Output options for region plots

These *b* bootstrap averages for each of the *g* groups are then displayed in a low-d *m*MDS space and you have control of whether to display any or all of: the *b*$\times$*g* bootstraps (✓Bootstrap averages); the overall averages for each group (✓Group averages); the smoothed envelopes (✓Bootstrap region (2D only)). You cannot easily change your mind about the choice of what is on the display after the run has completed so you may find yourself running the routine more than once, with differing display options. The (✓Group averages) are not the centre of a group's points in the (usually) 2-d *m*MDS space of the final display, but the centre of gravity in the m-dimensional space in which the bootstrap averages were calculated, and which are then ordinated into 2-d along with the bootstrap averages. The theoretical unbiasedness of bootstrap averages ensures that this is essentially the same as the centre of gravity of the original samples for that group, after they have been placed in the m-dimensional *m*MDS space. These group average points can only therefore fail to lie in the centre of the displayed bootstrap averages if there is some distortion in going down from the m-dimensional space of the calculations to the 2-d (say) space of the display, which is potentially useful information (and might suggest looking at the structure in 3-d). This also highlights another important consequence to carrying out the bootstrapping in the reduced m-dimensional *m*MDS space: because these are simple averages of points in Euclidean space, unequal replication across the groups is not a problem – it will not give the bias that bootstrap averaging in the species space is likely to face (i.e. larger samples produce more species and this changes similarity structures).

Revision #1
Created 11 November 2024 20:22:53 by Arden
Updated 11 November 2024 20:27:11 by Arden