

EDUARDO FERNANDEZ PASCUAL

From: David Jenkins <David.Jenkins@ucf.edu>
Sent: jueves, 18 de enero de 2018 17:37
To: Emma Ladouceur; Eduardo Fernandez Pascual
Subject: Re: Invitation for collaboration
Attachments: Andreucci etal 2016.pdf; Quinn 2017.pdf; Bytnerowicz & Carruthers 2014.pdf; Parmoon etal 2015.pdf

Hello Emma and Eduardo,

Thank you very much for the invitation to collaborate - I am flattered.

I agree that segmented regression (e.g., the segmented package in R) would be an improvement over methods used in the papers you provided. But my further brief exploration in the literature indicates that others have been using more sophisticated models - some quite complex. And I already found some interesting results, such as:

- Parmoon et al. (2015) find a beta function (smooth unimodal peak) is more plausible than a segmented model by AIC. Simple paper but legitimate model comparisons and a few sophisticated curves.
- Bytnerowicz & Carruthers (2014) use a rough equivalent of segmented regression and the Logan function but do not compare via AIC. They favor the Logan model.
- Though for arthropod larval development and fitting different functions than cardinal temperatures, Quinn (2017) evaluates 33 different models (!), including Logan models and derivatives.
- Andreucci et al. (2016) preferred the Lactin model (a derivative of the Logan model) to the bilinear model. But their Table 6 shows this was not always justified.

And so I can't help but wonder - why aim to develop a package aimed at segmented regression, when people can simply use one that already exists in R (<https://cran.r-project.org/web/packages/segmented/segmented.pdf>)? I know some do not (will not), but the option already exists.

And: I have been wrestling with related regressions, but didn't know such a diversity of functions existed. And: I bet others are like me - we know of some of these functions, but wish there was a way to implement and compare them in R that is easier than building them by hand.

So I suggest a more full comparison among all reasonable models for ecologists interested in nonlinear model fitting, based on AIC weights, etc., and aimed to list thresholds (including cardinal temperatures), confidence intervals, etc. as output. Alternative models could even be selected from subsets - e.g., linear, peaked, asymptotic, etc., where model choice could come from a list that includes indicators of model complexity (number of equation terms) and shape (e.g., peaked and left-skewed, or something like that). And I think segmented regressions could serve as a base for every subset. For example, a sigmoidal set would include a segmented model with two breakpoints. This might actually have broader application than to just the seeds world (see Quinn 2017), and thus have more appeal to a journal, and as an R package of more general utility, especially given the exponential accumulation of R packages.

Finally, I should tell you that unlike David Zeleny, I have never developed an R package, nor do I aspire to. I am more at the end-user side of the stats world. So I expect my role in this potential collaboration would more likely be related to finding appropriate algorithms to include, testing code with example data, writing, etc.

Please let me know your thoughts, and if the potential direction suggested above is beyond where you wish to go, I fully understand and would be content to exit stage left and wish you well.

Thanks again for writing me!

Sincerely,
Dave Jenkins

~

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~

From: Emma Ladouceur <emmala@gmail.com>
Sent: Wednesday, January 17, 2018 12:35:21 PM
To: David Jenkins; Eduardo Fernandez Pascual
Subject: Invitation for collaboration

Dear David Jenkins,

As you know, because i wrote you an informal note before, my colleague Eduardo Fernández-Pascual (Cc: attached) and I have been working on an analysis method to standardize the measurement of seed germination traits in R.

In brief review, the methodology is the physiological thermal time approach, which is frequently used in seed research. The implementation is through segmented models to calculate the three cardinal germination temperatures: base (i.e. minimum), optimum and ceiling (i.e. maximum). Current implementations in seed biology introduce user bias and are time-consuming, holding back the use of these germination traits in other fields of plant ecology. We submitted an early application, in the form of a script, to Methods in Ecology & Evolution. The reviewers and editor said that the application had potential, but ultimately rejected it, asking us to make it a package, and get some people who are more statistically minded on board. We would like to take another try at submitting with the changes they have suggested.

We have discussed it, and we think the next step is to get co-authors on board to help us with this. We are writing emails today to ask both you, and David Zelený (<http://www.davidzeleny.net/doku.php>) if you would like to be formally involved, and if you think you could help add value to the task at hand. Eduardo has a new position at the University of Oviedo (Spain) focused on analysis tools for seed germination. I have a new position at the German Centre for Integrative Biodiversity Research (iDiv) in Leipzig, Germany. We will both have resources for some logistical support, open access publishing, etc. Once the initial cardinal temperatures package is fully developed and published, we intend to continue expanding the suite of tools the package might offer.

If you would like to see more detail before you commit to anything, please do not hesitate to ask. Again I think I sent this before, but just for your convenient reference, I attach the first classic paper introducing this method, and a modern paper using other software. If interested, I can send along the material we have so far. Let us know what you think.

Best wishes,

Emma Ladouceur & Eduardo Fernández-Pascual

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