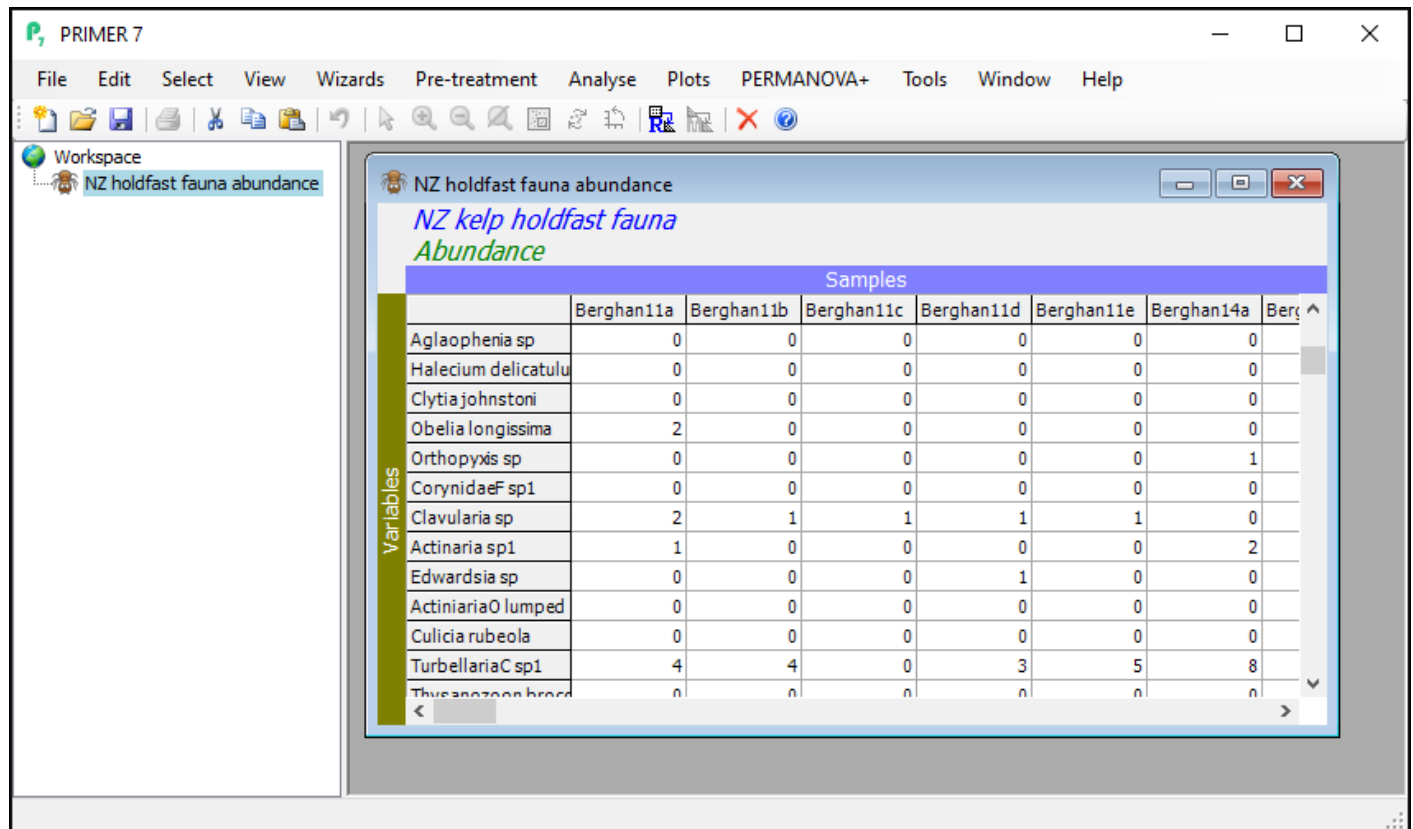


# Step 1: Data selection

## Open up the example data file

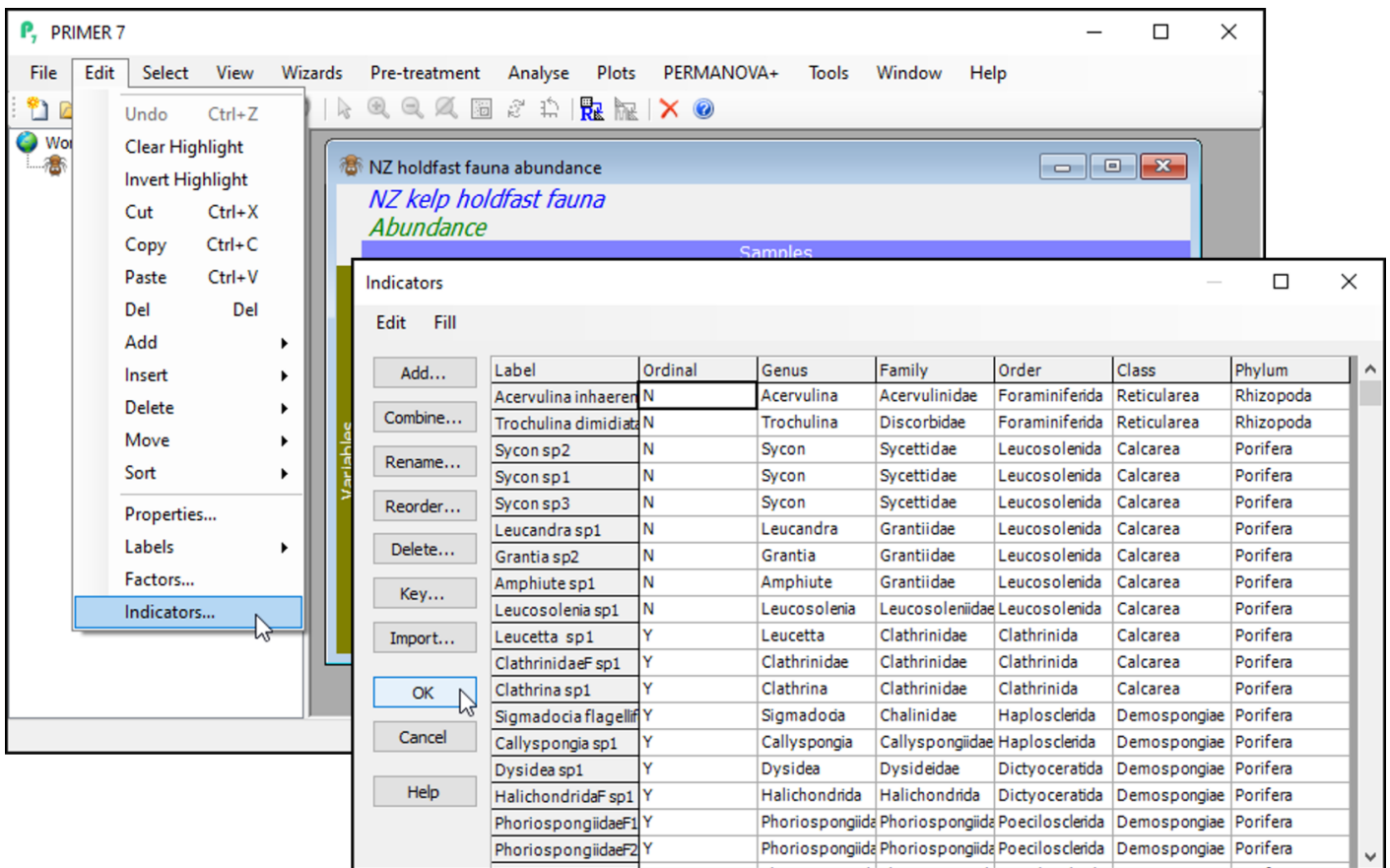
Launch PRIMER, then click **File > Open...** from the main menu, navigate to the folder named 'NZ holdfast fauna' in the 'Examples v7' directory, and select 'NZ holdfast fauna abundance.pri'. Click **Open** to display the species matrix.



The screenshot shows the PRIMER 7 software interface. The main window displays a species matrix titled 'NZ holdfast fauna abundance'. The matrix lists various species (variables) on the left and their abundance across different samples on the right. The samples are labeled Berghan11a, Berghan11b, Berghan11c, Berghan11d, Berghan11e, Berghan14a, and Berghan14b. The species listed include Aglaophenia sp, Halecium delicatulum, Clytia johnstoni, Obelia longissima, Orthopyxis sp, CorynidaeF sp1, Clavularia sp, Actinaria sp1, Edwardsia sp, ActinariaO lumped, Culicia rubeola, TurbellariaC sp1, and Thysanozoa broad.

	Samples						
	Berghan11a	Berghan11b	Berghan11c	Berghan11d	Berghan11e	Berghan14a	Berghan14b
Aglaophenia sp	0	0	0	0	0	0	0
Halecium delicatulum	0	0	0	0	0	0	0
Clytia johnstoni	0	0	0	0	0	0	0
Obelia longissima	2	0	0	0	0	0	0
Orthopyxis sp	0	0	0	0	0	1	0
CorynidaeF sp1	0	0	0	0	0	0	0
Clavularia sp	2	1	1	1	1	0	0
Actinaria sp1	1	0	0	0	0	2	0
Edwardsia sp	0	0	0	1	0	0	0
ActinariaO lumped	0	0	0	0	0	0	0
Culicia rubeola	0	0	0	0	0	0	0
TurbellariaC sp1	4	4	0	3	5	8	0
Thysanozoa broad	0	0	0	0	0	0	0

Click on **Edit > Indicators...** and you will see that the data includes information about whether individual taxa were counted (enumerated) or quantified on an ordinal scale ('Ordinal' = 'N' or 'Y', respectively). Also shown are indicators showing the taxonomic groups in which each species (or taxon) variable belongs, with different levels of the taxonomic hierarchy being provided as different indicators (i.e., 'Genus', 'Family', 'Order', 'Class' and 'Phylum').

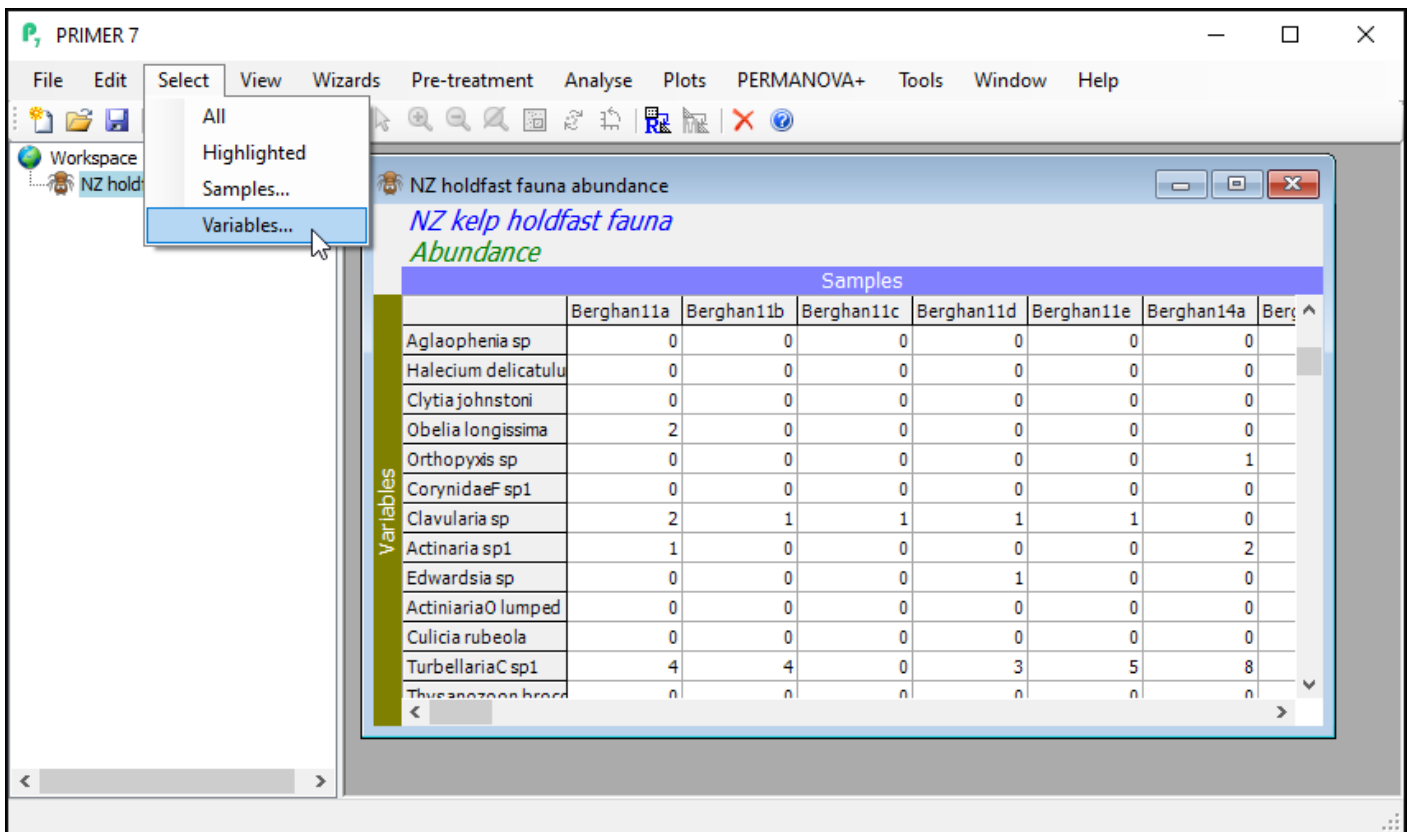


Click **OK** on the 'Indicators' dialog, so the data matrix is the active item in the workspace again.

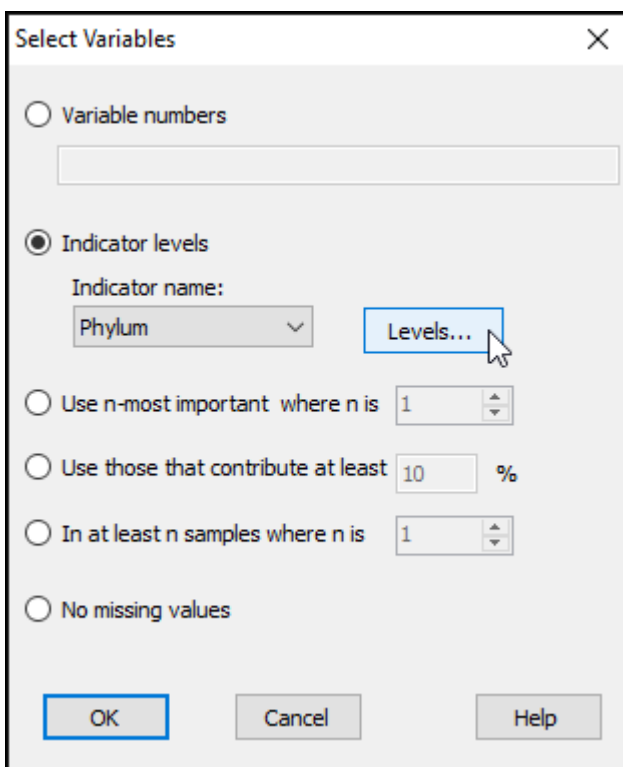
## Select a subset of variables, using an indicator

We wish to select just the mollusc species for the analysis.

1. From the 'NZ holdfast fauna abundance' data sheet, click **Select > Variables...**

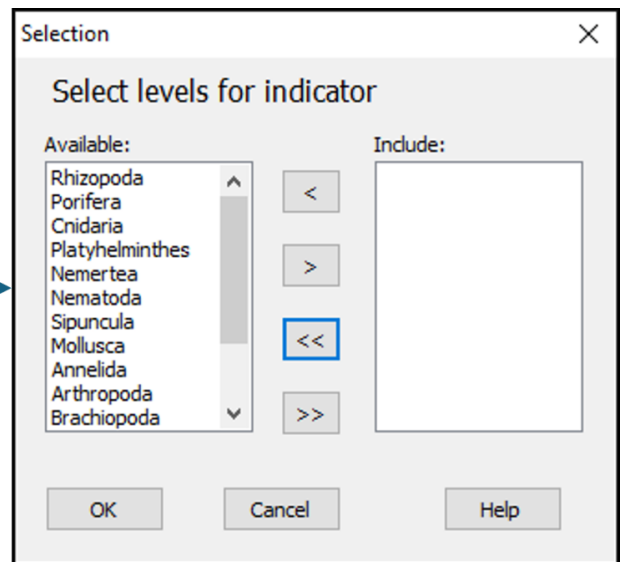
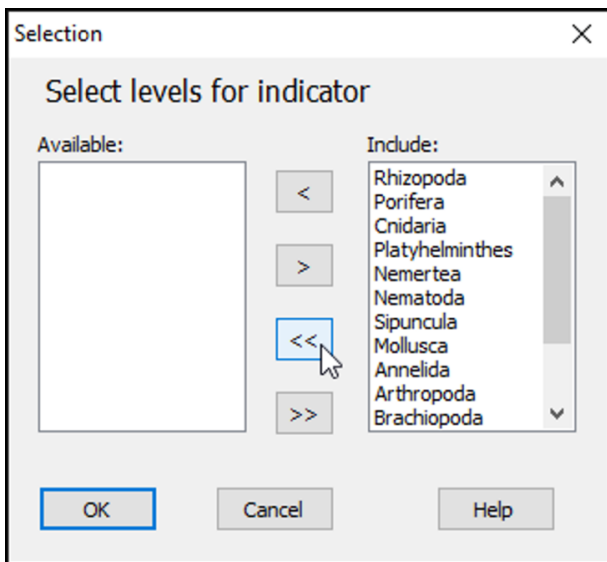



- In the 'Select Variables' dialog, choose (Indicator levels > Indicator name: **Phylum**) and click **Levels....**

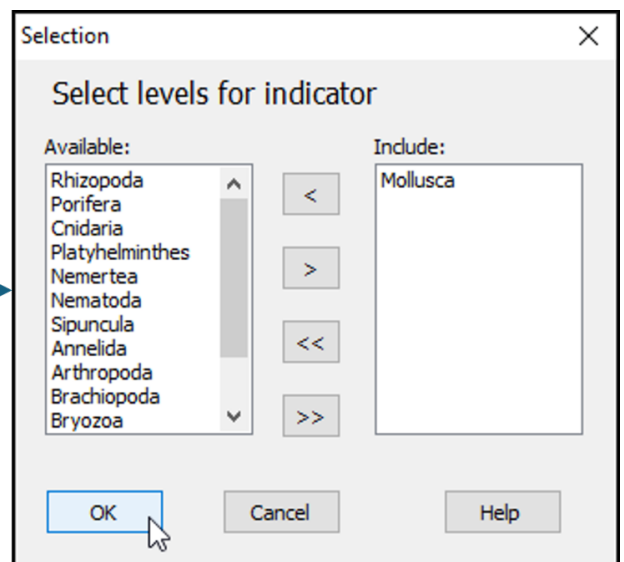
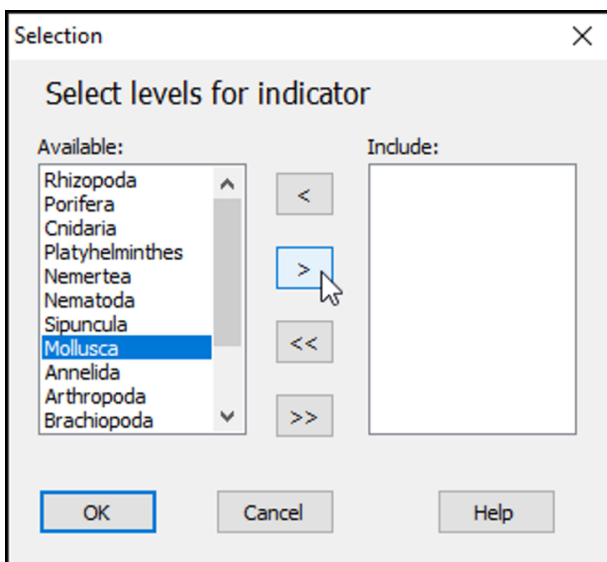


- In the 'Selection' dialog, first move all of the phylum categories from the 'Include:' box (on the right) to the 'Available:' box (on the left) by clicking on the double-left-arrow button:





4. Next, click on the word 'Mollusca' in the list of 'Available' phylum categories, and click on the single-right-arrow button: . This will move it to the 'Include:' box (right-hand side) of the 'Selection' dialog.



5. Click **OK** on the 'Selection' dialog, then click **OK** on the 'Select Variables' dialog.

Voila! Whenever you have selected a subset of data (this might be a subset of variables, as done here, or a subset of samples, or both), then the data matrix will have a turquoise background colour to indicate that you have done this, like so:

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Workspace

NZ holdfast fauna abundance

NZ kelp holdfast fauna  
Abundance

	Samples						
	Berghan11a	Berghan11b	Berghan11c	Berghan11d	Berghan11e	Berghan14a	Berghan14b
Onithochiton neglectus	2	0	0	2	0	0	0
Rhyssoplax sp	0	0	0	0	0	0	0
Notoiplax violacea	2	2	1	1	1	0	0
Asteracmea suteri	1	0	0	1	1	0	0
Incisura rosea	1	1	1	1	2	0	0
Scissurella prendre	1	0	1	4	1	0	0
Haliotis sp	0	0	0	0	0	0	0
Emarginula striatula	0	0	0	0	0	0	0
Tugali suteri	0	0	0	0	0	0	0
Cantharidus purpur	0	0	2	0	1	0	0
Herpetopoma bella	0	0	0	0	0	0	0
Herpetopoma laroc	0	0	0	0	0	0	1
Liotella polypeura	0	0	0	0	0	0	0
Trochus viridus	0	0	0	0	0	0	0
Trochus sp	0	0	0	0	0	0	0

Any analyses done on a selected subset of data will only be performed on that subset. It is usually a good idea to **duplicate and rename** a selected subset of data, so as to keep any analysis done on that subset of data clear and separate from the (full) original dataset. Note that subsetting does not affect the original full data matrix of information in any way, which is still always there. You can clear any subset selection (of variables and/or samples) by clicking on **Select > All** to return to the full data matrix in its entirety. (The turquoise background colour will go away when you do that, and the formerly selected data will yet be highlighted in a purple-ish hue. Clicking on **Select > Highlighted** can then be used to re-instate the selection from before, if desired.)

## Duplicate and rename a selected subset of data

From the subsetting data matrix, click **Tools > Duplicate**.



Click, hover and click again on the name 'Data1' in the Explorer tree window (or click **File > Rename Data** or hit the 'F2' key) and type in a new name for the subsetted data sheet: **Molluscs**.

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Workspace

- NZ holdfast fauna abundance
  - Molluscs

Data1

*NZ kelp holdfast fauna Abundance*

		Samples							
		Berghan11a	Berghan11b	Berghan11c	Berghan11d	Berghan11e	Berghan11f	Berghan11g	Berghan11h
Variables	Onithochiton neglectus	2	0	0	2	0	0	0	0
	Rhyssoplax sp	0	0	0	0	0	0	0	0
	Notoplax violacea	2	2	1	1	1	0	0	0
	Asteracmea suteri	1	0	0	1	1	0	0	0
	Incisura rosea	1	1	1	1	2	0	0	0
	Scissurella prende	1	0	1	4	1	0	0	0
	Haliotis sp	0	0	0	0	0	0	0	0
	Emarginula striatula	0	0	0	0	0	0	0	0
	Cantharidus purpur	0	0	2	0	1	0	0	0
	Herpetopoma bella	0	0	0	0	0	0	0	0
Herpetopoma laroc	0	0	0	0	0	0	1	0	
Liotella polypheura	0	0	0	0	0	0	0	0	
Trochus viridus	0	0	0	0	0	0	0	0	
Trochus sp	0	0	0	0	0	0	0	0	

Row 1 Col 1

At this point, you might like to save your workspace. Click **File > Save Workspace As... >** (Filename: **NZ\_holdfast\_molluscs.pwk**).

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