It is made available under a CC-BY 4.0 International license. **(which was not certified by peer review)** is the author/funder, who has granted medRxiv a license to display the preprint in perpetuity. medRxiv preprint doi: [https://doi.org/10.1101/2020.08.15.20175786.](https://doi.org/10.1101/2020.08.15.20175786)this version posted August 17, 2020. The copyright holder for this preprint

\overline{a} $\frac{A_{11} + A_{22} + A_{32}}{A_{12} + A_{22}}$

\overline{a} SUPPLEMENTARY METHODS

1A. Testing the upper bound on the true number of infections

To test the upper bound on the true number of infections (via
probability of observing $x=0$ cases, conditional on there being of
size N (of which we tested n). We assume that the sensitivity
diagnostic test are known コドくしー probability of observing x=0 cases, conditional on there being exactly K cases in our po
of size N (of which we tested n). We assume that the sensitivity (Se) and specificity (Sp)
diagnostic test are known and fixed probability of observing x -o cases, conditional of there being exactly K cases in our population
of size N (of which we tested n). We assume that the sensitivity (Se) and specificity (Sp) of the
diagnostic test ar diagnostic test are known and fixed at 80% and 100%, respectively. We assume that the *n* individuals were sampled at random and so are representative of the entire population *N*. We use the hypergeometric distribution s individuals were sampled at random and so are representative of the entire population N.
use the hypergeometric distribution since we have a finite population size so trials are not
independent, and binomial distributions individuals were sampled at random and so are representative of the entire population N. We
use the hypergeometric distributions ince we have a finite population size so trials are not
independent, and binomial distributi

independent, and binomial distributions to account for Se and Sp.
\n
$$
Pr(X = 0; K, N, n, Se, Sp) = \sum_{y=0}^{K} \frac{{\binom{K}{y}} {\binom{N-K}{n-y}}}{{\binom{N}{n}}} \cdot (1 - Se)^y \cdot Sp^{n-y}
$$
\nCode available at:
\nhttps://github.com/EPPlcenter/bolinas-analysis/blob/master/1A_Figure_1R.

 $\frac{1}{1}$

https://github.com
1B. Estimation of F
We estimated PCR
prevalence (n) and https://gammatom/EPPICenter/Politicality.com/Philosofty-EPPIC game Carry
18. Estimation of PCR prevalence
Prevalence (p) and second, by using the hypergeometric distribution to mode
latter is more appropriate in this scena ここ トーキ We estimated PCR prevalence in t
prevalence (p) and second, by usint
latter is more appropriate in this s
the total population (upwards of 8
estimates of uncertainty. We again \
|F|
|t ∈ prevalence (p) and second, by using the hypergeometric distribution to model prevalence. The
latter is more appropriate in this scenario since testing was performed on a large proportion of
the total population (upwards latter is more appropriate in this scenario since testing was performed on a large proportion of the total population (upwards of 80%), so the hypergeometric distribution will yield narrower
estimates of uncertainty. We again assume that the *Se* and *Sp* of the diagnostic test are known
and fixed at 80% and 100%, re estimates of uncertainty. We again assume that the *Se* and *Sp* of the diagnostic test are known
and fixed at 80% and 100%, respectively. As the binomial distribution is more frequently used
for prevalence estimation, we and fixed at 80% and 100%, respectively. As the binomial distribution is more frequently used for prevalence estimation, we provide Stan code to implement both models.

$$
x \sim \text{Hypergeometric}\left(n, \left(p \cdot Se + (1 - p) \cdot (1 - Sp)\right) \cdot N, N - \left(\left(p \cdot Se + (1 - p) \cdot (1 - Sp)\right)\right) \cdot N\right)
$$
\n
$$
x \sim \text{Binomial}(N, p \cdot Se + (1 - p) \cdot (1 - Sp))
$$
\nCode available at:

\nhttps://github.com/SPDlerator/holise, and his this is the fact that the problem is 1000.

$$
x \sim \text{Binomial}\big(N, p \cdot Se + (1-p) \cdot (1-Sp)\big)
$$

っ
(トー $\frac{1}{2}$ https://github.com
https://github.com
2A. Estimation of s https://github.com/EPPIcenter/bolinas-analysis/blob/master/1B.2_PCR_prevalence_binomia
2A. Estimation of seroprevalence (one test)

https://gathacenter.com/EPPIcenter.com/EPPIcenter/prevalence.com/
2A. Estimation of seroprevalence (one test) $\frac{2}{3}$ 2A. Estimation of seroprevalence (one test)

It is made available under a CC-BY 4.0 International license. **(which was not certified by peer review)** is the author/funder, who has granted medRxiv a license to display the preprint in perpetuity. medRxiv preprint doi: [https://doi.org/10.1101/2020.08.15.20175786.](https://doi.org/10.1101/2020.08.15.20175786)this version posted August 17, 2020. The copyright holder for this preprint

We use the binomial distribution, which will yield conservative intervals as compared to the
hypergeometric distribution used as above. The difference from the estimation of PCR
prevalence is that we also estimate *Se* an We use the binomial distribution, which will yield conservative intervals as compared to the hypergeometric distribution used as above. The difference from the estimation of PCR prevalence is that we also estimate Se and prevalence is that we also estimate *Se* and *Sp* of the assays using validation data. The p
predictive values (PPV) are calculated directly from the estimates.
 $x_j \sim \text{Binomial}(N, p_j \cdot Se_j + (1 - p_j) \cdot (1 - Sp_j))$ prevalence is that we also estimate Se and Sp of the assays dsing validation data. The positive
predictive values (PPV) are calculated directly from the estimates.
 $x_j \sim \text{Binomial}(N, p_j \cdot Se_j + (1 - p_j) \cdot (1 - Sp_j))$
Positive controls tes

$$
x_j \sim \text{Binomial}\left(N, p_j \cdot Se_j + (1 - p_j) \cdot (1 - Sp_j)\right)
$$

Positive controls testing positive $j \sim \text{Binomial}\left(\text{Pos}$
Negative controls testing negative $j \sim \text{Binomial}\left(N\right)$

 $x_j \sim \text{Binomial}(N, p_j \cdot Se_j + (1 - p_j) \cdot (1 - Sp_j))$
Positive controls testing positive $j \sim \text{Binomial}(\text{Positive controls}_j, Se_j)$
Negative controls testing pogative. $\approx \text{Binomial}(\text{Negative controls} - S_n)$ Positive controls testing positive $_j \sim \text{Binomial}\big(\text{Positive controls}_j, \text{ Se}_j\big)$

Negative controls testing negative, \sim Binomial(Negative controls, Sp_i)

Positive controls testing positive_j ~ Binomial (P
Negative controls testing negative_j ~ Binomial(
PPV_j =
$$
\frac{Se_j \cdot p_j}{(Se_j \cdot p_j) + ((1 - Sp_j) \cdot (1 - p_j))}
$$
Code available at:
https://github.com/EPPlcenter/bolinas-

 $\frac{1}{2}$ $\frac{1}{2}$ $\frac{1}{2}$ $\frac{1}{2}$ Code available at:

https://github.com/EPPIcenter/bolinas-

analysis/blob/master/2A Ab prevalence separate binomial.R

2B. Estimation of seroprevalence (two tests)

We extended the approach in 2A above to jointly model the results of both assays x_{jk} , using the multinomial distribution as the generalization of the binomial distribution and now estimating a single seroprevalence p analysis/massis/2021-2022 presents and the separation of seroprevalence (two tests)
We extended the approach in 2A above to jointly model the res
multinomial distribution as the generalization of the binomial d
single sero U
V
I
S We extended the approach in 2A above to jo

multinomial distribution as the generalization

single seroprevalence p. We necessarily assue

assays *j* and *k*. For samples that were only test

contribute to the binomial lik \
r < c < multimomental distribution as the generality assumed conditional independence between the two
assays *j* and *k*. For samples that were only tested on one platform, we allowed them to
contribute to the binomial likelihood single seroprevalence p. we necessarily assumed conditional independence between the two
assays j and k. For samples that were only tested on one platform, we allowed them to
contribute to the binomial likelihood for the contribute to the binomial likelihood for the platform that they were tested on. The posi-
predictive values, which are now based on the results of both assays, are calculated direction
from the estimates.
 $\begin{pmatrix} x_{++} \\ x_{$ predictive values, which are now based on the results of both assays, are calculated directly from the estimates.

from the estimates.
\n
$$
\begin{pmatrix}\nx_{++} \\
x_{-+} \\
x_{--}\n\end{pmatrix} \sim \text{Multinomial}\begin{pmatrix}\np \cdot Se_1 \cdot Se_2 + (1-p) \cdot (1 - Sp_1) \cdot (1 - Sp_2) \\
p \cdot Se_1 \cdot (1 - Se_2) + (1 - p) \cdot (1 - Sp_1) \cdot Sp_2) \\
p \cdot (1 - Se_1) \cdot Se_2 + (1 - p) \cdot Sp_1 \cdot (1 - Sp_2) \\
p \cdot (1 - Se_1) \cdot (1 - Se_2) + (1 - p) \cdot Sp_1 \cdot Sp_2\n\end{pmatrix}
$$
\nPositive controls testing positive, \sim Binomial (Positive controls, *Se*.)

Positive controls testing positive $_i \sim$ Binomial (Positive controls_i, Se_i)

Negative controls testing negative $_i \sim$ Binomial(Negative controls $_i$, S p_i)

Positive controls testing positive_j ~ Binomial (Positive controls_j, *S*.
Negative controls testing negative_j ~ Binomial (Negative controls_j,
PPV₊₊ =
$$
\frac{Se_j \cdot Se_k \cdot p}{(Se_j \cdot Se_k \cdot p) + ((1 - Sp_j) \cdot (1 - Sp_k) \cdot (1 - p))}
$$

It is made available under a CC-BY 4.0 International license. medRxiv preprint doi: [https://doi.org/10.1101/2020.08.15.20175786.](https://doi.org/10.1101/2020.08.15.20175786)this version posted August 17, 2020. The copyright holder for this preprint
(**which was not certified by peer review)** is the author/funder, who has granted

$$
PPV_{+-} = \frac{Se_j \cdot (1 - Se_k) \cdot p}{(Se_j \cdot (1 - Se_k) \cdot p) + ((1 - Sp_j) \cdot Sp_k \cdot (1 - p))}
$$

$$
PPV_{-+} = \frac{(1 - Se_j) \cdot Se_k \cdot p}{((1 - Se_j) \cdot Se_k \cdot p) + (Sp_j \cdot (1 - Sp_k) \cdot (1 - p))}
$$

$$
Code available at: \frac{\text{https://github.com/EPPlcenter/bolinas-}}{\text{https://github.com/EPPlcenter/bolinas-}}}
$$

 $\frac{1}{2}$ Code available at:

https://github.com/EPPIcenter/bolinas-

analysis/blob/master/2B Ab prevalence joint multinomial.R analysis/block/master/2B_Abachemial. \overline{R}