This chapter reviews and discusses the implications of assuming a homogeneous point process. This chapter is important because many ecologists are deterred from using SCR because of this assumption. Additionally this chapter discusses how SCR can be used to assess habitat associations between activity centers and environmental covariates (habitat) which is a goal of many ecological studies.

Lines 1052: Example

I don’t think it’s obvious from this example what you are trying to show unless you point out somewhere that the nP <- rpois(1, muP\*Area) is going to produce a different number of points each time, while the Binomial is fixed. Because there is no output from the code, you have to know what to look at and I don’t think everyone will. Also if you are unlucky you might get a four the only time you run the model for the Poisson. Maybe run a loop save the nP’s and plot of histogram of them? Maybe run a loop and plot the PPP everytime a new one is made so the reader can see that a different number of P’s is produced for every run?

Line 10234: Why is the data augmentation rate and thinning rate the same? I think this is the point you are trying to demonstrate but I missed it (it made a whooshing sounds as it went by).

Again I think this example suffers a little because there is nothing to see in the R window when you are done and ecologists (like me) like pictures.

Lilne 10333: an extra “the”

10361: I’d move up the point that you need to use the R2Cuba package or hapless ecologists will go searching for it on their own before reading ahead.

10395 if you add the line plot(s) then the reader will see that they get the plot from Fig 11.2

10410 : I get the error “Error in solve.default(fm$hessian) : Lapack routine dgesv: system is exactly singular” after running

nll <- function(beta) { # negative log-likelihood

beta0 <- beta[1]

beta1 <- beta[2]

EN <- cuhre(2, 1, mu, beta0=beta0, beta1=beta1)$value -(sum(beta0 + beta1\*elev.fn(s)) - EN) **###is this correct as one line??**

}

starting.values <- c(-10, 0)

fm <- optim(starting.values, nll, hessian=TRUE)

cbind(Est=fm$par, SE=sqrt(diag(solve(fm$hessian))))

If I run the binomial function I get the right results but an error that In dbinom(x, size, prob, log) : NaNs produced

Line 10471: K seems to be missing…..

fm1 <- scrIPP(yz, X, M, 10000, xlims=c(0,100), ylims=c(0,100),

space.cov=elev.fn, tune=c(0.4, 0.2, 0.3, 0.3, 7))

plot(mcmc(fm1$out))

10495 “parameters” instead of “parameter” ?

Line 10501 : composed “of” and Chap ?? should probably be filled in

Fig 11.5 and Fig 11.6 you have a note about changing to gray scale.