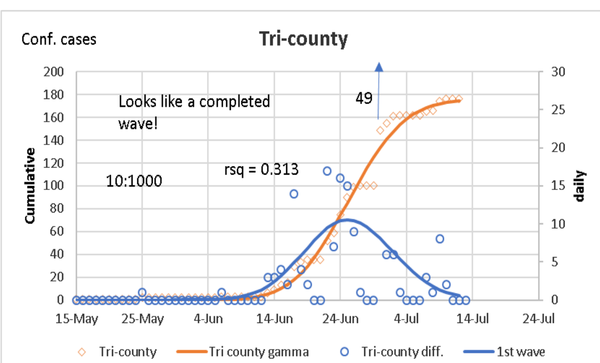
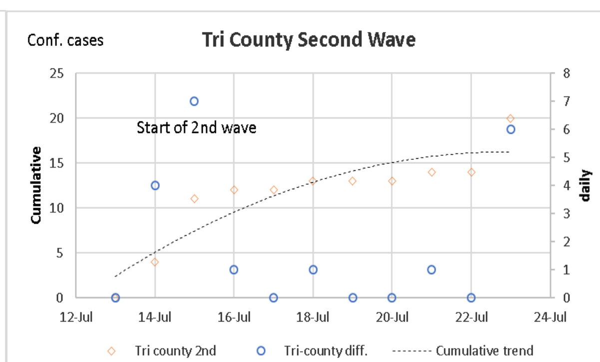
Please refer to accompanying two pdf files of graphs. The estimated number, and the related incidence relative to population, is based on maximums estimated from curve fits. They are subject to change of course, and should not be taken as precise projections, since there is no such thing. Another way to interpret them is as relative indices, that show a locale's progress relative to the others.[1]

As far as Tri-County (Brewster, Jeff Davis and Presidio counties in Texas) goes, the following tabulation shows what happens if the proposed US or Texas projections for confirmed cases are scaled to our population:

max US daily	79,881	persons
equiv. max Tri-County	4.4	persons
max TX daily	10,538	persons
scaled to Tri-County	704.1	persons
max US cumulative	8,509,931	persons
equiv. max Tri-County	464	persons
incidence	26:1000	
max TX cumulative	1,095,282	persons
scaled to Tri-County	704	persons
incidence	39:1000	
Tri-County (current)	11:1000	7/23/2020

Tri-County has just completed a wave, and may be starting a new one. This is the time for everyone here to work together to avoid another wave.

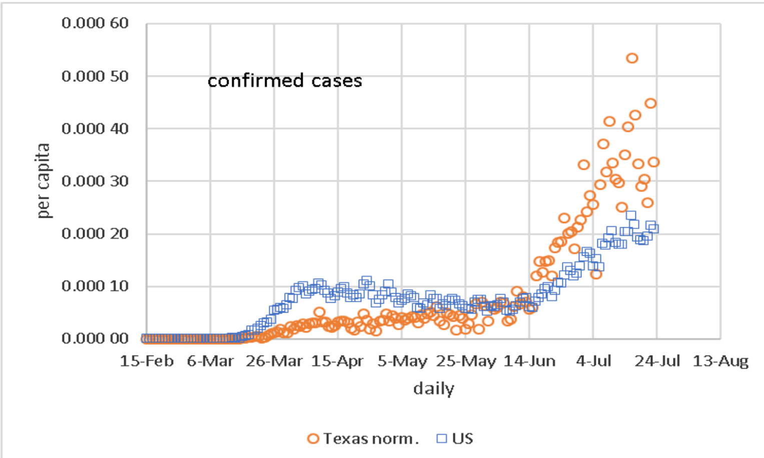




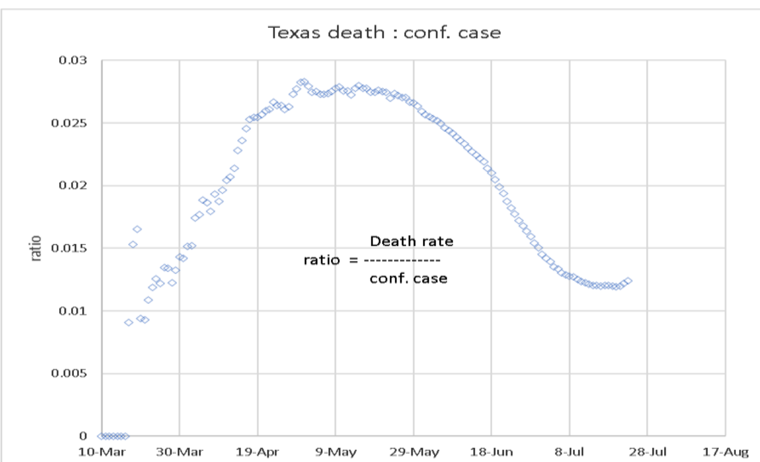
[1] Data all from publicly available Github site: https://github.com/CSSEGISandData/COVID-19

Comments

If Texas and the USA data are plotted as daily data concurrently, on a per capita basis, here is what you see:

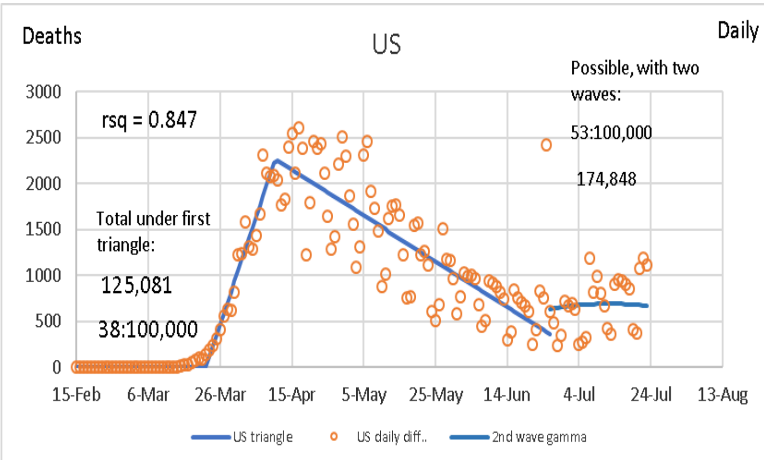


Texas is showing faint signs of turn around finally, as well as the US. It's interesting that the Texas ratio of deaths to confirmed cases has been dropping, but now leveling off, and always has been significantly less than the US numbers, which could mean better treatment of a growing number of confirmed cases, or more testing finding more cases, or some combination of that. Arizona has a similar curve.



COVID-19 deaths

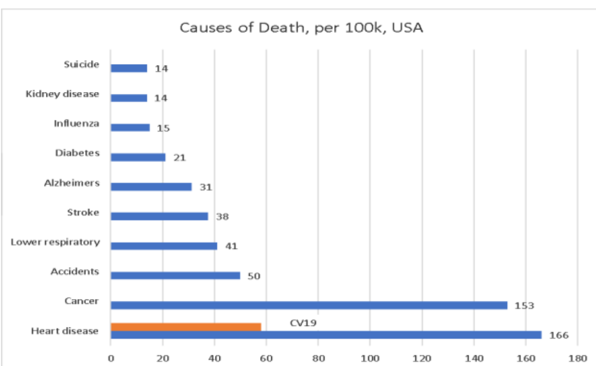
A few months ago the Wall Street Journal published data on annual causes of death which I have plotted with the USA CV-19 death statistics. The USA CV-19 death statistic is based on a triangular distribution, combined with a later gamma distribution curve fit of USA deaths that generates a cumulative maximum for the two combined (minus their overlap).

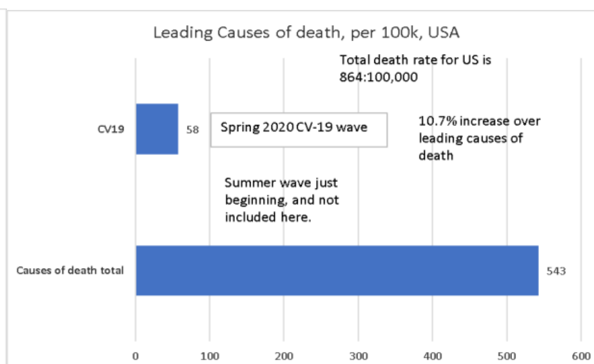


A point of comparison:

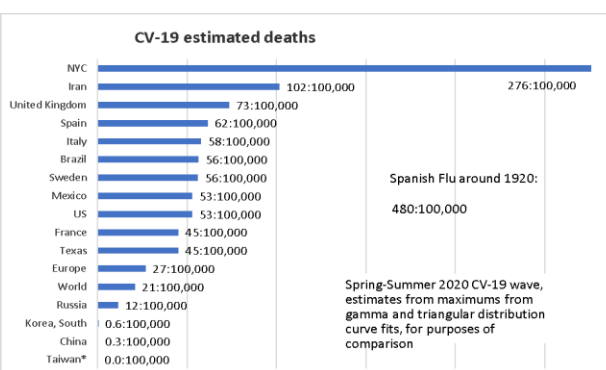
In 1920, the population of the US was 105 million. It is estimated that 500,000 people in the US died from the Spanish Flu epidemic in those years. This is a death rate of around 480 per 100k.

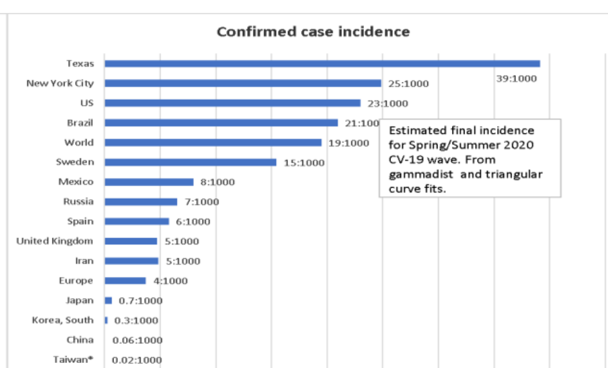
The possible value is plotted as deaths per 100,000 with WSJ data of annual averages of leading causes:





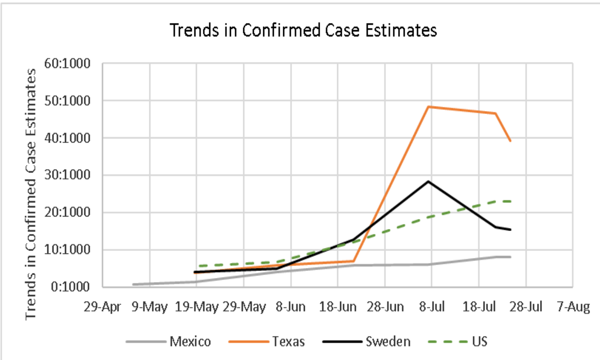
It's right up there with the major killers, although it's known many who died from CV-19 already had these potentially fatal issues. It's not clear where dying from old age fits in here, either. I suspect old age deaths would deduct from all these more or less equally, so the relative size remains unchanged.

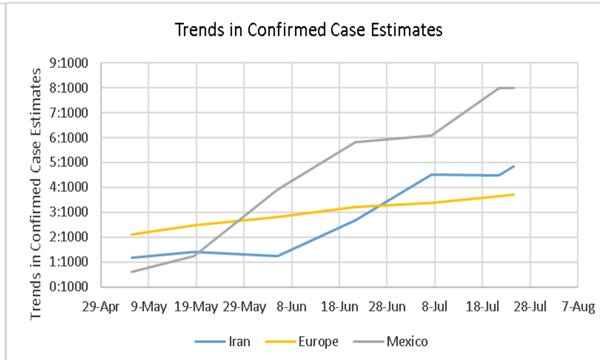




Trends in Confirmed Case Estimates

The confirmed case estimates are based on the maximum value parameter of a curve fit for a *completed* epidemic wave. The US was changed from a triangular distribution to a combination curve. The curve fit has been based on data that was in the process of being completed for the Spring/Summer 2020 CV-19 wave, so it's to be expected that the estimates might change. Here are confirmed case trends for a few select countries:



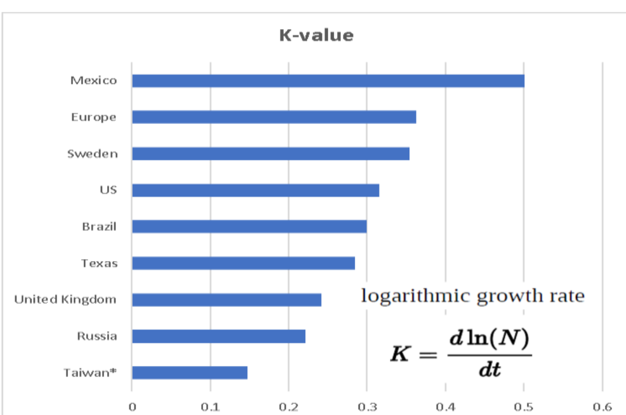


Explanation of statistic used for comparative purposes:

Often the generation of confirmed cases or deaths tend to be in a gamma distribution, which is a slightly skewed bell-shaped curve. Other times a triangular distribution better describes what's happening. A least squares procedure is used to get the closest fit to the data. Generally, the data is provided in a *cumulative* format, so the number increases each day, until the wave is over, at which point it is at its maximum and no longer changes. This can be converted to a daily format just by finding the difference between each pair of successive days. In mathematical terms, the daily format is the time derivative of the cumulative format. In any case, the area under the daily curve is identical to the last, largest and unchanging value in the cumulative format. This is the value that is used here as a comparative statistic, on a per capita basis. Each locale's "wave" has a different beginning, develops at a different rate, so comparison of values on a particular date among any given datasets doesn't tell you much.

Cases are usually described as incidents per thousandths; deaths are described as incidents per hundred thousandths. In this way, one can get a better feel for the relative performance of locales, as long as the current population figure is available. It's also a way to gauge one's own personal risk. Keep in mind this statistic can and will change over time, not as a direct result of increasing cases or deaths, but because of the possible change in shape of the distribution. In some cases, particularly with the US, the distribution was changed from a gamma to a triangular because it fit better, which also changed the comparative statistic. It should be thought a qualitative measure, since it's impossible to put error bounds on it, at least in its earlier stages before its inflection point.

R_o[2]: If one can find the exponential part of the cumulative growth curve (a short section near the beginning of the curve that loses validity if less than N = 100 people), one finds the growth rate constant for an exponential, which is $K = d\ln(N) / dt$. (If plotted on semi-log paper, look for a straight line section near the beginning; K is its slope.) $R_o = e^{K\tau}$ where τ is the average infectious period for each person. Reduce K by reducing contacts, reduce τ by isolation of infected individuals, for example. Here are some K values:



Example ($R_o = 2.6$, $K_{TX} = 0.284$ / day)

$$R_o = e^{K\cdot\tau}$$

$$\tau = \frac{\ln(R_o)}{K} \quad , \quad \frac{\ln(2.6)}{0.284} = 3.4 \quad \text{days infectivity}$$

Example ($R_o = 1.0$, $K_{TX} = 0.284$ / day)

$$\tau = \frac{\ln(1.0)}{0.284} = 0 \quad \text{days infectivity}$$

[2] Basic Reproduction Rate. R_o is a measure of transmissibility: $R_o < 1$, disease disappears; $R_o = 1$, it's endemic; $R_o > 1$, epidemic. R_o is mentioned a lot in this epidemic, along with flattening of curves, with not a lot of understanding.