# The effectiveness of population-wide, rapid antigen test based screening in reducing SARS-CoV-2 infection prevalence in Slovakia

## Authors

Martin Pavelka [1,2,3], Kevin Van-Zandvoort [4,5], Sam Abbott [4,5], Katharine Sherratt [4,5], Marek Majdan [7], CMMID COVID-19 working group [5], Inštitút Zdravotných Analýz [6], Pavol Jarčuška [7], Marek Krajčí [1+], Stefan Flasche [4,5]*, Sebastian Funk [4,5]*

[1] Slovak Ministry of Health, Bratislava, Slovakia

[2] Inštitút Zdravotných Analýz, Bratislava, Slovakia

[3] Department of Public Health and Policy, London School of Hygiene & Tropical Medicine, London, UK

[4] Department for Infectious Disease Epidemiology, London School of Hygiene & Tropical Medicine, London, UK

[5] Centre for Mathematical Modelling of Infectious Diseases, London School of Hygiene & Tropical Medicine, London, UK

[6] Inštitút Zdravotných Analýz (Institute of Health Analyses), Bratislava, Slovakia

[7] Faculty of Medicine, Pavol Jozef Šafárik University, Košice, Slovakia

[7] Institute for Global Health and Epidemiology, Faculty of Health Sciences and Social Work, Trnava University, Trnava, Slovakia

[+] on behalf of all Slovak medical staff who have helped in the mass testing campaigns
* authors contributed equally, order decided by coin toss
Address correspondence to: Martin Pavelka <martin.pavelka@health.gov.sk>

## Abstract

Non-pharmaceutical interventions have been extensively used worldwide to limit the transmission of SARS-CoV-2, but they also place an enormous social and economic burden on populations . We report the results of recent mass testing for SARS-CoV-2 in Slovakia where rapid antigen tests were used to screen the whole population and to isolate infectious cases together with their household members. Prevalence of detected infections decreased by 58% (95% CI: 57-58%) within one week in the 45 counties that were subject to two rounds of mass testing. Adjusting for geographical clustering and differences in attendance rates and the epidemiological situation at the time of the first round, this changed to 61% (95% CI: 50-70%). Adjusting for an estimated growth rate in infections of 4.4% (1.1-6.9%) per day in the week preceding the mass testing campaign and the corresponding expected growth in infection prevalence, the estimated decrease in prevalence compared to a scenario of unmitigated growth was 70% (67-73%). Using a microsimulation model we find that this decrease can not be explained solely by infection control measures that were introduced in the weeks preceding the intervention, but requires the additional impact of isolation as well as quarantine of household members of those testing positive during the mass testing campaign.

**NOTE: This preprint reports new research that has not been certified by peer review and should not be used to guide clinical practice.**

## Introduction

Non-pharmaceutical interventions have been extensively used worldwide to limit the transmission of SARS-CoV-2 (*1–4*). These have included travel restrictions, mandating face masks, closure of schools and non-essential businesses, and nationwide stay-at-home orders. While all the measures were aimed at mitigating ill-health due to COVID-19 (*3*, *5*) they also place an unprecedented economic and social burden on people (*6–9*), the majority uninfected. Testing of reported symptomatic cases and tracing their contacts aims to provide a more targeted measure but in many settings has proven insufficient for containing transmission (*10*, *11*).

Mass testing campaigns are an alternative way to identify infectious individuals and allow targeting of interventions without much added burden to those uninfectious (*12*). However, they have been limited until recently by the dependence on Polymerase Chain Reaction (PCR) for the diagnosis of a SARS-CoV-2 infection. While laboratory capacities have been upscaled in record time, PCR testing remains expensive and can seldom achieve a turnaround time of less than one day (*13*, *14*). In comparison, recently developed rapid antigen tests are cheap and can be quickly produced in large quantities offering results on site in 15-30 mins without the need for a laboratory. They are less sensitive in detecting infections with low viral load but have been found to detect the vast majority of infectious infections, and hence may make mass testing a viable part of the portfolio of non-pharmaceutical interventions (*15–17*).

In October 2020, Slovakia became the first country in the world to use rapid antigen tests in a campaign targeting the whole population in order to identify infections at scale, rapidly reduce transmission and allow quicker easing of lockdown measures(*18*). A pilot took place between 23 and 25 October in the four most affected counties, followed by a round of national mass testing on 31 October and 1 November (henceforth: round 1). High prevalence counties were again targeted with a subsequent round on 7 and 8 November (round 2).

We evaluated the impact of mass testing in Slovakia, in combination with other measures put in place around the time, by comparing infection prevalence in each round of testing.

## Results

In total, 5,276,832 rapid antigen tests were used in the mass testing campaigns, with 65% of the respective populations tested in the pilot, 66% in mass testing round 1 and 62% round 2. This corresponded to 87%, 83% and 84% of the age-eligible population in each round, respectively, and does not include another 534,300 tests that were conducted through additional testing sites for medical, military and governmental personnel and not included in geographical county data.

A total of 50,466 tests indicated the presence of a currently infectious SARS-CoV-2 infection. The proportion of positive tests was 3.91% (range across counties: 3.12 to 4.84%) in the pilot, 1.01% (range: 0.13-3.22%) in round 1 and 0.62% (range: 0.28-1.65%) in

round 2 (Figure 2C and D). We estimate that with 95% certainty the specificity of the SD Biosensor Standard Q antigen test was exceeding 99.85%.

In the four counties where the pilot was conducted, prevalence decreased by 56% (95% Confidence Interval, CI: 54-58%) between the pilot and round 1 of the mass testing campaign and a further 60% (95% CI: 56-63%) between rounds 1 and 2, totalling a decrease of 82% (95% CI: 81-83%) over two weeks. There was little heterogeneity between counties (Figure 2B).

Among the 45 counties that were included in round 2 of the mass testing campaign, infection prevalence decreased by 58% (95% CI: 57-58%) in the crude analysis and by 61% (95% CI: 50-70%) if adjusted for differences in region, attendance rates, reproduction number and round 1 prevalence. The estimated reduction varied by county from 29% in county Považská Bystrica to 79% in county Medzilaborce but with little regional differences (Figure 2A). Neither region, attendance rates, prevalence in round 1 or the estimated growth rate prior to mass testing were found to be significantly associated with county specific reductions.

At the time of round 1 of the mass testing campaign incidence of confirmed cases was rising in non-pilot counties with an estimated infection growth rate of 4.4% (1.1%-6.9%) per day. When adjusting for this growth trend, we estimated a self-adjusted prevalence ratio (saPR) of 0.30 (0.27-0.33) . In the pilot counties, reported infection incidence showed signs of levelling in the week before the mass testing campaign with an estimated infection growth rate of 1.3% (-7.4-7.8%), yielding a respective saPR of 0.31 (0.26-0.33).

In a microsimulation model, only the scenario that assumed a substantial impact of both the lockdown and the mass testing was able to generate reductions in test positivity rates between testing rounds that were similar to those observed (Figure 3). The requirement for quarantine for the whole household following a positive test was essential for the effect of mass testing; predicted prevalence ratio between the first two testing rounds of 0.41 (0.38-0.45) with and 0.90 (0.84-0.96) without household quarantine.


## Discussion

The reduction in prevalence achieved in Slovakia through a combination of restrictions on movement and the first ever large scale rapid antigen mass testing is striking, with reductions of over 50% achieved within a week between two rounds of testing. While we could not with certainty disentangle the effects, simulations from a mathematical model suggested that both the restrictions and mass testing likely contributed substantially to the observed impact and that quarantining of household contacts was a crucial contribution to the effectiveness of mass testing.

Potentially large numbers of false positive tests have been a point of criticism for mass testing campaigns. While multiple studies have found high specificity of the Biosensor test kit they are not powered to exclude specificity levels that on population level would yield an overwhelming amount of false positives (15, 22). We show that indeed specificity is very likely exceeding 99.85% and therefore not of major concern in this study.

While we observed a dramatic reduction in test positivity between mass testing campaigns, the observed change in daily case incidence reported through standard

surveillance was not the rapid collapse in test-positive cases that would correspond to the drastic reductions in prevalence. This may be due to a variety of reasons. Foremost, national mass testing campaigns are likely to have a major disruptive effect on passive syndromic surveillance. In addition, starting mid-September the incidence surveillance has been operating at capacity with long waiting lists for testing and stricter eligibility criteria, which in the post mass testing period reduced substantially, and hence may have artificially reduced the observable change in such data. In contrast, data on hospital bed occupancy shows sudden flattening from mid-November suggesting a sharp decrease in new admissions consistent with a sizable reduction in new infections at the time of the mass testing campaigns (Figure S6).

The most important limitation of this observational study is that we were unable to clearly distinguish the effect of the mass testing campaigns from that of the other non-pharmaceutical interventions introduced at a similar time, that have led to a reduction in contacts and mobility, albeit much less than during the Spring lockdown (Figure S4). We are unaware of any other context in which a COVID-19 intervention has resulted in a 60% decline in infection prevalence within one week (or 80% in two weeks), particularly while primary schools and workplaces were mostly open. This would suggest that indeed a large share of the impact can be attributed to the mass testing campaigns. Similarly, our analysis using mathematical modelling suggests that even with what would be considered as one of the most impactful lockdowns observed so far, it would be impossible to replicate such rapid drop in test positivity without a substantial contribution from the mass testing campaign.

The need to mobilise sufficient medical personnel to conduct the nasopharyngeal swabs could be a major obstacle to countries. Other rapid antigen tests kits are available that have achieved similarly high sensitivity in detecting likely infectious infections in lab conditions but are also licensed for use with nasal swabs (*32*, *33*). Nasal swabs can be self-administered and therefore reduce demand on trained personnel and transmission risk in the process of sample collection or even may enable testing at home. However, these benefits have to be carefully weighed against the potential loss of sensitivity if self administered (*34*).

In conclusion, the combination of nationwide restrictions and mass testing with quarantining of household contacts of test positives rapidly reduced the prevalence of infectious residents in Slovakia. While impossible to disentangle the precise contribution of control measures and mass testing, the latter is likely to have had a substantial effect in curbing the pandemic in Slovakia and may provide a key tool in the containment of SARS-CoV-2.

## Material and Methods

### Study population

Slovakia is a country with a population of 5.5 million, consisting of 79 counties grouped into 8 administrative regions. Slovak residents aged between 10 and 65 years and older adults in employment were eligible for mass testing (about 4 million people). Those

quarantining at the time or who had recovered from COVID-19 in the past three months were excluded.

The pilot was conducted in three counties in the Orava subregion (Námestovo, Tvrdošín, Dolný Kubín) and Bardejov county, which had the highest infection incidence at the time. The first round of mass testing was conducted nation-wide and the second round of mass testing was restricted to 45 counties, mostly in the northern part of Slovakia, with infection prevalence in the first mass testing round exceeding 7 per 1,000 tests.

## Interventions

Slovakia implemented a series of infection control measures throughout October, which included closing schools for pupils aged 14 or above on 15 Oct and for pupils aged 10 and above on 26 October. They remained closed throughout the period of the mass testing campaigns and thereafter. Indoor gastronomy and indoor leisure activities were also restricted. Residents were further asked to limit their movement for one week between 24 October and 1 November only to: going to work, taking children to school, shopping for essential items and going for recreational walks (Figures 1 and S4). Although these rules were legally enforceable, Slovakia relied mostly on people's civil responsibility to adhere to restrictions.

On the days of mass testing, participants attended testing centres run by healthcare professionals, armed forces and volunteers. Overall, Slovakia deployed around twenty thousand medical staff and forty thousand non-medical personnel. Testing procedures followed as recommended by the manufacturer, with nasopharyngeal samples obtained by trained medical personnel using flexible, aluminum-shaft, calcium alginate swabs (19).

Testing was not obligatory, but residents who did not attend the mass testing were instructed to stay home for ten days or until the next round of mass testing. A medical certificate was issued to every participant confirming their infection status. A test-negative certificate was required by employers to enter workplaces. Various venues and public institutions inspected peoples' certificates at random. Private PCR tests were also accepted if no older than the most recent mass testing campaign. Citizens whose test results were positive were asked to enter a 10-day long quarantine together with all members of the same household and their self-traced contacts in the preceding two days in an attempt to reduce secondary transmission.

## Data

No participant information was collected during either of the mass-testing campaigns. However, information on the number of tests used as well as the number of positive tests has been tracked and made openly available by the Slovak Government (18). The SD Biosensor Standard Q antigen test that was used exclusively has high specificity, with point estimates typically in excess of 99.5%. Sensitivity exceeded 70% in most validation studies, and exceeded 90% among samples with a cycle threshold below 25, a threshold commonly associated with effective transmission (15, 20–22).

To assess trends in the local epidemiology of SARS-CoV we used routine syndromic and PCR confirmed surveillance for the daily incidence of infections as reported by the Slovak Ministry of Health (23).

## Analyses

We calculated crude prevalence ratios (cPR) to estimate the change in test positivity between mass testing campaigns, including Wald-Normal confidence intervals. Binomial confidence intervals were calculated for prevalence estimates. Test positive rates provide a natural upper bound for false positive rates of a test. We thus estimated the minimum test specificity *ms* as the probability of observing a test positivity of at least 1-*ms* in at least one county, assuming the test positivity to be binomially distributed.

To explore heterogeneity between counties in the estimated reduction in test positivity in subsequent rounds of mass testing, we used a quasi-Poisson regression model. The number of positive tests in each county was modelled with a county specific intercept, an indicator variable for the round 2 of mass testing, and interactions of the latter with attendance rates in round 1, round 1 test positivity, the reproduction number leading up to round 1 and region as covariates as well as the log number of tests as an offset variable. The three continuous variable interaction terms were centered and standardised (see supplement).

We used the EpiNow2 model (24, 25) for the calculation of trends in local epidemiology prior to mass testing based on routinely reported infection incidence. EpiNow2 uses observed delay distributions in combination with a renewal equation model to probabilistically infer the infection date for each reported case as well as the population-wide time varying reproduction number (26–28) , allowing a smoothed extrapolation of infection incidence and prevalence and extrapolation beyond the observed study period under an assumption of no change.  We define the self-adjusted prevalence ratio (saPR) as the cPR divided by the prevalence ratio at the times of  round 2 vs round 1 as estimated through EpiNow2. The saPR is an estimate for the effect of the intervention that takes into account that infection prevalence would have changed in the time between observations (see supplement).

To explore scenarios for the relative effect of mass testing and lockdown we used a microsimulation model. We focused on three scenarios in which mass testing takes place, i) an epidemic growth rate of $R_e$=1.4 (as in early October) that is unchanged by lockdown measures, ii) a reduced growth rate of $R_e$=1 from 15th October (similar to many parts of Europe in the weeks following autumn lockdowns) and iii) the growth rate reduced to $R_e$=0.6  from 15th October (the smallest observed reproduction number nationally during the COVID-19 pandemic) but no effect of mass testing. A detailed model description is provided in the supplementary material, but in brief: Individuals are grouped in households according to Slovak census data (29),  and make contact with individuals outside their household at age-specific rates(30). To account for social distance measures, we assumed absence of at-school contacts for children 10 years and over, and that contacts at work and contacts not at the home, school, or workplace, were reduced by 25% and 75% from pre-epidemic levels, respectively. We simulated infections among 78,000 susceptible individuals, representative of the population size of a typical pilot county. When infection prevalence reached 3.2% (approximating a typical observed

prevalence during the testing pilot), up to 3 rounds of weekly mass testing were initiated and the week before that restrictions equivalent to those enacted in Slovakia were implemented. In the model, we assumed perfect test sensitivity for detection of currently infectious infections, specificity, and compliance with quarantine. Observed test attendance rates were used assuming that individuals in quarantine did not attend mass-testing.

## Open Access

Daily incidence of positive COVID-19 test reports and the results of the mass testing are available through governmental websites (*18*, *23*). All analyses were conducted in R (*31*) and can be found at www.github.com/sbfnk/covid19.slovakia.mass.testing (data analyses) and https://github.com/kevinvzandvoort/covid_svk (simulation model).

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## Conflicts of interest

All authors declare that they have no conflicts of interest

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# Tables and Figures

**Table 1:** Overview of county specific test numbers and reductions for the 79 counties in Slovakia. R: median estimate of the reproduction number on 22 October. %: proportion positive out of those attending mass testing.

| County | Region | Population | R | Round 1 | | | Round 2 | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | Positive | Attendance | % | Positive | Attendance | % |
| Bánovce nad Bebravou | Trenčiansky | 36282 | 1.4 | 457 | 23264 | 1.96 | 192 | 22248 | 0.86 |
| Banská Bystrica | Banskobystrický | 110828 | 1.2 | 687 | 64127 | 1.07 | 231 | 66544 | 0.35 |
| Banská Štiavnica | Banskobystrický | 16086 | 0.7 | 33 | 11725 | 0.28 | | | |
| Bardejov | Prešovský | 77771 | 0.7 | 740 | 44197 | 1.67 | 366 | 43983 | 0.83 |
| Bratislava I | Bratislavský | 44798 | 1.2 | 108 | 29047 | 0.37 | | | |
| Bratislava II | Bratislavský | 108139 | 1.2 | 345 | 80958 | 0.43 | | | |
| Bratislava III | Bratislavský | 61418 | 1.2 | 175 | 49788 | 0.35 | | | |
| Bratislava IV | Bratislavský | 93058 | 1.2 | 81 | 63857 | 0.13 | | | |
| Bratislava V | Bratislavský | 141259 | 1.2 | 268 | 68139 | 0.39 | | | |
| Brezno | Banskobystrický | 61450 | 1.4 | 450 | 37339 | 1.21 | 242 | 38515 | 0.63 |
| Bytča | Žilinský | 30917 | 1.6 | 328 | 21419 | 1.53 | 164 | 20931 | 0.78 |
| Čadca | Žilinský | 90080 | 1.0 | 1736 | 53907 | 3.22 | 506 | 52304 | 0.97 |
| Detva | Banskobystrický | 32051 | 1.3 | 211 | 19704 | 1.07 | 79 | 23255 | 0.34 |
| Dolný Kubín | Žilinský | 39456 | 1.0 | 345 | 24251 | 1.42 | 138 | 24170 | 0.57 |
| Dunajská Streda | Trnavský | 122358 | 1.3 | 840 | 87329 | 0.96 | 577 | 110083 | 0.52 |
| Galanta | Trnavský | 94076 | 1.3 | 349 | 71243 | 0.49 | | | |
| Gelnica | Košický | 31868 | 1.3 | 131 | 18331 | 0.71 | 72 | 19087 | 0.38 |
| Hlohovec | Trnavský | 45012 | 1.4 | 171 | 28892 | 0.59 | | | |
| Humenné | Prešovský | 61986 | 1.1 | 598 | 32962 | 1.81 | 197 | 32750 | 0.60 |
| Ilava | Trenčiansky | 59188 | 1.4 | 442 | 37604 | 1.18 | 291 | 35931 | 0.81 |
| Kežmarok | Prešovský | 75235 | 1.4 | 845 | 43959 | 1.92 | 390 | 43252 | 0.90 |
| Komárno | Nitriansky | 101712 | 1.5 | 343 | 61268 | 0.56 | | | |
| Košice - okolie | Košice | 129544 | 1.2 | 196 | 32849 | 0.60 | | | |
| Košice I | Košice | 67513 | 1.2 | 295 | 39314 | 0.75 | | | |
| Košice II | Košice | 82288 | 1.2 | 41 | 11109 | 0.37 | | | |
| Košice III | Košice | 28748 | 1.2 | 135 | 26992 | 0.50 | | | |
| Košice IV | Košice | 60126 | 1.2 | 487 | 80426 | 0.61 | | | |
| Krupina | Banskobystrický | 22182 | 1.4 | 66 | 13388 | 0.49 | | | |
| Kysucké Nové Mesto | Žilinský | 32914 | 1.6 | 384 | 20605 | 1.86 | 177 | 20491 | 0.86 |
| Levice | Nitriansky | 110824 | 1.4 | 375 | 70155 | 0.53 | | | |
| Levoča | Prešovský | 33702 | 1.0 | 373 | 18344 | 2.03 | 172 | 17747 | 0.97 |
| Liptovský Mikuláš | Žilinský | 72260 | 1.2 | 667 | 47172 | 1.41 | 267 | 46827 | 0.57 |
| Lučenec | Banskobystrický | 73466 | 1.0 | 213 | 40655 | 0.52 | | | |
| Malacky | Bratislavský | 74323 | 1.3 | 285 | 54657 | 0.52 | | | |
| Martin | Žilinský | 96338 | 1.5 | 771 | 56533 | 1.36 | 381 | 57513 | 0.66 |
| Medzilaborce | Prešovský | 11842 | 1.1 | 91 | 6980 | 1.30 | 17 | 6142 | 0.28 |
| Michalovce | Košický | 110705 | 1.0 | 512 | 58929 | 0.87 | 211 | 62790 | 0.34 |
| Myjava | Trenčiansky | 26356 | 0.9 | 249 | 17753 | 1.40 | 68 | 18599 | 0.37 |
| Námestovo | Žilinský | 62664 | 0.9 | 668 | 37029 | 1.80 | 207 | 37659 | 0.55 |
| Nitra | Nitriansky | 161560 | 1.3 | 674 | 99175 | 0.68 | | | |
| Nové Mesto nad Váhom | Trenčiansky | 62554 | 1.5 | 363 | 40829 | 0.89 | 198 | 46269 | 0.43 |
| Nové Zámky | Nitriansky | 139004 | 1.3 | 478 | 79234 | 0.60 | | | |
| Partizánske | Trenčiansky | 45596 | 1.5 | 494 | 26492 | 1.86 | 186 | 27585 | 0.67 |
| Pezinok | Bratislavský | 65145 | 1.3 | 240 | 45801 | 0.52 | | | |
| Piešťany | Trnavský | 62802 | 1.3 | 183 | 40122 | 0.46 | | | |
| Poltár | Banskobystrický | 21471 | 2.0 | 71 | 12455 | 0.57 | | | |
| Poprad | Prešovský | 104914 | 1.4 | 1059 | 59072 | 1.79 | 364 | 58098 | 0.63 |
| Považská Bystrica | Trenčiansky | 62438 | 1.4 | 505 | 37822 | 1.34 | 343 | 36092 | 0.95 |
| Prešov | Prešovský | 175610 | 1.0 | 724 | 84781 | 0.85 | 472 | 108271 | 0.44 |
| Prievidza | Trenčiansky | 133980 | 1.3 | 1497 | 76457 | 1.96 | 576 | 77170 | 0.75 |
| Púchov | Trenčiansky | 44310 | 1.3 | 782 | 29455 | 2.65 | 461 | 28017 | 1.65 |
| Revúca | Banskobystrický | 39636 | 1.7 | 58 | 21419 | 0.27 | | | |
| Rimavská Sobota | Banskobystrický | 84159 | 1.7 | 197 | 46872 | 0.42 | | | |
| Rožňava | Košický | 62208 | 1.2 | 100 | 34307 | 0.29 | | | |
| Ružomberok | Žilinský | 56702 | 1.6 | 682 | 34000 | 2.01 | 236 | 33056 | 0.71 |
| Sabinov | Prešovský | 60518 | 1.4 | 804 | 35366 | 2.27 | 295 | 34757 | 0.85 |
| Šaľa | Nitriansky | 51685 | 1.2 | 199 | 31993 | 0.62 | | | |
| Senec | Bratislavský | 89832 | 1.4 | 314 | 66052 | 0.48 | | | |
| Senica | Trnavský | 60446 | 1.2 | 384 | 40675 | 0.94 | 194 | 46000 | 0.42 |
| Skalica | Trnavský | 47104 | 1.2 | 368 | 29223 | 1.26 | 168 | 31200 | 0.54 |
| Snina | Prešovský | 36240 | 1.3 | 345 | 19122 | 1.80 | 111 | 19396 | 0.57 |
| Sobrance | Košický | 22819 | 0.9 | 135 | 12986 | 1.04 | 43 | 12966 | 0.33 |
| Spišská Nová Ves | Košický | 99765 | 1.3 | 739 | 54279 | 1.36 | 361 | 53712 | 0.67 |
| Stará Ľubovňa | Prešovský | 53954 | 1.2 | 805 | 28749 | 2.80 | 354 | 27234 | 1.30 |
| Stropkov | Prešovský | 20532 | 1.1 | 125 | 10494 | 1.19 | 63 | 10764 | 0.59 |
| Svidník | Prešovský | 32564 | 1.1 | 220 | 16631 | 1.32 | 85 | 16705 | 0.51 |
| Topoľčany | Nitriansky | 70132 | 1.4 | 748 | 44627 | 1.68 | 330 | 50253 | 0.66 |
| Trebišov | Košický | 105353 | 0.9 | 400 | 68503 | 0.58 | | | |
| Trenčín | Trenčiansky | 114523 | 1.2 | 832 | 73424 | 1.13 | 434 | 72546 | 0.60 |
| Trnava | Trnavský | 132454 | 1.2 | 557 | 92215 | 0.60 | | | |
| Turčianske Teplice | Žilinský | 15884 | 1.7 | 112 | 11287 | 0.99 | 54 | 12210 | 0.44 |
| Tvrdošín | Žilinský | 36180 | 1.3 | 369 | 18541 | 1.99 | 164 | 20502 | 0.80 |
| Veľký Krtíš | Banskobystrický | 43473 | 1.2 | 76 | 24652 | 0.31 | | | |
| Vranov nad Topľou | Prešovský | 80766 | 1.4 | 460 | 43552 | 1.06 | 281 | 45424 | 0.62 |
| Žarnovica | Banskobystrický | 26152 | 1.4 | 105 | 16272 | 0.65 | | | |
| Žiar nad Hronom | Banskobystrický | 46862 | 0.8 | 108 | 26260 | 0.41 | | | |
| Žilina | Žilinský | 158043 | 1.5 | 1392 | 111155 | 1.25 | 512 | 103898 | 0.49 |
| Zlaté Moravce | Nitriansky | 40572 | 0.9 | 156 | 26180 | 0.60 | | | |
| Zvolen | Banskobystrický | 68758 | 1.4 | 276 | 39422 | 0.70 | 136 | 47764 | 0.28 |

**Figure 1: Overview of interventions and pre mass testing epidemiology.** Top panel: description of timing and extent of national contact restriction in Slovakia (color intensity indicates intensity of the measures) and timing and extent of the mass testing campaigns. Dots and lines in respective colors show the start and duration of the contact restrictions and the blue dots show the days on which mass testing was conducted, though the highest turnout was usually on the first day. The additional box illustrates contact reducing measures for test positives and those who did chose not to get tested. Bottom panel: SARS-CoV-2 infection incidence as reported by the Slovak Ministry of Health and collected through passive symptom triggered PCR testing. Using the same color coding as in the top panel contact interventions are displayed by horizontal and mass testing campaigns by vertical lines. Data following the respective first mass testing campaign is omitted as mass testing is likely to have interfered with passive surveillance.
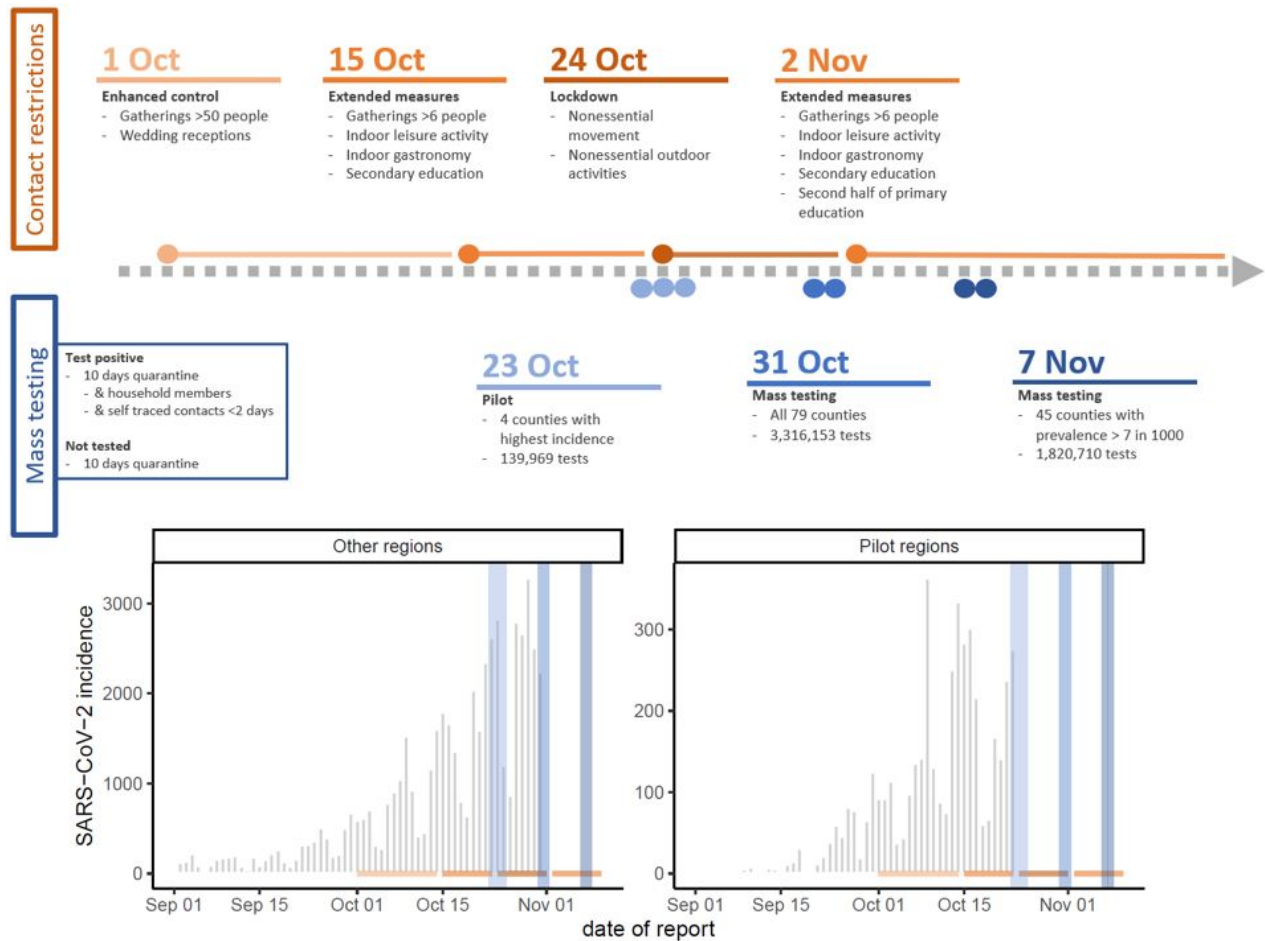
**Figure 2: The change in test positivity between mass testing campaigns**. Panel A: change in test positivity (1 - cPR) observed from mass testing round 1 to round 2 in the 45 counties that were eligible for both rounds of mass testing. Counties are grouped and color coded into regions. The crude pooled estimate and its 95% confidence bounds are shown as red vertical lines. Panel B: change in test positivity (1 - cPR) observed from the pilot mass testing round to either the first (green) or the second (orange) national round and from the first to the second mass testing round (blue) in the 4 counties that were included in the pilot. Panel C and D: county level test positivity in the first (C) and second (D) round of mass testing. Grey areas indicate counties that were not part of the second round because their test positivity rate was less than 7 per 1000 and hence have no estimates.
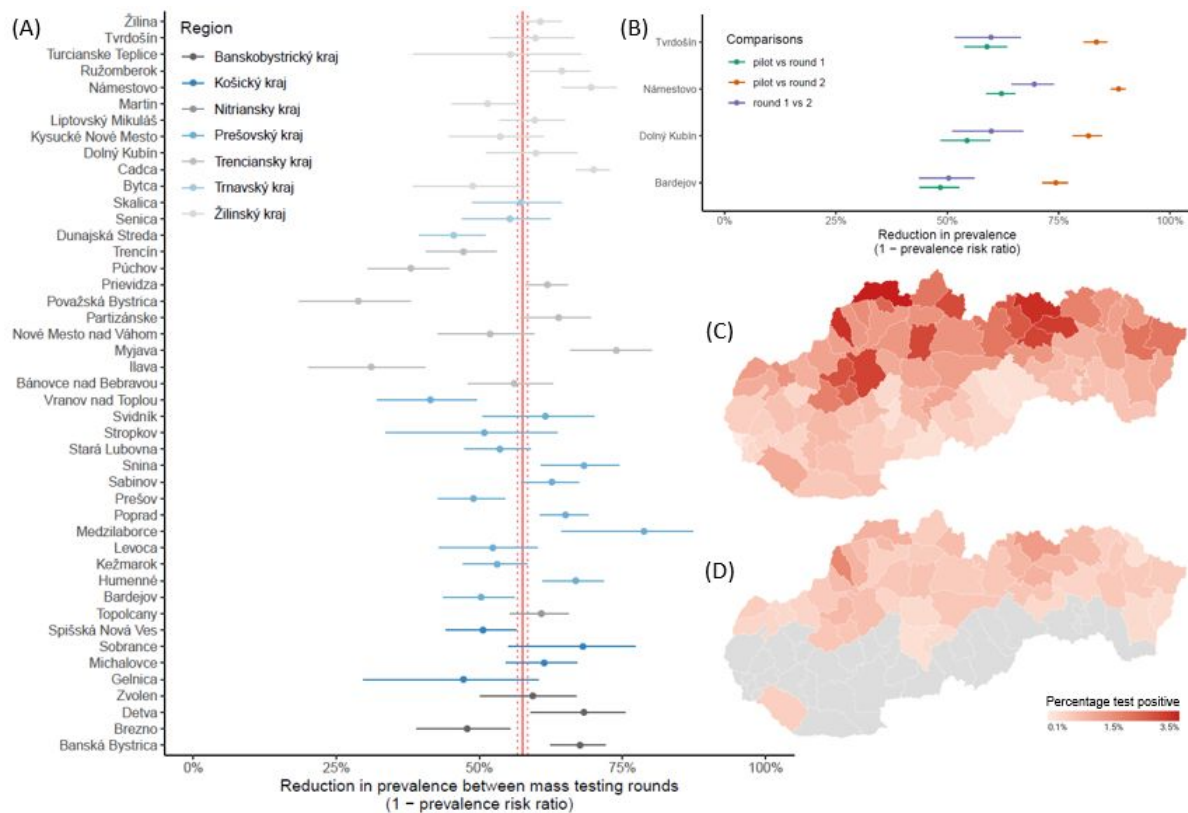
**Figure 3: Simulated relative effectiveness of the lockdown and the mass testing.** Top panel: the change in prevalence of infectious non-quarantining individuals between 10 and 65 years of age as predicted by the microsimulation model. For comparison the observed test-positivity rate is shown in blue. The facets show changes from the pilot to the first round of mass testing (left) and from the pilot to the second round of mass testing (right). Shown scenarios compare the effect of (top to bottom) no additional interventions that limit the growth rate of $R_e=1.4$, the national lockdown drastically reducing the growth rate to $R_e=0.6$ and no mass testing being conducted, the national lockdown reducing the growth rate to $R_e=1.0$ and no mass testing being conducted, no change in growth rate but mass testing, and the national lockdown reducing the growth rate to $R_e=1$ and mass testing. Bottom panel: Simulated infection incidence of alternative intervention strategies. Simulations are aligned by the date of the first mass test (t=0). The dashed line indicates the timing of the lockdown and the solid lines the timing of the mass testing campaigns. Colors indicate the simulations stratified into whether no mass testing or 1, 2 or 3 testing rounds were performed and the effectiveness of the lockdown measures. Red and yellow dots indicate the prevalence of infectiousness observed among the non-quarantining age-eligible population, corresponding to the scenarios in the top panel.
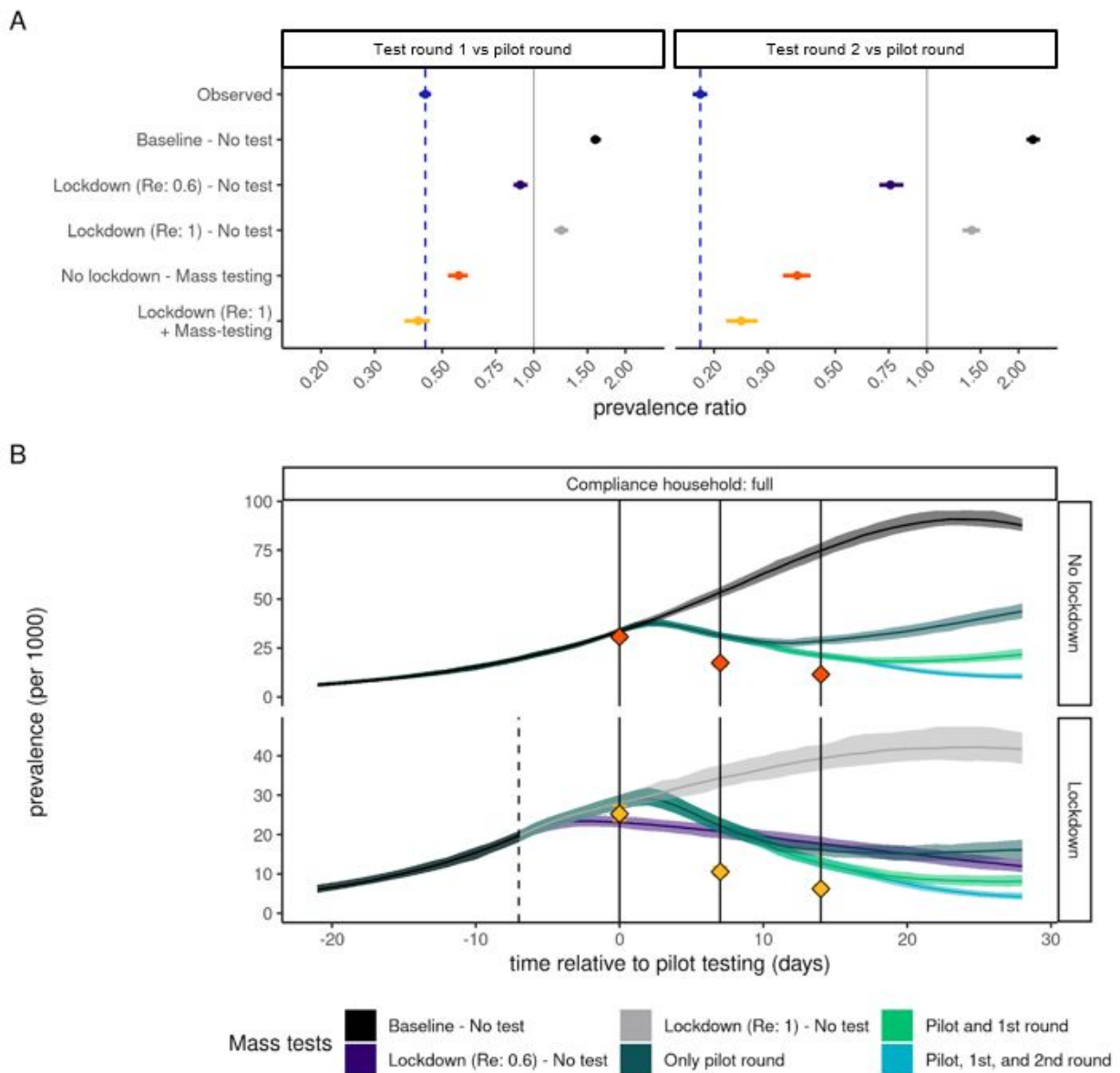
# Supplementary material to "The effectiveness of population-wide screening in reducing SARS-CoV-2 infection prevalence in Slovakia"

by Martin Pavelka, Kevin Van-Zandvoort, Katharine Sherratt, Sam Abbott, Marek Majdan, CMMID COVID-19 working group, Pavol Jarčuška, Marek Krajčí , Stefan Flasche*[$], Sebastian Funk*[$]

## Supplementary Tables and Figures

**Figure S1: Proportion of positive tests**. Test positivity grouped by different mass testing rounds. Given a sufficiently large sample size, one minus test specificity would be the lowest observable proportion of positive test. The absence of apparent clustering of observations at the lower end of the observed range suggests that even lower value could have been observed and test specificity was not a limiting factor.
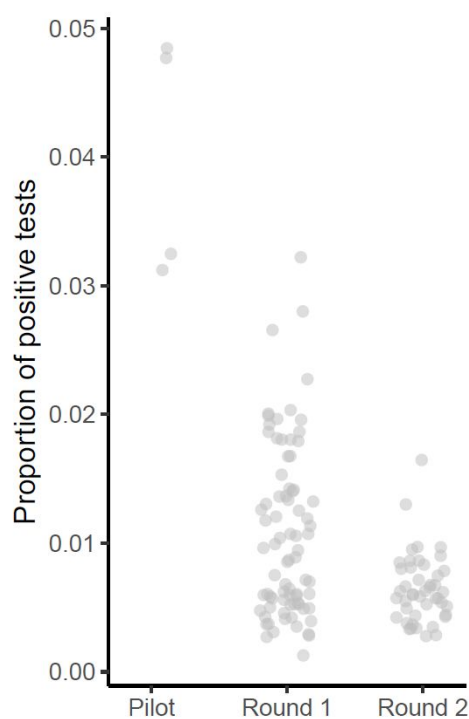
**Figure S2: Simulated relative effectiveness of the lockdown and the mass testing without adherence to quarantine for household members of test-positives.** The change in prevalence of infectious non-quarantining individuals between 10 and 65 years of age as predicted by the microsimulation model. For comparison the observed test-positivity rate is shown in light green. The facets show changes from the pilot to the first round of mass testing (top) and from the pilot to the second round of mass testing (bottom). Shown scenarios compare the effect of (top to bottom) no additional interventions that limit the growth rate of $R_e$=1.4, the national lockdown drastically reducing the growth rate to $R_e$=0.6 and no mass testing being conducted, no change in growth rate but mass testing, and the national lockdown substantially reducing the growth rate to $R_e$=1 and mass testing.
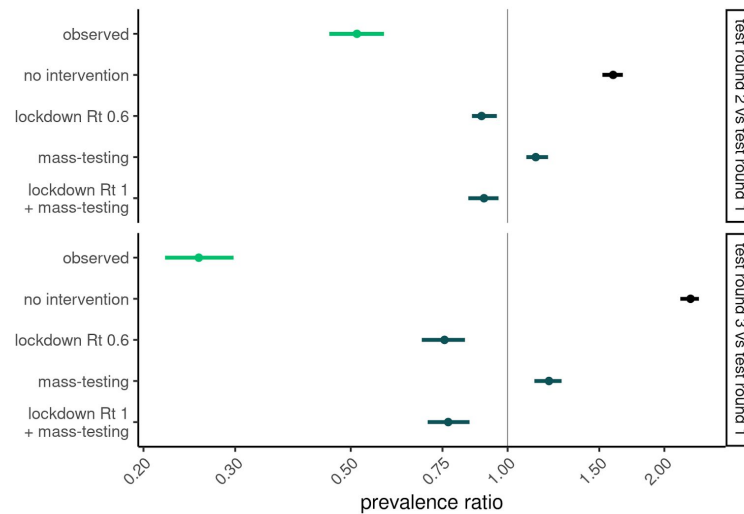


**Figure S3: Simulated relative effectiveness of the lockdown and the mass testing over time.** Simulated infection incidence of alternative intervention strategies. Simulations are aligned by the date of the first mass test (t=0). The dashed line indicates the timing of the lockdown and the solid lines the timing of the mass testing campaigns. Colors indicate the simulations stratified into whether no mass testing or 1, 2 or 3 testing rounds were performed. In the full household compliance facets all household members quarantine for 10 days if a member was tested positive and in the non compliance facet they did not. In Scenario 1 lockdown had no effect on the reproduction number and in Scenario 2 the reproduction number was reduced to 1. The additional grey line in scenario 2 indicates a scenario where no mass testing was done but the reproduction number was reduced to 0.6.
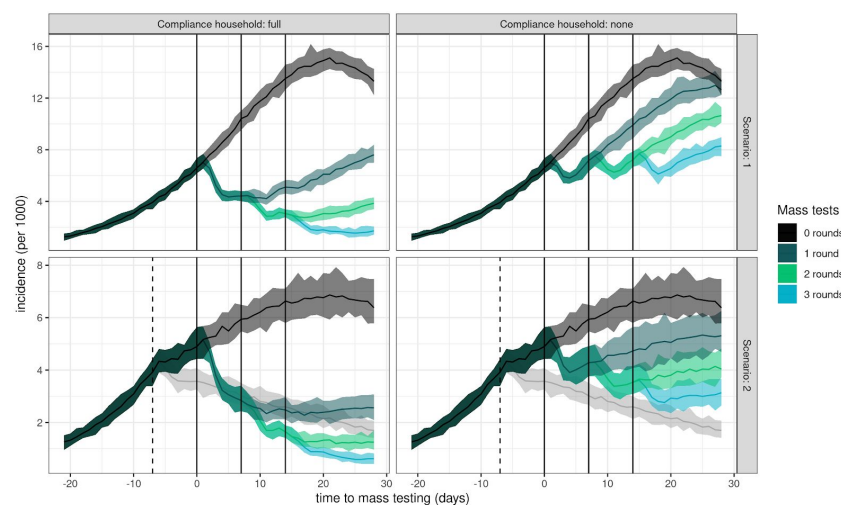


**Figure S4: Google mobility index for Slovakia.** The change in mobility in comparison to baseline for a number of settings during 2020 in Slovakia. The mobility data is as provided by Google (https://www.google.com/covid19/mobility/ ).
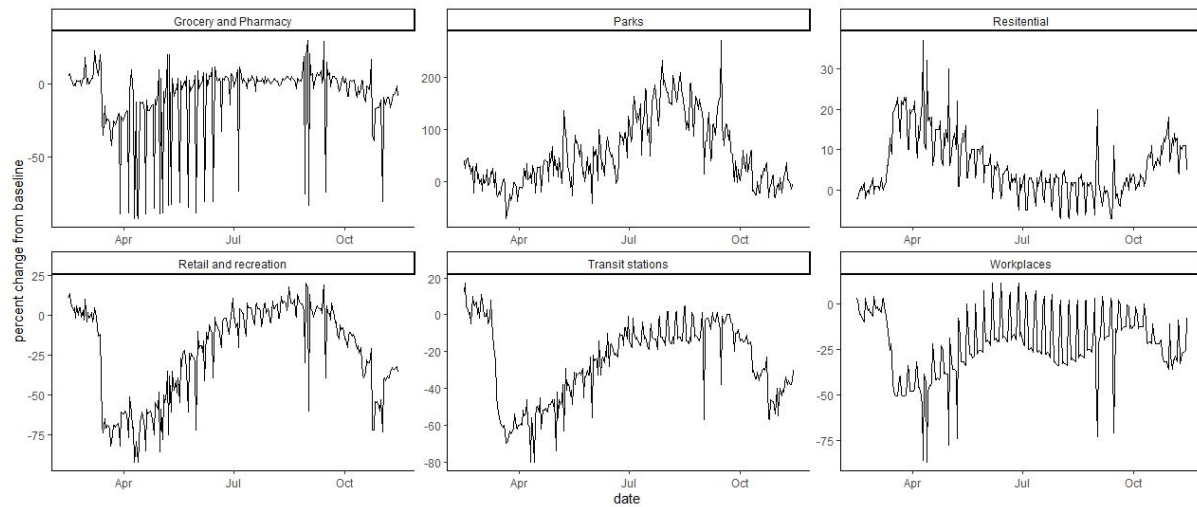
**Figure S5: Comparing the microsimulation model population to observed structures in Slovakia.** Panel A shows the median relative population distribution across all model runs (dark-green) compared to the UNWPP population estimates for Slovakia in 2020 (light-green), by age-group. Panel B shows the median household contact matrix (left; assuming all household members make one contact per day) compared to the synthetic household contact matrix (right), adjusted for UNWPP population size. Panel C shows the median non-household contact matrix (left) compared to the synthetic non-household contact matrix (right), adjusted for lockdown measures and UNWPP population size.
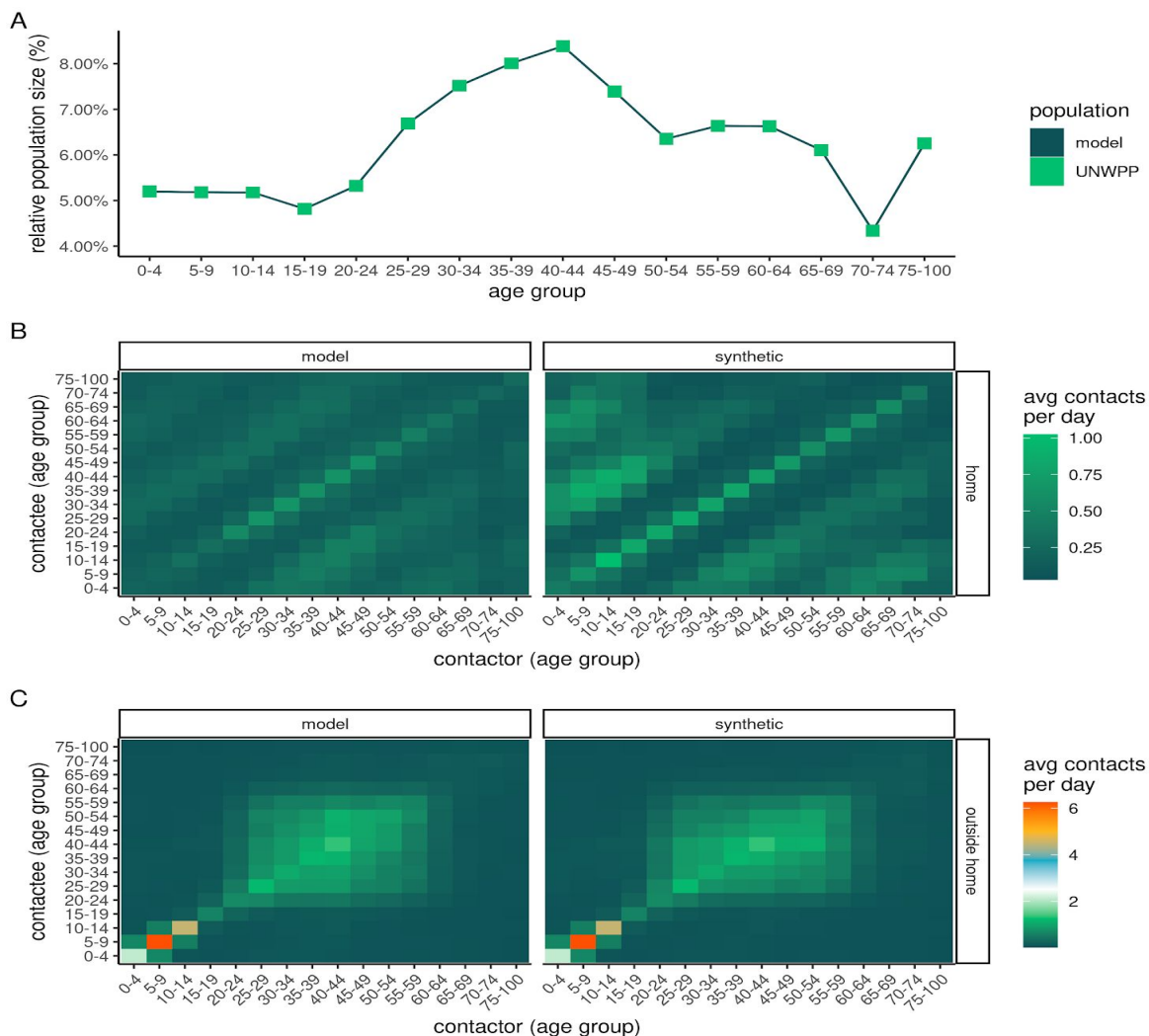
**Figure S6: Hospital bed occupancy with COVID-19 patients in Slovakia during the autumn of 2020**.
Following an increase particularly during October a sharp the abrupt levelling off in the first week of November suggests a sharp decrease in new admissions coinciding with the timing of the mass testing. Data presented are available from the European Centre for Disease Prevention and Control (https://www.ecdc.europa.eu/en/publications-data/download-data-hospital-and-icu-admission-rates-and-current-occupancy-covid-19)
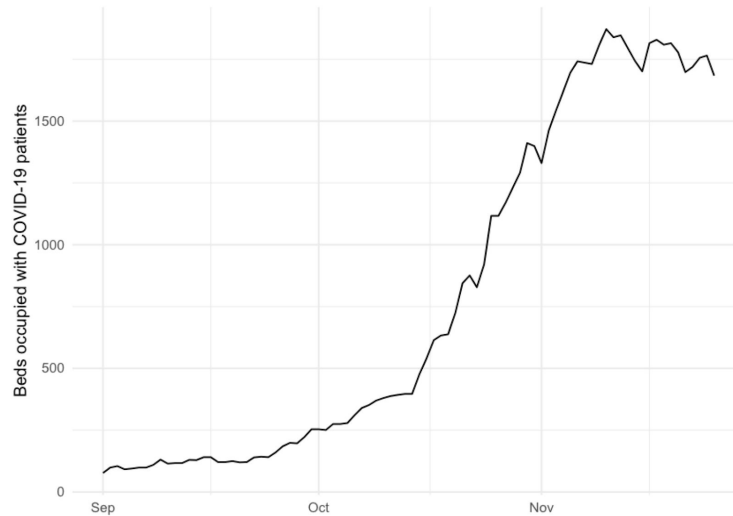


## Additional details for the study

## Detailed timeline of national SARS-CoV-2infection control measures adopted in Slovakia

### Pre - 1 October

- Compulsory face coverings indoors, in enclosed public places and inside mass transport vehicles
- 1000 limit on number of people in aquaparks
- 1000 outdoors and 500 indoors limit on mass gatherings
- Travellers returning from "high risk" countries or regions are requested to take a PCR test after the fifth day of their arrival or remain in quarantine for 10 days
- Shopping hours between 9am and 11am reserved for the elderly

### 1 October

- Gatherings limited to max 50 people
- Wedding receptions banned

### 15 October

- Gatherings limited to max 6 people (indoors or outdoors)
- Online schooling for pupils aged 14 years or older
- Compulsory face coverings including outdoors, if within city limits
- Wake receptions banned
- Indoor gastronomy closed
- Theatres and cinemas closed
- Pubs, clubs and bars closed

- Gyms, swimming pools, aquaparks, spas and other wellness and fitness facilities closed
- Church and religious services suspended

**24 October - 1 November**

- National stay at home order (lockdown) with the following exceptions:
    - travel to and from place of work
    - accompanying children to and from school
    - the first four grades of elementary schools, nurseries and creche stayed open
    - essential travel and activities (i.e. groceries, pharmacy, doctor surgeries, caring for a family dependant, animal husbandry, walking pets within 100 meter distance from home, funerals, post office, bank, insurance company, cleaning services, car repair services, petrol stations)
    - recreational nature walks

**2 November**

- same restrictions as 15 October with the addition of closing school for pupils aged 10 year or older.

## EpiNow2

We used EpiNow2 to backcalculate infection curves in pilot and non-pilot regions. These were converted to infection prevalence using a detection window of 2-6 days after exposure. This allowed us to estimate the infection prevalence of reported cases at the time of mass testing (*p1*) and in the subsequent mass testing round (*p2*). Thus we define the self adjusted prevalence ratio as the crude prevalence ratio observed in the mass testing campaigns adjusted for the predicted change in prevalence if no mass testing or other interventions were conducted:

$$saPR = cPR * p_1/p_2$$

## Regression model

We used a quasi Poisson model that was a priori defined by a choice of available covariates that could have plausibly altered the observed impact of the intervention:

$$log(x) = \sum \beta_{0,i} c_i + \beta_1 r + \beta_2 r a_2 + \beta_3 r p_2 + \beta_4 r R_2 + \sum \beta_{5,i} r g_i + log(N) + \epsilon$$

where

| | |
|---|---|
| $x$ | = number of positive tests in each county |
| $N$ | = number of samples |
| $r$ | = round indicator; 0 for first and 1 for second round |
| $c_i$ | = county (categorical) |
| $a_2$ | = attendance rate of the first national survey (FNS) |
| $p_2$ | = prevalence observed in the FNS |
| $R_2$ | = net reproduction number estimated from EpiNow2 for the day of the FNS |
| $g_i$ | = region (categorical) |

The model was set up to use the county specific intercept to exactly model the test positivity observed in the first national testing campaign. The round indicator measures the adjusted prevalence ratio (aPR) and the remaining covariates are centered and standardised interaction terms with round to estimate the effects of these variables on the prevalence ratio between the first and second round of mass testing. The number of tests was included as an offset.

## Microsimulation model

### Model structure

We used an individual-based, probabilistic microsimulation model (IBM) to study the expected reduction in prevalence of (detected) infectiousness under different assumptions.

We up our model to represent an average county of Slovakia     .

In our IBM, individuals fall within $a$ age strata (where $i$ is a given age stratum) with relative proportions $p_i$. They belong to  households of mean size $m_h$ (we combine different datasets to simulate a population). The simulation starts when the model population of size $N$  is seeded with at least one SARS-CoV-2 infection, and runs for 365 days.

Births, non-COVID-19 deaths, ageing and migration are omitted from the model given its short timeframe. The study's endpoint of interest is infection, we did not include hospitalisation or clinical outcome status of cases. Infectiousness is assumed to be unaffected by clinical severity, but does differ for asymptomatic, pre-symptomatic and symptomatic cases (see below).

### Infection states and transitions

At any time $t$, individuals  within the IBM are within one of the following classes: $S$ (susceptible), $E$ (exposed and latent, i.e. infected but not yet infectious), $I_P$ (infectious but pre-symptomatic), $I_C$ (infectious and symptomatic), $I_S$ (infectious and asymptomatic throughout the infection), or $R$ (removed: recovered and assumed to be immune or deceased). The age-specific probability of becoming a symptomatic case when infected is $y_i$ .

Over any $\Delta t$  time unit, any given individual  has the following binomial probabilities of transitioning to a subsequent state:

$$P_r(S_x \rightarrow E_x) Binomial(1, 1 - e^{-\lambda_{i,x,t}})$$

$$P_r(E_x \rightarrow I_{P,x}) Binomial(1, d_E(t_{E,x}) y_{i,x})$$

$$P_r(E_x \rightarrow I_{S,x}) Binomial(1, d_E(t_{E,x})(1 - y_{i,x}))$$

$$P_r(I_{P,x} \rightarrow I_{C,x}) Binomial(1, d_P(t_{P,x}))$$

$$P_r(I_{C,x} \rightarrow R_x) Binomial(1, d_C(t_{C,x}))$$

$$P_r(I_{S,x} \rightarrow R_x) Binomial(1, d_S(t_{S,x}))$$

where $1 - e^{-\lambda_{i,x,t}}$  is the age-specific instantaneous force of infection experienced by a susceptible individual, as detailed below; and , $d_E$ , $d_P$ , $d_C$ , and $d_S$  are cumulative

distribution functions (CDFs) for the duration of the corresponding states: $d_E(t_{E,x})$ denotes the CDF for the duration of the pre-infectious state evaluated at the time already spent by individual $x$ in that state, and so on.

## Transmission dynamics

Over any $\Delta t$ time unit, susceptible individuals of any age $i$ within each household $h$ move from $S$ to $E$ based on an individual-specific instantaneous force of infection that is the sum of $\lambda$ due to contacts within the household and $\lambda$ due to extra-household contacts:

$$\lambda_{i,t,x} = \beta w \frac{I_{P,t,h}+I_{C,t,h}+I_{S,t,h}}{N_{t,h}-1} + \beta \sum_{j=1}^{j=a} U_{ij} \frac{I_{P,t,h'}+I_{C,t,h'}+I_{S,t,h'}}{N_{t,h'}}$$

where $\beta$ is the probability of infection per contact between a susceptible and infectious person, $f$ is the relative infectiousness of asymptomatic infections, compared to cases that do develop symptoms, $w$ is the mean per-capita intra-household contact rate, assuming random mixing within the household. $U$ is the contact matrix outside the household for the total number of contacts made between individuals aged i with individuals aged j. $h$ denotes individuals within the household itself, while $h'$ denotes individuals in the population excluding the household itself). $I_{P,t}$, $I_{C,t}$, and $I_{S,t}$ represent the total number of infectious individuals not in quarantine at time $t$.

We assume that all individuals within the household make one contact per day, and calculate the expected population-wide intra-household contact matrix $W$ where $W_{ij}$ is the sum of all aged individuals aged $i$ living together with household members of age $j$, divided by the model population size aged $i$. We ensure that the average contact rates are such that the total number of extra-household contacts are symmetric between age-groups, and calculate the population-level contact matrix, $Z = W + U$ .

The basic reproduction number $R_0$ is then defined as the average number of secondary infections generated by a typical infected individual in a fully susceptible population, and is computed as the dominant eigenvalue of the next generation matrix (NGM) of the corresponding compartmental model structure to our IBM model, defined as:

$$NGM_{ij} = \beta Z_{ij}(y_i(\overline{d_P + d_C}) + (1 - y_i)f\overline{d_S})$$

where accents indicate the expected (average) values. Lastly, $\beta$ is the ratio of this eigenvalue and the $R_0$ value assumed in the simulation (see below).

We validated the calculated $R_0$ value through this method by running multiple iterations of the model using a different seed for the random number generator, and calculating the average number of secondary cases derived from all infectious individuals who completed their period of infectiousness in the first 30 days of the simulation.

## Testing and lockdown

We simulate an epidemic using a timestep of $\Delta t = 1 day$ . The first round of mass testing is introduced at time $t_g$ when the prevalence of infectiousness in the model reaches a predefined threshold (as observed in the pilot round of mass testing in the county). If introduced, the second and third rounds of testing are introduced on days $t_g + 7$ and $t_g + 14$ .

When testing is introduced, we assume that any individual $x$ attends mass-testing with probability $z_t$. We calculated this probability as $z_t = \frac{N_{attend,t}}{N_{eligible}} \frac{1}{P_{quarantine}}$ , where $N_{attend,t}$ is the observed attendance for the test round introduced at time $t$ , $N_{eligible}$ is the total model population size that is eligible for testing (any individual between the ages of 10 and 65), and $P_{quarantine}$ is the proportion of the model population size that is in quarantine at time $t$ .

Individuals already in quarantine do not attend testing. We assume 100% sensitivity to detect an infectious individual (in state $I_P$ , $I_S$ , or $I_C$ ), 0% sensitivity to detect an infected but not yet infectious individual (in state $E$ ), and 100% specificity for any individual not currently infected. Those who test positive are assumed to comply with quarantine measures with probability $C_p$ , and any of their household members not already quarantining are assumed to comply with probability $C_h$. We also assume the same probability $C_h$ to quarantine individuals who do not attend mass-testing, but are eligible (between the ages of 10 and 65).

To implement scenarios with lockdown, we first calculated the effective reproduction number in the two weeks before the first round of mass-testing would be implemented, between $t_g - 14$ and $t_g$ . We then started a new model run using the same seed for the random number generator, and implemented a lockdown scenario by changing the value for the probability of effective contact $\beta$ from the time of implementation of lockdown with $\beta^* = \beta \frac{R_E^*}{R_E}$ , where $R_E$ is the estimated effective reproductive number in the period before lockdown and $R_E^*$ is the target value for the effective reproduction number after implementation of lockdown. We assumed the reduced $\beta^*$ would remain in place for the remainder of the simulation.

**Population structure**

We simulate a new population within each model iteration by combining estimates for the 2020 Slovak population size, household size by age, and the estimated number of daily contacts made in the household per day.

We simulated a population with target size $N$ by simulating new households until the sum of individuals in all households reached $N$ .

To simulate a household, we randomly sampled $i$ , the age of one individual living in the new household, and drew a value for $Y$ , the household size (ranging from 1 to 6) for those living in the household, from a multinomial distribution where the age-specific distribution of household sizes as estimated in the 2011 Slovak census were used as probabilities for the household size (Eurostat, 2020).

We assumed that normalized age-specific at-home contact rates, $W_{ij}^*$ , calculated as $W_{ij}^* = \frac{W_{ij}}{\sum_{j=1}^{j=a} W_{ij}}$ , were proportional to household age distribution (Prem et al, 2020).

We then sampled $Y - 1$ age-groups of household members from a multinomial distribution with age-specific probability of sampling age-group $j$ , $P(j|i) = W_{ij}^* p_j$ , where $P_j$ is the probability of sampling any individual from age-group $j$ , following age-specific UNWPP estimates for the population size (UNWPP, 2019).

The median average household size across all modelled populations is 3.7 (3.6-3.7). This is slightly lower than the average household size across all age groups (4.0) as reported in the 2011 Slovak household census (2020, Eurostat - Population by sex, age group, size of household and NUTS 3 regions). Figure S5 compares other key model parameters for the simulated populations with the empirical datasets used. Panel A compares the UNWPP population distribution for Slovakija in 2020 with the median population distribution across all simulated populations. A black area underneath the median population size shows the 95% interval of estimates across all populations, but is not visible in the plot as there is barely any variability across simulated populations, due to the algorithm that was used.

Panel B compares the median household contact matrix across all simulated populations to the synthetic at home contact matrix, where the synthetic matrix has been adjusted with the UNWPP population size estimates to ensure symmetry in the total number of contacts (i.e. total number of contacts of those aged i with j = total number of contacts of those aged j with i). We used the dominant eigenvalue of all matrices to select the matrix representing the median model matrix. The matrices are very similar, though there are slightly less child-adult contacts in the median model matrix compared to the synthetic matrix. The synthetic matrix is generated through extrapolation of contact surveys done in the mid 2000s in other European countries, and may therefore not reflect actual household contact patterns in Slovakia. In addition, the surplus of contacts in the synthetic contact matrix could be due to inclusion of extra-household contacts occurring at the home, which are not included in the model household contact matrix.

Panel C compares the median contact matrix for contacts made outside of the household used in the model, with the contact matrix for non-home contacts in the synthetic matrix for Slovakija (adjusted to represent a change in contact patterns due to Covid-19 interventions). The model contact matrices have been made symmetric for the population distribution used in the model, while the synthetic contact matrix has been made symmetrical for the UNWPP 2020 Slovakija contact matrix, but are otherwise identical. As these population distributions are very similar (Panel A), the contact matrices are as well.

## Parameter values
The table below lists all parameter values used in the model

| Parameter | Description | Value | Source |
|---|---|---|---|
| $H$ | Number of households | See text | Computed within the model |
| $i,j$ | Age strata in years (number of age strata = ) | 0-4, 5-9, 10-14, 15-19, 20-24, 25-29, 30-34, 35-39, 40-44, 45-49, 50-54, 55-59, 60-64, 65-69, 70-74, 75+ | n/a |
| $p_i$ | Proportion of people in each age stratum | Resampled within each model iteration | (UNWPP, 2019) |
| $m_h$ | Mean household size | Resampled within each model iteration | (Eurostat, 2020) |
| $N$ | Total population size | 78,000 | Representative for a typical Slovak county |
| $N_h$ | Number of people in each household | Resampled within each model iteration | (Eurostat, 2020) |
| $\Delta t$ | Time step for discrete-time simulation | 1 day | n/a |
| $d_E$ | Latent period in days | ~ gamma($\mu$ = 2.5, k = 4) | |
| $d_P$ | Duration of pre-symptomatic infectiousness in days | ~ gamma($\mu$ = 2.5, k = 4) | |
| $d_C$ | Duration of symptomatic infectiousness in days | ~ gamma($\mu$ = 2.5, k = 4) | |

| | | | |
|---|---|---|---|
| $d_S$ | Duration of asymptomatic infectiousness in days | ~ gamma($\mu = 5$, $k = 4$) | Assumed to be the same as duration of total infectious period for clinical cases |
| $y_i$ | Probability of becoming a symptomatic case, if infected, for age group | Age-dependent, as estimated in Davies et al. | (Davies et al, 2020) |
| $R_0$ | Basic reproduction number | 1.5 | Assumption, based on EpiNow2 estimates for in time before testing |
| $f$ | Relative infectiousness of asymptomatic cases | 50% | Assumption |
| $w$ | Within-household per-capita daily contact rate | 1 | Assumption |
| $W$ | Age-dependent contact matrix inside the household | Resampled within each model iteration | (Prem, 2020; UNWPP, 2019; Eurostat, 2020) |
| $U$ | Age-dependent contact matrix outside the household | | (Prem, 2020) |
| $\beta$ | Probability of transmission per contact with an infectious individual | See text | Computed within the model |
| $z_t$ | Proportion of people eligible for testing who are tested | As estimated in mass-testing (0.85, 0.78, 0.78) | (Slovakia MOH, 2020) |
| $c_p$ | Compliance with quarantine for those who test positive | Variable: 0.0, 1.0 | Assumption |
| $c_h$ | Compliance with quarantine for household members of those who test positive | Variable: 0.0, 1.0 | Assumption |
| $R_E^*$ | Target $R_E$ after lockdown | Variable: 0.6, 1.0 | Assumption |
| $P_E$ | Sensitivity of SARS-CoV-2 laboratory test among individuals in latent class | 0 | Assumption |
| $P_P$ | Sensitivity of SARS-CoV-2 laboratory test among individuals in pre-symptomatic infectious class | 100% | Assumption |
| $P_C$ | Sensitivity of SARS-CoV-2 laboratory test among individuals in symptomatic infectious class | 100% | Assumption |
| $P_S$ | Sensitivity of SARS-CoV-2 laboratory test among individuals in asymptomatic infectious class | 100% | Assumption |

## Simulations

We ran a total of 15 scenarios and 200 iterations for each:

| Scenario | Lockdown effectiveness ($R_E^*$) | Number of test rounds | Compliance household members ($c_h$) |
|---|---|---|---|
| 1 | N/A | 0 | N/A |
| 2 | N/A | 1 | 100% |
| 3 | N/A | 2 | 100% |
| 4 | N/A | 3 | 100% |
| 5 | N/A | 1 | 0% |
| 6 | N/A | 2 | 0% |
| 7 | N/A | 3 | 0% |
| 8 | 1 | 0 | N/A |
| 9 | 1 | 1 | 100% |
| 10 | 1 | 2 | 100% |
| 11 | 1 | 3 | 100% |
| 12 | 1 | 1 | 0% |
| 13 | 1 | 2 | 0% |
| 14 | 1 | 3 | 0% |
| 15 | 0.6 | 0 | N/A |