Journal: Is lambda related to r?

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Is lambda related to the value of r in the original population?

While I previously found that the amount of smoothing needed to recover the value of r from dimensionless data was much higher than I had expected, now I want to find out how r, the population intrinsic growth rate, relates to λ^* , the optimal smoothing value. I have three main hypothesis:

- 1. The value of λ^* is constant for all r,
- 2. The value of λ^* is proportional to r, or
- 3. The value of λ^* is chaotic with respect to the value of r.

Right now, I am leaning towards hypothesis 2: I think there will be a linear relationship between the value of r and the value of λ^* .

Eventually I will wrap this up into a function, but right now I just want to do the experiment, so I will be copy-pasting most of my code from the previous experiment and wrapping it inside another loop. First I will source the necessary scripts and set a random seed, as well as setup variables I need.

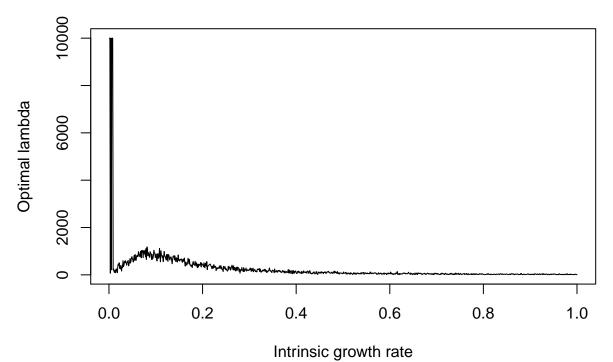
Note here that I added the functions from the previous test to the Helpers.R script, so I didn't have to redefine them here.

```
source(here::here("Scripts", "Dimensionless_exploration.R"))
## Loading required package: MASS
source(here::here("Scripts", "Helpers.R"))
source(here::here("Scripts", "Least_squares_methods.R"))
rs \leftarrow seq(0.001, 1, 0.001) # Values of r to test
lambdas <- seq(10, 10000, 10) # Values of lambda for each r
k <- 3 # k-fold cross validation constant
lstar <- numeric(length(rs))</pre>
for (r in rs) {
  # Generate and partition data
  df <- generate_dimensionless_logistic_data(.1, r, 50, 0.1)</pre>
  parts <- random_partition(df, k)</pre>
  combos <- combn(1:k, k-1, simplify = F)</pre>
  # Empty vector to contain cross-validation error values
  cves <- numeric(length(lambdas))</pre>
  # Do all of this stuff for each lambda using the current data.
  for (a in 1:length(lambdas)) {
    1 <- lambdas[[a]]</pre>
    errors <- numeric(length(parts))</pre>
```

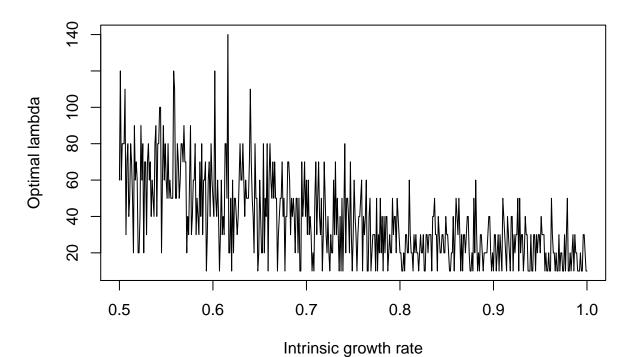
```
# Need to do this k number of times (# of parts)
  for (i in 1:k) {
    # Grab the first combo of indices to use
    to use <- combos[[i]]
    # Make a blank dataframe
    train <- data.frame()</pre>
    # This part has to be done k-1 times to build training data.
    for (j in to use) {
      # Get the next data frame.
      new_dat <- parts[[j]]</pre>
      # Add this data frame to the bottom of the rest.
      train <- rbind(train, new_dat)</pre>
    }
    # Now train has k-1 of the parts in it.
    # Set test to be the part that wasn't selected.
    not_used <- (1:k)[!(1:k %in% to_use)]</pre>
    test <- parts[[not_used]]</pre>
    # Prep and model the data, specify time step manually.
    prepped <- prep_data(train, 0.1)</pre>
    mod <- model logistic data dimensionless smoothing(prepped, 1)
    # Next need to calculate predicted values using the estimated growth rate from the model.
    \#P = (P0e^{(rt)})/(1+P0(1-e^{(rt)}))
    t <- test$t
    pred <- (0.1*exp(mod*t))/(1+0.1*(exp(mod*t)-1))
    errors[i] <- calculate_SSE(test$P,pred)</pre>
  cves[a] <- mean(errors)</pre>
lstar[match(r,rs)] <- lambdas[which(cves == min(cves))]</pre>
```

Now we need to collect the values of r and λ^* together and we can visualize the results.

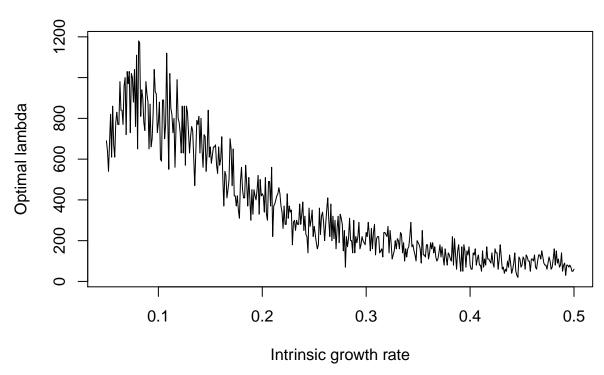
Optimal lambda vs. R



1 > r > 0.5

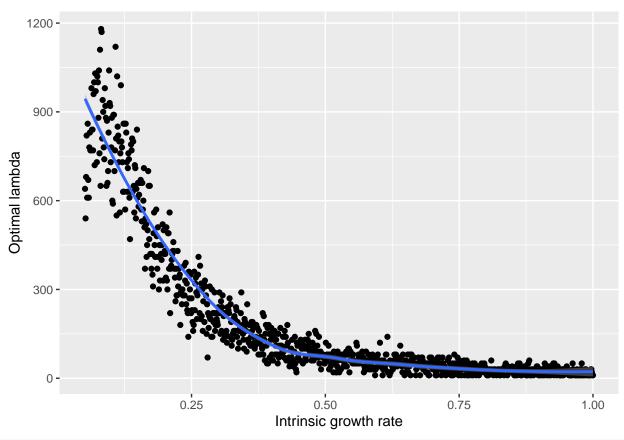


0.5 > r > 0.05



THis curve (starting at around r = 0.05 to exclude the major outliers) can probably be modeled well by an exponential decay curve. Here, I have just modeled it with a LOESS curve but an exponential fit might be worth examining.

```
library(tidyverse)
res %>%
  filter(res$r > 0.05) %>%
  ggplot(aes(x = r, y = 1)) +
    geom_point() +
   labs(x = "Intrinsic growth rate", y = "Optimal lambda") +
   geom_smooth(method = "loess")
```



```
res %>%
filter(res$r > 0.05) %>%
ggplot(aes(x = r, y = 1)) +
   geom_point() +
   scale_y_log10() +
   labs(x = "Intrinsic growth rate", y = "log10(optimal lambda)") +
   geom_smooth(method = "lm")
```

