**MATLAB code details for model of SARS-Cov-2 transmission in remote Australian Aboriginal and Torres Strait Islander communities**

**M-files**

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| **File** | **Description** |
| Transmission only | |
| parameters\_base.m | Defines simulation set up and population parameters |
| parameters\_infection.m | Defines infection-related parameters |
| initialise\_demographics.m | Initialises age, dwelling set, current dwelling, unique agent ID for all agents |
| initialise\_infection\_status.m | Initialises infection and vaccination status of all agents |
| simulator.m | Simulates model |
| Response | |
| parameters\_response.m | Defines response parameters |
| manage\_agents\_with\_symptoms.m | Simulates isolation pathway |
| manage\_quarantine.m | Simulates quarantine pathway |
| lockdown.m | Simulates lockdown pathway |
| trace\_contacts.m | Simulates contact tracing (input is array of agent IDs that are having their contacts traced). If symptomatic, back trace from (parameters.LengthofTracing) before date of symptom onset to test date. If asymptomatic, back trace (parameters.LengthofTracing) days before test date |
| test\_sensitivity.m | Calculates test sensitivity, given time since symptom onset (input is array of times since symptom onset) |
| reactive\_vaccination.m | simulates reactive vaccination (receiving first dose) |
| Simulating batches of scenarios and generating output files for tables, figures, and data for clinical pathways model | |
| run\_preemptive.m | * Runs a single preemptive scenarios n=100 times. * Called by preemptive\_scenarios\_batch.m * Saves model outputs from n runs of scenario i in cpw\_outputs/batch\_preemptive\_i.mat |
| run\_reactive.m | * Runs a single reactive scenarios n=100 times. * Called by reactive\_scenarios\_batch.m * Saves model outputs from n runs of scenario i in cpw\_outputs/batch\_reactive\_i.mat |
| preemptive\_scenarios\_batch.m | Runs a batch of scenarios with various preemptive vaccination set ups. Parameters defining the scenarios are in 'data/preemptive\_scenarios.xlsx'. Each scenario is run n=100 times. |
| reactive\_scenarios\_batch.m | Runs a batch of scenarios with various reactive vaccination set ups. Parameters defining the scenarios are in 'data/reactive\_scenarios.xlsx'. Each scenario is run n=100 times. |
| create\_cpw\_data.m | Run this script to generate data for clinical pathways model from transmission model mat files (cpw\_outputs/batch\_preemptive\_i.mat, cpw\_outputs/batch\_reactive\_i.mat)   * Set reactive=1 on line 3 before running if generating data from reactive scenarios * Set reactive=0 on line 3 before running if generating data from preemptive scenarios * Generates a csv file for each response scenario I in folder cpw\_outputs/clinical\_pathways\_model\_inputs, either:   + - remote\_communities\_cpw\_reactive\_i.csv     - remote\_communities\_cpw\_preemptive\_i.csv |
| Generate figures and tables from transmission model | |
| generate\_tables\_figures\_reactive.m | Creates prevalence figures and saves cumulative infections in vaccinated and unvaccinated subpopulations in age groups in spreadsheet for reactive vaccination scenarios |
| generate\_tables\_figures\_preemptive.m | Creates prevalence figures and saves cumulative infections in vaccinated and unvaccinated subpopulations in age groups in spreadsheet for preemptive vaccination scenarios |
| Model calibration | |
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**Main structure arrays**

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| **Structure** | **Description** |
| parameters | Stores all model parameters (some of these are updated throughout the simulations, but most are static) |
| AgentCharacteristics | Stores the current infection state, age, vaccination state, dwelling set, current household, contact data, details related to outbreak response of agents |
| SummaryStatistics | Stores statistics of interest for model outputs |

**AgentCharacteristics structure**

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| --- | --- | --- |
| **Field** | **Description** | **Size** |
| Age | Age of each agent | (parameters.PopSize, 1) |
| HouseholdList | Stores set of dwelling IDs (parameters.HHIDs) of each agent’s dwelling set:  HouseholdList(i,:) = [core, regular, on/off] HHID | (parameters.PopSize, 3) |
| CurrentHousehold | Stores dwelling ID (parameters.HHIDs) of each agent’s current dwelling | (parameters.PopSize, 1) |
| ID | Stores unique agent ID for each agent (birth/death can lead to a row in AgentCharacteristics.x being replaced by that of a new agent, but when this happens a new ID is created) | (parameters.PopSize, 1) |
| InfectionStatus | Stores array of details of infection status for each agent:  InfectionStatus(i,1) = 0: susceptible,  1: exposed, E  2: presymptomatic infectious, PI  3: symptomatic infectious, I  4: presymptomatic, asymptomatic infectious, PA  5: asymptomatic infectious, A  6: recovered, R    InfectionStatus(i,2) = Time to leave E (time unity days for all durations here)  InfectionStatus(i,3) = Time to leave PI/PA  InfectionStatus(i,4) = Time to leave I/A | (parameters.PopSize, 4) |
| VaccinationStatus | Stores array of details of vaccination status for each agent:  VaccinationStatus(i,1): # of doses of Pfizer  VaccinationStatus(i,2): proportional effect of VE given # of doses of Pfizer  VaccinationStatus(i,3): # of doses of AZ  VaccinationStatus(i,4): proportional effect of VE given # of doses of AZ  Proportional effect of VE has a range of [0,1]. E.g.,   * if 1 dose: effective VE = (proportional effect of VE) \* max\_VE\_dose 1 * if 2 doses: effective VE = max\_VE\_dose 1 + (proportional effect of VE) \*   (max\_VE\_dose 2 - max\_VE\_dose 1)  VaccinationStatus(i,5): Relevant when all or nothing vaccination considered. With all or nothing, VE effect is either 0 or fully protective.  = 0 if agent has no reduction in infection/sympt frac  = 1 if agent is fully protected (not susceptible). | (parameters.PopSize, 5) |
| ReactiveVaccination | Stores details about timing of scheduled vaccinations and vaccine hesitancy.  ReactiveVaccination (i,1): if awaiting second dose, time until can have second dose (units days)  ReactiveVaccination (i,2): if had second dose during simulation, this is 0.  This is set to -1 for fully vacced at start of simulation. (only relevant for double vacced)  ReactiveVaccination(i,3): = 1: vaccine hesitant,  0: otherwise | (parameters.PopSize, 3) |
| Contacts | Stores contact data for agents during their infectious period  Contacts{j,1} = [ (unique agent IDs of contacts of agent j while infectious) binary value timestep]  Where the binary value =1 if it is a household contact, 0 otherwise | parameters.PopSize \* 1 cell array, where each cell is a k\*3 matrix, k is number of contact events |
| Symptoms | Stores array of details of agents who develop symptoms:  AgentCharacteristics.Symptoms(i,1)=  0: no symptoms  1: self isolating, awaiting test result  2: self isolating, have test result, awaiting move to isolation  3: isolating  4: isolating, awaiting clearance test result, will leave  5: isolating, awaiting clearance test result, will restart isolation  AgentCharacteristics.Symptoms(i,2)=time left in case state (if a case, time units is days)  AgentCharacteristics.Symptoms(i,3)=time since end of incubation period (time units is days) | (parameters.PopSize, 2) |
| TestSensitivity | Stores array of details of current test sensitivity of agents  AgentCharacteristics.TestSensitivity(i,1) = 1 if probability of true positive test for agent i is >0, 0 otherwise | (parameters.PopSize, 1) |
| Quarantine | Stores array of details of agents who are contact traced:  AgentCharacteristics.Quarantine(i,1)=  0: not currently being traced/managed  1: identified, awaiting entry into quarantine  2: in quarantine, going to isolation, waiting on test result  3: in quarantine, going to isolation, have test result, waiting on entering isolation  4: in quarantine, going to remain in quarantine, waiting on test result  5: quarantining  6: quarantining, awaiting clearance test result, will leave  AgentCharacteristics.Quarantine (i,2)=time left in quarantine state (if being managed, time units is days) | (parameters.PopSize, 2) |
| Lockdown | Stores array of details of agents who are in lockdown:  AgentCharacteristics.Lockdown(i,1)=  0: not currently in lockdown  1: identified, awaiting entry into lockdown  2: in lockdown, going to isolation, waiting on test result  3: in lockdown, going to isolation, have test result, waiting on entering isolation  4: in lockdown, going to remain in lockdown, waiting on test result  5: lockdown  6: lockdown, awaiting clearance test result, will leave  AgentCharacteristics. Lockdown (i,2)=time left in lockdown state (if in lockdown) | (parameters.PopSize, 2) |

**Parameters structure**

(grey1=defined in parameters\_base.m, white1: defined in parameters\_infection.m, grey2=calculated in initiliase\_demographics.m, white2=defined in simulator.m (pregenerate\_random\_numbers)), grey3: defined in parameters\_response.m

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| **Field** | **Description** | **Size** |
| dt | Duration of time step in days | 1 |
| dt\_years | Duration of time step in years | 1 |
| T | Duration of simulation in years | 1 |
| Ntimesteps | Number of discrete time steps per simulation | 1 |
| time | Time array | (1, Ntimesteps) |
| PopSize | Population size | 1 |
| NumberHouses | Number of dwellings in community | 1 |
| HHIDs | Array of unique IDs for each dwelling | (NumberHouses,1) |
| HHMobilityPD | Cumulative probability distribution for movement between an agent’s dwelling set | (1,4) |
| NumberAgeClassesContacts | Number of age categories with different contact rates | 1 |
| NumberAgeClassesDeath | Number of age categories with different death rates | 1 |
| AgeClassDividersContacts | Array of min/max ages of age groups that determine community contact rates | (1, NumberAgeClassesContacts+1) |
| AgeDeath | Maximum age of an agent | 1 |
| Ncontacts | Matrix of age-dependent contact rates (per time step) Ncontacts(i,j) = for agent in age group i, this is the rate of contact with agents in age group j. | (NumberAgeClassesContacts, NumberAgeClassesContacts) |
| NE0, NPI0, NI0, NPAI0, NA0, NR0 | Initial number of agents in each infection compartment | 1 |
| VP10, VP20, VAZ10, VAZ20 | Initial percentage of all agents in each vaccination compartment (may make this dependent on age) | 1 |
| Ptransmission | Base probability of transmission per contact | 1 |
| SymptomsACD | Array of min/max ages of age groups that determine relative susceptibility and probability of onset of symptoms (10 year age groups) | (1,9) |
| ProbabilitySymptoms | Array of age-dependent probabilities of symptoms given infection | (1,8) |
| RelativeTransmissibilityCom | Matrix of age-dependent relative transmission probabilities between age groups for community contacts | (17,17) |
| RelativeTransmissibilityHH | Matrix of age-dependent relative transmission probabilities between age groups for household contacts | (17,17) |
| ReductionOnwardTAsymptomatic | Relative contribution to force of infection of asymptomatics, compared to symptomatics | 1 |
| MeanDurationLatency, SDLatency | Latency period is assumed to follow a lognormal distribution with mu= MeanDurationLatency, sigma = SDLatency | 1 |
| MeanDurationIncubation, SDIncubation | Incubation period is assumed to follow a lognormal distribution with mu= MeanDurationIncubation, sigma = SDIncubation | 1 |
| MeanDurationSymptoms, SDSymptoms | Symptomatic period is assumed to follow a lognormal distribution with mu= MeanDurationSymptoms, sigma = SDSymptoms | 1 |
| Max\_VE\_Reduction\_Infection\_Pfizer\_Dose1, Max\_VE\_Reduction\_Infection\_Pfizer\_Dose2 | Maximum reduction in susceptibility, given 1 or 2 doses of Pfizer | 1 |
| Max\_VE\_Reduction\_SymptomaticInfection\_Pfizer\_Dose1, Max\_VE\_Reduction\_SymptomaticInfection\_Pfizer\_Dose2 | Maximum reduction in probability of symptoms, given 1 or 2 doses of Pfizer | 1 |
| Max\_VE\_Reduction\_Infection\_AZ\_Dose1, Max\_VE\_Reduction\_Infection\_AZ\_Dose2 | Maximum reduction in susceptibility, given 1 or 2 doses of AZ | 1 |
| Max\_VE\_Reduction\_SymptomaticInfection\_AZ\_Dose1, Max\_VE\_Reduction\_SymptomaticInfection\_AZ\_Dose2 | Maximum reduction in probability of symptoms, given 1 or 2 doses of AZ | 1 |
| Max\_VE\_Reduction\_OnwardsT\_Pfizer\_Dose1, Max\_VE\_Reduction\_OnwardsT\_Pfizer\_Dose2 | Maximum reduction in probability of onwards transmission, given 1 or 2 doses of Pfizer | 1 |
| Max\_VE\_Reduction\_OnwardsT\_AZ\_Dose1, Max\_VE\_Reduction\_OnwardsT\_AZ\_Dose2 | Maximum reduction in probability of onwards transmission, given 1 or 2 doses of AZ | 1 |
| Max\_VE\_Reduction\_Infection\_Pfizer\_Dose1\_AON,  Max\_VE\_Reduction\_Infection\_Pfizer\_Dose2\_AON | VE for all or nothing vaccination, given 1 or 2 doses of Pfizer | 1 |
| parameters.Max\_VE\_Reduction\_Infection\_AZ\_Dose1\_AON, parameters.Max\_VE\_Reduction\_Infection\_AZ\_Dose2\_AON | VE for all or nothing vaccination, given 1 or 2 doses of AZ | 1 |
| allornothingve | = 0 if leaky vaccine protection,  = 1 if all or nothing vaccine protection | 1 (only tested for pre-emptive scenarios, not reactive scenarios) |
| ProbabilityPerTimeStep0to1VE\_Pfizer\_Dose1,  ProbabilityPerTimeStep0to1VE\_Pfizer\_Dose2 | Probability per timestep (during time dependent VE stage) of obtaining full protection for 1 or 2 doses of Pfizer (relevant for all or nothing vaccine protection) | 1 |
| ProbabilityPerTimeStep0to1VE\_AZ\_Dose1,  ProbabilityPerTimeStep0to1VE\_AZ\_Dose2 | Probability per timestep (during time dependent VE stage) of obtaining full protection for 1 or 2 doses of AZ (relevant for all or nothing vaccine protection) | 1 |
| OnwardsTCorrection | (i,j) Correction factor for VE onwards transmission for age group i (5 year age groups)  j=1: Pfizer dose 1  2: Pfizer dose 2  3: AZ dose 1  4: AZ dose 2 | (17,4) |
| VE\_Effect\_Over\_Time\_Dose1 | Array that tracks the increase in effect of VE from first dose over time. Starts at 0 on day of vaccination, and reaches 1 after 3 weeks. | (1, 21/ dt+1) |
| VE\_Effect\_Over\_Time\_Dose2 | Array that tracks the increase in effect of VE from second dose over time. Starts at 0 on day of vaccination, and reaches 1 after 2 weeks. | (1, 14/dt+1) |
| nahh | Number of agents currently in each dwelling | (1, NumberHousees) |
| countID | Maximum unique ID of agents | 1 |
| UniformRand | Stores pre-generated uniformly distributed random numbers | (10^5, 1) |
| countUR | Stores index of first un-used uniformly distributed random number (updated when a uniformly distributed random number is used) | 1 |
| ContactsNumberRand | Stores pre-generated matrices of Poisson distributed random numbers of number of contacts for each age group | (NumberAgeClassesContacts, NumberAgeClassesContacts, 10^5) |
| countCNR | Stores index of first un-used contact matrix (updated after a matrix is used) | 1 |
| DurationInfectionRand | Stores pre-generated arrays of lognormally distributed random numbers for latency, incubation and symptomatic periods | (10^5, 3) |
| countDIR | Stores index of first un-used array of infection durations (updated after an array is used) | 1 |
| response | 1: response switched on  0: response switched off | 1 |
| qpolicy | 1: CTP2, quarantined and isolated removed from community  2: CTP1, isolated removed from community, quarantined can contact core HH members | 1 |
| MinDurationQua | Minimum duration of quarantine | 1 |
| MinDurationIso | Minimum duration of isolation | 1 |
| MinDurationLoc | Minimum duration of lockdown | 1 |
| DelayOnsetSymptTestResult | Delay to self-isolated receiving test results (days) | 1 |
| QuarantineClearanceTestDay | Delay to quarantined receiving clearance test results (days) | 1 |
| LockdownClearanceTestDay | Delay to agents in lockdown receiving clearance test results (days) | 1 |
| EffectivenessContactTracing | Proportion of contacts found by tracers | 1 |
| LengthofTracing | Length of time can backtrace contacts from specified time (days) | 1 |
| EffectivenessSelfIsoH | Proportional reduction in household contact rates of agents in self-isolation | 1 |
| EffectivenessSelfIsoC | Proportional reduction in community contact rates of agents in self-isolation | 1 |
| EffectivenessIsoH | Proportional reduction in household contact rates of agents in isolation | 1 |
| EffectivenessIsoC | Proportional reduction in community contact rates of agents in isolation | 1 |
| EffectivenessQuaH | Proportional reduction in household contact rates of agents in quarantine | 1 |
| EffectivenessQuaC | Proportional reduction in community contact rates of agents in quarantine | 1 |
| EffectivenessLocH | Proportional reduction in household contact rates of agents in lockdown | 1 |
| EffectivenessLocC | Proportional reduction in community contact rates of agents in lockdown | 1 |
| TestSensitivity | Array of 1/0 for each infection state (S,E,PI,I,PA,A,R) that determines whether it is possible (1) or not possible (0) to return a positive test result | (1,7) |
| lockdown | 1: lockdown response switched on  0: lockdown response switched off | 1 |
| reactivevacc | 1: reactive vaccination response switched on  0: reactive vaccination response switched off | 1 |
| DelayStartReactiveVaccination | Delay from case identification to start of reactive vaccination response (days) | 1 |
| DailyMaxVaccination | Rate of first dose reactive vaccination (doses per day) | 1 |
| Hesitancy | Proportion of unvaccinated who will not receive vaccination through reactive vaccination response | 1 |
| OlderFirst | 1: reactive vaccination gives surge vaccines to oldest unvaccinated first  0: reactive vaccination gives surge vaccines in random order to unvaccinated | 1 |
| DoseIntervalP | Interval between first and second dose of Pfizer for surge vaccinations (days) | 1 |
| DoseIntervalAZ | Interval between first and second dose of AstraZeneca for surge vaccinations (days) | 1 |
| MinAgeVaccination | Minimum age of vaccination | 1 |
| MinVEForSeverityDose1 | Corresponding value of VE\_Effect\_Over\_Time\_Dose1 when dose 1 severity protection takes effect (this delay is specified in TimeToSeverityEffectDose1, which is the delay from receiving first dose of vaccine to gaining protection against severity (days)) | 1 |
| MinVEForSeverityDose2 | Corresponding value of VE\_Effect\_Over\_Time\_Dose2 when dose 2 additional severity protection takes effect (this delay is specified in TimeToSeverityEffectDose2, which is the delay from receiving second dose of vaccine to gaining further protection against severity (days)) | 1 |

**SummaryStatistics structure**

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| **Field** | **Description** | **Size** |
| InfectorInfecteePairs | Stores array of  [unique agent ID for infector,  unique agent ID infectee,  age of infectee,  whether household transmission {1,0}  dwelling of infectee,  timestep,  number susceptible in infectors dwelling,  number susceptible in infecteds dwelling,  ]  (note, time here is in timesteps, not necessarily days) | (Cumulative number of transmission events, 7) |
| CaseData | [unique agent ID of case, CurrentHousehold at time of notification, Age of case, time of notification (days) 1/2/3 VaccStatus]  1: case enters iso from self-iso  2: case enters iso from quarantine  3: case enters iso from lockdown  \*\*Extra column added after timeloop: day of onset | (Cumulative number of cases, 9) |
| TestDate | [unique agent ID for agent with +ve test, time of test (days)] | (Cumulative number of +ve tests, 2) |
| TimeSymptomOnset | Stores array of [unique agent ID, time of symptom onset] for symptomatic infections.  (note, time here is in timesteps, not necessarily days) | (Cumulative number of symptomatic infections, 2) |
| NumberInfectionVaccinationAgeStatusTime | Stores 7\*5\*84 array each timestep. (i,j,k,t) is the number of agents in infection state i, in vaccine state j, in age group k, at day t.  Infection states:  1: exposed,  2: presymptomatic infectious,  3: symptomatic infectious,  4: presymptomatic asym infectious,  5: asym infectious,  6: recovered  7: susceptible  Vaccination states  1: 1 dose Pfizer  2: 2 dose Pfizer  3: 1 dose AZ  4: 2 dose AZ  5: 0 doses  Age Status  k: k-1 to k years old | (7,5,84,Ntimesteps) |
| AgeVaccIncidence | Stores 84\*5 array each day. (k,j,t) stores number of infections in each age group k, in vaccine state j, at day t  Vaccination states  1: 1 dose Pfizer  2: 2 dose Pfizer  3: 1 dose AZ  4: 2 dose AZ  5: 0 doses  Age Status  k: k-1 to k years old | (84,5, number of days in simulation) |
| NumberInQTime | Number of agents in quarantine over time | (1,Ntimesteps) |
| NumberInITime | Number of agents in isolation over time | (1,Ntimesteps) |
| NumberInLTime | Number of agents in lockdown over time | (1,Ntimesteps) |

**Pseudo code for simulator.m**

(E: exposed, PI: pre-symptomatic infectious, I: symptomatic infectious, PA: presymptomatic infectious to become asymptomatic, A: asymptomatic infectious, R: recovered, S: susceptible)

* Calculate summary statistics for t=0 from AgentCharacteristics
* For each time step
  + Store temporary current infection, vaccination and response status of agents, and use these to update AgentCharacteristics in the following steps
  + If no infected agents left, stop simulation
  + For each agent in E, check their time remaining in E
    - If time remaining in E < 0,
      * if uniform random number < probability of developing symptoms
        + move to PI
      * else
        + move to PA
    - else
      * update time remaining in E
  + For each agent in PI or PA
    - If time remaining in PI / PA < 0,
      * move to I / A
      * store time of symptom onset
      * move agents with symptoms into isolation pathway
    - else
      * update time remaining in PI / PA
  + For each agent in I or A
    - If time remaining in I / A < 0,
      * move to R
    - else
      * update time remaining in I / A
  + Determine relative susceptibility of all agents based on response status
  + Calculate relative infectiousness of infected agents based on vaccination, age and symptom status
  + For each infectious agent
    - Determine their relative infectiousness to household and community contacts based on their response status
    - Find current household members and add to household contact list
    - Find non-household contacts and add to community contact list
    - Store contact list for infectious agent for contact tracing
    - Determine whether transmission occurs to any of these contacts, based on susceptibility of contacts, infectiousness of infectious agent, location of contact
    - For each transmission event
      * Sample infection durations and set timers for infectees
      * Store infector-infectee pair data
      * Store data for clinical pathways model
  + If it is a new day in the simulation, for each agent determine whether their current dwelling is their core dwelling, regular dwelling, on/off dwelling, or a dwelling chosen uniformly at random
  + For each agent
    - If age of agent is greater than parameters.AgeDeath
      * Replace with susceptible, unvaccinated agent with age 0.
  + For each vaccinated agent who has not reached the full effect of given vaccine dose
    - Update relative VE
  + If reactive vaccination is switched on
    - Find agents who have had only one vaccine dose
    - For each of these agents
    - If they and who are due for second dose this time step.
      * Give second dose and update their vaccination status
    - else
      * Update their second dose timers
  + If response is switched on
    - Manage agents who are in the isolation pathway (see figure A1(a) in technical appendix)
    - Manage agents who are in the quarantine pathway (see figure A1(b) in technical appendix)
    - If first case has been identified
      * If lockdown not currently switched on
        + Initiate lockdown after a delay
      * else
        + Manage agents who are in the lockdown pathway (see figure A1(c) in technical appendix)
      * If reactive vaccination is not currently switched on
        + Initiate reactive vaccination after a delay
      * else
        + If new day in simulation

Find non vaccinated agents who are currently susceptible, not vaccine hesitant, and old enough to be vaccinated

Of these agents, select agents to be vaccinated based on vaccination rate and order of vaccination

Update vaccination status of these agents and set time to receive second dose

* + Update summary statistics
* Collate data for clinical pathways model
* Collate case data

end