GDISTSAMP DISCUSSION

Using year-stacked gdistsamp analysis to determine density trend.

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Rory Macklin

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Hello all,

Firstly, just wanted to share appreciation for this board. I've been working through an analysis over the past few weeks and this board has been immensely helpful. The information shared here has certainly shaved weeks off of my analysis time.

Secondly, I wanted to ask a question regarding the interpretation of a year-stacked gdistsamp analysis. I have a dataset of 22 avian point count sites that were visited twice per year for 5 years and have stacked these data, modeling availability against a categorical "Year" variable to account for inter-year variation (as suggested here: <https://groups.google.com/g/unmarked/c/VWJfixK6Z2k/m/RqHQDjrqd8cJ>). I've estimated density by multiplying lambda by the year-specific phi (again, suggested in the previously linked thread).

I'm interested in the potential for using these year-specific density estimates as a way to measure trends in density. Although it's unlikely a trend would be detected over 5 years, I am trying to set up my analysis such that as data accumulates through this monitoring program, it can be applied to the expanded dataset. Would it be appropriate to interpret changes in the density estimate year to year (lambda \* year-specific phi) as changes in population size?

It's also mentioned in the linked thread that you could get standard errors on density/abundance estimated this way using the "delta" function or bootstrap. Would anyone be able to outline the process to compute these?

Again, much appreciation in advance for the input. Totally invaluable!

Rory

Jeffrey Royle's profile photo

Jeffrey Royle

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to unma...@googlegroups.com

hi Rory,

 I think the best thing to do here is just to introduce a year as a "site variable" (i.e., value = 1 for the first 22 rows of the matrix, value  = 2 for the next 22 rows, value = 3 for the following 22 rows, etc...) and then you can just model trend explicitly on lambda.  If I'm understanding your question correctly then I think this will work.

regards

andy

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\*\*\* Three hierarchical modeling email lists \*\*\*  
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(2) SCR: for design and Bayesian or non-bayesian analysis of spatial capture-recapture  
(3) HMecology: for everything else, especially material covered in the books by Royle & Dorazio (2008), Kéry & Schaub (2012), Kéry & Royle (2016, 2021) and Schaub & Kéry (2022)  
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Rory Macklin

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Hi Jeffery,

That sounds like a good solution to me. If I was to implement this, would I remove Year as a categorical predictor on phi and just take lambda as a direct estimate of abundance rather than multiplying it by phi? Or, would it make more sense to maintain a year-specific phi and calculate density the same way.

Thanks very much,

Rory

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Jeffrey Royle

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hi Rory, I'm not sure. In principle I think models with trend in lambda and year-specific phi should be identifiable.  So you could keep doing it that way, although personally I would think hard about having 5 parameters to describe phi. That's a lot of parameters for 22 sites per year.

regards

andy

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Rory Macklin

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Hi Jeffery,

Thanks for the input. I think accounting for year in the lambda model should be enough as I don't expect too much variation in by-year availability since the time span I'm currently working with is quite small.

Just one clarifying question, since the local population at a site *N\_i*~ Binomial (*M\_i, phi*), the predicted *N\_i* would be the expected value of this distribution: E(*N\_i*) = E(*M\_i*)\*phi = *lambda\_i \* phi*. Thus, to predict density at a site, I should multiply the predicted lambda and phi for that site's values. Am I understanding this correctly?

Thanks very much,

Rory

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Jeffrey Royle

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Jul 13, 2022, 7:51:36 AM

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to unma...@googlegroups.com

hi Rory,

 I think that is correct. You should obtain predictions of phi and lambda for all sites and then multiply them.

regards

andy

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And what about the standard errors for these derived quantities, Andy ? I presume, bootstrap them ?

What about the following ?

* Nonparametric: repeatedly (e.g., 1000 times) draw a sample (with replacement) of n sites out of your real data set containing n sites, fit the model and estimate phi and lambda, multiply them and save that product. The SD of the 1000 products will then be the SE of the desired quantity
* But what about the following ? Simply draw a large sample (e.g., again 1000) from a Normal distribution with mean equal to the MLE of lambda and sd equal to its SE, and do the same for phi as well, and then multiply these pairs of values for every draw and obtain a resampling distribution of the product in this way… Would this be a valid approach ? Could it be called a parametric bootstrap (because it assumes normality) ? What simplifying assumptions does it make (e.g, zero covariances between the estimates) ?

Thanks, and best regards --- Marc

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