## Benford analysis of Covid-19 data

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## 1 Summary

In the effort to react appropriately to the spread of Covid-19 it is essential to have access to data concerning the effects of the virus; the two most commonly reported statistics are persons known to have tested positive for the virus (called "Cases") and persons who have succumber to the virus ("Deaths"). It is important that the data are timely and accurate; in the case of the latter, how can this be checked? Here we show that datasets such as the cumulative case and death data from different countries can be analysed by comparing the reported integers to the expected distribution for such rapidly-growing statistics, which are expected to have a Benford-law type distribution. Only the leading digit is of importance in such an analysis. We show that there is an expected good agreement between theory and reported values, although there are occasional strange deviations.

## 2 Analysis

Data for all countries analysed were obtained from https://github.com/mhandley/COVID19/ on 9/4/20 (courtesy Prof. M. Handley, UCL, UK), who has distributed data from national authorities and occasionally from the WHO daily briefing. These data tend to be more up-to-date than the definitive Johns Hopkins data. We take as data for each country the cumulative cases or cumulative deaths as reported in the country files and neglect the date, so that the only numbers are the growing cumulative totals. We create two "All countries" datasets for cases and for deaths by concatenating the country data. These dataset consist of 2185 and 2070 integers respectively. The latter is slightly smaller than the former because on some days when there are cases, no death information is reported. The data we acquired contained no death information for China.

We begin by analysing the two "All counties" datasets for cases and deaths in Figures 1a and 1b. In all figures the dashed curve represents the expected Benford 1st digit distribution, in which there are around 30% leading digits that are "1"s and around 5% that are "9"s.

We see a clear adherence from all the data to the expected distribution. We can see this also at a country level (Figure 2). We take as examples the European countries France, Germany, Spain, UK, Switzerland, Italy. All these countries have experienced large growths in numbers. Since the datasets are smaller, we expect to see more variability around the expected distribution. Such variability would diminish as the datasets increase in size. We have examined the plots of 53 countries, and find general agreement in their behaviour, similar to in Figure 2.

There are, however, very rare outliers that signal a behaviour far from expected. An example is given in Figure 3. The likelihood of having so many data with "9"s is very low, and one can now trace this back to the original data. Subsequent days reported 9 deaths, and then two weeks later, subsequent days reported 90 and 99 deaths. Figure 4 shows the correlection coefficient for all countries' case data when compared to the theoretical curve.

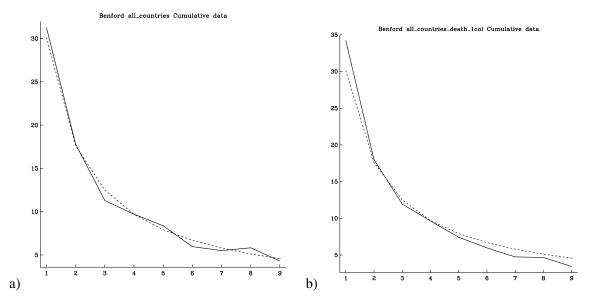


Figure 1: Comparison of data from all countries together with the expected distribution (dashed). a) Cases. b) Deaths.

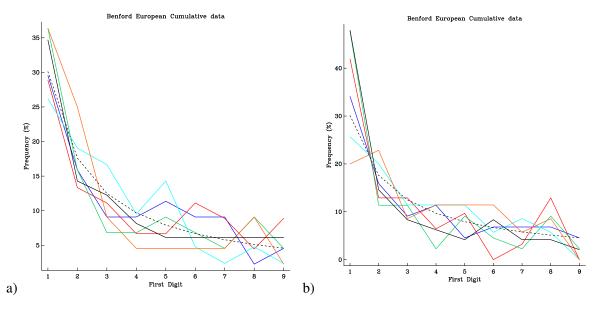


Figure 2: Comparison of data from selected European countries together with the expected distribution (dashed). Countries are France (blue), Germany (red), Spain (green), UK (cyan), Switzerland (Orange) and Italy (black). a) Cases. b) Deaths.

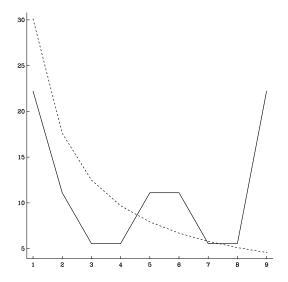


Figure 3: Death data reported by a single country (name withheld).

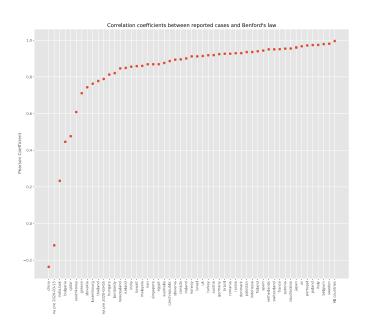


Figure 4: Correleation coefficient for each of the countries' case data that was analysed.



