(Original reviewer comments are quoted in purple)

**Question 1: Testing the existence of a breakpoint**

*On page 6 lines 16-17, the authors write: `The final germination.. Figure 1, which needs to be inspected visually for evidence that the temperature treatments used in the experiment do represent the full germination temperature range'. Rather than relying on visual (subjective) inspection (that should be avoided as stressed by the authors) I am wondering if a statistical test could be used. The point is to test if the germination- temperature relationship is linear or piecewise linear (i.e. segmented). The package segmented should include functions to test for the existence of the breakpoint.*

The reviewer suggests using a statistical test implemented in *segmented* to check the existence of a breakpoint, rather than visually inspecting Figure 1. While this step was meant also for users to decide if their experiment was sufficient or not, we agree that explicitly testing this would be helpful, and maybe it could be a checkpoint that automatically decides whether to forward data to step 3a or 3b. Could you point out the best way to implement this test?

**Question 2: Confidence of the breakpoint calculation**

*Page 5, line 12.  I don’t see how R inherently removes bias given that a person had to create the algorithm that was programmed into R.  Rather, this procedure just automates what the person programmed and any inherent bias of the programmer is going to still be manifest in the procedure.*

*[…]*

*Page 9, line 5.  Your description of how the procedure identifies the breaking point is insufficient.  This seems to be the key procedure given that once identified, the sub and supra-optimal linear regressions are pretty straight forward.*

On a question related to the previous one, the other reviewer argued that the algorithms implemented to determine the breakpoint could be as biased as a person deciding on a case-by-case basis. How can we refute this, and is there any output that we can include to support the confidence of the breakpoint estimation?

**Question 3: Fitting a linear model when there is no breakpoint**

*The proposed STEP 3b is to fit separate linear models in the sub- or supra-optimal germination temperature ranges. I am wondering if (and why) it is really necessary. I think it is not.*

*For the panels where breakpoint has been estimated, the fits could be very similar to the fits from segmented models. Note very similar and not the same. In fact fitting two separate regression models for covariate values less or more than the breakpoint does not imply the intersection point is the breakpoint. Rather it will be different!*

*The linear fits could be added in the appropriate panels of Figure 3. In other words, Figure 4 (and relevant code) could be removed or the authors should motivate it carefully.*

We did not explain the reasons for step 3b / Figure 4 well in the manuscript, and perhaps this point warrants discussion before we reach a decision on whether to keep it or eliminate it. We have proposed step 3b, related to Figure 4, for the following motivations;

* It eliminates the need to ‘throw out’ data when common problems are encountered in germination data, and allows for an option for partial analysis when the experiment was not successful in identifying the full temperature range of a given species, or a full piecewise regression, as a discussion point for next steps;
* It demonstrates the difference between a segmented model that might not fit perfectly (often germination data can be irregular), and two linear models;
* It can give the statistical fit of each line (R2), as is sometimes necessary for publication or requested by reviewers;

It has been suggested that instead of Figure 4, the linear fits could be added to the appropriate panels in Figure 3. We are not sure how to accomplish this, and wonder if you might have a suggestion. Maybe a single step can be implemented within segmented, in which a linear or a piecewise linear model is fitted, depending on the test commented in the previous question?

**Question 4: Weights in the dose-response models**

*In step 2 the authors use the function drc to fitt dose response models. In the source file the authors define the function CGfun in turn calling, for instance*

*m1 <- drm(G/PG ~ Time, data = x, type = "binomial", fct = LL.2())*

*I see no weights argument is specified (which should be 25 in the example in the manuscript). Please make sure if such argument should be specified (I think so.., see ?drm).*

We would like to implement this is a way that makes the value of weight dependent on the data being analysed. However, we are not sure what would be more correct to consider as weight value, given the characteristic of the experiments. These experiments are usually done by sowing a number of seeds in a number of containers. So, would the correct value be the number of seeds per container, the number of containers, or the total number of seeds?