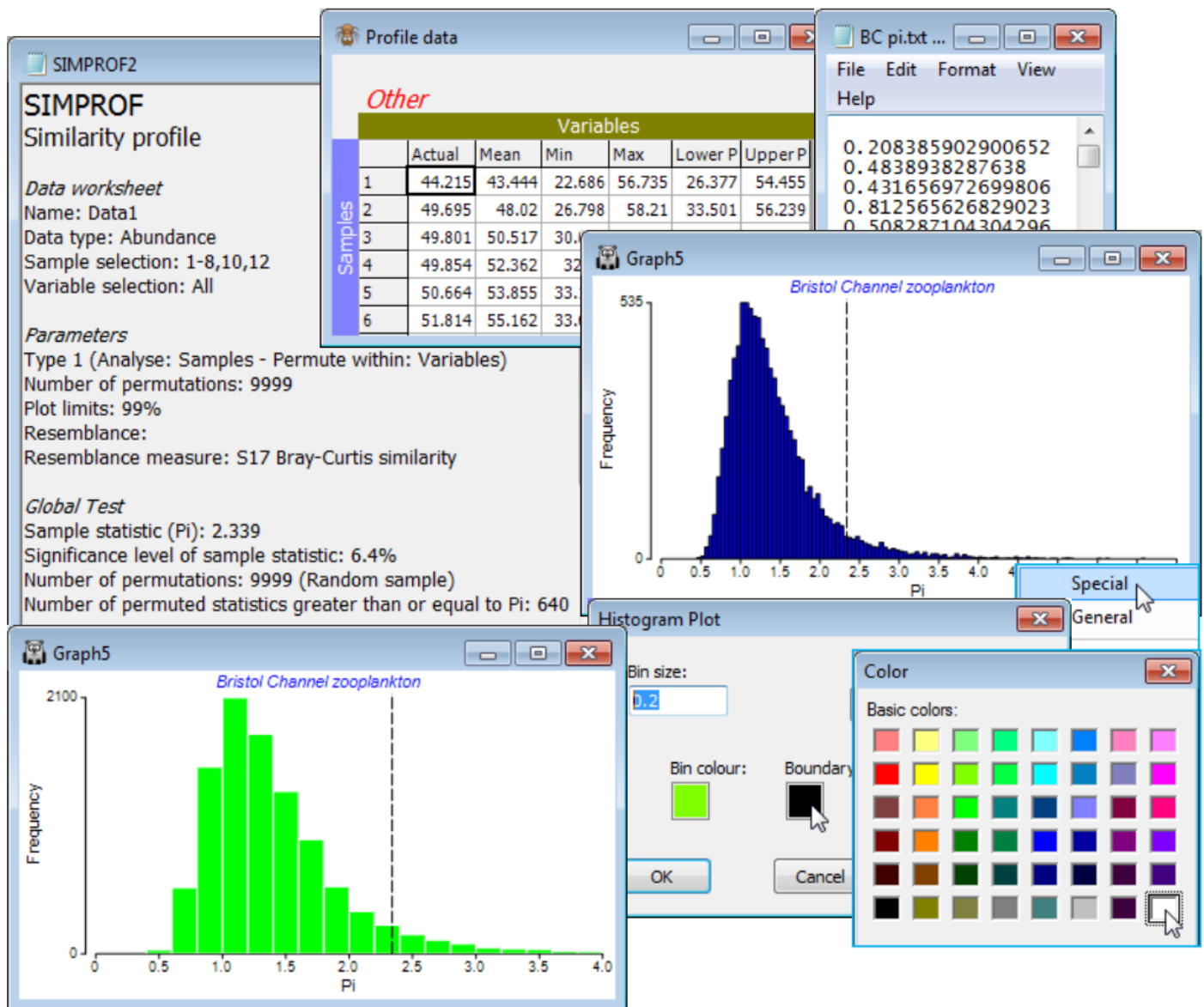# Histograms of null distributions

As in all permutation tests in PRIMER v7 (e.g. in ANOSIM, RELATE, BEST etc), a further output from **Analyse>SIMPROF** is thus a histogram of the values of the test statistic (π, here) for the null hypothesis conditions, under permutation, with the real value (π = 2.3) also indicated. The relevant p value is given in the SIMPROF results window – not 'significant' but borderline here, $p \approx$ 6.5%. Minor variations of both π and p values, from those in the results window for the earlier CLUSTER run, are to be expected because the permutations are random – each new run gives slightly different answers. Previously, the default of 999 permutations was selected. If greater precision is needed in significance levels, then the number of permutations should be increased, as here to 9999 (there are a vast number of possible permutations for this particular test). Binomial calculations show that tests with a true p of 5% will return a p in the range (3.5%, 6.5%) with 999 permutations, and in (4.6%, 5.4%) for 9999 permutations – this is true for all tests employing random permutations.

As previously seen (Section 4) with direct plotting of histograms, via **Plots>Histogram Plot**, the **Special** menu (right click when over the plot) allows changes to bin width, colour, axis scales etc. A final option on the SIMPROF dialog (✓Pi values to file) is to export the π values from all the permutations to a text file (*.txt). This is not commonly used but is again an option with most permutation tests in PRIMER; e.g. it would allow the user to redraw the null distribution histogram of π with other software, or perhaps examine its parametric form etc.

SIMPROF2

SIMPROF
Similarity profile

Data worksheet
Name: Data1
Data type: Abundance
Sample selection: 1-8,10,12
Variable selection: All

Parameters
Type 1 (Analyse: Samples - Permute within: Variables)
Number of permutations: 9999
Plot limits: 99%
Resemblance:
Resemblance measure: S17 Bray-Curtis similarity

Global Test
Sample statistic (Pi): 2.339
Significance level of sample statistic: 6.4%
Number of permutations: 9999 (Random sample)
Number of permuted statistics greater than or equal to Pi: 640

Profile data

Other

		Variables				
		Actual	Mean	Min	Max	Lower P	Upper P
Samples	1	44.215	43.444	22.686	56.735	26.377	54.455
	2	49.695	48.02	26.798	58.21	33.501	56.239
	3	49.801	50.517	30.6			
	4	49.854	52.362	32			
	5	50.664	53.855	33.			
	6	51.814	55.162	33.			

BC pi.txt ...

File Edit Format View Help

```
0.208385902900652
0.4838938287638
0.431656972699806
0.812565626829023
0.508287104304296
```

Graph5

Bristol Channel zooplankton

Frequency / Pi

Graph5

Bristol Channel zooplankton

Frequency / Pi

Histogram Plot

Bin size:
0.2

Bin colour: Boundary

OK   Cancel

Special
General

Color

Basic colors:

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