



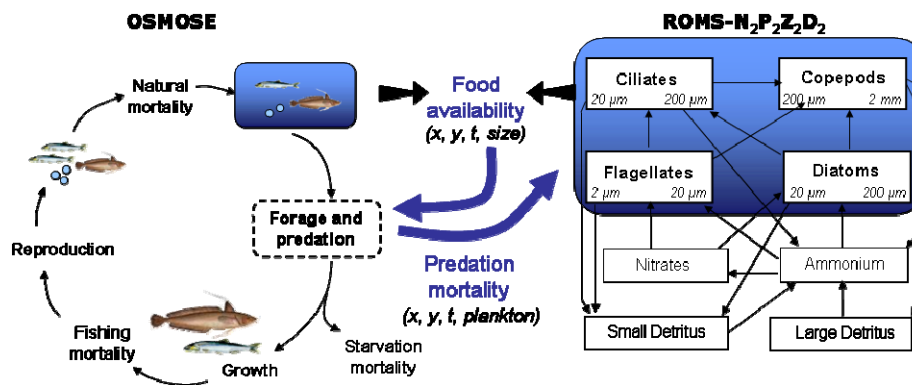
## 1. General Information

### Developer contacts:

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**Model name:** OSMOSE (coupled to ROMS-NPZD-, BFM-, ERSEM- )

**MEECE Area of implementation:** Southern Benguela-South Africa (implemented), Northern Humboldt-Peru (implemented), Strait of Georgia-Canada (ongoing), Adriatic Sea (Meece project), Aegean Sea (Meece project), North Sea (Meece project), Gulf of Lions-France (in project)



### Model description, key publications:

OSMOSE is a multispecies and Individual-based model (IBM) which focuses on fish species. This model assumes opportunistic predation based on spatial co-occurrence and size adequacy between a predator and its prey (size-based opportunistic predation). It represents fish individuals grouped into schools, which are characterized by their size, weight, age, taxonomy and geographical location (2D model), and which undergo major processes of fish life cycle (growth, explicit predation, natural and starvation mortalities, reproduction and migration) and a fishing mortality distinct for each species (Shin and Cury 2001, 2004). Osmose, uncoupled version, has been first applied to the Benguela upwelling ecosystem for which 12 fish species have been specified, from small pelagic fish to large demersal species (Shin et al. 2004, Travers et al. 2006). The model needs basic parameters that are often available for a wide range of species, and which can be found in FishBase for instance ([www.fishbase.org](http://www.fishbase.org)). In output, a variety of size-based and species-based ecological indicators can be simulated and confronted to in situ data (surveys and catch data) at different levels of aggregation: at the species level (mean size, mean size-at-age, max size, trophic level etc), and at the community level (slope and intercept of size spectrum, Shannon diversity index etc). The model can be calibrated to observed biomass, using genetic algorithms.

The coupling process used to link OSMOSE to LTL models (NPZD, BFM) models is the predation process (Travers et al. . The LTL model is used as a prey field for the HTL model (concentration of nitrogen/carbon concentrations, converted into wet biomass) and the HTL model provides a predation mortality field for the LTL model. In a second step, other processes linked to detritus or nutrients boxes will be explicated for the coupling (egestion, excretion, natural mortality).

Different scenarios have been run, including the simulations of Marine Protected Areas (Yemane et al. 2009, Shin et al. 2001b), fishing moratoriums (Marzloff et al. 2009), overexploitation scenarios (Shin et al. 2004, Travers et al. accepted), combined effects of climate change and overexploitation.

### Relevant publications:

Travers M., Shin Y.-J., submitted 21 January 2009. An end-to-end model coupling OSMOSE and ROMS-N2P2Z2D2 for representing marine food webs in a changing environment. *Ecological Modelling*.  
[http://www.elsevier.com/wps/find/journaldescription.cws\\_home/503306/description#description](http://www.elsevier.com/wps/find/journaldescription.cws_home/503306/description#description)

- Travers M., Watermeyer K., Shannon L.J., Shin Y.-J., accepted. *Changes in food web structure under scenarios of overfishing in the southern Benguela: comparison of the Ecosim and OSMOSE modelling approaches*. *Journal of Marine Systems* <http://dx.doi.org/10.1016/j.jmarsys.2009.07.005>.
- Travers M., Shin Y.-J., Jennings S., Machu E., Huggett J.A., Field J., Cury P., accepted. *Two-way coupling versus one-way forcing of plankton and fish models to predict ecosystem changes in the Benguela*. *Ecological Modelling*.
- Marzloff M., Shin Y.-J., Tam J., Travers M., Bertrand A., 2009. *Trophic structure of the Peruvian marine ecosystem in 2000–2006: Insights on the effects of management scenarios for the hake fishery using the IBM trophic model Osmose*. *Journal of Marine Systems*, 75(1-2): 290-304.
- Yemane D., Shin Y.-J., Field J., 2009. *Exploring the effect of marine protected areas on the dynamics of fish communities in the southern Benguela: an Individual Based Modelling approach*. *ICES Journal of marine Science*, 66: 378-387.
- Travers M., Shin Y.-J., accepted. *Spatio-temporal variability in fish-induced predation mortality on plankton. A simulation approach using a coupled trophic model of the Benguela ecosystem*. *Progress in Oceanography*.
- Travers M., Shin Y.-J., Shannon L.J., Cury, P. 2006. *Simulating and testing the sensitivity of ecosystem-based indicators to fishing in the southern Benguela ecosystem*. *Canadian journal of Fisheries and Aquatic Sciences*. 63: 943-956.
- Shin Y.-J., P. Cury, 2004. *Using an individual-based model of fish assemblages to study the response of size spectra to changes in fishing*. *Canadian Journal of Fisheries and Aquatic Sciences*, 61: 414-431.
- Shin, Y.-J., Shannon L.J., Cury, P.M. 2004. *Simulations of fishing effects on the southern Benguela fish community using an individual-based model: learning from a comparison with ECOSIM*. In *Ecosystem Approaches to Fisheries in the Southern Benguela*. Shannon, L.J., Cochrane, K.L. and S.C. Pillar (Eds). *African Journal of marine Science* 26: 95-114.
- Shin Y.-J., P. Cury, 2001a - *Exploring fish community dynamics through size-dependent trophic interactions using a spatialized individual-based model*. *Aquatic Living Resources*, 14(2): 65-80. <http://dx.doi.org/10.1051/alr:2005001>
- Shin Y.-J., P. Cury, 2001b - *Simulation of the effects of Marine Protected Areas on yield and diversity using a multispecies, spatially explicit, individual-based model*. In: Kruse, G. H.; Bez, N.; Booth, A.; Dorn, M. W.; Hills, S.; Lipcius, R. N.; Pelletier, D.; Roy, C.; Smith, S. J., and Witherell, D., (eds.). *Spatial processes and management of marine populations*. University of Alaska Sea Grant ed. Fairbanks; 2001; pp. 627-642.

### Weblink for Further Information:

Code available at <https://svn.mpl.ird.fr/osmose/code>

## 2. Technical & Driver Information

**Programming language:** JAVA. 2D on workstations, cluster required for calibration of the model (genetic algorithms in PYTHON).

### Solution algorithms:

#### Specific Setups

Spatial resolution:

16-24.4°E, 28.8-37.7°S  
0.15°, 9 nm

Temporal resolution:

time step 2 weeks

Vertical resolution

### Details of current / planned simulations:

25 year hindcast , 1978-present, future snapshots

### Purpose for development (i.e. original rationale for model development)

Originally focused on fish, detailed life cycle, multispecies and size-based.  
Addressing fishing and management scenarios.

Now coupled to BGC models.  
Addressing climate combined with fishing scenarios

**Source of External Forcing (climate runoff)**

*The ROMS-NPZD model (to which OSMOSE is coupled) is forced by monthly climatology fields derived from the Comprehensive Ocean-Atmosphere Data Set (COADS) (Da Silva et al., 1994), including notably wind stress and heat flux at sea surface.*

**How is the model initialised?**

*From observations then spin up for 30 years in 1-way coupling*

**3. Model detail:**

*We only detail here the upper trophic levels, as the low trophic levels are represented by BGC models to which OSMOSE can be coupled*

**List all state variables and currency per trophic level:**

(correct if inappropriate!)

Trophic Level 0 (nutrients and tracers):

Trophic Level 1 (phytoplankton, bacteria(!!!)):

Trophic Level 2 (zooplankton):

Trophic Level 3 (fish):

*Kg wet biomass m<sup>-2</sup>*

Trophic Level 4 (sea birds):

**Key species (PFT groups, genera, spp) of the model:**

*OSMOSE is species-based, fish species and some invertebrate species are explicitly modelled (whole life cycle). Other functional groups such as birds, marine mammals etc are implicitly modelled through a predation mortality term. Plankton groups are modelled in the BGC models.*

*In the southern Benguela application, there are 11 species modelled in OSMOSE, see table 1 below.*

**Key physiological rates as well where new information is required for those species AND units:**

Table1 (from Travers and Shin submitted): Input parameters of OSMOSE for the 11 species of high trophic level.  $L^\infty$ ,  $K$ , and  $t_0$  are the parameters of the von Bertalanffy growth model;  $c$  is Fulton's condition factor and  $b$  the exponent of the Length-Weight allometric relationship;  $\phi$  is relative fecundity;  $a_{mat}$  is age at maturity;  $a_{max}$  is longevity;  $M_{nat}$  is an additional mortality rate (resulting from predation by other species of the ecosystem that are not explicitly modelled);  $F$  is the annual fishing mortality rate;  $a_{rec}$  is age of recruitment;  $F_{max}$  is the maximum ration of food for predators,  $\xi_{crit}$  is the critical threshold of predation efficiency below which maintenance function is not fulfilled and  $M_{\xi_{max}}$  is the maximum starvation mortality rate.

Species	Growth					Reproduction			Survival			Predation		
	$L_{\infty}$ cm	K $y^{-1}$	$t_0$ y	c $g.cm^{-3}$	b	$\phi$ eggs.g <sup>-1</sup>	$a_{mat}$ y	$a_{max}$ y	$M_{nat}$ y <sup>-1</sup>	$a_{rec}$ y	F y <sup>-1</sup>	$F_{max}$ g.body g <sup>-1</sup> .y <sup>-1</sup>	$\xi_{crit}$	$M_{\xi_{max}}$ y <sup>-1</sup>
Euphausiids	1.84	1.682	-0.1975	0.00738	3.16	42254	0.3	1	0.1	-	0	3.5	0.57	1
Anchovy	14.8	1.37	-0.03	0.007	3	8000	1	5	0.403	1	0.23	3.5	0.57	1
Sardine	26	0.26	-1.5	0.009	3	2400	2	10	0.365	1	0.16	3.5	0.57	1
Redeye	30.1	0.71	0.28	0.009	3	750	1	6	0.208	1	0.04	3.5	0.57	1
Lanternfish	7	1.66	0.06	0.008	3	646	0.5	2	0.226	1	0.0003	3.5	0.57	1
Lightfish	6	1.15	0.06	0.008	3	334	0.5	2	0.226	1	0.0003	3.5	0.57	1
Horse mackerel	54.5	0.183	-0.65	0.009	3	250	3	8	0.314	2	0.06	3.5	0.57	1
Shallow water hake	270.6	0.039	-0.73	0.006543	3.0425	500	4	15	0.228	3	0.23	3.5	0.57	1
Deep water hake	219.4	0.049	-0.914	0.007846	2.9759	500	4	15	0.174	3	0.33	3.5	0.57	1
Snoek	115.3	0.294	-0.1	0.018	3	130	3	10	0.132	2	0.25	3.5	0.57	1
Silver kob	116	0.12	-1.47	0.007	3	150	2	25	0.228	3	0.181	3.5	0.57	1

**Life history driven distribution ...i.e. life history closure**

*Life history is modelled for each species of OSMOSE: predation, growth, reproduction, mortality (predation, starvation, fishing, larval specific mortality)*

**Model output AND units:**

*Csv files*

*Every 2 weeks or less*

*State variables and derived indicators at different aggregation levels (schools, age/size class, species, community):*

*- Biomass, numbers (x,y,t, by school, age/size class, species), catches*

*- size-based indicators (mean and max size for each species, size at age, size spectrum, diversity spectrum)*

*- tropho-dynamic indicators (mean trophic level of species, trophic spectrum, diets matrices per size/age/species)*

**Conservation of mass?**

*80% of HTL biomass is explicitly modelled.*

**Principle methods & data sets to calibrate your model**

*A genetic algorithm algorithm has been specifically developed to calibrate OSMOSE model.*

*Phenotype vector (target observed data): observed species biomass*

*Genotype vector (estimated parameters): larval additional mortalities, plankton accessibilities*

**Principle data sets currently used for evaluation**

*Validation of OSMOSE using pattern-oriented modelling (Travers and Shin, submitted)*

**Validation data needs AND units:**

*Any multivariate data sets at different hierarchical levels (size-based and trophodynamic indicators at individual, population and community levels)*

**Closure terms**

**4. Implementation of MEECIAN Modules:**

**MEECE Drivers being addressed at present (current capability)**

*Ocean circulation*

*Climate patterns*

*Fishing*

## **MEECE Drivers under development**

### **Modules targeted for Implementation in your system (end-2-end coupling purposes):**

- In Meece, OSMOSE will be coupled to:*
- ROMS-NPZD in the Benguela ecosystem
  - BFM in the Adriatic and Aegean Seas
  - ERSEM in the North Sea

### **Key Species or PFT in the anticipated modules**

- to be determined by Chris Smith (Aegian, [csmith@her.hcmr.gr](mailto:csmith@her.hcmr.gr)) and Marco Zavatarelli (Adriatic, [marco.zavatarelli@unibo.it](mailto:marco.zavatarelli@unibo.it))*

### **Status of Key Species or PFT parameterization.**

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