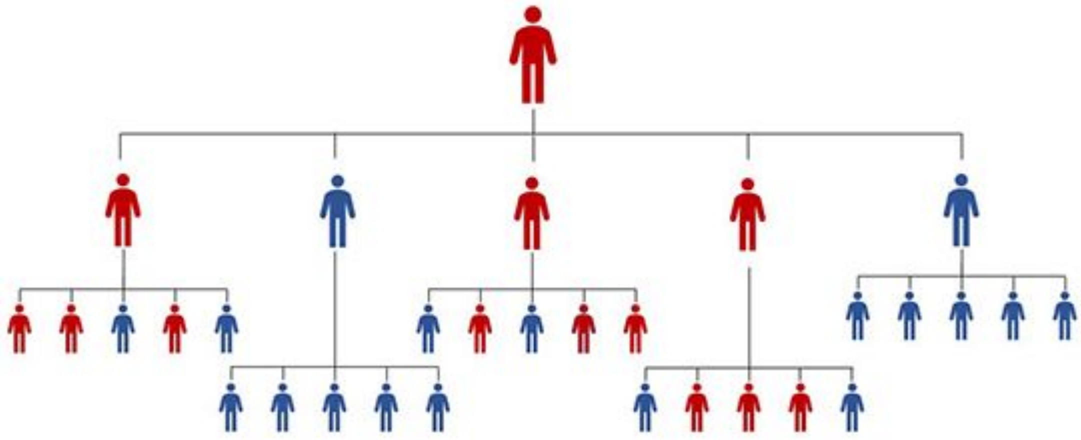

Approximate Bayesian Computation for Disease Outbreaks

S610 Final Project
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Introduction

- **Objectives**: Apply Approximate Bayesian Computation (ABC) method to model the spread of different strains of influenza

- **Data**:
  - 1st dataset: Table 2
  - 2nd dataset: Table 3

Table 2: Influenza A (H3N2) infection in 1977-78 (middle column) and 1980-81 (right column) epidemics, Tecumseh, Michigan [1].

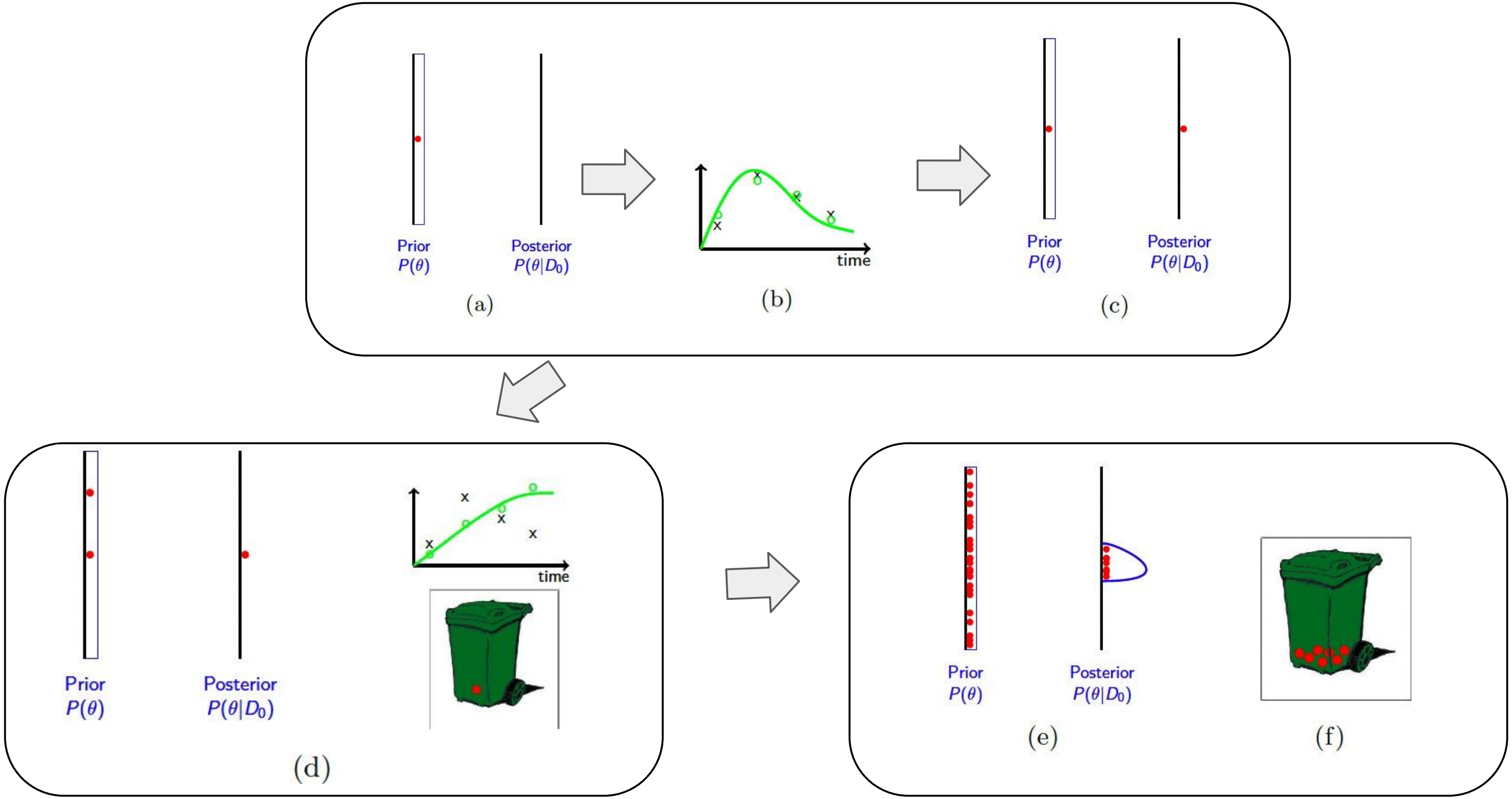
Nr. infected individuals	1	2	3	4	5	1	2	3	4	5
0	66	87	25	22	4	44	62	47	38	9
1	13	14	15	9	4	10	13	8	11	5
2		4	4	9	1		9	2	7	3
3			4	3	1			3	5	1
4				1	1				1	0
5					0					1

Table 3: Influenza B infection in 1975-76 epidemic (middle column) and influenza A (H1N1) infection in 1978-79 epidemic (right column), Seattle, Washington [2].

Nr. infected individuals	1	2	3	4	5	1	2	3
0	9	12	18	9	4	15	12	4
1	1	6	6	4	3	11	17	4
2		2	3	4	0		21	4
3			1	3	2			5
4				0	0			
5					0			

Method

Schematic representation of ABC rejection



Function to Generate Probability Matrix

- First, generate a probability matrix that we then use to simulate data
- The probability matrix formula takes two parameters:
  - q_c = the probability that a susceptible individual does **not** get infected from their community
  - q_h = the probability that a susceptible individual does **not** get infected from their household
- w_{js} , the probability that j out of s susceptibles in a household become infected, is given by:

$$w_{js} = \binom{s}{j} w_{jj} (q_c q_h^j)^{s-j},$$

Notes about Probability Matrix

- The probability that 0 out of s susceptibles in a household become infected is:

$$w_{0s} = q_c^s, \quad s = 0, 1, 2, \ldots$$

- w_{jj} (in the formula on the previous slide) is equal to 1 minus the sum of the elements in column j from the first row (where there are 0 infections) to the jth row (where there are j-1 infections as j=0 occurs at row 1)

$$w_{jj} = 1 - \sum_{i=0}^{j-1} w_{ij}$$