

Topic 2

January 11, 2022

Compare epidemiological parameters, including patterns of viral spread between health regions and hotspots/non-hotspots within each province (phylogenetic studies with simple compartmental epidemic models linked to viral genealogies).

- Fit model to populations in Ontario + Quebec, use estimates of epidemiological parameters to conclude something about effects of different NPIs on transmission
- Can extend to include spatial spread, other heterogeneity if the data is sufficient

1 Model

Compartmental differential equation models have been used extensively to model competing viral strains (see e.g. [1,4,6,8]). We can further subdivide population into high-SES vs low-SES. This raises some further questions that are difficult to answer. E.g. What is the extent of transmission between high and low SES groups?

Another approach that seems to be used more widely with Sars-CoV-2 is a semi-mechanistic, renewal equation based approach as in [2,3,5,7,9].

Some assumptions:

- Distinguish infections as VOC and non-VOC (possibly more detail?)
- VOC and non-VOC have different infection rates, recovery times
- Co-infection negligible
- Time scale short enough that recovery from either infection grants immunity
- Vaccination immunity does not wane over model timescale ?
- Immunity from vaccination commutes with immunity from infection
- Vaccination reduces all infection parameters by the same proportion ?

- Vaccination rate is constant (not necessary since we have data on exact vaccination rates)

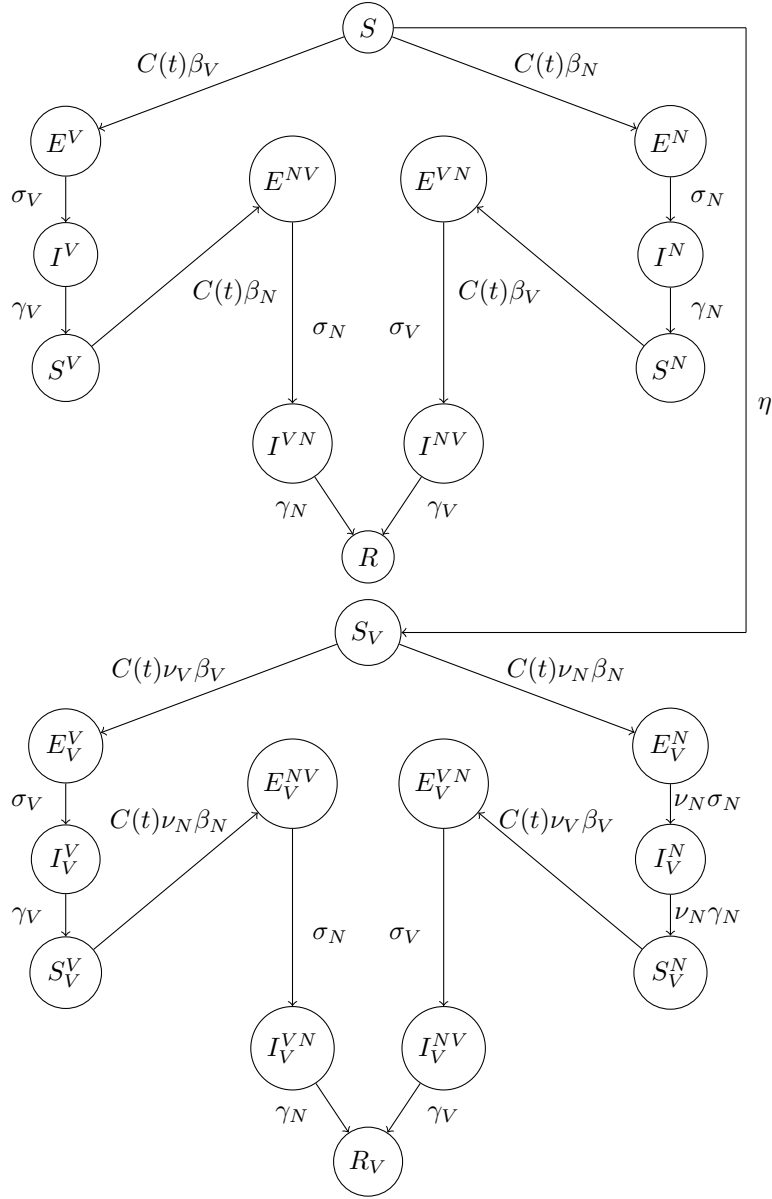


Figure 1: State diagram of model with vaccination and explicit competition

symbol	description	source
β_N	Transmission rate (Non-VoC)	
σ_N	Inverse of latent period (Non-VoC)	
γ_N	Recovery rate (Non-VoC)	
β_V	Transmission rate (VoC)	
σ_V	Inverse of latent period (VoC)	
γ_V	Recovery rate (VoC)	
η	Vaccination rate (time dependent?)	
$C(t)$	Time varying contact rate due to lockdown protocol	
S	Susceptible	
I^V	Infected with VoC	
I^N	Infected with Non-VoC	
I^{VN}	Recovered from Non-VoC, infected with VoC	
I^{NV}	Recovered from VoC, infected with non-VoC	
E^{VN}	Recovered from Non-VoC, exposed to VoC	
E^{NV}	Recovered from VoC, exposed to non-VoC	
R	Recovered	
E^V	Exposed to VoC	
E^N	Exposed to Non-VoC	
S^V	Recovered from Non-VoC, susceptible to VoC	
S^N	Recovered from VoC, susceptible to non-VoC	
S_V	Vaccinated, Susceptible	
I_V^V	Vaccinated, Infected with VoC	
I_V^N	Vaccinated, Infected with Non-VoC	
I_V^{VN}	Vaccinated, Recovered from Non-VoC, infected with VoC	
I_V^{NV}	Vaccinated, Recovered from VoC, infected with non-VoC	
E_V^{VN}	Vaccinated, Recovered from Non-VoC, exposed to VoC	
E_V^{NV}	Vaccinated, Recovered from VoC, exposed to non-VoC	
R_V	Vaccinated, Recovered	
E_V^V	Vaccinated, Exposed to VoC	
E_V^N	Vaccinated, Exposed to Non-VoC	
S_V^V	Vaccinated, Recovered from Non-VoC, susceptible to VoC	
S_V^N	Vaccinated, Recovered from VoC, susceptible to non-VoC	

Table 1: Table of symbols

2 Useful Data

2.1 General

- RePositive
- Investigation_Lineage
- Investigation_Mutation
- Accurate_Episode_Date
- Case_Reported_Date
- Client_Postal_Code
- Client_Province
- Client_Address_City
- Age_At_Time_of_Illness
- Likely_Acquisition
- Outbreak_Number
- Setting_Combined
- Epidemiologic_Linkage
- Epidemiologic_Link_Status

2.2 Social determinants of health

- Res_AdultDevServices
- Res_AdultYouthAddiction
- Res_ChildrensRes_Site
- Res_CorrectionalF
- Res_HomelessShelter
- Res_LTCH
- LTCH_Resident
- LTCH_HCW
- Res_RetirementHome
- Res_SupportiveHousing

- Res_OtherCongregateCare
- Res_VAWorAHT_Site
- Ses_Income
- SES_HHSize_Num
- Occ_LTCH
- Ses_Race_Black
- Ses_Race_East_Southeast_Asian
- Ses_Race_South_Asian
- Ses_Race_White
- Ses_Race_Middle_Eastern
- Ses_Race_Latino
- Immunocompromised

References

- [1] Samuel Alizon and Minus van Baalen. Multiple infections, immune dynamics, and the evolution of virulence. *The American Naturalist*, 172(4):E150–E168, Oct 2008.
- [2] Simon Cauchemez, Pierre Nouvellet, Anne Cori, Thibaut Jombart, Tini Garske, Hannah Clapham, Sean Moore, Harriet Linden Mills, Henrik Salje, Caitlin Collins, Isabel Rodriguez-Barraquer, Steven Riley, Shaun Truelove, Homoud Algarni, Rafat Alhakeem, Khalid AlHarbi, Abdulhafiz Turkistani, Ricardo J. Aguas, Derek A. T. Cummings, Maria D. Van Kerkhove, Christl A. Donnelly, Justin Lessler, Christophe Fraser, Ali Al-Barrak, and Neil M. Ferguson. Unraveling the drivers of mers-cov transmission. *Proceedings of the National Academy of Sciences*, 113(32):9081–9086, Aug 2016.
- [3] Christophe Fraser. Estimating individual and household reproduction numbers in an emerging epidemic. *PLoS ONE*, 2(8):e758, Aug 2007.
- [4] Marc Lipsitch, Caroline Colijn, Ted Cohen, William P. Hanage, and Christophe Fraser. No coexistence for free: Neutral null models for multistrain pathogens. *Epidemics*, 1(1):2–13, Mar 2009.
- [5] Swapnil Mishra, Tresnia Berah, Thomas A. Mellan, H. Juliette T. Unwin, Michaela A. Vollmer, Kris V. Parag, Axel Gandy, Seth Flaxman, and Samir Bhatt. On the derivation of the renewal equation from an age-dependent branching process: an epidemic modelling perspective. *arXiv:2006.16487 [q-bio, stat]*, Jun 2020. arXiv: 2006.16487.

- [6] Emily J. Nicoli, Diepreye Ayabina, Caroline L. Trotter, Katherine M.E. Turner, and Caroline Colijn. Competition, coinfection and strain replacement in models of bordetella pertussis. *Theoretical Population Biology*, 103:84–92, Aug 2015.
- [7] Pierre Nouvellet, Anne Cori, Tini Garske, Isobel M. Blake, Ilaria Dorigatti, Wes Hinsley, Thibaut Jombart, Harriet L. Mills, Gemma Nedjati-Gilani, Maria D. Van Kerkhove, Christophe Fraser, Christl A. Donnelly, Neil M. Ferguson, and Steven Riley. A simple approach to measure transmissibility and forecast incidence. *Epidemics*, 22:29–35, Mar 2018.
- [8] Minus van Baalen and Maurice W. Sabelis. The dynamics of multiple infection and the evolution of virulence. *The American Naturalist*, 146(6):881–910, Dec 1995.
- [9] J Wallinga and M Lipsitch. How generation intervals shape the relationship between growth rates and reproductive numbers. *Proceedings of the Royal Society B: Biological Sciences*, 274(1609):599–604, Feb 2007.