The manual forward selection has the objective to identify environmental parameters where each # explains a separate dimension of variance in the taxa data (i.e. that show no collinearity between # each other). By following this procedure, we will obtain a set of independent forcing variables that # drive the taxa assemblage.

Ranking the 6 parameters by eigenvalue (the amount of taxa variance they explain):

rda(TAXA ~ PARAMETER.X, data=ENVI)

Result: SSTsummer (12.7%), Sealce (9.7%), SSSsummer (6.9%), PPsummer (4.6%), PPannual # (4.2%), PPspring (2.5%)

Evaluating the independence between all 6 parameters:

To this end we calculated Variance Inflation Factors (VIF), expressing how much of the taxa # variance explained by one environmental variable is already explained by another parameter. The # VIF of a variable is calculated from the multiple correlations (r) among the environmental variables # (ter Braak and Smilauer 2002), using the equation VIF=1/(1-r2). We chose a cut-off value of VIF \leq 2 # for all parameters as also suggested in other studies (e.g., Lopes et al. 2010). Such a VIF value only # allows collinearities of r2 \leq 0.5 and thus not more than half of the variance in the taxa data explained # by one variable to also be explained by another variable.

Now we start with the actual forward selection:

After ranking the 6 variables by their eigenvalue we start with the first one and add step-by-step # another variable and check if the VIF's < 2.

n.rda <- rda(TAXA ~ SSTsummer+Sealce, data=ENVI) vif.cca(n.rda)

VIF < 2? YES
Result: SSTsummer Sealce
1.78 1.78
Taxa variance explained: 18.7%</pre>

Proceede with the above model and add the next parameter:

n.rda <- rda(TAXA ~ SSTsummer+Sealce+SSSsummer, data=ENVI) vif.cca(n.rda)

VIF < 2? NO

Result:SSTsummerSealceSSSsummer#2.132.601.46

We find that two parameters show too much collinearity. To decide which parameters to keep and # which to exclude from the set of independent forcing variables, we check which model explains more # taxa variance and how large the VIFs are:

n.rda<-rda(TAXA ~ SSTsummer+Sealce, data=ENVI) # Taxa variance explained: 18.7% VIFs: SSTsummer 1.78 Sealce 1.78

n.rda<-rda(TAXA ~ SSSsummer+Sealce, data=ENVI) # Taxa variance explained: 17.5% VIFs: SSSsummer 1.23 Sealce 1.23

n.rda<-rda(TAXA ~ SSSsummer+SSTsummer, data=ENVI) # Taxa variance explained: 19.6% VIFs: SSTsummer 1.00 SSSsummer 1.00

The model including SSTsummer and SSSsummer (excluding Sealce) is the better model explaining # the largest amount of taxa variance and showing the highest amount of independence.

Note:

We exclude Sealce from our dataset because it does not explain a separate dimension of variance # in taxa assemblages within the regional Baffin Bay dataset. This does not mean, that it cannot be # reconstructed or does not explain taxa variance! However, our analysis suggests that SSTsummer # and Sealce "play the same part" in driving assemblage compositions, meaning that by # reconstructing one we actually reconstruct a "mixture" of SSTsummer and Sealce. This is # strengthened by the result of the MFA where we detected SST on the one end of the first dimension # and Sealce on the other end. However, to calibrate an independent dataset, we need to decide # between SSTsummer and Sealce. Statistics favour SSTsummer. But, we have to bear in mind when # applying the independent calibration dataset that the SSTsummer parameter is a place holder for # several temperature parameters like SSTsummer, Sealce and presumably others.

Proceede with the best performing model and add the next variable

n.rda <- rda(TAXA ~ SSTsummer+SSSsummer+Ppsummer, data=ENVI) vif.cca(n.rda)

VIF < 2? NO

Result:SSTsummerSSSsummerPpsummer#1.871.222.08# We follow the same procedure as above: Which model explains more variance and how large are# the VIFs?

n.rda <- rda(TAXA ~ SSSsummer+Ppsummer, data=ENVI) # Taxa variance explained: 10.2% VIFs: SSSsummer 1.11 Ppsummer 1.11

n.rda <- rda(TAXA ~ SSTsummer+SSSsummer, data=ENVI) # Taxa variance explained: 19.6% VIFs: SSTsummer 1.00 SSSsummer 1.00

n.rda <- rda(TAXA ~ SSTsummer+Ppsummer, data=ENVI) # Taxa variance explained: 17.6% VIFs: SSTsummer 1.71 Ppsummer 1.71

Proceede with the best performing model and add the next variable

n.rda <- rda(TAXA ~ SSTsummer+SSSsummer+Ppannual, data=ENVI) vif.cca(n.rda)

VIF < 2? NO</th># Result:SSTsummerSSSsummerPpannual#2.111.092.19# We follow the same procedure as above: Which model explains more variance and how large are# the VIFs?

n.rda <- rda(TAXA ~ SSSsummer+Ppannual, data=ENVI) # Taxa variance explained: 10.4% VIFs: SSSsummer 1.04 Ppannual 1.04

n.rda <- rda(TAXA ~ SSTsummer+SSSsummer, data=ENVI) # Taxa variance explained: 19.6% VIFs: SSTsummer 1.00 SSSsummer 1.00

n.rda <- rda(TAXA ~ SSTsummer+Ppannual, data=ENVI) # Taxa variance explained: 17.7% VIFs: SSTsummer 2.01 Ppsummer 2.01

Proceede with the best performing model and add the next (last) variable

n.rda <- rda(TAXA ~ SSTsummer+SSSsummer+Ppspring, data=ENVI) vif.cca(n.rda)

VIF < 2? YES
Result: SSTsummer SSSsummer Ppspring
1.81 1.00 1.81
Taxa variance explained: 23.6%</pre>

Final results:

- # The final model is SSTsummer+SSSsummer+PPspring
- # Each of the three parameters explain an independent part of the variance in the assemblage# composition, while together explaining 23.6% of the total taxa variance
- #- Sealce is excluded as it presumably explains the same part of the variance as SSTsummer
- # SSTsummer reconstructions will reflect Sealce reconstructions (if we had decided to keep
 # Sealce, Sealce reconstructions would reflect SSTsummer changes)
- # PPannual and PPspring are excluded as they presumably explain the same part of the# variance as PPspring does
- # In the local calibration dataset we find three "signals" in the taxa variance regarding the 6
 # parameters we took into account.

References:

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