

Range Expansion: High Intrinsic Growth Rate (r) Outpaces High Carrying Capacity (K)

Abstract

Range expansion is a vital ecological process shaped by the intrinsic growth rate (r) and carrying capacity (K) of a population. Using simulations we compared a high r and low K population against a low r and high K population to determine which expands their range faster in a 1-dimensional habitat. Our results showed that high r and low K populations were consistently able to expand their range faster.

Introduction

Range expansion is a critical ecological process that drives species dispersal, colonization of new habitats and maintains the stability of ecosystems. The speed by which populations are able to expand their range is heavily influenced by traits of the population such as its intrinsic growth rate (r) and the carrying capacity of the population (K)¹. Previous research has shown that while populations with higher r values are better able to utilize new resources, populations with higher K values tend to be more stable over time². For instance by using a simulation modelling range expansion, Bohn et al.³ found that r -selected species made better colonizers, while K -selected species made better competitors. However, it is still unknown how the values of r and K directly impact the speed of range expansion.

Our study aims to address this gap by comparing a population with a high r -value and lower K -values against a population with a low r -value but higher K -values, to see which one is able to expand their range faster. To do this we created a simulation that models range expansion across a 1-dimensional series of habitat patches. The simulation allows for precise control of r and K , as well as the effect of migration, isolating their affections on range expansion in a way that real-world studies cannot replicate. We hypothesize that the results of our simulation will show that a population with a higher r -value but lower K -value will be able to expand their range faster.

Methods

Data Description

To answer this question we created a simulation with a nested list containing 20 'habitat patches' to act as our world. Within each habitat patch the population of n_1 and n_2 were contained, the parameters (r and K) for each population were contained on a separate nested list. We began each run of the simulation with both n_1 and n_2 having a population of 10 in patch one. A `growth` function was created using a discrete time version of the logistics growth equation taken from the University of British Columbia's BIO301⁴ course, to simulate population growth in each time step. A `migration` function was created using a random binomial draw in order to select the number of immigrants in each time step, the `sample` function was used to create `direction_generator` function which randomly picks 1 or -1, which was used to determine the direction of migrations. We created a larger simulation function in which the `growth` function, `migration` function, and `direction_generator` function, were all called in a `while loop` order to simulate population growth and migration until one population reaches patch 20 and is considered the winner of the simulation at which point the final state of the world will be saved to a data frame. The simulator function was looped over 400 times for each set of parameters to generate our data.

Data Analysis

To analyze the results produced by our simulation, we created plots showing the number of wins for n_1 and n_2 on the y-axis, with the number of timesteps to each win being the x-axis. This visualization allows us to examine how fast each population was able to expand their range

as well as the population that was able to win the most simulations under a given set of parameters. By comparing the plots produced using different parameters we examined the combined and individual effects of r and K on the speed of range expansion.

Results

The results of our simulation showed that the population with the higher r -value was able to expand their range faster, reaching the edge patch first more frequently than the population with the lower r -value (Figure 1a). On the other hand, changing the K -value showed that the greater K -value also results in more frequent wins (Figure 1c), however, only by a smaller margin when compared to a change in r -value which shows that changing the r -value had greater impact on range expansion than altering K (Figure 1a vs 1b).

Discussion

Biological conclusions

The bottom right plot of Figure 1 shows the results of the control simulation where both populations have the same r and K values. As can be seen, each population wins roughly half of the total number of simulations at the control parameters with the majority of wins for each being concentrated around $t = 20$. When the r value for Population 1 is halved (top right panel of Figure 1) a very clear change can be observed. Population 1 experiences significantly fewer wins with a higher median win time and Population 2 experiences a significant increase in wins overall. In contrast, when the K value for Population 2 is halved, the decrease in number of wins is noticeable but not nearly as extreme (bottom left panel of Figure 1). In a simulation where both these changes in r and K are implemented, the resulting plot (top left panel of Figure 1) appears most similar to the only halved r plot, likely indicating a lower impact of the K on a population's dispersal.

It should also be noted that in each set of parameters where either one or both of r and K are halved the median win rate and spread of win times for both populations increases. This is likely due to one population having a reduced win ability, resulting in a higher number of long simulations occurring.

Limitations

Many simplifications were made when building this model that impacted the conclusions we were able to draw from the simulations. One method of further exploration would be to expand the model to examine movement in a 2-dimensional space. This would allow the model to be applied to a wider range of habitats and dispersal strategies. The model in its current state assumes individuals only move one patch at a time and in a random direction aligning with a binomial distribution.

There are also a multitude of other pressures driving dispersal, one being climate change which has been linked to range shifts and shrinking habitats. Taking into account how different factors of patch quality affect dispersal patterns may allow for the more effective use of resources in conservation efforts.

Conclusions

We believe this study to be a preliminary step in the exploration of factors of dispersal. Through the simulations presented, we found the intrinsic growth rate, r , to have a powerful impact on the rate a population can expand their range.

Figures

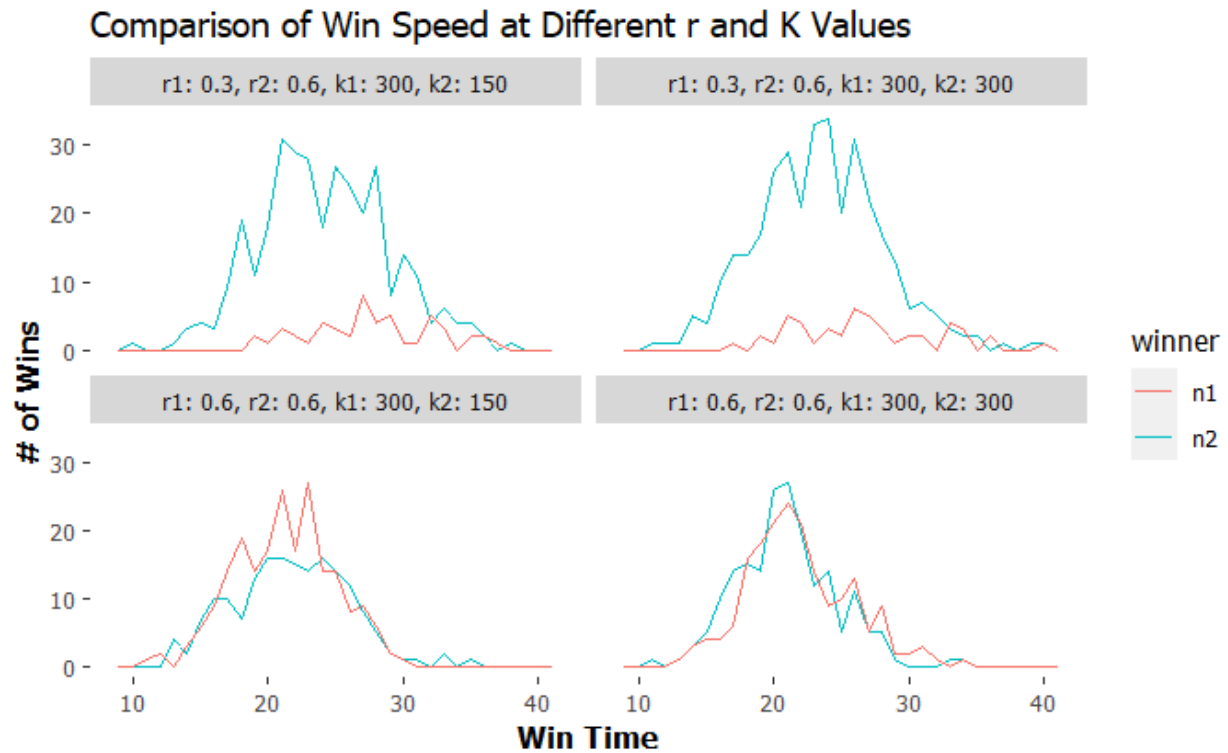


Figure 1. Number of simulation wins for n1 and n2 across different combinations of r and K values. The top-left(a) plot shows n2 winning the majority of the simulation runs when n1 has a low r-value of 0.3 and a high K-value of 300 and n2 has a high r-value of 0.6 and low K-value of 150. The top-right plot shows that n2 still wins the majority of simulation runs when n1 has a low r-value of 0.3 and n2 has a high r-value of 0.6 at the same K-value (meaning the K-value has smaller effect on dispersal speed). The bottom-left(c) shows n1 wins more of the simulations when n1 higher K-value of 300 than n2 K-value of 150 but the same r-value, however the magnitude of difference is much smaller. The bottom-right(d) plot is a control plot showing an even distribution of wins when n1 and n2 have identical parameters ($r = 0.6$ and $K = 300$) where the win frequencies across different speeds are roughly the same.

References

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