


$R_0=3$



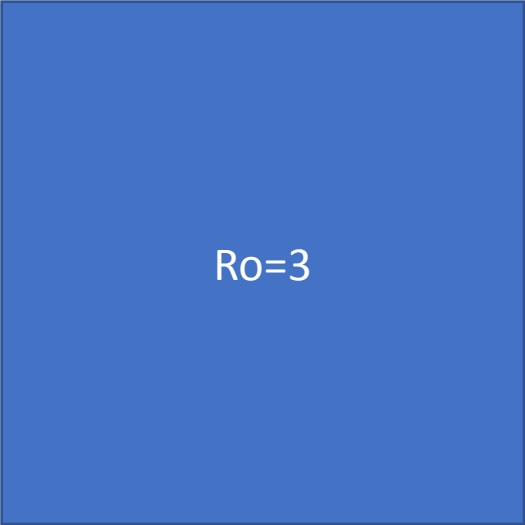
$R_0=7$

Let's begin this module by looking at the two simulations to the left.


Both reflect the transmission of a disease through a population.

You may notice, however, that these two diseases do not spread as the same rate.

Ed. Note: Luis's simulations



$R_0=3$

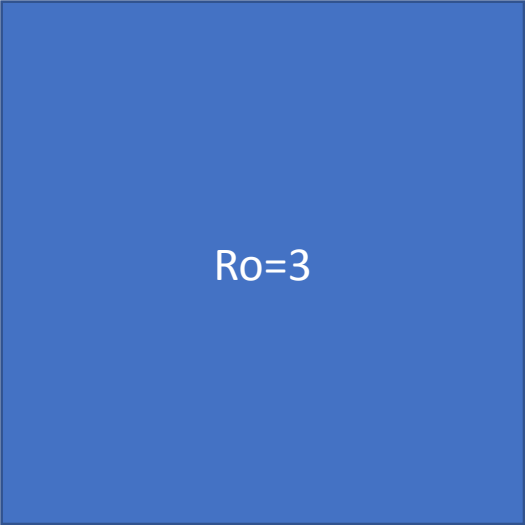


$R_0=7$


The one on the left passes from person to person slowly, while the one on the right infects people quickly.

We see this difference reflected by the speed at which people turn from susceptible to infected, and by the shape of the curves for the Infected population.

Ed. Note: emphasize curves



$R_0=3$

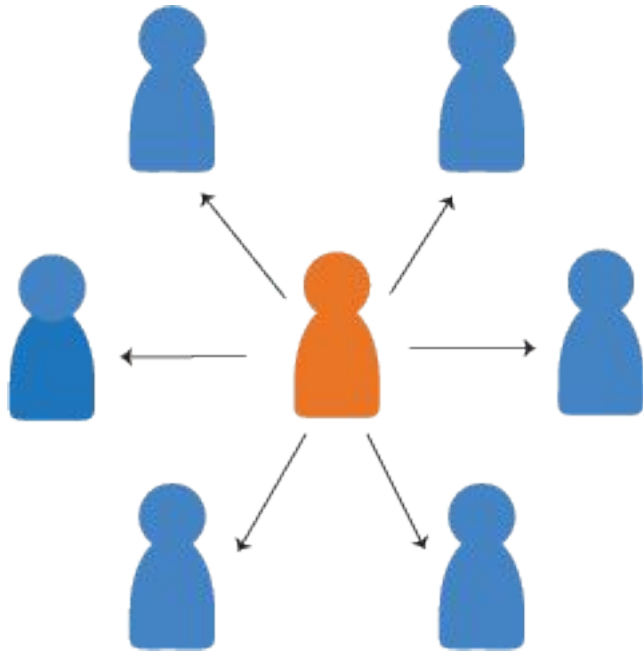


$R_0=7$

These diseases are not the same, clearly, but how do we talk about their differences?

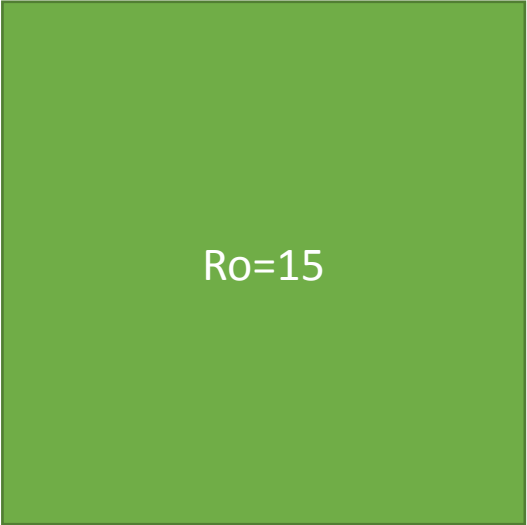
How can we take information from the S,I, and R curves and condense it into something that is easy to interpret and can give us some bearing on how contagious the disease is?

Ed. Note: emphasize curves



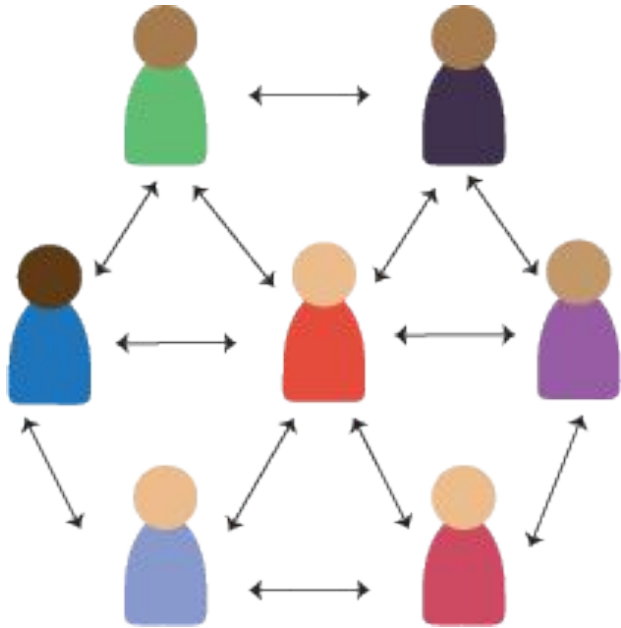
R_0 (R- naught) is one way to do this.

R_0 represents the average number of additional cases that will arise from 1 case if the disease spread in population made entirely of susceptible people.



$R_0=15$

This is why measles is concerning to epidemiologists, its R_0 is **15**!

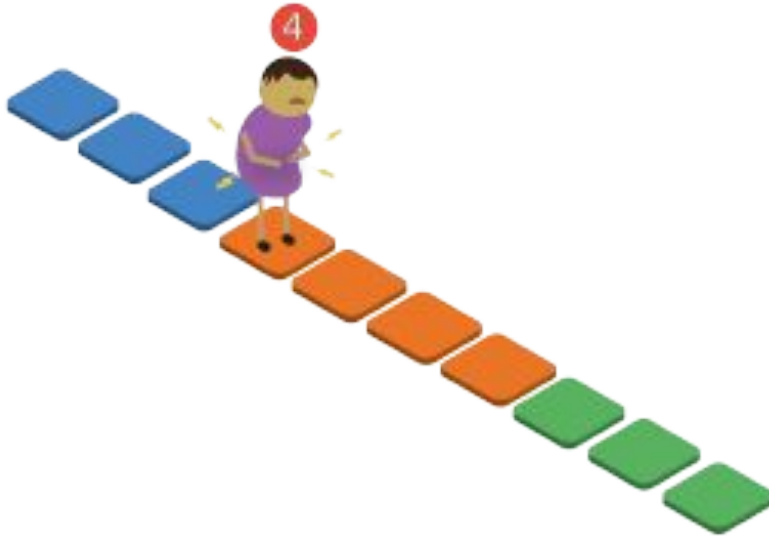


As we saw in the last section, there are 3 aspects that determine a disease's spread:

1. The rate at which people interact with each other. (In our model it was once per time step)



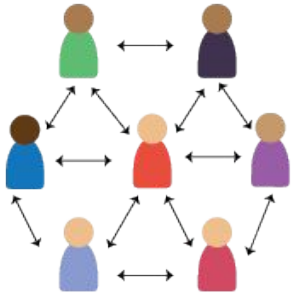
2. The probability that a disease is transmitted during an encounter between a susceptible and infection person.



3. The length of time a person is infectious. (In our model it was 4 days)

R_0

=



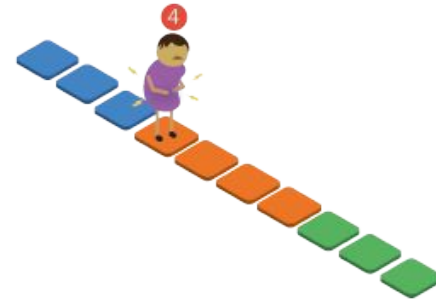
Rate of Interaction
with Others

X



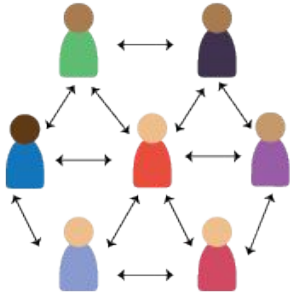
Chance of Encountering
an Infected Person *and*
Becoming Infected

X



Duration of Illness

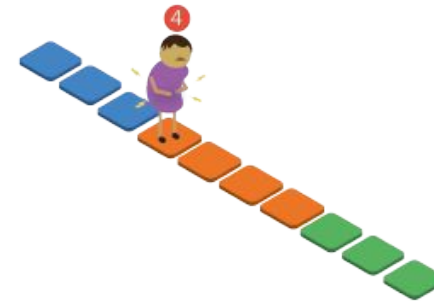
R_0 is calculated
using these 3
pieces of
information!

R_0 $=$ 

Rate of Interaction
with Others

 \times 

Chance of Encountering
an Infected Person and
Becoming Infected

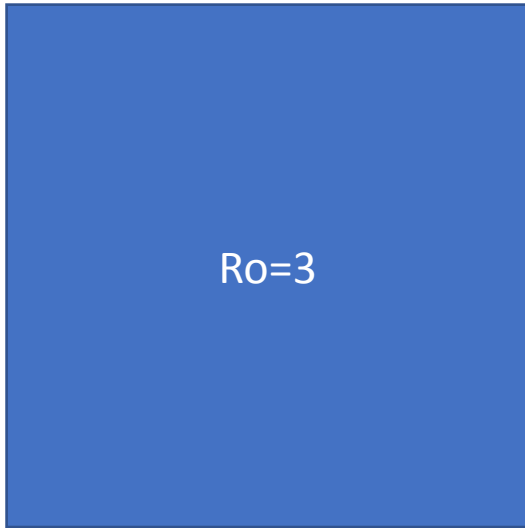
 \times 

Duration of Illness

R_0 is useful because it distills the information from our SIR model into an easier to interpret, standardized measure, that can be used directly to guide policy decisions and public health practice.

Ed. Note: After much consideration, I propose showing this figure again. I don't think having it on one slide is enough. And I think it's a lot to take in. I had considered showing SIR curves for different diseases- but the connection between those and policy decisions is not overt. I had considered making a connection between the R_0 components and the parts of the model they

The Complexity, Nuance, and Caveats of R_0 .



Since two components of our R_0 equation relate to movement and interaction, differences in behavior between two groups of people in a community can result in different reproductive numbers for the same disease.

The simulations to the left reflect this. Both have the same community size, and the same infection duration, but one group interacts with each other often, while the other group does not.

Ed Note: show something similar to these? Same population size, same illness duration Except for these- the only parameter that changes is the contact rate?

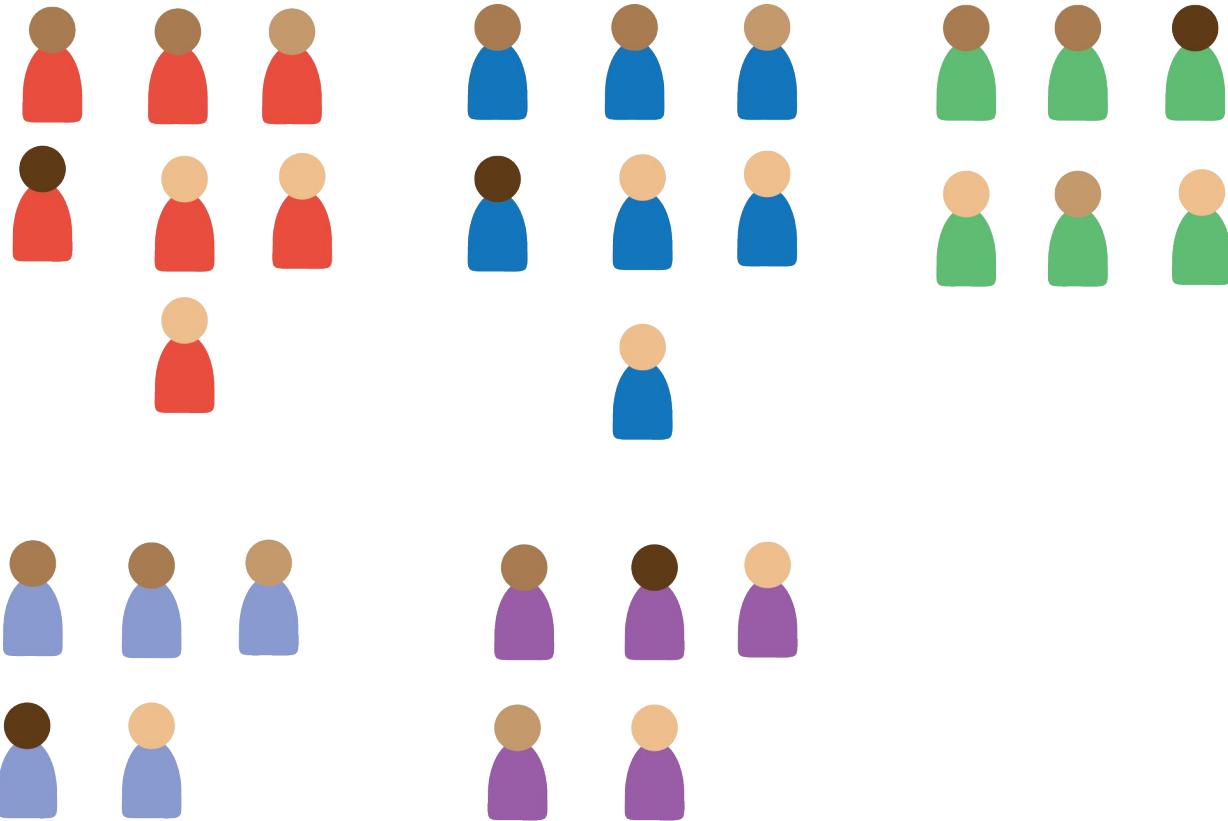
The Complexity, Nuance, and Caveats of R_0 .



For instance, you might expect that a physician working during the day at a hospital will interact with a greater number of people, than a baker who works overnight to make bread for a deli.

Ed Note: I am drawing the background for these characters currently.

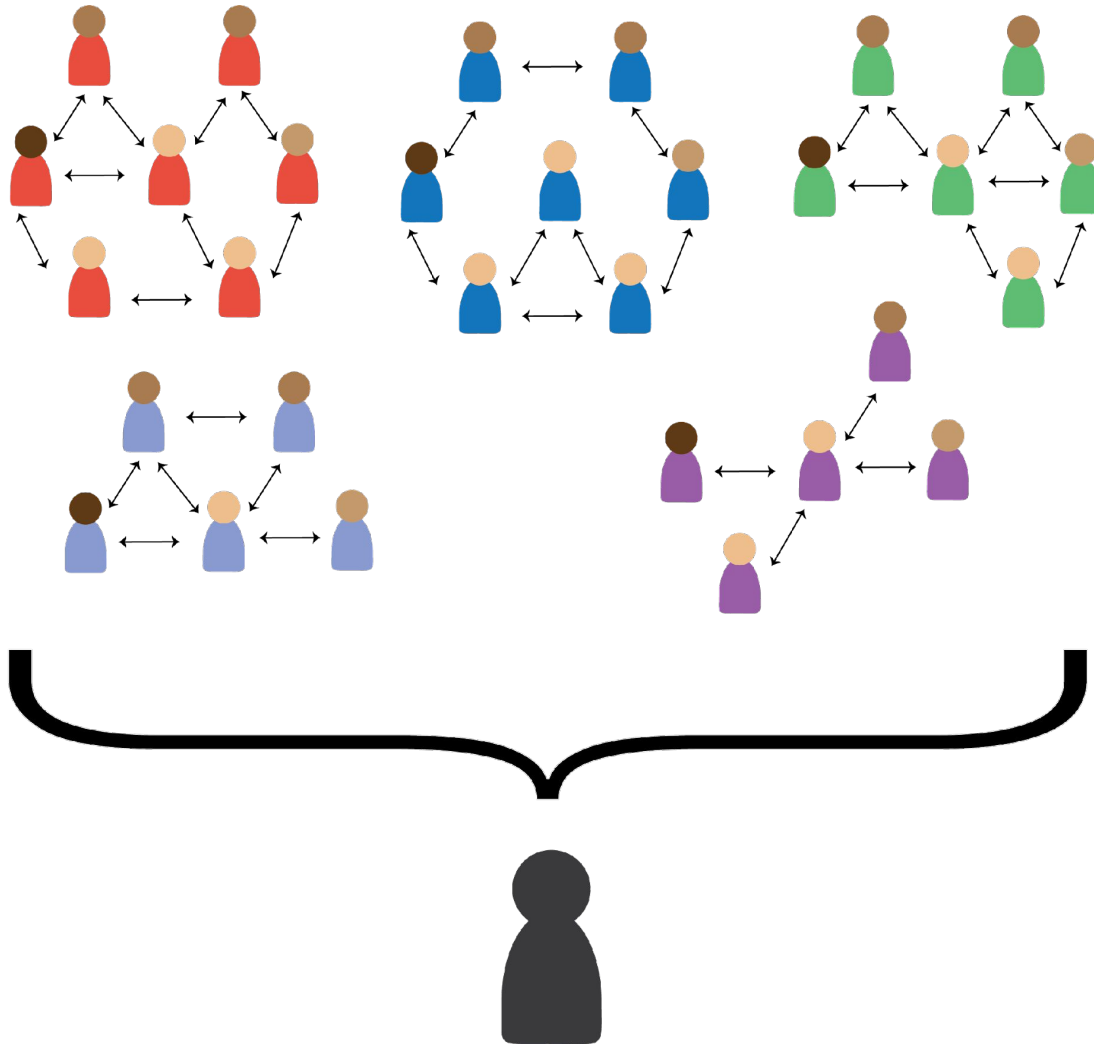
The Complexity, Nuance, and Caveats of R_0 .



How then do we trust a R_0 value if they are likely to be so variable?

By combining all of the subgroups within a population together (medical staff, farmers, retail workers, lawyers, teachers, students, retired people, old people, young people, etc..)...

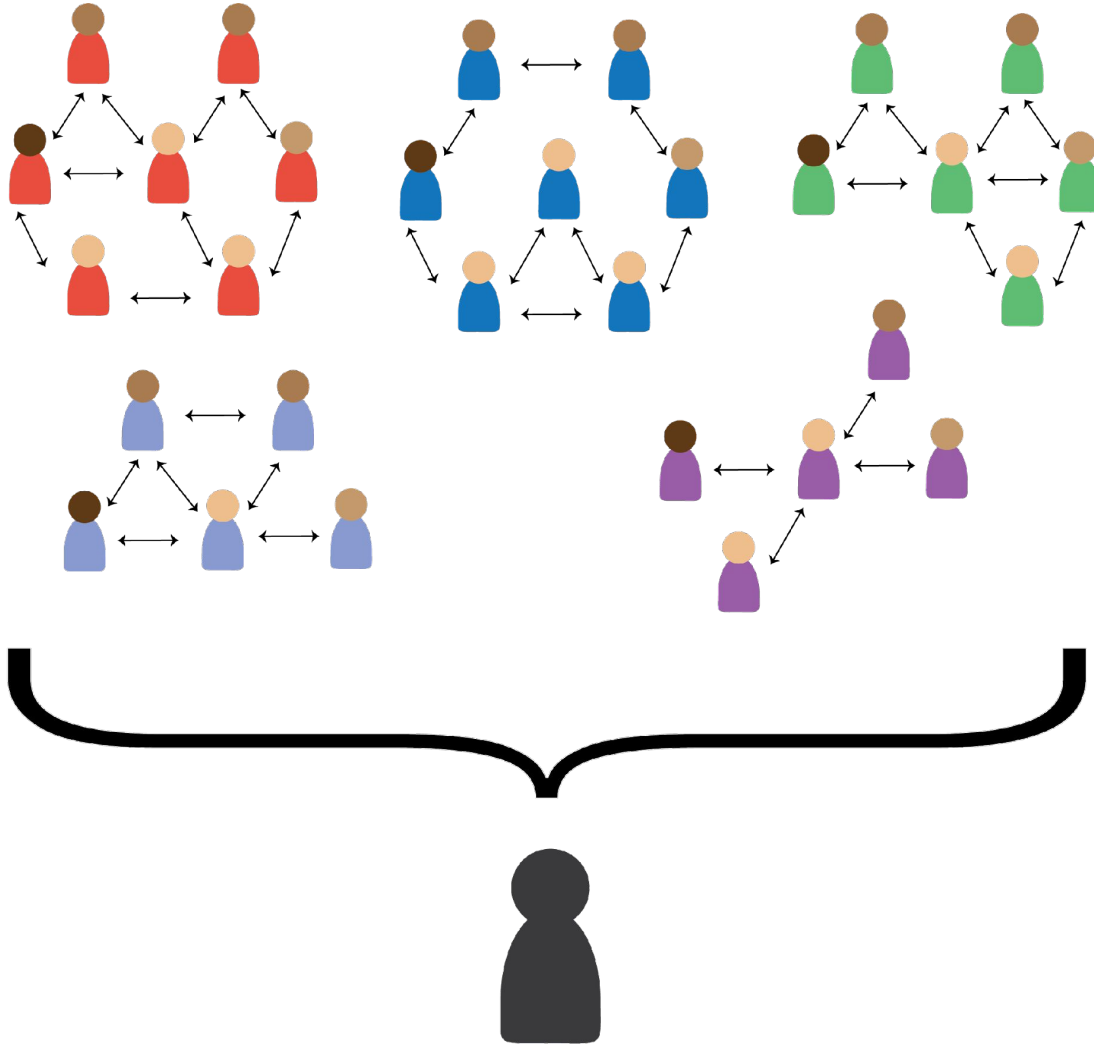
The Complexity, Nuance, and Caveats of R_0 .



... and finding the average contact rate and probability of infection across them.

The resulting values represent the “average experience” of someone living in a community and they yield the *mean or average* R_0 for a disease.

The Complexity, Nuance, and Caveats of R_0 .



The benefit of using “the average experience” to calculate R_0 is that it allows us to compare mean R_0 s to one another, since the population used to calculate them is broadly the same.

CONSTRAINED DIMENSIONS WIDGET

Fixed R_0 , adjust two sliders, the other one moves to keep R_0 constant

Let's see this equation in action!

Here you will find a set of widgets: In the first one we have fixed R_0 at 5. You can move up to two sliders to see how the third changes as the first two change.

Adjust all three sliders to see how R_0 changes/ or select a disease and see the parameters?

In this widget you can adjust all 3 parameters and see how R_0 changes. Alternatively you can select from a list of disease to see estimates of its R_0 and parameters.

How do we get the first two parameters, because they are not always available. Third

How has R_0 for Covid changed?