

March 7, 2007

FW663 Midterm II Exam

This exam is a take-home, open-book exercise. There are 3 sets of questions; you must answer all of them. You may use any reference material (class notes, assigned reading, library material, WWW site, etc.). Under NO circumstances are you to discuss this exam with classmates or any other individual. You are to work independently and you should not confer with others. If you need clarification on a question, please email gwhite@cnr.colostate.edu or doherty@cnr.colostate.edu and ask for clarification by 3:00pm Thursday, 8 March. This exam is to be turned in by 4:00 pm Friday, 9 March to Dr. Doherty's **mailbox** in Wagar 108. Turn in this sheet and your answers and computer files on CDs, or USB drives. **Question 1 should be stapled in a separate bundle with its own CD from Questions 2 and 3 because each bundle will be graded by a different individual. Identify each page of your answer sheets and your computer files with your student number only.** Only put your name (via your signature) on this sheet.

By my signature below, I certify that I have not collaborated with anyone concerning any material related to this examination.

Student Number

Signature

Date

Question 1 (50 points): Sea turtle breeding ages. Real problem, simulated data.

Long-lived species often have delayed maturity, where not all individuals breed in the following breeding season after birth. Estimates of first-time breeding probabilities (i.e., the probability that an individual will first breed at a particular age) are of interest both to parameterize population models, as well as investigating life history trade-offs between reproductive parameters (such as age of first breeding) and survival.

Such interests motivated a 20-year study of sea turtles. This particular species of sea turtle is long-lived and has delayed breeding. Individuals may delay breeding up to five years (i.e., there is a probability that an individual will first breed at age 1, age 2, age 3 or age 4, but if the animal has not attempted to breed by age 5 it is assumed to do so with probability = 1). Note: breeding at age 1 means breeding on the turtle's first birthday, breeding at age 2 means breeding on its second birthday, etc. This delayed breeding can also be thought of a "transition" from the hatchling, or pre-breeding state, to the adult, or breeding, state. Generally, first-time breeding probabilities are thought to increase with age.

Turtles are marked with PIT tags, flipper tags, and photo-identified. Turtles are either marked as hatchlings coming out of nests, or as breeding adults of unknown age (i.e., 2 states). Since hatchling turtles can not be observed again until they return to first breed, survival of hatchling turtles is considered constant until they return to first breed. This means that pre-breeder survival should be considered constant across all time and ages (**Big Hint – if not, you will run into parameter identifiably problems**). Also no temporal variation can be modeled for age-specific transitions to the breeding population.

Assume $\hat{c} = 1$.

The input file (**SeaTurtle.inp**) consists of 2 groups;

A = the hatchling turtles, and

B = adult breeders

Provide your MARK files on a CD along with your written answers to the following questions.

- a) Which parameters would you consider fixing? (10 pts)

- b) Describe and identify four models that you would construct and run these. Present a table of model results (20 pts).

- c) Graph survival and the age-specific first breeding probabilities (15 pts).

- d) What is the pre-breeding survival rate? (5 pts)

Question 2 (35 points). Grizzly bear population size estimates. Real species with simulated data.

Grizzly bears (*Ursus arctos*) in the western US are dangerous for researchers to capture, but hair samples containing DNA can be collected with barbed wire “traps” baited with scents (e.g., rotten beef blood, rotten fish). Bears are not actually given a reward, i.e., no food is actually given to them. See the picture below. The DNA sampling technique is obviously less invasive than historical methods. Each hair sample on the barbed wire is collected and the DNA sequenced to assign each bear an identity. Because genetics labs have had considerable experience sequencing bear DNA, the identification errors are assumed non-existent.



Credit: Stefan Himmer and John Boulanger

To estimate bear populations in Montana, a large hair trapping grid containing 400 grid cells (20 x 20) was established, with each grid cell 10 x 10 km². One hair snag trap was placed in each of the 400 cells. However, even this large grid was not big enough to completely cover all of the potential grizzly bear range in the state. As a result, some bears were only observed (meaning DNA collected) on the edge of the grid, whereas other bears apparently had home ranges located completely on the grid.

Hair samples were collected for 7 occasions, with hair snag traps moved within the grid cell on each occasion to keep the traps novel to the bears (although there is suspicion by the biologists that bears lose interest in the scents when not given a food reward). To correct for some bears with home ranges completely located on the grid, and others with home ranges only on the edge of the grid, an individual covariate has been included in the input file. This individual covariate is the distance from the edge of the grid for first capture location of each bear. The input file is **Grizzly.inp**. Provide your MARK DBF and FPT files on a CD along with your written answers.

- A. (20 pts) Compute the population estimate for this grid. Explain why you used or did not use model averaging.
- B. (15 pts) Did the distance covariate provide useful information to estimate population size? Provide a graph of the initial capture probability (p) (and recapture probability c if necessary) as a function of distance from edge of the grid.

Question 3 (15 points). Same data as Question 3 from Midterm I. Population dynamics of Northern Spotted Owls. Real species and simulated data.

The northern spotted owl (*Strix occidentalis caurina*) owl is a medium-sized, nocturnal owl that inhabits coniferous forests along the Pacific Coast of North America from southern British Columbia to central California. Because of the association between northern spotted owls and old forests, conservation of the owl and its habitat has been extremely contentious among environmentalists, the timber industry, land managers, and scientists since the early 1970s. This species is particularly amenable to monitoring via capture-resighting techniques. Adult territorial birds (both sexes) are easily captured by “mousing”, i.e., holding out a domestic mouse for the owl to take, and capturing them with a noose pole or net. Birds are then marked with colored plastic leg bands, giving each owl a unique identity.

Owls have been marked and monitored on multiple study areas in Washington, Oregon, and California from 1990 to the present. Here, we are going to analyze just 2 of these study areas, one from Oregon and one from Washington. Because of differences in the timber harvesting policies of the 2 states, we are interested in whether there are differences in the rate of population change between the 2 study areas. Each study area is monitored annually to detect previously marked owls, as well as to mark both members of pairs that are new territory holders. Although occasionally males will defend a territory without a female present, this is an uncommon situation.

Live encounter data are provided in the file **NSO.inp** for 17 occasions (1990-2006), with 4 groups (Oregon females, Oregon males, Washington females, Washington males). As part of your answer, provide the MARK DBF and FPT files, and copies of other relevant output.

- A. (10 pts) Using the model $\{\phi(\text{State} \times \text{Year}) p(\cdot) \lambda(\text{State} \times \text{Year})\}$, compute the geometric mean value of lambda and its associated 95% confidence interval for each state. Also, compute the process standard deviation of $\log(\lambda)$ for each state.
- B. (5 pts) Assume that the process standard deviation of $\log(\lambda)$ for each state is identical, and compute the geometric mean values of the 2 λ estimates for each state.