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metaMDS output
global Multidimensional Scaling using monoMDS

Data:      community[, 1:10]
Distance:  bray shortest

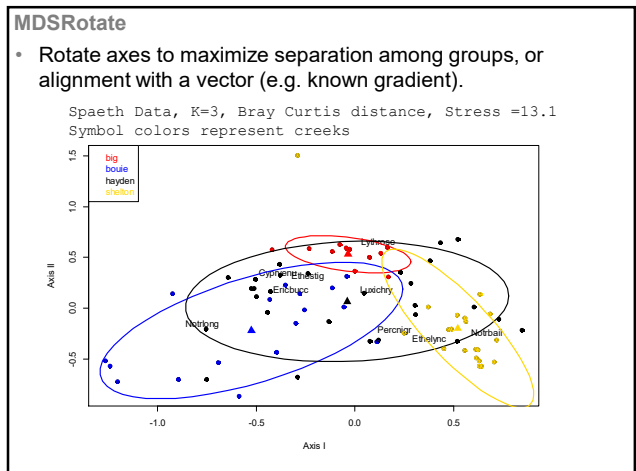
Dimensions: 2
Stress:    0.01561306
Stress type 1, weak ties
Two convergent solutions found after 4 tries
Scaling:   centring, PC rotation, halfchange scaling
Species:  expanded scores based on 'community'

> names(metamds)
[1] "nobj"      "nfix"      "ndis"      "ndis"      "nggp"      "diss"      "lidx"      "jidx"      "kinit"
[10] "istart"   "iform"    "fics"     "lreq"     "lsc1"     "maita"    "sizam"   "stmdia"   "edgms"
[19] "dist"     "dhat"     "points"   "stress"   "gstress"  "iters"    "lcause"  "call"     "model"
[28] "distmethod" "distcall" "data"     "distance" "converged" "tries"    "engine"  "species"
    
```

- ### Scaling and Rotation
- NMDS axes are not in any particular order, values are arbitrary.
 - By convention
 - all axes are centered (means=0)
 - Axes rotated to PCA axes. This will "order" them by importance
 - Halfchange scaling – ordination scores are scaled to match the scale of the similarity matrix used (typically 0-1)
 - Function `MDSrotate()` will rotate the axes to any vector (e.g. environmental variable).

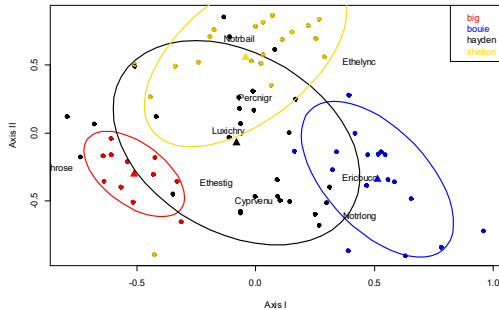
Scaling defined by your distance metric

- NMDS performed on the same data (Spaeth dataset)
- Below, Bray Curtis matrix was multiplied by 5.
- Axes are scaled differently, everything else is the same.



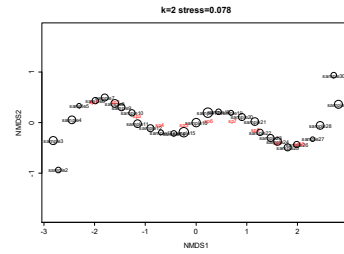
MDSrotate

- Same analysis after: `MDSrotate(nmds_object, creek)`
 - In this case, axes are being rotated to maximally differentiate groups in 2 dimensions. The third axis would then contain residual variation. Based on linear discriminant analysis (`lda`)
 - Doing this with $K=2$ would have no effect



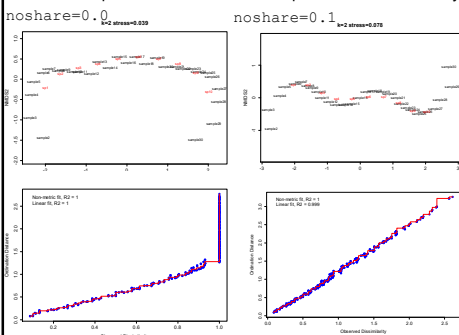
Goodness of Fit

- Function `goodness()` returns goodness of fit statistics for each site. Relative measure of the total stress linked to each point.
- Higher values = more uncertainty and more stress



noshare option

- Using this option will invoke a function that will estimate dissimilarity for sites that do not share any species.
 - T/F – us or do not use
 - Value 0 to 1 – cutoff for when to use (proportion of sites with no shared species)
- Zerodist option – what to do with samples with no dissimilarity (ties)




NMDS stopping point

- `isoMDS` uses a stable stress value as a stopping point
 - Set tolerance as an option
 - “converged” when done

```

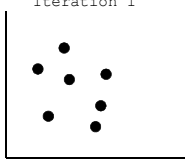
initial value 4.200889
iter 5 value 9.263973
iter 10 value 7.920977
iter 15 value 7.734398
iter 15 value 7.726740
final value 7.701990
converged
> nmds<-isoMDS(distance,k=3)
initial value 7.939925
iter 5 value 4.118777
iter 10 value 3.973427
iter 15 value 3.870255
final value 3.822107
converged
> nmds<-isoMDS(distance,k=5)
initial value 1.595218
iter 5 value 1.371944
iter 10 value 1.210386
iter 15 value 1.137483
iter 20 value 1.060814
iter 25 value 1.026373
iter 30 value 1.019002
iter 30 value 1.018286
iter 35 value 1.004853
iter 35 value 1.003870
iter 35 value 1.003204
final value 1.003204
converged
> nmds<-isoMDS(distance,k=10)
initial value 1.110138
iter 5 value 0.765316
iter 10 value 0.664021
iter 15 value 0.610260
iter 20 value 0.552149
iter 25 value 0.490166
iter 30 value 0.453501
iter 35 value 0.408528
iter 40 value 0.366260
iter 45 value 0.340277
iter 50 value 0.324808
final value 0.324808
stopped after 50 iterations
    
```

Procrustes Distance

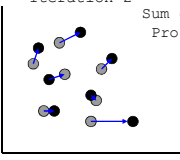


- metaMDS uses a **Procrustean analysis** instead of stress values to assess differences in configurations for each iteration
 - Procrustes – son of Poseidon, had an iron bed that all visitors had to sleep in. He would stretch or cut limbs so they all fit.
 - Procrustes analysis – how much “cutting” and “stretching” is necessary to get one configuration (ordination) to match another.

Iteration 1



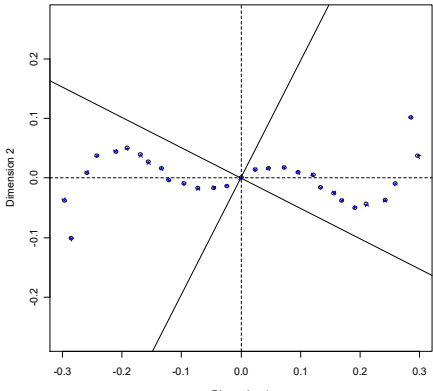
Iteration 2



Sum of line lengths ~
Procrustes distance

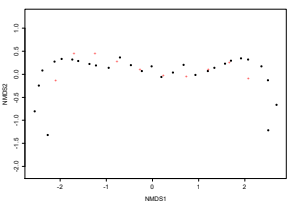
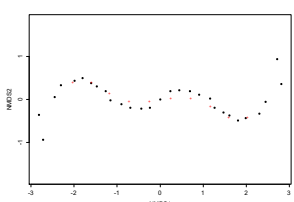
Procrustes

Plot=TRUE option will plot the Procrustes errors at each iteration.



Procrustes Statistic

- Any two configurations can be compared and their differences quantified with a Procrustes statistic –sum of squares of the residuals.

- How different are these two configurations?

Procrustes Statistic

- You can also test the significance of Procrustes values (function `protest` compares observed vs. permuted values). This is testing for non-random concordance between two configurations.

```

Call:
procrustes(X = metanmids$points, Y = metanmids_without_noshare$points)

Number of objects: 29   Number of dimensions: 2

Procrustes sum of squares:
9.477623
Procrustes root mean squared error:
0.571677
Quantiles of Procrustes errors:
      Min       3Q      Median       Max
0.03398588 0.14887655 0.25752112 0.53496706 2.15866845

Rotation matrix:
      [,1] [,2]
[1,] 0.99978430 -0.02076904
[2,] 0.02076904 0.99978430

Translation of averages:
      [,1] [,2]
[1,] 3.450472e-17 -4.280952e-18

Scaling of target:
[1] 0.9371033
    
```

