Estimating abundance and density of populations

Question Answer

With regard to slide 22, I'm not sure I get it right. If I understand correctly, n10 refers to the individuals that were marked but not recaptured, and n11 are the individuals marked AND recaptured?
Yes it's correct: 1 means captured and 0 means not captured.

Would the pleger's mixed model not require more sampling to compensate the estimation of more parameter estimations?
Yes it does, more parameters would induce wider confidence intervals and require more data
At the same time, ignoring heterogeneity would cause bias in abundance estimates, guess it's a matter of what's more important to you (unbiased or precise estimates)

is there a test you can use to approximate the required sample numbers then pre-study
You can perform power analysis using simulations to assess the requirements of your models
for capture-recapture simulations, have a look to the "Applied Hierarchical Modeling in Ecology data" (Kery & Royle) books,
https://onlinelibrary.wiley.com/doi/abs/10.2193/0091-7648%282006%2934%5B1028%3APCSSPB%5D2.0.CO%3B2

In models without heterogeneity, shouldn't pi be fixed =1?
you don't need to fix it, it will not be estimated in the model and will remain at the initial value in the Rmark model output

Can you please explain a little more why in pi SE was not stimated?
because pi was fixed pi = 1. Because it is fixed, it means it is not being estimated, so there is no SE
SE is only relevant for parameters that are estimated. Fixed means we already "know" the value. It is the same for any model WITHOUT heterogeneity

You can not have individuals with "unkwnon" sex?
yes you can. Here, it will estimate a value for 3 groups: male, female and unknown.
Some other models (more complex) can also be used to assign unknown sex individuals to the most likely real sex (male or female)
These models won't be treated here
you can check this paper : Nichols et al Estimation of sex-specific survival from capture–recapture data when sex is not always known. Ecology. 2004 Dec;85(12):3192-201.
https://onlinelibrary.wiley.com/doi/10.1002/cjs.5550360105
https://besjournals.onlinelibrary.wiley.com/doi/10.1111/j.1365-2656.2012.01991.x

I thought pi would be the proportion of males and females?
PI stands here for proportion of individuals per category when you include heterogeneity in the model

Is there any matrix models for Tree species?
there is no example on trees. There is one quick example on peonies tomorrow afternoon, but the principles of matrix models (Leslie matrix) can be applied to any species, trees included

Is there a reason why the sum of the two sex population size estimates is lower than the single population size estimate?
that's not the same dataset used

I think I misunderstood the meaning of pi. I thought it was the proportion of the groups specified, ie in this case the 2 sexes. But it's not. So what does pi stand for?
in a model without heterogeneity, parameter PI is not estimated, so it will appear fixed at 0.5 (initial value) without standard error.

Can we do the same for tree population ?
you can use population models for tree species as well, ususally using models with "stades", Aurelien will say a few words about that
see for example authors of this paper https://besjournals.onlinelibrary.wiley.com/doi/abs/10.1111/1365-2745.13533

Thank you for this first module! I was wondering, wouldn't you normally assume that the number of missed individuals f0 DIFFERS between groups?
yes you are correct. Typically, we should always include the group effect on f0
that's what I was thinking too. But shouldn't yoy include it in the pi too then?
but now we included heterogeneity by including sex, so why is PI not estimated?
here we included a sex effect as a group, which means you know the category of each individual
you need PI when you account for unknown heterogeneity : imagine if you could not measure sex on the field, but you know you have two unknown groups in your data
Ah, ok. So the difference is that you expect heterogeneity, but you don't know which individual belongs to which group. Thank you!
no, even in models with heterogeneity you get only one estimate of f0 = number of unmarked individuals in the population

are moving targets in the transect counted? where will you measure the perpendicular distance?
yes, you take them into account ; and measure the perpendicular distance from the INITIAL position

are we still assuming the population demography and geography are closed?
Yes population is closed during the time of the sampling.

do the lenght of transect have to be the same?
Yes, the transect length can be included as a "sampling effort" covariate.

could you also apply this to a fixed point such as a centroid of a radius?
Yes you can count individuals from a point and estimating radius distance from the center 🙂

trying to think how to apply this to aquatic systems where we test density without discrete zones such as MPAs
within descrete zones, sorry typo
there is no problem to apply it to aquatic ecosystems ;-)
https://peerj.com/articles/5066/

will population estimation using camera traps be discussed?
No, not specifically. Most models can also be applied to camera trap. You can find a lot of literature on the topic if you're interested to help ou apply these models on CT data.

the methods covered can also be applied to camera trap data eg capture recapture of individually identifiable species
can camera traps be used as a method of point transects?
specially in crytic and shy animals which run away by human presence.
Some papers on DS on CT : https://besjournals.onlinelibrary.wiley.com/doi/10.1111/2041-210X.12790tps://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/1365-2664.13602
send the links again (there is an error) : https://besjournals.onlinelibrary.wiley.com/doi/10.1111/2041-210X.12790
https://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/1365-2664.13602
links for distance sampling on cam trap papers

is each row an individual? if there are flocks of birds, when will we insert the number of individuals?
In Aurélien's example, indeed each row is an individual. There is a way to implement directly groups (or bird flock). @coline canonne will direct you to the Distance package manual

For more details about options

here each row is an individual. but you can also have 1 row = 1 group, in which cas you will have another variable in your data specifying the group size

Does "no death" include mortalities caused by predators? or does it refer to only natural mortalities?
It includes any mortality
natural anthropogenic mortality - all mortalities combined

As a novice, I see a lot of intrinsic and extrinsic uncertainties in this field. I'm wondering how one would be able to account for these meaningfully, especially in rapidly changing habitats
What do you mean by uncertainties here ? Are you talking about sources and variations of detection probabilities ?
if you want to deal with further complexities in detection probabilities, you can do so by including covariates, with other types of mark-recapture models.
But you need to have measured these covariates on the fields

What if a population is highly dense, and recapture probabilities are close to zero?
For very low detection probability, probably you might increase the number of sessions to get a good precision in your estimations.

Is it possible that the trap-happy effect increases with repeated recaptures?
yes it can as individual learn

what's the implication of the second assumption for individuals of different age?
it will be discussed a bit later (individual hetergeneity on detection)

In the L-P estimator, we assume that m/n_2 accurately reflects the proportion of marked animals in the population.
However with, say, half of the population marked in the first sample, we could still get 7/10 marked individuals in the second sample just by chance.
Is it correct to say that this is due to binomial variation $Np(1-p)$ that we don't always get the expected count Np?
exactly, you get it right! you will not sample exactly m/n_2, the estimator accounts for the uncertainty - the lower the number of marked individuals is, the wider the confidence interval will be
Also Aurélien will talk about mixture models for dealing with heterogeneity later which may be useful.

Do I understand it correctly that that the study area is defined using the maximum distance of individuals detected?
no, the study area is defined a priori, and the transect are then placed adequately in the study area, then you get the abundance for the entire study area

Okay, thank you! ... Could there be cases where it makes sense to combine capture-recapture and distance sampling methods? Or is it per definition for different contexts?
yes, makes sense, see e.g. https://www.biorxiv.org/content/10.1101/2021.02.01.429097v1 en references therein ;-)

In the mouse example for abundance estimation, can we have NA in capture history ? if marked individuals are dead or killed after their first recapture for example
in the example model dead individuals are not dealt with. In the case you would like to add dead individuals you could chose to use another model type, such as Live-dead recovery model
a quick and dirty way to accomodate dead individuals is to censor them by adding a -1 so that the 0's after the last capture are not used in the estimation procedure.

Estimation of demographic parameters using capture-recapture models

Question Answer

Is it possible to estimate demographic parameters using unmarked animals?

For example, could you determine survivorship for a particular demographic class of a species from calculating changes in density over time?

there are several ways to do that. you can do open N-micture Dail&Madsen models (2011), see for exemple : https://esajournals.onlinelibrary.wiley.com/doi/pdf/10.1890/13-1131.1

using the Dail & Madsen model you can also look at https://esajournals.onlinelibrary.wiley.com/doi/10.1002/ecy.1831

To add to your response, would this be possible using camera traps rather than direct counts?

it may be possible, but camera-traps will generate a lot of heterogeneity (i.e. will capture different individual home-ranges etc.)

If my data comes from citizen science (5 years worth of CR data) and I know basically nothing about the individuals in the population (i.e. I do not know age or sex), which model would be best?
Or how do i choose a model?
I was looking at CJS and POPAN. But I do not know how to choose between them.

if you want to estimate survival, CJS or POPAN would do the job, pending underlying assumptions are satisfied

Ok, thank you. Are you going to talk about those? I already tried working with the POPAN JS model, but I had some problems

not in this workshop sorry, maybe look at this paper : https://journals.plos.org/plosone/article?id=10.1371%2Fjournal.pone.0076574

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0166650

what about if I want to estimate abundance changes over time? From what I read, survival in my case (dolphins) can even be assumed constant over time..

the best is Robust Design (if you have several session each year) or Jolly-Seber model

How are survival and detection decomposed in the CJS model, given the unimodal type of data (just detection)? Or have I missed something from the presentation?

you have some 0 between two 1, so you can estimate detection (as you know individual is alive) and then with detection prob you can get survival

if we do not know the sex of a bird, can we make a third group of "unknown"?

no because the birds are males or females. You have to use "multi-event CR models". look at this paper https://besjournals.onlinelibrary.wiley.com/doi/10.1111/j.1365-2656.2012.01991.x

In that case, can we use mixture models when we want to use sex as a covariate but we are unsure about the sex of some of the individuals?

 it seems a bit tricky because you then have to have the mixture only to the unknown sex and force them to have the same values as the known males/females

What do you take into account when choosing between time as a factor (formula=~time) or continuous (formula=~Time)? Is running a model with both (formula=~Time+time) nonsense?

Time is a regression over years, while time consider each year separately , so you canonot put both in the same model

So there cannot be a linear (or more complex even, e.g. polynomial) response as well as a categorical?

I understand that there's some collinearity risk, but still I could imagine situations where both may apply

you would need to put time as a random effect and not as categorical

OK, thank you, that makes sense, although I guess then I wouldn't be able to tell which levels (sessions) cause a potential significant random FX.
Comparing models with either of both (time or Time, not both) with the model without both probably reveals a lot too.

yes exactly, by comparing AIC you know what model is the best. And by using a categorical time effect, this will give you an idead of what year is far from the mean

In the results we just saw, where are the parameters for the group "M"?

the models we saw before (constant and time-dependant), there is no sex effect

In line with what Thibaut says, for the model that is shown here, the estimates are the same for M and F. The output just shows the alphabetically first group level.

What approach is more suited to analyse capture recapture data of multiple years with multiple capture sessions in each year? So with closed population in each year and open population between years?

you can use robust design

you can look at this paper for example : https://journals.plos.org/plosone/article?id=10.1371%2Fjournal.pone.0076574

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0166650

could I determine survivorship for a lemur speciess from calculating changes in density over time period ?

if you have individual data from marked individuals you can apply capture-recapture methods to estimate survival, otherwise you should use for unmarked individuals (described above)

Among others, we refered to this paper using counts to assess survival https://esajournals.onlinelibrary.wiley.com/doi/10.1002/ecy.1831

If you have more than two discrete variables (ie. juvenile, sub-adult, adult) would you use 0, 1 and 2 ?

you have to use two variables (the intercept will be for juv and then you will have two covariates for sub-adults(0/1) and adults (0/1). You will estimate three parameters

What about binary covariates that change with time? i. e., permanent plots that initially weren't protected area then a protected area was established. How to incorporate that change in the model?

then you'll have to make one column per year

 after what i have to make a column?

if your occasions are years, you then put an interaction between time and columns with information about the protection status

In the "Explore results (3)" slide, what do g1, c1, and a0 mean in reference to Phi?

In the parameter estimate summary, what does a0, a1, etc stay for?

c stands for cohort, g for group, a for age and t for time. Here as it is a simple model values are by default the first

you can find some example here : https://rdrr.io/cran/RMark/man/make.design.data.html

age is the time since capture

If I have two discrete covariate columns (age and sex), how do you group them to determine survival for adults, adult male, adult female, sub adults, sub adult female, sub adult male and juvenile ?

you cand fit a model with age, a model with sex, and a model with their interaction using *

you have to use two variables (the intercept will be for juv and then you will have two covariates for sub-adults(0/1) and adults (0/1). You will estimate three parameters

With this statistical framework to estimate the survival probability, does it allow the observed data to have irregular observation intervals?

you can have sessions with irregular time intervals (if you did not conduct field work one year, in this situation you can also leave 0 for all individuals and fix p=0)

Can you explain how to get the wing value that optimizes survival?

When you predict the survival as in slides #52 and #53 you can extract the wing_length value that maximize the predicted survival.

Then you have to "unscale" the value multiplying the scaled value by the standard deviation of the original vector, and the adding the mean of the orignial vector

What about binary covariates that change with time? i. e., permanent plots that initially weren't protected area then a protected area was established. How to incorporate that change in the model?

then you'll have to make one column per year

after what i have to make a column?

if your occasions are years, you then put an interaction between time and columns with information about the protection status

The automatic age assumes we start with a single cohort?

they are here marked as juvenils, so there is an age effect, but you could also add a cohort effect (different years of capture)

So far we've seen how to estimate survival and detection rates, but how does one estimate population size for open populations at each survey year? (Have I missed it?)

Models called "Closed Robust design Multistate" combine both approaches : estimates of N, phi and psi parameters. You should find more information in the Mark book.

phi and psi parameters pertain to intervals, p parameters pertain to sampling occasions, right?

absolutely right !

Can multistate CR model handle latent states (e.g. infected but asymptomatic) if only a subset of individuals are tested using some procedure where Pr(+|infected) is between 0 and 1?
Yes. Using what are called multi-event models. They allow modelling uncertainty in individual state
For multi-event models, you can check this paper https://onlinelibrary.wiley.com/doi/10.1111/j.1541-0420.2005.00318.x
https://oliviergimenez.github.io/pubs/Gimenezetal2012TPB.pdf

but age/dvlpmt stage seems very fixed to me and predictable with the knowledge we have on the species and there is no retrun possible to previous stage...
Yes, but that's not a problem. We can fix the probability of those transition to zero
for sure, but you can fix some transitions probabilities to 0, and some individuals will stay longer than other in somes stages

What is the best source to check for different models? To get some background information. Directly in Mark?
what do you mean by "check for different models" ?? to do model selection ?
No, sorry, to check for model = "Multistrata" for example. TO find out, when it is appropriate
the best option is to look into the Rmark help files (vignette, etc) provided with the package
Following a previous question about the models in RMark, here is a list of all models you can implement and how to call them : https://pdixon.stat.iastate.edu/stat534/RMark/MarkModels.pdf

Thanks. And how does one estimate population size for each state/site at each survey year? Yesterday @Thibaut Couturier suggested a robust-design approach. How to implement it in R?
https://github.com/oliviergimenez/bayesRD

Regarding R2ucare, once the overall GOF test results not significant, the other tests (for trap-dependency and transience for example) should not be even looked at, right?
if the GOF tests are not significant, you don't need to proceed to other tests.
https://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/2041-210X.13014 and https://oliviergimenez.github.io/R2ucare/index.html

Could multisite modles give adequate results if I have only 2 observation occasions and several sites?
no you always need at least three occasions in CR if you want to separate capture prob and survival prob

so you do not need to replace the numbers with letters?
(as in MARK)
No, you can run directly with detection histories made with numbers.

can you make survival conditional on movement? Ie animals that move to a different stratum have a lower survival
Yes, it that case survival will be conditionnal on the state (eg, state at t-1)
And how do you make it conditional?
you can do it when building the design matrix. You will find good examples in the MARK book or on the phidot website. it would be a bit hard to explain the procedure here

Are the psi parameters conditioned on the phi parameters? Else phi should be included when summing parameters to 1, right?
yes the transition probabilities are conditionnal to survival

Goodmorning all. What's the difference between coding -1 + stratum:tostratum and just stratum:tostratum? In other words, what's the difference between a model without intercept and a model with it?
the -1 remove the intercept so you directly have the estimates of each transition, if not then you get an intercept and the other parameters are the differences with other transitions

What if there are more than 10 sites. Does it confuse the model? E.g. With 20 sites a capture history of 1, 5, 18, 0 would read after folding 15180. The interpretation could be also 15,1,8,0
if you have a large number of sites you may go for multi-event models, check thta paper https://oliviergimenez.github.io/pubs/Lagrangeetal2014Ecology.pdf
20 sites ! that's a lot of states !! and a lot of parameter transitions. I doubt the model will run with so many states. But to answer your question, you could use letters instead (A, B, C,....)

What is the minimum amount of years required to determine an accurate rate of increase over years?

it will depends on the inter-annual variance, if high need more years

I don't think this was mentionned before but are any of the methods we went rhough are applicable to cryptic species? If we have lots of sampling efforts but low detection (or low abundance)?
use "site occupancy models"
for rare species, here is an interesting paper to look at : https://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/2041-210X.12842
Thanks - I do'-n't think I can use occupancy modelligg, because of the asumptions for detection. But will check that paper!

Population projection models

Question Answer

could you also use this method to compare reference values=
similiar to a relative difference and interval increases or decreases
if we look at management goals, typically the are in relation to reference states. So I wonder if instead of extinction rate, if we could use lamba and population growth trajectories relative to reference states
yes you can easily do that
sorry, in place of extinction thresholds
was also trying to think of how to implement environmental covariates
you can model the lambda as a function of covariates, that's not hard. you would use a linear relationship for instance

Shouldn't you also constrain the pop growth rate to a maximum, related to the biology of the species? (max number of cubs etc)
you could, but usually you don't need to, here you would have to constraint the whole lambda, as it's not decomposed
why do you not need to? I would expect less extremely positive growth trajectories and higher extinction probability
if your distribution stays in plausible values
because of the observed distrbution of mu that the simulation is based on?
if the variance of the distribution is estimated from the data then it should be right...but we will see later that density-dependence is important too

If you're doing a for-loop with a random number generator, shouldn't you use set.seed()?
it's better practice, but you dont have to. R will set it based on current day/time

Is it possible to use abundance values instead of actual population size?
Do you mean RELATIVE abundance values ?
Yes
Like "Abundance Index" ?
Yes, no problem, as long as your index is reliable
I have RAI values for my focal species and won't be able to determine actual counts. Is it possible to still model pop growth rates for the next "50" years?
I wonder: would it make sense to perform PVA on the number of grid cells (presence-absence data) instead of census data (when population abundance and distribution align well). Such models available?
Yes, if your RAI is relaible. Be careful with variation in your index due to variation in detection. Often, abundance index are not reliable from one year to the next
because detection probability is not constant

Do you have any suggestions on what would be more reliable? i have continuous data collected from 40 camera traps over 4 years on unmarked animals.
there are several methods (REM, STE, TTE) but all have drawbacks. Have a lokk at this paper : https://conbio.onlinelibrary.wiley.com/doi/full/10.1111/cobi.13517
analysis unmarked data from CT is still a topic in active developement - so no easy answer on this one. This specific topic won't be tackled in this course
thank you. I have really been struggling to find literature on it. Unfortunately, I did not get to choose my project design and must now do the best I can with the data.
have a look at the different methods presented in this paper and you should be able to find the one best suited to your case (and you will know what the limitations are)

I can see the paralell you are making between occupancy et pop dynamic, but there are not quite the same, and there is no easy way to transfer the PVA methods to occupancy
It might be feasible but doing so would require some careful thinking because the interpretation of the lambda is not the same as the colonization/extinction dynamic of occupancy
In occupancy, the number of sites is fixed which puts a big constraint on what you would think of as the equivalent of the "lambda" -- so it makes hard to use the same logic
I am not saying it's not feasible, just harder than we would think of at first glance. I don't think anyone has done it in the literatur. But maybe you can try to check the literature
thought so... Thank you

Hi there ! I don't really understand why the environemental variance correspond for the mean sq residuals in the ANOVA analysis
because it's the variance around the average slope (here just tje mean lambda)
In other words, it's the variance around average lambda

how many years of data we have in order to use PVA?
 it will depends on the inter-annual variance, if high need more years

If we want to look at the demographic structure of a population at t+1, could you incorporate the different survival rates (N0 and u) for each demographic class?
yes sure, we will see that a bit later with matrix models

is chick survival the survival until fledging? ie a shorter time period? or survival in the 1st year?
survival in the 1st year

assuming a 50:50 sex ratio
is th sex-ratio is not 50:50 you can add this parameter in the cycle
thank you. I think my focal spp. all have 50:50 sex ratios.

are there any good papers or we will discuss populations with sex biased ratios that you may know of ?
Kendall et al. 2019 on Ecological Modelling explain why newborns reproduce as Sarah explained
This one I guess : https://www.sciencedirect.com/science/article/pii/S0304380019301085
you can look at this paper (and cited refs), with both sexes and unbalanced sexe ratio : https://onlinelibrary.wiley.com/doi/pdf/10.1111/ecog.05738

You are only considering females in the population right?
yes
this is modeling females only

With F1, would this refer to the females that are still less than 1yo or does it refer to the # of offspring produced when they are 1yo (ie. when they enter adult class)?
I'm looking at juveniles, sub-adults and adults but according to my classes, only adult females can reproduce.
Oh, I see it depends on pre- or post- breeding census. I understand now.
ok, good.

If you have a 3 to 4 year life cycle and only count adults (which live a few weeks only), can you then relate Nt as a function of Nt-3 and Nt-4?
can you specify what you want to do ? You mean an autoregressif model of adults counts ?
I want to asses population size changes and we yearly count the number of adults along transects
yes you can do that (look at papers on cycles on salmon populations for ex)
Thanks, I will use it on insect so it shouldn't be uncommon there as well for beetles, dragonflies
it can be done on insects no problem as long as you know the life cycle (stages and parameters values : survivals et fecundities)

This projection is assuming a stable age distribution, right?
at the beginning of the projection, not necessarily. Stable Age dist is reahced asymptotically

yes, after the transition phase

I wonder: would it make sense to perform PVA on the number of grid cells (presence-absence data) instead of census data (when population abundance and distribution align well). Such models available?
Yes, if your RAI is relaible. Be careful with variation in your index due to variation in detection. Often, abundance index are not reliable from one year to the next
because detection probability is not constant

is there a way of doing this kind of analysis but on a 2d grid model for exemple ?
with the popbio package i mean
what is your 2nd dimension ?
sorry my question was unclear
my two dimensions are X and Y on a map for exemple
a standard grid model
like the "game of life" for exemple
you then need to use spatially explicit approaches
i see, but my question was : can this package do it ? ahah
but do you have 1 pop per cell in your grid ? do individual exchange between cells ? it is unclear
No it cannot
okay thank you everyone !

I'm not sure if I missed it, but where did the survival values come from for the Barn swallow example?
they come from the litterature - it's just a pedagogic example
thought so... Thank you

how do we calculate the inital population size in a open population for the Matrix population models? Can we use the superpopulation obtained from the POPAN analysis?
yes you can use a POPAN estimate. Any mean of estimating pop size will do (as long as it's reliable) - like the methods that were shown yesterday in the class

Is there a stochastic version of the projection in popbio?
yes you can perform environmental stochasticity in popbio

The calculated population sizes at the various timesteps in the last example were the numbers for females, as we were only looking at females?
Total population size is the number of femal animals?
yes only females here
yes as the model is female-only
if the sexratio is 50% and stable in time yes (rarely the case in practice)

Just to clarify, this is based on pre-breeding census right?
yes pre-breeding with 2 age classes
if it were based on post breeding, would you just describe the 3 age classes in the same manner?
thanks, only wanted to make sure. So in the end I can double the value due to a balanced sex ratio
yes

What kind of sampling is performed for parameters in vitalsens? Is it "one-at-a-time" or global ?
not sure exactly how it's done in the bg, bu it's a global evaluation of each parameter. Probably based on derivative math functions
Ok thanks, so it takes into account possible interactions between parameters varying both fecundity and survival from their reference value simultaneously, for instance?
there is no interaction between parameters here. The sensitivity is specific to each parameter. Basically, parameters are independent of each other.
sensitivity is only conditional on combination of the "fixed" values of parameters you specified in the matrix

within function `vitalsens()`, by how much are parameters preturber? Or it does not matter as we look not on the (elasticity) values themselves but compare the ranks in parameters?
parameters are not "perturbed" by some arbitrary value - the calculation of sensitivity is based on derivative math functions

How would you introduce or estimate the covariance of parameters within the Leslie matrix?
dealing with covariance imply to code your own stochastic projection (popbio does not permit that)
 Thank you, I didn
t think popbio had a way but was hopeful 😊 coding on my own it is
or use yearly matrices
if you want to code it then you can use the covariance matrix when you draw annual values (as Sarah now)

is there also a function to calculate the sensitivities of lower level demographic parameters (eg nest success in fecundity)?
yes, if you decompose survival and/or fecundity parameters in the matrix.
eg if yiou write fecundity as the product of lower levels parameters

Would an increase in predation be considered as environmental stochasticity ?
if you have a trend in predation or abrupt change then it is not stochastic as it is structured over time
so I could use deterministic modelling then?
not really because the parameter schange over time but you should code a loop with a change in some vital rates over years

Thank you! With a normal distribution, how are you keeping rates between 0 and 1?
you can use a logit transformation
you should work on logit scale but it is a bit tricky to get the covariance then
Easier to use beta distribution and then covariance is easier?
yes exactly

Couldn't predation be treated as stochastic if you used a gamma distribution of time to the abrupt change caused?
not sur to understand but if the change is a trend or a before/after then it is not stochasticity per se
if there is a real trend of predation, not really. you should model the trend or the abrupt event separately from the stochastic variation

how do we calculate the inital population size in a open population for the Matrix population models? Can we use the superpopulation obtained from the POPAN analysis?
yes you can use a POPAN estimate. Any mean of estimating pop size will do (as long as it's reliable) - like the methods that were shown yesterday in the class

Is there literature you would recommend on two sex models?
you'll find interessting refs in this papers : https://besjournals.onlinelibrary.wiley.com/doi/pdf/10.1111/1365-2664.12177
or : https://onlinelibrary.wiley.com/doi/pdf/10.1111/ecog.05738

is it possible to estimate sensitivity from the stochastic models?
I think sensitivity remains the same regardless whether it is a deterministic or stochastic model. So yes, it is the same sensitivity as before

Do you know of a way to include both sexes if e.g. the males are the only ones that provide parental care (thinking of emus and cassowaries).
The females then guide fecundity through clutch size, but the males guide it through hatching rate and juvenile survival. So if a male dies at that point the juveniles' survival would also be impacted
Just out of curiosity
in a PVA exercise you do not model the effect of parents on offspring survival. PVA are more general models of pop dynamics. You can include both sexes. Refer to the paper sent

is Caswell a good reference for all matrix models, including those with demographic stocasticity? or any other recommendations on that?

Caswell is definitely a very good book