Nonlinear evaluation of stock assessment and marine ecosystem models

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Nonlinear evaluation of stock assessment and marine ecosystem models

Abstract
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Keywords
Agriculture, Fisheries and Aquaculture
NONLINEAR EVALUATION OF STOCK ASSESSMENT AND MARINE ECOSYSTEM MODELS

BY

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BA Boston University (2009)

Submitted to the University of New Hampshire in partial fulfillment of the requirements for the degree of Master of Science in Natural Resources: Environmental Conservation

May 2011
This thesis has been examined and approved.

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Date
5/8/2011
ACKNOWLEDGMENTS

First, I would like to thank my thesis advisor Andy Rosenberg and committee members Tom Lee and Kevin Short. Andy has provided me with the necessary resources and guidance during my transition from an astronomical background to natural resources, while also allowing me to select my own project out of the larger CAMEO research group. Tom Lee and Kevin Short have served as the ecological and mathematical basis of a project that spans both fields.

Without Sarah Glaser, I would not have a Masters project. With extensive knowledge and endless patience, she taught me how to use the models and answered my incessant barrage of questions. Emily Klein, Irit Altman, Hao Ye, Isaac Kaplan, and Alec MacCall have also contributed significant amounts of their time and provided me with invaluable knowledge and feedback.

Additionally, I would like to thank the remaining members of the office, including (but not limited to) Lynn Rutter, Lina Saavedra Diaz, Karen Alexander, Bill Leavenworth, Jessie Knapp, and Jamie Cournane for their support (and supply of snacks).

Last but not least, I must thank my parents. Despite wishing that I had pursued a more lucrative career path, they still supported me, financially and otherwise.
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ABSTRACT
NONLINEAR EVALUATION OF STOCK ASSESSMENT AND MARINE ECOSYSTEM MODELS
by
Laura Storch
University of New Hampshire, May, 2011

In fisheries management, single-species stock assessment models use fisheries-dependent catch and landings data along with fishery-independent estimates of relative or absolute abundance to make estimates of species biomass for a given area. This output is used by the Atlantis marine ecosystem model as input. Atlantis uses an array of physical, biological, and anthropogenic factors to predict biomass for individual species or functional groups of species. Nonlinear analysis was used to assess the output for both the stock assessment and Atlantis models for the marine ecosystem off the California coast. The number of time series displaying nonlinear characteristics decreases from raw (landings) data to model output, which suggests that models may not be conserving underlying data signals. Relationships between species in Atlantis functional groups (determined by the Atlantis modelers) were also analyzed using the nonlinear analysis, and relationships assumed by the Atlantis modelers were in disagreement with relationships that appeared out of the nonlinear analysis.
CHAPTER 1
INTRODUCTION

Ecosystem models are becoming increasingly important as both scientists and policy makers realize the need for ecosystem-based management. In 2010 it was estimated that approximately 50% of fish stocks were fully exploited and 28% were overexploited [5] and in 2008, it was estimated that top predator biomass (e.g. Bluefin Tuna) had decreased by 50% since 1950 [11]. Such overexploitation has occurred during the era of single-species models and management practices. Ecosystem-based management is described as a management practice that aims to consider the connectedness of all ecosystem components including humans, along with the full array of ecosystem services, when making policy decisions [3]. Ecosystem-based management becomes increasingly important as target species populations decline and collapse due to the presence and interaction of multiple factors including overfishing of target species, losses to bycatch, habitat loss, and environmental degradation.

It has been argued that fishing is the primary reason for modern decline in fish populations, as opposed to other factors such as climate change [35]. Fishing also impacts species population abundance by increasing their yearly fluctuations [15, 1]. In addition, the direct and indirect effects of fishing activities likely contribute to changes in overall ocean productivity [27] by altering the ecosystem of the fish being exploited [24]. Such alterations can take the form of habitat destruction or changes in species abundances. Evidence for this is presented in historical fishery research studies, where it was found that the fishermen of the 1800s were catching more fish than modern fishermen despite increased efforts and improved gear (Rosenberg 2005).
Fishing impacts can also cascade through the ecosystem. For example, changes in trophic structure have been observed which result in jellyfish swarms as discussed by Longhurst [20]. Although the definitive reason for recent explosions in jellyfish populations is unknown, one hypothesis suggests that for the northern Benguela ecosystem, the once-dominant anchovy and sardine suffered enough of a biomass decrease due to fishing that it allowed for the jellyfish to become the dominant species in the region.

The success of current management plans is often limited because they manage on local scales, are single-species focused, and consider only short-term effects. Policies such as the Magnuson-Stevens Fishery Conservation and Management Act place economically reasonable time limits on recovery acts for biological systems. Such time scales may be ecologically unreasonable for the managed system and this hinders recovery [29]. Additionally, management practices focus on economic development and catch maximization instead of restoring and maintaining ecosystem integrity and ecosystem services [28]. While recent attempts have been made to consider human impacts on marine ecosystems, each impact is usually considered in isolation. This approach underestimates the effect of human impacts which act synergistically and whose cumulative impact is therefore larger than an additive framework would presume [10].

Ecosystem functioning depends on complex interactions among and between species and environmental factors. Furthermore, because ocean biodiversity leads to greater ecosystem stability [36], every species is valuable to the whole, and commercially uninteresting species should have a role in fisheries management. Understanding the nature of key relationships among ecosystem components is also a critical element of ecosystem-based management. Recent evidence suggests that many biological systems are nonlinear by nature [14], and biological systems modeling has seen great improvement in forecasting ability with the switch from linear to nonlinear mod-
els. In a nonlinear system, variables can have complicated interactions with each other [16]. This is further evidence that the removal of an apparently inconsequential species may have detrimental effects on a commercial species of interest due to unknown interactions. For these reasons, a whole-ecosystem view, and the application of this view to analytical models, may be critical for successful management.

Tools for understanding the relationships and functioning of whole ecosystems are critical for developing ecosystem-based management. In this context ecosystem models can be an integral part of ecosystem-based management. Models that address whole systems incorporate sometimes hundreds of variables that single-species models do not. As more species and parameters are included, the models become increasingly complex and this could detract from their usefulness as higher levels of complexity lead to higher levels of error [6].

Few attempts have been made to analyze model performance in terms of the models structure or level of complexity [6]. The way variable relationships are structured influence model output. In the case of well studied systems or relatively simple models (i.e. few variables and relationships to parameterize), scientific information may be substantial and can be used directly to inform management decisions. On the other hand when models become very complex, it is oftentimes left to the individual modelers judgment to decide the best structure for the model [25]. For example, functional groups are used in ecosystem models to reduce dimensionality. Creation of a functional group is often a qualitative exercise in which species with similar traits (e.g. diet, life history characteristics, or other factors) are aggregated. The way these functional groups are assembled affects the output of the model [25].

This research seeks to determine whether complex models preserve underlying raw data signals. In an attempt to understand what happens to data as it moves from model input to model output, this research compares the input and output via
nonlinear forecasting models. The results will help determine whether the models have passed the optimal error/complexity tradeoff as described by Fulton [6].

1.1 Background Information

1.1.1 Study Area

The data employed in this research is from California ports, or in the case of the Atlantis model, the California current. The California current travels north to south along the west coast of the United States. It is characterized by substantial upwelling that is responsible for transporting deep-water nutrients (and cold water) to the surface. Such upwelling processes are responsible for highly productive systems and are therefore associated with major fishing activity [23].

The most abundant species in the California current are sardine, anchovy, hake, and mackerels [23]. Heavy exploitation of the major California fisheries in the early 1900s led to moratoriums or substantial management actions in the later part of the century. A moratorium was introduced in 1967 on sardine fishing due to overexploitation [23]. Similarly, a 1965 depletion of Pacific Mackerel led to a moratorium in the 1970s [22]. Rockfishes followed in the 1980s, with increasingly strict management plans that eventually led to the 2000 declaration of the west coast as a federal fishery disaster with mandatory rebuilding plans for many stocks [19].

Landings data are available for California ports as far back as the late 1800s, but survey data, which are frequently of more interest to research scientists, are far less abundant. The California Cooperative Oceanic Fisheries Investigations (CalCOFI) program, which began in 1950, provides larval abundance survey data (see www.CalCOFI.org for data). Such data have greatly aided in the understanding of the California current ecosystem [22].
1.1.2 Stock Assessment Models

Fisheries stock assessment models use fisheries dependent data such as catch and catch per unit effort (CPUE) to make estimations of a stock's total biomass. In addition to the available fisheries data, biomass is calculated using estimated parameters of abundance, natural mortality, and myriad other factors, depending on the complexity of the model. In their simplest form, stock assessment models make predictions about number of fish alive at year (t) based on number alive at year (t-1) minus natural and fishing mortality. Abundance is converted to biomass via estimations of size/weight at age. Fishing mortality depends on fishing effort, gear type, and number of fish available [12].

Any given target fishery is usually considered a closed system, though some stock assessment models can allow for multiple geographic locations and migration between these locations. Along with relative geographic isolation, stock assessment models are also single-species focused and do not have variables to account for interactions between species. The fact that species interactions are ignored in traditional stock assessments is justified by Hilborn and Walters [12] for the following reasons:

1. If dynamics of a stock can be reliably predicted using only parameters pertaining to that species and perhaps physical environment parameters, there is no need to add further complication to the model

2. Parameters of stock/species interactions may not be estimated well enough to add to model predictability

3. Future conditions of other species may be unknown

The authors admit that these arguments have serious weaknesses, and as the popularity of the ecosystem-based management (EBM) concept increases, single-species models are increasingly scrutinized. Such scrutiny will be discussed in the following subsection. A widely used stock assessment model for US west coast fisheries is the
stock synthesis model, developed by Richard Methot in 1989. The synthesis model uses catch, catch per unit effort, and age-structure data (length/weight at age, numbers at age) to estimate a fishery biomass. It can be run as an age-structure model or an age-size model. The larger model consists of three sub-models: a population model, observation model, and statistical model.

The population model produces biomass estimates by specifying a starting abundance at age, number of recruits per year, and survival rate of recruits. Variables include natural mortality, fishing mortality, selectivity for the fishery at a given age, and total abundance. Initial numbers-at-age and recruitment can be user-defined with multiple independent parameters, or estimated based on a spawner-recruitment (S-R) function (or a combination of user-defined values and S-R function estimation). Fishing mortality can be user-defined, estimated as a free model parameter, or defined as a linear function of fishing effort. Actual catch numbers can be mimicked by continuously varying the fishing mortality parameter to match data [26].

Selectivity can be specified in several ways. A single age may be selected, one parameter can be assigned per age, or selectivity patterns can be based on logistic functions. Time steps occur on a yearly basis but the model can account for up to four time periods per year for increased accuracy when modeling seasonal fisheries. Migration between regions is an additional feature available in the population model. The modeler can choose up to three geographic locations with individual migration patterns. Geographic structure is not available in the model [26].

The population model feeds into the additional two sub-models. The observation model compares the population model estimates with observed values for fishery and survey data. Biomass estimates are expected to be proportional to survey abundance data. The statistical model is used as a framework from which to estimate stock dynamics. Log-likelihood functions are used to compare observed and expected val-
ues, with individual log-likelihood functions for different data sources and observation types [26]. Because the stock synthesis model allows for a wide variety of input data, it is useful in its ability to exhibit inconsistencies across different data types and illustrate limitations due to lack of available or consistent data [26].

1.1.3 Limitations of Stock Assessment Models

As mentioned previously, single-species management efforts (and therefore single-species modeling) have received increasing scrutiny in light of the rise of EBM, but stock assessment models have additional limitations beyond their lack of ability to model species interactions.

In many stock assessment models CPUE, a fisheries dependent metric, is used to inform natural abundance of species. While CPUE is often considered to be proportional to abundance in a modeling framework, examination of this relationship, when sufficient data is available, suggests that in many cases direct proportionality is not the correct relationship [12]. Thus the relationship between CPUE and abundance is a contentious topic in fisheries sciences, and the way it is estimated in many stock assessment models may not be true to life.

In theory, the relationship between Abundance and CPUE could take on a variety of forms, yet, as mentioned previously, it is most commonly assumed to be proportional in stock assessment models (center line in figure 1.1). In contrast, fisheries data sets most often indicate a hyperstable relationship (top line in figure 1.1) where fishermen can maintain catch past sustainable levels even when actual stock abundance is in rapid decline [12].

A more fundamental problem in attempting to estimate stock abundance from catch data is the fact that fisherman go where the fish are [12]. Fisherman themselves are a dynamic variable in fisheries modeling (although they are not always modeled as such) and will inevitably concentrate their efforts on areas of high stock density [12].
Therefore, using CPUE and other fisheries-dependent data can greatly overestimate actual population abundances.

In addition to the introduction of fishermen bias, landings and catch data are themselves imprecisely measured/reported and this introduces errors into stock assessment models at the start. Landings data are only as accurate as the fishermen or observers reporting them. Although this is a larger problem for global fisheries management than for domestic management in the US, catch data are not always indicative of total fishing mortality due to illegal, unreported, or unregulated fishing [20]. It is difficult to estimate true fishing mortality due to data inaccuracies and underreported kills.

Even with the limitations listed above, many stock assessment models succeed in closely replicating historical data. Yet, Hilborn and Walters [12] warn against assuming historical replication means good parameter estimation:

"... the ability of a model to fit past data says absolutely nothing about whether it will make correct policy predictions! It is quite possible to construct a model that fits
past data very well, but whose individual parameter values are so poorly determined that the parameters most important to policy are in fact very badly estimated.”

While it cannot automatically be assumed that all stock assessment models have poorly fit parameters (or the opposite, that all have well fitted parameters), for both modelers and those wishing to create management plans based on the models, precautions must be taken when interpreting the results of stock assessment outputs.

### 1.1.4 Atlantis Ecosystem Model

The Atlantis ecosystem model was developed by Beth Fulton at the Australian Commonwealth Scientific and Research Organization (CSIRO). The model incorporates physical, biological, and anthropogenic factors. Each section of ocean is separated into a 3-dimensional polygon of generally physically homogeneous features. Additionally, the polygon has a vertical depth structure, with one sediment layer at the bottom of the ocean and up to five water layers [7]. It uses nutrient cycling (nitrogen) to model biological activities for 60+ invertebrate and vertebrate groups [17]. Vertebrate species are further categorized by age structure. Some species are aggregated into functional groups while select commercially important species have individual output. Abundance at a given age class is dependent on movement, predation, fishing mortality, and additional linear and quadratic mortality terms [13].

Atlantis models use differential equations to step forward in half-day or full-day increments [17], although input and output is in the form of yearly biomass. These biomass estimates are obtained from stock assessment models for individual species. Large parameter files set the conditions for environmental, species-by-species, and human interactions. These parameters are manipulated by the user, and are adjusted so that the output matches actual data. Parameters can be year-specific so that model conditions match known historical conditions. During the calibration process, the modeler adjusts the most uncertain parameters. This gives insight into the sen-
sivities of those parameter values and what role those parameters may play in the ecosystem [13].

Calibration of Atlantis is a three-step process. The model is first run forward in time without fishing, and populations are expected to recover to historical levels of unfished biomasses. The unfished biomass values are based on 1950 biomass estimates. If the output range is within 0.5 - 1.5 times that of input, calibration continues to the next step. Next, different scenarios with varying degrees of fishing pressure are run through the model. If biomass response to fishing pressure is too severe or too robust (in comparison to historical knowledge of fishing pressure responses), productivity via recruitment is adjusted. Lastly, historical fishing pressure (1950s to 2000s) is used to see if the model can replicate historical biomass values. For this research, the California Current Atlantis Model (CCAM) output was used. CCAM experienced success with replication for 14 out of 18 groups with available historical data [13].

1.1.5 Limitations of the Atlantis Ecosystem Model

"...the accumulated uncertainty about ecological states and economic outcomes associated with any EBFM [ecosystem based fisheries management] procedure increases as the number and complexity of indices required by the procedure themselves increase" [20].

As stated above in the quote by Alan Longhurst, the errors and uncertainty of a single-species model are compounded in a multi-species model. Multi-species models are very complex (e.g. thousands of parameters estimating relationships between species, humans, and the environment) and at the same time a gross oversimplification of nature. Any given species may have tens to hundreds of linkages in its local community, but modelers have no way to accurately quantify or even detect all of these linkages and incorporate them into an ecosystem model [20]. Moreover, inclusion of such a large number of linkages per species is not (generally) advisable in a modeling
framework, as increasing complexity does not always lead to increase in performance (and may quickly lead to increase in error), as was discussed previously (i.e. [6]). This leaves the Atlantis modeler to estimate which linkages in the ecosystem are most worthy of inclusion and to find a balance between oversimplification and an overly complex model.

The majority of Atlantis outputs are in the form of functional groups created by the Atlantis modelers (via food web analysis and taxonomic similarities, Isaac Kaplan, pers. comm.), and so the validity of the functional grouping is dependent on the decisions of the modeler. Each regional Atlantis team has its own modelers to assess the given regional ecosystem. As a part of the research in this thesis, Atlantis functional groups are assessed via nonlinear models to see if the individual species comprising the groupings are capable of predicting each other with success (high correlation coefficients when comparing observed versus predicted values).

1.1.6 Nonlinear Modeling in the Biological Sciences

Modeling of a nonlinear system is less obvious than modeling a linear system because the time series of such a system can appear to be random. Furthermore, ecological data provide additional complications because they are relatively short (~several decades) and noisy and thus dynamic signals can be even harder to detect. One characteristic of a nonlinear system is that predictive power rapidly drops as one increases the length of time the model must predict into the future [32]. It is important to identify a nonlinear system as such, or analysis and policy decisions could be misguided. If a system is nonlinear instead of linear stochastic, it is possible (in principle) to devise a simple model explaining the behavior of the system [16].

To devise a model of a nonlinear system, it must first be identified as nonlinear. Hsieh et. al. [16] provide several methods for identification of nonlinearity. This research employs simplex projection and s-maps (see methods). These nonlinear
forecasting techniques employ Takens theorem [34] in an attempt to uncover the underlying system dynamics. Takens theorem states that using time-lagged coordinates as a forecasting tool preserve the underlying dynamics of the system [34]. Time-lagged coordinates involve moving all of the data points in a time series one year forward, so e.g. 1993 of the time-lagged time series is 1992 of the original time series. Lagged coordinates enable the modeler to obtain a shadow image of the system attractor. An attractor is described as the point, line, or general shape that a system tends towards over time. This trajectory is perfectly deterministic in the proper number of dimensions, but the modeler does not know how many dimensions are appropriate for the given data set [32]. For example, a time series of Bluefin Tuna may appear completely random because it is a one-dimensional picture of a system which in reality exists in more than one dimension [32]. In theory, if one can reconstruct the shape of the system attractor using Takens’ embedding theorem in the proper number of dimensions, a seemingly random time series can become predictable.

As a classic example, Figure 1.2 exhibits the Lorenz attractor [21] in X-Y-Z coordinates (σ=10, b=8/3, r=26). The driving equations are:

\[ \dot{x} = \sigma(y - x), \quad \dot{y} = r x - y - x z, \quad \dot{z} = xy - bz \]  

(1.1)

Although a one-dimensional graph of this three-dimensional system would appear completely random, the boundaries of movement as defined by the attractor are well defined in the proper number of dimensions. If this attractor represented the biomass of a species, its form and the number of dimensions in which it resides can help identify the number and identity of environmental or anthropogenic factors that direct its dynamics. Moreover, through this understanding, effects of environmental or anthropogenic forcings on the biomass can be predicted.
Figure 1.3 exhibits the Lorenz attractor built with lagged coordinates. Instead of graphing $X(t)$ versus $Z(t)$ and $Y(t)$, $X(t)$ is graphed against $X(t-6)$ and $X(t-12)$. The attractor shape is obviously distorted, but the essential behavior is preserved. The two wings of the Lorenz attractor are still clearly visible, and one can still estimate the system behavior. Further, the system can be modeled with no knowledge of the driving equations.

The aforementioned forecasting techniques have already been used on fisheries data sets, particularly for the California current ecosystem [8, 9, 14, 16]. These studies found that physical factors in a system can be modeled via linear models, but forecasting ability was greatly improved for biological fisheries data when nonlinear models were employed [14]. Nonlinear biological modeling will be an integral part of future fisheries research, both for scientists working to make accurate predictions and for policy makers who need to consider the effect of management actions on complex and often nonlinear ecosystems.
1.2 Objectives

This project analyzes fisheries models on several different levels of organization. The project can be separated into two main questions:

1) Are the raw catch data that form the basis of stock assessment and ecosystem models nonlinear? If so, is this nonlinearity conserved in the output of the stock assessment or Atlantis models?

2) Are the functional groups created by Atlantis modelers similar to the functionally coupled units identified with multivariate nonlinear analysis?

The rationale for these questions follows:

1. Using univariate nonlinear analysis, Glaser has found discrepancies in the percent of nonlinear data sets between landings data and stock assessment estimated biomass data [8]. Seven of 36 stock assessment data sets were found to have nonlinear signals, while 22 of 49 California Commercial Landings data sets were nonlinear. This
result is of interest because landings are used as raw data for stock assessment models. Nonlinear analysis was repeated for the California commercial landings data sets and west-coast stock assessment data sets for training purposes. Additionally, the same univariate analysis was performed on Atlantis output.

Because the Atlantis models have such large parameter files that are heavily manipulated by the modeler, signal conservation does not occur as data transfers from input to output. The complicated nature of Atlantis means that parameters are adjusted so that input matches output. This project explores the implications of this modeling procedure to see if the model is capturing the underlying dynamics of the ecosystem.

2. Functional groups in Atlantis are based on dietary or taxonomic similarities (Isaac Kaplan, pers. comm.) (e.g. large rockfish, midwater flatfish) and do not match with Functionally Coupled Units (FCUs) identified through the multivariate analysis. The multivariate analysis identifies species that follow the same attractor or are dynamically coupled in time but are not necessarily taxonomically similar.
CHAPTER 2

METHODS

2.1 Data

California commercial landings data, stock assessment output, and California Current Atlantis Model (CCAM) output were used as time series for analysis by nonlinear methods. Landings consist of yearly aggregated landings at the dock. The data for 50+ species are stored on the University of San Diego CAMEO server and were accessed from that location. A total of 49 landings time series were used, with 48 unique species (shrimp is separated into "bay" and "ocean" groups). Stock assessment data are also stored on the CAMEO server and time series for 36 individual species stocks were used. In several cases when server data were not adequate, data were acquired from the Pacific Fisheries Information Network (PacFIN) or the Southwest Fisheries Science Center (SWFSC). Stock assessment output consists of yearly biomass estimates.

For this project, yearly aggregated biomass across all age classes was utilized when available. For a select number of species, spawning stock biomass was used. Additionally, some species have biomass estimates for specific regions. When evaluating Atlantis functional groups, stock assessment output of the same type and region were used for each individual species that forms the functional group. One exception to this was for a single Atlantis functional group comprised of six species (the other functional groups tested in this analysis consist of two to three species). Because data of the same region were unavailable for all six species associated with this functional group, available data from neighboring regions were used. Results related to
this functional group therefore may be dissimilar to analysis performed using data from a single region.

CCAM data were obtained from Isaac Kaplan at the Northwest Fisheries Science Center. CCAM output is in the form of yearly age aggregated biomass estimates for both individual species and modeler determined functional groups. Thirteen individual species and 46 functional group time series were analyzed using the nonlinear forecasting model.

Landings and stock assessment time series were trimmed for each species individually in order to reflect a best estimate of the time period where the fishery was fully developed (S. Glaser, pers. comm.). CCAM time series run from 1900 to 2008, but fishing is activated in the model beginning in the year 1950 (Isaac Kaplan, pers. comm.). For this reason, CCAM time series were trimmed to the years 1950-2008.

Atlantis future projections were also obtained from Isaac Kaplan. Projections with status quo fishing were obtained for the years 2010-2060. Status quo is defined as continuation of current (2007) mortality and closure areas. Closures serve to regulate catch/fishing mortality while also preserving the ecosystem in the closure area by forbidding harmful fishing practices such as extensive bottom trawling [18]. Historical physical conditions (water flux, temperature) were used for the future projections. In the status quo scenario, the overwhelming majority of species experience growth from initial levels after 20 years, mainly due to rebuilding measures in the current fishery management plans [18].

2.2 Forecasting Model

The nonlinear forecasting models used for this project include simplex projection and s-maps, and are described in more detail below. Simplex projection is used to
find an optimal embedding dimension for a time series, and s-maps is used to detect nonlinearity in a time series.

Both simplex projection and s-maps have been pioneered by George Sugihara [32, 33] as a way of testing nonlinearity in biological systems, and are based on Takens’ theorem of lagged coordinates [34]. As discussed in the introduction, lagged coordinates can be used to obtain a shadow image of a system attractor. This is the technique used in univariate simplex projection.

In a lagged coordinates system, a data point of one species is plotted against past data points of that same species, where coordinate axes are x(t), x(t-1), etc. In essence, the past is used to predict the future. In simplex projection, half of the data set is used as a library set which the model is built on. The other half of the data set is the predictive set which is used to evaluate the accuracy of the models predictions [16]. The library and prediction sets may also include the same data points, in which case the model will automatically use cross-validation. For cross-validation, the predictee, along with any vectors containing the predictee, are removed from the prediction set. This option can be used for analyzing short time series, and for this reason all data in this research were analyzed via cross-validation.

Figure 2.1 is a conceptualized illustration of simplex projection with an embedding of two, looking one step into the future (two dimensional lagged space of X(t) and X(t-1)). \( \hat{Y}_{t+1} \) is the value to be predicted. Three library vectors (\( X_t \)) representing the three closest (euclidean distance) values, surround the previous year, \( Y_t \). These three nearest neighbors are used to make the prediction. When the library and prediction sets are the same, future values may be the closest neighbors, but a year will never be used in a prediction of itself. Each library point is weighted differently (represented by \( w_j \)) depending on its distance from the predictee [14]. The weighting of each
Figure 2-1 Illustration of simplex projection for one step forward in time [14]

\[ \hat{Y}_{t+1} = \sum_{j=0}^{E} w_j X_t(j) \]  

(2.1)

neighbor is governed by equation 2.1. The number of library points used to predict the future depends on the dimensionality, \( E \), of the model.

\( E \) corresponds to the number of time lags used in the model, which can be represented by separate coordinate axes. Guided by previously completed analysis, \( E \) is given values between 1 and 10 [9]. The number of library points (nearest neighbors) used for prediction is \( E+1 \), as \( E+1 \) is the smallest number of neighbors able to surround a predictee in \( E \)-dimensional space. The model with the best predictive accuracy and lowest error is then selected and the corresponding \( E \) value is recorded. Simplex projection output provides error in terms of both root mean square error (RMSE) and mean absolute error (MAE), but past research conducted using simplex projection has favored MAE and this was continued for consistency [8, 9].
After E has been determined, the degree of nonlinearity of the system can be evaluated using s-maps. S-maps is short for sequentially locally weighted global linear maps. S-maps again employs a library set of nearest neighbors, but unlike simplex projection, s-maps does not selectively remove any of the library points. Instead, library points are weighted differently depending on their proximity to the predictee.

The embedding of a time series from simplex projection is represented by the vectors:

\[ x_t \in \mathbb{R}^{E+1} \]

(2.2)

where \( x_t(0) = 1 \) is the constant term in the solution of eq. 2.5. This serves the purpose of correcting for target variables that have not been standardized to a mean of zero (Hao Ye, pers. comm.).

Stepping forward in time through the prediction set yields:

\[ Y_{t+T_p}(1) = Y(t) \]

(2.3)

where \( T_p \) is a time step forward (set to one) and the forecast for \( Y(t) \) is:

\[ \hat{Y}_t = \sum_{j=0}^{m} C_t(j)x_t(j) \]

(2.4)

where \( C \) is a constant, calculated as:

\[ B = AC \]

(2.5)

\[ B_i = w(\| x_i - x_t \|)Y_i \]

(2.6)

\[ A_{ij} = w(\| x_i - x_t \|)x_{i}(j) \]

(2.7)
Subscript ”i” is a library set. Finally, the weighting is given by:

\[ w(d) = e^{-\frac{d\theta}{\bar{d}}} \]  \hspace{1cm} (2.8)

where \( d \) is the euclidean distance to the predictee, \( \bar{d} \) is a scaling factor (average distance between neighbors), and \( \theta \) is the variable local weighting factor. For \( \theta \) of zero, the system is linear and all points are weighted the same. As \( \theta \) increases, local points become more heavily weighted [33].

Figure 2.2 illustrates an s-map for sample linear and nonlinear data sets. In this example, the embedding dimension \( E \) equals two. The lower squares (left red and right blue) are representations of \( w(d) \). For the left graph, theta equals zero and so the geometric shape is completely flat. Each of the library vectors (blue points surrounding the red predictee) contribute equally to the prediction. For the right graph, theta is greater than zero. The library vectors closest to the predictee contribute more heavily to the forecast. As a result, the shape is three dimensional and cone-like. The higher the elevation of a library coordinate on the three-dimensional map, the more heavily it is weighted and the greater the underlying nonlinearity in the data [14]. The degree of nonlinearity is dependent on the value of theta (see equations above).

For this project, nonlinearity of the model input (landings) was compared with nonlinearity of the model output for stock assessment models and the Atlantis ecosystem model. This was done by running landings, stock assessment, and Atlantis time series through the s-maps model and determining how many time series of each data type exhibited nonlinearity.

For all of the data used in this analysis, time lag spacing (tau) was set to one. For example, if an \( E \) of three is chosen, the model employs \( x(t), x(t-1), \) and \( x(t-2) \) to predict \( x(t+1) \). If a tau of two is used for an \( E \) of three, the model employs \( x(t), x(t), \) and \( x(t-2) \) to predict \( x(t+1) \).
Figure 2-2 S-map comparing linear (left) and nonlinear (right) results [14]. The bottom two planes are representations of the weighting function $w(d)$.

$x(t-2)$, and $x(t-4)$ to make the prediction. To test modeling ability with different time lag spacings a subset of 20 landings time series were chosen, where ten of the chosen time series displayed very erratic, rapidly changing values from year to year, and ten time series had smoother, more constant or gently changing values from year to year. Tau of two, three, and four were tested. The taus were compared with a tau of one in terms of maximum achieved rho in s-maps.

To develop a multivariate approach from these methods, the library vectors represent different fish species instead of time-lagged coordinates. In this way, the technique can identify functionally coupled units, FCUs [2]. These FCUs are defined as groupings of species that are highly cross- and co-predictable and follow the same attractor. These two types of predictions will be described in the following paragraphs. Here, this multivariate analysis is used to analyze the relationships of the species in predefined Atlantis functional groups. California commercial landings and stock assessment data for species of the Atlantis functional groups are run through the multivariate analysis to see if they are members of FCUs.
The two previously mentioned prediction types, cross-prediction and co-prediction, were used to analyze the modeler-defined [13] Atlantis functional groups using both landings data and stock assessment data. Every species in a functional group was tested via pair-wise predictions with every other species in that group. Co-prediction works the same way as univariate simplex projection, but uses the time series of one species X as the library file and the time series of another species Y as the prediction file. In this way, one can test whether or not the X and Y time series are governed by similar dynamics and originate from similar attractors (Hao Ye, pers. comm.).

Cross-prediction employs multivariate simplex projection. This differs from univariate simplex projection in that the user must specify, from a matrix, which columns to use for prediction (in other words, E must be predefined). These columns could be time series of multiple species, or time lags of the same species’ time series. For the pair-wise cross-prediction methods, the columns represent time lags of a single species. Cross-prediction searches for a time-dependent influence of species X on species Y. For example, X(t), X(t-1), and X(t-2) are used to predict the target variable Y(t), where X(t-1) and X(t-2) are -1 and -2 time lags of the X(t) time series. If cross-prediction results achieve good predictability, then the two species have a time-dependent influence on each other. Cross-prediction does not determine the nature of this relationship, which could be predator-prey interactions or myriad other factors (Hao Ye, pers. comm.).

California region landings time series for all 22 species of the Atlantis functional groups were analyzed using the nonlinear forecasting model and a search function was used that allowed the model to create optimal groupings (highest predictability and lowest error) of species for a given E. The search function yields groupings of species with time-dependent relationships, (i.e. the same methods as cross-prediction are employed, but the matrix contains time series of many different species) (Hao Ye,
pers. comm.). Such groupings render possible FCUs. Optimal combinations were tested for an embedding dimension of three species predicting the target species. Up to three time lags of each time series were allowed, and the top 100 combinations for each embedding dimension were displayed as output. Out of those 100 embeddings, the top three most frequently appearing species were recorded for each of 22 target species.

Scaling issues involved with using time series of multiple species are addressed by using exclusively standardized or standardized first differenced data. First differenced data involves subtracting year X of datum from year X+1. For example, subtracting the biomass associated with 1931 from the biomass associated with 1932 would yield a first differenced data point for 1932. The data is then standardized to a mean of zero and standard deviation of one.

Simplex projection and s-maps are available as executables on the UCSD CAMEO server under the programs lnlp (univariate) and block lnlp (multivariate). The programs were written in C++ by Hao Ye, University of California San Diego, Scripps Institute of Oceanography. For this project, the modeling process was automated for multiple data sets via Matlab wrappers (written by Hao Ye, Chih-Hao Hsieh, and Sarah Glaser).

### 2.3 Statistical Methods

Nonlinear model output provides a correlation coefficient, rho (observed values versus predicted model values), along with MAE and RMSE, for each value of E. The correlation coefficient determines the strength of the linear relationship between random variables X and Y, and is defined as the covariance of X and Y over the product of their standard deviations [4]. It can range in value from negative one to one.
Rho is described as the predictability of the model, where higher rho indicates that more predicted values share the same sign as observed values. Negative rho indicates poor model fit (S. Glaser & H. Ye, pers. comm.). As mentioned previously, MAE was favored over RMSE as a measure of error because it is less sensitive to outliers. For simplex projection, best E was determined via a combination of lowest MAE, highest rho, highest N, and lowest RMSE [9]. These four components are listed in descending order of importance.

P-values for rho were calculated as a preliminary test of data significance using Microsoft Excel. Time series with rho P-values ≥ 0.05 may be too short or too noisy to perform useful analysis.

To test nonlinearity, delta MAE and delta rho were calculated for each time series. Delta MAE is the difference between MAE at theta zero (linearity) and minimum MAE (from the selection of output thetas). Similarly, delta rho is the difference between rho at theta zero and maximum rho (maximum nonlinearity). P-values for delta rho were calculated in Microsoft Excel, while p-values for delta MAE were obtained by performing a randomization test [8]. This procedure was automated using Matlab wrappers obtained from Sarah Glaser. The results are then the degree of nonlinearity for the time series as represented by Delta MAE and Delta Rho including tests of significance for each.
CHAPTER 3
RESULTS

Results are presented for standardized first differenced data. Results for standardized data can be found in the appendix. Data is presented in 6 categories:

(1) Landings  California commercial landings time series for individual species
(2) Stock Assessment  Stock assessment biomass outputs for individual species
(3) Atlantis - Atlantis biomass outputs for individual species, years 1950-2008
(4) Atlantis FG  Atlantis biomass outputs for modeler-defined functional groups, years 1950-2008
(5) Atlantis Future  Atlantis biomass outputs for individual species, future projections years 2010-2060
(6) Atlantis Future FG  Atlantis biomass outputs for modeler-defined functional groups, future projections years 2010-2060

Data was used for both univariate and multivariate analyses, where univariate is the case of a time series used to predict itself, and multivariate is the use of multiple species to predict a target species. Results of the univariate and multivariate analyses are presented in the following two subsections.

3.1 Univariate Analyses

Table 3.1 displays the percent of nonlinear data sets (number of time series) for each of the six data types. Here, nonlinearity is defined by significant p value ($\leq 0.05$) for delta MAE, where delta MAE is the difference in error between results with \theta
Table 3.1. Presence of nonlinearity. The first column indicates whether the data type is raw data or manipulated model output.

<table>
<thead>
<tr>
<th>Data Type</th>
<th># Data Sets (n)</th>
<th>% Nonlinear</th>
</tr>
</thead>
<tbody>
<tr>
<td>Raw Data</td>
<td>Landings</td>
<td>49</td>
</tr>
<tr>
<td>Model Output</td>
<td>Stock Assessment</td>
<td>36</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis</td>
<td>13</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis FG</td>
<td>46</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis Future</td>
<td>13</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis Future FG</td>
<td>47</td>
</tr>
</tbody>
</table>

Table 3.2. Average maximum rho for s-maps results. The first column indicates whether the data type is raw data or manipulated model output.

<table>
<thead>
<tr>
<th>Data Type</th>
<th># Data Sets (n)</th>
<th>Average Rho</th>
</tr>
</thead>
<tbody>
<tr>
<td>Raw Data</td>
<td>Landings</td>
<td>0.277±0.180</td>
</tr>
<tr>
<td>Model Output</td>
<td>Stock Assessment</td>
<td>0.699±0.217</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis</td>
<td>0.867±0.152</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis FG</td>
<td>0.865±0.147</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis Future</td>
<td>0.846±0.199</td>
</tr>
<tr>
<td>Model Output</td>
<td>Atlantis FG Future</td>
<td>0.812±0.263</td>
</tr>
</tbody>
</table>

of zero and results with theta unequal to zero. Theta is the s-maps tuning parameter used to determine degree of nonlinearity (see methods). Across all the data types, standardized data has a lower percentage of nonlinear time series (see appendix). First differenced data has the highest nonlinearity for landings and Atlantis future projections, and lowest nonlinearity for the Atlantis functional groups, years 1950-2008.
Table 3.3. Average Embedding Dimension (E) in Different Data Types

<table>
<thead>
<tr>
<th>Data Type</th>
<th># Data Sets</th>
<th>Average E</th>
</tr>
</thead>
<tbody>
<tr>
<td>Landings</td>
<td>49</td>
<td>3.8±2.5</td>
</tr>
<tr>
<td>Stock Assessment</td>
<td>36</td>
<td>4.7±2.6</td>
</tr>
<tr>
<td>Atlantis</td>
<td>13</td>
<td>4.6±2.6</td>
</tr>
<tr>
<td>Atlantis FG</td>
<td>46</td>
<td>5.0±2.6</td>
</tr>
<tr>
<td>Atlantis Future</td>
<td>13</td>
<td>5.1±3.3</td>
</tr>
<tr>
<td>Atlantis FG Future</td>
<td>47</td>
<td>5.4±2.9</td>
</tr>
</tbody>
</table>

Table 3.4. Number of data sets with significant improvement in maximum rho over Tau 1 maximum rho, n=10.

<table>
<thead>
<tr>
<th>Tau Smooth</th>
<th>Erratic</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>3/10</td>
</tr>
<tr>
<td>3</td>
<td>2/10</td>
</tr>
<tr>
<td>4</td>
<td>2/10</td>
</tr>
</tbody>
</table>

Table 3.2 displays average maximum rho from s-maps results for the six data types. Standardized data consistently have higher predictability than first differenced data (see appendix), and model outputs have higher predictability than raw data.

Table 3.3 displays average embedding dimension (E) for the six data types. The embedding dimension is the number of time series (either independent species or time lags of the same species) used to predict the target species. Embedding dimensions were similar across data types, and do not appear to increase for functional group output versus individual species output.

Results of the time lag spacing analysis are displayed in Table 3.4. Time lag spacing (tau) of two, three, and four were tested on a subset of 20 landings time
Figure 3-1 Example of an "erratic" time series, albacore landings. The x-axis is time in years and the y-axis is landed pounds of fish.

Figure 3-2 Example of a "smooth" time series, cabezon landings. The x-axis is time in years and the y-axis is landed pounds of fish.
series, where ten time series are smooth and ten erratic. Tau of two, three, and four were compared with tau of one in terms of maximum achieved rho in s-maps results. Significant difference in rho is described as difference with a p-value p $\leq 0.05$.

For smooth, first differenced data with tau of two, three data sets experienced significant improvement in maximum rho over results for tau of one. Generally, smooth time series experienced more improvement than erratic time series. The terms smooth and erratic are subjective for such data sets as fisheries landings, but an attempt was made to classify data sets as one or the other based on yearly fluctuations in landings. Figures 3.1 and 3.2 are examples of smooth and erratic time series. The albacore time series experiences large fluctuations from year to year, while the cabezon time series has smaller yearly fluctuations.

### 3.2 Multivariate Analyses

#### 3.2.1 Functional Group Testing

Results are presented for both cross- and co-prediction. Cross-prediction seeks to find time-dependent coupling between species, while co-prediction looks for overall similarity in dynamics between species that would indicate that they come from similar attractors. Co-prediction does not test for time-dependent coupling.

The Atlantis functional groups are comprised of the following species, with Atlantis model abbreviations listed before the species. Functional groups selected for testing are comprised exclusively of fish, and are a small subset of the total number of Atlantis functional groups. Atlantis contains functional groups of whales, sharks, plankton, birds, and other marine animals. Fish groups were selected to allow for comparison with landings and stock assessment data.

1. Small flatfish (FDF): English Sole, Starry Flounder
2. Deep large rockfish (**FDO**): Darkblotched Rockfish, Blackgill Rockfish, Short-spine Thornyhead

3. Midwater rockfish (**FDS**): Pacific Ocean Perch, Boccaccio, Chilipepper Rockfish, Vermillion Rockfish, Widow Rockfish, Yellowtail Rockfish

4. Large planktivorous fish (**FPL**): Pacific Mackerel, Jack Mackerel

5. Small planktivorous fish (**FPS**): Northern Anchovy, Pacific Sardine

6. Shallow large rockfish (**SHR**): Black Rockfish, Kelp Greenling

7. Large demersal predators (**FVS**): Cabezon, Lingcod

8. Large flatfish (**FVD**): Petrale Sole, Arrowtooth Flounder, Pacific Halibut

Nonlinear time series methods of pairwise cross- and co-prediction were used to examine whether species associated with user-defined functional groups (outlined above) exhibit evidence for strong coupling. Both landings and stock assessment data were used. Results of the pairwise cross- and co-prediction testing using simplex are presented below.

Optimal E varied for each pair-wise test in co-prediction and was selected out of E between one and ten (as with the univariate analysis). The cross-prediction model requires that E be selected prior to running the model, so E of one through four were tested for each pair-wise relationship in a functional group and results across all E were averaged. E of one indicates that cross-prediction uses X(t) to predict Y(t), while E of four indicates that cross-prediction used X(t), X(t-1), X(t-2), and X(t-3) to predict Y(t). Rhos are then averaged across all pair-wise results for each functional group.

Table 3.5 exhibits co- and cross- prediction results for eleven functional groups. Eight functional groups were created out of landings data and three were created out of stock assessment data, and those created out of stock assessment data have consistently higher rho than the landings functional groups of the same species. Stan-
Table 3.5. Average rho for both co- and cross-prediction. The bottom row calculates the average of all co-prediction results versus the average of all cross-prediction results.

<table>
<thead>
<tr>
<th>Data Used</th>
<th>Functional Group</th>
<th># Species</th>
<th>Average Rho Co-prediction</th>
<th>Average Rho Cross-prediction</th>
</tr>
</thead>
<tbody>
<tr>
<td>Landings</td>
<td>FDF</td>
<td>2</td>
<td>0.181±0.073</td>
<td>-0.035±0.036</td>
</tr>
<tr>
<td>Landings</td>
<td>FDO</td>
<td>3</td>
<td>0.264±0.120</td>
<td>-0.169±0.093</td>
</tr>
<tr>
<td>Stock Assessment</td>
<td>FDO</td>
<td>3</td>
<td>0.628±0.071</td>
<td>0.795±0.071</td>
</tr>
<tr>
<td>Landings</td>
<td>FDS</td>
<td>6</td>
<td>0.315±0.197</td>
<td>-0.159±0.366</td>
</tr>
<tr>
<td>Landings</td>
<td>FPL</td>
<td>2</td>
<td>0.617±0.259</td>
<td>0.083±0.064</td>
</tr>
<tr>
<td>Landings</td>
<td>FPS</td>
<td>2</td>
<td>0.202±0.188</td>
<td>-0.041±0.098</td>
</tr>
<tr>
<td>Landings</td>
<td>SHR</td>
<td>2</td>
<td>0.066±0.241</td>
<td>-0.142±0.072</td>
</tr>
<tr>
<td>Stock Assessment</td>
<td>SHR</td>
<td>2</td>
<td>0.708±0.084</td>
<td>0.566±0.250</td>
</tr>
<tr>
<td>Landings</td>
<td>FVS</td>
<td>2</td>
<td>0.287±0.054</td>
<td>-0.119±0.085</td>
</tr>
<tr>
<td>Stock Assessment</td>
<td>FVS</td>
<td>2</td>
<td>0.504±0.283</td>
<td>-0.003±0.117</td>
</tr>
<tr>
<td>Landings</td>
<td>FVD</td>
<td>3</td>
<td>0.346±0.099</td>
<td>-0.032±0.095</td>
</tr>
<tr>
<td>Average</td>
<td></td>
<td></td>
<td>0.374±0.209</td>
<td>0.068±0.316</td>
</tr>
</tbody>
</table>

Standardized data has consistently higher rho than standardized first differenced data (standardized data available from author).

For cross-prediction, nine of 62 (15%) standardized first differenced and 42 of 62 (68%) standardized data sets had significant rhos (p < 0.05). This indicates that there is excessive noise in the data and/or the species being tested together result in a poor model. In order to test species relationships, additional raw data sources should be used. For many functional groups, useable time overlap of species rendered very short data sets (less than 30 years) and this inevitably contributed to poor predictability.

For co-prediction, 31 of 62 (50%) standardized first differenced and 46 of 62 (65%) standardized data sets had significant rho values. Again, this is indicative of the amount of noise in the data and/or poor modeling ability of tested species.
3.2.2 FCU Search Results

Search function results are presented for E=3, standardized first differenced data. For the search function, E=3 implies that the model matched three species with a given target species. The results for standardized data are available upon request, as are results for E=4. In table 3.6, the target species is in the first column, with the top three most frequently occurring species in the following columns. If a species name is followed by (t-1), etc, then a time lag of that species time series was used. The percent column yields how many times a given species occurred out of the top 100 search results.

Groundfish appear more frequently as predictors than other species, particularly widow rockfish and yellowtail rockfish. Both of these time series display a large spike 2-4 standard deviations from the mean during the year 1982/1983. Sensitivity testing was performed to see if the frequent occurrence of widow rockfish was due to the spike in the time series. The value of the data point composing the spike was changed to the mean of the data set, and the search function was run again for a select number of species with high occurrence of widow rockfish. Pacific mackerel, lingcod, English sole, shortspine thornyhead, and halibut were used as target species for the sensitivity testing.

Sensitivity testing results for standardized first differenced data can be found in table 3.7. Two of five target species retained widow rockfish as one of their top three frequently occurring species.

The search function was also used on Stock assessment data, both standardized and standardized first differenced data. This analysis was performed as an additional exploratory exercise. The motivation was to test the functional groups using linearized stock assessment data, as this is the data that Atlantis uses as input. Stock assessment biomass output for California was unavailable for cabezon, halibut, anchovy,
vermillion rockfish, and jack mackerel, so the search function used 17 species instead of the full set of 22 species used for the landings data. For this reason, these results are excluded from the formal analysis. There was little agreement between groupings created with landings data and groupings created with stock assessment data. The maximum number of matches between landings and stock assessment groupings for any given target species was two species out of the top five most frequently occurring. Neither the stock assessment search results or landings search results matched Atlantis functional groups.
Table 3.6. Nonlinear search results for optimal species groupings, listing the top three most frequently occurring species for each target species.

<table>
<thead>
<tr>
<th>Target</th>
<th>Species 1</th>
<th>%&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Species 2</th>
<th>%&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Species 3</th>
<th>%&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Average Rho</th>
<th>Average N&lt;sup&gt;b&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pacific Mackerel</td>
<td>Widow RF</td>
<td>39</td>
<td>Black RF(t-3)</td>
<td>30</td>
<td>Arrowtooth(t-3)</td>
<td>22</td>
<td>0.58±0.06</td>
<td>18.80±4.33</td>
</tr>
<tr>
<td>Jack Mackerel</td>
<td>Yellowtail RF</td>
<td>37</td>
<td>Kelp Greenling</td>
<td>20</td>
<td>Blackgill RF(t-1)</td>
<td>17</td>
<td>0.55±0.04</td>
<td>25.35±9.89</td>
</tr>
<tr>
<td>Anchovy</td>
<td>Blackgill RF</td>
<td>35</td>
<td>Bocaccio(t-3)</td>
<td>29</td>
<td>Petrale sole</td>
<td>18</td>
<td>0.63±0.02</td>
<td>30.91±3.31</td>
</tr>
<tr>
<td>Sardine</td>
<td>Yellowtail RF(t-1)</td>
<td>59</td>
<td>Yellowtail RF(t-2)</td>
<td>28</td>
<td>Widow RF(t-2)</td>
<td>18</td>
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<td>20.85±6.34</td>
</tr>
<tr>
<td>Black RF</td>
<td>Black RF</td>
<td>100</td>
<td>Arrowtooth(t-2)</td>
<td>40</td>
<td>Arrowtooth (t-3)</td>
<td>25</td>
<td>0.70±0.03</td>
<td>21.64±0.81</td>
</tr>
<tr>
<td>Kelp greenling</td>
<td>Cabezon(t-2)</td>
<td>99</td>
<td>Starry flounder</td>
<td>22</td>
<td>Jack Mackerel</td>
<td>20</td>
<td>0.79±0.01</td>
<td>22.90±0.76</td>
</tr>
<tr>
<td>Cabezon</td>
<td>Kelp greenling(t-1)</td>
<td>75</td>
<td>Arrowtooth(t-1)</td>
<td>31</td>
<td>Black RF</td>
<td>27</td>
<td>0.72±0.04</td>
<td>23.40±3.77</td>
</tr>
<tr>
<td>Lingcod</td>
<td>Yellowtail RF(t-3)</td>
<td>87</td>
<td>Widow RF</td>
<td>35</td>
<td>Pacific Mackerel</td>
<td>17</td>
<td>0.70±0.04</td>
<td>17.86±3.62</td>
</tr>
<tr>
<td>Darkblotted RF</td>
<td>Darkblotted RF</td>
<td>48</td>
<td>Arrowtooth(t-3)</td>
<td>46</td>
<td>Starry flounder</td>
<td>35</td>
<td>0.55±0.03</td>
<td>25.23±6.24</td>
</tr>
<tr>
<td>Blackgill RF</td>
<td>Petrale Sole</td>
<td>60</td>
<td>Kelp greenling</td>
<td>19</td>
<td>Yellowtail RF(t-1)</td>
<td>19</td>
<td>0.68±0.04</td>
<td>22.86±4.60</td>
</tr>
<tr>
<td>Shortspine thornyhead</td>
<td>Starry flounder</td>
<td>35</td>
<td>Widow RF</td>
<td>30</td>
<td>Shortspine(t-3)</td>
<td>29</td>
<td>0.61±0.04</td>
<td>20.44±3.69</td>
</tr>
<tr>
<td>Halibut</td>
<td>Halibut</td>
<td>26</td>
<td>Darkblotted RF</td>
<td>20</td>
<td>Widow RF</td>
<td>20</td>
<td>0.51±0.04</td>
<td>24.56±5.04</td>
</tr>
</tbody>
</table>

<sup>a</sup> Percentage values rounded to one decimal place.

<sup>b</sup> Average values rounded to one decimal place.
<table>
<thead>
<tr>
<th>Target</th>
<th>Species 1</th>
<th>Species 2</th>
<th>Species 3</th>
<th>%&lt;sup&gt;a&lt;/sup&gt;</th>
<th>%&lt;sup&gt;a&lt;/sup&gt;</th>
<th>%&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Average Rho</th>
<th>Average N&lt;sup&gt;b&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Petrale Sole</td>
<td>Black RF(t-3)</td>
<td>Darkblotched RF</td>
<td>Chilipepper</td>
<td>32</td>
<td>19</td>
<td>16</td>
<td>0.58±0.04</td>
<td>28.38±6.57</td>
</tr>
<tr>
<td>Arrowtooth flounder</td>
<td>Shortspine(t-3)</td>
<td>Shortspine(t-3)</td>
<td>Starry</td>
<td>46</td>
<td>27</td>
<td>21</td>
<td>0.61±0.05</td>
<td>21.63±3.07</td>
</tr>
<tr>
<td>Starry Flounder</td>
<td>Chilipepper RF</td>
<td>Petrale sole(t-1)</td>
<td>Blackgill</td>
<td>36</td>
<td>24</td>
<td>14</td>
<td>0.65±0.03</td>
<td>27.86±6.30</td>
</tr>
<tr>
<td>English Sole</td>
<td>Shortspine(t-2)</td>
<td>Widow RF</td>
<td>Vermillion(t-3)</td>
<td>38</td>
<td>30</td>
<td>19</td>
<td>0.61±0.04</td>
<td>25.22±6.89</td>
</tr>
<tr>
<td>Pacific Ocean Perch</td>
<td>Blackgill(t-2)</td>
<td>Lingod(t-3)</td>
<td>Black RF</td>
<td>31</td>
<td>24</td>
<td>19</td>
<td>0.66±0.04</td>
<td>27.63±6.13</td>
</tr>
<tr>
<td>Widow RF</td>
<td>Darkblotched</td>
<td>Yellowtail RF(t-1)</td>
<td>Kelp Greenling(t-3)</td>
<td>97</td>
<td>57</td>
<td>23</td>
<td>0.73±0.02</td>
<td>13.35±0.89</td>
</tr>
<tr>
<td>Yellowtail RF</td>
<td>Yellowtail</td>
<td>Arrowtooth flounder</td>
<td>Widow RF</td>
<td>54</td>
<td>45</td>
<td>21</td>
<td>0.62±0.02</td>
<td>20.48±2.41</td>
</tr>
<tr>
<td>Bocaccio</td>
<td>Starry(t-2)</td>
<td>Halibut(t-3)</td>
<td>Kelp Greenling</td>
<td>25</td>
<td>21</td>
<td>20</td>
<td>0.59±0.05</td>
<td>25.17±6.08</td>
</tr>
<tr>
<td>Chilipepper RF</td>
<td>Blackgill(t-2)</td>
<td>Yellowtail RF</td>
<td>Kelp Greenling</td>
<td>77</td>
<td>32</td>
<td>14</td>
<td>0.59±0.03</td>
<td>24.99±6.03</td>
</tr>
<tr>
<td>Vermillion RF</td>
<td>Vermillion RF</td>
<td>Blackgill RF(t-3)</td>
<td>Darkblotched(t-3)</td>
<td>64</td>
<td>32</td>
<td>21</td>
<td>0.72±0.03</td>
<td>23.97±1.02</td>
</tr>
</tbody>
</table>

<sup>a</sup>The percent columns indicate how many times each species appeared out of the top 100 search results for a given target species.

<sup>b</sup>Average N indicates average length of time series used for prediction.
Table 3.7. Results for sensitivity testing of widow rockfish. A spike in the widow rockfish time series was averaged out and the nonlinear search function was rerun. Two of five tested species retained widow rockfish in their top three most frequently occurring species results.

<table>
<thead>
<tr>
<th>Target</th>
<th>Species 1</th>
<th>%a</th>
<th>Species 2</th>
<th>%a</th>
<th>Species 3</th>
<th>%a</th>
<th>Average Rho</th>
<th>Average N</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pacific mackerel</td>
<td>Widow RF</td>
<td>44</td>
<td>Black RF(t-3)</td>
<td>28</td>
<td>Yellowtail RF(t-2)</td>
<td>19</td>
<td>0.58±0.06</td>
<td>18.23±4.05</td>
</tr>
<tr>
<td>Lingcod</td>
<td>Yellowtail RF(t-3)</td>
<td>85</td>
<td>Widow RF</td>
<td>39</td>
<td>Pacific Mackerel</td>
<td>17</td>
<td>0.70±0.04</td>
<td>17.54±3.62</td>
</tr>
<tr>
<td>English sole</td>
<td>Vermillion RF(t-3)</td>
<td>23</td>
<td>Shortspine(t-2)</td>
<td>22</td>
<td>Bocaccio</td>
<td>18</td>
<td>0.60±0.04</td>
<td>26.83±6.21</td>
</tr>
<tr>
<td>Shortspine thornyhead</td>
<td>Starry flounder</td>
<td>40</td>
<td>Yellowtail RF(t-2)</td>
<td>22</td>
<td>Shortspine(t-3)</td>
<td>21</td>
<td>0.61±0.04</td>
<td>20.99±3.51</td>
</tr>
<tr>
<td>Halibut</td>
<td>Halibut</td>
<td>26</td>
<td>Darkblotched RF</td>
<td>21</td>
<td>Chilipepper RF(t-3)</td>
<td>17</td>
<td>0.52±0.04</td>
<td>24.37±5.21</td>
</tr>
</tbody>
</table>

aThe percent columns indicate how many times each species appeared out of the top 100 search results for a given target species.

bAverage N indicates average length of time series used for prediction.
CHAPTER 4
DISCUSSION

4.1 Univariate Analyses

Although results are available for both standardized and standardized first differenced data, first differenced results are preferred over standardized results because standardized data is sensitive to linear trends in the time series [9]. This is illustrated by the higher predictability observed in standardized data across all data types. Investigating standardized results alone can lead to overconfidence in forecasting abilities or strength of relationships between species, as the high predictability could simply be tracking linear trends in the time series of uncorrelated species.

Univariate analysis was performed on landings, stock assessment, and Atlantis data to determine if nonlinearity and predictability are consistent across these different data types. In addition, because both Atlantis and stock assessment models rely on landings and other raw data as input, analyses help distinguish whether key features of this data are preserved in model output.

Landings data has a higher percentage of nonlinear time series and lower predictability (rho) than both stock assessment and Atlantis data. This indicates that the models estimation processes alter the raw data signals. Some parameters of both the stock assessment and Atlantis models are inevitably estimated better than others, and each estimation adds additional errors. Stock assessment models also employ modified logistics equations [26] to calculate stock abundances, and the equations themselves are estimations of the dynamics of natural populations. With myriad es-
timations, these fisheries models are filtering out nonlinearity and uncertainty, and driving the system towards linearity and higher predictability.

Roughly speaking, the models use nonlinear data with low predictability as input and output linear results with high predictability. Because of differences in both predictability and nonlinearity between raw landings data and model output, policy makers should use caution when employing stock assessment or Atlantis output for quota estimation or other management purposes. Because the model output is linearized, the models may be underestimating natural variation in the data. Such underestimation can then lead to overconfidence in forecasting ability because the system is assumed to be more well behaved than it actually is.

Some nonlinear systems have the characteristic of exponential divergence of nearby trajectories [31] which means that neighboring starting points can have completely different trajectories when the system moves forward in time. In terms of model accuracy, this implies that if parameter estimation slightly diverges from the true relationship being modeled, the end results (model output) can be completely different from what actually occurs in nature. The fisheries models employ some nonlinear equations, and this principle could be applied to the Atlantis future projections, where there is no opportunity to check model output with historical records.

Atlantis future projections for the years 2010-2060 had higher occurrence of nonlinear time series than Atlantis historical runs for the years 1950-2008. Future and historical Atlantis data have the same physical parameters, but Atlantis historical output has year-specific catch rates and closure areas, while Atlantis future projections have a constant mortality rate and constant closure areas [18]. Atlantis historical output is more reliable in that it contains yearly input of actual catch and closure information. Modelers also have the additional ability to calibrate parameters using known historical information. In this way, the modeler is able to set more detailed
parameter values for the Atlantis historical projections than Atlantis future projections. Future projections cannot be checked for error because there are no base values with which to check them against, so errors are allowed to compound after each time step. In this case, it is likely that the compounding error leads to nonlinear signals in model output.

A small number (less than 10) of fish species had individual outputs for two or more of the three data types (landings, stock assessment, and Atlantis data). There was no consistency among this small sample set with regards to nonlinearity across multiple data types. Six species retained their linear/nonlinear status in Atlantis and stock assessments as was observed in their raw form. There was no consistency with regards to species type exhibiting this trend. Species of rays, flounder, rockfish, and tuna were included in the subset of six species retaining linearity/nonlinearity. Three species switched their linear/nonlinear status found in model output. While the sample set is too small to make strong conclusions, such inconsistencies are likely due to slight differences in methodologies associated with species specific stock assessment models. This issue is an obvious avenue for further exploration, and data sets with more overlap between species are required for a complete analysis.

### 4.2 Multivariate Analyses

Three different model approaches were used to test whether species included in Atlantis functional groups exhibit evidence of dynamic similarity using methods of nonlinear time series analysis. Co- and cross- prediction were used to test the pairwise relationships between all of the members of a functional group. The nonlinear search function was used to determine original species groupings for 22 different target species.
First differenced cross-prediction data yielded poorer predictability than first differenced co-prediction data. Poor cross-prediction results (average rho = \(0.068 \pm 0.316\)) suggest that the species being tested together do not have a time-dependent relationship, or that the data were too noisy to use in the analysis. Nine of 62 tested pairings had significant rhos (\(p \leq 0.05\)). To test whether the poor predictive ability is due to noise in the data or poor species pairings, longer time series are required. Different types of raw data could also be tested other than landings, such as research abundance surveys or CPUE. These data types are numerous enough to use as a comparison, but for this particular study, species overlap was not large enough to employ these data sets. Recent investigations [8] have demonstrated that these types of raw/input data do have different dynamical characteristics and it is therefore possible that fisheries-independent measures of species populations could reveal different patterns.

Cross- and co-prediction results for the group SHR comprised of stock assessment data were much higher than results for SHR comprised of landings data (see table 3.5). Similar patterns were observed for the groups FDO and FVS. Higher predictability in stock assessment pairings over landings pairings is again indicative of data signal alteration by the stock assessment models, as the same species with low landings predictability have high stock assessment predictability. An important caveat must be discussed regarding this result. Stock assessment models are attempting to model population abundance, while landings data are fishery-dependent. Although landings are certainly tracking management actions, such data is also indicative of “changes in resource abundance, market demand, [and] species- and size-selective harvesting practices...” [8]. Landings data is a manifestation of biological variations in addition to management actions, and these variables are inevitably confounded. Additionally, species abundance is dependent on ecological/environmental factors but is also
inevitably affected by fishing. It is possible that two species may not be highly predictable with regard to their fishing management practices but may be highly predictable in an ecological context, but because these two factors are always confounded in the various data types, a highly predictable relationship in one data type could indicate high predictability in another data type. To test this, additional raw data sources must be employed. With multiple data types, one could test whether or not the relationship between two species is simply an artifact of the fisheries model or an actual dynamical dependence.

The nonlinear model FCU search yielded very different species pairings from the Atlantis functional groups. For example, in Atlantis, the FPS functional group consists of northern anchovy and pacific sardine. Anchovy and sardine share similar food sources, and there has been an observed increase in anchovy with decline of sardine [22]. Long-term fish scale records have questioned this relationship, as historically anchovy is consistently abundant while sardine varies in abundance [23]. The nonlinear model did not pair anchovy with sardine or vice versa. The most frequently occurring species in the anchovy search output were blackgill rockfish, bocaccio, and petrale sole (see table 3.6). The most frequently occurring species in the sardine search results were yellowtail rockfish and widow rockfish (see table 3.6). To explain some of the species found in the search results, MacCall [22] cites bocaccio as a probable predator of anchovy, and suggests that pelagic rockfish have possible interactions with pelagic schooling fish such as anchovy and sardine. Additionally, anchovy and sardine experienced low predictability with both cross- and co-prediction results, suggesting that perhaps these two species do not belong in a functional group.

Because the functional groups in Atlantis are comprised of species with taxonomic similarities, one would not necessarily expect the species to be co- or cross-predictable. Highly predictable couplings could result from species that are sensitive to the same
environmental forcings, are coupled via a predator-prey relationship, or occupy similar niches in an ecosystem [2]. While species of the same taxonomic group could share these characteristics, it is not required that they share them.

Similar analysis can be applied to the remaining functional groups. For the majority of Atlantis functional groups, there was no overlap of species found in the FCU search output. The lack of species overlap in the FCU search output, combined with poor co- and cross-prediction results may indicate a need for reexamination of Atlantis functional groups. Because this research employed fishery-dependent landings data as the only source of raw data, additional testing should be performed to either validate or question the findings of the FCU search results. Research survey abundances and CPUE data should be tested using the nonlinear search function to search for consistency among raw data types.

Importance of the Atlantis functional groupings also depends on what the data is being used for. For the sake of model simplicity, many species with taxonomical or dietary similarities are combined in Atlantis, while a select number of commercially important species are given individual outputs. If the Atlantis modelers wish to focus on the behavior of those commercially important species, then correct aggregation of the less pertinent species into functional groups is not of principle importance. Conversely, if the modelers wish to test the effect of a management plan, etc, on a functional group and assume that all species will act in a similar fashion, this could lead to dangerous results.

As indicated by the cross- and co-prediction results, the species in Atlantis functional groups do not necessarily belong in the same attractor or exhibit time-dependent relationships. For this reason, one would not expect the species to react in the same way to a given environmental or anthropogenic forcing. This is a particularly important consideration in a management context. In aggregated species scenarios, a
species with higher levels of uncertainty or vulnerability may be at higher risk of adverse effects if management decisions are made based on the reactions of a more robust member of the group [30].

General trends found in the search results include frequent occurrence of Widow and Yellowtail Rockfish as predictor species, and low occurrence of pelagics such as mackerel, anchovy, and sardine as predictors. Rockfish in the California current ecosystem have been heavily managed since the early 1980s [18], and frequent occurrence of rockfish as predictor species may indicate that the functional groups created out of landings data are better tracking fishing than ecological factors.

4.3 Limitations and Avenues for Future Exploration

The simplex and s-maps forecasting models are useful tools for assessment of fisheries data. The models do not require any biological input parameters. The most variable input parameters are selection of the embedding dimension (E) and time lag spacings. Despite the many strengths of simplex projection and s-maps, there are inevitably drawbacks. Most notably, selection of E is a subjective process. Efforts were made to maintain consistency among results by ranking importance of the output (lowest MAE, highest rho, highest N, lowest RMSE). For outputs where these four variables were in agreement, selection of optimal E was straightforward. However, many data sets had no agreement between lowest error and highest rho. In such cases, selection of optimal E required both ranking of output importance and judgment of the researcher.

Model forecasting ability is best for time series with at least 30 data points [9]. The majority of univariate data sets satisfied this minimal length requirement, but many of the data sets used for the FCU testing did not. Each individual species time series was cropped according to the best guess of time period when the fishery was
active (see methods). Grouping multiple species for cross- and co-prediction analysis required additional cropping so that all time series within a functional group were of the same length. Such cropping led to some time series of less than 30 years, which may have contributed to poor cross- and co-prediction results for many species.

As mentioned previously, California commercial landings data was the only form of raw data (unprocessed by models) used in this research. The results would be greatly strengthened by use of multiple raw data sources.

Additionally, the majority of Atlantis functional groups were not tested during the course of this research project. Atlantis output consists mostly of functional groups (approximately 50 groups), and many of these groups are comprised of dozens of species [13]. This research chose to focus on fish-based functional groups with available stock assessment and landings data, but Atlantis also has planktonic functional groups, bird functional groups, whale groups, and so on. Future research can test the relationships in these larger functional groups.

Additional exploration is also required with the nonlinear search function output, as results were not consistent between E of three and E of four, nor were they consistent between standardized and standardized first differenced data. Some preliminary testing performed by Alec MacCall indicates that slight improvement of rho with E of four is not significant, and that groupings created with an E of three are more relevant. For this reason, this research chose to focus on results of E=3, standardized first differenced data.

Testing of different time lag spacings (tau) indicated that some time series experienced significant improvement in predictability (rho) with tau greater than one. Further testing of variable time lag spacings is required, as only a subset of 20 landings time series were analyzed during the course of this project. Tau of two, three, four, and higher should be tested on all of the landings, stock assessment, and Atlantis
data, as determination of optimal time lag spacing is an important factor in non-linear modeling. Time lag spacings should also be considered for all future research performed using the simplex and s-maps forecasting models.
BIBLIOGRAPHY


APPENDIX
Table A.1. Percent nonlinearity in standardized versus standardized first differenced

<table>
<thead>
<tr>
<th>Data Type</th>
<th># Data Sets (n)</th>
<th>% Nonlinear Standardized</th>
<th>% Nonlinear First Differenced</th>
</tr>
</thead>
<tbody>
<tr>
<td>Landings</td>
<td>49</td>
<td>14%</td>
<td>49%</td>
</tr>
<tr>
<td>Stock Assessment</td>
<td>36</td>
<td>0%</td>
<td>22%</td>
</tr>
<tr>
<td>Atlantis</td>
<td>13</td>
<td>0%</td>
<td>23%</td>
</tr>
<tr>
<td>Atlantis FG</td>
<td>46</td>
<td>2%</td>
<td>13%</td>
</tr>
<tr>
<td>Atlantis Future</td>
<td>13</td>
<td>15%</td>
<td>46%</td>
</tr>
<tr>
<td>Atlantis Future FG</td>
<td>47</td>
<td>8.5%</td>
<td>32%</td>
</tr>
</tbody>
</table>

Table A.2. Average rho in standardized versus standardized first differenced data

<table>
<thead>
<tr>
<th>Data Type</th>
<th>Average Rho Standardized</th>
<th>Average Rho First Differenced</th>
</tr>
</thead>
<tbody>
<tr>
<td>Landings</td>
<td>0.670±0.242</td>
<td>0.277±0.180</td>
</tr>
<tr>
<td>Stock Assessment</td>
<td>0.973±0.067</td>
<td>0.699±0.217</td>
</tr>
<tr>
<td>Atlantis</td>
<td>0.998±0.002</td>
<td>0.867±0.152</td>
</tr>
<tr>
<td>Atlantis FG</td>
<td>0.926±0.175</td>
<td>0.865±0.147</td>
</tr>
<tr>
<td>Atlantis Future</td>
<td>0.961±0.065</td>
<td>0.846±0.199</td>
</tr>
<tr>
<td>Atlantis FG Future</td>
<td>0.878±0.217</td>
<td>0.812±0.263</td>
</tr>
</tbody>
</table>
Table A.3. Average E in standardized versus standardized first differenced data

<table>
<thead>
<tr>
<th>Data Type</th>
<th>Average E Standardized</th>
<th>Average E First Differenced</th>
</tr>
</thead>
<tbody>
<tr>
<td>Landings</td>
<td>4.6±2.3</td>
<td>3.8±2.5</td>
</tr>
<tr>
<td>Stock Assessment</td>
<td>4.6±2.8</td>
<td>4.7±2.6</td>
</tr>
<tr>
<td>Atlantis</td>
<td>5.3±2.7</td>
<td>4.6±2.6</td>
</tr>
<tr>
<td>Atlantis FG</td>
<td>4.8±2.8</td>
<td>5.0±2.6</td>
</tr>
<tr>
<td>Atlantis future</td>
<td>4.3±3.6</td>
<td>5.1±3.3</td>
</tr>
<tr>
<td>Atlantis FG future</td>
<td>4.9±3.1</td>
<td>5.4±2.9</td>
</tr>
</tbody>
</table>

Table A.4. Number of data sets with significant improvement in maximum rho over Tau 1 maximum rho, n=10. Standardized data versus standardized first differenced

<table>
<thead>
<tr>
<th>Tau</th>
<th>Standardized Smooth</th>
<th>Standardized Erratic</th>
<th>First Differenced Smooth</th>
<th>First Differenced Erratic</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>2/10</td>
<td>0/10</td>
<td>3/10</td>
<td>1/10</td>
</tr>
<tr>
<td>3</td>
<td>1/10</td>
<td>0/10</td>
<td>2/10</td>
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