Note: The following is a tongue-in-cheek piece written to provide an overview of mark-recapture and distance sampling approaches for abundance estimation. It was originally written for students in the PRIMES program at Colorado State University where I was invited to speak on the subject. Since then I have updated some of the material including the reference to Borchers et al (2006) which has now been published and the reference to DISTANCE software. 13 Dec 2006.

A Biologist's Nightmare Fairy Tale of Mark-Recapture Distance Sampling

by

Jeff Laake

Once upon a time, two field biologists transited the same set of well-marked lines randomly placed throughout a field containing duck nests. The second biologist started the sampling after the first biologist finished so they were unaware of each other's observations. Thus, both independently made observations of duck nests on either side of the line out to a perpendicular distance W. When they detected a nest they measured the perpendicular distance to the nest from the line and they also recorded the type of vegetation and a measure of vegetation density. Each observer also recorded a GPS position for each observed nest that would enable them to determine if the observers saw the same nests or different nests. The two biologists eagerly returned from the field wanting to "get" their data analyzed so they could estimate how many nests were in the area that they sampled (note: we are ignoring making an inference to a larger non-sampled area). Now like most biologists they didn't really think that they missed any nests but they decided to check so they could get the study published. They had some vague idea about mark-recapture and distance sampling but in reality they had no clue how they were going to analyze the data before they collected it. So they visited the Analysis-R-Us hot-line and started asking analysts what they should do with their data. Below are some of the responses that the biologists received from the analysts.

Analyst 1: Well it is obvious to me that you have a classic mark-recapture problem and you should use the 2-sample Petersen estimator as follows:

$$\hat{N} = \frac{n_1 n_2}{n_{11}}$$

where n_j is the number of nests seen by the j^{th} biologist and n_{11} is the number of nests that both saw in common (note: n_{11} is typically denoted as m_2 in capture-recapture notation and it is subscripted as n_3 in the Borchers et al submission to Biometrics). Now you may want to use the small-sample bias correction but you can do it all with a calculator and you can look up the variance estimator in Seber's book "The Estimation of Animal Abundance" or in the Otis et al Wildlife Monograph 62 on Statistical Inference from Capture Data on Closed Animal Populations". It's all cookbook equations! Piece of cake! Next question!

Analyst 2: Well it is obvious to me that this is a classic distance sampling problem. Even though you both ran the transects, we can ignore that because the nests didn't move and new nests weren't created or destroyed during the time you sampled so you should just pool your data as if they had done the sampling as a team and use only the unique nests $n_. = n_1 + n_2 - n_{11}$. Clearly the estimator you want to use is:

$$\hat{N} = \frac{n_{.}}{\hat{p}}$$

where

$$\hat{p} = \int_0^W \hat{g}(y) \frac{1}{W} dy .$$

You can use the software DISTANCE [http://www.ruwpa.st-and.ac.uk/distance/] to derive an estimate for the detection probability function $\hat{g}(y)$ using the observed distances $y_1, y_2, \ldots, y_{n_.}$. You should examine several different forms for $g(y)$, but from what you said about the visibility of duck-nests you may want to consider initially the half-normal model $g(y) = e^{-y^2/(2\sigma^2)}$. And if you really want to be clever you may want to use the vegetation covariates as an explanatory variable for the detection function. You can do that by using the vegetation measures as covariates in the scale parameter, $\sigma = e^{\beta_0 + \sum \beta_i z_i}$ where z_i are the vegetation covariates. Treat vegetation type as a factor variable and since there are only two types you can code it as $z_i = 0$ or 1. Vegetation density can be entered as a continuous variable. I don't know what analyst 1 was thinking, my answer is clearly better. Distance sampling rocks!

Analyst 3: Well those two analysts are clueless. I know the right way to analyze these data. I agree with analyst 1 that this is a mark-recapture problem but that analyst is clearly unsophisticated because they didn't suggest using the vegetation or distance data in the mark-recapture analysis. And analyst 2 is clueless because he believes you saw everything on the line ($y=0$). No disrespect fellows but I think that is unlikely even though they were duck nests. That vegetation is really thick out there and I'm sure you overlooked some nests close to the line. Distance sampling sucks, it doesn't rock! What you really need to do is a more sophisticated mark-recapture analysis using the vegetation and distance covariates. And because you are using distance as a covariate, I THINK it really is distance sampling within the mark-recapture framework. You can do this analysis using the closed Huggins model in MARK [http://www.cnr.colostate.edu/~gwhite/mark/mark.htm]. The observer-specific detection function based on the logit transformation is:

$$p_j(y, z_1, z_2) = \frac{e^{\alpha_j + \beta_1 y + \beta_2 z_1 + \beta_3 z_2}}{1 + e^{\alpha_j + \beta_1 y + \beta_2 z_1 + \beta_3 z_2}}$$

where z_1 is a 0/1 coding for vegetation type and z_2 is vegetation density. You want to estimate abundance with a Horvitz-Thompson-like estimator (note this isn't strictly H-T because the probabilities are estimated):

$$\hat{N} = \sum_{i=1}^{n_.} \frac{1}{\hat{p}_{i.}}$$

where

$$\hat{p}_{i.} = p_1(y_i, z_{1i}, z_{2i}) + p_2(y_i, z_{1i}, z_{2i}) - p_1(y_i, z_{1i}, z_{2i}) p_2(y_i, z_{1i}, z_{2i})$$

MARK will estimate all of the parameters for you and will give you an abundance estimate and a variance. All you have to do is figure out those crazy design matrices. You can get help by reading an on-line electronic book written by Evan Cooch and Gary White (http://www.phidot.org/software/mark/docs/book/) or you can attend Gary White's class on MARK this June. Or if you are really brave, try to survive FW663 (fondly known by the survivors as the class from hell). Now go analyze your data and quit bothering me! I'm busy!

Analyst 4: Well I mean no disrespect to my fellow analysts and I'm not really name dropping (yeah right) but my uncle is Bryan Manly and he and Lyman McDonald and others had a very similar problem with some polar bear survey data in which they had 2 independent observers in the airplane observing from the same side but different windows. They wrote it up in Manly, B.F.J., L.L. McDonald & G.W. Garner 1996. Maximum likelihood estimation for the double-count method with independent observers. J. Agr. Bio. Env. Stat. 1:170-189. Last Christmas when Uncle Bryan and I were sitting around the fireplace drinking spirits, he told me that the papers by Chen and others (Chen, S.X. 2000. Animal abundance estimation in independent observer line transect surveys. Envir. Ecol. Stat. 7:285-299 and Chen, S.X. and C.J. Lloyd. 2000. A nonparametric approach to the analysis of two-stage mark-recapture experiments. Biometrika 87:633-649) were quite similar to his paper.

My Uncle Bryan, who isn't usually very talkative, went on to say that the paper by his colleague Ken Pollock and his student Russell Alpizar-Jara (Alpizar-Jara, R. & K.H. Pollock 1996. A combination line transect and capture-recapture sampling model for multiple observers in aerial surveys. *Env. Ecol. Stat*. 3:311-327) wasn't quite the same because what they did was similar to the suggestion of the clever Analyst 3. Uncle Bryan thinks his method is better.

Uncle Bryan went on to tell me about David Borchers. He said David Borchers is a very clever sort who published his dissertation on this subject (Borchers, D.L. 1996. *Line transect abundance estimation with uncertain detection on the trackline.* Ph.D. dissertation, Univ. of Cape Town, South Africa.)and subsequently published 2 papers in Biometrics (Borchers, D.L., S.T.Buckland, P.W Goedhart, E.D.Clarke and S.L. Hedley. Horvitz-Thompson estimator for double-platform line transect surveys. *Biometrics* 54:1221-1237. and Borchers, D.L., W. Zucchini & R. Fewster 1998. Mark-recapture models for line transect surveys. *Biometrics* 54:1207-1220.). He said that David had worked on this subject with the International Whaling Commission and that there is a lot of literature in their reports on this subject. He told me that even though David had devised the correct full likelihood, he didn't understand why David only used the mark-recapture part of the likelihood like his colleagues Russell and Ken. He did say that David did use the full likelihood with some whale data and he noted that the estimated abundance increased in comparison to using only the mark-recapture component of the likelihood.

By this time I was nearly asleep, but Uncle Bryan kept on talking. He went on to say that the same thing happened when he looked at the papers of Chen (2000) and Alpizar-Jara and Pollock (1996) who analyzed the same set of stake data that some crazy fellow from Utah collected eons ago. He said that Chen's estimate was higher and closer to the known number of stakes than Russell's estimate. He said that convinced him that he was correct to include both the distance sampling and mark-recapture components of the likelihood like he and Lyman did in their polar bear paper. He followed with the comment that it can't really be mark-recapture distance sampling if you exclude the distance sampling component of the likelihood. By that time, I had dozed off but I got Uncle Bryan's message loud and clear.

Now wake up biologists! I know that was a long boring diatribe but you've got to wake up for the bad news. You have to hire me as a programmer because the only way you can get your abundance estimate is by numerically optimizing the likelihood and there isn't any generalized code like MARK or DISTANCE to do it. Just to impress you with my intelligence and show you how complicated it is (so you'll know that you are getting good value with your money), I'm going to show you the 2 pieces of the likelihood. You remember likelihoods don't you? You probably saw them in Stats 101, right? The biologists' faces appeared blank and they nodded in a knowing fashion. Oh well, you don't really need to know because that's why you are paying me.

The mark-recapture likelihood component is:

$$L_{\omega}(\theta)=\prod_{i=1}^{n_{\cdot}}\frac{\Pr\{\underline{\omega}_i \mid y_i,\underline{z}_i)}{p_{\cdot}(y_i,\underline{z}_i)}$$

Now this isn't really as complicated as it looks. $\underline{\omega}_i=(\omega_{i1},\omega_{i2})$ is a capture-history (simply a pair of indicator variables) and the possible observable pairs are: seen only by biologist 1 (1,0), seen only by biologist 2 (0,1), seen by both biologists (1,1). The other capture-history (0,0) is unobservable and is what we want to estimate. Now you need a generic detection function that could be like the one analyst 3 suggested (although I don't really want to give them any credit). I'll call the generic function $p_j(y_i,\underline{z}_i)$ where j indexes the biologists 1 and 2. The dot-subscript represents the union of the observations and $p_{i.}=p_{\cdot}(y_i,\underline{z}_i)=p_1(y_i,\underline{z}_i)+p_2(y_i,\underline{z}_i)-p_1(y_i,\underline{z}_i)p_2(y_i,\underline{z}_i)$. I'm sure you can work out the values of $\Pr\{\underline{\omega}_i \mid y_i,\underline{z}_i)$ for the 3 observable histories. This is the likelihood that MARK uses for the Huggins closed model.

But you can't use MARK after I include the distance sampling component of the likelihood:

$$L_{y|\underline{z}}(\theta)=\prod_{i=1}^{n_{\cdot}}\frac{p_{\cdot}(y_i,\underline{z}_i)\pi(y_i \mid \underline{z}_i)}{p_{\cdot}(\underline{z}_i)}$$

Now because this is distance sampling we assume that $\pi(y_i \mid \underline{z}_i)$=1/W, based on random line placement the perpendicular distances of all nests (not just observed ones) are distributed uniformly. Thus, the simpler version of the distance sampling likelihood is:

$$L_{y|\underline{z}}(\theta)=\prod_{i=1}^{n_{\cdot}}\frac{p_{\cdot}(y_i,\underline{z}_i)}{\int_0^W p_{\cdot}(y,\underline{z}_i)dy}$$

Youch! That is where it really gets ugly. You have to integrate that blasted function and while you can choose some generic functions to get analytical results for the integral, you are still stuck with numerically optimizing the likelihood.

No wonder, David Borchers chose to ignore the distance sampling component. Instead of using the Huggins model in MARK he used logistic regression with standard software to maximize the mark-recapture likelihood component using a little-known trick of Buckland et al. (*Buckland, S.T. J.M. Breiwick, K.L. Cattanach, and J.L.Laake. 1993. Estimated population size of the California gray whale. Marine Mammal Science 9:235-249*) to adjust for the conditioning on the observed set of capture histories. No ugly integration! No muss, no fuss!

But, you don't want to do that. Remember dropping the distance sampling component of the likelihood can lead to negative bias in the abundance estimator. I'm not certain why but it seems to do that. Also, then I wouldn't get paid to write the code. I'll use the same abundance estimator as analyst 3 but computing the numerical MLE for the parameter vector θ to get $\hat{p}_{i.}$ for each of the observations is going to take some work (at least for my computer). So give me your data and come back in six weeks with a check and I'll give you the answer. You may not understand it, but it will be better than what analyst 3 suggested.

Analyst 5: I don't work for Analysis-R-Us, but I like working the hot-line and I'm going to tell you how you should analyze your data. My fellow analysts were close but each of their models can have problems.

I know a little about distance sampling and I read this paper by Palka (Palka, D. 1995. Abundance estimate of the Gulf of Maine harbor porpoise. *Rep. Int. Whaling Comm. Special Issue* 16:27-50.) in the literature of the International Whaling Commission and I thought to myself she is onto something. Her estimator for abundance is this:

$$\hat{N} = \frac{\hat{N}_1 \hat{N}_2}{\hat{N}_{11}}$$

Now I know that looks a lot like the Petersen estimator and it is except that it uses abundance estimates derived independently using distance sampling with the nests seen by observer 1, the nests seen by observer 2 and the nests that both observers saw.

Now wait a minute you say. Analyst 3 said that distance sampling assumed that detection on the line was 1, so how will this help. Well, consider for a minute what the estimator for distance sampling would look like if g(0) isn't 1. Well since other analysts have already described g(y) such that g(0)=1, I'll use p(y) for detection functions in which p(0) may be less than 1. If you write out the expectation for the distance sampling estimator you'll find that: $E[\hat{N}] = Np(0)$. So if we assume that $p_{11}(0) = p_1(0)p_2(0)$ and plug in each expectation we get N. Or you can think of it this way:

$$\hat{N} = \frac{\hat{N}_1}{\hat{N}_{11}/\hat{N}_2} = \frac{\hat{N}_1}{\hat{p}_1(0)}$$

Hmm! So what makes me like this idea? Well, with no disrespect to Uncle Bryan's nephew and all of the folks that have worked on this problem, I don't like the assumption that $p_{11}(y_i, \underline{z}_i) = p_1(y_i, \underline{z}_i) p_2(y_i, \underline{z}_i)$. That assumes independence of the observer's detection probabilities for a given distance and set of covariates. Yes, I know that you observed at different times so you observed independently but that isn't the only problem. Heterogeneity in detection probability will induce dependence and it is the bane of mark-recapture problems. As David Borchers showed in his dissertation, if there is unmodelled heterogeneity (covariates not in the model) then you can write the following equality:

$p_{11}(y, \underline{z}) = \delta(y, \underline{z}) p_1(y, \underline{z}) p_2(y, \underline{z})$ where $\delta(y, \underline{z}) = 1 + \dfrac{\mathrm{cov}[p_1(y, \underline{z}), p_2(y, \underline{z})]}{p_1(y, \underline{z}) p_2(y, \underline{z})}$. Note that $p_j(y, \underline{z})$ and $\mathrm{cov}[p_1(y, \underline{z}), p_2(y, \underline{z})]$ are expectations with regard to variables that affect detection probability but are not in the modeled covariates. If there is positive dependence (covariance) then $\delta(y,\underline{z})>1$ and the probability of a duplicate (seen by both observers) is higher than what it would be based on independence. If there is negative dependence (covariance) then $\delta(y,\underline{z})<1$ and the probability of a duplicate (seen by both observers) is less than what it would be based on independence. Positive dependence is the more normal situation in which the covariate (not in the model) affects the observer in the same way, making it easier or harder for both observers to detect.

So what is the relevance of all that mathematics you say? If you assume that detection probabilities are independent and they are not, you can get a biased estimator. The most likely occurrence with mark-recapture is to get negative bias in abundance due to positive covariance in detection probabilities.

But how did the Palka estimator avoid that assumption that you call "full independence"? She avoided it by fitting a separate detection $p_{11}(y,\underline{z})$ for the duplicates. She did not restrict it to be the product of the detection functions $p_1(y,\underline{z})$ and $p_2(y,\underline{z})$ like analysts 3 and 4 suggested. It wasn't restricted because those detection functions were fit separately.

No hold on a second, the biologist interjected. I may be just a dumb biologist but couldn't that be a problem and didn't she assume independence. She did assume that $p_{11}(0)=p_1(0)p_2(0)$. You have made a very good observation on both points. By fitting the detection functions separately it is quite possible to get a situation in which $p_{11}(y,\underline{z})>p_j(y,\underline{z})$ which is nonsense logically because the probability of the intersection of 2 events can't be larger than the probability of either event. Also, Palka(1995) does assume independence but really only at y=0.

That is where Laake(1999) (Laake, J.L. 1999. Distance sampling with independent observers: Reducing bias from heterogeneity by weakening the conditional independence assumption. In: G. W. Garner, et al., editors, Marine mammal survey and assessment methods. A.A. Balkema, Rotterdam; Brookfield. 287p.) comes in. He just happened to be in the right place at the right time and recognized that 1+1=2 (at least on some days). Borrowing heavily from Borchers and all those that published before him, Laake(1999) recognized that Palka's estimator could be cast into a likelihood framework using 3 separate detection functions and 2 restrictions: 1) he structured the probabilities $\Pr\{\underline{\omega}_i \mid y_i,\underline{z}_i)$ based on the 3 detection functions rather than using 2 with the independence assumption and he required them to be non-negative in the optimization and 2) he used detection functions designed to enforce the independence at y=0. He analyzed the stake data from the crazy guy in Utah and showed that full independence was not a good assumption and assuming independence at y=0(which he called trackline conditional independence and what we now call point independence) was better. He also showed that if you assumed full independence, it was possible to get lower abundance estimates from mark-recapture distance sampling (which he called distance-sight-resight) than just distance sampling. He also showed that couldn't occur if you used the weaker assumption of point independence.

Now it is reasonable to argue that if Laake(1999) had used covariates other than distance that maybe full independence would have worked better and maybe it would be more likely that point independence at zero would hold. Fair point! Laake expanded on his work to include covariates in (Innes, S., M.P. Heide-Jorgensen, J.L. Laake, K.L. Laidre, J.J. Cleator, P. Richard, and R.E.A. Stewart. 2002. Surveys of belugas and narwhals in the Canadian High Arctic in 1996. NAAMCO Sci. Publ. 4:169-190.) while analyzing some data on beluga and narwhal surveys for a colleague (Innes) who was tragically killed while surveying (this is not always a safe business). While the code he developed was a little quirky and testy because of the numerical constraints, all seemed well.

He then took on the task of analyzing some independent observer murrelet data from small boats. Alas, the code he so cleverly designed had real problems converging in the optimization and was taking forever on his spiffy new computer. Slowly, he came to the realization that there must be a better way to formalize point independence. Well after a month of emails back and forth to David Borchers and much head scratching while lounging in the hot-tub, the obvious answer (in hindsight) finally appeared. Merge the solutions of analysts 2 and 3.

Well wait a minute isn't that what analyst 4 did. Well yes, but merge them without sharing detection functions in the 2 likelihoods. Use the distance sampling likelihood to estimate $p_{\cdot}(y,\underline{z})$ except that you can't really get $p_{\cdot}(y,\underline{z})$ and all you really get is $g_{\cdot}(y,\underline{z}) = \dfrac{p_{\cdot}(y,\underline{z})}{p_{\cdot}(0,\underline{z})}$ because the intercept $p_{\cdot}(0,\underline{z})$ cancels out in the likelihood for distance sampling which is why you have to assume that $g_{\cdot}(0,\underline{z}) = 1$. By using the solution of analyst 3, you are estimating conditional detection functions (i.e., $p_{1|2}(y,\underline{z})$ and $p_{2|1}(y,\underline{z})$ - the probability that the first observer saw it given that the second observer did and vice versa). The appendix of Borchers et al (2006) (Borchers, D.L., Laake, J.L., Southwell, C.. Paxton. C.G.M. 2006. Accommodating unmodelled heterogeneity in double-observer distance sampling surveys. Biometrics 62: 372-378.) shows that if you accept that there is unmodelled heterogeneity, then in reality you can only estimate the conditional detection functions with the mark-recapture likelihood and they won't equal true unconditional detection functions $p_j(y,\underline{z})$ unless all heterogeneity is correctly modeled (how likely do you think that is). Point independence amounts to assuming that $p_{1|2}(0,\underline{z}) = p_1(0,\underline{z})$ and $p_{2|1}(0,\underline{z}) = p_2(0,\underline{z})$ and $p_{\cdot}(0,\underline{z}) = p_{1|2}(0,\underline{z}) + p_{2|1}(0,\underline{z}) - p_{1|2}(0,\underline{z})p_{2|1}(0,\underline{z})$.

By re-posing the problem, the mark-recapture and distance sampling likelihoods don't share parameters, so the parameters of each can be obtained independently. Thus, there are no problems with constraints and existing software can be used. Hard to believe but what was once a difficult problem to solve numerically because of the constraints becomes a much easier problem (note: numerical optimization is still required for distance sampling). If however, you were to assume full independence (a much stronger assumption) parameters are held in common and the likelihood components must be optimized jointly.

The example in Borchers et al (2006) demonstrates an analysis of some survey data of crabeater seals in the Antarctic using only the mark-recapture likelihood and then using both mark-recapture and distance sampling with point independence. A very large number of covariates were examined but still they could not remove all the heterogeneity. Because $p_{\cdot}(0,\underline{z})$ is close to 1 in this example, the solution of analyst 2 would have worked nearly as well but that is not always the case. This example also illustrates that the estimated abundance can be lower than distance sampling (solution of analyst 2) if you use only the mark-recapture likelihood (solution of analyst 3) and there is unmodelled heterogeneity. That problem would have been lessened with the solution of analyst 4 (full independence with both components of the likelihood). Logically, using mark-recapture distance sampling should not lead to a lower estimate than using distance sampling because $p_{.}(0,\underline{z}) \le 1$. That logical inconsistency can't occur with point independence.

After the biologist's awoke from their nightmare fairy tale they discussed their adventure and decided they were thankful that they weren't working on whales. Can you imagine how much more mathematics those analysts would have thrown at us if they had to consider that whales dive and are not always visible. *The End.*

From the author:

Now that was a much longer fairy tale that I intended. Believe me, I could go on even longer but I'm sure your head is getting close to hitting the table by now. I hope that you find this story useful in sorting through the myriad of papers that exist in the literature on estimation of detection probability (visibility bias or an assortment of other names). Before you nod off (not that I'd blame you), I want to say that this is a very real problem confronted by biologists that want to collect visual survey data. What method should I use?

There have been two concurrent streams of methods being used in the literature seemingly ignoring one another: one using distance sampling and the other double-count mark-recapture ideas. For the last decade or so these methods have been merging. And yet, all you have to do is look in the current issue of the Wildlife Society Bulletin and you'll find a paper on surveying deer solely by double-observer with no inclusion of distance sampling concepts (Potvin, F., L. Breton and L-P. Rivest. 2004. Aerial surveys for white-tailed deer with the double-count technique in Quebec: two 5-year plans completed. Wildl. Soc. Bull. 32:1099-1107). Other biologists confronted with different techniques try them all and see which one works "best" (Walter, M.J. and J. Hone. 2003. A comparison of 3 aerial survey techniques to estimate wild horse abundance in the Australian Alps. Wildl. Soc. Bull. 31:1138-1149). "Best" can't be determined without a known population. Walter and Hone (2003) presume that "best" is "highest" based on the premise that visibility bias and heterogeneity will reduce the abundance estimate. Walter and Hone (2003) provide a good field example of the effects of heterogeneity especially in their comparison of the Petersen estimator with a widening strip.

Unfortunately, Walter and Hone (2003) didn't take the next step to do an integrated mark-recapture distance sampling analysis. Probably they didn't do so because software wasn't readily available. That has been corrected. The analysis ideas I have described here have been coded using the R statistical programming language and they are available in the DISTANCE software v5.0. There is still work to do but hopefully in the not too distant future, mark-recapture distance sampling will become the norm for the situations in which it is applicable.

Veracity disclaimer:

Hopefully no one will take my ribbing seriously and realize that any good fairy tale is both factual and fictional. I find that math is easier to swallow with a good laugh. But to be sure I'll make the following corrections.

1) Analysis-R-Us is not a real company as far as I know.
2) None of the statements about or attributed to Bryan Manly were truthful. I only picked on him because he was the senior author on the polar bear paper which I think was an important advancement. He is a quiet and unassuming fellow and it

is unlikely that he has a niece or nephew that works for Analysis-R-Us. Also, I have no idea whether he drinks spirits around a fire at Christmas time.

3) I'm the crazy guy from Utah with the stake data.
4) None of the analysts described here are real and I'm sure that none of the real analysts would be quite as bold and obnoxious as my fictitious analysts. Nor are the biologists real and I'm sure they aren't as clueless as I made them appear.
5) The comments about MARK were truthful. In my opinion, design matrices are a pain especially if they get large, but MARK is an extremely valuable software package.
6) Hell may be a strong adjective for FW663. I guess it depends on your mathematical level. It certainly pales in comparison to some Stats theory courses. If you are interested in estimation of animal abundance and survival estimation, I highly recommend FW663.
7) Since I'm a federal government employee, I should say that I did not receive any monetary or other benefit from my blatant advertising of DISTANCE, MARK, Gary's MARK workshop and FW663.