

# JIMAR, PFRP ANNUAL PROGRESS REPORT: FY 2004

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Project Proposal Title: Development of a hierarchical model to estimate sea turtle rookery contributions to mixed stocks in foraging habitats

Funding Agency: JIMAR

## 1 Purpose of the project and indicative results:

The purpose of the project is to develop general methods for incorporating ecological covariates in genetic stock analysis models. Stock analysis attempts to estimate the proportion of the individuals in a mixed population that come from each of a number of possible source populations: for example, comparing data from breeding grounds and an open-ocean population that combines individuals from many breeding grounds to figure out the importance of particular breeding grounds to the overall population. In the past, stock analysis has been based only on individual morphological or genetic measurements, such as the mitochondrial DNA haplotypes of individuals found in rookeries and in mixed-stock foraging grounds. Other ecological information such as the size of the breeding population or the distance from the breeding population to the foraging ground is often available (and ignored). We are using stock analysis of Atlantic sea turtle populations (loggerhead and green turtles) to test and develop models that include ecological covariates such as rookery size and location, and drawing initial conclusions about the more powerful or different conclusions that come from incorporating this information. In particular, we are developing hierarchical Bayesian models, which are a flexible but rigorous way to add rookery size and geographic location to stock analysis methods that have traditionally used only genetic data to try to infer the contributions from each rookery. We are also developing important auxiliary statistical tools, such as model selection methods that can determine whether adding particular ecological covariates to an analysis actually increases the precision and accuracy of our estimates, or whether (if we mistakenly try to add irrelevant information to the model) it actually dilutes the power of the analysis; these tools are necessary before one can confidently start using hierarchical Bayesian methods as a general tool to add information to stock analyses. We are building software tools that implement these methods and that can be used by a broader audience of researchers. Finally, we hope to apply these general methods to some broader questions in stock analysis: for example, where should we define boundaries between populations for the purpose of stock analysis? How do we know when we have enough information to justify analysis at a very fine spatial scale or using very detailed genetic differences, and when should we be satisfied with analyses on a coarser scale?

## 2 Progress through December 31 2004

- Two mss. published (see below),
- We have continued to develop our methods for estimating contributions in a “many-to-many” stock analysis situation, where data are available from many sources (rookeries) and many destinations. In this case, we can incorporate rookery and feeding-ground size directly (rather than hierarchically, although we are also exploring hierarchical versions of this model), and we can express contributions in either a “rookery-centric” way — percentages of individuals leaving each rookery for different

foraging grounds — or in the more traditional “foraging ground-centric” way — percentages of individuals in each foraging ground coming from different rookeries. We have found that approaching this problem naively, by running a series of separate stock analyses for each foraging ground, give misleading answers.

In addition to our paper in *Molecular Ecology* applying this technique to stranding data, we have applied these techniques to green turtle data from the Atlantic and have a manuscript in prep. (also for submission to *Molecular Ecology*).

- We will continue to work to make the procedures we have developed robust and to incorporate them into a relatively user-friendly package running on top of the R programming environment (and possibly tying in the BUGS statistical estimation package as well). (An initial version of the package is available at <http://www.zoo.ufl.edu/bolker/turtle>.)
- We have continued (and will continue) to develop and support our R package for stock analysis, available from <http://www.zoo.ufl.edu/bolker/R/windows>.

### **3 Papers published in refereed journals**

- B. W. Bowen and A. L. Bass and S.-M. Chow and M. Bostrom and K. A. Bjorndal and A. B. Bolten and T. Okuyama and B. M. Bolker and S. Epperly and E. LaCasella and D. Shaver and M. Dodd and S. R. Hopkins-Murphy and J. A. Musick and M. Swingle and K. Rankin-Baransky and W. Teas and W. N. Witzell and P. H. Dutton (2004) Natal homing in juvenile loggerhead turtles (*Caretta caretta*). *Molecular Ecology*, 13:3797–3808. doi:10.1111/j.1365-294X.2004.02356.x
- Toshinori Okuyama and Benjamin M. Bolker (2005) Combining genetic and ecological data to estimate sea turtle origins. *Ecological Applications*, 15(1):315–325.

### **4 Students graduating**

None

### **5 Budget for next fiscal year:**

None: grant ended on 31 December 2004