Online Appendix to Accompany:

Risk-driven responses to COVID-19 eliminate the tradeoff between lives and livelihoods

Contents

S1 – Estimation method

The estimation equation for our model (equation 14 in the main paper) is replicated below:

$$E\left(r_{IM}(t)\right) =$$

$$\beta_0\left(1-\frac{\gamma_D}{f}\sum_{s=0}^{s=t} d_{NM}(s)\right)e^{-\left(\alpha_0+(\alpha_f-\alpha_0)\frac{1}{1+e^{\frac{-(t-t_0)}{\theta}}}\right)\left(\int_{s\geq 0} d_{NM}(t-s)\frac{2}{\lambda}s^2 e^{\frac{2s}{\lambda}}ds\right)}\sum_{k=1}^{k=\tau} r_{IM}(t-k)$$

This equation predicts the expected number of new infections for day t as a function of past infections (to calculate stock of infectious individuals) and past death rates (to calculate the response function). We assume the observed infections follow a negative binomial distribution with the given mean from this equation and a scale parameter, ϵ, that is estimated to replicate observed error distributions. The negative binomial distribution provides the flexibility to account for heteroscedasticity, over-dispersion, and fat tails, allowing a robust estimation despite substantial randomness in the data-generating process.

The model includes the following unknown parameters: $\boldsymbol{\omega} = [\beta_0, \alpha_0, \alpha_f, t_0, \theta, \lambda_u, \lambda_d, \gamma_D, \epsilon]$ – 4 $(\alpha_0, \alpha_f, t_0, \theta)$ quantify responsiveness and how it changes over time, 2 (λ_u, λ_d) specify the risk perception delays, β_0 estimates the initial rate of infectious contacts per day per index case, and γ_D estimates the potential under-valuation of Infection Fatality Rates (*f* values) for each country . Besides the f values (see IFR calculation below for details) the model includes two other given parameters, the duration of disease (10 days) and the order of the perception delay (2).

More compactly, the model yields a (log)likelihood for observing the daily reported cases ($r_{IM}(t)$), given a vector of unknown model parameters $\boldsymbol{\omega}$ and the reported daily cases and death rate for each country prior to the current date ($d_{NM}(t-)$) and $r_{IM}(t-)$): $LL_{NegBin}(r_{IM}(t)|\boldsymbol{\omega}, r_{IM}(t-), d_{NM}(t-))$

The estimation process seeks to identify the values for $\boldsymbol{\omega}$ that maximise this likelihood or are likely to be observed given that peak.

We estimate the model separately for each country. Separating countries significantly speeds up estimation and makes it feasible to conduct the full analysis within days on a 48-core server. For each country, we estimate the parameter vector $\boldsymbol{\omega}$ using the Powell direction search method implemented in Vensim™ DSS simulation software, restarting the optimization at 20 random points in the feasible parameter space. From the resulting optimum, we use MCMC to explore the payoff landscape to identify the high-likelihood region of parameter space. The MCMC algorithm used is designed for exploring high-dimensional parameter spaces; for more details see (Vrugt et al. 2009). We draw a total of 500000 samples for each country, of which the first 300000 are discarded (the burn-in period); by the end of the burn-in, the chains are well-mixed and stable (Gelman-Rubin PSRF statistic < 1.1). We use the remaining 200000 samples to derive credible intervals for parameter and outcome estimates.

S2 – Data processing

Data on daily confirmed cases and deaths come from the OurWorldInData (OWID) global COVID-19 database (Roser et al. 2020), which draws on the Johns Hopkins University CSSE COVID

dashboard (Dong et al. 2020). The CSSE dashboard in turn aggregates its data primarily from official sources such as the US Centres for Disease Control and Prevention (CDC), the European CDC, the World Health Organization, and national health ministries, updating at least daily.

We use OWID's 7-day rolling averages for new cases ('new_cases_smoothed') and deaths per million population ('new_deaths_smoothed_per_million'). COVID-19 case and death reporting data show strong weekly cycles in many countries, as well as occasional anomalous spikes due to e.g. irregularities in test reporting or redefinitions by government statistical agencies; using the rolling average data smooths out these cycles, which we are not attempting to model here, to better reflect underlying trends.

Our analysis includes all countries in the dataset with at least 10000 cumulative cases reported, and at least 20 days of data. We exclude countries with fewer than 10000 cumulative cases to avoid skewing the results with outliers. The minimum datapoint requirement helps ensure robust estimation. In total, 118 countries meet these criteria as of 02 December 2020.

For countries included, we utilise data starting from the date when they exceed 100 cumulative cases reported. Excluding early data entails a tradeoff. Excluding it makes estimating the true basic reproduction number (R_0) more difficult – as discussed in the main text, after forceful outbreaks in the first countries, most others adopted various precautions that brought down R_0 below its pre-pandemic level. Furthermore, excluding the early data may cut out the initial dynamics of infection. As a result, our estimated values for initial reproduction number are likely underestimates of basic reproduction number, and thus the g estimates may tend to be larger than the true changes in the contact rates compared to pre-pandemic levels. On the other hand, many of the early cases reported in most countries were due to travellers, and often identified and isolated early on. The data during this earliest 'importation' stage therefore do not accurately reflect community transmission dynamics we are modelling. Rapid changes in the testing coverage also impact our ability to use assume ascertainment rates are stable in the τ time horizon as needed in our derivations (see equation 12 in the main text). We selected the 100 case cut-off to balance reasonably estimating R_0 with correctly reflecting transmission dynamics rather than travel networks, which are out of scope for this model.

For mobility data we use Google's COVID-19 Community Mobility Reports (https://www.google.com/covid19/mobility). We access this data as compiled by OWID (https://ourworldindata.org/covid-mobility-trends) which provides consistent mapping for country names to other data we use.

Data are downloaded and processed with Python 3 code, using Pandas and NumPy packages. For the full data processing code, see https://github.com/tseyanglim/CovidRiskResponse.

IFR calculation

Most countries' reported case counts substantially under-estimate the true magnitude of the epidemic (Rahmandad et al. 2020). To estimate the remaining susceptible fraction (S_j) for each country over time, we therefore rely on reported deaths, which while still variable are more reliable, multiplying cumulative reported deaths by an estimated country-specific under-reporting ratio (γ_D) and using country-specific infection fatality rates (IFR) to calculate cumulative infections.

Age strongly influences IFR, with older patients far more likely to die of COVID-19 (Verity et al. 2020). We therefore calculate country-specific IFRs based on each country's age structure.

We use data from the World Bank's World Development Indicators (World-Bank 2014) on the age distribution of each country's population in 10-year age strata to calculate an age-weighted average of the IFRs for COVID patients by 10-year age group estimated in (Verity et al. 2020). The resulting demography-adjusted country-specific IFRs range from 0.14% (Uganda) to 1.51% (Japan), with a mean of 0.54% and median of 0.44% (Lebanon). For the handful of countries for which up-to-date demographic data are unavailable, we use a baseline IFR of 0.50%.

We incorporate an estimated multiplier for actual to calculated deaths, γ_D, to account for potential undercounts of death and reductions in IFR compared to early values estimated from the methods we used. In estimation we restrict this multiplier to be between 1 and 4.

S3 – Full results

Figure S1 shows fits to data for simulated infection rates for all 118 countries. Blue lines show model-generated daily infection rates, while red lines show 7-day rolling average infection rates from OWID. The correspondence between model and data is very close for most countries, with a few outliers bringing down the quality of fit a bit; yet over the full sample of 118 countries, R^2 for infections against data is 0.936, while the mean absolute errors normalized by mean (MAEN) are 13.2%. The quality of fit should not come as a total surprise: the model uses infection rates from the past 10 days to predict current-day infections, and thus to the extent that infections are auto-correlated, the estimation process can use this anchor to offer close approximations for the number of new cases. However, the behavioural response function does add significant value in terms of quality of fit, which we demonstrate in the sensitivity analysis section by comparing results against estimates that do not account for behaviour responses.

Table S1 summarises estimated parameter values across the 115 countries which met the quasi-equilibrium condition ($S_f > 1/R_0$). 3 of the 118 total countries estimated (ARG: Argentina, JOR: Jordan, OMN: Oman) no longer meet this condition as of 02 December 2020, and were excluded from further analyses. For the full table of country-by-country parameter estimates, see https://github.com/tseyanglim/CovidRiskResponse.

Figure S2 shows 90% credible intervals estimated for each country for the two main outcome measures, quasi-equilibrium normalized contact rate (g^{eq}) and quasi-equilibrium daily death rate per million (d_{NM}^{eq}).

Figure S3 shows reported daily death rates per million against change in visits to workplaces and retail & recreation venues respectively, relative to pre-pandemic levels, averaged over 180 days from 05 June 2020-02 December 2020. (The figure showing the combined index is in the main paper.) The correlation between deaths and relative daily visits is non-positive in all cases: Pearson's R^2 for averaged index = -0.371 (p = 0.0002); workplaces = -0.516 (p = 1.01E-07); retail & recreation venues = -0.249 (p = 0.016).

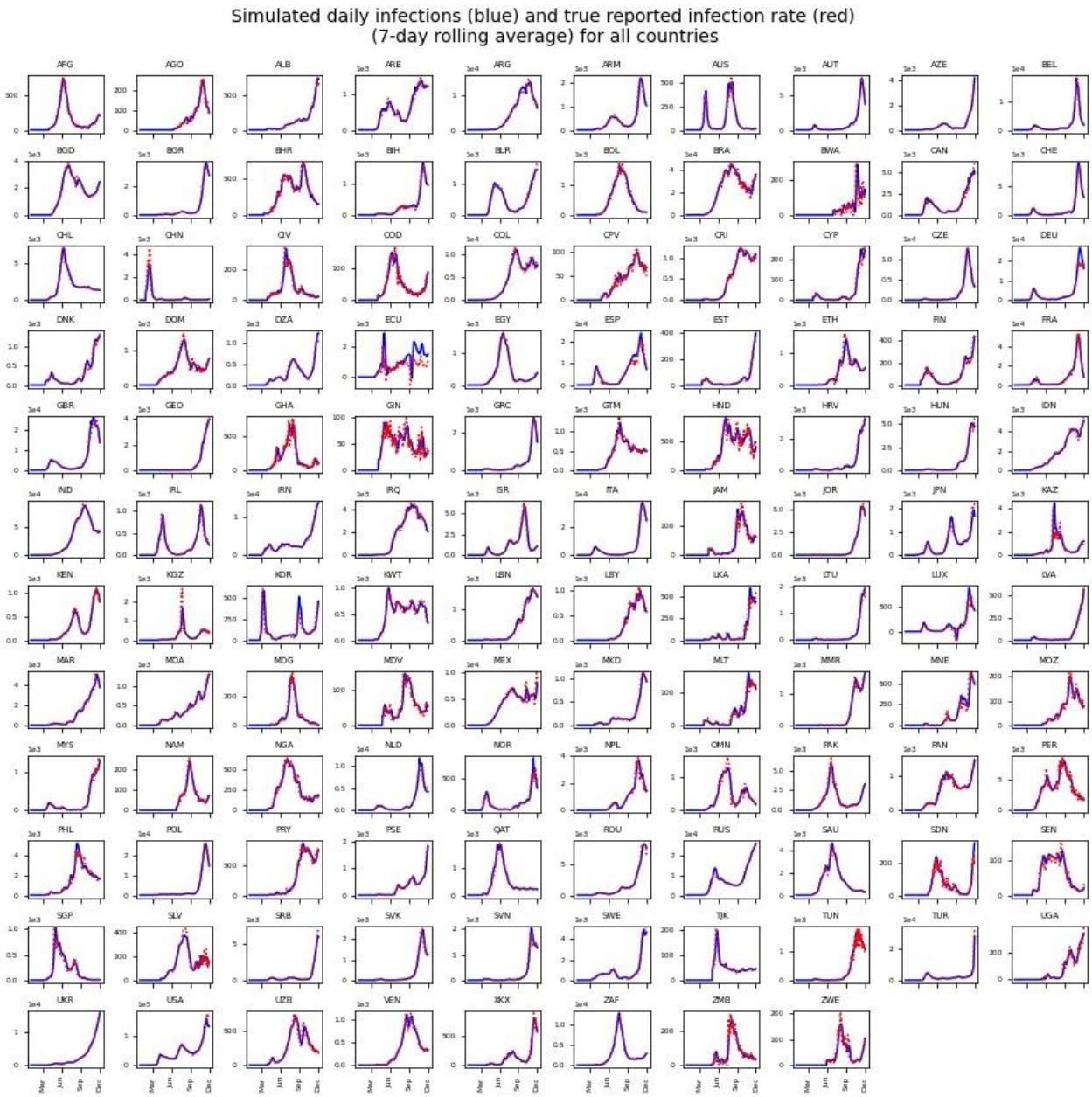

Figure S1 - Comparison of simulated infection rates with data across all 118 countries

Table S1 - Summary statistics of estimated parameter values

Parameter	Symbol	Mean	StDev	Median	Med. IQR
Reference effective contact rate	$\beta 0$	0.17	0.034	0.16	0.008
Initial responsiveness	$\alpha 0$	3.87	4.01	1.91	0.97
Final responsiveness	αf	1.46	2.79	0.19	0.064
Responsiveness inflection point	t0	197	84	211	13
Responsiveness scaling factor	θ	16.1	22.0	5.1	5.4
Time to upgrade risk	λU	12.2	9.8	8.9	3.9
Time to downgrade risk	λD	58	38	61	11
Death underreporting multiplier	γD	2.52	1.29	2.35	1.66
Likelihood scaling factor	ϵ	0.058	0.150	0.022	0.004

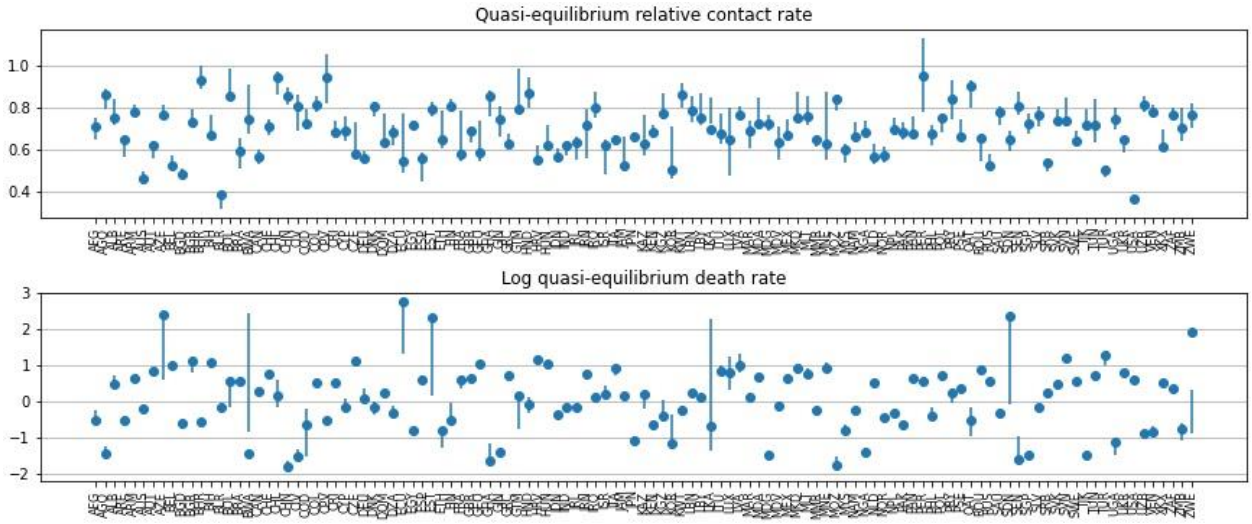

Figure S2 - 90% credible intervals for estimates of normalized contact rate and log10 daily deaths per million in quasi-equilibrium.

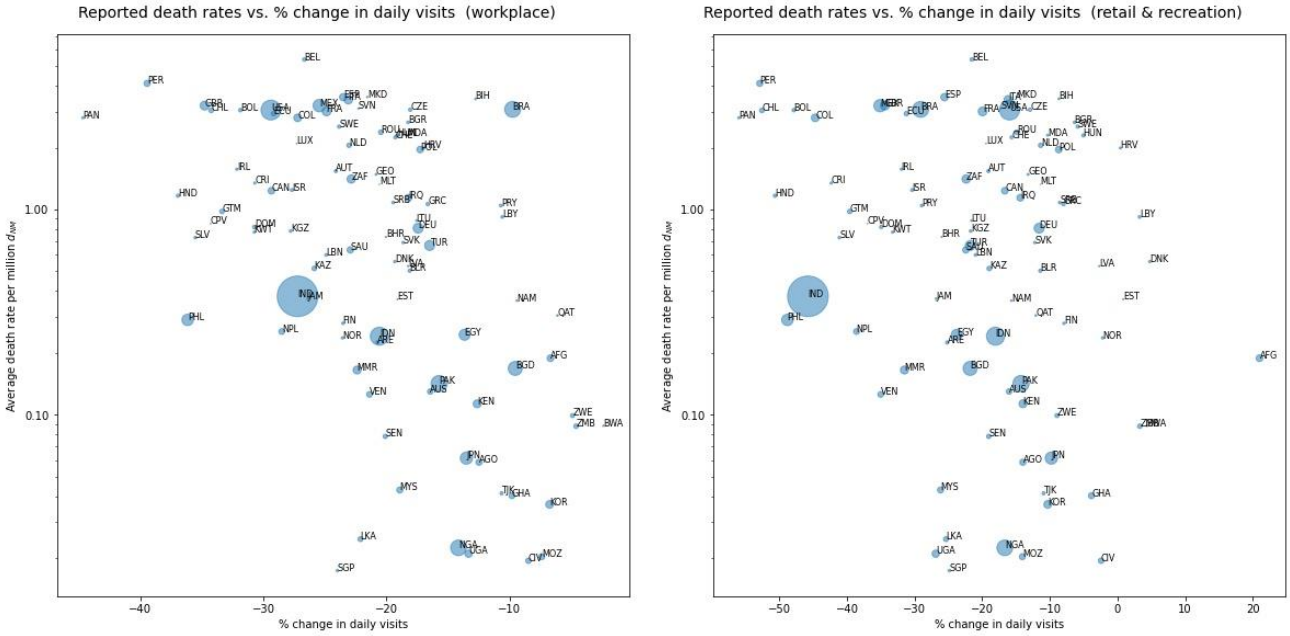

Figure S3 – Reported daily death rates per million against change in daily visits to workplaces (left) and retail & recreation venues (right) relative to pre-pandemic levels, averaged over the last 180 days from 05 June 2020-02 December 2020.

S4 – Sensitivity results

Disease Duration

We specify the average disease duration (τ) at 10 days, constant across all countries. This duration is consistent with prior findigns (He et al. 2020, Wolfel et al. 2020). To test for sensitivity to this parameter, we re-ran model estimation and analysis with τ = 8 and 14 days.

Figure S4 and Figure S5 show the main result for τ = 8 and 14 days respectively. The primary insight has not changed – expected deaths and normalized contact rates in quasi-equilibrium conditions have no positive correlation (for τ = 8 and 14 days respectively, Pearson's r = -0.044, p = 0.647 and r = 0.099, p = 0.303; for $\log(d_{NM}^{eq})$, r = -0.130, p = 0.177 and r = -0.238, p = 0.012), with if anything a slight negative correlation as per the main result.

The model is still able to fit the data reasonably well with changes in disease duration. Table S2 and Table S3 summarise estimated parameter values with τ = 8 and 14 days respectively. On average, reducing τ to 8 days results in a 10.0% absolute change in estimated parameter values, while increasing it to 14 days results in a 7.4% absolute change. The fit between simulated infections and data deteriorates slightly at τ = 14 days (R^2 = 0.930, MAEN = 14.7%) compared to baseline (R^2 = 0.936, MAEN = 13.2%). Fit improves slightly at τ = 8 days (R^2 = 0.950, MAEN = 11.5%). The primary driver of infection rates is the number of currently infected people, which is calculated exogenously from the data based on the specified disease duration. As such, some inverse relationship between quality of fit and disease duration is to be expected, as shorter durations allow autocorrelation in the [smoothed] infection data to exert a stronger influence on the accuracy of model predictions.

These results indicate that both overall model performance, and more importantly, the main results of this analysis, are robust to alternative specifications of average disease duration within a broadly reasonable range.

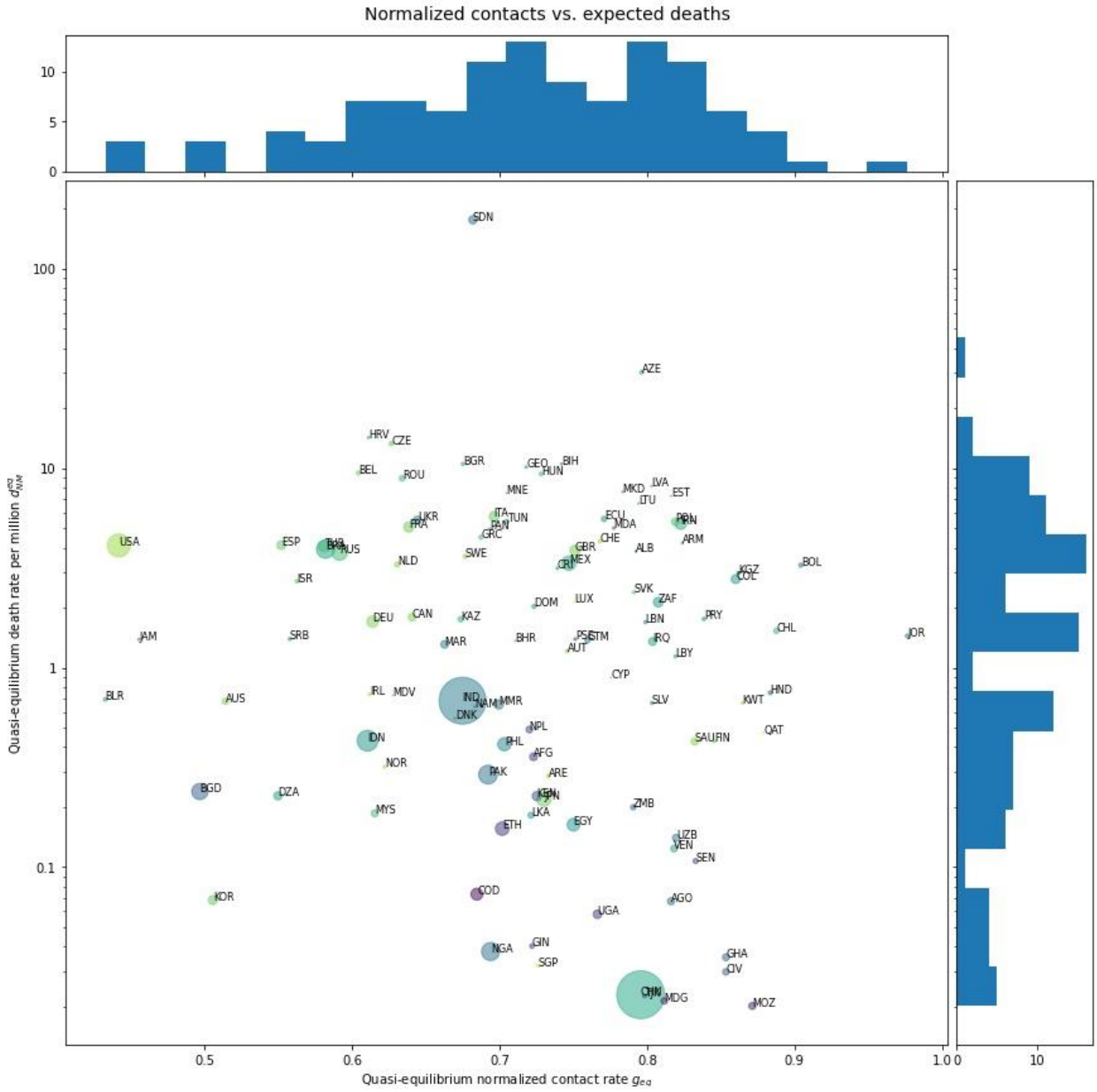

Figure S4 - Normalized contacts vs. expected deaths for $\tau = 8$ days

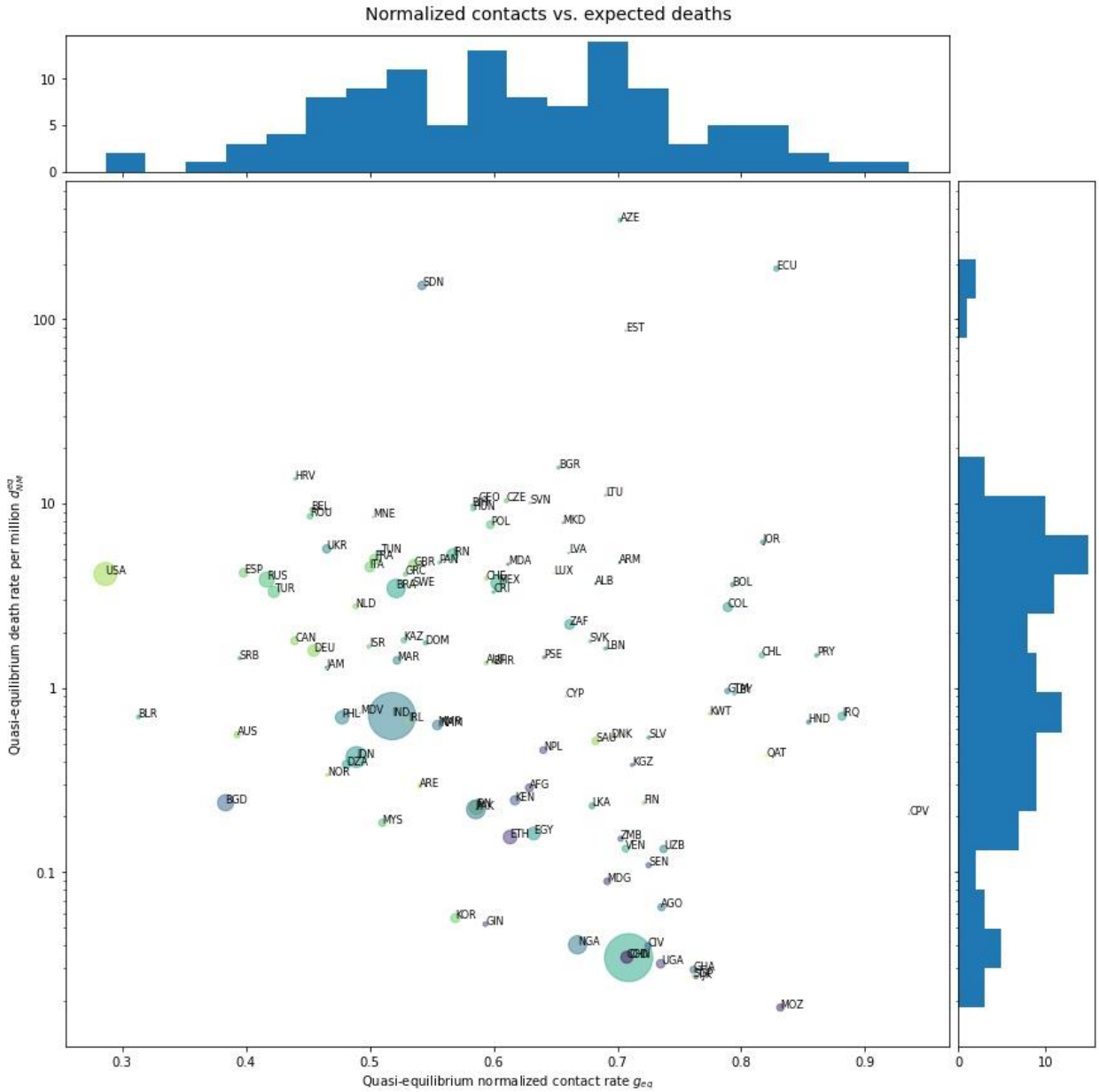

Figure S5 - Normalized contacts vs. expected deaths for $\tau = 14$ days

Table S2 - Summary of parameter estimates for τ = 8 days, with change in mean & median estimates

Parameter	Symbol	Mean	Change	Median	Change
Reference effective contact rate	$\beta 0$	0.20	0.187	0.19	0.195
Initial responsiveness	$\alpha 0$	4.30	0.111	2.12	0.109
Final responsiveness	αf	1.30	-0.114	0.21	0.098
Responsiveness inflection point	t0	190	-0.031	197	-0.068
Responsiveness scaling factor	θ	14.1	-0.127	5.0	-0.012
Time to upgrade risk	λU	11.6	-0.052	7.4	-0.175
Time to downgrade risk	λD	60	0.036	63	0.030
Death underreporting multiplier	γD	2.42	-0.039	2.21	-0.059
Likelihood scaling factor	ϵ	0.046	-0.202	0.017	-0.205

Table S3 - Summary of parameter estimates for τ = 14 days, with change in mean & median estimates

Parameter	Symbol	Mean	Change	Median	Change
Reference effective contact rate	$\beta 0$	0.14	-0.16	0.13	-0.174
Initial responsiveness	$\alpha 0$	3.95	0.02	1.70	-0.109
Final responsiveness	αf	1.65	0.13	0.35	0.848
Responsiveness inflection point	t0	201	0.02	214	0.016
Responsiveness scaling factor	θ	13.3	-0.18	5.0	-0.013
Time to upgrade risk	λU	12.7	0.04	10.3	0.160
Time to downgrade risk	λD	59	0.02	61	0.007
Death underreporting multiplier	γD	2.66	0.06	2.85	0.214
Likelihood scaling factor	ϵ	0.060	0.04	0.030	0.386

Estimation without behavioural response

We estimate the model with the endogenous behavioural response deactivated, i.e. $\alpha = 0$. In the absence of behavioural response, the fit of simulated infections to data deteriorates by 38% (R^2 = 0.914, MAEN = 18.2%), as expected, indicating that the behavioural response mechanism does improve the quality of fit. As the primary driver of infection rates is the number of currently infected people, which is calculated exogenously from the data, overall model fit remains notably good.

S5 – Model equations listing

1) AdjIFR[Rgn] = GET VDF CONSTANTS('InputConstants.vdf', 'AdjIFR[Rgn]', 1)
2) alp[Rgn] = 0.1 This parameter is 1 over the number of failures in negative binomial before experiment is stopped. A value between 0 and 1 (excluding zero) is legitimate calibraiton parameters here.
3) alpha[Rgn] = alpha 0[Rgn] + 1 / (1 + exp (timesens[Rgn])) * (alpha f[Rgn] - alpha 0[Rgn])
4) alpha 0[Rgn] = 1
5) alpha f[Rgn] = 2
6) BaseIFR = 0.005
7) beta[Rgn] = 0.1
8) CumulativeDpm[Rgn] = INTEG(DeathsOverTime[Rgn] , 0)
9) DataFlowOverTime[Rgn] = if then else (new cases[Rgn] = :NA:, :NA:, new cases[Rgn])
10) DataIncluded[Rgn] = 1
11) DataStartTimeCases[Rgn] = INITIAL(GET DATA FIRST TIME (new cases[Rgn]))
12) DataStartTimeDeaths[Rgn] = INITIAL(GET DATA FIRST TIME (new dpm[Rgn]))
13) DeathReportingRatio[Rgn] = 500
14) DeathsOverTime[Rgn] = if then else (Time < DataStartTimeDeaths[Rgn] , 0, new dpm interpolated[Rgn])
15) DeathsOverTimeRaw[Rgn] = if then else (new dpm[Rgn] = :NA:, :NA:, new dpm[Rgn])
16) Di[Rgn] = DataFlowOverTime[Rgn]
17) DiseaseDuration = 10
18) dn[Rgn] = SMOOTH N (DeathsOverTime[Rgn] , if then else (dn[Rgn] < DeathsOverTime[Rgn] , PMean[Rgn] , PMeanRelax[Rgn]) ,0, PMeanOrder)
19) eps = 0.01
20) eqDeath[Rgn] = ZIDZ (ln (beta[Rgn] * DiseaseDuration * SFrac[Rgn]) , alpha[Rgn])
21) FINAL TIME = 334 The final time for the simulation.
22) g death[Rgn] = exp (- alpha[Rgn] * dn[Rgn])
23) IFR[Rgn] = INITIAL(if then else (AdjIFR[Rgn] = -1, BaseIFR , AdjIFR[Rgn])) Note: -1 is placeholder value for missing data in InputConstants.vdf
24) inf exp[Rgn] = beta[Rgn] * roll[Rgn] * g death[Rgn] * SFrac[Rgn]
25) InfShift[Shft] := - Shft
26) INITIAL TIME = 0 initial time for the simulation.
27) Mu[Rgn] = Max (eps , inf exp[Rgn])
28) NBL1[Rgn] = if then else (DataFlowOverTime[Rgn] = 0, - ln (1 + alp[Rgn] * Mu[Rgn]) / alp[Rgn] , 0) This is the part of negative binomial distribution calcualted when outcomes are zero.
29) NBL2[Rgn] = if then else (DataFlowOverTime[Rgn] > 0, GAMMA LN (Di[Rgn] + 1 / alp[Rgn]) - GAMMA LN (1 / alp[Rgn]) - GAMMA LN (Di[Rgn] + 1) - (Di[Rgn] + 1 / alp[Rgn]) * ln (1 + alp[Rgn] * Mu[Rgn]) + Di[Rgn] * (ln (alp[Rgn]) + ln (Mu[Rgn])) , 0) This is the second piece in the loglikelihood for negative binomial which only applies to non-zero data points.
30) NBL3[Rgn] = if then else (Di[Rgn] > 0, - GAMMA LN (Di[Rgn] + 1) - (Di[Rgn] + 1 / alp[Rgn]) * ln (1 + alp[Rgn] * Mu[Rgn]) + Di[Rgn] * (ln (alp[Rgn]) + ln (Mu[Rgn])) , 0)
31) NBLLFlow[Rgn] = (NBL1[Rgn] + NBL2[Rgn]) * DataIncluded[Rgn]
32) new cases[Rgn] :RAW:
33) new dpm[Rgn] :RAW:
34) new dpm interpolated[Rgn] := new dpm[Rgn]
35) PMean[Rgn] = 5
36) PMeanOrder = 2
37) PMeanRelax[Rgn] = 20
38) Pssn : (p1-p100)
39) Re[Rgn] = beta[Rgn] * g death[Rgn] * DiseaseDuration * SFrac[Rgn]
40) Rgn : AFG, AGO, ALB, ARE, ARG, ARM, AUS, AUT, AZE, BEL, BGD, BGR, BHR, BIH, BLR, BOL, BRA, BWA, CAN, CHE, CHL, CHN, CIV, COD, COL, CPV, CRI, CYP, CZE, DEU, DNK, DOM, DZA, ECU, EGY, ESP, EST, ETH, FIN, FRA, GBR, GEO, GHA, GIN, GRC, GTM, HND, HRV, HUN, IDN, IND, IRL, IRN, IRQ, ISR, ITA, JAM, JOR, JPN, KAZ, KEN, KGZ, KOR, KWT, LBN, LBY, LKA, LTU, LUX, LVA,

MAR, MDA, MDG, MDV, MEX, MKD, MLT, MMR, MNE, MOZ, MYS, NAM, NGA, NLD, NOR, NPL, OMN, PAK, PAN, PER, PHL, POL, PRY, PSE, QAT, ROU, RUS, SAU, SDN, SEN, SGP, SLV, SRB, SVK, SVN, SWE, TJK, TUN, TUR, UGA, UKR, USA, UZB, VEN, XKX, ZAF, ZMB, ZWE

41) roll[Rgn] = if then else (Time < DataStartTimeCases[Rgn] , 0, sum (SelectRoll[Shft!] * ShiftedInfection[Rgn,Shft!]))
42) SAVEPER = TIME STEP [0,?] The frequency with which output is stored.
43) SelectRoll[Shft] = if then else (Shft > DiseaseDuration , 0, 1)
44) Series : Infection
45) SFrac[Rgn] = Max (1e-06, 1 - (CumulativeDpm[Rgn] * DeathReportingRatio[Rgn] / IFR[Rgn]) / 1e+06)
46) Shft : (S1-S20)
47) ShiftedInfection[Rgn,Shft] := TIME SHIFT (new cases[Rgn] , InfShift[Shft])
48) t0[Rgn] = 20
49) theta[Rgn] = 1
50) TIME STEP = 1 [0,?] The time step for the simulation.
51) timesens[Rgn] = MIN (50, - (Time - t0[Rgn]) / theta[Rgn])

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