> library(vegan)

> library(MASS)

> data(varespec)

> vare.dis <- vegdist(varespec)

> vare.mds0 <- isoMDS(vare.dis)

The results of isoMDS is a list (items points, stress)

Stress S is a statistic of goodness of fit, and it is a function of and non-linear monotone transformation of observed dissimilarities θ(d) and ordination distances ˜d.

> stressplot(vare.mds0, vare.dis)

As a rule of thumb, an NMDS ordination with a stress value around or above 0.2 is deemed suspect and a stress value approaching 0.3 indicates that the ordination is arbitrary. Stress values equal to or below 0.1 are considered fair, while values equal to or below 0.05 indicate good fit. Allowing the algorithm to ordinate in more dimensions can reduce the stress; however, allowing more than 3 dimensions quickly makes interpretation more challenging.

> vare.mds <- metaMDS(varespec, trace = FALSE)

> vare.mds