1 Question 1:

Write some code that runs 1000 simulated ER epidemics on the network `er_net_example` with beta of 0.3. Make a histogram that shows how much variation there is in the total number of people infected in each simulation. (Recall that we generated `er_net_example` above, using the ER random network model.)

```
In [ ]: num_infected = make_array()
        for _ in range(1000):
            num_infected = np.append(num_infected, np.sum(sim_epidemic(er_net_example, beta=.3)))
        Table().with_column('num_infected', num_infected).hist()
```

2   Question 3

Now make a scatter plot of the value of beta (x axis) to the average number of people infected across the simulations for each value of beta (y axis).

Hint: If you don't know what "group" does, you can review previous assignments or check out the python documentation: https://docs.python.org/3/howto/regex.html

```
In [ ]: beta_sim_res.group('beta', np.mean).scatter('beta', 'num_infected mean')
```

3 Question 4

Now let's visualize the results in a second way. Make a scatterplot that compares the value of beta (x axis) to the number of people infected in each simulation (y axis). (Use the `alpha` parameter to avoid misleading results due to overplotting.)

```
In [ ]: beta_sim_res.scatter('beta', 'num_infected', alpha=.05)
```

4   Question 5

What do you conclude from the two plots above? How does increasing beta affect the number of people who are infected in an SIR model on the network `er_net_example`? Describe the effects separately for the two plots.

Type your answer here, replacing this text.

5 Question 8

Which metric of centrality (degree or betweenness centrality) appears to be a better guide to targeting nodes for innoculation in the ER network?

Type your answer here, replacing this text.