

## Exercise 4: Reproduction number

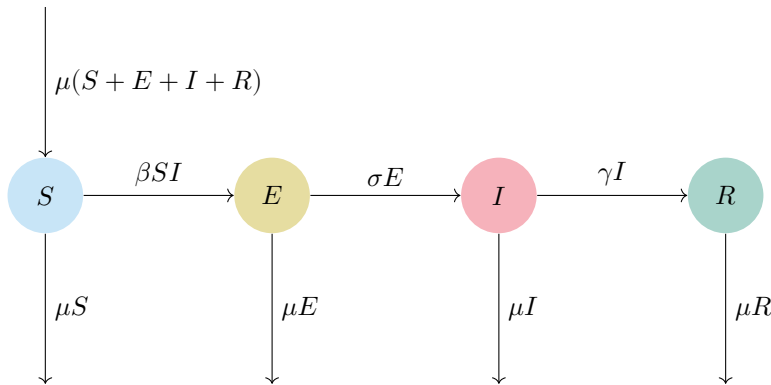
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Complete Exercise 3a and either 3b or 3c.

### Exercise 3a

Following is the state diagram for an SEIR model with balanced birth and death.  $\mu$  is the birth and death rate, indicating zero population change.  $\beta$  is the transmission rate,  $\sigma$  is the progression rate from exposed to infected, and  $\gamma$  is the recovery rate.



$\mathcal{R}_0$  for this model can be estimated as:

$$\mathcal{R}_0 = \frac{\beta\sigma}{(\mu + \gamma)(\mu + \sigma)},$$

where  $\mu \ll \gamma$  and  $\sigma$  is of the order of  $\gamma$ .

Your task is to design a plot to explore variation in  $\mathcal{R}_0$  across a range of  $\gamma$  and  $\sigma$ .

#### Step 1:

Begin by fixing  $\mu$  and  $\beta$  and preparing a grid of  $\gamma$  and  $\sigma$ . (You can use `expand.grid()` for this.)

Calculate  $\mathcal{R}_0$  for all values of the grid.

Transform your data into a matrix of  $\mathcal{R}_0$  values, with rows = levels of  $\gamma$ , and columns = levels of  $\mu$ .

```

library(tidyverse)
# Example with fixed beta, fixed mu, and grid of gamma and sigma
beta <- .15
mu <- .01
gamma <- seq(1/10, 1/3, length.out=20)
sigma <- seq(1/10, 1, length.out=20)
results <- expand.grid(gamma = gamma, sigma = sigma)

# Calculate  $R_0$ 
# Note: In tidyverse, use all_of(varname) to refer to an object outside the dataframe.
# Use varname to refer to column of the dataframe.

results <- results %>%
  mutate(R0 = all_of(beta) * sigma / ((all_of(mu) + gamma)*(all_of(mu) + sigma)))

# Prepare a matrix
results.wide <- results %>%
  pivot_wider(names_from = sigma, values_from = R0)
results.matrix <- results.wide %>%
  select(c(-gamma)) %>%
  as.matrix()
dimnames(results.matrix) <- list(gamma = results.wide$gamma,
                                sigma = colnames(results.matrix))

```

## Step 2:

Visualize.

A matrix of smoothly changing values can be visualized as a “level plot” (with values mapped to colors), or as a “contour plot” (with contours drawn at set intervals), or both.

A level plot can be made with the `lattice::levelplot()` or `graphics::filled.contour`. Both functions can add contours to the level plot.

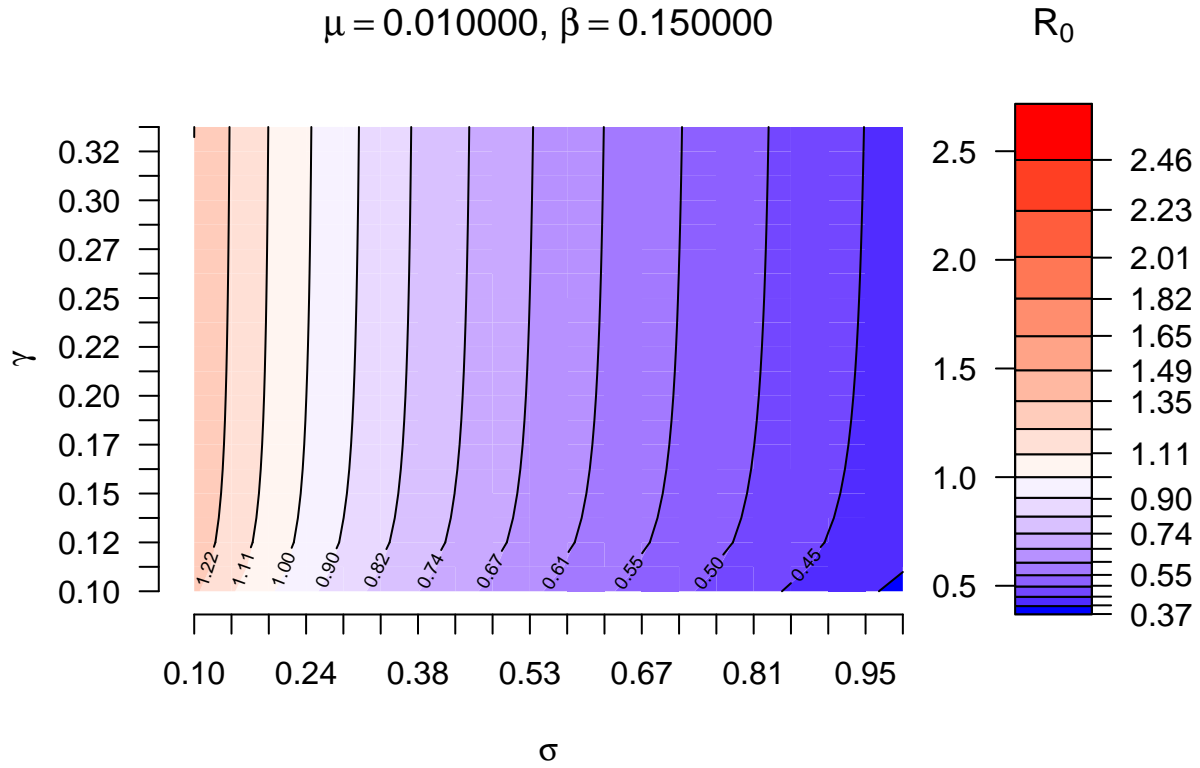
### Questions to consider:

How fine of a grid do you need? What should the bounds be?

What kind of color scale would be appropriate to represent  $\mathcal{R}_0$ ? (Think carefully about what  $\mathcal{R}_0$  represents, the critical value(s), boundaries, etc.)

Does a log scale make sense for the independent variables?

Does a log scale make sense for the dependent variable ( $\mathcal{R}_0$ )? If so, how would you construct a log color scale?



### Exercise 3b

$\mathcal{R}_0$  for a model with both environmental and direct transmission can be estimated as

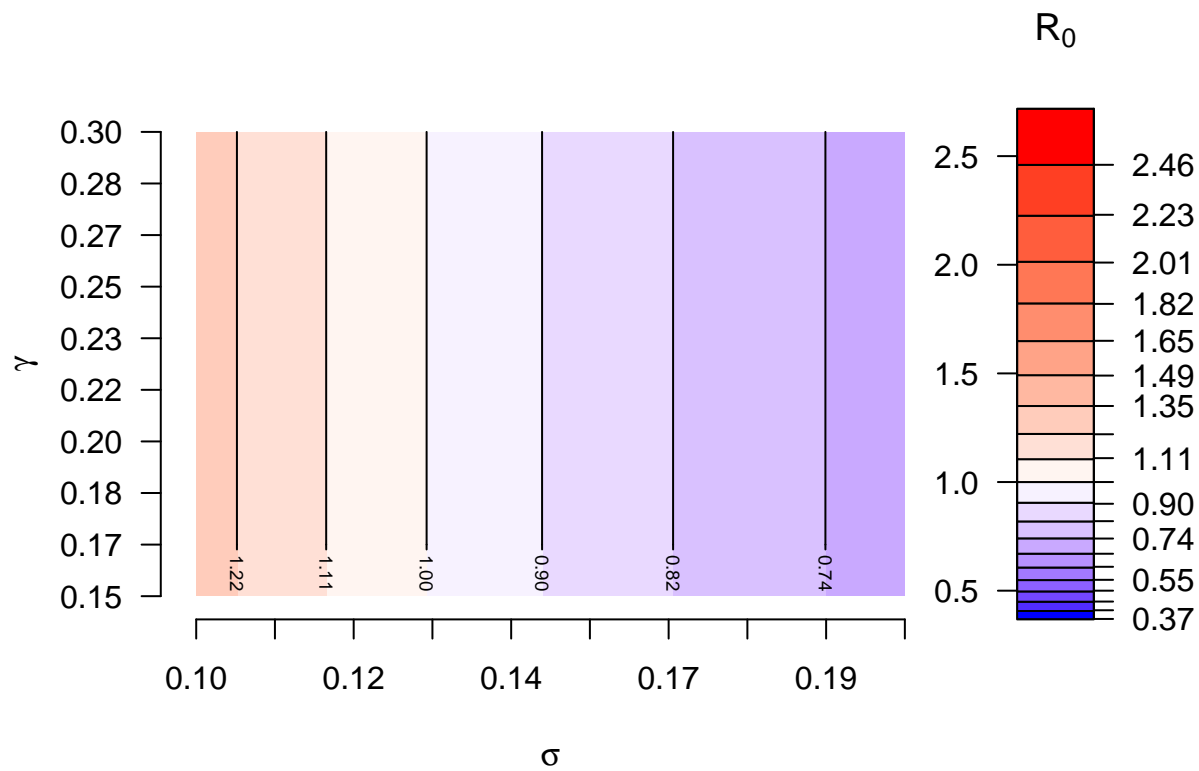
$$\mathcal{R}_0 = \frac{\beta}{(\mu + \gamma)} + \frac{\beta_v \omega}{\rho(\mu + \gamma)},$$

where  $\beta$  is the basic transmission rate,  $\beta_v$  is the environmental transmission rate,  $\omega$  is ? , and  $\rho$  is ? .

How can you use the level plot approach to explore  $\mathcal{R}_0$  across this parameter space?

Can you imagine alternate ways to visualize  $\mathcal{R}_0$  across this parameter space? Sketch your ideas on paper.

$\mu = 0.01, \beta = 0.2, \beta_v = 0.2, \rho = 0.1, \omega = 0.1$



### Excercise 3c

For a simple COVID model with asymptomatic transmission

$$\mathcal{R}_0 = \frac{\kappa\beta}{\gamma_A} + \frac{(1-\kappa)\beta}{\gamma}$$