testing_mortality_simulation

June 1, 2020

0.1 Assessment using first principles simulation

In another notebook we have analyzed the relationship between coronavirus testing data and mortality counts using Poisson regression. This is a statistical approach rather than an explicitly mechanistic approach. Viral epidemics are generally modeled using first principles mathematical models that reflect the assumed disease dynamics. Here we will simulate data from a simple compartmental model for a viral epidemic, fit Poisson regression to it, and assess the extent to which Poisson regression captures mechanistic features of the epidemic.

A common formalism is to view the population as being partitioned into compartments of "susceptible", "infected", "recovered", and "dead" individuals. In a discrete-time approach, on each day, the following can happen: (i) currently infected people can recover, (ii) currently infected people can die, and (iii) currently infected people can infect susceptible people. By specifying probability distributions for the duration that a newly infected person remains infected, the probability that an infected person dies (the "infection/fatality rate"), the duration from infection to recovery or death, and the number of new infections arising from each infected person (the "r0", or more precisely, "rt" parameter), we can generate data following this formalism.

Below we will carry out a simulation using the very simple compartmental model described above, aiming to roughly capture the situation for Michigan. We will model the rt parameter as a piecewise linear function that starts at 2.2 (a high value) and remains there for one month. Then, due to the effect of mitigation measures, we have the rt decrease linearly from 2.2 to 0.9 over a duration of 20 days. The rt remains at 0.9 thereafter.

The main goal here is to see how the Poisson regression model performs when fed data generated according to a commonly-utilized probability model for epidemics.

[1]:

```python
import pandas as pd
import numpy as np
import statsmodels.api as sm
import matplotlib.pyplot as plt
```

Make the notebook reproducible.

[2]:

```python
np.random.seed(3443)
```

[3]:

```python
# Simulate for this number of days
ntime = 85

# Infection fatality rate
ifr = 0.01

# Information characterizing one person
```

```python
class person:

    # Day on which the person was infected
    infection_day = 0

    # True if the person recovers, False if they die
    recover = True

    # The time duration from infection to recovery or death
    duration = 0

    # The number of people infected by this person
    infects = 0

    def get_rt(self, d):

        # The initial rt and final rt
        r0 = 2.5
        r1 = 0.9

        # Due to mitigation, the rt value drops from r0 to r1
        # between days d0 and d1.
        d0, d1 = 20, 40

        # Calculate the rt value on day d
        if d <= d0:
            rt = r0
        elif d <= d1:
            rt = r0 - (r0 - r1) * (d - d0) / (d1 - d0)
        else:
            rt = r1
        return rt

    # Generate a random person who is infected on day d.
    def __init__(self, d):

        rt = self.get_rt(d)

        # Day of infection
        self.day = d

        # Does the person recover or die?
        self.recover = np.random.uniform() > ifr
        if self.recover:
            # Duration to recovery
            self.duration = int(np.ceil(-7*np.log(np.random.uniform())))
        else:
            # Duration to death
            self.duration = int(np.ceil(-21*np.log(np.random.uniform())))

        # Number of people infected by this person, give it heavier
        # tails to approximate "super-spreading".
        # b = v/m
        # a = m^2/v
        m = rt
        v = 10.0 * m**2
        self.infects = int(np.round(np.random.gamma(m**2/v, v/m)))
```

The columns of the array ‘sird’ correspond to the number of new infections, new recoveries, new deaths, and active infections on a given day. The rows of sird correspond to consecutive days since the beginning of the epidemic.

The following function updates the numbers rows of ‘sird’ based on a set of infected people in ‘active’.

[4]:
```
def update_mat(active, sird):
    for k, p in enumerate(active):
        if p.day >= ntime:
            continue

        # Update the new infection column
        sird[p.day, 0] += 1

        # The end of the infectious interval
        t = p.day + p.duration

        # Update the active cases column
        sird[p.day:min(t, ntime), 3] += 1

        # The person's outcome occurs in the future
        if t >= ntime:
            continue

        # Update the outcome columns
        if p.recover:
            sird[p.day + p.duration, 1] += 1
        else:
            sird[p.day + p.duration, 2] += 1

    return sird
```

The following function advances one generation, taking all the currently infected people and simulating data for the people infected by them.

[5]:
```
def update_people(active):
    active1 = set({})
    for a in active:
        for k in range(a.infects):
            delay = np.random.poisson(4)
            active1.add(person(a.day + delay))
    return active1
```

[6]:

```
np.random.seed(34234)
```

The following function generates the ‘sird’ array as described above.

[7]:

```
def gen_sird():

    sird = np.zeros((ntime, 4))

    # Start with 10 seeds on day 0.
    active = set({person(0) for k in range(10)})

    # Loop over ntime/4 generations of transmission (the serial
    # interval is thought to be around 4 days).
    for itr in range(ntime // 4):
        sird = update_mat(active, sird)
        active = update_people(active)

    sird = pd.DataFrame(sird, columns=["I", "R", "D", "A"])

    return sird
```

Next we need to simulate daily positive and negative test results. We use a gamma distribution, centered on a value equal to 1/100 of the population of active cases to produce the positive test results, and we simulate the negative test results as random values independent of the disease. Note that detecting 1/100 of the active cases on a single day implies that the case/ascertainment ratio is around 10, if people would test positive for around 10 days during the course of their illness.

[8]:

```
def attach_testing(sird):
    # The relationship between the mean/variance and
    # the gamma distribution parameters.
    # m = a*b
    # v = a*b^2
    # b = v/m
    # a = m^2/v

    # Positive tests
    m = sird.A / 100
    v = 1.0 * m**1.5
    sird["dpositive"] = np.random.gamma(m**2/v, v/m, ntime)

    # Negative tests
    m = 20000
    v = 1.0 * m**1.5
    sird["dnegative"] = np.random.gamma(m**2/v, v/m, ntime)
    return sird
```

Next we construct the covariates we need, so as to be able to fit the same model used above for the actual Covid tracking project data.

[9]:
```python
# Sum x from d2 days back in time to d1 days back in time, inclusive of
# both endpoints.  d2 must be greater than d1.
def wsum(x, d1, d2):
    w = np.ones(d2 + 1)
    if d1 > 0:
        w[-d1:] = 0
    y = np.zeros_like(x)
    y[d2:] = np.convolve(x.values, w[::-1], mode='valid')
    return y

def attach_covariates(sird):
    for j in range(4):
        sird["cumpos%d" % j] = wsum(sird.dpositive, 7*j, 7*j+6)
        sird["cumneg%d" % j] = wsum(sird.dnegative, 7*j, 7*j+6)
        sird["logcumpos%d" % j] = np.log(sird["cumpos%d" % j] + 1)
        sird["logcumneg%d" % j] = np.log(sird["cumneg%d" % j] + 1)
    return sird
```

The following function puts everything together:

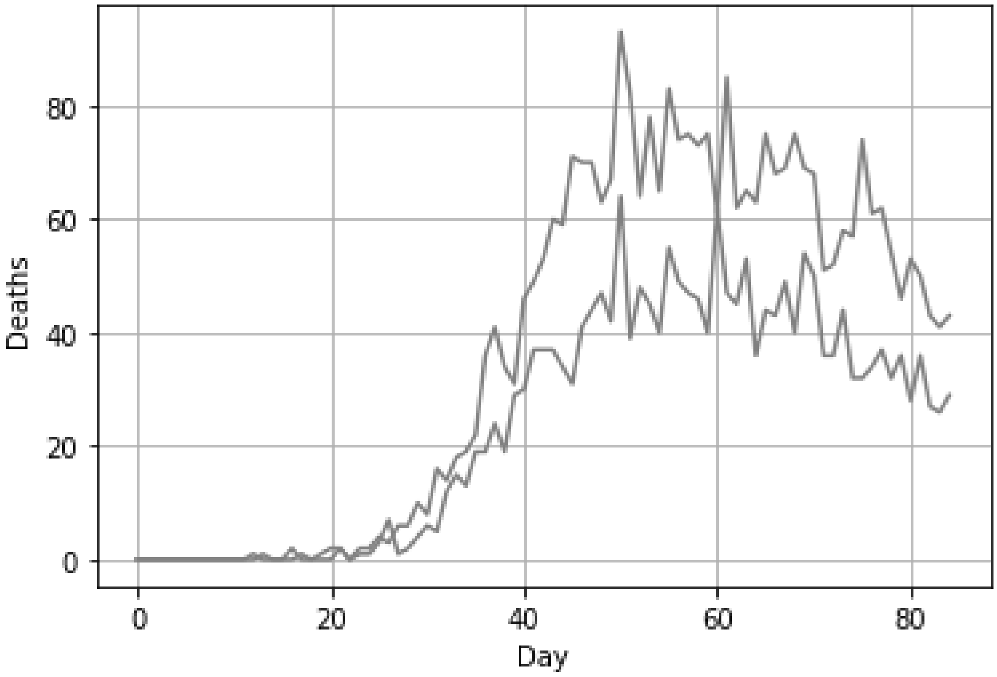
[10]:
```python
def generate():
    sird = gen_sird()
    sird = attach_testing(sird)
    sird = attach_covariates(sird)
    return sird

sird = [generate() for k in range(2)]
```

Below are plots of the simulated number of daily deaths, the simulated number of active cases, and the simulated number of positive tests. The stochastic nature of the daily deaths and testing data is evident, but the number of active cases appears non-stochastic. In fact this is not the case, but at the population level it appears to be so.

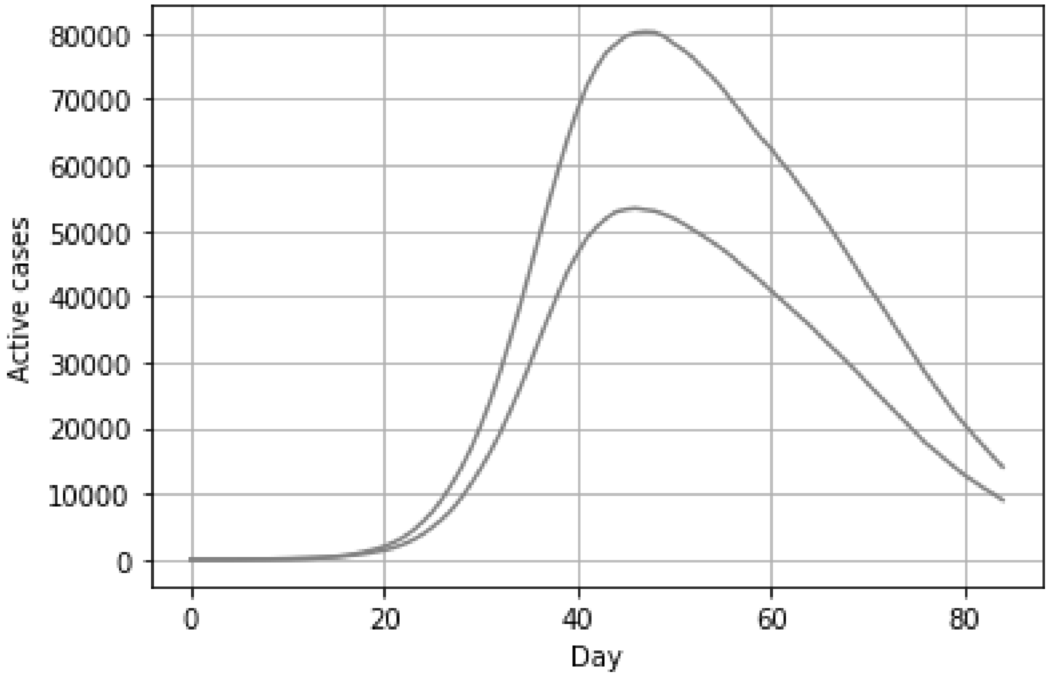
[11]:
```python
plt.clf()
plt.grid(True)
for x in sird:
    plt.plot(x.D.values, '-', color='grey')
plt.xlabel("Day")
plt.ylabel("Deaths")
```

[11]:
```
Text(0, 0.5, 'Deaths')
```



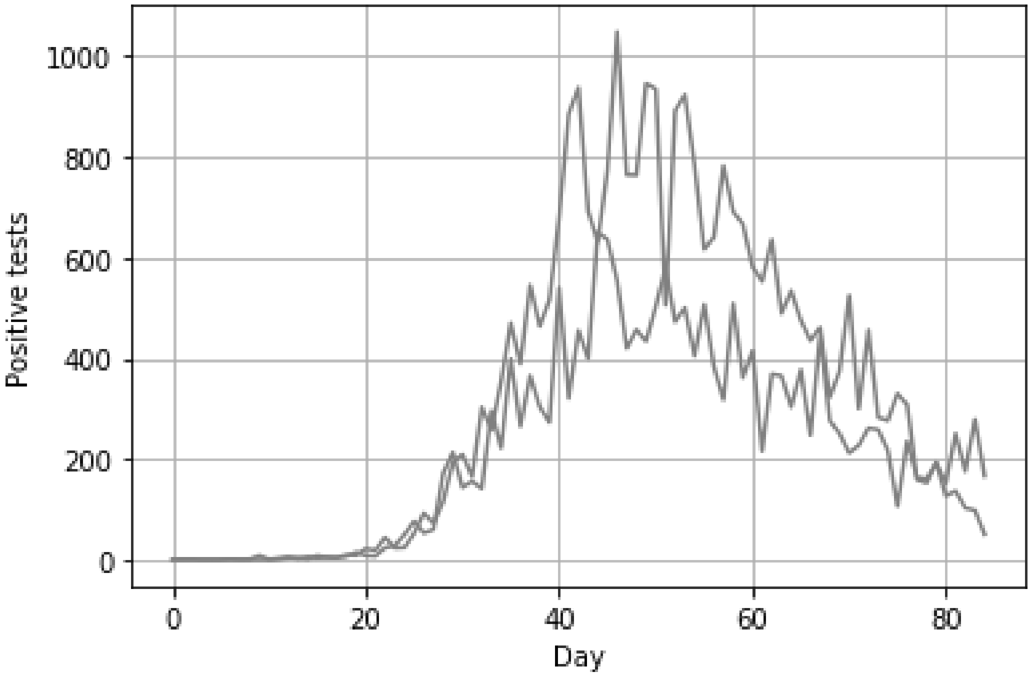
[12]:
```
plt.clf()
plt.grid(True)
for x in sird:
    plt.plot(x.A.values, '-', color='grey')
plt.xlabel("Day")
plt.ylabel("Active cases")
```

[12]:
```
Text(0, 0.5, 'Active cases')
```



[13]:
```
plt.clf()
plt.grid(True)
for x in sird:
    plt.plot(x.dpositive.values, '-', color='grey')
plt.xlabel("Day")
plt.ylabel("Positive tests")
```

[13]:
```
Text(0, 0.5, 'Positive tests')
```



Now we can fit the same model used above to see what we get:

[14]:

```
fml = "D ~ "
fml += " + ".join(["logcumpos%d" % j for j in range(4)])
fml += " + "
fml += " + ".join(["logcumneg%d" % j for j in range(4)])
r4 = []
for x in sird:
    m4 = sm.GLM.from_formula(fml, data=x, family=sm.families.Poisson())
    r = m4.fit(scale="X2")
    print(r.summary())
    print(r.scale)
    r4.append(x)
```

```
                 Generalized Linear Model Regression Results
==============================================================================
Dep. Variable:                      D   No. Observations:                   85
Model:                            GLM   Df Residuals:                       76
Model Family:                 Poisson   Df Model:                            8
Link Function:                    log   Scale:                         0.84139
Method:                          IRLS   Log-Likelihood:                -248.68
Date:                Mon, 01 Jun 2020   Deviance:                       66.067
Time:                        14:43:10   Pearson chi2:                     63.9
No. Iterations:                    14
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept     -6.7249      5.827     -1.154      0.248     -18.145       4.695
logcumpos0     0.3274      0.192      1.702      0.089      -0.050       0.704
logcumpos1     0.3047      0.232      1.313      0.189      -0.150       0.759
logcumpos2    -0.1131      0.198     -0.572      0.568      -0.501       0.275
logcumpos3     0.0902      0.109      0.829      0.407      -0.123       0.303
logcumneg0     0.3915      0.481      0.814      0.415      -0.551       1.334
logcumneg1    -0.0452      0.088     -0.514      0.607      -0.217       0.127
logcumneg2     0.0792      0.058      1.371      0.171      -0.034       0.193
logcumneg3     0.0729      0.022      3.243      0.001       0.029       0.117
==============================================================================
0.8413859140104512
                 Generalized Linear Model Regression Results
==============================================================================
Dep. Variable:                      D   No. Observations:                   85
Model:                            GLM   Df Residuals:                       76
Model Family:                 Poisson   Df Model:                            8
Link Function:                    log   Scale:                         0.89880
Method:                          IRLS   Log-Likelihood:                -216.70
Date:                Mon, 01 Jun 2020   Deviance:                       69.669
Time:                        14:43:11   Pearson chi2:                     68.3
No. Iterations:                    16
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept     -8.1909     14.200     -0.577      0.564     -36.022      19.640
logcumpos0     0.2268      0.167      1.361      0.174      -0.100       0.553
logcumpos1     0.4360      0.157      2.771      0.006       0.128       0.744
logcumpos2     0.0208      0.115      0.181      0.856      -0.205       0.246
logcumpos3     0.0056      0.071      0.080      0.936      -0.133       0.144
logcumneg0    -0.0815      0.788     -0.103      0.918      -1.626       1.463
logcumneg1     0.5604      0.800      0.700      0.484      -1.008       2.129
logcumneg2     0.0522      0.053      0.994      0.320      -0.051       0.155
logcumneg3     0.0194      0.029      0.660      0.509      -0.038       0.077
==============================================================================
0.8987985447019455
```

Qualitatively, the results are fairly similar to what we saw with the actual Covid Tracking project data. Note that the simulation reflects data for a single state, whereas the actual data is for all US states. As a result, the actual data analysis has much greater power. In the simulated data, the coefficients for the log number of positive tests are not always statistically significant. As in the actual data, their sum is around 0.8.