

DRIVERS OF *CALANUS FINMARCHICUS*: THE TOP, THE BOTTOM, AND THE QUEST FOR A HOLISTIC APPROACH

Danny J. Papworth ^{1*}, Simone Marini ² and Alessandra Conversi ³

¹ Faculty of Science and Technology, School of Marine Science and Engineering, University of Plymouth, United Kingdom - dpapworth@hotmail.co.uk

² ISMAR – Marine Sciences Institute, CNR, Lerici (SP), Italy

³ ISMAR – Marine Sciences Institute, CNR, Lerici (SP), Italy; Faculty of Science and Technology, University of Plymouth, United Kingdom PL4 8AA.

Abstract

Ecosystems dynamics are an integrated response of the ecosystem's biological components to drivers. A long, unsolved ecological question is whether top-down trophic drivers (i.e. predation) or bottom-up drivers (often intended as climate, hydrography, food) control populations and ecosystems. Current methods for analysing drivers of ecosystems can have varying degrees of bias, giving rise to conflicting views in published research. In this study, we use an unbiased approach based on Genetic Programming for selecting drivers of a key species, *Calanus finmarchicus*, in the North Sea. This species has been widely discussed due to its importance for the food chain and its link to an ecosystem-wide regime shift in the late 1980's. The results suggest that both bottom-up and top-down drivers are involved in driving this species abundance.

Keywords: North Atlantic, Zooplankton, Warming, Time series, Models

Abrupt changes in ecosystems, termed regime shifts, are the cumulative response to drivers, which act on and within the ecosystem. A holistic, unbiased method for determining drivers of marine regime shifts would greatly improve our understanding and future management capabilities [1].

Genetic Programming (GP) is a methodology capable of generating solutions to a given problem without any strong *a-priori* knowledge or assumptions about the problems solution, hence unbiased [2]. GP has been used successfully in a wide range of applications, including economics and robotics; however, analyses approaches based on GP are yet to be fully utilised within an ecological setting, although they have been used to investigate copepod variability in the English Channel [2].

The approach we propose is a statistical analysis of ecological data, based on a GP-symbolic-regression method coupled with a cross-validation framework. We used 26 variables, ranging from local to large scale, from climatic, hydrographic, to food and predation (Fig. 1), over the period 1972 to 2011, to validate and highlight the potential future use of the GP procedure. Our target species was *Calanus finmarchicus*, a key species in the North Sea food chain, which has seen a decline in abundance over the past 40 years [3].

identified as likely drivers during the 40 years period [4]. This work highlights the complexity and multiplicity of population drivers and the need for analysing them without *a-priori* assumptions.

References

- 1 - Conversi A. et al., 2015. A holistic view of marine regime shifts. *Philosophical Transactions of the Royal Society B*, 370:20130279. <http://dx.doi.org/10.1098/rstb.2013.0279>.
- 2 - Marini S. and Conversi A., 2012. Understanding Zooplankton Long Term Variability through Genetic Programming. In: Giacobini M, Vanneschi L, and Bush W. (eds) *Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics*, Springer, Berlin Heidelberg, pp. 50–61. DOI: 10.1007/978-3-642-29066-4_5.
- 3 - Alheit J., Moellmann C., Dutz J., Kornilovs G., Loewe P., Mohrholz V. and Wasmund N., 2005. Synchronous ecological regime shifts in the central Baltic and the North Sea in the late 1980s. *ICES J Mar Sci*:62(7):1205-15.
- 4 - Papworth D., Marini S. and Conversi A. Declining *Calanus*: What is driving *Calanus finmarchicus* abundance in the central North Sea? A new model based on Genetic Programming. Submitted to *PLOSone*, under revision (Apr 2016).

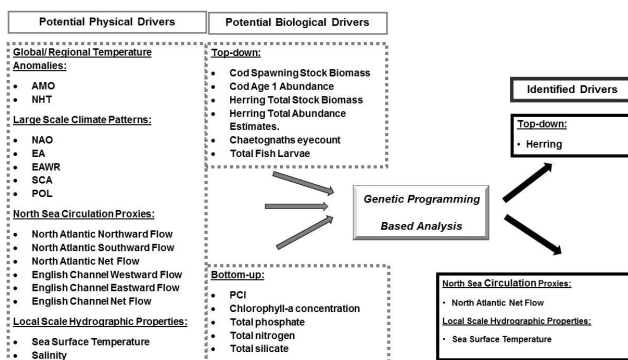


Fig. 1. Drivers of *Calanus finmarchicus*. On the left, in the gray dashed boxes, the potential drivers selected for this study, subdivided in physical and biological (bottom-up, top-down) drivers. On the right, in the black boxes, the drivers identified after Genetic Programming-based analysis.

The GP procedure, combined with a cross validation framework and with relevance analysis highlighted 9 statistically relevant variables for the approximation of *C. finmarchicus* abundance. Of these, 6 variables from 3 main groups: ocean circulation, sea surface temperature and predation (Fig. 1), were