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ShellSIM modelling shellfish growth

Marine Matters

ShellSIM™: a user-friendly software tool predicting growth and environmental effects in bivalve shellfish

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USDA United States Department of Agriculture

Background, validation and applications

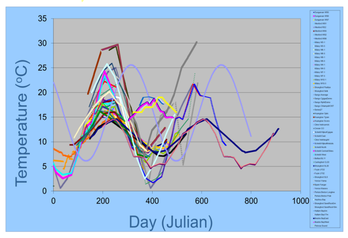
ShellSIM™ is a computer-based tool for bivalve shellfish aquaculture with outputs tailored as required for integrated applications helping to manage aquaculture production, including internalisation of wastes within multi-trophic systems and effects of aquaculture on wider ecosystem services, each according to the EU Water Framework Directive and FAO guidelines for ecosystem approach.

1. Individual growth, population dynamics and environmental effects are simulated in real-time within variable environments

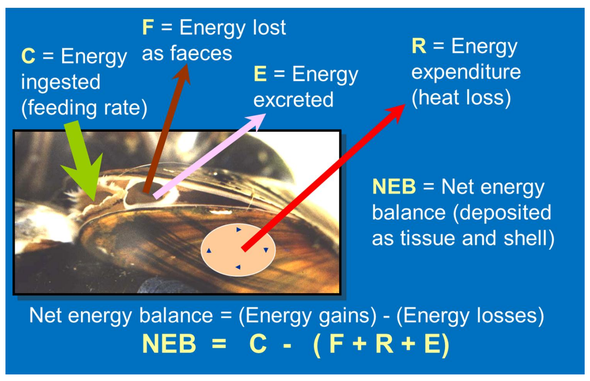
Forcing Functions

- Temperature
- Salinity
- Food availability
- Aerial exposure
- Current speed
- Dissolved oxygen

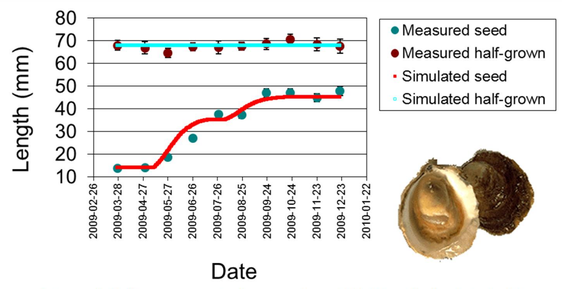
Simulated Responses



2. Each physiological component of dynamic energy balance is iterated using established relations

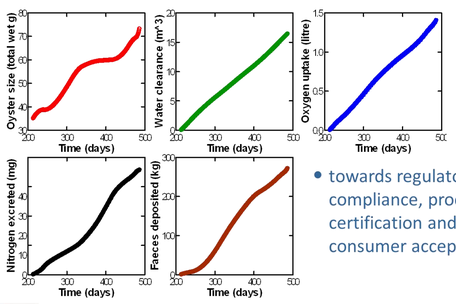


3. Simulations are accurate over full ranges of natural variability, accounting for shellfish size and age



Ostrea edulis (European oyster): comparison of shell length simulated with that observed (mean ± 2 SE) following deployment as either seed or ½ grown oysters during normal trestle culture in Strangford Lough, N. Ireland

4. Outputs that define dynamic environmental effects enable integrated ecosystem modeling



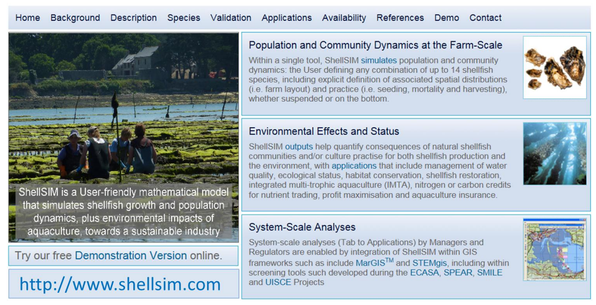
- towards regulatory compliance, product certification and consumer acceptance

One *Crasssostrea gigas* individual cultured from half-grown size in Dungarvan Bay over 272 d from Aug 2007 to May 2008 cleared 16 m^3, deposited 200 kg wet faeces, excreted 50 mg N and consumed 1.5 l O_2

5. ShellSIM™ has been validated in 13 species to date; accurate to within 25% when optimised for a single species across contrasting environments

Species	Type	Site	Error (%)	Culture
Mytilus edulis	Mussel	Oosterscheldt, Netherlands	6	*Bottom*
Mytilus edulis	Mussel	Carlingford Lough, N. Ireland	0	*Bottom*
Mytilus edulis	Mussel	Lough Foyle, N. Ireland	8	*Bottom*
Mytilus edulis	Mussel	Belfast Lough, N. Ireland	19	*Bottom*
Mytilus edulis	Mussel	Clew Bay, Ireland	22	*Rope*
Mytilus edulis	Mussel	Killary Harbour, Ireland	16	*Rope*
Crassostrea gigas	Oyster	Fangar Bay, Spain	9	*Trestle*
Crassostrea gigas	Oyster	Sanggou Bay, China	17	*Rope*
Crassostrea gigas	Oyster	Oosterscheldt, Netherlands	5	*Bottom*
Crassostrea gigas	Oyster	Strangford Lough, N. Ireland	17	*Trestle*
Crassostrea gigas	Oyster	Carlingford Lough, N. Ireland	25	*Trestle*
Crassostrea gigas	Oyster	Clew Bay, Ireland	10	*Trestle*
Crassostrea gigas	Oyster	Loch Creran, Scotland	3	*Trestle*
Crassostrea virginica	Oyster	Damariscotta River , U.S.A	4	*Floating*
Crassostrea virginica	Oyster	Long Island Sound, U.S.A	7	*Bottom*
M. galloprovincialis	Mussel	Venice Lagoon, Italy	<5	*Rope*
Perna canaliculus	Mussel	Pelorus Sound, New Zealand	<5	*Rope*
Modiolus modiolus	Mussel	Strangford Lough, N. Ireland	<5	*Bottom*
Crassostrea plicatula	Oyster	Huangdun Bay, China	<5	*Rope*
Ostrea edulis	Oyster	Strangford Lough, N. Ireland	<5	*Trestle*
Chlamys farreri	Scallop	Sanggou Bay, China	<5	*Lantern*
Pecten maximus	Scallop	Strangford Lough, N. Ireland	<5	*Bottom*
Tegillarca granosa	Cockle	Huangdun Bay, China	<5	*Bottom*
Tapes philippinarum	Clam	Venice Lagoon, Italy	<5	*Bottom*
Sinonovacula constricta	Clam	Huangdun Bay, China	<5	*Bottom*

6. Compiled using the Microsoft.NET Framework, ShellSIM™ is easily linked to other models, with online Demo version, where our track record of applications in coastal zone management is described



Novel approaches and key findings

Novel approaches both when calibrating ShellSIM™ and in simulating feeding behaviour have enhanced model versatility when challenged by different environments, whilst also evidencing adaptations that are key to understanding preferred habitats and geographic distributions for each species.

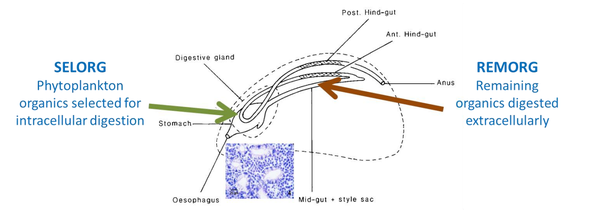
1. Identical protocols are ensured when calibrating ShellSIM™ in different locations and species

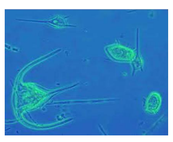
Standard protocols

Seston availability
- Chl a, POM or POC

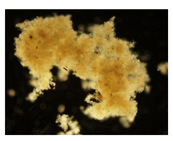
Feeding responses
- retention efficiency
- filtration rate
- rejection rate
- ingestion rate
- absorption efficiency
- absorption rate

2. Simulation resolves chlorophyll-rich food selected for intracellular digestion (SELORG) versus the remaining food digested extracellularly (REMORG)

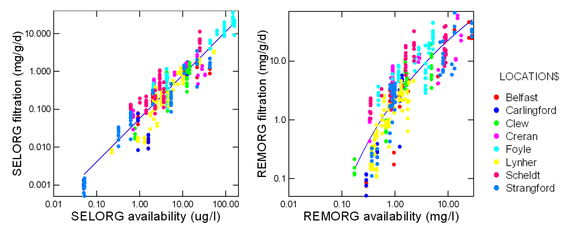




Hawkins, A. J. S., Bayne, B. L., Mantoura, R. F. C., Llewellyn, C. A. & Navarro, E. (1986) Chlorophyll degradation and absorption throughout the digestive system of the blue mussel *Mytilus edulis* L. *Journal of Experimental Marine Biology and Ecology*, 96: 213-223



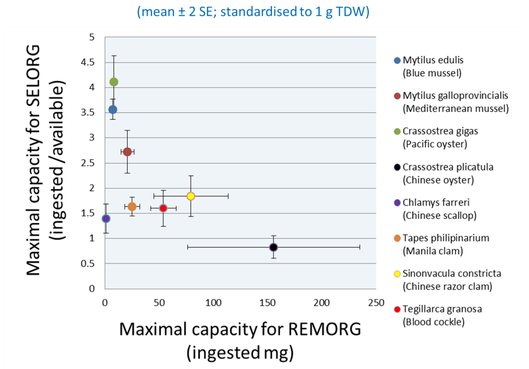
3. Different feeding responses for SELORG and REMORG are consistent across contrasting environments, enabling a single set of equations for each species



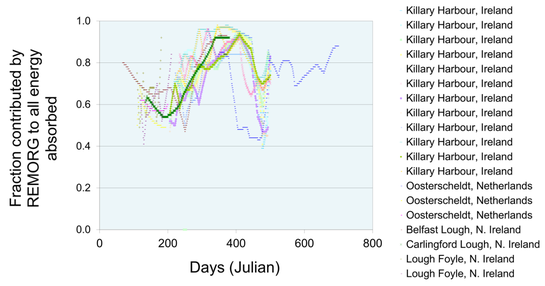
Mytilus edulis (Blue mussel): comparative filtration of SELORG and REMORG at all sites to date

4. Fitted equations establish very different capacities for SELORG and REMORG between bivalve species

(mean ± 2 SE; standardised to 1 g TDW)

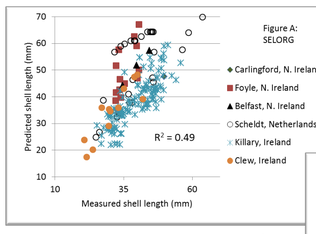


5. Outputs confirm significant and variable contributions of REMORG

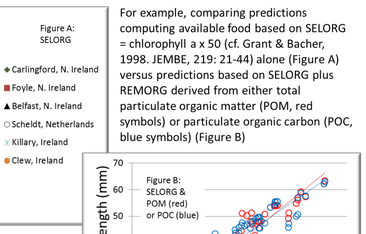


Mytilus edulis (Blue mussel): comparison of fraction contributed by REMORG to all energy absorbed during normal culture over between 8 and 24 months at all sites to date

6. Options establish when chlorophyll alone is adequate to simulate food available at different locations



For example, comparing predictions computing available food based on SELORG = chlorophyll a x 50 (cf. Grant & Bacher, 1998. JEMBE, 219: 21-44) alone (Figure A) versus predictions based on SELORG plus REMORG derived from either total particulate organic matter (POM, red symbols) or particulate organic carbon (POC, blue symbols) (Figure B)



Mytilus edulis (blue mussel): comparison of shell length simulated with that observed (mean for cohort) during normal culture over between 8 and 24 months at all sites to date

Summary and conclusions

- ShellSIM™ simulates growth and environmental effects across contrasting environments in wide range of species
- Such versatility has in part been enabled upon using standardised protocols which resolve feeding responses across full natural ranges of both chlorophyll-rich (SELORG) and remaining (REMORG) organic matter, as may vary in relative abundance between different locations
- Resulting findings show very different feeding behaviours such that, even within the same genus, there can be no "representative" species
- Practical and cost-effective application is facilitated by:
  - a common model structure with defined list of parameters ready for calibration in new species
  - options that establish the minimal set of environmental drivers required to simulate effectively at different locations
  - easy linkage using the Microsoft.NET Framework with other models such as include ShellGIS™
  - tailored outputs as needed for integrated system modelling
- We welcome hearing of collaborative interest, ready to help develop underlying science and outputs to satisfy further requirements

afbi Agri-Food and Biosciences Institute

BIM Bord Iascaigh Mhara Irish Sea Fisheries Board

SARF Scottish Aquaculture Research Forum

Loughs Agency

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