

A probabilistic representation of fish diet compositions from multiple data sources: A Gulf of Mexico case study



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ABSTRACT

Trophic ecosystem models are interactive tools that allow decision makers to analyze how a management decision can impact an ecosystem on a multi-species level, and are increasingly being used as a supplement to the current single species approach to fisheries management. The functionality of such a model is dependent upon an accurate representation of the trophic interactions occurring within a study area. Typical methods for developing a diet matrix to be used in ecosystem models often fail to account for uncertainty associated with sampling; this is especially relevant when dealing with small diet data sets. In this case study of the Gulf of Mexico ecosystem, we have conducted a laboratory diet analysis to define predator–prey interactions for non-commercially important predator species resident to the study area, and then expounded on this laboratory data by assimilating two, more robust data sets. By applying a maximum likelihood estimation method, we combine these data sets and produce maximum likelihood estimates (MLEs) and associated error ranges, which describe the likely diet contribution that a given prey item contributes to a predator's diet. We use the resultant mode values to develop a preliminary food web diagram, depicting the trophic interactions occurring between aggregated groups of species within our model study area. These results will be used to parameterize the availabilities (diet) matrix of an Atlantis ecosystem model of the Gulf of Mexico.

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1. Introduction

Commercial and recreational fisheries in the United States are a multimillion dollar asset (Nipper et al., 2004), providing food and jobs for many of the region's coastal communities (NOAA Fact Sheet, 2010; Marshall, 2013). Improperly managing the harvest of these fisheries can stress the ecosystem, possibly leading to the collapse of important marine resources (Backlund et al., 2008; Millennium Ecosystem Assessment, 2005). Moreover, the loss of functionally important species can have indirect impacts on the rest of the ecosystem with consequences for system resiliency and biodiversity. As marine uses intensify and diversify, it is essential that we begin applying ecosystem-based fisheries management strategies (EBFM) (Brodziak and Link, 2002; Garcia et al., 2003; NOAA, 2003; FAO, 2003) if we hope to account for trophodynamic relationships occurring within a complex marine ecosystem.

In accordance with the Magnuson–Stevens Fishery Conservation and Management Act (Anonymous, 2006), the Integrated Ecosystem Assessment (IEA) program at the National Marine Fisheries Service (NMFS/NOAA) is obligated to develop EBFM strategies in order to supplement the current single-species approach to fisheries management. One way to incorporate EBFM is through the use of trophodynamic ecosystem simulation software. For example, we can use trophic ecosystem models to assess how a simulated ecosystem responds to a management strategy that increases the harvest of an important commercial fishery. Many ecosystem simulators exist that can be used to address a wide range of conceptual, strategic and tactical objectives (e.g., Walters et al., 1997; Fulton et al., 2004a; Kazanci, 2007). However, the behavior of these models hinges on an accurate representation of the predator–prey interactions occurring between model functional groups (i.e., aggregated species sharing similar diet and/or habitats, or that are commercially important in the study area). These interactions greatly influence how the ecosystem responds to simulated management decisions (Pinnegar et al., 2005).

Diet data has been assembled by various agencies and researchers, many of which are available for public use. However, some difficulties arise for ecosystem modelers when collating diet

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information from just a single data set as these data sets are often limited to a narrow range of species that are of interest to the organization conducting the survey. To gain a comprehensive overview of species dependencies, ecosystem modelers must combine multiple diet studies into a single aggregated data set, and in doing so must also accurately represent the uncertainty surrounding these data to reflect variable sample size (Plagányi, 2007; Ainsworth et al., 2010). Failing to account for this uncertainty could lead to discreditable model predictions and undermine the movement toward EBFM.

The purpose of this research is to provide critical diet information for an Atlantis ecosystem model of the Gulf of Mexico (GoM) ecosystem. Atlantis (Fulton, 2001; Fulton et al., 2004a, 2004b, 2005, 2007) is a spatially explicit, 3-dimensional trophic ecosystem model that can dynamically simulate the physical, chemical and biological interactions occurring within a marine ecosystem. We first perform a laboratory analysis of stomach samples with the intent to better understand the trophic interactions of data deficient fish species within the GoM study area. We then expound on our laboratory results through the assimilation of available diet data sets. Following the methodology of Ainsworth et al. (2010), we perform a statistical analysis to provide a probabilistic representation of major predator–prey linkages for the GoM ecosystem. The statistical analysis first bootstraps the synthesized diet composition data, and then fits the data to a Dirichlet distribution. This produces maximum likelihood estimates (MLEs), or joint probability density functions (PDFs), and corresponding 95% confidence intervals. The peak of the obtained PDF is the mode, and was taken as the fraction of the prey's contribution to a predator's diet for each predator–prey interaction.

Although Atlantis can only use a point value for diet input, other modeling systems like Ecoranger (Christensen et al., 2008) are able to accept probabilistic diet compositions directly. Furthermore, the error ranges offered by this method are still very useful for validating the realized diet compositions after tuning our Atlantis model (Fig. 1). This is because after spatial co-occurrence of predators and

prey, and gape limitations are taken into account in Atlantis (Fulton et al., 2001) the realized diet composition of a given predator can be expected to fall within the error ranges offered by the Dirichlet distribution (Ainsworth et al., 2010). The multinomial distributions created using our statistical approach normalize the variance in the predicted diet outcomes, allowing us to account for co-variation between prey items. Thus, using this statistical method we are able to represent the uncertainty surrounding these diet data sets, making this an ideal tool for describing the diets in a multispecies context.

The synthesized diet data we present in this study is the largest amount of diet data to ever be used in the parameterization of an ecosystem model for the Gulf of Mexico. The resulting diet compositions are used to develop a preliminary food web diagram, which characterizes trophic interactions between predator and prey species within the model study area. The statistical method is applicable to any study that would require combining multiple data sets spanning a number of species, while accounting for variable sample sizes. Furthermore, this methodology is easily adaptable to other modeling systems, like Ecoranger (Christensen et al., 2008) that are able to accept probabilistic diet compositions directly.

2. Methods

2.1. Sampling

In an effort to define trophic interactions for our non-commercial consumer functional groups in the GoM Atlantis model, we acquired 101 fish stomachs that were collected in 2011 from sampling locations throughout the GoM (Fig. 2) by local, state and federal agencies. These agencies include the National Marine Fisheries Service (NOAA), Florida Fish and Wildlife Conservation Commission (FWC) and the University of South Florida (USF). Collecting fish stomachs from these various agencies and locations allows for analysis across a broad range of gear types (trawls,

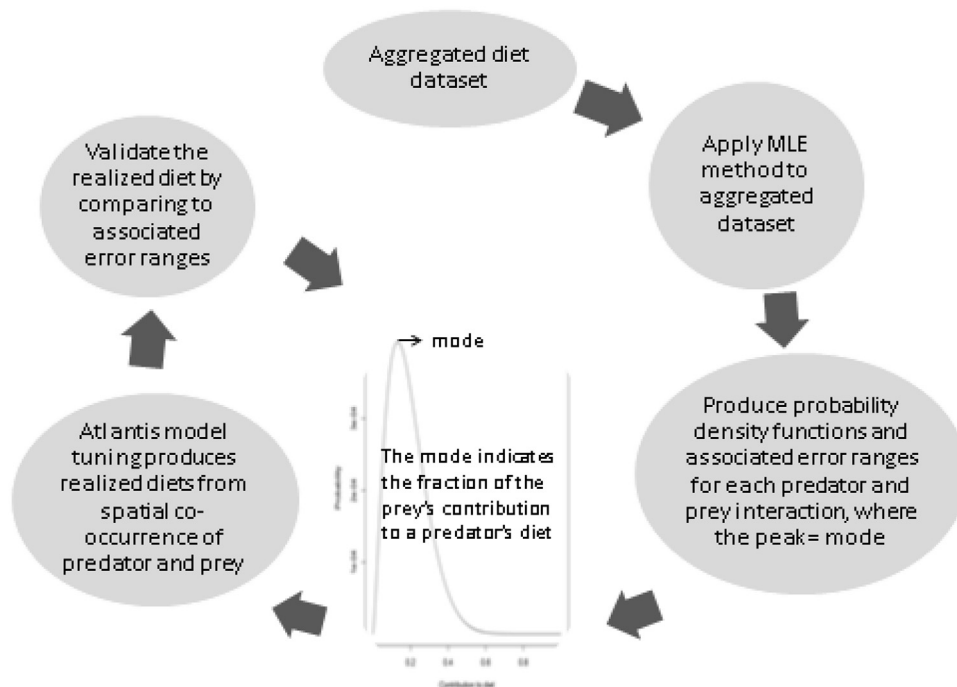


Fig. 1. Conceptual model showing data amalgamation, the MLE method used to produce joint probability density functions (PDFs), where the mode of the PDF indicated the fraction of the prey's contribution to a predator's diet, and finally the model tuning and realized diet composition validation process.

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