NVS Express:

Summary and Analysis software

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NVS Express Interface Version: 1.18.0

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Shirley Vickers, Susan Wiser, Nick Spencer, Hamish Maule, Hazel Broadbent, Anna Marburg, Sarah Richardson, Graeme Hall, Elise Arnst

Manaaki Whenua – Landcare Research

Reviewed by:	Approved for release by:

Manaaki Whenua – Landcare Research

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NOTE TO ALL USERS OF THIS SOFTWARE

Although this software has been tested, we cannot guarantee that it is bug-free. If you find bugs please contact us at: nvs@landcareresearch.co.nz

We also welcome suggestions for future enhancements.

The Validation and Temporal Trends routines are slow and you will need to be patient when you run them. We are working on improving performance.

1   Introduction

The plot-based vegetation data stored in the National Vegetation Survey (NVS) Databank can offer unique insights into vegetation distribution and dynamics over regional and national scales. The NVS team have developed a freely available software package called 'NVS Express' which is specifically designed for the purpose of entering and analysing permanent plot and Recce data which has been collected using standard methodology (as per Hurst & Allen 2007a & b). This manual contains instructions on using the analysis module of NVS Express (hereafter referred to as 'NVS-Analysis') to validate and assist with the summary and analysis of these data. NVS-Analysis is a Windows-based program, designed for ease of use and interpretation of data. It is similar in appearance and function to the NVS Express data entry module (hereafter referred to as 'NVS-Data Entry'). Terminology in this manual follows that of the manual for NVS-Data Entry (formerly known as NVS Lite; Vickers et al. 2018). Users of NVS-Analysis are expected to be familiar with NVS-Data Entry.

NVS-Analysis contains functions to validate, summarise, and analyse data stored in the standard NVS-Data Entry formats. NVS-Analysis can also convert both raw data and processed results into a range of formats for export. Data summaries are produced in tabular and graphical form. Basic temporal trend analyses can be performed. NVS-Analysis provides analysis routines for the following dataset types:

- Recce – records total species composition and abundance within height tiers

- Diameter – records diameter of individual trees by species

- Sapling – records density of saplings within subplots by species

- Seedling – records density of seedlings within height tiers within subplots by species

The target audience for NVS-Analysis is conservation practitioners (e.g. Department of Conservation or regional council staff), resource management and biodiversity consultants, policymakers, and any others who measure and monitor vegetation using standard plot-

based methods. NVS-Analysis will help these people summarise and better understand their data, without having to use advanced statistical packages.

NVS-Analysis was developed by Landcare Research, based on G.M.J. Hall's DOS-based 'PC packages', PC-RECCE, PC-DIAM and PC-USTOREY (Hall 1992, 1994a and 1994b, respectively) which were extensions of Allen & McLennan (1983).

2 Getting Started

2.1 Installation

NVS –Analysis is included in the NVS Express tool. The NVS Express installation package can be downloaded via the Internet (see http://nvs.landcareresearch.co.nz/Data/dataentry). NVS Express is a Windows application and will run on Windows 2000 and above.

Users need to register and log in to the NVS Databank before being able to download NVS Express. A valid email address and self-selected password are needed for registration. Registration allows us to notify all NVS Express users when new versions of NVS Express or the authority lists are available, and also means that the NVS Databank is ready to accept data deposits uploaded via the NVS website.

In some cases NVS Express may be available from your organisation's computer support staff. Please contact the appropriate support person in your organisation to find out how to get the application installed (e.g. Department of Conservation staff should contact their network system administrator).

Any previous version of NVS Express must be removed before a new version can be installed. In a network environment, NVS Express must be installed directly on all local drives of those computers from which it will need to be accessed.

- The NVS Express tool requires that the Microsoft .net framework is loaded on your computer. If the .Net framework is not present on your computer you will be asked to download this as part of the installation process.

- The installation package contains the file 'setup.exe'. This is the application file. Double-click on this file and accept the default options to install NVS Express to the default Program files folder. To install NVS Express elsewhere, navigate to the appropriate folder.

- When installation is complete, a shortcut icon will be added to your desktop, if not, navigate to the folder to start the application or save NVS.exe as a shortcut to the

desktop or pin the program to the start menu. The default location for the application is at C:\Program Files (x86)\Landcare Research\NVS Express.

2.2   Location of NVS Express project files

The NVS-Analysis module of NVS Express operates on data stored in the NVS-Data Entry module of NVS Express. NVS Express projects are stored as files on the hard drive of the computer. Analysis can be performed on project files that users have created themselves using NVS-Data Entry (Vickers et al. 2018) or those that have been downloaded from the NVS Databank. However if analysis is to be performed on multiple projects at once then all but one of them must have been downloaded from NVS Databank, in order to have distinct IDs. It is also advisable to upload projects to the NVS Databank before beginning data summaries or analyses, to gain the full benefit of validated data.

Project files are stored locally on the same computer where NVS-Data Entry is installed and can be found by viewing the project list in the NVS-Data Entry tool. See the NVS-Data Entry manual (Vickers et al. 2018) for more information about finding, navigating, and selecting NVS-Data Entry projects (see Glossary). Both new project files created by the user and those imported from the NVS Databank will automatically be saved into the correct location for NVS-Analysis to access.

If you receive data as NVS Express project files you need to put these files in the correction location so that the tool can recognise them. This location is ... Documents\NVS Projects. Note that although these files have the extension .mdb, you will not be able to open then using MSAccess. NVS Express projects can only be recognised by NVS Express, although the data can be exported into other formats from the program.

CAUTION: If you move between computers you also need to move all the NVS projects and associated party data that you want to analyse and they need to be loaded into the subdirectory C:\ Documents\NVS Projects.

NVS Express projects are stored as files on the hard drive of the computer used for data entry. This means that it is recommended that only one computer is used for entering data for any particular project. If it is necessary to move NVS Express project files onto another computer, you will need to move the project file (with extension .mdb) found at:

........Libraries\ Documents\NVS Projects\

and the party data, usually found at:

C:\Program Files\Landcare Research\NVS Express\Resources\ NVS_PartyData.mdb

Ensure that the NVS Express program is closed before moving these files. Note that these programs are only recognized by the NVS Express program and cannot be opened directly. If you wish to use the data in another program you will need to open the file in NVS Express and export it in a suitable file format.

2.3   NVS Express program updates

Periodic updates to NVS Express authority data are needed to update default methods and species code lists. Updates will be periodically released from the NVS Databank to registered users of NVS Express.

- Updates will be installed onto local versions of NVS Express via the file called 'NVS_AuthorityData.mbd'.

- Select 'Import Authority Data' from the File menu, and navigate to the folder in which you have saved the updated 'NVS_AuthorityData.mbd' file from the NVS Databank.

2.4   Running the program

NVS Express opens at a Main form. This is the launch point for all other operations including data entry, validation, and the analysis features. The form has five pages or sections that are accessed by clicking the tabs located on the lower left-hand side. Select the Analysis tab and a page resembling the following will appear:
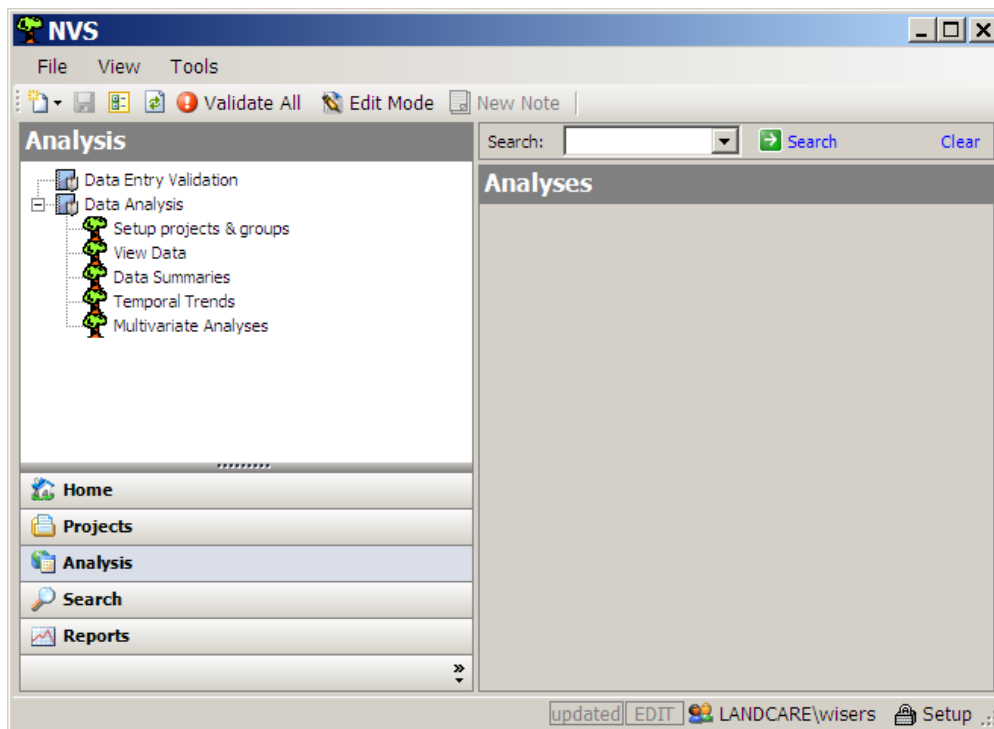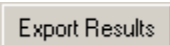
2.5 Global options

Several options are common to all the analyses. These may be selected at any point in the Analysis program where they appear:

Export Data Allows the user to export data in a range of selected formats, e.g. delimited text files, Excel spreadsheets, the PC-Packages, CANOCO, to a user-defined destination. This option is described in more detail is section 4 below.

Select Used to select projects or files that have been created by NVS-Analysis.

Analyse Clicking this button runs the chosen analyses.

Export Results After processing data, this option allows the user to export the results as delimited text files or Excel spreadsheets.

3 Data Entry Validation

High data quality is dependent on effectively identifying mistakes and sensibly correcting them (Wiser et al. 1999). NVS-Data Entry validates many fields at the point of entry, but additional validation rules can be applied once data entry is complete. Historical data downloaded from the NVS Databank will not necessarily have been through such extensive data validation. In any case, no downloaded data is guaranteed to be error-free and it is up to users to decide whether they want to use the data and what error-loading they think they can tolerate.

To ensure data is as error-free as possible NVS-Analysis includes options for validating datasets and these can identify any errors that will cause data summaries or analyses to fail. From the Analysis page, select the 'Data Entry Validation' option in the 'Analysis' menu (on the left-hand side of the screen below) and the 'Data Entry Validation' window will appear on the right-hand side. All the data within a particular project file can be checked at the same time.

Use the 'Select Project' button to select the project and methods (see Glossary) to be validated. The project name will appear on the top of the screen and a list of all the methods used in the project will appear in the left-hand window.
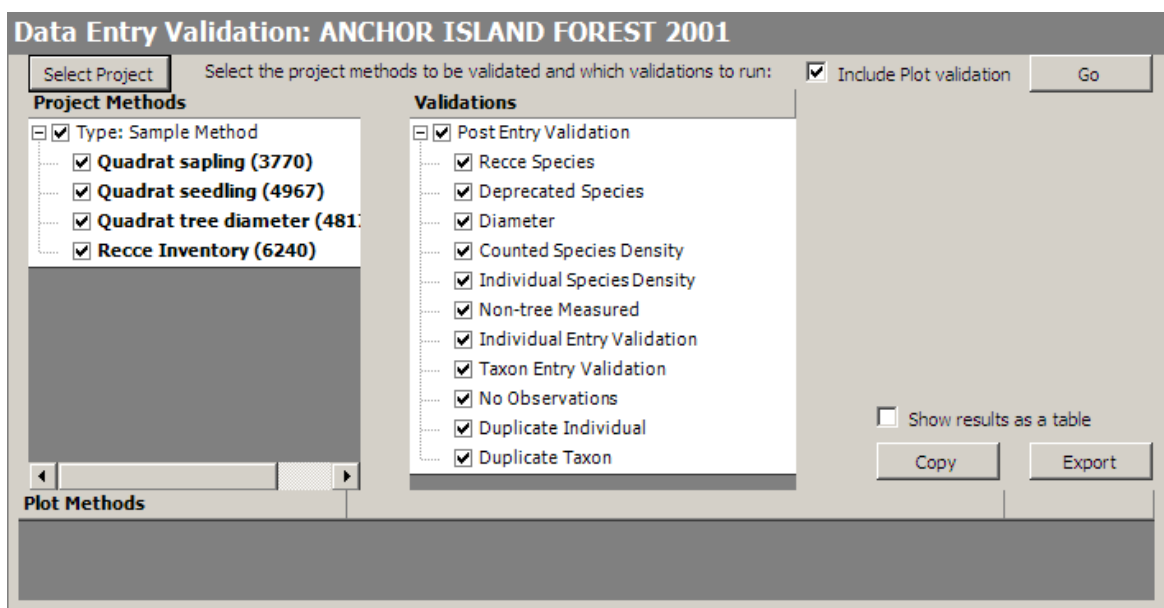
By default all project methods and all validation tests are selected – unselect any that you do not wish to run.

By default, the Include Plot Validation checkbox will be selected. This option repeats the validations done on plots during data entry and reports any warnings (not errors as the data would not have been allowed to be saved if it had errors). This includes validation of number

ranges (values that seem high or low), missing values, dates, plot area vs dimensions, coordinates, etc.

Click on the 'Go' button.

Validation can take some time, particularly for large datasets, so go make yourself a cup of tea or check your email.

When validation is completed, the results are displayed at the bottom of the form:
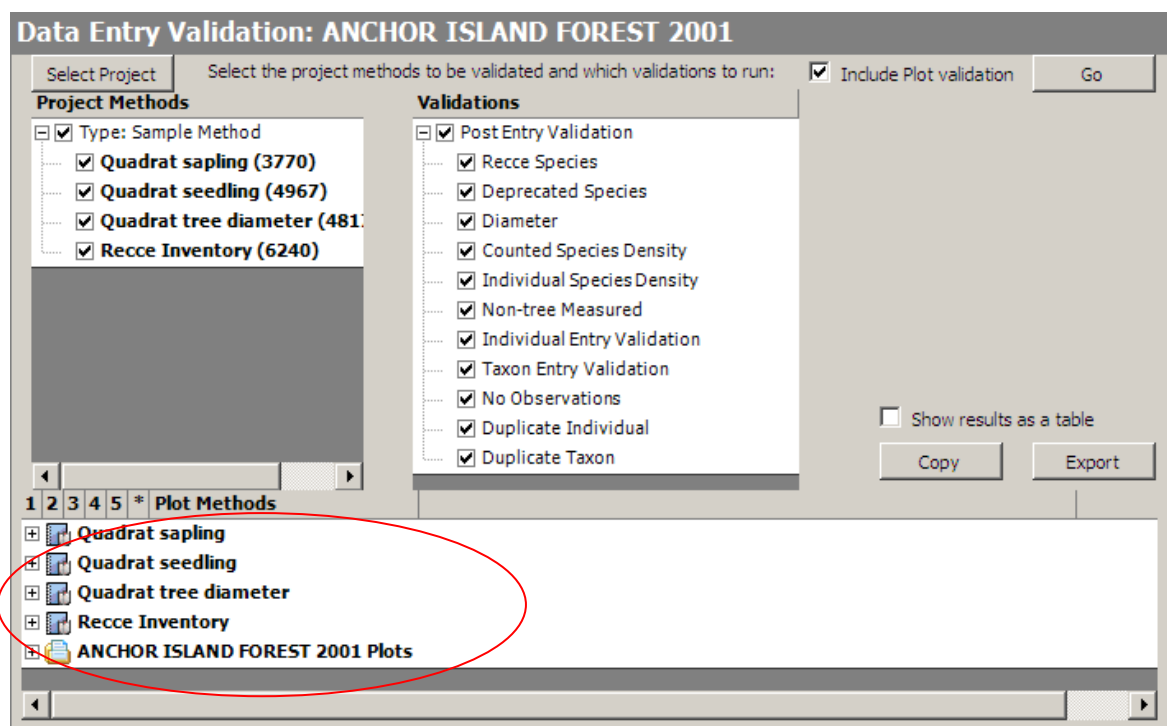
Expanding the node for any plot method will display a sorted list of any plots in the dataset that have a warning, and similarly expanding a plot node will display a list of sub-plots with warnings. You can then view the specific warning messages under each plot. If the 'Include Plot Validation' checkbox is ticked, there may also be a node for plot validations.

If the dataset is one of your own, you can immediately correct data errors by double-clicking on the plot or subplot node. If the dataset has already been uploaded to the NVS Databank, please let us know so that we can correct any errors in this version of the data. The NVS-Data Entry form for editing that method is displayed for the plot (see Vickers et al. 2018):

Errors and warning are highlighted immediately in the data.

The Validation window displays immediately (before editing) – some validations relate to missing rows that, as a consequence, cannot be highlighted.

After closing the Entry form, the post-entry validation of that plot and method is repeated and the display is updated.

Remember to upload your corrected dataset into the NVS databank for secure storage.

If the dataset is not your own or you are unsure how to proceed, contact the NVS Databank Administrator (nvs@landcareresearch.co.nz).

By ticking the Show results as Table checkbox the validations results are displayed in a table, which useful for sorting and looking at validations in groups.


ErrorLevel	Error Title	Error Description	Messages	SampleMethodID	MethodName	ParentPlotObsID	ParentPlotname	Plotname
0	Non-tree Measu...	Species entered ...		3770	Quadrat sapling	4539	4	E
0	Non-tree Measu...	Species entered ...		3770	Quadrat sapling	4539	4	L
0	Non-tree Measu...	Species entered ...		3770	Quadrat sapling	4539	4	L
0	Verbatim species...	Verbatim code C...		3770	Quadrat sapling	4539	4	L
0	Non-tree Measu...	Species entered ...		3770	Quadrat sapling	4541	6	H
0	Non-tree Measu...	Species entered ...		3770	Quadrat sapling	4541	6	I
0	Non-tree Measu...	Species entered ...		3770	Quadrat sapling	4543	8	I
0	Non-tree Measu...	Species entered ...		3770	Quadrat sapling	4543	8	P
0	Verbatim species...	Verbatim code C...		4967	Quadrat seeding	4539	4	10
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	J
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	O
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	H
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	H
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	I
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	I
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	C
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	C
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	C
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	P
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	P
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	K
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	A
0	Item Obs missin...	Item Obs has mi...		4817	Quadrat tree dia...	4543	8	N

A complete list of Data Entry Validation errors, and recommendations on how to solve them, is provided in Appendix 1. You can exit Data Entry Validation by closing NVS Express or by choosing a new menu option.

4   Exporting Data

Before or after analysis, raw data can be exported from any screen within NVS-Analysis.

- **Data Selection:** The whole project can be downloaded or data can be selected by plot and/or method:

- To export all data from a project, right-click on the dataset name in the Projects column and select 'Export Project data'
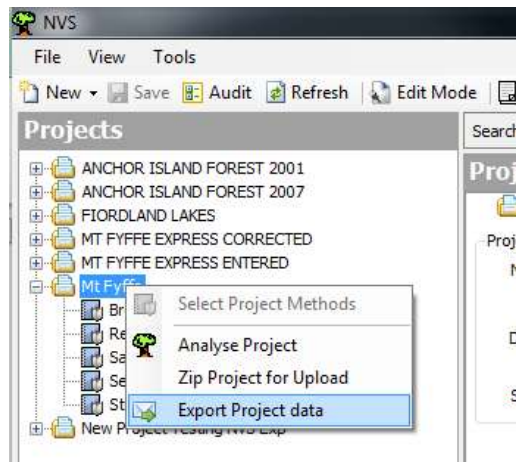
- By Plot -To export data from a single plot, click on the project name in the Projects column, right click on the plot name under the Plots tab and select 'Export data for Plot: x'. The export form has a Use Plot Group checkbox showing the name of the selected plot, ticked by default. To export a subset of plots create a plot group in the analysis tab (see NVS Express analysis manual).

- By Method- To export data from a single method for all plots within a Project, right-click on the method in the Projects column and select 'Export Sample Method data'.

- To export data from a single method from a single plot, click on the method in the Projects column, the plots that have that method will appear under the plots tab, right-click on the plot and select 'Export data for x method (plot: x)'

- Data can be exported for multiple projects and by using the Export function from within the Analysis tab.

- A form will appear:

- Using this form you can choose to export all the data in the project (if you've chosen the export from the whole project option) or by ticking & unticking boxes, limit your export to only that data you are interested in.

- Adding a method keyword to the Method field in the data selection box will limit the exported data to the method containing that keyword, e.g. 'debris' for coarse woody debris.

Table Types:

Tables are grouped into Project data, Plot data and Vegetation data.

- Table types for which the project has no measures are not listed for export.

- Tables types which are selected but have no data entered will be excluded from the results.

- Checkboxes can be used to select or unselect tables individually or by group, to change the default selections.

- The table type of each method in a project is shown in the Type column of its Measures (in the description tab). For example seedling and sapling methods have type Taxon Simple Value.

Formats:

Options for the format of the exported data are also given.

Column Formats:

- For the main three formats data is exported in columns:

- CSV produces one comma-delimited text file per table/dataset

- TXT produces one tab-delimited text file per table/dataset

- Excel produces a single excel file with one worksheet per table/dataset

- The 'Zip results' option puts all exported files into a single ZIP file. This option is the default for CSV and TXT files.

- The 'Cross-tabulate' option affects Vegetation data only. With cross-tabulation tables are formatted like a plotsheet:

- one row per observed species or individual

- a column for each tier, each attribute, and each diameter or orthogonal width.

- Since tiers and attributes can differ between methods, each sample method is exported as a separate file or worksheet.

- Without cross-tabulation tables are exported as they are stored in the database:

- one row per observed value (cover class, count, diameter etc).

- a single column for each type of value (usually only one, except two widths for orthogonal width)

- each table contains all datasets of that type, such as seedling and sapling together in TaxonCategoryValue, with columns to identify the dataset ID and method name.

- attributes must be exported separately

Other Formats
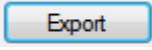
Other export formats are for special purposes

- Formatted:

- Plotsheet/Species List produces an excel file with one worksheet per table type.

- For diameter and orthogonal with methods, the plotsheet lists tagged individuals.

- For aggregate methods:

- NVS Express

- PC Packages

- Intermediate Files –These are only used when exporting for multivariate analysis (see the NVS Express: Summary and Analysis software manual).

Other Documents

- The option to **Include NVS documents and Definitions** adds three standard documents to the export:

  1. NVS Data Use Protocol,

  2. NVS Terms of Use and Copyright Statement,

3. Read Me

- It also adds a file containing definitions of all tables and columns that were exported. The **Detailed Definitions** option determines whether dataset-specific information is included, such as the definitions of each tier.

- **Exporting:** Once you have chosen your options, click the Export button [Export], navigate to where you want to save the exported file then click Save. If you've chosen to export the data as non-zipped .csv or .txt files, each method will export as a separate file. A confirmation message box will appear once the export is complete.

5   Data Analysis Overview

NVS-Analysis is composed of five major utilities:

Setup Projects & Groups – This page is used to select projects for viewing and analysis.

View Data – This page allows the user to view raw site description and vegetation data.

Data Summaries – This page allows the user to analyse site and vegetation data and to produce one-way, two-way and three-way tabular and graphical summaries.

Temporal Trends – This page allows the user to investigate changes in the data when plots have been remeasured.

Multivariate Analyses – Also known as community analysis, this page allows the user to create intermediate files which can then be used in analysis software.

6   Set up projects and groups

Before you can begin to analyse data, you must first select the dataset you plan to use. Within NVS-Analysis there are two ways to do this: by Selecting projects from a list or by Importing a project set file that you exported in a previous session.

Clicking on the Setup Projects & Groups node initiates the selection process:
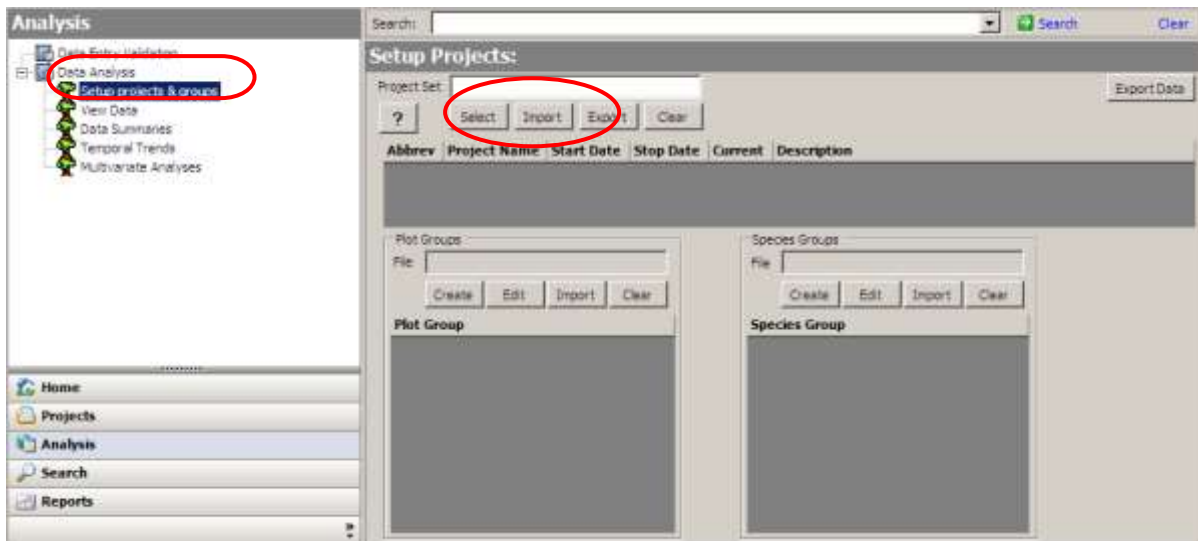
To set up a new analysis:

1.   Click on the Select button (or type Alt + s).

2.   The Select Project box will appear displaying a list of projects stored on your computer:
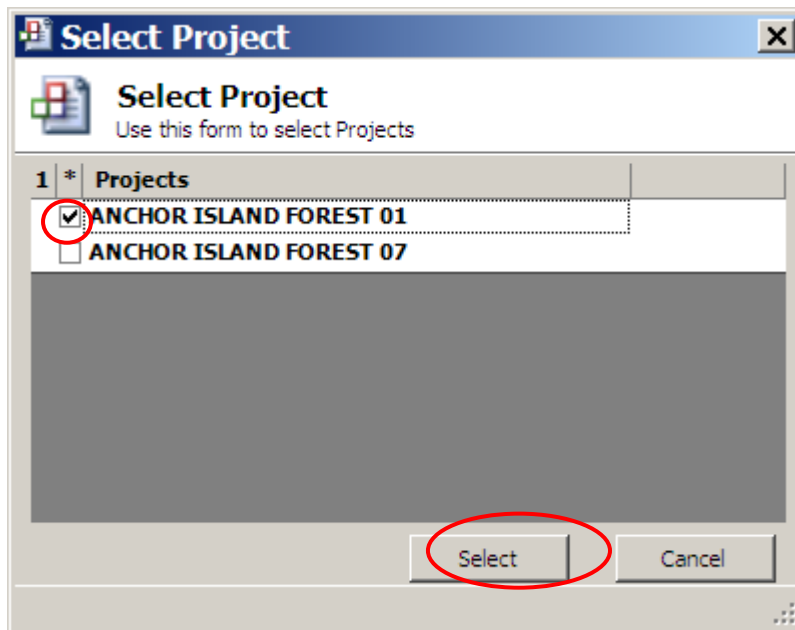
3.   Tick the checkbox to the left of the required project/s and click on 'Select'.
        Alternatively, double-click a single project to select it.

This process makes the data available to the NVS-Analysis program as indicated in the **Project Set** list. The **Project Set** name is defaulted from the first project selected, but it can be changed by typing the new name in the **Project Set** box.

To resume working on an analysis that was saved from a previous session use the **Import** button to search for the file containing the project set for that session (see **Export** below).

Analysis can also be initiated from the Projects tab (outside NVS-Analysis):

Right-click on a project name (in the list of projects) and choose 'Analyse project' from the menu. That project becomes the project set.

6.1 Options in the 'Setup Projects' window

Once projects have been selected for analysis there are several options available. These include changing whether projects are 'Current' (see below) and specifying plot or species groups. You may also Clear all projects from the project set or Export a file containing the Project Set.

Analyses involving trends over time require projects in the Project Set to be marked as either Previous (first measurement period) or Current (second measurement period, i.e. the

repeated measurements). By default, all projects are marked as Current – click in the Current column to untick a project and thus mark it as Previous. Make sure only one project is marked as Current. Data Summaries and Multivariate Analyses can be done on either the Current or Previous projects (if any) in the Project Set.

Note that **<u>only two</u>** measurements can be compared for temporal anlysis.

Warning: A project set can only contain multiple projects if all but one of the projects have been downloaded from NVS Databank, in order to have distinct IDs. For trend analyses, all of the projects must have been downloaded, in order to have plot and stem IDs that can be matched.
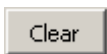
Clear   This removes **<u>all</u>** projects from the Project Set.

Export   This exports the Project Set to a file that holds the identifier details (but not the underlying data) of the project/s currently in the set. The next time you wish to work on this set, you can use the **Import** command to load the projects into the Project Set list.

6.2   Plot and Species Groups

Plot Groups and Species Groups are lists that define a classification of plots or species within your selected projects. They are used throughout the package as input to the analyses, which make use of groups in different ways to sort or subtotal the data. Setting up and using groups is optional. Groups that are set up can be temporarily disabled at any time, and can be stored for later reuse.

Plot Groups may be used, for example, to define groups of plots belonging to the same plant community (as defined by TWINSPAN), or groups of plots subject to different experimental treatments (e.g. exclosures and controls). Species Groups may be used, for example, to separate species that are palatable to browsers from those that are not or to separate indigenous from introduced species.

Creating Plot and Species Group files:

1.   At the bottom of the Setup Projects & Groups page are the panes:
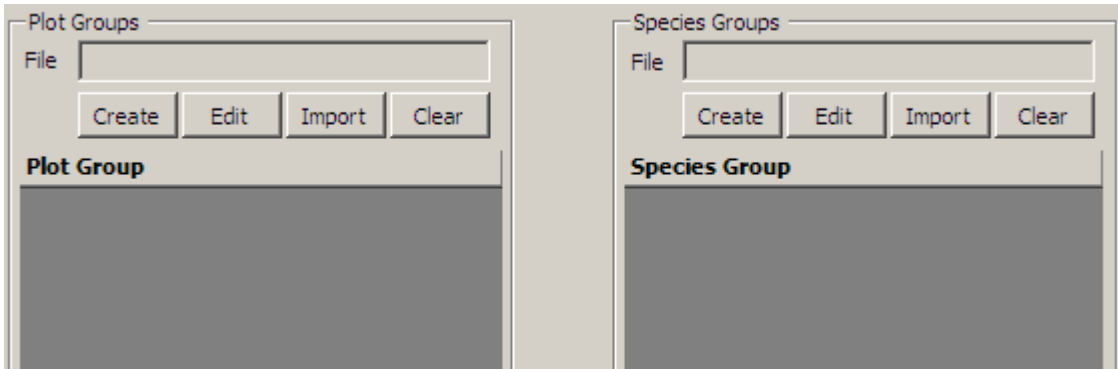
2.   To create a file listing all plots or species within the project set (which can then be edited to create groups), click on the 'Create' button. An 'Export … List' box will then appear, asking where you wish to store the list once you create it. Navigate to the desired folder, name your file (or use the default comprising 'project name' + 'plots.csv' or 'species.csv'), then click 'Save'.

3.   An advice box will appear:
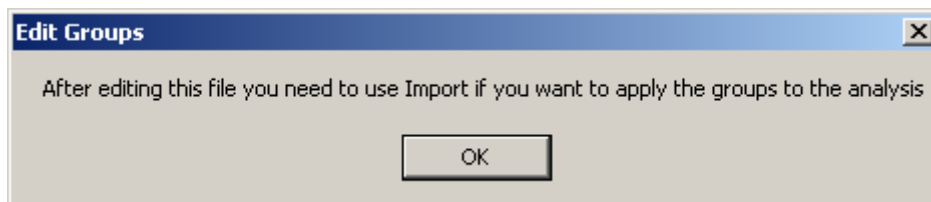
4.   Click 'OK' and an editable .csv (comma-separated values) file will open in Notepad.

For plot groups, both Plot IDs and Plot Names are provided to create a unique identifier for each plot, as combining data from multiple projects may result in duplicate plot names.
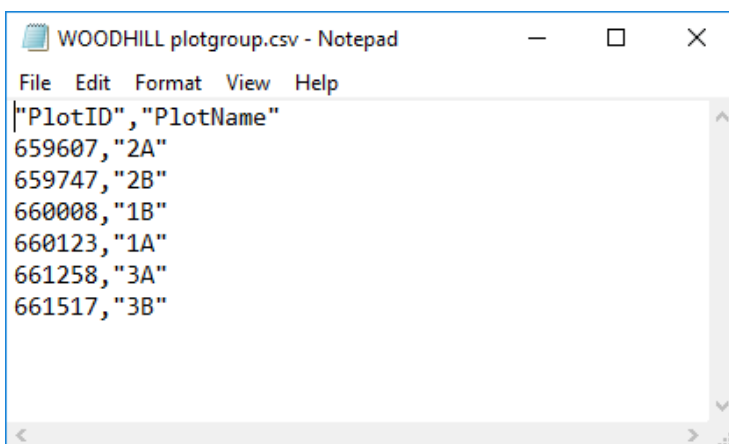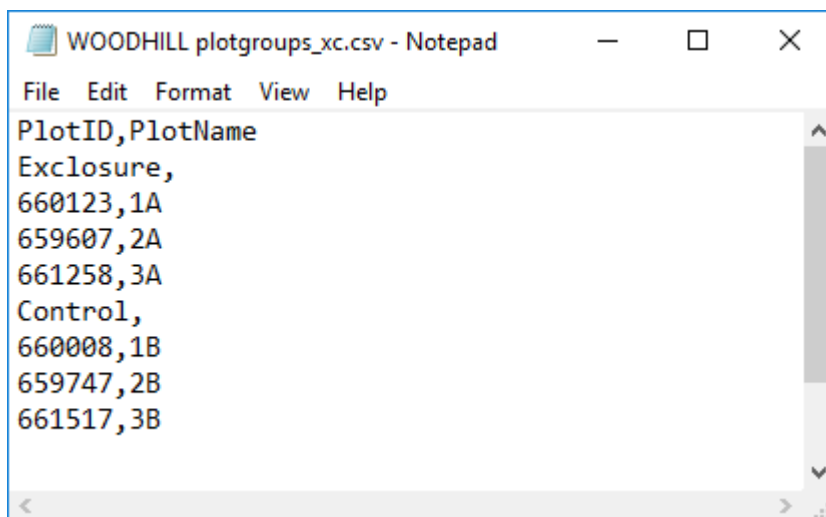
Groups of plots or species are defined by separating them with blank lines or lines containing group names. Blank lines can be inserted, removed or changed with Notepad.

Lines with Plot IDs and Plot Names can also be rearranged, but should not be changed. Anything in the first column of the file not recognised as an ID or Name is treated as a Group Name. If there is no group name after a blank line then a default name of 'Plot Group #' is assigned. To exclude a species or plot from the analysis, delete that line from the file.

Tip: The Plot and Species Groups facilities can be used to delete specific plots or species from the analysis by creating a single group with those plots or species removed.

In this example the entries in the file have been rearranged to form one group for all plots identified with a 'A' as the last character of the plot name and a second group for all plots identified with an 'B' as the last character of the plot name. These groups have been named 'Exlosure' and 'Control' respectively:

5.   Click 'File -> Save' (or 'Save As', if you wish to keep the original file). This will save the modified file.

6.   Close the file, then, as the advice box above suggested, import your file.

7.   The Import button opens the folder in which you just saved a plot group file (otherwise My Documents). If your .csv file is located elsewhere, navigate to the correct folder. Highlight the file you want to use, then click 'Open' to load the plot group file into the current analysis. The Plot Group list will be populated with your defined groups as shown below:
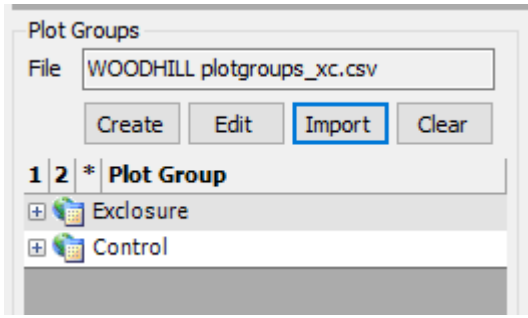
8.   Species Groups can be created in the same way. Note that if you create a species group containing a given species then all of its sub-species, varieties etc. are automatically added to the group during the import (unless they have been specifically assigned to a different group).

If you want to create a species group from the entire NVS list you can download the full NVS species list from the NVS website (https://nvs.landcareresearch.co.nz/Resources/NVSNames) and select only those species you want. The fields "Taxon ID" and "Species Code Current" are required for the Species group file.

7   Viewing data

To view the raw data as digitised from field-sheets, click on the Project Data item of the Data Analysis tree. All standard NVS data collection methods used in the current project are displayed.

Site Description – This contains most of the data recorded on the first page of the Recce field-sheet: Plot name, location and physical features such as altitude, slope, etc.

Recce – This contains the species composition data collected on the Recce survey of the plot: species present, the height tiers they occupy, cover values within height tiers, etc.

Diameter – This contains data pertaining to tagged trees in permanent plots: tree tag, species code, species name, diameter, etc.

Understorey – This contains the data from the understorey subplot measurements, which comprise counts of saplings within subplots by species and counts of seedlings within seedling subplots by species and height class.

The example below displays all data methods used in the project:
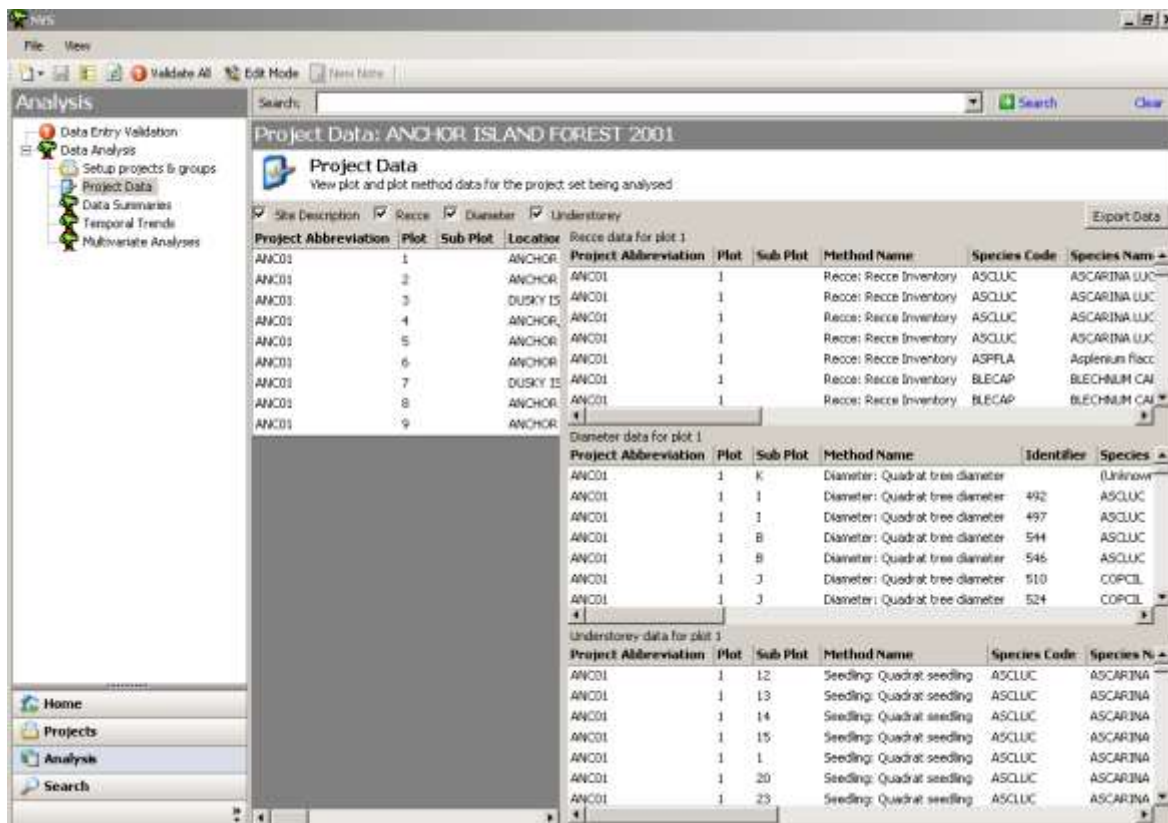
Each method can be added or removed from view by ticking or unticking its checkbox. To view method data for an individual plot, click on its row in the Site Description window. To view method data over all plots, untick the Site Description checkbox. The size of each window can be adjusted, as can the column widths, by using standard Windows techniques.

By right-clicking on a plot or row in any window, you can open a new window to view the data via the data entry template.

8 Data summaries

This comprehensive set of functions allows the user to produce one-way, two-way, and three-way cross-tabulations and summary graphs based on the project data. Summary results depend on the variables selected, the nature of the cross-tabulation (dimensions), sorting and filtering options, and general settings. Summaries may be made across all plots or species, by individual plots or species, or by plot or species groups.

Data Summaries: ANCHOR ISLAND FOREST

Data Summaries
Perform summary analyses on the project set, by data type

Analysis Options
Plots ☐ Use Groups ☐ Analyse by Plot where optional ☐ Prompt for site factor cross-tabs
Species ☐ Use Groups ☐ Use Preferred ☐ At Species level ☐ Prompt for cover classes & tiers
○ Previous Projects ⦿ Current Projects

Export Data
Analyse

1	2	3	*	Analysis	Description
☐ All Analyses					
⊞ ☐ Species Summaries, General					
⊞ ☐ Site Factors					
⊞ ☐ Species by Site Factor					
⊞ ☐ Recce Summaries, Detail					
⊞ ☐ Seedling/Sapling Summaries, Detai					
⊞ ☐ Diameter Summaries, Detail					

Select the summaries you wish to calculate by ticking the boxes next to their name in the **Data Summaries** window. Clicking on the node will expand or contract the list of summaries. You can select just one specific summary, e.g. Site Factors: Ground Cover Percentage, as shown below, or you can select all possible summaries. Ticking a box next to an analysis automatically selects all the summaries nested within it (e.g. Species Summaries, General, as shown below).

Data Summaries: ANCHOR ISLAND FOREST 2001

Data Summaries
Perform summary analyses on the project set, by data type

Analysis Options

| Plots | Use Groups | Analyse by Plot where optional | Prompt for site factor cross-tabs |
| Species | Use Groups | Use Preferred | At Species level | Prompt for cover classes & tiers |

Previous Projects ● Current Projects

Export Data

Analyse

| 1	2	3	*	Analysis	Description
				All Analyses	
				Species Summaries, General	
				Species - Recce	Plot Freq,Plot % Freq,Obs Freq,Obs % Freq BY Species Group
				Species - Understorey	Sub Plot Freq,Sub Plot % Freq,Taxon Obs Freq,Taxon Obs % Freq BY Species Group
				Species - Continuous Cover	Plot Freq,Plot % Freq,Taxon Obs Freq,Taxon Obs % Freq BY Species Group
				Species - Orthogonal Width	Sub Plot Freq,Sub Plot % Freq,Stem Freq,Stem % Freq BY Species Group
				Species - Diameter	Sub Plot Freq,Sub Plot % Freq,Stem Freq,Stem % Freq BY Species Group
				Species - Biostatus	Plot Freq,Plot % Freq,Obs Freq,Obs % Freq BY Bio Status X Bio Status Detail X Species
				Species - Palatability (Forsyth)	Plot Freq,Plot % Freq,Obs Freq,Obs % Freq BY Palatability X Species
				Species - Growth Form	Plot Freq,Plot % Freq,Obs Freq,Obs % Freq BY Growth Form X Species
				Growth Form by BioStatus	Obs % Freq BY Growth Form X Bio Status
				Site Factors	
				Aspect	Plot Freq BY Aspect /d (45 ° bands, with statistics) X other Site Factors (opt)
				Slope	Plot Freq BY Slope (10 ° bands, with statistics) X other Site Factors (opt)
				Top Height	Plot Freq BY Top Height (2 m bands, with statistics) X other Site Factors (opt)
				Physiography Distribution	Plot Freq BY Physiography X other Site Factors (opt)
				Drainage Distribution	Plot Freq BY Drainage X other Site Factors (opt)
				Surface Cover Percentage	Plot Freq,G Cover % Mean AP BY Ground Cover SurfaceCategory X other Site Factors (opt)
				Ground Cover Percentage	Plot Freq,G Cover % Mean AP BY Ground Cover GroundCoverCategory X other Site Factors (opt)
				Plot Ground Cover	G Cover % Mean AP BY Plot X Ground Cover
				Species by Site Factor	
				Recce Summaries, Detail	
				Seedling/Sapling Summaries, Detail	
				Diameter Summaries, Detail	

8.1   Options for running data summaries

Before running summaries, there are a set of universal options you can apply:

Use Plot Groups indicates whether summaries make use of the currently loaded Plot Groups. If this option is greyed out it means that no plot groups have been loaded. Different summaries make use of groups in different ways and some do not use groups at all. In general, if this option is selected, a summary that would otherwise be by Plot will subtotal or sort by Plot Group instead.

Use Species Groups indicates whether summaries make use of the currently loaded Species Groups. If this option is greyed out it means that no species groups have been loaded. Different summaries make use of groups in different ways and some do not use groups at all. In general, if this option is selected, a summary that would otherwise be by Species will subtotal or sort by Species Group instead.

Analyse per Plot where optional indicates whether to produce the summaries by individual plots as well as across all plots, for those analyses which are 'Optional per Plot'.

Prompt for cover classes & tiers results in a window appearing before analyses of Recce data to allow cover class percentages and tier heights to be viewed and the 'Sum Cover Percentages' option to be changed. The default for this option is 'Midpoint' – i.e. the value used in analysis for percent cover is taken from the midpoint of the cover class. If the option is set to 'Lower' then both midpoints and lower values are used in analyses: midpoints are used for cross-tabulation of individual tiers and species, lower values are used when summing across tiers and species. Weights, which are edited in the same window, are used for Multivariate Analyses rather than Data Summaries.
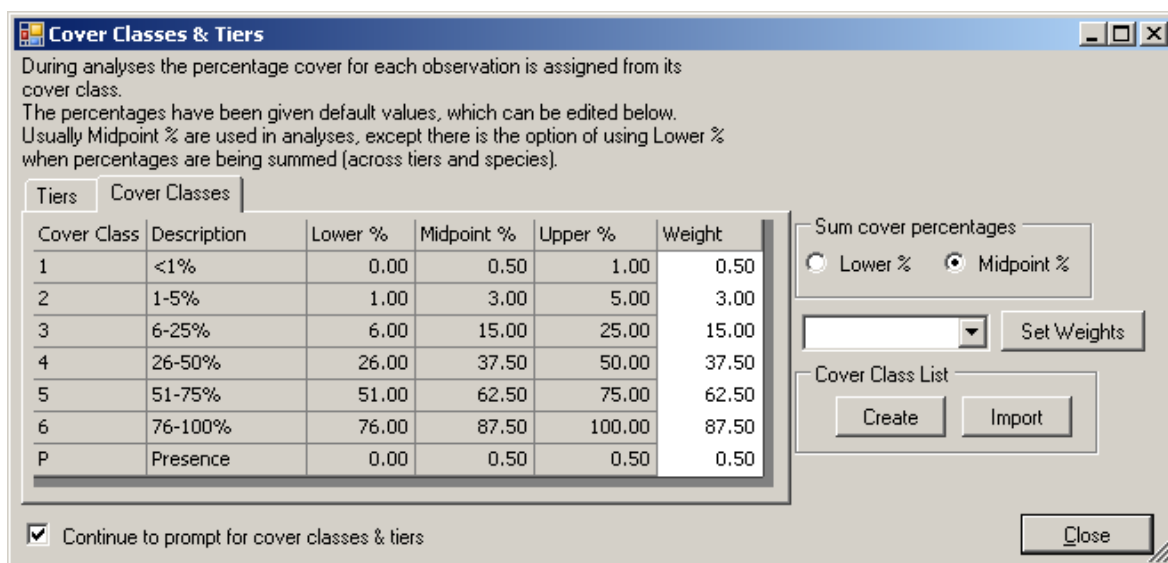

Prompt for site factor cross-tabs applies only to the 'Site Factor' summaries and is described under the Site Factor section.

Current Projects/Previous Projects indicates whether summaries are to use data from Current or Previous projects.

Use Preferred Species assigns current names to species where a one-to-one taxonomic name change has been made since the data was entered (e.g. *Podocarpus ferrugineus* is now known as *Prumnopitys ferruginea*). This is based on information from the Ngā Tipu Aotearoa – New Zealand Plants database (http://nzflora.landcareresearch.co.nz). In summary tables, species which have a preferred name applied are indicated with '*'.

Users can create and use their own preferred species to override the defaults. This is similar to creating plot or species groups as described in section 6.
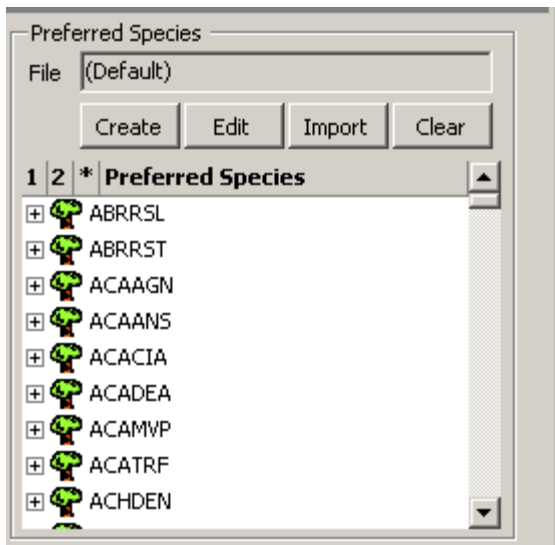
After creating the new file a window will pop up asking if you would like to define your preferred species from a standard list, or only using the species present in the project.
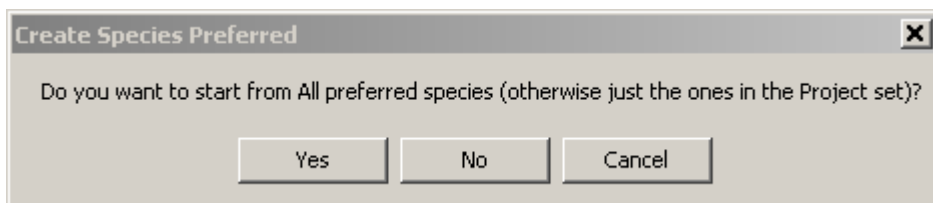
The file will then open and you can make adjustments to the preferred species. Once you have finished, save the file and then import it to apply the new species rules you have created. If you decide you would prefer to use the default list, click **Clear**.

At Species level assigns all subspecies and varieties to the species name. Note that if both 'Use Preferred Species" and "At Species level' are checked then the preferred species function is applied first, i.e. each observation is first switched to its Preferred species and then moved up to Species Level.
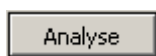
 Clicking this button runs the chosen analyses. Alternatively, double-click anywhere in the list of analyses to run that analysis, or all the analyses below if it is a heading (e.g. Species Summaries). A new window will be opened to display the results.

8.2 Format of data summary displays

The Analysis Results window shows each requested summary as a separate tab at the top of the window. To view a given summary, click on the appropriate tab.

All summary tables share a common layout:

The Project Set name and Analysis name are shown in the top of the left-hand pane ('ANCHOR ISLAND FOREST', 'Species – Recce' in the example above).

The Notes section contains a summary of what data were analysed (number of plots, groups used etc.), how the analysis was done (including default settings used), definitions of abbreviations used in the output, values for coded variables (e.g. cover classes, height tiers), conditions applied to specific columns, where preferred species names have been applied and anything else required to document the analysis.

The Warning button will be active if there are values in the data that may be suspect, such as some plot areas being missing when calculating densities. In non-trend analyses this can be a result of the same plot occurring in more than one project in a Project Set – only the first instance of such plots is included in the analysis. In time series data this can be a result of unmatched plots in the two projects being analysed.

The arrangement in the left-hand column shows the hierarchy of the analysis, usually the species or plots being summarised and any groupings that have been applied. This hierarchy can be fully expanded to any level using the numbers in the top-left corner. The top of the hierarchy shows whether the data is from Current or Previous projects, and from which method (e.g. 'Current - Recce' in this example).

The right-hand columns show the calculated values with descriptive column headers. Overall calculations (across all species in this example) are shown in the top row. If the summary is displayed as a cross-tabulation then the last dimension of the hierarchy is shown as sets of

columns and there are separate columns for overall calculations. An example of this can be seen in 'Species Freq By Tier' Recce summary.

ⓘ **What plant is that?** Placing the cursor on the species code in the species list will bring up the Latin binomial and, if you're working online, double-clicking on the code will take the user to that species' entry in the Manaaki Whenua – Landcare Research New Zealand Plants Database.

## 8.3   Viewing underlying data

Double-clicking or right-clicking on any cell in a summary table will drill down to the underlying data for that cell. From there you can right-click to view the data within the data entry template or to copy the data to the clipboard.

8.4   Options for displaying data summaries

Once the data are summarised there are a range of options to change the appearance of the tables and graphs.

8.4.1   Sorting & Filtering
Each dimension in the analysis hierarchy is sorted alphabetically (if categorical) or numerically, or some analyses are pre-set to sort by values of one of the variables. You can change the sort order by choosing from the 'Sort by' drop-down list. When the summary has more than one dimension, you can use the 'Within' option to further specify the sorting (e.g. sort species by mean cover, separately within each height tier).
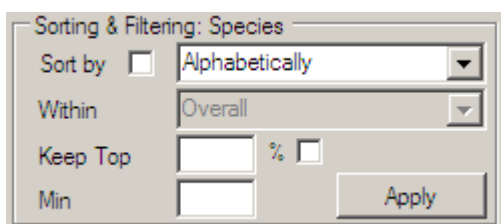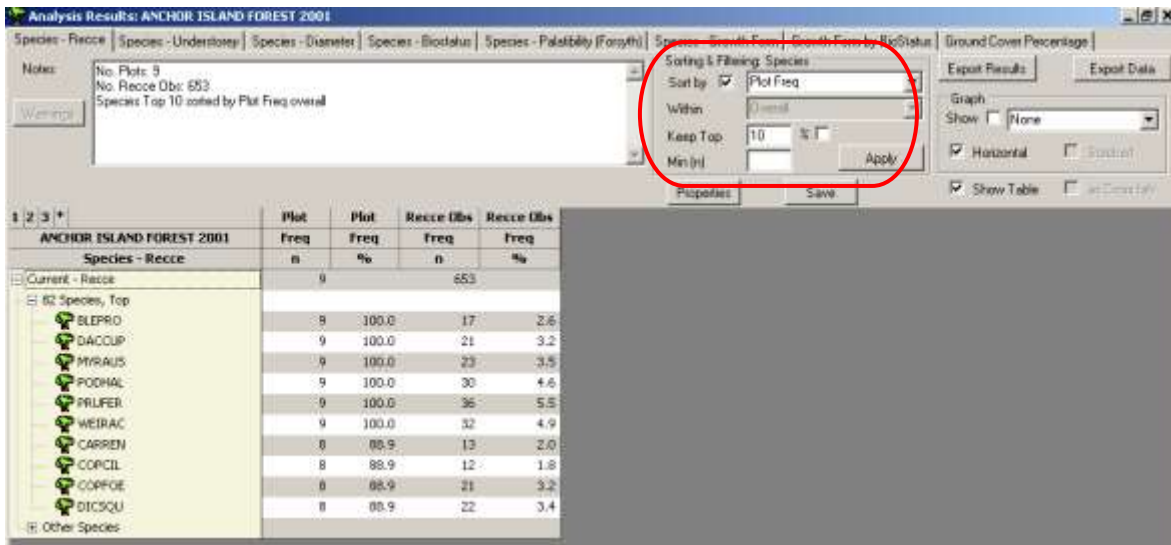
When the summary table has been sorted numerically, it can be simplified to display a restricted range of values. The display can be restricted to a limited number of values (by typing the number of values to display into the 'Keep Top' box), an upper percentage of values (by typing in the percentage amount in the 'Keep Top' box and ticking the **%** checkbox) or to results above and including a specified minimum value (by typing the minimum value required in the **Min** box). The remainder of the data is hidden within the 'Other Species' node at the bottom of the species list.

The example screen shot below shows species sorted alphabetically (default):
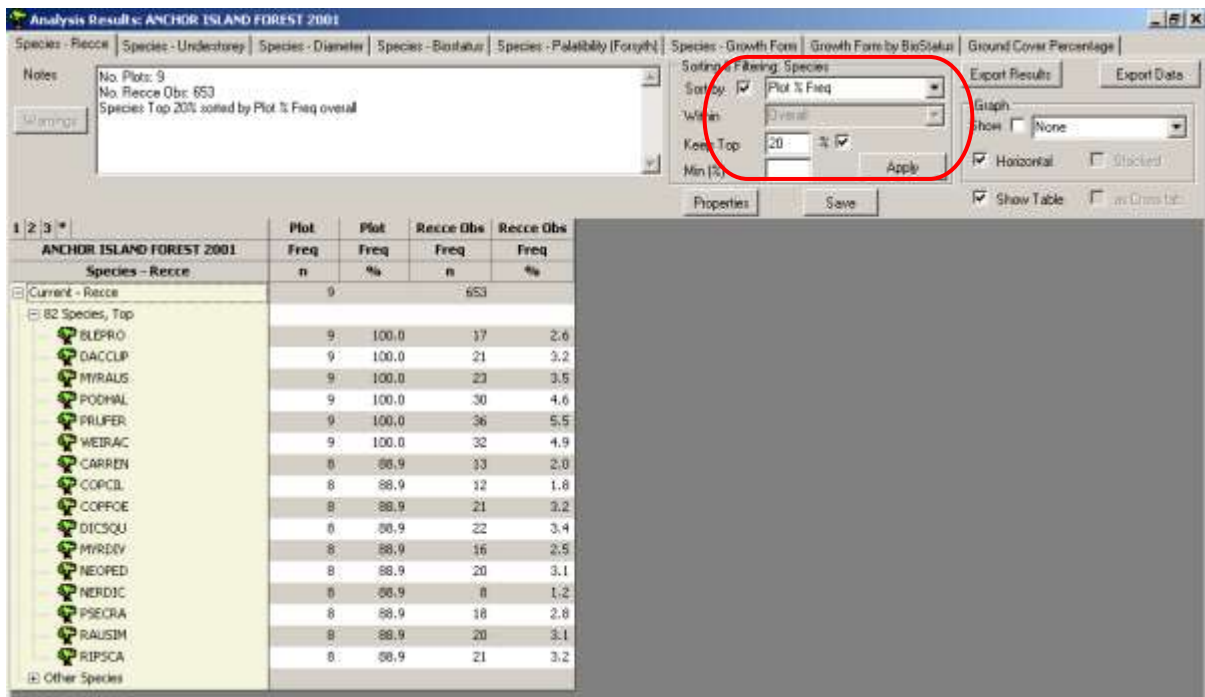

The screen shot below shows species sorted by percent plot frequency (Plot % Freq) and restricted to displaying only the top ten species (Keep Top):

The screen shot below shows species sorted by percent plot frequency (Plot % Freq) with the **%** checkbox ticked, resulting in only the top 20 (Keep Top) <u>percent</u> of species being displayed:

The screen shot below shows species sorted by percent plot frequency (Plot % Freq) with 100 typed in the Min value box, displays only those species with a plot frequency of 100 % (i.e. present in all plots surveyed):
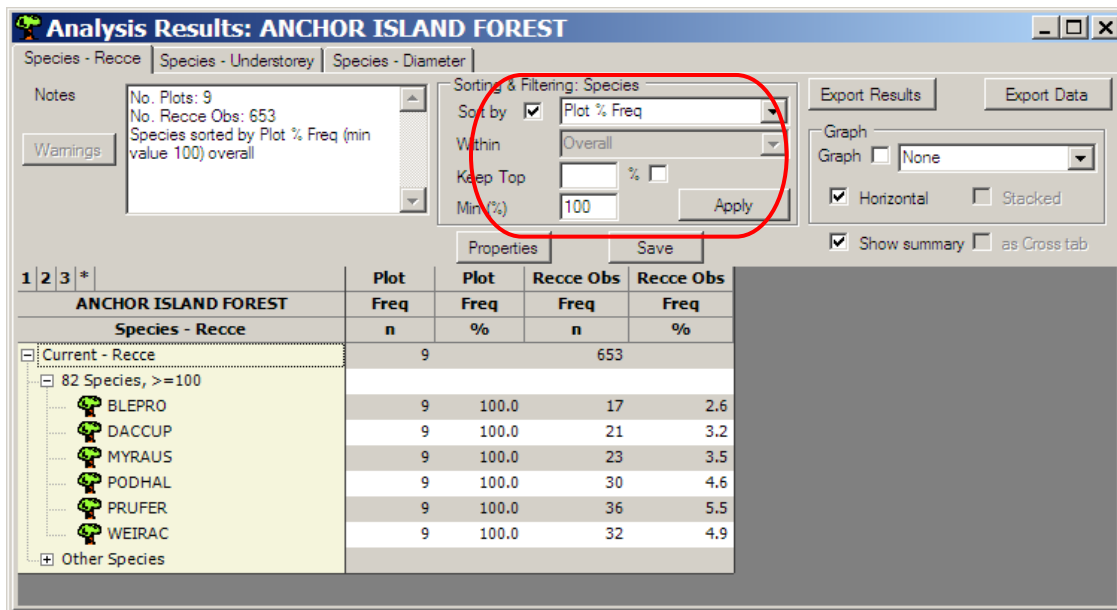
8.4.2   Graph Options

Some analyses are preset to display a bar graph immediately – otherwise tick the **Graph** checkbox or (if there are multiple variables in the analysis) choose from the drop-down menu which column from the table you wish to graph. A shortcut is to click the cell of the top (overall) row of the column you wish to graph once you have ticked the **Graph** checkbox. The left/right arrows can be used to change cells and immediately display graphs of the other columns. When the summary is a cross-tabulation this only works for the first set of columns.

Graphs can display the overall results or, where the summaries are hierarchical, the results for each step of the first level of the hierarchy can be displayed separately. For example in an analysis displaying seedling frequency by plot, each plot can be graphed separately by clicking on it in the hierarchy. You can then use the up and down arrows to quickly graph others.

Graphs can be displayed with the bars either horizontal or vertical and, where the data is cumulative (e.g. tree diameters within size classes), as a stacked bar graph, by ticking the appropriate checkboxes.

The **Graph Options** and **Sort: Species** functions work together in that only the 'exposed' data in the Results table will display as a graph, not that hidden within the 'Other Species' node. Therefore to reduce or increase the amount of data in the graph, you can use the **Sort: Species** options or open the 'Other Species' node.

The relative sizes of the summary table and the graph can be changed by dragging the line between them. To show the graph only, untick the **Show Summary** checkbox. To zoom in on the graph, use the mouse to draw a box around the are you would like to zoom in on. Rick-click and select **Un-zoom** to restore the screen to the previous resolution, or **Undo all zoom/pan** to return to the original resolution.

The example below shows a graph, with vertical bars, of observation frequency of all 82 species recorded in this dataset, sorted by descending observation frequency. Note that it is not possible to display all species codes. The species code associated with an individual bar can be displayed by positioning the mouse over that bar.
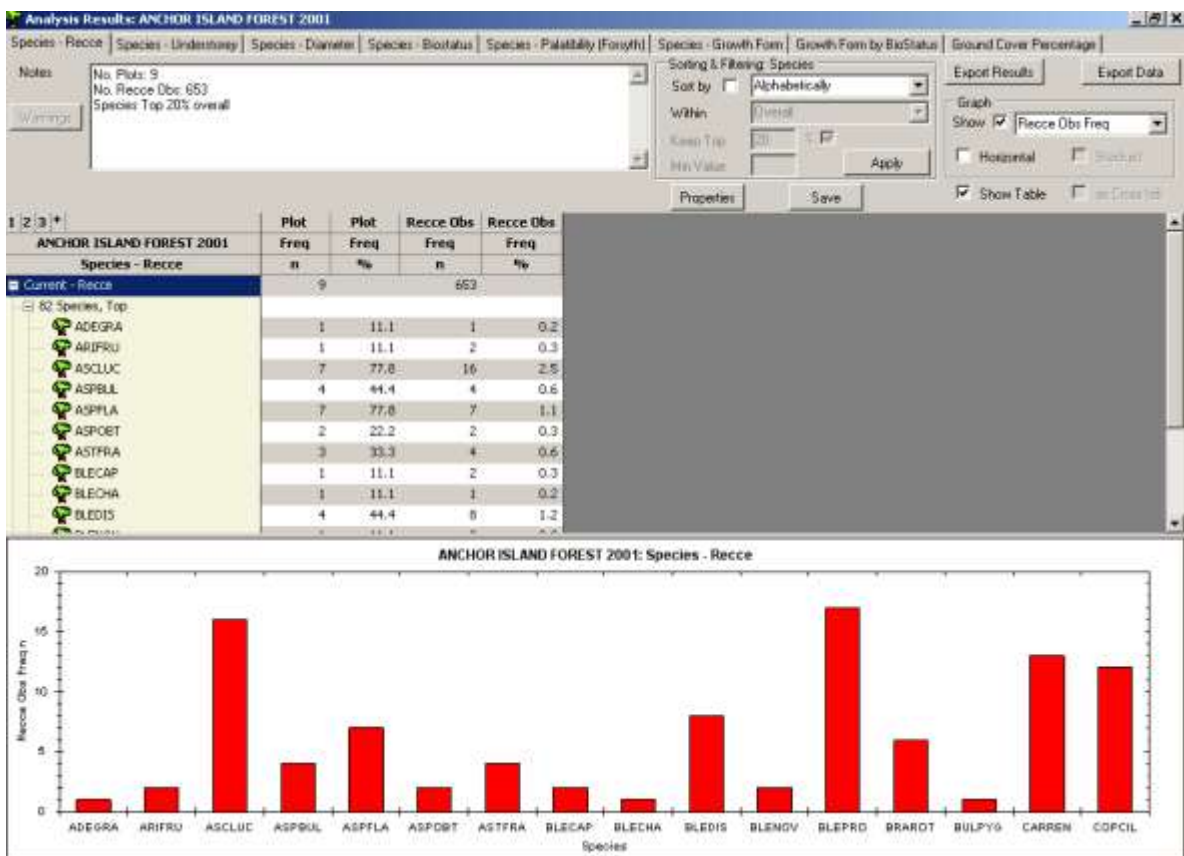
The example below shows a table and associated graph of only the top five species (Keep Top) by observation frequency.
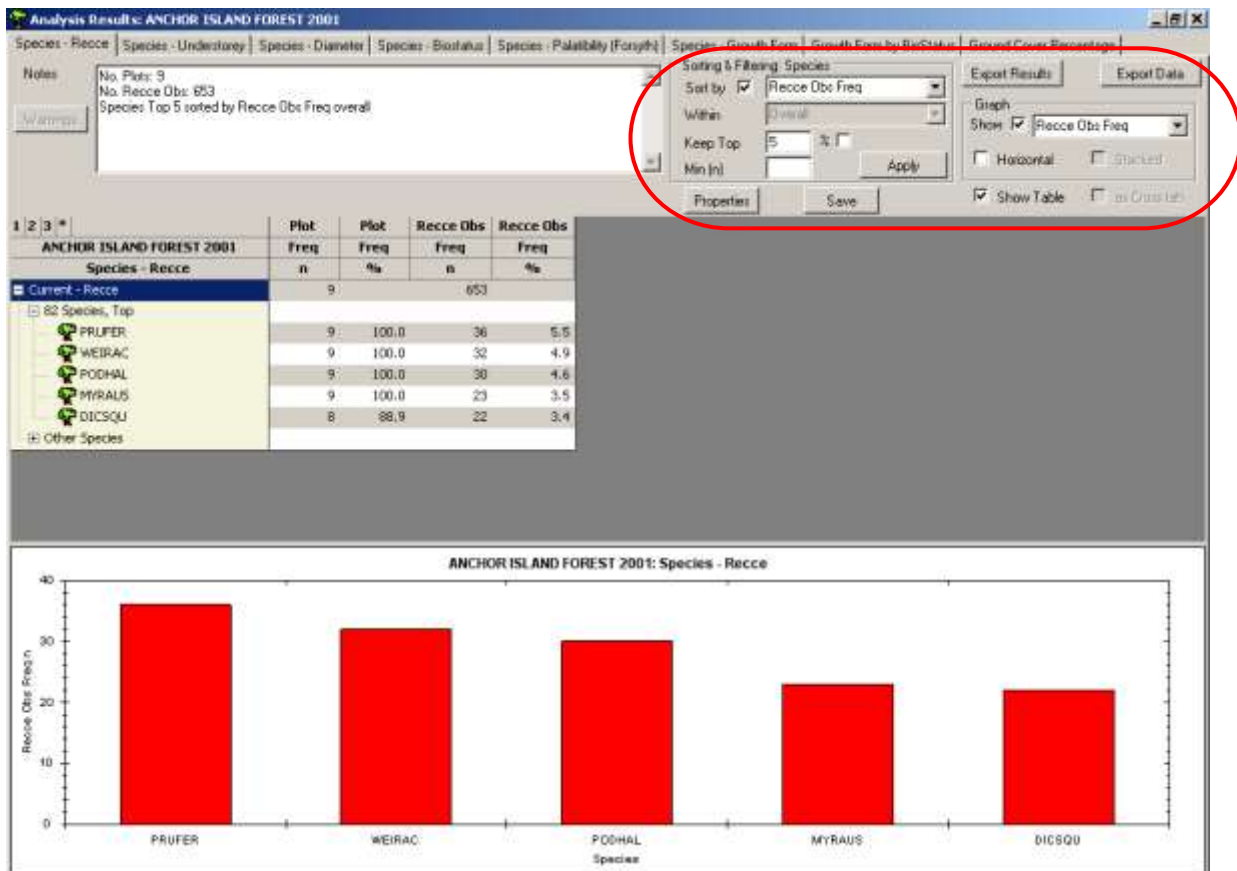
Data summaries can be customised by changing default options using the **Properties** button. These are detailed in Appendix 2. Changed options can be saved to a file for later use by using the **Save** button.

Options for displaying results for specific types of summaries are described in more detail in the following sections.

8.4.3 Export Results

The results of analysis can be exported by using the Export Results button. A selection of file options can be selected, as shown below:
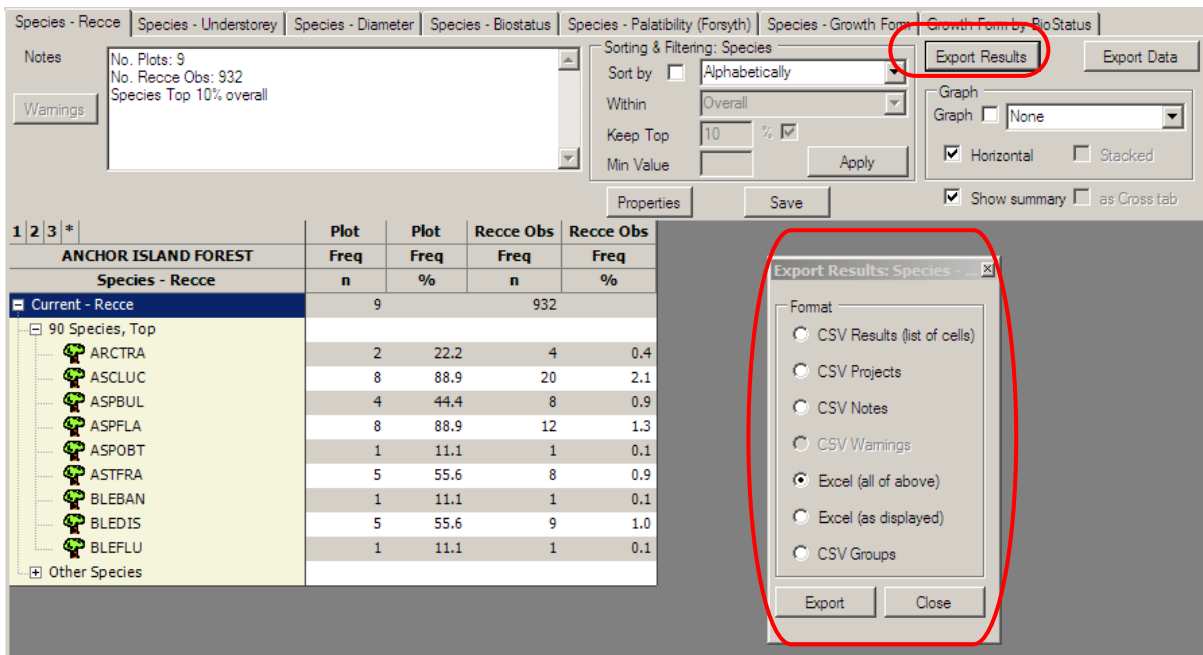
All data summaries and graphs can be copied to be pasted into other software packages by right clicking with the mouse and selecting Copy.

8.5 Species Summaries, General

The analyses under **Species Summaries, General** displays, for each species, the number of plots where it was recorded (Plot Freq n), the percentage of plots where it was recorded (Plot Freq %), and other columns depending on the data. There are separate analyses for Recce, Understorey and Diameter species data.

Species - Recce

For Recce data, the third column (Recce Obs Freq n) is the number of plot/height tiers where the species was recorded. The fourth column (Recce Obs Freq %) is the percentage plot/height tier/species observations which were that species.

1 2 3 *	Plot Freq n	Plot Freq %	Recce Obs Freq n	Recce Obs Freq %
ANCHOR ISLAND FOREST 2001				
Species - Recce				
⊟ Current - Recce	9		653	
⊟ 82 Species				
ADEGRA	1	11.1	1	0.2
ARIFRU	1	11.1	2	0.3
ASCLUC	7	77.8	16	2.5
ASPBUL	4	44.4	4	0.6
ASPFLA	7	77.8	7	1.1
ASPOBT	2	22.2	2	0.3
ASTFRA	3	33.3	4	0.6
BLECAP	1	11.1	2	0.3
BLECHA	1	11.1	1	0.2
BLEDIS	4	44.4	8	1.2
BLENOV	1	11.1	2	0.3
BLEPRO	9	100.0	17	2.6
BRAROT	4	44.4	6	0.9

Species – Understorey

For Understorey data the third column (Taxon Obs Freq n) is the number of subplots where the species occurred. The fourth column (Taxon Obs Freq %) is the percentage of subplot/species observations which were that species:

1 2 3 *	Sub Plot Freq n	Sub Plot Freq %	Taxon Obs Freq n	Taxon Obs Freq %
ANCHOR ISLAND FOREST				
Species - Understorey				
⊟ Current - Understorey	360		2,274	
⊟ 76 Species				
ARCTRA	4	1.1	4	0.2
ASCLUC	40	11.1	40	1.8
ASPBUL	9	2.5	9	0.4
ASPFLA	1	0.3	1	<0.1
ASPOBT	1	0.3	1	<0.1
ASTFRA	4	1.1	4	0.2
BLEDIS	6	1.7	6	0.3
BLEFLU	1	0.3	1	<0.1
BLENOV	21	5.8	21	0.9
BLEPRO	133	36.9	133	5.8
BRAROT	10	2.8	10	0.4

Species - Diameter

For Diameter data, the third column (Stem Freq n) is the total number of stems recorded of the species. The fourth column (Stem Freq %) is the percentage all stems that were that species.

1 2 3 *	Sub Plot	Sub Plot	Stem	Stem
ANCHOR ISLAND FOREST	**Freq**	**Freq**	**Freq**	**Freq**
Species - Diameter	**n**	**%**	**n**	**%**
Current - Diameter	144		640	
25 Species				
ASCLUC	2	1.4	4	0.6
COPCIL	1	0.7	2	0.3
COPFOE	14	9.7	19	3.0
CYASMI	3	2.1	3	0.5
DACCUP	8	5.6	8	1.3
DICSQU	35	24.3	106	16.6
DRALON	6	4.2	15	2.3
ELAHOO	7	4.9	8	1.3
GRILIT	2	1.4	2	0.3
HEDARB	2	1.4	3	0.5

There are three further species attributes that have been included in the general data summaries: **Biostatus** (as per Ngā Tipu Aotearoa – New Zealand Plants), **Palatability** (to ungulates as per Forsyth et al. 2002) and **Growth Form** (preliminary list as compiled by NVS staff and as per McGlone et al. 2009). These are displayed as categorical lists at the top of the Recce summary.

Species - Biostatus

The biostatus summary displays the frequencies and percentages for each biostatus category. Each category node can be expanded to display the list of species, as shown below. Biostatus is designated as:

- Indigenous: a taxon that occurs naturally in the region. This is further defined as:

  - Indigenous Endemic: an indigenous taxon that occurs naturally only in the region.

  - Indigenous Non-endemic: an indigenous taxon that occurs naturally in this and other regions

- Indigenous Unspecified: an indigenous taxon which has not been specified as being either endemic or non-endemic.

- Exotic: a taxon that has been accidentally or deliberately introduced into the region.

- Uncertain: a taxon for which the biostatus has not yet been determined or coded.

- Unknown: a taxon for which there is no biostatus information.

The 'Species - Biostatus' analyses at two levels: Bio Status (which combines all Indigenous categories together) and Bio Status Detail.

1 2 3 4 5 6 7 * ANCHOR ISLAND FOREST 2001 Species - Biostatus	Plot Freq n	Plot Freq %	Recce Obs Freq n	Recce Obs Freq %
Current - Recce	9		653	
Bio Status				
Indigenous	9	100.0	650	99.5
Bio Status Detail				
Indigenous Endemic	9	100.0	530	81.2
50 Species				
Indigenous Non-Endemic	9	100.0	62	9.5
20 Species				
Indigenous Unspecified	9	100.0	58	8.9
10 Species				
BLECAP	1	11.1	2	0.3
BLEPRO	9	100.0	17	2.6
CARREN	8	88.9	13	2.0
GRABIL	7	77.8	10	1.5
HYMBIV	1	11.1	1	0.2
HYMENO	1	11.1	1	0.2
HYMMUL	1	11.1	1	0.2
PHYPUS	6	66.7	8	1.2
PYRROS	2	22.2	2	0.3
PYRSER	3	33.3	3	0.5
Unknown	3	33.3	3	0.5

Species - Palatibility (Forsyth)

The palatability summary displays the frequencies and percentages for each palatability category. Each category node can be expanded to display the list of species, as shown below.

1 2 3 4 5 *	Plot	Plot	Recce Obs	Recce Obs
ANCHOR ISLAND FOREST	**Freq**	**Freq**	**Freq**	**Freq**
Species - Palatibility (Forsyth)	**n**	**%**	**n**	**%**
⊟ Current - Recce	9		653	
⊟ Palatibility				
⊞ Avoided	9	100.0	236	36.1
⊞ Not Selected	9	100.0	166	25.4
⊟ Preferred	9	100.0	122	18.7
⊟ 10 Species				
ASPFLA	7	77.8	7	1.1
COPLUC	4	44.4	4	0.6
GRILIT	5	55.6	6	0.9
MYRAUS	9	100.0	23	3.5
NEOCOL	2	22.2	2	0.3
PHYPUS	6	66.7	8	1.2
PSECRA	8	88.9	18	2.8
RIPSCA	8	88.9	21	3.2
SCHDIG	1	11.1	1	0.2
WEIRAC	9	100.0	32	4.9
⊞ Unclassified	9	100.0	129	19.8

Species - Growth Form

The growth form summary displays the frequencies and percentages for each growth form category. Each category node can be expanded to display the list of species, as shown below.

1 2 3 4 5 * ANCHOR ISLAND FOREST Species - Growth Form	Plot Freq n	Plot Freq %	Recce Obs Freq n	Recce Obs Freq %
⊟ Current - Recce	9		653	
⊟ Growth Form				
⊞ Fern	9	100.0	136	20.8
⊞ Forb	8	88.9	17	2.6
⊟ Graminoid	7	77.8	19	2.9
⊟ 8 Species				
ASTFRA	3	33.3	4	0.6
GAHNIA	1	11.1	1	0.2
LIBPUL	1	11.1	1	0.2
MICAVE	1	11.1	1	0.2
PHOCOO	1	11.1	1	0.2
UNCFIL	3	33.3	4	0.6
UNCRUP	4	44.4	4	0.6
UNCUNC	2	22.2	3	0.5
⊞ Shrub	9	100.0	56	8.6
⊞ SubShrub	9	100.0	15	2.3
⊞ Tree	9	100.0	359	55.0
⊞ Treefern	9	100.0	30	4.6
⊞ Vine	8	88.9	21	3.2

Growth Form by BioStatus

Recce data can be further summarised by constructing a cross tabulation of growth form by biostatus.

1 2 3 * Bio Status: ANCHOR ISLAND FOREST Growth Form by BioStatus	Endemic Recce Obs Freq %	Exotic Recce Obs Freq %	Indigenous Recce Obs Freq %	Non-endemic Recce Obs Freq %	Unknown Recce Obs Freq %	Overall Recce Obs Freq %
⊟ Current - Recce						
⊟ Growth Form						
Fern	27.2		42.6	28.7	1.5	100.0
Forb	94.1			5.9		100.0
Graminoid	47.4	5.3		42.1	5.3	100.0
Shrub	91.1			8.9		100.0
SubShrub	53.3			46.7		100.0
Tree	99.7			0.3		100.0
Treefern	100.0					100.0
Vine	100.0					100.0

1 2 3 *	Bio Status:	Indigenous	Unknown	Overall
	ANCHOR ISLAND FOREST 2001	Recce Obs	Recce Obs	Recce Obs
	Growth Form by BioStatus	Freq	Freq	Freq
		%	%	%
☐ Current - Recce				
☐ Growth Form				
Fern		98.5	1.5	100.0
Forb		100.0		100.0
Graminoid		94.7	5.3	100.0
Shrub		100.0		100.0
SubShrub		100.0		100.0
Tree		100.0		100.0
Treefern		100.0		100.0
Vine		100.0		100.0

The details of the records can be seen by right clicking on a value and selecting drill down:

8.6   Site Factors

The analyses under **Site Factors** produce summary statistics (mean, standard deviation and standard error), and one-way or two-way summaries of site factors. One-way summaries show plot frequency within specific ranges (or bands) of continuous variables such as altitude and slope, or levels of categorical variables such as physiography or drainage. Frequency histograms are also produced.

Site factors that can be summarised include:

- Altitude

- Aspect (corrected for magnetic declination by the program and displayed as Aspect /d)

- Slope

- Top Height

- Physiography Distribution

- Parent Material Distribution

- Disturbance Distribution

- Drainage Distribution

- Surface Cover Percentage

- Ground Cover Percentage

One-way summaries

For each numeric site factor, summary statistics (mean, standard deviation and standard error) are displayed then the number of plots (Plot Freq n) within the bands of that site factor. An example of the display for Slope (in 10° bands) is given below.

1 2 3 4 *	Plot
ANCHOR ISLAND FOREST	**Freq**
Slope	**n**
Current - Site Description	9
Slope (°)	
Statistics	
Mean: 20.00	
StdDv: 2.0	
StdErr: 0.10	
0<10	1
10<20	3
20<30	1
30<40	1
50<60	1
Missing	2

If the **Graph** checkbox is ticked a histogram is also displayed:
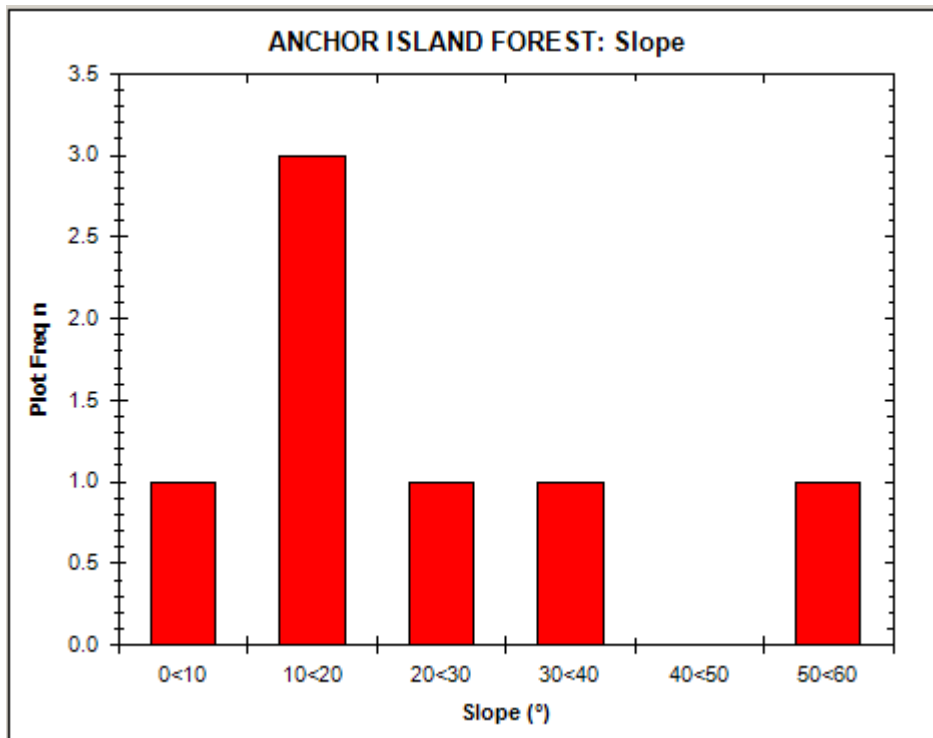
Note that Aspect has a circular distribution, so its mean and standard deviation are calculated by using circular distribution formulae (Zar 1974).

For each categorical site factor the number of plots (Plot Freq n) within each category level is displayed. An example for Physiography is shown below.

Two-way summaries

To produce two-way summaries you need to tick the **Prompt for site factor cross-tabs** checkbox in the Data Summaries page. The following window then appears before the analysis is run, with a title indicating the first site factor selected and you can then tick the other factor you wish to add.
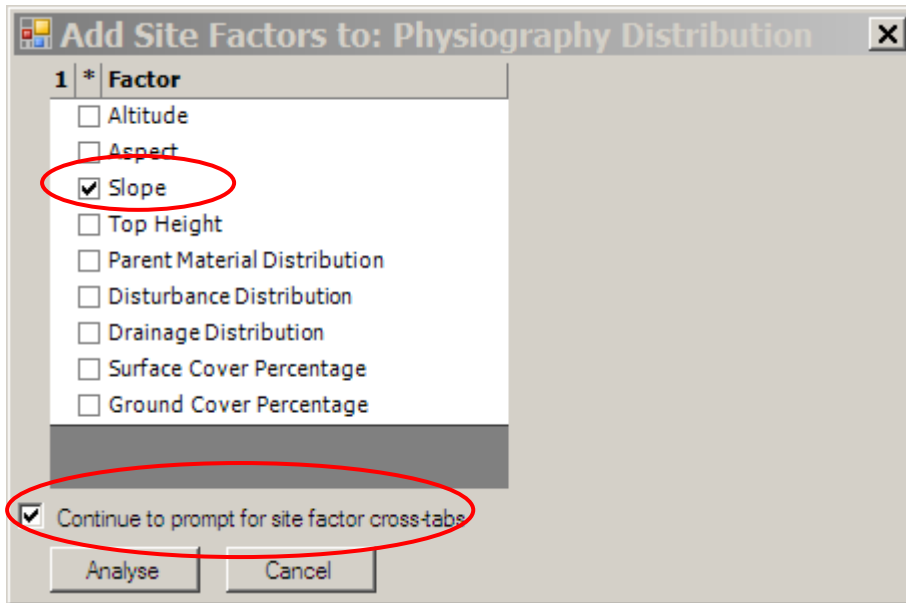
If the checkbox **Continue to prompt for site factor cross-tabs** is ticked the window will reappear for the next site factor analysis.

In this example, Slope has been selected to cross tabulate with the initially selected Physiography. The main display shows the number of plots (Plot Freq n) within each combination of Slope range and Physiography category level. The right-hand column displays the total number of plots within each Physiography category level (Overall Plot Freq n):

1 2 3 * Slope (°):	0<10	10<20	20<30	30<40	40<50	50<60	Missing	Overall
ANCHOR ISLAND FOREST	**Plot**	**Plot**	**Plot**	**Plot**	**Plot**	**Plot**	**Plot**	**Plot**
Physiography Distribution	**Freq**	**Freq**	**Freq**	**Freq**	**Freq**	**Freq**	**Freq**	**Freq**
	n	**n**	**n**	**n**	**n**	**n**	**n**	**n**
⊟ Current - Site Description								9
⊟ Physiography								
Face	1	2		1			1	5
Gully		1	1					2
Ridge							1 1	2

8.7 Species by Site Factor

The analyses under **Species by Site Factor** calculate species distributions by the site factors. The initial display is a high-level summary of the number of plots in each Site Factor category or numerical band range. Expanding a node displays the number of plots (Plot Freq n) and percentage of plots (Plot Freq %) within that Site Factor band or level where the species was recorded.

Species by Physiography

1 2 3 4 5 * ANCHOR ISLAND FOREST Species by Physiography	Plot Freq n	Plot Freq %
⊟ Current - Recce	9	
⋮⋯⊟ Physiography		
⋮⋯⊟ Face	5	
⋮⋯⊟ 70 Species		
🌳 ADEGRA	1	20
🌳 ARIFRU	1	20
🌳 ASCLUC	4	80
🌳 ASPBUL	2	40
🌳 ASPFLA	4	80
🌳 ASPOBT	1	20
🌳 ASTFRA	2	40
🌳 BLECAP	1	20

In the example displayed, there were five plots on faces; ADEGRA was found on one (or 20%) of those plots.

8.8 Recce Summaries, Detail

These summaries and graphs can be used to answer questions about the composition and structure of individual plots or plot groups. For example, a height tier summary with canopy species poorly represented in lower height tiers could reflect current pressure from animal browsing or increased competition from other plants. A height tier diagram of higher elevation plots with similar species to those of low elevation plots may show structural differences in the height tiers, with canopy species being scrub-like in the lower height tiers at higher elevations. A summary for disturbed sites may be composed of faster growing and quickly established species, with small numbers of the final canopy species.

These summaries can be used with plot groups to interpret a classification of plots into communities (see Multivariate Analysis section), by allowing the user to compare composition and structure of different communities.

In all the summaries, statistics (frequency, averages) are calculated across just the plots in which the species was recorded (usually the first in a set of columns) and then across all plots (signified by the abbreviation 'AP' in the column heading, usually the second in a set of columns). Cover means are calculated by averaging cover class midpoints (i.e. midpoint of the percentage cover range signified by the cover-class – as indicated in the Notes box). Species in all tables are sorted by descending order of abundance across all plots.

8.8.1   Species Freq & Cover

This analysis displays the percent frequency (Plot Freq %) and mean percentage cover (Cover Mean AP %) of each species calculated across all plots. The default display is of the top 20 species that are over the minimum of 0.1% overall mean percentage cover. This display can be changed in the Sorting and Filtering box. Species are listed in order of descending overall mean cover:

8.8.2   Species Freq & Cover by Tier

This analysis displays percent frequency (Plot Freq %) and mean percentage cover (Cover Mean AP %) of each species within each height tier where the species was recorded. The details of the height tier ranges are recorded in the notes box. The two right-hand columns

display the percent frequency (Overall Plot Freq %) and mean percentage cover (after summing across height tiers) (Overall Cover Mean AP %) calculated across all plots, as above. Species are listed in order of descending overall percentage frequency, with a minimum value of 20% (default):

123* Tier: ANCHOR ISLAND FOREST Species Freq & Cover by Tier	2 Plot Freq %	Cover Mean AP %	3 Plot Freq %	Cover Mean AP %	4 Plot Freq %	Cover Mean AP %	5 Plot Freq %	Cover Mean AP %	6 Plot Freq %	Cover Mean AP %	7 Plot Freq %	Cover Mean AP %	Overall Plot Freq %	Overall Cover Mean AP %
Current - Recce														172.7
81 Species, >=20														
BLEPRO							100.0	8.9	88.9	4.5			100.0	13.4
DACCUP	44.4	9.2			11.1	0.1	77.8	0.4	100.0	0.5			100.0	10.1
MYRAUS			66.7	1.2	55.6	0.3	11.1	0.1	88.9	0.4	33.3	0.2	100.0	2.1
PODHAL	66.7	7.5	22.2	0.7	33.3	0.4	100.0	5.2	100.0	3.5	11.1	0.1	100.0	12.2
PRUPER	77.8	7.7	66.7	3.3	55.6	1.4	100.0	1.6	100.0	0.8			100.0	14.8
WEIRAC	66.7	11.2	88.9	12.7	33.3	2.1	22.2	0.4	100.0	0.5	44.4	0.2	100.0	27.1

8.8.3   Species Freq by Tier

This analysis displays the number of plots (Plot Freq n) and the percentage of all plots (Plot Freq %) where the species were recorded, within height tiers. The two 'overall' columns display the total number of plots (Overall Plot Freq n) and the percentage frequency calculated across all plots (Overall Plot Freq %). Species are listed in order of descending overall percentage frequency, with a minimum value of 3% (default):

123* Tier: ANCHOR ISLAND FOREST Species Freq by Tier	2 Plot Freq n	Plot Freq %	3 Plot Freq n	Plot Freq %	4 Plot Freq n	Plot Freq %	5 Plot Freq n	Plot Freq %	6 Plot Freq n	Plot Freq %	7 Plot Freq n	Plot Freq %	Overall Plot Freq n	Overall Plot Freq %
Current - Recce													9	
81 Species, >=3														
BLEPRO							8	100.0	8	88.9			9	100.0
DACCUP	4	44.4			1	11.1	7	77.8	9	100.0			9	100.0
MYRAUS			6	66.7	5	55.6	1	11.1	8	88.9	3	33.3	9	100.0
PODHAL	6	66.7	2	22.2	3	33.3	9	100.0	9	100.0	1	11.1	9	100.0
PRUFER	7	77.8	6	66.7	5	55.6	9	100.0	9	100.0			9	100.0
WEIRAC	6	66.7	8	88.9	3	33.3	2	22.2	9	100.0	4	44.4	9	100.0

8.8.4   Species Cover by Tier

This analysis displays mean percentage cover of each species within height tiers across plots where the species was recorded (Cover Mean %) and across all plots (Cover Mean AP %). The two 'overall' columns display the mean cover (after summing across height tiers) on plots where the species was recorded (Overall Cover Mean %) and across all plots (Overall Cover Mean AP %). Species are listed in order of descending overall mean cover, with a minimum value of 3% (default):

123* Tier: ANCHOR ISLAND FOREST Species Cover by Tier	2 Cover Mean %	Cover Mean AP %	3 Cover Mean %	Cover Mean AP %	4 Cover Mean %	Cover Mean AP %	5 Cover Mean %	Cover Mean AP %	6 Cover Mean %	Cover Mean AP %	7 Cover Mean %	Cover Mean AP %	Overall Cover Mean %	Overall Cover Mean AP %
Current - Recce													172.7	172.7
81 Species, >=3														
WEIRAC	16.8	11.2	14.3	12.7	6.2	2.1	1.8	0.4	0.5	0.5	0.5	0.2	27.1	27.1
NOTCLI	3.0	1.0	50.0	11.1	15.0	1.7	0.5	0.2	0.5	0.3			25.7	14.3
METUMB	22.5	7.5	9.0	4.8	15.0	1.7	0.5	0.2	0.5	0.3	0.5	0.2	17.9	13.8
PRUFER	8.9	7.7	5.0	3.3	2.5	1.4	1.6	1.6	0.4	0.8			14.8	14.8
BLEPRO							8.9	8.9	5.1	4.5			13.4	13.4
PODHAL	11.0	7.5	3.0	0.7	1.3	0.4	3.2	5.2	0.5	0.5	0.5	0.1	12.2	12.2
NOTMEN	20.2	4.5	0.5	0.1			0.5	0.1	0.5	0.2			18.9	4.8

8.8.5 Species Layers

The 'Species Layers - All Plots' analysis displays total cover across all species (Cover Mean AP %) and the total number of species (Species Freq n) within each height tier across all plots in the project:

1 2 3 4 5 * ANCHOR ISLAND FOREST Species Layers - All Plots	Cover Mean AP %	Species Freq n
⊟ Current - Recce	172.7	81
⊟ Tier		
⊞ Tier 2	49.0	9
⊞ Tier 3	37.7	16
⊞ Tier 4	18.6	20
⊞ Tier 5	39.1	45
⊞ Tier 6	22.9	67
⊞ Tier 7	5.4	36

Expanding the node of a height tier displays the mean percentage cover across all plots (Cover Mean AP %) and the percent frequency (Species Freq n) for each species occurring in that height tier. By default, species are listed in descending order of their mean percentage cover across all tiers and these values are displayed in the 'Notes' box for the top 10 species. In the example below, species are sorted by their 'Cover Mean AP %' within each tier by picking 'Tier' from the drop-down menu of the **Within** box:

1 2 3 4 5 * ANCHOR ISLAND FOREST Species Layers - All Plots	Cover Mean AP %	Species Freq n
⊟ Current - Recce		90
⊟ Tier		
⊞ Tier 1	0.3	1
⊟ Tier 2	41.5	9
⊟ 9 Species, Top		
🌳 DACCUP	9.2	1
🌳 WEIRAC	8.3	1
🌳 PRUFER	6.0	1
🌳 METUMB	5.8	1
🌳 PODHAL	4.7	1
🌳 NOTMEN	4.5	1
🌳 NOTCLI	2.3	1
🌳 ELAHOO	0.3	1
🌳 RIPSCA	0.3	1
⊞ Tier 3	46.8	19

This summary is graphed by tier (as shown below) and clicking on another tier will change this display. Each tier graph will have a different scale on the x axis, depending on the range of cover values.
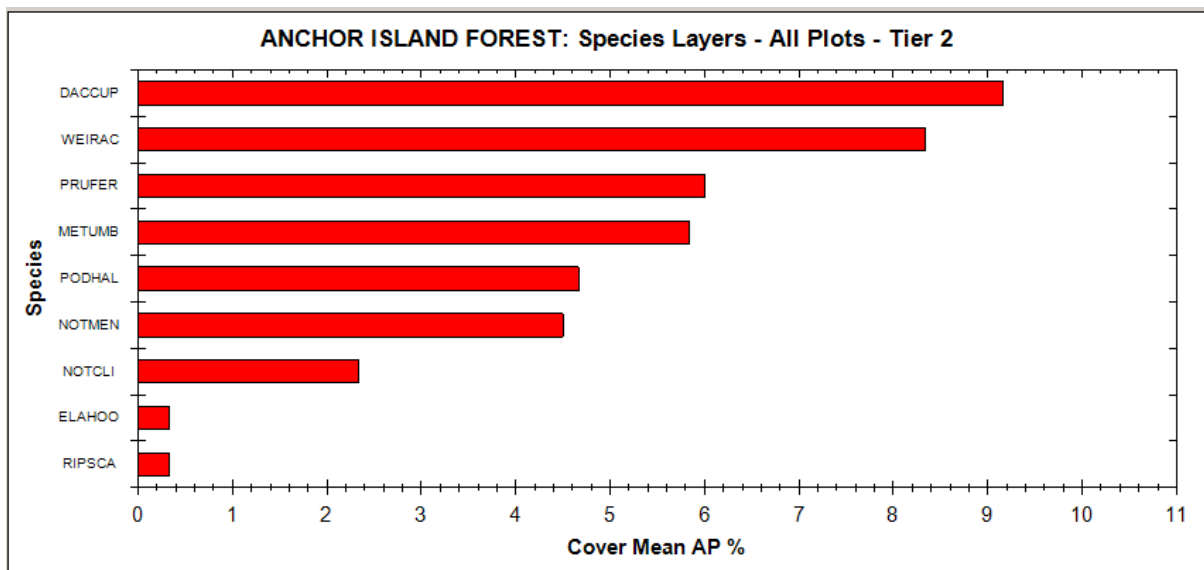
The 'Species Layers – Per Plot' analysis displays the mean percentage cover (after summing across all species and all height tiers) (Cover Mean AP %) and the total number of species (Species Freq n) across all plots in the project, listed by individual plots or plot groups:

1 2 3 4 5 6 7 *	Cover	Species
ANCHOR ISLAND FOREST	**Mean AP**	**Freq**
Species Layers - Per Plot	**%**	**n**
⊟ Current - Recce	172.7	81
⊟ 9 Plots		
⊞ 1 ANC01	258.5	40
⊞ 2 ANC01	154.0	41
⊞ 3 ANC01	154.5	47
⊞ 4 ANC01	162.5	41
⊞ 5 ANC01	142.5	33
⊞ 6 ANC01	167.5	29
⊞ 7 ANC01	211.5	41
⊞ 8 ANC01	161.0	27
⊞ 9 ANC01	142.5	42

Expanding a plot node displays mean percentage cover (after summing across all species) (Cover Mean AP %) and the total number of species (Species Freq n) within height tiers. Expanding the tier nodes, in turn, displays mean percentage cover (Cover Mean AP %) and percent frequency (Species Freq n) for each species recorded from those height tiers. Species are listed in order of descending overall mean cover:

1 2 3 4 5 6 7 *	Cover	Species
ANCHOR ISLAND FOREST	**Mean AP**	**Freq**
Species Layers - Per Plot	**%**	**n**
⊟ Current - Recce	172.7	81
⌐⊟ 9 Plots		
⊟ 1 ANC01	258.5	40
⌐⊟ Tier		
⊞ Tier 2	111.0	6
⊟ Tier 3	51.0	5
⊟ 5 Species, Top		
🌳 WEIRAC	15.0	1
🌳 PRUFER	15.0	1
🌳 RIPSCA	3.0	1
⊞ Other Species		
⊞ Tier 4	40.5	12

Ticking the **Graph** checkbox displays this expanded summary as a stacked bar graph depicting the relative cover of different species in each tier:

ANCHOR ISLAND FOREST: Species Layers - Per Plot - Plot 1 ANC01
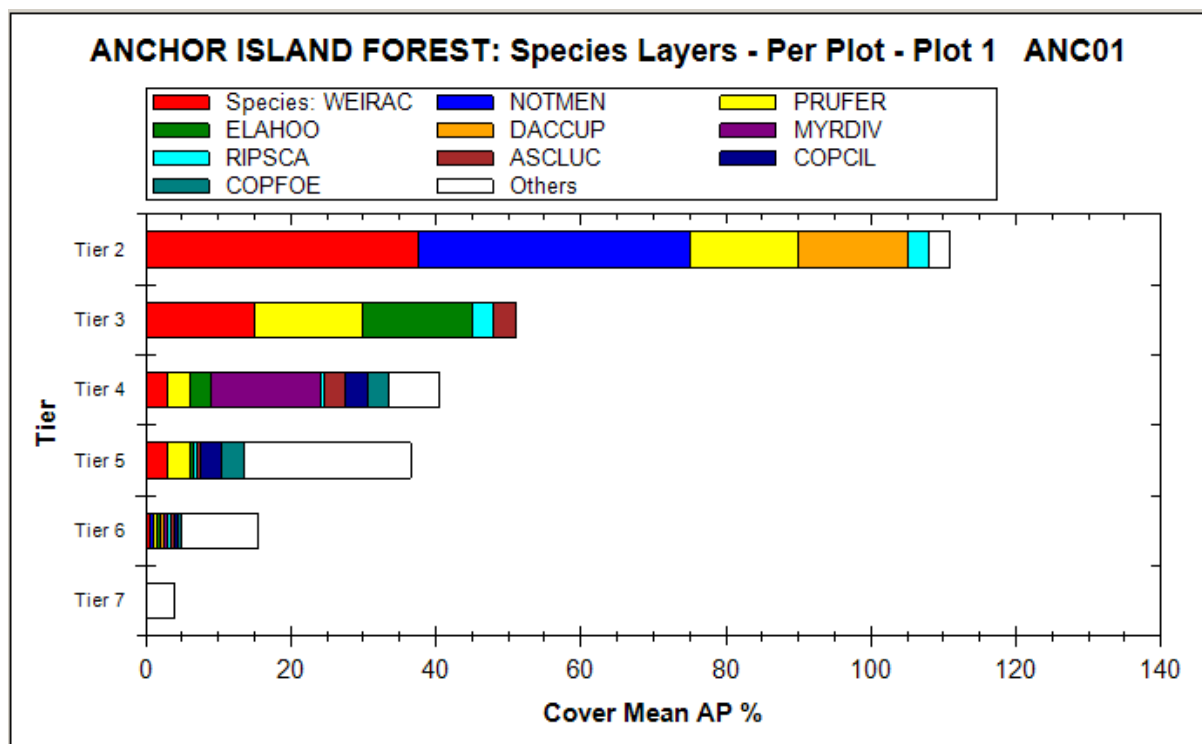
8.8.6 Species Cover by Plot

This analysis displays the mean percentage cover (after summing across height tiers) (Cover Mean AP %) of each species recorded, arranged in columns for each plot or plot group. The 'overall' column displays the mean cover (after summing across height tiers) of each species across all plots (Overall Cover Mean AP %). Species are listed in order of descending overall mean cover:

1 2 3 * 9 Plots:	1 ANC07 Cover Mean AP %	2 ANC07 Cover Mean AP %	3 ANC07 Cover Mean AP %	4 ANC07 Cover Mean AP %	5 ANC07 Cover Mean AP %	6 ANC07 Cover Mean AP %	7 ANC07 Cover Mean AP %	8 ANC07 Cover Mean AP %	9 ANC07 Cover Mean AP %	Overall Cover Mean AP %
Overall - Recce										246.4
90 Species										
WEIRAC	61.5	34.0	20.0	73.5	34.5	33.5	22.5	1.5	54.0	37.2
BLEPRO	6.0	18.0	18.0	6.0	18.0	75.0	6.0	150.5	3.5	33.4
PRUFER	19.5	36.5	10.0	22.0	36.5	15.0	22.5	12.0	7.5	20.2
METUMB	0.5	17.0	20.0		42.5	19.5		21.5	53.5	19.4
DACCUP	15.5	46.0	1.0	31.5	3.5	4.0	39.5	1.0	1.5	15.9
PODHAL	5.5	21.5	18.5	11.0	25.0	12.5	19.5	1.5	3.5	13.2

8.8.7 Species Presence by Plot

This analysis displays the presence of each species recorded in each plot (or Plot Group). Species presence is denoted by a '1' in each plot column. The 'overall' column displays a '1' for every species recorded in the project. Species are listed alphabetically:

1 2 3 * 9 Plots: ANCHOR ISLAND FOREST Species Presence by Plot	1 ANC01 Species Presence	2 ANC01 Species Presence	3 ANC01 Species Presence	4 ANC01 Species Presence	5 ANC01 Species Presence	6 ANC01 Species Presence	7 ANC01 Species Presence	8 ANC01 Species Presence	9 ANC01 Species Presence	Overall Species Presence
Current - Recce										1
81 Species										
ADEGRA				1						1
ARIFRU							1			1
ASCLUC	1	1	1	1	1	1	1			1
ASPBUL		1	1		1			1		1
ASPFLA	1		1		1	1	1	1	1	1
ASPOBT		1		1						1
ASTFRA		1	1				1			1
BLECHA		1								1
BLEDIS	1	1		1			1			1

8.8.8 Tier Cover Profile

This analysis displays the mean percentage cover (after summing across species) across all plots (Cover Mean AP%) and the number of species recorded (Species Freq n), within each combination of height tier and cover class. The two 'overall' columns display the mean percentage cover (after summing across species and cover classes) across all plots, and the total number of species, for each height tier.

It may be useful to drill down on particular items in the table. For example, there are four species (Species Freq n) with cover class '3' in tier 3. By right-clicking on the species frequency value '4' in the table, you can determine which species were recorded for that tier and cover class and on which plot each species occurred.

This summary may be more readily understood when displayed as a stacked histogram. This graph is an abstract representation of forest or vegetation structure and as such can be used to compare groups of plots by their different profiles. Definitions of the cover class categories are displayed in the notes field.

ANCHOR ISLAND FOREST: Tier Cover Profile
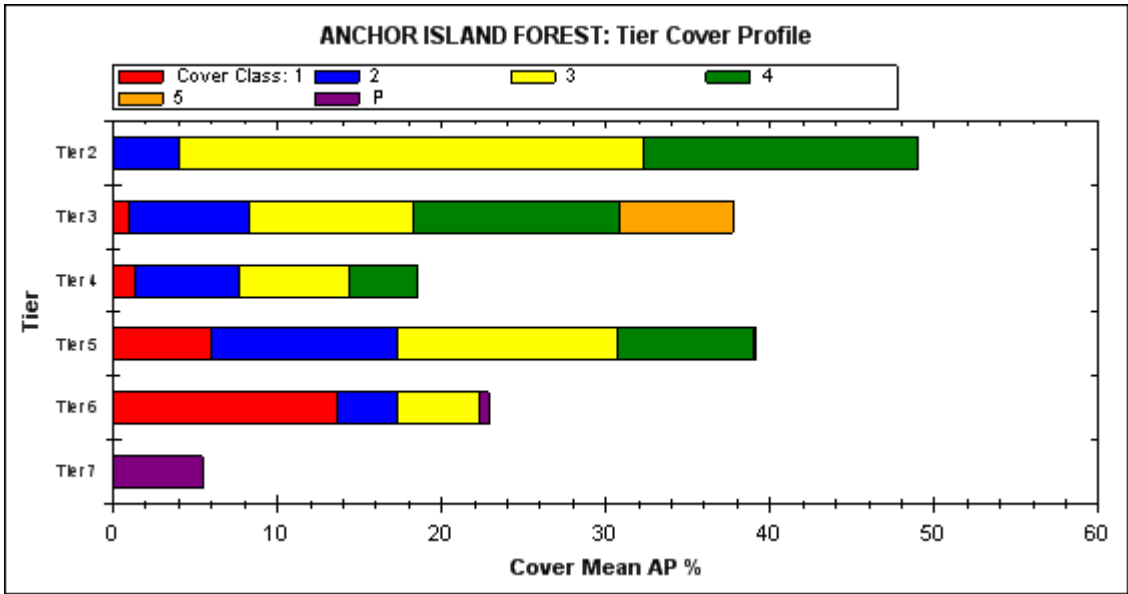
8.9 Seedling/Sapling Summaries, Detail

8.9.1 Seedling Frequency

The 'Seedling Frequency - All Plots' analysis displays the percentage of all seedling plots (SubPlot Freq %) where the species was recorded. Expanding a species node displays the percentage of all seedling plots where the species was recorded for each height tier. Species are listed in order of descending overall frequency:

1 2 3 4 5 *	Sub Plot
ANCHOR ISLAND FOREST	**Freq**
Seedling Frequency - All Plots	**%**
⊟ Current - Seedling	
⊟ 74 Species	
⊞ 🌳 BLEPRO	61.0
⊞ 🌳 PRUFER	55.9
⊞ 🌳 COPFOE	46.0
⊞ 🌳 NEOPED	38.5
⊞ 🌳 PODHAL	36.2
⊞ 🌳 MYRDIV	32.4
⊞ 🌳 MYRAUS	30.5

1 2 3 4 5 *	Sub Plot
ANCHOR ISLAND FOREST	**Freq**
Seedling Frequency - All Plots	**%**
⊟ Current - Seedling	
⊟ 74 Species	
⊟ 🌳 BLEPRO	61.0
⊟ Height Class	
0-15 cm	34.7
16-45 cm	39.4
46-75 cm	15.0
76-105 cm	0.9
> 135 cm	0.5
⊟ 🌳 PRUFER	55.9

If the **Analyse per Plot where optional** checkbox has been ticked on the Data Summaries page, an additional tab displays a summary table for 'Seedling Frequency - Per Plot', which can be expanded. Expanding a plot node displays, for each tier, the percentage of the plot's seedling plots where each species was recorded (SubPlot Freq %). Again, expanding a species node displays the percentage frequencies for each height class.

1 2 3 4 5 6 7 *	Sub Plot
ANCHOR ISLAND FOREST	**Freq**
Seedling Frequency - By Plot	**%**
⊟ Current - Seedling	
⊟ 9 Plots	
⊞ 📋 1	
⊞ 📋 2	
⊞ 📋 3	
⊞ 📋 4	
⊞ 📋 5	
⊞ 📋 6	
⊞ 📋 7	
⊞ 📋 8	
⊞ 📋 9	

1 2 3 4 5 6 7 *	Sub Plot
ANCHOR ISLAND FOREST	**Freq**
Seedling Frequency - By Plot	**%**
⊟ Current - Seedling	
⊟ 9 Plots	
⊟ 📋 1	
⊟ 41 Species	
⊟ 🌳 BLEPRO	37.5
⊟ Height Class	
0-15 cm	20.8
16-45 cm	33.3
⊞ 🌳 PRUFER	37.5
⊞ 🌳 COPFOE	12.5
⊞ 🌳 NEOPED	54.2

8.9.2 Seedling Density

The 'Seedling Density - All Plots' analysis displays the mean seedling density (per square metre; Density Count Mean AP n/sq m) of each species and the standard deviation (Density Count StdDv AP n/sq m), calculated by seedling height class. The density calculation uses subplot areas and includes all subplots that were observed for the seedling method, even if no seedlings of the species were observed. It is based on the numerical Count of seedlings, so is not a valid density if only the Presence of seedlings was recorded.

Expanding a species node displays the mean seedling density and standard deviation for the individual height classes. Species are listed in order of descending mean seedling density.

1 2 3 4 5 *	Density Count	Density Count
ANCHOR ISLAND FOREST	**Mean AP**	**Std Dv AP**
Seedling Density - All Plots	**n/sq m**	**n/sq m**
⊟ Current - Seedling	5.149	5.674
└⊟ 44 Species		
└⊟ 🌳 NEOPED	0.933	1.967
└⊟ Height Class		
⋯ 16-45 cm	0.532	1.166
⋯ 46-75 cm	0.194	0.705
⋯ 76-105 cm	0.081	0.408
⋯ 106-135 cm	0.044	0.283
⋯ > 135 cm	0.081	0.408
⊞ 🌳 PRUFER	0.842	1.938
⊞ 🌳 COPFOE	0.513	1.078
⊞ 🌳 PODHAL	0.462	1.440
⊞ 🌳 NOTCLI	0.316	1.426

If the **Analyse per Plot where optional** checkbox is ticked, an additional tab displays a summary table for 'Seedling Density - Per Plot', which can be expanded. Expanding a plot's node displays the mean seedling density for each species in that plot, calculated by seedling height class (per square metre; Density Count Mean AP n/sq m) and the standard deviation of this mean (Density Count StdDv AP n/sq m). Again, expanding a species node displays the mean seedling density and standard deviation for the individual height tiers. Species are listed in order of descending mean seedling density.

1 2 3 4 5 6 7 *	Density Count	Density Count
ANCHOR ISLAND FOREST	**Mean AP**	**Std Dv AP**
Seedling Density - By Plot	**n/sq m**	**n/sq m**
⊟ Current - Seedling	5.149	5.674
└⊟ 9 Plots		
└⊟ 📦 1	3.333	2.638
└⊟ 16 Species		
└⊟ 🌳 NEOPED	0.556	0.872
└⊟ Height Class		
⋯ 16-45 cm	0.278	0.553
⋯ 46-75 cm	0.111	0.376
⋯ 76-105 cm	0.056	0.272
⋯ 106-135 cm	0.056	0.272
⋯ > 135 cm	0.056	0.272
⊞ 🌳 PRUFER	0.111	0.544
⊞ 🌳 COPFOE	0.111	0.376
⊞ 🌳 MYRDIV	0.333	0.709
⊞ 🌳 COPCOL	0.611	1.470

8.9.3 Sapling Frequency & Density

The 'Sapling Frequency & Density - All plots' analysis displays, for each species, the percentage of all sapling plots where the species was recorded (SubPlot Freq %), the mean sapling density (per square metre; Density Count Mean AP n/sq m) and the standard deviation (Density Count StdDv AP n/sq m). The density calculation uses subplot areas and includes all subplots that were observed for the sapling method, even if no saplings of the species were observed. . It is based on the numerical Count of saplings, so is not a valid density if only the Presence of saplings was recorded. Species are listed in order of descending frequency:

1 2 3 * ANCHOR ISLAND FOREST Sapling Frequency & Density - All Plots	Sub Plot Freq %	Density Count Mean AP n/sq m	Density Count Std Dv AP n/sq m
⊟ Current - Sapling		0.391	0.387
⊟ 28 Species			
NEOPED	50.8	0.138	0.221
PODHAL	44.3	0.046	0.091
PSECOL	27.0	0.038	0.079
COPFOE	25.4	0.019	0.044
DICSQU	24.6	0.015	0.030
MYRDIV	23.0	0.018	0.041
PRUFER	23.0	0.022	0.060
RIPSCA	18.9	0.041	0.113
WEIRAC	15.6	0.016	0.050

If the **Analyse per Plot where optional** checkbox is ticked, the 'Sapling Frequency & Density - Per Plot' analysis displays, for each plot, the percentage of all sapling plots where any plants were recorded (SubPlot Freq %), the mean sapling density (per square metre; Density Count Mean AP n/sq m) across all species and the standard deviation of the mean (Density Count StdDv AP n/sq m).

1 2 3 4 5 *	Sub Plot	Density Count	Density Count
ANCHOR ISLAND FOREST	Freq	Mean AP	Std Dv AP
Sapling Frequency & Density - Per Plot	%	n/sq m	n/sq m
☐ Current - Sapling		0.391	0.387
☐ 9 Plots			
⊞ 1 ANC01		0.335	0.209
⊞ 2 ANC01		0.301	0.287
⊞ 3 ANC01		0.504	0.349
⊞ 4 ANC01		0.650	0.511
⊞ 5 ANC01		0.177	0.148
⊞ 6 ANC01		0.173	0.215
⊞ 7 ANC01		0.868	0.357
⊞ 8 ANC01		0.080	0.043
⊞ 9 ANC01		0.097	0.071

Expanding the plot node displays the percentage of each plots' sapling plots where each species was recorded, (SubPlot Freq %), the mean sapling density (per square metre; Density Count Mean AP n/sq m) of each species and the standard deviation of the mean (Density Count StdDv AP n/sq m).

1 2 3 4 5 *	Sub Plot	Density Count	Density Count
ANCHOR ISLAND FOREST	Freq	Mean AP	Std Dv AP
Sapling Frequency & Density - Per Plot	%	n/sq m	n/sq m
☐ Current - Sapling		0.391	0.387
☐ 9 Plots			
☐ 1 ANC01		0.335	0.209
☐ 12 Species			
NEOPED	62.5	0.088	0.099
PODHAL	6.3	0.008	0.030
PSECOL	25.0	0.028	0.058
COPFOE	31.3	0.013	0.019
MYRDIV	50.0	0.030	0.043
RIPSCA	31.3	0.070	0.145
WEIRAC	62.5	0.063	0.073
COPCIL	37.5	0.023	0.033
COPCOL	6.3	0.003	0.010
CYASMI	12.5	0.005	0.014
ELAHOO	6.3	0.003	0.010
MYRAUS	12.5	0.005	0.014
⊞ 2 ANC01		0.301	0.287
⊞ 3 ANC01		0.504	0.349

8.10 Diameter Summaries, Detail

8.10.1 Diameter statistics

This analysis displays, for each species, the mean stem density per hectare (Stem Mean AP n/ha), the mean plot stem diameter, in centimetres (Diameter Mean cm (Plot mean)), mean plot stem circumference in metres per hectare (Circum Mean AP m/ha) and mean plot basal area in square metres per hectare (Basal Area Mean AP sq m/ha), across all plots and the standard deviations of these means (Stem StdDv AP n/ha, Diameter StdDv cm (Plot mean); Circum. StdDv AP m/ha; Basal Area Std Dv AP sq m/ha). Dead stems are excluded from all calculations. The density calculation uses plot areas (not sub plot areas) and includes all plots that were observed for the diameter method, even if no stems of the species were observed. Species are listed in order of descending mean plot stem diameter.

1 2 3 4 5 *	Stem	Stem	Diameter	Diameter	Circum.	Circum.	Basal Area	Basal Area
ANCHOR ISLAND FOREST	Mean AP	Std Dv AP	Mean	Std Dv	Mean AP	Std Dv AP	Mean AP	Std Dv AP
Diameter Statistics - All Plots	n/ha	n/ha	cm (Plot mean)	cm (Plot mean)	m/ha	m/ha	sq m/ha	sq m/ha
☐ Current - Diameter	1,652.8	526.3	16.5	3.1	824.7	232.8	58.52	12.2
☐ 25 Species								
⊞ DACCUP	22.2	34.1	56.9	21.4	32.7	41.7	6.08	7.7
⊞ NOTMEN	22.2	45.8	41.0	10.9	27.3	54.4	3.49	7.0
⊞ NOTCLI	83.3	161.5	30.5	16.1	85.1	162.7	8.30	16.0
⊞ METUMB	169.4	245.8	30.4	15.5	108.7	103.3	8.59	7.5
⊞ PODHAL	94.4	74.8	22.4	14.9	72.9	66.6	6.83	7.4
⊞ PRUFER	150.0	118.6	21.4	11.2	76.7	46.2	4.80	2.4
⊞ GRILIT	5.6	11.0	20.4	10.0	3.6	7.6	0.20	0.5
⊞ WEIRAC	519.4	357.7	18.4	8.4	253.6	145.3	15.85	11.2
⊞ CYASMI	8.3	17.7	13.5	0.7	3.5	7.3	0.12	0.2
⊞ PENCOR	2.8	8.3	10.4		0.9	2.7	0.02	0.1
⊞ HEDARB	8.3	25.0	10.1		2.7	8.0	0.10	0.3
⊞ ELAHOO	19.4	32.5	9.8	2.7	6.4	11.3	0.20	0.4
⊞ DICSQU	238.9	464.7	9.6	2.6	88.4	187.3	2.74	6.2
⊞ RAUSIM	25.0	30.6	9.4	1.9	8.1	11.1	0.22	0.3

Expanding a species node displays the same statistics within size classes:

1 2 3 4 5 *	Stem	Stem	Diameter	Diameter	Circum.	Circum.	Basal Area	Basal Area
ANCHOR ISLAND FOREST	Mean AP	Std Dv AP	Mean	Std Dv	Mean AP	Std Dv AP	Mean AP	Std Dv AP
Diameter Statistics - All Plots	n/ha	n/ha	cm (Plot mean)	cm (Plot mean)	m/ha	m/ha	sq m/ha	sq m/ha
☐ Current - Diameter	1,652.8	526.3	16.5	3.1	824.7	232.8	58.52	12.2
☐ 25 Species								
⊞ DACCUP	22.2	34.1	56.9	21.4	32.7	41.7	6.08	7.7
☐ NOTMEN	22.2	45.8	41.0	10.9	27.3	54.4	3.49	7.0
☐ Diameter (cm)								
0<10	2.8	8.3	7.7		0.7	2.0	0.01	<0.1
10<20	2.8	8.3	11.5		1.0	3.0	0.03	0.1
20<30	2.8	8.3	29.7		2.6	7.8	0.19	0.6
30<40	2.8	8.3	34.2		3.0	9.0	0.26	0.8
40<50	2.8	8.3	41.0		3.6	10.7	0.37	1.1
50<60	2.8	8.3	54.2		4.7	14.2	0.64	1.9
60<70	2.8	8.3	62.5		5.5	16.4	0.85	2.6
70<80	2.8	8.3	72.2		6.3	18.9	1.14	3.4
⊞ NOTCLI	83.3	161.5	30.5	16.1	85.1	162.7	8.30	16.0
⊞ METUMB	169.4	245.8	30.4	15.5	108.7	103.3	8.59	7.5

Histograms can be produced for any statistic. The example below displays the mean plot basal area by species, sorted by decreasing basal area. It is not possible to display all species names on the axis but they can be seen by hovering over the appropriate bar.
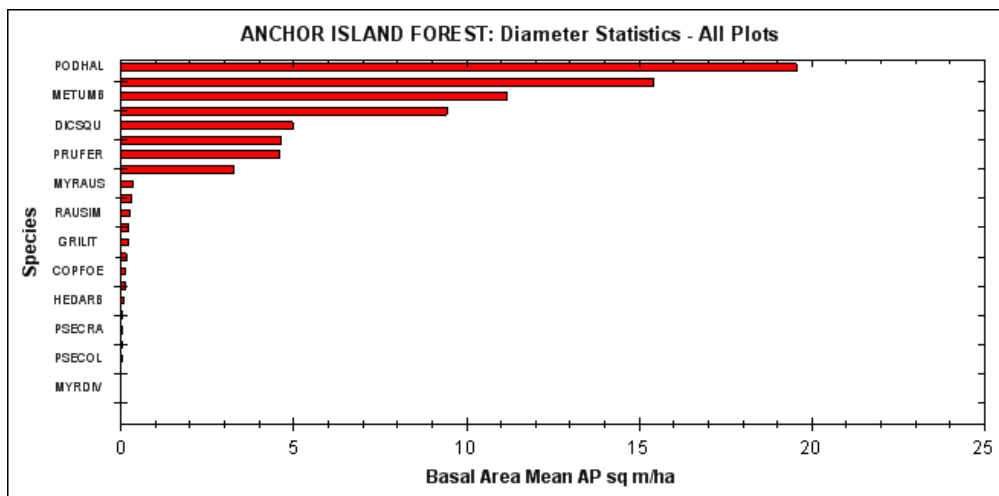
Ticking the 'Stacked' option produces the same graph except that each bar is broken down by diameter class:
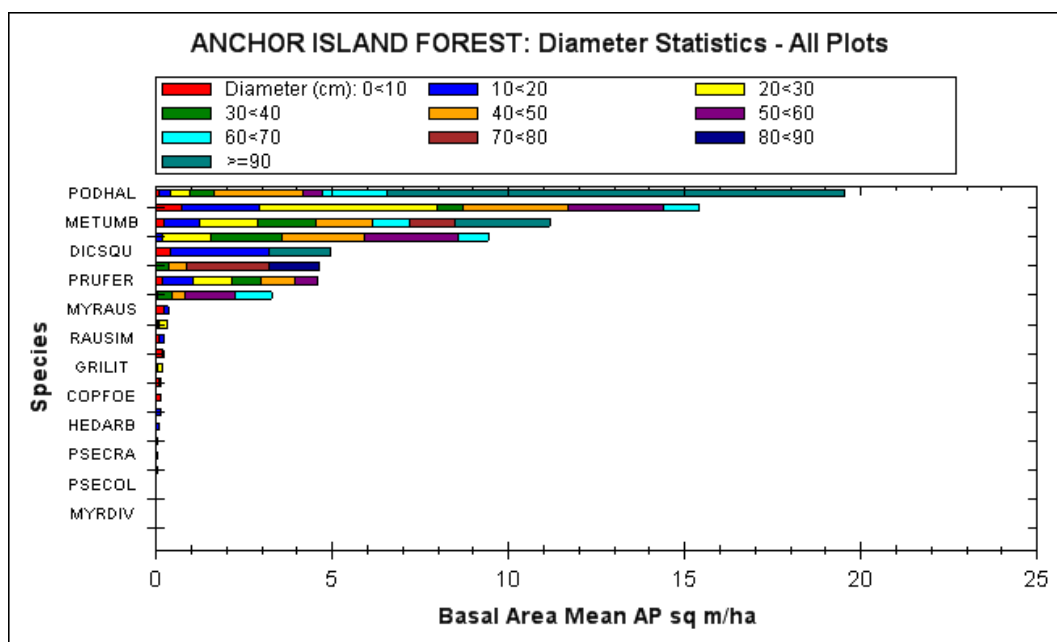
By clicking on individual species, histograms of diameter distributions within species can be produced:

ANCHOR ISLAND FOREST: Diameter Statistics - All Plots - Species PODHAL
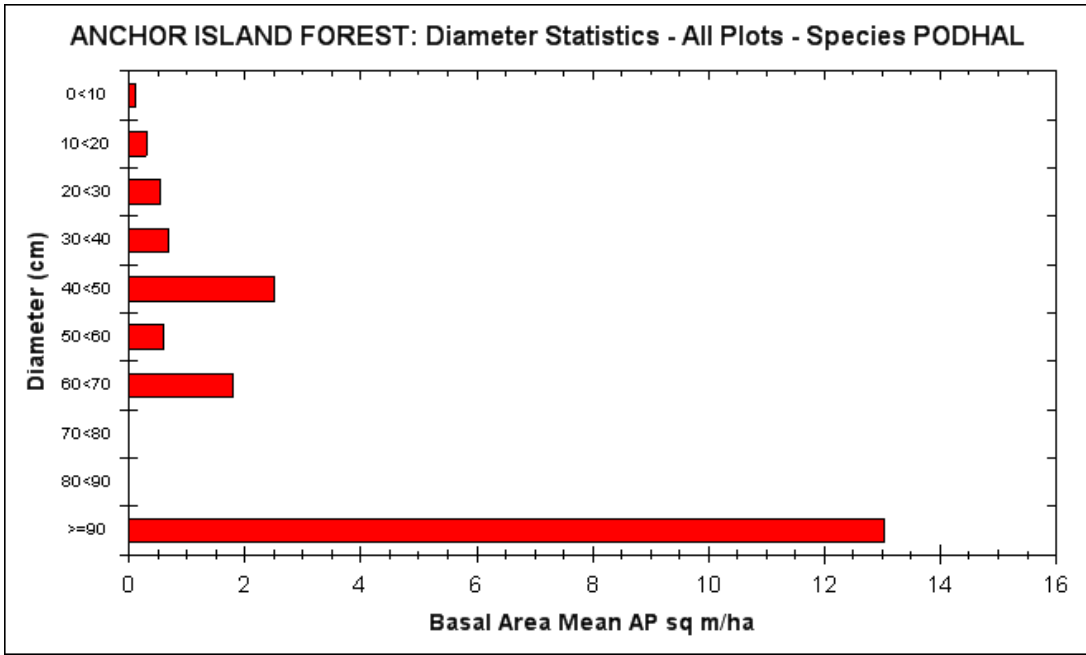
An additional tab for 'Diameter Statistics - By Plot' appears in the results. This analysis displays the same statistics as above for each plot (across all species):

1 2 3 4 5 6 7 *	Stem	Stem	Diameter	Diameter	Circum.	Circum.	Basal Area	Basal Area
ANCHOR ISLAND FOREST	Mean AP	Std Dv AP	Mean	Std Dv	Mean AP	Std Dv AP	Mean AP	Std Dv AP
Diameter Statistics - By Plot	n/ha	n/ha	cm (Plot mean)	cm (Plot mean)	m/ha	m/ha	sq m/ha	sq m/ha
⊟ Current - Diameter	1,652.8	526.3	16.5	3.1	824.7	232.8	58.52	12.2
⊟ 9 Plots								
⊞ 1 ANC07	1,975.0		11.9		737.3		49.73	
⊞ 2 ANC07	1,400.0		18.9		829.4		74.98	
⊞ 3 ANC07	1,200.0		16.4		616.9		51.14	
⊞ 4 ANC07	1,900.0		12.9		771.1		49.46	
⊞ 5 ANC07	800.0		21.6		541.8		45.24	
⊞ 6 ANC07	1,250.0		18.8		738.4		60.09	
⊞ 7 ANC07	2,150.0		14.5		982.4		72.55	
⊞ 8 ANC07	1,750.0		15.7		864.4		49.28	
⊞ 9 ANC07	2,450.0		17.4		1,340.6		74.20	

Expanding a plot node allows the site factors for the plot to be examined, and beneath that are listed the above statistics for each species on the plot. Expanding a species node, in turn, displays the statistics by size classes of that species. Site Factors can also be displayed:

1 2 3 4 5 6 7 *	Stem	Stem	Diameter	Diameter	Circum.	Circum.	Basal Area	Basal Area
ANCHOR ISLAND FOREST	Mean AP	Std Dv AP	Mean	Std Dv	Mean AP	Std Dv AP	Mean AP	Std Dv AP
Diameter Statistics - By Plot	n/ha	n/ha	cm (Plot mean)	cm (Plot mean)	m/ha	m/ha	sq m/ha	sq m/ha
⊟ Current - Diameter	1,652.8	526.3	16.5	3.1	824.7	232.8	58.52	12.2
⊟ ■ 9 Plots								
⊟ 🔵 1 ANC07	1,975.0		11.9		737.3		49.73	
⊟ Site Factors								
Area:400 m								
Altitude:60 m								
Aspect /d:99 °								
Slope:30 °								
Top Height:16 m								
⊟ 14 Species								
⊞ 🌳 DACCUP	25.0		74.0		58.1		10.75	
⊟ 🌳 NOTMEN	75.0		48.7		114.8		18.17	
⊟ Diameter (cm)								
10<20	25.0		11.5		9.0		0.26	
60<70	25.0		62.5		49.1		7.67	
70<80	25.0		72.2		56.7		10.24	
⊞ 🌳 PODHAL	125.0		23.2		91.0		5.64	

8.10.2 Diameter summary

This analysis displays the number of plots where each species was recorded (Plot Freq n), the percent frequency across all plots (Plot Freq %), and other statistics similar to the 'Diameter Statistics' above, with no analysis per plot.

9   Temporal trends

Temporal Trends is a facility for analysing changes in vegetation over time. It takes two projects (i.e. datasets collected from the same set of plots) and matches the observations in order to analyse changes. Make sure that you only have two measurements loaded for this analysis and have marked the latest one as 'current'. With **Diameter** data, the program matches plots and tagged stems between measurements and calculates change in basal area and stem density, rates of stem recruitment and mortality, and annual diameter growth. With **Recce** data, it matches plots and summarises changes in species richness and occupancy over time.

Warning: For trend analyses, all of the projects must have been downloaded from NVS Databank, in order to have plot and stem IDs that can be matched.

9.1 Running Temporal Trends

1. From the **Setup projects & groups** page import the two projects of interest into NVS-Analysis as in section 3. Check that the datasets contain data appropriate for the analysis (i.e. that they are the same type of data collected from the same plots).

2. Specify the most recent measurement as 'Current' using the checkbox in Setup Projects. The **Current** checkbox must be unticked for the first measurement (i.e. 'Previous' project).

3. Click on the **Temporal Trends** tree under **Data Analysis**; a page resembling the following will appear:

The Extreme Change Thresholds are used in some diameter trend analyses to exclude or separately analyse stems with large changes in size. Default limits are set for maximum annual growth and shrinkage. Users can change these limits if they wish.

If there have been changes in species names between the two measurements, tick the Use Preferred checkbox to ensure comparisons between the two datasets actually reflect change, rather than taxonomic usage.

4. To perform all available analyses, tick the **All Analyses** checkbox; to perform only selected analyses, tick only the relevant checkboxes.

9.2 Recce Trends

9.2.1 Recce Species Change

The 'Recce Species Change - All Plots' analysis is used to describe changes in species richness and vegetation composition. It displays the number of species found at each measurement, and, for each species, its presence (designated by a '1', Species Freq n), percent frequency across all plots (Plot Freq %) and mean percentage cover across all plots (Cover Mean AP %) at each measurement. In the example below, there were 87 species in the initial (Previous) measurement and 81 species in the Current measurement. For the species displayed, frequency across plots is unchanged, but cover has increased for some (e.g. NOTCLI) and decreased for others (e.g. WEIRAC, BLEPRO). Species are arranged in order of decreasing mean cover in the current measurement.

1 2 3 * ANCHOR ISLAND FOREST Recce Species Change	Species Previous Freq n	Species Current Freq n	Plot Previous Freq %	Plot Current Freq %	Cover Previous Mean AP %	Cover Current Mean AP %
☐ Trend - Recce	87	81			246.4	172.7
☐ 100 Species						
🌳 WEIRAC	1	1	100.0	100.0	37.2	27.1
🌳 PRUFER	1	1	100.0	100.0	20.2	14.8
🌳 NOTCLI	1	1	55.6	55.6	8.2	14.3
🌳 METUMB	1	1	77.8	77.8	19.4	13.9
🌳 BLEPRO	1	1	100.0	100.0	33.4	13.4
🌳 PODHAL	1	1	100.0	100.0	13.2	12.2
🌳 DACCUP	1	1	100.0	100.0	15.9	10.1
🌳 DICSQU	1	1	88.9	88.9	11.8	8.9
🌳 NEOPED	1	1	100.0	88.9	11.0	8.2

If the **Analyse per Plot where optional** checkbox has been ticked, an additional tab for 'Recce Species Change - Per Plot' appears in the results. This analysis displays the same statistics as above for each plot and each plot node can be expanded to display the species:

1 2 3 4 5 * ANCHOR ISLAND FOREST Recce Species Change - By Plot	Species Previous Freq n	Species Current Freq n	Plot Previous Freq %	Plot Current Freq %	Cover Previous Mean AP %	Cover Current Mean AP %
☐ Trend - Recce	81	87				
☐ 9 Plots						
☐ 📦 1	40	52				
☐ 57 Species						
🌳 WEIRAC	1	1	100.0	100.0	59.0	61.5
🌳 BLEPRO	1	1	100.0	100.0	3.5	6.0
🌳 PRUFER	1	1	100.0	100.0	36.5	19.5
🌳 METUMB		1		100.0		0.5
🌳 DACCUP	1	1	100.0	100.0	15.5	15.5
🌳 PODHAL	1	1	100.0	100.0	6.5	5.5
🌳 DICSQU		1		100.0		1.0
🌳 NEOPED	1	1	100.0	100.0	6.5	6.5
🌳 NOTCLI	1	1	100.0	100.0	1.0	0.5

9.3 Seedling/Sapling Trends

9.3.1 Seedling Change

The 'Seedling Change - All Plots' analysis displays, by species, the current (SubPlot Current Freq %) and previous mean subplot frequency (SubPlot Previous Freq %) and current (Density Count Current Mean AP n/sq m) and previous seedling density (Density Count Previous Mean AP n/sq m), across all plots. Density calculations use subplot areas and include all subplots that were observed for the seedling method, even if no seedlings of the species were observed. They are based on the numerical Count of seedlings, so are not valid densities if only the Presence of seedlings was recorded. Species are arranged in order of descending current frequency.

1 2 3 * ANCHOR ISLAND FOREST Seedling Change - All Plots	Sub Plot Previous Freq %	Sub Plot Current Freq %	Density Count Previous Mean AP n/sq m	Density Count Current Mean AP n/sq m
⊟ Trend - Seedling			5.149	7.095
⊟ 89 Species				
🌳 BLEPRO	61.0	62.1	0.106	0.019
🌳 PRUFER	55.9	62.1	0.842	1.083
🌳 COPFOE	46.0	52.3	0.513	0.657
🌳 NEOPED	38.5	35.0	0.933	1.008
🌳 PODHAL	36.2	31.3	0.462	0.403
🌳 MYRDIV	32.4	41.1	0.243	0.460
🌳 MYRAUS	30.5	34.1	0.006	0.056
🌳 RIPSCA	27.2	33.2	0.013	0.055
🌳 COPCOL	26.3	24.3	0.211	0.298
🌳 RAUSIM*	25.4	29.0	0.106	0.204

If the **Analyse per Plot where optional** checkbox has been ticked, an additional tab for 'Seedling Change - Per Plot' appears in the results. This analysis displays the same statistics as above for each plot and each plot node can be expanded to display the species:

1 2 3 4 5 * ANCHOR ISLAND FOREST Seedling Change - By Plot	Sub Plot Previous Freq %	Sub Plot Current Freq %	Density Count Previous Mean AP n/sq m	Density Count Current Mean AP n/sq m
⊟ Trend - Seedling			5.149	7.095
└⊟ 9 Plots				
⦙⦙⊟ 🗐 1			3.333	4.611
⦙⦙└⊟ 52 Species				
⦙⦙⦙🌳 BLEPRO	37.5	41.7	0.111	
⦙⦙⦙🌳 PRUFER	37.5	54.2	0.111	0.111
⦙⦙⦙🌳 COPFOE	12.5	37.5	0.111	0.111
⦙⦙⦙🌳 NEOPED	54.2	37.5	0.556	1.056
⦙⦙⦙🌳 PODHAL	25.0	20.8		
⦙⦙⦙🌳 MYRDIV	50.0	75.0	0.333	0.778
⦙⦙⦙🌳 MYRAUS	33.3	16.7		
⦙⦙⦙🌳 RIPSCA	20.8	37.5		
⦙⦙⦙🌳 COPCOL	62.5	70.8	0.611	1.000

9.3.2   Sapling Change

The 'Sapling Change - All Plots' analysis displays, by species, the current (SubPlot Current Freq %) and previous mean subplot frequency (SubPlot Previous Freq %) and current (Density Count Current Mean AP n/sq m) and previous sapling density (Density Count Previous Mean AP n/sq m), across all plots. Density calculations use subplot areas and include all subplots that were observed for the sapling method, even if no saplings of the species were observed. They are based on the numerical Count of saplings, so are not valid densities if only the Presence of saplings was recorded.

1 2 3 * ANCHOR ISLAND FOREST Sapling Change - All Plots	Sub Plot Previous Freq %	Sub Plot Current Freq %	Density Count Previous Mean AP n/sq m	Density Count Current Mean AP n/sq m
⊟ Trend - Sapling			0.391	0.423
└⊟ 32 Species				
⦙⦙🌳 NEOPED	50.8	47.8	0.138	0.121
⦙⦙🌳 PODHAL	44.3	41.3	0.046	0.066
⦙⦙🌳 PSECOL	27.0	23.9	0.038	0.044
⦙⦙🌳 COPFOE	25.4	41.3	0.019	0.035
⦙⦙🌳 DICSQU	24.6	26.1	0.015	0.018
⦙⦙🌳 MYRDIV	23.0	18.8	0.018	0.020
⦙⦙🌳 PRUFER	23.0	28.3	0.022	0.041
⦙⦙🌳 RIPSCA	18.9	5.8	0.041	0.005
⦙⦙🌳 WEIRAC	15.6	15.2	0.016	0.013

If the **Analyse per Plot where optional** checkbox has been ticked, an additional tab for 'Sapling change - Per Plot' appears in the results. This analysis displays the same statistics as above for each plot and each plot node can be expanded to display the species:

1 2 3 4 5 *	Sub Plot	Sub Plot	Density Count	Density Count
ANCHOR ISLAND FOREST	Previous Freq	Current Freq	Previous Mean AP	Current Mean AP
Sapling Change - By Plot	%	%	n/sq m	n/sq m
⊟ Trend - Sapling			0.391	0.423
⊟ 9 Plots				
⊟ 🌳 1			0.335	0.260
⊟ 13 Species				
🌳 NEOPED	62.5	68.8	0.088	0.080
🌳 PODHAL	6.3	12.5	0.008	0.010
🌳 PSECOL	25.0	25.0	0.028	0.015
🌳 COPFOE	31.3	18.8	0.013	0.008
🌳 MYRDIV	50.0	31.3	0.030	0.023
🌳 RIPSCA	31.3	37.5	0.070	0.030
🌳 WEIRAC	62.5	56.3	0.063	0.070
🌳 COPCIL	37.5	18.8	0.023	0.015
🌳 COPCOL	6.3		0.003	
🌳 CYASMI	12.5	6.3	0.005	0.003
🌳 ELAHOO	6.3		0.003	
🌳 MYRAUS	12.5	12.5	0.005	0.005
🌳 PSECRA		6.3		0.003
⊞ 🌳 2			0.301	0.318

9.4 Diameter Trends

Note that stems which are recorded as Dead, Not Found or Unknown are excluded from matching and from calculations involving growth over time. Stems with no status recorded are regarded as Alive.

9.4.1 Diameter Change per Plot

This analysis displays the mean diameter across all surviving (Matched) stems in each plot in the current project (Matched Diameter Current Mean cm) and the previous project (Matched Diameter Previous Mean cm) per plot.

1 2 3 *	Matched Diameter	Matched Diameter
ANCHOR ISLAND FOREST	Previous Mean	Current Mean
Diameter Change per Plot	cm	cm
� Trend - Diameter	16.4	16.4
◻ 9 Plots		
1	12.2	11.6
2	18.9	21.2
3	17.3	16.5
4	13.1	12.8
5	22.3	23.0
6	18.8	16.7
7	16.5	15.6
8	16.0	16.7
9	17.6	17.7

9.4.2   Stem Count Changes

This analysis produces a summary of the number of stems that were found alive at both measurements (Matched Stem Current Freq n), the number of stems that have died between measurements (Unmatched Stem Previous Freq n), and the number of new stems (Recruit Stem Current Freq n). These numbers are summarised by species across all plots (or by plot groups, if specified). This analysis also shows the number of stems that exceed the **Extreme Change Thresholds** for growth (Extreme+ Stem Current Freq n) and shrinkage (Extreme− Stem Current Freq n) to alert the user to potential errors in the data. Double-clicking on cells displaying Extreme values allows the user to examine the 'current' measurement data for these stems.

1 2 3 4 5 *	Recruit Stem	Unmatched Stem	Matched Stem	Extreme + Stem	Extreme - Stem
ANCHOR ISLAND FOREST	Current Freq	Previous Freq	Current Freq	Current Freq	Current Freq
Stem Count changes - All Plots	n	n	n	n	n
▬ Trend - Diameter	38	51	557	3	7
◻ 25 Species					
⊞ ASCLUC		2	2		
⊞ COPCIL			2		
⊞ COPFOE	1	3	15		
⊞ CYASMI			3		
⊞ DACCUP	2		6	1	
⊞ DICSQU	7	21	79		
⊞ DRALON			15		
⊞ ELAHOO		1	7		
⊞ GRILIT			2		

Expanding a species node displays these statistics by 10-cm size class within the species:

	Recruit Stem	Unmatched Stem	Matched Stem	Extreme + Stem	Extreme - Stem
ANCHOR ISLAND FOREST	Current Freq	Previous Freq	Current Freq	Current Freq	Current Freq
Stem Count changes - All Plots	**n**	**n**	**n**	**n**	**n**
Trend - Diameter	38	51	557	3	7
25 Species					
ASCLUC		2	2		
COPCIL			2		
COPFOE	1	3	15		
CYASMI			3		
DACCUP	2		6	1	
Current Diameter (cm)					
0<10	2		1		
40<50			1		
70<80			3		
>=90			1	1	
DICSQU	7	21	79		

9.4.3 Basal Area Changes

The 'Basal Area Changes - All Plots' analysis displays changes in stem basal area (BA, sq m/ha or $m^2\,ha^{-1}$) across all plots for all species, and across all plots for individual species. The analysis calculates BA from the initial measurement and BA from the final measurement and summarises change in BA attributable to four processes:

- **Decrease Basal Area:** these are matched stems between measurements that have shrunk in size.

- **Increase Basal Area:** these are matched stems between measurements that have grown in size.

- **Ingrowth Basal Area:** these are new stems.

- **Mortality Basal Area:** these are stems that have died from the initial measurement.

These four processes are summarised as follows:

Net growth: Increase Basal Area + Decrease Basal Area

Growth: Net growth + Ingrowth Basal Area

Net: Growth − Mortality Basal Area. This is the absolute change in BA between measurements.

1 2 3 4 5 *	Initial Basal Area	Decrease Basal Area	Increase Basal Area	Net Growth	Ingrowth Basal Area	Growth	Mortality Basal Area	Net	Final Basal Area
ANCHOR ISLAND FOREST	Previous Mean AP	Mean AP Chg	Mean AP Chg		Current Mean AP		Previous Mean AP		Current Mean AP
Basal Area changes - All Plots	sq m/ha	sq m/ha	sq m/ha		sq m/ha		sq m/ha		sq m/ha
Trend - Diameter	55.57	2.57	0.61	-1.97		2.55	0.59	1.19	-0.60	57.53
25 Species									
ASCLUC	0.01	<0.01		<0.01		<0.01		<0.01	0.05
COPCIL	<0.01	<0.01		<0.01		<0.01		<0.01	<0.01
COPFOE	0.12	<0.01	<0.01	<0.01		<0.01	<0.01	<0.01	0.14
CYASMI	0.12	<0.01	<0.01	<0.01		<0.01		<0.01	0.11
DACCUP	4.17	0.11	0.07	-0.04		-0.04	0.01	-0.05	4.12
DICSQU	2.74	0.05	0.18	0.13	1.77	1.90	0.20	1.70	4.97
DRALON	0.23	0.03		-0.03		-0.03		-0.03	0.21
ELAHOO	0.20	0.01		-0.01		-0.01		-0.01	0.31
GRILIT	0.20	0.01	<0.01	-0.01		-0.01		-0.01	0.20

These calculations exclude dead stems and stems beyond the **Extreme Change Thresholds.**

Expanding a species node displays these statistics by 10-cm size class within the species as in Stem Count Changes above.

Changes can be displayed in histograms. For example, the histogram below displays net growth by species. Note that the graphing facility does not allow all species codes to be displayed. Holding the cursor over any bar displays the associated species code.
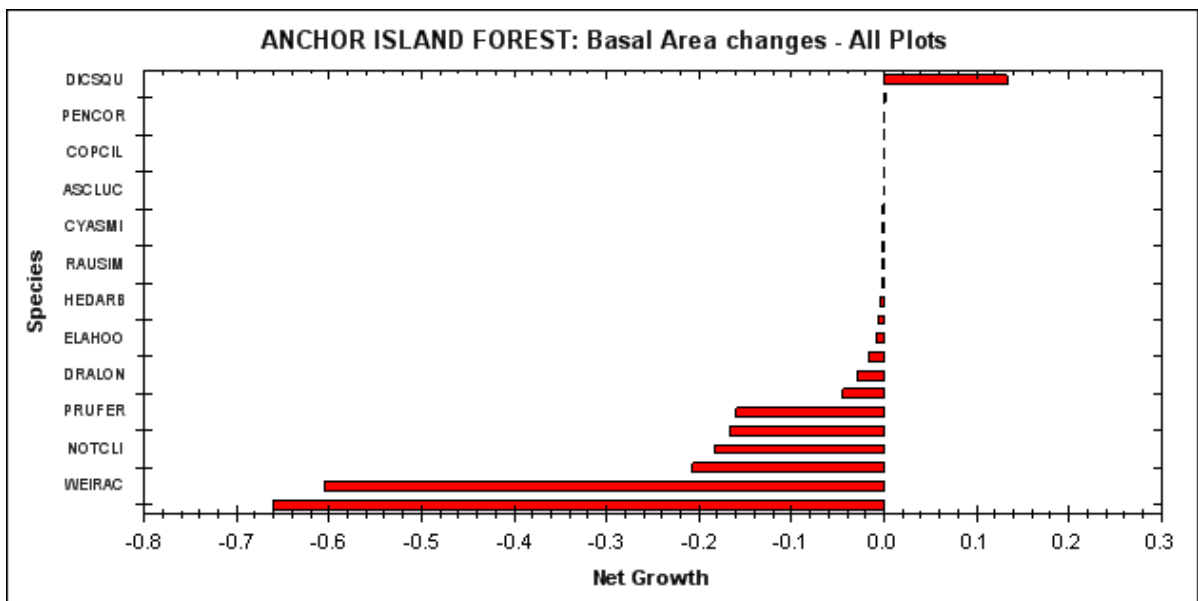
If the **Analyse per Plot where optional** checkbox has been ticked, an additional tab for 'Basal Area Changes - Per Plot' appears in the results. This analysis displays the same statistics as above for each plot (across all species):

1 2 3 4 5 6 7 *	Initial Basal Area	Decrease Basal Area	Increase Basal Area	Net Growth	Ingrowth Basal Area	Growth	Mortality Basal Area	Net	Final Basal Area
ANCHOR ISLAND FOREST	Previous Mean AP	Mean AP Chg	Mean AP Chg		Current Mean AP		Previous Mean AP		Current Mean AP
Basal Area changes - Per Plot	sq m/ha	sq m/ha	sq m/ha		sq m/ha		sq m/ha		sq m/ha
Trend - Diameter	55.57	2.57	0.61	-1.97	2.55	0.59	1.19	-0.80	57.53
9 Plots									
1	49.71	3.43	0.06	-3.37	0.43	-2.94	0.48	-3.43	47.72
2	73.70	5.18	0.21	-4.97	5.18	0.21	5.33	-5.13	69.32
3	50.95	2.47	0.32	-2.14	15.90	13.76	0.75	13.00	64.00
4	49.46	2.92	1.34	-1.58		-1.58	0.23	-1.81	47.66
5	44.98	1.02	0.31	-0.71		-0.71	0.39	-1.10	45.03
6	55.85	3.06	0.24	-2.81		-2.81		-2.81	54.12
7	55.30	1.62	0.36	-1.27	0.03	-1.24	1.09	-2.33	53.06
8	45.95	1.62	0.89	-0.74		-0.74	0.10	-0.84	56.34
9	74.16	1.85	1.74	-0.11	1.44	1.33	2.33	-1.00	80.55

Expanding a plot node displays the above statistics for each species on the plot. Expanding the species node, in turn, displays the statistics by size classes of that species:

1 2 3 4 5 6 7 *	Initial Basal Area	Decrease Basal Area	Increase Basal Area	Net Growth	Ingrowth Basal Area	Growth	Mortality Basal Area	Net	Final Basal Area
ANCHOR ISLAND FOREST	Previous Mean AP	Mean AP Chg	Mean AP Chg		Current Mean AP		Previous Mean AP		Current Mean AP
Basal Area changes - By Plot	sq m/ha	sq m/ha	sq m/ha		sq m/ha		sq m/ha		sq m/ha
Trend - Diameter	57.53	0.61	2.57	1.97	1.19	3.16	5.12	-1.96	55.57
9 Plots									
1	47.72	0.06	3.41	3.36	0.48	3.84	1.85	1.99	49.71
14 Species									
ASCLUC	0.46		<0.01	<0.01		<0.01	0.35	-0.35	0.11
COPCIL	0.04		<0.01	<0.01		<0.01		<0.01	0.04
COPFOE	0.23	0.01	0.01	<0.01	0.02	0.02	0.03	<0.01	0.23
CYASMI	0.63		0.02	0.02		0.02		0.02	1.66
DACCUP	10.35		0.40	0.40		0.40		0.40	10.75
ELAHOO	1.10		<0.01	<0.01		<0.01	0.99	-0.99	0.11
MYRAUS	0.03	0.01		-0.01		-0.01		-0.01	0.03
NEOPED	0.07		<0.01	<0.01		<0.01		<0.01	0.07
NOTMEN	16.63		1.53	1.53		1.53		1.53	18.17
Current Diameter (cm):									
10<20	0.23		0.03	0.03		0.03		0.03	0.26
60<70	7.02		0.65	0.65		0.65		0.65	7.67
70<80	9.38		0.86	0.86		0.86		0.86	10.24
PENCOR	0.22	<0.01		<0.01		<0.01		<0.01	0.21

9.4.4 Annual Diameter Growth

The 'Annual Diameter Growth - All Plots' analysis summarises the mean (Diameter Mean Chg/year cm) and standard deviation (Diameter StdDv Chg/year cm) of annual diameter growth of tagged stems between measurements across all plots (or plot groups, if specified). Data is presented across all species, and by individual species. These calculations exclude dead stems and stems beyond the **Extreme Change Thresholds.** The default units for annual diameter growth are centimetres but this may be inappropriate for surveys with slow-growing tree species. The units can be changed to millimetres using the **Units** tool found by clicking the **Properties** button (see Appendix 2 for further instructions on editing properties).

1 2 3 4 5 *	Diameter	Diameter
ANCHOR ISLAND FOREST	**Mean Chg/year**	**Std Dv Chg/year**
Annual Diameter Growth - All Plots	**cm**	**cm**
⊟ Trend - Diameter	0.04	0.15
⊟ 25 Species		
⊞ ASCLUC	0.02	0.02
⊞ COPCIL	0.01	0.01
⊞ COPFOE	<0.01	0.05
⊞ CYASMI	0.02	0.06
⊟ DACCUP	0.07	0.25
⊟ Current Diameter (cm)		
0.0<10.0	0.00	
40.0<50.0	0.19	
70.0<80.0	0.05	0.34
⊞ DICSQU	-0.06	0.11
⊞ DRALON	0.09	0.06

Expanding a species node displays these statistics by 10-cm size class within the species as in Stem Count Changes above.

If the **Analyse per Plot where optional** checkbox is ticked, an additional tab for 'Annual Diameter Growth - Per Plot' appears in the results. This analysis displays the same statistics as above for each plot (across all species):

1 2 3 4 5 6 7 *	Diameter	Diameter
ANCHOR ISLAND FOREST	**Mean Chg/year**	**Std Dv Chg/year**
Annual Diameter Growth - By Plot	**cm**	**cm**
⊟ Trend - Diameter	0.04	0.15
⊟ 9 Plots		
⊟ 1	0.07	0.10
⊟ 14 Species		
⊞ ASCLUC	0.02	0.02
⊞ COPCIL	0.01	0.01
⊞ COPFOE	-0.01	0.06
⊞ CYASMI	0.04	0.06
⊞ DACCUP	0.24	
⊞ ELAHOO	0.02	
⊞ MYRAUS	-0.07	
⊞ NEOPED	0.01	0.01
⊟ NOTMEN	0.36	0.23
⊟ Current Diameter (cm)		
10<20	0.10	
60<70	0.46	
70<80	0.52	
⊞ PENCOR	-0.02	
⊞ PODHAL	0.12	0.12
⊞ PRUFER	0.06	0.10
⊞ PSECOL	0.01	0.01
⊞ WEIRAC	0.07	0.06
⊞ 2	0.07	0.28

9.4.5 Diameter Growth Intervals

The 'Diameter Growth Intervals - All Plots' analysis summarises the amount of diameter growth per stem, so that the range of values measured for each species can be examined. For each species, the mean number of individuals per hectare (Stem Current Mean AP n/ha) is displayed. Expanding a species node displays the mean number that have grown by each diameter-growth interval (i.e. <0 cm, 0 to <0.5 cm, etc.). These calculations exclude dead stems and stems beyond the **Extreme Change Thresholds.**

1 2 3 4 5 * ANCHOR ISLAND FOREST Diameter Growth Intervals - All Plots	Stem Current Mean AP n/ha
☐ Trend - Diameter	1,777.8
☐ 25 Species	
⊞ 🌳 ASCLUC	11.1
⊞ 🌳 COPCIL	5.6
⊞ 🌳 COPFOE	52.8
⊞ 🌳 CYASMI	8.3
☐ 🌳 DACCUP	22.2
☐ Diameter (cm) Chg/year	
<0	2.8
0<0.5	16.7
>=2.0	2.8
⊞ 🌳 DICSQU	294.4
⊞ 🌳 DRALON	41.7
⊞ 🌳 ELAHOO	22.2

The results may be more readily interpreted by displaying a stacked bar graph (note that hovering the mouse over a bar will display the species name):
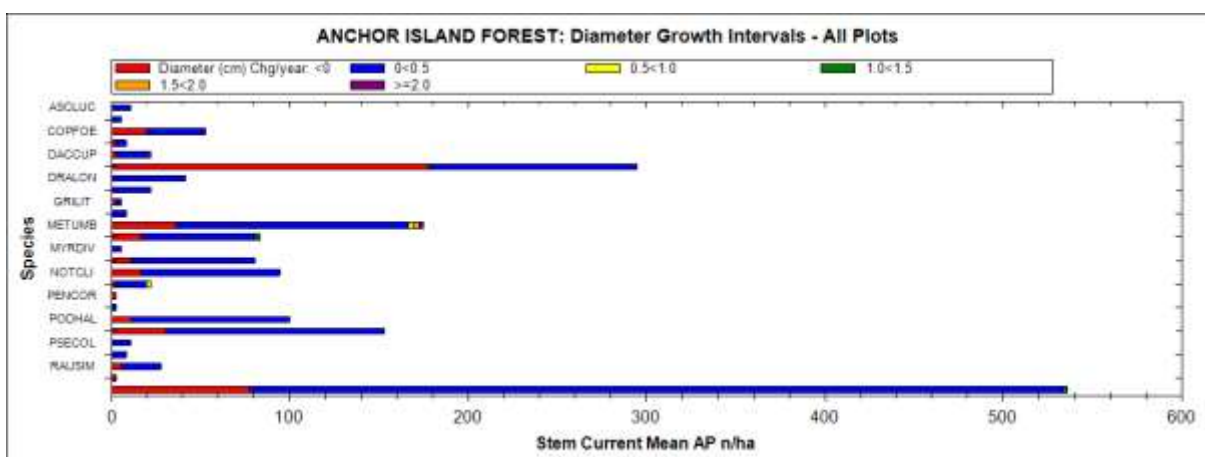
If the **Analyse per Plot where optional** checkbox is ticked, an additional tab for 'Diameter Growth Intervals - Per Plot' appears in the results. This analysis displays the same statistics as above for each plot (across all species):

1 2 3 4 5 6 7 *	Stem
ANCHOR ISLAND FOREST	Current Mean AP
Diameter Growth Intervals - By Plot	n/ha
☐ Trend - Diameter	1,777.8
☐ 9 Plots	
☐ 1	2,100.0
☐ 14 Species	
☐ ASCLUC	100.0
☐ COPCIL	50.0
☐ COPFOE	200.0
☐ CYASMI	50.0
☐ DACCUP	25.0
☐ ELAHOO	50.0
☐ MYRAUS	25.0
☐ NEOPED	50.0
☐ NOTMEN	75.0
☐ Diameter (cm) Chg/year	
0<0.5	50.0
0.5<1.0	25.0
☐ PENCOR	25.0
☐ PODHAL	125.0
☐ PRUFER	225.0
☐ PSECOL	50.0
☐ WEIRAC	1,050.0
☐ 2	1,575.0

9.4.6   Stem Changes

The 'Stem Changes - All Plots' analysis summarises the mean number of new stems that have been tagged (i.e. recruitment) onto the plots since the previous measurement, and the mean number of stems that have died (i.e. mortality) on the plots since the previous measurement.

For recruitment, the analysis displays the mean number of new stems across all plots, expressed per hectare (New Stem Current Mean AP n/ha), the overall recruitment rate (the mean number of new stems divided by the mean number of stems in the previous measurement; % Recruitment) and the annualised recruitment rate (% Recruitment pa) after McCune & Cottam (1985):

% recruitment per year = $(1 + B_x)^{1/x} - 1$, where B_x is the proportion of new stems for period x.

For mortality, the analysis displays the mean number of stems across all plots that have died since the previous measurement (Dead Stem Previous Mean AP n/ha), the overall mortality rate (the mean number of dead stems divided by the mean number of stems in the first measurement; % Mortality) and the annualised mortality rate (% Mortality pa) after McCune & Cottam (1985) and Runkle (1990):

$$\% \text{ mortality per year} = 1 - (1 - Q_x)^{1/x}, \text{ where } Q_x \text{ is the proportion of dead stems for}$$
period x.

In the example below, the display has been sorted by % Recruitment (descending). Species with no recruitment are displayed at the bottom of the list:

1 2 3 4 5 * ANCHOR ISLAND FOREST Stem Changes - All Plots	New Stem Current Mean AP n/ha	Original Stem Previous Mean AP n/ha	% Recruitment	% Recruitment pa	Dead Stem Previous Mean AP n/ha	% Mortality	% Mortality pa
Trend - Diameter	105.6	1,688.9	6.3	1.0	141.7	8.4	1.4
25 Species							
HEDARB	2.8	5.6	50.0	7.8			
NEOPED	22.2	58.3	38.1	5.5	2.8	4.8	0.8
DACCUP	5.6	16.7	33.3	4.9			
PSECOL	2.8	8.3	33.3	4.9			
PRUFER	11.1	141.7	7.8	1.3	2.8	2.0	0.3
DICSQU	19.4	277.8	7.0	1.1	58.3	21.0	3.9
MYRAUS	5.6	80.6	6.9	1.1	5.6	6.9	1.2
PODHAL	5.6	97.2	5.7	0.9	8.3	8.6	1.5
COPFOE	2.8	50.0	5.6	0.9	8.3	16.7	3.0
WEIRAC	25.0	516.7	4.8	0.8	22.2	4.3	0.7
NOTCLI	2.8	91.7	3.0	0.5	11.1	12.1	2.1
ASCLUC		11.1			5.6	50.0	
COPCIL		5.6					

The graphing option only displays those species for which there was recruitment:

ANCHOR ISLAND FOREST: Stem Changes
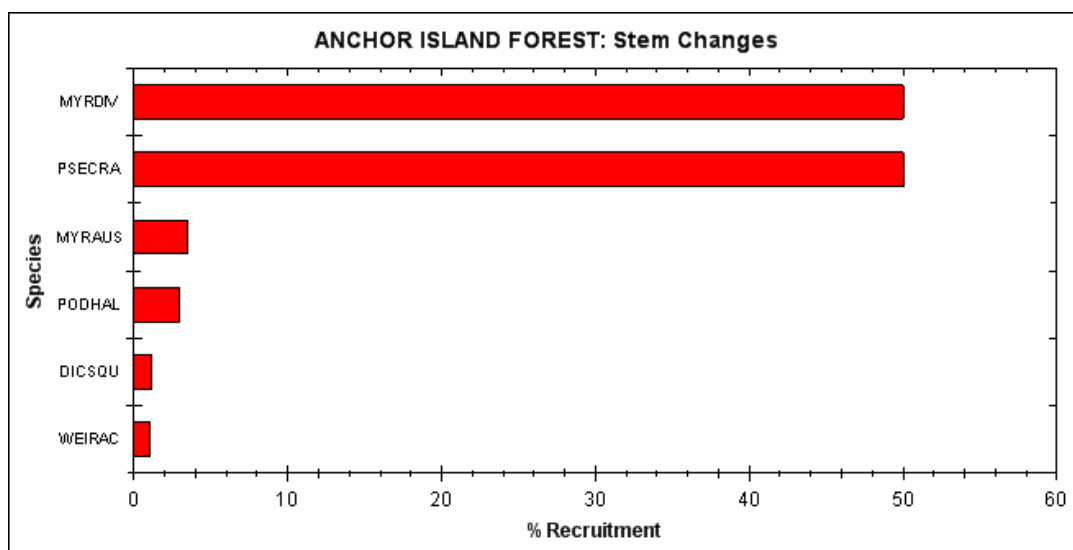
If the **Analyse per Plot where optional** checkbox has been ticked, an additional tab for 'Stem Changes - Per Plot' appears in the results. This analysis displays the same statistics as above for each plot and each node can be expanded to display further details:

1 2 3 4 5 6 7 * ANCHOR ISLAND FOREST Stem Changes - By Plot	New Stem Current Mean AP n/ha	Original Stem Previous Mean AP n/ha	% Recruitment	% Recruitment pa	Dead Stem Previous Mean AP n/ha	% Mortality	% Mortality pa
Trend - Diameter	105.6	1,688.9	6.3	1.0	141.7	8.4	1.4
9 Plots							
1	75.0	2,050.0	3.7	0.6	150.0	7.3	1.3
14 Species							
ASCLUC		100.0			50.0	50.0	
COPCIL		50.0					
COPFOE	25.0	175.0	14.3	2.2	25.0	14.3	2.5
CYASM1		50.0					
DACCUP		25.0					
Current Diameter (cm)							
70<80		25.0					
ELAHOO		50.0			25.0	50.0	

10 Multivariate analyses

Classification and ordination are multivariate techniques used to reduce large, multidimensional datasets to meaningful entities or to manageable dimensions that the ecologist can examine, interpret, and describe. It is possible to do this manually to some extent by comparing species patterns and collating plot sheets with similar species associations, but as the number of plots and species increases, this task becomes time-consuming and the need for computational assistance becomes more necessary. For more details about the theory behind multivariate analyses or how they work mathematically see McCune et al. (2002).

There are a number of algorithms for classifying and ordinating vegetation composition data and some excellent commercial software packages that are easy to use and provide the ability to produce publication-quality graphs. Example of these are CANOCO (ter Braak & Šmilauer 2002), and PC-Ord (McCune & Mefford 1999). For R-Language users, the package Vegan (Oksanen et al. 2013) is recommended. The NVS Express Summary and Analysis software package can export data in the formats required by these more sophisticated packages.

10.1 Generating an input file for multivariate analyses

Multivariate analyses require an **Intermediate File,** which contains species importance values. When the 'Multivariate Analyses' item is selected, the initial screen allows the user to select options for generating this file.

10.1.1 What are Importance Values?

Multivariate analyses require one value of abundance, or ecological importance, for each species on each plot. Where there are multiple values collected for a species on a plot (e.g. cover scores in different height tiers, density values in different subplots, etc.), an overall value for ecological importance must be constructed for the plot. Constructing these values is a critical step in the analysis. 'Importance Values' act as mathematical weights, whose relative sizes measure how similar or dissimilar one plot may be to another and hence what community classifications or ordination gradients are produced. By changing height tier or cover class weights or by applying different data transformations, results can vary considerably. See Van der Maarel (1979), McCune et al. (2002) and Leps & Smilauer (2003) for more detail.

For a **Recce** plot, an individual species' Importance Value S_j in a plot is calculated by summing the height tier (t) weights by the cover (c) weights, i.e.

$$S_j = \sum_{i=1}^{7} (t_i \times c_k)$$

where i=1, ...,7 are height tier weights, one per height tier, and k=1, ...n are the cover weights, one per class.

S_j is calculated for every species in a plot.

For **tree diameter** data, an individual species' Importance Value in a plot may be calculated in the following ways:

Basal area per hectare:

$$S_j = \sum_{i} \pi \, (d_{ij}/2)^2 / \text{plot\_area} \,,$$

where d_{ij} is the ith diameter (in metres) of species j and *plot_ area* is the plot area in hectares.

Relative basal area:

$$S_j = BA/(j) / \sum_j BA(j) \times 100 \, ,$$

where $BA(j)$ is the basal area of the jth species.

Stem density per hectare

$$S_j = n_j / plot\_area \, ,$$

where n_j is the number of diameters for species j and $plot\_area$ is the plot area in hectares.

For **seedling or sapling** data an individual species' Importance Value in a plot may be calculated in the following ways:

Frequency:

$$S_j = \sum_i f_{ij}$$

where f_{ij} is 1 if the species j was recorded in seedling or sapling subplot i, or 0 otherwise.

Relative frequency:

$$S_j = \sum_i f_{ij} / \sum \sum f_{ij} \times 100$$

where f_{ij} is 1 if the species j was recorded in seedling or sapling subplot i, or 0 otherwise.

Density per square metre is the number of seedlings or saplings of a species converted to a standard area:

$$S_j = \sum_i n_{ij} / \sum_i subplot\ area_i$$

where n_j is the number of stems of species j in seedling or sapling subplot i, *subplot_area$_i$* is the subplot area in metres.

Relative density is the percentage density of the species over the total density of all species:

$$S_j = \sum_i n_{ij} / \sum_{ij} \sum n_{ij}$$

where n_j is the number of stems of species j in seedling or sapling subplot i.

Combined relative frequency and density is the mean of the two relative measures for a species:

$$\left(\left(\sum_i f_{ij} / \sum_{ij} \sum f_{ij} \right) + \left(\sum_i n_{ij} / \sum_{ij} \sum n_{ij} \right) \right) \times 50$$

where f_{ij} is 1 if the species j was recorded in seedling or sapling subplot i, or 0 otherwise and is the number of stems of species j in seedling or sapling subplot i.

10.1.2 Creating a file for multivariate analysis

When the '**Multivariate Analyses**' item is selected, this screen appears:
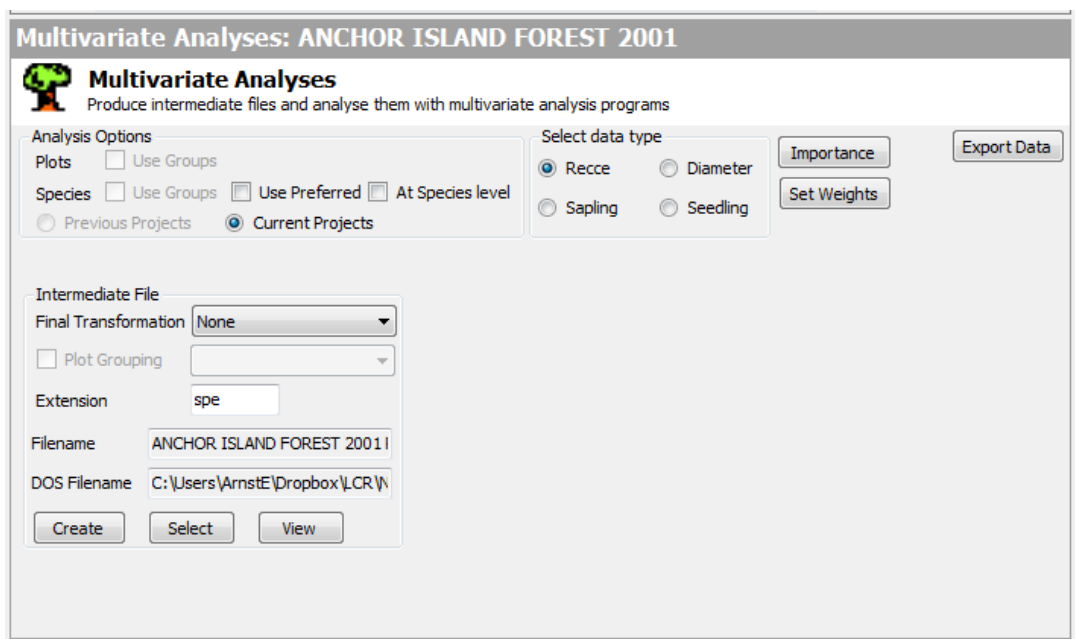
The workflow process is as follows:

1   Select the data to be used under **Analysis Options**.

2   Select the data type (measurement method) to be used under **Select data type**.

3   If desired, set the Importance Values to be used by using the **Set Weights** button.

4   Select the final transformation type required (if any)

5   Enter the extension

6   Create an Intermediate File.

7   Export the intermediate file to appropriate package for analysis.

As a first step the user selects the method (Recce, Seedling, Sapling and/or Diameter) of the data being analysed. Once the method is selected, the remaining options on the screen become available.

If 'Recce' is selected:
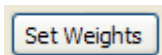
Set Weights   Allows cover class or height tier weightings to be changed. Users can enter their own weights or use those generated by choosing an option from the following picklists for tiers and covers and pressing 'Select Weights':

Default: cover classes are weighted by their midpoints and all height tiers are weighted equally

Equal: all cover class/height tiers weighted equally

Numerical: weights equal numeric value of cover class/height tier

Lower bound: weights set to lower bound of cover class/height tier

Mid point: weights set to midpoint of cover class/height tier

Upper bound: weights set to upper bound of cover class/height tier

To remove an individual cover class or height tier from the analysis, set its weight to zero by typing this into the 'Set Weights' table.

If 'Seedling', 'Sapling' or 'Diameter' is selected, users can select the Importance Value method to apply (see above) using a picklist.

The cover class list used to generate the weighted values can then be saved for future use by using the 'Create' option under 'Cover Class List' in the **Set Weights** screen. Cover class weights can then be imported using the 'Import' option, as shown below.
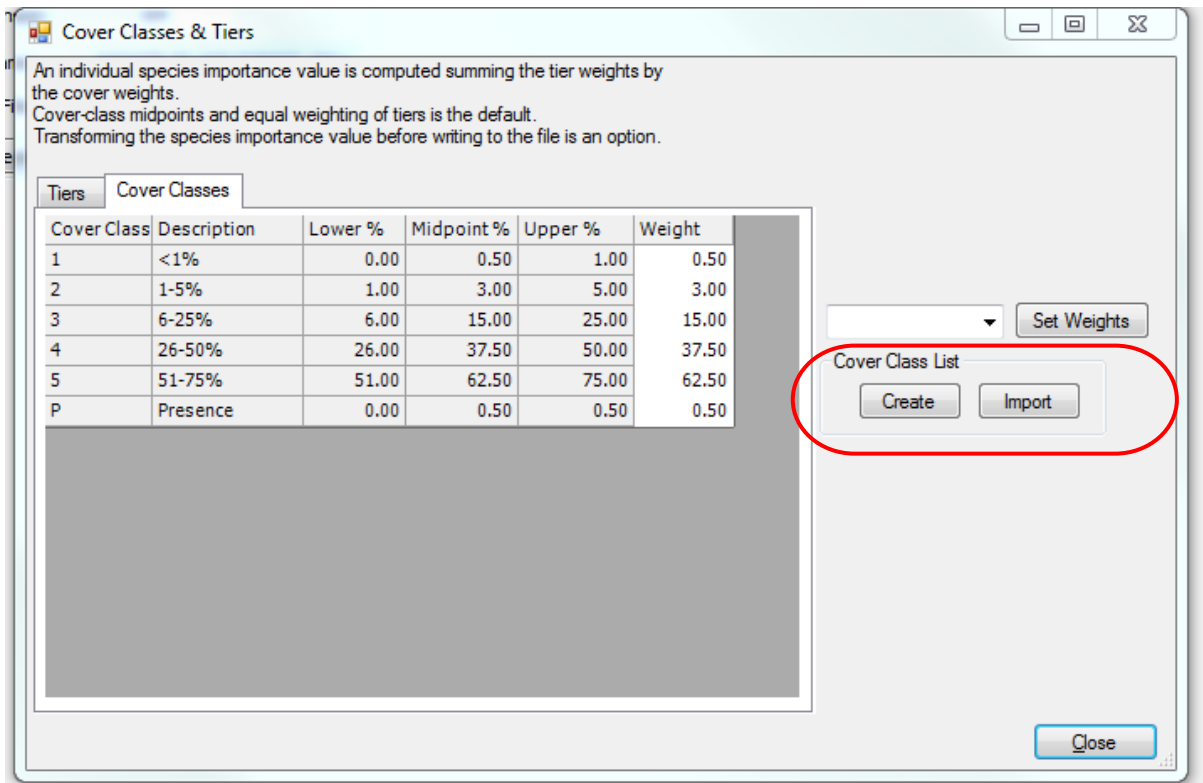
For all methods, users can view the initial stage of calculating the Importance Values by pressing the **Importance** button, as displayed below.

123* 9 Plots: ANCHOR ISLAND FOREST Recce Importance	1 ANC07 Importance Mean AP	2 ANC07 Importance Mean AP	3 ANC07 Importance Mean AP	4 ANC07 Importance Mean AP	5 ANC07 Importance Mean AP	6 ANC07 Importance Mean AP	7 ANC07 Importance Mean AP	8 ANC07 Importance Mean AP	9 ANC07 Importance Mean AP	Overall Importance Mean AP
Current - Recce										
90 Species, Top, >=0.1										
WEIRAC	61.50	34.00	20.00	73.50	34.50	33.50	22.50	1.50	54.00	37.22
BLEPRO	6.00	18.00	18.00	6.00	18.00	75.00	5.00	150.50	3.50	33.44
PRUPER	19.50	36.50	10.00	22.00	36.50	15.00	22.50	12.00	7.50	20.17
METUMB	0.50	17.00	20.00		42.50	19.50		21.50	53.50	19.39
DACCUP	15.50	46.00	1.00	31.50	3.50	4.00	39.50	1.00	1.50	15.94
PODHAL	5.50	21.50	18.50	11.00	25.00	12.50	19.50	1.50	3.50	13.17
DICSQU	1.00	6.50	18.50		21.00	1.50	1.00	1.00	55.50	11.78
NEOPED	6.50	33.00	1.50	33.00	1.00	1.00	21.00	1.00	1.00	11.00
NOTCLI	0.50			7.00		36.50	5.00	24.50		8.17
COPFOE	7.00	19.00	5.00	6.50	7.00	4.50	1.50	18.00	1.50	7.78
NOTMEN	38.00			1.50			5.00			4.94
BLEDIS	6.00	1.00		18.00		0.50	18.00			4.83
RAUSIM	1.50	2.00	7.00	1.00	1.50	1.00	2.00	1.00	16.50	3.72
MYRAUS	1.50	10.00	5.00	0.50	4.50	4.50	2.50	1.50	1.50	3.50
PSECOL	4.00	1.00	13.50		0.50		4.00	0.50		2.83
RUMADI			1.50			1.00			18.50	2.33
ASCLUC	4.50	6.00	2.00	1.00	1.00	3.50	1.50	0.50		2.22
COPCIL	3.50		1.50	1.00	3.50	1.00	1.50	6.00	1.50	2.17
CYASMI	6.50	1.00	1.00	0.50	0.50	0.50	0.50		9.00	2.17
MYRDIV	3.50	1.50	1.50		0.50	0.50	4.00	7.00	0.50	2.11
Other Species										

Clicking the **Importance** button generates the weighted values by species using the cover class and height tier weight settings displayed (Recce) or raw density and frequency values (Seedlings and Saplings) and raw diameter and stem density values (Trees) to produce a species-by-plot table of these values. Relativisation is not done until the importance values are written to the intermediate file.

The next step is to create the **Intermediate File**, using the section of the form below.

As the name suggests, the **Intermediate file** is the go-between file between the raw data and multivariate analyses. It must be created before the data can be analysed. The Intermediate File contains 'Importance Values', which may or may not be transformed and may or may not be based on plot groups. If the data has been loaded with plot groups (the 'Use Groups' box has been checked under 'Analysis Options') then the **Plot Grouping** option will be enabled. If the **Plot Grouping** checkbox is ticked, then importance values are calculated across plot groups rather than by individual plots.

NOTE: If 'Use Plot Groups' or 'Use Species Groups' is ticked but 'Plot Grouping' is not then the plots or species analysed are limited to those predefined in the groups. In this case the generated Intermediate Files are still organised by Plot or Species for the actual analyses.

Transformations affect the Importance Value distribution and range, with the general aim being to prevent any species or species attribute from dominating the multivariate analyses. There are no general rules about which transformation will lead to the clearest interpretation of the data. For further information see Jensen (1978) or van der Maarel (1979).

The following transformations may be selected from the 'Final Transformation' drop-down list:

None no transformation of the data.

ArcsineSquareRoot is used to normalise data in percentages or proportions whose distributions fit the binomial distribution.

Natural Log applies a natural logarithmic transformation. This reduces relative differences between the highest and lowest species Importance Values so presences are not swamped by the higher dominant species.

Common Log$_{10}$ performs a base-10 logarithmic transformation, to lessen the relative differences between the largest and smallest Importance Values. This stresses the presence/absence component of the Importance Value at the expense of the structural information. After applying this transformation, a factor of 100 difference between two values becomes a factor of 2. Values are compressed more by this than by a natural logarithmic transformation.

Presence/Absence avoids problems with constructing Importance Values by ignoring the cover and height tier data. Only the species presence in each plot is used.

Square Root is best applied to count data such as seedling, sapling or tree   density

The default **Intermediate File** extension is .spe.

After any transformations or plot groups are applied and the file extension has been specified:
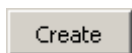
| Create | creates the Intermediate File and allows the user to save it to a specified directory. |

| Select | allows the user to select an Intermediate File that has previously been saved. |

| View | allows the user to view the intermediate file in Notepad. |
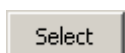
11 Troubleshooting

If you experience any difficulty in the use of this program please feel free to contact the NVS Database Administrator (nvs@landcareresearch.co.nz) for advice.

NVS Express we are interested in any feedback that you may have. If you get any error messages whilst using this program please contact us. Knowing exactly what was being done and receiving the text of the error will help us isolate the problem. If you get a message that includes the note "Full details have been copied to the clipboard" the error details have been copied onto the windows clipboard. This means that the error can be pasted into an email or word document.

12 References

Allen RB, Bellingham PJ, Wiser SK 1999. Immediate damage by an earthquake to a temperate montane forest. Ecology 80: 708–714.

Bellingham PJ, Stewart GH, Allen RB 1999. Tree species richness and turnover throughout New Zealand forests. Journal of Vegetation Science 10: 825–832.

Richardson S, Wiser S, Cooper J, Spencer N 2005. Adding value to the National Vegetation Survey (NVS) Databank: development of software tools for the analysis of vegetation data. Landcare Research Contract Report: LC0405/073; prepared for the Terrestrial and Freshwater Biodiversity Information System programme, Department of Conservation.

Wiser SK, Allen RB, Clinton PW, Platt KH 1998. Community structure and forest invasion by an exotic herb over 23 years. Ecology 79: 2071–2081.

Wiser SK, Rose AB 1997. Two permanent plot methods for monitoring changes in grasslands: A field manual. 51p. Manaaki Whenua Landcare Research NZ Ltd, Christchurch, New Zealand)

13   Glossary

% Mortality -- the overall mortality rate. The percentage of the mean number of dead stems over the mean number of stems in the first measurement, across all plots. [percentage]

% Mortality pa -- annualised mortality rate (% Mortality pa) after McCune & Cottam (1985) and Runkle (1990):

% mortality per year = 1 − (1 − Qx)1/x, where Qx is the proportion of dead stems for period x. [percentage per year]

% Recruitment -- overall recruitment rate. A percentage of the mean number of new stems over the mean number of stems in the first measurement (across all plots). [percentage]

% Recruitment pa -- annualised recruitment rate after McCune & Cottam (1985):

% recruitment per year = (1 + Bx)1/x − 1, where Bx is the proportion of new stems for period x. [percentage per year]

AP -- all plots

Aspect /d -- aspect corrected for magnetic declination

BA -- basal area in m^2/ha or m^2ha-1

Basal Area Mean AP sqm/ha -- mean plot basal area in metres squared per hectare. [square metres per hectare]

Basal Area StdDv AP sqm/ha -- standard deviation of plot basal area. [square metres per hectare]

CANOCO -- software package for constrained and unconstrained ordination in ecological applications. (ter Braak & Šmilauer 2002).

Chg -- Change (abbreviation)

Circum -- circumference

Circum Mean AP m/ha -- mean plot stem circumference [metres per hectare]

Circum. StdDv AP m/ha -- standard deviation of mean plot stem circumference. [metres per hectare]

Cover Current Mean AP % -- mean percentage cover across all plots for the project marked as current. [percentage]

Cover Mean % -- mean percentage cover across all plots. [percentage]

Cover Mean AP % -- mean percentage cover of a species calculated across all plots. [percentage]

Cover Previous Mean AP % -- mean percentage cover across all plots for the project marked previous, should normally be the earlier measure of two. [percentage]

Data Summaries -- section in NVS-Analysis designed to retrieve and manipulate subsets of the raw data and to produce one-way, two-way and three-way tabular and graphical summaries.

Dead Stem Previous Mean AP n/ha -- mean number of stems that have died since the previous measurement across all plots [number per hectare]

Decrease Basal Area Mean AP Chg sq m/ha -- basal area of matched stems that have shrunk in size between measurements for all plots. [square metres per hectare]

Density Count Current Mean AP n/sq m -- density of individuals across all plots for the current measure. [number per square metre]

Density Count Mean AP n/sq m -- mean density per square metre. [number per square metre]

Density Count Previous Mean AP n/sq m -- mean density per square metre for the earliest measure. [number per square metre]

Density Count StdDv AP n/sq m -- standard deviation of the mean density. [number per square metre]

Diameter -- Field methodology for measuring trees as per Hurst & Allen 2007.

Diameter Mean Chg/Year cm -- mean of annual diameter growth of tagged stems since the previous measurement across all plots. [centimetres]

Diameter Mean cm (Plot mean) -- mean plot stem diameter [centimetres]

Diameter StdDv cm (Plot mean) -- standard deviation of plot stem diameter. [centimetres]

Diameter StDv Chg/Year cm -- standard deviation of the mean of annual diameter growth of tagged stems since the previous measurement across all plots. [centimetres]

Extreme Change Thresholds -- function to highlight unusually large changes in diameter. The program checks the data for possible errors using limits set for maximum annual growth and shrinkage.

Extreme- Stem Current Freq n -- number of stems that exceed the Extreme Change Thresholds for shrinkage. [number]

Extreme+ Stem Current Freq n -- number of stems that exceed the Extreme Change Thresholds for growth. [number]

Final Basal Area Current Mean AP sq m/ha -- basal area of the current (most recent) measure for all plots. [square metres per hectare]

Freq -- Frequency (abbreviation)

Growth -- Net growth + Ingrowth Basal Area [square metres per hectare]

Importance Values -- mathematical weights, whose relative sizes measure how similar or dissimilar one plot may be to another and hence what community classifications or ordination gradients are produced. Used in multivariate analyses. See Van der Maarel (1979), McCune et al. (2002) and Leps & Smilauer (2003) for more detail.

Increase Basal Area Mean AP Chg sq m/ha -- basal area of matched stems that have grown in size between measurements for all plots. [square metres per hectare]

Ingrowth Basal Area -- basal area of new (recruited) stems.

Ingrowth Basal Area Current Mean AP sq m/ha -- basal area of new (recruited in re-measurement) stems for all plots. [square metres per hectare]

Initial Basal Area Previous Mean AP sq m/ha -- basal area of previous (initial) measure for all plots. [square metres per hectare]

Matched -- stems that have survived between measurements.

Matched Diameter Current Mean cm -- mean diameter across all surviving (Matched) stems in each plot in the most recent measure. [centimetres]

Matched Diameter Previous Mean cm -- mean diameter across all surviving (Matched) stems in each plot in the earlier measurement. [centimetres]

Matched Stem Current Freq n -- number of stems that were found at both measurements. [number]

Method -- A method defines a general research or survey technique, e.g. Quadrat tree diameter (following Hurst & Allen 2007) or plot ground cover. A method may have many individual measured attributes, e.g. height, diameter, status, bare ground, soil. A measured attribute may be categorical or continuous.

Mortality Basal Area Previous Mean AP sq m/ha -- basal area of stems that have died after the initial measurement for all plots. [square metres per hectare]

Net -- Growth – Mortality Basal Area. This is the absolute change in BA between measurements. [square metres per hectare]

Net growth -- Increase Basal Area + Decrease Basal Area. [square metres per hectare]

New Stem Current Mean AP n/ha -- mean number of stems tagged since the previous measurement, expressed per hectare across all plots. [number per hectare]

NVS Species Code -- The NVS species code that uniquely links to a species name

Obs -- Observation (abbreviation), refers to a single measurement in time.

Opt -- Optional (abbreviation).

Original Stem Previous Mean AP n/ha -- mean number of stems per hectare from the earlier measurement across all plots. [number per hectare]

Overall Cover Mean % -- mean cover (after summing across height tiers) on plots where the species was recorded. [percentage]

Overall Cover Mean AP % -- mean cover (after summing across height tiers) across all plots. [percentage]

Overall Plot Freq % -- percentage frequency across all plots. [percentage]

Overall Plot Freq n -- total number of plots within each category level. [number]

Overall Species Freq n -- total number (i.e. richness) of species across all plots. [number]

Palatability - - Palatability to ungulates, as categorised by: Forsyth, D.M.; Coomes, D.A.; Nugent, G.; Hall, G.M.J. 2002: Diet and diet preferences of introduced ungulates (Order: Artiodactyla) in New Zealand. New Zealand Journal of Zoology 29: 323-343

PC-Ord   -- software package for multivariate analysis (McCune & Mefford 1999).

Plot % Freq --   percentage frequency of a variable across all plots. [percentage]

Plot Current Freq % -- percentage frequency of a variable across plots on the project designated current (normally the latest measure). [percentage]

Plot Freq n -- number of plots in the project where a variable was recorded. [number]

Plot Groups -- list that defines a classification of plots pertaining to a specific project.

Plot ID-- a unique NVS database ID for a particular plot

Plot Names or **Plot --** the name for a plot as assigned by the data providers.

Plot Previous Freq % -- percentage frequency of a variable across plots on the earlier measurement [percentage]

Preferred Species -- a function to update all taxonomy to preferred names as per Ngā Tipu Aotearoa – New Zealand Plants (http://nzflora.landcareresearch.co.nz/)

Previous -- measurement not marked as current in an analysis, should be the earlier of two measurements.

Project   -- all data and associated notes for a survey of a group of vegetation plots. Plots are usually in a restricted geographical region and were measured over a specific time period. Usually a project will cover a single season, but occasionally it will span two. When permanent plots are remeasured, that is considered a new project.

Recce -- Field methodology for measuring vegetation composition as per Hurst & Allen (2007).

Recce Obs – an observation of a species in a plot and height tier, corresponding to one cell in a Recce plot sheet or data entry screen.

Recce Obs Freq % -- percentage of Recce Obs that were the listed species. [percentage]

Recce Obs Freq n -- number of Recce Obs of a species. [number]

Recruit Stem Current Freq n -- number of new stems that have been taggged since the previous measurement. [number]

Site Description -- Abiotic factors for a plot, as per Hurst & Allen 2007.

Species Current Freq n -- total number of species in the project designated current (i.e. the most recent). [number]

Species Freq n -- total number of species. [number]

Species Groups -- list that defines a classification of species associated with a specific project.

Species Previous Freq n -- total number of species in the earlier of two projects. [number]

Std Dv – Standard Deviation (abbreviation)

Stem Current Mean AP n/ha -- mean number of individuals per hectare in the more recent of two projects. [number per hectare]

Stem Freq % -- percentage frequency of stems of each species across all stems recorded in all plots. [percentage]

Stem Freq n -- total number of stems recorded of each species [number]

Stem Mean AP n/ha -- mean stem density per hectare [number per hectare]

Stem StdDv AP n/ha -- standard deviation of stem density per hectare. [number per hectare]

SubPlot Current Freq % -- percentage of subplots where the species was recorded in the most recent of two projects. [percentage]

SubPlot Freq % -- percentage of subplots where a species was recorded. [percentage]

SubPlot Previous Freq % -- percentage of subplots where the species was recorded for the earliest of two projects. [percentage]

Taxon – Taxonomic name (abbreviation)

Taxon Obs – an observation of a species in a plot, corresponding to one row in a plot sheet or data entry screen. Applies to Recce, Seedling and Sapling data.

Taxon Obs Freq % -- percentage of Taxon Obs that were the listed species. [percentage]

Taxon Obs Freq n -- number of Taxon Obs of a species [number]. Applies to Recce, Seedling and Sapling data.

Temporal trends -- a section in NVS-Analysis for investigating changes in the data when plots have been remeasured.

Understorey -- understorey methods, comprising both counts of saplings within subplots by species (Quadrat sapling) and counts of seedlings within seedling subplots by species and height class (Quadrat seedling)(as per Hurst & Allen 2007).

Unmatched Stem Previous Freq n -- number of stems that have died between measurements. [number]

Vegan -- software package for multivariate analysis using R-Language.

Verbatim Species Code -- the species code as recorded on the original datasheet. This may not be a valid NVS code. It also may not resolve ambiguous species codes.

Appendix 1 – Data Entry Validation Errors and Their Resolution

There are a number of data entry validations that have been included in the NVS Express tool. The following is a list of the Data Entry Validation Messages:

Area is missing

> Reason: No area has been recorded for a plot or sub plot.

> Solution: Check the area and enter where possible.

Area differs from calculated value

> Reason: The area calculated using the tape lengths from the plot layout differs from that indicated by the size; e.g. a plot may be entered as 20 m × 20 m but have a calculated size of >400 due to differing tape lengths.

> Solution: Check that the tape lengths are entered correctly and that the difference is not significant. This validation is bringing this difference to your attention but it is not always a problem as the actual tape lengths are affected by terrain.

Counted Species Density - Species had density greater than the maximum

> Reason: The counts in Quadrat sapling or Quadrat seedling data exceed the maximum expected density for the species, which has been derived from existing data in the NVS databank.

> Solution: Check that the relevant data is entered correctly.

Deprecated Species – Species names no longer in use

> Reason: You have entered a species code that is in the NVS list but is no longer in active usage.

> Solution: Check the entry of this species. If this code is entered correctly, check that this is a recognised name through searching the New Zealand Plants Database at http://nzflora.landcareresearch.co.nz/

Diameter – Observations had diameter greater than their species maximum

> Reason: A stem has been entered with a diameter greater than the expected maximum size for the particular species, which has been derived from existing data in the NVS databank.

> Solution: Check that the stem has been entered correctly.

Duplicate Individual

Reason: There are duplicate tags within a plot or sub plot (stems without tags are excluded).

Solution: Check duplicates to see if they can be resolved. Sometimes duplicate tags can be resolved by reference to the tag sequence or previous measurements.

Duplicate Taxon

Reason: There are duplicate taxon rows within a plot or sub plot (for Recce, Quadrat seedling, Quadrat sapling). This validation will normally prevent saving the record after entry or editing.

Solution: Edit the first record of the species to include the data for both records. For example, if there are two Recce records for the same species, enter the species using the higher cover class recorded for each tier. For sapling and seedling data counts can be summed.

Individual Entry Validation – Item duplicate tag – Item has duplicate tag indicated: (* or ?)

Reason: There are multiple tags in a plot with the same tag number. One of these tags should be entered with a * followed by the last three tag digits (in older projects) or as the full tag number followed by ??

Solution: Check whether the tags were entered properly, whether it is a problem with reading the handwriting or with the use of two similar tag sequences. If it looks like an obvious recording error, please make an operator note against the tag.

If it is not possible to resolve these as being different numbers then leave them marked as duplicates.

Individual Entry Validation – Item Obs has missing tag

Reason: An individual item (normally a stem diameter) has been entered without a tag number

Solution: Check whether a tag number has been recorded. If it has been recorded, enter the tag number, otherwise a note should be made. This note can be a general note against the entire method (using the Notes option on the toolbar) in the case where no stems were tagged. Alternatively a specific operator note can be made against the individual stem (in the Notes column) where this is a single omission, e.g. [no tag recorded].

Taxon Entry Validation – Taxon Obs no data – Taxon Obs has no data entered, note: (if any)

See description under "Individual Entry Validation – Item Obs no data – Item Obs has no data entered, note: (if any)"

Individual Entry Validation – Item Obs query – Text of note ?

Reason: The note for an item observation (i.e. diameter or orthogonal width) contains '??'. This is usually used to denote a duplicate tag or another problem to be checked.

Solution: Check the reason for the note and resolve if possible.

Individual Entry Validation – Item Obs remeasure note – Remeasure note: Text of note $

Reason: A remeasurement note has been recorded (as described in the NVS-Data Entry manual (Vickers et al. 2009).

Solution: This is an operator note that is designed to bring a remeasurement issue to the attention of the NVS Administrator when the data is uploaded into the main NVS database. Appropriate notes include:

- $Tag corrected from xxx$ denotes a tag correction for an existing tag
- $Retag of xxx$ denotes a retag of an existing tag
- $ReID from xxx$ denotes the re-identification of a tagged individual
- $Subplot corrected from xxx$ denotes a change in the subplot that a tagged individual is measured in.
  Please see section 8.3.1 for further details.

Individual Entry Validation – Item Obs verbatim species code – Verbatim code is different to the species code

Reason: The 'verbatim' code entered differs from the species code selected for an individual item. This can occur for a couple of different reasons:

1. Where there are mis-spellings and the verbatim code is entered as recorded but a different code has been selected as the NVS code.

2. Where a tagged stem is remeasured with a different species identification. In this case the verbatim code represents what was recorded in the current year and the NVS species code shows what was recorded in previous year(s).

Solution: Check the reason for this difference.

1. It is acceptable to retain a different verbatim code where there is a mis-spelling as this shows where any assumptions have been made by the data entry operator.

2. Where there are two different identities for a tagged individual the NVS code can be changed when there was a clear note recorded stating that the new identification was checked and correct. This can only be done in the main NVS database. NVS Express Data Entry users need to record a remeasurement note in the following format: $ReID from [previous code]$

Individual Entry Validation – Missing Taxon – Taxon is missing
Taxon Entry Validation - Missing Taxon – Taxon is missing

Reason: A row has been entered without any species being recorded.

Solution: First check whether this is a data entry error.

Sometimes people will create a new row for a note, e.g. Seedling plot 13 'in stream'. This is not appropriate. Any such note should either go against an observation or into the general notes found on the toolbar.

If using the general notes remember to record which plot this refers to, e.g. Plot 1EX, seedling plot 13, in stream.

If there is a note that there are no species in a particular subplot then the code 'NOSPEC – No species on plot' can be used, rather than leaving the species blank. Be careful not to make assumptions where there are no recorded notes, as it is possible that a subplot may not have been measured rather than having no species present.

Individual Entry Validation – Species Mapping – Species is not the default for ...
Taxon Entry Validation – Species Mapping – Species is not the default for ...

Reason: Where there is a duplicate code (the intuitive six-letter code matches more than one species), one of the options has been selected as the default species for the project. Whenever this duplicate code is entered subsequently, the default species will be automatically selected. This validation is generated where there is a default selection but the same code has been used elsewhere in the project to represent one of the other duplicate options.

e.g. COPPSE is the intuitive code for two species: *Coprosma pseudocuneata* (NVS code = COPPSE) & *Coprosma pseudociliata* (NVS code = COPPSC). If a default selection has been made so that all entries of COPPSE default to COPPSE *Coprosma pseudocuneata* then a validation will be brought up if COPPSC *Coprosma pseudociliata* is selected for the duplicate code COPPSE.

Solution: Check that the correct species has been selected for this duplicate code – you may have to check with the field staff. If you have selected the incorrect species, you can correct all entries in one action by using the 'Species Defaults' option on the

toolbar. Edit the species in the Species Default list and select the appropriate species. You should be asked if you want to update all occurrences of this species code.

It is also possible that both species might be present in the one project, in which case it is not appropriate to set a default code.

Individual Entry Validation – Unknown Taxon Verbatim – Taxon is unknown for Verbatim code

Reason: An unknown six-letter code has been entered. The code entered is not in the current NVS code list.

Solution: Check the recorded code with the field staff to obtain the full species name. If the recorded code is a misspelling, then enter the correct code in the NVS code field, leaving the Verbatim code as it is (unless a correction has been made to the original plotsheets). If the species is not on the NVS code list, please send the full species name to the NVS database administrator [Hazel Broadbent, nvs@landcareresearch.co.nz], who will generate a new code for you. In the interim, type the full species name into the Notes column.

If no definite species can be obtained for the recorded code, you may wish to discuss with the field staff whether this record should be removed. If this is the case, please make a note regarding this. When using the general notes remember to record which plot this refers to, e.g. Plot 1EX seedling plot 1: unknown code 'hairy herb' not entered.

Alternatively, if you wish to retain the species but it is not identified, you may assign it to a general descriptive NVS code, e.g. FERN, HERB, GRASS, TREEFE, ORCHID, DANDEL, THISTL. Note that we do not recommend the routine use of these codes – all possible attempts should be made to resolve species to specific or generic level.

Individual Species Density - Species had density greater than their maximum

Reason: The values of individuals, such as tagged stems, exceed the maximum expected density for the species, which has been derived from existing data.

Solution: Check that the relevant data is entered correctly.

Non-tree measured – Species entered is not on the validation list for this type of data – please check that the species code is correct

Reason: A species has been entered for a method where it is not on the list of validated species for the method.

Solution: Check that the species was recorded under the particular method. It may also be necessary to consider whether the inclusion of the species is consistent with the standard methodology, for example if a crown fern has been recorded as a sapling.

Operator note: Text of note []
Taxon Entry Validation – Taxon Obs operator note – Operator note: Text of note []

Reason: An operator note has been entered in the Notes field. This validation displays the content of the operator note.

Solution: Check to see whether this note requires any action.

Plot has no observations entered

Reason: This occurs in a subplot-based method (diameters, saplings, seedlings) when nothing has been recorded against a subplot.

Solution: Where there is a note that there were no individuals (e.g. 'no saplings in A') this validation can be removed by adding the code 'NOSPEC No species in plot' to the appropriate subplot (A in this example).

Recce Species – Some species measured in other Methods were not included in Recce

Reason: This occurs when a species was recorded on another method but was not recorded on the Recce.

Solution: To correct this omission please add the species as 'present' to the Recce as follows:

*For species in diameters – add as a presence in the 2-4 m tier with an operator note: [Added to Recce as recorded in diameter method]

*For Species in saplings – add as a presence in the 0.3–2 m tier with an operator note: [Added to Recce as recorded in sapling method]

*For species in seedlings – add as a presence in the appropriate tier (with reference to seedling tier, for seedlings 0-15 cm and 15-45 cm add as a presence in the 0–0.3 m tier and for seedlings >45 cm add as a presence in the 0.3–2 m tier on Recce) with an operator note: [Added to Recce as recorded in seedling method]

 Some things to watch for:

- Genera recordings: only add these if there is not a species in this genus already on the Recce.

- Synonyms (e.g. PSESIM = RAUSIM).

- Previous tag identifications will also come through on this validation so you may already have these under the current identification.

- Watch out for duplicate codes. If a duplicate is already present, determine whether both or only one of the duplicates are present before adding.

Individual Entry Validation – Missing Taxon – Taxon is missing

See description under " Taxon Entry Validation - Missing Taxon – Taxon is missing"

Taxon Entry Validation – Taxon Obs operator note – Operator note: Text of note []

See description under "*Operator note: Text of note []*"

Taxon Entry Validation – Taxon Obs no data – Taxon Obs has no data entered, note: (if any)
Individual Entry Validation – Item Obs no data – Item Obs has no data entered, note: (if any)

Reason: A species or tag has been entered with no data against it.

Solution: Check whether this data has been entered correctly. If no data was recorded for the species, you can make an operator note, e.g. [no data recorded for this species]. For sapling and seedling records it is often possible to make an assumption, as long as the assumption is recorded. For saplings it is often assumed that if a species has no count recorded then there was at least one sapling. In this case a count of 1 can be entered and an operator note recorded in the notes column: [no count recorded, assumed 1]. Likewise, if no seedlings were recorded but a species was written then it can often be assumed that the particular species was present in the <15 cm tier. In this case a 'P' is entered in the <15 cm tier and an operator note recorded in the Notes column: [no count recorded, assumed presence in <15 cm tier].

Taxon Entry Validation – Species Mapping – Species is not the default for …

See description under " Individual Entry Validation – Species Mapping– Species is not the default for …"

Taxon Entry Validation - Taxon Obs query - Text of note ?

Reason: The note for an item observation (i.e. Recce, Quadrat sapling or Quadrat seedling) contains '??'. This is usually used to denote a problem to be checked.

Solution: Check the reason for the note and resolve if possible.

Taxon is unknown for Verbatim code
Taxon Entry Validation – Unknown Taxon Verbatim – Taxon is unknown for Verbatim code

Reason: An unrecognised six-letter species code has been entered.

Solution: Check that the species was entered correctly. The field recorder should be contacted to provide the full species name. If the code is misspelled, the Verb. code should be left as recorded and the correctly spelled code should be entered under the NVS code. For example if 'WAIRAC' is recorded and found to be a misspelling of 'WEIRAC' then the Verb. code should be WAIRAC and the NVS code should be WEIRAC.

If the species is not on the NVS list then the full species name should be entered in the Notes field next to the species. This name should be sent to the NVS Administrator so that a new NVS code can be created. An email will be returned specifying the new code.

Taxon Obs verbatim code is different to the species code

Reason: This occurs when a NVS code different to the Verbatim code is selected.

In many methods this can be deliberately used for when there is a spelling error on the plotsheets. For example if 'WAIRAC' is recorded and found to be a misspelling of 'WEIRAC' then the Verbatim code should be WAIRAC and the NVS code should be WEIRAC.

In remeasured diameters this can occur when a project is uploaded into the main NVS database and the current species recorded (Verb. code) is different to the tag species ID from the past measures (NVS code). Corrections will be made to the NVS code in the main NVS database where there is a specific remeasurement note detailing that the previous ID was incorrect.

Solution: Check the reason for this difference and correct any entry errors.