



Assessing goodness of fit for ECASA

27 July 2007

ShellSIM has been validated to date against field measures of actual growth during normal culture in nine different species of bivalve shellfish (Table 1).

It is not difficult to tune a model of shellfish growth so as to perform well in any given environment, or in similar environments. For example, excellent predictions are achieved by ShellSIM for the clam *Tapes philippinarum*, based upon very limited tuning of calibrations undertaken during ECASA in the Venice Lagoon, Italy, where the actual error in predicted growth was much less than 5%, given that the proportion of variance explained by ShellSIM was as high as 98% ($r^2 = 0.98$, $n = 24$) (Figure 1). In practice, as is indicated in Table 1 for species calibrated and validated to date at a single site, an error of less than 15% is acceptable for most purposes.

Of far greater value, ShellSIM is able to simulate effectively upon calibration in separate species, and which can then be applied using the same calibration for each species reared in contrasting coastal and estuarine environments, thereby saving significant time and resources.

Such adaptability in the face of different and contrasting environments has been established separately for *Crassostrea gigas* and *Mytilus edulis*, which are among the most widely cultured bivalve shellfish. When exactly the same set of functional interrelations that comprise ShellSIM are optimized for each of these species across wide ranges of environment and culture practice, then applying the resulting single standard set of parameters in each of those species, ShellSIM simulates to < 25% error across those ranges of environment and culture practice (Table 1).

To help further establish ShellSIM's credibility, we have undertaken analyses of goodness of fit based upon comparisons between simulated growth and observed growth using linear regression as described by Portilla and Tett (ECASA Internal Paper, 2007). First, for both *C. gigas* and *M. edulis*, we illustrate collective relations between predicted growth and measured growth during normal culture at all sites described in Table 1 (Figures 2 and 3, respectively). Second, for both *C. gigas* and *M. edulis*, we illustrate fitted linear regressions plus 95% confidence and 95% prediction bands between

predicted growth and measured growth during normal culture at all sites described in Table 1 (Figures 4 and 5, respectively). Third, we summarize assessments of ShellSIM's performances for *C. gigas* and *M. edulis* according to (i) the proportion of variance explained by each regression and (ii) the closeness of slopes to one including the closeness of intercepts to zero, upon which basis, models can be judged as 'excellent', 'good', 'fair' or 'poor' according to Oreskes et al. (1994) (Tables 2 and 3, respectively).

Trans-site analysis of all measured and predicted data, using a single standard set of ShellSIM parameters, for *C. gigas* during normal culture in Sanggou Bay (China), the Oosterscheldt (Netherlands), Strangford Lough (Northern Ireland), Carlingford Lough (Northern Ireland), Clew Bay (Republic of Ireland) and Loch Creran (Scotland) indicated that the slope and intercept of fitted regression were both different from zero ($p < 0.05$), and that the slope is significantly different from 1 ($p < 0.05$) (Table 2).

Similarly, trans-site analysis of all measured and predicted data, using a single standard set of ShellSIM parameters, for *M. edulis* during normal culture in the Pertuis Breton (France), Oosterscheldt (Netherlands), Strangford Lough (Northern Ireland), Carlingford Lough (Northern Ireland), Lough Foyle (Northern Ireland), Belfast Lough (Northern Ireland) and Clew Bay (Republic of Ireland) indicated that the slope and intercept of fitted regression were both different from zero ($p < 0.05$), and that the slope is significantly different from 1 ($p < 0.05$) (Table 3).

On which basis, according to Oreskes et al. (1994), ShellSIM's generic performance when applying a single standard set of parameters to predict growth across a broad range of culture environments and practices throughout Europe and Asia is classified as "**Fair**" when used for both *C. gigas* and *M. edulis*.

It should be remembered that state variables and derivations in ShellSIM include soft tissue energy, soft tissue weight, shell energy, shell weight, total dry weight, total wet weight and shell length. Functions predicted in the calculation of those state variables include separate calculations of the rates with which inorganic matter, phytoplankton organics and non-phytoplankton detrital organics are each filtered, rejected prior to ingestion as pseudofaeces, ingested and defecated as true faeces. Associated interrelations predict rates of energy absorption, excretion as ammonium, oxygen consumption, heat losses, reproductive losses and net energy balance. All of these predictions are based upon significant established interrelations, likely to be much of the same accuracy and precision as reported here for animal size, and which are collectively enabling analyses of the complex feedbacks, both positive and negative, whereby suspension feeding shellfish interact with ecosystem processes in dynamic environments.

We consider ShellSIM's ability to simulate effectively using the same calibration for each species reared in contrasting coastal and estuarine environments to be a significant step forward given the diversity of culture sites, additional variance conferred through the inclusion of different shellfish

stocks and varying protocols employed in the measurement of environmental drivers.

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27 July 2007

Table 1. Summary of species and sites for which ShellSIM has been validated. Percentage errors are those observed between final predicted and final observed sizes after between 8 and 24 months of growth under normal culture practice at each site, the model having been initialised for sizes upon seeding at the beginning of each growth cycle.

Species	Type	Site	Error in predicted growth (%)	Culture	Context
Single standard set of parameters, optimised per species across sites					
<i>Mytilus edulis</i>	Mussel	Pertuis Breton, France	7	<i>Pole</i>	<i>Literature</i>
<i>Mytilus edulis</i>	Mussel	Oosterscheldt, Netherlands	6	<i>Bottom</i>	<i>KEYZONES</i>
<i>Mytilus edulis</i>	Mussel	Strangford Lough, N. Ireland	6	<i>Rope</i>	<i>SMILE</i>
<i>Mytilus edulis</i>	Mussel	Carlingford Lough, N Ireland	0	<i>Rope</i>	<i>SMILE</i>
<i>Mytilus edulis</i>	Mussel	Lough Foyle, N. Ireland	4	<i>Rope</i>	<i>SMILE</i>
<i>Mytilus edulis</i>	Mussel	Belfast Lough, N. Ireland	19	<i>Bottom</i>	<i>SMILE</i>
<i>Mytilus edulis</i>	Mussel	Clew Bay, Ireland	12	<i>Rope</i>	<i>KEYZONES</i>
<i>Crassostrea gigas</i>	Oyster	Sanggou Bay China	17	<i>Rope</i>	<i>SPEAR</i>
<i>Crassostrea gigas</i>	Oyster	Oosterscheldt, Netherlands	5	<i>Bottom</i>	<i>KEYZONES</i>
<i>Crassostrea gigas</i>	Oyster	Strangford Lough, N. Ireland	17	<i>Trestle</i>	<i>SMILE</i>
<i>Crassostrea gigas</i>	Oyster	Carlingford Lough, N Ireland	25	<i>Trestle</i>	<i>SMILE</i>
<i>Crassostrea gigas</i>	Oyster	Clew Bay, Ireland	10	<i>Trestle</i>	<i>KEYZONES</i>
<i>Crassostrea gigas</i>	Oyster	Loch Creran, Scotland	3	<i>Trestle</i>	<i>KEYZONES</i>
Calibrated and validated at single sites					
<i>Chlamys farreri</i>	Scallop	Sanggou Bay, China	<15	<i>Lantern net</i>	<i>SPEAR</i>
<i>M. galloprovincialis</i>	Mussel	Venice Lagoon, Italy	<15	<i>Rope</i>	<i>ECASA</i>
<i>Tapes philippinarum</i>	Clam	Venice Lagoon, Italy	<15	<i>Bottom</i>	<i>ECASA</i>
<i>Tegillarca granosa</i>	Cockle	Huangdun Bay, China	<15	<i>Bottom</i>	<i>SPEAR</i>
<i>Ostrea plicatula</i>	Oyster	Huangdun Bay, China	<15	<i>Rope</i>	<i>SPEAR</i>
<i>Sinonvacula constricta</i>	Clam	Huangdun Bay, China	<15	<i>Bottom</i>	<i>SPEAR</i>

Table 2: Assessment of ShellSIM model outputs predicting growth (g total fresh weight) in *Crassostrea gigas*, compared with collective observations of growth made over between 8 and 24 months during normal culture in six contrasting environments described in Table 1. A linear regression was fitted investigating the 1to1relationship. Results for the test are values different from 0 for both coefficients, i.e. slope and intercept, when the slope is significantly different from 1.

Model description			
Model name		ShellSIM	
State variable		Size of individual <i>Crassostrea gigas</i> measured as total fresh weight (TFW, g)	
Sites at which tested		Trans-site analysis of all measured and predicted data, using a single standard set of ShellSIM parameters, for <i>C. gigas</i> during normal culture in the Sanggou Bay (China), Oosterscheldt (Netherlands), Strangford Lough (Northern Ireland), Carlingford Lough (Northern Ireland), Clew Bay (Republic of Ireland) and Loch Creran (Scotland).	
n, number of independent observations used in test		48	
Model Performance			
r^2 , % of variance	0.973	p , on null hypothesis	<0.001
β_0 , regression intercept	-5.178	$se\beta_0$	2.122
$t = (\beta_0 - 0)/se\beta_0$	-2.440	p	0.019
β_1 , regression slope	1.132	$se\beta_1$	0.039
$t = (\beta_1 - 1)/se\beta_1$	28.792	p	<0.001
Model Conclusion			
Model explains a significant part of variance in observations		YES	
Model reliability Class		Fair	

Table 3: Assessment of ShellSIM model outputs predicting growth (mm shell length) in *Mytilus edulis*, compared with collective observations of growth made over between 8 and 24 months during normal culture in six contrasting environments described in Table 1. A linear regression was fitted investigating the 1to1 relationship. Results for the test are values different from 0 for both coefficients, i.e. slope and intercept, when the slope is significantly different from 1.

Model description			
Model name		ShellSIM	
State variable		Size of individual <i>Mytilus edulis</i> measured as shell length (mm)	
Sites at which tested		Trans-site analysis of all measured and predicted data, using a single standard set of ShellSIM parameters, for <i>M. edulis</i> during normal culture in the Pertuis Breton (France), Oosterscheldt (Netherlands), Strangford Lough (Northern Ireland), Carlingford Lough (Northern Ireland), Lough Foyle (Northern Ireland), Belfast Lough (Northern Ireland) and Clew Bay (Republic of Ireland).	
n, number of independent observations used in test		72	
Model Performance			
r^2 , % of variance	0.874	p , on null hypothesis	<0.001
β_0 , regression intercept	6.564	$se\beta_0$	2.299
$t = (\beta_0 - 0)/se\beta_0$	2.854	p	0.006
β_1 , regression slope	0.807	$se\beta_1$	0.053
$t = (\beta_1 - 1)/se\beta_1$	15.079	p	<0.001
Model Conclusion			
Model explains a significant part of variance in observations		YES	
Model reliability Class		Fair	

Figure 1. Comparison of measured growth with that predicted by ShellSIM for *Tapes philippinarum* cultured over 3 y in the Venice Lagoon. The reduction in predicted weight upon about day 660 occurred upon simulated spawning.

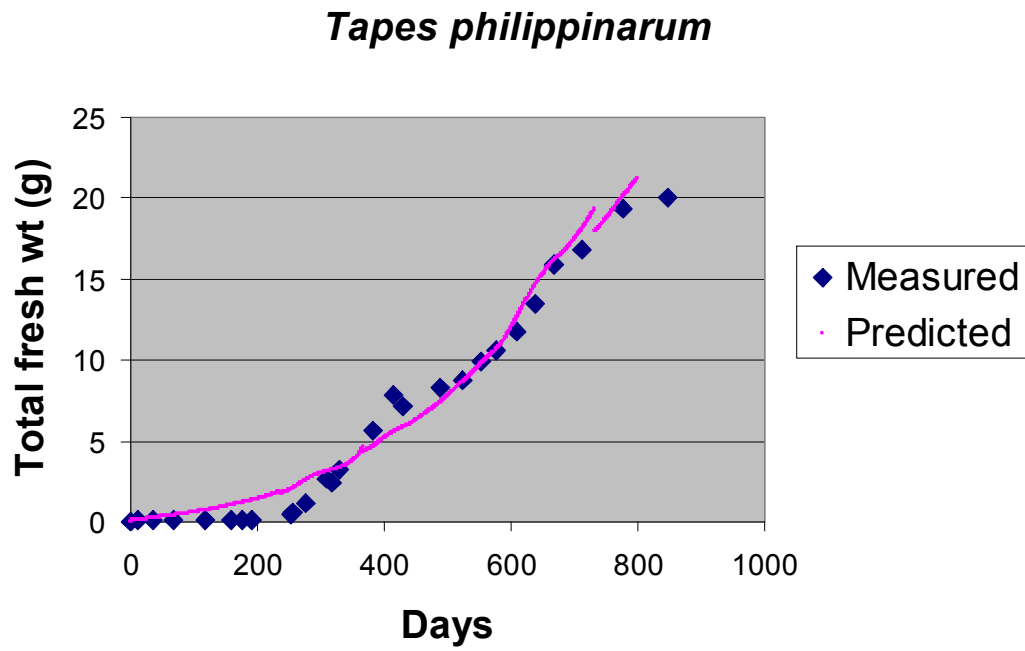


Figure 2. Collective relations between predicted growth and growth measured as total fresh weight (TFW, g) during normal culture of *Crassostrea gigas* over between 8 and 24 months at all sites described in Table 1.

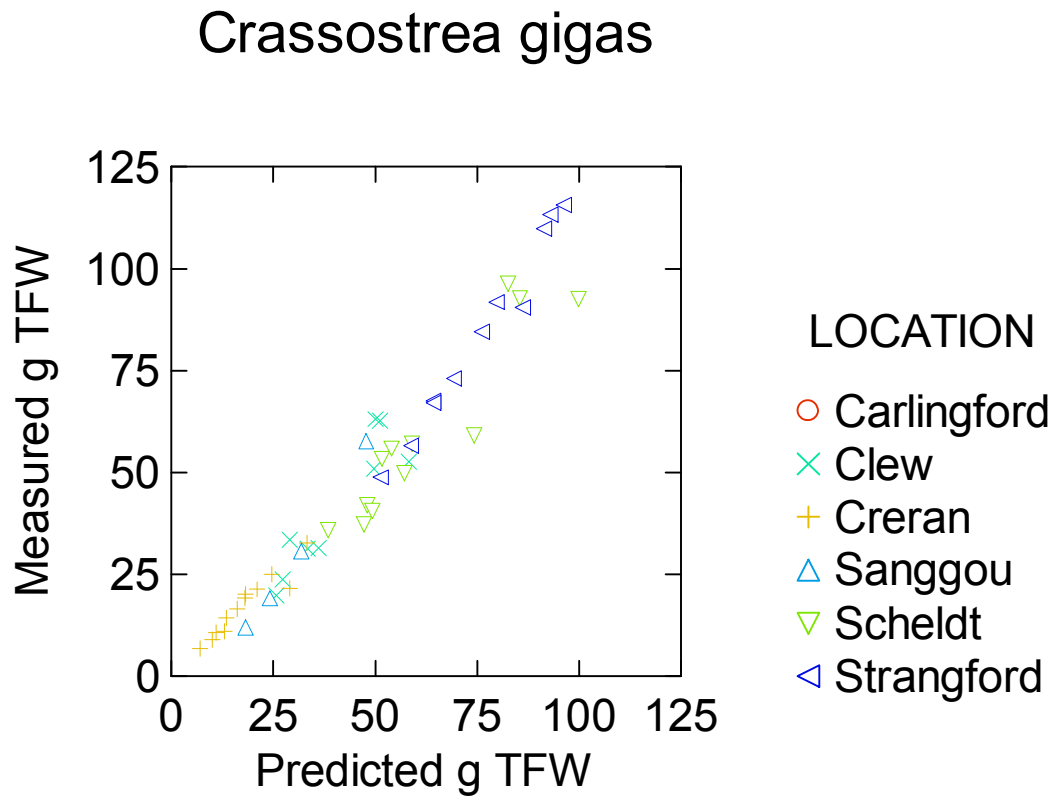


Figure 3. Collective relations between predicted growth and growth measured as shell length (mm) during normal culture of *Mytilus edulis* over between 8 and 24 months at all sites described in Table 1.

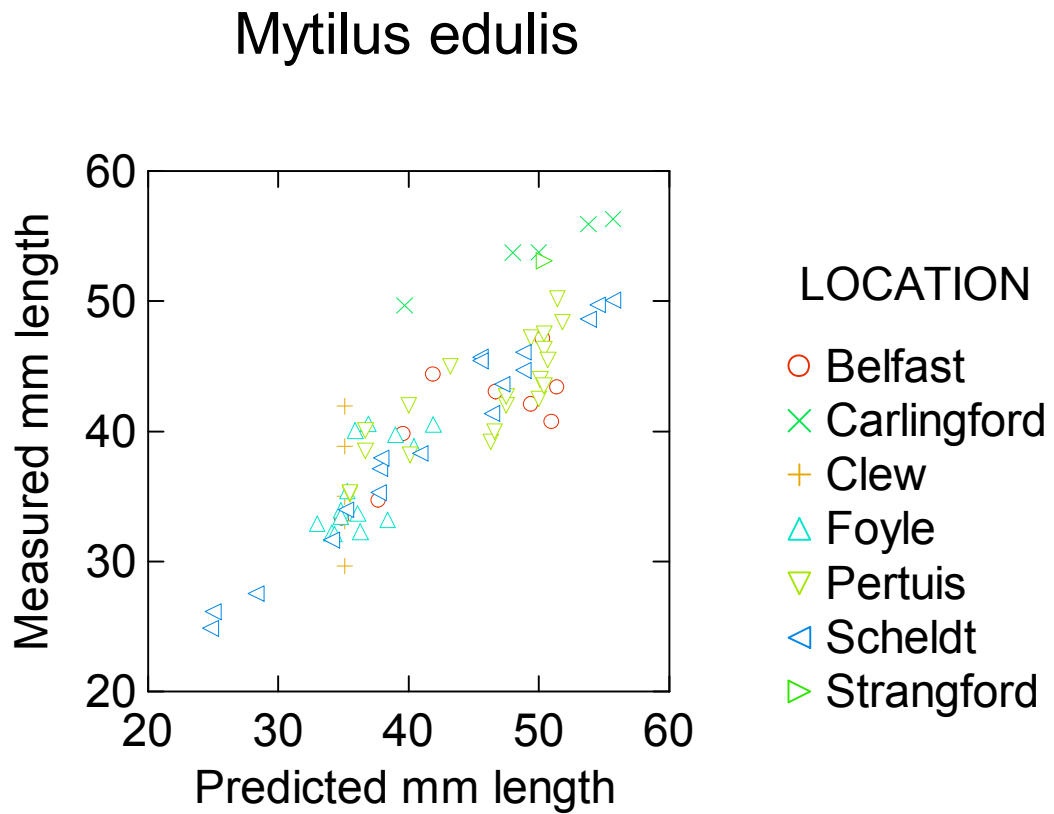


Figure 4. Fitted linear regressions plus 95% confidence and 95% prediction bands between predicted growth and growth measured as total fresh weight (TFW, g) during normal culture of *Crassostrea gigas* over between 8 and 24 months at all sites described in Table 1.

Crassostrea gigas

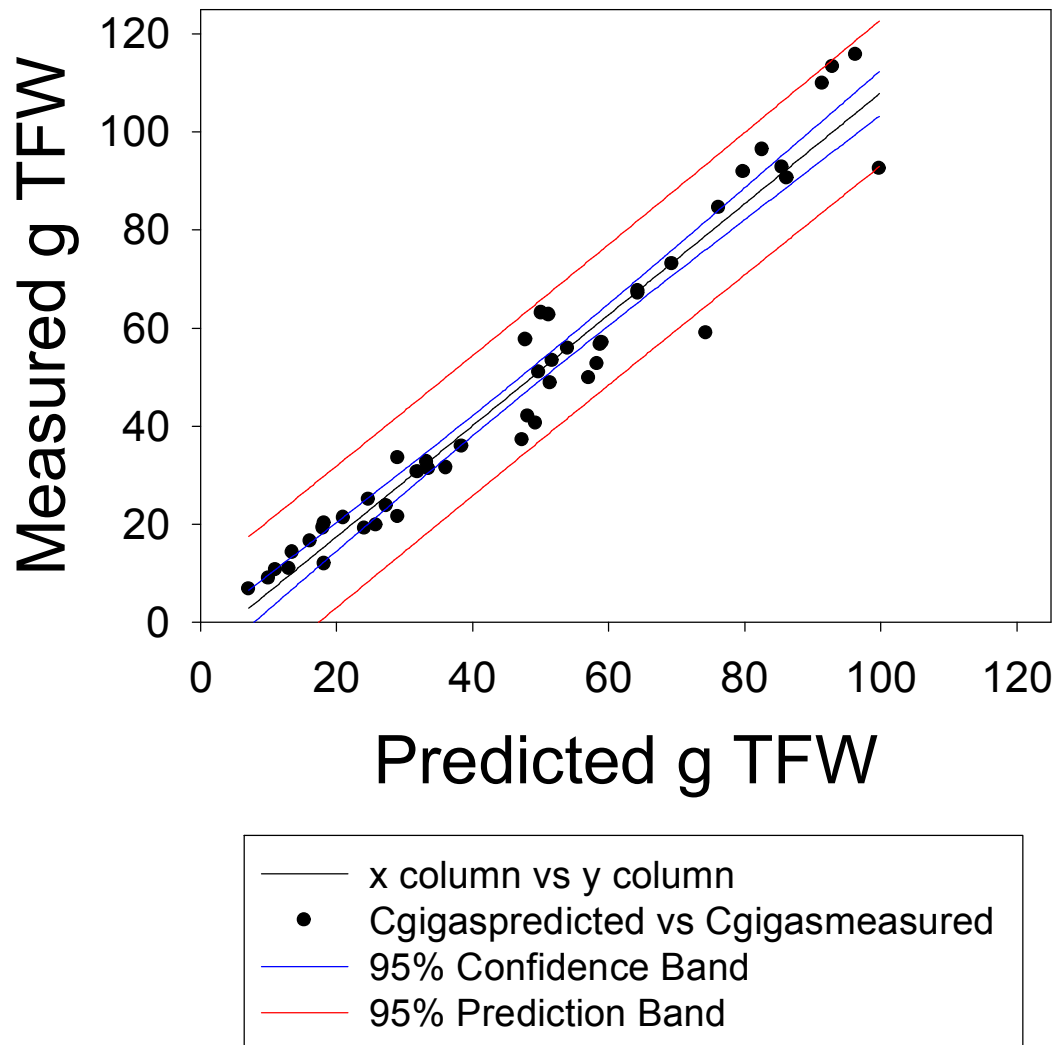


Figure 5. Fitted linear regressions plus 95% confidence and 95% prediction bands between predicted growth and growth measured as shell length (mm) during normal culture of *Mytilus edulis* over between 8 and 24 months at all sites described in Table 1.

Mytilus edulis

