Investigating COVID-19 dynamics with individual-based models

NORDITA

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Pandemic response at NIPH

Situational awareness

- Forecast of epidemiological indicators
- Methods: SEIR models with changepoints SMC-ABC, SMC
- 150+ reports

Scenarios analyses

Scenario analyses

Pharmaceutical interventions

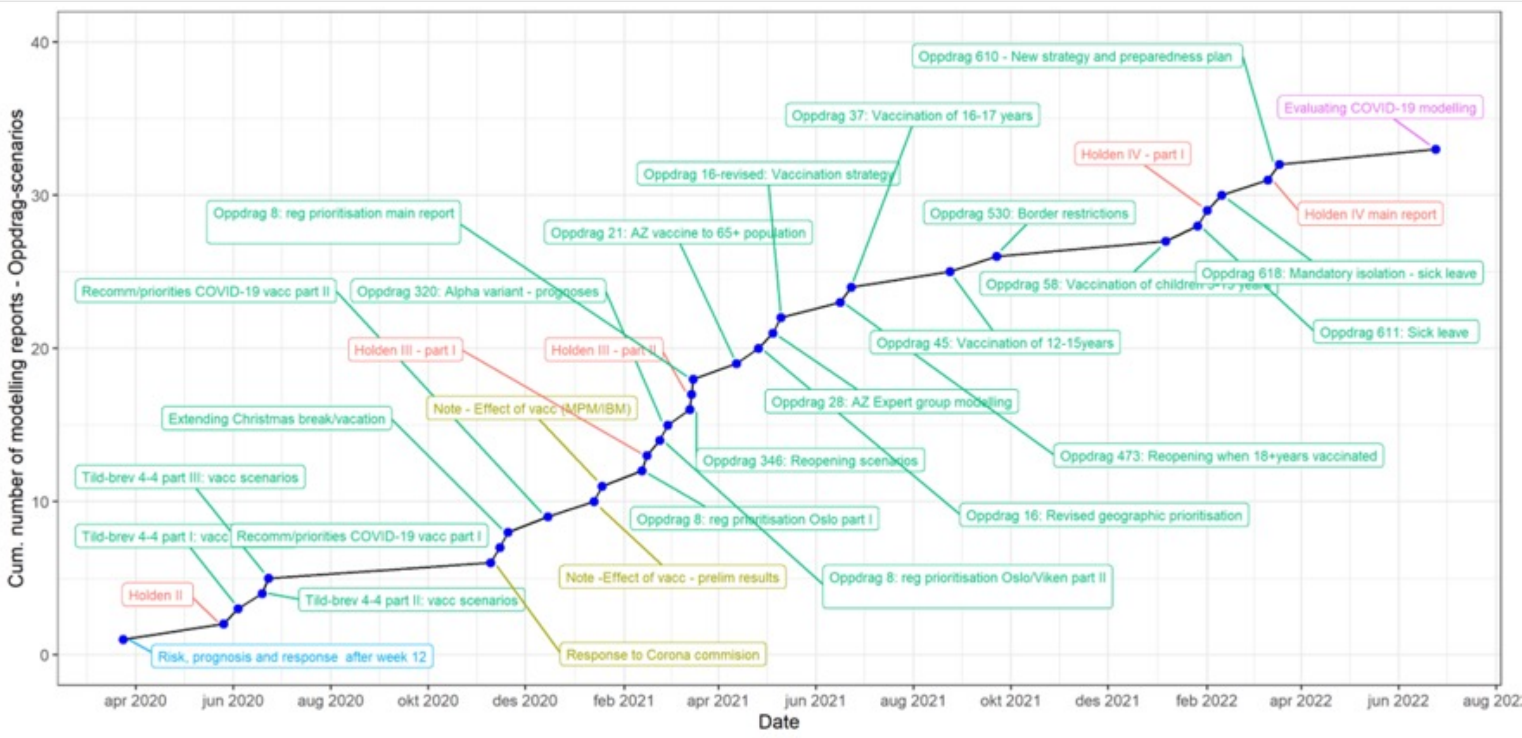
- National vs. Regional vaccine distribution
- Age and risk-group prioritization
- Vaccination of children (12-15)
- Increase uptake

Non-pharmaceutical interventions

- Individual behaviour (e.g. self-isolation)
- Quarantine measures
- Lockdowns

Epidemiological uncertainties

- New variants
- Seasonal effects



Mathematical models

- Meta-population model (MPM)
- Individual-based model (IBM)

[FHI MODELLING WEB PAGE: https://www.fhi.no/en/id/infectious-diseases/coronavirus/coronavirus-modelling-at-the-niph-fhi/](https://www.fhi.no/en/id/infectious-diseases/coronavirus/coronavirus-modelling-at-the-niph-fhi/)

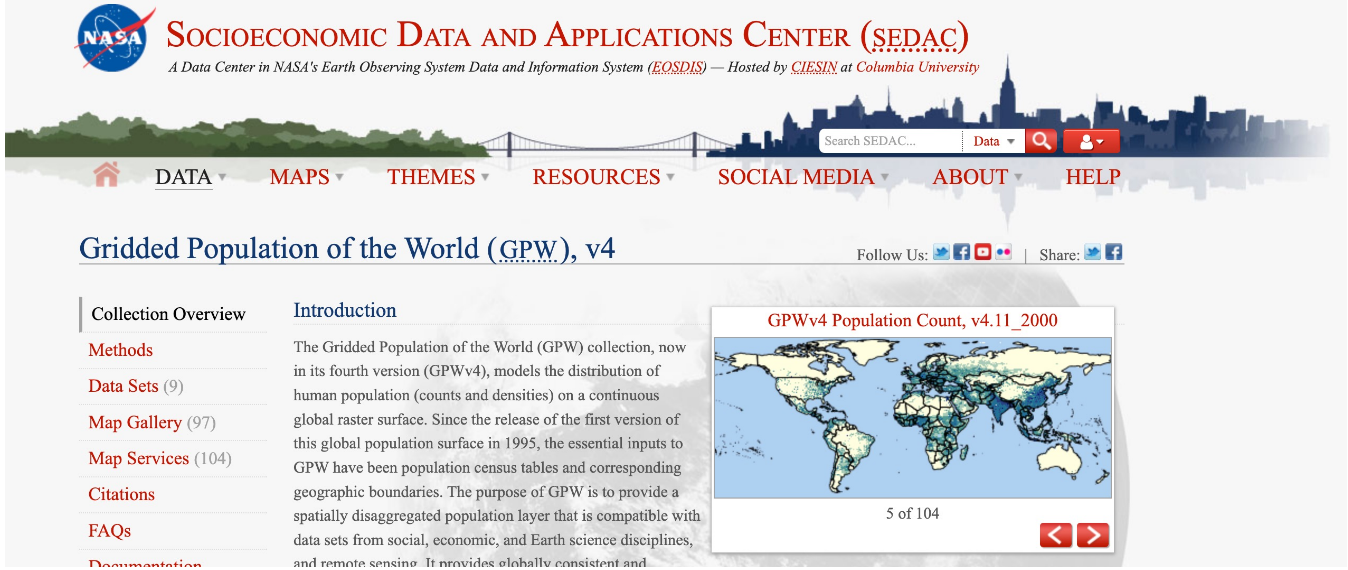
IBM structure

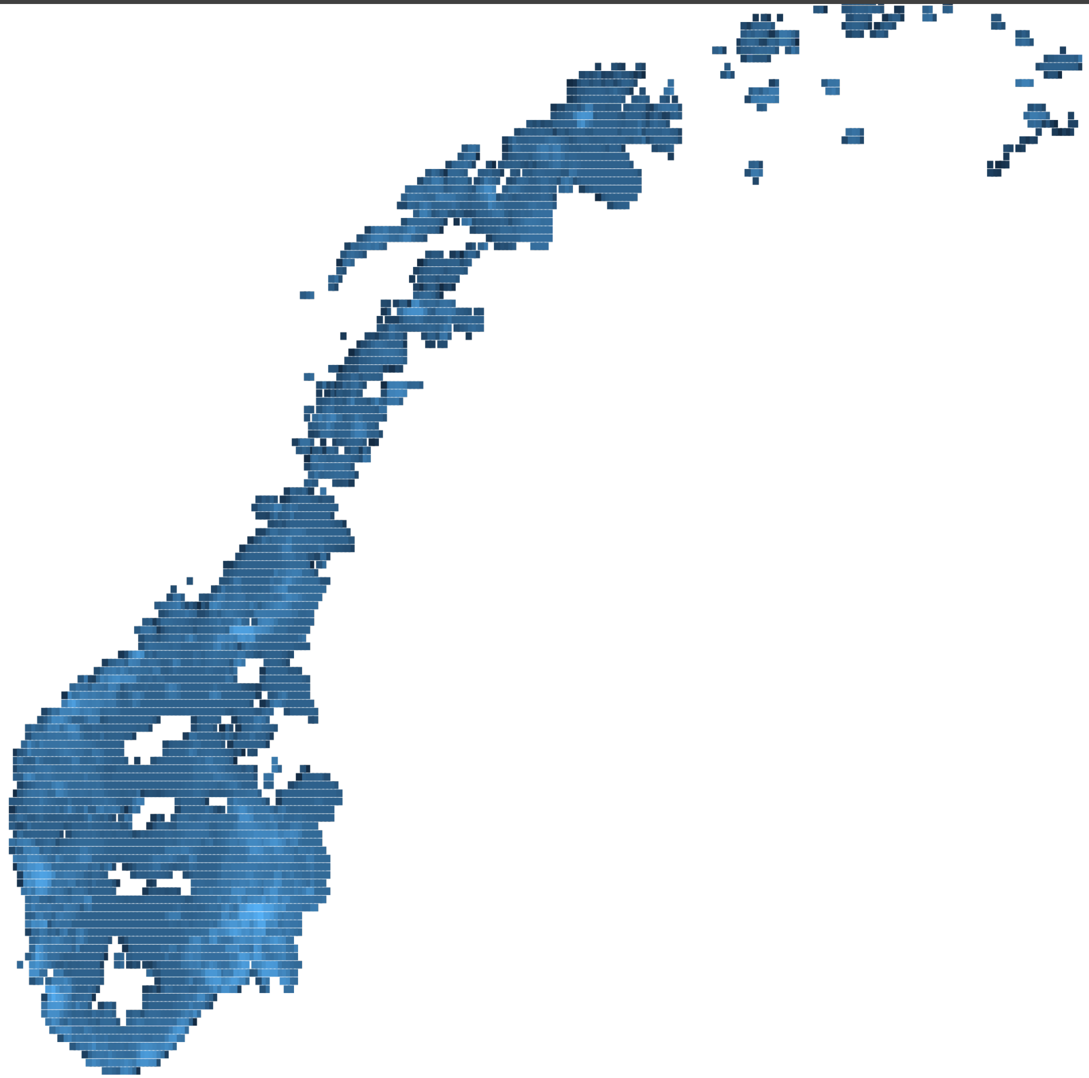
Norwegian IBM: Geo-spatial features

Gridded population data

Version 1 (GPW data)

- Approximately 5.4 mln individuals
- 4978 cells



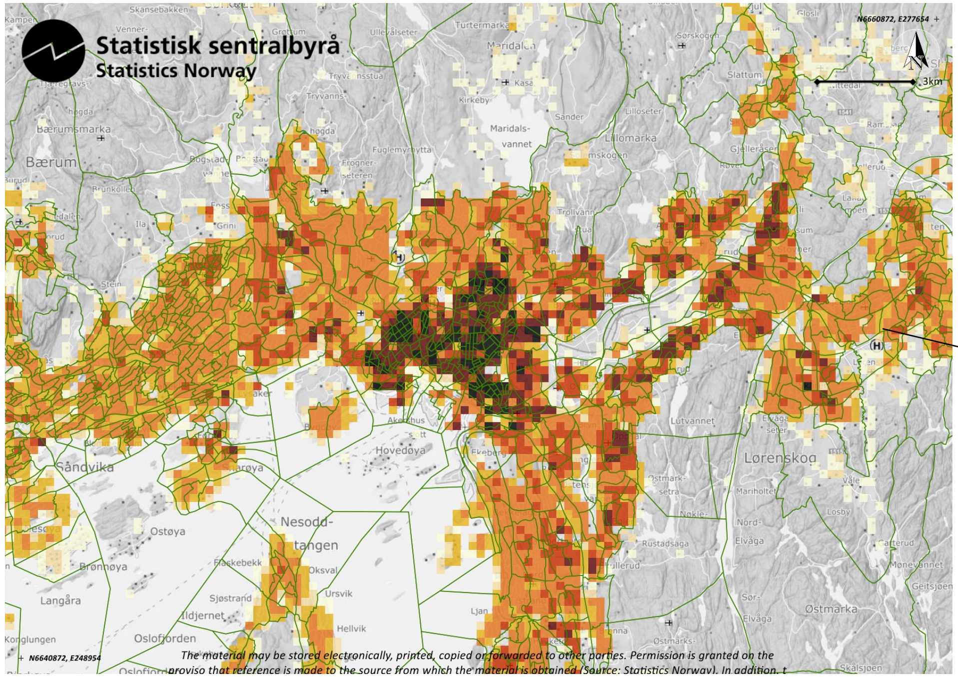


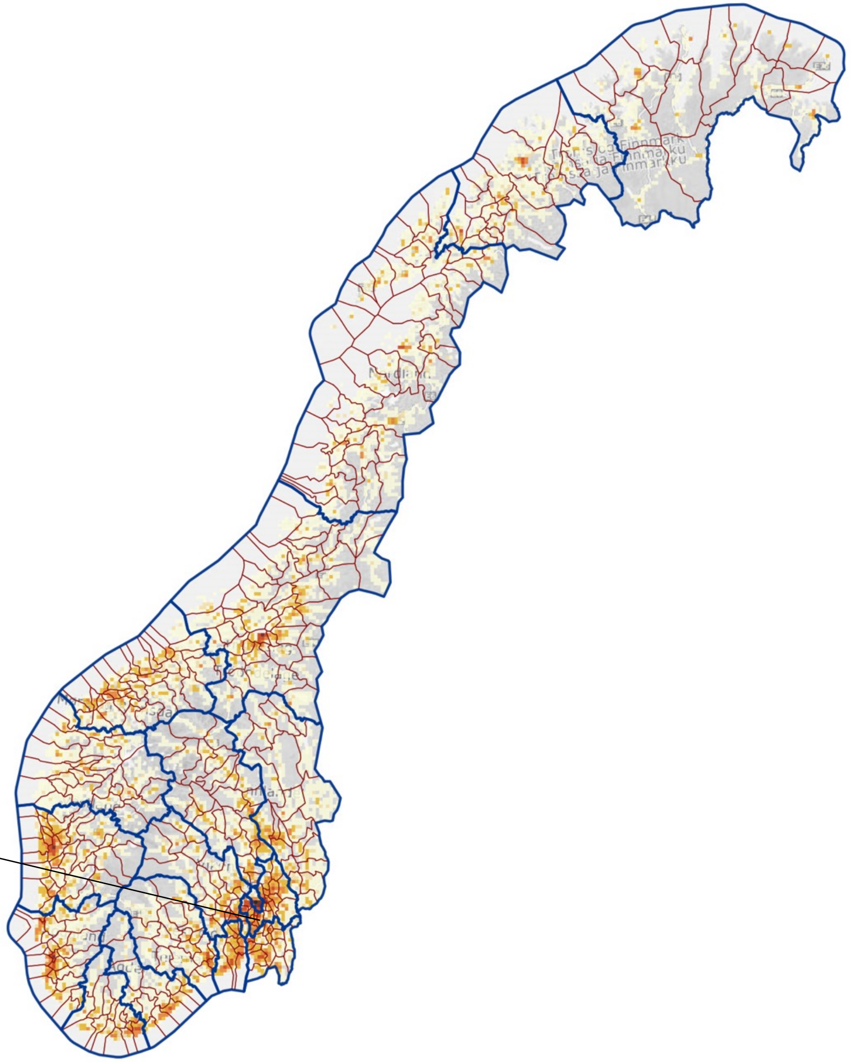
Norwegian IBM: Geo-spatial features

<u>Gridded population data</u>

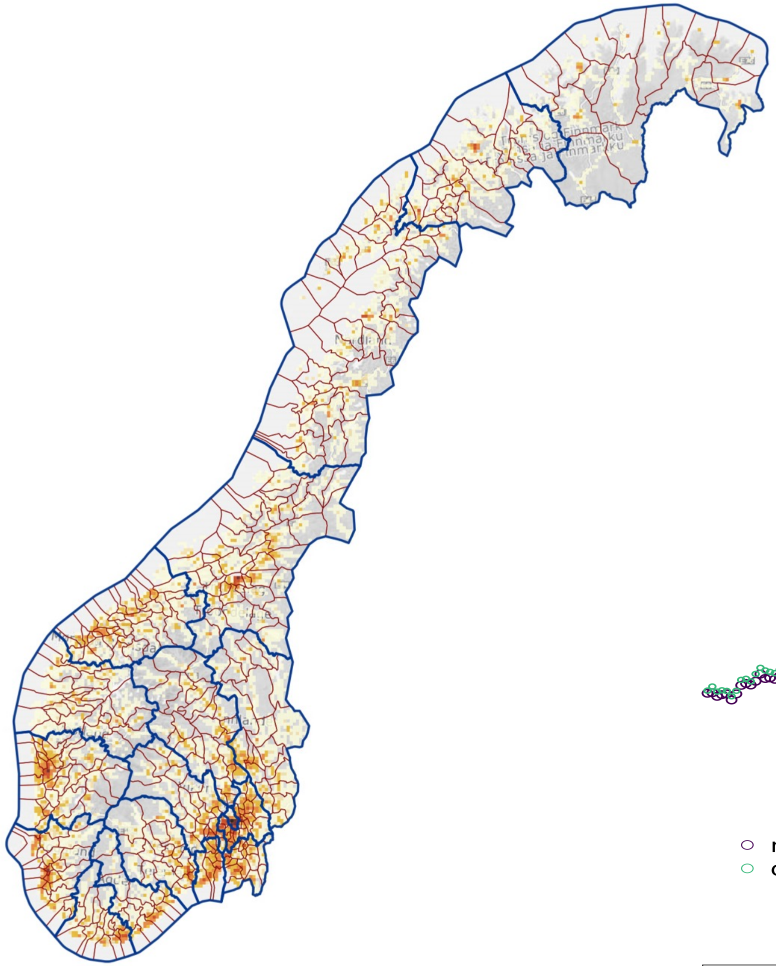
Version 2 (Statistics Norway data)

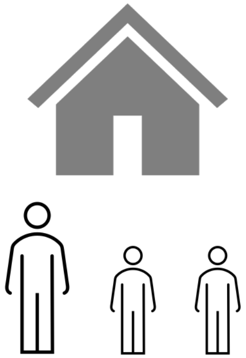
- Approximately 5.4 mln individuals
- 13521 cells, 356 municipalities / 11 counties





Norwegian IBM: Synthetic population



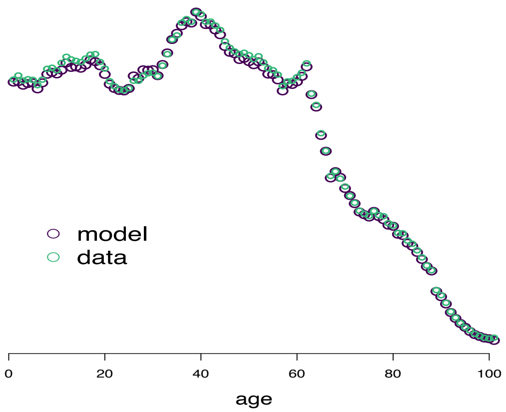


Census data (SSB, FHI)

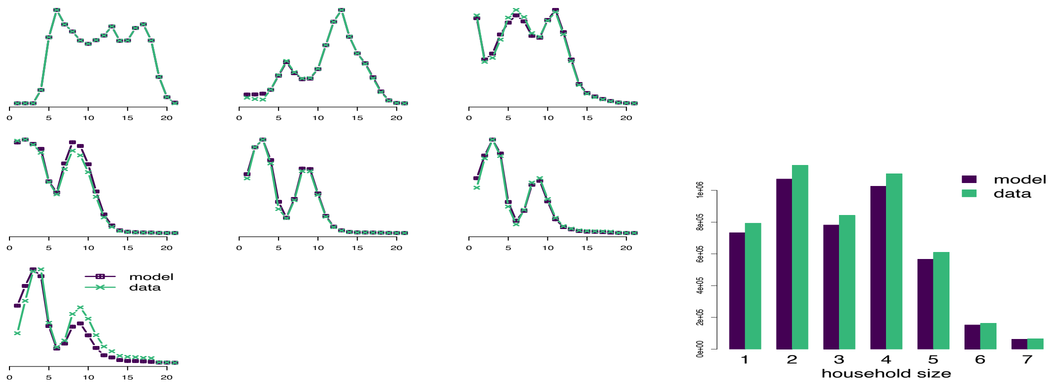
Algorithm to build households (hhs):

1. Sample hh size from the distribution
2. Sample the age of the hh head from the age-distribution of that hh size
3. Define if there are more adults or kids in the hh
4. Sample the age of the other members

Age profile



Household size by age



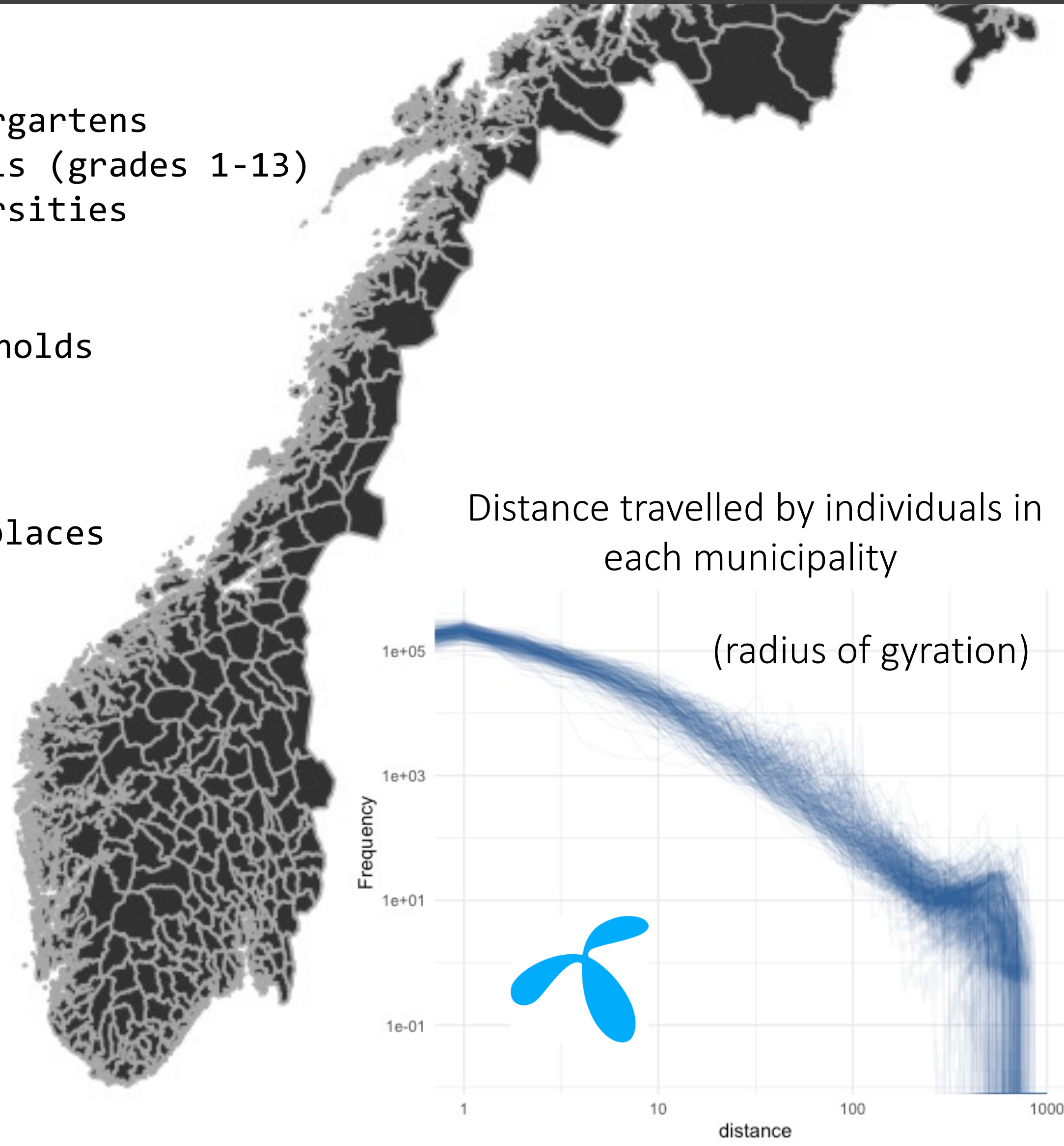
Individuals, settings and mobility

- Location
- Age
- Occupation
- Ethnic background
- Vaccination status
- Risk group
- Epidemiological status
- Hospitalization status

kindergartens
Schools (grades 1-13)
Universities

Households

Workplaces



Distance travelled by individuals in each municipality

(radius of gyration)

Mobility patterns: informed by mobile phone data data from Telenor Norway

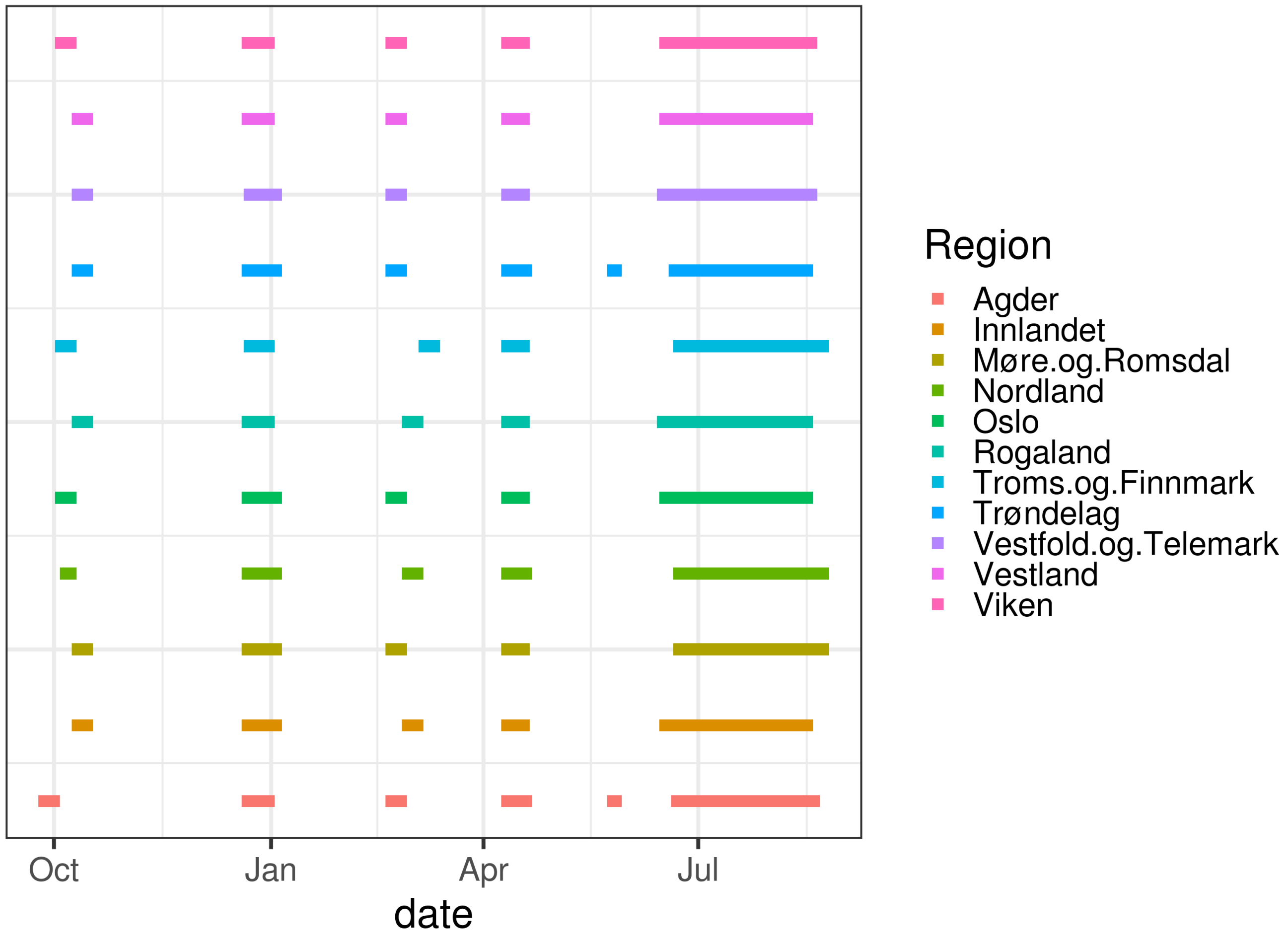
Understanding individual human mobility patterns

Marta C. González[1], César A. Hidalgo[1,2] & Albert-László Barabási[1,2,3]

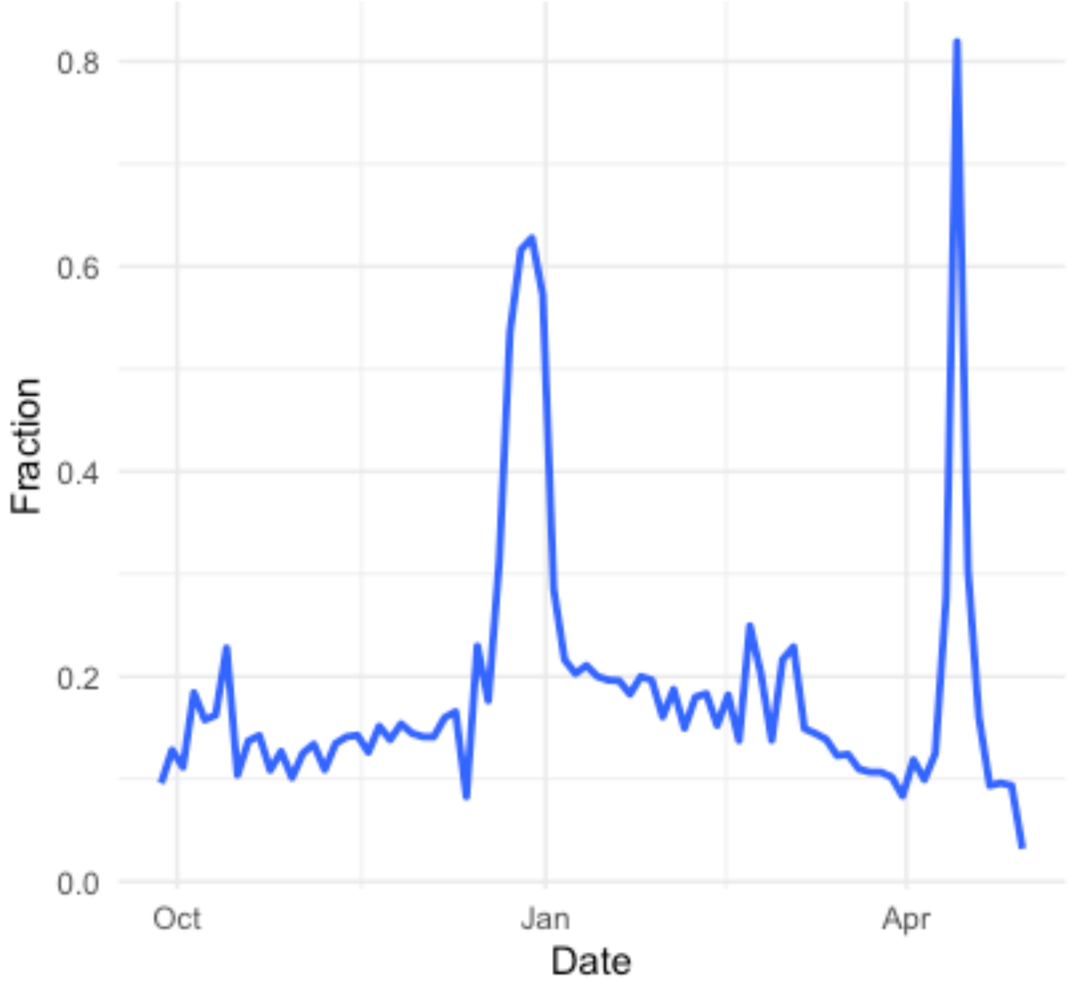
$$P(r_g) = \left(r_g + r_g^0\right)^{-\beta_r} \exp\left(-r_g/\kappa\right)$$

School holidays and home office

School holidays



Home office (Google data)



Synthetic population

5.3 mln individuals

Real socio-demography

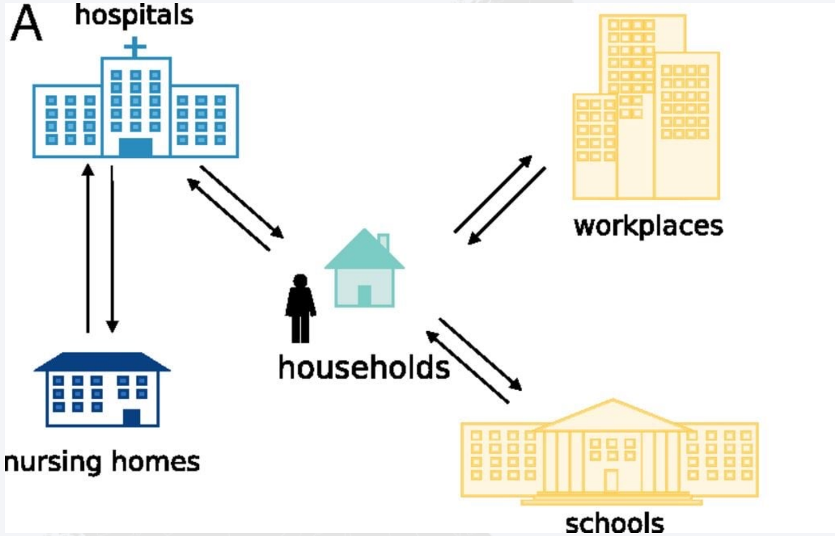
Mobility patterns

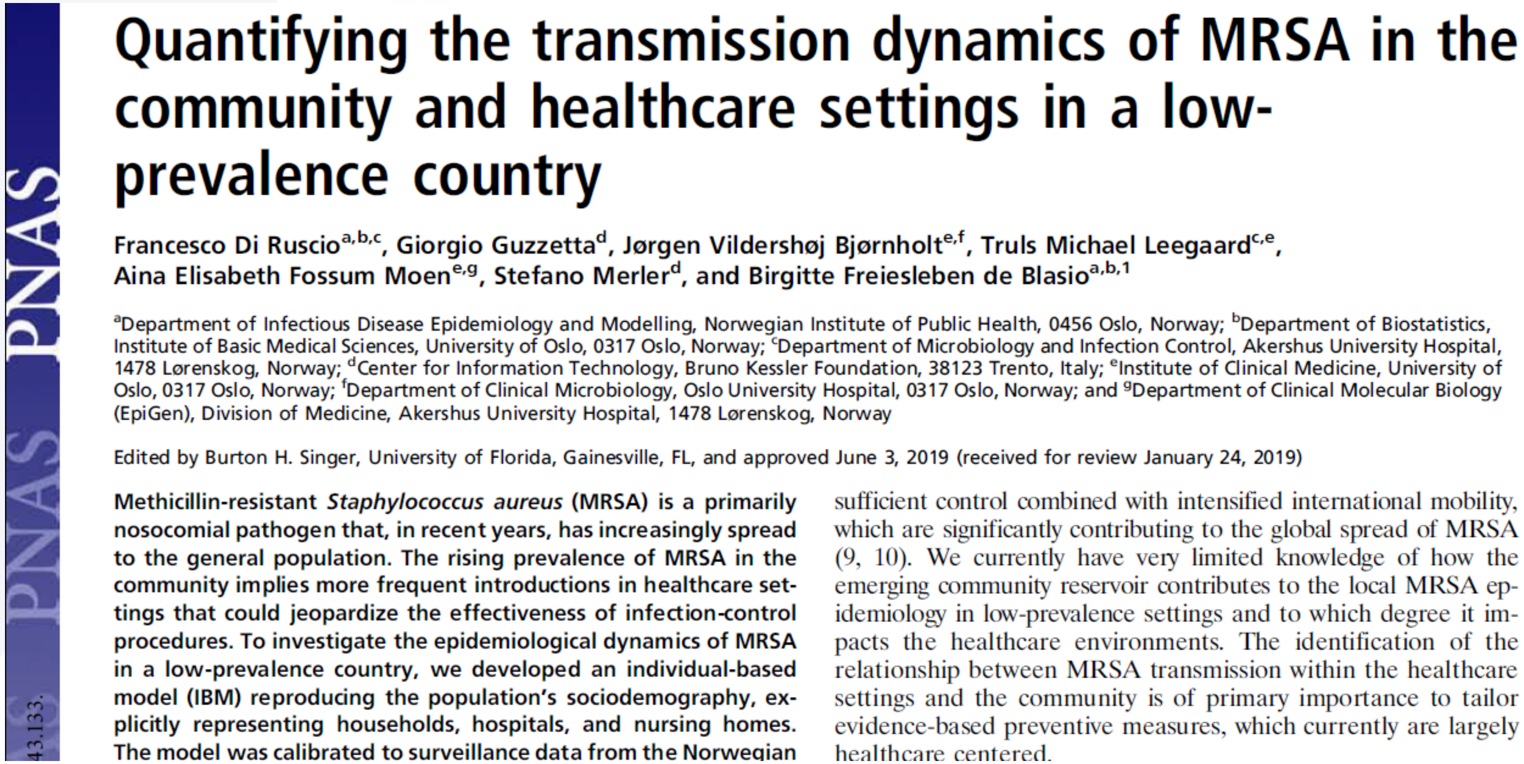
Schools
Workplaces
Community

Hospitalizations

Epidemiological model

Spread of AMR bacteria





PNAS PNAS

Quantifying the transmission dynamics of MRSA in the community and healthcare settings in a low-prevalence country

Francesco Di Ruscio[a,b,c], Giorgio Guzzetta[d], Jørgen Vildershøj Bjørnholt[e,f], Truls Michael Leegaard[c,e], Aina Elisabeth Fossum Moen[e,g], Stefano Merler[d], and Birgitte Freiesleben de Blasio[a,b,1]

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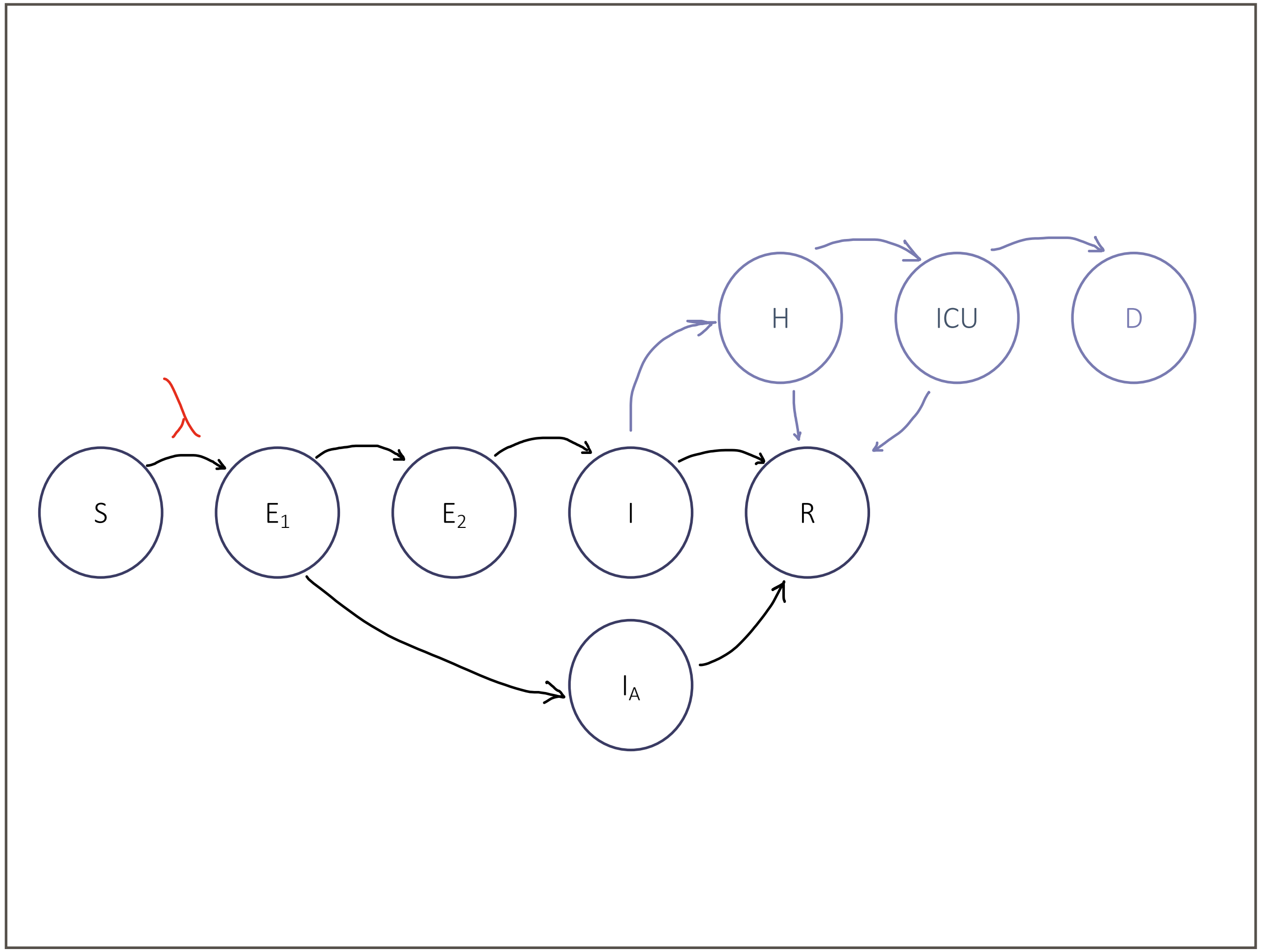
Edited by Burton H. Singer, University of Florida, Gainesville, FL, and approved June 3, 2019 (received for review January 24, 2019)

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a primarily nosocomial pathogen that, in recent years, has increasingly spread to the general population. The rising prevalence of MRSA in the community implies more frequent introductions in healthcare settings that could jeopardize the effectiveness of infection-control procedures. To investigate the epidemiological dynamics of MRSA in a low-prevalence country, we developed an individual-based model (IBM) reproducing the population's sociodemography, explicitly representing households, hospitals, and nursing homes. The model was calibrated to surveillance data from the Norwegian

sufficient control combined with intensified international mobility, which are significantly contributing to the global spread of MRSA (9, 10). We currently have very limited knowledge of how the emerging community reservoir contributes to the local MRSA epidemiology in low-prevalence settings and to which degree it impacts the healthcare environments. The identification of the relationship between MRSA transmission within the healthcare settings and the community is of primary importance to tailor evidence-based preventive measures, which currently are largely healthcare centered.

An *in-silico* laboratory that we can use to study the transmission of different pathogens

COVID-19 epidemiological model



Main Parameters

- Gamma distributions - transition time
- Transmission rates β (setting dependent)
- Susceptibilities by age
- Proportion of asymptomatics by age
- Relative infectiousness of P,I and A
- Risk of hospitalizations by age
- Risk of death by age
- LOS in hospital and ICU by age
- Vaccine efficacies + waning by dose and age

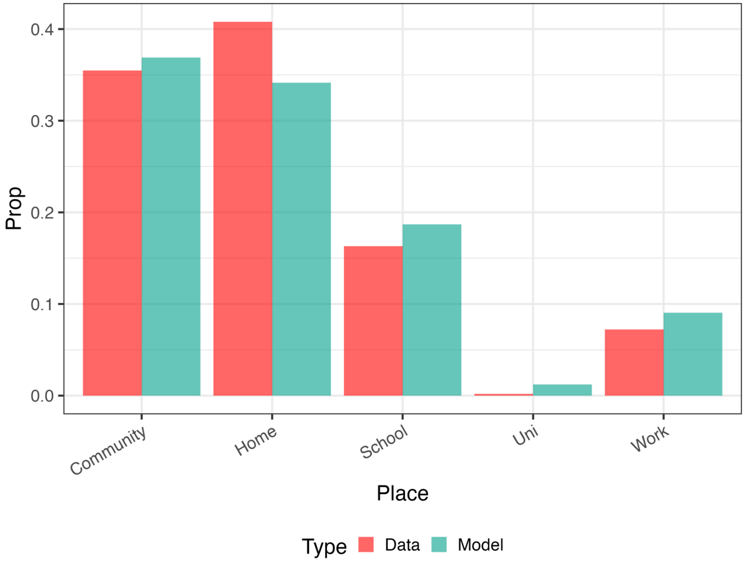
Total

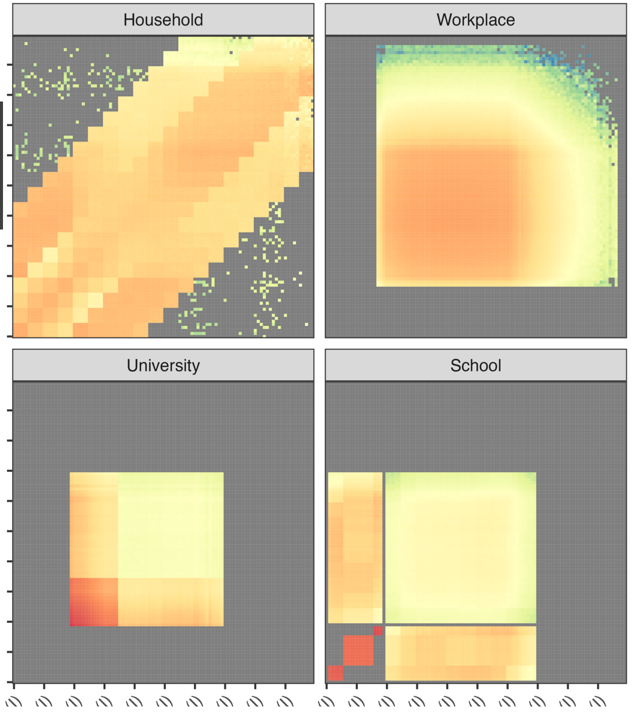
> 100 parameters

Force of infection

$$\lambda = \lambda_h + \lambda_w + \lambda_s + \lambda_c$$

~35-40% ~20% ~35-40%



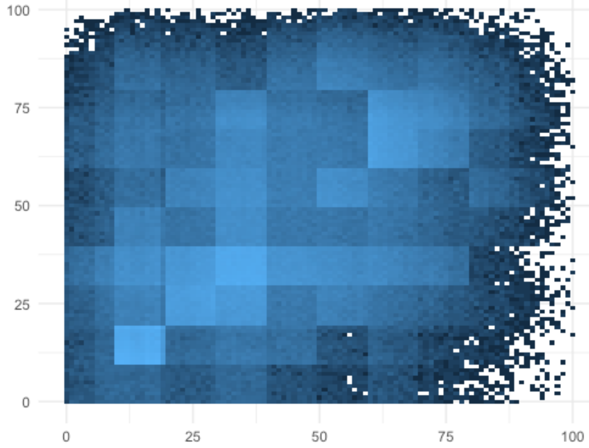


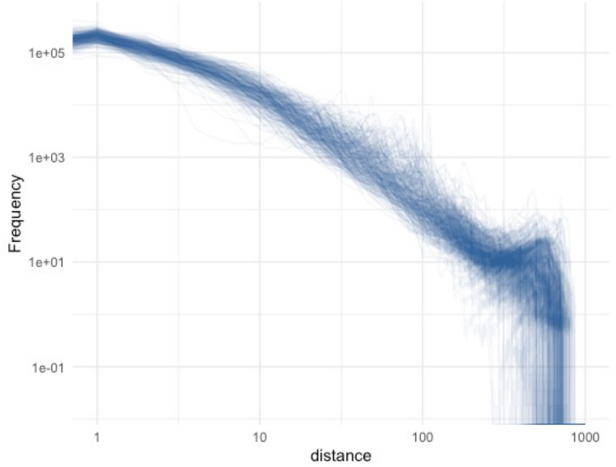
Community

We use a **negative binomial distribution** to take into account super-spreading events. (Lloyd-Smith, Nature, 2005)

The model simulates age-dependent contacts in the community (based on Norwegian *contact data*) and *a spatial kernel* derived from mobility data from Telenor Norway.

Susceptibility factors capture behavioral changes in specific periods of time.



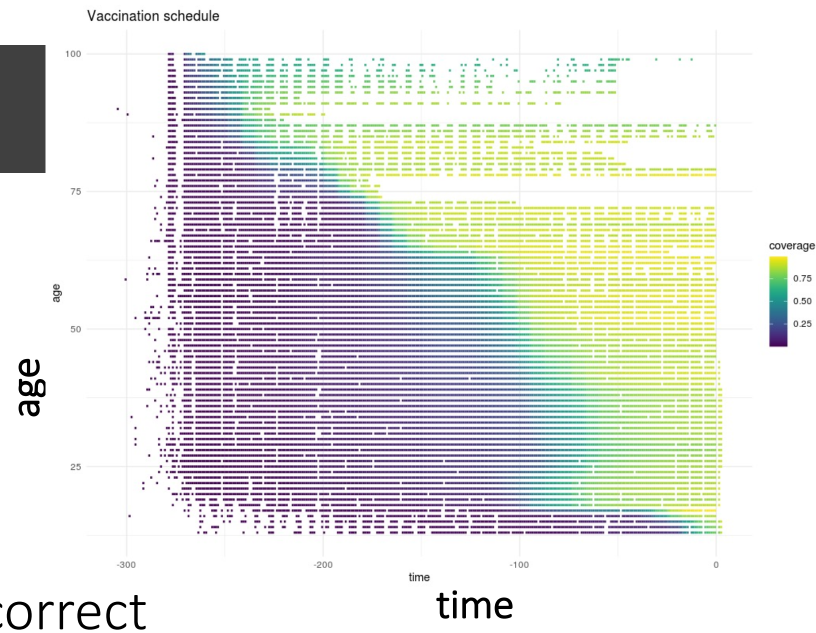


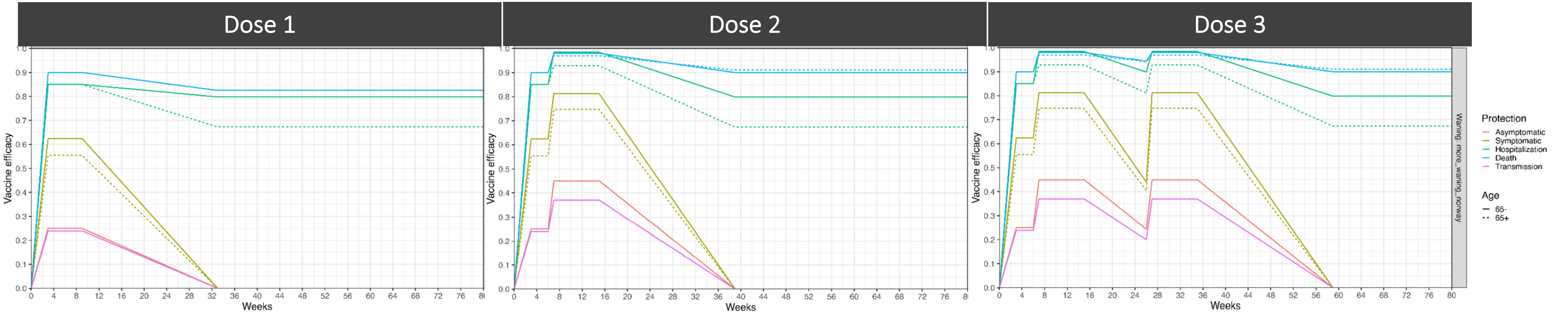
Vaccination model

Single shots of vaccine

Waning dynamics with different functional forms (linear, exponential)

Historical registry data (SYSVAK) used to initialize the model with the correct number of doses by age and municipality in time.





Model calibration

Computationally expensive stochastic model:

Simulation time: ~ 5-15 min (on a 2.6 GHz; programming language C)

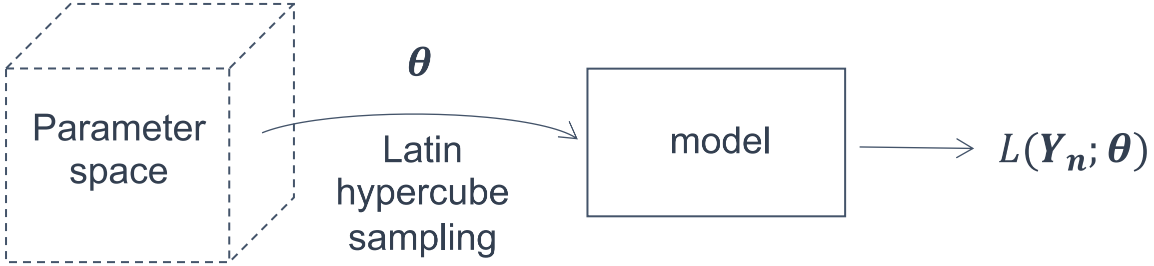
Parameter exploration unfeasible with methods that rely upon large numbers of sequential model evaluations (e.g. MCMC).

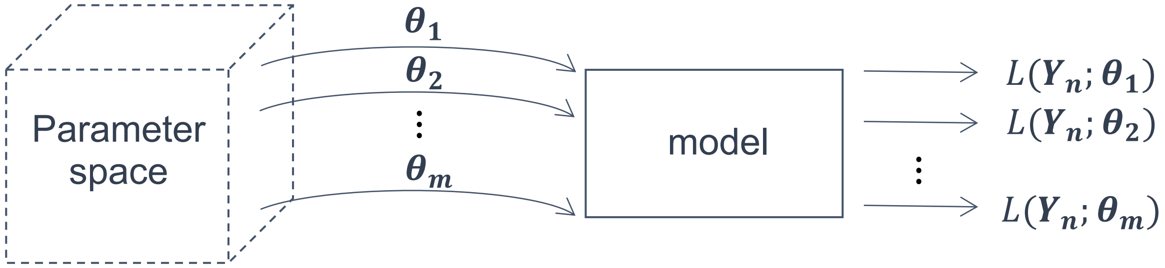
HPC infrastructure are needed to run different simulations in parallel

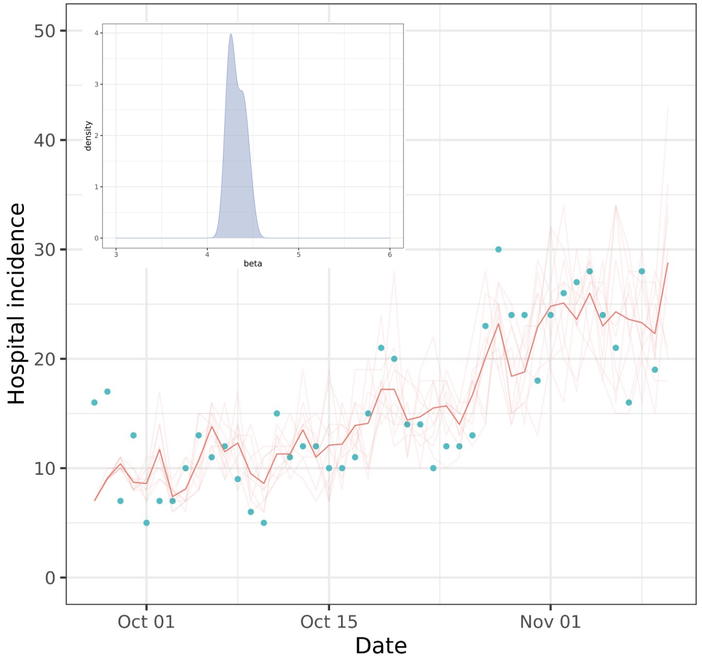
Model calibration – *Latin Hypercube Sampling*

Data - e.g. hospital incidence

Set θ of free parameters - e.g. transmission rates β, susceptibility parameters



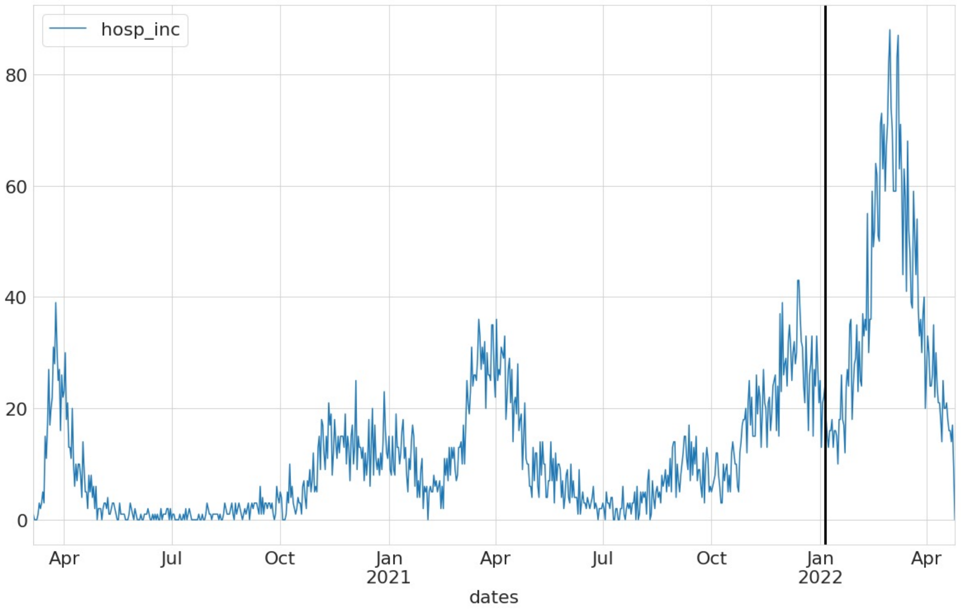


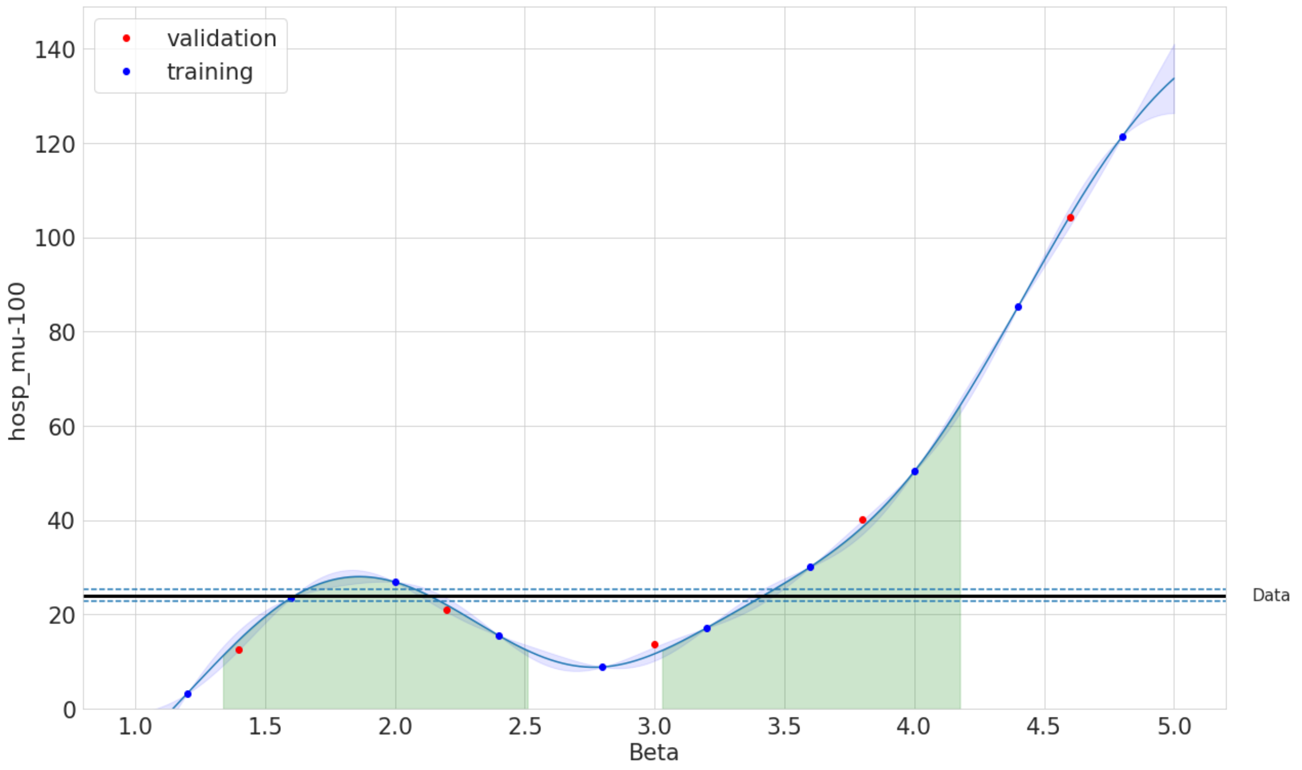


- Simulations can be run in parallel
- 10k -100k simulations –Computationally and financially expensive (HPC infrastructure needed).

Model calibration – *Emulators*

Given a set of model runs (training dataset) it is possible train an ***emulator*** (statistical model) and use it as a surrogate of the model, allowing for a more cost-effective exploration of the parameter space.





A retrospective study of the spread of the Omicron variant

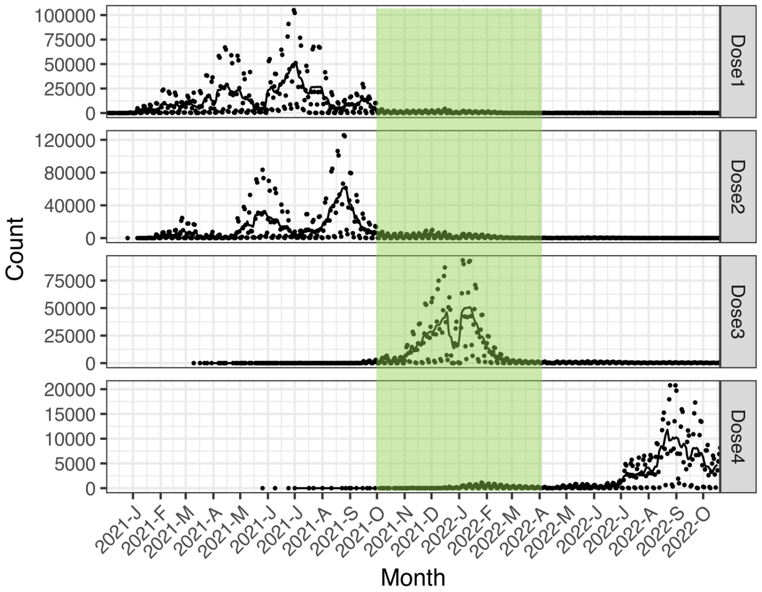
(Preliminary results)

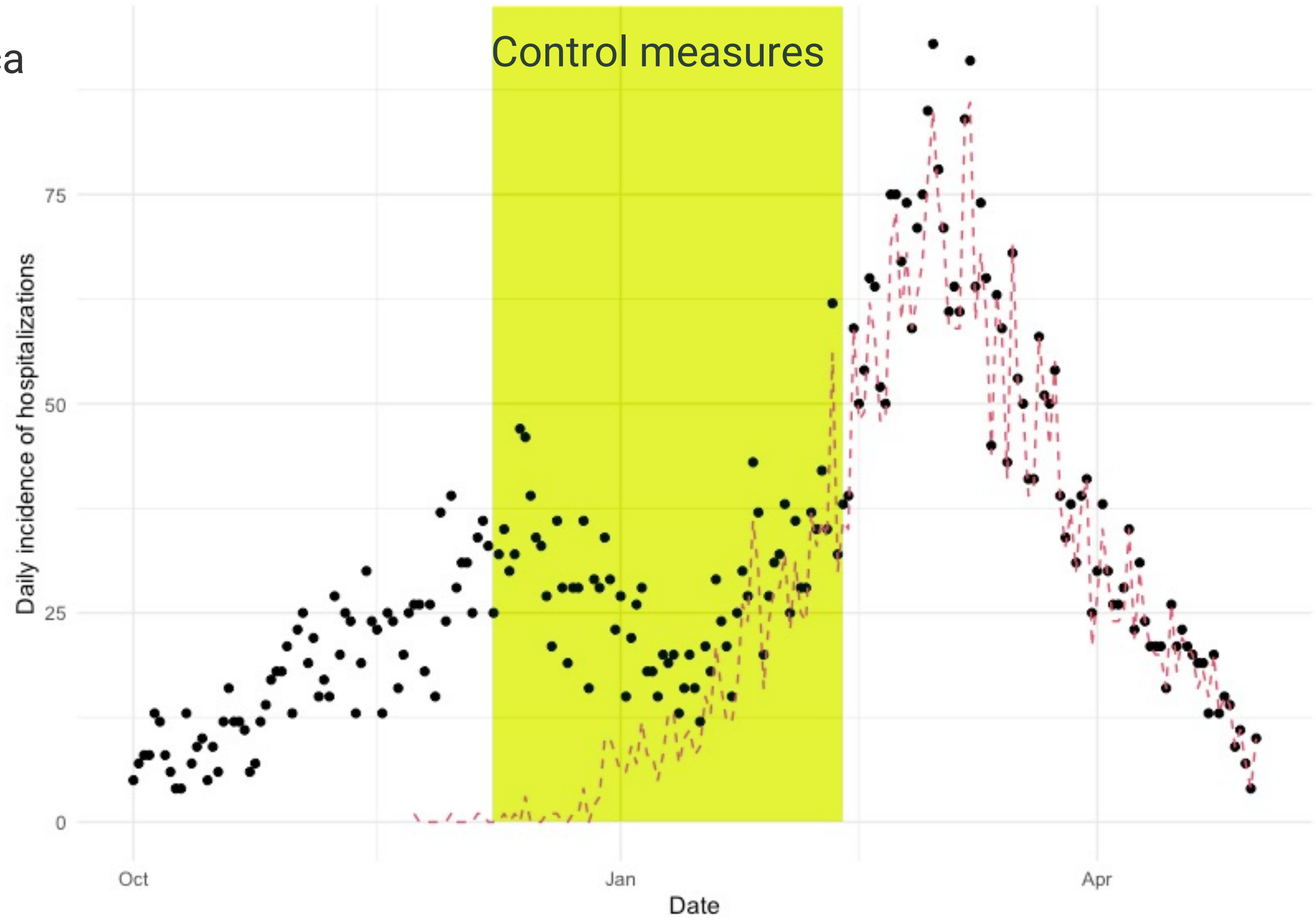
Omicron emergence - background

24 November 2021
First case detected in Norway from South Africa

Quick take over of the Omicron variant

Primary vaccination series completed
Booster campaign started in October

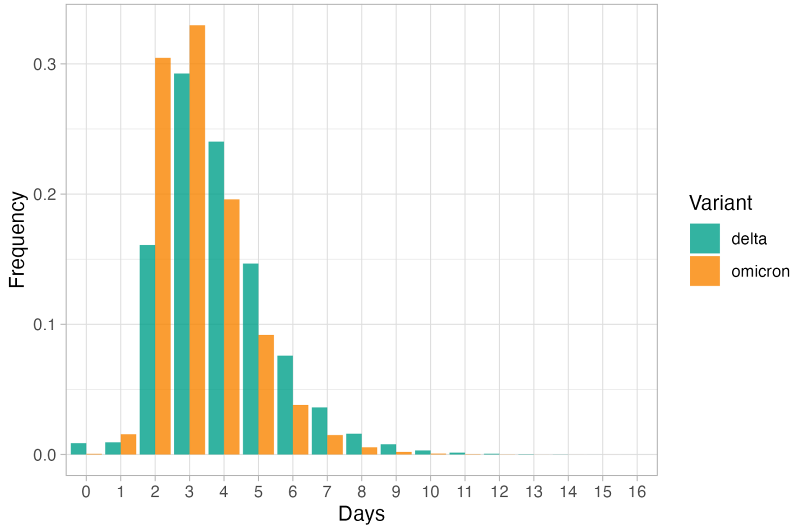




Epidemiological model with 2 strains

Omicron vs. Delta

- Higher transmissibility, lower generation time
- Ability to evade natural immunity from previous infections
- Milder symptoms
- Lower vaccine efficacy against infection



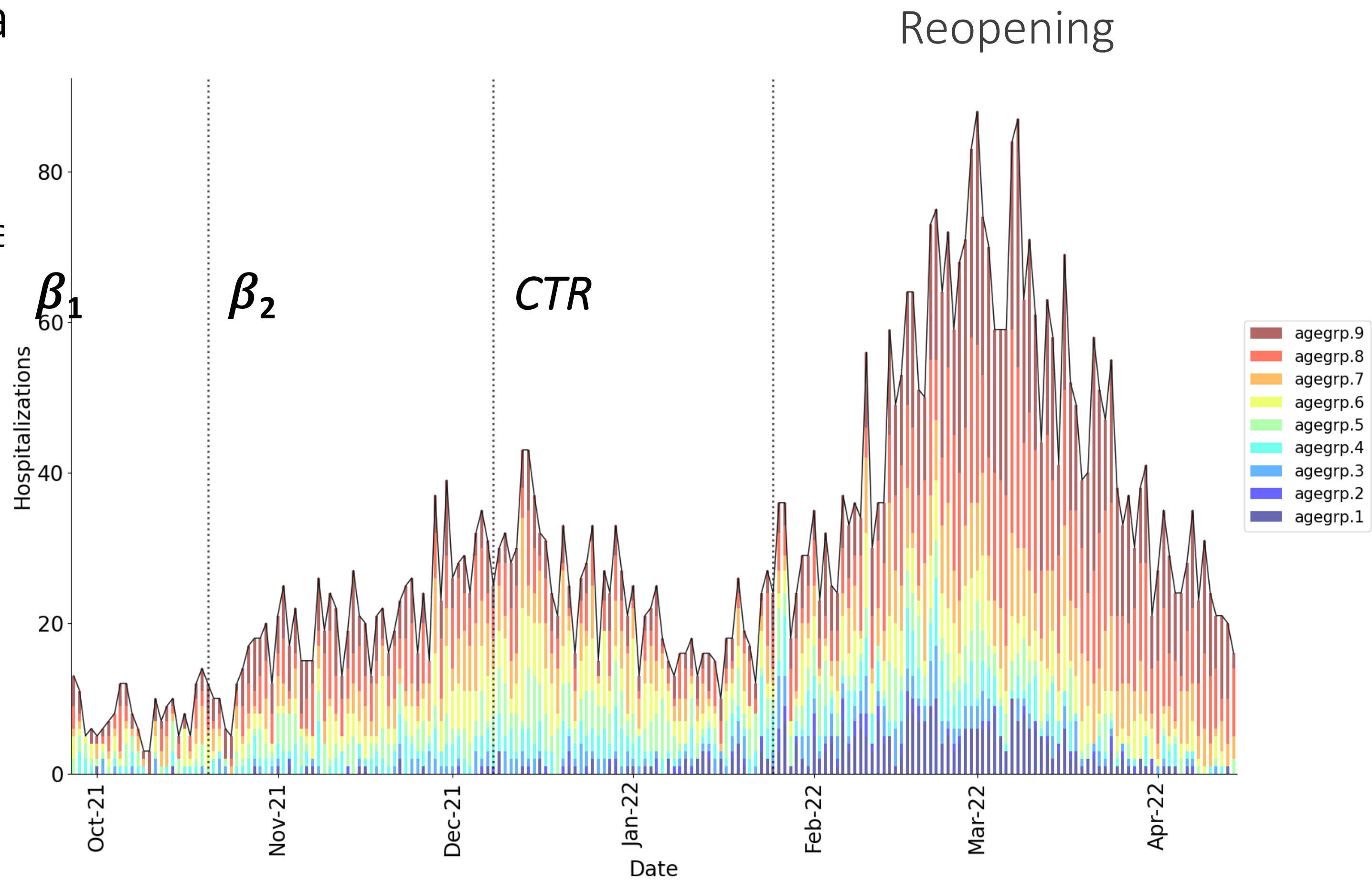
Calibration

Refined VE values and other parameters
from the litterature and Norwegian data

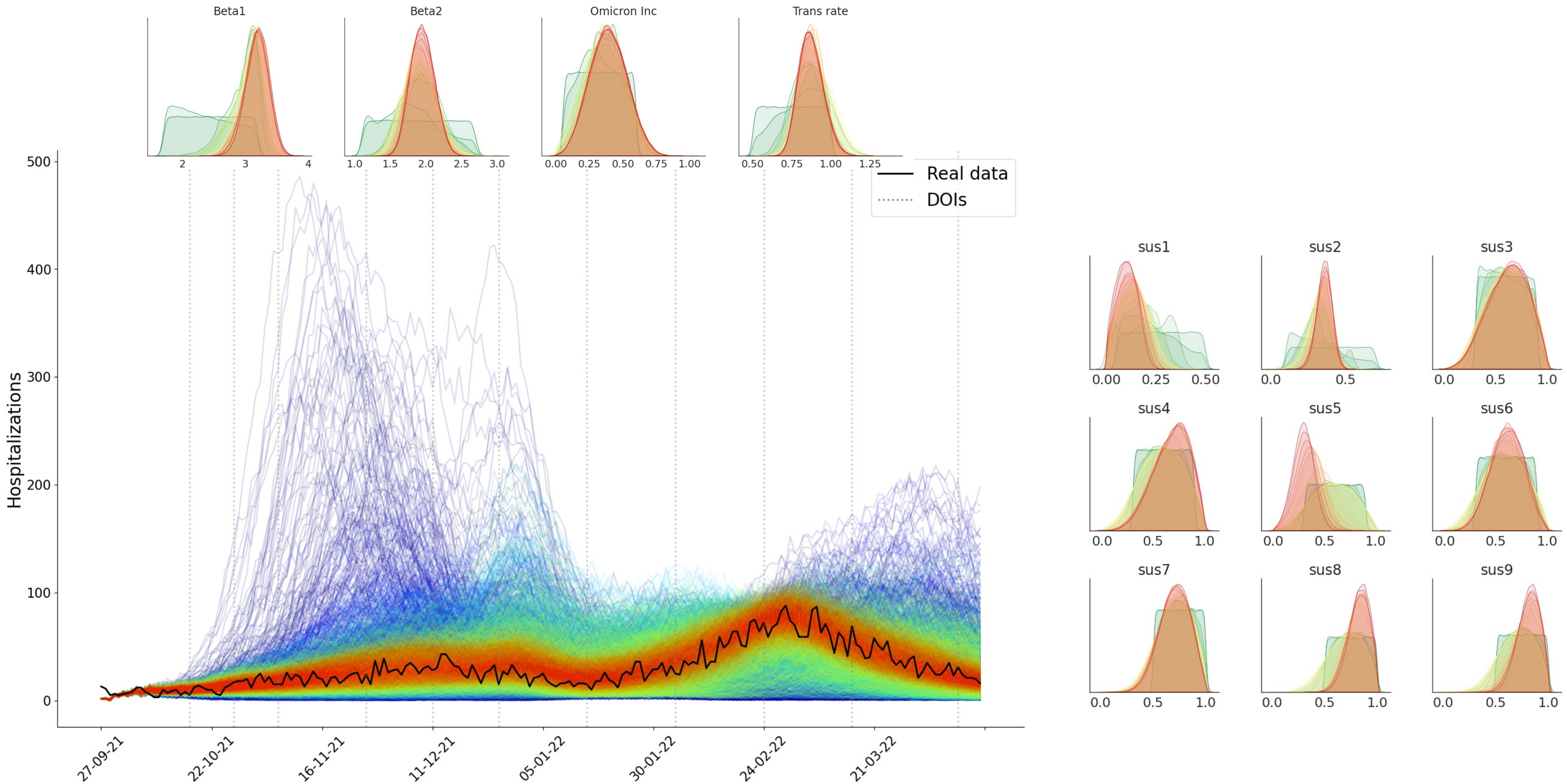
Free parameters (13):

- CTR : change in the ransmission rate due to inte
- β_1: Transmissibility t_0:Oct 19th
- β_2: Transmissibility from Oct 20th
- $\Delta_{omicron}$: Omicron advantage
- Sus : Susceptibility factors (9)

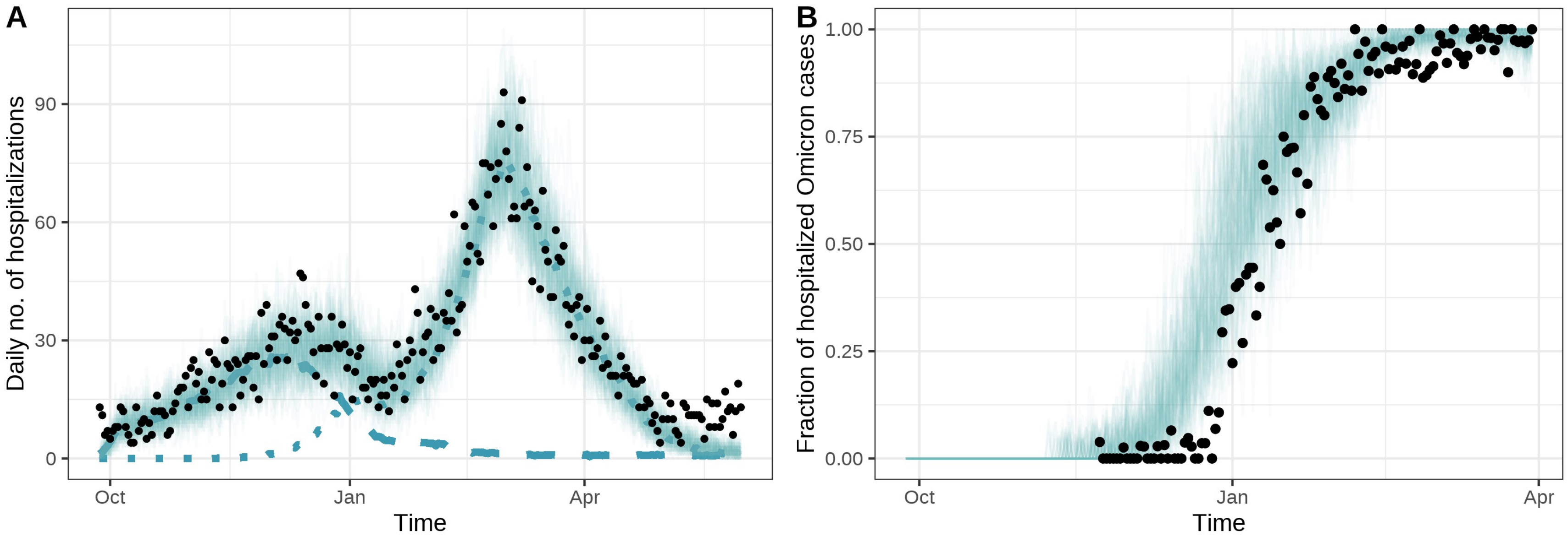
Data: incidence of hospitalization by age



Calibration – Emulation and history matching

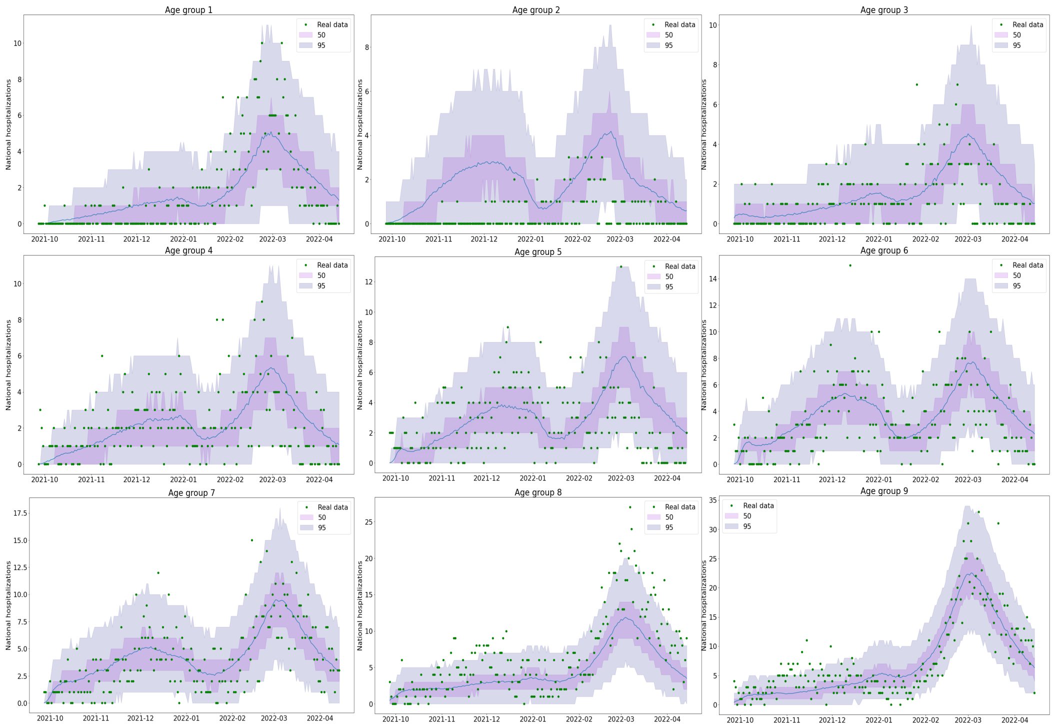


Baseline



Omicron importation

The model suggests that the first Omicron cases arrived in Norway in the first weeks of November (earlier than the first detected cases).



"… Omicron was present in Europe 10 days before its discovery in South Africa …"

Reviews in Medical Virology

REVIEW | Open Access

Evolution of the SARS-CoV-2 omicron variants BA.1 to BA.5: Implications for immune escape and transmission

Lok Bahadur Shrestha, Charles Foster, William Rawlinson, Nicodemus Tedla, Rowena A. Bull

First published: 20 July 2022 | https://doi.org/10.1002/rmv.2381 | Citations: 98

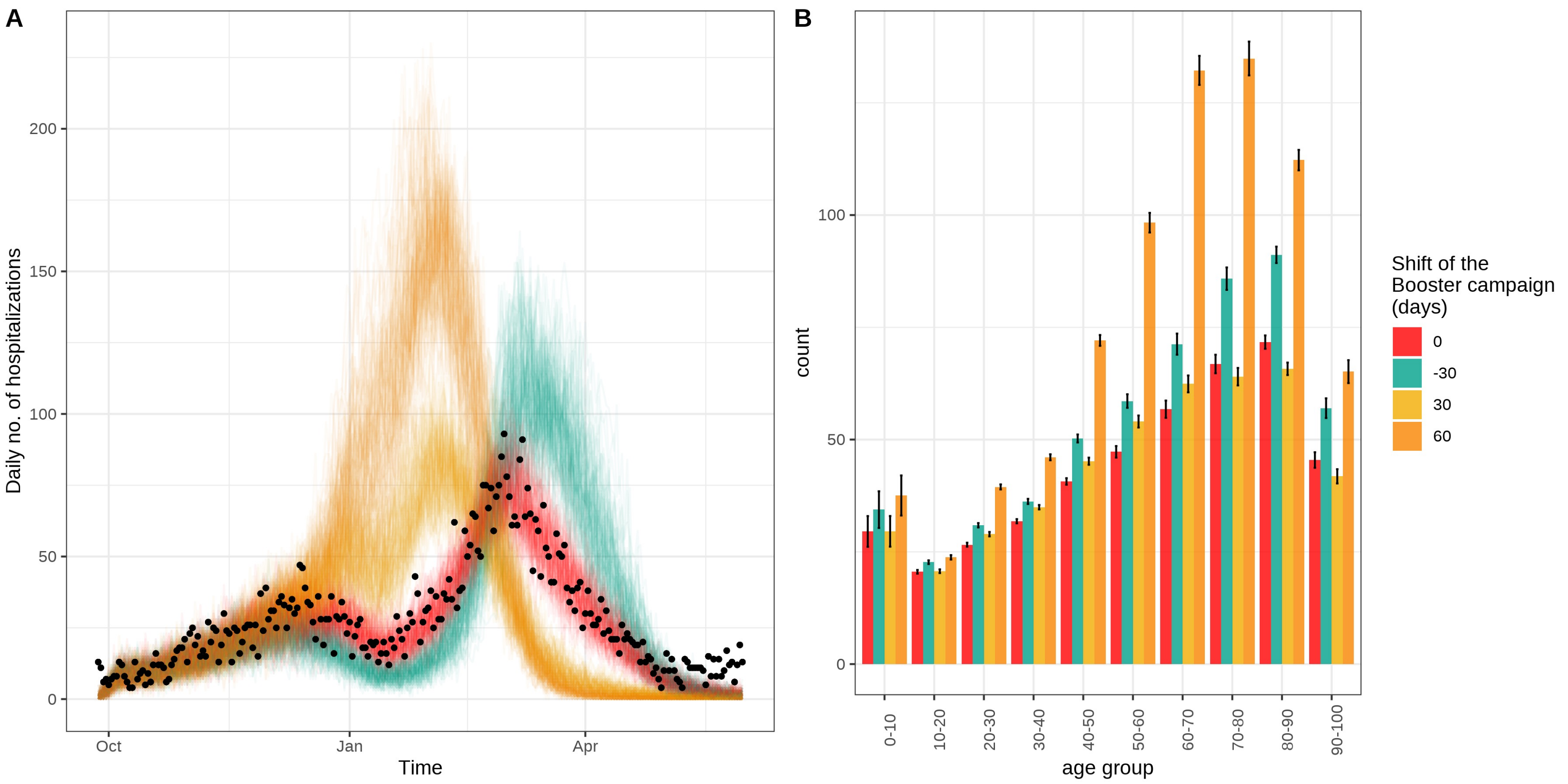
SECTIONS PDF TOOLS SHARE

Scenario analyses

- Timing of the booster dose
- Non-pharmaceutical interventions: timing of reopening the society
- School holidays
- Individual behavior

Scenario analyses

Timing of the booster dose

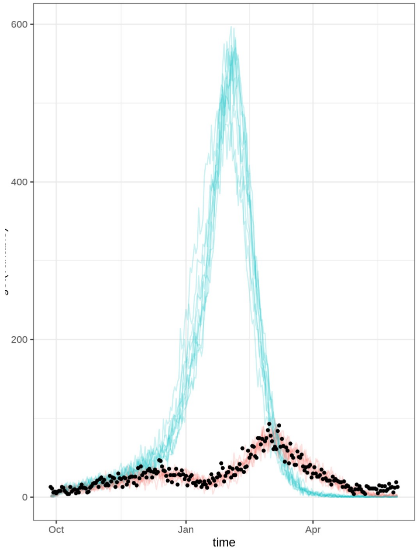


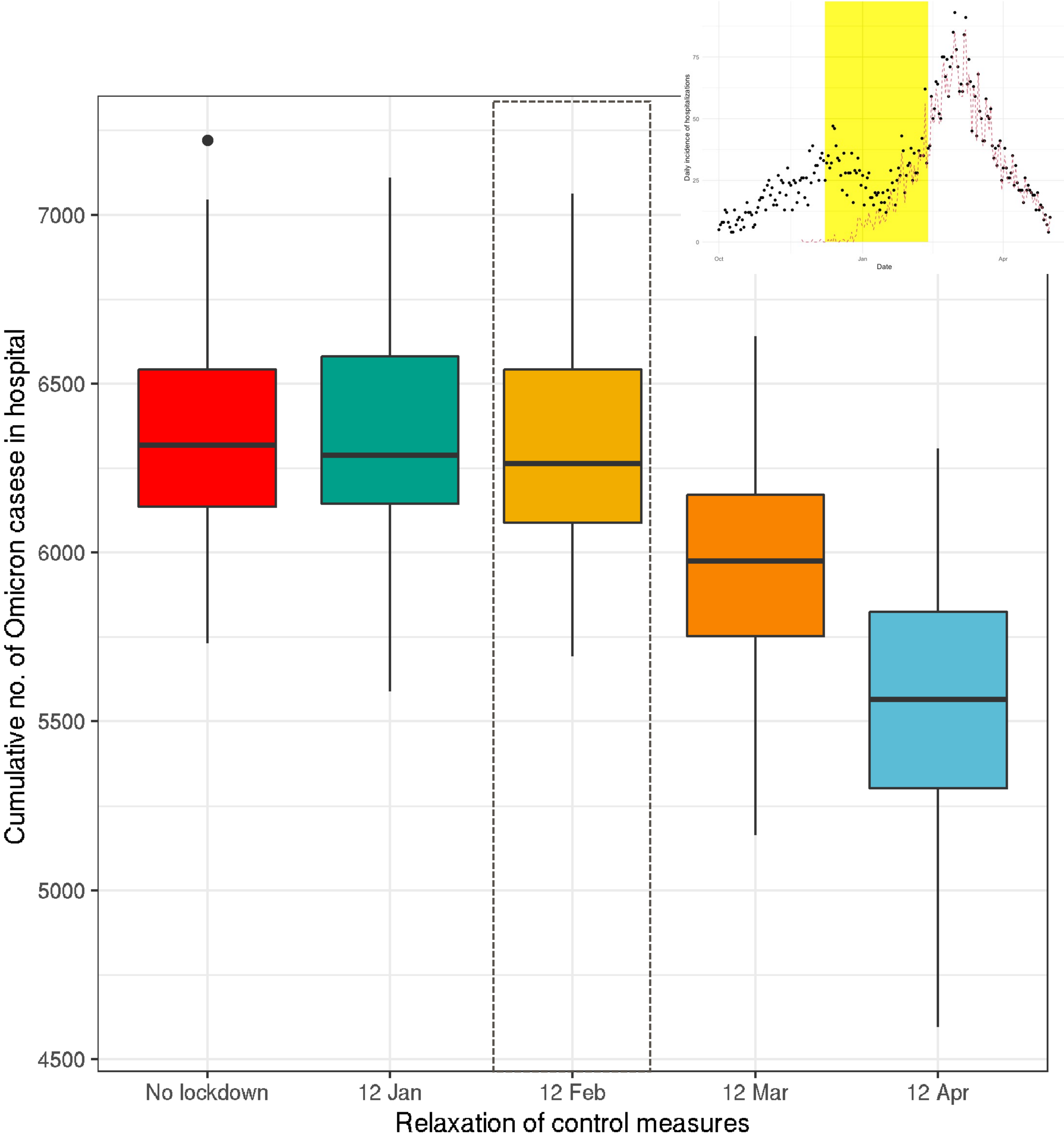
Scenario analyses

Lockdown and relaxation time of the control measures

10% reduction in the contact rate estimated

Scenario without the second dose





Reflections

The COVID-19 pandemic has provided an **unprecedented level data**.

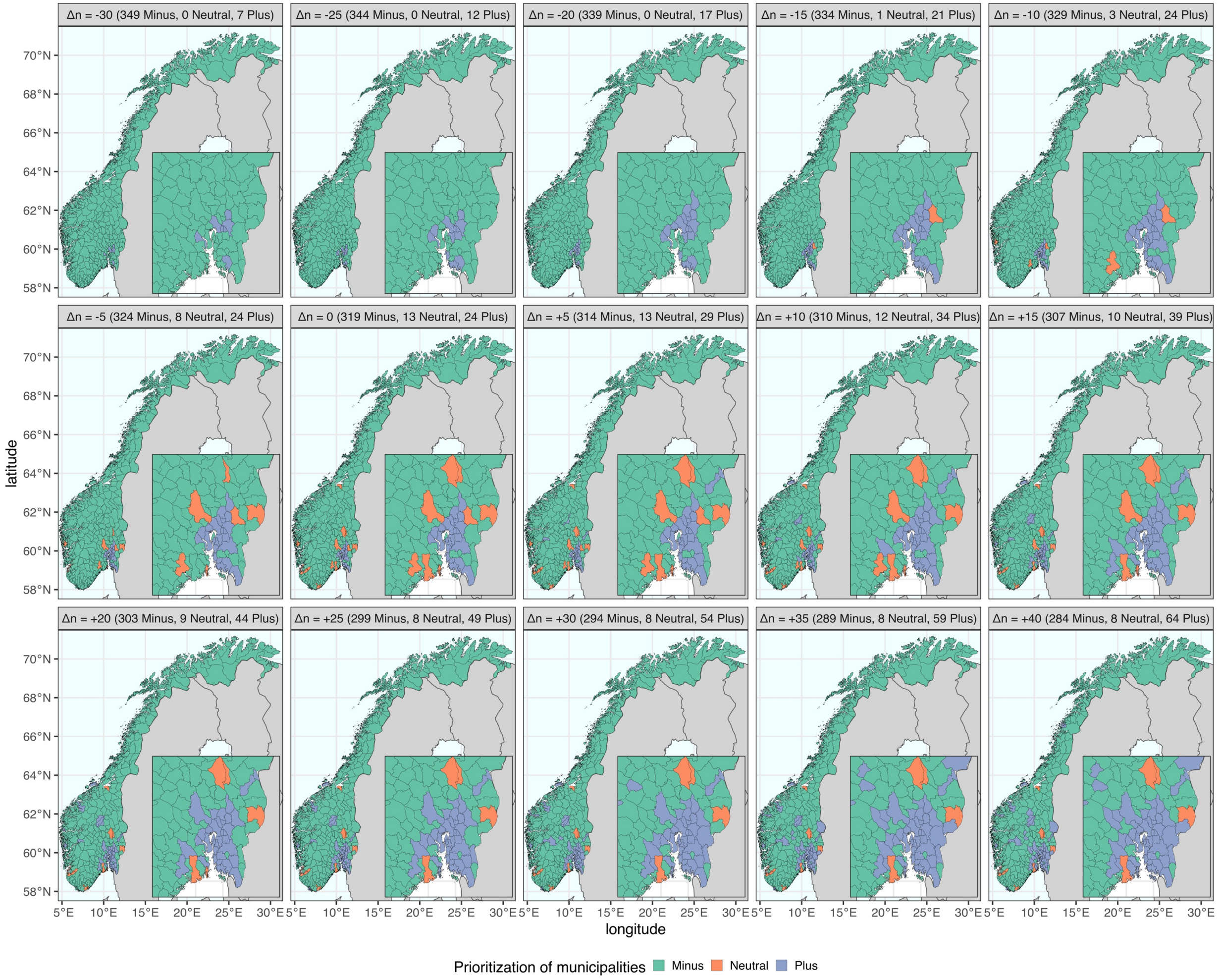
IBMs are **data hungry models** that greatly benefit from the extensive information available in registries, as well as behavioral and mobility data from sources such as social media and telecommunication companies.

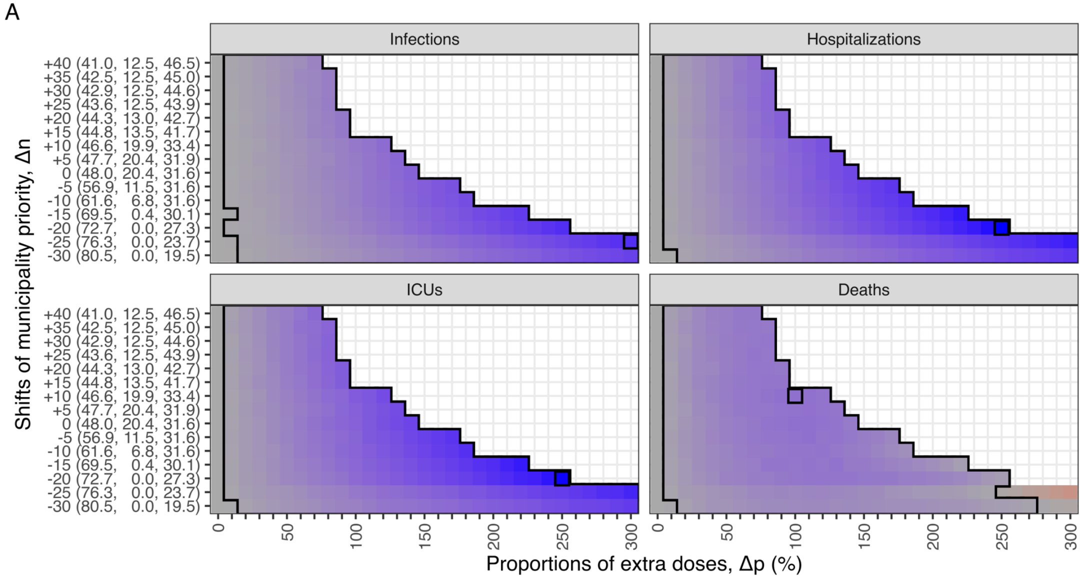
Retrospective analyses can give important insights into the spreading dynamics and the impacts of pharmaceutical and non-pharmaceutical interventions.

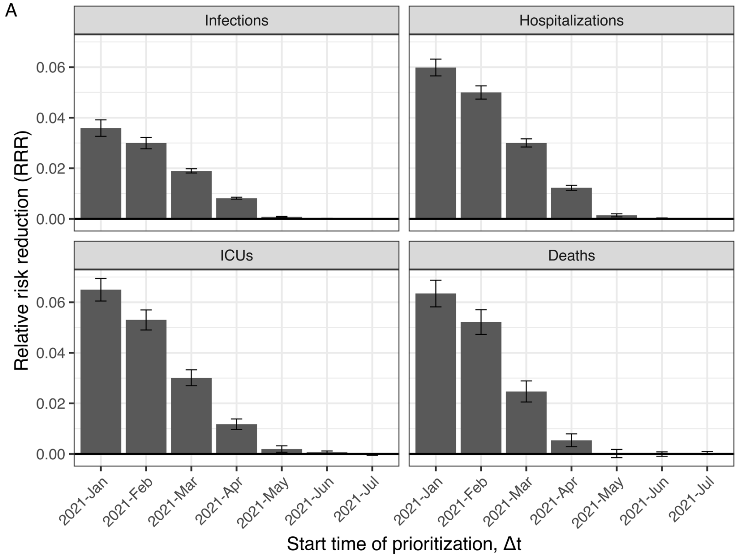
These insights are important for developing effective preparedness plans.

Vaccination strategy in Norway

Regional vs. national vaccination strategy







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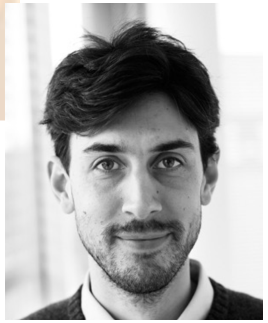





Thank you

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