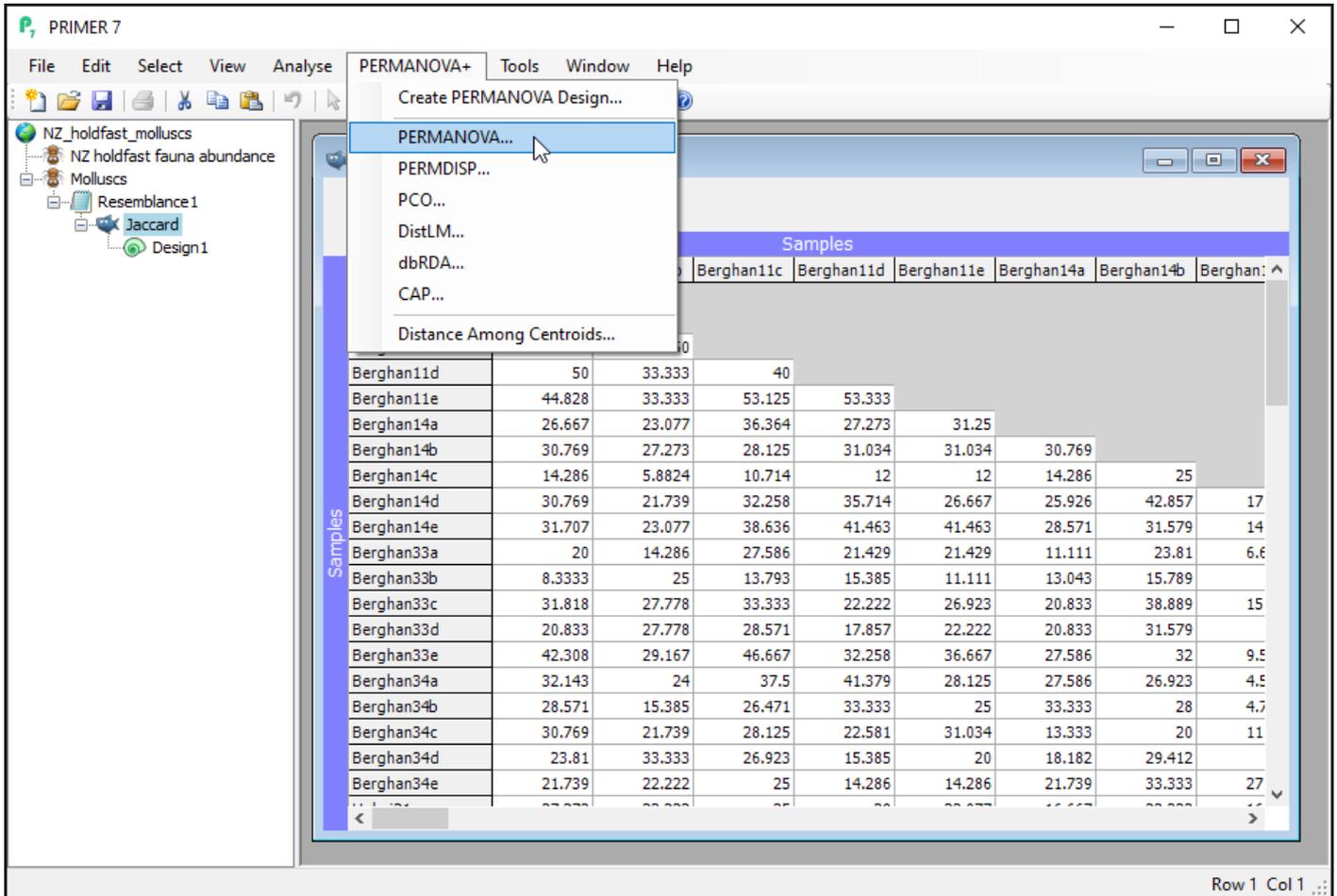


Step 4: Run PERMANOVA

Once the design file is created, we are ready to go ahead with the PERMANOVA analysis.

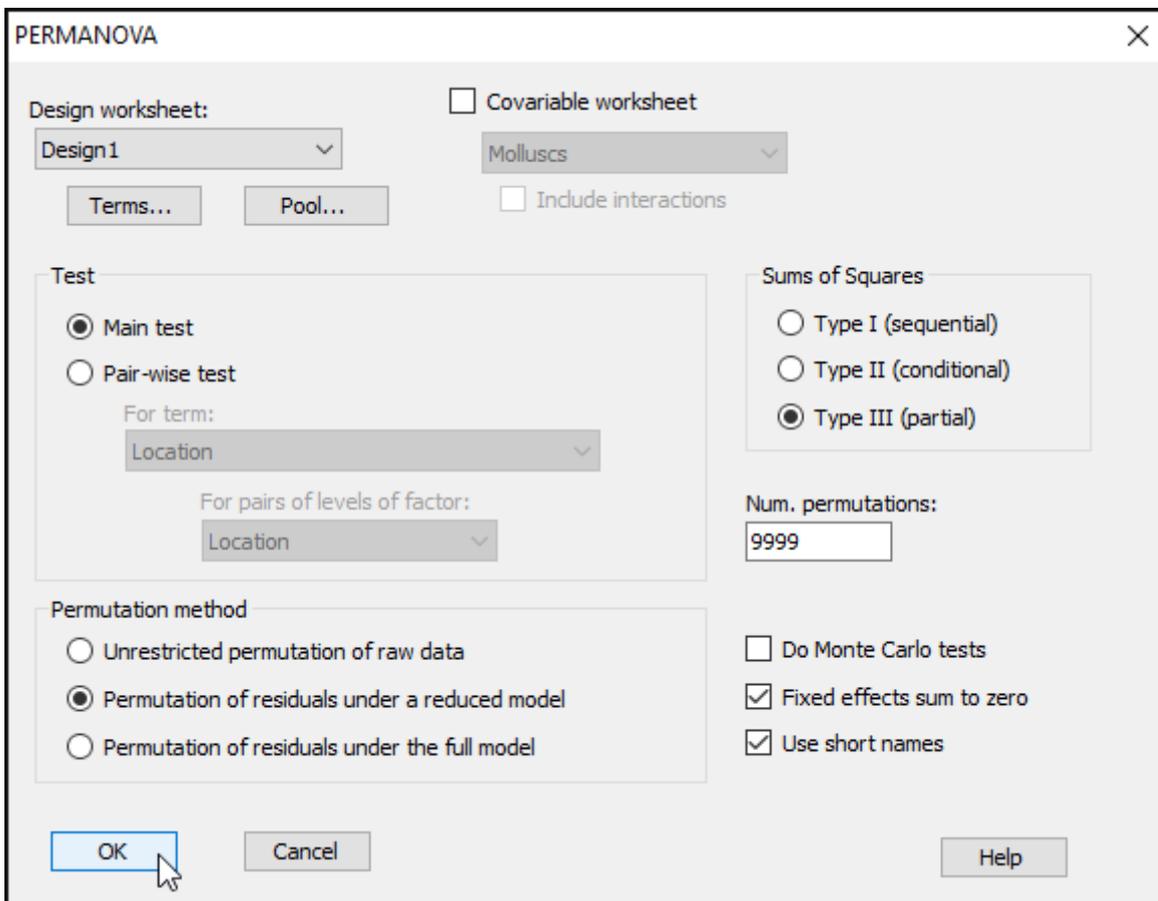
1. Click on the 'Jaccard' resemblance matrix in the Explorer tree so that it is the active item in the workspace, then click **PERMANOVA+ > PERMANOVA...**



The screenshot shows the PRIMER 7 interface. The 'PERMANOVA+' menu is open, with 'PERMANOVA...' selected. The Explorer tree on the left shows 'Jaccard' as the active item. The main window displays a distance matrix table with the following data:

	Berghan11c	Berghan11d	Berghan11e	Berghan14a	Berghan14b	Berghan14c	Berghan14d	Berghan14e	Berghan33a	Berghan33b	Berghan33c	Berghan33d	Berghan33e	Berghan34a	Berghan34b	Berghan34c	Berghan34d	Berghan34e
Berghan11d		50	33.333	40														
Berghan11e		44.828	33.333	53.125	53.333													
Berghan14a		26.667	23.077	36.364	27.273	31.25												
Berghan14b		30.769	27.273	28.125	31.034	31.034	30.769											
Berghan14c		14.286	5.8824	10.714	12	12	14.286	25										
Berghan14d		30.769	21.739	32.258	35.714	26.667	25.926	42.857	17									
Berghan14e		31.707	23.077	38.636	41.463	41.463	28.571	31.579	14									
Berghan33a		20	14.286	27.586	21.429	21.429	11.111	23.81	6.6									
Berghan33b		8.3333	25	13.793	15.385	11.111	13.043	15.789										
Berghan33c		31.818	27.778	33.333	22.222	26.923	20.833	38.889	15									
Berghan33d		20.833	27.778	28.571	17.857	22.222	20.833	31.579										
Berghan33e		42.308	29.167	46.667	32.258	36.667	27.586	32	9.5									
Berghan34a		32.143	24	37.5	41.379	28.125	27.586	26.923	4.5									
Berghan34b		28.571	15.385	26.471	33.333	25	33.333	28	4.7									
Berghan34c		30.769	21.739	28.125	22.581	31.034	13.333	20	11									
Berghan34d		23.81	33.333	26.923	15.385	20	18.182	29.412										
Berghan34e		21.739	22.222	25	14.286	14.286	21.739	33.333	27									

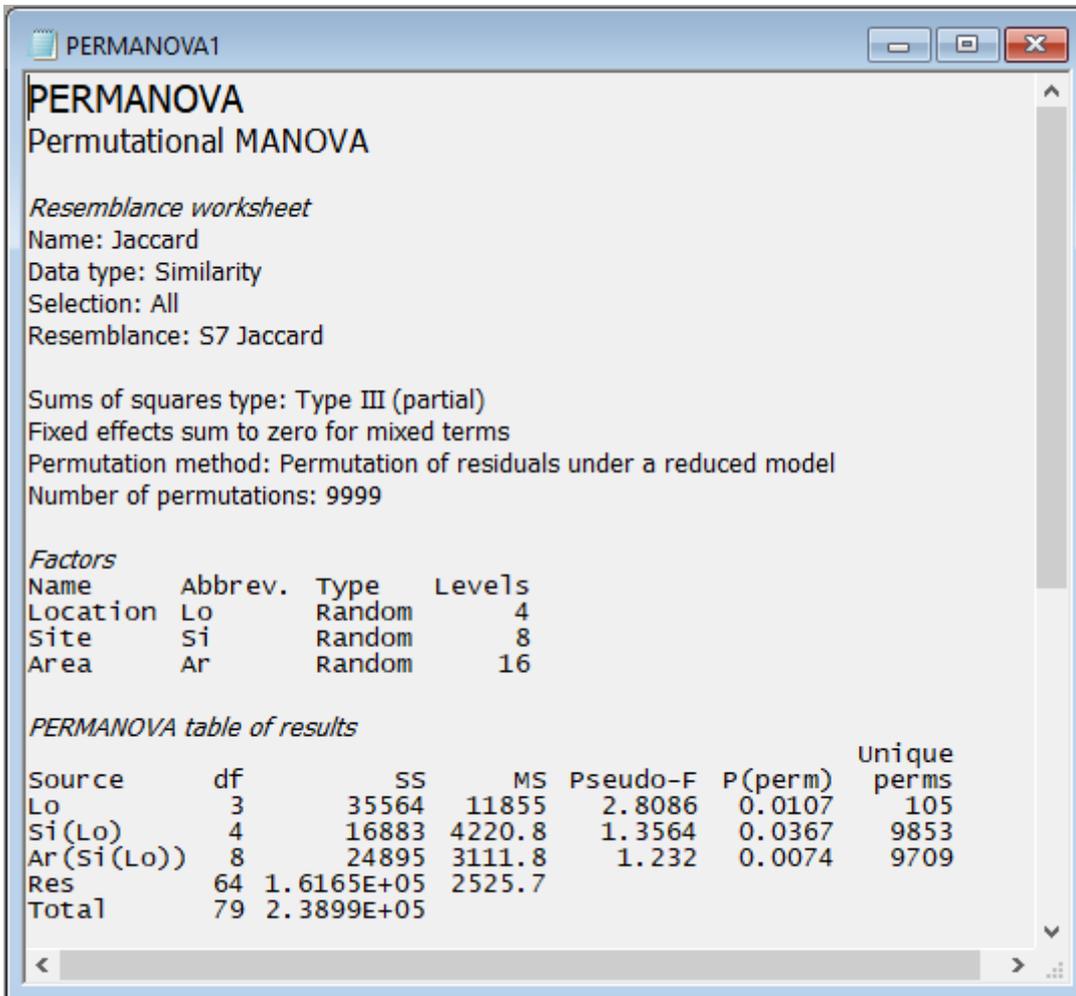
2. Check to see that the 'Design worksheet:' is **Design1**; this is the design file we created in the previous step that contains the three-way nested design. For the rest, we will keep most of the defaults in the PERMANOVA dialog, but it is wise to increase 'Num. permutations:' from **999** to **9999**, as shown below, then click **OK**.



3. This produces an output file (called 'PERMANOVA1') in the Explorer tree. It shows:

- the details of the choices you made in the PERMANOVA dialog to run the analysis;
- the details of your experimental design; and
- the PERMANOVA table of results

as follows:



Interpretation

These results show that there is statistically significant variability in the identities of molluscs among holdfasts at each of the three spatial scales in the experimental design: **Areas** ($F_{8,64} = 1.23$, $P < 0.01$), **Sites** ($F_{4,8} = 1.36$, $P < 0.05$) and **Locations** ($F_{3,4} = 2.81$, $P < 0.05$). Note that the p-value for Locations is somewhat limited by the number of unique values of the pseudo-F statistic under permutation that are available here. Specifically, when we permute 2 samples per group (i.e., the 8 Sites) randomly across 4 groups (the Locations), there are just 105 unique values of pseudo-F that can be obtained, so the minimum possible p-value here is $1/105 = 0.0095$).

Revision #23

Created 19 April 2024 01:17:33 by Marti

Updated 22 April 2024 04:22:38 by Marti