Help files

## community.md

Community contacts are defined as any contact that does not live with the index case.

## household.md

Household contacts are defined as any contact that lives with the index case.

## name.md

This is the name of the community that your contact tracing program serves, for example “Baltimore City Health Department”.

## prepared\_by.md

This is your name, we only use for your convenience to this to add to your report.

## s1.md

This can’t be measured directly. We can estimate it for you, using an estimated infection fatality rate and proportion of positive tests, or you can input an estimate directly.

## s1\_ifr.md

The infection fatality ratio (IFR) is the proportion of all people infected (not just those who have symptoms) who die, and will depend on:

* The average age of the population \* The prevalence of underlying comorbidities \* Access to medical care

The best way to choose the IFR for your population is to use a measurement from your population and input that directly into this calculator. However, if you do not have access to an estimate, we provide some options here. The highest estimate is 1%, which comes from a modeling study of an older adult population. The 0.75% estimate is close to the estimate for France, where the average age is 41 years. A recent model suggests that the IFR from China was close to 0.5%, and the average age of their population is 37 years. If the average age of your population is in the 20s, the best IFR to choose might be 0.25%.

## s1\_n\_detect.md

We calculate number of infections detected this week as

(total tests in the past month / 4.345)

We have you input the total number of infections over the past month and take the average as an imperfect way to help account for the exponential growth of cases and lagging indicator of deaths.

## s1\_n\_detect\_month.md

How many people have tested positive in your community in the past **month**.

We have you input the total number of infections over the past month and take the average as an imperfect way to help account for the exponential growth of cases and lagging indicator of deaths.

## s1\_n\_infections.md

We calculate the estimated number of infections in your community this week as:

(number of deaths in the past week) x (100 / IFR)

This is an imperfect estimation, since death is a lagging indicator of number of cases.

## s1\_n\_isolate.md

We want to know how many people who have tested positive for COVID-19 in your community were contacted and told to isolate in the past **month**.

## s1\_perc\_detect.md

We calculate percent detected as:

(number of infections detected in the past week) / (number of infections in the past week)

(number of infections detected in the past month / 4.345)

and number of infections in the past week is estimated by:

(number of deaths in the past week) x (100 / IFR)

If you indicate that the number of deaths x (100 / IFR) is less than the total number of infections, we assume your detection is 100%.

## s3.md

An “index case” is another word for a person detected via surveillance. We want to know the average length of time (in days) between when someone exhibits symptoms and when they are tested for COVID-19 in your community. Symptoms may include:

* Fever or chills\* Cough\* Shortness of breath or difficulty breathing\* Fatigue\* Muscle or body aches\* Headache\* New loss of taste or smell\* Sore throat\* Congestion or runny nose\* Nausea or vomiting\* Diarrhea

## s4.md

An “index case” is another word for a person detected via surveillance. We want to know the average length of time (in days) between when someone exhibits symptoms and when they are contacted and told to isolate. The yellow slider symbol here represents the number of days from symptom onset to being tested (as indicated in S3), drag the **blue slider on the right** to update the number of days from symptom onset to isolation.