

28/11/2024

How prior immunity impacted the deadly second wave of SARS-CoV-2 in Manaus

By: Jan Paul van Meenen



Who am I?

Master's: currently a 2nd-year Master's student in Bioinformatics and Biocomplexity at Utrecht University

Bachelor's: Molecular and Biophysical Life Sciences (MBLS, formerly MLS) at Utrecht University

Took the Biological Modeling course in 2021: one of my favorite courses! (*unbiased opinion*)

- Especially enjoyed the disease spread modeling (Chapter 6)



Jan Paul van Meenen



Who am I?

Research Interests: Exploring immunology and epidemiology through computational methods

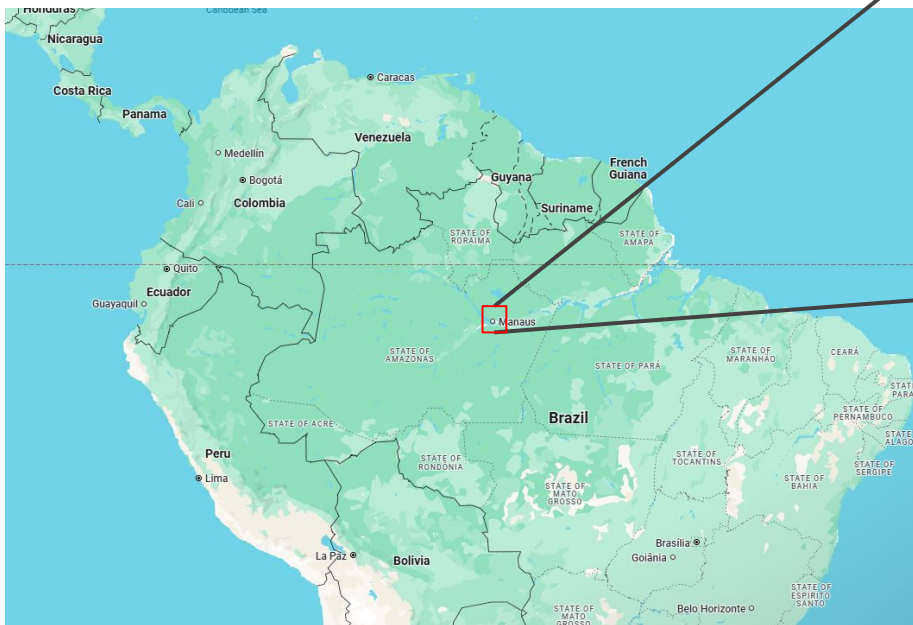
Goal this lecture:

- Explaining our research
- Walking you through the ideas and concepts behind it
- Show how material covered in Chapter 6 has real-world application

The story of Manaus

Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates
→ Counterfactual

The case of Manaus



Population: 2.2 million

More than the population of
Amsterdam, Rotterdam, The Hague and
Utrecht combined!

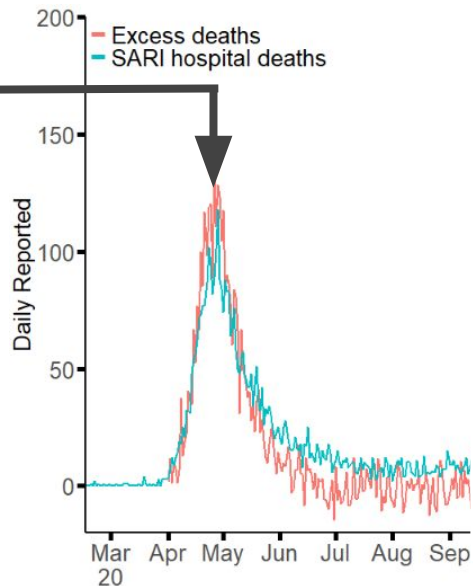
Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates
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The case of Manaus: devastating initial wave of COVID-19 deaths ...



B.1.195 strain



SARI: Severe Acute Respiratory Infection

21

Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates
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The case of Manaus: devastating initial wave of COVID-19 deaths ...

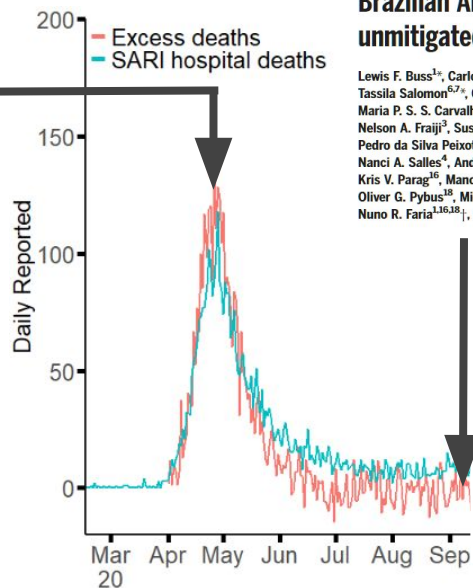


RESEARCH

CORONAVIRUS

B.1.195 strain Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic

Lewis F. Buss^{1*}, Carlos A. Prete Jr.^{2*}, Claudia M. M. Abraham^{3*}, Alfredo Mendrone Jr.^{4,5*}, Tassila Salomoni^{6,7*}, Cesar de Almeida-Neto^{8,9*}, Rafael F. O. França⁸, Maria C. Belotti², Maria P. S. S. Carvalho², Allyson G. Costa¹, Myuki A. E. Crispim², Suzete C. Ferreira^{4,5}, Nelson A. Fraijó¹, Susie Gurzenda⁹, Charles Whittaker¹⁰, Leonardo T. Kamaura¹¹, Pedro L. Takecian¹¹, Pedro da Silva Peixoto¹¹, Marcio K. Oikawa¹², Anna S. Nishiyama^{1,5}, Vanderson Rocha^{4,5}, Nanci A. Salles⁴, Andreza Aruska de Souza Santos¹³, Martirene A. da Silva³, Brian Custer^{14,15}, Kris V. Parag¹⁶, Manoel Barral-Netto¹⁷, Moritz U. G. Kraemer¹⁸, Rafael H. M. Pereira¹⁹, Oliver G. Pybus¹⁸, Michael P. Busch^{4,15}, Márcia C. Castro⁹, Christopher Dye¹⁹, Vitor H. Nascimento², Nuno R. Faria^{1,16,18}†, Ester C. Sabino¹‡



76% of the population infected

Herd-immunity?

21

Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates
→ Counterfactual

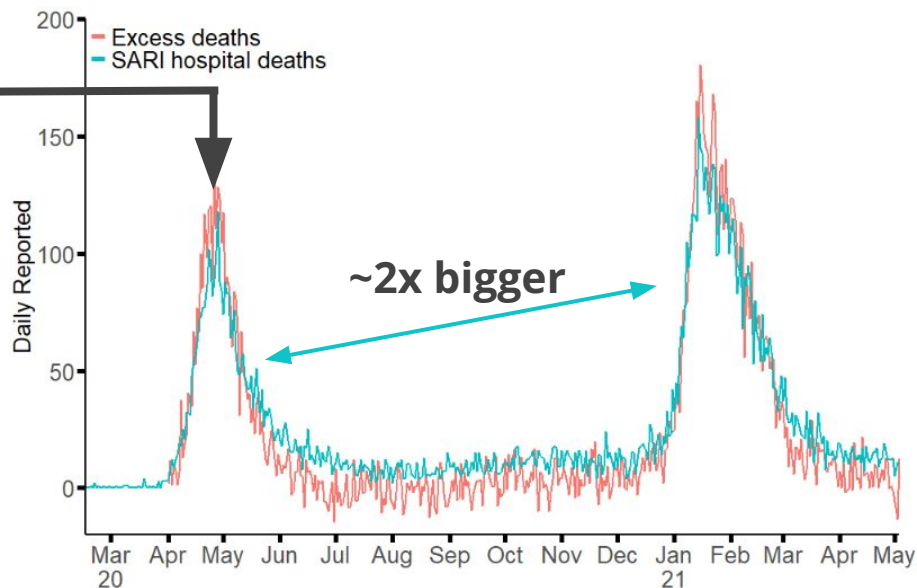


The case of Manaus: devastating initial wave of COVID-19 deaths followed by an even larger secondary wave



B.1.195 strain

Gamma P.1 strain



Manaus → Previous models → Available data → Experimental data → Full model → Fit → Parameter estimates → Counterfactual



The case of Manaus: devastating initial wave of COVID-19 deaths followed by an even larger secondary wave

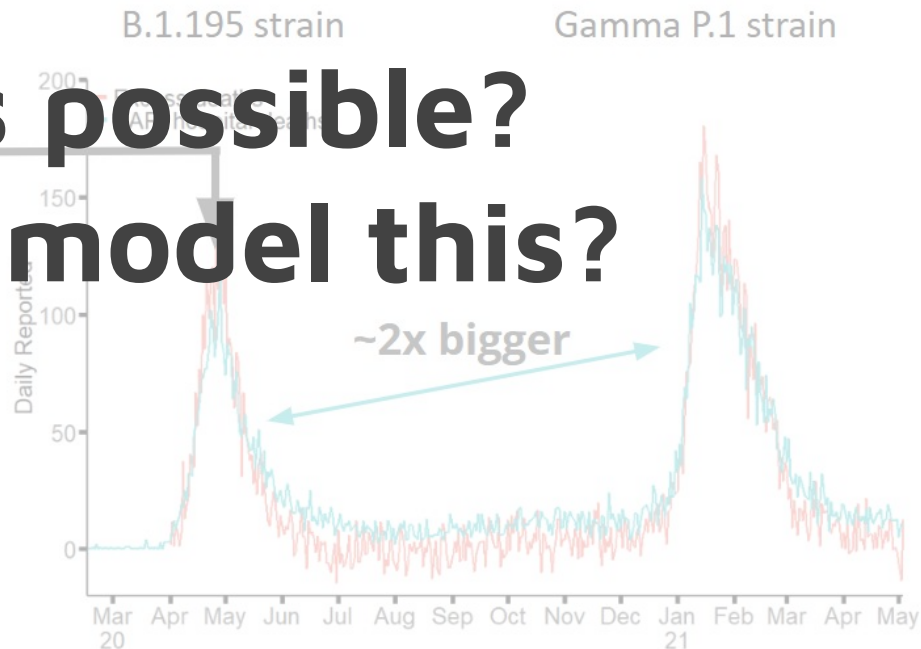
from
2020

The
Guardian

How is this possible? How can we model this?



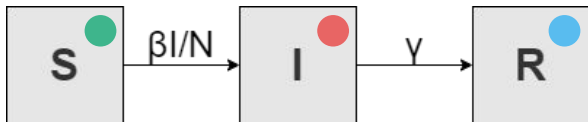
'Utter disaster': Manaus fills mass graves as Covid-19 hits the Amazon





Classic epidemiological models

Simple SIR model



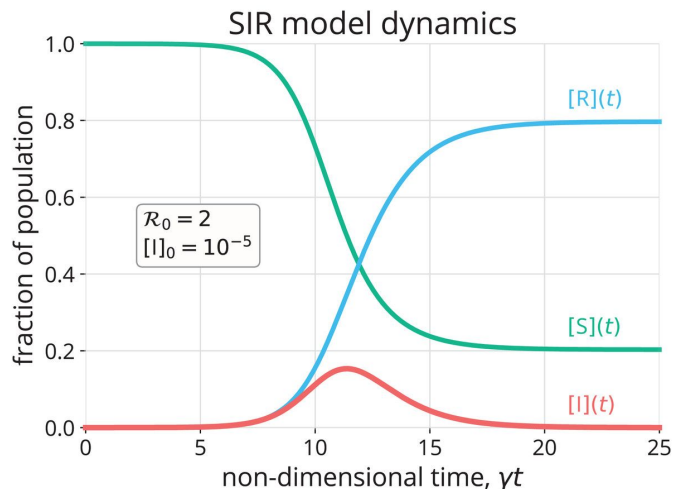
Three states:

- Susceptible
- Infected
- Recovered

$$N = S + I + R$$

Transition rates:

- Force of infection, $\beta I/N$
- Removal rate, γ



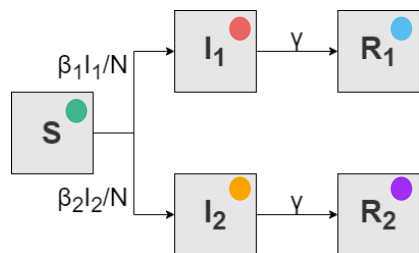
Ordinary Differential Equations (ODE's)

$$\begin{aligned} \frac{dS}{dt} &= -\beta \frac{I}{N} S \\ \frac{dI}{dt} &= \beta \frac{I}{N} S - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned}$$



Classic epidemiological models: multiple waves

Simple two strain model

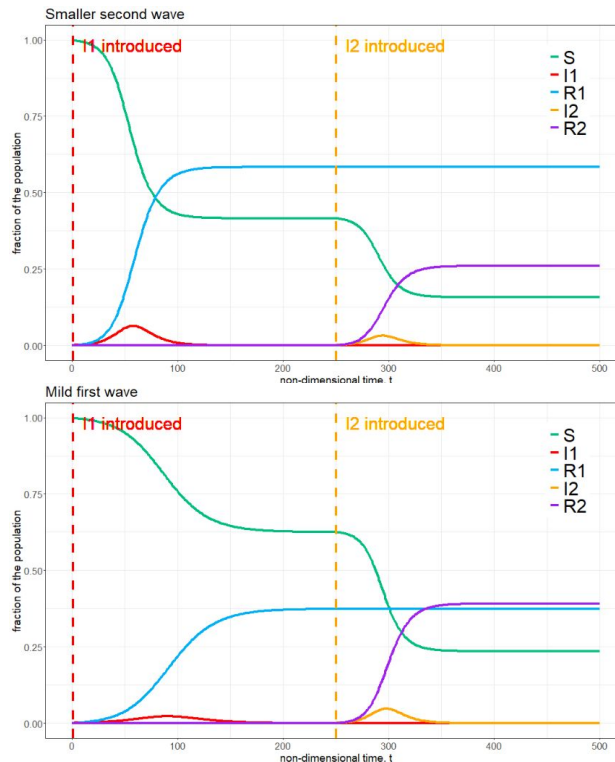


$$R_{0,1} < R_{0,2}$$

When sequentially introducing strains:

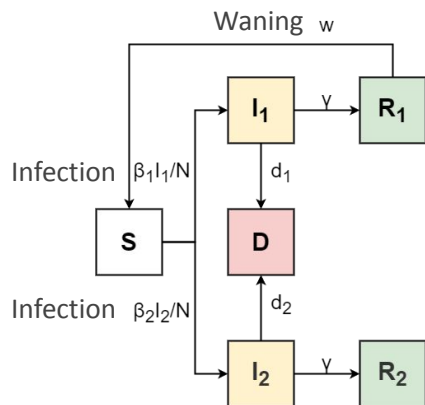
- Secondary waves are generally smaller
- Larger secondary waves are preceded by milder first waves

How can we generate large secondary waves following large primary waves?



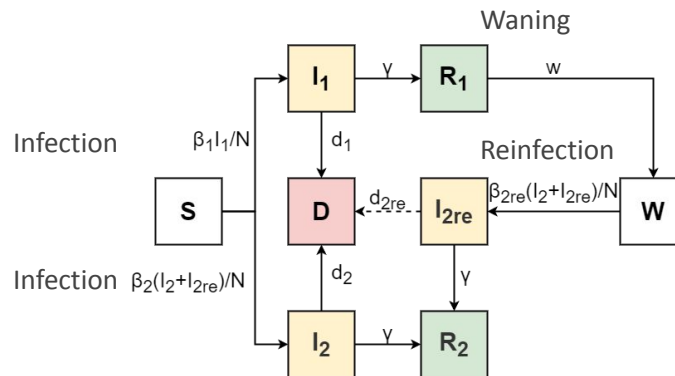


Idea: waned and reinfected individuals may have (very) different properties



SIRS-like model (He et al., 2023)


- Become naive after waning ($R_1 \rightarrow S$)
- Reinfections behave equally to primary infections



Our model (pilot version)

- Second susceptible class (**W**)
- Reinfection class (**I_{2re}**)
- Waning precedes reinfection:
 - Waning ($R \rightarrow W$)
 - Reinfection ($W_1 \rightarrow I_{2re}$)

**To what data can we fit our
model?**

A decorative pattern at the bottom of the slide consisting of a series of overlapping, semi-transparent circles in various shades of teal and light blue, arranged in a horizontal line.

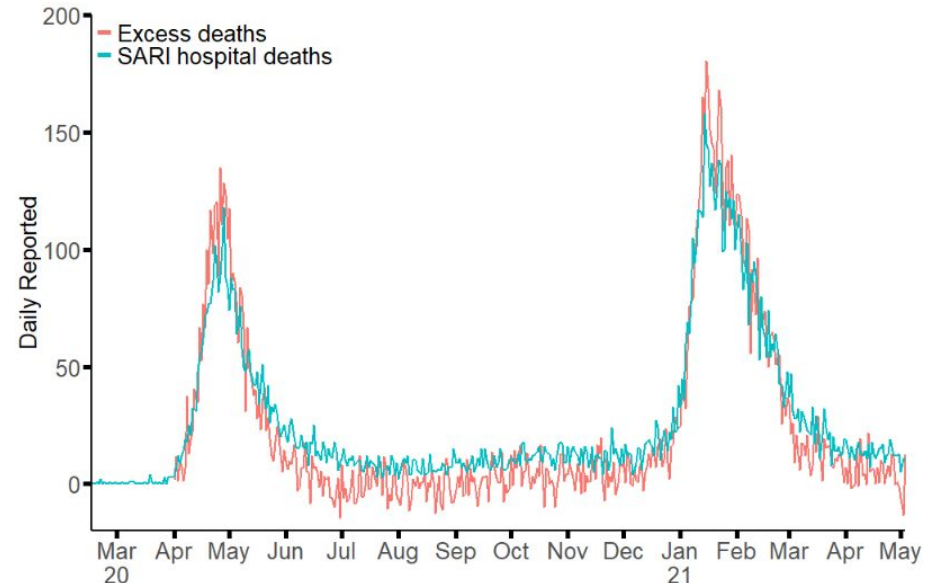
Manaus → Epidemiological modeling → **Available data** → Full model → Fit → Parameter estimates
→ Counterfactual



Available data: disease burden

Disease burden:

- Nelson, 2021:
 - Reported burials & cremations
 - Excess deaths
- SIVEP-Gripe database:
 - Severe acute respiratory infection (SARI) admissions
 - Reporting mandatory in Brazil
 - SARI deaths:
 - Confirmed COVID-19 deaths
 - Excluding known other etiologies



Manaus → Epidemiological modeling → **Available data** → Full model → Fit → Parameter estimates
→ Counterfactual

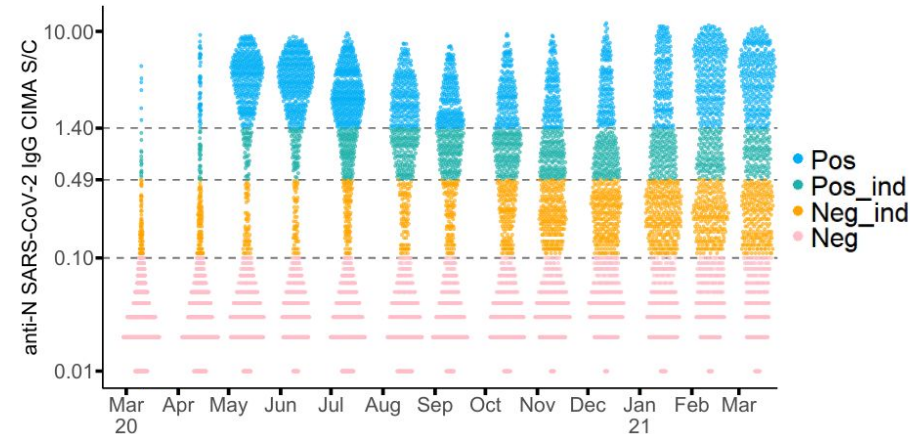


Available data: Antibody levels ...

Prete et al., 2022

Antibody data:

- HEMOAM Blood bank in Manaus
- Serial cross-sectional anti-nucleocapsid (anti-N) antibody levels



Manaus → Epidemiological modeling → **Available data** → Full model → Fit → Parameter estimates
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Available data: Antibody levels and seroprevalence

Prete et al., 2022

Antibody data:

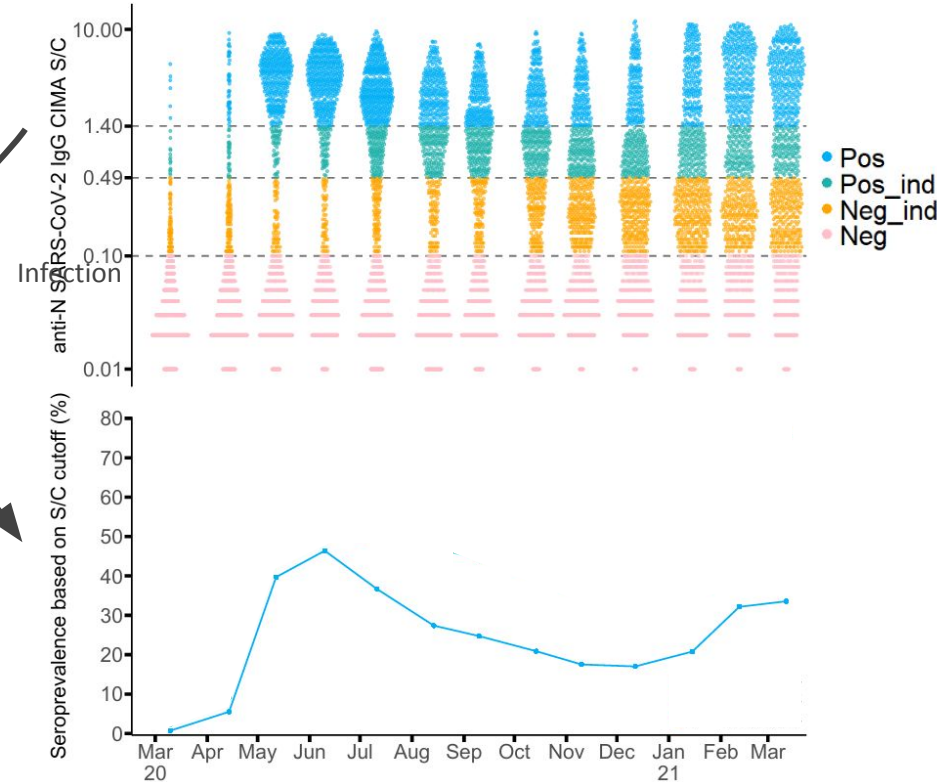
- HEMOAM Blood bank in Manaus
- Serial cross-sectional anti-nucleocapsid (anti-N) antibody levels

Seroprevalence:

- Fraction of sampled individuals with positive antibody results
- Proxy of fraction Recovered

Pos/total

R



Manaus → Epidemiological modeling → **Available data** → Full model → Fit → Parameter estimates
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Available data: Antibody levels and seroprevalence

Prete et al., 2022

Antibody data:

- HEMOAM Blood bank in Manaus
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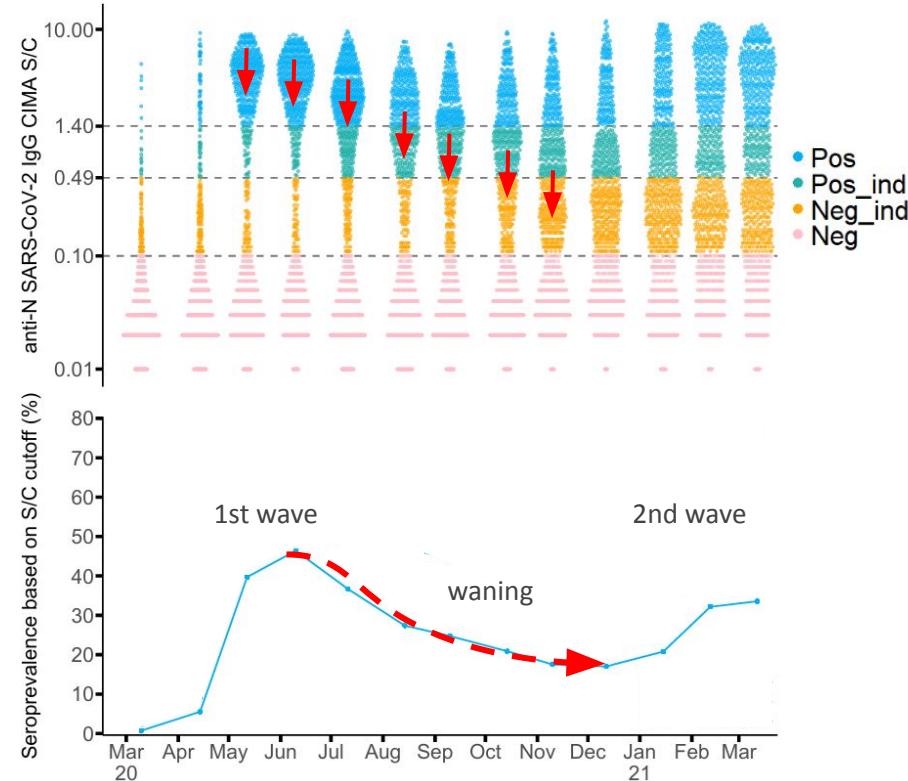
Seroprevalence:

- Fraction of sampled individuals with positive antibody results
- Proxy of fraction Recovered

R

Declining antibody levels indicative could indicate waning immunity

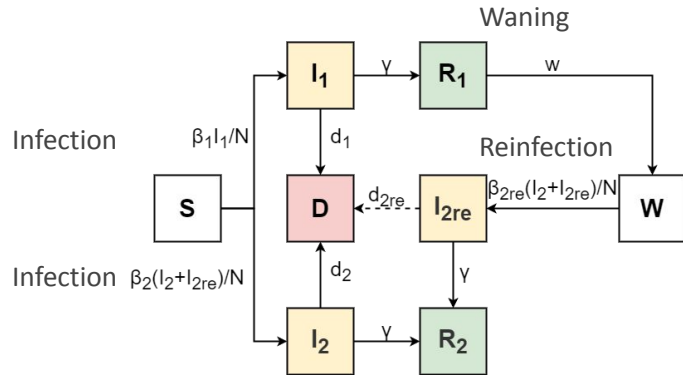
Pos/total



Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates
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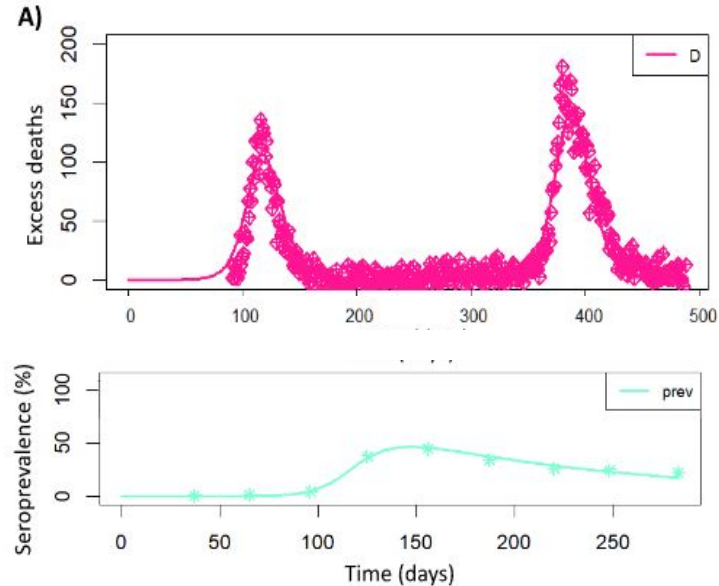


Our model: fits excess deaths and seroprevalence data better than SIRS-like models



Our model (pilot version)

- Second susceptible class (W)
- Reinfection class (I_{2re})
- Waning precedes reinfection:
 - Waning (R₁ → W)
 - Reinfection (W → I_{2re})

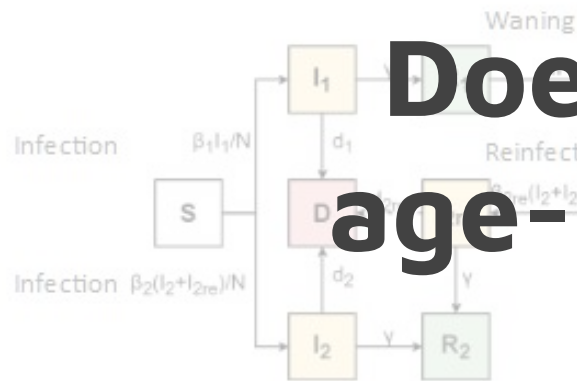


Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates → Counterfactual



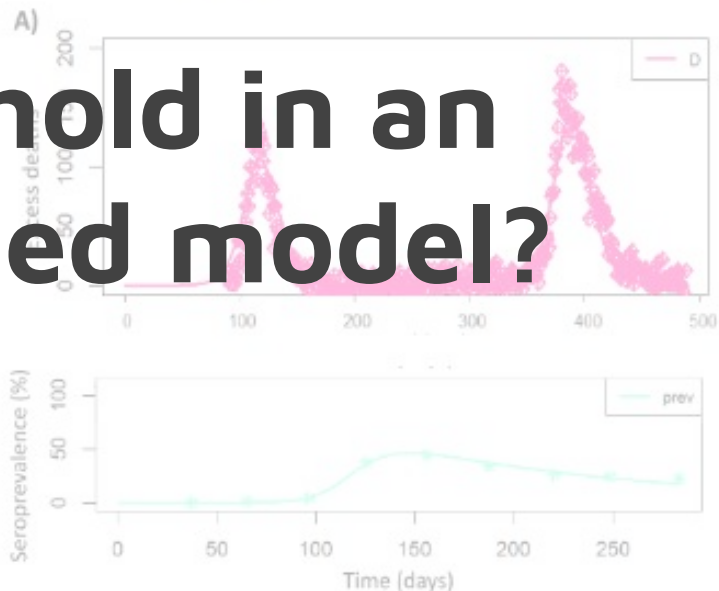
Our model: fits excess deaths and seroprevalence data better than SIRS-like models

Does this hold in an age-stratified model?



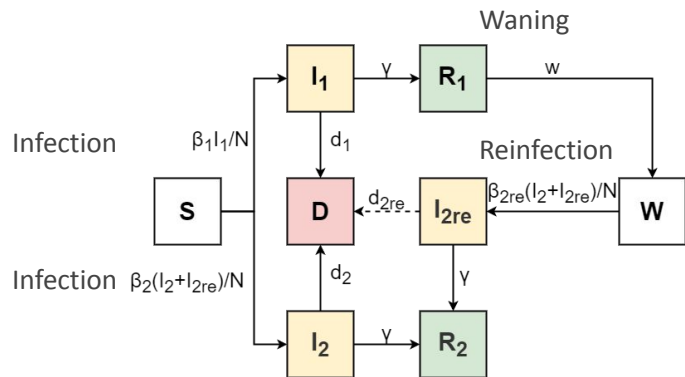
Our model (pilot version)

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- Waning precedes reinfection:
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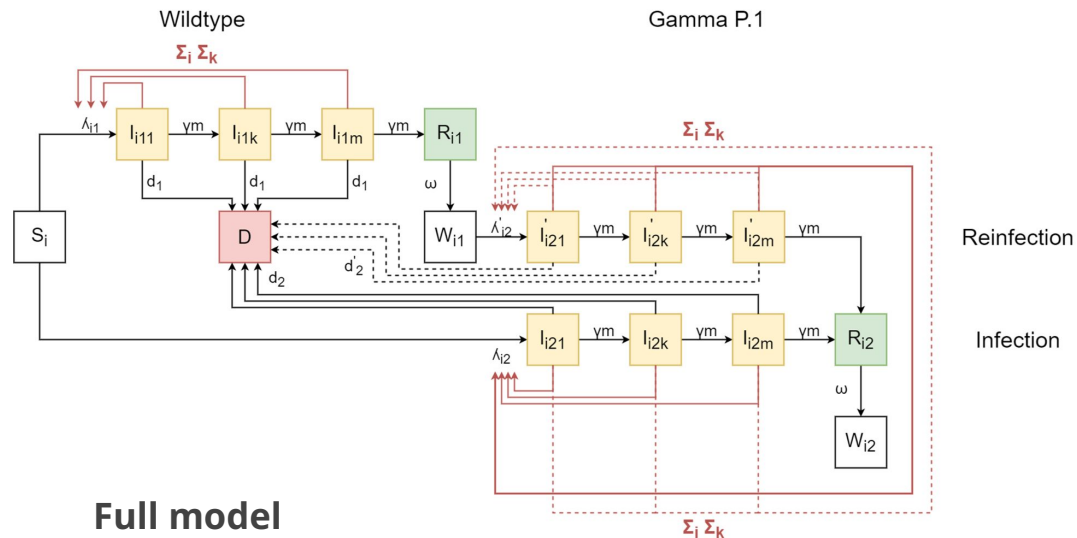


Our model: waning immunity preceding reinfection



Our model (pilot version)

- Second susceptible class (**W**)
- Reinfection class (**I_{2re}**)
- Waning precedes reinfection:
 - Waning (**R₁ → W**)
 - Reinfection (**W₁ → I_{2re}**)



Full model

- + Stratified by age (8 age groups)
- + Erlang-distributed infectious period (l infection stages)
- + Contact matrix

Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates
→ Counterfactual

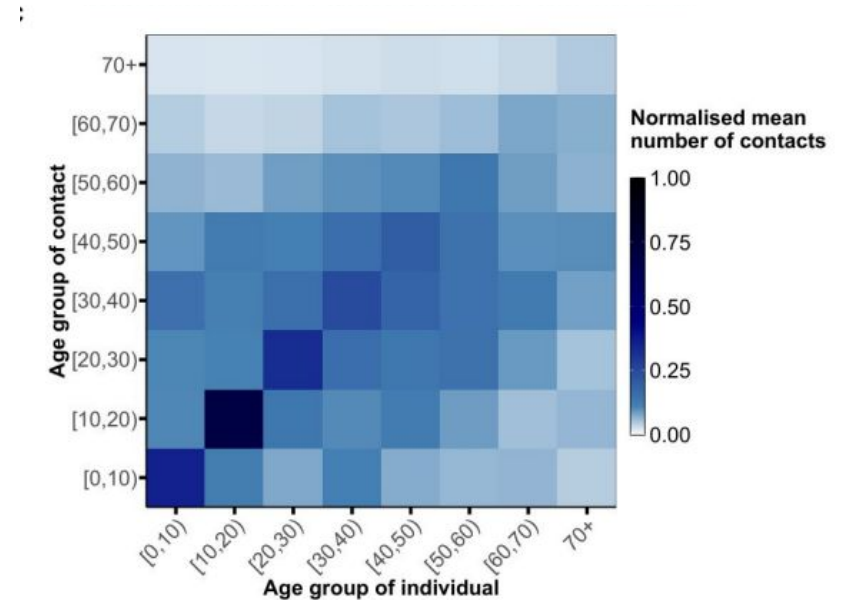


Our model: including demography with age stratification, contact-matrices and age-dependent infection fatality rate

Age-specific contact matrix with entries $\{c_{ij}\}$

Describing contact pattern from a person in group j to persons in age group i

Older persons have fewer contacts than younger persons (loneliness epidemic among older adults)

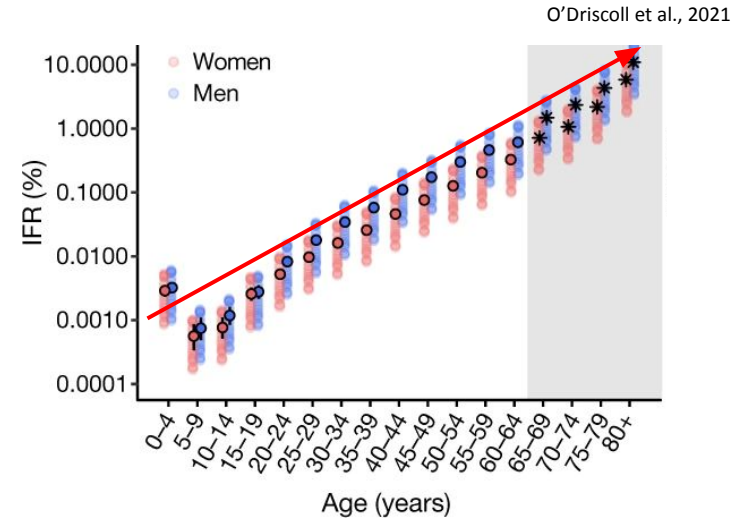


Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates
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Our model: including demography with age stratification, contact-matrices and age-dependent infection fatality rate

Infection fatality rate (IFR) increases log-linearly with age ↑



Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates
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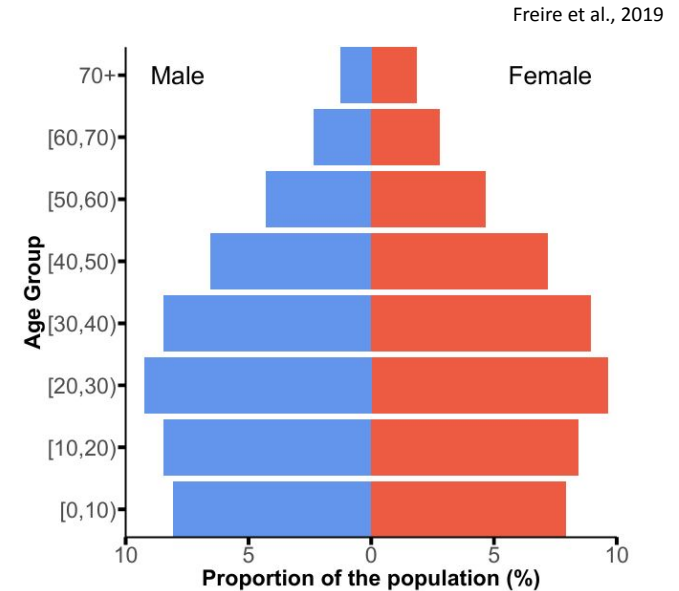


Our model: including demography with age stratification, contact-matrices and age-dependent infection fatality rate

Infection fatality rate (IFR) increases log-linearly with age

~90% IFR variation across geographical locations due to age composition (Levin et al. 2020)

- 82.8% is under 50



Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates
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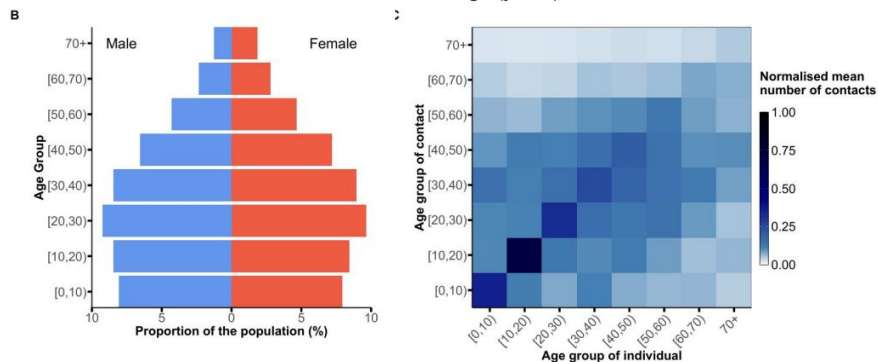
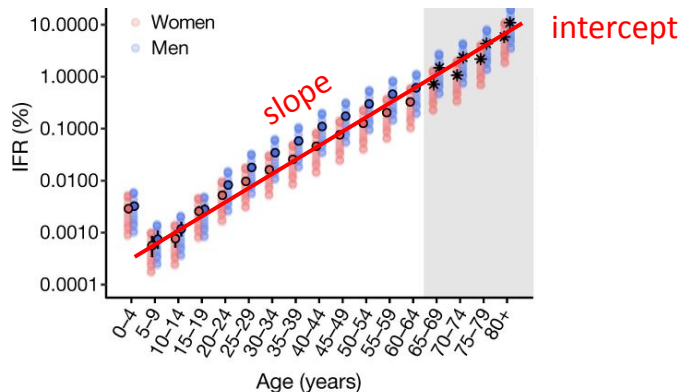


Our model: estimate 12 parameters

Fit model to seroprevalence and hospital deaths data, estimate:

- Infectious period: $1/\gamma$
- Infection rates: $\beta_1, \beta_2, \beta'_2$
- Waning time, $1/\omega$
- Intercepts and slopes of both IFR
 - Scalar for reduction of IFR

Incorporates the population structure for the starting state and uses a fixed age-dependent contact rate



Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates
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Our model: fit the data with MCMC methods using Stan

Coded using C++

Bayesian inference using Markov chain Monte Carlo (MCMC) with Hamiltonian Monte Carlo (HMC) sampling

- Similar to gradient descent

Relies on assumptions about how observations (data) are generated




Stan

Carpenter et al., 2017

$$\# \text{daily deaths} \sim \text{Poisson} \left(d_{i1} \sum_{k=1}^m I_{i1k} + d_{i2} \sum_{k=1}^m I_{i2k} + d'_{i1} \sum_{k=1}^m I'_{i2k} \right)$$

$$\# \text{ daily positive samples} \sim \text{Binom} \left(Y_i, \frac{R_{i1}(\tau) + R_{i2}(\tau)}{N_i(\tau)} \right), \quad i \in [2, 7]$$

**How well does our full
model describe the
available data?**

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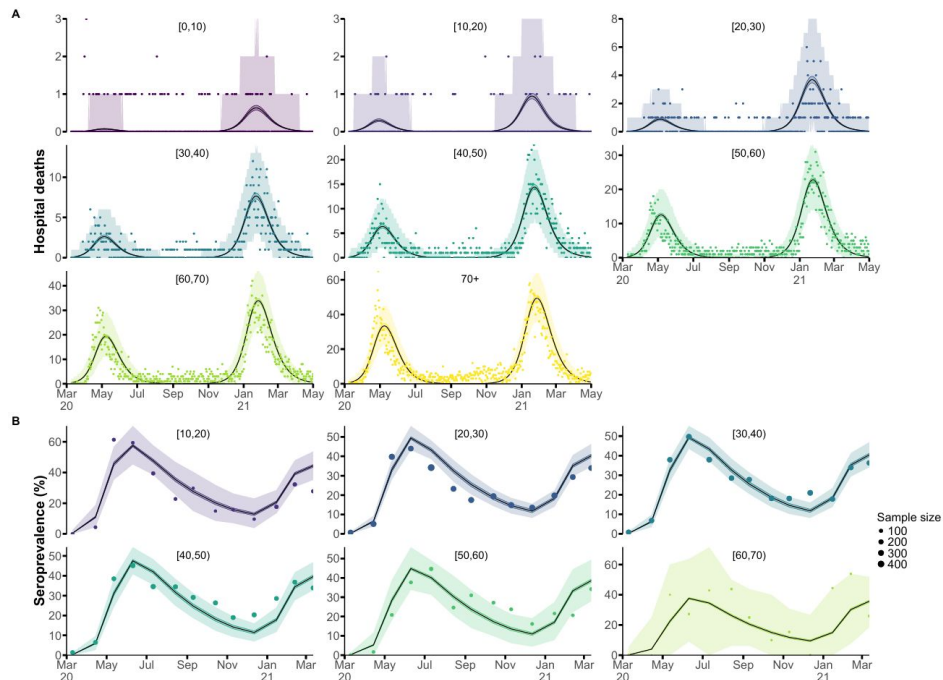
Manaus → Epidemiological modeling → Available data → Full model → **Fit** → Parameter estimates
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Result: model fits death and seroprevalence very well

Our model can describe both waves:

- A.** Mortality data
 - all 8 age groups
- B.** Seroprevalence data
 - 6 available age groups



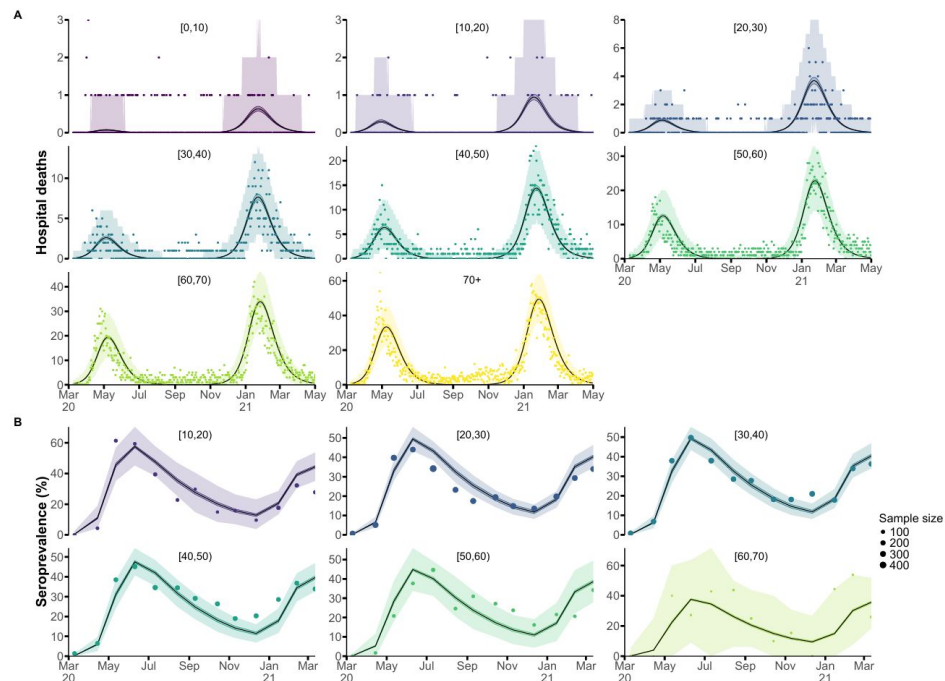
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Our model vs. SIRS-like: SIRS-like fails to fit the seroprevalence of the second wave

SIRS-like:

- A.** Fits mortality data equally well
- B.** Fails to fit seroprevalence data of the second wave.



Manaus → Epidemiological modeling → Available data → Full model → **Fit** → Parameter estimates
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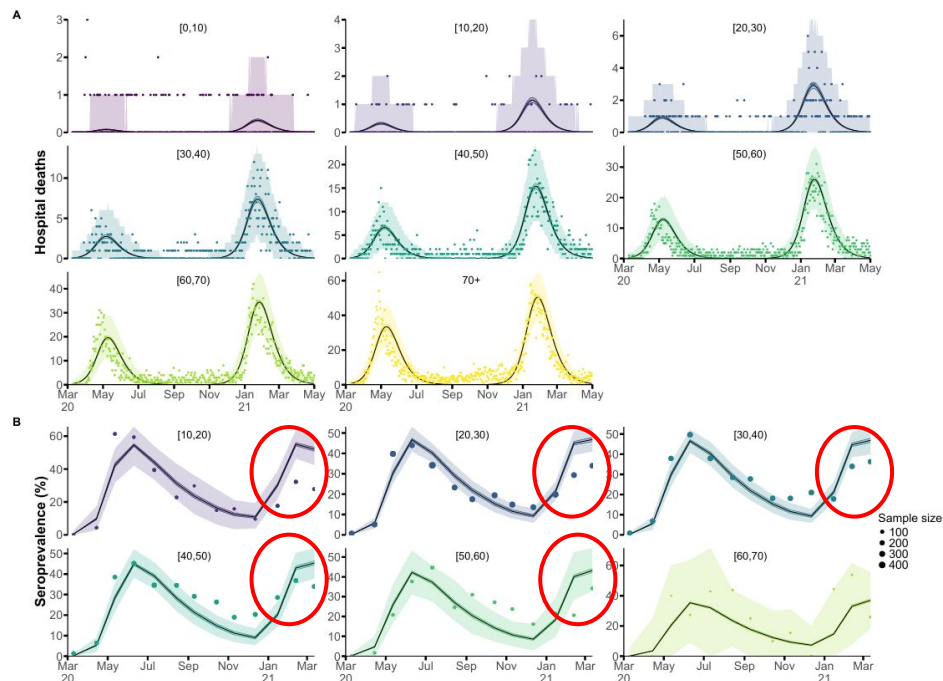


Our model vs. SIRS-like: SIRS-like fails to fit the seroprevalence of the second wave

SIRS-like:

- A.** Fits mortality data equally well
- B.** Fails to fit seroprevalence data of the second wave..

Seroprevalence is important as different assumptions about immunity can result in the similar mortality fits.

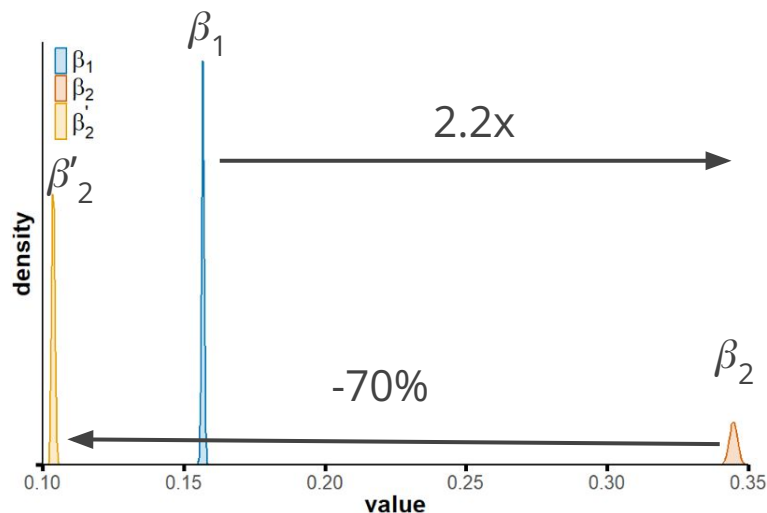


Manaus → Epidemiological modeling → Available data → Full model → Fit → **Parameter estimates**
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Result: Gamma P.1 more transmissible,
previous infection reduces susceptibility

- Gamma P.1 ~2.2 times more transmissible than the
- First strain
- Cross-immunity reduces Gamma P.1 susceptibility by 70%

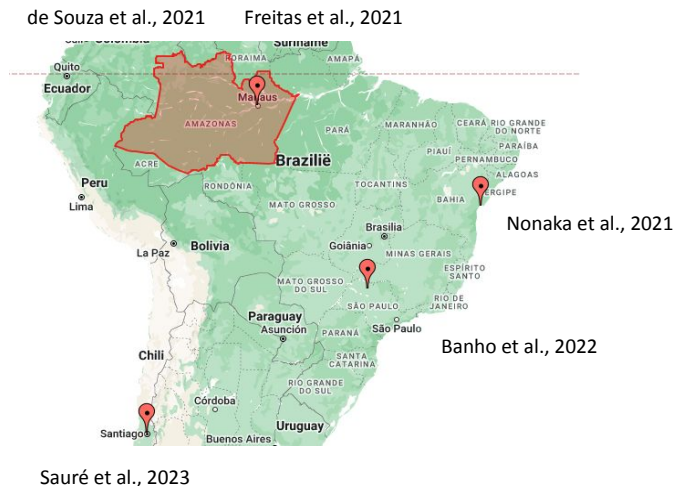
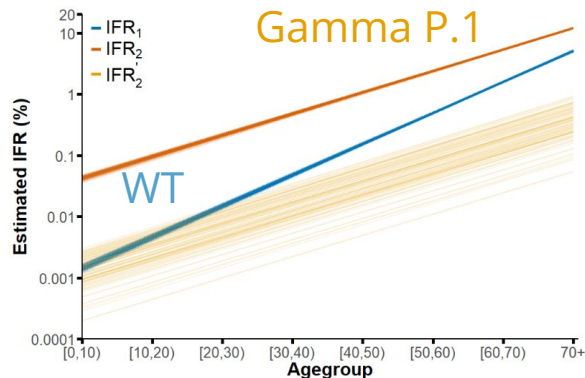




Result: Gamma P.1 has increased mortality rates, notably in younger age groups

- First strain IFR:
 - 0.0014% [0,10)
 - 5.1% 70+

- Second strain IFR: (Gamma P.1)
 - 0.037% [0,10)
 - 12.1% 70+
- Notably affects younger age groups





Result: Previous immunity reduces IFR by **100-fold**

● First strain IFR:

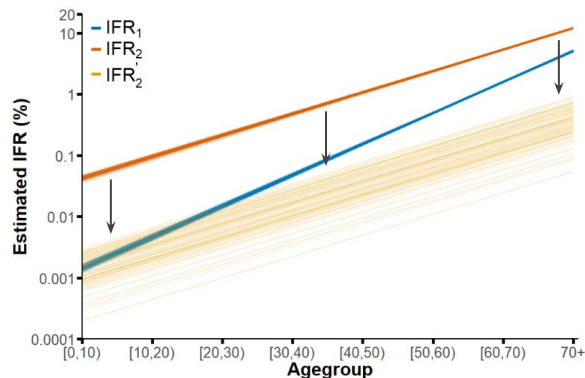
- 0.0014% [0,10)
- 5.1% 70+

● Second strain IFR: (Gamma P.1)

- 0.037% [0,10)
- 12.1% 70+

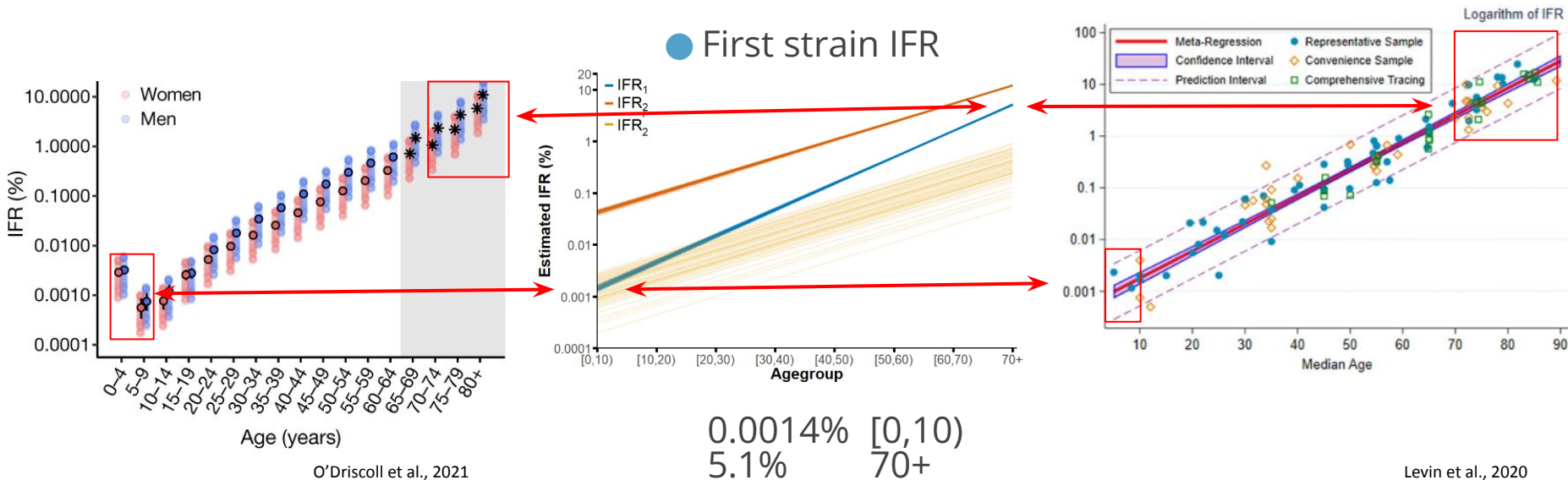
Notably affects younger age groups

● Previous immunity reduces Gamma P.1 IFR by **93.4 to 99.7%**



Meta-analysis: 90.2% (69.7-97.5%)
(COVID-19 Forecasting Team, 2023)


Result: First strain IFR estimates in line with meta-analysis IFR estimates



O'Driscoll et al., 2021

Levin et al., 2020

**How prior immunity
impacted the deadly second
wave of SARS-CoV-2 in
Manaus**

A decorative pattern at the bottom of the slide consisting of numerous vertical bars of varying heights and shades of teal, creating a stylized bar chart or data visualization effect.



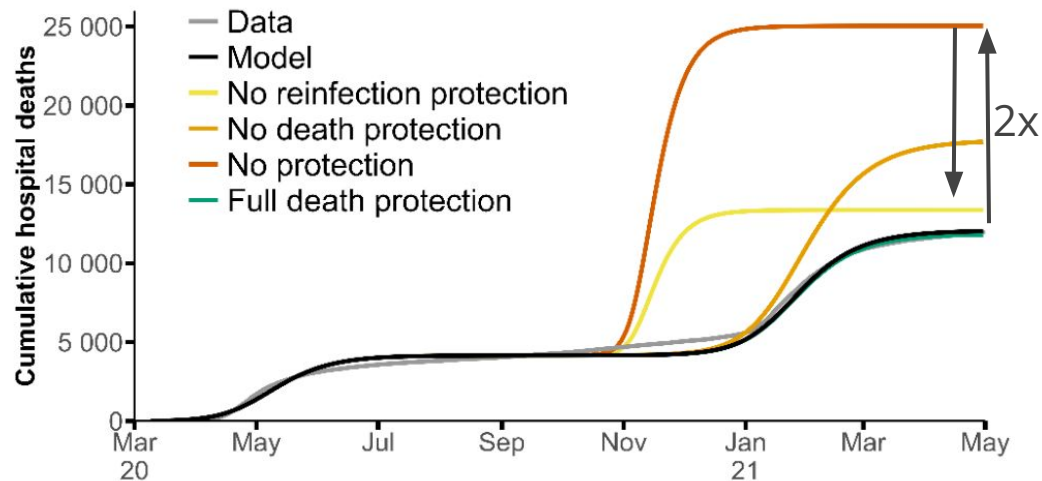
Counterfactual: First wave protected against an even deadlier second wave by reducing the infect

What if previous immunity does not provide protection against reinfection and/or deaths

Three scenarios:

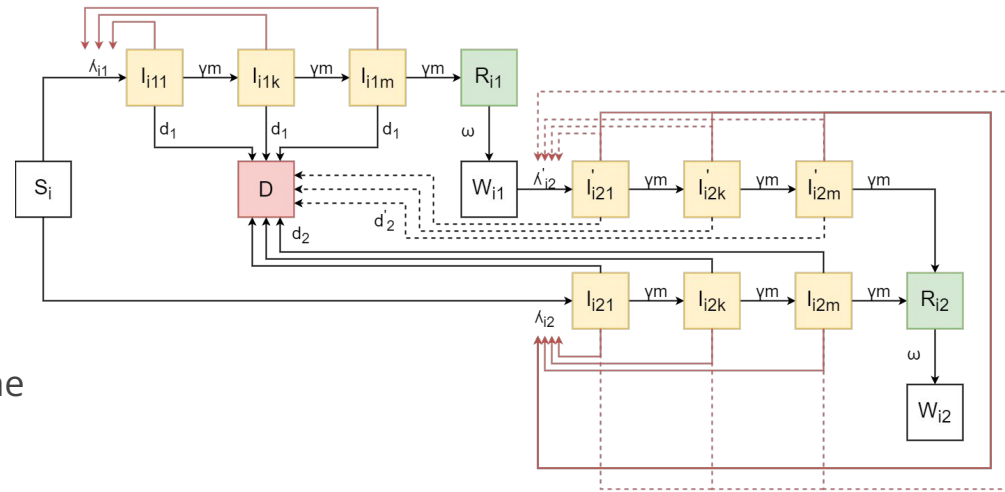
- No protection
- No protection against death
- No protection against reinfection

Without any protection, the cumulative number of deaths would have **doubled**, with about **13 000** additional deaths.



Conclusions

- Adding waning compartment greatly improves the fit:
 - mortality data
 - seroprevalence data
- Model reproduces IFR1 estimates in line in line with literature:
- Gamma P.1 variant:
 - more infectious
 - higher infection fatality rate,
 - affected younger age groups
- Long lasting protective cross-immunity mitigated an even deadlier second wave by greatly reducing the infection fatality rate
 - Even if cross-immunity does not prevent reinfection itself



Stan

Carpenter et al., 2017

Special thanks to:



Prof. dr. R.J. (Rob J.) de Boer



**Utrecht
University**



Dr. M. (Michiel) van Boven



UMC Utrecht



Dr. C.H. (Christiaan H.) van Dorp



Questions?





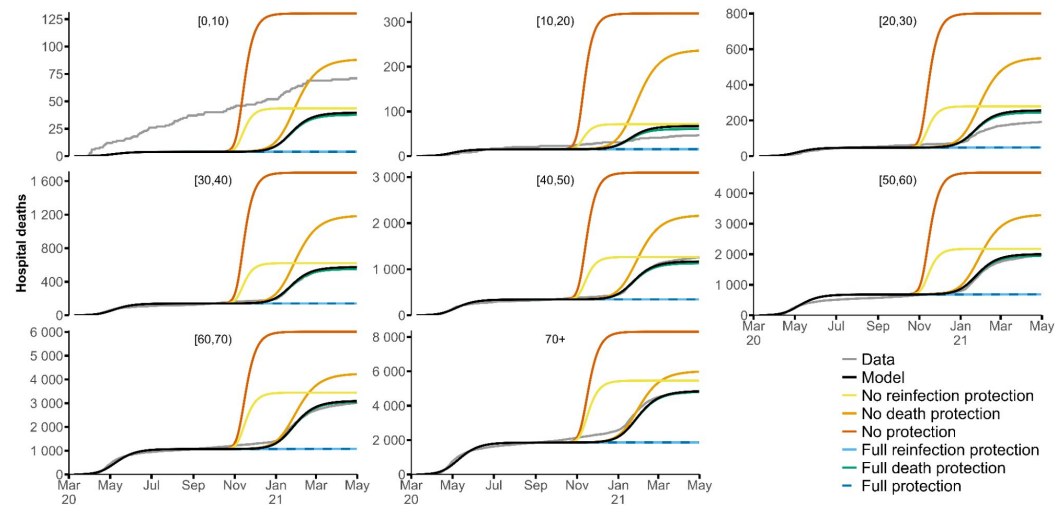
Counterfactual: First wave protected against an even deadlier second wave

What if previous immunity does not provide protection against reinfection and/or deaths

Three scenarios:

- No protection
- No protection against death
- No protection against reinfection

Increased deaths are not equally distributed over the age groups





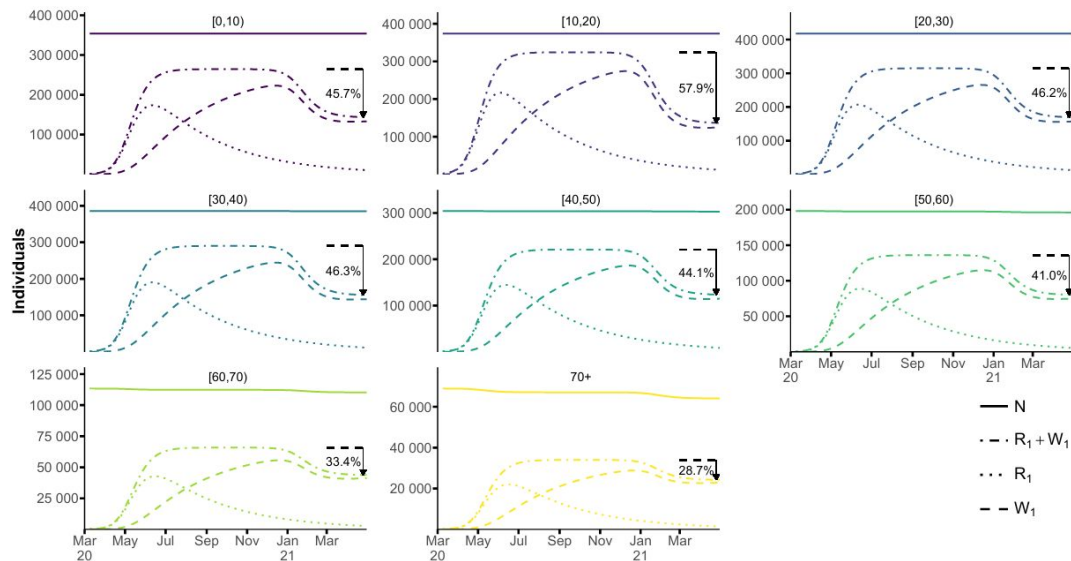
Result: High attack rate after the first wave

First wave attack rate:

- Model: 74.7%
- Buss et al., 2021: 76.0%

Attack rate depends on age group

After first wave: sizeable number of susceptible individuals in older age group





Result: Reinfection is common and a driving force in the epidemic of Manaus

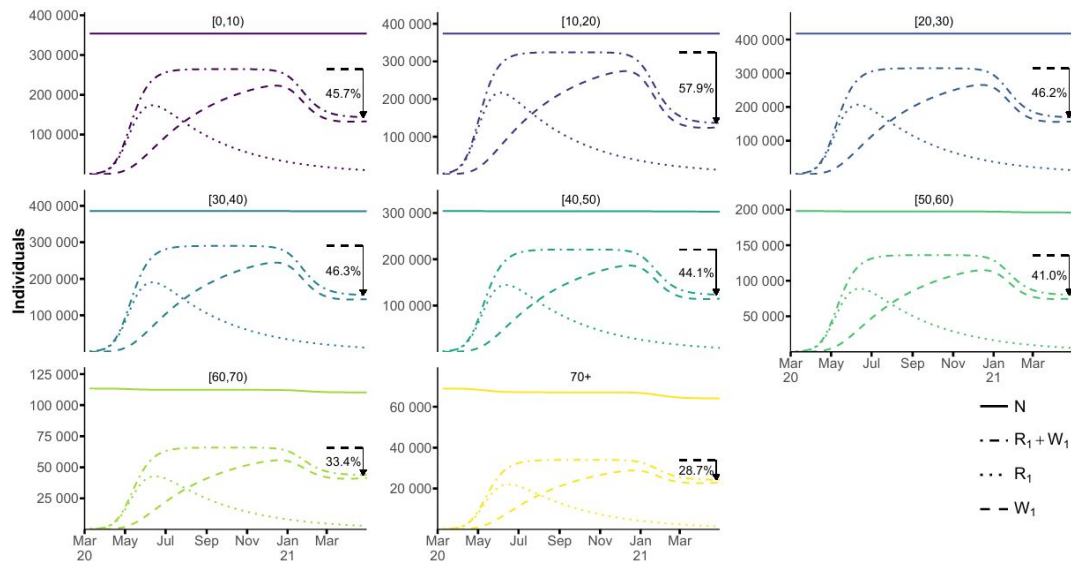
Reinfection levels depend on age group

Gamma P.1 reinfection:

- Model: 46.9%
- Prete et al., 2021: 14-50%

Reinfections need not be symptomatic:

- Asymptomatic individuals have similar viral loads
- Gamma P.1 reinfections display viral loads comparable to primary infections (Naveca et al., 2023)

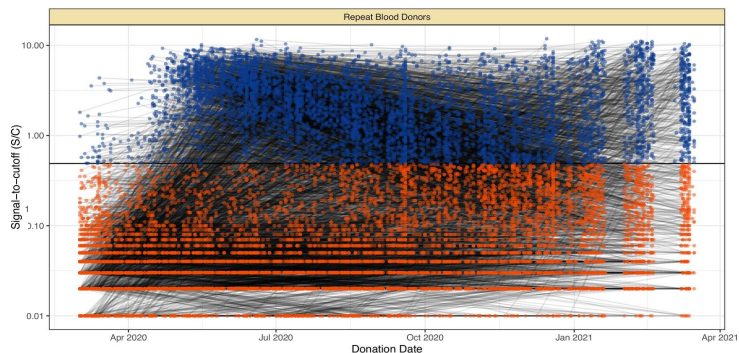


Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates → Counterfactual



Experimental data: Reinfection results in v-shaped antibody curves

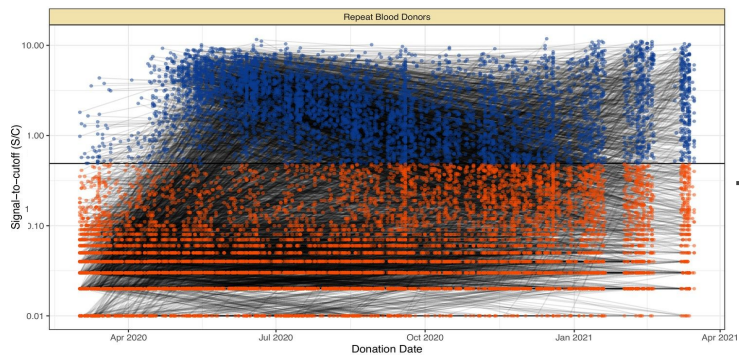
Longitudinal signal-to-cutoff (S/C) antibody levels (Prete et al. 2022a)



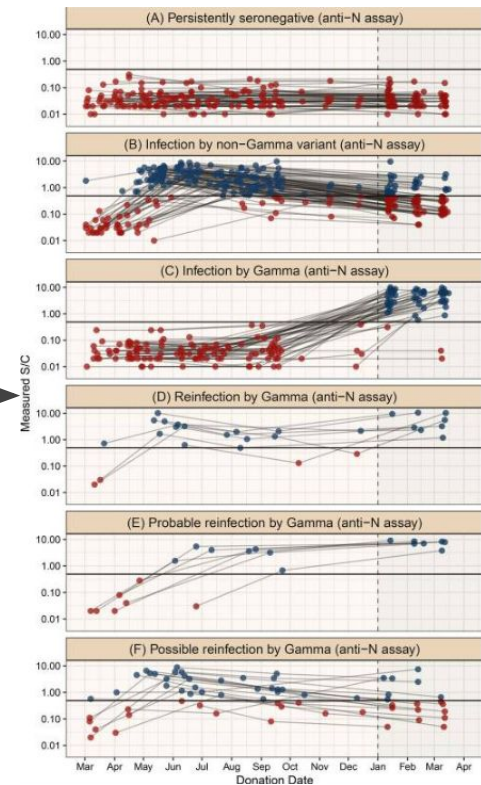
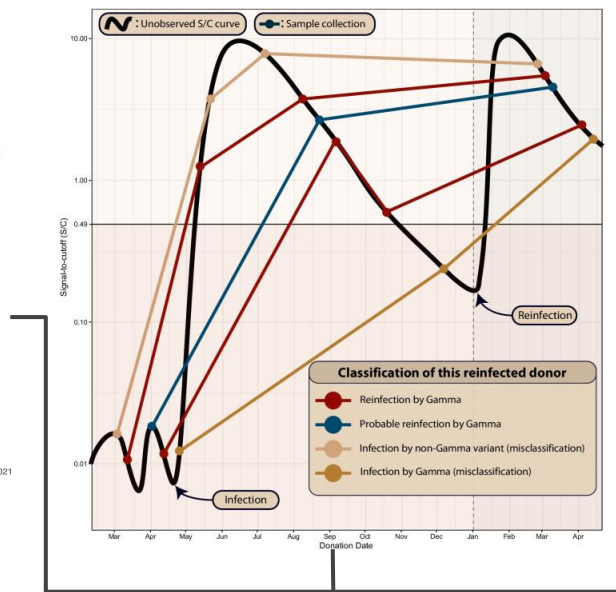
Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates → Counterfactual

Experimental data: Reinfection results in v-shaped antibody curves

Longitudinal signal-to-cutoff (S/C) antibody levels (Prete et al. 2022a)



Repeat blood donor classification (Prete et al. 2022b)





Experimental data: cellular response remains strong and protects against severe outcomes

92% still positive for SARS-CoV-2 memory **CD4⁺ T** cells up to 8 months

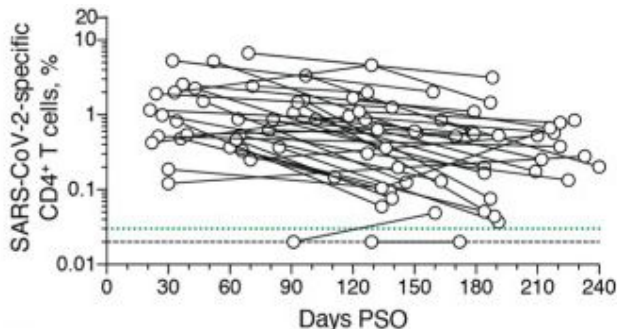
(Dan et al., 2021)

Similarly, **CD8⁺ T** cell responses remain robust 8 months after infection (Dan et al., 2021)

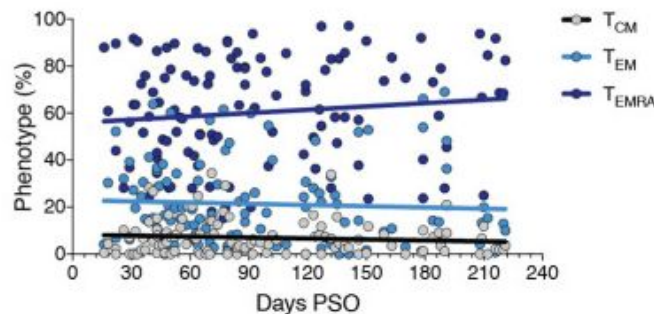
- **CD8⁺ T_{EMRA}** cells associated with protection against severe disease in humans increase in proportion

In ~45% with CD4⁺ and CD8⁺ T cell responses, antibody levels decline to pre-pandemic levels in 8 months (Vo et al., 2022)

Longitudinal CD4⁺ T-cell analysis with paired samples



Cross-sectional CD8⁺ T-cell phenotype (%)



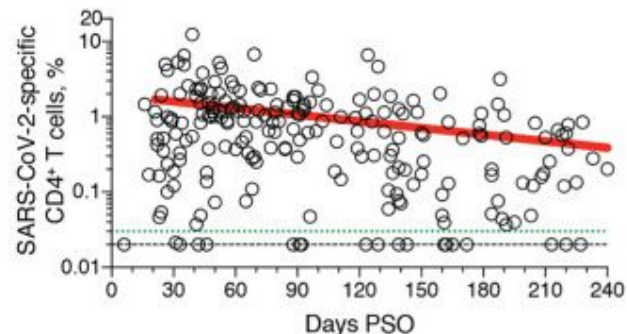


Experimental data: cellular response remains strong and protects against severe outcomes

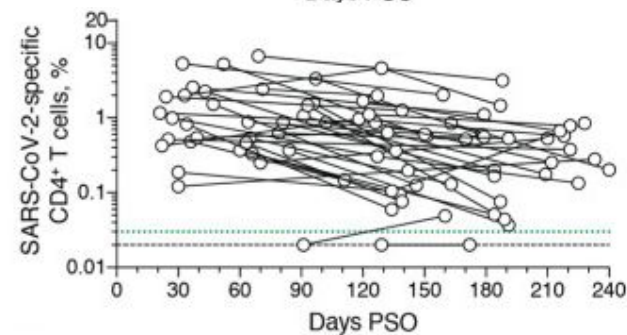
SARS-CoV-2 memory **CD4⁺ T** cell responses, up to 8 months after infection (Dan et al., 2021)

- half life of 94 days
- 92% still positive at ≥ 6 months post-symptom onset (PSO) for SARS-CoV-2 memory CD4⁺ T cells

Cross-sectional analysis



Longitudinal analysis with paired samples



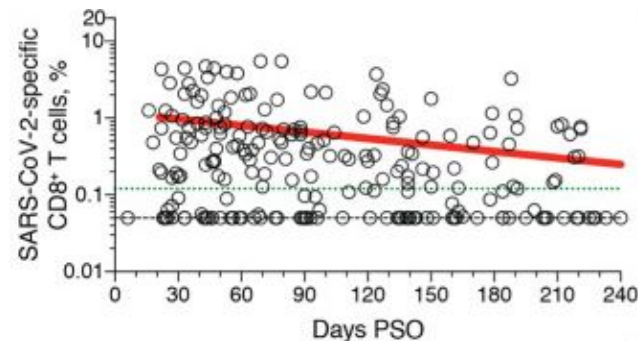


Experimental data: cellular response remains strong and protects against severe outcomes

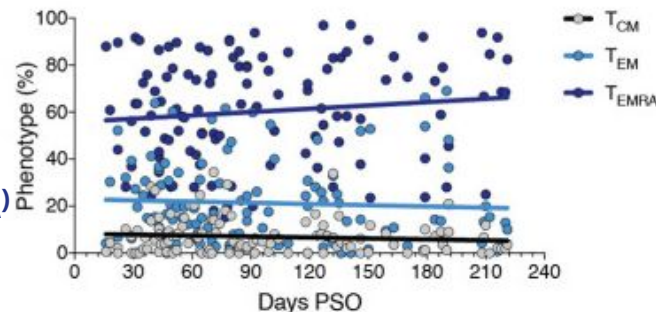
Similarly, **CD8⁺ T** cell responses remain robust 8 months after infection (Dan et al., 2021)

- half life of 125 days
- Proportion T_{EMRA} increases over time
- $CD8^+$ T_{EMRA} cells associated with protection against severe disease in humans

Cross-sectional analysis



Distribution of central memory (T_{CM}), effector memory (T_{EM}), and terminally differentiated effector memory cells (T_{EMRA})



Manaus → Epidemiological modeling → Available data → **Full model** → Fit → Parameter estimates
→ Counterfactual



Our model: including demography with age stratification, contact-matrices and age-dependent infection fatality rate

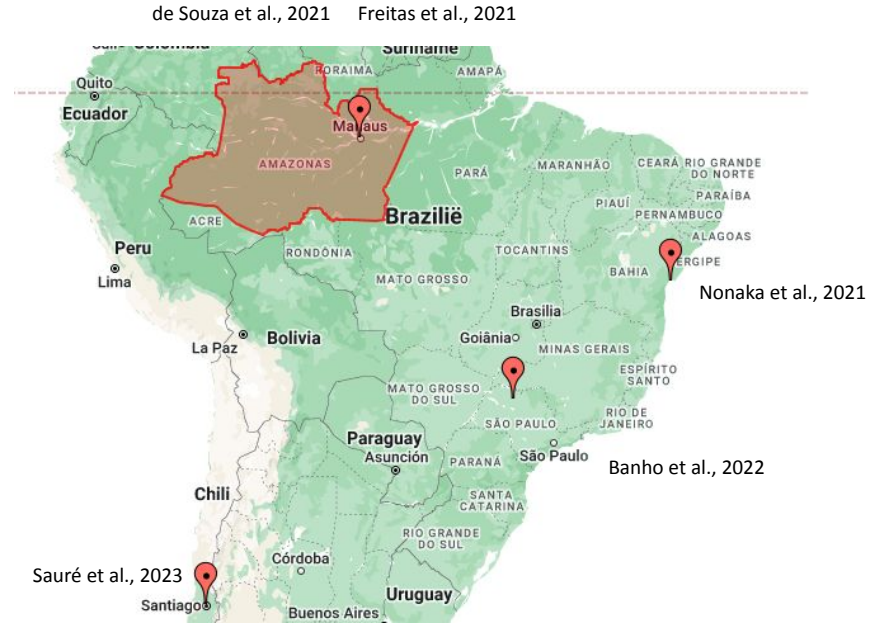
Infection fatality rate (IFR) increases log-linearly with age

~90% IFR variation across geographical locations due to age composition (Levin et al. 2020)

- 82.8% is under 50

Gamma (P.1) variant:

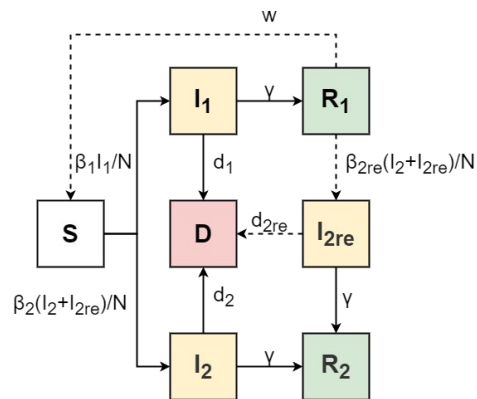
- Dominated second wave
- Emerged in Amazonas
- Higher mortality rate
- **Affected younger age groups**



Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates → Counterfactual



Epidemiological modeling: cannot describe both observed deaths and seroprevalence well

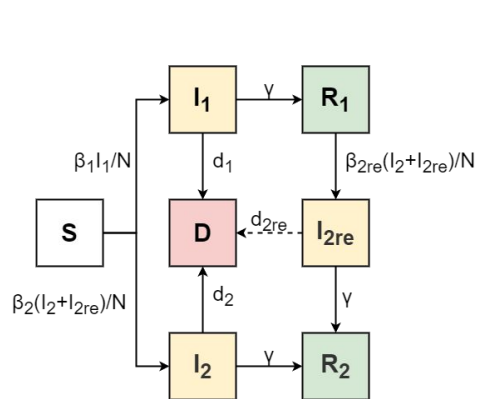


Previous Manaus models

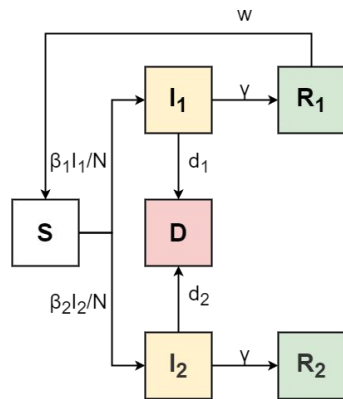
- Waning and/or reinfection independent
- Waning ($R \rightarrow S$)
- Reinfection ($R \rightarrow I$)



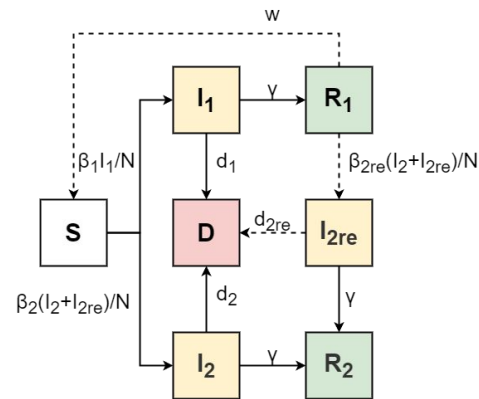
Epidemiological modeling: cannot describe both observed deaths and seroprevalence well



Direct reinfection (R→I_{re})
(Coutinho et al., 2023)



Waning only (R→S)
(He et al., 2023)



Both (R→S) & (R→I)
(Ferrante et al., 2022)

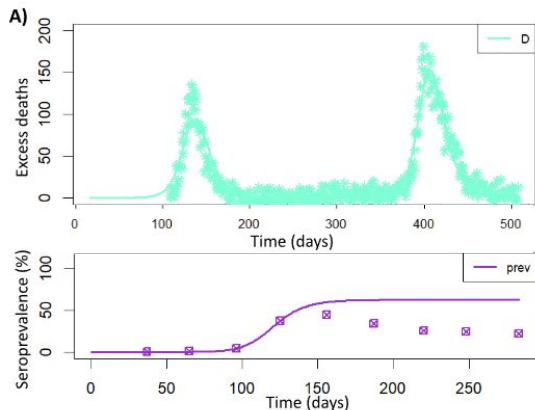
Become naive after waning
Can't track reinfections

Only track direct reinfections

Manaus → Epidemiological modeling → Available data → Full model → Fit → Parameter estimates → Counterfactual



Epidemiological modeling: cannot describe both observed deaths and seroprevalence well

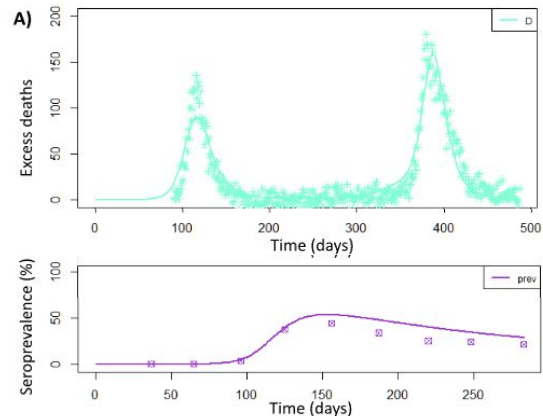


Direct reinfection (R→I_{re})
(Coutinho et al., 2023)

Can't describe decline in seroprevalence

Waning only (R→S)
(He et al., 2023)

Become naive after waning
Can't track reinfections



Both (R→S) & (R→I)
(Ferrante et al., 2022)

Only track direct reinfections
Fit to seroprevalence not great

Manaus → Epidemiological modeling → Available data → Full model → Fit → **Parameter estimates**
→ Counterfactual



Result: Gamma P.1 more transmissible, previous infection reduces susceptibility

- Gamma P.1 ~1.6 times more transmissible than the first strain
- first strain
- Previous immunity reduces Gamma P.1 susceptibility by 70%

