Simulating Dynamical Systems

load packages
library(tidyverse)
library(deSolve)
library(ggthemes)

Consider the data set lynxhare.csv - provided with this mini-assignment. This data set was from Whitman College. This data is from a study of predator-prey interactions, a data set of snowshoe hare and lynx pelts, hare-lynx data by the Hudson's Bay Company of Canada.

The data set contain population estimates by year of Snowshoe Lynx and Hare. The variables includes:

- year The year when the Lynx and Hare was obtained.
- *lynx* Lynx population (in thousands) by year.
- *hare* Hare population (in thousands) by year.

```
# load the lynx hare population data set
df <- read_csv("lynxhare.csv")</pre>
```

```
# pivot for easy plotting
df_pivot <- df %>%
pivot_longer(
    cols = c("hare","lynx"),
    names_to = "species",
    values_to = "population")
```

Below shows a visualization of the population dynamics of Lynx and Hare. Considering that lynx are predators that preys on hares, the assumption here is that the population of lynx are regulated and influenced by how many hares are there available. You can read more about this data and model we are about to introduce here.

Yearly Population of Snowshoe Hare and Lynx



We can model the population dynamics of lynx and have populations using a system of differential equations. Specifically we use the Lotka-Volterra model. This is defined mathematically below.

$$\frac{dX(t)}{dt} = X(\alpha - \beta Y)$$
$$\frac{dY(t)}{dt} = -Y(\gamma - \delta X)$$

where X(t) is the population size of the prey species at time t and Y(t) is the population size of the predator species. Here, $\frac{dX(t)}{dt}$ is the change in the prey population in time while $\frac{dY(t)}{dt}$ is the change in the predator population in time.

This model has four parameters:

- α the growth rate of the prey population,
- β the death rate of the prey population relative to the product of the population sizes,
- γ the death rate of the predator population, and
- δ the growth rate of the predator population as a factor of the product of the population sizes.

Below we define the system of differential equations.

```
# define the Lotka-Volterra system of differential equation
LV_ode_model <- function (Time, State, Pars) {
    with(as.list(c(State, Pars)), {
        dx = x*(alpha - beta*y)
        dy = -y*(gamma - delta*x)
        return(list(c(dx, dy)))
    })
}</pre>
```

We solve this system numerically using the ode function from the deSolve package. While we are not focusing on the details of the solution, we are focusing on interpreting the parameters of the model to describe and understand the given data. 1. Graphically estimating the parameters. Below are a series of code blocks that solves the differential equation with a set of parameters and initial population sizes, and plots the model against the data.

Your task is to set the initial population sizes the same as the data, and find a set of parameters of the model that creates a simulation that closely match the data. Note that it is helpful to understand what this parameters mean in order to successfully simulate the data.

```
### [BEGIN] - CHANGE PARAMETERS HERE
# parameters of the model
LT_parameters <- c(alpha = 0.55, # hare birth rate
                   beta = 0.028, # hare death rate
                   gamma = 0.84, # lynx death rate
                   delta = 0.026) # lynx birth rate
# initial population sizes
initial_state <- c(x = 19.1, y = 30.1) # updated from data
### [END] - CHANGE PARAMETERS HERE
# time vector
time <- seq(1845,1935,1)
# solve the system of differential equations
LT_sim <- as.data.frame(ode(func = LV_ode_model,</pre>
                            y = initial_state,
                            parms = LT_parameters,
                            times = time))
# convert to dataframe
df_sim_LV <- as_tibble(LT_sim) %>%
  mutate(year = as.numeric(time),
         hare_sim = as.numeric(x),
         lynx_sim = as.numeric(y)) %>%
  select(-time,-x,-y)
# join the data and the simulated data using the models
df_all <- df %>%
 left_join(df_sim_LV, by = c("year" = "year"))
# transform the data for plotting
df_all_pivot <- df_all %>%
 pivot_longer(
   cols = c("lynx", "hare", "hare sim", "lynx sim"),
   names_to = "species",
   values_to = "population")
ggplot(data = df_all_pivot, aes(x = year, y = population, color = species)) +
 geom_point() +
  geom_line() +
  scale_color_colorblind() +
  scale_x_discrete(limits = seq(1845,1935,10)) +
  labs(x = "year",
       y = "population (in thousands)",
       title = "Yearly Population of Snowshoe Hare and Lynx")
```



- 2. Trying out cases of initial population sizes and model parameters. Copy the series of code blocks from problem 1 and paste it below. Produce two sets of plots as described below.
- a. Have your parameters fixed from problem 1 and try two sets of initial conditions where one of them is 0. Plot your results. Provide a paragraph that describe your observations.
- b. Have your initial conditions fixed from problem 1 and try two sets of parameters where one of the species have negative growth rate. Plot your results. Provide a paragraph that describe your observations.

[BEGIN] - PASTE R CODES HERE

[END] - PASTE R CODES HERE