ASKEM Final Evaluation (February 2025):
Epidemiology Independent Questions (IQ) Part 1

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These problems are intended to be more like independent textbook problems. Each Set will have 2-3 questions of varying difficulty/complexity. All problems are intended to be independent of each other, except for the Stratification questions which will build upon one another, from simple to complex.

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Section 1: Technical Area 1 Functionality

Set 1.1: Model Extraction and Unit Tests, for COVID Domain

Given a paper, extract the model with human-in-the-loop (HITL) curation, so that it can reproduce the unit test.

Three papers describing COVID-19 models of increasing complexity will be provided to ingest. The inputs will be a paper to extract a model from, and a model configuration to execute a unit test. The outputs expected will be a compartmental diagram and set of equations describing the extracted model, and some basic simulation plots demonstrating that the extracted model is executable and is correct enough to satisfy the unit test.

For baseline modelers, model extraction is defined as the following:

- Writing out or capturing the equations describing the model and drawing out the model structure. (You can write them out by hand but be sure to capture the image for the work product).
- Gathering definitions of all variables and parameters, with units
- Getting model into executable state (you may need to find and install code or write your own code to do this)
- Configuring model and running unit test, and iterating as required to satisfy the unit test criteria

For workbench modelers, model extraction is defined as the following:

- Ingesting the model from source paper or code, into the workbench
- Capturing the set of equations describing the model in the workbench
- Gathering definitions of all variables and parameters, with units
- Configuring model and running unit test, and iterating as required to satisfy the unit test criteria

General format of inputs, tasks, and outputs

Inputs	Tasks	Outputs
• Paper containing model description and equations • Model configuration (initial conditions, parameter values, simulation parameters) for unit test	• Extract model from paper with HITL curation • Configure model • Run unit test; iterate until expected unit test outputs are achieved	• Model in executable state • Compartmental diagram of the model and set of equations • Definitions of all variables and parameters, with units • Unit test results showing they match expected output

(Q1.1.1) *Set 1.1, Question 1: Model Extraction For Simple COVID-19 Model*

Inputs:

- Paper: "Identification and estimation of the SEIRD epidemic model for COVID19.pdf"
- Model configuration (initial conditions, parameter values, simulation parameters) for unit test (use the proportion of people in the population for each compartment – e.g., convert the numbers to a proportion of total population):
  (S, E, I, R, D, α, σ, β, λ, γ, dt, simulation length)
  = (2000 people, 50 people, 0 people, 0 people, 0 people, 0.01 (unitless proportion), 0.2 (day^{-1}), 3/18 (unitless proportion), 0.2 (unitless proportion), 1/18 (day^{-1}), dt = 1 day, simulation length = 100 days).

Tasks:

- Extract the model from the paper into an executable format, curating as necessary to ensure correctness. Extract or find variable and parameter definitions and units.
- As a unit test to ensure extraction was done correctly, configure the model using the initial conditions and parameter values described above. These parameter values are the minimum values of the ranges provided in the paper. Simulate the model using the proportion of total population in your simulation (e.g., convert the numbers to a proportion of total population) with these values for 100 days with dt = 1 day.

Outputs:

- Extracted model in executable state
- Compartmental diagram of the model with all transitions, and set of equations
- Definitions of all variables and parameters, with units
- Unit test results:
  - Single plot of state variables S and I (on same plot) as shown in the following plot. You should expect the peak of I to occur around day 81.

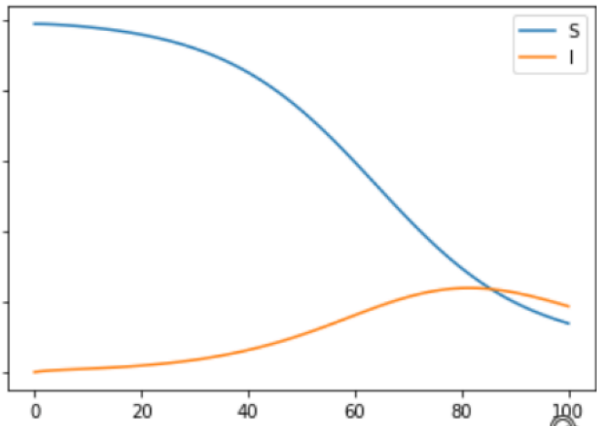

Figure 1 Example plot of state variables S and I

  - Single plot of state variable R

(Q1.1.2) *Set 1.1, Question 2: Model Extraction For Medium-Complexity COVID-19 Model*

Record how long it takes you to complete the following task:

Inputs:

- ***Mathematical Model 1*** from paper titled "Extended SEIQR type model for COVID19 epidemic and data analysis.pdf"
- Model configuration (initial conditions, parameter values, simulation parameters) for unit test: (S, E_1, E_2, I_a, I_s, Q, J, R, dt, simulation length) = (10000 people, 200 people, 100 people, 0 people, 0 people, 0 people, 0 people, dt = 1 day, simulation length = 100 days). For parameter values, see Table 1.For parameter values, see Table 1.

Table 1: Q1.1.2 Table of Parameters

Parameter	Value	Parameter	Value
β	0.5 day^{-1}	σ	0.25 (unitless)
η	0.5 day^{-1}	δ	0.75 day^{-1}
μ	0.29 day^{-1}	ζ_1	0.07 day^{-1}
ξ_1	0.14 day^{-1}	ζ_2	0.1 day^{-1}
ξ_2	0.075 day^{-1}	ζ_3	0.14 day^{-1}
p_1	0.195 (unitless)	ρ_1	0.075 day^{-1}
p_2	0.195 (unitless)	ρ_2	0.07 day^{-1}
p_3	0.195 (unitless)	ν	0.05 day^{-1}
p_4	0.195 (unitless)		

Tasks:

- Extract the model from the paper into an executable format, curating as necessary to ensure correctness. This paper starts with a base SEIQR model and extends the compartments to include two exposed populations, two infected populations, and a hospitalized population, creating an $SE_1E_2 I_a I_s$ QJR model. Note that the paper further extends the model beyond this, but we want to use the initial model provided in the section titled ***Mathematical Model 1***.
- Extract relevant metadata, including variable and parameter definitions, values, and units.
- Configure the model as described in the input configuration, and run the unit test

Outputs:

- Extracted model in executable state
- Compartmental diagram of the model with all transitions, and set of equations
- Definitions of all variables and parameters, with units
- Unit test results:
    - Plot of state variables I_a and I_s (on same plot)

- Plot of state variable Q. You should expect the peak of Q to occur around day 13, as shown in the following plot

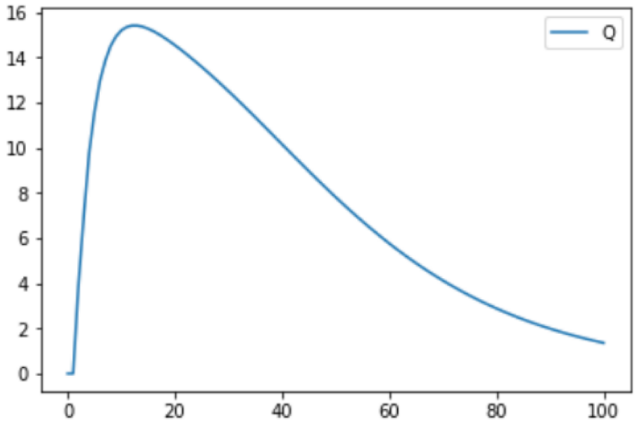

Figure 2 Example plot of state variable Q

(Q1.1.3) *Set 1.1, Question 3: Model Extraction For High-Complexity COVID-19 Model*

Inputs:

- Paper titled "A new SEAIRD pandemic prediction model.pdf"
- Model configuration (initial conditions, parameter values, simulation parameters) for unit test: Use initial values of S = 10000 people, E = 100 people, N = E+S = 10100 people, all other state variables = 0 initially. Use simulation length of 15 days and dt = 1 day. Use parameter settings as given in Table 2.

Table 2: Q1.1.3 Table of Parameters

Parameter	Value	Parameter	Value
β	0.002 day^{-1}	γ	0.15 day^{-1}
β_1	0.4 day^{-1}	γ_R	0.3 day^{-1}
α	1/5 day^{-1}	γ_Q	0.1 day^{-1}
μ	0.05 day^{-1}	γ_I	0.7 day^{-1}
ξ	0.1 (unitless)	ρ	0.1 (unitless)
φ	0.2 (unitless)	η	0.6 (unitless)
θ_1	0.2 (unitless)	ε	0.3 day^{-1}
θ_2	0.8 (unitless)	ω	0.2 day^{-1}
$p_1 (= 1 - p2)$	0.6 (unitless)	ν_1	0.005 day^{-1}
p_2	0.4 (unitless)	ν_2	0.005 day^{-1}

Tasks:

- Extract the model from the paper into an executable format, curating as necessary to ensure correctness. The model in this paper is an SEAIRD model with quarantining in stages S, E, and I.
- Configure the model according to initial conditions listed in the inputs, and the parameters in Table 2. Simulate the model for 15 days, with dt = 1 day.

Outputs:

- Extracted model in executable state
- Compartmental model diagram and set of equations
- Definitions of all variables and parameters (with units)
- Unit test results:
    - Plot of A over the simulation period. You should expect the peak to occur around day 9.
    - Plot of Sq and Iq (the quarantined and susceptible compartment and the quarantined and infected compartment) over the simulation time (on the same plot). The plot should look similar to the following plot:

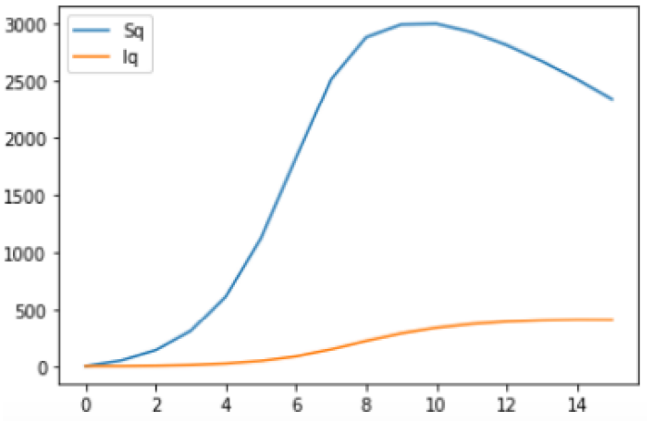

Figure 3 Example plot of state variables Sq and Iq

    - Plot of I_1 and I_2 over the simulation period on the same plot

Set 1.1 Summary Table

Question	Inputs (Both Teams)	Task	Outputs
Q1	• "Identification and estimation of the SEIRD epidemic model for COVID19.pdf" • Unit test configuration	Extract the SEIRD model and pass unit tests.	• Executable model • Compartmental diagram and set of equations • Definitions of variables and parameters with units • Plot of S and I • Plot of R

Q2	• "Extended SEIQR type model for COVID19 epidemic and data analysis.pdf" • Unit test configuration	Extract the SEIQR model and pass unit tests.	• Executable model • Compartmental diagram and set of equations • Definitions of variables and parameters with units • Plot of I_a and I_s • Plot of Q
Q3	• "A new SEAIRD pandemic prediction model.pdf" • Unit test configuration	Extract the SEAIRD model and pass unit tests.	• Executable model • Compartmental diagram and set of equations • Definitions of variables and parameters with units • Plot of S_q and I_q • Plot of A • Plot of I_1 and I_2

Set 1.2: Model Extraction and Unit Tests, for New Epi Domain

Given a paper, extract the model with human-in-the-loop (HITL) curation, so that it can reproduce the unit test.

Three papers describing epidemiology models of increasing complexity in domains other than COVID-19 will be provided to ingest. The inputs will be a paper to extract a model from, and a model configuration to execute a unit test. The outputs expected will be a compartmental diagram and set of equations describing the extracted model, and some basic simulation plots demonstrating that the extracted model is executable and is correct enough to satisfy the unit test.

Model extraction is defined as it was in **Set 1.1: Model Extraction and Unit Tests, for COVID Domain**. General format of inputs, tasks, and outputs for this set of questions matches the ***General format of inputs, tasks, and outputs*** for Set 1.1 as well.

(Q1.2.1) *Set 1.2, Question 1: Model Extraction For Simple Model in New Epi Domain*

Inputs:

- Paper: "The SIRC model and influenza A.pdf"
- Model configuration (initial conditions, parameter values, simulation parameters) for unit test (use the proportion of people in the population for each compartment – e.g., convert the numbers to a proportion of total population):
  (S, I, R, C, $\beta, \sigma, \alpha, \mu, \delta, \gamma$, simulation length, dt) = (1000 people,5 people,0 people, 0 people, 4/12 year^{-1}, 0.2 [unitless], 25/365 year^{-1}, 1/80 year^{-1}, 1/8 year^{-1}, 1/200 year^{-1}, 100 days, 1 day).

Tasks:

- Extract the SIRC model of Influenza A from the paper given, curating as necessary to ensure correctness. Use the prevalence of disease in your model (e.g., the proportion of population).
- Configure the model according to initial conditions and parameters listed in the inputs.
- Run unit test

Outputs:

- Extracted model in executable state
- Compartmental diagram of the model with all transitions, and set of equations
- Definitions of all variables and parameters, with units
- Unit test results:
    - Plot of state variables S and I (in the same plot) over the simulation period. You should expect the peak of I to occur somewhere around day 30, as shown in the following plot:

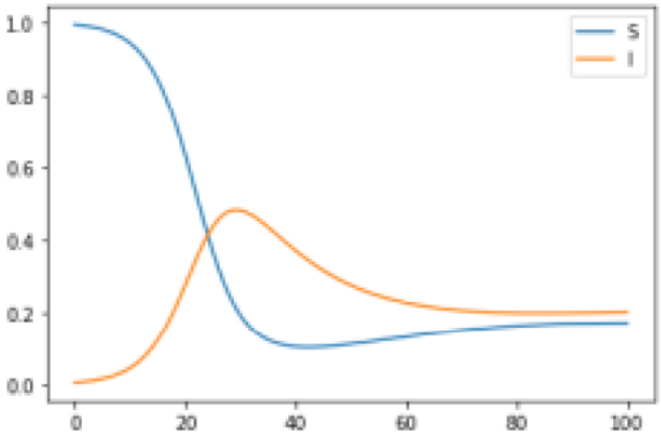

Figure 4 Example plot of state variables S and I

    - Plot of state variable C over the simulation period

(Q1.2.2) *Set 1.2, Question 2: Model Extraction For Medium-Complexity Model in New Epi Domain*

Inputs:

- Paper: "A Mathematical Model of Chikungunya Dynamics.pdf"
- Initial values for unit test (use the proportion of people in the population for each compartment – e.g., convert the numbers to a proportion of total population): S = 1000 people, E = 5 people, I = I_a = R = 0 people, X = 1000 mosquitoes, Y = 5 mosquitoes, Z = 0 mosquitoes. For parameter values, see
-
- Table 3. Simulation length is 100 days, with dt = 1 day

Table 3: Q1.2.2 Table of Parameters

Parameter	Value	Parameter	Value
β_1	0.14 day^{-1}	λ_1	0.5 day^{-1}
β_2	0.4 day^{-1}	λ_2	0.5 day^{-1}
ϕ	0.97 (unitless)	γ	0.25 day^{-1}
μ	0.05 day^{-1}		

Tasks:

- Extract the model of transmission of Chikungunya virus from mosquitos to humans from the paper. Curate as necessary to ensure correctness.
- Configure the model with the initial conditions and parameters described in the inputs. Use the proportion of people in the population for each compartment – e.g., convert the numbers to a proportion of total population.
- Run the unit test.

Outputs:

- Extracted model in executable state
- Compartmental diagram of the model and set of equations
- Definitions of all variables and parameters (with units)
- Unit test results:
    - Plot of S and R (on same plot), as shown in the following plot:

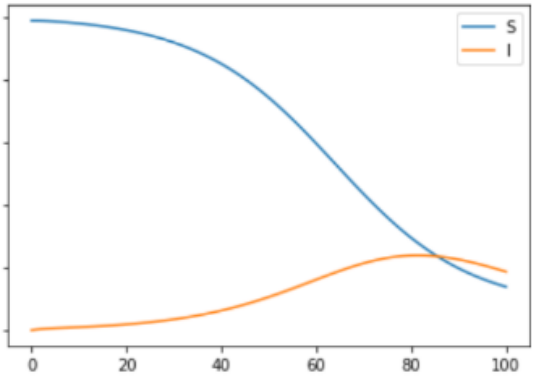

Figure 5 Example plot of state variables S and I

    - Plot of X. You should expect the minimum value of X to occur around day 81

(Q1.2.3) *Set 1.2, Question 3: Model Extraction For High-Complexity Model in New Epi Domain*

Inputs:

- Paper: "Modeling the spread of the Zika virus by sexual and mosquito transmission.pdf"
- For the unit test, use initial values of proportion of the human and mosquito populations: $S_w = 0.475$, $S_m = 0.475$, $E_w = E_m = 0.025$, $S_v = 0.913$, $E_v = 0.087$ (all values are unitless proportions of the population). All other initial values are 0.) Set parameter values according to Table 4. Simulation length is 150 days with dt = 1 day.

Table 4: Q1.2.3 Table of Parameters

Parameter	Value	Parameter	Value
λ_h	1/6.8 day^{-1}	ρ	0.07 (unitless)
λ_v	1/10 day^{-1}	ν	1/14 day^{-1}
β_{WM}	0.055 day^{-1}	ϕ	0.185 (unitless)
β_{MW}	0.0505 day^{-1}	γ_1	1/15 day^{-1}
β_{HV}	0.295 day^{-1}	γ_2	1/20 day^{-1}
β_{VH}	0.205 day^{-1}	γ_3	1/10.5 day^{-1}

Tasks:

- Extract the SEIRV model from the paper, and extract all definitions and units, curating as necessary to ensure correctness.
- As a unit test to ensure extraction was done correctly, configure the model using the initial conditions and parameter values described above.

Outputs:

- Extracted model in executable state
- Compartmental diagram of the model with all transitions, and set of equations
- Definitions of all variables and parameters, with units
- Unit test results:
  - Plot of I_V. You should expect the peak to occur around day 80, as show in the plot below

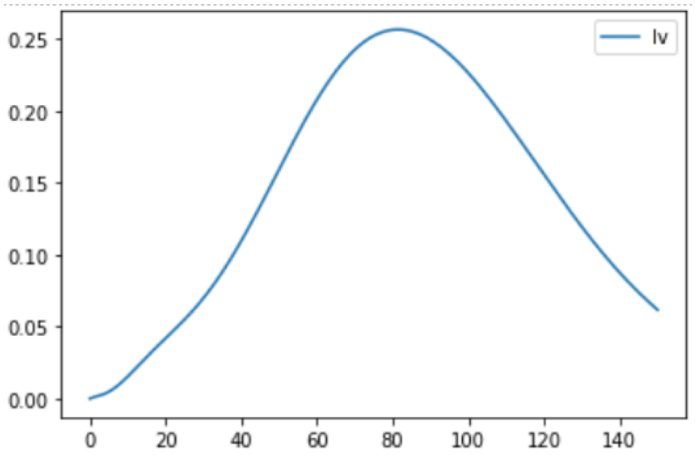

Figure 6: Example plot of state variable I_v

  - Plot of S_m and S_w on the same plot

Set 1.2 Summary Table

Question	Inputs (Both Teams)	Task	Output
Q1	• "The SIRC model and influenza A.pdf" • Unit test configuration	Extract the SIRC model of Influenza A and pass unit tests	• Executable model • Compartmental diagram and set of equations • Definitions of variables and parameters with units • Plot of S and I • Plot of C
Q2	• "A Mathematical Model of Chikungunya Dynamics.pdf" • Unit test configuration	Extract the Chikungunya model and pass unit tests	• Executable model • Compartmental diagram and set of equations • Definitions of variables and parameters with units • Plot of S and R • Plot of X
Q3	1. "Modeling the spread of the Zika virus by sexual and mosquito transmission.pdf" 2. Unit test configuration	Extract the Zika SEIRV model and pass unit tests	• Executable model • Compartmental diagram and set of equations • Definitions of variables and parameters with units • Plot of I_v • Plot of S_m and S_w

Section 2: Technical Area 2 Functionality

Set 2.1: Multi-model Structural Comparison

Compare the structures of 2-3 related models

Given multiple grounded compartmental models of a similar system or set of processes, do a structural comparison and provide output that clearly illustrates the similarities and differences between them (with respect to parameters, state variables or compartments, and transition pathways)

General format of inputs, tasks, and outputs

Inputs	Tasks	Outputs
2-4 models to be compared	Do a structural model comparison with the input models	A diagram that illustrates common and differing structural components of the models, along with any complementary text summary

(Q2.1.1) *Set 2.1, Question 1: Simple Model Comparison*

Inputs:

- Model A: Unstratified SIRD model in executable but unconfigured form as "ModelA" in the workflow titled "Q2.1.1" (Workbench) and in Q2.1.1 in the code notebook (Baseline)
- Model B: SIRD stratified by 3 age groups, in executable but unconfigured form in "ModelB" in the workflow titled "Q2.1.1" (Workbench) and in Q2.1.1 in the code notebook (Baseline)

Tasks:

- Do a structural model comparison

Outputs:

- A diagram and any accompanying description (which could include equations or not) that illustrates common and differing structural components of the models, along with any complementary text summary

(Q2.1.2) *Set 2.1, Question 2: Complex Model Comparison*

Inputs:

- Model A: Main model from Pinky et. al[1]. This model is in executable but unfigured form as "ModelA" in the workflow titled "Q2.1.2" (Workbench), and in Q2.1.2 in the code notebook (Baseline)
- Model B: Second model from Pinky et. al. This model is in executable but unfigured form as "ModelB" in the workflow titled "Q2.1.2" (Workbench), and in Q2.1.2 in the code notebook (Baseline)
- Model C: Third model from Pinky et. al. This model is in executable but unfigured form in "ModelC" in the workflow titled "Q2.1.2" (Workbench), and in Q2.1.2 in the code notebook (Baseline)

Tasks:

- Do a structural model comparison

Outputs:

- A diagram and any accompanying description (which could include equations or not) that illustrates common and differing structural components of the models, along with any complementary text summary

Set 2.1 Summary Table

	Inputs (Baseline)	**Inputs (Workbench)**	**Task**	**Output**
Q1	"ModelA" and "ModelB" in section Q2.1.1 in the code notebook	"ModelA" and "ModelB" in the workflow titled "Q2.1.1"	Do a structural model comparison	A diagram that illustrates common and differing structural components of the models, along with any complementary text summary
Q2	• "ModelA", • "ModelB", and "ModelC" in "Q2.1.2" in the code notebook • Pinky et al. paper describing the 3 models	• "ModelA", "ModelB", and "ModelC" in the workflow titled "Q2.1.2" • Pinky et al. paper describing the 3 models	Do a structural model comparison	

[1] L. Pinky, H. Dobrovolny, 'Epidemiological Consequences of Viral Interference: A Mathematical Modeling Study of Two Interacting Viruses', Front. Microbiol., 10 March 2022, https://doi.org/10.3389/fmicb.2022.830423. Note the supplementary file for this publication.

Set 2.2: Model Editing

Perform a variety of model edits to compartmental models

General format of inputs, tasks, and outputs

Inputs	Tasks	Outputs
• Base model • Instructions on what edits need to be made, with a diagram of the target model	• Make model edits of varying complexity according to instructions • Configure model	• Modified model in executable state and that meets the structure of the target model diagram

(Q2.2.1) *Set 2.2, Question 1: Simple Model Edits*

Inputs:

- SIR model in unconfigured but executable form in the workflow titled "Q2.2.1" (Workbench), and in section Q2.2.1 in the code notebook (Baseline).

Tasks:

- Split infection compartment into symptomatic infections and asymptomatic infections, and add a reinfection pathway from R to S. The edited model should match the structure shown in Figure 7.

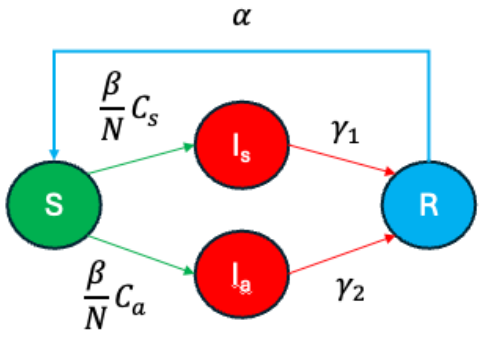

Figure 7. Target model structure for Q2.2.1

Outputs:

- Edited model whose structure can be visually inspected

(Q2.2.2) *Set 2.2, Question 2: Medium Complexity Model Edits*

Inputs:

- SEIRHD model in unconfigured but executable form in the workflow titled "Q2.2.2" (Workbench), and in Q2.2.2 in the code notebook (Baseline).

Tasks:

- Start with the SEIRHD model for a single virus. Extend this into a 2-virus model by combining it with an SIR model (representing virus 2).

- Add reinfection pathways for the recovered populations for both viruses.
- The combined model should have a single susceptible compartment, and match the diagram in Figure 8.

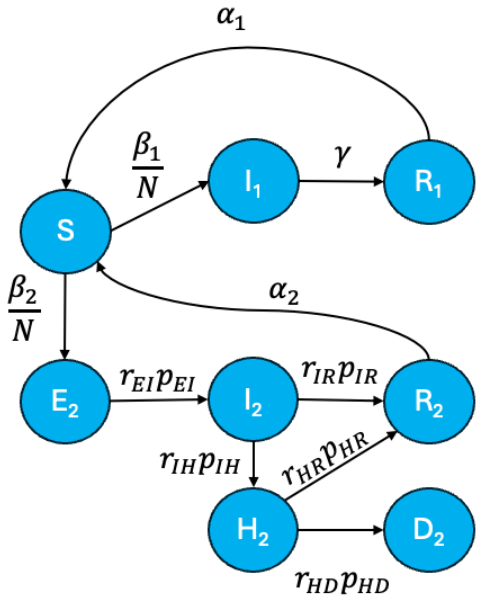

Figure 8. Target model structure for Q2.2.2

Outputs:

- Edited model in executable state and whose structure can be visually inspected

(Q2.2.3) *Set 2.2, Question 3: Complex Model Edits*

Inputs:

- Begin with the model described in Zafarnejad et. al[2], which is in unconfigured but executable form in the workflow titled "Q2.2.3" (Workbench), and in section Q2.2.3 in the code notebook (Baseline).

Tasks:

- Add hospitalization states for each category of infection (H_f, H_c, H_{fc}), and add new hospitalization parameters h_f, h_c, h_{fc} to describe the transitions from $I_f \rightarrow H_f$, $I_{fc} \rightarrow H_{fc}$, and $I_c \rightarrow H_c$.
- Add a single deceased state (do not delineate by virus type), and move the existing death rate outflows (with α_c, α_f, α_{fc}), to flows between the new hospitalization compartments, and the deceased compartment. Your edited model should match the structure in Figure 9.

[2] R. Zafarnejad, P. Griffin, M. Ventresca, 'A Joint Compartmental Model for The Co-infection of SARS-CoV-2 and Influenza', medRxiv 2022.08.26.22279281; doi: https://doi.org/10.1101/2022.08.26.22279281

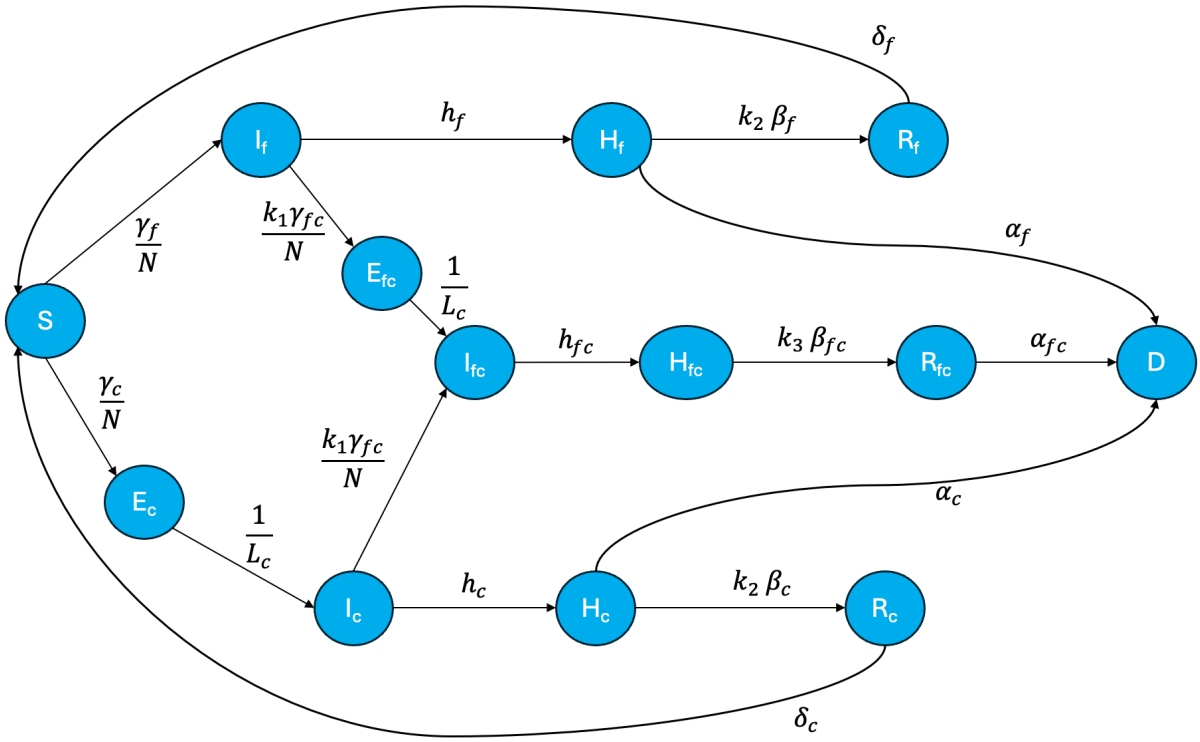

Figure 9. Target model structure for Q2.2.3

Output:

- Edited model in executable state and whose structure can be visually inspected

Set 2.2 Summary Table

Question	Inputs (Baseline)	Inputs (Workbench)	Task	Output
Q1	SIR	SIR link in Terarium	• Split infection compartment into symptomatic and asymptomatic infections • Add a reinfection pathway from R to S	Executable model that matches required structure
Q2	SEIRHD	SEIRHD in Terarium	• Extend this into a 2-virus model by combining it with an SIR model for virus 2 • Add reinfection pathway from R to S for both viruses	
Q3		Zafarnejad model in Terarium	• Add hospitalization states for each category of infection • Add a single Deaths state	

Set 2.3: Model Stratification

General format of inputs, tasks, and outputs

Inputs	Tasks	Outputs
• Configured executable model • Instructions on how to stratify the model	• Stratify the model as instructed • Configure stratified parameters as appropriate • Execute model	• Configured executable stratified model • Plots confirming successful execution of the model

For all questions, use the following SEIR model as the starting input model. It can be found in the workflow title "Q2.3" (Workbench), and in section 'Q2.3' in the RMarkdown file titled "Set 2" (Baseline)

$$dS/dt = -\beta/N * S * I$$
$$dE/dt = \beta/N * S * I - \sigma * E$$
$$dI/dt = \sigma * E - \gamma * I$$
$$dR/dt = \gamma * I$$

Table 5. Parameter Values for Set 2.3

Parameter	Value	Description
β	0.4 /day	Transmission rate
σ	0.2 /day	Incubation rate
γ	0.14 /day	Recovery rate

Initial conditions:

- S = 49,980
- E = 20
- I = 0
- R = 0

After each question, continue to build on the same model, adding additional layers of stratification.

(Q2.3.1) *Set 2.3, Question 1: Simple Stratification*

Inputs:

- SEIR model, configured according to specification above

Tasks:

- Stratify the model by vaccination status for all compartment.
- Simulate the stratified model for 100 days.

- 10,000 people start off vaccinated, 0.5% of the unvaccinated population gets vaccinated per day, and the vaccine effectiveness is 85% (meaning the transmission rate is 85% lower for vaccinated people). Assume other transition parameters for the vaccinated population, are similar to the unvaccinated population.
- Plot model outcomes for both vaccinated and unvaccinated populations.

Outputs:
- Stratified model in executable state
- Simulation plots for stratified model

(Q2.3.2) *Set 2.3, Question 2: Medium Complexity Stratification*

Inputs:
- Model from Q2.3.1, already stratified by vaccination status and configured

Tasks:
- Stratify the model by age and sex as follows:
    1. 0-5 year olds and 65+ year olds have twice the transmission rate of 6-64 year olds. 5% of the population is 5 or under, and 18% are 65 or older. (Keep the average for the total population at 0.4)
    2. Women tend to recover 2 days faster than men on average (and each make up half the population). (Again, keep the average at 0.14 per day)
    3. 0-5 year olds are vaccinated at a rate of 1.5% per day. People over 65 are vaccinated at a rate of 1% per day. (The overall vaccination rate is still 0.5% per day)
- Simulate the stratified model for 200 days and plot the model outcomes for infectious unvaccinated women over 65.

Outputs:
- Stratified model in executable state
- Simulation plots for stratified model

(Q2.3.3) *Set 2.3, Question 3: Challenging Stratification*

Inputs:
- Model from Q2.3.2, already stratified by vaccination status, age, and sex

Tasks:
- Further stratify the model by location. The region is divided into 16 locations with equal population, such that they form a 4x4 grid. Contact rate within a grid is 100% of the baseline. The contact rate drops to 50% one square away, 25% two squares away, 10% three squares away, and 0% four or more squares away. (“Squares away” refers to the Manhattan distance. That is, squares are adjacent if they share an edge. Corners do not count)

- Simulate the stratified model for 200 days and plot the model outcomes for recovered unvaccinated men between 6-64 years of age, located in the top left grid location over time.

Outputs:
- Stratified model in executable state
- Simulation plots for stratified model

Set 2.3 Summary Table

Question	Inputs	Tasks	Outputs
Q1	(Workbench) Q2.3 workflow in Terarium (Baseline) RMarkdown file titled "Set 2", section Q2.3	Stratify by vaccination status	Configured executable stratified model Plot showing exposed over time for both vaccinated and unvaccinated populations.
Q2		Stratify by age and sex	Configured executable stratified model Plot showing infectious unvaccinated women over 65 over time.
Q3		Stratify by location	Configured executable stratified model Plot showing recovered unvaccinated men between 6-64 located in the top left grid location over time.

Section 4: Technical Area 4 Functionality

Set 4.1: High Level Model Summarization and Comparison

Given a decision-maker objective, compare candidate models, provide a high-level summary of each, determine the gap between model capabilities and decisionmaker objectives, and rank fit-for-purpose.

Perform comparisons of SIR-types of compartmental models for COVID-19. In terms of complexity, we will vary the number of models and the subtlety of the differences between them. The output will be a table describing each model's distinguishing characteristics, assumptions, strengths, limitations, and fit-for-purpose ranking.

General format of inputs, tasks, and outputs

Inputs	Tasks	Outputs

• 2 or more candidate models (papers with model descriptions contained) to be compared
• Decision-maker objective(s)
	• Summarize each model, including distinguishing characteristics, assumptions, strengths, and limitations
	• With respect to the decision-maker objective(s), perform gap analysis of each model
	  ○ Describe whether the model is sufficient for meeting the objective
	  ○ If not sufficient, describe what is missing and what could be modified/added to meet the objective(s)
	  ○ Rank each model with respect to fit-for-purpose for decisionmaker objective(s) and provide reasoning
		• Fill out a copy of Table 6 summarizing each model
		• Fill out a copy of Table 7 with the gap analysis for each model

Table 6. Set 4.1 Summarization Table Template

Model	Distinguishing Characteristics	Assumptions	Strengths	Limitations
A				
B				

Table 7. Set 4.1 Gap Analysis Template

Model	Gap Analysis relative to objective(s)	Proposed remedies for gaps	Rank fit-for-purpose (1 = most suitable; 3 = least suitable), with reasoning
A			
B			

(Q4.1.1) *Set 4.1, Question 1: Simple Summarization and Comparison*

Inputs:

- **Candidate models**:
    1. *Model A*: Sowole, S. O., Sangare, D., Ibrahim, A. A., & Paul, I. A. (2019). On the existence, uniqueness, stability of solution and numerical simulations of a mathematical model for measles disease. *Int. J. Adv. Math*, *4*, 84-111. https://adv-math.com/wp-content/uploads/2019/07/adv-manuscript.pdf.pdf
    2. *Model B*: Stojkovic, N., Kukuseva, M., Stojanova, A., & Koceva Lazarova, L. (2024). SEIRV Model of Measles. *International Journal of Applied Mathematics*, *37*(6), 615-626. https://eprints.ugd.edu.mk/35047/
- **Decision-maker Objective**: You are an analyst in a state health agency that is investigating whether or not to continue to require measles vaccines. Which of the two models would best be able to predict the impacts of this decision?

Tasks:

- Summarize each model, including distinguishing characteristics, assumptions, strengths, and limitations, and fill out a table similar to Table 6.
- With respect to the decision-maker objective(s), perform gap analysis with each model, describing whether the model is sufficient for meeting the objective, and if not, what is missing. If there is functionality missing, determine what could be modified/added to meet the objective(s). Rank each model with respect to fit-for-purpose and provide reasoning. Fill out a table similar to Table 7.

Outputs:

- Tables describing each model's distinguishing characteristics, assumptions, strengths, and limitations, gap analysis, and fit-for-purpose ranking

(Q4.1.2) *Set 4.1, Question 2: Medium-Complexity Summarization and Comparison*

Inputs:

- **Candidate models**:
    - *Model A*: Kamrujjaman, M., Saha, P., Islam, M. S., & Ghosh, U. (2022). Dynamics of SEIR model: A case study of COVID-19 in Italy. Results in Control and Optimization, 7, 100119. https://doi.org/10.1016/j.rico.2022.100119
    - *Model B*: Giordano, G., Blanchini, F., Bruno, R., Colaneri, P., Di Filippo, A., Di Matteo, A., & Colaneri, M. (2020). Modelling the COVID-19 epidemic and implementation of population-wide interventions in Italy. Nature medicine, 26(6), 855-860. https://doi.org/10.1038/s41591-020-0883-7
- **Decision-maker objective**: You are the Chief Medical Officer of a hospital in Italy facing a potential surge in COVID-19 cases. You are tasked with determining whether to allocate resources toward expanding ICU capacity or investing in widespread community testing and isolation efforts. Your goal is to ensure the hospital can manage an immediate surge while also mitigating the longer-term strain on healthcare resources. Which of the two models would best be able to support your decision?

Tasks:

- Summarize each model, including distinguishing characteristics, assumptions, strengths, and limitations, and fill out a table similar to Table 6.
- With respect to the decision-maker objective(s), perform gap analysis with each model, describing whether the model is sufficient for meeting the objective, and if not, what is missing. If there is functionality missing, determine what could be modified/added to meet the objective(s). Rank each model with respect to fit-for-purpose and provide reasoning. Fill out a table similar to Table 7.

Outputs: Tables describing each model's distinguishing characteristics, assumptions, strengths, and limitations, gap analysis, and fit-for-purpose ranking

(Q4.1.3) *Set 4.1, Question 3: Challenging Summarization and Comparison*

Inputs:

- **Candidate models**:
  - *Model A*: O'Reilly, K. M., Sandman, F., Allen, D., Jarvis, C. I., Gimma, A., Douglas, A., ... & Edmunds, W. J. (2021). Predicted norovirus resurgence in 2021–2022 due to the relaxation of nonpharmaceutical interventions associated with COVID-19 restrictions in England: a mathematical modeling study. *BMC medicine*, *19*, 1-10. https://doi.org/10.1186/s12916-021-02153-8
  - *Model B*: Rocklöv, J., Sjödin, H., & Wilder-Smith, A. (2020). COVID-19 outbreak on the Diamond Princess cruise ship: estimating the epidemic potential and effectiveness of public health countermeasures. *Journal of travel medicine*, *27*(3), taaa030.https://doi.org/10.1093/jtm/taaa030
- **Decisionmaker objective**: You are the director of a cruise line in charge of creating a policy to contain potential norovirus outbreaks on the ship. There are two non-pharmaceutical intervention strategies under consideration:
  1. Enhanced pre-board screening and prevention
  2. Enhanced on-board containment measures

  In general, both strategies will be used at some level, but you must decide which to emphasize. To assist your decision, you'll need to understand the health impacts of each strategy, among other criteria. Analysts have presented two models for consideration. Which of the two would best be able to support your decision?

Tasks:

- Summarize each model, including distinguishing characteristics, assumptions, strengths, and limitations, and fill out a table similar to Table 6.
- With respect to the decision-maker objective(s), perform gap analysis with each model, describing whether the model is sufficient for meeting the objective, and if not, what is missing. If there is functionality missing, determine what could be modified/added to meet the objective(s). Rank each model with respect to fit-for-purpose and provide reasoning. Fill out a table similar to Table 7.

Outputs: Tables describing each model's distinguishing characteristics, assumptions, strengths, and limitations, gap analysis, and fit-for-purpose ranking

Set 4.1 Summary Table

Question	Inputs	Tasks	Outputs
Q1	*Model A*: Sowole, S. O., Sangare, D., Ibrahim, A. A., & Paul, I. A. (2019). https://adv-math.com/wp-content/uploads/2019/07/adv-manuscript.pdf.pdf *Model B*: Stojkovic, N.Kukuseva, M., Stojanova, A., & Koceva Lazarova, L. (2024). https://eprints.ugd.edu.mk/35047/ Decision-maker Objective: Whether to continue measles vaccines	Summarize each model, including distinguishing characteristics, assumptions, strengths, and limitations. With respect to the decision-maker objective(s), perform gap analysis with each model, describing whether the model is sufficient for meeting the objective, and if not, what is missing. If there is functionality missing, determine what could be modified/added to meet the objective(s). Rank each model with respect to fit-for-purpose and provide reasoning	Completed copies of Table 6 and Table 7 describing each model's distinguishing characteristics, assumptions, strengths, and limitations, gap analysis, and fit-for-purpose ranking
Q2	*Model A*: Kamrujjaman, M., Saha, P., Islam, M. S., & Ghosh, U. (2022). https://doi.org/10.1016/j.rico.2022.100119 *Model B*: Giordano, G., Blanchini, F., Bruno, R., Colaneri, P., Di Filippo, A., Di Matteo, A., & Colaneri, M. (2020). https://doi.org/10.1038/s41591-020-0883-7 Decision-maker Objective: Hospital resource allocation		
Q3	*Model A*: O'Reilly, K. M., Sandman, F., Allen, D., Jarvis, C. I., Gimma, A., Douglas, A., ... & Edmunds, W. J. (2021). https://doi.org/10.1186/s12916-021-02153-8 *Model B*: Rocklöv, J., Sjödin, H., & Wilder-Smith, A. (2020). https://doi.org/10.1093/jtm/taaa030 Decision-maker Objective: Cruise ship non-pharmaceutical interventions		

Set 4.2: Visualization and Comparison Against Data

Create decision-maker-friendly visualizations.

Generate requested charts and annotations to compare forecasts against data or thresholds, compare interventions, examine optimization results, etc.

General format of inputs, tasks, and outputs

Inputs	Tasks	Outputs
• Observational data to plot model output against and measure error metrics • Annotations to include in plots (e.g. peak of an infection curve and time of peak, threshold values, etc.)	Generate plots according to input specifications	Output 'ready for report' plots and visualization artifacts

During the early stages of COVID, mitigations had competing objectives of minimizing lives lost while also minimizing economic damage and maximizing liberty. A model (Mitcham & Keisler 2022) was run with 100,000 sets of parameters in an SEIRD model with 4 mitigation strategies each: Base (or do nothing), masks only, light lockdown, heavy lockdown. The outputs of these runs are provided as a dataset, to be used for Set 4.2 questions.

(Q4.2.1) *Set 4.2, Question 1: Simple Visualization*

Inputs:
- "Set 4.2 COVID_model_data.csv"

Tasks:
- For each set of disease parameters, a utility value was calculated (in the dataset columns 'Base Utility', 'Mask utility', etc.) Identify which strategy maximized the utility for each set of disease parameters and plot the number of times that strategy was the best in a bar chart.

Outputs:
- Bar chart

(Q4.2.2) *Set 4.2, Question 2: Medium-Complexity Visualization*

Inputs:
- "Set 4.2 COVID_model_data.csv"

Tasks:
- Plot the number of deaths for each mitigation strategy as a frequency polygon. Use a log scale for the y-axis.

Outputs:
- Frequency polygon

(Q4.2.3) *Set 4.2, Question 3: Challenging Visualization*

Inputs:

- "Set 4.2 COVID_model_data.csv"

Tasks:

Create a heatmap for each of the following strategies: **Masks**, **Light Lockdown**, and **Heavy Lockdown**, showing the **percent reduction in deaths** compared to the **Base** (do nothing) strategy across a range of **R0** and **Untreated Fatality Rate** values.

To create the heatmaps, follow these steps:

1. **Divide the parameter space**:
    - Split the range of **R0** and **Untreated Fatality Rate** each into 20 grid cells.
2. **Compute the percent reduction**:
    - For each grid cell, calculate the **percent reduction in deaths** for the given strategy compared to the **Base** strategy.
3. **Create and color the heatmaps**:
    - Color each grid cell based on the calculated percent reduction in deaths.
4. **Ensure your heatmaps include**:
    - A legend indicating what the colors represent.
    - Clearly labeled axes for **R0** and **Untreated Fatality Rate**.
    - A descriptive title for each heatmap.

Outputs:

- 3 heatmaps

Set 4.2 Summary table

Question	Input	Task	Output
Q1	"Set 4.2 COVID_model_data.csv"	Identify which strategy maximized the utility for each set of disease parameters and plot the number of times that strategy was the best in a bar chart.	Bar chart
Q2		Plot the number of deaths for each mitigation strategy as a frequency polygon. Use a log scale for the y-axis.	Frequency polygon
Q3		Create a heatmap for each of the following strategies: Masks, Light Lockdown, and Heavy Lockdown, showing the percent reduction in deaths compared to the Base (do nothing) strategy across a range of R0 and Untreated Fatality Rate values.	3 heatmaps