Exercise 4: Reproduction number

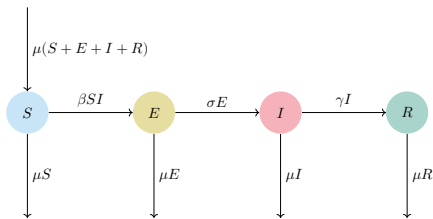## Éric Marty

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Complete Exercise 4a. If you have time, look at exercise 3b.

Exercise 4a

Following is the state diagram for an SEIR model with balanced birth and death. μ is the birth *and* death rate, implying zero net population change. β is the transmission rate, σ is the progression rate from exposed to infected, and γ 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 σ is of the order of γ.

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

You should complete the exercise in a new Rmarkdown document.

Step 1:

Begin by fixing μ and β and preparing a grid of γ and σ. (You can use `expand.grid()` for this.) Consider the question(s) are you trying to answer about the model. How fine of a grid you will need? What should the bounds be?

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

Transform your data into a matrix of $\mathcal{R}_0$ values, with row indices = levels of γ, and column indices = levels of μ.

To see a solution, open the Rmd version of this file ("exercises/4_reproduction_number.Rmd") and look at the hidden code chunk at this point in the document.

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 might aspects of the visual design help reveal answers to questions you have about the model?

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?

Here is a default plot of a matrix of $\mathcal{R}_0$ by σ and γ using `filled.contour()`:

```
filled.contour(results.matrix)
```
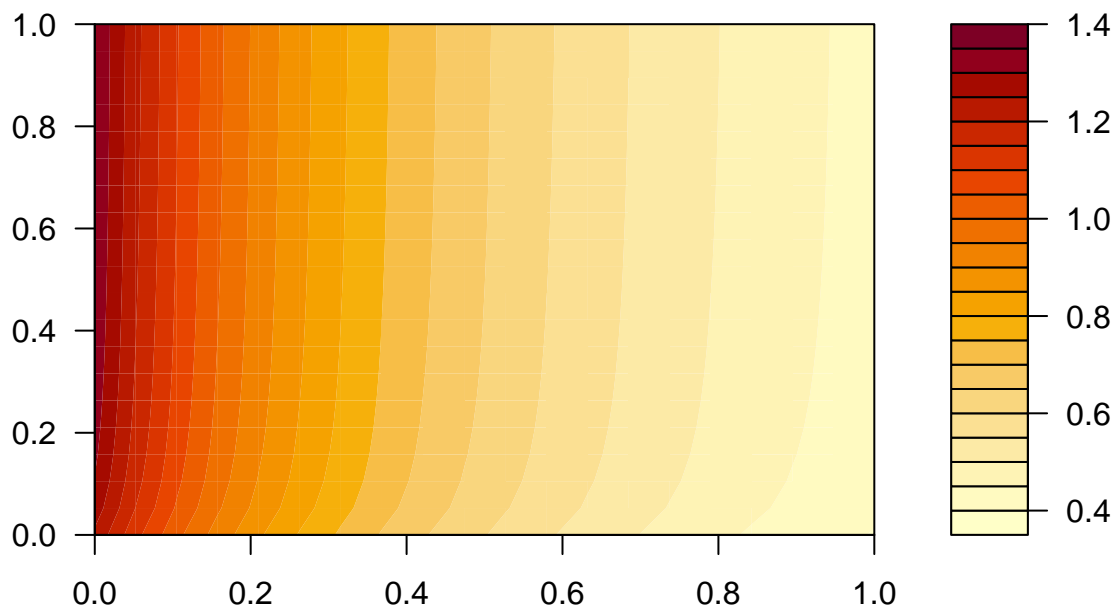

Problems with the default plot:

1. Axes are not labeled and do not display the actual parameter values.
2. It is difficult to read data off the plot.
3. The color scale does not have an obvious semantic relationship to $\mathcal{R}_0$. It is not immediately apparent where the critical value of $\mathcal{R}_0$ lies. It is not immediately intuitive what the colors mean. (Could you guess at the R_0 values without the legend?)

To see a solution, open the Rmd version of this file ("exercises/4_reproduction_number.Rmd") and look at the hidden code chunk at this point in the document.

Exercise 4b

Consider models with more complex parameter spaces.

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

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

$\mathcal{R}_0$ for a **simple COVID model with asymptomatic transmission** can be estimated as

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

How could you use the level plot approach to explore $\mathcal{R}_0$ across these parameter spaces?

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