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Abstract for an Invited Paper
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A spherical cow model of Covid-19 epidemiology and applications¹

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In late 2019, a coronavirus called SARS-CoV-2 appeared in Wuhan, China. This virus has since caused a worldwide pandemic, which is still ongoing. The associated respiratory illness, called COVID-19, ranges in severity from a symptomless infection, to common-cold like symptoms, to viral pneumonia, organ failure, neurological complications and sometimes, death. While mortality rates from SARS-CoV-2 infections are significantly lower than from the earlier pandemic in 2003 from the SARS-CoV-1 virus, it has more favorable transmission characteristics, a higher reproduction number, and a long incubation period, when the patient may be asymptomatic but infective. Each country/region instituted varying measures to reduce the rates of infections using lockdown, quarantine, use of masks, reduced movement of people etc. In this paper, after a brief introduction to the origins and spread of the virus, I will describe a simple mathematical epidemiological SIR model for the pandemic, where S = Susceptible, I = Infected, R = Removed: Recovered or Dead. This model accurately describes the initial rise of cases in a pandemic, up to and beyond the initial peak in daily cases. I will then discuss two applications of the model, using public data on caseloads and deaths. The first application was to understand daily caseloads and deaths in the United Kingdom and eight European counties: Norway, Sweden, Denmark, The Netherlands, Italy, France, Germany, and Spain. The results can be used to determine where mitigation effects worked and where they did not. In the second application I will show how to use Change of Address data to understand how the virus spread from its epicenter in the five boroughs of New York City into counties of the tri-state area of New Jersey, Connecticut and New York to cause a second wave in cases because of movements of households. This analysis shows that tracking household movements may be a simple way to predict where new cases are likely to appear. I will end with some caveats on the limitations of the model and prospects for future work.

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