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Role	Name	Organisation	Date	File suffix ³
Authors	Montse Pérez	IEO	18/11/2014	MP
Authors	Sarah Helyar	MATIS	18/11/2014	SH
WP leader/Authors	Santiago Cervino	IEO	18/11/2014 (rev 25/11/2015)	SC
Coordinator	Anna K. Daniélsdóttir	Matis	25/11/2014	AKD
Administrative Coordinator	Oddur M. Gunnarsson	Matis		OMG
Scientific Coordinator	Gunnar Stefánsson	UI		GS

¹ Document will be a draft until it was approved by the coordinator

² PU: Public, PP: Restricted to other programme participants (including the Commission Services), RE: Restricted to a group specified by the consortium (including the Commission Services), CO: Confidential, only for members of the consortium (including the Commission Services)

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Deliverable D2.1

On relevant novel information and data available for integration into new models

08/12/2014

(rev 25/11/2015)



Executive Summary

The first deliverable in WP2 is related with the first task (Task 2.1) dealing with the compilation of novel information from all Case Studies (CSs). The workshop at the Kick-off meeting (see report in annex I) in Reykjavik February 2014, was useful to WP2 in 3 ways: (1) to define a template to report Case specific data; (2) to identify a potentially useful source of data (e.g. FishPopTrace, etc.) and (3) to set priorities in terms of WP2 data. This emphasise new technological data as the main priority.

All Case studies presented information to work with in WP2. This information was presented by completing the template (Appendix I). Some CSs have used the FishPopTrace project to search for information. All CSs have presented new technological data, although the amounts of data collected are different in different CS. Many CSs have also provided other types of data such as landings, abundance indices, age-length keys, etc. It is necessary to clarify what information is going to be used in WP2 and what information is not. However, given that new technological data have been prioritized and all CSs have reported new technological data, all CSs are in a position to determine how to integrate this data, and to initiate work in Task 2.2.

Furthermore, given that the analysis of these data can be extended until month 18 (June 2015) all CSs may have new information added to their model analysis if such relevant information becomes available in the meantime.



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Introduction

The aim of this WP is to identify, collect, and evaluate information not usually considered for assessment and management, mainly (not only) focusing on making the best use of new tools and technologies to create new knowledge.

The first deliverable in WP2 is related with the first task (Task 2.1) dealing with the compilation of novel information (Task 2.1: Compilation of novel information. Lead: IEO, all WP2 partners contributing with additional contribution from SLU, NRC and ICES. Explore available novel information in existing DBs that potentially could contribute to the assessment of the key species identified in WP5 for each Case Study. WP2 will then identify new data types available.)

This report aims to describe the information that is going to be used in all the WP2 tasks. The information identified and selected in this task will be evaluated (Task 2.2; Lead: MATIS, UI and IEO, all WP2 partners contributing), discarded or selected to be implemented in models (Task 2.3; Lead: UI, MATIS and IEO, all WP2 partners contributing), and finally, after model implementation their utility for management will be evaluated.

During the kick-off meeting WP2 was introduced and tasks and goals were discussed. Representatives from the External Advisory Group provided WP2 evaluation heightening critical questions. Following the presentations, a WP workshop in parallel with WP3, WP4, WP5 and WP6 was undertaken (see Annex I Minutes for kick-off meeting workshop). The definition of data to be used in WP2 is broad and, given the limitation of resources and the need to address Objective 1 of the call, data to prioritise was decided during the kick-off meeting. This priority is the “new technological data”. These are genetics, proteomics, otolith microchemistry, isotope analysis, fatty acid analysis, tagging, oceanography, etc. Tagging and oceanography are in this group only if they refer to new technologies (pop-ups, satellites, etc.). Not all Case Studies would have to deal with all kind of new technological data in all models. However all Case Studies should try to explore the implementations of some of these new data at least in one model.

In this report WP2 presents the work performed for task 2.1 that finalises with the selection of new information to be used in each Case Study.

Methods

Three activities regarding compilation of novel information (task 2.1) were initialized in the kick-off meeting: reporting and analysis of data compilation status at Case Study level; identification of potentially useful data sources and design of a template for deliverable 2.1.

Not all Case Studies have availability of “new technological data”. Given that the access to new information is different in each case study; two additional sources of information have been considered apart of existing data sets by Case Studies partners. These are: literature review and also from FishPopTrace project (<https://fishpoptrace.jrc.ec.europa.eu/>).

FishPopTrace was selected because it sampled and analysed new technological data including genetics (SNPs), otolith microchemistry, fatty acid profiles; in addition it has priority species in common with MareFrame (Atlantic cod, Atlantic herring and European hake) and common areas (North Atlantic, Mediterranean, and Baltic sea). A meeting was scheduled with Prof. Gary Carvalho to discuss options



for accessing FishPopTrace data (see Meeting minutes are presented as Annex II). It was decided that the FishPopTrace (FPT) database will be a useful source of data to the project. At this stage the data might be most useful at an aggregated, rather than an individual level. If this changes, then FPT is open to further discussion regarding how to best provide access to the wider database. The sources of FPT data that are most relevant to MareFrame at this point are:

The Geobrowser: https://fishpoptrace.jrc.ec.europa.eu/map/genetics_geobrowser/

The Web crawler: <https://fishpoptrace.jrc.ec.europa.eu/crawler> (this is not currently functional, but JRC are looking into it).

Published papers from the project (full current list attached in Annex II).

With these resources, every Case Study has compiled the useful information relevant for them. This information is presented in the Appendix 1. A summary by Case Study is presented in “Results” section. When Case Studies provided ideas about the implementation of these new data into models, these are also included in the “Results” section.

Results

A summary of the information provided by each Case Study is presented here. A detailed description of these data is presented in the Appendix I.

Baltic Sea.

Baltic Sea Case Study reported different kinds of data including data of general use such as catches (landings and discards), effort, CPUE or biological data; data for ecosystem model implementation such as stomach content (proportion of different prey species by predator length) and genetic data (F_{ST} estimates) in different areas.

North Sea.

North Sea case study reported data of stable isotope studies as indicators of trophic levels that may feed ecosystem models (simple size and EwE type models). This data is potentially useful for determining other food, primary productivity requirements. Data was taken from Jennings et al (2008) although raw data may be available on request.

Northern and Western Waters – Iceland Waters

Northern Waters provided minke whale data on stable isotopes, genetics and fatty acids, as well as stomach content. This information might help the model to define stock structure or develop spatial hypothesis, been used as likelihood data or to model species interactions.

Northern Waters – West Scotland

Data provided are mainly basic such as survey abundance, age-length key (ALK), maturity or seal population size for different species (cod, haddock, whiting, saithe, hake, herring, mackerel, Norway pout, sprat, anglerfish, megrim, etc.); stomach content data and oceanographic data are also available. Genetic data from FishPopTrace might be used to define the hake stock boundaries and possibly



document migrations, although only 2 years of data are available. This data will most probably not be used directly in the implementation and parameterisation of ecosystem model, but will provide novel insight on stock definition and/or migration.

South-Western Waters – Iberian Peninsula

Cs provides data for the main species in case study model (hake, sardine, anchovy, common dolphin and bottlenose dolphin) as well as other species. There are four main sources of new information that can be considered for their incorporation into GADGET models, namely: genetics/genomics, otolith microchemistry, stable isotopes and biology. These new technological data will be used to feed the ecosystem model implemented in GADGET with information about spatial and trophic processes.

- Genetics data: Bayesian inference made on multilocus genotypic data (microsatellites) of *Merluccius merluccius* populations provides evidence that a large genetic connectivity exists among Atlantic grounds and is mediated by significant migration rates stepping up from the Celtic Sea towards its adjacent Atlantic grounds (Pita et al, 2014). Therefore, the spawning biomass of the northern hake population could play a crucial role at ensuring the sustainability of southern hake fish grounds (Pita et al, 2011; Pita et al, 2014). SNPs analysis shows similar results (Milano et al., 2014). In general, all data show the same pattern of connectivity among Atlantic populations of *Merluccius merluccius*.
- Otolith microchemistry: Both otolith core and edge geochemical signatures provided strong evidence of movement of European hake between the local populations in the Atlantic Ocean and the Mediterranean Sea (Tanner et al, 2012). Information on microchemistry might be used to estimate the proportion of anchovy recruits that occupies estuarine waters while juveniles. This will inform the model on habitat conditions (open sea versus estuarine waters) to incorporate in the environmental forcing of anchovy life cycle.
- Stable isotopes data: Information on isotopic composition of small cetaceans will add understanding on the trophic level of their food in connection with their pelagic and demersal preys. This will help in the parameterization and/or validation of models.
- Biological data: sex ratio at length data might be used to calibrate a sex separated model. It requires a design of a new likelihood in GADGET.

Mediterranean Waters – Strait of Sicily

There are three main sources of information that the Mediterranean Case Study can consider for their incorporation into Atlantis and Gadget models for the Strait of Sicily (SS) ecosystem, namely: genetics/genomics, stable isotopes, vessel monitoring system data.

-Genetics data: genomics of hake juveniles (*Merluccius merluccius*) from the two main persistent nursery grounds (Adventure Bank on the eastern side of the SS, Malta Bank on the western side of SS). The two groups of juveniles displayed genetics discontinuities that might be interpreted as an evidence of reduced connectivity and mixing between the two areas (Milano et al., 2014). Genetic data available for *Parapenaeus longirostris* also clearly show a gradual discrepancy along a west-east gradient, with some geographical areas with some degree of isolation (Lo Brutto et al., 2013).



We can argue that the two nurseries basically depends on two different groups of spawning fish distributed upstream from the nursery grounds. This aspect can be explicitly implemented into ATLANTIS to separate the effects of anthropogenic (e.g. fishing) and environmental sources (e.g. climate forcing) on the two sub-groups of specimens.

-Stable isotope measurements of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ for 42 species from three different Sicilian coastal areas (Fanelli et al., 2009, 2010, 2011; Sinopoli et al., 2012). This data combined with stomach content data are used to define functional groups and assign species accordingly based on their trophic role. In addition, ontogenetic changes in isotopic composition of target commercial species (e.g. hake, red mullet) were used to better separate specimens in size classes to be incorporated into Atlantis food web structure.

-Vessel Monitoring System (VMS) data: VMS were introduced in 2002 by the European Union for the remote monitoring of fishing vessels and the data has been collected within Data Collection Framework since 2006. Specifically, the VMS data, available for about 300 vessels operating in the area, covers the years 2006–2010 (Russo et al., 2014). Data for 2011-2013 still needs to be gathered and elaborated. The VMS data were processed following the methodology described in Russo et al., 2013 and combined with landing/discards data for the spatial allocation of fishing pressure. In addition this data will be used in area closure scenarios to simulate the effects of changes in the spatial distribution of the fleets on catches / fishing mortality of the main commercial stocks.

Black Sea

They presented data for single species assessment models and also genetic data.

Chatham Rise – New Zealand

Provide information on stable isotopes and stomach content for most abundant fish species in the ecosystem. This information is being used to investigate trophic level and niche structure.

Discussion

All Case Studies have reported information to be used in WP2. The level of detail regarding data of interest for WP2 is different for each Case Study. Many CS have also presented information that is not the main area of main interest for WP2 such as landings, effort, abundance indices or ALK. Further discussions are needed to delimit which information will be analysed in WP2. Given the time limitation in WP2 it is important to prioritize data to be analysed, to enable the other data to be analysed in WP5 (Case Studies). This decision should be agreed between WP2 and WP5.

New technological data already compiled include: genetics (allozymes, microsatellites, SNPs), stable isotopes, otolith microchemistry for different species including hake, anchovy, cod, herring, etc. Information from FishPopTrace project was taken in consideration by some CSs. However is not clear now how to consider this information in the models. Further analysis is needed and will be carried out in T2.2. Some CSs have reported that this information is not useful in their case and rejected their use. In any case FishPopTrace is open to discuss it in case we need more disaggregated information.



Given that the analysis of these data can be extended until month 18 (June 2015) all CSs may have new information added to their model analysis if such relevant information becomes available in the meantime.

Conclusion

New technological data such as genetics, stable isotopes, otolith microchemistry, fatty acids and Vessel Monitoring Systems, were presented by different CSs. This data will be the main information to develop the WP2 tasks. In addition to this information, partners have also presented different types of new data such as landings, abundance indices, age-length keys, etc. However, given that new technological data have been prioritized and all CSs have reported new technological data, all CSs are in a position to determine how to integrate this data, and to develop the WP2 objectives.

Acknowledgement

We have to thank Gary Carvalho (FishPopTrace coordinator) for his help identifying new technological data analysed in FishPopTrace.



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Appendix I - Data tables by Case Study

Baltic Sea.

Species / Functional group	Cod
Data	Stomach content, proportion of different prey species by predator length
Suggested data use in MareFrame	Trophic interaction
Area (add ICES SD)	Baltic Proper
Spatial resolution	ICESrect?
Year	2012-2014
Season / resolution	Q1, Q4?
Reference	EU program Mare/2012/02, stomach sampling program coordinated with the BITS survey
Where the data can be retrieved	
Access	available?
What's new (data, use)	new data
Comments	data should be available under the EU program Mare/2012/02 in which both SLU and NMFRI are involved
Species / Functional group	Cod
Data	Stomach content, proportion of different prey species by predator length
Suggested data use in MareFrame	Trophic interaction
Area (add ICES SD)	Baltic Proper
Spatial resolution	ICES sub-div.
Year	2006-2007
Season / resolution	Q1, Q4
Reference (paper, project, DB?)	Internal project of NMFRI (Poland)
Where the data can be retrieved	NMFRI,
Access	available to the project on request
What's new (data, use)	new data, so far not used for ecosystem/assessment models
Comments	ready available at ICES sub-div, it would need extra work to have them by ICES rect
Species / Functional group	Cod
Data	Bottom trawl survey CPUE
Suggested data use in MareFrame	Index of abundance, spatial distribution
Area (add ICES SD)	Baltic Proper
Spatial resolution	individual haul
Year	
Season / resolution	Q1, Q4
Reference (paper, project, DB?)	SGSPATIAL, BONUS Inspire (WP1), LOT1, Tian et al. in prep.
Where the data can be retrieved	ICES, WGBFAS
Access	available
What's new (data, use)	spatial dimension



Species / Functional group	Cod
Data	Drift models output
Suggested data use in MareFrame	Movement
Area (add ICES SD)	
Spatial resolution	
Year	
Season / resolution	
Reference (paper, project, DB?)	BONUS Inspire (WP2)
Where the data can be retrieved	
Access	?
What's new (data, use)	new data
Comments	the actual content and availability of the data to be verified
Species / Functional group	Cod/Herring/Sprat
Data	Commercial landings
Suggested data use in MareFrame	Distribution landings (excl. discards)
Area (add ICES SD)	Baltic
Spatial resolution	ICESrect
Year	2003-2013
Season / resolution	Annual/Quarter?
Reference (paper, project, DB?)	http://stecf.jrc.ec.europa.eu/data-reports
Where the data can be retrieved	STECF
Access	available
What's new (data, use)	spatial dimension
Comments	
Species / Functional group	Cod/Herring/Sprat
Data	Fishing effort
Suggested data use in MareFrame	distribution effort
Area (add ICES SD)	Baltic
Spatial resolution	ICESrect
Year	2003-2013
Season / resolution	Annual/Quarter?
Reference (paper, project, DB?)	http://stecf.jrc.ec.europa.eu/data-reports
Where the data can be retrieved	STECF, ICES?
Access	available
What's new (data, use)	spatial dimension
Comments	
Species / Functional group	Cod
Data	Acoustic survey CPUE (BIAS and BASS)
Suggested data use in MareFrame	Pelagic cod component
Area (add ICES SD)	Baltic



Spatial resolution	ICESrect
Year	~2008-2013
Season / resolution	Q2, Q4
Reference (paper, project, DB?)	
Where the data can be retrieved	ICES, WGBFAS, SLU
Access	available
What's new (data, use)	spatial dimension
Comments	Indices for cod have been computed for the last 5-6 years, but they should be available for the whole survey period. Likely worked out in the BONUS Inspire project.
<hr/>	
Species / Functional group	Herring/Sprat
Data	Acoustic survey CPUE (BASS)
Suggested data use in MareFrame	Index of abundance, spatial distribution
Area (add ICES SD)	Baltic, SD25-26 (~28)
Spatial resolution	ICESrect
Year	1999-2013
Season / resolution	Q2
Reference (paper, project, DB?)	
Where the data can be retrieved	ICES, WGBFAS, NMFRI?
Access	available
What's new (data, use)	spatial dimension
Comments	
<hr/>	
Species / Functional group	Herring/Sprat
Data	Acoustic survey CPUE (BIAS)
Suggested data use in MareFrame	Index of abundance, spatial distribution
Area (add ICES SD)	Baltic, SD24-29 (~30-32)
Spatial resolution	ICESrect
Year	1991-2013
Season / resolution	Q4
Reference (paper, project, DB?)	
Where the data can be retrieved	ICES, WGBFAS, SLU
Access	available
What's new (data, use)	spatial dimension
Comments	
<hr/>	
Species / Functional group	Herring/Sprat
Data	Acoustic survey CPUE (BIAS)
Suggested data use in MareFrame	historical abundance and spatial distribution
Area (add ICES SD)	Baltic, SD24-29 (~30-32)
Spatial resolution	ICESsubd / ICESrect
Year	1978-1984 / 1985-1990
Season / resolution	Q4
Reference (paper, project, DB?)	



Where the data can be retrieved	ICES, WGBFAS, SLU
Access	available
What's new (data, use)	historical perspective
<hr/>	
Species / Functional group	Cod
Data	Commercial catch
Suggested data use in MareFrame	Total catch (incl. discards)
Area (add ICES SD)	Baltic Proper
Spatial resolution	ICESsubd
Year	1966
Season / resolution	Annual
Reference (paper, project, DB?)	ICES DB
Where the data can be retrieved	ICES, WGBFAS
Access	available
What's new (data, use)	spatial dimension
<hr/>	
Species / Functional group	Cod
Data	Biological data (length, weight, maturity, ...) from bottom trawl survey
Suggested data use in MareFrame	Growth and maturity
Area (add ICES SD)	same as BITS
Spatial resolution	
Year	
Season / resolution	Q1, Q4
Reference (paper, project, DB?)	
Where the data can be retrieved	ICES, WGBFAS
Access	
<hr/>	
Species / Functional group	Herring/Sprat
Data	Biological data (length, weight, maturity, ...) from pelagic trawl associated to acoustic survey
Suggested data use in MareFrame	Growth and maturity
Area (add ICES SD)	same as BIAS and BASS
Spatial resolution	
Year	
Season / resolution	Q2, Q4
Reference (paper, project, DB?)	
Where the data can be retrieved	ICES, WGBFAS
Access	
<hr/>	
Species / Functional group	Cod
Data	genetics
Suggested data use in MareFrame	F _{ST} estimates
Area (add ICES SD)	Baltic Proper
Spatial resolution	samples from Gotland, Gdańsk Bornholm basins, Western Baltic, Sound, Kattegat, North Sea



Year	1996-1998
Season / resolution	NA
Reference (paper, project, DB?)	Einar E. Nielsen, Michael M. Hansen, Daniel E. Ruzante, Dorte Meldrup and Peter Gronkjaer (2003) Evidence of a hybrid-zone in Atlantic cod (<i>Gadus morhua</i>) in the Baltic and the Danish Belt Sea revealed by individual admixture analysis <i>Mol. Ecol.</i> (2003) 12: 1497-1508
Where the data can be retrieved	rough data (genotypes) from the authors on request
Access	FST estimates available in the paper
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Species / Functional group	Sprat
Data	genetics
Suggested data use in MareFrame	F _{ST} estimates
Area (add ICES SD)	Baltic Proper
Spatial resolution	sample from Baltic Sea, Gotland
Year	2006
Season / resolution	NA
Reference (paper, project, DB?)	Kevin A. Glover, Øystein Skaala, Morten Limborg, Cecilie Kvamme, and Else Torstensen (2011). Microsatellite DNA reveals population genetic differentiation among sprat (<i>Sprattus sprattus</i>) sampled throughout the Northeast Atlantic, including Norwegian fjords. <i>ICES J. Mar. Sc.</i> 68: 2145-2151
Where the data can be retrieved	rough data (genotypes) from the authors on request
Access	FST estimates available in the paper
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Species / Functional group	Sprat
Data	genetics
Suggested data use in MareFrame	F _{ST} estimates
Area (add ICES SD)	Baltic
Spatial resolution	samples from Gotland, Gdanska, Bornholm, Arkon basin, Belt Sea, Kattegat, German Bight
Year	2004-2006
Season / resolution	NA
Reference (paper, project, DB?)	Morten T. Limborg, Jes S. Pedersen, Jakob Hemmer-Hansen, Jonna Tomkiewicz, Dorte Bekkevold (2009) Genetic population structure of European sprat (2009) <i>Mar. Ecol. Prog. Ser.</i> 379: 213-224
Where the data can be retrieved	rough data (genotypes) from the authors on request
Access	FST estimates available in the paper
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Species / Functional group	Herring
Data	genetics
Suggested data use in MareFrame	F _{ST} estimates
Area (add ICES SD)	Southern Baltic
Spatial resolution	samples from Rügen and Gdansk Bay
Year	2002-2003
Season / resolution	Q1, Q2



Reference (paper, project, DB?)	H.B.H. Jørgensen, M.M. Hansen, V. Loeschcke (2005). Spring-spawning herring (<i>Clupea harengus</i> L.) in the southwestern Baltic Sea: do they form genetically distinct spawning waves? ICES J. Mar. Sci. (2005) 62: 1065-1075
Where the data can be retrieved	rough data (genotypes) from the authors on request
Access	FST estimates available in the paper
Species / Functional group	Herring
Data	genetics
Suggested data use in MareFrame	F _{ST} estimates
Area (add ICES SD)	Baltic
Spatial resolution	samples from Bothnian Bay and Sea, Gulf of Finland, Aland Archipelago, Gulf of Riga, Hanö Bay, Gdask Bay Rügen
Year	2002-2003
Season / resolution	NA
Reference (paper, project, DB?)	H.B.H. Jørgensen, M.M. Hansen, D. Bekkevold, D.E. Ruzzante & V. Loeschcke (2005) Marine landscapes and population genetic structure of herring (<i>Clupea harengus</i> L.) in the Baltic Sea. Mol. Ecol. (2005) 14: 3219-3234
Where the data can be retrieved	rough data (genotypes) from the authors on request
Access	FST estimates available in the paper
Species / Functional group	Herring
Data	genetics
Suggested data use in MareFrame	F _{ST} estimates
Area (add ICES SD)	Baltic
Spatial resolution	samples from Bothnian Bay, Aland Archipelago, Gulf of Riga, Rügen
Year	2002-2003
Season / resolution	NA
Reference (paper, project, DB?)	H.B.H. Jørgensen, C. Pertoldi, M.M. Hansen, Daniel Ruzzante & V. Loeschcke (2008) Genetic and environmental correlates of morphological variation in a marine fish: the case of Baltic Sea herring (<i>Clupea harengus</i> L.) J. Fish. Aquat. Sci. (2008) 65: 389-400
Where the data can be retrieved	rough data (genotypes) from the authors on request
Access	FST estimates available in the paper
Species / Functional group	Herring
Data	genetics
Suggested data use in MareFrame	F _{ST} estimates or genotypes
Area (add ICES SD)	Southern Baltic
Spatial resolution	Western, Central, Eastern Baltic
Year	2003
Season / resolution	NA
Reference (paper, project, DB?)	
Where the data can be retrieved	rough data (genotypes) NMFRI - Poland
Access	not published



Species / Functional group	zooplankton
Data	taxa, abundance and biomass
Suggested data use in MareFrame	fish prey availability, element of the foodweb
Area (add ICES SD)	SD 25 & 26
Spatial resolution	3 stations
Year	2002-2013
Season / resolution	usually 5 times a year (3/4, 6, 8,9, 11)
Reference (paper, project, DB?)	Polish National Monitoring, HELCOM Combine
Where the data can be retrieved	NMFRI, Piotr
Access	yes
What's new (data, use)	this dataset was not widely used so far

Baltic references

Einar E. Nielsen, Michael M. Hansen, Daniel E. Ruzante, Dorte Meldrup and Peter Gronkjaer (2003) Evidence of a hybrid-zone in Atlantic cod (*Gadus morhua*) in the Baltic and the Danish Belt Sea revealed by individual admixture analysis *Mol. Ecol.* (2003) 12: 1497-1508.

Kevin A. Glover, Øystein Skaala, Morten Limborg, Cecilie Kvamme, and Else Torstensen (2011). Microsatellite DNA reveals population genetic differentiation among sprat (*Sprattus sprattus*) sampled throughout the Northeast Atlantic, including Norwegian fjords. *ICES J. Mar. Sc.* 68: 2145-2151.

Morten T. Limborg, Jes S. Pedersen, Jakob Hemmer-Hansen, Jonna Tomkiewicz, Dorte Bekkevold (2009) Genetic population structure of European sprat (2009) *Mar. Ecol. Prog. Ser.* 379: 213-224.

H.B.H. Jörgensen, M.M. Hansen, V. Loeschcke (2005). Spring-spawning herring (*Clupea harengus* L.) in the southwestern Baltic Sea: do they form genetically distinct spawning waves? *ICES J. Mar. Sci.* (2005) 62: 1065-1075.

H.B.H. Jörgensen, M.M. Hansen, D. Bekkevold, D.E. Ruzante & V. Loeschcke (2005) Marine landscapes a population genetic structure of herring (*Clupea harengus* L.) in the Baltic Sea. *Mol. Ecol.* (2005) 14: 3219-3234.

H.B.H. Jörgensen, C. Pertoldi, M.M. Hansen, Daniel Ruzante & V. Loeschcke (2008) Genetic and environmental correlates of morphological variation in a marine fish: the case of Baltic Sea herring (*Clupea harengus* L.) *J. Fish. Aquat. Sci.* (2008) 65: 389-400.



North Sea. (Partner 20)

Spatial dimension	Northern North Sea 57.5° N–61.5° N and 1° W–4° E,
Time dimension	August-September 2002-2005
Data Type	Trophic Level by nitrogen stable isotope composition
Data description	detailed Regression Results of Trophic level by length
N° samples	145 fish
Aggregation level	Aggregated but raw data can be available (by application to S. Jennings CEFAS)
Reference	Regression results of trophic level on size from S. Jennings et al. / Journal of Sea Research 60 (2008) 74–88
Data Licensing Terms	Published results. Raw data available on request.
Description about implementation models	on Use directly in simple size and EwE type models. Potentially useful for determining other food, Primary productivity requirements
Notes	Provides perspective on trophic level of dominant (by biomass) species in area
Species	<i>Trisopterus marki</i> (Norway pout) <i>Hippoglossoides platessoides</i> (Long rough dab) <i>Limanda limanda</i> (Common dab) <i>Eutrigla gurnardus</i> (Grey gurnard) <i>Merlangius merlangus</i> (whiting) <i>Microstomus kitt</i> (Lemon sole) <i>Pleuronectes platessa</i> (plaice) <i>Amblyraja diata</i> (starry ray) <i>Melanogram musaeglefinus</i> (Haddock) <i>Pollachius virens</i> (saithe) <i>Gadus morhua</i> (cod)

North Sea references

Jennings, S., R. van Hal, J.G. Hiddink and T. A.D. Maxwell. 2008. Fishing effects on energy use by North Sea fishes. Journal of Sea Research 60 74 – 88.



Northern and Western Waters – Iceland Waters

Species	Minke whale
Spatial dimension	Icelandic waters
Time dimension	2003- 2007
Data Type	Stomach contents, fatty acid, stable isotopes, genetics
Data detailed description	Data sample from the special scientific whaling of minke whales in Icelandic waters
N° samples	N/A
Aggregation level	raw data
Reference	Special scientific permit whaling, described in Víkingsson et. Al 2014, Pampoulie 2014
Data Licensing Terms	Available in MRI databases
Description about implementation on models	Different stock structures, likelihood data, spatial hypothesis, species interaction.

Iceland waters References

Víkingsson, G. A., Elvarsson, B.T., Ólafsdóttir, D., Chosson, V. and Galan, A. 2014. Recent changes in the diet composition of common minke whales (*Balaenoptera acutorostrata*) in Icelandic waters. A consequence of climate change? *Marine Biology Research* 10.2: 138-152.

Pampoulie, C. et al. Stock structure of North Atlantic common minke whale (*Balaenoptera acutorostrata*): a multidisciplinary review of the Icelandic Research Program results.

Elvarsson, Bjarki Þór. 2014. Evaluating stock structure hypotheses using genetically determined close relatives: a simulation study on North Atlantic fin whales. *ICES Journal of Marine Science*.doi:10.1093/icesjms/fsu140



Northern Waters – West Coast of Scotland (INIABDN)

Scientific survey abundance observations

Species	cod, haddock, whiting, saithe, hake, herring, mackerel, Norway pout, sprat
Spatial dimension	ICES area Via
Time dimension	1985 to 2013
Data Type	length frequency observations
Data detailed description	Data consist in number at length observed for each species at each sampling station. The number and location of sampling is defined by the ICES standard sampling protocol which applies to scientific surveys.
N° samples	Variable, minimum is 1 sample per ICES statistical rectangle per year for the area covered.
Aggregation level	Raw data
Reference	DATRAS database on ICES website
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	The amount, quality and time series of data can vary among species. In some cases the data may need raising/scaling before being used in models

Notes

Scientific survey abundance observations

Species	cod, haddock, whiting, saithe, hake, herring, mackerel, Norway pout, sprat, anglerfish, megrim
Spatial dimension	ICES area VIa
Time dimension	2005 to 2013
Data Type	length frequency observations
Data detailed description	Data consist in number at length observed for each species at each sampling station. The number and location of sampling is defined by the ICES standard sampling protocol which applies to scientific surveys.
N° samples	Variable, minimum is 1 sample per ICES statistical rectangle per year for the area covered.
Aggregation level	Raw data
Reference	Scottish surveys carried by Marine Scotland
Data Licensing Terms	Available on request, data source needs referencing
Description about implementation on models	The amount, quality and time series of data can vary among species. In some cases the data may need raising/scaling before being used in models



Age length keys

Species	cod, haddock, whiting, saithe, Norway pout
Spatial dimension	ICES area VIa
Time dimension	1985 to 2013
Data Type	length-at-age observations
Data detailed description	Otolith age reading of stratified sub-sample taken at each length class of each species for each station sampled. The number and location of sampling is defined by the ICES standard sampling protocol which applies to scientific surveys.
Nº samples	Variable, not all samples contain individuals from all length classes for all species
Aggregation level	Raw data
Reference	DATRAS database on ICES website
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	The amount, quality and time series of data can vary among species. In some cases the data may need raising/scaling before being used in models

Age length keys

Species	cod, haddock, whiting, saithe, hake, herring, mackerel, Norway pout, sprat, anglerfish, megrim
Spatial dimension	ICES area VIa
Time dimension	2005 to 2013
Data Type	length-at-age observations
Data detailed description	Otolith age reading of stratified sub-sample taken at each length class of each species for each station sampled. The number and location of sampling is defined by the ICES standard sampling protocol which applies to scientific surveys.
Nº samples	Variable, not all samples contain individuals from all length classes for all species
Aggregation level	Raw data
Reference	Scottish surveys carried by Marine Scotland
Data Licensing Terms	Available on request, data source needs referencing
Description about implementation on models	The amount, quality and time series of data can vary among species. In some cases the data may need raising/scaling before being used in models

Notes

Sex maturity age length keys

Species	cod, haddock, whiting, saithe, Norway pout
Spatial dimension	ICES area VIa
Time dimension	1985 to 2013



Data Type	length-at-age and maturity status observations
Data description	Maturity stage are observed from the state of the gonads from Otolith age reading of stratified sub-sample taken at each length class of each species for each station, on top of length-at-age measurements. The number and location of sampling is defined by the ICES standard sampling protocol which applies to scientific surveys.
N° samples	Variable, not all samples contain individuals from all length classes for all species
Aggregation level	Raw data
Reference	DATRAS database on ICES website
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	The amount, quality and time series of data can vary among species. In some cases the data may need raising/scaling before being used in models

Notes

Sex maturity age length keys

Species	cod, haddock, whiting, saithe, hake, herring, mackerel, Norway pout, sprat, anglerfish, megrim
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Spatial dimension	ICES area VIa
Time dimension	2005 to 2013
Data Type	length-at-age and maturity status observations
Data description	Maturity stage are observed from the state of the gonads from Otolith age reading of stratified sub-sample taken at each length class of each species for each station, on top of length-at-age measurements. The number and location of sampling is defined by the ICES standard sampling protocol which applies to scientific surveys.

N° samples	Variable, not all samples contain individuals from all length classes for all species
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Aggregation level	Raw data
Reference	Scottish surveys carried by Marine Scotland
Data Licensing Terms	Available on request, data source needs referencing
Description about implementation on models	The amount, quality and time series of data can vary among species. In some cases the data may need raising/scaling before being used in models

Seal population size

Species	Grey seal, harbour seal
Spatial dimension	Inner and outer Hebrides
Time dimension	1996 to 2009



Data Type	Number of individuals
Data detailed description	Estimation of number of individuals based on visual surveys
N° samples	Variable, not all years have been sampled
Aggregation level	Raw data
SCOS	Advice from Special Committee On Seals (SCOS) of the Sea Mammal Research Unit (SMRU)
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	The number of individuals is estimated by counting individuals on land, not the ones at sea. This number is therefore an minimum estimate of population size

Notes

Stomach content

Species	cod, haddock, whiting, saithe, hake, Norway pout, megrim, herring, mackerel, anglerfish, grey gurnard, spurdog, lesser spotted dogfish
Spatial dimension	ICES area VIa
Time dimension	Varies among species
Data Type	Stomach content in % of prey
Data detailed description	Observed stomach content of predator fishes, raised to %
N° samples	2319 across all species
Aggregation level	Raw data
Reference	DAPSTOM database available on CEFAS website
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	Although covering a wide range of species, the number and quality of observations is highly heterogeneous among species and in some cases might require some adjustment/assumptions

Notes The DAPSTOM database consist of data from several different surveys as well as historical records which may not have all been obtained via the same sampling protocol. The database is patchy for some species and varies greatly in quantity

Temperature

Species	All species in the considered area
Spatial dimension	ICES area VIa
Time dimension	1991 - 2011
Data Type	Monthly mean sea surface temperature



Data description	Gridded monthly mean sea surface temperature data on a 1° latitude by 1° longitude grid extrapolated from a model calibrated on satellite observations
N° samples	16329600
Aggregation level	Gridded data
Reference	Met Office Hadley Centre Data
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	Information about the data format can be found online when downloading the data
Notes	

Primary production

Species	All species in the considered area
Spatial dimension	ICES area VIa
Time dimension	2002 - 2014
Data Type	Estimated chlorophyll concentrations
Data description	Chlorophyll concentrations estimated from a Vertically Generalized Production Model
N° samples	Varies with preferred spatial and temporal coverage
Aggregation level	Gridded data
Reference	Ocean Productivity Group, Oregon University
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	Information about the data format can be found online when downloading the data
Notes	

Genetic information

Species	European hake
Spatial dimension	ICES area VIa
Time dimension	2008-2009
Data Type	Genetic
Data description	Genetic SNP markers
N° samples	Unknown
Aggregation level	ICES area VIa
Reference	FishPopTrace
Data Licensing Terms	Publicly available, data source needs referencing
Description about implementation on models	This data will most probably not be used directly in the implementation and parameterisation of ecosystem model, but will provide novel insight on stock definition and/or migration
Notes	Data only available for European hake in ICES area VIa



South-Western Waters – Iberian Peninsula (CSIC and IEO)

1

Species	European hake
Spatial dimension	Atlantic Ocean and Mediterranean Sea
Time dimension	May 2010-November 2010
Data Type	otoliths microchemistry, age 1
Data description	detailed Otolith geochemistry of European hake showed a strong ontogenetic signal that must be considered when using them as natural tags in connectivity or migration studies. Both otolith core and edge geochemical signatures provided strong evidence of movement of European hake between the local populations in the Atlantic Ocean and the Mediterranean Sea. Nonetheless, the results were still insufficient to provide unequivocal information on population structure and connectivity of European hake.
Nº samples	7 pops, 10 individuals each
Aggregation level	aggregated data
Reference	Tanner S.E., Vasconcelos R. P., Cabral H. N., Thorrold S. R. 2012. Testing an otolith geochemistry approach to determine population structure and movements of European hake in the northeast Atlantic Ocean and Mediterranean Sea. Fisheries Research 125– 126: 198– 205
Data Licensing Terms	Publicly available, but data source needs referencing, etc
Description about implementation on models	different stock structure, evidence of movement
Notes	In the Atlantic Ocean, samples from the northern stock (Celtic Sea and Armorican Shelf) were grouped together while individuals collected from locations within the southern stock (Galician Shelf , Portugal and Gulf of Cádiz) were segregated into two groups. Little exchange was observed between Balearic Islands and Sardinia, while the Gulf of Cádiz did not seem to be connected to the Mediterranean populations by larval dispersal.

2

Species	European hake, cod, herring, common sole
Spatial dimension	Distribution area of each species



Time dimension	2009??
Data Type	SNPs
Data description	detailed SNPs Forensically informative. The most powerful markers will be used to form SNP panels for each species that are capable of unambiguously assigning an individual to its geographic origin
N° samples	https://fishpoptrace.jrc.ec.europa.eu/web/fishpoptrace/sampling/gis
Aggregation level	raw data, aggregated data
Reference	Martinsohn and Ogden 2009 FishPopTrace—Developing SNP-based population genetic assignment methods to investigate illegal fishing. Forensic Science International: Genetics Supplement Series 2: 294–296. FISHPOPTTRACE
Data Licensing Terms	Gary Carvalho MOU
Description about implementation on models	Atl-Med split.
Notes	Technical note

3

Species	<i>Merluccius merluccius</i> , <i>Gadus morhua</i> , <i>Melanogram musaeglefinus</i> , <i>Merlangius merlangus</i> , <i>Micromesistius poutassou</i> and <i>Clupea harengus</i>
Spatial dimension	NE Atlantic
Time dimension	Depends on the species
Data Type	Genetic data from published papers
Data description	detailed The mismatch between genetic population structure and the current management units found for six species (<i>Gadus morhua</i> , <i>Melanogrammus aeglefinus</i> , <i>Merlangius merlangus</i> , <i>Micromesistius poutassou</i> , <i>Merluccius merluccius</i> and <i>Clupea harengus</i>), emphasizes the need for a revision of these units and questions the appropriateness of current management measures. The implementation of complex and dynamic population structures into novel and less static management procedures should be a primary task for future fisheries management approaches.
N° samples	
Aggregation level	aggregated data



Reference Reiss, Hoarau, Dickey-Collas & Wolff. 2008. Genetic population structure of marine fish: mismatch between biological and fisheries management units. Fish and fisheries, DOI: 10.1111/j.1467-2979.2008.00324.x

Data Licensing Terms published papers

Description about implementation on models

4

Species European hake

Spatial dimension

Time dimension May2008-July 2008

Data Type Proteomics

Data detailed description The liver and brain extracts of 18 hake (N = 36) captured in the Mediterranean Sea, Cantabrian Sea, and Atlantic Ocean were examined by 2D/DIGE and mass spectrometry.

Nº samples Liver and brain 18 hakes (36 samples)

Aggregation level

Reference Gonzalez, Krey, Espiñeira, Diez, Puyet and Bautista. 2010. Population Proteomics of the European Hake (*Merluccius merluccius*). Journal of Proteome Research 2010, 9, 6392–6404. [FISHPOPTRACE](#)

Data Licensing Terms Published paper

Description about implementation on models

Notes Through a comparative analysis of qualitative data (present or absence of protein spots in gels), the Atlantic Ocean and Cantabrian Sea populations were found to have more proteins in common compared to the Mediterranean Sea population.

5

Species European hake



Spatial dimension	in the ICES areas VI (north Ireland), VIIj (south Ireland or Celtic Sea), VIIIa,b,d (north Bay of Biscay), and IX (Portuguese coast), and in 3 Mediterranean areas: MED (southeast Spanish coast), ION (Ionic Sea), and AEG (Aegean Sea).
Time dimension	2001
Data Type	Genetics
Data description	detailed 5 Microsatellites
Nº samples	9 pops
Aggregation level	
Reference	Ana G.F. Castillo, Jose L. Martinez, and Eva Garcia-Vazquez. 2004 Fine Spatial Structure of Atlantic Hake (<i>Merluccius merluccius</i>) Stocks Revealed by Variation at Microsatellite Loci. Mar. Biotechnol. 6, 299–306,
Data Licensing Terms	
Description about implementation on models	The first relevant result of our study is the existence of a fine spatial substructure of hake stocks, both in Atlantic and Mediterranean waters.
Notes	For assessing the temporal stability of the genetic structure of hakes, we chose 2 samples genetically different but geographically close: VIIIc-2 and VIIIc-3. The hierarchical AMOVA showed that the main component of the genetic variance was spatial, not temporal (Table 5). The v^2 values for testing the genetic differentiation between the adults and the juveniles within region (VIIIc-2 or VIIIc-3) were not statistically significant. The fine spatial substructure of hake stocks can be interpreted as connectivity

6

Species	European hake
Spatial dimension	Whole distribution area
Time dimension	1998-1999
Data Type	Genetics
Data description	detailed Allozymes
Nº samples	15 samples (11 Mediterranean), 1306 European hakes



Aggregation level

Reference R. Cimmaruta, P. Bondanelli and G. Nascetti 2005 Genetic structure and environmental heterogeneity in the European hake (*Merluccius merluccius*). *Molecular Ecology* 14, 2577–2591

Data Licensing Terms

Description about implementation on models Table 4 Wright's genetic diversity parameters FST calculated over all the polymorphic loci.

Notes The levels of genetic variability were found to be slightly lower in the depleted Atlantic stock than in the Mediterranean one. Clinal variation related to salinity. Most important results in Mediterranean Sea.

7

Species European hake

Spatial dimension Four hundred and eighty-three individuals were sampled from Trondheims fjord in Norway, the Celtic Sea, the southern Bay of Biscay, Faro off Portugal, the Mediterranean Sea north of the coast of Tunisia and the Adriatic Sea.

Time dimension DATA PRESENTED REPRESENT ONLY 1 YEAR'S SAMPLING

Data Type genetic data

Data detailed description 6 microsatellites and mitochondrial DNA

N° samples 6 pops

Aggregation level

Reference Lundy et al. 1999 Macrogeographical population differentiation in oceanic environments: a case study of European hake (*Merluccius merluccius*), a commercially important fish. *Molecular Ecology* 8, 1889–1898

Data Licensing Terms Published paper

Description about implementation on models The Atlantic population structure appears to be more complex than previously suggested by the placement of stock boundaries by the International Council for the Exploration of the Seas (ICES).



Notes Analyses based on various models of microsatellite evolution all suggest that differentiation exists between Bay of Biscay and Portuguese samples, $q = 0.013$ ($P < 0.001$), $R_{ST} = 0.036$ ($P < 0.001$) which are currently managed as one stock. By contrast, fixation indices indicated no differentiation between southern Bay of Biscay samples and Celtic Sea samples, $q = 0.003$ ($P = 0.02$), $F_{ST} = 0.007$ ($P = 0.10$) which are managed as separate stocks. These results suggest that if the observed trends are stable through time, current management policy of European hake may need revision.

8

Species	European hake
Spatial dimension	during scientific surveys
Time dimension	from 2008 to 2009
Data Type	Genetics
Data description	detailed SNPs. Outlier loci separated North Sea and Northern Portugal populations from all other Atlantic samples and revealed a strong differentiation among Western, Central and Eastern Mediterranean geographical samples. Significant correlation of allele frequencies at outlier loci with seawater surface temperature and salinity supported the hypothesis that populations might be adapted to local conditions. Such evidence highlights the importance of integrating information from neutral and adaptive evolutionary patterns towards a better assessment of genetic diversity
N° samples	Nineteen geographical population samples (5 from Atlantic and 14 from Mediterranean)
Aggregation level	
Reference	Milano et al, 2014. Outlier SNP markers reveal fine-scale genetic structuring across European hake populations (<i>Merluccius merluccius</i>) Molecular Ecology (2014) 23, 118–135 and Milano et al 2011 (SNPs library). FISHPOPTRACE
Data Licensing Terms	
Description about implementation on models	correlation of allele frequency at outlier loci with seawater surface temperature and salinity. Local adaptations?
Notes	299 putatively neutral SNPs confirmed the genetic break between basins (FCT = 0.016) and weak differentiation within basins, outlier loci revealed a dramatic divergence between Atlantic and Mediterranean populations (FCT range 0.275–0.705) and fine-scale significant population structure. Outlier loci separated North Sea and Northern Portugal populations from



all other Atlantic samples and revealed a strong differentiation among Western, Central and Eastern Mediterranean geographical samples.

9

Species	European hake
Spatial dimension	The whole distribution area
Time dimension	2000
Data Type	Genetics
Data detailed description	microsatellites and Cytochrome b
Nº samples	27 samples, 5610 individuals,
Aggregation level	
Reference	Pita, Presa, Pérez 2010. Gene flow, multilocus assignment and genetic structuring of the European hake (<i>Merluccius merluccius</i>). <i>Thalassas</i> , 26 (2): 129-133.
Data Licensing Terms	Published
Description about implementation on models	connectivity between N and S stocks.
Notes	Preliminary study. See Pita et al, 2014

10

Species	European hake
Spatial dimension	
Time dimension	Autumn 2000, 2001 and 2002
Data Type	Genetics
Data detailed description	microsatellites



N° samples	52 samples (1123 mature individuals)
Aggregation level	
Reference	Pita, Perez, Cerviño, Presa 2011. What can gene flow and recruitment dynamics tell us about connectivity between European hake stocks in the Eastern North Atlantic? Continental Shelf Research 31(2011) 376–387
Data Licensing Terms	
Description about implementation on models	F _{ST} data per year (table 4), and putative number of migrants. Gene flow, number of migrants per year
Notes	Population dynamics of the NE-Atlantic European hake fishery seems to fit a pattern of connectivity where biomass production and environmental facilitation would determine the intensity of southerly gene flow from central grounds to southern grounds of the Bay of Biscay. This scenario is congruent with an inter-annual gene-flow from central grounds of the northern stock (Porcupine and Great Sole) to Iberian grounds inhabited by the southern stock.

11

Species	European hake
Spatial dimension	Europe (distribution area)
Time dimension	2000-2001
Data Type	Genetic
Data detailed description	Microsatellites (5), cytochrome b (ADNmit)
N° samples	27+outgroup (13 from Pita et al, 2011+15 news including Mediterranean)
Aggregation level	
Reference	Pita, Pérez, Balado, Presa 2014. Out of the Celtic cradle: The genetic signature of European hake connectivity in South-western Europe. Journal of Sea research 93, 90-100
Data Licensing Terms	Published paper
Description about implementation on models	Connectivity between N and S stocks. Table 3. Estimates of gene flow. Table 5 migration rates



Notes

Bayesian inference made on multi-locus genotypic data provides evidence that a large genetic connectivity exists among Atlantic grounds and is mediated by significant migration rates stepping up from the Celtic Sea towards its adjacent Atlantic grounds. Therefore, the spawning biomass of the northern hake population could play a crucial role at ensuring the sustainability of southern hake fish grounds.

12

Species	European hake
Spatial dimension	Europe (in the northeast Atlantic Ocean and the western Mediterranean Sea) Collection locations of <i>Merluccius merluccius</i> in the northeast Atlantic Ocean and the western Mediterranean Sea: Celtic Sea, Armorican Shelf, Galician Shelf, Portugal, Gulf of Cádiz, Balearic Islands, Sardinia.
Time dimension	May-November 2010
Data Type	genetics and microchemistry
Data description	detailed Five microsatellites were sequenced and otolith core geochemical composition was determined from age-1 hake collected in the northeast Atlantic Ocean and the Mediterranean Sea.
Nº samples	7 pops
Aggregation level	
Reference	Susanne E. Tanner, Montse Pérez, Pablo Presa, Simon R. Thorrold, Henrique N. Cabral. 2014. Integrating microsatellite DNA markers and otolith geochemistry to assess population structure of European hake (<i>Merluccius merluccius</i>). Estuarine, Coastal and Shelf Science 142 (2014) 68-75
Data Licensing Terms	
Description about implementation on models	Table 2. F_{ST} between pops
Notes	Different spatio-temporal scales. Otolith geochemistry provides information over an ecological time frame and on a fine spatial scale, while microsatellite DNA markers report on gene flow over evolutionary time scales and therefore act on a broader spatio-temporal resolution.

13



Species	European hake
Spatial dimension	Europe
Time dimension	(1990) Annual
Data Type	genetics
Data description	detailed Allozymes
Nº samples	910 tissue samples from 6 North Atlantic Ocean and 4 Mediterranean Sea locations.
Aggregation level	
Reference	Roldán, García-Marín, Utter and Pla. 1998. Population genetic structure of European hake, <i>Merluccius merluccius</i> . Heredity 81: 327-334
Data Licensing Terms	
Description about implementation on models	Population spatial distribution
Notes	Complexity in Atlantic ocean.

14

Species	European hake
Spatial dimension	Iberian peninsula
Time dimension	1980-2014
Data Type	sex ratio at length
Data description	detailed sex sampling of landings and survey
Nº samples	58145
Aggregation level	raw data
Reference	Cerviño, S. 2014. Estimating growth from sex ratio-at-length data in species with sexual size dimorphism. Fisheries Research. 160: 112-119.
Data Licensing Terms	available



Description about implementation on models

info needed to develop a sex separated model for hake

15

Species European anchovy (*Engraulis encrasicolus*)

Spatial dimension IXa south

Time dimension 1988 - 2014

Data Type Landings, CPUE, acoustics, Easterlies strength, River discharges, Sea Surface Temperature, microchemistry of otolith

Data detailed description Stock size and environmental forcing of the life cycle dynamics. Microchemistry of adults and juveniles of anchovy is available for one year to evaluate the proportion of the population that occupies the estuary

Nº samples 104 records of landings, 26 of CPUE, 3 of acoustics, 312 for each of the environmental covariates and one sampling of otolith microchemistry

Aggregation level raw data, with some estimations of the size of the individuals in the population

Reference ICES reports, Ruiz et al (2006), Ruiz et al (2009), Rincón et al (submitted)

Data Licensing Terms Publicly available

Description about implementation on models

Environmental data and microchemistry used to embed the life cycle of anchovy into the variability of the physical habitat

Notes

REFERENCES

Ruiz, J., E. Garcia-Isarch, I. Emma Huertas, L. Prieto, A. Juárez, J. L. Muñoz, A. Sánchez-Lamadrid, S. Rodríguez-Gálvez, J. M. Naranjo and F. Baldó. (2006) Meteorological and oceanographic factors influencing *Engraulis encrasicolus* early life stages and catches in the Gulf of Cádiz. *Deep-Sea Research II* 53: 1363–1376.

Ruiz, J., R. González-Quirós, L. Prieto and G. Navarro. (2009) A Bayesian model for anchovy: the combined pressure of man and environment. *Fisheries Oceanography*. 18(1): 62–76.

Margarita María Rincón, Ignacio Alberto Catalán, Samu Mantyniemi, Diego Macías, and **Javier Ruiz** Embedding anchovy survival in the environment with a dual time resolution : A Bayesian state-space size-structured population dynamics model. Submitted Canadian Journal of Fisheries and Aquatic Sciences.



16

Species	Sardine (<i>Sardinapilchardus</i>)
Spatial dimension	IXa south
Time dimension	1988 – 2014
Data Type	Landings, CPUE, acoustics,
Data detailed description	Stock size
Nº samples	104 records of landings, 26 of CPUE, 3 of acoustics
Aggregation level	raw data, with some estimations of the size of the individuals in the population
Reference	ICES reports
Data Licensing Terms	Publicly available
Description about implementation on models	Stakeholders requested to include in our model to sardine as an alternative resource to anchovy

17

Species	Small cetaceans
Spatial dimension	IXa south (35.00Km of sighting)
Time dimension	2002-2010
Data Type	More than 1000 observations. Stomachs available: <i>Tursiops truncatus</i> (11), <i>Delphinus delphis</i> (50), <i>Stenella coeruleoalba</i> (6) and <i>Phocoena phocoena</i> (5). Stable isotopes available : <i>Delphinus delphis</i> (43), <i>Tursiops truncatus</i> (59), <i>Phocoena phocoena</i> (5)
Data detailed description	Observations in the area during spatial transects for several years as well as stomachs and isotopes to help understanding the position of small cetaceans in the trophic network
Nº samples	Enumerated above
Aggregation level	Raw data
Reference	CIRCE



Data Licensing Terms To be public soon in a Ph D dissertation

Description about implementation on models Small cetaceans are top predators in the area and their interaction with fish and fisheries in the area is to be resolved through modelling

Iberian Peninsula References

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Mediterranean Waters – Strait of Sicily

Species	33 shelf species + 9 slope species (see the list attached below)
Spatial dimension	Gulf of Castellammare, Termini Imerese and Santa Agata (NW Sicily). Slope and continental shelf.
Time dimension	Spring 2005
Data Type	Carbon and Nitrogen stable isotopes
Data detailed description	Carbon and Nitrogen stable isotopes were measured on the most important species of the trawlable assemblages in the continental shelf of three Gulfs of the Northern Sicily. Species were selected of similar size (i.e. 60/80% of the maximum total length)
N° samples	87 records
Aggregation level	aggregated data
Reference	Fanelli et al., 2009, 2010, 2011, Sinopoli et al., 2012

Data Licensing Terms

Description about implementation on models	Functional groups identification
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Slope

Centrophorus granulosus
Dalatia slichia
Etmopterus spinax
Galeus melastomus
Heptranchias perlo
Hexanchus griseus
Raja radula
Scyliorhinus canicula
Torpedo marmorata

Continental shelf

Alloteuthis media
Arnoglossus laterna
Callionymus maculatus
Capros aper
Cepola rubescens
Dicentrarchus labrax
Diplodus annularis
Eledone cirrhosa
Engraulis encrasicolus
Epinephelus aeneus
Gadiculus argenteus
Gobiidae
Illex coindetii
Lepidotrigla cavillone
Loligo vulgaris
Lophius budegassa
Merluccius merluccius
Mullus barbatus
Octopus vulgaris
Pagellusa carne
Pagellus erythrinus
Parapenaeus longirostris



Sardina pilchardus
Serioladu merili
Serranus cabrilla
Sparus aurata
Serranus hepatus
Spicara flexuosa
Spicara spp
Torpedo torpedo
Trachurus trachurus
Trisopterus sminutus
Uranoscopus scaber

Strait of Sicily references

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Black Sea

Species	Information (genetics, microchemistry, isotopes, other)	Data type	Area	Year	Reference	Access
Turbot	dynamic of catches, long-time data series		WBS	1950-2013		a
Turbot	fishing effort		WBS	2003-2013		a
Turbot	population structure by size classes		WBS	2003-2013		a
Turbot	sex ratio		WBS	2003-2013		a
Turbot	the degree of maturation of the gonads		WBS	2003-2013		a
Turbot	stomach contents		WBS	2013		a
Turbot	fecundity		WBS	2013		a
Turbot	growth parameters		WBS	2008-2013		a
Turbot	mortality rate		WBS	2008-2013		a
Turbot	distribution of the fishing agglomeration		WBS	2008-2013		a
Turbot	indices of abundance and biomass		WBS	2008-2013		a
Turbot	temperature, salinity		WBS	2003-2013		a
Turbot	genetic analyses of molecular markers: <i>ADNr</i> and <i>COI</i>	scientific report	WBS	2010-2011	Romanian national project PNII_Partnerships_52-133/2008	unpublished data

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Chatham Rise (New Zealand)

Species	A wide range of commercial and bycatch species
Spatial dimension	Chatham Rise region to east of New Zealand
Time dimension	summer 2004-2014 (from summer trawl surveys)
Data Type	Fish diet (stomach contents) data to inform food web Stable isotope data (most abundant 25 species from trawl surveys)
Data detailed description	Fish diet (stomach contents) information. Details of diet composition in relation to species. Location and predator size. This is being used to investigate niche structure. This data is being used to generate a balanced food web for the Chatham Rise region. Stable isotope data to estimate trophic level. For the most abundant 25 species caught in the trawl survey, TL from stable isotope analysis will be used to check against the TL estimated from the balanced food web.
N° samples	
Aggregation level	aggregated data
Data Licensing Terms	NIWA held data, NIWA and MPI owned data
Description about implementation on models	Diet information to inform development of food web Stomach contents for hoki hake ling orange roughy oreo (black and smooth) Alfonsino Chimaeroid fishes (multiple species) Warehou (silver, white) Red cod, sea perch Southern Ray's Bream Orange perch Macrouridae (multiple species) Squaliforme sharks (multiple species)

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Annex I. WP2 - Kick-off meeting Workshop Report.

Santiago Cerviño (WP leader), Montse Pérez (reporteur) and Sara Helyar (reporteur)

Summary

WP2 was introduced the first day of the meeting when tasks and goals were discussed. Representatives from the External Advisory Group provided WP2 evaluation heightening critical questions. Following the presentations, a WP workshop in parallel with WP3, WP4, WP5 and WP6 was performed. Three activities regarding compilation of novel information (task 2.1) were also performed: (1) report on data compilation progress and (2) identification of data sources and (3) Del 2.1 template. These minutes also have taken in consideration information coming from CSs and WPs leaders and Partners during the meeting and the workshop as well as through e-mail discussions after that.

Work Package Leaders introduction and discussions

The priority of WP2 in terms of data compilation is the “new technological data”

What data type may be considered ‘new technological data’ as mentioned in Objective 1? Genetics, proteomics, otolith microchemistry, isotope analysis, fatty acid analysis, tagging, oceanography, etc. Tagging and oceanography only if they refer to new technologies. Other data like stomach contents or VMS might be useful for new implementation in models even if their value to address the Objective 1 in the call is limited.

Not all CSs would have to deal with all kind of new technological data in all models. However all CSs should try to explore the implementations of these new data at least in one model. At this time not all CSs are in the same position to start to work. Some have already available data and others not. All CSs should continue exploring sources of new data in literature, data from EU projects like FishPopTrace (<https://fishpoptrace.jrc.ec.europa.eu/>).

The team of scientists in WP2 includes experts on genetics, ecology or modelling, however there are no experts on ATLANTIS or EwE. Model experts are important in the implementation of new information in these models. Their presence in the month 18th workshop (data implementation into models) is needed.

At this time we have identified two main ways to implement data into ecosystem models: through spatial process (genetic, microchemistry) and trophic process (isotopes, fatty acids). Not all models are able to deal with these processes, e.g. EwE is not a spatial model, however, the novel information may be used to inform the location of biologically meaningful spatial boundaries for the model.

Evaluation and critical questions from the External Advisory Group (EAG)

WP2 task 2.1 ‘Compilation of novel information’ has to be finished by 15th June. EAG advises to not procrastinate and start work now. Ensure and check accuracy, validity and comparability of data (historical and new). Other EAG recommendations are related to expected problems with data implementation in models (such as model modifications, interactions among data and process, model limitations, etc).



Activities

During the kick-off meeting there were three activities regarding Task 2.1 (Compilation of novel information): (1) reporting and analysis of data compilation status at CS level and (2) identification of potentially useful data sources and (3) Deliverable 2.1 template. Task 2.1 started the 1st month and finish with Del 2.1 (month 6) that have to be submitted to WP2 leader by 15th June.

(1) Table 1 summarized the current work status of different Case Studies regarding new data.

Case Study	Partners	genetic	micro	isotop	other	species	model
Iberian Waters	IEO, CSIC	*	*	*	*	hake, anchovy, cetaceans	GADGET
Icelandic Waters	MATIS, IU, MRI	*	*	*	*	multispecies	GADGET, EwE, Atlantis
Baltic Sea	SLU, NMFRI, UH	*				Cod, herring, sprat	GADGET, EwE, MultiProduction
Black Sea	INCMD					turbot	GADGET, EwE
Mediterranean	CNR	*		*		multispecies	GADGET, ATLANTIS
Chatham rise	NIWA			*	*	multispecies	ATLANTIS
West Scotland	UNIABDN					seals, gadoids, nephrops	EwE, FishSums
North Sea	NRC					multispecies	GADGET, EwE, Prod., size spectra

There are 4 CS with data already available (Iberian Waters, Icelandic Waters, Mediterranean and Chatham Rise) that eventually might allow their implementation into models. The Baltic Sea CS has already partial data (herring genetics in Polish area). Other 3 CS have not reported already 'new' data. Black Sea CS is not now at position to develop a spatial or multispecies model making more difficult the option to implement 'new data'. North Sea CS only has one partner contributing (NRC) and this partner does not have time allocated to work in WP2. West Scotland CS has not started to work in WP2. In all CS (except Black Sea) it is expected that the exploration of data sources might provide more information useful to CSs.

(2) Identification of potentially useful data sources.

EU projects list was explored previous to the meeting and 3 projects were identified as potentially useful: FishPopTrace, CodTrace and OTOMIC. Among these only FishPopTrace (<https://fishpoptrace.jrc.ec.europa.eu/>) has an up to data web page with a well structured data base with useful information to MareFrame. FishPopTrace has collected different novel data types (genetics, otoliths microchemistry, fatty acids, proteomics, gene expression); from different areas (North Atlantic, Mediterranean and Baltic); and 4 ecologically important species (Atlantic cod, Atlantic herring, European hake, and sole) which are relevant for MAREFRAME work. Gary R. Carvalho is the project coordinator and should be contacted officially to study the option of collaborates. A.K. Daniëlsdóttir proposes to discuss it first with PMG.

(3) Deliverable 2.1 template.

This template is needed to report Del 2.1. It is also needed to report to WP3 about DB structure (Del 3.1; month 6), both deliverables are due in month 6. It was therefore decided to produce a common template for both deliverables. The format of this template was discussed with WP 3 leader and is presented in annex I.

Conclusions



Del 2.1 On relevant novel information and data available for integration into new models: Workshop report [month 6]. 30 June. The goals of Task 2.1 for this meeting were addressed through the activities described before.

Data should be delivered to WP2 coordinator by 15th June with the formats described in annex I. Furthermore every Case Study has to present a table with the fields for the Data Base developed in WP3 (e.g. time, area, data type, amounts).

WP 2 Workshop. It is scheduled a Workshop in month 18 to discuss this implementation with WP4 and WP5. Participation of all CSs and model experts are required. Venue to be decided.

A formal contact with FishPopTrace coordinator (Gary Carvalho) is required. Anna Kristín Daníelsdóttir will discuss it with PMG before contacting him.



Annex II. Minutes of skype meeting regarding MareFrame collaboration with the FishPopTrace consortium.

Date: 26/6/14

Gary R Carvalho (GRC), Santiago Cerviño (SC), Sarah Helyar (SJH), Gunnar Stefánsson (GS).

This meeting was to introduce the projects and participants to each other; to this end, GRC introduced FPT and the projects aims and outcomes, and SC introduced Mareframe (with particular emphasis on WP2) and the projects aims. This led to a positive and fruitful discussion on how best the collaboration should proceed, and touched on topics such as useful sources and scales of data, species, areas and model integration.

It was decided that:

- The FPT database will be a useful source of data to the project.
- Both parties were positive about the collaboration, and a MoU will be produced by SH for consideration by all parties.
- At this stage the data is most useful at an aggregated, rather than an individual level.
- If this changes, then FPT is open to further discussion regarding how to best provide access to the wider database.
- Sources of data with FPT that are most relevant to MF at this point are:
 - The Geobrowser: https://fishpoptrace.jrc.ec.europa.eu/map/genetics_geobrowser/
 - The Web crawler: <https://fishpoptrace.jrc.ec.europa.eu/crawler> (this is not currently functional, but GRC are looking into it).
 - Published papers from the project (full current list attached).



FPT publications:

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