

Average body mass matrix (B/A)

A useful variation of this, but one which needs more care, is to compute average body mass of each species in each sample. This is simply B/A , but needs to cater for the many cases when A (and B) are zero and a simple ratio is undefined. With active sheet **Clyde macrofauna counts**, so that V is again the counts, **Pre-treatment>Transform(individual)>Expression:** `Work("Clyde macrofauna biomass")/(V - (V=0))` will do the trick, because when $V>0$ the expression $(V=0)$ gives the value 0 (false), so that the correct ratio of B/A is calculated. However, when $V=0$ the expression $(V=0)$ returns the value -1 (true). The bottom line is then 1 and the result of the ratio is a reasonable value of 0. This assumes that $B=0$ when $A=0$ of course! [This, incidentally, is something that can be checked by running Abundance-Biomass Comparison curves, described in Section 16, since the **Analyse>Dominance Plot** (ABC) routine explicitly checks for incorrect matrix entries which have $A=0$ but $B>0$; the converse is perfectly permissible – the weight of all organisms of a species in a sample might be too small to register – but this does not cause a problem with a B/A calculation).]

An illustration of error trapping and relaxation of strict matching, in **Pre-treatment>Transform(individual)** with matching of entries, is obtained by copying **Clyde macrofauna biomass** with **Tools>Duplicate**, then **Edit>Labels>Variables** on this to delete all the species labels (click the Label header and hit the delete key or **Edit>Delete**). A sheet cannot function without labels so PRIMER substitutes its own defaults of (V1), (V2), etc. Now run the above calculation on **Clyde macrofauna counts**, but with the relabelled biomass sheet (**Data10** below) replacing the original biomass sheet. A warning message says that it could not find (variable) labels to match, but the two matrices are the same size so the option is given of proceeding anyway, on the assumption that the species order matches. We know it does here, so continue, to give the desired B/A matrix, and the original species labels will be present in the resulting new sheet because these are always taken from the active matrix, in a case such as this. Re-run having deselected one of the rows in **Data10**, however, and an irrecoverable error message occurs – a match is impossible because the variable labels do not match and neither does the number of variables in the A and B matrices.

Labels

Edit

Fill

Cut

Ctrl+X

Copy

Ctrl+C

Paste

Ctrl+V

Delete

Del

OK

Data10

Clyde macrofauna biomass (Biomass)

Samples - Sites along transect

	S1	S2	S3	S4	S5	S6	S7	S8
(V16)	0	0	128	0	0	0	0	0
(V17)	0	0	0	1	59	3	12	6
(V18)	0	0	0	7	17	0	3	7
(V19)	0	0	1	0	0	0	0	0

Clyde macrofauna counts (Abundance)

Samples - Sites

	S1	S2	S3	S4
Calocaris macandrea	0	0	1	0
Capitella capitata	0	0	1	2
Caulerliella sp.	0	0	0	24
Chaetoderma sp.	0	0	1	0
Chaetozone setosa	1	56	38	13

TRANSFORM

Selected data taken. Only highlighted data transformed.

Expression:

WORK("Data10")/(V-(V=0))

Pick

Type

☐ Cell value
 ☐ Function
 ☐ Sample
 ☐ Variable
 ☐ Formula
 ☐ Index
 ☒ Worksheet

Item:

Clyde environment
 Clyde log abiotic
 Clyde macrofauna biomass
 Data1
 Data10
 Data2

Renam

PRIMER

?

Delete data values?

OK

Data11

Clyde macrofauna - average body mass of an individual (B/A) (Abundance)

Samples - Sites along transect

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12
Calocaris macandrea	0	0	128	0	0	0	0	0	0	0	55	0
Capitella capitata	0	0	0	0.5	0.80	0.75	0.56	0.18	0	0	0	0
Caulerliella sp.	0	0	0	0.29	1.04	0	0.75	0.46	0	0	0	0
Chaetoderma sp.	0	0	1	0	0	0	0	0	0	2	1	0
Chaetozone setosa	0	2	0.55	0.30	0	0	0	0	0.11	0.35	1	9
Cirratulidae	0	0.16	0	0	0	0	0	0	0	0	0	0.5
Cirratulus cirratus	0	0	2.33	2	2.42	0	7.42	0	0.25	2.18	0	0

PRIMER

!

Some labels not matched
Matching to worksheet: 'Data10'

Skip matching and take same order as worksheet selections?

OK

Cancel

PRIMER

!

Some labels not matched
Cannot match labels, even relaxed
Matching to worksheet: 'Data10'

OK

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