The topic and results are important to biological theory. The article is nicely written, the methodology is clear and mathematically elegant, but many of the assumptions of the model go beyond biological reality. Setting parameters within a reasonable range is important to (1) show that the results are not artifacts of poor parameter selection and (2) show that the results can be applied to real biological examples.

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1. Problem with definition and values of intrinsic growth rate

Line 119: „where r > 0 and k > 0 are respectively the intrinsic growth rate and the carrying capacity on the natural logarithmic scale".

However, this sentence is misleading because only the carrying capacity is on a logarithmic scale, while r is on an arithmetic scale. Please correct.

For further considerations let carrying capacity K = exp(k) <=> k=log(K).
Here is a simple code that uses eq. 1 to demonstrate the population growth which I found helpful to understand the role of parameters:

```
GompertzGrowth<-function(Y0, r, k , n){
  res<-rep(NA,n)
  res[1]<-Y0
  for (j in 2:n){
    res[j]<-res[j-1] * exp(r * (1 - log(res[j-1]) / k))
  }
  res
}
PopTrajectory <- GompertzGrowth(56, r=1, k=log(55), n=1e2)
plot(PopTrajectory,ylab='population size',xlab='time',type='l')
abline(h=55,lty=2)
plot(log(PopTrajectory[-1]/PopTrajectory[-length(PopTrajectory)]),
ylab='empirical r',xlab='time',type='l')
abline(h=1,lty=2)
```

I think it is clear that r is intrinsic population growth rate in the absence of density dependence. In the Gompertz or Ricker models, r is constant, but "empirical intrinsic population growth rate" decreases with population size (m_e = ln [N (t2) / N (t1)] / (t2 - t1)). I think this difference should be mentioned somehow in the article as it could be misleading for non-theoretical biologists.

(major issue)

You only use r=1 in your examples, I would try different values.

3. Carrying capacities are too small (major issue)

Lines 240-241: You assume unrealistically small carrying capacities, e.g. k = 1.333 gives K = exp (1.333) = 3.8. The greatest carrying capacity you have is ~ 55. They certainly do not describe large populations compared to what you have suggested in various places in the manuscript

By the way, why not use log(K) instead of k throughout the paper?

2. Selected betas are unrealistic.

In numeric examples, you use beta = {0.25, 0.5, 0.75}.
Usually in nature r is rather small, probably r <2 for most of the population, while the carrying capacity (K) can be huge. Imagine a population with a very high intrinsic growth rate (r = 2) and low capacity (K = 55) then beta = 1 - r / log (K) = 0.5, but this is an extreme situation. I would expect realistic beta values in the range 1> beta> 0.6.

The model works very fast, so I would also explore other betas and connect them with exemplary r and K pairs."Field" biologists may be used to thinking in terms of r and K (e.g., r

and K selection), so such an approach would make it easier to imagine real biological scenarios.

4. Assumed noise variance is huge! (major issue)
In your code used to generate the data, you assume sd = 1 (sdr). sdr is used to model the epsilon variable, which acts additively to the population size on a logarithmic scale. Knowing that the carrying capacity is around 55, your population estimate is often up to 20 times higher than that! Such noise is very unreal.

This simple code demonstrates the problem with your assumption:

```
set.seed(123)
Pop<-dataGompertz(1e4, 1, 4, 1)
cat('Data 95% range:\n')
# Data 95% range:
quantile(Pop,c(0.025,0.975))

#      2.5%     97.5%
#  2.827847 993.983621
cat('Carrying capacity K =',exp(4),'\n')
# Carrying capacity K = 54.59815
plot(Pop,pch=19,cex=0.5); abline(h=exp(4),col=2,lwd=3)
```

In other words, at steady state, the logarithm of the population is 4 (55 on an arithmetic scale), and the epsilon ~ N (0.1) can often increase this value by 2 or more, leading to huge population sizes, for example exp (4 + 3)> 1000.

5. Demographic stochasticity and other sources of variability

It would be good to define what demographic stochasticity is. By demographic stochasticity, do you mean only the "sampling" variance? What about the stochasticity resulting from past population dynamics / trajectory?

Even in large populations, this stochasticity can be big. Previous models (e.g., Caswell) have shown that a population can enter a "series" of bifurcations that can move it far from carrying capacity. I think it would be good to mention about it.

The role of a stable age distribution is not discussed. I think, even if it is not explicitly written / modeled, the model assumes a stable age distribution. However, this distribution may not reach equilibrium due to environmental variability. The lack of a stable age distribution may lead to even greater variation in the size of the population.

6. Biological context and reliability

The biological context is poorly explored in both the introduction and the discussion. The paper dramatically missing biological examples.

Gompertz growth models have been successfully used to model the growth of tumors, but not necessarily of biological organisms. It would be nice if you could give some biological examples of the uses of these models.

The model does not explicitly take into account the density-dependency mechanism (e.g. see Kozłowski 1980 Evolutionary Theory 5: 89-101 for criticism). I understand that this is not a feature of the Ricker and Gompertz models, but it would be good to mention in the text that models that take into account life history and the way density dependence affects populations better describe reality.

The carrying capacity must also be placed in a biological context. For example, for many birds (see also nesting lottery models) the number of the population is determined by the number of

nests, so the K cannot be greatly exceeded and therefore your model cannot be used. Please write about biological situations that are relevant to your model.

For a theoretical biologist like me it, would be more interesting to model the variability of K and r rather than using epsilon added to log population sizes, which may have difficult biological explanation when there are density dependence effects. However, I understand that in such a case the current model would lose its elegance.

7. Minor issues and comments

108: „Ricker model Ricker (1954)" - please correct the format of citation
327: „underlying value" - Not clear
167: The case -1 < beta < 0 can be written equivalently as k < r < 2k (using equation from line 134) or log(K) < r < 2log(K). This case is unrealistic because the internal rate of population growth would have to be greater than the log carrying capacity. In other words, the capacity would have to be very small.