.
- Press **<SHIFT>+ENTER** to move backwards to the previous fields.
- Use arrows or the scrollbar to move up and down records.
- Press the **F12** key to go to column 1
- When in the first column, you can press the left arrow to go to the last column.

! The Navigation toolbar on the top right side of the screen can be used for record navigation.

Locating records using

- In the main species file, use the toolbar to locate the species name *Pinus devoniana*. Entering 'pin dev' in the **search for** box should be enough. *Pinus devoniana* is an accepted name and has 'acc' in the TAXSTAT field.



Locate / select a species

TAXSTAT	SPNUMBER	FAMILY	SPECIES	UNIQUE	YEAR	SYNCAT	DEL
syn	2594	Pinaceae	Picea nigra	0	1831	HOM	
syn	2748	Pinaceae	Picea nigra var. brevifolia	0	1901	HOM	
syn	2735	Pinaceae	Picea nigra var. rubra	0	1879	HOM	
syn	2595	Pinaceae	Picea nobilis (Douglas ex D. Don) Loudon	0	1838	HOM	
syn	2596	Pinaceae	Picea nordmanniana	0	1842	HOM	
syn	2753	Pinaceae	Picea notabilis (Rehd. & E.H. Wilson) Lacass.	0	1932	HOM	
syn	2597	Pinaceae	Picea numidica (de Lannoy ex Carrière) Gordon	0	1875	HOM	
acc	2598	Pinaceae	Picea obovata	0	1833		
syn	2745	Pinaceae	Picea obovata ssp. petschorica	0	1952	HET	

Search mode: ● Genus+sp ○ Species ID code

Species name includes:

Family includes:

Search for:

☐ Hide synonyms when searching ☑ Goto accepted name when a synonym is selected

☑ Goto last selected species when this form is opened

Citation: Trav. Lab. Forest. Toulouse T. 1 (3, 1): 180. 1932.

Type notes:

Nomenc note:

Accepted name: Picea asperata var. notabilis

The species search form with Goto accepted name option selected. If you choose a synonym, the system will direct you to the accepted name. Options such as 'Goto accepted name' on the above form are saved as a personal preference.

- Now use the toolbar to locate the species name *Widdringtonia caffra.* Make sure the option **Hide synonyms** is not selected and the option **Goto accepted** is selected. This should guide you to the correct name.

Locating records using

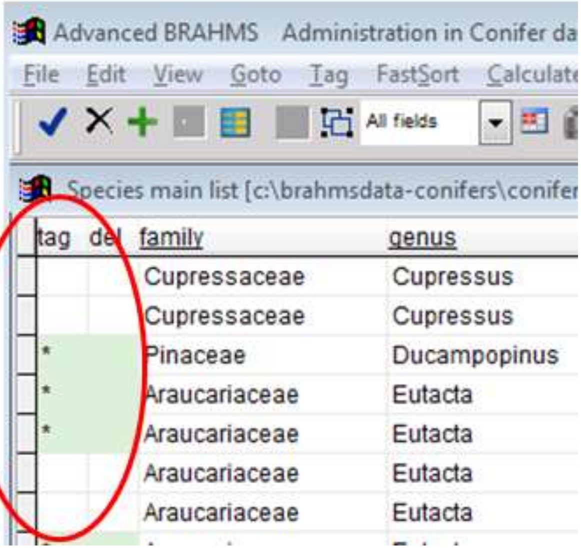
The tree view control is used to display your taxa in a searchable tree. In the main species file,

- Select the toolbar to build a tree view.

- Click on a family name to go to and filter on that family.
- Click '+' to list genera in that family and click on a genus name to go to and filter on that genus.
- Click '+' again to list species in the selected genus and click on a species name to go to that species.
- Using the tree view option, navigate to the species *Fitzroya cupressoides* in the Cupressaceae.

Tag options introduced

Record tagging is used **throughout BRAHMS** for marking/selecting records. When you tag a record, '*****' is added to the TAG field.



tag	del	family	genus
		Cupressaceae	Cupressus
		Cupressaceae	Cupressus
*		Pinaceae	Ducampopinus
*		Araucariaceae	Eutacta
*		Araucariaceae	Eutacta
		Araucariaceae	Eutacta
		Araucariaceae	Eutacta

Most files have a TAG field at the start of the record

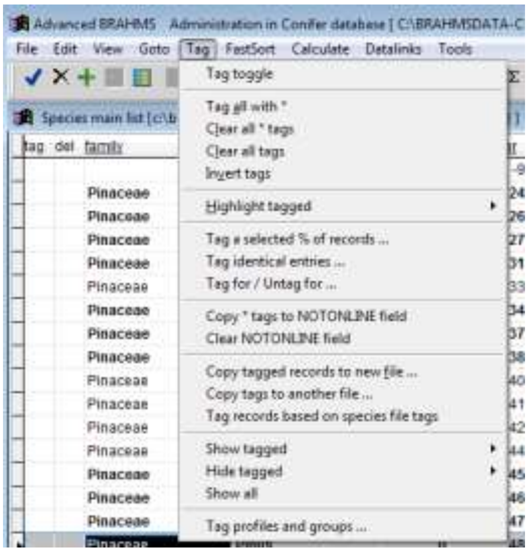
Some example uses of tags: to create groups of records (a tag profile); to copy selected records to a new file; to extract/query data; to restrict an analysis to tagged records; to restrict a map to include tagged records.

- Select **Taxa > View/edit species in database** to open the main species file.
- Click ✓ or press **F6** several times to tag some records. If a record is already tagged, the tag will be removed.
- Select **Tag > Invert tags** to invert the current tag settings.

- Select **Calculate > Count tagged with ***
- Select **Calculate > Count untagged**

- Select **Tag > Show tagged > Show tagged with ***
  Select **Tag > Show all** (which removes all filters)

- Select **Tag > Tag all with *** to tag all records.
- Select **Tag > Clear all * tags** to clear all tags.



Screen shot of the Tag menu options

Tag custom commands

You can use custom commands to tag records. For example, the main species file includes the field YEAR (=year of publication). We want to tag all records published before 1900

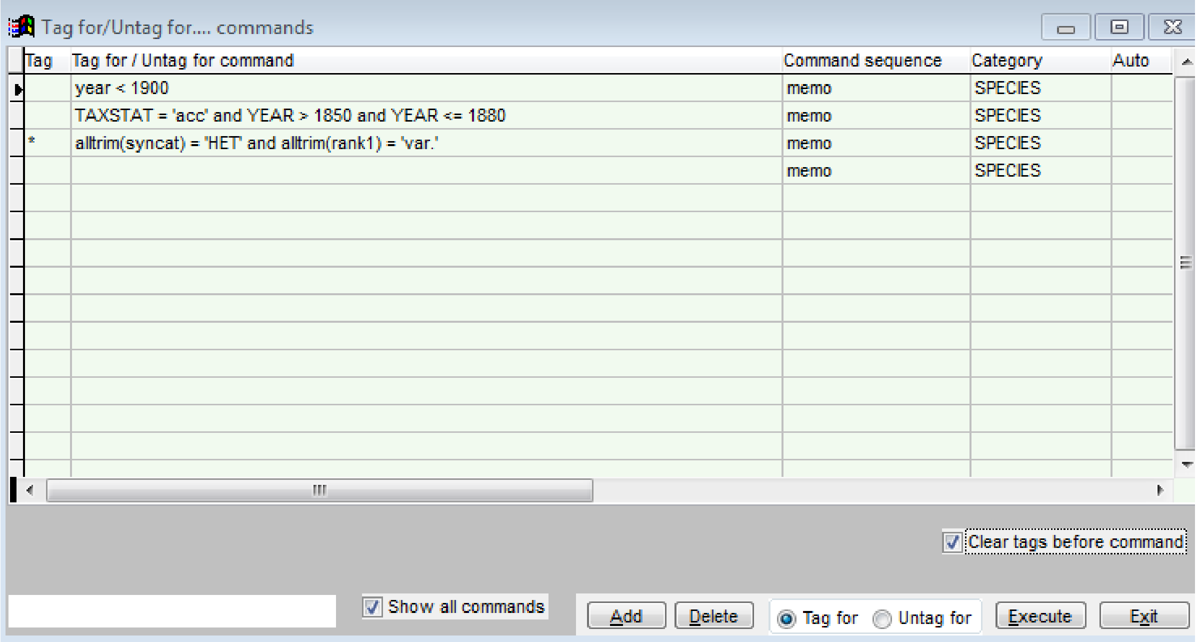
- Select **Taxa > View/edit species in database** to open the main species file.
- Select **Tag > Tag for/Untag for …** and enter the command as prompted: YEAR < 1900
- Ensure that you have the option **Clear tags before command** selected.
- Execute the command.

Try a more complex example:

- Select **Tag > Tag for/ Untag for …**and enter the command as prompted:

  TAXSTAT = 'acc' and YEAR > 1850 and YEAR <= 1880

  The operator **<=** means ‘ less than or equal to’. Also that ‘acc’ is surrounded by quotes as it is text. Numbers such as 1850 are not.



Tag	Tag for / Untag for command	Command sequence	Category	Auto
	year < 1900	memo	SPECIES	
	TAXSTAT = 'acc' and YEAR > 1850 and YEAR <= 1880	memo	SPECIES	
*	alltrim(syncat) = 'HET' and alltrim(rank1) = 'var.'	memo	SPECIES	
		memo	SPECIES	

☑ Clear tags before command

☑ Show all commands

● Tag for ○ Untag for

Some example ‘Tag for’ commands.

Learning to use more function keys

Many tasks are faster using function keys rather than your mouse. For example, **F6** can be used instead of ✓ to tag records.

Key	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12
	Help	Open form	Open file	Copy field	Sort form	Tag toggle	Delete mark toggle	Field view	Lookup		Filter form	Go to first column
Shift	Open shortcut help template			Increment last field value	Sort ascending	Tag all		Autofit	External file lookup		Filter on selection	Go to last column
Ctrl	Find	FoxPro commands		Copy record		Count tagged		Reduce column width		Zoom toggle or **Ctrl+Z**	Filter includes selection	
Alt	Add record or **Alt+A**		Close screen or **Alt+X**		Clear sort	Clear tags		Increase column width			Clear filters	

The BRAHMS **Function Key** template is available in the folder BRAHMS7\template\function key template.

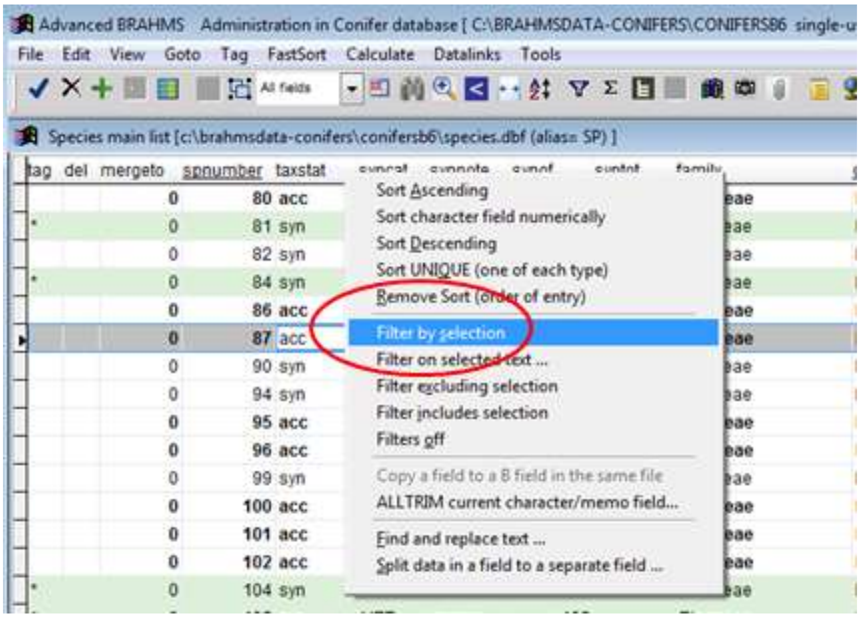
- Select **BotanicalRecords > View/edit botanical records in database.**
- Enter **Alt+A** several times to add blank records.
- In the LOCALITY field, press **F9** to activate the lookup option for that field.
- Use **F6** to tag the new records.
- Use **F7** to mark all these new records for deletion. Although note a useful option is **Edit > Delete options > TAG -> DEL**.
- Select **Edit > Delete options > Remove records marked for deletion**.
- Enter **Alt+X** to close the screen.

! The template form can be opened in a separate window using SHIFT+F1.

Setting simple filters

Filters restrict your view of the data to a selected group of records.

- In the main species file, locate and click once on the text ‘acc’ in the field TAXSTAT (choose any record).
- Now **right-click** on the TAXSTAT **column header** and choose **Filter by selection**. This will set a filter to show only ‘acc’ names *i.e.* accepted names.



tag	del	mergeto	spnumber	taxstat
		0	80	acc
*		0	81	syn
		0	82	syn
*		0	84	syn
		0	86	acc
		0	87	acc
		0	90	syn
		0	94	syn
		0	95	acc
		0	96	acc
		0	99	syn
		0	100	acc
		0	101	acc
		0	102	acc
*		0	104	syn

Filter by selection is one way to quickly filter/restrict records on the selected text in any field

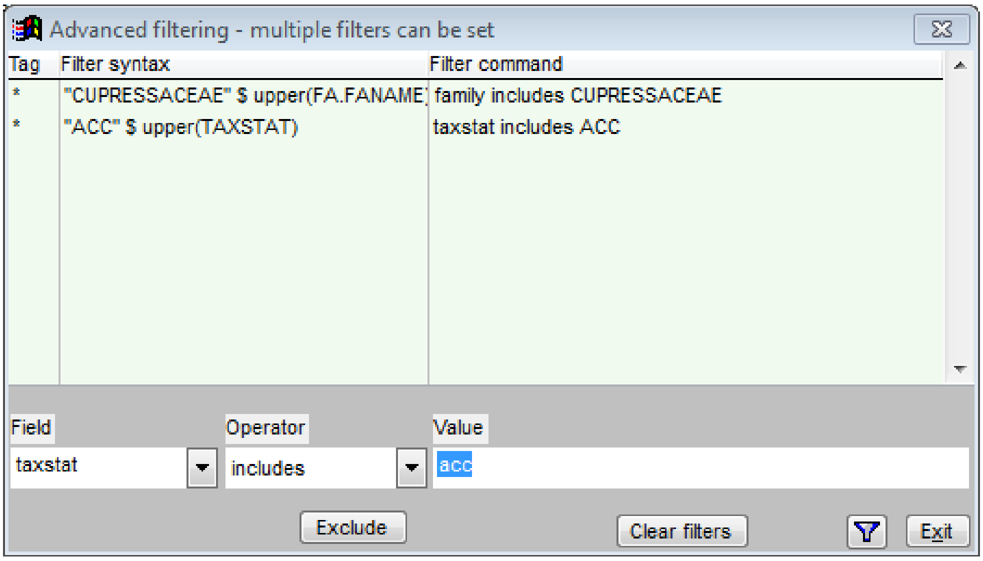
- Then choose **Tag > Tag all with ***. This will tag all the accepted names.
- To remove the filter, **right-click** on the toolbar.
- Try setting filters on some other fields.

! To quickly set a filter on tagged records, use **Tag > Show tagged**.

Setting compound filters

You can add multiple filters at the same time using the toolbar.

- Select **Taxa > View/edit species in database** to open the main species file.
- Use the toolbar to open the main filter form.
- Edit the form so that the option reads **field**=family, **operator**=includes; **value**=cupr.
- Now click the button on the form to apply this filter.
- Re-open the filter form and add a second command: **field**=taxstat, **operator**=includes; **value**=acc.
- Apply the filter. This will set the filter to accepted names in the Cupressaceae.



Tag	Filter syntax	Filter command
*	"CUPRESSACEAE" $ upper(FA.FANAME	family includes CUPRESSACEAE
*	"ACC" $ upper(TAXSTAT)	taxstat includes ACC

Field: taxstat
Operator: includes
Value: acc

Simple record sorting

Sorting records in files is vital – especially when generating reports. Sorting is also useful in other ways, for example to locate data or for finding and correcting errors.

Most files can be easily sorted on a single column by choosing a header **Right-click** option. There is also a **FastSort** menu with some commonly used sort options – some of which sort of multiple fields.

Still in the main species file:

- Select **FastSort > Family + species** to sort the file A-Z by species within family.
- Select **FastSort > Species name** to sort this file by the species name only.
- **Right-click** on the column header for the field SP1 and choose **Sort Ascending**.
- **Right-click** on the column header for the field FAMILY and choose **Sort Unique** to show one record per different family.
- To remove the current file sort, **right-click** on the toolbar.

More complex sorting

You may need to build your own sort commands which sort your records in a more way. These can be added (and saved) using the ↕ toolbar.

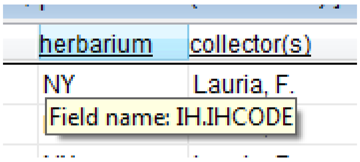
Task one. Sort the main species file by year of publication + full species name

- Select **Taxa > View/edit species in database**.
- Select the ↕ toolbar and add a new record. Into the command line, enter the command str(year) + substr(fullname,1,60) and then **Sort** the file

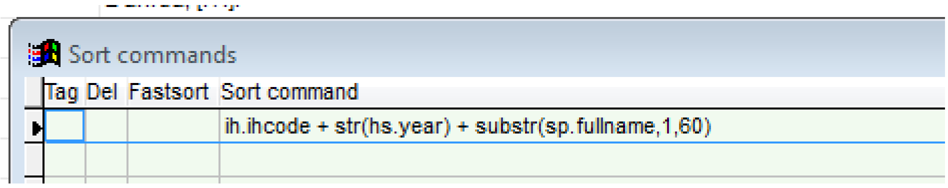
The str() function converts a numeric field to character which enables you to combine year with the character field FULLNAME. The substr() function allows you to select part of a long character string, here the first 60 characters. Long strings (above *c.*100 characters) can cause problems when creating indexes.

- Select **Botanical Records> View/edit specimens in database**. The challenge here is to sort of the file on herbarium + collection year + species.
- Select the ↕ toolbar and add a new record. . Into the command line, enter the command ih.ihcode + str(hs.year) + substr(sp.fullname,1,60) and then **Sort** the file.

This command has to refer so fields that are in other files, hence the field name is prefixed with the short file alias name. You can hover your mouse over the field header to see the full field names needed for sorting.



Hover your mouse over a field header to get the correct sorting reference.



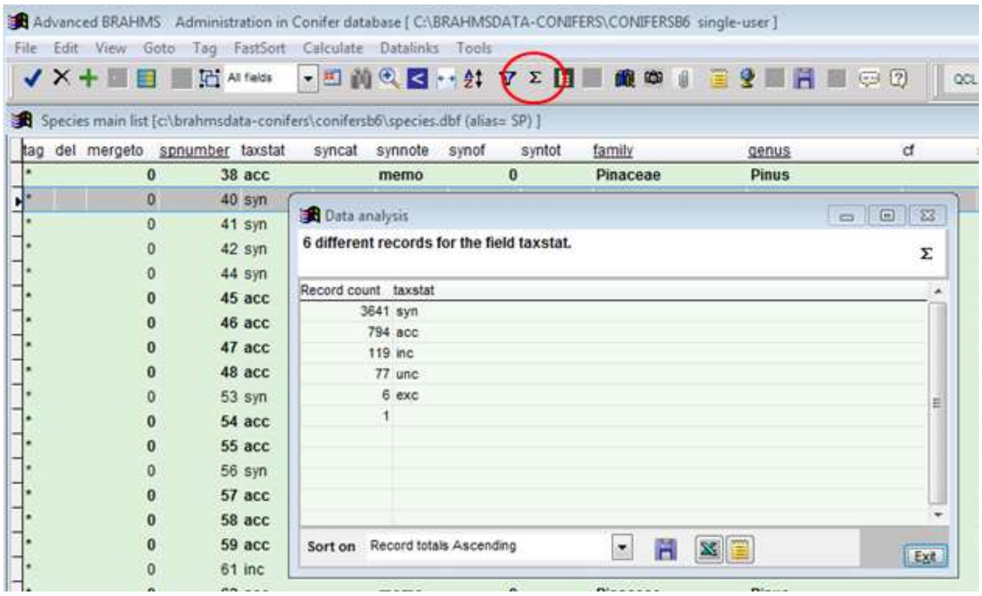
ih.ihcode + str(hs.year) + substr(sp.fullname,1,60)

An example compound sort command.

Calculate menu and toolbar options

Calculate options provide counts and summaries of your data. Aside from using count tagged and untagged as above, the most commonly used option is **Calculate > Analyze data in selected column**, also activated using the Σ toolbar.

- Open the main species file.
- **Right-click** the ▽ toolbar to ensure no filters are set.
- Click anywhere in the TAXSTAT field (data or header).
- Click on the Σ toolbar**.**



6 different records for the field taxstat.

Record count	taxstat
3641	syn
794	acc
119	inc
77	unc
6	exc
1	

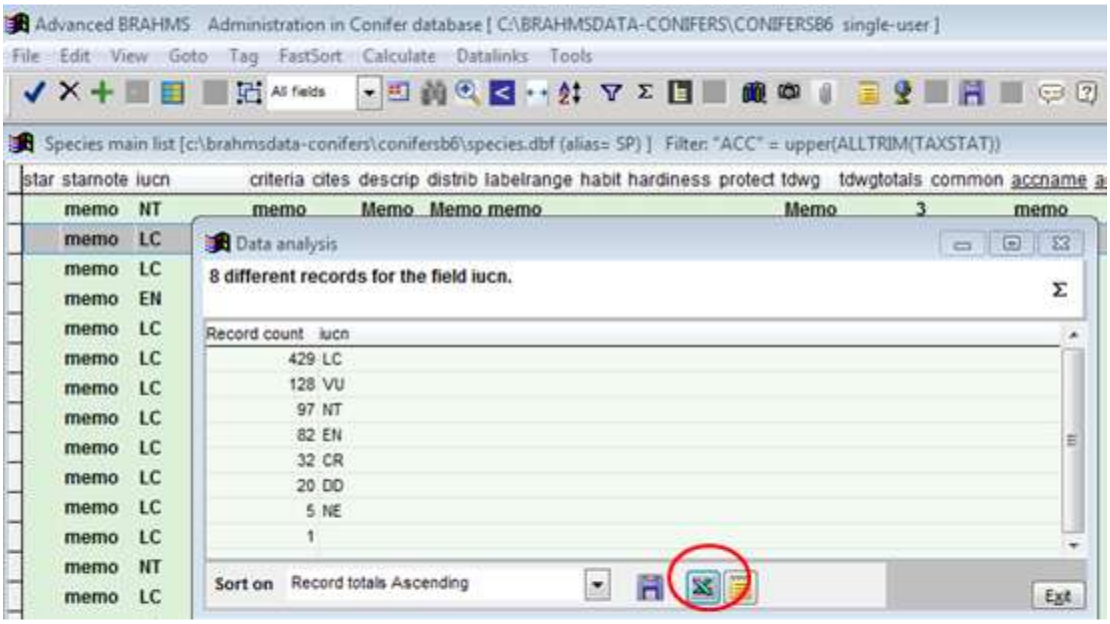
The record counts here refer to the number of species records for each TAXSTAT value.

Try the following:

- Use Σ in the FAMILY field to calculate the total number of taxa per family.
- Use Σ in the GENUS field to calculate the total number of taxa per genus.
- Use Σ in the YEAR field to calculate the total number of taxa per publication year.

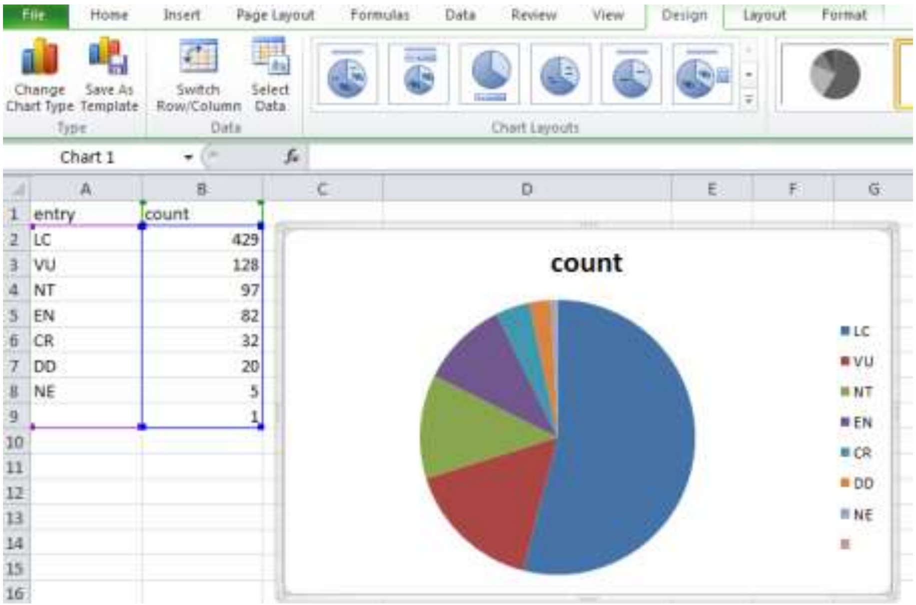
- Apply a simple filter on the FAMILY field to filter on the family Podocarpaceae.
- With this filter set, click once in the AUTHOR1 field and then use Σ to display the total number of taxa in this family published per different author.
- To clear all filters, right-click on the ▽ toolbar.

- Apply a simple filter on the TAXSTAT field to show only **acc** names (as described earlier). Locate the field IUCN in the main species file. Click in this column and then use Σ to display the total number of taxa per IUCN category. Also open the analysis result in Excel using the option provided on the Σ form.



8 different records for the field iucn.

Record count	iucn
429	LC
128	VU
97	NT
82	EN
32	CR
20	DD
5	NE
1	



entry	count
LC	429
VU	128
NT	97
EN	82
CR	32
DD	20
NE	5
	1

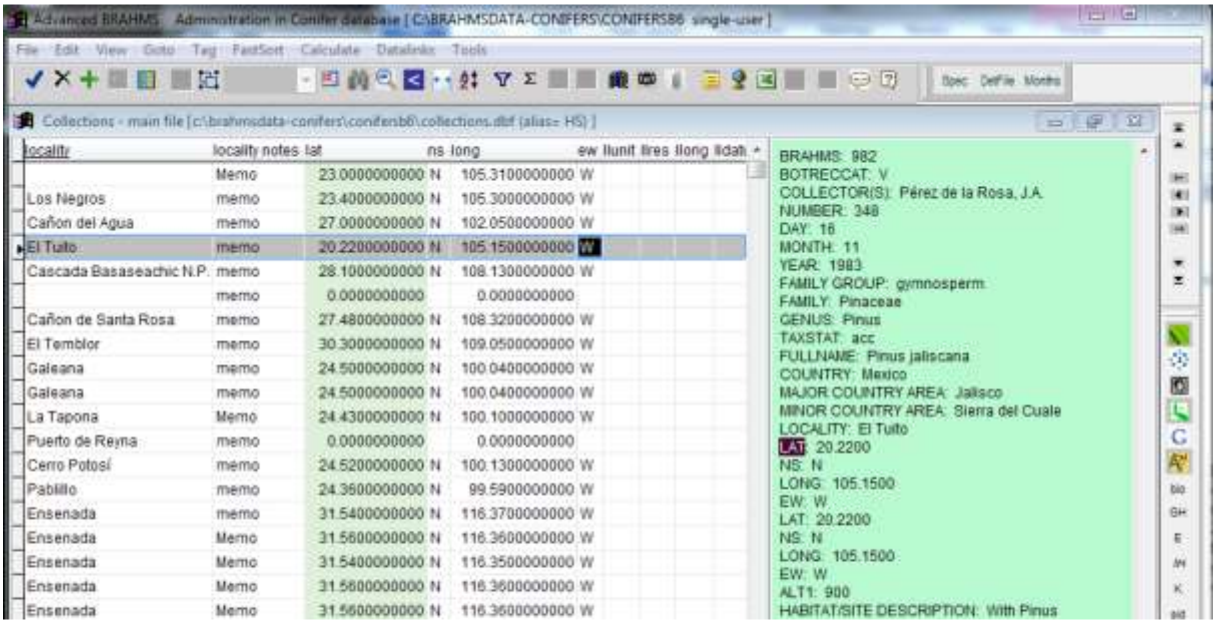
*Results generated by the Σ toolbar can be open in Excel and used to prepare **charts** and **graphs**.*

- Open the main genus file (option on the **Taxa** menu). Using the Σ toolbar option, produce a summary table of the total numbers of genera per family. Which family has the most genera?

The Zoom window

The 🔍 toolbar displays all non-empty fields in a mouse-sensitive window to the right of the main window. Clicking on the **Zoom** button a second time closes the Zoom window.

- Select **Taxa > View/edit species in database** to open the main species file.
- Click on the 🔍 toolbar to open the zoom pane.
- Double click on a field name in the **Zoom pane** to go to and highlight that column.



locality	locality notes	lat	ns	long	ew	llunit	lres	llong	lldat
	Memo	23.0000000000	N	105.3100000000	W				
Los Negros	memo	23.4000000000	N	105.3000000000	W				
Cañon del Agua	memo	27.0000000000	N	102.0500000000	W				
El Tuito	memo	20.2200000000	N	105.1500000000	W				
Cascada Basaseachic N.P.	memo	28.1000000000	N	108.1300000000	W				
	memo	0.0000000000		0.0000000000					
Cañon de Santa Rosa	memo	27.4800000000	N	108.3200000000	W				
El Temblor	memo	30.3000000000	N	109.0500000000	W				
Galeana	memo	24.5000000000	N	100.0400000000	W				
Galeana	memo	24.5000000000	N	100.0400000000	W				
La Tapona	Memo	24.4300000000	N	100.1000000000	W				
Puerto de Reyna	memo	0.0000000000		0.0000000000					
Cerro Potosí	memo	24.5200000000	N	100.1300000000	W				
Pablillo	memo	24.3600000000	N	99.5900000000	W				
Ensenada	memo	31.5400000000	N	116.3700000000	W				
Ensenada	Memo	31.5600000000	N	116.3600000000	W				
Ensenada	Memo	31.5400000000	N	116.3500000000	W				
Ensenada	Memo	31.5600000000	N	116.3600000000	W				
Ensenada	Memo	31.5600000000	N	116.3600000000	W				

BRAHMS: 982
BOTRECCAT: V
COLLECTOR(S): Pérez de la Rosa, J.A.
NUMBER: 348
DAY: 16
MONTH: 11
YEAR: 1983
FAMILY GROUP: gymnosperm
FAMILY: Pinaceae
GENUS: Pinus
TAXSTAT: acc
FULLNAME: Pinus jaliscana
COUNTRY: Mexico
MAJOR COUNTRY AREA: Jalisco
MINOR COUNTRY AREA: Sierra del Cuale
LOCALITY: El Tuito
LAT: 20.2200
NS: N
LONG: 105.1500
EW: W
LAT: 20.2200
NS: N
LONG: 105.1500
EW: W
ALT1: 900
HABITAT/SITE DESCRIPTION: With Pinus

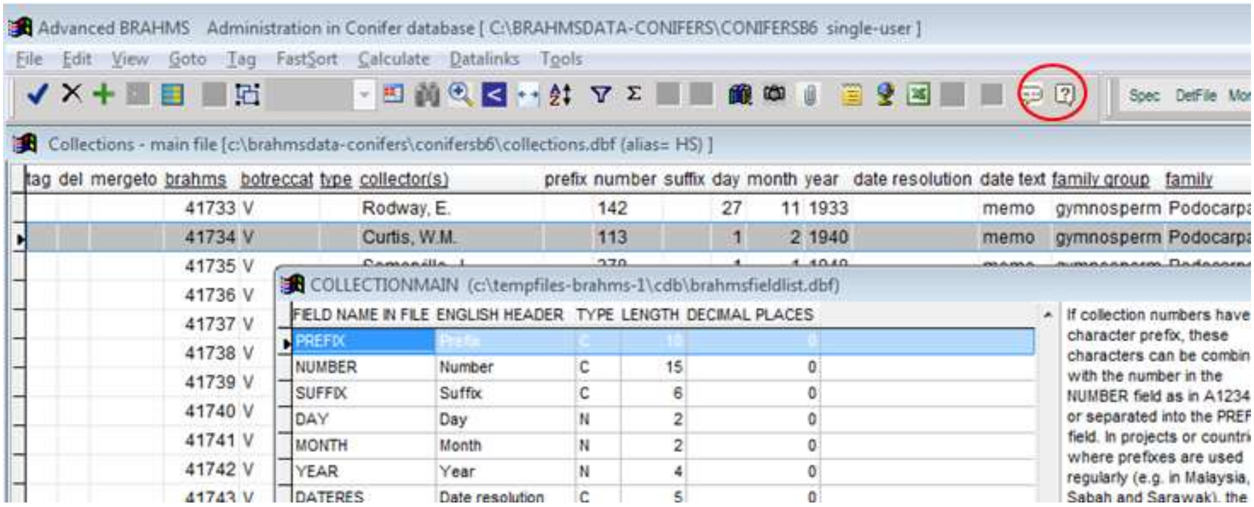
When you move to a new record in the main file, the Zoom window is updated.

- Click on the 🔍 toolbar to close the zoom window.

! If you **right-click** in the Zoom window, you can adjust window properties. One of the options is to include blank fields (these are excluded by default).

Using the ? toolbar to get field level help

- Select **BotanicalRecords > View/edit botanical records in database**. Click in the PREFIX field and then on the ? toolbar to read about this field.
- Open one of the taxon files (family, genus or species) and, using ? toolbar, read about the SYNOF field.



Collections - main file [c:\brahmsdata-conifers\conifersb6\collections.dbf (alias= HS)]

tag	del	mergeto	brahms	botreccat	type	collector(s)	prefix	number	suffix	day	month	year	date resolution	date text	family group	family
			41733	V		Rodway, E.		142		27	11	1933		memo	gymnosperm	Podocarpa
			41734	V		Curtis, W.M.		113		1	2	1940		memo	gymnosperm	Podocarpa
			41735	V												
			41736	V												
			41737	V												
			41738	V												
			41739	V												
			41740	V												
			41741	V												
			41742	V												
			41743	V												

COLLECTIONMAIN (c:\tempfiles-brahms-1\cdb\brahmsfieldlist.dbf)

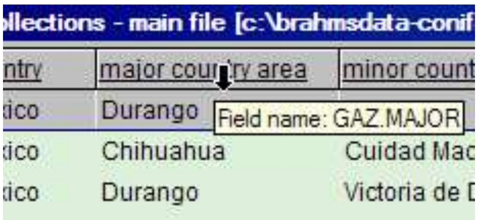
FIELD NAME IN FILE	ENGLISH HEADER	TYPE	LENGTH	DECIMAL PLACES
PREFIX	Prefix	C	10	0
NUMBER	Number	C	15	0
SUFFIX	Suffix	C	6	0
DAY	Day	N	2	0
MONTH	Month	N	2	0
YEAR	Year	N	4	0
DATERES	Date resolution	C	5	0

If collection numbers have character prefix, these characters can be combin with the number in the NUMBER field as in A1234 or separated into the PREF field. In projects or countri where prefixes are used regularly (e.g. in Malaysia, Sabah and Sarawak), the

Physical and translated field names

The field headings you see on the screen are sometimes different to the real field names in the data file. This makes them more readable. However, with some functions (*e.g.* creating reports and using Foxpro commands), you must know and use the real field names.

- Select **BotanicalRecords > View/edit botanical records in database** and locate the field name with the name MAJOR COUNTRY AREA.
- Hover your mouse over the column header and note that the physical field name here is GAZ.MAJOR. This means that the field is in a related file with short name GAZ and in that file, the true field name is MAJOR.



llections - main file [c:\brahmsdata-conif

ntry	major country area	minor count
ico	Durango	
ico	Chihuahua	Cuidad Mac
ico	Durango	Victoria de I

Field name: GAZ.MAJOR

Memo fields

Memo fields hold text of any length. They are used for notes and descriptions. You can copy and paste text into memo fields or drag selected text from your word processor files.

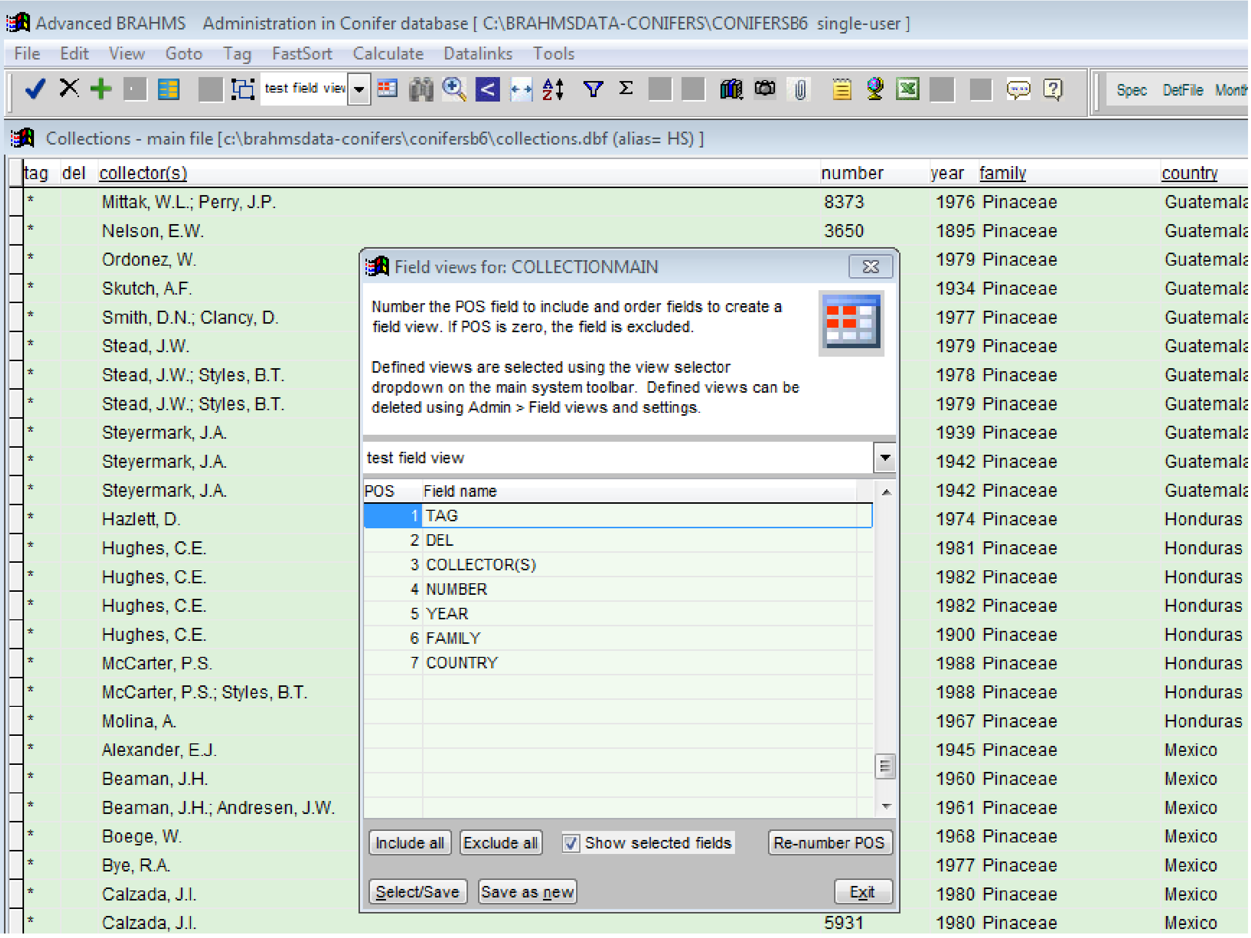
- Select **BotanicalRecords > View/edit botanical records in database.**
- Locate the field PLANT DESCRIPTION.
- Double-click on a memo to open it or use **Ctrl+M.**
- Enter **Ctrl+W** to close and save - or **Esc** to close a memo and abandon edits.

! Memo fields with ‘Memo’ rather than ‘memo’ have data. You can open and edit several memo fields at the same time in a file.

Field Views

Field views are used to restrict the fields you see when viewing data grids. You can create and save multiple views for each type of data (species, collections, extract files, RDE files, *etc.*). They are useful for different editing tasks or simply viewing your data.

- Select **BotanicalRecords > View/edit botanical records in the database**.
- Select the toolbar to define/select field views.
- Initially, select **Exclude all** to remove all fields then choose fields by numbering in the **POS** column.
- Create a field view to show the fields TAG, DEL, COLLECTOR(S), NUMBER, YEAR, FAMILY and FULLNAME.



Number the POS field to include and order fields to create a field view. If POS is zero, the field is excluded.

Defined views are selected using the view selector dropdown on the main system toolbar. Defined views can be deleted using Admin > Field views and settings.

test field view

POS	Field name
1	TAG
2	DEL
3	COLLECTOR(S)
4	NUMBER
5	YEAR
6	FAMILY
7	COUNTRY

tag	del	collector(s)	number	year	family	country
*		Mittak, W.L.; Perry, J.P.	8373	1976	Pinaceae	Guatemala
*		Nelson, E.W.	3650	1895	Pinaceae	Guatemala
*		Ordonez, W.		1979	Pinaceae	Guatemala
*		Skutch, A.F.		1934	Pinaceae	Guatemala
*		Smith, D.N.; Clancy, D.		1977	Pinaceae	Guatemala
*		Stead, J.W.		1979	Pinaceae	Guatemala
*		Stead, J.W.; Styles, B.T.		1978	Pinaceae	Guatemala
*		Stead, J.W.; Styles, B.T.		1979	Pinaceae	Guatemala
*		Steyermark, J.A.		1939	Pinaceae	Guatemala
*		Steyermark, J.A.		1942	Pinaceae	Guatemala
*		Steyermark, J.A.		1942	Pinaceae	Guatemala
*		Hazlett, D.		1974	Pinaceae	Honduras
*		Hughes, C.E.		1981	Pinaceae	Honduras
*		Hughes, C.E.		1982	Pinaceae	Honduras
*		Hughes, C.E.		1982	Pinaceae	Honduras
*		Hughes, C.E.		1900	Pinaceae	Honduras
*		McCarter, P.S.		1988	Pinaceae	Honduras
*		McCarter, P.S.; Styles, B.T.		1988	Pinaceae	Honduras
*		Molina, A.		1967	Pinaceae	Honduras
*		Alexander, E.J.		1945	Pinaceae	Mexico
*		Beaman, J.H.		1960	Pinaceae	Mexico
*		Beaman, J.H.; Andresen, J.W.		1961	Pinaceae	Mexico
*		Boege, W.		1968	Pinaceae	Mexico
*		Bye, R.A.		1977	Pinaceae	Mexico
*		Calzada, J.I.		1980	Pinaceae	Mexico
*		Calzada, J.I.	5931	1980	Pinaceae	Mexico

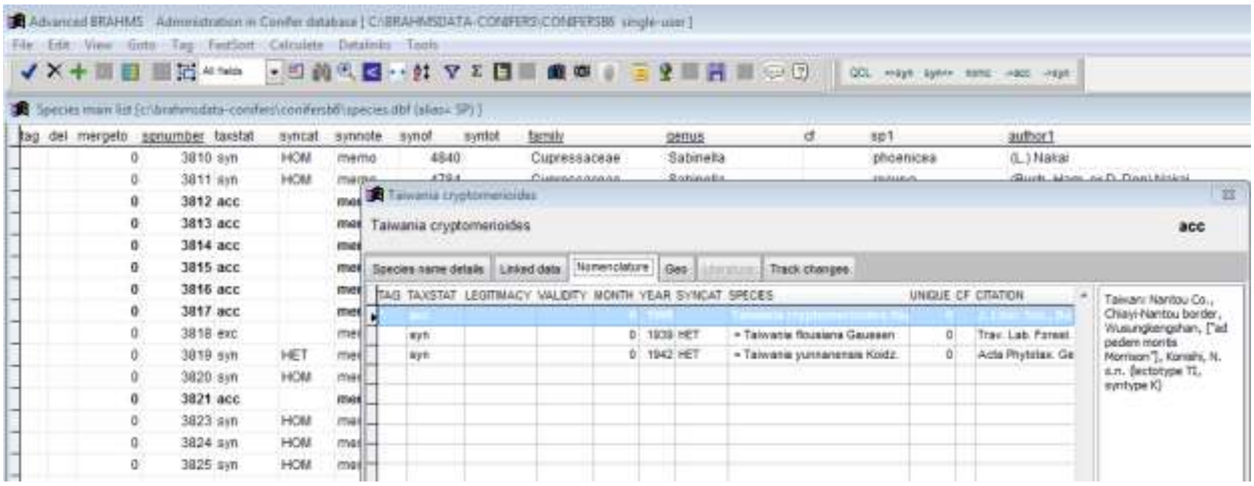
*The field selection form with the option **Show selected fields** ticked.*

- Select **Save as new** to save and select this view, choosing an appropriate name for this field selection as prompted.

You can add and save many field views per file. The required view is selected using the dropdown field view list on the main toolbar. All field views are registered centrally under **Admin > Field views and settings**. You can remove views here.

Edit data in form mode

Experienced BRAHMS users usually find working in data grids faster and more flexible than working with forms. However, with some files, especially those with many fields, data can also be edited using tabbed dialogue screen forms.



Advanced BRAHMS Administration in Conifer database [C:\BRAHMSDATA-CONIFERS\CONIFERSB6 single-user]

Species main list [c:\brahmsdata-conifers\conifersb6\species.dbf (alias= SP)]

Taiwania cryptomerioides **acc**

TAG	TAXSTAT	LEGITIMACY	VALIDITY	MONTH	YEAR	SYNCAT	SPECIES	UNIQUE	CF	CITATION
	syn			0	1939	HET	= Taiwania flousiana Gaussen	0		Trav. Lab. Forest.
	syn			0	1942	HET	= Taiwania yunnanensis Koidz.	0		Acta Phytotax. Ge

Taiwan: Nantou Co., Chiayi-Nantou border, Wusungkengshan, ["ad pedem montis Morrison"], Konishi, N. s.n. (lectotype TI, syntype K)

- In the main species file, locate the name *Taiwania cryptomerioides* using the toolbar.
- Select the toolbar to open the data form.
- Click on the **Nomenclature** tab to view/edit synonyms of this species.

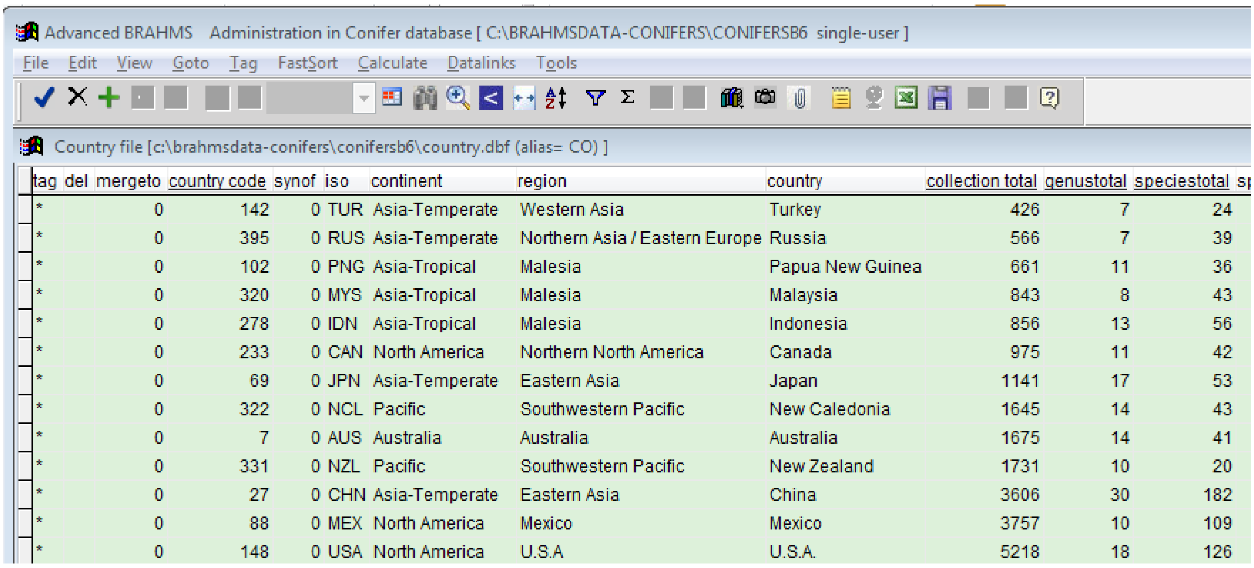
Calculated fields

Calculated fields are summaries of data, often handy for reporting and data checking. These fields are not auto-updated – they must be updated periodically using the **Calculate** menu options provided. Calculated field options are available in most of the main files.

- Open the main country list by selecting **Geo > View/edit countries in database**.
- Select **Calculate > Update calculated fields….**
- Select **Select all** then **Process**.

Calculated totals are added to fields such as COLLECTION TOTAL, SEED TOTAL, SPECIES TOTAL, *etc.*

- Locate the column COLLECTION TOTAL, right-click the column **header** name and choose **Sort Ascending**. Go to the bottom of the file to see the highest values.
- Close the country file.



Advanced BRAHMS Administration in Conifer database [C:\BRAHMSDATA-CONIFERS\CONIFERSB6 single-user]

Country file [c:\brahmsdata-conifers\conifersb6\country.dbf (alias= CO)]

tag	del	mergeto	country code	synof	iso	continent	region	country	collection total	genustotal	speciestotal
*		0	142	0	TUR	Asia-Temperate	Western Asia	Turkey	426	7	24
*		0	395	0	RUS	Asia-Temperate	Northern Asia / Eastern Europe	Russia	566	7	39
*		0	102	0	PNG	Asia-Tropical	Malesia	Papua New Guinea	661	11	36
*		0	320	0	MYS	Asia-Tropical	Malesia	Malaysia	843	8	43
*		0	278	0	IDN	Asia-Tropical	Malesia	Indonesia	856	13	56
*		0	233	0	CAN	North America	Northern North America	Canada	975	11	42
*		0	69	0	JPN	Asia-Temperate	Eastern Asia	Japan	1141	17	53
*		0	322	0	NCL	Pacific	Southwestern Pacific	New Caledonia	1645	14	43
*		0	7	0	AUS	Australia	Australia	Australia	1675	14	41
*		0	331	0	NZL	Pacific	Southwestern Pacific	New Zealand	1731	10	20
*		0	27	0	CHN	Asia-Temperate	Eastern Asia	China	3606	30	182
*		0	88	0	MEX	North America	Mexico	Mexico	3757	10	109
*		0	148	0	USA	North America	U.S.A	U.S.A.	5218	18	126

The country file showing some calculated fields, sorted on collection total.

- Now open the main people file by selecting **People > View/edit people in database**.
- Select **Calculate > Update calculated fields** and select the option ‘Collection totals’ and then **Process**. Locate and then and sort on that column.

ADDING AND DELETING RECORDS

Adding records

- Open the main species file using **Taxa > View/edit SPECIES in database,** click the + toolbar several times to add some blank records. You don't need to add any data at this stage. Close this file.

- Open the main country file using **Geo > View/edit countries in database,** click the + toolbar several times to add several blank records. Close this file

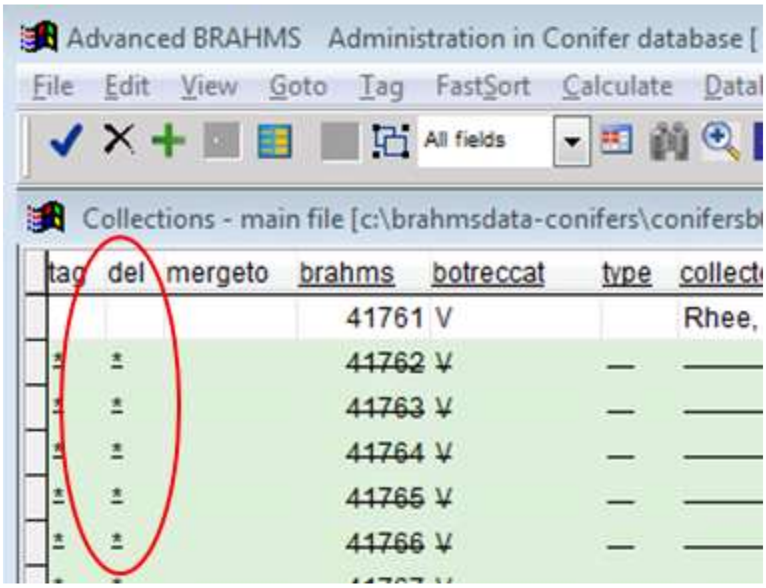
- Now add blank records to the botanical records, family and genus files.

Deleting records

- Delete all the new records added to the various files edited above. To delete a record, go to that record and then either click on the ✕ toolbar or press the **F7** key. This adds * to the DEL field for each record that you want to delete.

- To finally remove these marked records, select **Edit > Delete options > Remove records marked for deletion**.

! Record deletion is always a **two-stage process** as described here.



tag	del	mergeto	brahms	botreccat	type	collect
			41761	V		Rhee,
*	*		~~41762~~	~~V~~		
*	*		~~41763~~	~~V~~		
*	*		~~41764~~	~~V~~		
*	*		~~41765~~	~~V~~		
*	*		~~41766~~	~~V~~		

*Pressing F7 of using the ✕ toolbar adds * to the DEL field but at this stage, records are only marked for deletion. In the above example, the records are also tagged.*

USING LINK FILES TO EXTEND DATABASE STRUCTURE

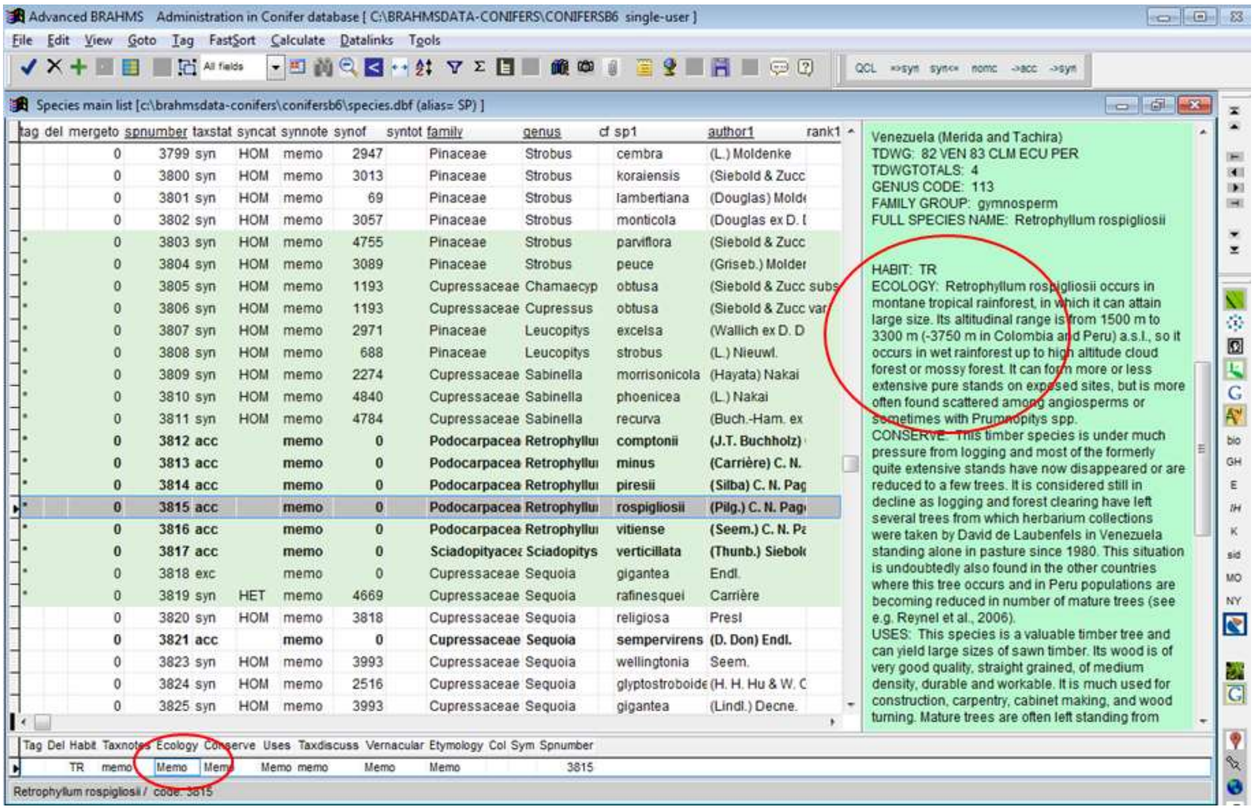
Link files introduced

BRAHMS database files are provided with default standard fields. If BRAHMS lacks fields that you require, you can add your own fields using linked data files. Link files extend the structure of your database and are available in most of the main database files including species and botanical records.

For example, if you want to indicate whether a species has spines or not, you could add a new field to the species link file called ‘SPINES’ and add ‘*’ to all species that have spines. In this case, the field would only need be 1 character in width.

Viewing link file fields from a main file

- Select **Taxa > View/edit species in database** to open the main species file.
- Click on the toolbar. This opens the link data file at the bottom of your data grid.
- Set a simple filter in the main species file to restrict the view to TAXSTAT = ‘acc’. Accepted names will tend to have linked data such as descriptions stored.
- Open the Zoom window using the toolbar.
- Link file data are included in the Zoom window and all the data in the Zoom window are updated as you move to a different record.
- Close the main species file.



tag	del	mergeto	spnumber	taxstat	syncat	synnote	synof	syntot	family	genus	cf	sp1	author1	rank1
		0	3799	syn	HOM	memo	2947		Pinaceae	Strobus		cembra	(L.) Moldenke	
		0	3800	syn	HOM	memo	3013		Pinaceae	Strobus		koraiensis	(Siebold & Zucc	
		0	3801	syn	HOM	memo	69		Pinaceae	Strobus		lambertiana	(Douglas) Mold	
		0	3802	syn	HOM	memo	3057		Pinaceae	Strobus		monticola	(Douglas ex D. I	
*		0	3803	syn	HOM	memo	4755		Pinaceae	Strobus		parviflora	(Siebold & Zucc	
*		0	3804	syn	HOM	memo	3089		Pinaceae	Strobus		peuce	(Griseb.) Molder	
*		0	3805	syn	HOM	memo	1193		Cupressaceae	Chamaecyp		obtusa	(Siebold & Zucc	subs
*		0	3806	syn	HOM	memo	1193		Cupressaceae	Cupressus		obtusa	(Siebold & Zucc	var
*		0	3807	syn	HOM	memo	2971		Pinaceae	Leucopitys		excelsa	(Wallich ex D. D	
*		0	3808	syn	HOM	memo	688		Pinaceae	Leucopitys		strobus	(L.) Nieuwl.	
*		0	3809	syn	HOM	memo	2274		Cupressaceae	Sabinella		morrisonicola	(Hayata) Nakai	
*		0	3810	syn	HOM	memo	4840		Cupressaceae	Sabinella		phoenicea	(L.) Nakai	
*		0	3811	syn	HOM	memo	4784		Cupressaceae	Sabinella		recurva	(Buch.-Ham. ex	
*		**0**	**3812**	**acc**		**memo**	**0**		**Podocarpacea**	**Retrophyllu**		**comptonii**	**(J.T. Buchholz)**	
*		**0**	**3813**	**acc**		**memo**	**0**		**Podocarpacea**	**Retrophyllu**		**minus**	**(Carrière) C. N.**	
*		**0**	**3814**	**acc**		**memo**	**0**		**Podocarpacea**	**Retrophyllu**		**piresii**	**(Silba) C. N. Pag**	
*		**0**	**3815**	**acc**		**memo**	**0**		**Podocarpacea**	**Retrophyllu**		**rospigliosii**	**(Pilg.) C. N. Pag**	
*		**0**	**3816**	**acc**		**memo**	**0**		**Podocarpacea**	**Retrophyllu**		**vitiense**	**(Seem.) C. N. Pa**	
*		**0**	**3817**	**acc**		**memo**	**0**		**Sciadopityace**	**Sciadopitys**		**verticillata**	**(Thunb.) Siebol**	
*		0	3818	exc		memo	0		Cupressaceae	Sequoia		gigantea	Endl.	
*		0	3819	syn	HET	memo	4669		Cupressaceae	Sequoia		rafinesquei	Carrière	
		0	3820	syn	HOM	memo	3818		Cupressaceae	Sequoia		religiosa	Presl	
		0	**3821**	**acc**		**memo**	**0**		**Cupressaceae**	**Sequoia**		**sempervirens**	**(D. Don) Endl.**	
		0	3823	syn	HOM	memo	3993		Cupressaceae	Sequoia		wellingtonia	Seem.	
		0	3824	syn	HOM	memo	2516		Cupressaceae	Sequoia		glyptostroboide	(H. H. Hu & W. C	
		0	3825	syn	HOM	memo	3993		Cupressaceae	Sequoia		gigantea	(Lindl.) Decne.	

Venezuela (Merida and Tachira)
TDWG: 82 VEN 83 CLM ECU PER
TDWGTOTALS: 4
GENUS CODE: 113
FAMILY GROUP: gymnosperm
FULL SPECIES NAME: Retrophyllum rospigliosii

HABIT: TR
ECOLOGY: Retrophyllum rospigliosii occurs in montane tropical rainforest, in which it can attain large size. Its altitudinal range is from 1500 m to 3300 m (-3750 m in Colombia and Peru) a.s.l., so it occurs in wet rainforest up to high altitude cloud forest or mossy forest. It can form more or less extensive pure stands on exposed sites, but is more often found scattered among angiosperms or sometimes with Prumnopitys spp.
CONSERVE: This timber species is under much pressure from logging and most of the formerly quite extensive stands have now disappeared or are reduced to a few trees. It is considered still in decline as logging and forest clearing have left several trees from which herbarium collections were taken by David de Laubenfels in Venezuela standing alone in pasture since 1980. This situation is undoubtedly also found in the other countries where this tree occurs and in Peru populations are becoming reduced in number of mature trees (see e.g. Reynel et al., 2006).
USES: This species is a valuable timber tree and can yield large sizes of sawn timber. Its wood is of very good quality, straight grained, of medium density, durable and workable. It is much used for construction, carpentry, cabinet making, and wood turning. Mature trees are often left standing from

Tag	Del	Habit	Taxnotes	Ecology	Conserve	Uses	Taxdiscuss	Vernacular	Etymology	Col	Sym	Spnumber
		TR	memo	Memo	Memo	Memo	memo	Memo	Memo			3815

Retrophyllum rospigliosii / code: 3815

The link file opened using the toolbar at the bottom of the main species file. Link file fields are displayed in the Zoom window. Link files are available for species, gazetteer, botanical records, seed collections, living collections, images and references.

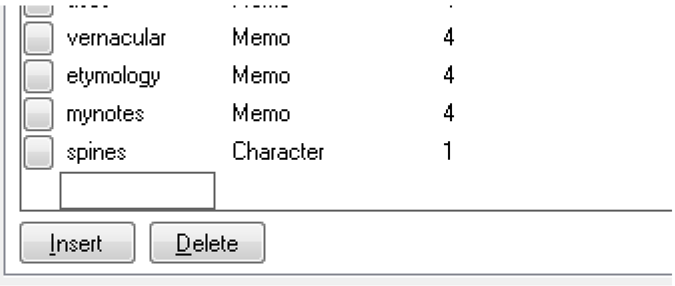
Opening and editing link files directly

You can also open link files directly from the main menu.

- Select **Taxa > Default linked data file (SPLINK)**. This opens the species link file. If you are doing a lot of editing of link file fields, it may be quicker to open it like this rather than at the bottom of the main species file.

Modify link file structure

- Select **Taxa > Default linked data file (SPLINK)** to re-open the link file.
- Select **File > Modify file structure…**
- In the open square at the bottom of the field list, type in **mynotes** and change the field type to Memo.
- Click on **Insert** to add another new field
- In the open square at the bottom of the field list, type in **spines** and change the field type to Character width 1



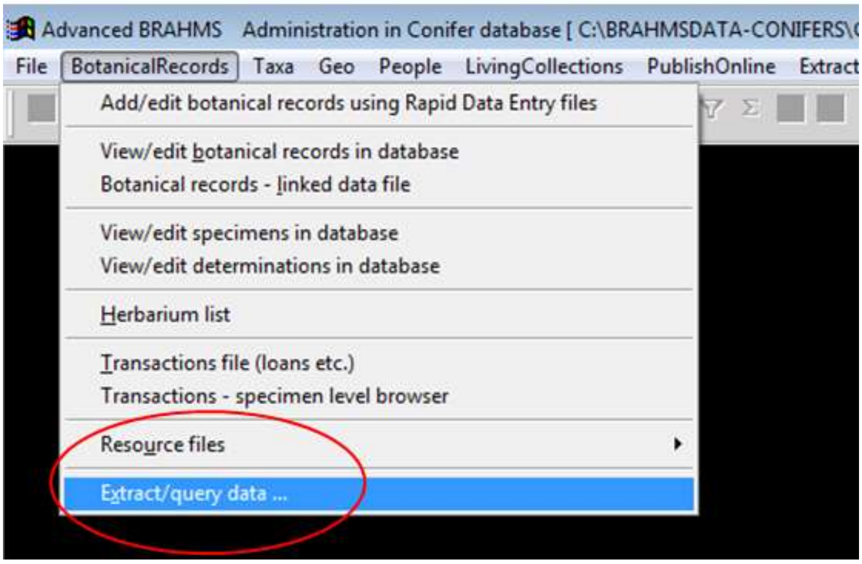
vernacular	Memo	4
etymology	Memo	4
mynotes	Memo	4
spines	Character	1

- Click **OK** to save this edit and respond **Yes** to the prompt ‘Make structure change permanent?’.
- Close the link file.
- Select **Taxa > View/edit species in database** to open the main species file.
- Click on the toolbar again to open the link file and note that these new fields are now available and can be edited.

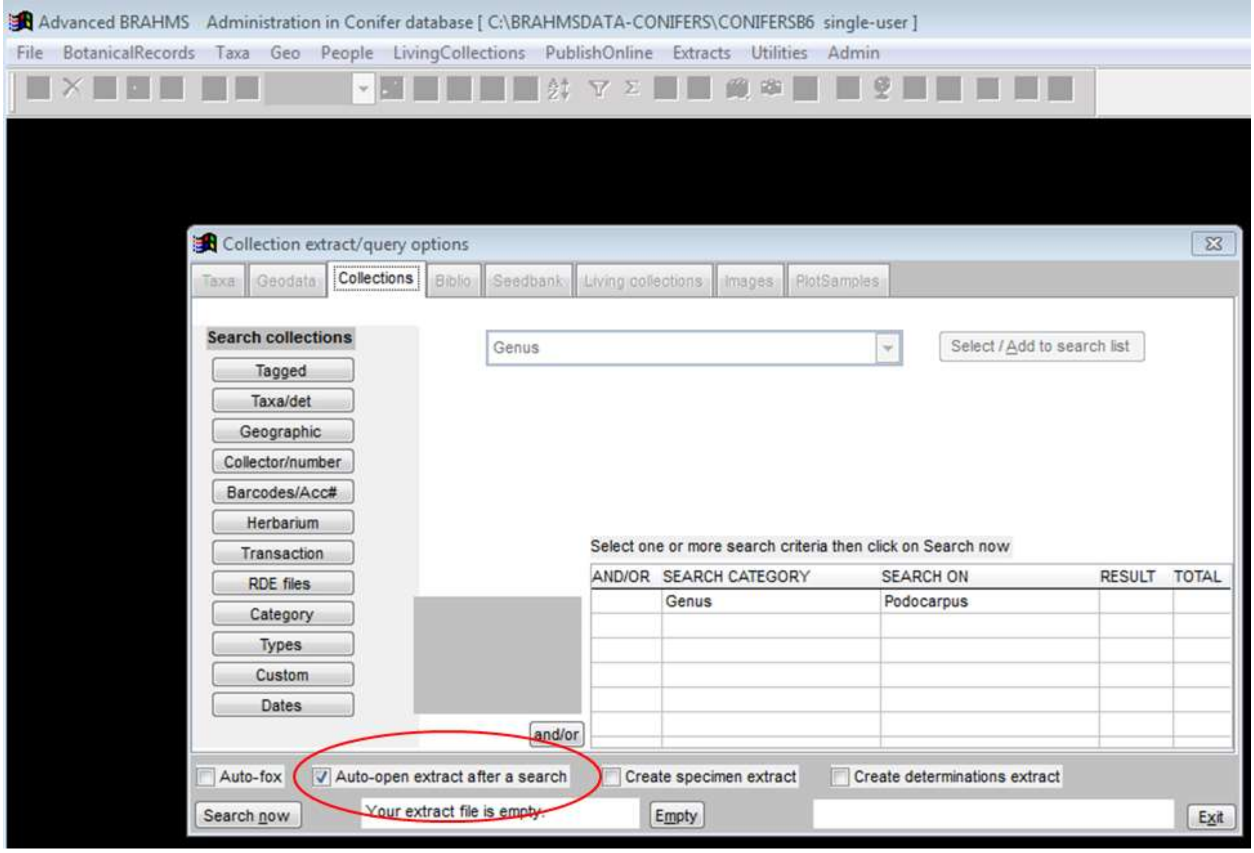
QUERYING DATA – MAKING EXTRACT FILES

About query (extract) files

Most categories of data have a menu option at the bottom of the respective menu: **Extract/query data.** The query commands provided vary depending on the category of data you are working with.



Extract menu option for botanical records



Genus

Select one or more search criteria then click on Search now

AND/OR	SEARCH CATEGORY	SEARCH ON	RESULT	TOTAL
	Genus	Podocarpus		

☐ Auto-fox ☑ Auto-open extract after a search ☐ Create specimen extract ☐ Create determinations extract

Your extract file is empty.

Extracting botanical records (collections) by genus. As the option ‘Auto-open extract file after a search’ is selected, the search result will be displayed after clicking ‘Search now’.

Extract collections by genus

- In the Conifer database, select **BotanicalRecords > Extract/query data...**
- Check the extract file is empty by clicking the **Empty** button.
- Select **Taxa/det > Genus > Select/Add to search list**.

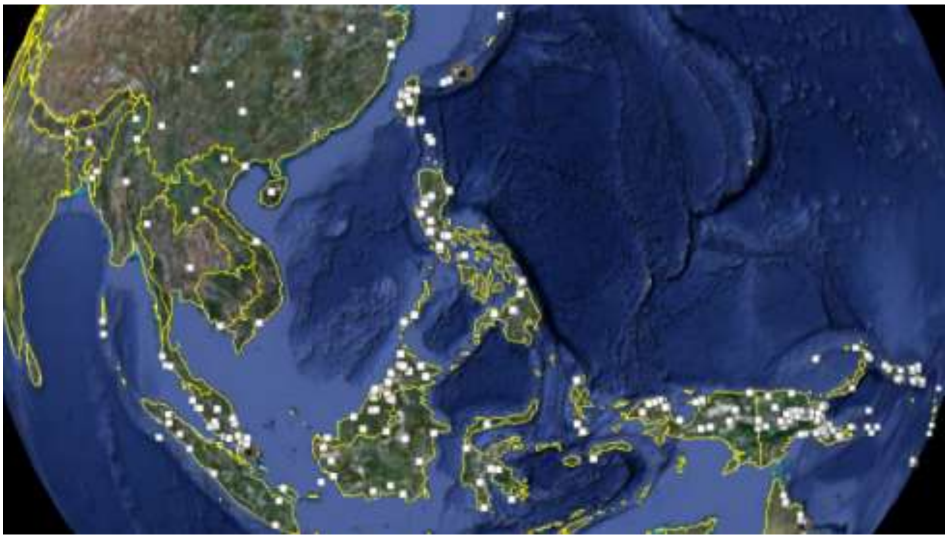
- To choose the genus *Podocarpus*, enter ‘pod’ in the search string box. In the Conifer database, this would be enough to locate the correct name. Click on **Select** to confirm the selected name.
- Click on **Search now** to extract the data.
- If the **Auto-open extract** option was selected, the extract will auto-open. Otherwise, close the form and select **Extracts > BotanicalRecords**.

You can now process these results in different ways, for example to make a report or a map, undertake an analysis or export the data for processing elsewhere.

- Click on the ↔ toolbar to auto-resize column widths.
- Click on the 🔍 toolbar to open the zoom pane.
- In the Zoom pane, locate and dbl-click on the COUNTRY column name to quickly locate and select that column.
- Then use the Σ toolbar to calculate the number of collections stored in this database per country for this genus in this database.

Mapping extracted collections to Google Earth

- If you are online and you have Google Earth installed, select the 🌐 toolbar, check the **Google Earth** option
- Make sure that the option **Restrict to tagged** is not selected (unless you only want to map tagged records).
- Click on **Map all**.



A snapshot of the Podocarpus collections in S E Asia region.

Extract collections by country

- In the Conifer database, select **BotanicalRecords > Extract/query data...**
- Check the extract file is empty by clicking the **Empty** button.
- Select **Geographic > Country** then **Select/Add to search list**.
- Choose a country that has conifers, for example China or Vietnam.
- Click on **Search now** to extract the data for the selected country.

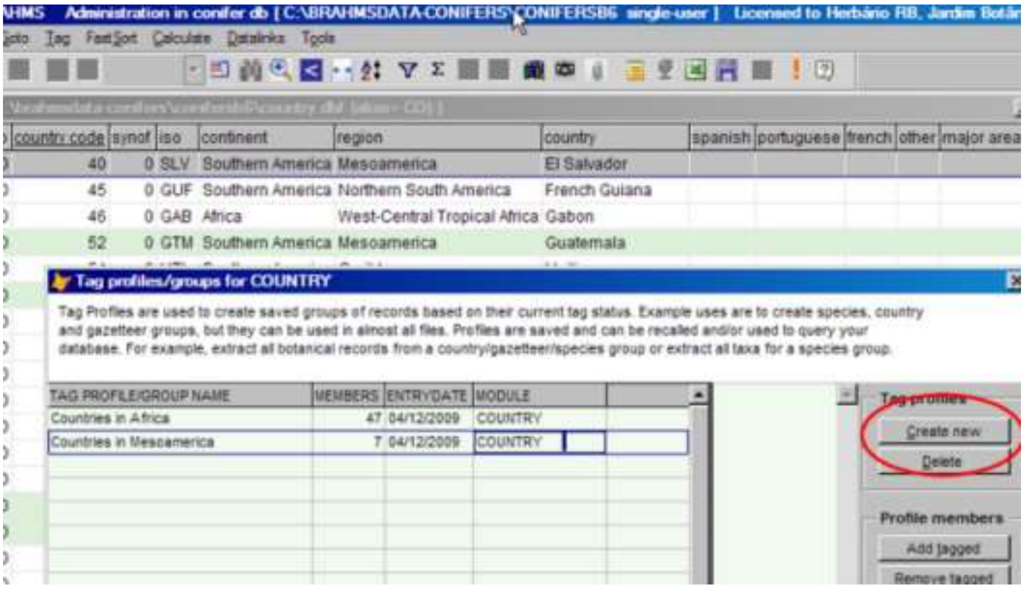
You can now process your extracted records in different ways. For example:

- Locate the SPECIES column and use the Σ toolbar to calculate the number of collections per species for that country.
- Use a **FastSort** menu option to sort the records.
- If online, use the 🌐 toolbar to map these data using Google Earth.

Creating and using a tag profile for countries

A further use of tagging in BRAHMS is to create and save groups or records, for example a group of countries that you may use frequently. You can use your groups to query your database, for example, to extract all specimens from Africa or all countries in southern Africa.

- Select **Geo > View/edit countries in database**.
- Clear all the tags using the **Tag** menu option.
- Locate and tag a series of countries in your region (you could do this manually or deploying some filter and tag menu options).
- Select **Tag > Tag profiles an groups** then **Create new** to save these tags to a named group e.g. 'Africa' or 'Indochina'.



HMS Administration in conifer db [C:\BRAHMSDATA-CONIFERS\CONIFERS86 single-user] Licensed to Herbário RB, Jardim Botân

country code	synof	iso	continent	region	country	spanish	portuguese	french	other	major area
40	0	SLV	Southern America	Mesoamerica	El Salvador					
45	0	GUF	Southern America	Northern South America	French Guiana					
46	0	GAB	Africa	West-Central Tropical Africa	Gabon					
52	0	GTM	Southern America	Mesoamerica	Guatemala					

Tag profiles/groups for COUNTRY

Tag Profiles are used to create saved groups of records based on their current tag status. Example uses are to create species, country and gazetteer groups, but they can be used in almost all files. Profiles are saved and can be recalled and/or used to query your database. For example, extract all botanical records from a country/gazetteer/species group or extract all taxa for a species group.

TAG PROFILE/GROUP NAME	MEMBERS	ENTRYDATE	MODULE
Countries in Africa	47	04/12/2009	COUNTRY
Countries in Mesoamerica	7	04/12/2009	COUNTRY

- Select **BotanicalRecords > Extract/query data...** . Then select **Geographic > Country Group** and extract all specimens from that group of countries.

! The same process could be used to save any logical group of records (*e.g.* endangered species or a group of locations in your main gazetteer).

Create a species list from extracted botanical records

Using your extracted botanical records, you can create a separate list of taxa. This is a useful tool when producing check lists based on collections.

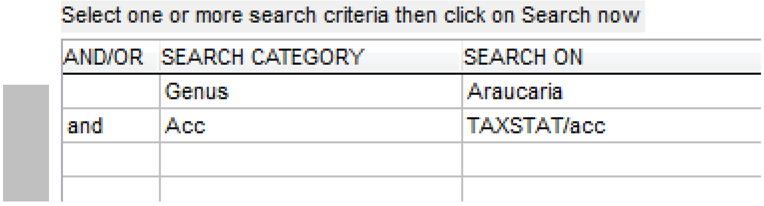
- In the opened extract file (created above), select **Tools > Convert extract file to another … > Botanical Record extract -> Taxon extract**.

- Close the current extract and select **Extracts > Taxa** to open this new taxon extract derived from your collections.

Extract accepted names of *Araucaria*

As described above, you can create a taxon extract from a botanical records extract. But you can also make taxon extracts directly – and this is the normal procedure when making checklists and other outputs based on a list of taxa.

- In the Conifer database, select **Taxa > Extract/query data...**
- Check the extract file is empty by clicking the **Empty** button.
- On the form, select **Taxa > Genus** > **Select/Add to search list** and the locate and select *Araucaria*.
- Now select the **Name status** option and choose the ‘acc’ to restrict to accepted names only. If you do not do this, you will extract a list of all Araucaria names (accepted + synonyms) which of course sometimes, you may want.

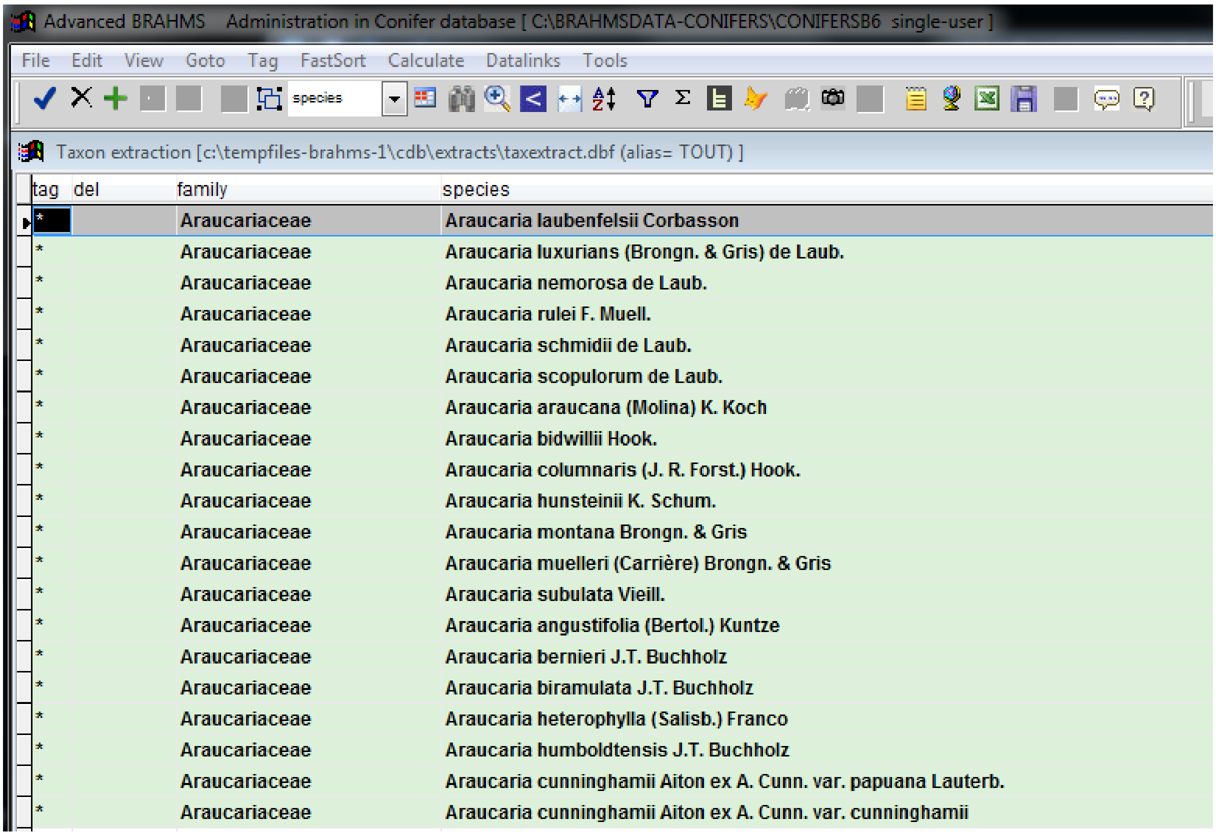


Select one or more search criteria then click on Search now

AND/OR	SEARCH CATEGORY	SEARCH ON
	Genus	Araucaria
and	Acc	TAXSTAT/acc

Two search options selected on the taxon extract form

- Finally, click on **Search now** to extract the data.
- Assuming the **Auto-open extract** option on the form was selected, the resulting table will be auto-opened. Otherwise, close the form and select **Extracts > Taxa**



Taxon extraction [c:\tempfiles-brahms-1\cdb\extracts\taxextract.dbf (alias= TOUT)]

tag	del	family	species
*		Araucariaceae	Araucaria laubenfelsii Corbasson
*		Araucariaceae	Araucaria luxurians (Brongn. & Gris) de Laub.
*		Araucariaceae	Araucaria nemorosa de Laub.
*		Araucariaceae	Araucaria rulei F. Muell.
*		Araucariaceae	Araucaria schmidii de Laub.
*		Araucariaceae	Araucaria scopulorum de Laub.
*		Araucariaceae	Araucaria araucana (Molina) K. Koch
*		Araucariaceae	Araucaria bidwillii Hook.
*		Araucariaceae	Araucaria columnaris (J. R. Forst.) Hook.
*		Araucariaceae	Araucaria hunsteinii K. Schum.
*		Araucariaceae	Araucaria montana Brongn. & Gris
*		Araucariaceae	Araucaria muelleri (Carrière) Brongn. & Gris
*		Araucariaceae	Araucaria subulata Vieill.
*		Araucariaceae	Araucaria angustifolia (Bertol.) Kuntze
*		Araucariaceae	Araucaria bernieri J.T. Buchholz
*		Araucariaceae	Araucaria biramulata J.T. Buchholz
*		Araucariaceae	Araucaria heterophylla (Salisb.) Franco
*		Araucariaceae	Araucaria humboldtensis J.T. Buchholz
*		Araucariaceae	Araucaria cunninghamii Aiton ex A. Cunn. var. papuana Lauterb.
*		Araucariaceae	Araucaria cunninghamii Aiton ex A. Cunn. var. cunninghamii

List of names in the taxa extract file with a field view set to show family and species.

Although reports can be created from any BRAHMS file, they are usually prepared from extract or RDE files. The following examples introduce the two main categories of reporting used in BRAHMS: **Text** and **Visual** reports.

REPORTING INTRODUCED

This section introduces some general facts about reporting in BRAHMS. A quick read here will provide some perspective on the sections ahead in this guide.

Text *vs* Visual reports

Aside from exporting data to Excel or elsewhere, BRAHMS has two main ways to produce reports: **Text and Visual reporting**.

Text reports format your data into text files with HTML tags. These files can be transferred to text or word processor documents. Text reports are, in general, used to produce checklists, monograph accounts and similar. Text reports may include graphics generated using HTML tags *e.g.* lines (<hr/>), images references (<img src>) and so on. Most BRAHMS users don't know much about HTML tags – which is fine. You do not need any special knowledge although it is useful to be aware that, should you want to elaborate reporting outputs with fonts, styles, colours, indents, *etc.* this is possible by adding valid html tags to your text reports.

Visual reports are generated using the Visual Report Designer. These reports are normally used to prepare lists, labels, det. slips, loan forms and other reports that are printed directly or sent to a PDF – rather than being passed to a word processor. Visual reports often include graphics (lines, boxes, images).

Learning curve

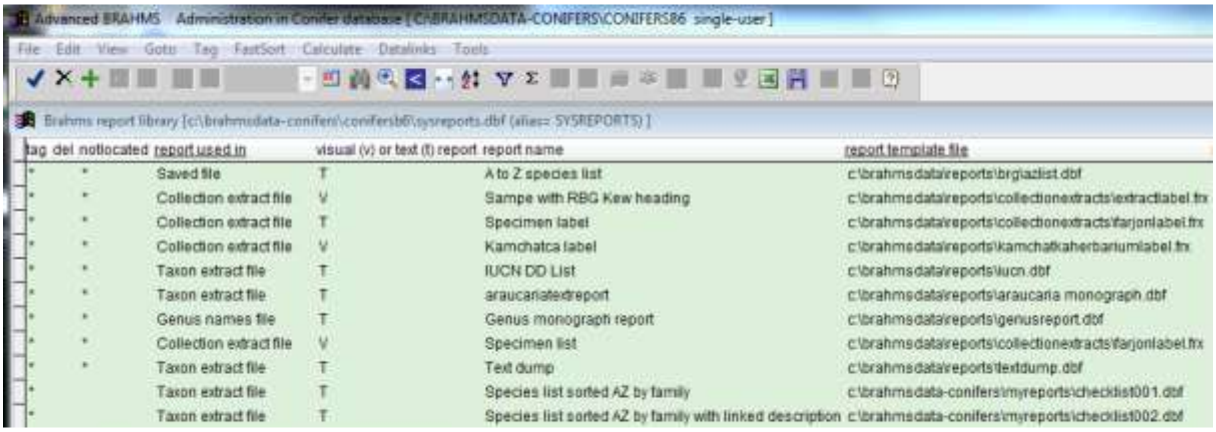
The BRAHMS report design options are flexible. You can achieve more or less any report you want using visual or text reports. However, there is quite a lot to learn about both report categories so it may take some time to conquer both. Don't be discouraged!

Templates?

When you design a report, you are designing a template that can be used for any data of the same type – not just one report. If you invest time to perfect a label report, this template will be saved and used as and when required.

Managing report template files

When you add a new report design, the saved report template is added to your central reports library. You can open this using **Utilities > View/edit all report templates**. Note that templates are associated with a particular type of data (or BRAHMS module). Thus, if you create a new design in a botanical record RDE file, that template can only be used with that file type. But of course, it can be used in any botanical record RDE file, not just the one you had open when you created the report. In the central reports library, you can delete and rename report templates.



Brahms report library [c:\brahmsdata-conifers\conifers86\sysreports.dbf (alias= SYSREPORTS)]

tag	del	notlocated	report used in	visual (v) or text (t) report	report name	report template file
*		*	Saved file	T	A to Z species list	c:\brahmsdata\reports\brgiazlist.dbf
*		*	Collection extract file	V	Sampe with RBG Kew heading	c:\brahmsdata\reports\collectionextracts\extractlabel.frx
*		*	Collection extract file	T	Specimen label	c:\brahmsdata\reports\collectionextracts\farjonlabel.frx
*		*	Collection extract file	V	Kamchatca label	c:\brahmsdata\reports\kamchatkaherbariumlabel.frx
*		*	Taxon extract file	T	IUCN DD List	c:\brahmsdata\reports\iucn.dbf
*		*	Taxon extract file	T	araucariatextreport	c:\brahmsdata\reports\araucaria monograph.dbf
*		*	Genus names file	T	Genus monograph report	c:\brahmsdata\reports\genusreport.dbf
*		*	Collection extract file	V	Specimen list	c:\brahmsdata\reports\collectionextracts\farjonlabel.frx
*		*	Taxon extract file	T	Text dump	c:\brahmsdata\reports\textdump.dbf
*			Taxon extract file	T	Species list sorted AZ by family	c:\brahmsdata-conifers\myreports\checklist001.dbf
*			Taxon extract file	T	Species list sorted AZ by family with linked description	c:\brahmsdata-conifers\myreports\checklist002.dbf

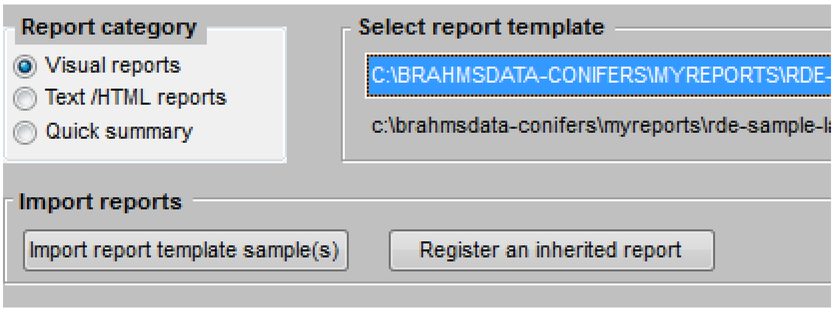
Report templates opened from the Utilities menu. Reports are specific to a project. Some samples are provided with BRAHMS.

Inheriting reports from another project

If you want to register a report provided from another database/project, use the **Register an inherited report** option on the reports form.

Importing report template samples

Some report sample templates are provided with BRAHMS. You can import these to your database using the **Import report template sample(s)** option on the reports form.



Report category

● Visual reports

○ Text /HTML reports

○ Quick summary

Select report template

C:\BRAHMSDATA-CONIFERS\MYREPORTS\RDE-

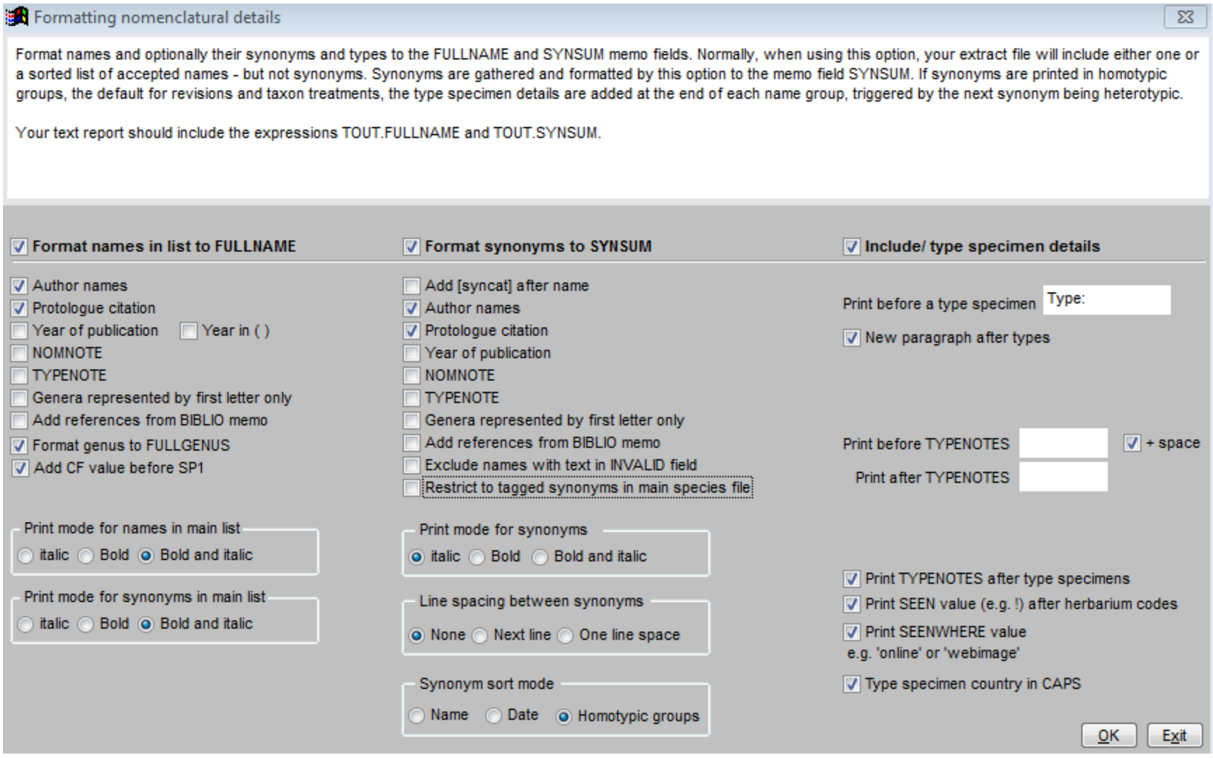
c:\brahmsdata-conifers\myreports\rde-sample-l

MORE EXTRACTS AND A START WITH REPORTING

Preparing a sample text report for *Araucaria*

Using Text Reports, reports can be formatted directly into your word processor.

- In your opened taxon extract prepared above for *Araucaria*, sort the names using **Fastsort > Family+species**.
- Select **Tools > Formatting for text reports > Names, synonyms and types to FULLNAME and SYNSUM**



Format names and optionally their synonyms and types to the FULLNAME and SYNSUM memo fields. Normally, when using this option, your extract file will include either one or a sorted list of accepted names - but not synonyms. Synonyms are gathered and formatted by this option to the memo field SYNSUM. If synonyms are printed in homotypic groups, the default for revisions and taxon treatments, the type specimen details are added at the end of each name group, triggered by the next synonym being heterotypic.

Your text report should include the expressions TOUT.FULLNAME and TOUT.SYNSUM.

☑ **Format names in list to FULLNAME**
☑ Author names
☑ Protologue citation
☐ Year of publication ☐ Year in ( )
☐ NOMNOTE
☐ TYPENOTE
☐ Genera represented by first letter only
☐ Add references from BIBLIO memo
☑ Format genus to FULLGENUS
☑ Add CF value before SP1

Print mode for names in main list: ○ italic ○ Bold ● Bold and italic

Print mode for synonyms in main list: ○ italic ○ Bold ● Bold and italic

☑ **Format synonyms to SYNSUM**
☐ Add [syncat] after name
☑ Author names
☑ Protologue citation
☐ Year of publication
☐ NOMNOTE
☐ TYPENOTE
☐ Genera represented by first letter only
☐ Add references from BIBLIO memo
☐ Exclude names with text in INVALID field
☐ Restrict to tagged synonyms in main species file

Print mode for synonyms: ● italic ○ Bold ○ Bold and italic

Line spacing between synonyms: ● None ○ Next line ○ One line space

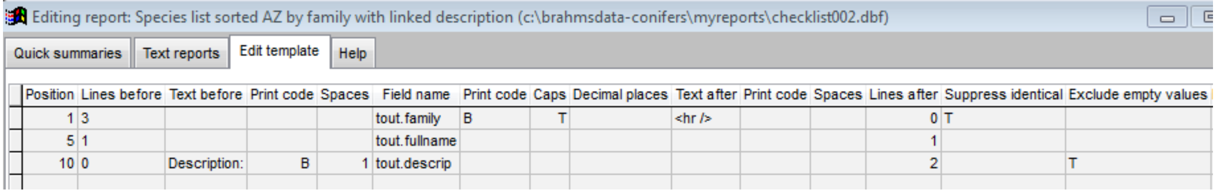
Synonym sort mode: ○ Name ○ Date ● Homotypic groups

☑ **Include/ type specimen details**
Print before a type specimen: Type:
☑ New paragraph after types
Print before TYPENOTES: ☑ + space
Print after TYPENOTES:
☑ Print TYPENOTES after type specimens
☑ Print SEEN value (e.g. !) after herbarium codes
☑ Print SEENWHERE value e.g. 'online' or 'webimage'
☑ Type specimen country in CAPS

You can use the above form to format your names and synonyms

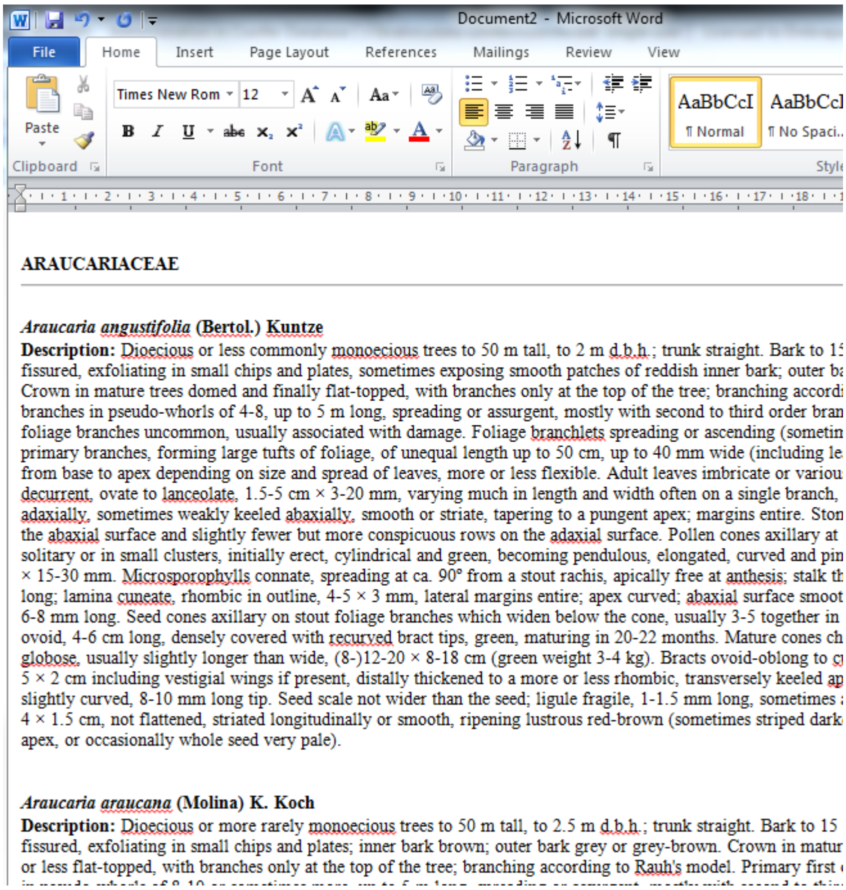
- Click the toolbar to open the **Text reports** form.
- Choose the report '*Species list sorted AZ by family with linked description*' from the listed text reports. If this report does not appear in your report list, use the option **Import sample** and **Add** the report as prompted.
- Select **Generate report.** By default, the report will open as an HTML document. You can close this and then use option to open the report in a word document.

- This sample report format, used to create the report shown below, is a simple one. If you click on **Edit report template**, you will see there are 3 command lines. You will learn how to edit these templates later in this guide.



Position	Lines before	Text before	Print code	Spaces	Field name	Print code	Caps	Decimal places	Text after	Print code	Spaces	Lines after	Suppress identical	Exclude empty values
1	3				tout.family	B	T		<hr />			0	T	
5	1				tout.fullname							1		
10	0	Description:	B	1	tout.descrip							2		T

The fields Text before and Text after optionally store text headings to print before/after the select item, for example "Description: ".The "<hr />" coding in the PUNC2 field creates a line after the family name.



ARAUCARIACEAE

***Araucaria angustifolia* (Bertol.) Kuntze**
Description: Dioecious or less commonly monoecious trees to 50 m tall, to 2 m d.b.h.; trunk straight. Bark to 15
fissured, exfoliating in small chips and plates, sometimes exposing smooth patches of reddish inner bark; outer ba
Crown in mature trees domed and finally flat-topped, with branches only at the top of the tree; branching accordi
branches in pseudo-whorls of 4-8, up to 5 m long, spreading or assurgent, mostly with second to third order bran
foliage branches uncommon, usually associated with damage. Foliage branchlets spreading or ascending (sometin
primary branches, forming large tufts of foliage, of unequal length up to 50 cm, up to 40 mm wide (including le
from base to apex depending on size and spread of leaves, more or less flexible. Adult leaves imbricate or variou
decurrent, ovate to lanceolate, 1.5-5 cm × 3-20 mm, varying much in length and width often on a single branch,
adaxially, sometimes weakly keeled abaxially, smooth or striate, tapering to a pungent apex; margins entire. Ston
the abaxial surface and slightly fewer but more conspicuous rows on the adaxial surface. Pollen cones axillary at
solitary or in small clusters, initially erect, cylindrical and green, becoming pendulous, elongated, curved and pin
× 15-30 mm. Microsporophylls connate, spreading at ca. 90° from a stout rachis, apically free at anthesis; stalk th
long; lamina cuneate, rhombic in outline, 4-5 × 3 mm, lateral margins entire; apex curved; abaxial surface smoot
6-8 mm long. Seed cones axillary on stout foliage branches which widen below the cone, usually 3-5 together in
ovoid, 4-6 cm long, densely covered with recurved bract tips, green, maturing in 20-22 months. Mature cones ch
globose, usually slightly longer than wide, (8-)12-20 × 8-18 cm (green weight 3-4 kg). Bracts ovoid-oblong to c
5 × 2 cm including vestigial wings if present, distally thickened to a more or less rhombic, transversely keeled ap
slightly curved, 8-10 mm long tip. Seed scale not wider than the seed; ligule fragile, 1-1.5 mm long, sometimes
4 × 1.5 cm, not flattened, striated longitudinally or smooth, ripening lustrous red-brown (sometimes striped dark
apex, or occasionally whole seed very pale).

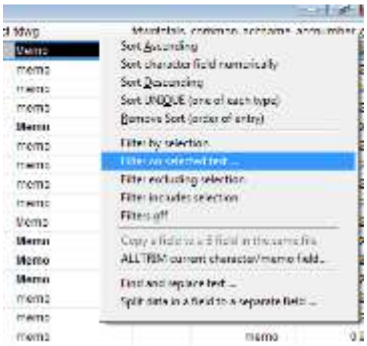
***Araucaria araucana* (Molina) K. Koch**
Description: Dioecious or more rarely monoecious trees to 50 m tall, to 2.5 m d.b.h.; trunk straight. Bark to 15
fissured, exfoliating in small chips and plates; inner bark brown; outer bark grey or grey-brown. Crown in matur
or less flat-topped, with branches only at the top of the tree; branching according to Rauh's model. Primary first

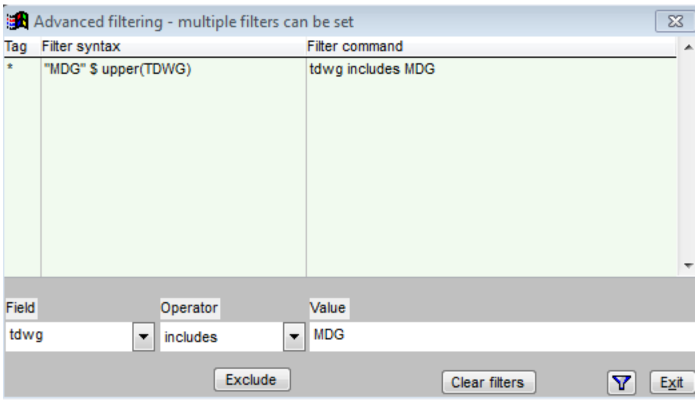
Sample text report

Tagging species to prepare a checklist of conifers for Madacasgar

The following exercise introduces the use of geographic coding in the species file. The TDWG field provides a standard, global geo-coding system based on the so called "taxonomic database working group" system as used in the conifer database. You may have your own coding system. All accepted taxa in the conifer database are coded in this way thus defining their known geographic distribution. Clearly, botanical records provide more distribution details. But only when available in a database.

- Select **Taxa > View/edit species in database** to open the main species file.
- Select **Tag > Clear all tags**.
- Locate the memo field TDWG in this file. Set a filter so that the memo field TDWG includes 'MDG' which is the geo-code for Madagascar. To do this, you could right-click on the TDWG column header and select **Filter on selected text** and edit as below:





Tag	Filter syntax	Filter command
*	"MDG" $ upper(TDWG)	tdwg includes MDG

Field: tdwg
Operator: includes
Value: MDG

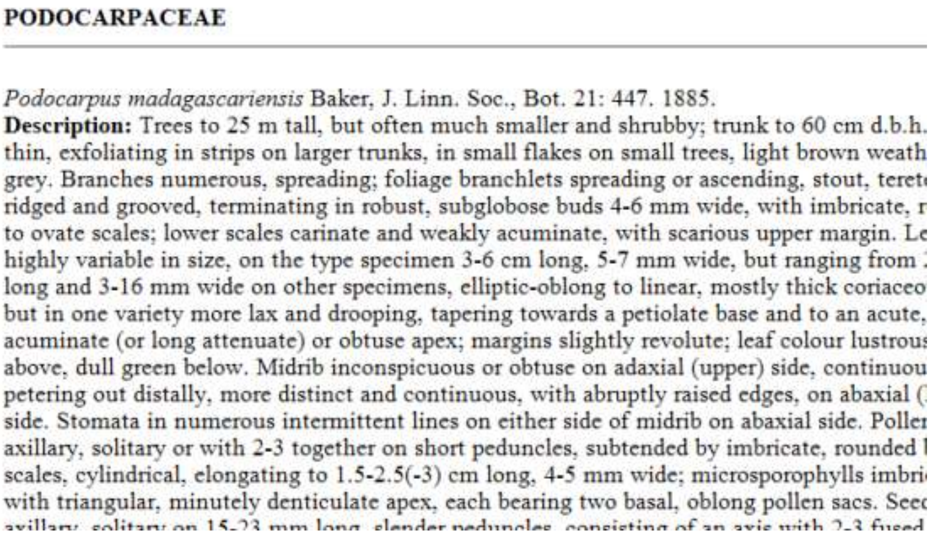
Enter MDG in the Value prompt. It's not case sensitive.

- Once the filter is set, tag all these records using **Tag > Tag all with ***.
- Close the species file.
- Select **Taxa > Extract/query data**.
- Check the extract file is empty by clicking the **Empty** button.
- On the query form, select **Tagged > Tagged species > Select/add to search list** then click on the **Search now** button.

This creates a query file of all conifer taxa known to be from Madagascar.

Preparing a sample text report for Madagascar conifers

- To produce this report, follow the same instructions provided above for the *Araucaria* text report.



PODOCARPACEAE

Podocarpus madagascariensis Baker, J. Linn. Soc., Bot. 21: 447. 1885.
Description: Trees to 25 m tall, but often much smaller and shrubby; trunk to 60 cm d.b.h.
thin, exfoliating in strips on larger trunks, in small flakes on small trees, light brown weath
grey. Branches numerous, spreading; foliage branchlets spreading or ascending, stout, teret
ridged and grooved, terminating in robust, subglobose buds 4-6 mm wide, with imbricate, r
to ovate scales; lower scales carinate and weakly acuminate, with scarious upper margin. Le
highly variable in size, on the type specimen 3-6 cm long, 5-7 mm wide, but ranging from
long and 3-16 mm wide on other specimens, elliptic-oblong to linear, mostly thick coriaceo
but in one variety more lax and drooping, tapering towards a petiolate base and to an acute,
acuminate (or long attenuate) or obtuse apex; margins slightly revolute; leaf colour lustrous
above, dull green below. Midrib inconspicuous or obtuse on adaxial (upper) side, continuou
petering out distally, more distinct and continuous, with abruptly raised edges, on abaxial (
side. Stomata in numerous intermittent lines on either side of midrib on abaxial side. Polle
axillary, solitary or with 2-3 together on short peduncles, subtended by imbricate, rounded
scales, cylindrical, elongating to 1.5-2.5(-3) cm long, 4-5 mm wide; microsporophylls imbri
with triangular, minutely denticulate apex, each bearing two basal, oblong pollen sacs. See
axillary, solitary on 15-23 mm long, slender peduncles, consisting of an axis with 2-3 fused

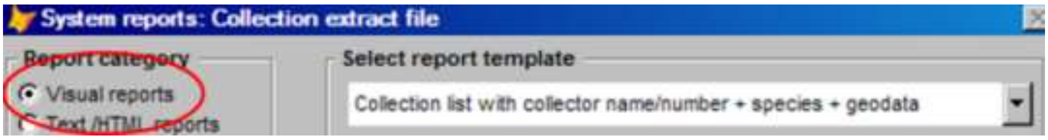
Section of the report, in this case opened as a word document

Extract botanical records by collector name

- In the Conifer database, select **BotanicalRecords > Extract/query data...**
- Check the extract file is empty by clicking the **Empty** button.
- Select **Collector/Number > Collector name > Select/add to search list**. As prompted enter ‘Farj’ and choose the collector ‘Farjon, A.’.
- On the next prompt form, click **OK** to choose the defaults although note that you could restrict to a selected number range for this collector. Click **Search now** to extract these data.

View extracted collections using a Visual Report list template

- In the opened extract file, select **FastSort > Collector+Number**.
- Click on the toolbar again to open the reports form.



System reports: Collection extract file

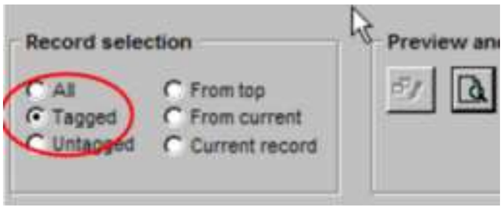
Report category: ● Visual reports ○ Text /HTML reports

Select report template: Collection list with collector name/number + species + geodata

*Choose the report ‘Collection list with collector name/number + species + geodata’ from the listed visual reports. If this report is **not available**, choose the option **Import report template sample(s)**. Make sure you select the correct report on the dropdown.*

- Click the button to view/print the report. You can restrict the report to tagged records:

- In the same extract file, select **Tag > clear all tags** then locate and tag the Farjon records with collection numbers 440 – 445.
- Click on the 🗒 toolbar. Select **Tagged** in the Record selection area to restrict the report to tagged records only.



Record selection

○ All
● Tagged
○ Untagged
○ From top
○ From current
○ Current record

- Close the preview by pressing **Esc**.

COLLECTION	SPECIES	DATE	COUNTRY/REGION
Farjon, A. 260	*Pinus muricata [1]*	1 October 1992	Mexico, Baja California Norte, Ensenada, San Vicente: along road to the coast, ca. 3 km from Ej. Eréndira
Farjon, A. 261	*Pinus quadrifolia*	2 October 1992	Mexico, Baja California Norte, Sierra San Pedro Martir, Cañon San Ramon: along the road into the mts. between Meling Ranch and the...
Farjon, A. 263	*Pinus lambertiana*	2 October 1992	Mexico, Baja California Norte, Sierra San Pedro Martir, Cerro de La Encantada
Farjon, A. 274	*Pinus monophylla*	16 October 1992	Mexico, Baja California Norte, Sierra de Juarez, P.N. "Constitucion de

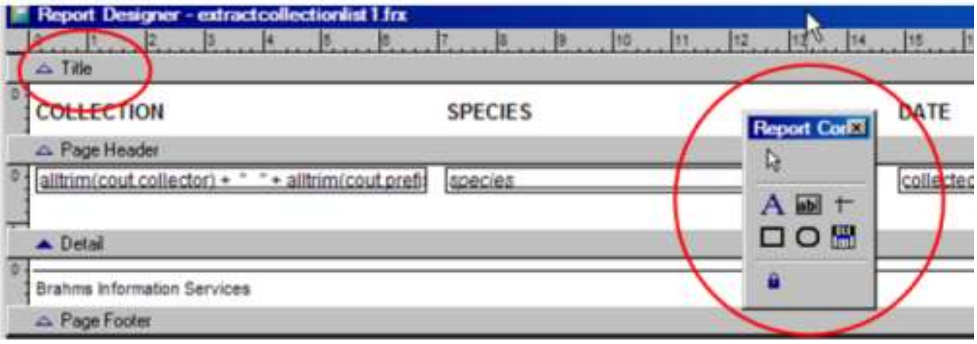
Sample report. Note that the report looks rather sad without a report title/banner. You will add one below.

Adding a title to the Visual Report

- Select **Extracts > BotanicalRecords** to open the last extract file.
- Click again on the 🗒 toolbar again to open the visual reports form. Choose the report '*Collection list with collector name/number + species + geodata*' from the listed visual reports (as used above).

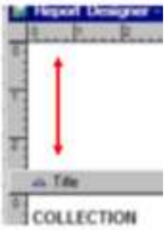
The next challenge is to add some text and images to the report **Title** section. The Title section is printed once at the beginning of the report.

- On the report form, select the **Edit Report Template** button.
- With the report edit screen open, select **View > Reports controls toolbar** on the main BRAHMS menu This opens the toolbar to assist with visual report editing.

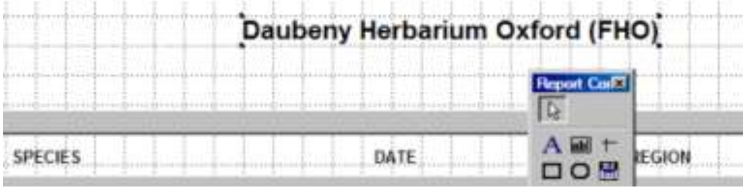


The visual report template opened for editing with the Report controls toolbar

- The first task is to create some space to add a title. To do this, drag the 'Title band' of the report down. It may already be used in your sample report.



- On the reports toolbar, click on the **A** button. Then click in the report title (top) band and write some text such as ‘Collection list’.
- If you now click on the toolbar **Arrow** then again on this text, the text is ‘selected’.
- Dbl-click the selected text, select **Style** and choose a font as required.
- Now select the menu option **Format > Align > Centre horizontally**.



- Note that you can use View > Grid Lines to show a graticule on the design surface.
- To save these changes so far, enter **Ctrl+W** or you can use **File > Close** and save the changes as prompted.
- Click the button to view/print the report (labels). Press Esc to close this preview.

Livening up a Visual Report template with images

- To continue editing, again select the **Edit Report Template** button and open the editing toolbar as above.
- On the Reports Controls toolbar, click the button. Then click and drag open a small square shape in the report title area, top left. The size of this square can be changed later. The dialogue that opens allows you to locate an image file.
- The **Control source type** will by default be set to ‘Image file name’. Click on the find button opposite the Control source text box and locate any image available on your computer. If you have none, locate the image ‘\brahms7\setupdata\report_samples\ plant sciences.jpg’.
- Set the **Frame size mode** to ‘*Scale contents, retain shape*’.
- Click **OK** to save these edits.
- Add more sample images to the report title band as you wish.
- To close and save the report template edits, enter **Ctrl+W**.
- Click the button to view/print the report.

Collection list

COLLECTION	SPECIES	DATE	COUNTR
Farjon, A. 260	*Pinus muricata [1]*	1 October 1992	Mexico, B coast, ca.
Farjon, A. 261	*Pinus quadrifolia*	2 October 1992	Mexico, B

! Visual reports are mostly used for labels and lists. They are printed directly, not sent to text files. You can ‘print’ a visual report to a PDF.

A sample label

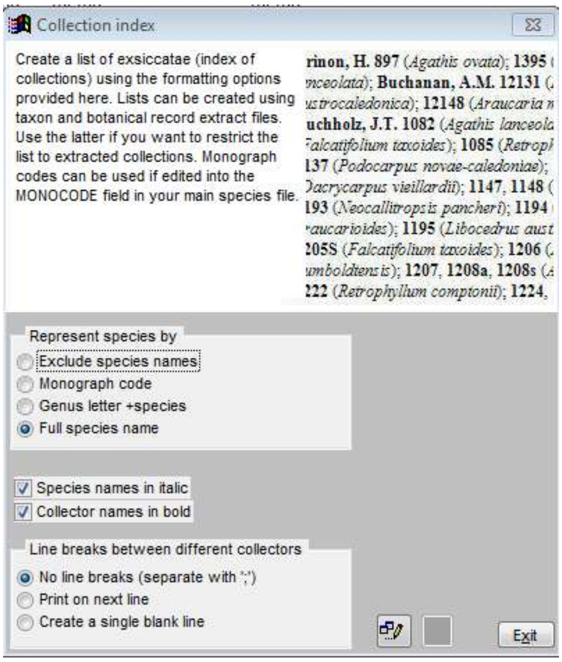
Continuing with the above extract file:

- If it not already selected, choose the report ‘*Label starter - A4, 6 per page surrounded by square box*’ from the listed visual reports. If this report is not available, choose the option **Import report template sample(s)**. Make sure you select the correct report on the dropdown.
- Click the 🔍 button to view/print the report (labels). Close this preview and the report form.

Creating an index of collections

Lists of exsiccatae, tedious to produce manually, can be created from the taxon or botanical record extract files.

- In the Conifer database, select **BotanicalRecords > Extract/query data...**
- Check the extract file is empty by clicking the **Empty** button.
- Select **Geographic > Country** then **Select/Add to search list**. Choose a country that has conifers, for example China or Vietnam. Click on **Search now** to extract the data for the selected country.
- In the extract file, select **Tools > Data summaries and indexes > List of exsiccatae.**



Create a list of exsiccatae (index of collections) using the formatting options provided here. Lists can be created using taxon and botanical record extract files. Use the latter if you want to restrict the list to extracted collections. Monograph codes can be used if edited into the MONOCODE field in your main species file.

Represent species by
○ Exclude species names
○ Monograph code
○ Genus letter +species
● Full species name

☑ Species names in italic
☑ Collector names in bold

Line breaks between different collectors
● No line breaks (separate with ';')
○ Print on next line
○ Create a single blank line

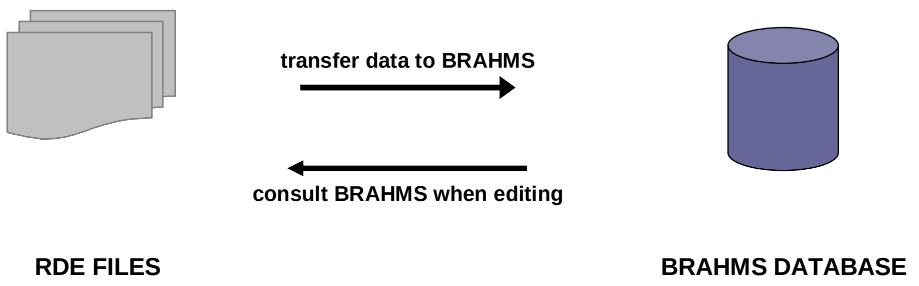
Lobbichler, F. 203, **241**, **292**, **428** (*Juniperus semiglobosa*); **Miehe, G. 17**, **18**, **48**, **226** (*Juniperus squamata*); **369**, **449**, **613** (*Juniperus excelsa ssp. polycarpos*); **780** (*Juniperus pseudosabina*); **1797** (*Juniperus excelsa ssp. polycarpos*); **1843** (*Juniperus semiglobosa*); **2064** (*Juniperus pseudosabina*); **2550** (*Juniperus semiglobosa*); **2663** (*Juniperus excelsa ssp. polycarpos*); **3538**, **3678**, **3679** (*Juniperus semiglobosa*); **4713** (*Juniperus pseudosabina*); **4718** (*Juniperus semiglobosa*); **4798**, **4843** (*Juniperus pseudosabina*); **4922** (*Juniperus semiglobosa*); **4927**, **4930** (*Juniperus excelsa ssp. polycarpos*); **4932**, **4947**, **4961** (*Juniperus semiglobosa*); **4968**, **4970**, **4971** (*Juniperus excelsa ssp. polycarpos*); **5025**, **5051**, **5058** (*Juniperus pseudosabina*); **6031**, **6372** (*Juniperus semiglobosa*); **6373**, **6396**, **6415** (*Juniperus excelsa ssp. polycarpos*); **6417**, **6418** (*Juniperus semiglobosa*); **6505** (*Juniperus pseudosabina*); **6670** (*Juniperus excelsa ssp. polycarpos*); **6686** (*Juniperus pseudosabina*); **6718**, **6770** (*Juniperus excelsa ssp. polycarpos*); **6798** (*Juniperus semiglobosa*); **6826**, **6883**, **7045** (*Juniperus pseudosabina*); **7057** (*Juniperus semiglobosa*); **7058** (*Juniperus excelsa ssp. polycarpos*); **7114**, **7115** (*Juniperus squamata*); **7116** (*Juniperus excelsa ssp. polycarpos*); **Nüsser, M. 1796** (*Juniperus squamata*); **2701**

USING RAPID DATA ENTRY (RDE)

Relationship between RDE and BRAHMS

Although data may be entered directly into BRAHMS, RDE is recommended for entering larger numbers of records. RDE can be used to enter botanical records (specimens), seed records, living collections, taxa, gazetteer names, references and images. RDE is a fast, flexible and safe - and you can make reports and maps directly from RDE.

RDE files, once ready, are transferred into a BRAHMS database. They can then be kept safely as backup files.



When typing data into RDE, you can consult your BRAHMS database to lookup and auto-copy available data. RDE files have settings and functions to optimize field and record lookups, verification and copying.

! RDE is also used as a data transfer mechanism when importing data from Excel, Access and elsewhere.

Create a new RDE file for botanical records

- Log into the Conifer database.
- Select **BotanicalRecords > Add/edit botanical records using Rapid Data Entry files** to open the RDE file manager.
- Select **File > Create a new RDE file....** Select **The system template** option to create the file and choose a path and RDE file name as prompted.
- Your new file will be auto-registered in the RDE file manager. The RDE file manager tracks all your RDE files.

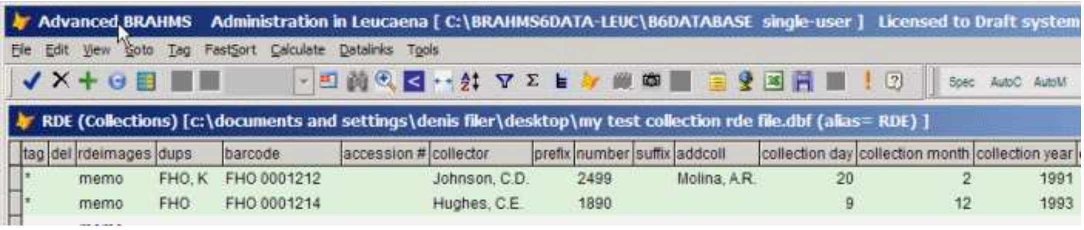
Adding records to RDE

- Select **BotanicalRecords > Add/edit botanical records using Rapid Data Entry files** to open the RDE file manager for collections. Then dbl-click on the file name to open your new file.
- Click on the ✚ toolbar to add a new record (or use ALT+A).
- Enter, as best you can, the data for a few specimens.

Most fields have an obvious meaning (e.g. COUNTRY and COLLECTOR) but others are less clear. For information on any field, click on the field name and then on the ? toolbar.

A few basic rules:

1. Any field can be left blank.
2. Enter personal names using the format Smith, A.B.
3. Separate multiple names using a semi-colon as in ‘Forzza, R.C.; Saavedra, M.M.; Zappi, D.; Freitas, L.
4. Longer text entries are added to memo fields. An example in locality notes if these are given.
5. The DUPS field is used to cite herbaria where the specimen is held. Use codes as in ‘K’ or ‘K, MO, FHO’.
6. Open memo fields quickly using Ctrl+M.



tag	del	rdeimages	dups	barcode	accession #	collector	prefix	number	suffix	addcoll	collection day	collection month	collection year
*		memo	FHO, K	FHO 0001212		Johnson, C.D.		2499		Molina, A.R.	20	2	1991
*		memo	FHO	FHO 0001214		Hughes, C.E.		1890			9	12	1993

Field and record copying using F4 and Ctrl+F4

- Use the toolbar to add a new record. Press F4 to copy fields from the previous record.
- Position the cursor on any record with data. Enter Ctrl+F4 to duplicate that record.

Selective field copying using the toolbar

This toolbar is used to edit **data copy** settings to selectively copy fields when you add records. The fields selected depend on the data entry task. For example, it may be useful to copy the collector name, country name, day, month and year and other fields that mostly remain constant after a field trip.

- Click on the toolbar, and edit some of the copy settings.
- In RDE, position the cursor on the last record with data and then add one or more new records to test field copying.

Using F9 lookup options

- Click on the toolbar to add a new record (or use ALT+A).
- In the COLLECTOR field, press F9 to look for data in BRAHMS. Using the ‘Name starts with’ prompt, locate and select the name ‘Farjon, A.’.
- In the SP1 field, press F9 to look for the species *Juniperus sabina var. sabina* – typing ‘ju sab’ in the Search for prompt will get you very close. Choose the correct name from the list and then press Enter. Note that the family and genus fields are also filled.
- In the GAZETTEER field, press F9 to look for a place. Note that all related geographic fields are also filled.

AutoComplete

The AutoComplete function attempts to fill in data fields as you type.

- In an open RDE file, click on the **AutoC** toolbar and ensure AutoComplete is enabled.
- Add a blank record to your file. In the FAMILY field, typing 'Cup' adds Cupressaceae. Typing 'J' in the GENUS field adds Juniperus. The names offered are restricted to the current family.
- Start typing into SP1. The names offered are restricted to the current genus.
- Try this in geographic fields.

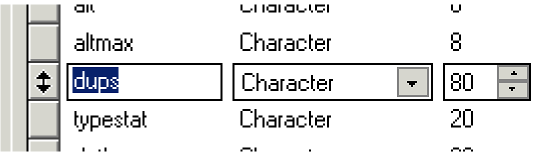
Editing file structure

Standard BRAHMS RDE templates are likely to include fields that you will not need and they may exclude one or more special fields that you want to add.

- To open the RDE file, **dbl-click** on the file name or use the toolbar.

To remove, edit or add fields:

- Select **File > Modify file structure….**
- Click on the field SUFFIX and the Delete button to remove that field.
- Click on the field COLLECTOR and then reduce the field Width to 40.
- To move a field, drag the small rectangle to the immediate left of the field name.



altmax	Character	8
dups	Character	80
typestat	Character	20

- Click on **OK** to save the file structure changes permanently.
- Close the RDE file and the RDE file manager.

! When you modify the structure of an RDE file, the system creates a .BAK version of the file. If the file includes memo fields, a .TBK file is also created. These files can be safely deleted using your windows file manager.

Opening the specimen level form

RDE is a simple 'flat file'. In some cases, the level of detail you may want to store for a record is more complex. For example, you may want to store accession numbers for other herbaria, old determinations and type status details. This level of individual specimen detail can be stored using the SPEC form.

- Click on the **Spec** toolbar (or use the toolbar and select the **Specimens** tab). Note that the specimen level data already added to your RDE file will be registered in this form.
- On this form, click on the top ➕ button adjacent to **Edit Specimens.**
- Use **F9** in the HERBARIUM field to choose a herbarium code from the available list. If the CATEGORY is blank, use **F9** to select 'Herbarium sheet'. This action registers a further duplicate for this collection.
- Close the specimen form.

! Using the Specimen form in RDE, you can add determination histories, type status and further details about one or more individual specimens of a botanical record.

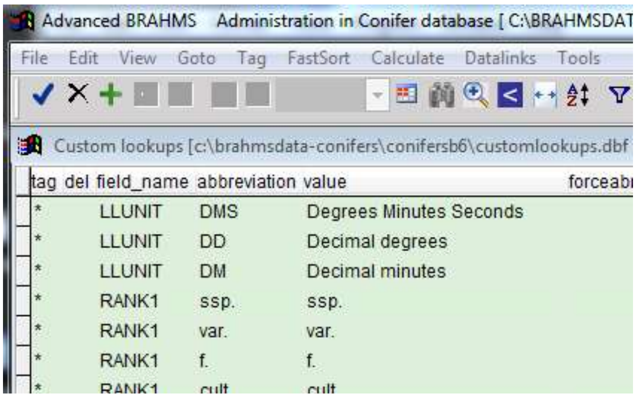
Custom lookups

BRAHMS has a separate file - the custom lookup dictionary - where you can store lists of values for fields used in RDE and BRAHMS. Data entered in this list helps speed up and standardize data by using lookups or AutoComplete.

Example fields are HABIT, IUCN, TAXSTAT and RANK1 – all of which have a relatively small number of potential values. Note that any field can be registered in this file with the field values by selecting **Admin > Custom lookups**. Note that large dictionaries that are built into BRAHMS (*e.g.* the main people, taxonomic and geographic lists) have their own special lookup options. Values for these dictionaries do not go into the custom lookup lists. To test how this works:

- Select **Admin > Custom lookups** to open the list. Your list will by default include some entries for the field RANK1. You can edit these values if necessary.
- Close this file after checking the various RANK1 values.
- Now open your new RDE file for botanical records, check AutoComplete is on, go to the RANK1 field and type "s" to auto fill to ssp. (or subsp.).

You can add any field you want to your RDE file, for example LEAFTYPE and register that field in your custom list with the values you want.



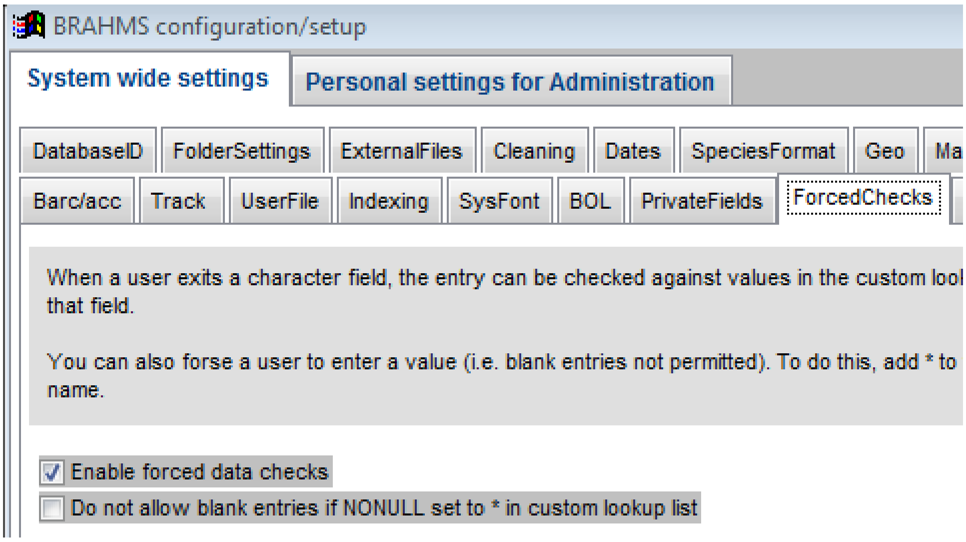
Custom lookups [c:\brahmsdata-conifers\conifersb6\customlookups.dbf

tag	del	field_name	abbreviation	value	forceab
	*	LLUNIT	DMS	Degrees Minutes Seconds	
	*	LLUNIT	DD	Decimal degrees	
	*	LLUNIT	DM	Decimal minutes	
	*	RANK1	ssp.	ssp.	
	*	RANK1	var.	var.	
	*	RANK1	f.	f.	
	*	RANK1	cult	cult	

Forced data checks

Forced checks are used to prevent users adding a value that is not in your custom list. This feature can be used with AutoComplete.

- Select **Admin > Project configuration > System wide settings > ForcedChecks** and tick the option **Enable forced data checks**.
- Now return to your RDE file and try entering a bad value into the RANK1 field. The data value must be valid before you can exit the field.



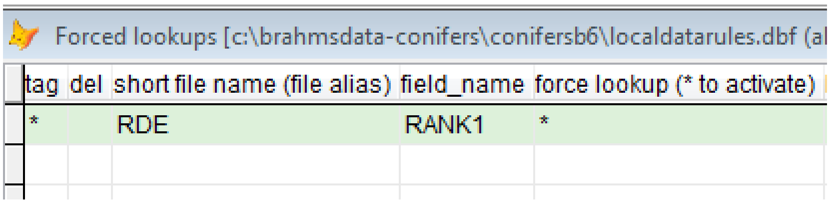
When a user exits a character field, the entry can be checked against values in the custom lool that field.

You can also forse a user to enter a value (i.e. blank entries not permitted). To do this, add * to name.

☑ Enable forced data checks
☐ Do not allow blank entries if NONULL set to * in custom lookup list

Forced lookup settings

A variation on the above is to set fields so that users must use a lookup function (no free text entry allowed). You can create a forced lookup field by using **Admin > Forced lookup settings**. You must enter the short file name (e.g. RDE), the field name and activate with "*".



tag	del	short file name (file alias)	field_name	force lookup (* to activate)
*		RDE	RANK1	*

This feature prevents the use of AutoComplete.

AutoMatching

AutoMatching auto-prompts you with collections **already stored** in the active database and/or designated external file when you exit a specified RDE field. This function minimizes double entry of specimens.

- In your RDE file, click on the **Onoff** toolbar until is reads 'On'.
- Click also on the **AutoM** toolbar and enable the option **Further checks on exiting the field** and set the field value to NUMBER.
- In the **Select field(s) to use for Matching** list, select the NUMBER field and ensure all the other field names are not selected. You can experiment with different settings later.
- Ensure that the **Data source(s) to check** includes the current (logged into) database.
- Close this form and test adding data to NUMBER and pressing ENTER. In the Conifer database, try adding any number *e.g.* 649 or 116.

Using the IMAGELIST memo

Some sample specimen images are provided in your brahmsdata-conifers\Other sample files\Images folder.

If you have images of specimens or the labels, you can **right-click** on the memo field IMAGELIST and locate these images. Image file names are added to the memo and can be viewed using the images using the 📷 toolbar. Alternatively, open the image viewer using the 📷 toolbar and drag images from Explorer onto the viewer.

! Image files are not stored in RDE or BRAHMS – only the reference to the file.

Transfer the RDE file to BRAHMS

Once you have added 5 or more practice records, transfer these data into the conifer database.

- Close the RDE file but stay in the RDE file manager and select the ⇥ toolbar.
- If the RDE file includes images, the **Image transfer** option will be enabled. Note that you can link the images to the botanical record as a whole or directly to the relevant specimen. If your images are of the plant habit, choose **Link to botanical record** - but if your images are of specimens/labels, choose the **Link to specimen at** option and ensure the correct herbarium code is selected.
- Ignore **Link to transaction** unless you want to auto-link the imported specimens to a loan or exchange.
- Select **Check RDE file**. This produces a summary of what is new in the RDE file and flags up errors.
- Assuming there are no serious errors (these will be reported in red), proceed to **Transfer all**.

Check your database files

As a final step in this exercise, you can check the data added to your main database. When an RDE file in transferred into BRAHMS, each category of data is checked and appended to the appropriate file if new. In all cases, new records will be found at the bottom of unsorted database files.

- Select **BotanicalRecords > View/edit BotanicalRecords in database** and confirm that the expected records have been appended.
- Select Taxa **> View/edit species in database** to check for any new taxa. Repeat for families and genera if you added new names.
- Select **People > View/edit people in database** to check for new personal names.
- Select Geo **> View/edit gazetteer in database** to check for place names.

RDE import problems

If you see a red message as shown below, this means that BRAHMS has rejected your RDE file.

- Open the RDE file and read the contents of the RDE_ERRTXT memo field (this will be added to the end of the record structure).

Processing: c:\documents and settings\denis filer\desktop\my test collection rde file.dbf

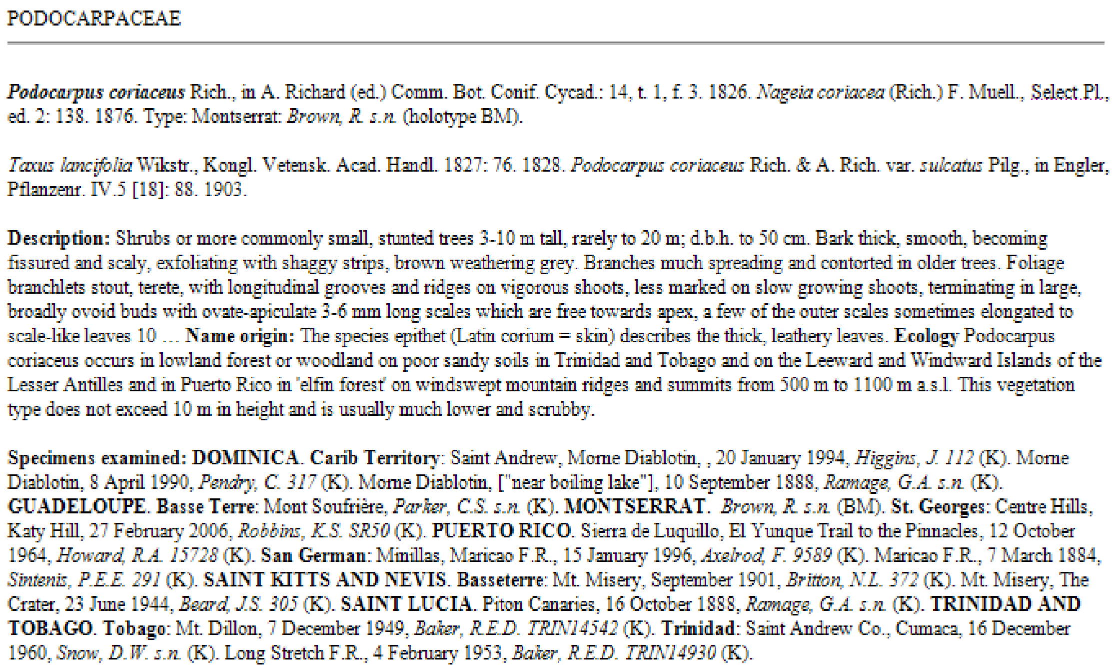
This file has one or more errors stopping the transfer to BRAHMS.

Open your RDE file and check the fields RDE_ERROR and RDE_ERRTXT.

TEXT REPORTS: A SAMPLE CHECKLIST

The objective of this exercise

The following exercise shows how to produce a checklist or text for revisions from BRAHMS using text reporting. You will create a text report template that generates examples similar to that shown below. In the sample database provided, data in the longer descriptive fields are truncated and may have '…' printed after shortening.



PODOCARPACEAE

Podocarpus coriaceus Rich., in A. Richard (ed.) Comm. Bot. Conif. Cycad.: 14, t. 1, f. 3. 1826. *Nageia coriacea* (Rich.) F. Muell., Select Pl., ed. 2: 138. 1876. Type: Montserrat: *Brown, R. s.n.* (holotype BM).

Taxus lancifolia Wikstr., Kongl. Vetensk. Acad. Handl. 1827: 76. 1828. *Podocarpus coriaceus* Rich. & A. Rich. var. *sulcatus* Pilg., in Engler, Pflanzenr. IV.5 [18]: 88. 1903.

Description: Shrubs or more commonly small, stunted trees 3-10 m tall, rarely to 20 m; d.b.h. to 50 cm. Bark thick, smooth, becoming fissured and scaly, exfoliating with shaggy strips, brown weathering grey. Branches much spreading and contorted in older trees. Foliage branchlets stout, terete, with longitudinal grooves and ridges on vigorous shoots, less marked on slow growing shoots, terminating in large, broadly ovoid buds with ovate-apiculate 3-6 mm long scales which are free towards apex, a few of the outer scales sometimes elongated to scale-like leaves 10 … **Name origin:** The species epithet (Latin corium = skin) describes the thick, leathery leaves. **Ecology** Podocarpus coriaceus occurs in lowland forest or woodland on poor sandy soils in Trinidad and Tobago and on the Leeward and Windward Islands of the Lesser Antilles and in Puerto Rico in 'elfin forest' on windswept mountain ridges and summits from 500 m to 1100 m a.s.l. This vegetation type does not exceed 10 m in height and is usually much lower and scrubby.

Specimens examined: DOMINICA. Carib Territory: Saint Andrew, Morne Diablotin, , 20 January 1994, *Higgins, J. 112* (K). Morne Diablotin, 8 April 1990, *Pendry, C. 317* (K). Morne Diablotin, ["near boiling lake"], 10 September 1888, *Ramage, G.A. s.n.* (K). **GUADELOUPE. Basse Terre**: Mont Soufrière, *Parker, C.S. s.n.* (K). **MONTSERRAT**. *Brown, R. s.n.* (BM). **St. Georges**: Centre Hills, Katy Hill, 27 February 2006, *Robbins, K.S. SR50* (K). **PUERTO RICO**. Sierra de Luquillo, El Yunque Trail to the Pinnacles, 12 October 1964, *Howard, R.A. 15728* (K). **San German**: Minillas, Maricao F.R., 15 January 1996, *Axelrod, F. 9589* (K). Maricao F.R., 7 March 1884, *Sintenis, P.E.E. 291* (K). **SAINT KITTS AND NEVIS. Basseterre**: Mt. Misery, September 1901, *Britton, N.L. 372* (K). Mt. Misery, The Crater, 23 June 1944, *Beard, J.S. 305* (K). **SAINT LUCIA.** Piton Canaries, 16 October 1888, *Ramage, G.A. s.n.* (K). **TRINIDAD AND TOBAGO. Tobago**: Mt. Dillon, 7 December 1949, *Baker, R.E.D. TRIN14542* (K). **Trinidad**: Saint Andrew Co., Cumaca, 16 December 1960, *Snow, D.W. s.n.* (K). Long Stretch F.R., 4 February 1953, *Baker, R.E.D. TRIN14930* (K).

Extracting and sorting the data

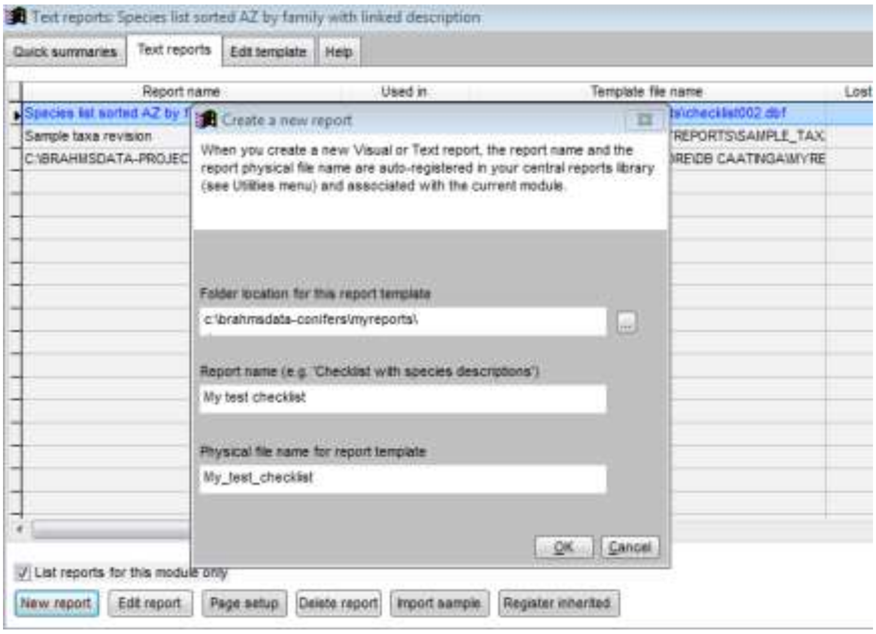
Although text reports can be created from any BRAHMS files, the most common use is from the **taxon extract file**. A first step is to extract the taxa you want to include in the report. In this example, you will extract all accepted names in the genus *Podocarpus*.

- In the Conifer database, select **Taxa > Extract/query data...** Empty the extract file if necessary.
- Choose **Taxa > Genus** and select *Podocarpus*. Also select **Name status** and choose 'acc'. Proceed to extract all the accepted names in the genus, just over 100 names.
- In your taxon extract file, select **FastSort > Species** to sort the list.

A quick checklist

At this stage, you can already produce a checklist based on the data you have extracted. First, you need to create a text report template that includes minimally a reference to the FULLNAME field and then generate the report.

- Click on the toolbar option to open the text reporting form.
- Select **New report**. The report file folder location will default to your Myreport folder unless set otherwise in your **Folder settings** setup options.
- Add a report template descriptive name as appropriate.



When you create a new Visual or Text report, the report name and the report physical file name are auto-registered in your central reports library (see Utilities menu) and associated with the current module.

Folder location for this report template: c:\brahmsdata-conifers\myreports\

Report name (e.g. 'Checklist with species descriptions'): My test checklist

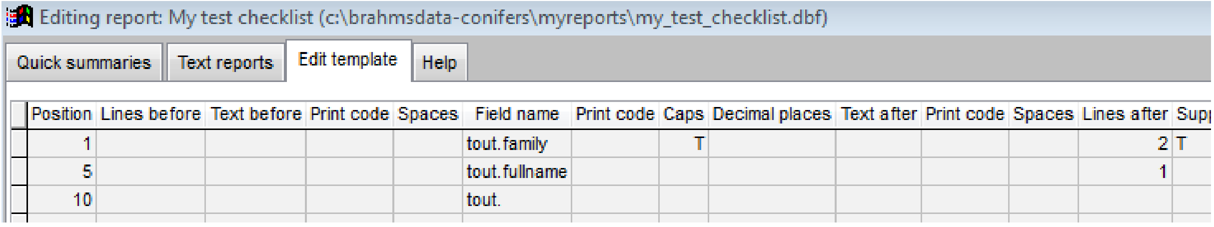
Physical file name for report template: My_test_checklist

☑ List reports for this module only

Dialogue for creating a new text report

- To open the new report template, select the **Edit report** option.

BRAHMS will automatically add expressions (items to be included in the report) for the FAMILY and FULLNAME fields similar to the below screen:



Position	Lines before	Text before	Print code	Spaces	Field name	Print code	Caps	Decimal places	Text after	Print code	Spaces	Lines after	Sup
1					tout.family		T					2	T
5					tout.fullname							1	
10					tout.								

In the text report template designer, fields are always added with the short file name as a prefix as in tout.fullname. The short file names are knows as file aliases (in this case 'tout' = taxon output). They are provided in the main browser caption bar (not seen here). The POS field control field order and can be edited. If POS is zero, the item is excluded.

- In this case, delete the last line as it refers to no proper field name.
- Click on **Generate report** to create the report. The result will auto-open.

PODOCARPACEAE

Podocarpus acuminatus de Laub., Novon 2 (4): 329. 1992.
Podocarpus acutifolius Kirk, Trans. & Proc. New Zealand Inst. 16: 370. 1
Podocarpus affinis Seem., Fl. Vitiensis: 266. 1868.
Podocarpus angustifolius Griseb., Cat. Pl. Cubensis: 217. 1866.
Podocarpus aracensis de Laub. & Silba, Phytologia 65: 330. 1988.
Podocarpus archboldii N.E. Gray, J. Arnold Arbor. 39: 452. 1958.
Podocarpus atjehensis (Wasscher) de Laub. ex Silba, Phytologia Mem.
Podocarpus borneensis de Laub., Blumea 30 (2): 266. 1985.
Podocarpus bracteatus Blume, Enum. Pl. Javae 1: 88. 1827.
Podocarpus brasiliensis de Laub., Fl. Venezuela 11 (2): 31. 1982.
Podocarpus brassii Pilg. var. ***brassii***
Podocarpus brassii Pilg. var. ***humilis*** de Laub., Blumea 30 (2): 274. 198
Podocarpus brevifolius (Stapf) Foxw., Philipp. J. Sci. 6: 160. 1911.
Podocarpus buchii Urb., Fedde's Repert. Sp. Nov. Regni Veg. 19 (16-21
Podocarpus capuronii de Laub., Adansonia 11 (4): 713. 1971.
Podocarpus celatus de Laub., Fl. Venezuela 11 (2): 35. 1982.
Podocarpus chingianus (N.E. Gray) S. Y. Hu, Taiwania 10: 32. 1964.

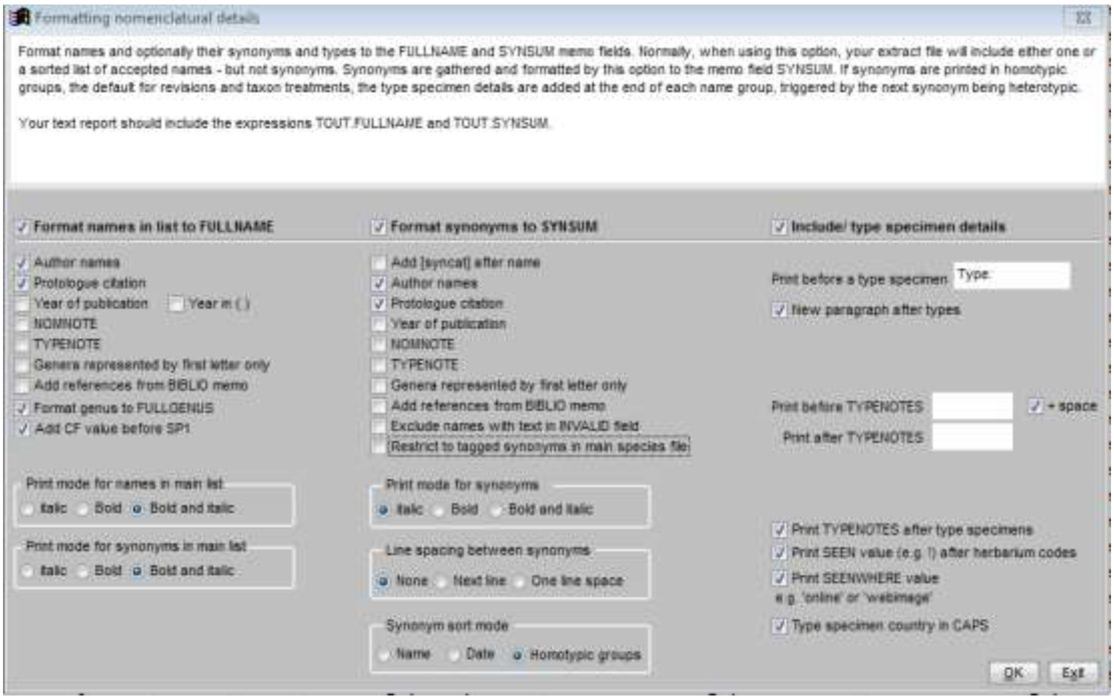
Example from basic list as generated above with names sorted and with some basic formatting.

- Close the preview screen before proceeding.

Formatting names and types

In the taxon extract file, tools are provided to format and/or add data summaries for each extracted name. These options format data in special extract file fields using HTML tags, preparing for inclusion in your text report.

- In your extract file, select **Tools > Formatting for text reports > Names, synonyms and types to FULLNAME and SYNSUM**. This provides formatting options for the accepted names including the assembly of synonyms and types.



Formatting nomenclatural details

Format names and optionally their synonyms and types to the FULLNAME and SYNSUM memo fields. Normally, when using this option, your extract file will include either one or a sorted list of accepted names - but not synonyms. Synonyms are gathered and formatted by this option to the memo field SYNSUM. If synonyms are printed in homotypic groups, the default for revisions and taxon treatments, the type specimen details are added at the end of each name group, triggered by the next synonym being heterotypic.

Your text report should include the expressions TOUT.FULLNAME and TOUT.SYNSUM.

☑ **Format names in list to FULLNAME**
☑ Author names
☑ Protologue citation
☐ Year of publication ☐ Year in ( )
☐ NOMNOTE
☐ TYPENOTE
☐ Genera represented by first letter only
☐ Add references from BIBLIO memo
☑ Format genus to FULLGENUS
☑ Add CF value before SP1

Print mode for names in main list
○ Italic ○ Bold ● Bold and italic

Print mode for synonyms in main list
○ Italic ○ Bold ● Bold and italic

☑ **Format synonyms to SYNSUM**
☐ Add [syncat] after name
☑ Author names
☑ Protologue citation
☐ Year of publication
☐ NOMNOTE
☐ TYPENOTE
☐ Genera represented by first letter only
☐ Add references from BIBLIO memo
☐ Exclude names with text in INVALID field
☐ Restrict to tagged synonyms in main species file

Print mode for synonyms
● Italic ○ Bold ○ Bold and italic

Line spacing between synonyms
● None ○ Next line ○ One line space

Synonym sort mode
○ Name ○ Date ● Homotypic groups

☑ **Include/ type specimen details**
Print before a type specimen: Type:
☑ New paragraph after types
Print before TYPENOTES: ☑ + space
Print after TYPENOTES:
☑ Print TYPENOTES after type specimens
☑ Print SEEN value (e.g. !) after herbarium codes
☑ Print SEENWHERE value
e.g. 'online' or 'webimage'
☑ Type specimen country in CAPS

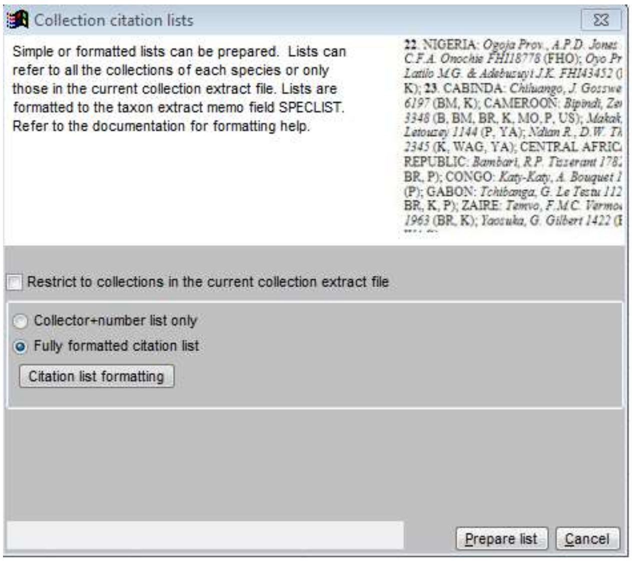
Experiment with the settings on this form. In the above example, the species names will be printed in bold+italic with their authors, protologue citations and any notes stored in the species file NOMNOTE and TYPENOTE fields. Synonyms, in italic, are also added to the SYNSUM memo in your extract file. Note that types are included and the formatting requested here is for types to be printed in homotypic groups.

Adding and formatting specimens for each species

Assuming you want to include a list of specimens in this report, you use another **Tools** option to do this. The specimen data will be assembled for each name in your list and formatted into the taxon extract field SPECLIST.

- In your taxon extract file, select **Tools > Formatting for text reports > Citation lists (Material examined) to SPECLIST**.

- Choose **Fully formatted citation lists.** Later, you can learn how to format lists exactly as required using the **Citation list formatting** options but for now, you can use the default format provided with the conifer database.



Simple or formatted lists can be prepared. Lists can refer to all the collections of each species or only those in the current collection extract file. Lists are formatted to the taxon extract memo field SPECLIST. Refer to the documentation for formatting help.

☐ Restrict to collections in the current collection extract file

○ Collector+number list only

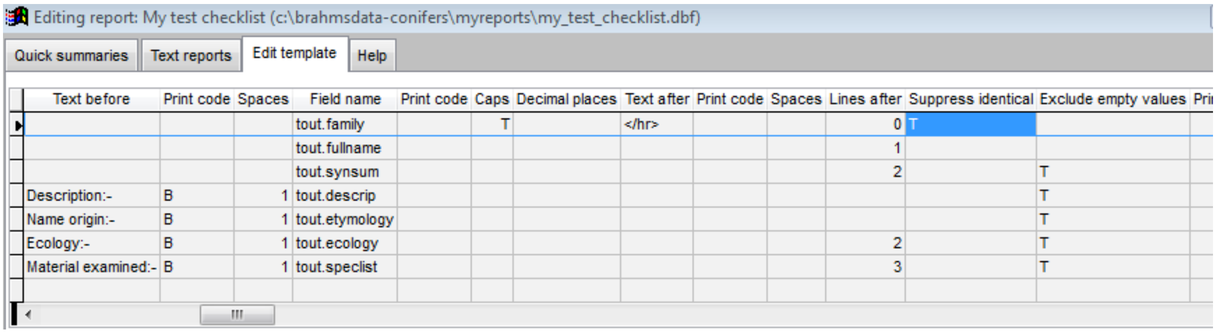
● Fully formatted citation list

Formatting specimens. Use this option to produce journal specific, fully formatted citation lists.

Designing the final text report

The last step is to add a few more expressions to the report template. In the screen below, you can see the new entries refer to field in the file ‘tout’ (taxon output) and ‘linked’ (species link file).

You need to carefully type the report structure shown below into your template file.


Editing report: My test checklist (c:\brahmsdata-conifers\myreports\my_test_checklist.dbf)

Text before	Print code	Spaces	Field name	Print code	Caps	Decimal places	Text after	Print code	Spaces	Lines after	Suppress identical	Exclude empty values	Pri
			tout.family		T		</hr>			0	T		
			tout.fullname							1			
			tout.synsum							2		T	
Description:-	B	1	tout.descrip									T	
Name origin:-	B	1	tout.etymology									T	
Ecology:-	B	1	tout.ecology							2		T	
Material examined:-	B	1	tout.speclist							3		T	

The above text report template was used to produce a report sample similar to the example at the start of this section.

All the expression entries refer to fields in either the main or the linked file. The POS field controls the order of printing. The gaps in numbering are deliberate and facilitate insertions. Anything set to POS = 0 is not printed.

! For an explanation of the various columns in the designer, click on the **Editing help on** option on the lower part of the design form.

A few design points are explained here:

The entry ‘T’ in fields such as **CAPS** signifies True; The entry ‘<hr/>’ in the **Text after** column (punctuation after printing the expression) in the HTML tag to draw a line; Note that as the **Lines after** value for the expressions linked.descrip and linked.etymology are set to 0, these items will be printed (also with linked ecology) in a single paragraph. The **Lines after** value 2 will print 1 blank line; The field **Exclude empty values**, if set to T, suppresses printing of expression (and the related punctuation) if there is no data; The field **Suppress identical** suppresses printing an item in a sorted file until it changes.

- Edit the your checklist text report template (created above) and add in the expressions and related punctuation as shown above. If you want to keep that basic list, you can create a new template for this more detailed one.
- Select **Generate report** to create the report. This should produce the sample shown at the start of this section in an HTML browser screen.
- Close the browser and then click on the W toolbar to open this in Word. In the example, the word document is formatted in 2 columns (**Format > Columns**).

VISUAL REPORTS: DESIGNING A SPECIMEN LABEL

Designing labels

To design a report template for labels, you need to learn about some of the Visual Reports design tools. The following exercise takes you through step by step. The result you want to achieve (or something similar to this) is shown below. There are countless different ways to design labels. Once the basics are mastered, you can choose your own designs.

Ghana Herbarium (GC)

Family Combretaceae
Species Combretum sp.
Locality Ghana, Northern Region, Tamale District, Sinsanbligbini Forest Reserve, 2km E. from Tugu, near road that runs along forest boundary.
9°14.04' N, 0°21.56' W
Notes Small tree 4-6m tall; youngest leaves slightly sticky; outer bark rough, fissured, with obvious cracks; slash fibrous, flexible, reddish.
Collector Ekpe, P. 62 16 March 2006
With Hawthorne, W.D.; Baba, J.; Mensah, M.
Specimens collected under the National Biodiversity Survey Project

Ghana Herbarium (GC)

Family Cochlospermaceae
Species Cochlospermum planchoni Hook.f.
Locality Ghana, Northern Region, Tamale District, Sinsanbligbini Forest Reserve, 2km E. from Tugu, near road that runs along forest boundary.
9°14.04' N, 0°21.56' W
Notes Bush with few stems at ground level. New shoots purplish and obvious flatoid twigs.
Collector Ekpe, P. 66 16 March 2006
With Hawthorne, W.D.; Baba, J.; Mensah, M.
Specimens collected under the National Biodiversity Survey Project

The above label sample is printed in 2 columns, with a shaded background, each displaying an image of the plant. Otherwise, the labels include standard fields expected on the typical specimen label. Each label is boxed. Any of these features can be removed from the design as you proceed. The special features are included here partly to illustrate what can be achieved.

Labels are usually created from RDE and/or botanical record extract files. Although very similar, you will need a separate label template for each file. This is explained further at the end of this section.

! While this section deals with labels, the procedures discussed can be applied to develop many further types of visual report template.

Getting ready with your RDE file

You need to have an RDE file which includes the common standard fields and has at least some data ready to print. If one or more fields (represented in the report template) are missing, you will get a warning message when you try or preview or print.

- To refresh any calculated RDE fields, open your RDE file and select **Tools > Refresh label fields**. This will update fields such as GEODATA, COLLECTED and LATLONG.

! The content of the calculated GEODATA memo can be configured from **Admin > Project configuration > System wide settings > Geo**. On the **Dates** tab on that form, you can also choose the date format for COLLECTED.

Creating a new visual report template

- Click on the ▤ reports toolbar.
- Select **Create new template**.
- The report file folder should default to your 'myreports' folder. As prompted, add a report file name (*e.g.* rdelabel01) and a report description (*e.g.* My sample label 1). Select **OK** to create the report template.
- At this stage, it is recommended that you enter **Ctrl+W** which is shortcut to save the work and close the template designer.
- To re-open and continue designing, ensure your label name (report description) is selected in the **Select report template** drop down at the top and then click on **Edit report template**.

Report bands and columns

The default visual report designer has 3 ‘bands’ Page Header, Detail and Page Footer. Of these, we only require the **Detail band**. To effectively remove the others:

- Drag the Header band up to the very top and the Footer band up to touch the Detail band.
- Also, to set this report to 2 columns, select **File > Page setup** and set the **Column number** to 2.
- You can also drag the Detail band down to the 9 cm mark as shown on the left side. (Note that a **right-click** on the Detail band provides access to a properties menu where, using the **General** tab, you can set the height precisely).

! Note that if you were preparing a visual report template to generate a list with columns, you would add text labels (e.g. “COLLECTOR”) to the header band. The header band is printed at the top of each page. You can also add a title band which is printed once at the start of the report.

The Report Controls Toolbar and editing grid

A special report design toolbar is needed for this task. The toolbar has options to add boxes and lines, text labels, and data and images from your file.

- Select **View > Report Controls Toolbar** to open the design toolbar.
- At this stage, also useful to select **View > Grid Lines** to enable an editing grid.

! For help on the Report Controls Toolbar, search for the text ‘Report Controls Toolbar’ in the help file. Each on the toolbar options is explained.

Setting a default font

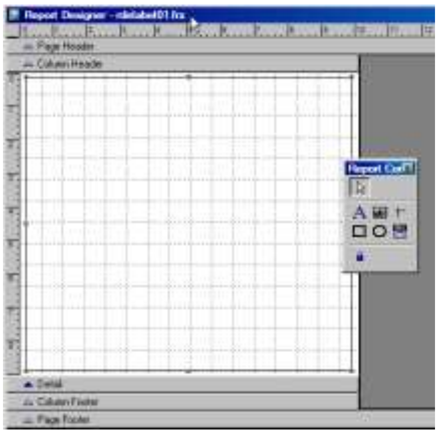
Before proceeding further, it will be useful to set a default font for your label. This will save time as you add labels and field expressions.

- Right-click on the blank label surface and choose Properties > Page layout and set the default font to Arial, Regular 9 point size – or another font/size as you prefer.

Adding a box surround for the labels

Adding a surround box can be useful when designing labels as it gives you a more defined area to work in and it helps when previewing your labels. The box can be easily removed later on.

- Click on the rectangle icon on the toolbar and then drag a box onto the label design surface, roughly from top left to bottom right. The exact position and size can be adjusted later.



Your screen up to this point should be similar to the above.

- Before going further, enter **File > Save.**

The next task is to set the background colour of the added rectangle. To do this:

- **Dbl-click** on any of the box edges and select the **Style** tab on the properties form.
- Remove the tick from the **Use default background (fill) colour** option.
- Select a colour using the lookup provided. You can define a custom colour.

! As you proceed to design your label, select **File > Save** frequently to avoid loss of your hard work …

Adding a text label

If at any stage the designing toolbar vanishes, select **View > Report Controls Toolbar** to re-open it.

- Now click A on the Report Controls Toolbar and then click once on the label surface inside your box area and type in the name of your herbarium or any text to appear at the top of the label.
- After typing the text, click ↖ on the Report Controls Toolbar (Select objects) and then click once on the text label you have just added. This will **select** this object and you will see handles (small selection marks) at the label corners.
- If you **dbl-click** on the label and select **Style**, you can increase the font point size for this as you wish, perhaps also setting it to bold.
- After doing this (the text label will still be selected), on the menu, select **Format > Align > Center Horizontally**.
- Also note that you use your up and down keyboard arrows to fine adjust the item position up/down/left/right.

Label previewing

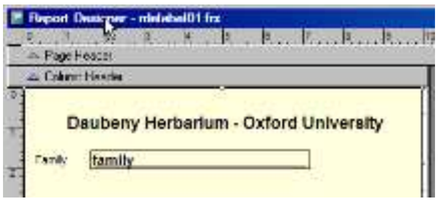
At any stage during the design, you can save and close your report template (using **Ctrl+W** is a fast way) and click on the 🔍 toolbar to view progress. If your RDE file has many records, tag a few and use the Restrict to tagged option on the reports form.

Adding the family name

Bear in mind that you can add report items in any order. As a next step here, you can add the family name. The family differs from the text label added above as it may change, record by record, in your data file. Thus, rather than adding a basic text label, you must add a field expression.

- Click abl on the Report Controls Toolbar, click on the label surface. In the Expression box, enter RDE.FAMILY (this can be in upper or lower case). 'RDE' is the short file name for RDE files and FAMILY is the name of the field in the RDE file. Note the '.' between the two words.
- Should you want to print the family name slightly larger than other label features and perhaps in bold, select **Style** (dbl-click on the expression box if the form was closed) and set accordingly.
- If you want to add the fixed text label 'Family' to the left of this, click A on the Toolbar and then click once on the label surface let of the family expression and add the text 'Family'.

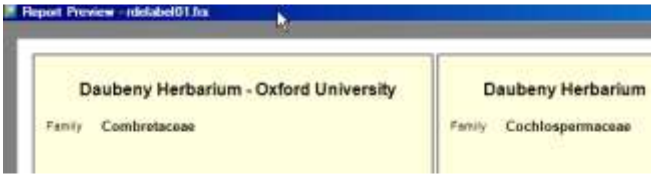
! At any stage, you can drag these label objects to refine their positions.



Daubeny Herbarium - Oxford University

Family family

The label so far - in design mode



Daubeny Herbarium - Oxford University

Family Combretaceae

Daubeny Herbarium

Family Cochlospermaceae

The label so far - in preview mode

Adding the species name

Species names are a bit tricky as names are composed of more than one field and they often require the mixing of italic and regular fonts. You cannot mix fonts within a single expression.

- If you don’t need italic font or are happy to print the species name and authors all in italic – you can add an expression to your label – following the same procedure used for the family name but using the expression: alltrim(rde.genus) + ‘ ‘ + alltrim(rde.sp1) + ‘ ‘ + alltrim(rde.author1).
- If you want to print the names with mixed format, the simplest option will be to select the option **Species names sample** on the report form and to copy the code there onto your label surface.

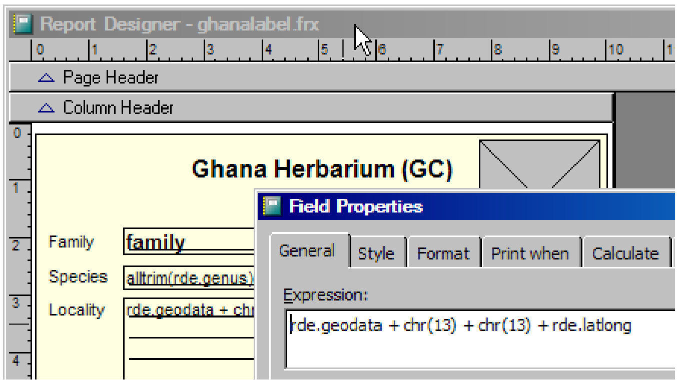
! The alltrim() function removes leading and trailing spaces from the fields. If you do not use it, you would end up with something like ‘Dioscorea   sagittifolia   Pax’.

Adding locality data

The easiest way to add locality data is to use the calculated memo field GEODATA. You can adjust your **Admin > Project configuration > Geo** options to control the content of the GEODATA memo. Remember to update this field using **Tools > Refresh label fields** after editing your RDE file.

- Click abl on the Report Controls Toolbar, click on the label surface. Drag the box to form a ‘paragraph sized’ area on the label surface – it can be resized later. In the **Expression** box, enter RDE.GEODATA.
- If you want to print the contents of the calculated field LATLONG together with GEODATA, you can edit the expression to ‘rde.geodata + rde.latlong’.
- If you want to force the latlong data onto the next line, use ‘rde.geodata + chr(13) + rde.latlong’.
- To leave a blank line, use ‘rde.geodata + chr(13) + chr(13) + rde.latlong’.
- Use the A toolbar to add the text label ‘Locality’ or similar - as for the family.

! Some experimentation will be needed to get the optimal size of this locality text box. You can drag the box lower edge up/down to resize. If it is not deep enough, longer text entries would be truncated.



Expression: rde.geodata + chr(13) + chr(13) + rde.latlong

Building a field expression, combing the geodata and latlong fields, forcing a blank line between them.

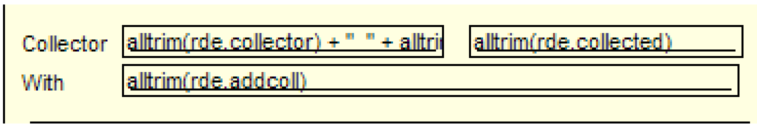
Adding other field notes

Using a similar procedure to the above, you can add a further paragraph sized expression to display the PLANTDESC memo, perhaps combined with HABITATTXT. Bear in mind that you have the choice about which fields to include, where they are located and how they are combined with other fields For example, you could equally combine HABITATTXT with GEODATA and LATLONG.

Adding the collector name and date

The collector name is added in very much the same way as the other fields discussed above, for example, the family name. In this label example the name and number are combined in a single field expression.

- Add a field expression to the label and set the expression text to alltrim(rde.collector) + " " + alltrim(rde.number).
- Add a further, separate expression set to alltrim(rde.collected). If you want the date to be printed on the right side of the label, drag the date expression box to the right side and also select on the menu **Format > text alignment > Right**.



Collector alltrim(rde.collector) + " " + alltri alltrim(rde.collected)

With alltrim(rde.addcoll)

In this example, additional collectors are added below the main collector in a separate expression.

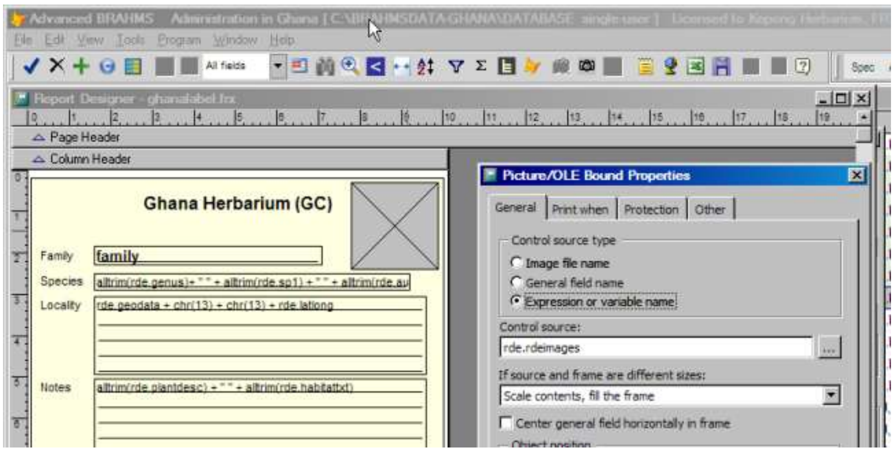
Adding images to your label

Skip this stage if you don't want to add any images to your labels. There are two categories of image addition considered here. You can add:

a) a **fixed image** to all your labels (perhaps an institutional logo or a small country map).

b) images that **vary record by record** – *e.g.* of the plant habit.

- Click on the OLE toolbar and then drag a small square top right of your design surface. The final size you can adjust later.
- To add a **fixed image**, set the **Control source type** to **'**Image file name' and locate an image file using the lookup provided.
- Most likely, the image will not be the same size as your label image area – and thus, you will benefit by setting the Source/Frame size to **Scale contents, retain shape**. If you do not, the image will be clipped.
- To add a variable image, set the **Control source type** to 'Expression or variable name' and add the RDE field name to the **Control source** text box.



Ghana Herbarium (GC)

Family family

Species alltrim(rde.genus)+" " + alltrim(rde.sp1) + " " + alltrim(rde.au

Locality rde.geodata + chr(13) + chr(13) + rde.latlong

Notes alltrim(rde.plantdesc) + " " + alltrim(rde.habitattxt)

Control source type

○ Image file name

○ General field name

● Expression or variable name

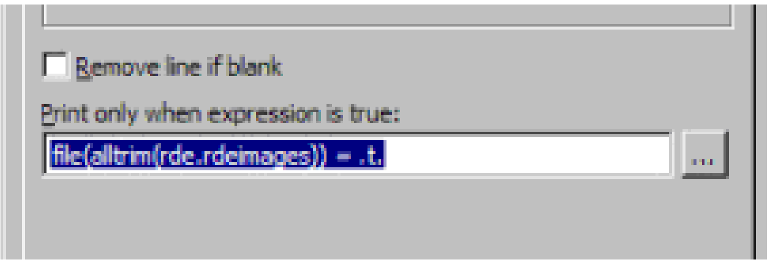
Control source: rde.rdeimages

If source and frame are different sizes: Scale contents, fill the frame

☐ Center general field horizontally in frame

You may have several images per record stored in IMAGELIST memo. As only one image is permitted for Visual Report image display, you would then need to create a new field called *e.g.* LABELIMAGE and copy the selected image filename here, editing the report expression to RDE.IMAGELABEL. You may want to print several images, in which case you could add to your RDE file the fields LABELIMG1, LABELIMG2, or equivalent.

Each record in the file must have a valid image - otherwise the reporter will generate an error. As one or more records may not have an image, the safe procedure is to add a **Print when** clause, using the tab provided, as follows:



☐ Remove line if blank

Print only when expression is true: file(alltrim(rde.rdeimages)) = .t.

The expression **file(alltrim(rde.imagelist)) = .t.** restricts processing to records where the image file is located.

Aligning fields

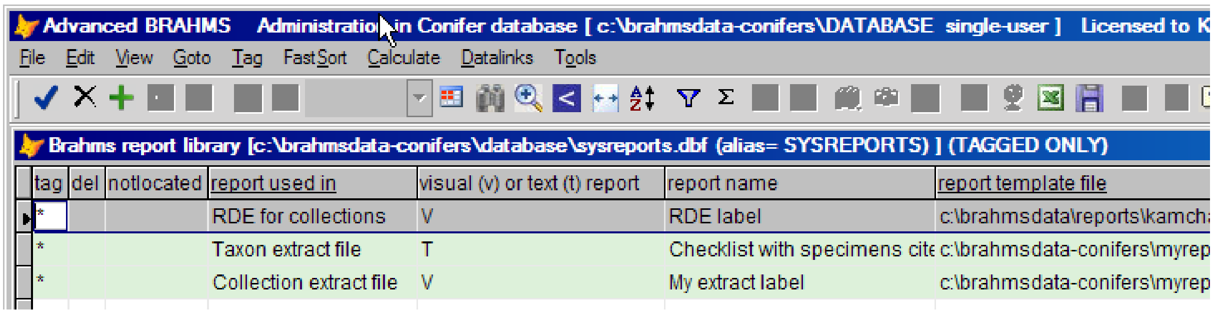
To tidy up your label design, use the options on the **Format** menu. In the example below, the left side text labels have been collectively selected (use **shift+click** to do multiple selections). You can then use **Format > Align > Align left sides**. Repeat this to align other fields as necessary.

Labels for RDE or extract files

If you want to print labels from RDE or extract files, you will normally need separate reporting templates for each – even if they are very similar. This is because when adding field expressions to templates, it is recommended you use the format *filealias.fieldname* where the filealias is the short name of the file you are reporting on and the fieldname is the name of the field in that file. Thus, 'rde.collector' and 'cout.collector' refer to the field collector in the RDE and COUT files respectively (COUT = Collection Out). File alias names are displayed at the top of each opened file in BRAHMS.

If you design a good label for an RDE file with a filename *e.g.* 'MYRDELABEL', when editing this, you use **File > Save as** to save a copy to *e.g.* 'MYEXTRACTLABEL' and then register this new label in your central reports library and edit the template as required.

To register a report template, select **Utilities > View/Edit all report templates**, add a blank record, **F9** in the Report template file field to locate the saved report template file. You must also a) set the report type to 'V' to indicate it is a visual report and b) Use **F9** in the Report used in field to choose Collection extract file.



tag	del	notlocated	report used in	visual (v) or text (t) report	report name	report template file
*			RDE for collections	V	RDE label	c:\brahmsdata\reports\kamch
*			Taxon extract file	T	Checklist with specimens cite	c:\brahmsdata-conifers\myrep
*			Collection extract file	V	My extract label	c:\brahmsdata-conifers\myrep

The central report library stores details on all your report templates

Printing to a PDF file

If you have software installed to print to a PDF file. Rather than printing your labels directly, you can create a PDF file. Example free software is available on http://www.primopdf.com/.

DEVELOPING THE SPECIES LIST

Families, genera and species

All BRAHMS databases includes lists of families, genera and species. A database may consist only of taxonomic names and information about these names.

In addition to a basic list of names, you can include detailed nomenclature at the family, genus and species level (synonomy, types, protologues, *etc.*) together with facts about species such as habit, IUCN status, local and global distribution, descriptions, ecology, uses, conservation notes and so on.

! If BRAHMS does not include a species field that you need, you can add this using the species link file.

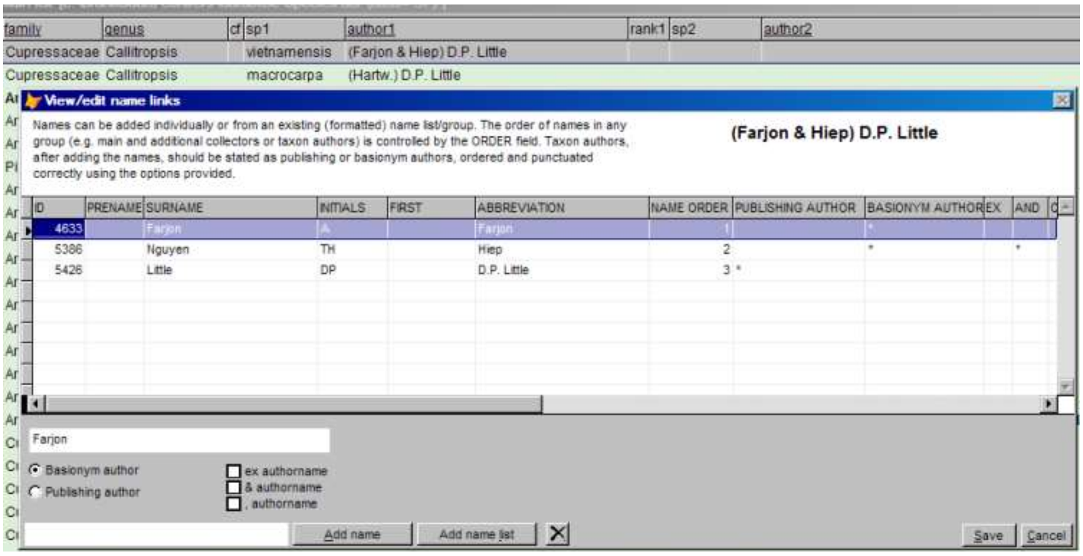
Manually adding family, genus and species records

Taxon names are usually added to BRAHMS when taxon, specimen or other RDE files that include the names are imported. However, from time to time, you may want to add names individually.

- Select **Taxa > View/edit FAMILIES in database**. Click on the + toolbar to add a blank record and type a name into the FAMILY field. Choose any name *e.g.* 'Anacardiaceae. It is not necessary at this stage to add any further details – but of you wish to, you can add in the author name (using a lookup), citation, publication year. Let's assume your new name is an accepted name – use a lookup in the TAXSTAT field to set to 'acc'.
- Select **Taxa > View/edit GENERA in database** to add a new genus name – *e.g.* 'Spondias' and using a lookup in the FAMILY field, link this name to your new family.
- Select **Taxa > View/edit SPECIES in database** to add a new species name. Use a lookup in the GENUS field to link this name to your new genus (and thus family) and enter in a species epithet to the SP1 field – *e.g.* 'testii'.
- Set the TAXSTAT of this new species to accepted ('acc').
- Now add a further new species in the same genus but with a different name.

Editing author names

To add the authors of taxa, use a lookup in the relevant AUTHOR field, click on **Add name** and locate an author name using the default abbreviation search – followed by **Save**. When adding multiple author names as In the complex example (Fisch. & C.A. Mey.) Lindl. & Gordon, you add each of the author names and edit their properties - Basionym or Publishing author + the punctuation 'ex', '&' or 'comma'.



family	genus	cf	sp1	author1	rank1	sp2	author2
Cupressaceae	Callitropsis		vietnamensis	(Farjon & Hiep) D.P. Little			
Cupressaceae	Callitropsis		macrocarpa	(Hartw.) D.P. Little			

Names can be added individually or from an existing (formatted) name list/group. The order of names in any group (e.g. main and additional collectors or taxon authors) is controlled by the ORDER field. Taxon authors, after adding the names, should be stated as publishing or basionym authors, ordered and punctuated correctly using the options provided.

(Farjon & Hiep) D.P. Little

ID	PRENAME	SURNAME	INITIALS	FIRST	ABBREVIATION	NAME ORDER	PUBLISHING AUTHOR	BASIONYM AUTHOR	EX	AND
4633		Farjon	A		Farjon	1		*		
5386		Nguyen	TH		Hiep	2		*		*
5426		Little	DP		D.P. Little	3	*			

Farjon

● Basionym author
○ Publishing author

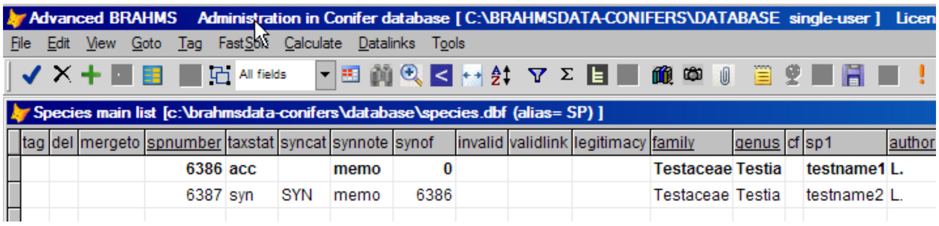
☐ ex authorname
☐ & authorname
☐ , authorname

Use a lookup (F9 or right-click) in the author field to open the above form. In this example, the species author is '(Farjon & Hiep) D. P. Little' . The names Farjon and Hiep are **basionym** authors while D.P.Little is the **publishing** author. Hiep is also indicated * in the '& authorname' select box.

Editing synonym links in the species file

Synonym links are most commonly made in the species file – but note that families and genera may also be linked as synonyms.

- Select **Taxa > View/edit SPECIES in database** to open your species file.
- Locate the last species you added above.
- Click on the **=>syn** toolbar and as prompted, locate the first of your 2 new species and make the a second name you added a synonym of this first name.



tag	del	mergeto	spnumber	taxstat	syncat	synnote	synof	invalid	validlink	legitimacy	family	genus	cf	sp1	author
			6386	acc		memo	0				Testaceae	Testia		testname1	L.
			6387	syn	SYN	memo	6386				Testaceae	Testia		testname2	L.

! When a synonym is added, the ID (spnumber) of the correct name is added to the SYNOF field. By default, the SYNCAT is set to 'SYN' although you can later edit this using the lookup option provided.

- To review the nomenclature of your new names, click on either of the names and then on the **nomc** toolbar.
- To remove a synonym link, click on the synonym record in the **nomc** screen and then click the **–syn** button.

Adding link file fields

- Select **Taxa > Default linked data file (SPLINK)** to open the species link file.
- Select **File > Modify file structure …** and add 2 new memo fields called LOCALDIST and LOCALECOL to store details on local distribution and ecology respectively.
- Save these changes
- Select **Taxa > View/edit SPECIES in database** to open your species file. Use the toolbar to open the link file.
- Add some sample text to these memo fields for your two new species.
- Open the Zoom window using the toolbar and check that your text is visible.

Import names from IPNI

For monographers, a useful first step may be to import a draft list of species names from the IPNI website. In this exercise, you will import a list of names from IPNI into BRAHMS via an RDE file.

! If you do not have an internet connection, use a download file provided to you on your training course.

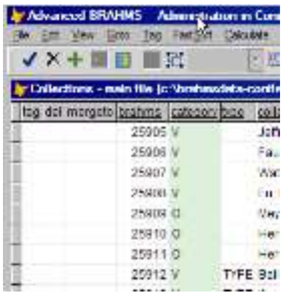
- Select **Taxa > Add/edit taxa using Rapid Data Entry files**. Here, select **File > Create a new RDE file …** and select the **System template** option and proceed to create a new RDE file for taxa.
- Open the BRAHMS help file and locate the option **Rapid Data Entry > RDE data import and convert tools > Taxon names from IPNI to BRAHMS**.
- Run through the steps in the help file to import the IPNI data to RDE.

! To check any species name in BRAHMS, go to that name in the species file, RDE or elsewhere and click on the toolbar.

BOTANICAL RECORDS

Botanical records and specimens

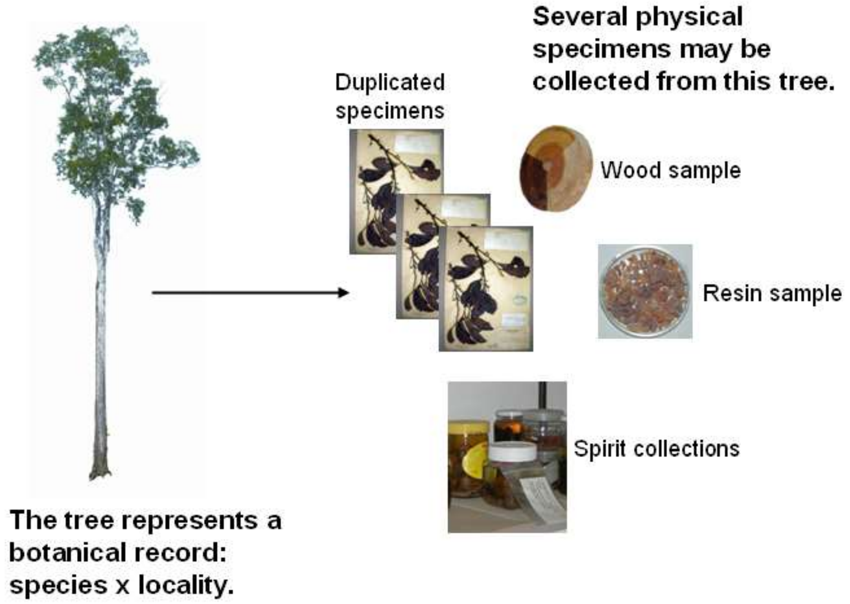
A botanical record represents the occurrence of a species in a locality. For some projects, this may be restricted to physical specimens stored in herbaria. On the other hand, some projects store information about field observations where there is no actual voucher (specimen) – perhaps just notes and one or more fotos. In other cases, a botanical record could be based on a literature reference.



brahms	category	type
25905	V	
25906	V	
25907	V	
25908	V	
25909	O	
25910	O	
25911	O	
25912	V	TYPE

The CATEGORY field in the main botanical records file indicates the type of record. "V" is for a vouchered collection while 'O' represents a field observation with no voucher. The default is 'V.

A botanical record may have one or more **specimens** – physical objects. Examples are herbarium sheets (the most common), spirit collections, silica dried leaf samples for DNA extracts, wood collections and bruchid beetles. A botanical record often has duplicate specimens that are distributed to different herbaria.



Specimens have data attributes that differ from that of the botanical record. These include herbarium location, specimen category, barcode, accession number, type status and determination histories.

! Botanical record categories can be edited using **BotanicalRecords > Resource files > Botanical Record categories**. The 3 default entries are 'V', 'O' and 'L'.

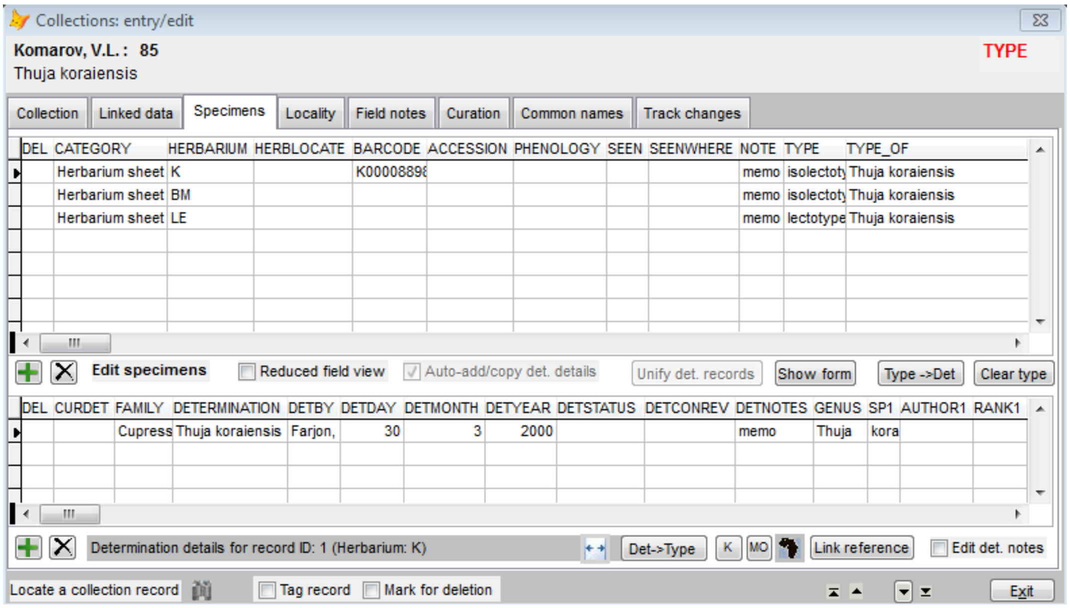
! Specimen categories can be edited using **BotanicalRecords > Resource files > Specimen categories**. The category 'Herbarium sheet' coded 'HS' is always added.

Manually adding a botanical record with 3 specimens

- Select **BotanicalRecords > View/edit botanical records in database.**
- Add a blank record using the + toolbar. A 'V' will be added by default to the CATEGORY field unless your setup instructs otherwise.

Many fields in this file must be edited using a lookup option as the fields cross-reference to data in other files.

- Use F9 in the COLLECTOR field to open the relevant lookup function. Use the **Add name** button to add one or more collector names.
- Enter some data for fields such as prefix, number, suffix, day, month and year. These can be freely edited. Leave fields blank as you wish.
- Using an F9 lookup in any of the species related field fields will open the **specimen level form**. You can also click on the **spec** toolbar.



Collections: entry/edit

Komarov, V.L.: 85
Thuja koraiensis

TYPE

DEL	CATEGORY	HERBARIUM	HERBLOCATE	BARCODE	ACCESSION	PHENOLOGY	SEEN	SEENWHERE	NOTE	TYPE	TYPE_OF
	Herbarium sheet	K		K0000889					memo	isolectoty	Thuja koraiensis
	Herbarium sheet	BM							memo	isolectoty	Thuja koraiensis
	Herbarium sheet	LE							memo	lectotype	Thuja koraiensis

☐ Reduced field view ☑ Auto-add/copy det. details

DEL	CURDET	FAMILY	DETERMINATION	DETBY	DETDAY	DETMONTH	DETYEAR	DETSTATUS	DETCONREV	DETNOTES	GENUS	SP1	AUTHOR1	RANK1
		Cupress	Thuja koraiensis	Farjon,	30	3	2000			memo	Thuja	kora		

Determination details for record ID: 1 (Herbarium: K)

☐ Edit det. notes

☐ Tag record ☐ Mark for deletion

The upper part of the specimen form lists the specimens, their category (here 3 Herbarium sheets) accession numbers/barcodes, type status if applicable as here and a few other facts. The lower part of the screen lists determinations for the individual specimens.

- Add one or more specimens to your new botanical record. Use F9 or right-click to lookup values in the CATEGORY and HERBARIUM field.
- In the lower part of this form, use a lookup in the DETERMINATION field to locate and select a species name. You may also add the DETBY name and date. If the name is new or a name change, you will be asked if you want to change the name.
- Use a lookup in any of the geographic place name fields to locate and select a country, area or place name. Locality free text notes are added into the LOCNOTES memo.
- Enter a map reference suitable for your country. Make sure you also fill in the NS and EW fields. Test your map reference using the or toolbar options.
- Notes describing the plant habit are normally added to the PLANT DESCRIPTION NOTES memo. Habitat notes can be added to HABITAT AND SITE DESCRIPTION.

THE MAPPING REVOLUTION

Recent advances

These days, very high quality map data is available on the web either to download to use with your own GIS or indeed to plot directly on Google Earth or Google Maps. Pinpoint accuracy is possible and BRAHMS provides you with up to10 decimal places in case you want to draw lines right in the middle of forest trails or plot plant positions in botanic gardens.

A vast amount of useful map data is available on the internet and, as one example, you can get excellent SHP file base maps from http://www.diva-gis.org/ following the **free spatial data** link.

Map style and Google Earth

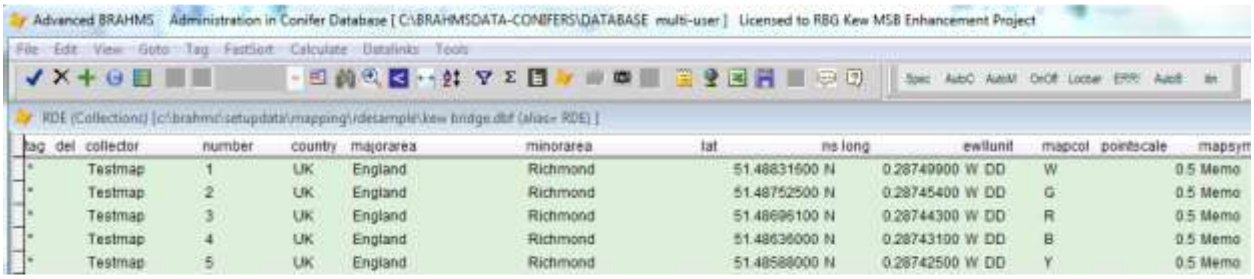
The following example is for users hooked up on the web with and Google Earth installed. As well showing how easy it is to make a map, it introduces map style setting.

You can change the data used in the example if you want.

A few colourful points plotted using Google Earth down the centre of Kew Bridge in London just next to the herbarium.

- Select **BotanicalRecords > Add/edit botanical records using Rapid Data Entry files** to open the RDE file manager for collections.
- Use the ✚ toolbar to add a new record and then use F9 in the FILE NAME columns to locate and register the sample RDE file Brahms7\Setupdata\Mapping\RDEsample\Kew bridge.dbf this file in your RDE manager.

- Open the RDE file.



Advanced BRAHMS   Administration in Conifer Database [C:\BRAHMSDATA-CONIFERS\DATABASE multi-user]   Licensed to RBG Kew MSB Enhancement Project

RDE (Collection) [c:\brahms\setupdata\mapping\rdesample\kew bridge.dbf (alias= RDE)]

tag	del	collector	number	country	majorarea	minorarea	lat	ns	long	ew	llunit	mapcol	pointscale	mapsym
*		Testmap	1	UK	England	Richmond	51.48831600	N	0.28749900	W	DD	W	0.5	Memo
*		Testmap	2	UK	England	Richmond	51.48752500	N	0.28745400	W	DD	G	0.5	Memo
*		Testmap	3	UK	England	Richmond	51.48696100	N	0.28744300	W	DD	R	0.5	Memo
*		Testmap	4	UK	England	Richmond	51.48636000	N	0.28743100	W	DD	B	0.5	Memo
*		Testmap	5	UK	England	Richmond	51.48588000	N	0.28742500	W	DD	Y	0.5	Memo

This RDE file has been edited with lat/long references already in decimal degrees (LLUNIT tells us this) and uses map the style fields MAPCOL, POINTSCALE and MAPSYM to control the colour, size and symbol of each point.

- Finally, select the 🌐 toolbar and choose Google Earth. Ensure the **All** option is selected and click **Map all.**

PRODUCING MAPS

Some notes on mapping

Maps are easily prepared from any RDE or BRAHMS file that has numeric LAT and LONG fields. If online, you can plot individual points using the 📌 or 📍 toolbar options (for Multimap and Google Maps respectively).

The 🌐 toolbar opens the main mapping form used to plot the points in the current file to your selected GIS.

Map precision check for online users

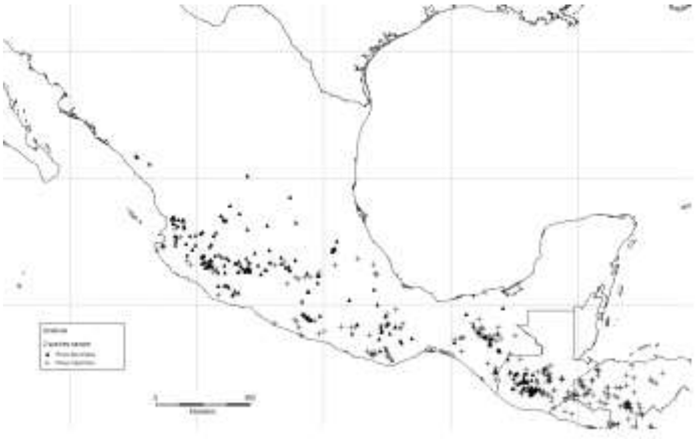
- Select **BotanicalRecords > View/edit botanical records in database**.
- Add a blank record using the + toolbar then press Enter until you reach the LAT field.
- Enter the coordinates of the kick-off mid-point in the Stade de Mahamasina, Antananarivo, Madagascar. LAT = 18.9193720 S and LONG = 47.525690 E.
- As these units are in decimal degrees, enter ‘DD’ in the LLUNIT field. This will override any general map unit configuration settings. Do not enter negative values.
- To check all records are untagged, select the menu option **Tag > Clear all tags**.
- Now tag your newly added record. Just that one record.
- Click on the 🌐 toolbar. Ensure Google Earth is selected.
- Select the option **Restrict map to tagged records**.
- Click on **Map tagged**.
- When you close Google Earth, **do not** save map items to temporary ‘My Places’ as prompted.

! You could also add this record to an RDE file and produce the map from there.

Preparing a map for 2 species using DIVA GIS

When publishing maps, you will normally need to map your data in black and white on a clear and sharp base map (not overly complicated). You can use ArcView or Diva to do this. The following exercises introduce DIVA. ArcView users can stick to ArcView.

- Open the BRAHMS help file and go to **Training exercises > Mapping > Creating a map using DIVA GIS**.
- Follow the step by step instructions in this exercise. You should complete the exercise with a completed map in a Word document similar to that shown below.



Introduction to style setting for Google Earth

The task now is to plot the same map in Google Earth, style set to show each species in a different colour and symbol.

- Return to the 2 species botanical record extract file created in the above exercise. If the file is closed, select **Extracts > BotanicalRecords** to re-open.

- Open the BRAHMS help file and go to **Training exercises > Mapping > Google Earth map and basic style setting**.
- Follow the step by step instructions in this exercise. You should complete the exercise with a completed map similar to that shown below.

If you do not see the two colours, close Google Earth, return to BRAHMS and make sure the filter set in the exercise is removed and try again.

IMAGING SPECIMENS AND THEIR LABELS

To image or not?

Herbaria undertaking large scale digitization of their specimens benefit enormously by integrating data entry with the imaging of specimens and their labels.

Using a modestly priced digital camera with flash, auto-focus and macro functions, images of entire specimens and images of the labels on specimens can be taken efficiently. Experience tells us that a trained specimen imager can take well over 1000 images per day, equivalent to more than 500 specimens.

Herbarium databases benefit from having images linked to the record in multiple ways. The ability to see an image of a specimen and especially its label provides by far the best way to verify and correct herbarium data, avoiding the need to hunt down specimens in the cabinets. Numerous errors are corrected in this way. Having images linked to specimens enlivens and enriches any herbarium database and facilitates going online.
With imaged labels linked up in the database, the entry of lengthy field note text becomes optional. Projects that have access to images of duplicates form other herbaria make yet further gains as images of duplicates can be compared often leading to a further wave of data correction.

Beyond strongly supporting specimen imaging, we go further to recommend data entry directly from the label images. Data entry from label images has certain advantages with respect to sorting data and thus being able to copy data from previous records. Specimens can be more quickly processed and returned to the cabinets. Data entry can take place anywhere, not necessarily physically next to bulky specimens.

Taxonomic vs database imaging

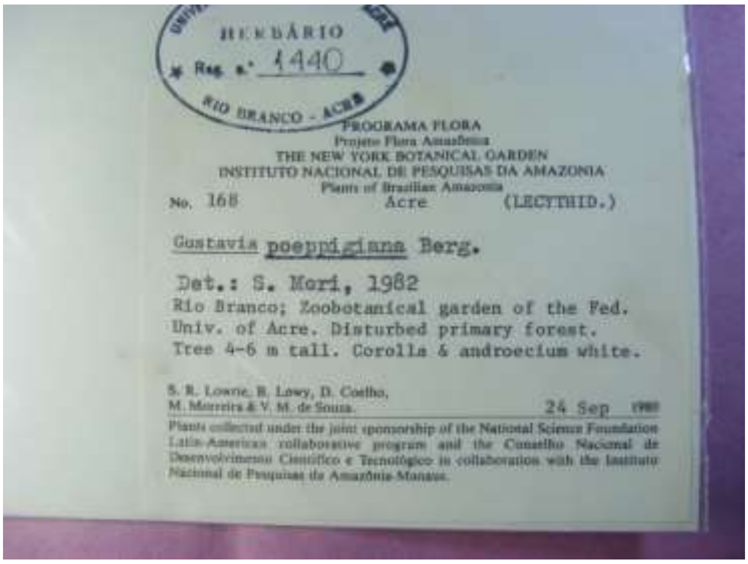
The rapid imaging methods discussed here should not be confused with the very high resolution images taken mostly for taxonomic purposes. Such images are often taken with special scanners or camera equipment. We encourage high resolution imaging for taxonomic purposes. However, imaging of this nature, often reserved for a subset of herbarium specimens including type specimens, is more time consuming and does not necessarily result in separate images of labels as advocated here.

Certainly, higher resolution images can subsequently be batch processed to make smaller resolution copies and if a herbarium has the resources to take large number of high resolution images of specimens and their labels (*e.g.* > 10Mbytes), this is fine.

We suggest using a camera setting of 2 Mbyte resolution. This size is more than adequate to see most details on any specimen. Label images can subsequently be batch reduced to < 500K per image.

Taking images of specimens and their labels

To optimize efficiency and speed, images can be taken with a hand held camera rather than using a fixed position tripod. This makes it far easier to reframe the images between specimen and label. Flash is recommended. If specimens are in plastic bags, flash is not practical unless specimens are removed. Use side lighting instead. Place a fixed size measure (ruler) on a blank part of the specimen.



HERBÁRIO
Reg. n.º 1440
RIO BRANCO - ACRE

PROGRAMA FLORA
Projeto Flora Amazônica
THE NEW YORK BOTANICAL GARDEN
INSTITUTO NACIONAL DE PESQUISAS DA AMAZONIA
Plants of Brazilian Amazonia
No. 168 Acre (LECYTHID.)

Gustavia poeppigiana Berg.

Det.: S. Mori, 1982
Rio Branco; Zoobotanical garden of the Fed.
Univ. of Acre. Disturbed primary forest.
Tree 4-6 m tall. Corolla & androecium white.

S. R. Lowrie, R. Lowy, D. Coelho,
M. Moreira & V. M. de Souza. 24 Sep [illegible]

Plants collected under the joint sponsorship of the National Science Foundation Latin-American collaborative program and the Conselho Nacional de Desenvolvimento Científico e Tecnológico in collaboration with the Instituto Nacional de Pesquisas da Amazônia-Manaus.

If the sheet has an accession number and/or barcode, include these with the label – or take a separate image if necessary. If you are adding barcodes at the same time as imaging, add the barcode first – then take the image.

In the next phase, these numbers will be typed in to rename the image files.

Assembly of image file names to RDE

The process described here captures images into a Botanical Record RDE file.

- Transfer the images from your camera to a folder on your hard drive. The images will have their default camera file names.
- Select **BotanicalRecords > Add/edit Botanical Records using Rapid Data Entry files**. Select **File > Create a new RDE file** copying the 'System Template' as prompted. Name this file IMAGETEST or equivalent.
- When making your new file, ensure that the option **Include IMAGELIST memo** is selected.
- Now select **Tools > Images in RDE > Append images to RDE file**. This will append all images from your selected folder, adding the complete image file name to the IMAGELIST memo. Each record will contain one image.
- To check this has worked, go to top of the file and click the 📷 toolbar and move through the file to view the images.

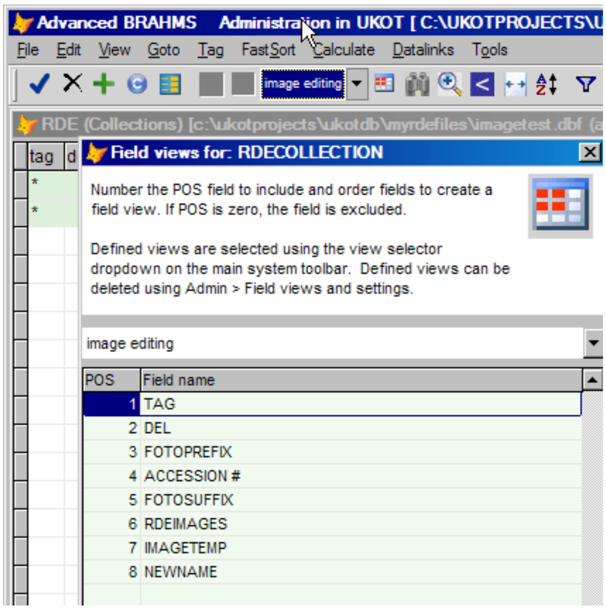
Initial entry of accession or barcode numbers

The next step is to enter sufficient data from your images to the RDE file to be able to rename the image files appropriately. The objective is to rename your image files to include:

1. your herbarium code
2. the herbarium accession number or barcode
3. and a suffix that indicates what type of image it is – specimen or label.

There are other ways to rename images but in this exercise, you will use accession number. To simplify and speed up this step, you should create a **field view** for the RDE file that includes the following fields: TAG, DEL, FOTOPREFIX, ACCESSION, FOTOSUFFIX, IMAGELIST, IMAGETEMP and NEWNAME. No other fields are required at this stage. Select BARCODE instead of ACCESSION as appropriate.

- Close and re-open your RDE file. This will ensure that the new FOTO fields are available for field selection.
- Click the ▦ toolbar to define a field view to include the fields listed above and save this with a suitable name *e.g.* 'Image editing'. The reason for setting up this field view is to speed up subsequent data entry.



Number the POS field to include and order fields to create a field view. If POS is zero, the field is excluded.

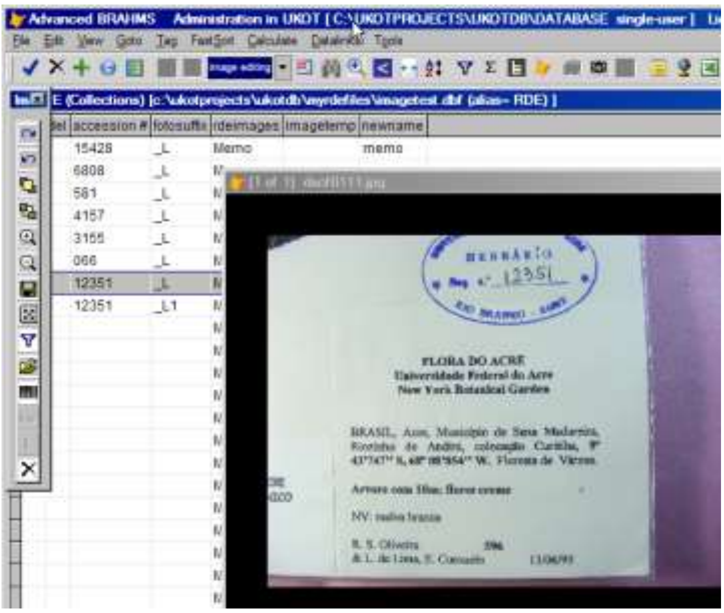
Defined views are selected using the view selector dropdown on the main system toolbar. Defined views can be deleted using Admin > Field views and settings.

image editing

POS	Field name
1	TAG
2	DEL
3	FOTOPREFIX
4	ACCESSION #
5	FOTOSUFFIX
6	RDEIMAGES
7	IMAGETEMP
8	NEWNAME

Field view set to show selected fields only and thus speed up data entry

- With this field view selected and the current image visible (using the 📷 toolbar), what you now need to do is enter the accession numbers by reading these off the images. Enter the barcode if using barcodes.



del	accession #	fotosuffix	rdeimages	imagetemp	newname
	15428	_L	Memo		memo
	6808	_L	M		
	561	_L	M		
	4157	_L	M		
	3155	_L	M		
	066	_L	M		
	12351	_L	M		
	12351	_L1	M		

Note that specimen with accession number 12351 has 2 records – there are 2 labels.

- Enter your herbarium code into the FOTOPREFIX field. As this will be standard, you will use F4 to copy next records. Alternatively, you could use a FoxPro command *Replace FOTOPREFIX with "ABC' all* at any stage (replace ABC with your herbarium code).

- Use the FOTOSUFFIX field as follows:

  1. if the image is a whole specimen, leave this field blank.
  2. If the image is of a label, enter "_L" (upper or lower case - but be consistent)
  3. If the image is of a second or further label for the same specimen, enter "_L1", "_L2", etc.

For example, a specimen may have 2 labels images. In this case, the first RDE record with the image of the whole specimen will have a blank FOTOSUFFIX, the next 2 records will have "_L" and "_L1". All 3 records will have the same ACCESSION number entry as they all refer to the same specimen. The actual character used in not important (e.g. in Brazil, they use '_e' for 'etiqueta').

Image file re-naming – step 1

The next task is to re-name the camera derived image files. Our objective here – and bear in mind you may want to re-name your images differently – is to convert the images files to be something like “ABC_123.JPG” and “ABC_123.JPG_L” where ABC is your herbarium acronym.

Once you have completed filling the ACCESSION and FOTOSUFFIX fields:

- Select **Tools > Images in RDE > Image file renaming > Generate IMAGETEMP from …** choosing the accession or barcode option as appropriate. This will compile the new ‘proposed’ image file name to replace the camera name.

The next task is to convert the IMAGETEMP to NEWNAME. The NEWNAME field adds the image file extension and the full path – this constructing the full image name. At this stage, if more than one image has the same name, warnings are given. Clearly, you cannot use the same name more than once.

- Select **Tools > Images in RDE > Image file renaming > Generate NEWNAMEs using the IMAGETEMP field for tagged records.**

If the same name is used more than once (i.e. generated from IMAGETEMP in turn from your prefix, accession/barcode and suffix fields), a warning is generated: “**!*! Duplicated new file name**” and added to the NEWNAME memo. For these records, an ‘X’ is added to the TAG field.

Image file re-naming – step 2

Once the NEWNAME field is filled, you are ready to proceed to the final re-naming stage which is to physically re-name the images on your disk.

- Tag the records you want to rename. The following option only processed tagged records.
- Select **Tools > Images in RDE > Image file renaming > Physically rename TAGGED image files on disk to NEWNAMEs**.
- Using your file manager, check that the images on the disk have in fact been correctly renamed.

Gathering same-specimen records

Most specimens will have 2 records in the RDE file (specimen + label). In some cases, more than 2. In the next step, you will merge same specimen images into one record, paving the way for data entry. We can match specimens using the accession number or barcode.

- Select **Tools > Images in RDE > Image file renaming > Gather images of same specimen …**
- Choose the field ACCESSION or BARCODE as used in the exercise.
- Tick the option ‘Delete records that have been merged’.
- Optionally restrict to tagged.

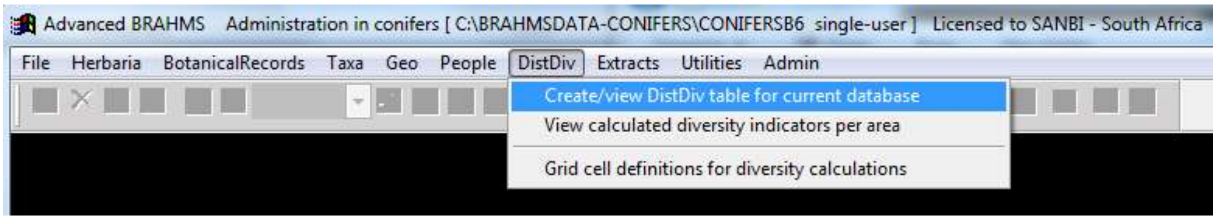
Data entry

Your course instructor will now explain how to proceed with data entry using the label images.

DIVERSITY ANALYSIS INTRODUCED

Notes on diversity analysis and DistDiv options

Distribution summary table (DST) options are all located on the main **DistDiv** menu option which is enabled using **Utilities > My Setup/Profile > Active modules**.



The purpose of these options is to calculate and display summary data about the distribution of taxa and to calculate diversity indicators. Summaries are executed for TAXON x AREA combinations. Example summaries are 'family x country', 'genus x majorarea' and 'species x gridcell'. In the last example, if grid cells were set to 1 degree square, the DistDiv options would generate tables with:

1. Distribution table: separate records for each degree square x species combination
2. Diversity indicators table: separate records for each grid cell with a sum of its content

Taxon quick codes

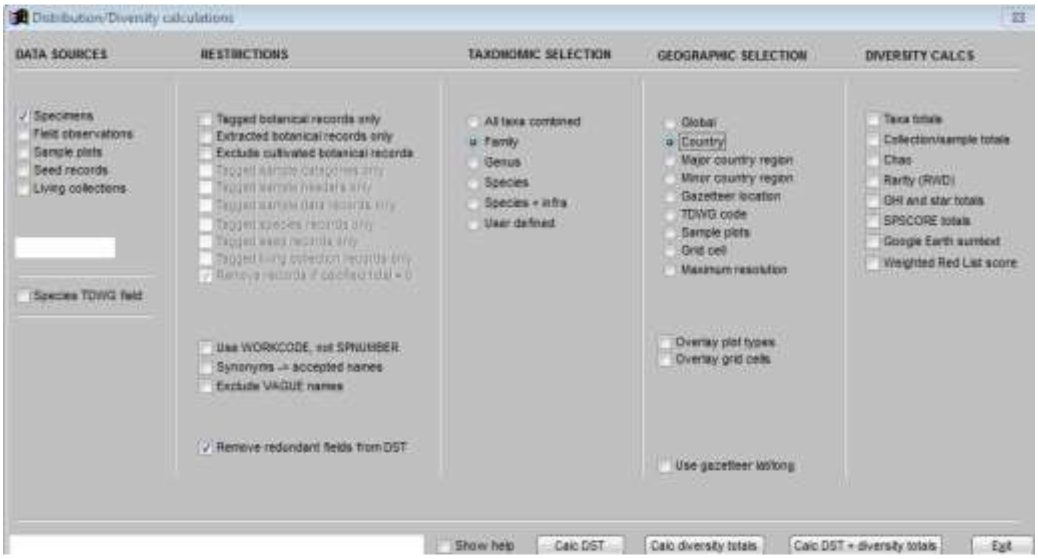
Some of the options associated with the **DistDiv** options (e.g. export to PC-ORD) require short codes for family, genus and/or species records. You can easily generate/refresh these.

- Select **Taxa > View/edit SPECIES in database** followed by **Tools > Generate species quick codes to SPQUICK**. Although you can adjust the settings, it's recommended you choose all the default and click on **Generate**. The results you will see in the field SPQUICK.
- Repeat this for the family and genus files.

! If any taxon records lack quick codes, you will be auto-prompted to re-generate these codes when you run the **DistDiv** options.

Generating DistDiv summary tables

- Select **DistSum > Create/View DistDiv for current database**.
- If the **DistDiv** form does not auto-open, click on the **Re-calc** toolbar.



DATA SOURCES

☑ Specimens
☐ Field observations
☐ Sample plots
☐ Seed records
☐ Living collections

☐ Species TDWG field

RESTRICTIONS

☐ Tagged botanical records only
☐ Extracted botanical records only
☐ Exclude cultivated botanical records
☐ Tagged sample categories only
☐ Tagged sample headers only
☐ Tagged sample data records only
☐ Tagged species records only
☐ Tagged seed records only
☐ Tagged living collection records only
☑ Remove records if coll/sub total = 0

☐ Use WORKCODE, not SPNUMBER
☐ Synonyms -> accepted names
☐ Exclude VAGUE names

☑ Remove redundant fields from DST

TAXONOMIC SELECTION

○ All taxa combined
● Family
○ Genus
○ Species
○ Species + infra
○ User defined

GEOGRAPHIC SELECTION

○ Global
● Country
○ Major country region
○ Minor country region
○ Gazetteer location
○ TDWG code
○ Sample plots
○ Grid cell
○ Maximum resolution

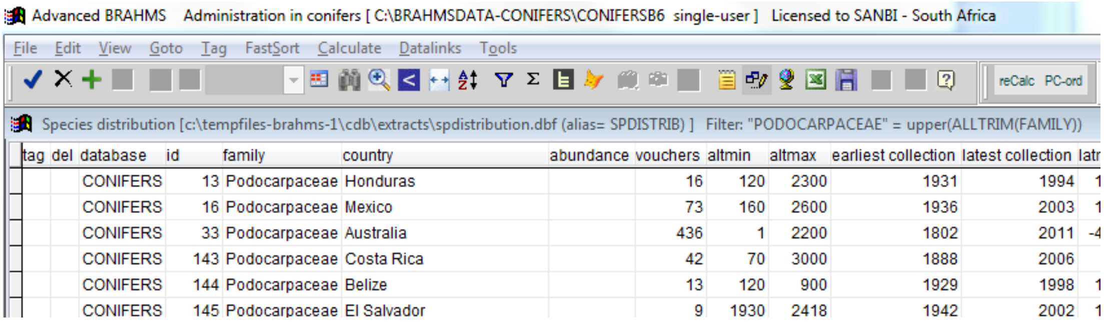
☐ Overlay plot types
☐ Overlay grid cells

☐ Use gazetteer lat/long

DIVERSITY CALCS

☐ Taxa totals
☐ Collection/sample totals
☐ Chao
☐ Rarity (RWD)
☐ GHI and star totals
☐ SPSCORE totals
☐ Google Earth avtext
☐ Weighted Red List score

- On this form, adjust the settings as seen above. Thus based on the data source “Vouched collections”, you will generate a table with one record for each family **x** country combination.
- Ensure none of the **Data restriction** options are selected and then click on the **Calc DST** option.



Advanced BRAHMS Administration in conifers [C:\BRAHMSDATA-CONIFERS\CONIFERSB6 single-user] Licensed to SANBI - South Africa

Species distribution [c:\tempfiles-brahms-1\cdb\extracts\spdistribution.dbf (alias= SPDISTRIB)] Filter: "PODOCARPACEAE" = upper(ALLTRIM(FAMILY))

tag	del	database	id	family	country	abundance	vouchers	altmin	altmax	earliest collection	latest collection	latr
		CONIFERS	13	Podocarpaceae	Honduras		16	120	2300	1931	1994	1
		CONIFERS	16	Podocarpaceae	Mexico		73	160	2600	1936	2003	1
		CONIFERS	33	Podocarpaceae	Australia		436	1	2200	1802	2011	-4
		CONIFERS	143	Podocarpaceae	Costa Rica		42	70	3000	1888	2006	
		CONIFERS	144	Podocarpaceae	Belize		13	120	900	1929	1998	1
		CONIFERS	145	Podocarpaceae	El Salvador		9	1930	2418	1942	2002	1

A sample result screen with a filter set on Podocarpaceae

- Sort the table on FAMILY column and/or set a filter on a selected family. Note that each record includes a summary of results, for example, the total number of vouchers and the map grid range.

If you want to calculate totals or other statistics for each resulting record (in this case each family per country), select one or more of the Diversity calcs options. Select **Calc DST+ diversity totals**. The summary diversity totals are opened using **DistDiv > View calculated diversity indicators per area.**

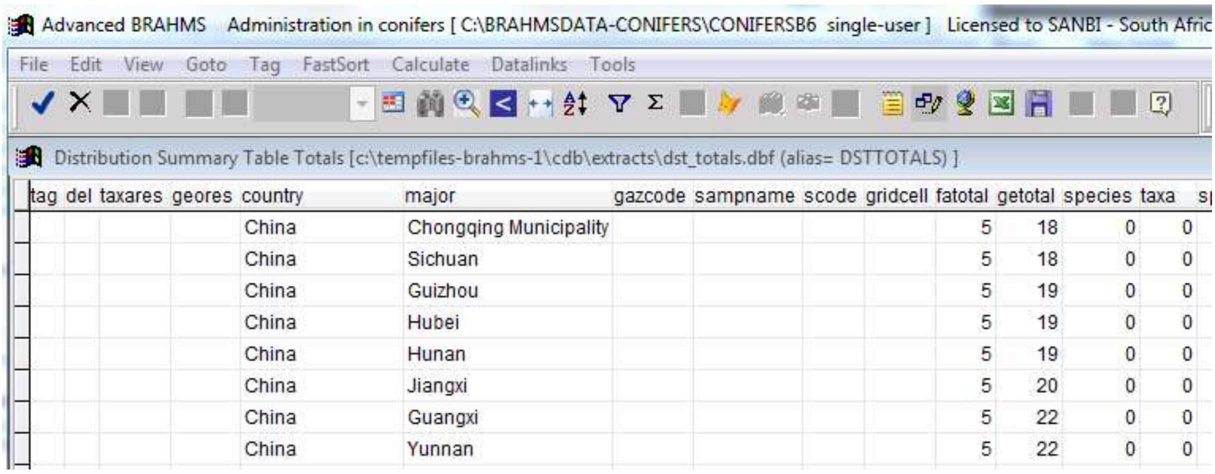
- You can repeat the recalculation for any combination of TAXA x GEOGRAPHIC RESOLUTION settings.
-

Advanced BRAHMS Administration in conifers [C:\BRAHMSDATA-CONIFERS\CONIFERSB6 single-user] Licensed to SANBI - South Africa

Species distribution [c:\tempfiles-brahms-1\cdb\extracts\spdistribution.dbf (alias= SPDISTRIB)] Filter: "RETROPHYLLUM" = upper(ALLTRIM(GENUS))

tag	del	database	id	family	genus	country	major	samptype	sampname	scode	abundance	vouchers	sampl
		CONIFERS	1316	Podocarpaceae	Retrophyllum	Fiji	Western Division					9	
		CONIFERS	1611	Podocarpaceae	Retrophyllum	Fiji	Viti Levu					9	
		CONIFERS	1613	Podocarpaceae	Retrophyllum	New Caledonia	Grande Terre					67	
		CONIFERS	1620	Podocarpaceae	Retrophyllum	Solomon Islands	Santa Cruz Is.					4	
		CONIFERS	1621	Podocarpaceae	Retrophyllum	Vanuatu	Torba Prov.					1	
		CONIFERS	1723	Podocarpaceae	Retrophyllum	Indonesia	Maluku					1	
		CONIFERS	1724	Podocarpaceae	Retrophyllum	Papua New Guinea	Central Province					2	
		CONIFERS	1725	Podocarpaceae	Retrophyllum	Indonesia	Papua					6	
		CONIFERS	1726	Podocarpaceae	Retrophyllum	Papua New Guinea	Bismarck Archipelago					3	
		CONIFERS	1727	Podocarpaceae	Retrophyllum	Fiji	Vanua Levu					2	

The above example is genus x majorarea



Advanced BRAHMS Administration in conifers [C:\BRAHMSDATA-CONIFERS\CONIFERSB6 single-user] Licensed to SANBI - South Afric

Distribution Summary Table Totals [c:\tempfiles-brahms-1\cdb\extracts\dst_totals.dbf (alias= DSTTOTALS)]

tag	del	taxares	geores	country	major	gazcode	sampname	scode	gridcell	fatotal	getotal	species	taxa	s
				China	Chongqing Municipality					5	18	0	0	
				China	Sichuan					5	18	0	0	
				China	Guizhou					5	19	0	0	
				China	Hubei					5	19	0	0	
				China	Hunan					5	19	0	0	
				China	Jiangxi					5	20	0	0	
				China	Guangxi					5	22	0	0	
				China	Yunnan					5	22	0	0	

The table here is opened using DistDiv > View calculated diversity indicators per area with the results sorted on getotal (genus total).

Checking grid cell definitions

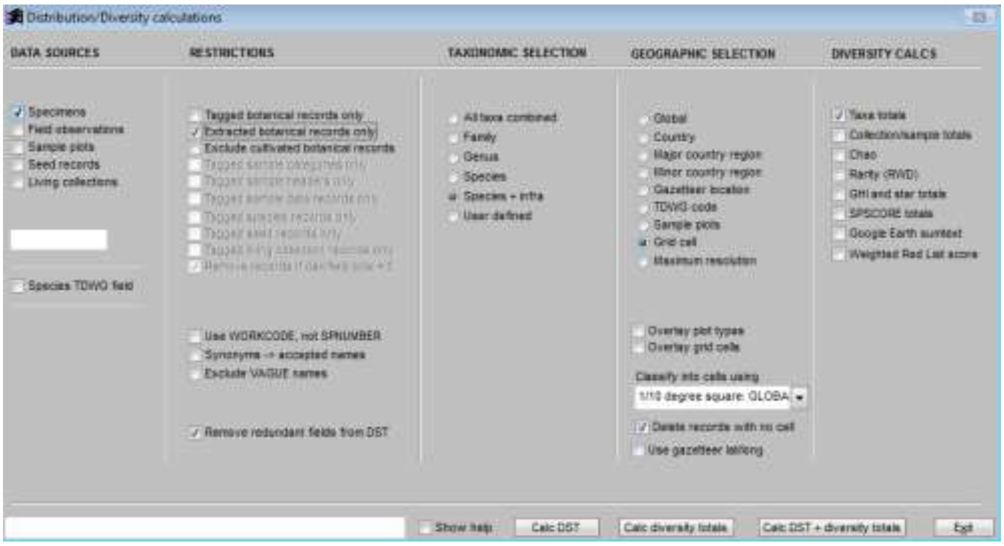
- Select **DistDiv > Grid cell definitions for diversity calculations**. If the file is empty, select **Tools > Add sample grid cell records**. You can add further definitions here if necessary.
- Meanwhile, note that the field CELLSIZE includes the cell dimensions. The value '1' represents 1 degree square cells. The value '1/10' represents 1/10th degree cells.

Recalculating the DistDiv for 1/10 degree cells and mapping on Google Earth

To speed up this next stage, you can restrict the calculation to a subset of your database.

- Select **BotanicalRecords > Extract/Query data,** choose **Geographic > Country** and proceed to extract all records from 'New Caledonia'. **Close** the extract file.

- Select **DistDiv > Create/view DistDiv for current database**. If the **DistDiv** form does not auto-open, click on the **Re-calc** toolbar.



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☐ Tagged sample data records only
☐ Tagged species records only
☐ Tagged seed records only
☐ Tagged living accession records only
☑ Remove records if [illegible]
☐ Use WORKCODE, not SPNUMBER
☐ Synonyms -> accepted names
☐ Exclude VAGUE names
☑ Remove redundant fields from DST

TAXONOMIC SELECTION
○ All taxa combined
○ Family
○ Genus
○ Species
● Species + infra
○ User defined

GEOGRAPHIC SELECTION
○ Global
○ Country
○ Major country region
○ Minor country region
○ Gazetteer location
○ TDWG code
○ Sample plots
● Grid cell
○ Maximum resolution
☐ Overlay plot types
☐ Overlay grid cells
Classify into cells using: 1/10 degree square: GLOBA
☑ Delete records with no cell
☐ Use gazetteer lat/long

DIVERSITY CALCS
☑ Taxa totals
☐ Collection/sample totals
☐ Chao
☐ Rarity (RWD)
☐ GHI and star totals
☐ SPSCORE totals
☐ Google Earth sumtext
☐ Weighted Red List score

- On this form, adjust the settings as seen above. Note that the Data restriction option **Extracted botanical records** is selected. Thus based on the data source "Vouched collections", you will generate a table with one record for each species+ssp/var **x** 1/10 degree grid cell – and the calculation will be restricted to the New Caledonia data subset.
- Examine then **close** the main **DistDiv** results table.
- Select **DistDiv > View calculated diversity indicators per area**. This file includes a summary of taxa and diversity indexes for each 1/10 degree cell area.

tag	del	taxares	geores	gazcode	sampname	scode	gridcell	tatotal	getotal	species	taxa	spscoretot	cr	en	vu	redlisttot	chao2	chao2r	rwd	rwdgroup	vouchers
*		Infra	Gridcell				6207091	1	2	2	2	0	0	0	0	0	0	3	9.000000	1	2
*		Infra	Gridcell				6207092	2	2	2	2	0	0	0	1	1	0	3	8.000000	1	2
*		Infra	Gridcell				6207093	3	6	7	7	0	1	1	1	5	9	8	82.000000	2	13
*		Infra	Gridcell				6207094	1	1	1	1	0	0	0	0	0	0	1	3.000000	1	1
*		Infra	Gridcell				6208889	1	1	1	1	0	0	0	1	1	0	1	3.000000	1	1
*		Infra	Gridcell				6208890	2	4	4	4	0	0	1	1	3	0	7	21.000000	1	6
*		Infra	Gridcell				6208891	1	1	1	1	0	0	0	0	0	1	1	5.000000	1	2
*		Infra	Gridcell				6208893	1	1	1	1	0	0	0	1	1	0	1	3.000000	1	1
*		Infra	Gridcell				6210686	1	1	1	1	0	0	1	0	2	1	1	6.000000	1	4
*		Infra	Gridcell				6210687	2	2	2	2	0	0	1	1	3	3	2	27.000000	1	3

Sample diversity indicators file sorted by species. This file includes one record per gridcell, tallies various paramaters (e.g. species and total taxa) and calculates various diversity indices. For further details refer to the help file.

- Now select **Tools > Map tools > Add/re-set map style fields**. This will add some extra columns useful for Google Earth mapping.

- Sort the file on the Column TAXA then go to the bottom of the file. Note that some cells have a value greater than or equal to 10 different taxa per cell.
- For each record where TAXA >= 10, add “R” to the field MAPCOL. This is a short code for the colour red.
- Click now on the 🌐 toolbar and ensure Google Earth is selected.
- On the map form, click on **Draw polygons for cell boundaries**. Then click on Map all.

```
TAG: *; TAXARES: Infra; GEORES: Gridcell; GRIDCELL: 6239478; CGRIDCELL:
GC6239478; CELLSIZE: 0.1000; FATOTAL: 3; GETOTAL: 11; SPECIES: 20; TAXA:
20; SPSCORE: 20; CHAO2: 21; CHAO2R: 20; RWD: 2.5402; VOUCHERS: 126;
LAT: -22.1500; LONG: 166.6500; CELLLATMIN: -22.1000; CELLLATMAX: -22.2000;
CELLLONMIN: 166.6000; CELLLONMAX: 166.7000; DSTTEXT: Acmopyle pancheri,
Agathis lanceolata, Agathis ovata, Araucaria bernieri, Araucaria biramulata,
Araucaria humboldtensis, Araucaria laubenfelsii, Araucaria muelleri, Araucaria
subulata, Callitris neocaledonica, Dacrycarpus vieillardii, Dacrydium araucarioides,
Falcatifolium taxoides, Libocedrus austrocaledonica, Neocallitropsis pancheri,
Podocarpus decumbens, Podocarpus gnidioides, Podocarpus sylvestris,
Retrophyllum comptonii, Retrophyllum minus; MAPCOL: FF0000FF
```

*Sample output showing the most diverse 1/10th degree cells in red. To open the text box, use **Ctrl+click** on a selected cell.*

THE POWER OF FOXPRO COMMANDS

Why use FoxPro commands?

The ability to use FoxPro commands in RDE (and elsewhere) opens up a further dimension of editing flexibility. It is never essential to use these commands. However, if you do, it makes some tasks much easier – both in RDE and in your database.

Imagine an RDE file with many records where you want to replace the mixed and incorrect text values ‘SN’ and ‘sn.’ in the NUMBER field to a uniform ‘s.n.’ . This could be done manually, record by record but it could take a long time! Using FoxPro commands, the task can be done in seconds.

Numerous data processing functions can be undertaken with one-line commands using a small number of programming keywords. The commands can be made to apply to one record, tagged or filtered records or all records in a file.

An example FoxPro command is: **Replace COUNTRY with ‘Malaysia’ all**. The replace command is the most commonly used. The **all** keyword tells BRAHMS to do this for all records in the open file.

You can execute FoxPro commands whenever the 🦊 button is activated on the toolbar. As FoxPro commands could be damaging, this button is usually only enabled in RDE, extract files and other temporary work files, but not in main database files. It is possible to enable FoxPro commands throughout BRAHMS using a configuration setting.

Command operators

Command	Notes
=	Equal to
>	Greater than
<	Less than
$	Is included in
<> or #	Not equal to

Some commonly used text string and numeric functions

Command	Does what
ALLTRIM()	Remove leading and trailing blanks
Upper(), Lower()	Convert to upper / lower case
Str()	Convert a numeric field to character format
Substr()	Extract a portion of a character field
Strtran()	search and replace characters within a text string
Val()	Convert a character field to numeric format

Some sample commands to try now

- Select **BotanicalRecords > Add/edit botanical records using Rapid Data Entry files.**
- Create a new file and add at least 20 blank records.

Using the ‘replace’, ‘upper’ and ‘lower’ commands

- Select the 🦊 toolbar and add a new command line Replace GENUS with “JUNIPERUS”
- Execute this command. This will add this genus name in upper case to the **current record**.

- Modify the above command to Replace GENUS with “JUNIPERUS” all

- Execute this command. This will add this genus name in upper case to all records.

Now Add and execute the commands (change the exact content of the commands if appropriate)

- Replace GENUS with lower(GENUS) all
- Replace GENUS with upper(GENUS) all
- Replace NUMBER with “12345” all
- Replace NUMBER with “A”+ alltrim(NUMBER)+”Z” all
- Replace COLLYY with 1899 all
- Replace COLLYY with COLLYY + 100 all
- Replace TAG with '*' for LAT = 0 and LONG = 0
- replace FAMILY with "Compositae" for FAMILY = "Asteraceae"

Using the ‘substr’ command

- Add and execute the command ‘Replace genus with upper(substr(GENUS,1,1)) + lower(substr(GENUS,2)) all

Experimenting with the strtran() function

- In the same RDE file, add and execute the command Replace COLLECTOR with “Smith, A.B.” all
- Now Replace COLLECTOR with strtran(COLLECTOR,”A.B.”,”C.D.”) all

Using ‘for’ to select records

- Tag some records in your RDE file then use Replace COLLMM with 12 for tag = “*”

CREATING A NEW DATABASE PROJECT

The template database

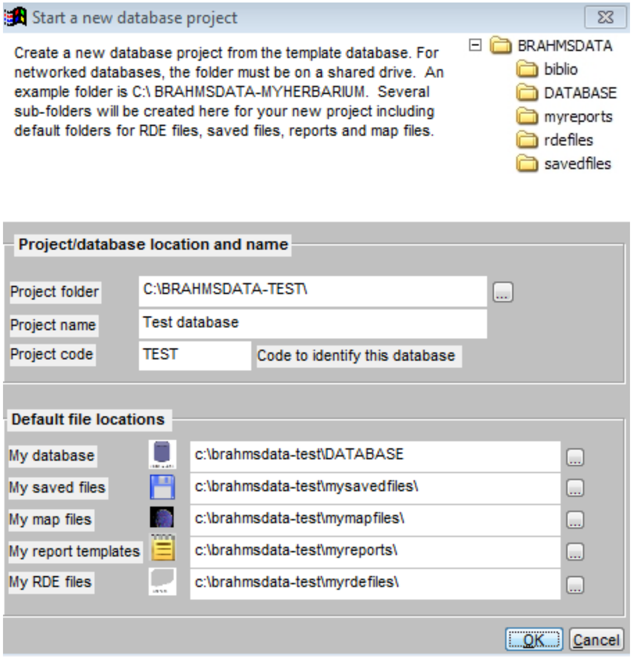
When you first install BRAHMS, you can log into the ‘Template database’ which is the empty database provided with BRAHMS. The template database is copied by the system to create new database projects. Do not enter data into the template database as these data would be lost when you next upgrade BRAHMS.

- Log into BRAHMS selecting the Template database.

Create a new database

Creating a new database is an essential first step when starting a new project. You can create and register as many separate databases as you need. To create your own database:

- Using your file manager, create a folder on any local or shared/networked drive. This folder will be where all files associated with the project will be stored. An example folder name is ‘c:\brahmsdata-mydatabase’.
- When logged into the template database, select **File > Create new database/project…**.
- Select your new folder name as prompted on the form.
- Give the project a name and a short code then select **OK** to proceed to create and login to the new database.



Create a new database project from the template database. For networked databases, the folder must be on a shared drive. An example folder is C:\ BRAHMSDATA-MYHERBARIUM. Several sub-folders will be created here for your new project including default folders for RDE files, saved files, reports and map files.

Project/database location and name

Project folder	C:\BRAHMSDATA-TEST\
Project name	Test database
Project code	TEST — Code to identify this database

Default file locations

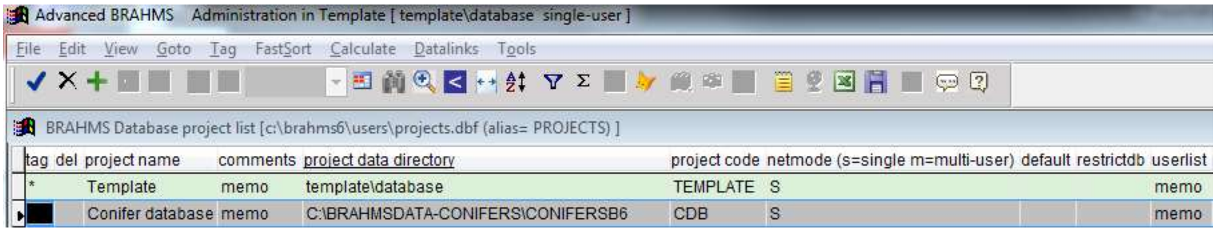
My database	c:\brahmsdata-test\DATABASE
My saved files	c:\brahmsdata-test\mysavedfiles\
My map files	c:\brahmsdata-test\mymapfiles\
My report templates	c:\brahmsdata-test\myreports\
My RDE files	c:\brahmsdata-test\myrdefiles\

When you create a new project, a series of subfolders is created under the main folder name. Of these, the most important is DATABASE. This is where your actual database is stored. The other subfolders are default locations for different BRAHMS files – these can be changed later.

The database manager

The database manager is a file in BRAHMS that stores details about the names, locations and some further properties concerning your database(s).

- Select **File > Database manager** to open this file.



BRAHMS Database project list [c:\brahms6\users\projects.dbf (alias= PROJECTS)]

tag	del	project name	comments	project data directory	project code	netmode (s=single m=multi-user)	default	restrictdb	userlist
*		Template	memo	template\database	TEMPLATE	S			memo
		Conifer database	memo	C:\BRAHMSDATA-CONIFERS\CONIFERSB6	CDB	S			memo

The NETMODE setting can be ‘S’ or ’M’ to indicate single or multi-user login for the project in question. Unless your BRAHMS configuration options and/or permissions prevent it, you can edit the netmode when logging in.

SOME ADMINISTRATION TOPICS

That pesky missing OCX file and/or OLE error

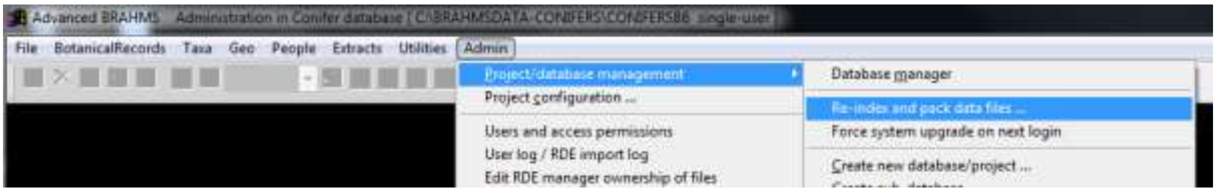
If you get an error message on opening a data file similar to "OLE error code 0x80040154: class not registered." (the actual message will vary but usually refers to a missing OCX or OLE), this means you need to register a missing OCX file.

Note that the file must be registered, not just copied into the folder. A readme file is provided in the brahms7\ocx files folder. The error message is quite typical on new BRAHMS installations on Windows7 and Windows 8 PCs.

Re-indexing your database

Database index files (.CDX files) allow rapid access to your data. These files are automatically kept up to date as you add or edit data. Nevertheless, periodic re-indexing can speed up system performance.

- Select **Admin > Project/database management > Re-index and pack data files...** and proceed to re-index your database.




Re-indexing and packing Conifer database database

This option deletes and then rebuilds the CDX index files for your database. It is recommended that you re-index periodically, for example once a month. Re-indexing can increase database performance with heavily edited datafiles. Always re-index after an abnormal system shutdown.

Using configuration options, your system collation may be set to MACHINE (=default) or GENERAL. This setting influences how accented characters are sorted (GENERAL is better for this). Refer to the help file for further details.

Large external files (>1m records) may take a few minutes to re-index. System files (e.g. the main menu and message files) cannot be re-indexed when the BRAHMS software folder is readonly. Re-set this property to re-index system files if necessary.

Last index 29/03/2012

Index mode: Machine

☑ Also re-index system files
☐ Also re-index external files (NB large files may take several minutes to reindex)
☐ Run DBF integrity checks after reindexing

When re-indexing, you can optionally select to run **Data integrity checks**. If problems are found in your database, these are reported in a separate file.

Backing up your data

- Have you located and read the help file text on backing up? If not, open the help file now and search for 'Backing up'.

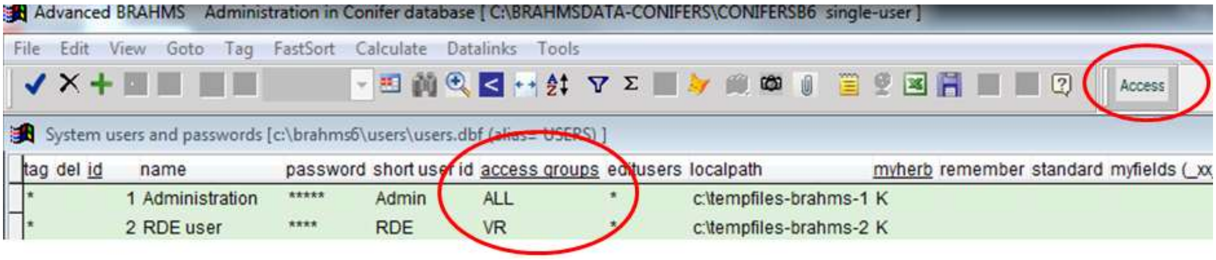
Backing up is the process of copying valuable files to a safe place. Copying your files to the same disk as the one your files are on is not recommended - all your eggs are in one basket. It is a nuisance to backup but this is a much better alternative than the loss of your data. Remember some key points:

- **There is only one way to absolutely ensure the safety of your data – rigorous adherence to a regular program of backing up of your data.**
- **Do not overwrite the same back up file. Keep a series of separate back up files. Why? Because you may overwrite a good back up with bad data.**

- **Create zip files to back up your data rather than copying the original files.**
- **Make sure you copy the DBF and the FPT files.**

User access permissions

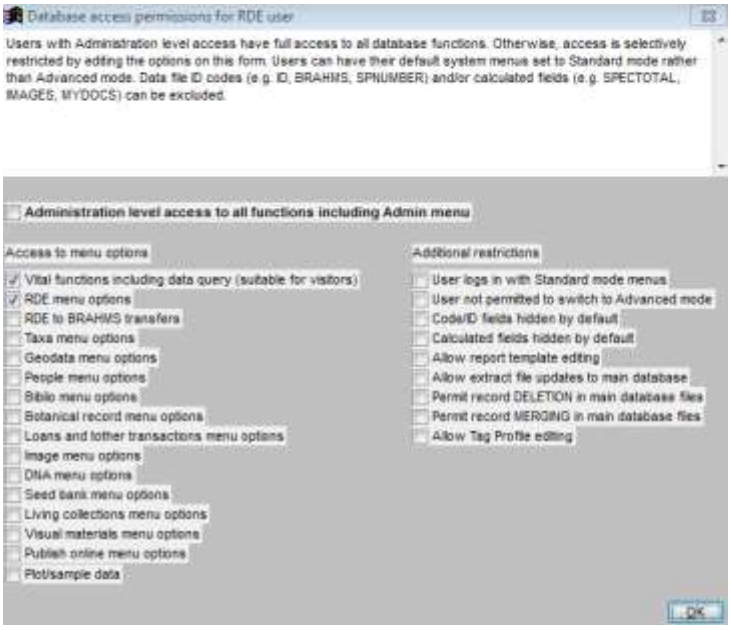
Each listed user can be assigned database access permissions. This is only important on networked systems with multiple users. If you are using your own research database, you would always have full admin level access. Access groups, discussed further in the BRAHMS help file, enable database administrators to select which options each user can access. The entry 'ALL' provides unrestricted access to all database options.



System users and passwords [c:\brahms6\users\users.dbf (alias= USERS)]

tag	del	id	name	password	short user id	access groups	editusers	localpath	myherb	remember	standard	myfields (_xx
*		1	Administration	*****	Admin	ALL	*	c:\tempfiles-brahms-1	K			
*		2	RDE user	****	RDE	VR	*	c:\tempfiles-brahms-2	K			

- Select the new record with your user name and click the **Access** extra toolbar.
- Remove the tick from the **Administration level access** box.
- On the displayed form, you can select the various user permissions.
- Now tick the **Administration level access** box AGAIN to ensure you have maximum access. The ACCESS GROUPS field will display 'ALL'.



Users with Administration level access have full access to all database functions. Otherwise, access is selectively restricted by editing the options on this form. Users can have their default system menus set to Standard mode rather than Advanced mode. Data file ID codes (e.g. ID, BRAHMS, SPNUMBER) and/or calculated fields (e.g. SPECTOTAL, IMAGES, MYDOCS) can be excluded.

☐ **Administration level access to all functions including Admin menu**

Access to menu options

☑ Vital functions including data query (suitable for visitors)
☑ RDE menu options
☐ RDE to BRAHMS transfers
☐ Taxa menu options
☐ Geodata menu options
☐ People menu options
☐ Biblio menu options
☐ Botanical record menu options
☐ Loans and /other transactions menu options
☐ Image menu options
☐ DNA menu options
☐ Seed bank menu options
☐ Living collections menu options
☐ Visual materials menu options
☐ Publish online menu options
☐ Plot/sample data

Additional restrictions

☐ User logs in with Standard mode menus
☐ User not permitted to switch to Advanced mode
☐ Code/ID fields hidden by default
☐ Calculated fields hidden by default
☐ Allow report template editing
☐ Allow extract file updates to main database
☐ Permit record DELETION in main database files
☐ Permit record MERGING in main database files
☐ Allow Tag Profile editing

Access permissions screen. In this example, user access is restricted to RDE and the user is unable to switch to Advanced mode. All users have Vital functions.

Software speed on networks

Inconveniently slower speeds are sometimes encountered on certain types of local network when running BRAHMS in multiple user mode. The slow speeds can be noted when using data grids, usually in the main species and people files but potentially elsewhere. Slower speeds are not noted in single user mode or when using RDE, even on the same network.

A typical networked installation of BRAHMS will have the software and database folder installed on a shared drive – e.g. N:\BRAHMS\BRAHMS7 and N:\BRAHMS\BRAHMSDATA-MYDATA\DATABASE. Several workstations will have access to these folders. The tempfiles-brahms folders are normally stored on the local workstation – e.g. C:\TEMPFILES-BRAHMS-A.

The symptoms of slow speed in multiple user mode are a) slow opening of files to display data grids b) a general stickiness of the cursor moving within the grid c) slow tag and filtering functions d) slow Fastsort operations.
If you encounter such problems, you can greatly speed up BRAHMS performance in general by selecting some or all of the following options:

Field views:

Using field views to reduce the number of columns displayed in data grids speeds up performance. Files such as the species file include many fields that you will not need day to day. Create a field view (using the ▦ toolbar) that removes these. You can probably reduce the number of fields by at least 50% without the loss of routine editing tasks. Note that you can set your preference on Utilities > My setup/profile > Data grids > Restore last used field view.

Disable dynamic formatting:

Dynamic formatting is when a row colour or font is edited in relation to something in that row, for example a different colour when a record is tagged. This formatting can slow up speeds are you can experiment by disabling one or more of these options by choosing:

- Utilities > My setup/profile > Data grids > Highlight tagged records : de-select
- Utilities > My setup/profile > Data grids > Disable strikeout font : select
- Utilities > My setup/profile > Data grids > Do not highlight accepted names: select

Private fields

The use of private fields (fields that can only be seen and/or edited by selected users) can cause a slowing of grid opening. See Admin > Project configuration > System wide settings > PrivateFields.

MY NOTES