

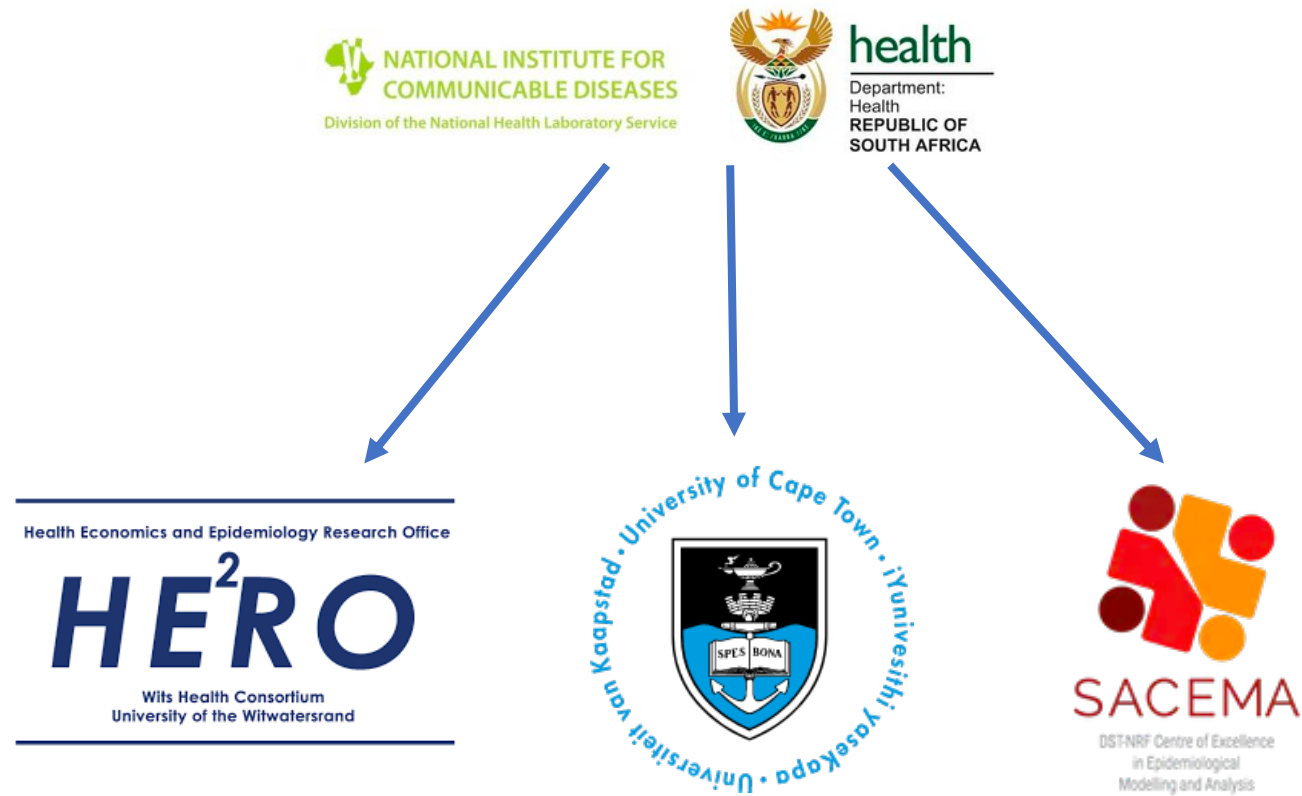
*A mathematical modeling consortium for COVID-19
epidemic prediction and resource allocation in:
South Africa*

8 April 2020

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Boston University School of Public Health, Boston, USA

Health Economics and Epidemiology Research Office, Johannesburg, South Africa



Epidemic modeling: cumulative cases, cases detected, hospitalized, ICU visits

Consortium structure

- Daily check-ins with modelers
 - Twice weekly model runs and testing of assumptions in a group
 - Open collaborative communication between lead modelers regarding refinement of assumptions
- Weekly updates with government
- Weekly input from the clinicians society of SA to discuss assumptions and scenarios

HE²RO model structure and data sources

Data inventory

Data point
GIS
GIS location of all healthcare facilities
GIS location of all labs
GIS location and capacity of laboratory equipment that can conduct COVID tests
Capacity
Hospital beds/ICU beds by facility
Testing capacity (including person-time required due to more lab-staff intensive front-end PCR)
Human resource capacity: national number of healthcare workers by cadre
Underlying population
Population by province by age & SVI/NLI
Burden of comorbidities
Number of people suppressed on ART by small area
Total number of people living with HIV by small area
TB burden
Costs*
Cost of laboratory tests
Rapid full costing of different test types
Hospitalization costs

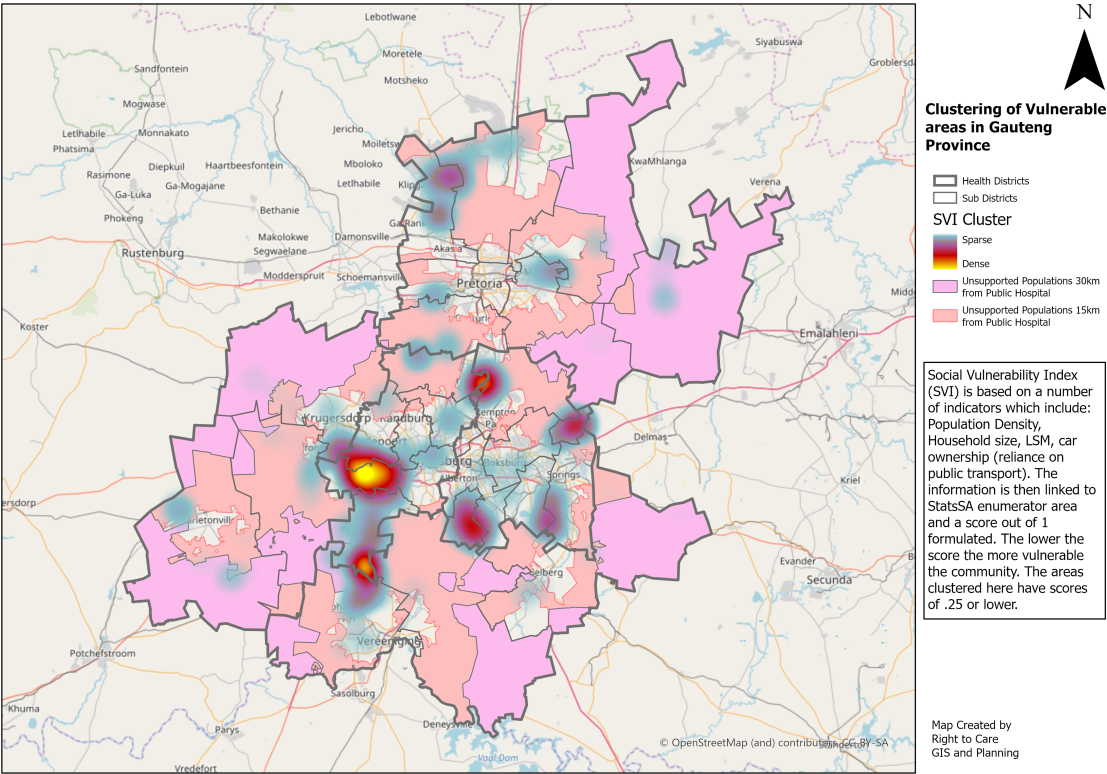
First: what can do we have and what can we use to make better predictions?

Assumptions and modeling strategy

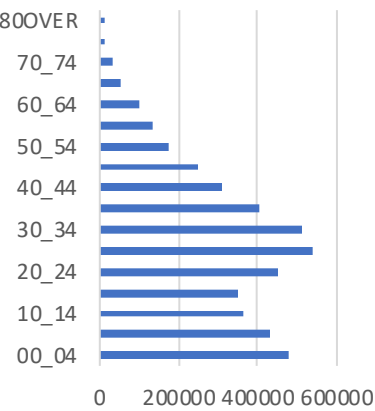
- Using South African data sources to update the pen source Covid-19 model developed by the Neher lab at Univ. of Basel (<https://neherlab.org/covid19/>)
- Need for hospitalisation/ critical care: differ by age strata (1)
- Data on social vulnerability index (SVI)
- Added separate sets of predictions and underlying assumptions regarding contact rate (and therefore transmission probability and effective reproductive number) (2), and resource availability for each SVI quintile, then recompiled

(1) Underlying population data by SVI

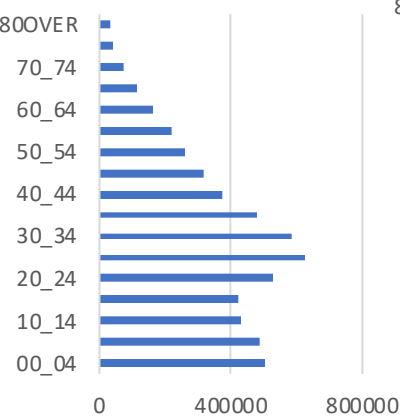
Population pyramids (absolute numbers, Gauteng) by SVI quintile



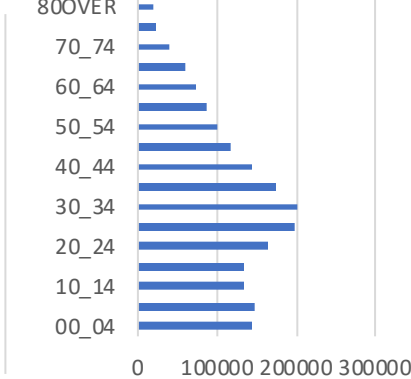
Lowest quintile



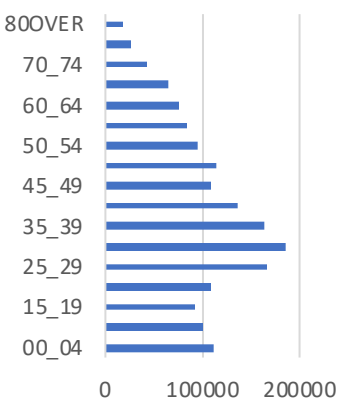
Quintile 2



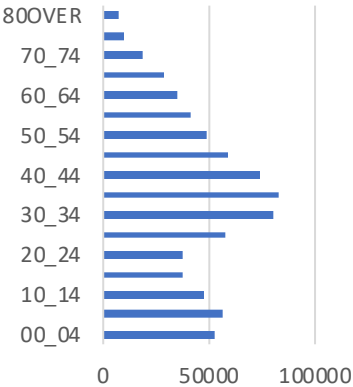
Quintile 3



Quintile 4



Highest quintile



(2) Reproductive number dependent on population density/communal spaces/etc. (which is also co-linear with SVI) ($\beta = c(\text{contact rate}) * p(\text{probability of transmission})$) $c(\text{contact rate})$ higher in areas with communal living and communal resources

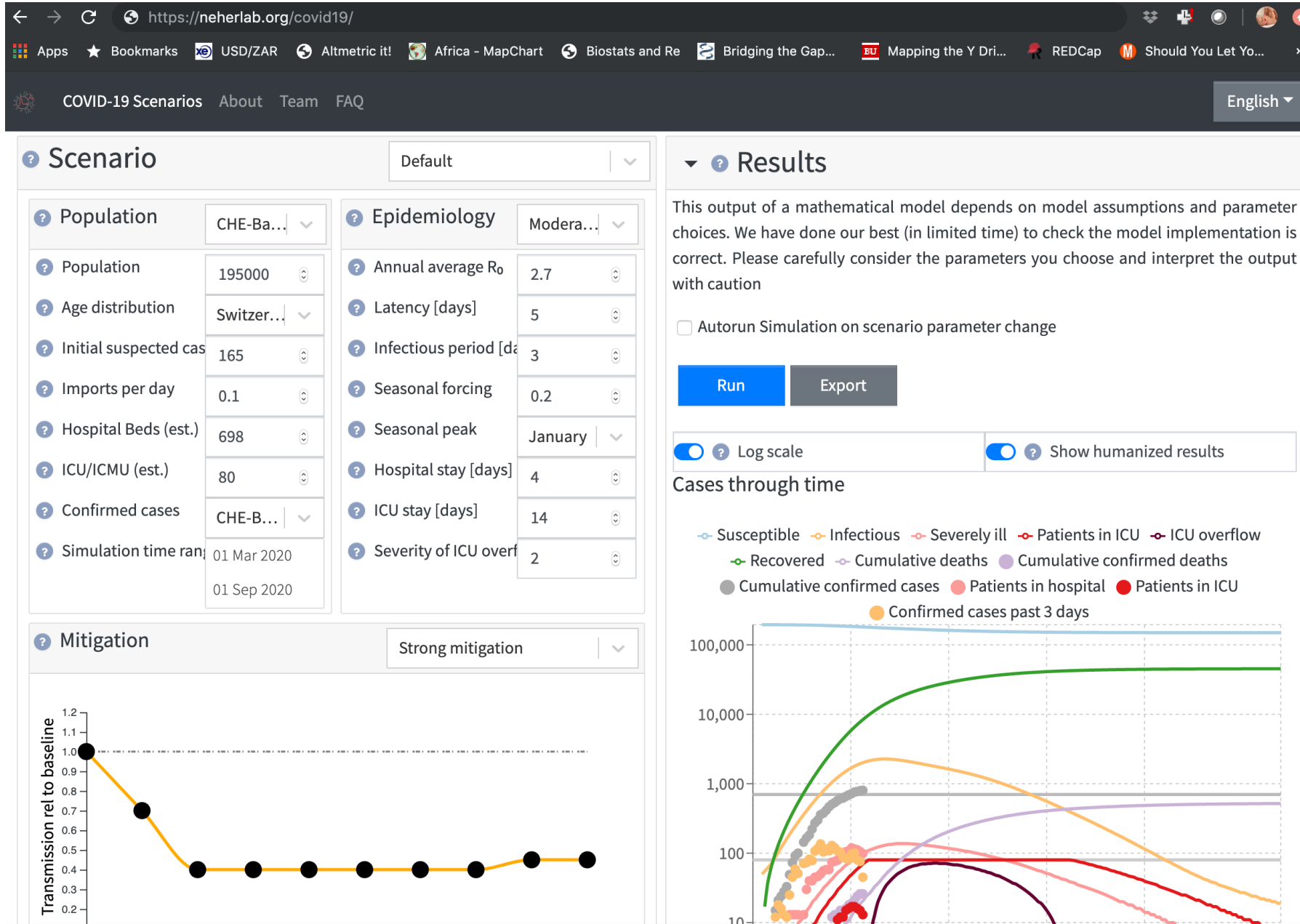
SVI quintile	Total population size	Reproductive number (no intervention)
1	4,497,939.00	3.2
2	5,226,576.00	2.7
3	1,735,753.00	2.2
4	1,496,456.00	2.2
5	664,002.00	2.2

Increasing contact rates

Reproductive number in different areas can be re-estimated regularly

**Contact rates by SVI estimated through prior work in flu*

Given timelines, wanted to use an infrastructure that had already been developed:



Neher lab
University of Basel, Switzerland

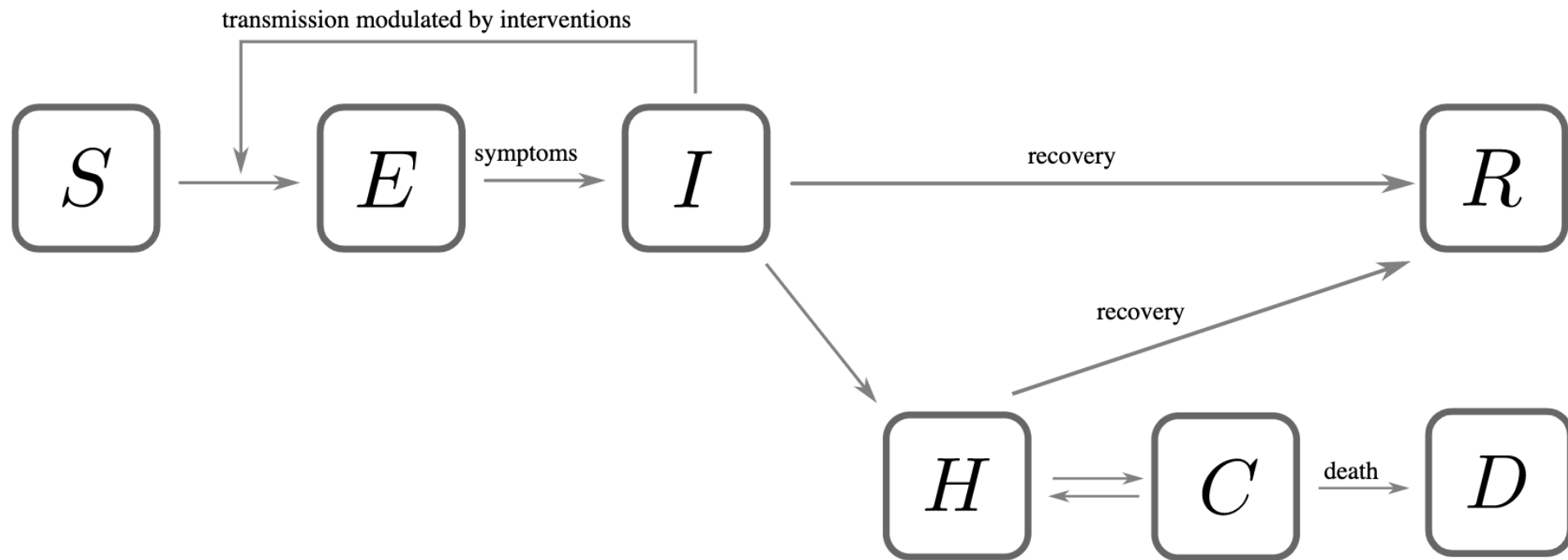
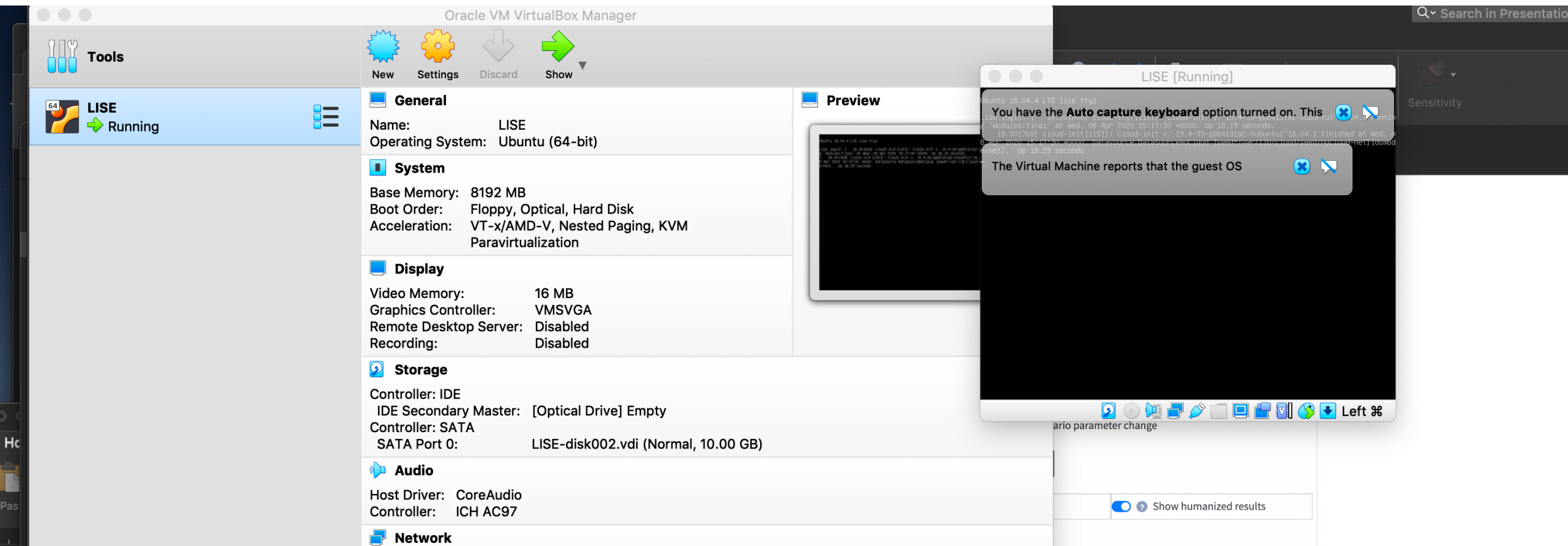


Figure 1. A schematic illustration of the underlying model. S corresponds to the 'susceptible' population, E is 'exposed', I is 'infectious', R 'recovered', H 'severe' (hospitalized), C 'critical' (ICU), and D are fatalities.

Since the Swiss group hadn't parameterized for South Africa in any sub-national way:
popped the hood on the model so we could re-parameterize for South Africa by provinces specifically



https://github.com/neherlab/covid19_scenarios

Scenario

Custom ▾

Population

Custom ▾

Population	1517944
Age distribution	WC -Low ▾
Initial suspected cases	5
Imports per day	1
Hospital Beds (est.)	2282
ICU/ICMU (est.)	53
Confirmed cases	WC -Low ▾
Simulation time range	23 Mar 2020 04 Oct 2020

Epidemiology

Custom ▾

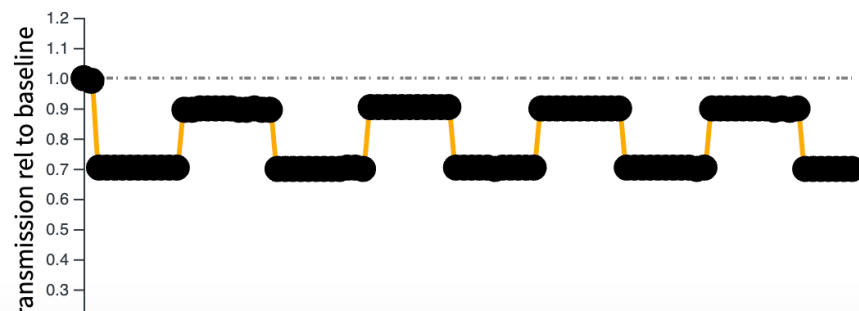
Annual average R_0	3.2
Latency [days]	3
Infectious period [days]	4
Seasonal peak	July ▾
Hospital stay [days]	12
ICU stay [days]	14
Severity of ICU overflow	2

Mitigation

Custom ▾

Number of points

100



Results

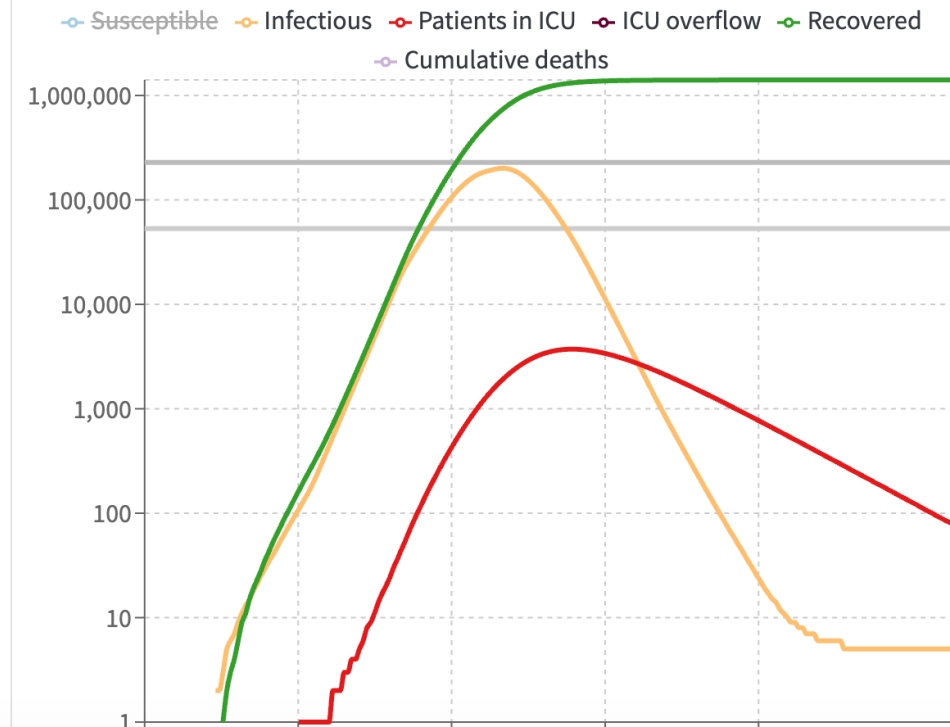
This output of a mathematical model depends on model assumptions and parameter choices. We have done our best (in limited time) to check the model implementation is correct. Please carefully consider the parameters you choose and interpret the output with caution

Run

Export

Built in underlying known data and flexibility

Cases through time



Scenario

Custom ▾

Population

Custom ▾

Population	1517944
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Epidemiology

Custom ▾

Annual average R_0	3.2
Latency [days]	3
Infectious period [days]	4
Seasonal forcing	0.1
Seasonal peak	July ▾
Hospital stay [days]	12
ICU stay [days]	14
Severity of ICU overflow	2

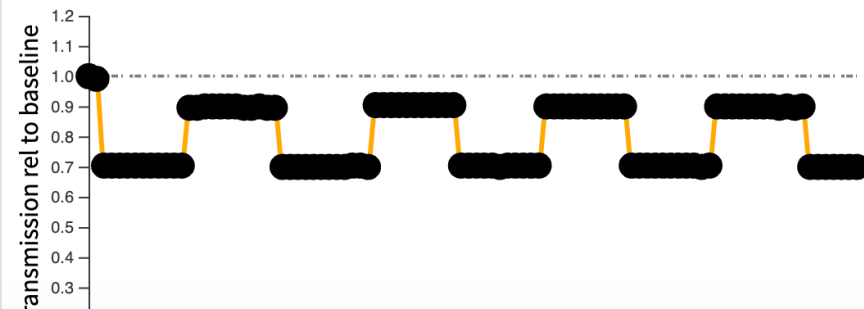
Literature and consensus expert opinion

Mitigation

Custom ▾

Number of points

100



Results

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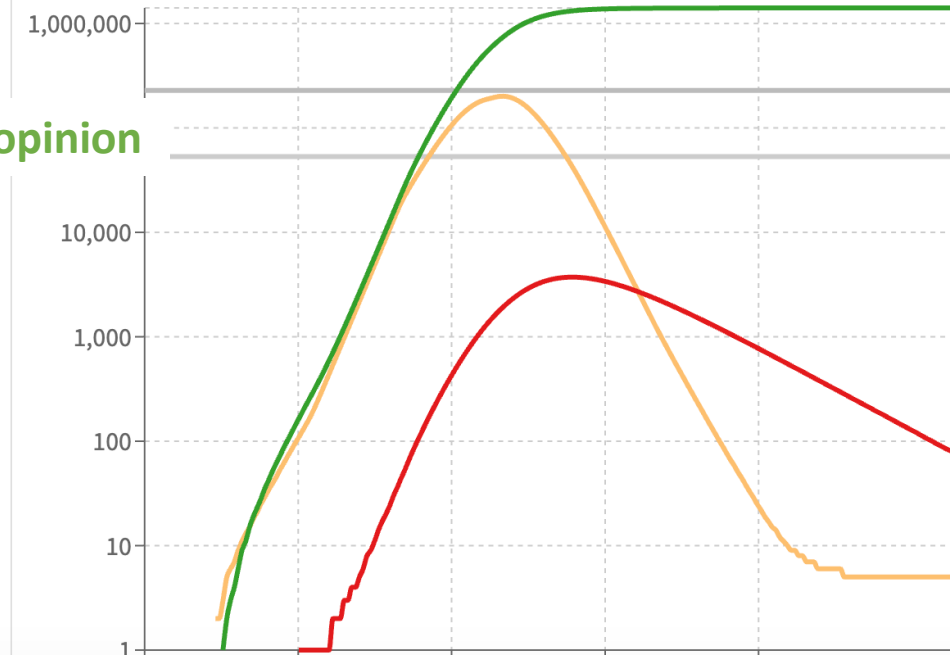
Run

Export

☒ Log scale

Cases through time

— Susceptible
— Infectious
— Patients in ICU
— ICU overflow
— Recovered
— Cumulative deaths



Scenario

Custom ▾

Population

Custom ▾

Population

1517944

Age distribution

WC -Low ▾

Initial suspected cases

5

Imports per day

1

Hospital Beds (est.)

2282

ICU/ICMU (est.)

53

Confirmed cases

WC -Low ▾

Simulation time range

23 Mar 2020

04 Oct 2020

Epidemiology

Custom ▾

Annual average R_0

3.2

Latency [days]

3

Infectious period [days]

4

Seasonal forcing

0.1

Seasonal peak

July ▾

ICU stay [days]

14

Severity of ICU overflow

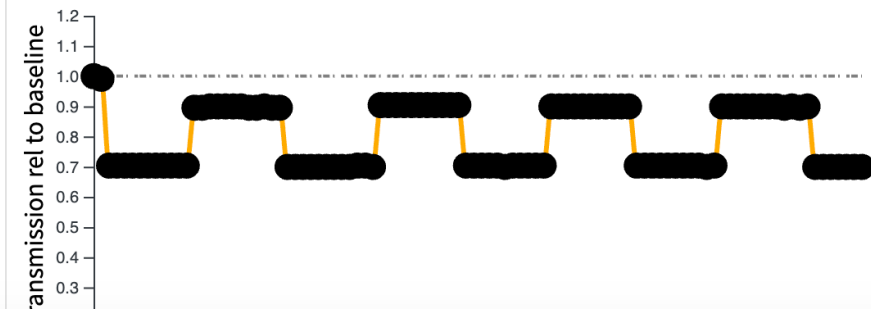
2

Mitigation

Custom ▾

Number of points

100



Results

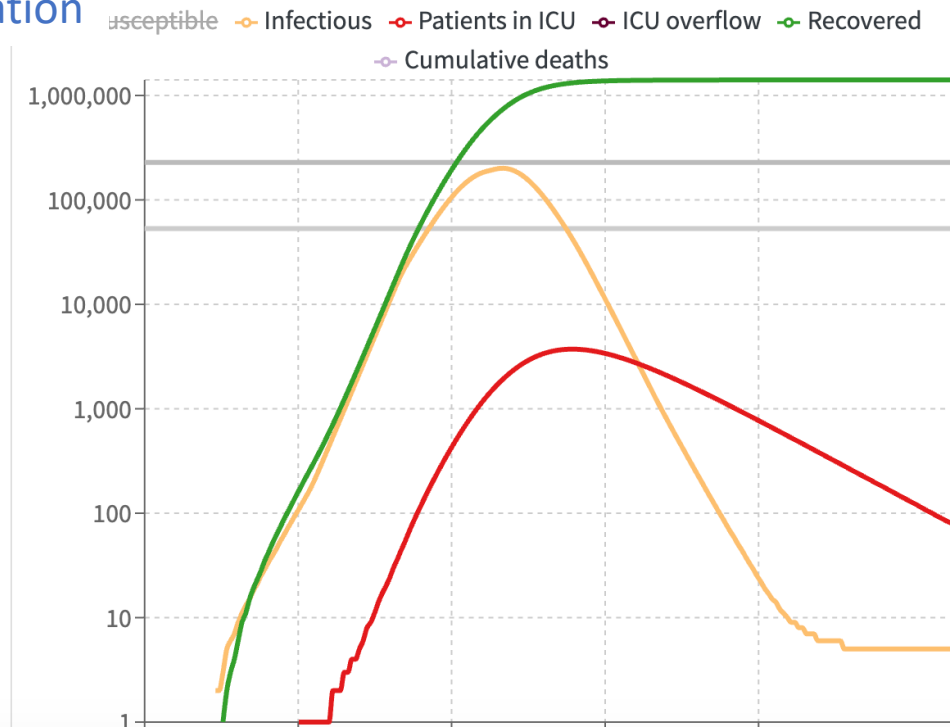
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☒ Log scale

Cases through time





Model for validation

Health Economics and Epidemiology Research Office

HERO²

Wits Health Consortium
University of the Witwatersrand



Model for validation



SACEMA

DST-NRF Centre of Excellence
in Epidemiological
Modelling and Analysis

Primary model for further development

- In depth parameter estimation
- National budgeting
- Resource needs estimation and tools
- Starting next week, direct programming of their model to increase capacity

Acknowledgements

Health Economics and Epidemiology Research Office

HERO²

Wits Health Consortium
University of the Witwatersrand



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