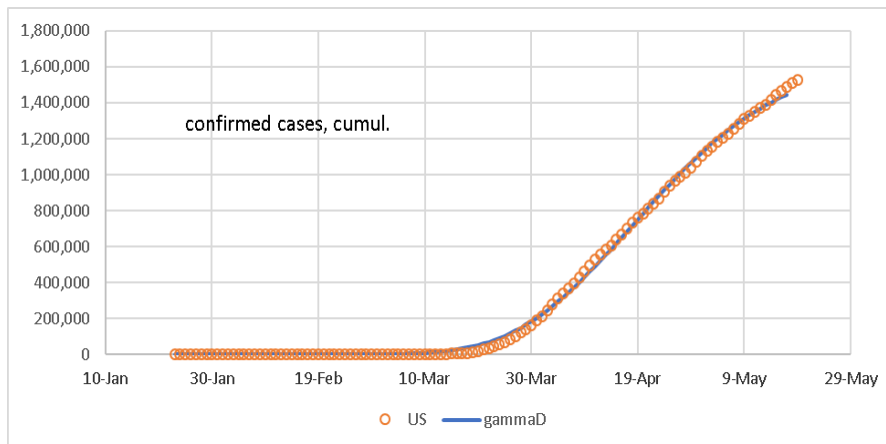
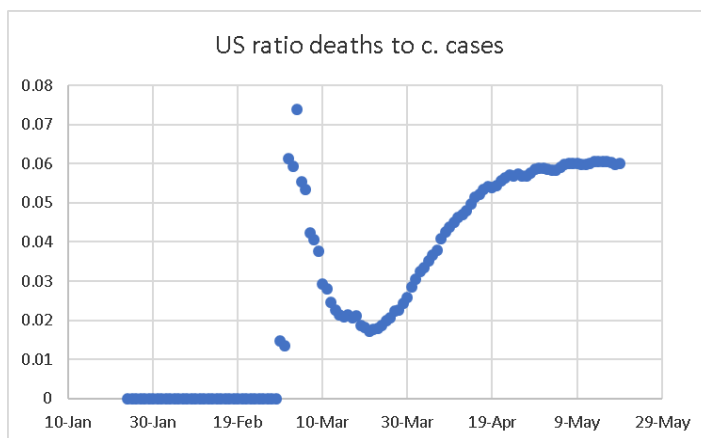


As of 20 May 2020, the US Covid-19 epidemic looks like this:<sup>1</sup>



The ratio of deaths to confirmed cases looks like this:



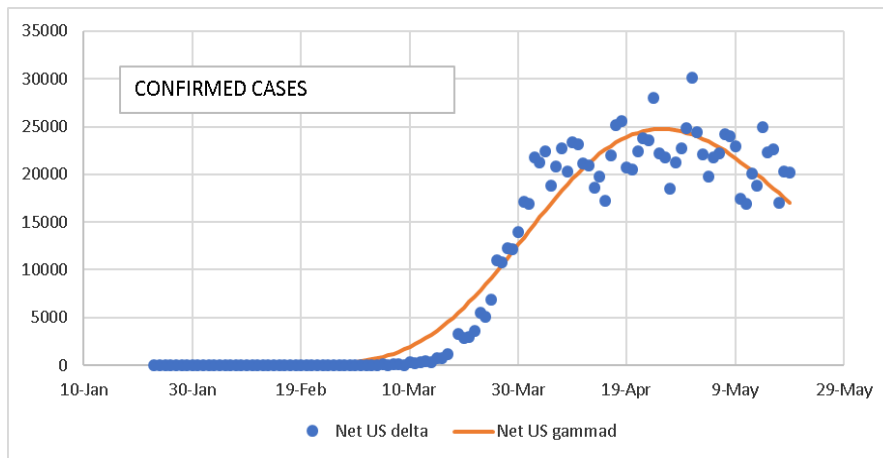
So, it appears that 6% of confirmed cases die, which proves this is no common flu.<sup>2</sup>

The distribution of this data could be applied locally, assuming the US case applies to the local situation. It makes sense to subtract out New York City confirmed cases, the urban extreme (and about 14% of total US cases), to arrive at a more applicable distribution, although still predominantly urban. Since here in the Big Bend we live more spread out, and don't crowd together on rapid transit, our "wave" is probably something less than the NET US (that is, US confirmed cases minus NYC). It also probably lags in time the urban populations by quite a bit. But since an epidemic is nothing but a deadly diffusion problem, sooner or later it reaches its equilibrium, no matter what we do (save a vaccine).

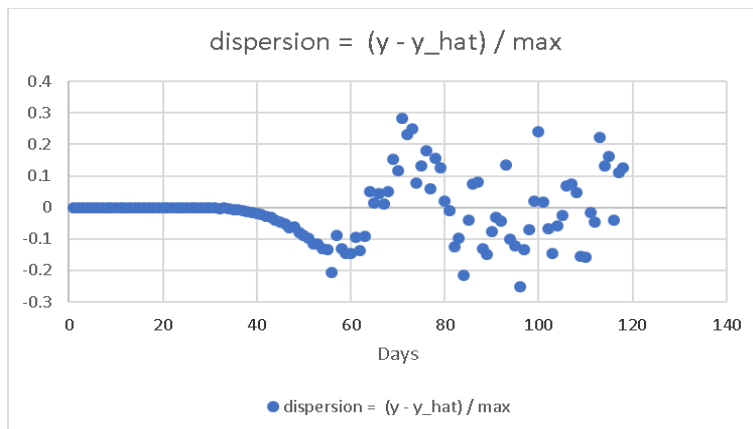
<sup>1</sup> <https://github.com/CSSEGISandData/COVID-19>

<sup>2</sup> A lot of useless discussion on actual vs. confirmed cases occurs, in my opinion, to minimize the deadliness of this virus. Why would you want to minimize the deadliness of something that is so obviously deadly?

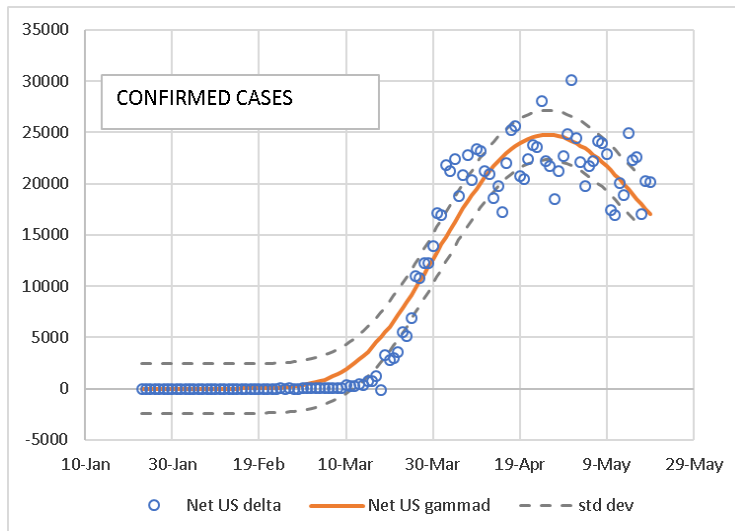
NET US appears like this, on a *daily* basis, not cumulative:



The curve fit is a gamma distribution, often used to characterize disease, population growth, and epidemics. A measure of dispersion is the standard deviation of  $(y - y_{\hat{}}) / y_{\hat{}}_{\max}$ .  $y$  is data recorded (in this case, the difference between each pair of successive values on the previously shown cumulative data),  $y_{\hat{}}$  (pronounced *wye hat*) is the value at each date of the gamma distributed curve fit, and  $y_{\hat{}}_{\max}$  is the maximum value of the gamma distributed curve fit. The dispersion looks like this (below) and gives an idea of the goodness of fit of the data around the gamma distribution.  $R^2$  is another, and is equal to 0.917.

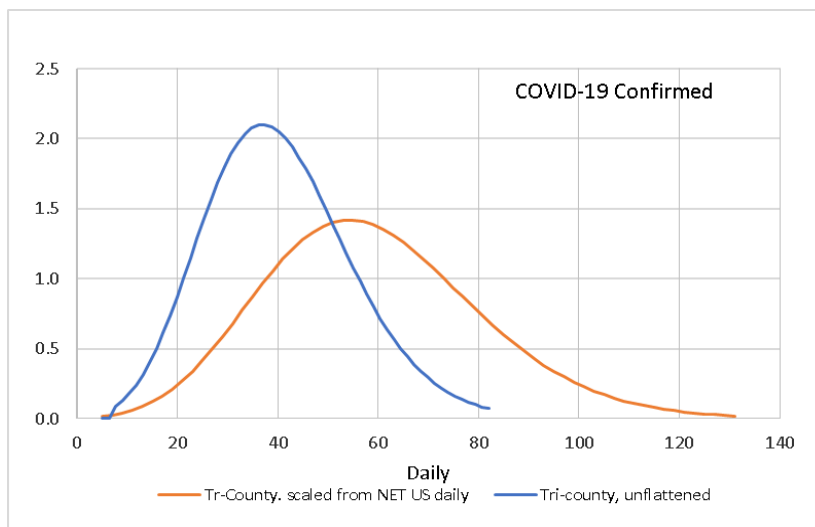


The standard deviation of the dispersion values (0.098) can be used to construct a 1 standard deviation boundary around the curve fit:

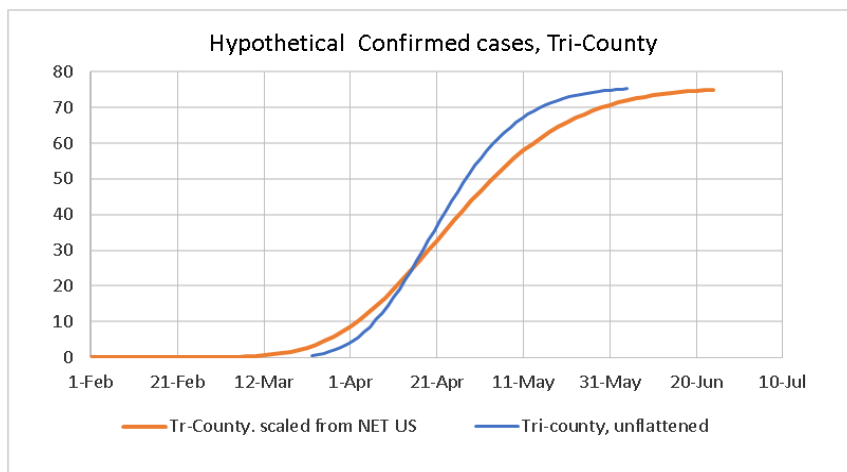


This data is for a population of 320 million (US population less NYC's), but why not scale it to a Tri-County population of 16,000, in order to have a better idea of what to expect here?

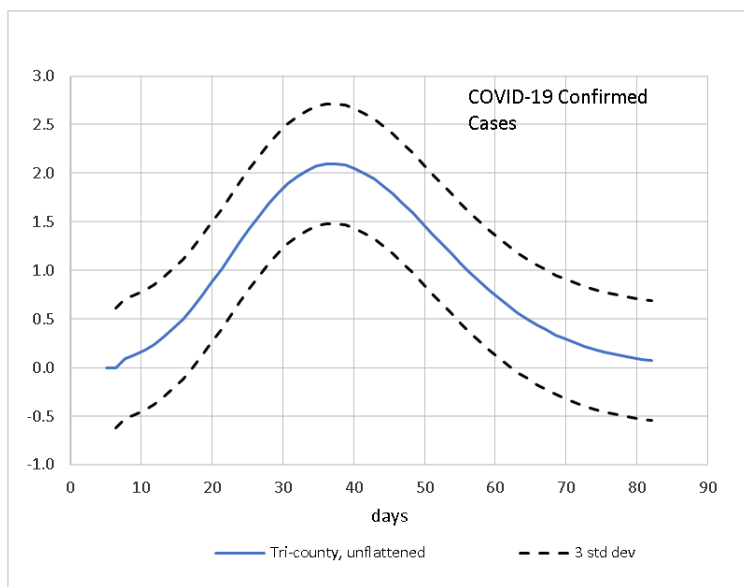
First, assume the above data represents a *flattened* curve—that is, all the restrictive measures that were put in place succeeded in lengthening its duration and reducing its peak (but not changing the total number of infections, the area under the curve). This was the original rationale given for the restrictive measures, to alleviate the burden on the medical facilities. It can be scaled by a simple population ratio to fit the Tri-County area. The resulting curve can also have its time scale compressed, to simulate an unflattened curve, presumably what would happen here without the restrictions. This is compressed by a factor 1.5. Here is what that looks like:



The area under each curve is the same, there is no change in total cases. It's also worth looking at the cumulative version of this distribution, to see what the time compression does to it. Notice it doesn't change the final, cumulative value, which is equivalent to 5 in 1000 being a confirmed case.<sup>3</sup>



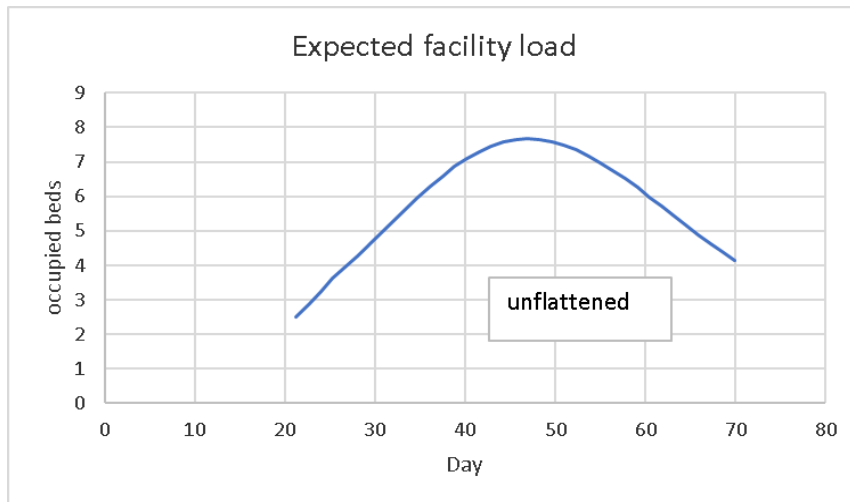
Secondly, taking the unflattened curve (blue), and applying the dispersion factor previously created, we can apply a three standard deviation bound—this could be a conservative design criteria to use for county-supplied COVID-19 treatment centers, to avoid sending any virus sufferers to the regional hospital. Three standard deviations should take care of 95% of the possibilities. The county could provide something less than this, and still do a lot of good, of course.



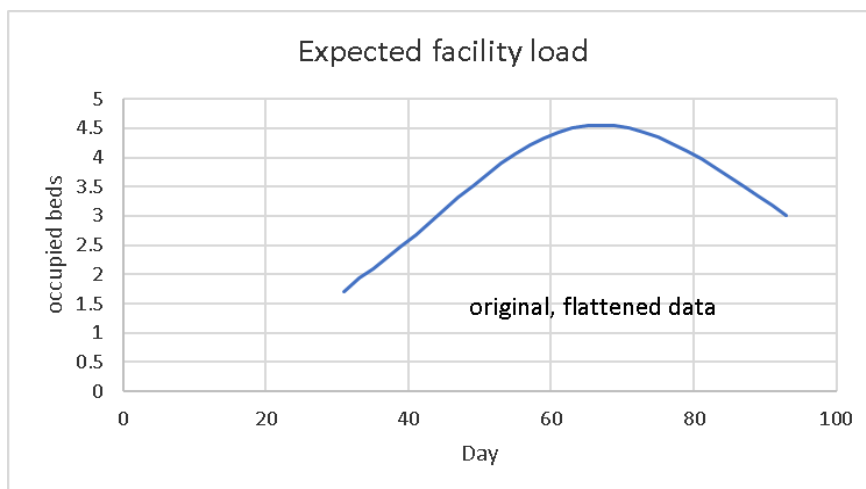
On first glance, it appears that *three* confirmed cases are what to expect for the maximum daily cases in the Tri-County during a virus wave. But, there will already be cases ongoing, with an average length of 14 days. A rolling sum of the two (new cases, plus cases lasting 14 days) can be constructed. To find the

<sup>3</sup> If one assumes the Tri-County is a sample of the US NET population, scaling it this way will likely increase its dispersion, since that is the nature of small samples. The rolling sum probably smooths that out enough that it is not significant, but that is not rigorously addressed here.

impact on medical care one needs to apply a 20% factor to the confirmed case estimate, since only about 10 to 20% of confirmed cases require medical care or hospitalization:



This peaks at 8, or about 3 beds per county, or to be apportioned by each counties' respective populations. A similar calculation can be done for the flattened curve case, where the expected facility load is 5, or about two beds per county:



Either case is one that the regional hospital could probably handle, or each county could undertake on their own, with separate medical facilities. It's worth reviewing the spread of both SARS-Covid-1 and SARS-Covid-2 (the current one) to see the key role of hospitals in initially *spreading* the disease, a good reason to *not* use the hospital if you can. Looked at this way, with life and economic restrictions, it would require two beds per county, while unrestricted liberty and economics costs three beds per county, for a net cost of one bed per county to preserve personal and economic liberty.

Remember, the area under the curve is the *same* in either flattened or unflattened case, which implies shutting everyone in *doesn't* reduce total cases. This was the original rationale, as was promoted when restrictions were introduced nation-wide. The restrictions were to help avoid inundating health facilities.