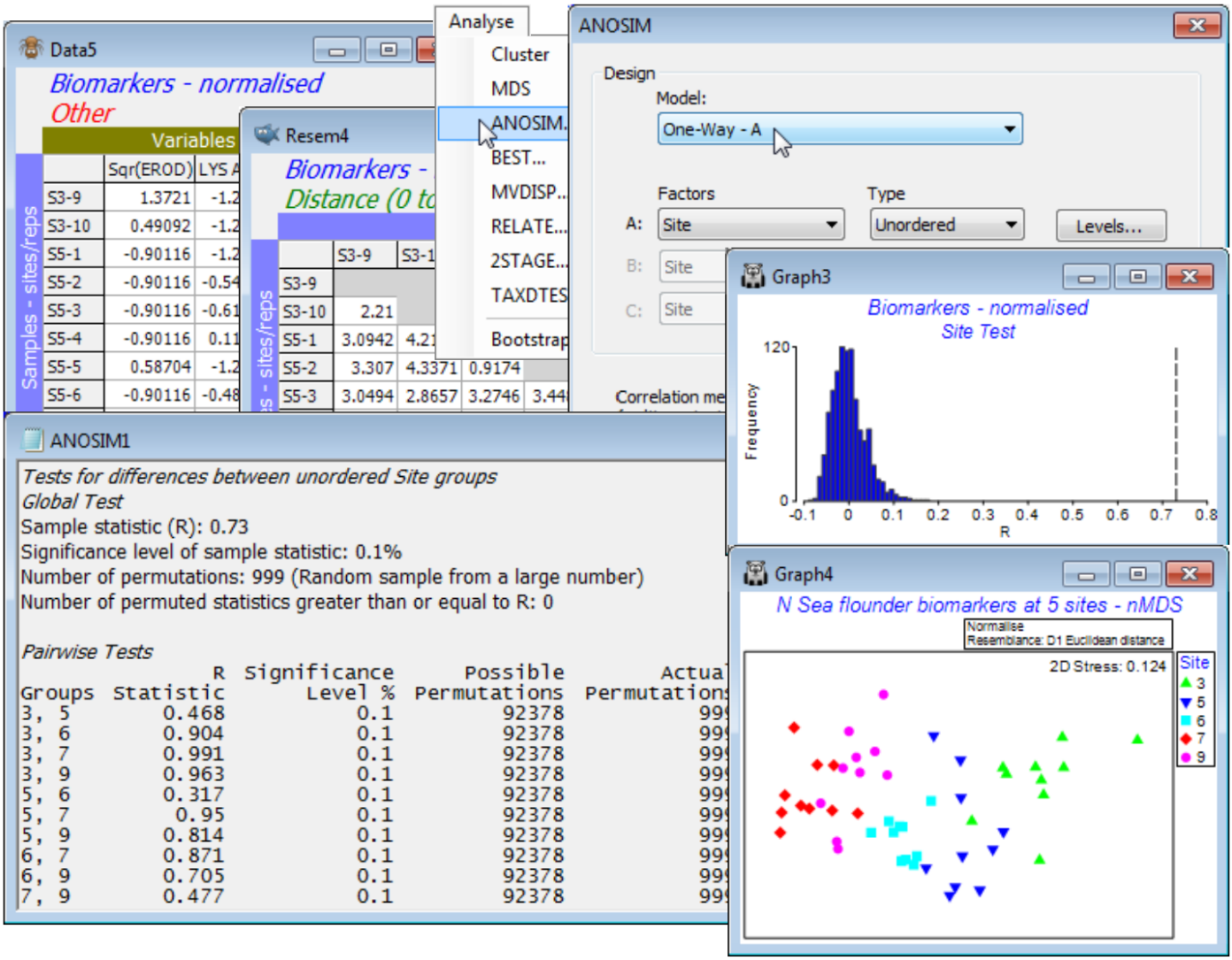
1-way layout (Biomarkers example)

ANOSIM applies equally well to data on environmental, biomarker or morphometric variables, which might be transformable to approximate normality; it is then a robust alternative to classical multivariate (MANOVA) tests such as Wilks' lambda. The inevitable slight loss in power of the non-parametric test, if the data really were multivariate normal (and had few enough variables in relation to sample sizes to allow proper estimation) is more than compensated for by its robustness, general applicability, and lack of assumptions such as constant variance-covariance structures.

Re open the N Sea ws workspace seen in Sections 4 & 5, with datasheet N Sea flounder biomarkers of 10 replicates from each of 5 N Sea sites, S3, S5, S6, S7, S9 (directory C:\Examples v7\N Sea biomarkers). Of the suite of 11 biomarkers it was previously suggested that EROD and LIPID VAC might benefit from square root transformation, being modestly right-skewed – earlier performed by highlighting them and **Pre-treatment>Transformation(individual)**>(Expression: SQR(V)). The variables are put on a common measurement scale with **Pre-treatment>Normalise Variables** and an appropriate resemblance calculation is **Analyse>Resemblance**>(Measure•Euclidean distance), before **Analyse>ANOSIM** on factor Site, as above. The results show a significant (mainly large) separation of the biomarker responses at all sites, seen clearly also in an *n*MDS plot (or *m*MDS would have nearly as good a stress here). Resave and close the workspace, N Sea ws.



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