Aquaculture 306 (2010) 205–210

Contents lists available at ScienceDirect

Aquaculture

journal homepage: www.elsevier.com/locate/aqua-online

A Bayesian hierarchical model for modeling white shrimp (*Litopenaeus vannamei*) growth in a commercial shrimp farm

Run Yu *, PingSun Leung

Department of Natural Resources and Environmental Management, University of Hawaii at Manoa, 3050 Maile Way Gilmore 111 Honolulu, HI 96822, United States

ARTICLE INFO

Article history:
Received 4 June 2009
Received in revised form 28 April 2010
Accepted 28 April 2010

Keywords:
Bayesian hierarchical model
Growth function
Shrimp
Forecasting

ABSTRACT

The paper explored the Bayesian hierarchical model as a possible way to incorporate growth variability in estimating shrimp growth function to enhance forecasting accuracy, using data from 16 growout ponds of a commercial shrimp farm in Hawaii. Based on a dataset of 571 weekly growth observations, the Bayesian hierarchical model is found to fit the data better than the simple nonlinear model that neglects growth variability, with respect to the deviance information criterion, root mean squared error and mean absolute percentage error. The Bayesian hierarchical model therefore could be a promising alternative for forecasting shrimp growth in commercial aquaculture practice.

1. Introduction

Forecasting growth of aquatic organisms bears great significance for any aquaculture enterprise. Many statistical models have been explored for modeling the growth of aquatic animals and plants. These models vary in the cultured species, explanatory factors, statistical methods employed, and the issues of interests. Shrimp is one of the most studied crustaceans (Wyban et al., 1995; Araneda et al., 2008). As for the statistical methods employed, various regression models have been widely applied in modeling shrimp growth (Tian et al., 1993). Yu et al. (2006) applied the neural network technique; and Whiting et al. (2000) adopted the empirical Bayes procedure. Recognized important factors influencing shrimp growth include water temperature, water exchange rate, feed supply, stocking density, oxygen concentration, salinity, and etc. (Leung and Rowland, 1989; Leung et al., 1990; Wyban et al., 1995; Wang, 1998; Jackson and Wang, 1998; Xiao, 1999; Tian and Dong, 2006). Focus of shrimp growth modeling has recently been shifted from studying growth performances in research experimental settings to commercial settings (Yu et al., 2006).

Commercial shrimp farm environment can differ considerably from that of research experiments. A commercial shrimp farm typically operates many growout facilities simultaneously. Consequently, the farm manager has to predict the growth performances for many growout units with limited observations in the beginning of the growout season. The growth performance of these growout units (e.g. ponds, pens, or raceways) usually vary and thus pose a particular challenge for shrimp growth modeling. For example, the shrimp farm in this study operated 40 growout ponds year round. While these ponds were constructed with the same physical characteristics such as depth and surface area, historical records indicated that growth performances were different across ponds even under similar cultivation conditions such as water temperature, stocking density, and feeding rate. Ideally, it is best to trace the growth curve for each pond individually. Unfortunately, sampling data from individual ponds were generally not sufficient to accomplish this task. The conventional solution is to fit a single growth curve with pooled data, assuming the parameter values of the growth function are the same for all the growout ponds. In other words, this approach neglects the variability in growout ponds and predicts an identical growth for all the growout ponds, given the same cultivation conditions.

In this paper, we explored the Bayesian method, in particular the Bayesian hierarchical model, as an alternative method for forecasting shrimp growth for commercial shrimp farms. We attempted to improve growth prediction through incorporating the across-ponds variability into the shrimp growth model[1].

The Bayesian method is based on the Bayes theorem. The mathematical representation of the Bayes theorem can be expressed as $P(H|D) = \frac{P(D|H)P(H)}{P(D)}$, where $P(H|D)$ is the conditional probability of the hypothesis H given evidence (data) D (i.e., the posterior

---

* Corresponding author. Tel.: +1 808 224 0503; fax: +1 808 956 9269.
E-mail addresses: run@hawaii.edu (R. Yu), psleung@hawaii.edu (P. Leung).

[1] The traditional frequentist method, for instance the random coefficients models, could also account for growth variability when sufficient data are available. The Bayesian method, on the contrary, is not generally restricted by the size of the data. It is ideally suited for analysis with limited data and is theoretically preferred to the frequentist method (Harvey, 1995).

0044-8486/$ – see front matter © 2010 Elsevier B.V. All rights reserved.
doi:10.1016/j.aquaculture.2010.04.028

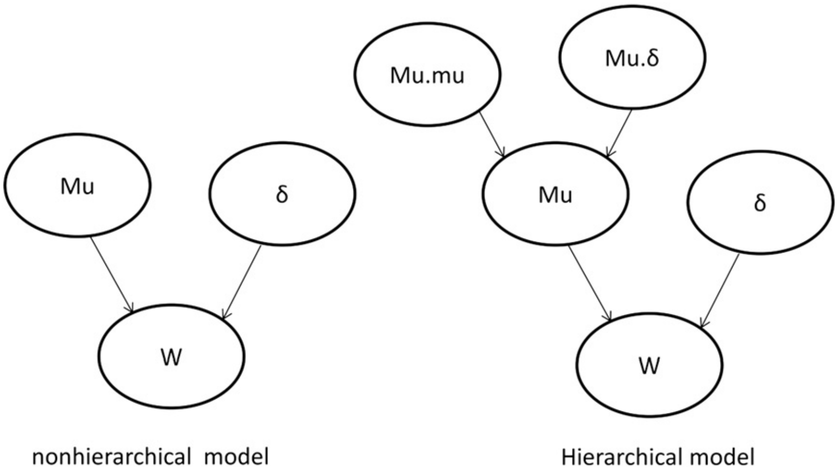

Fig. 1. Illustration of the Bayesian nonhierarchical and hierarchical structure.

probability); $P(D|H)$ is the "inverse" conditional probability of the observed data D given hypothesis H (i.e., the likelihood function); $P(H)$ is the marginal probability of hypothesis H (i.e., prior) ; and $P(D)$ is the marginal probability of observed data D (i.e., normalized constant). The likelihood function expresses the degree to which the hypothesis H predicts the evidence (data) given the probability. In other words, it postulates the linkage between the explanatory variable and the response variable. The Bayes theorem provides a mean to update the relationship between the explanatory variable and the response variable through validating the data observed against the prior (Draper, 1995). The application of the Bayesian method however gains popularity only recently because of the computational breakthrough known as the Markov Chain Monte Carlo (MCMC) simulation.

For our specific purpose of admitting growth variability in a shrimp growth function, we used the Bayesian hierarchical model, a special class of Bayesian models designed for dealing with parameter variability. Under the Bayesian hierarchical framework, the observations are assumed to be a distribution conditional on the explanatory parameters. The explanatory parameters in turn are assumed to be the distributions conditional on additional parameters, called the "hyper-parameters". The hyper-parameters characterize the distributional patterns of the values of the corresponding explanatory parameters. As illustrated in Fig. 1, a nonhierarchical model has a very simple structure. The response variable W is stochastically dependent on a deterministic term Mu and an error term δ. The basic idea of a hierarchical model is that the deterministic term (Mu) may also depend on some stochastic parameters (the hyper-parameters). In many cases, the hyper-parameters themselves may also (or may not) depend on some new parameters. Fig. 1 provides an example of a two-tier hierarchical structure.

The power of the Bayesian hierarchical model lies in its ability to modeling homogeneity and retaining its ability to characterize specific individuals (Rossi et al., 2006). For the shrimp growth model, the Bayesian hierarchical approach will construct a common growth function for individual growout units and postulate that the corresponding individual growth parameters come randomly from a population distribution. Using this multiple levels (hierarchical) structure, estimation of the unit-specific parameters could borrow strength (information) from other growout units through the assumed population distribution. The growth curve of individual growout units therefore can be modeled, using limited unit-specific data.

While the Bayesian method has been widely applied in admitting individual variability in a variety of models (Gelman et al., 2003; Helser and Lai, 2004; Zhang et al., 2009), including fishery (Alos et al., 2010a; 2010b), we are not aware of its applications in modeling the growth performance for aquatic organisms in aquaculture operations. In this paper, we compared the predictive performance of the Bayesian hierarchical model and the nonhierarchical (simple nonlinear) model, using data from a commercial shrimp farm in Hawaii.

2. Materials and methods

2.1. Data

Shrimp growth could be affected by various factors such as water temperature, feed supply, and stocking density (Leung and Rowland, 1989; Leung et al., 1990; Tian et al., 1993; Wyban et al., 1995). In this study we modeled the shrimp growth function by relating average shrimp weight with age of shrimp, water temperatures, density, and feed supply. The data was provided by a commercial shrimp farming

Table 1
Descriptive statistics of the data.

Variables	Modeling dataset				Validation dataset			
	Mean	Min	Max	Median	Mean	Min	Max	Median
Weight($t-1$)	13.38	0.70	24.60	13.91	12.66	1.38	23.53	13.33
Density	3.36	0.19	6.82	3.49	3.27	0.44	5.92	3.51
Feed	1.29	0.00	3.80	1.28	1.39	0.00	2.93	1.39
AM	24.06	21.74	27.14	24.04	24.24	21.74	27.14	24.22
PM	26.15	22.77	29.19	26.13	26.36	22.77	29.19	26.30
VAM	0.47	0.03	6.15	0.18	0.50	0.03	6.15	0.18
VPM	0.55	0.07	1.73	0.41	0.59	0.07	1.73	0.49
Age	12.84	1.00	36.00	12.00	11.91	2.00	30.00	11.00
Weight (t)	14.32	1.12	25.63	15.08	13.86	2.02	24.25	14.62