



Genomic research on South Africa's sardine stocks

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Ecological Genomics & Wildlife Conservation





2023 panel: key suggestions

P-values vs. magnitude of correlation coefficient

Extract more information from the genomic dataset by using more environmental variables (not only SST)

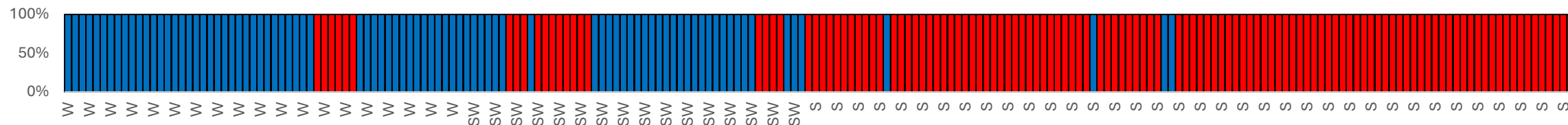
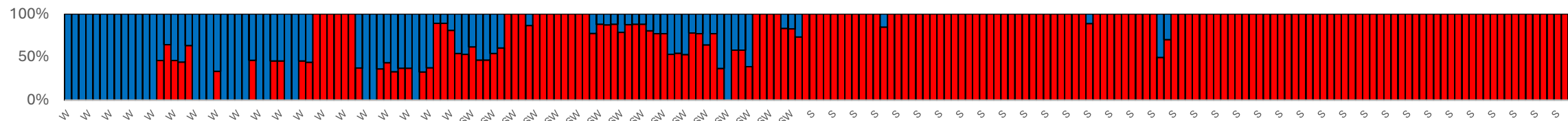
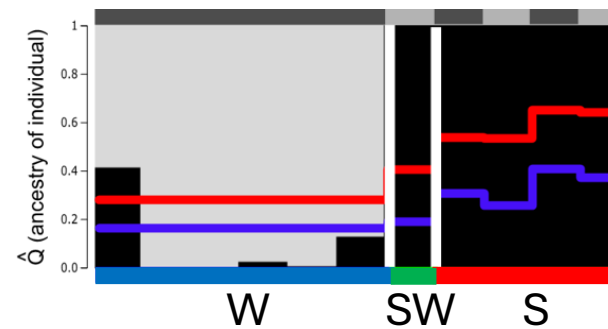
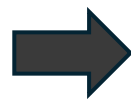
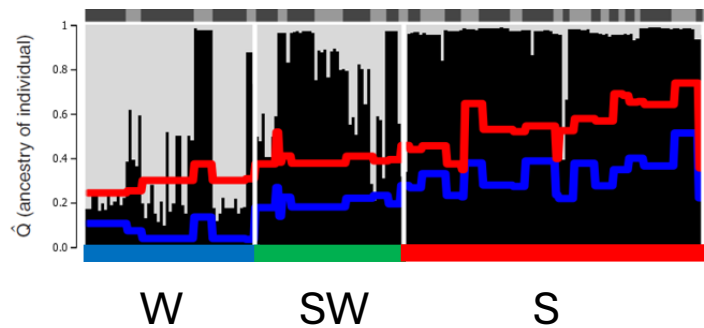
Explore selection

Finding genetic structure in such a high-dispersal species means there is strong selection (low genetic drift means fewer adaptive loci are stochastically lost)

Exome data vs. Genomic data

Generate more data using the more informative approach

Sardine/P5

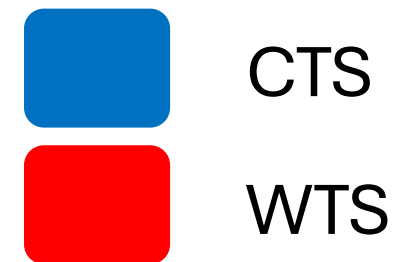
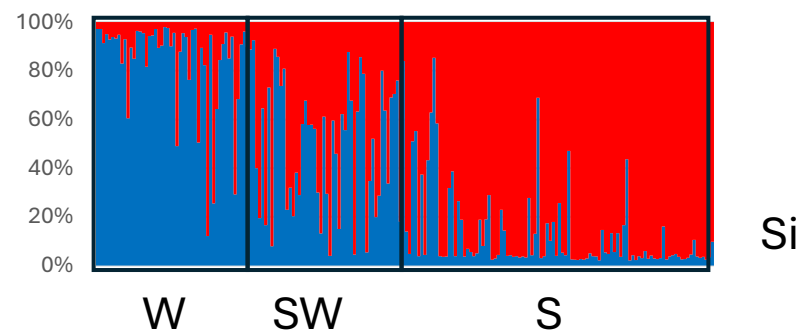
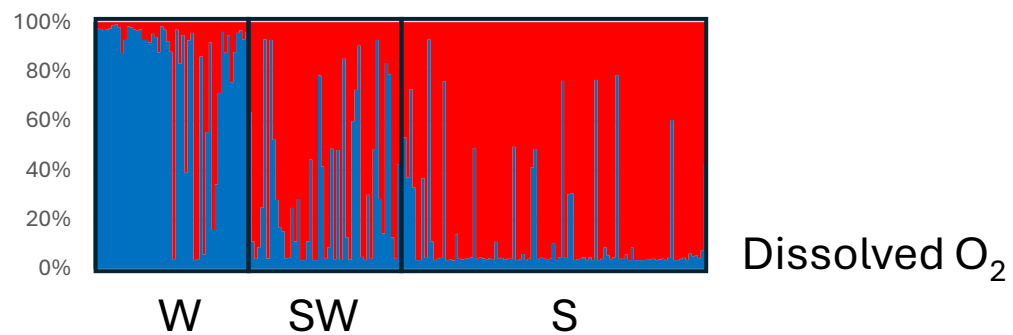
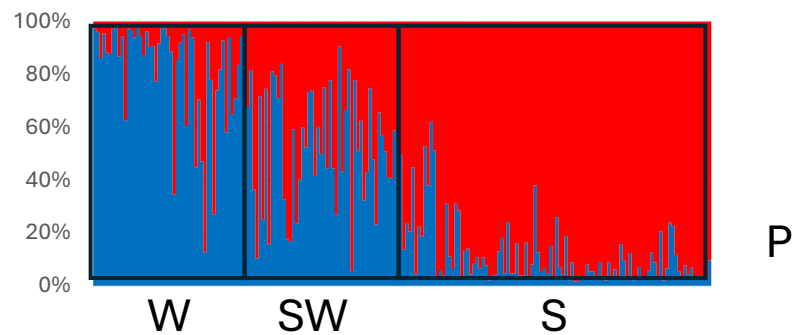
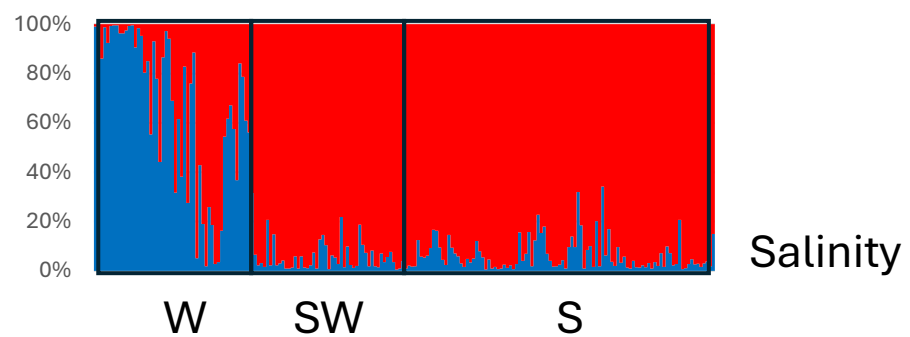
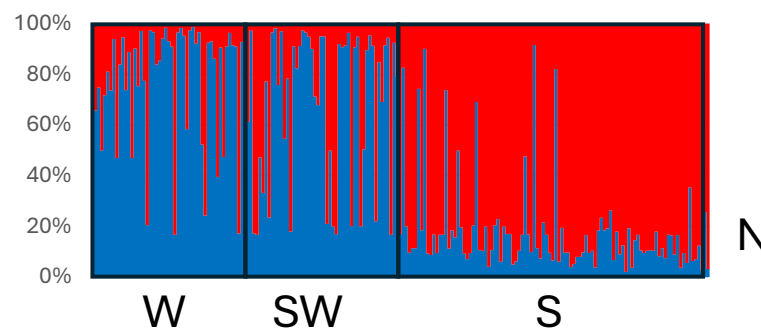
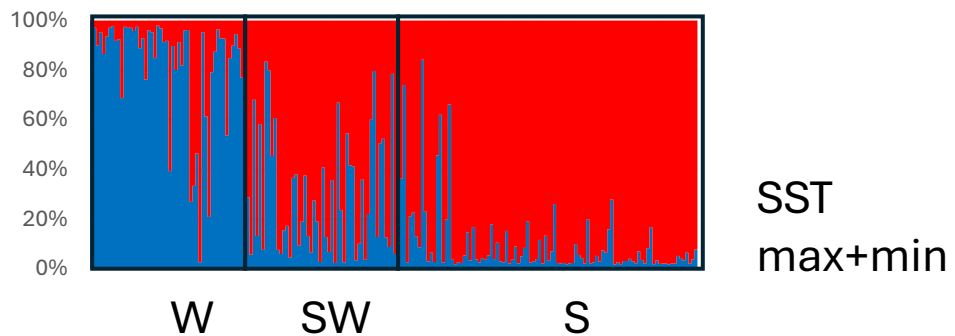


	Counts	%
CTS in W:	50	89
WTS in W:	6	11
CTS in SW:	34	69
WTS in SW:	15	31
CTS in S:	4	4
WTS in S:	105	96

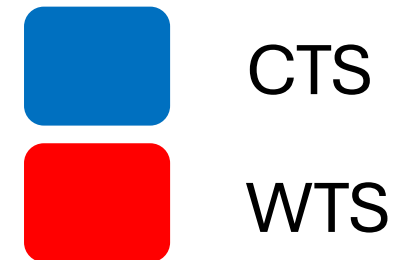
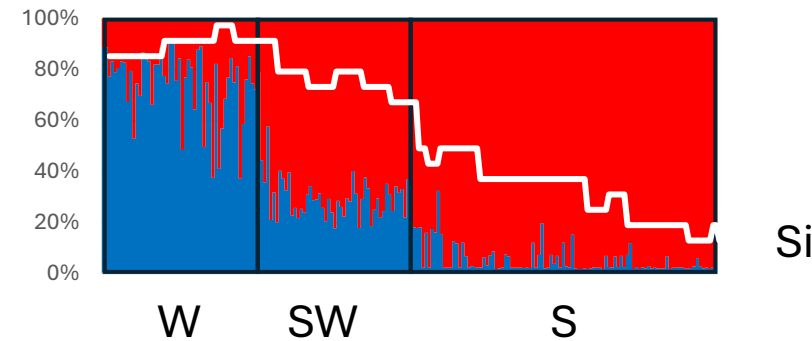
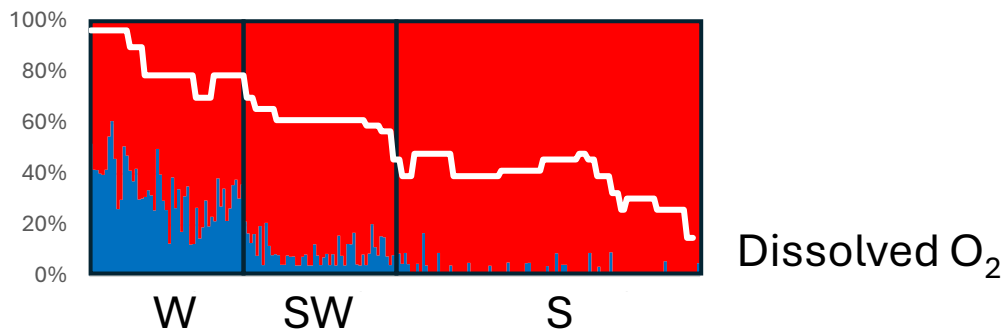
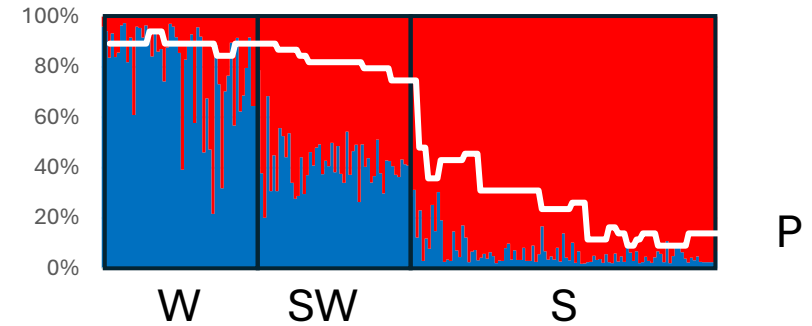
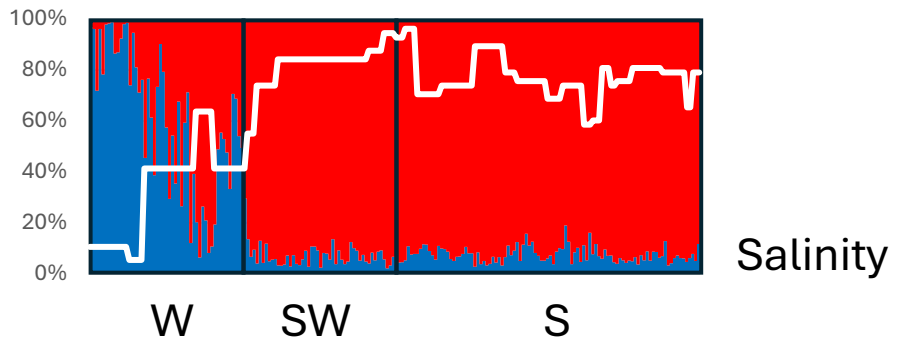
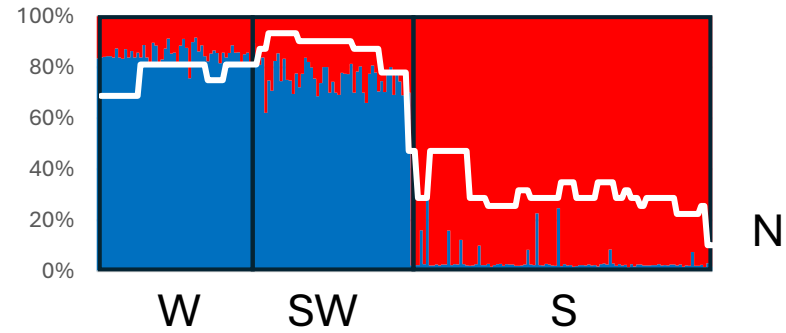
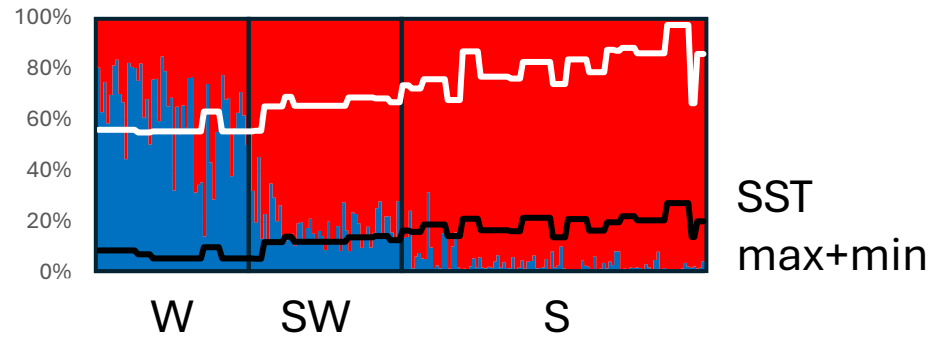
gINLAnd outliers

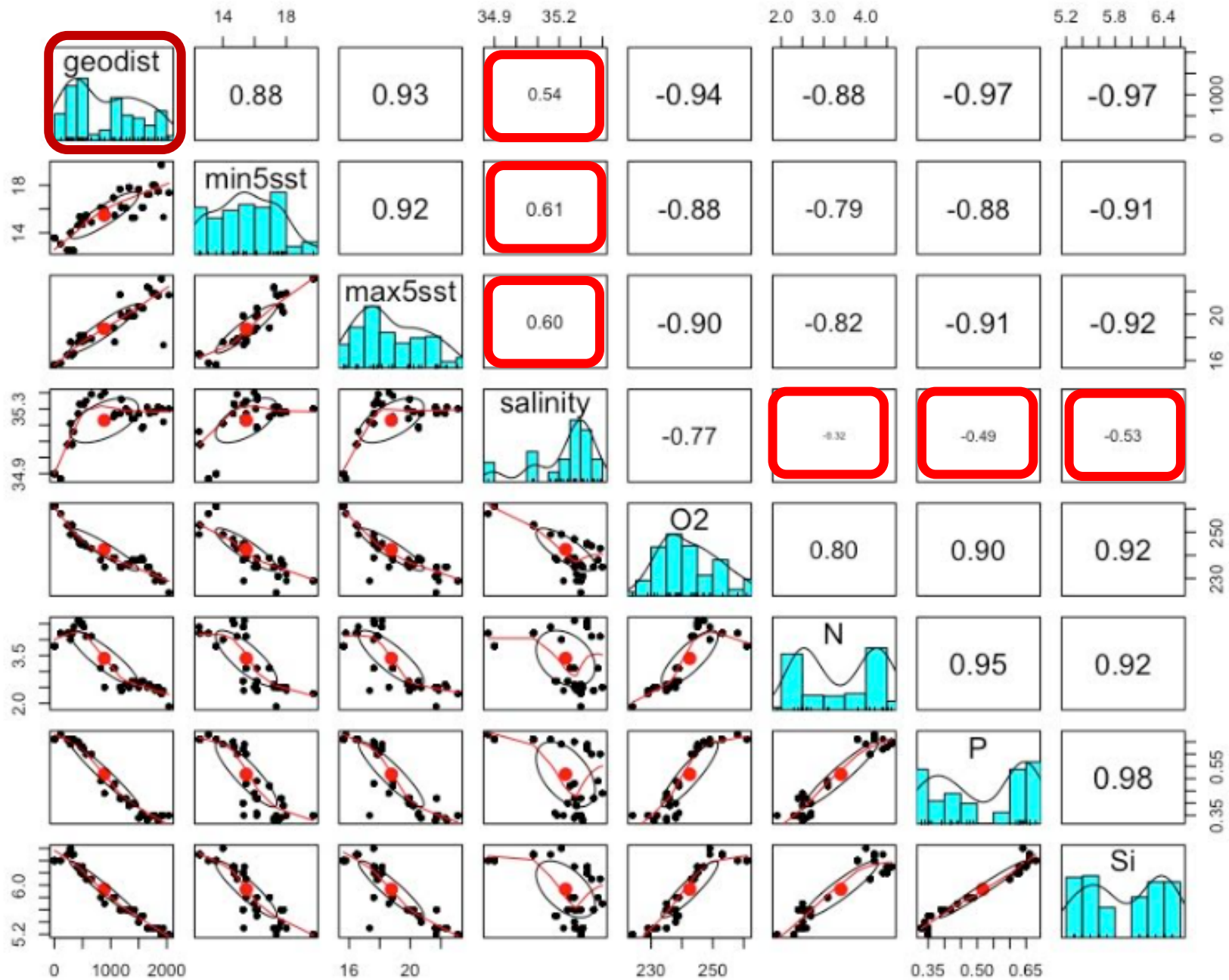


STRUCTURE barplots



gINLAnd outliers → STRUCTURE barplots (locprior)

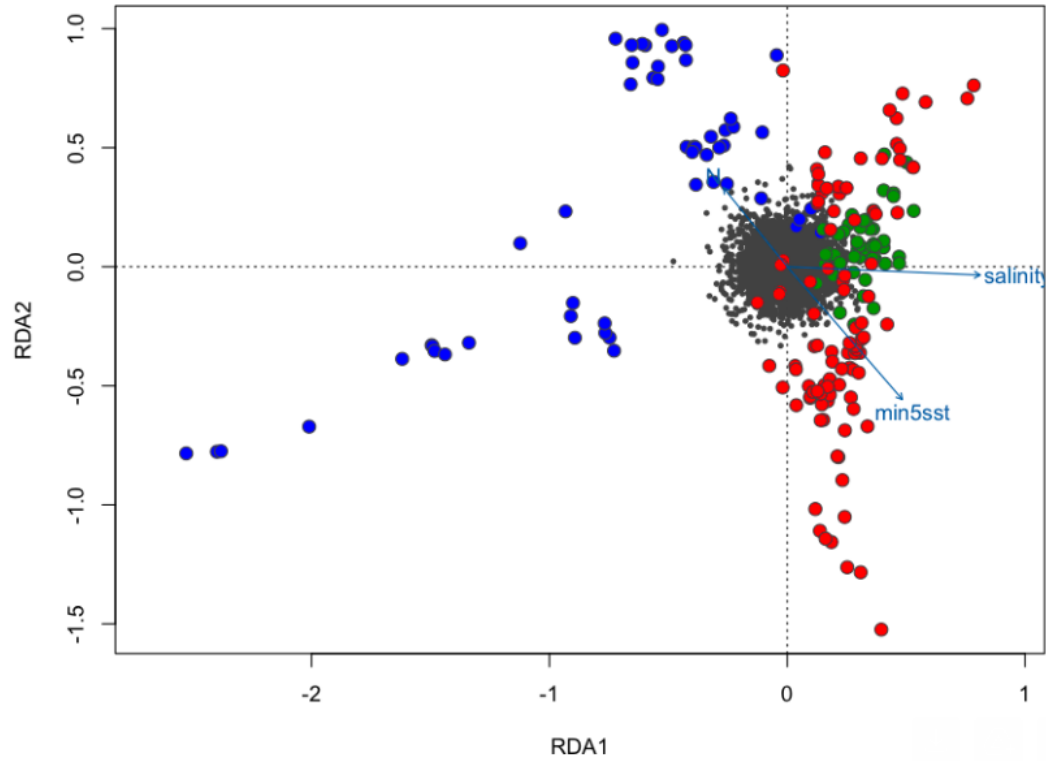




 $|r| < 0.7$

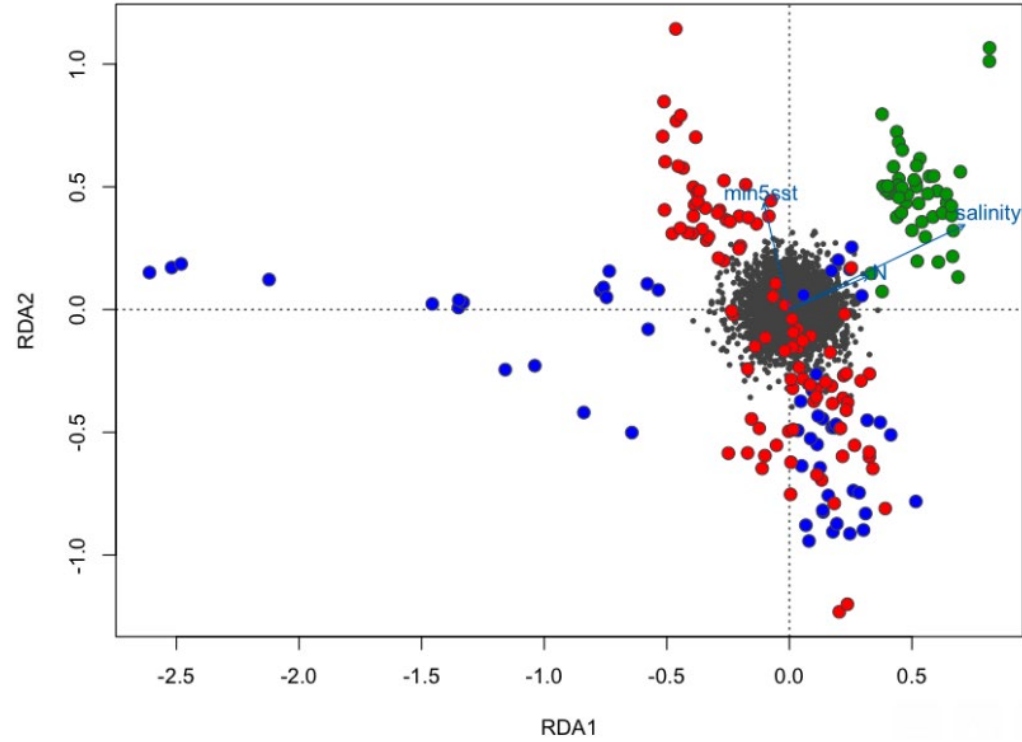
Pairwise correlation coefficients calculated using 'vegan'.

Redundancy Analysis (RDA)

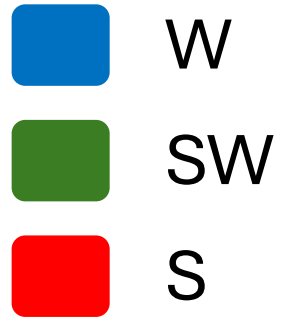


min5sst + salinity + N

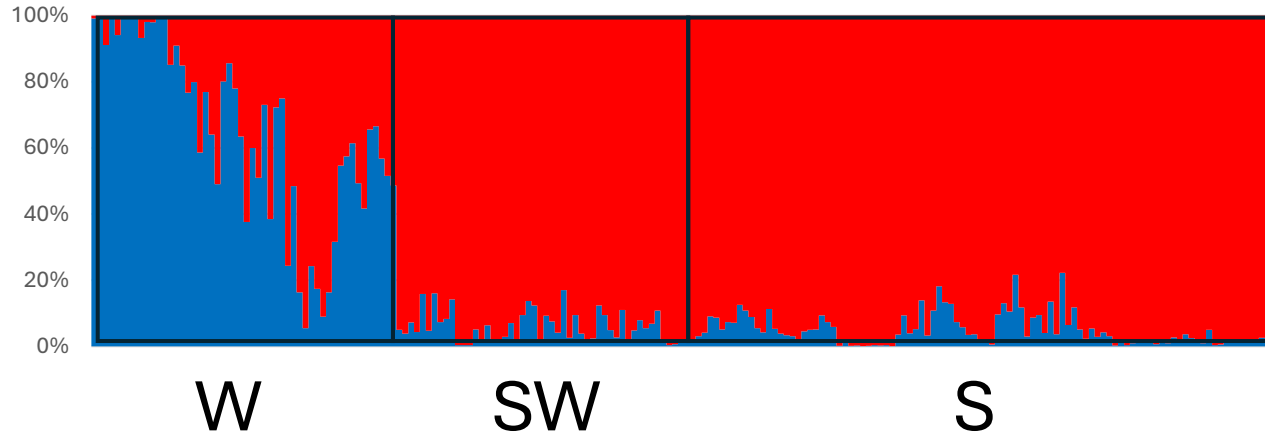
Partial Redundancy Analysis (pRDA)



min5sst + salinity + N



gINLAnd + RDA
(min5sst + salinity + N, not consensus)



Consensus SNPs
(1 GEA + 1 genome scan)

SNP_249
SNP_726
SNP_4448
SNP_4828
SNP_4938
SNP_5169
SNP_5422
SNP_5850
SNP_6772
SNP_6790
SNP_7435

Consensus SNPs
(gINLAnd + RDA + 1 genome scan)

SNP_5850

		W	SW	S
Outlier F_{ST}	W	-		
	SW	0.056**	-	
	S	0.063**	0.004**	-
Neutral F_{ST}	W	-		
	SW	0.009**	-	
	S	0.009**	0.001	-

Migration rates (BA3-SNPs)

