COSC150: Explorations in Pandemic Modeling with Vensim: Laboratory 5: 26 Oct 2021

This is an exploration of a "generic" pathogen/virus/disease that is transmitted by human-to-human contact. It is not intended to replace actual medical advice for specific cases.

By the end of the lab explorations today, or on your own time, you will have:
   a)   Built a simple Disease Model (Susceptible → Infected) producing a graph and a table
   b)   Modified your simple Disease Model to add "social distance compliance"
   c)   Modified your simple Disease Model to add Recovered, (save as…) to explore fuller SIR (Susceptible → Infected →Recovered) model in epidemiology
   d)   Modified or downloaded pre-built model to add more realism (Exposure) producing SEIR model.

1.   Follow the instructor to build a simple Disease Model. Record all steps needed to reproduce the procedure for any other model expressed as a difference (differential) equation or set of coupled equations. Include building/modifying a graph and a table.

2.   Modify your simple model to include effect of "social distance compliance." What is the main effect of compliance?

3.   Save your model, then build or download: http://shodor.org/~rpanoff/COSC150/VensimModels/SIR.mdl to add recovery

         a.   Develop some driving questions and
         b.   Use the model to investigate the answers
         c.   Record your observations
         d.   Reflect upon your observations

4.   Download: http://shodor.org/~rpanoff/COSC150/VensimModels/SEIR.mdl

         a.   Write as complete a "story" as you can by examining the model.
         b.   Develop some driving questions and
         c.   Use the model to investigate the answers
         d.   What strategies could you use to minimize how the disease spreads?
         e.   Record your observations
         f.   Reflect upon your observations

General questions:
         a)   How could you calibrate these models to "real world data"?
         b)   How high does "social distance compliance" have to be to truly flatten the curve?
         c)   How could you account for mutations in the pathogen?
         d)   How would death or quarantine affect your models?