The authors discuss a standardised statistical framework to estimate germination cardinal temperatures. The framework relies on a couple of statistical models, including nonlinear and segmented models.

The proposed model avoids subjective assessments to identify sub- or supra-optimal temperature ranges, and thus it could turn out quite useful for practitioners in applied Ecology. Some issues of mine are reported below. The manuscript is, in my opinion, worth publishing, however it could benefit greatly from a statistician that could be involved in the paper/project. Currently there are several mistakes and inaccuracies typical of people 'able' to using sophisticated statistical models but with no sound statistical background.

Major Points

- I apologizes for the probably silly question, but I am not familiar with such application. I am wondering what is the connection between step 2 and step 3a. It seems to me that step 3a (the most important) can be carried out with no information gained in step 2. The authors should discuss this point clearly.

- 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.

- In step 2 the authors use the function `drc` to fit 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`).

- Figure 3 is not exactly correct (and likewise object `BLfig` in the code file). In fact in some panels (t20, t60,...) the fit is not piecewise linear, and thus 2 breakpoints (erroneously) appear! The issue depends on the function `BLfun()`. In that function I suggest to replace the line

  ```
  data.frame(Treatment=unique(x)$Treatment, Rates=broken.line(seg)$fit)
  ```

  with

```
new.x<- sort(c(unique(x)$Treatment, seg$psi[,2]))
data.frame(Treatment=new.x,
Rates= predict(seg, newdata=data.frame(Treatment=new.x)))
```

- 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.

Minor Points

- On page 5 line 5: 'keeping the columns, their order, and their column names'. i don't think the order is necessary, provided the names are correct.

- At line 43 in the source code file (i.e. 'supplementary_information_2.R'), name in read.table() is wrong (it misses underscores and a capital letter..)

- At lines 46 and 55 in the code file: there is no reason to print on the console the whole dataframe `dat1` or `dat1[,2]`. the same at line 172 (`GR`). I suggest to use `View` (e.g. `View(dat1)`) to have a look at the dataframes.

- Please explain the column names in the output files ('Table-S2-Germination-rates.txt' and 'Table_S3_Segmented_model.txt', 'Table S4 Linear models.txt')

- It seems the reference of the segmented package is wrong (on page 6, line 9: '(Vito, 2008)'. In fact by typing in R `?segmented`, I get
  Muggeo, V.M.R. (2003) Estimating regression models with unknown breakpoints. Statistics in Medicine 22, 30553071.
  Muggeo, V.M.R. (2008) Segmented: an R package to fit regression models with broken-line relationships. R News 8/1, 2025.
  The authors should include both (right) references in their manuscript.