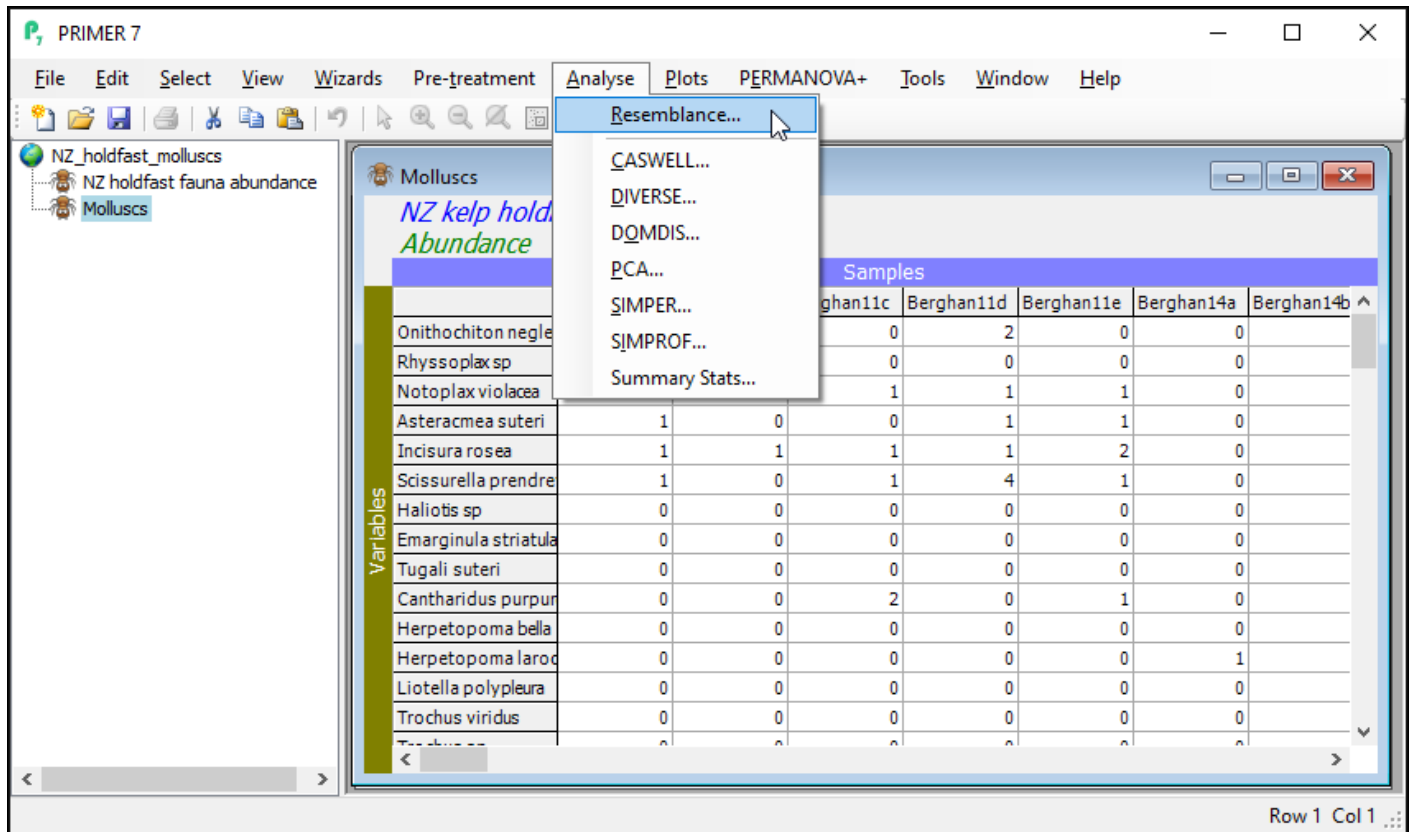


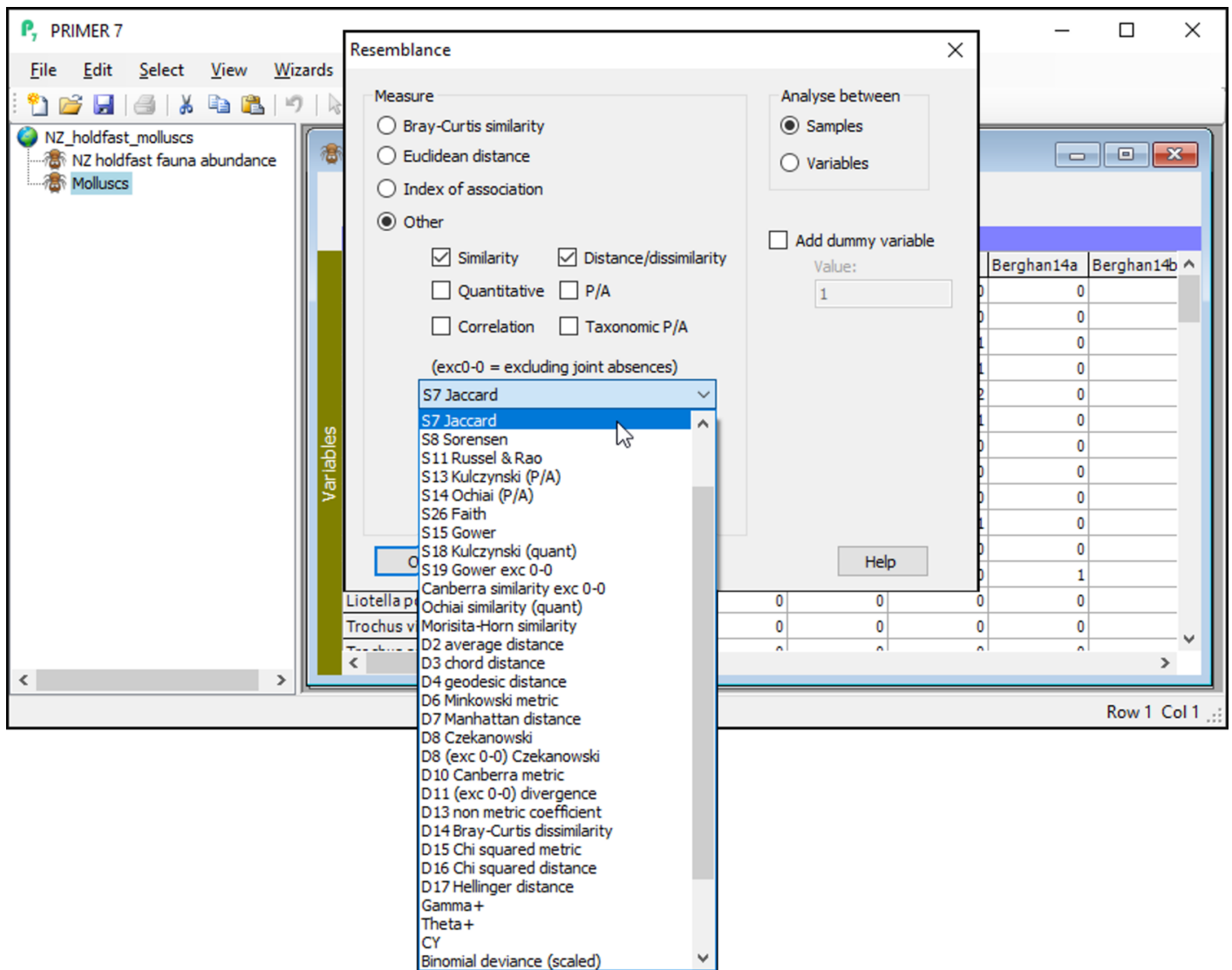
Step 2: Jaccard resemblance

Calculate the Jaccard resemblance

From the 'Molluscs' data sheet, click **Analyse > Resemblance....**

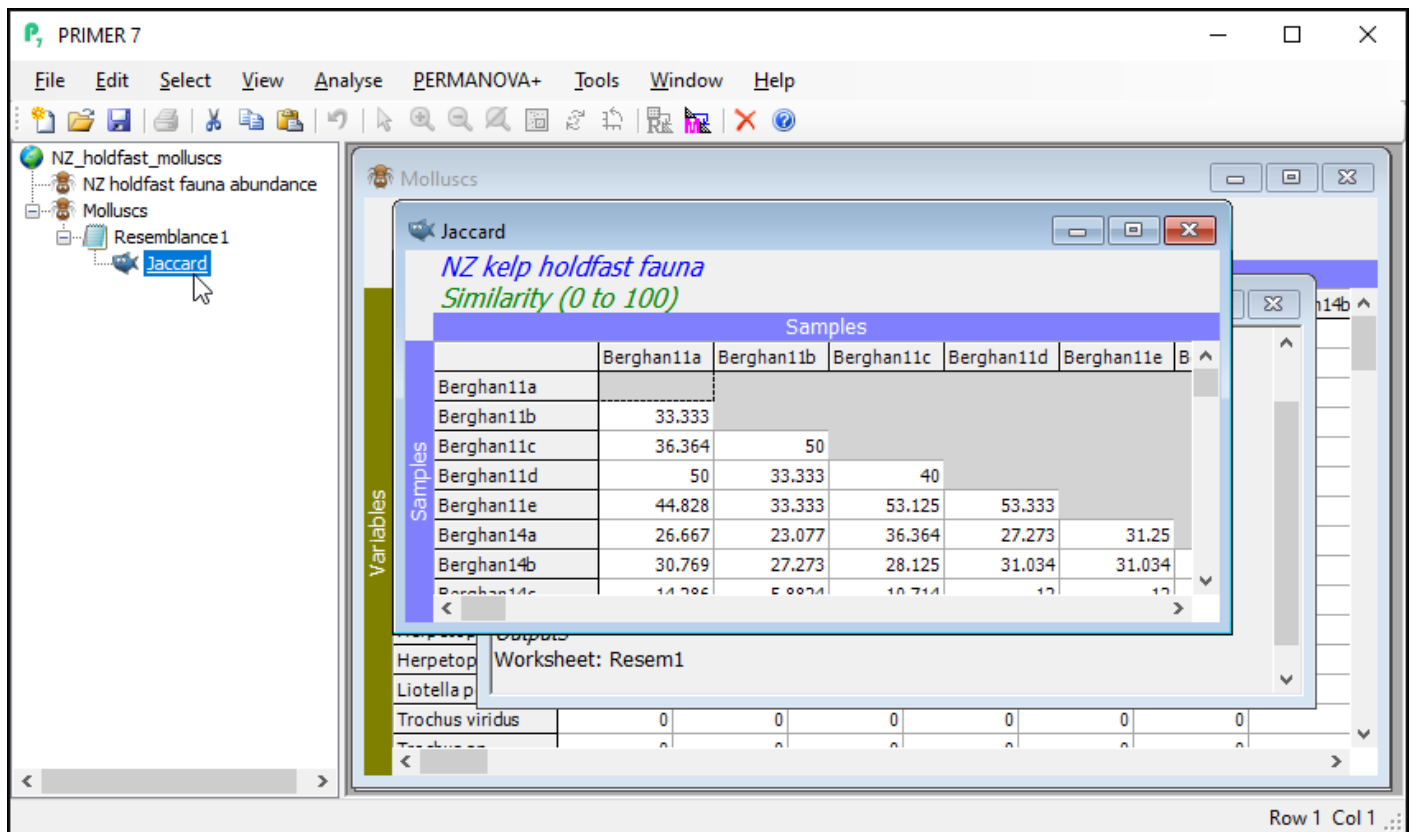


In the 'Resemblance' dialog, choose (\$\bullet\$Other) and then click on the drop-down menu to find 'S7 Jaccard', then click **OK**. (Note: 'S7' refers to the nomenclature used by [Legendre & Legendre \(2012\)](#) in their Chapter 7 on measures of ecological resemblance).



This produces a Jaccard similarity matrix among all pairs of holdfasts, called 'Resem1' by default. A nice feature of the Jaccard similarity measure is that it is directly interpretable as the percentage of shared species. For example, the first two holdfasts in the data matrix have a Jaccard similarity of 33.33%, so approximately one-third of the species that occur in either one or the other holdfast occur in both of them (i.e., are jointly present).

You can re-name this 'Jaccard' (click on the name 'Resem1' in the Explorer tree and hit the 'F2' key to re-name it), for clarity in what follows.



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