**COVID-19 treatment disparities**

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For any risk quantile *k*, we can express the number of adverse COVID-related events *E* (*e.g.*, hospitalizations or deaths) in terms of the number of COVID cases C and the number of treatments *T* with the following equation:

*Ek* = (*Ck* – *Tk*) P(*Ek*|*Ck*) + *Tk* (1-*σ*) P(*Ek*|*Ck*)

Here, P(*E*|*C*) is the probability that the event occurs given a symptomatic COVID-19 case, and *σ* is the treatment effectiveness (*i.e.*, the proportion reduction in risk due to treatment). In plain words, this equation says that the number of adverse events *E* is equal to (a) the number of untreated COVID cases times the baseline probability that the event occurs given a case, plus (b) the number of treated COVID cases times the treatment-adjusted probability that the event occurs given a case.

However, we know that we don’t observe all the cases, so we need to adjust this for imperfect ascertainment. Let *ck* (lowercase) denote the observed number of cases and *ak* denote the ascertainment rate, so that

*ak Ck* = *ck*

Thus, we can re-write the first equation as

*Ek* = (*ck*/ak – *Tk*) P(*Ek*| *ck*, *ak*)+ *Tk* (1-*σ*) P(*Ek*| *ck*, *ak*)

We can also simplify the equation:

*Ek* = P(*Ek*| *ck*, *ak*) [*ck*/ak – *σ Tk* ]

If we assume that we observe all treatments *T* and all adverse events *E*, we are left with two key unknowns:

* *ak*, the case ascertainment rate. This may vary across risk groups *k.*
* *σ*, the treatment efficacy. We will assume that this is constant across risk groups, though we can relax this assumption if needed.

If we make informed guesses about these values, it is possible to calculate P(*Ek*| *ck*, *ak*) (the risk of adverse outcomes) from the available data. Furthermore, with a slight adjustment to the main equation, we can also estimate the number of adverse events that would have occurred with a different number of treatments:

Here, is the alternate number of treatments in group *k* and is the expected number of adverse events that would have occurred with treatments.

**I think we should plot as a function of ascertainment rather than treatment efficacy…**

**Preliminaries.** For each risk group, there are two key unknowns: (1) the probability of (hospitalization/death) in the absence of treatment, and (2) the effectiveness of treatment against (hospitalization/death). These quantities are related to the observed cases/hospitalizations/deaths according to the following equations:

*# hospitalizations* = (*# untreated cases) (phosp)* + *(# treated cases) (phosp) (1-TEH)*

*# deaths* = (*# untreated cases) (pdeath)* + *(# treated cases) (pdeath) (1-TED)*

Here, the key unknowns are:

* *phosp* (probability of hospitalization in the absence of treatment)
* *TEH* (treatment effectiveness against hospitalization)
* *pdeath* (probability of death in the absence of treatment)
* *TED* (treatment effectiveness against death).

In terms of the available data, we have:

inpatientCovid = (covid22 – anydrug)\***phosp** + anydrug\***phosp**\*(1-**TEH**)

covidDeath = (covid22 – anydrug)\***pdeath** + anydrug\***pdeath**\*(1-**TED**)

Quantities in bold are unknown.

A few important points:

* *phosp* and *pdeath* are (by definition) expected to be different across risk groups: those in higher risk groups should have higher *phosp* and *pdeath.*
* *TEH*, and *TED* may also differ across risk groups. For example, treatment may be less effective in high-risk groups than in low-risk groups.

Some things we can do about this:

* At baseline, we can assume that the probability of hospitalization from COVID in the absence of treatment (*phosp*) is proportional to the probability of hospitalization from any other cause within each risk group. Same for *pdeath*.
* Furthermore, we can vary *phosp* and *pdeath* to “extreme” values to see how different they’d have to be from our baseline assumption to yield no effect.