

**Annual Progress Report to:**

**Pollock Conservation Cooperative  
Research Center  
School of Fisheries and Ocean Sciences  
University of Alaska Fairbanks  
Fairbanks, AK 99775-7220**

**for Project:**

**Combining genetics and population dynamics to improve management  
of Pacific ocean perch (*Sebastes alutus*).**

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**Summary of Work from 1 January 2009 to 30 September 2009.**

**Prepared by K. Palof**

**A.J. Gharrett  
and T.J. Quinn II  
Principal Investigators  
and  
K. Palof  
School of Fisheries and Ocean Sciences**

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## **Abstract**

Pacific ocean perch (POP) are the most abundant *Sebastes* rockfish species in Alaskan waters in both biomass and catch. An assumption made for many marine species, such as POP, which have pelagic larvae and apparently mobile adults, is that their population structures extend over very broad reaches, possibly including much of the natural range. Genetic studies of POP population structure have demonstrated that relatively strong divergence occurs between collections that were sampled at locations spaced about 400 km apart along the Gulf of Alaska (GOA) and Bering Sea (BS) continental slopes (Palof 2008). The degree of divergence suggests that, although population structure is not defined by geographic or oceanographic boundaries, the limited net dispersal that occurs in both pelagic larvae and adults restricts the spatial scale of POP production to areas that are related to the average distance moved between birth and reproduction called neighborhoods. The spatial scale of neighborhoods (productivity units) is the geographic scale on which management should focus. Incorporating demographic information from our genetic studies requires an evaluation of the current POP survey and fishery data. In this study we plan to develop a robust estimate of neighborhood size, determine if there is natural spatial variability that can be detected in standard survey measurements, and incorporate spatial structure into population dynamics and harvest models for POP.

## **Introduction**

In this PCCRC project, we are developing and applying quantitative models to examine the influence of population subdivision on population dynamics models that are used to evaluate sustained production of exploited resources. The project arose because an assumption made for many marine species, which have pelagic larvae and apparently mobile adults, is that their populations extend over very broad reaches, possibly including much of their natural ranges. However, this may often not be the case.

From the results of research conducted in our laboratory, we have preliminary estimates of the extent of substantial dispersal, and of neighborhood size. The questions that we will address are the effects that harvest patterns exert on the production and genetic structure of POP and, by extension, other species for which limited dispersal results in a neighborhood models for population structure, and for which the neighborhoods are much smaller than the management areas. To evaluate these effects, we are developing quantitative models that include information about dispersal, population dynamics, and exploitation and, with simulations, testing the effects of different spatially-based harvesting strategies, which will range from harvesting over the entire management area to harvests in a few limited locations within the area.

Since our last report to PCCRC in January 2009, we have made substantial progress in developing our quantitative modeling approach, refining our estimates of neighborhood size, and exploring current survey data for POP in Alaskan waters. Our exploration of the survey growth data has shown variability between spatial areas and over time, and we are currently conducting further evaluations to determine if the variability is random or deterministic. We are planning on completing both spatial and time series analysis on the growth data this fall, and continuing work on additional spatial and harvest models.

## **Approach**

### *Data Quality*

Although assessment of the quality of our genetic data was a subobjective for this project, it was vital to moving forward with our modeling objectives with quality population structure parameter estimates. In our previous annual reports, we thoroughly explained the theoretical role

of null alleles, and we used simulations to determine their influence on population genetic calculations. In the lab we designed new PCR primer pairs and reanalyzed the homozygotes in our POP samples in order to determine the incidence of null alleles. Addressing the presence of null alleles is important to the robustness of our genetic data and the models into which we incorporate these data. We also used SNP technology to verify that all of the samples analyzed in this study were Pacific ocean perch, because occasional misidentifications do occur during sample collection at sea.

### *Modeling*

We have established, using genetic information, that the geographic scale of the management areas is probably much larger than the scale of the productivity units. We need to further evaluate how the composition of these productivity units, or neighborhoods, is affected by a range of harvest plans. The methods of harvesting can range spatially as fish distributions change and as management areas expand or shrink and can also vary with respect to fishing pressure and the number of fish removed from an area. We do not know how these processes influence the genetic components of a population, which may be important for long-term abundances.

We will begin by determining if there are natural geographic breaks in Alaskan POP that are detectable from the survey and catch data. Based on estimates of neighborhood size from the genetic data, we can establish levels of spatial groupings – regional, statistical area, and smaller neighborhood size areas – to examine the variability present. Multiple statistical approaches will be used to determine if natural variation is detectable at any of these levels. The results of this analysis will aid us in determining the spatial scale at which further analyses should be focused.

We will then generally look at the interactions between harvest rates, spatial distributions, and population dynamics. Spatial models are described in depth in Quinn and Deriso (1999, chapter 10). An application of a spatial model to fishery harvest policy (Heifetz and Quinn 1998) described the necessary model features and showed that spatial considerations can alter the optimal harvest policy.

Simple models are needed to identify influential components in genetic processes and to determine the extent of each component's influence. We will use multiple simulations to fully investigate how general productivity units are affected by a range of processes. These simulations will be conducted in Excel, and with programs written in R. These extensive simulations will provide basic information as to how the variables interact without introducing specific parameters.

We will also use simple models, similar to those by Hastings (1993), in an attempt to understand how connectivity between demographic units affects population processes. Using only 2 demographic units Hastings showed that at levels of connectivity 10% and below, units were demographically independent. We hope to extend these simulations to three or more demographic units, which as far as we can tell has not been reported in the literature. The species-specific extension of this modeling, which is described below, depends on the results of this initial simulation period.

After the many aspects of the complex interactions and processes are fully explored, we plan to use this knowledge on Pacific ocean perch. We hope to use routine dispersal models to estimate POP abundance and apply both varying spatial and harvest considerations based on our initial explorations and simulations. Spatial considerations for our model will be established using previous knowledge of the species (Hanselman et al. 2003, Hanselman and Quinn 2004),

which included two years of scientific surveys. Information from regular AFSC surveys will also be synthesized.

Once the background of a spatial model is developed, the proportional density of POP will be measured under a constant spatial harvest model, where fishing efforts are equally distributed throughout each spatial area, and a patchy harvest model, where efforts will be randomly distributed throughout the spatial areas. The goal of these models will be to see how the concentration of fishing effort affects the density of the species, specifically at varying spatial scales. The models that will be used here are similar to those used in research for marine protective areas with respect to spatial considerations, but do not necessarily make all of the assumptions of marine reserves such as perfect management and zero harvest in the reserve (Rodwell and Roberts 2004, Hart 2006).

## **Results**

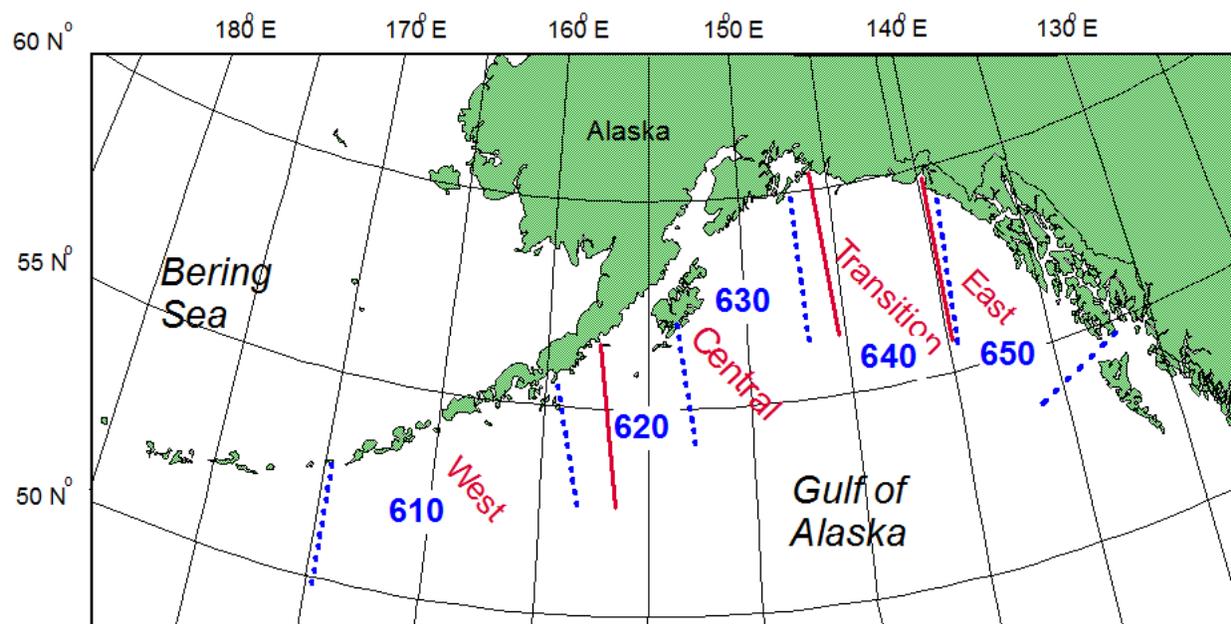
### *Previous accomplishments*

Our previous reports summarized the data quality portion of this project. We concluded, from the results of our simulations and laboratory observations, that our data has very low frequencies of null alleles at most of the loci that we applied and that null alleles have had little influence on our analyses of population genetics structure or on the estimation of parameters derived from the data. Therefore, we can conclude that our genetic data is of high quality and it can be relied to estimate demographic parameters. We also used SNP technology to positively ID 994 of our sample individuals as Pacific ocean perch. The other 4 individuals resulted in failed reactions.

### *Current accomplishments*

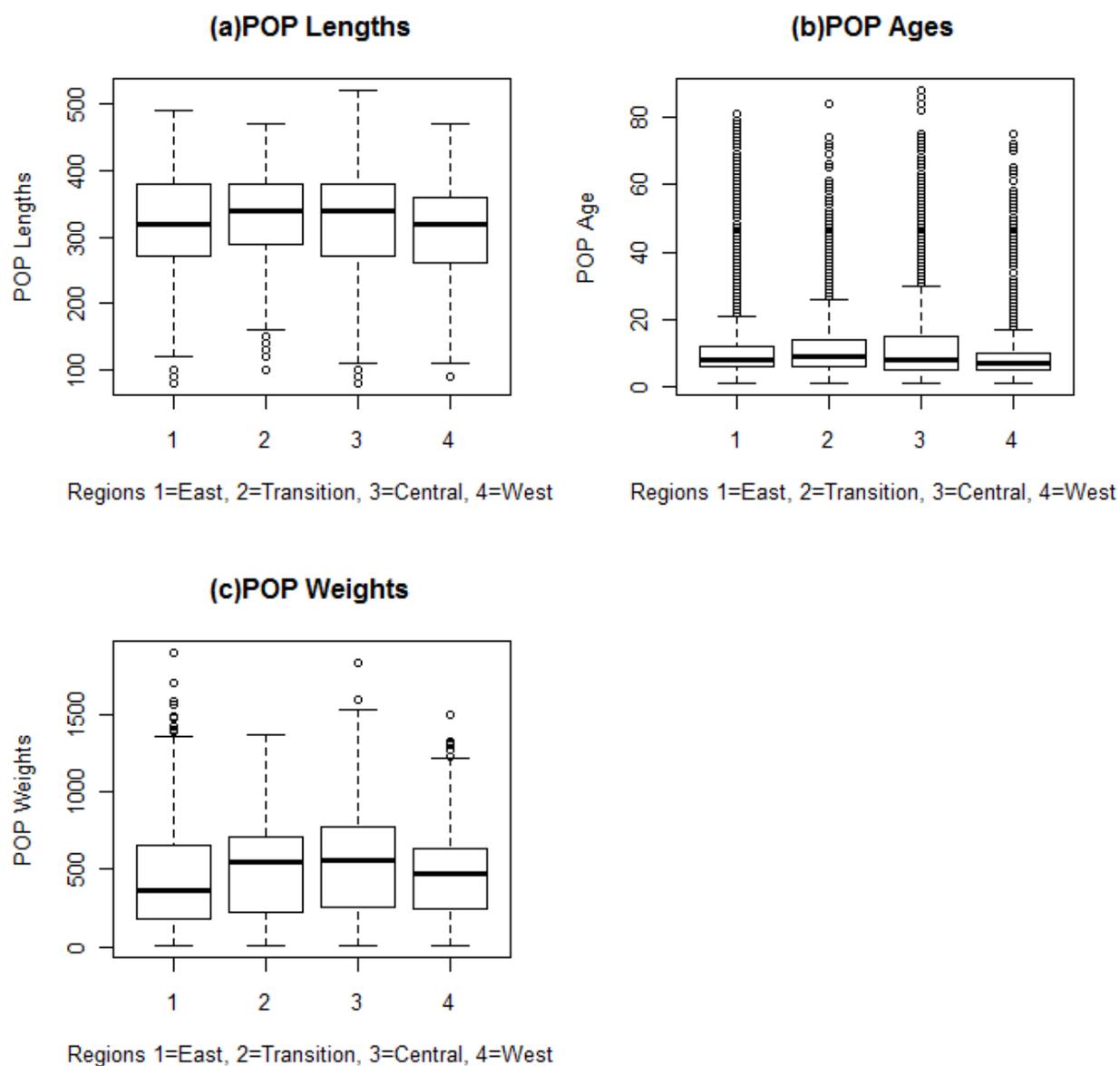
During this reporting period, we conducted extensive data explorations on available POP survey data, and we hope to be able to do the same on the catch (fishery) data. Obtaining the survey data with specific spatial reference points (latitude and longitude of trawls) was not difficult; however, we are still in the process of obtaining this same information for the fishery data. Obtaining spatial information from the fishery is a complicated process that requires consideration of liability and privacy rights. The fine scale spatial information for both the survey and fishery data is a prerequisite to running the proposed models. Additionally, we have consulted with other population geneticists to improve our genetic estimate of the neighborhood size for POP. These estimates will be used in our models, as the approximate size of a “demographic unit” for POP.

We have established preliminary levels of spatial scales and are working to determine which levels, if any, have statistical importance for the survey and catch data. The three spatial scales chosen are based on broad geographic areas, statistical reporting areas, and areas similar in size to the estimated neighborhood size for POP (Figure 1). Exploratory analysis of these spatial regions has shown variation (Figures 2-4) however, analyses are underway to determine if this variation is deterministic or random. These analyses will determine the most statistically significant spatial scale to focus our modeling efforts on. Based on this exploratory analysis we hypothesize that, at the largest spatial scale, fish in the center of the distribution appear to be older and larger (Figure 2). Also, at the finest spatial scale there are large differences in size and age in adjacent areas (Figure 4).

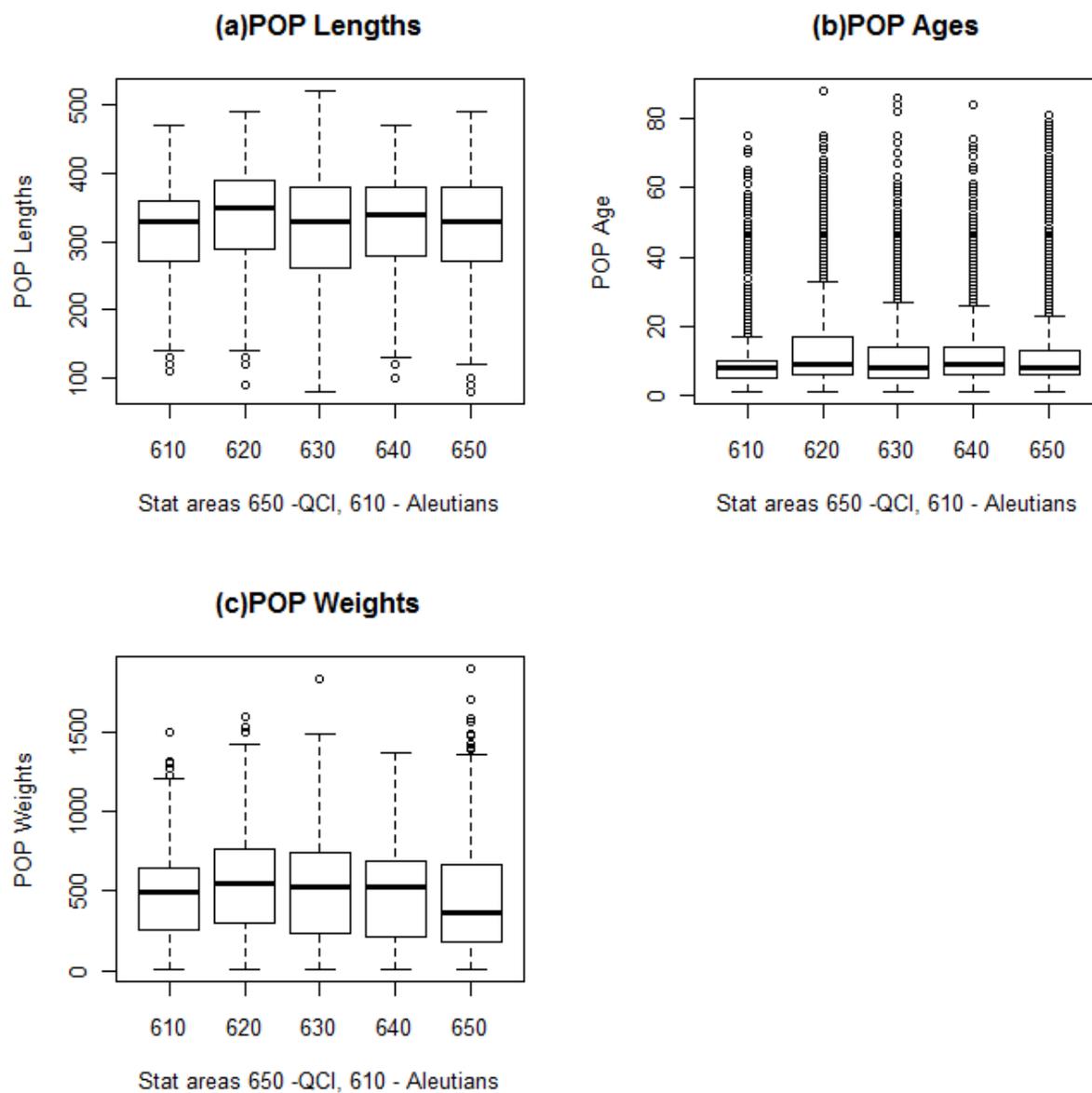


**Figure 1.**

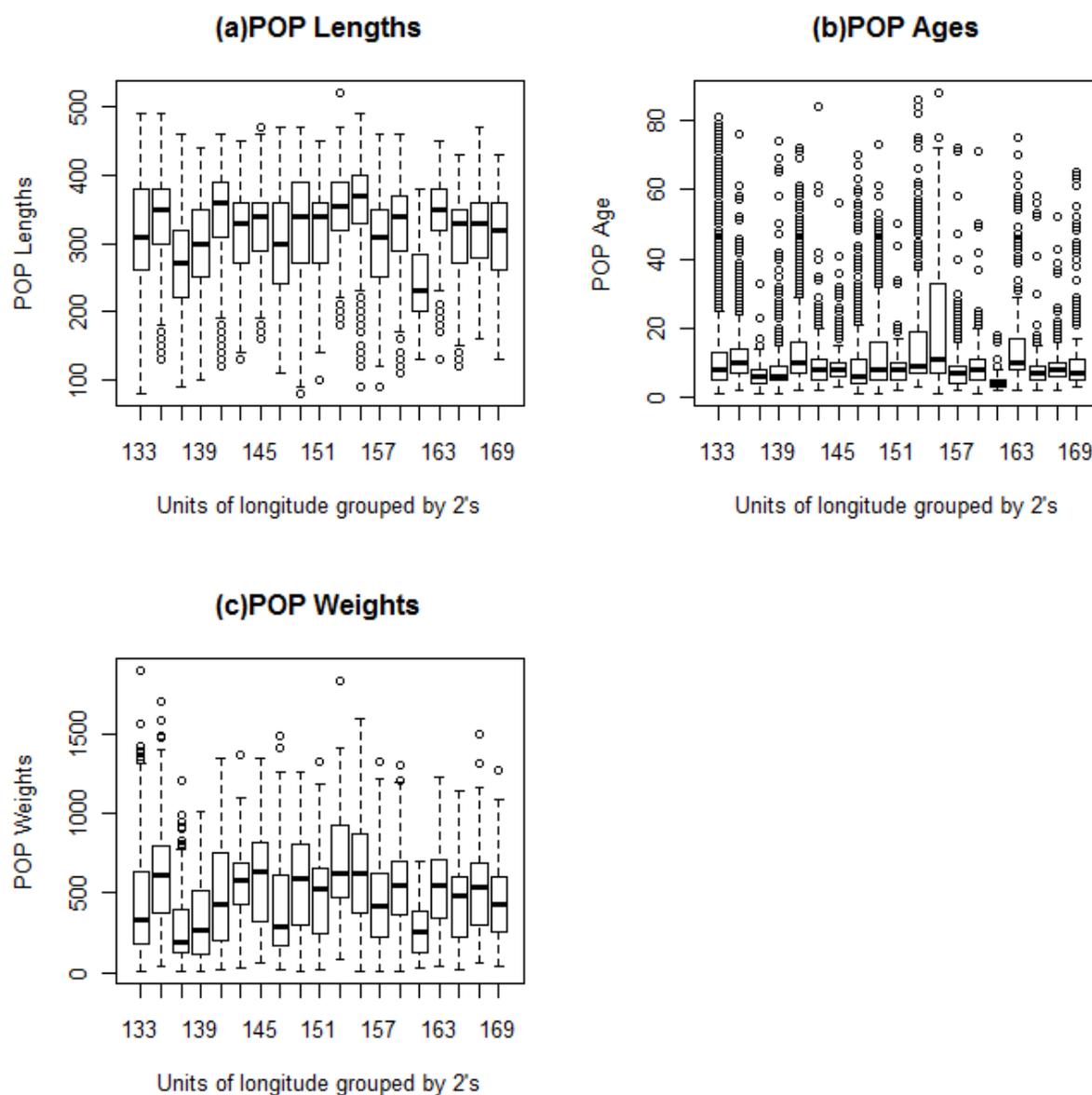
Map of the Gulf of Alaska with spatial groupings. The red boundaries and red labels (East, Transition, Central, and West) refer to the largest geographic spatial groups. The blue boundaries and blue labels (650, 640, 630, 620, 610) refer to the statistical reporting areas, which is the second spatial grouping. The third spatial grouping groups by intervals of two lines of longitude starting at 133E, these are not shown but intervals of longitude by 5 degrees are labeled in black.



**Figure 2.** Distribution of lengths, ages, and weights from 1981 to 2007 using the NMFS Pacific ocean perch (POP) growth data by large scale geographic groupings.



**Figure 3.** Distribution of lengths, ages, and weights from 1981 to 2007 using the NMFS Pacific ocean perch (POP) growth data by statistical reporting areas.



**Figure 4.**

Distribution of lengths, ages, and weights from 1981 to 2007 using the NMFS Pacific ocean perch (POP) growth data by units of longitude grouped by 2, approximately 120km in each group.

We are also conducting an extensive literature review of spatial models, especially those used in the area of marine protected areas. This will ensure that our models take advantage of the most recent findings in this area of research, since it is currently an area of ever expanding research. In this review we came across the work of Hastings (1993) which concludes that at a 10% level of connectivity two populations are demographically the same, but at levels less than 10% two populations are demographically independent. Hastings did a very thorough job of exploring this relationship with two populations, but we would like to extend this idea to three or more populations. Understanding a threshold of demographic independence is important for the incorporation of spatial structure into management practices, therefore we have modified our approach to include extending the work of Hastings.

Ms. Palof, the doctoral student on this project, has continued to take coursework, which includes both increasing her knowledge of statistical approaches (STAT 652: Statistical Theory II and STAT 611: Time Series) and learning the quantitative program ADMB (which she will apply in developing models). In addition, both Ms. Palof and Dr. Gharrett participated in a genetic stock structure working group for the BSAI Plan team during this time.

### **Future plans**

In the next few months we plan to apply spatial and time series analyses to the survey data and further formulate our overall modeling approach. The knowledge that Ms. Palof has gained from her literature review and courses is essential to the successful development and application of these models.

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