The authors have significantly improved the manuscript, but there are still some (mostly minor) problems. References to biological examples are still missing.

#1 (Problem in naming and interpreting the beta parameter)

Line 153: “We refer to the parameter as the density dependence parameter or density dependent effect since it quantifies the strength of density feedback on the population growth rate.”
Line 225: “depend on the strength, beta, of density regulation.”
Also other lines.

I don’t think calling Beta “strength of density dependence feedback“ / “strength of density regulation” is neither precise nor “intuitive” for biologists.

The strength of density dependence should depend on Y_t. It should be weakest with Y_t close to zero and increase with Y_t. It can measured as a “force” against population growth r. In the Gompertz model, it is 1 - log(Y_{t-1}) / log (K). For Y_{t-1}=K it takes value 0, so a population has r*0 =0 growth rate. When Y_{t-1}>K it takes negative values leading to a reduction of population.

You define Beta as: Beta = 1 - r / k. It is clear from lines 173/183 (equation 4 and 6) that Beta does indeed describe the feedback in the Gompertz model. However, Beta is not only (solely) related to the effects of density dependence, but describes both the effects of density dependence and the intrinsic population growth rate r at the same time (Beta is a function of r). Therefore, in my opinion, your interpretation/naming of Beta is misleading. An short explanation similar to the above should be included in the article.

Yes, by fixing r you can compare different density dependence (feedback) effects using different Betas but you should mention (also in the figures) that the results are specific to a single r value. Showing that your results are qualitatively similar for r values other than 1.2 would be great.

See also #12

#2 (Clarification needed)

Line 133: You wrote that “realized growth rate Y_t/Y_{t-1} decreases with increasing population size”. So, increasing Y_t or increasing Y_{t-1} ? Is this effect independent on r and K values? Please clarify what do you mean in the manuscript.

#3 (Typo in equation)

Line 147: Probably a typo in your equation. Change t-1 to t.

#4 ("Sdr" is an important parameter in your model, but there is no sensitivity analysis, only a single large value is used without any reference to the literature. Lack of biological realism/references)

Please run the code below.

A set of parameter values, such as those used in your model:

```
set.seed(1234)
k = 3
sdr = sqrt(0.55)
r = 1.2
```

```
n_iter = 1e4
K = exp(k)
```

Generate some data using your function

```
Y<-dataGompertz(n_iter, r, k, sdr)
```

Check how many times Y is higher than K measured on a common scale

```
plot(Y); abline(h=K, col='red',lwd=3)

hist(Y/K,0:100,xlim=c(0,20),freq=FALSE)

AT<-c(-2,log10(0.05),-1,log10(0.25),log10(0.5),0,log10(c(1:5,7)),1,lo
g10(25),log10(50),2)
hist(log10(Y/K),100,freq=!FALSE,xaxt='n',xlab= 'Y/K');
axis(1,at=AT, labels=round(10^AT,2), cex.axis=0.7)

table(Y>K)/iter*100 # symetric as expected
sum(Y>K*5)/iter*100
sum(Y>K*8)/iter*100
```

The chance for a ratio of 5 is still quite probable (4.22%), even 8 times higher Y than K occurs on average every 100 iterations. For most organisms, I don't think this is very realistic. From a biological point of view, it could be the world of bacteria or insects (???).

Moreover, it seems that a higher r reduces the variance in Y / K, and a higher sdr increases the variance of Y / K. Have you checked how different values of r and sdr affect the results of your model?

Is there any theory / empirical data behind sdr = sqrt (0.55)? It was never explained why do you use this value / Where does this value come from ?

The high sdr value limits the application of the results of this model to very specific organisms. This should be discussed, i.e. to which organisms can your model be applied? Note that for some organisms (e.g. some birds) the K cannot be exceeded almost at all ("sulprus" individuals has to migrate or die, see also nest-site lottery models).

#5 (Minor R-code notation problem)
"y" in "`dataGompertz()`" function should be changed to "Y". "Y" is on a common scale, while "y" is on a log scale. This can be confusing.

#6 (Minor R-code problem)
Set initial seed for "BRugsFit" (or earlier via `set.seed()` function) to make your results replicable.

#7 (Probably minor R-code problem, but check carefully)
"vs" and Bugs results are calculated using different data.

```
vs[i]<-var(log(simData))
DataToBUGS=list(y=log(simData[201:m]), n=length(201:m))
```

#8 (Minor R-code problem - in your case probably negligible, but check)
I am not an expert in OpenBugs. However it seems you wanted to use truncation, but you use old deprecated syntax that performs censoring instead of truncation.

You use

```
r ~ dnorm(0,1)%_%I(0,)
```

It probably should be
`r ~ dnorm(0,1)%_%T(0,)`

See
https://www.mrc-bsu.cam.ac.uk/software/bugs/openbugs/openbugs-versus-winbugs/
"OpenBUGS can handle both censored and truncated distributions. Previous versions of BUGS, e.g. WinBUGS, could only handle censoring, using the I(,) notation, although this could sometimes be exploited to trick BUGS into truncating. To avoid any confusion, OpenBUGS allows truncation via the notation T(lower, upper) and censoring via C(lower, upper). The I(lower, upper) notation is still allowed for censoring (for the sake of backwards compatibility) but is deprecated."

and
https://www.jiscmail.ac.uk/cgi-bin/webadmin?A2=ind0909&L=BUGS&P=R2080&1=BUGS&9=A&J=on&d=No+Match%3BMatch%3BMatches&z=4

 # 9 (Minor/negligible modeling problem)
`tau.y~dgamma(1,1)` seems not to be completely uninformative (weak) prior (run `hist(rgamma(1e5,1,1),100)` to see). Although it can be assumed that it probably does not matter for the qualitative results, it is worth checking it using e.g. `tau.y~dgamma(0.1,0.1)` or truncated uniform distribution.

 # 10 (Minor modeling problems: testing different aspects of convergence)

Line 294: How did you check that you only need to discard the first 200 observations?

Is 4000 iterations sufficient to get the convergence (nBurnin = 4000)?
Have you performed any convergence tests (similar to e.g. Gelman, Rubin or Geweke tests)? Several R packages can do this (related to JAGS at least).

Why are there different "nThin" values for the Gompertz and Rickert models (10 and 4 respectively)? Make sure how to set this parameter if you want to measure the "variance" of the parameters of an auto-regressive model.

#11 (Another option exists)
Lines 234-235: If r=0 then Beta=1 and there is a random-walk without drift.

#12 (Interpretation of Beta under Ricker model does not make sense)
Figure 2&3, Lines 382-385, other places in the manuscript: You use Beta to interpret the results of the Ricker model, but Beta only has an interpretation in terms of the Gompertz model. This should be clearly stated (figures and manuscript).