

# Responses of the Intertidal Key Species *Fucus serratus* to North Atlantic Warming



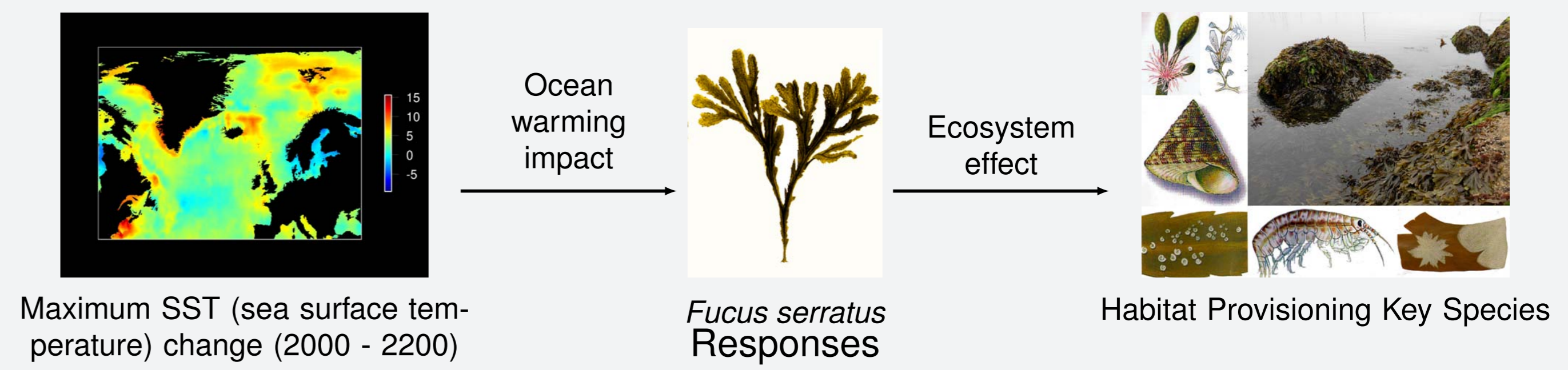
Jueterbock A.<sup>1</sup>, Coyer J.A.<sup>2</sup>, Tyberghein L.<sup>3</sup>, Olsen J.L.<sup>2</sup>, Hoarau G.<sup>1</sup>

<sup>1</sup> University of Nordland, Norway  
<sup>2</sup> University of Groningen, The Netherlands  
<sup>3</sup> University of Ghent, Belgium



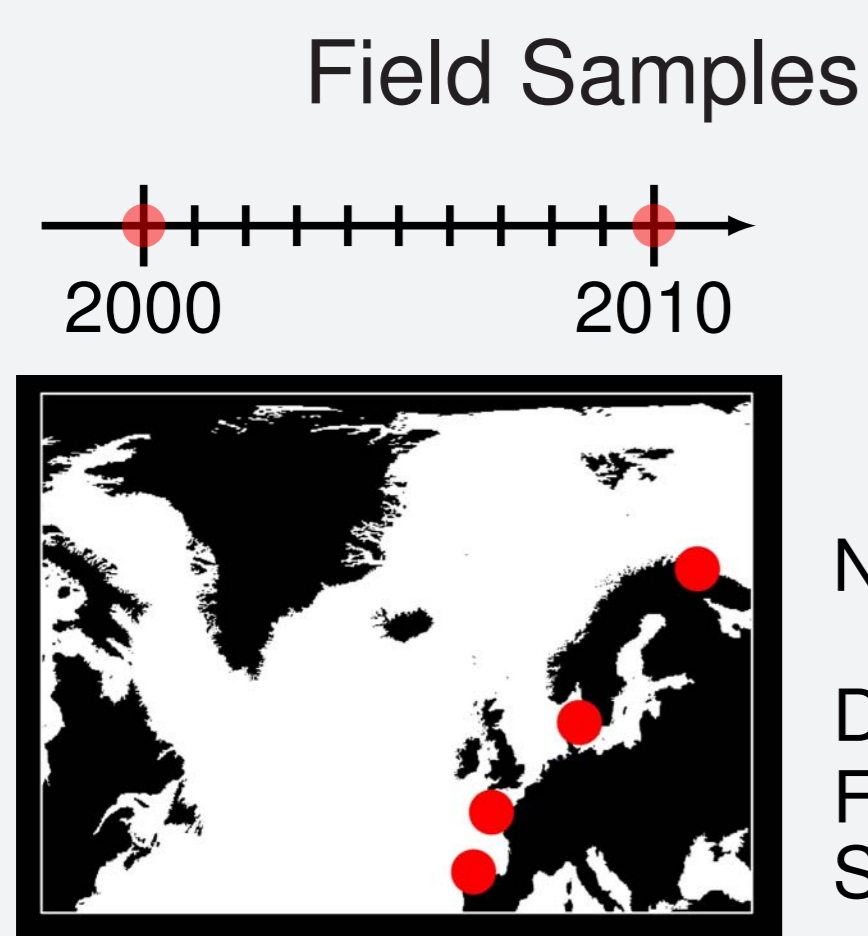
## Introduction

Climate change is likely to profoundly affect marine intertidal ecosystems since human impacts have already undermined their capacity to buffer additional stresses. Global environmental change invokes two basic responses of organisms: ecological (range shift, phenotypic plasticity) and evolutionary (genetic change), both of which are integrated into a “move, be plastic, or evolve” strategy. We investigate ocean warming responses in the seaweed *Fucus serratus*, a key ecosystem engineer of North Atlantic rocky shores, with focus on: (1) distributional changes under rising temperatures and (2) genetic changes over the past decade.



## Methods

### Genome Scan



Each of the four locations were sampled (50–70 individuals) in ~ 2000 and ~ 2010.

### Genotyping

▶ 31 Microsatellites, of which 20 are linked to ESTs

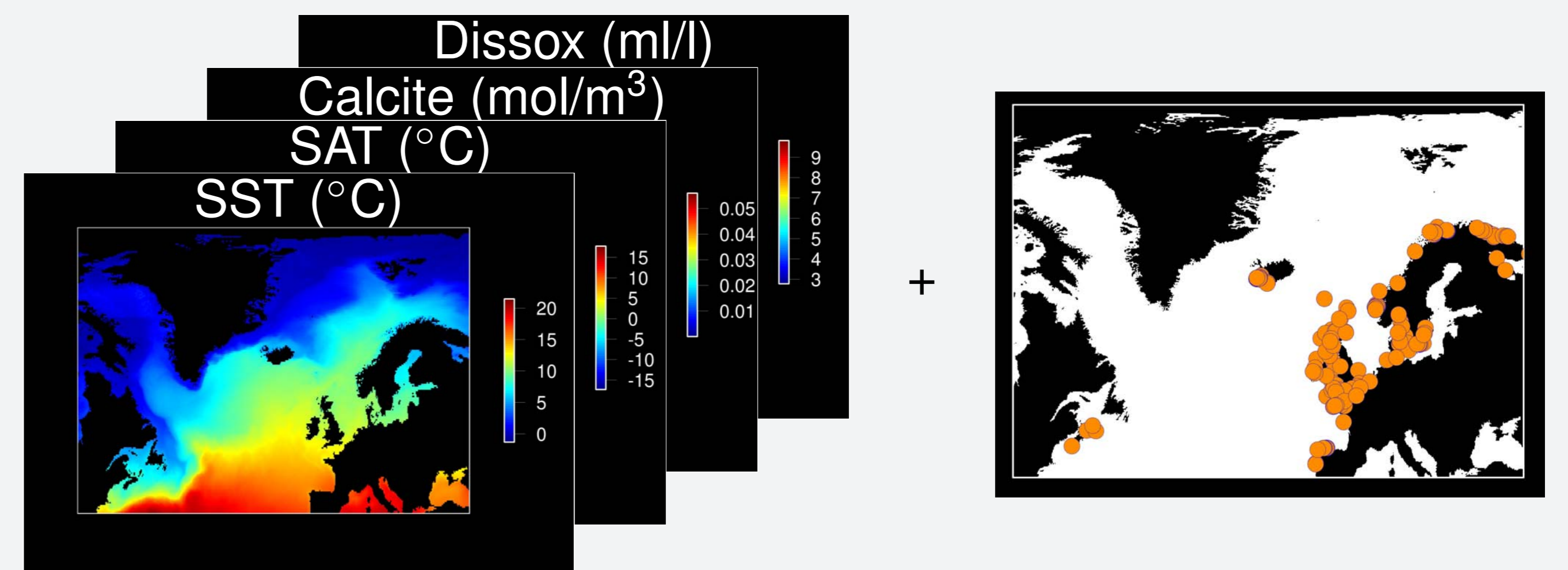


ABI 3500xl Genetic Analyzer.

### Data analysis

Variability *Genetix* (Belkhir et al., 1997); *ADZE* (Szpiech et al., 2008)  
Differentiation *Genetix* (Belkhir et al., 1997); *DEMETics* (Gerlach et al., 2010)  
Effective population size *MLNe* (Wang & Whitlock, 2003); *TMVP* (Beaumont, 2003)  
Outlier Loci *Arlequin* (Excoffier & Lischer, 2010); *Bayescan* (Beaumont & Nichols, 1996)

### Ecological Niche Modelling



Environmental variables (from the Bio-ORACLE database (Tyberghein et al., 2011)) at georeferenced occurrence sites specify the ecological niche of *Fucus serratus*. Locations fitting this niche are predicted to be of suitable habitat.

### Predicted environmental conditions for 2100 and 2200

- ▶ sea surface temperature and surface air temperature
- ▶ based on three IPCC scenarios (A2, A1B, B1)

### Future projection of habitat suitability

- ▶ Program MAXENT (Phillips et al., 2006)

## Results

### Genetic response

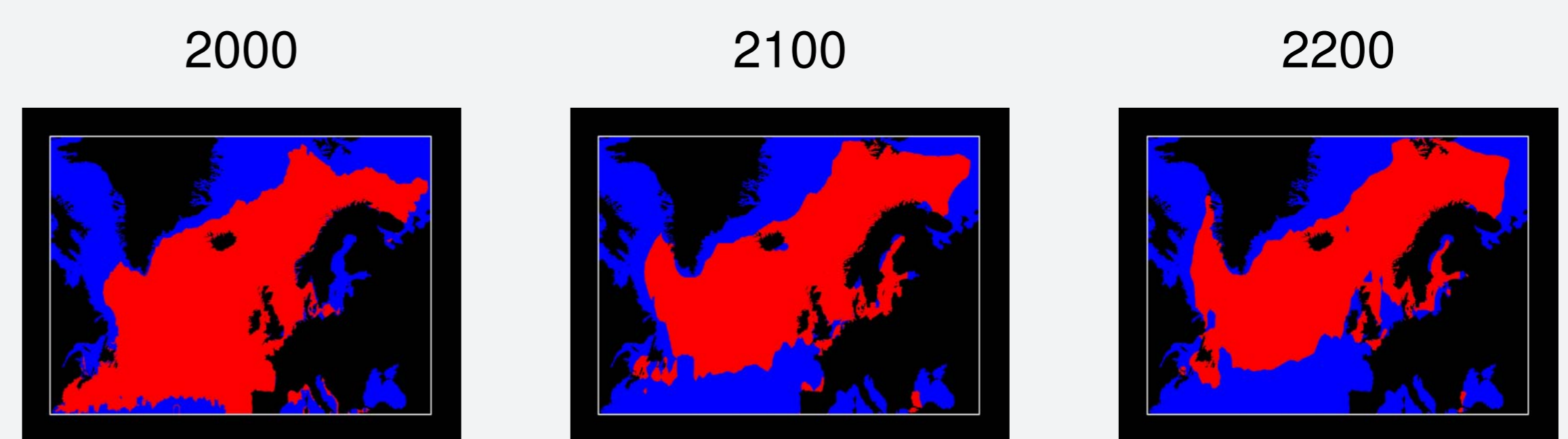
Population genetic changes of *F. serratus* over the past decade. **A**: Allelic richness, **H<sub>exp</sub>**: Expected heterozygosity, **N<sub>e</sub>**: Effective population size, **O**: Proportion of loci being outliers.

Location	Diversity		Differentiation		Population size			O		
	H <sub>exp</sub>	A	F <sub>ST</sub>	D <sub>est</sub>	N <sub>e</sub>					
	2000	2010	2000	2010	2000	2010	Average			
Norway	0.27	0.28	3.18	3.10	0.044 <sup>a</sup>	0.031*	22	33	91	5%
Denmark	0.50	0.48	4.55	4.19	0.010*	0.014*	51	54	613	0%
France	0.70	0.69	8.61	8.72	0.008*	0.022*	140	115	526	24%
Spain	0.41	0.38	4.24	3.68*	0.008*	0.007*	37	33	551	14%

<sup>a</sup>p < 0.05: significant change between temporarily paired population samples

### Distributional change

Drastic northward niche shift over the next two centuries



Predicted habitat suitability in present day and future conditions. Red areas depict the fundamental niche of *F. serratus*.

## Conclusion

Within the past decade, *F. serratus* suffered significant loss of allelic richness in Spain, where extreme summer temperatures already exceed its upper temperature tolerance limit. Under the predicted northward niche shift until 2200, populations of highest genetic diversity are at risk to become extinct. Disappearance of this key species may trigger substantial

ecosystem restructuring on North Atlantic rocky shores with potential societal and economic impacts. Whole genome scans for loci under selection are the first step to clarify whether the population of highest genetic diversity in France can adapt to climate change and thus mitigate the predicted northward retreatment.

## Bibliography

Beaumont, M.A. & Nichols, R.A. (1996): Evaluating loci for use in the genetic analysis of population structure. *P. Roy. Soc. B-Biol. Sci.* **263**(1377):1619–1626  
Beaumont, Mark A. (2003): Estimation of Population Growth or Decline in Genetically Monitored Populations. *Genetics* **164**(3):1139–1160  
Belkhir, K.; Borsa, P.; Goudet, J.; Chikhi, L. & Bonhomme, F. (1997): Genetix v. 5.0, logiciel sous Windows TM pour la génétique des populations.  
Excoffier, L. & Lischer, H.E.L. (2010): Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Mol. Ecol. Resour.* **10**(3):564–567  
Gerlach, G.; Jüterbock, A.; Krämer P.; Deppermann, J. & Harmand, P. (2010): Calculations of population differentiation based on G<sub>ST</sub> and D: forget G<sub>ST</sub> but not all of statistics! *Mol. Ecol. Notes* **19**(18):3845–3852

Phillips, S.J.; Anderson, R.P. & Schapire, R.E. (2006): Maximum entropy modeling of species geographic distributions. *Ecol. Model.* **190**(3–4):231–259  
Szpiech, Z.A.; Jakobsson, M. & Rosenberg N.A. (2008) ADZE: a rarefaction approach for counting alleles private to combinations of populations. *Bioinformatics* **24**(21):2498–2504  
Tyberghein, L.; Verbruggen, H.; Pauly, K.; Troupin, C.; Mineur, F. & De Clerck, O. (2011): Bio-ORACLE: a global environmental dataset for marine species distribution modelling. *Global Ecol. Biogeogr.*: 1–10  
Wang, J. & Whitlock, M.C. (2003): Estimating Effective Population Size and Migration Rates From Genetic Samples Over Space and Time. *Genetics* **163**(1):429–446