Simple disease models

"Even a bad model may be useful in providing some kind of intellectual foothold…"

Harris, 1960; cited in Miller, 1976

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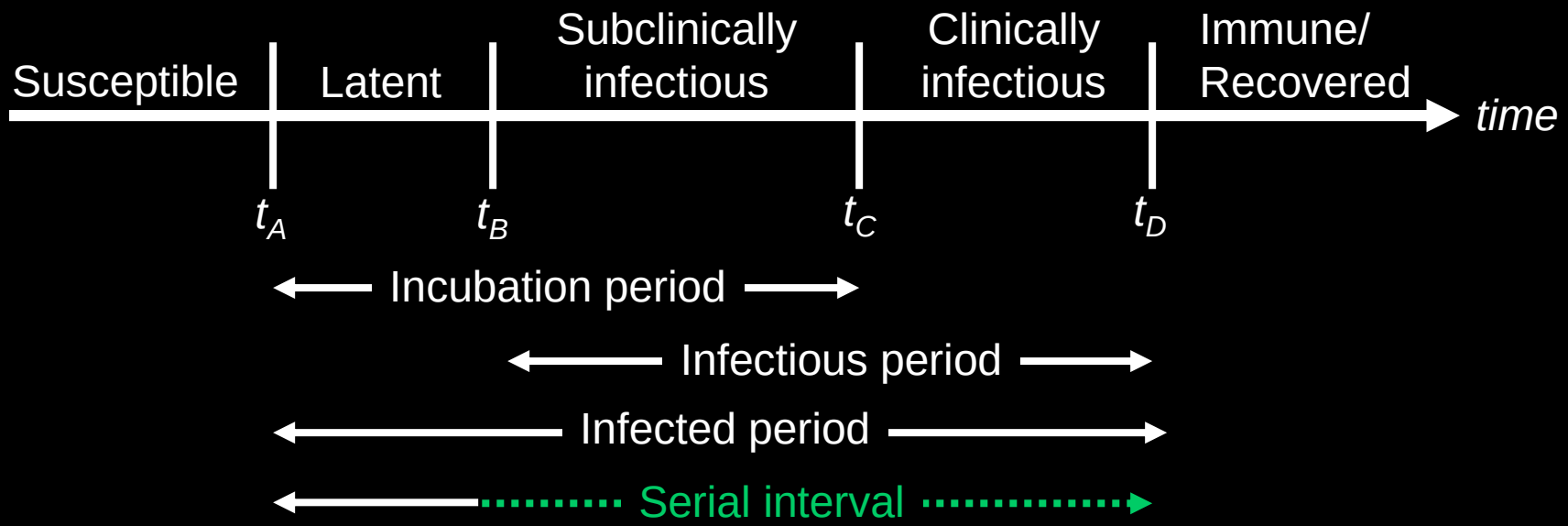
Disease states (I)

- Virtually all models incorporate the concept of *disease states*
- At any given point in time, every individual in a population exists in a disease state (which may be absence of disease)
- Individuals cannot have more than one disease state
- Upon infection, individuals progress through a series of disease states in a predictable manner

Disease states (II)

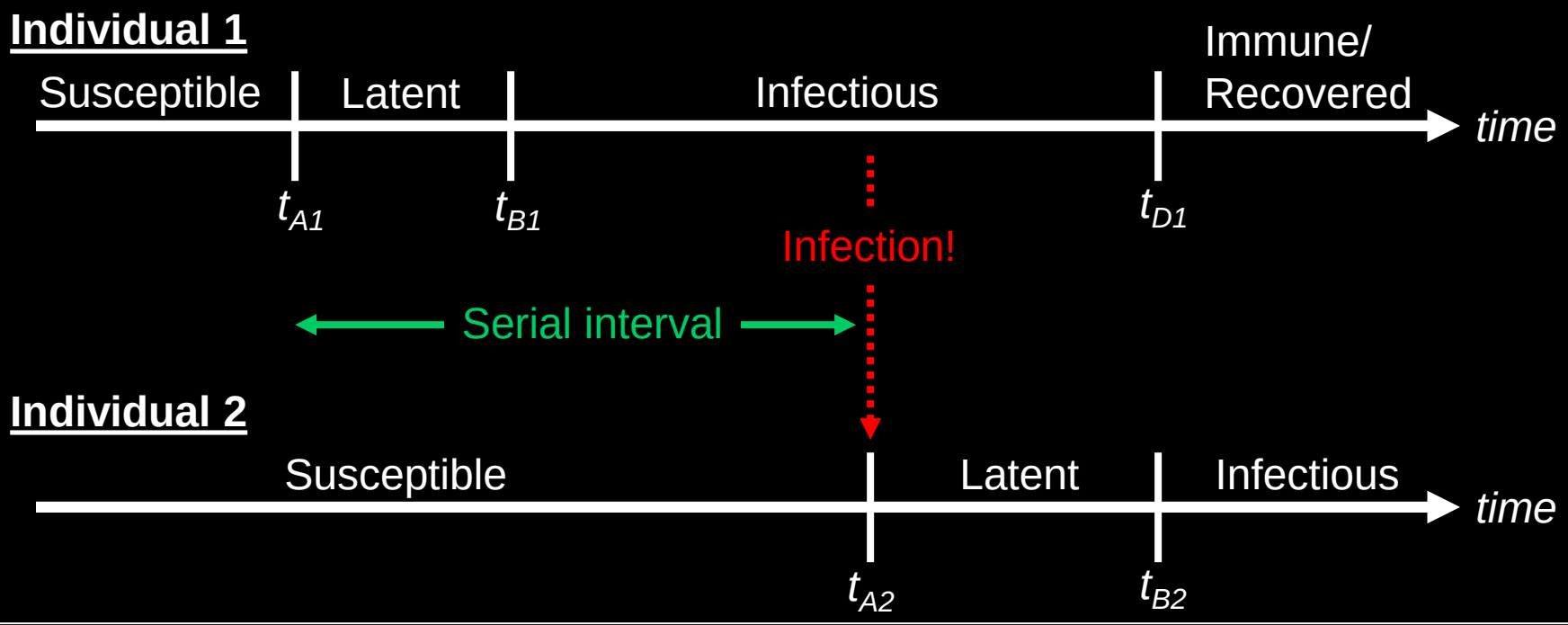


t_A: Infection occurs
t_B: Latency to infectious transition
t_C: Symptoms (clinical signs) appear
t_D: Individual is no longer infectious

Modified from Daley and Gani, 1999

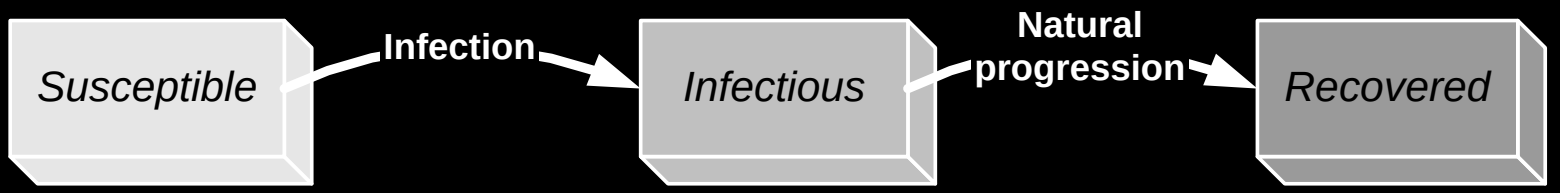
The serial interval

- Defined as the duration between the time when an individual is infected, and the time when that individual first infects another



SIR: A simple disease model

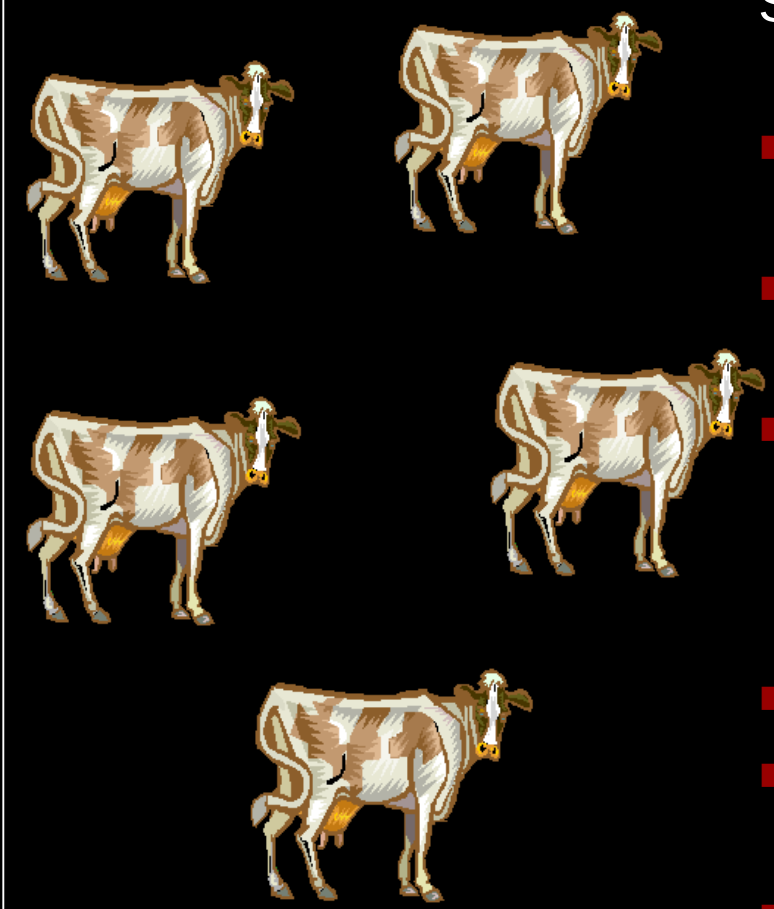
- *S* = Susceptible
- *I* = Infectious
- *R* = Recovered or Removed



- Equivalent Reed-Frost notation:
  - *S* = Susceptible = Susceptible in SIR
  - *C* = Case or Contagious = Infectious in SIR
  - *I* = Immune = Recovered in SIR

Size of the population = # Susceptible + # Cases + # Immune

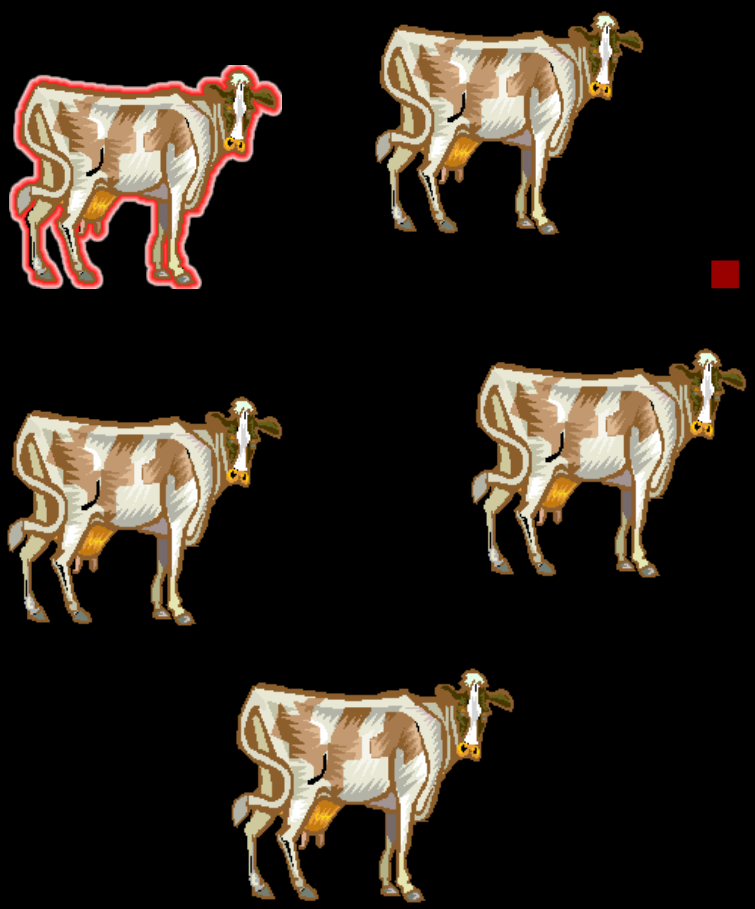
Disease in a simple population: Before infection



Some assumptions about the population and the disease:

- The population is *closed*: individuals neither enter nor leave
- Every individual in the population is *equally susceptible* to disease
- *Random mixing* occurs within the population: individuals are equally likely to come into contact with any other individual
- Disease spreads only by direct contact
- An infected individual is a “case” for 1 time period
- Immunity lasts indefinitely

Disease in a simple population: Initial infection (time period 0)



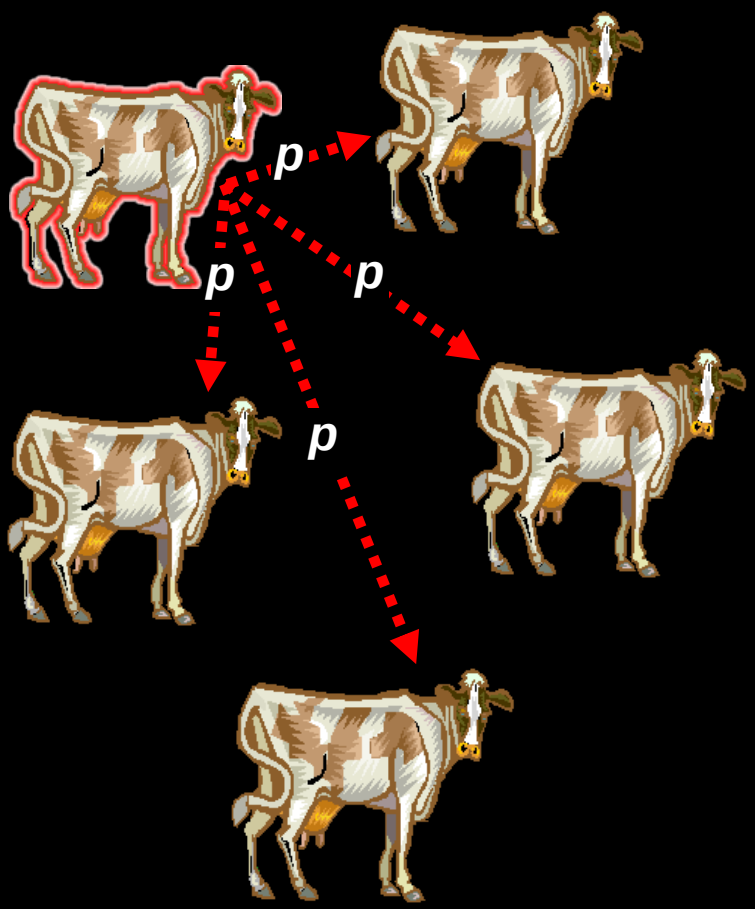
- The number of cases $C = 1$
- The number of susceptibles $S = 4$
- The total population size $N = 5$

- How will disease progress in this population?
  - The same question, rephrased: how many cases will there be in each subsequent time period?
  - The answer will depend on the *probability of adequate contact*

Adequate versus effective contact (I)

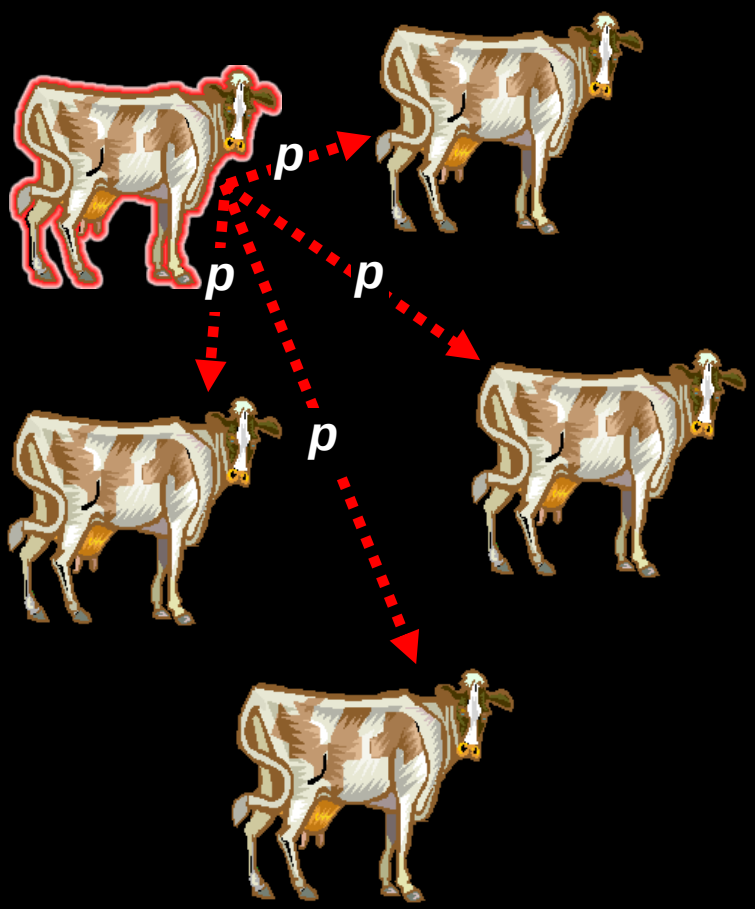
- Adequate contact: a contact between individuals that would lead to the transmission of disease, *if one individual is infectious and the other is susceptible*
- Effective contact: a contact between individuals that leads to disease
  - An *adequate* contact will be *effective* if it occurs between an infectious and a susceptible individual
  - Adequate contact will not be effective if:
    - Both individuals are infectious
    - Both individuals are susceptible
    - One is infectious, the other is immune
    - *etc.*

Probability of adequate contact (I)



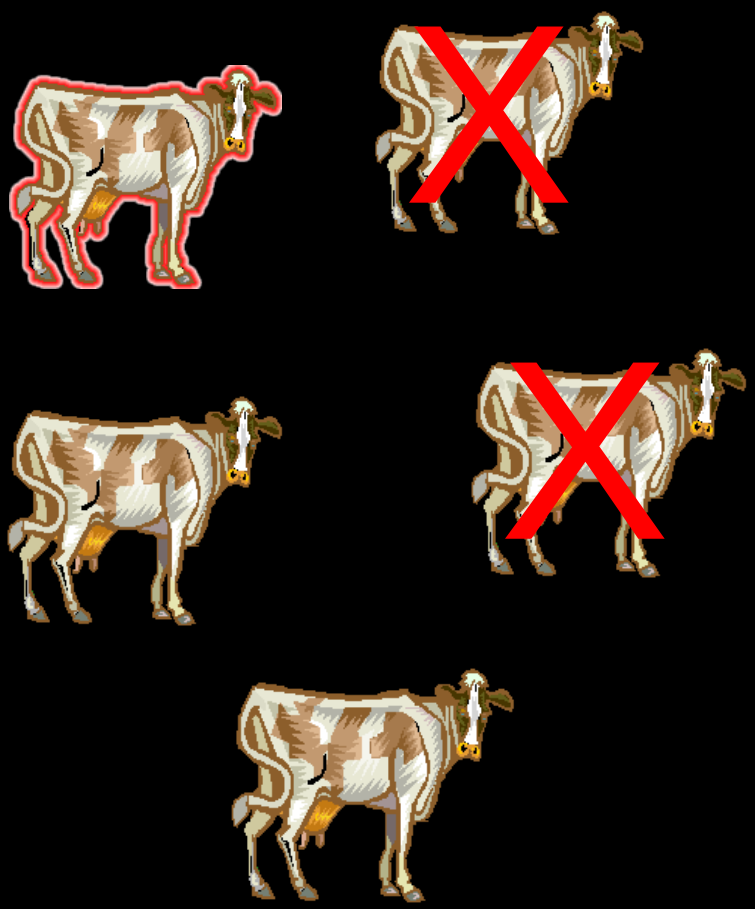
- Because the population is homogenously mixing, the *probability that an individual will have adequate contact with another individual in the population* is constant
- We'll use the symbol *p* to indicate this probability
- The probability that adequate contact *will not occur* between any two individuals is (1 – *p*), which we'll call *q*
- Suppose *p* = 0.4…

Probability of adequate contact (II)



- If $p = 0.4$…
- The probability that any particular individual will receive adequate contact (and will be infected) is 0.4
- Equivalently, the proportion of the population that will receive adequate contact is 0.4
- The probability that any particular individual will *avoid* adequate contact (equivalently, the proportion of the population that will avoid adequate contact) is
  $q = 1 - 0.4 = 0.6$

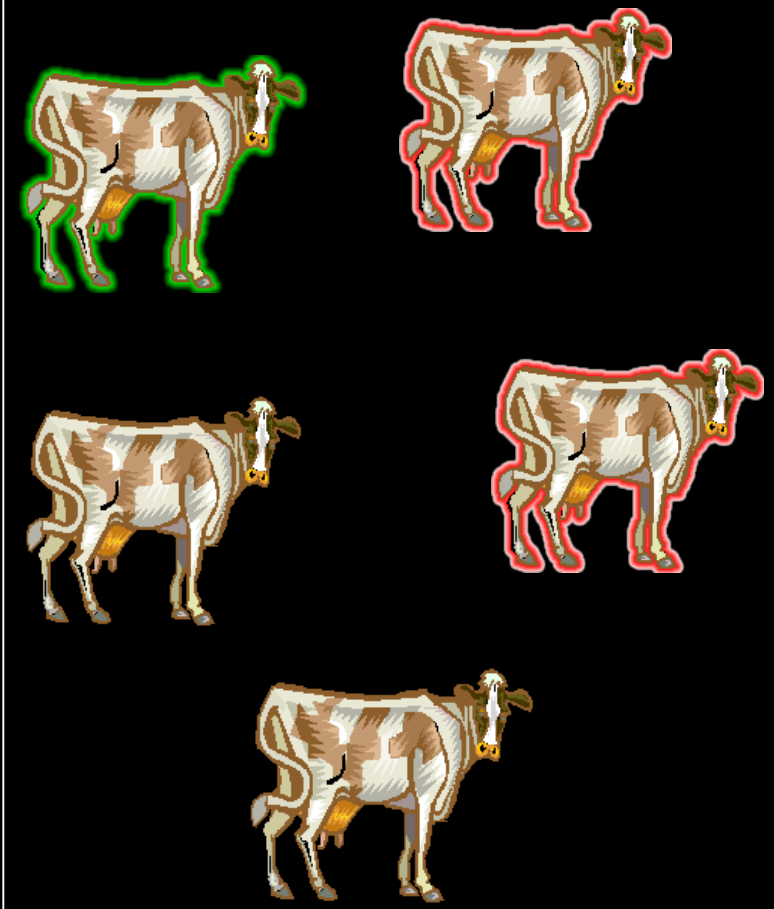
Probability of adequate contact (III)



- If $p = 0.4$…
- In a population of 5 with 1 infectious individual, there are 4 individuals which can receive adequate contact from the 1 infected
- Of those 4, we expect on average that $4 \times 0.4 = 1.6$ individuals will have adequate contact
- Because all 4 are susceptible, we expect that 1.6 will become infected (contact is effective, as well as adequate)
  - For convenience and simplicity, we'll round this to 2 for now

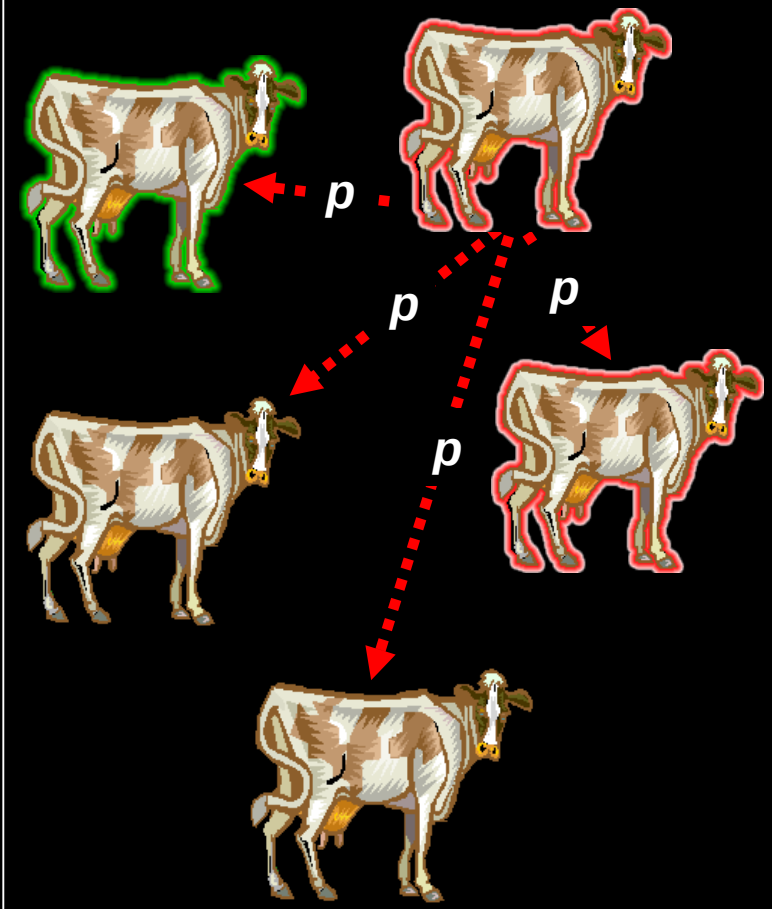
Time passes…

Disease states in time period 1



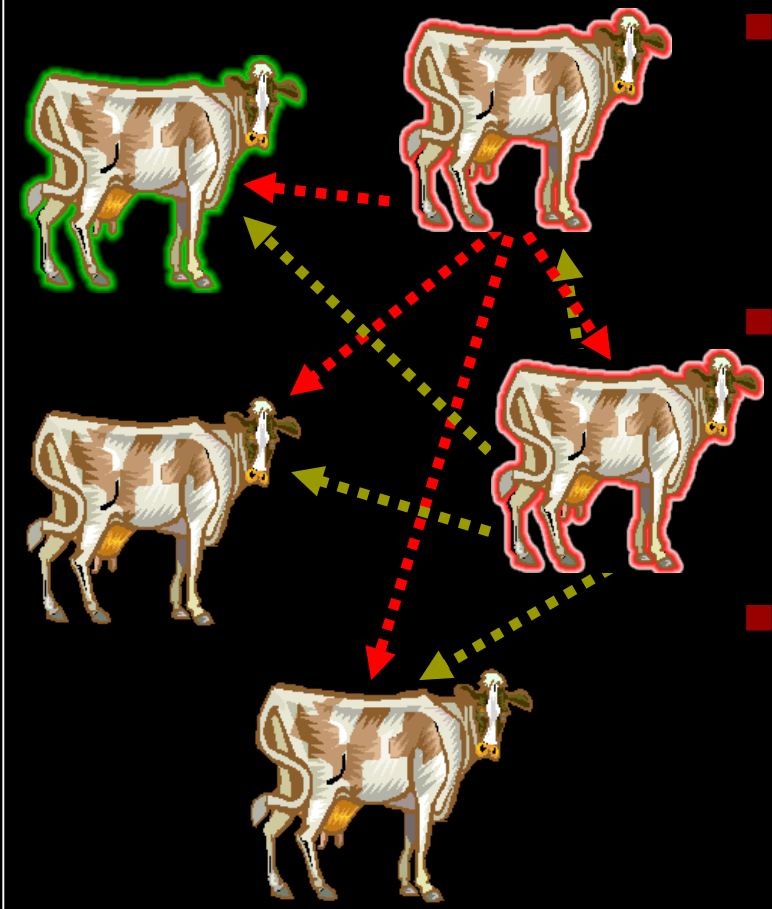
- The individual which was infectious in time period 0 is now immune (recovered)
- The two individuals which received adequate contact in time period 0 are now infectious

Disease spread in time period 1



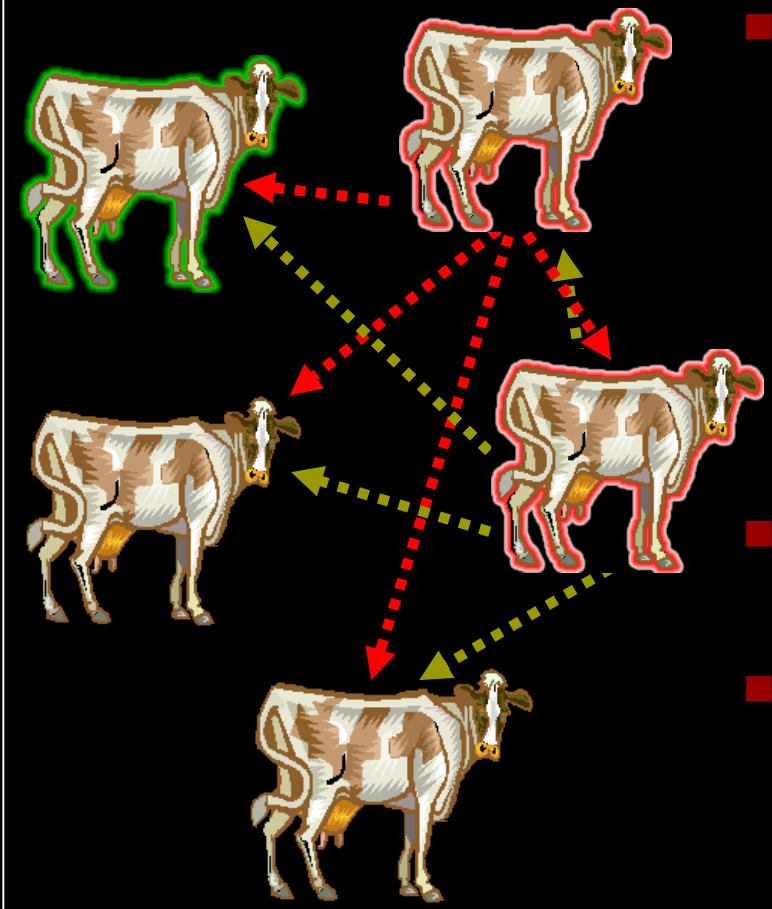
- As before, $p = 0.4$ (remember: p is constant!)
- So…
  - The probability that any single individual will avoid adequate contact is $q = 1 - 0.4 = 0.6$
  - Of 2 remaining susceptibles, we expect on average that $2 \times 0.4 = 0.8$ will receive adequate contact
  - Right?

No, that's not right!!



- The probability that any single individual will avoid adequate contact from *one possible source* is $1 - 0.4 = 0.6$
- The probability that any single individual will avoid adequate contact *from both possible sources* is $(1 - 0.4) \times (1 - 0.4) = 0.36$
- Of 2 susceptibles, we expect on average that there would be $2 \times (1 - 0.36) = 1.28$ new cases

Adequate versus effective contact (II)



- Note that the expected number of new cases in this time period (1.28) is not the same as the expected number of new cases in the previous time period (1.6), even though the probability of adequate contact is unchanged
- The ratio of infectious to susceptible individuals is different
- Some *adequate* contacts are not *effective*

A slightly less simple population (I)

- At time 0: 1 case, 100 susceptibles
- Probability of adequate contact $p = 0.04$
- Probability of avoiding adequate contact from 1 infectious individual: $q = (1 - 0.4) = 0.96$
- Probability of avoiding all adequate contacts: $q^{(\#\ \text{cases})} = (0.96)^1 = 0.96$
- Probability of having at least 1 adequate contact: $1 - q^{(\#\ \text{cases})} = 1 - 0.96 = 0.04$
- Number of expected new cases in the next time period: (# susceptibles) × (Probability of having at least 1 adequate contact) = 100 × 0.04 = 4

Time period	*Cases*	*Immune*	*Susceptible*
0	1	0	100
1	100 × [1 - (1-0.04)] = 4	1	96

A slightly less simple population (II)

- At time 1: 4 cases, 96 susceptibles
- Probability of adequate contact $p = 0.04$ *(Unchanged!)*
- Probability of avoiding adequate contact from 1 infectious individual: $q = (1 - 0.4) = 0.96$
- Probability of avoiding all adequate contacts: $q^{(\#\ \text{cases})} = (0.96)^4 = 0.85$
- Probability of having at least 1 adequate contact: $1 - q^{(\#\ \text{cases})} = 1 - 0.85 = 0.15$
- Number of expected new cases in the next time period: (# susceptibles) × (Probability of having at least 1 adequate contact) = 96 × 0.15 = 14

Time period	*Cases*	*Immune*	*Susceptible*
1	100 × [1 - (1-0.04)] = 4	1	96
2	96 × {1 - [(1-0.04) × (1-0.04) × (1-0.04) × (1-0.04)]} = 14	5	82

A slightly less simple population (III)

Time period	*Cases*	*Immune*	*Susceptible*
0	1	0	100
1	$100 \times [1 - (1-0.04)] = 4$	1	96
2	$96 \times \{1 - [(1-0.04) \times (1-0.04) \times (1-0.04) \times (1-0.04)]\} = 14$	5	82
3	$82 \times [1-(1-0.04)^{14}] = 36$	19	46
4	$46 \times [1-(0.96^{36})] = 35$	56	10
5	$10 \times [1-(0.96^{35})] = 8$	90	3
6	$2 \times [1-(0.96^{8})] = 1$	98	2
7	$1 \times [1-(0.96^{1})] = 0$	99	2

The Reed-Frost model in mathematical notation

- The probability of avoiding adequate contact *from any single source* is:
  $1 - p = q$
- The probability of avoiding *all* adequate contact is:
  $(1 - p)^C = q^C$
- The probability of *not* avoiding all adequate contact (*i.e.*, the probability of *at least one* adequate contact) is:
  $(1 - q^C)$
- The expected number of cases in the next time period is:
  $\boldsymbol{C_{t+1} = S_t(1 - q^{C_t})}$

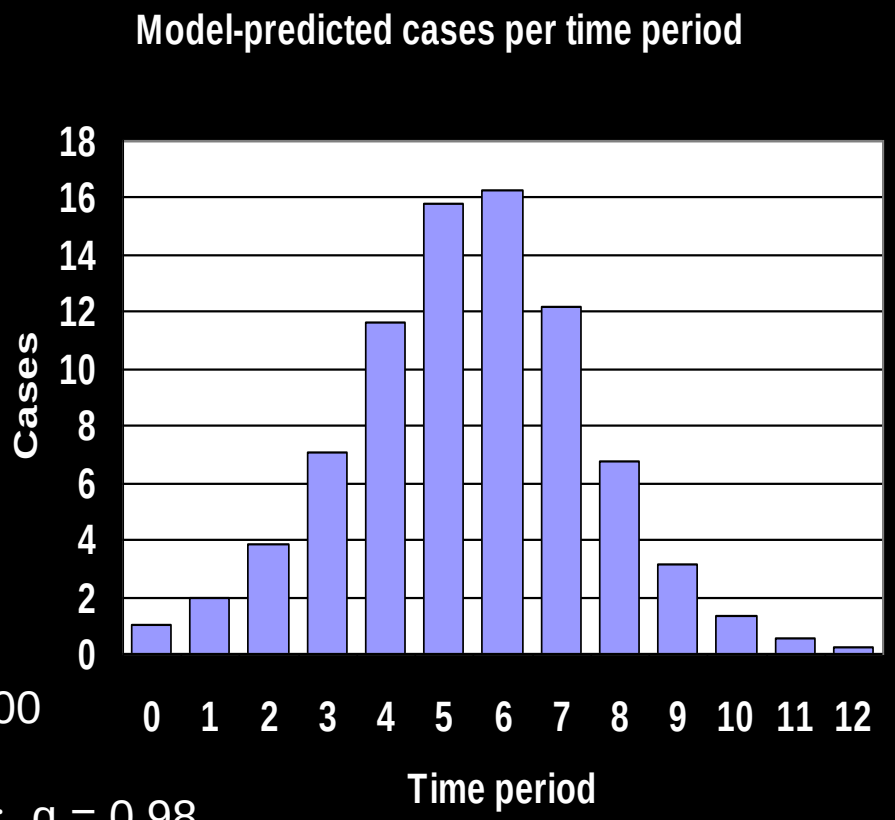
Time in a Reed-Frost model

- *p* is the probability that adequate contact will occur between two individuals during a single time period
- The model proceeds in time steps equal in length to a typical or average *serial interval* for the disease
- The duration of the average incubation period is often used for this serial interval
- The number of susceptibles, cases, and immune individuals in any one time period is dependent on those numbers from the previous time period
- After a time interval has passed, a case individual recovers, and is immune from re-infection
- In a simple *SIR* model, immunity after infection is assumed to last forever

Results of a simple Reed-Frost model

Time	*Cases*	*Immune*	*Susceptible*
0	1	0	100
1	2	1	98
2	4	3	94
3	7	7	87
4	12	14	75
5	16	26	60
6	16	41	43
7	12	58	31
8	7	70	24
9	3	77	21
10	1	80	20
11	1	81	19
12	0	82	19

- Does this chart show prevalence or incidence?

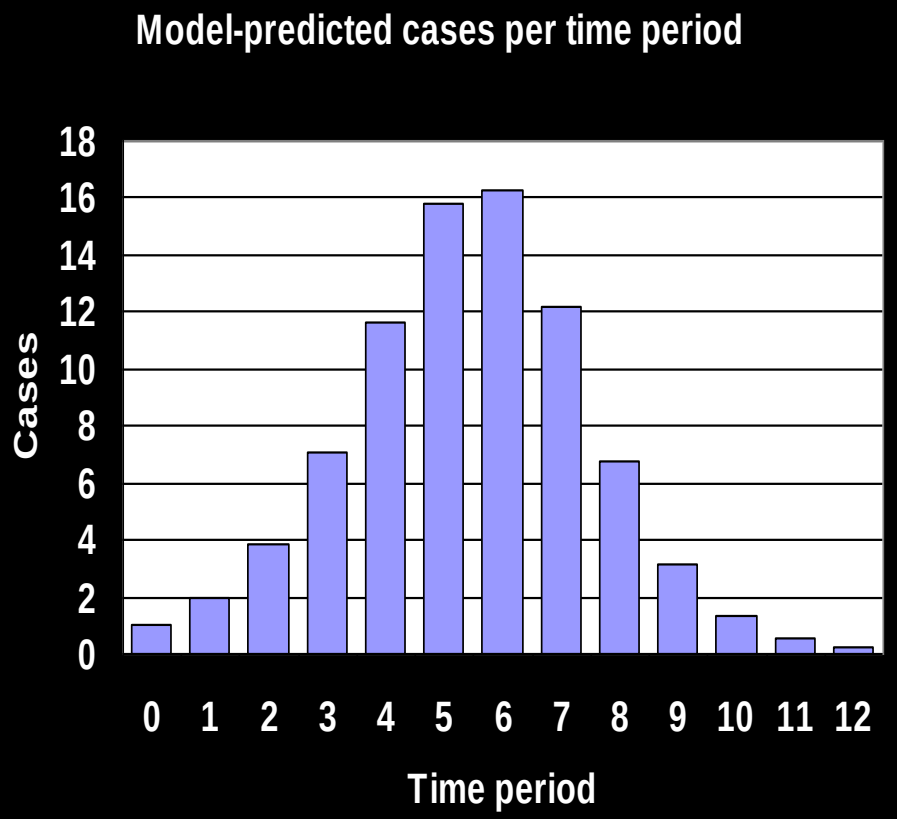


Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$ ∴ q = 0.98

The Reed-Frost model: Calculating the number of new cases

Time	*Cases*	*Immune*	*Susceptible*
0	1	0	100
1	2	1	98
2	4	3	94
3	7	7	87
4	12	14	75
5	16	26	60
6	16	41	43
7	12	58	31
8	7	70	24
9	3	77	21
10	1	80	20
11	1	81	19
12	0	82	19

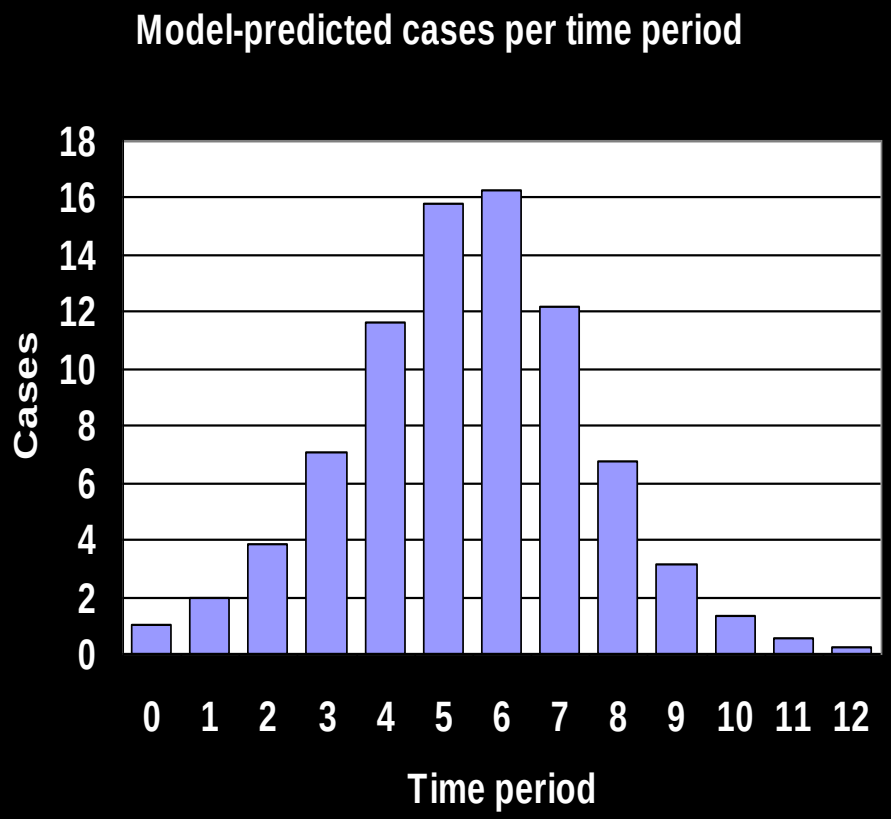


Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$ $\therefore$ $q = 0.98$

The Reed-Frost model: Calculating the number of immune individuals

Time	*Cases*	*Immune*	*Susceptible*
0	1	0	100
1	2	1	98
2	4	3	94
3	7	7	87
4	12	14	75
5	16	26	60
6	16	41	43
7	12	58	31
8	7	70	24
9	3	77	21
10	1	80	20
11	1	81	19
12	0	82	19



Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$ ∴ $q = 0.98$

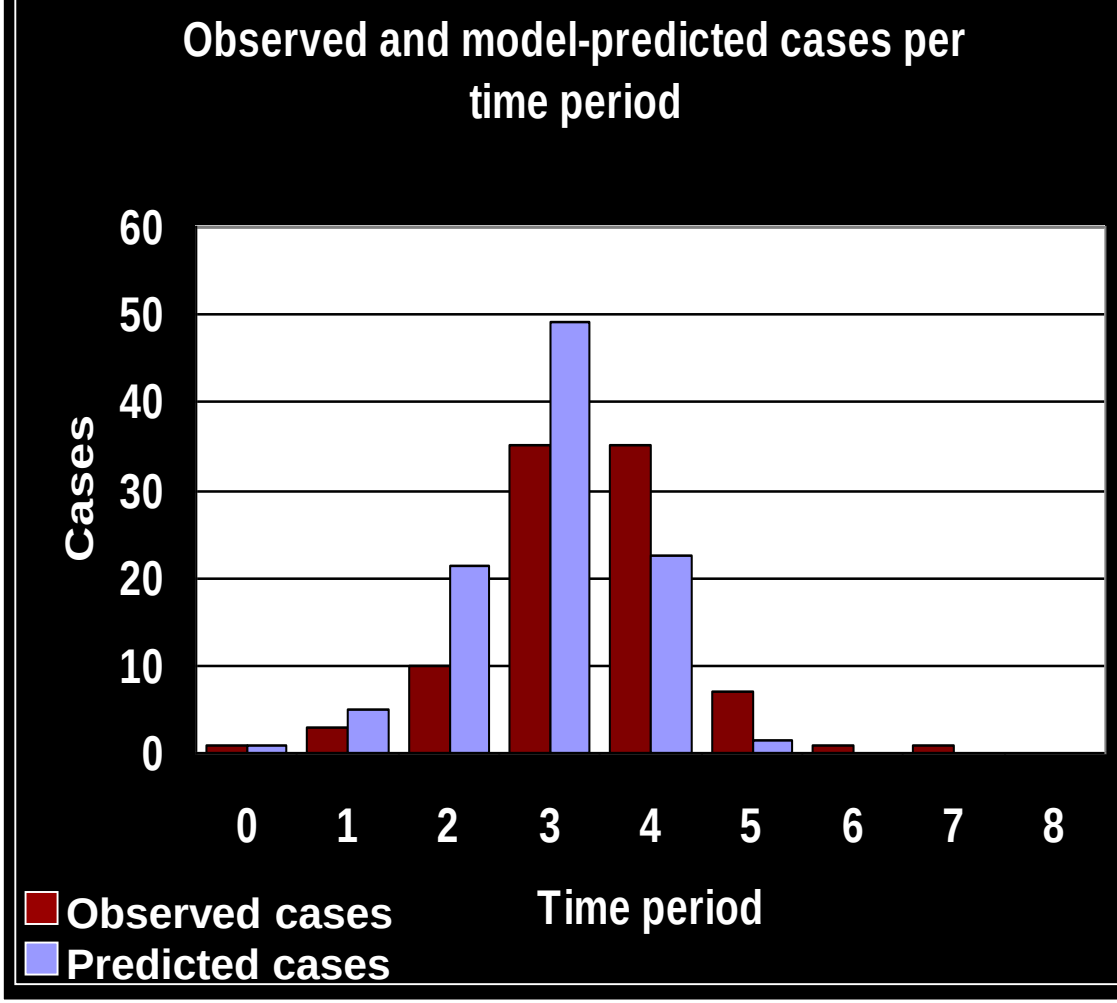
Some assumptions of the basic Reed-Frost model

- The population is closed, homogenously mixing, and does not change in size
  - Disease does not result in death
- All disease spread occurs by direct contact
- All susceptible individuals are equally likely to be infected
- All infected individuals are equally likely to spread infection
- The infectious period is short relative to the incubation period
- Animals infected in a particular time period become infectious in the following time period
- Individuals are infectious for only one time period
- Immunity after infection is complete and permanent

Dissecting the probability of adequate contact

- The probability of adequate contact (*p*) can be calculated as follows:
  $p = k / (N - 1)$
  where:
  - N = the size of the population
  - k = the average number of adequate contacts made by an individual during a single time period
- Estimates of *k* produce estimates of *p*, and *vice versa*
- *p* and *k* are difficult to measure directly, but can be estimated from real outbreak data

Assessing model fit to outbreak data (I)



Model parameters:

- $N = 101$
- $C_0 = 1 \therefore S_0 = 100$
- $k = 5 \therefore p = 0.05$, $q = 0.95$

Time	*Observed*	*Predicted*
0	1	1.00
1	3	5.00
2	10	21.49
3	35	49.10
4	35	22.44
5	7	1.35
6	1	0.04
7	1	0

The chi-square goodness of fit test

- The chi-square test can be used to determine the goodness of fit of an observed distribution to a theoretical or expected distribution
- Calculating the chi-square statistic:

$$\chi^2 = \sum \frac{(\text{Observed} - \text{Expected})^2}{(\text{Expected})}$$

- The smaller the value of the chi-square statistic, the better the fit
- Degrees of freedom: *df* = (# of categories) - 1
- Level of significance: we'll use $\alpha = 0.05$
- The hypothesis that will be tested:
  H_0: The observed values fit the expected distribution
  H_A: Observations in at least one category do not fit the expected distribution

Assessing model fit to outbreak data (II)

- Calculating the chi-square value:

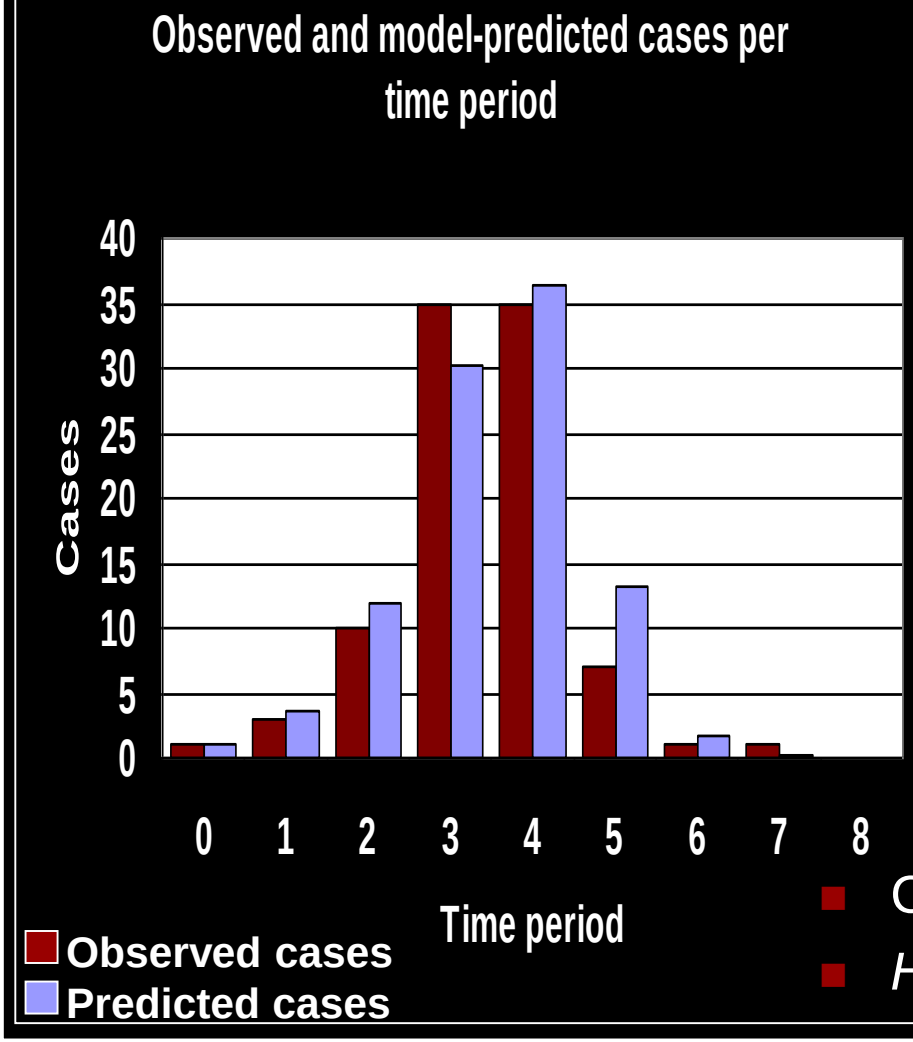
Time period	*Observed*	*Expected*	*(Obs – Exp)^2 / Exp*
0	1	1.00	
1	3	5.00	0.80
2	10	21.49	6.14
3	35	49.10	4.05
4	35	22.44	7.02
5	7	1.35	23.77
6	1	0.04	22.15
		χ^2:	63.93

- Critical value of the χ^2 distribution with $df = 5$, $\alpha = 0.05$: 11.07
- Critical value < χ^2 statistic $\therefore$ H_0 is rejected ($p < 0.00001$)
- The model is not a good fit to the observed data

Optimizing model fit to observed data (I)

- Using the Solver add-in in Microsoft Excel, the value of k (and p) that optimizes the fit of the observed data to the model-predicted values
- In this case, the Solver produces the following solution:
  $k = 3.62 \ \therefore p = 0.0362, q = 0.9638$

Optimizing model fit to observed data (II)



Time	*Obs.*	*Exp.*	*(Obs - Exp)²/Exp*
0	1	1.00	
1	3	3.62	0.10
2	10	12.02	0.34
3	35	30.18	0.77
4	35	36.36	0.05
5	7	13.16	2.88
6	1	1.80	0.35
7	1	0.18	3.61
		χ^2:	8.11

- Critical value (df = 6, α = 0.05): 12.59
- H_0 cannot be rejected (p = 0.23)

What is *k*?

- *k* is the typical or average number of adequate contacts each individual has with others in the population during a single time period
- If the population is entirely susceptible to disease, then every adequate contact will be effective
  - ∴ *k* is the average number of secondary cases that will arise from one initially infectious case during a single time period
- The basic Reed-Frost model assumes that individuals are infectious for no more than 1 time period
  - ∴ *k* is the average number of secondary cases that will arise from one initially infectious case
- In the basic Reed-Frost model, $k = R_0$
- When we estimate *k* in a basic Reed-Frost model (as we've just done), we are estimating R_0

A note about the χ^2 test

- As a rule of thumb, every cell (observed value and expected value) should be at least 5 for the χ^2 test to be valid
- In the example just shown, this rule was violated
- We will continue to violate it, for purposes of illustration
- It would be more appropriate to use a different test (*e.g.*, the G test: Sokal and Rohlf, 1994)

Revisiting some assumptions of the Reed-Frost model

- Assumption: There are three disease states: susceptible, infectious, and recovered
  - But many diseases have additional states, *e.g.*, a latent state
- Assumption: Each disease state has the same duration (1 time period)
  - But some diseases may have prolonged latent or infectious stages
- Assumption: Immunity after infection lasts forever
  - But for some diseases, immunity wanes over time, and individuals become susceptible to re-infection
  - For some diseases, there is no lasting immunity, and individuals become susceptible again very soon after recovery

If the existing model is too simplistic, build a more realistic model…

Modified Reed-Frost models: *SLIR* (I)

- Incorporating a latent period introduces a *delay* or *lag* between the time of infection and the time that individuals become infectious
- In the relatively simple Reed-Frost framework, that delay lasts for some multiple of the time period
- These models are sometimes referred to as *SEIR* models, where the *E* stands for “exposed”

Modified Reed-Frost models: *SLIR* (II)

- Upon infection, an individual will be latent for some specified number of time periods before becoming infectious itself

Time	*Latent incidence*	*Latent prevalence*	*Cases*	*Immune*	*Susceptible*
0	0	0	1	0	100
1	2	2	0	1	98
2	0	2	0	1	98
3	0	0	2	1	98
4	4	4	0	3	94
5	0	4	0	3	94
6	0	0	4	3	94
7	7	7	0	7	87
8	0	7	0	7	87
9	0	0	7	7	87

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Latency lasts for 2 time periods

Incidence and prevalence in an SLIR model

- Because of the lag, incidence is not necessarily equal to prevalence

Time	*Latent incidence*	*Latent prevalence*	*Cases*	*Immune*	*Susceptible*
0	0	0	1	0	100
1	2	2	0	1	98
2	0	2	0	1	98
3	0	0	2	1	98
4	4	4	0	3	94
5	0	4	0	3	94
6	0	0	4	3	94
7	7	7	0	7	87
8	0	7	0	7	87
9	0	0	7	7	87

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Latency lasts for 2 time periods

Reed-Frost *SLIR*: Calculating incidence of latent individuals

- The number of newly infected individuals is calculated based on the previous numbers of infectious cases and susceptible individuals, just as before

Time	*Latent incidence*	*Latent prevalence*	*Cases*	*Immune*	*Susceptible*
0	0	0	1	0	100
1	2	2	0	1	98
2	0	2	0	1	98
3	0	0	2	1	98
4	4	4	0	3	94
5	0	4	0	3	94
6	0	0	4	3	94
7	7	7	0	7	87
8	0	7	0	7	87
9	0	0	7	7	87

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Latency lasts for 2 time periods

Reed-Frost *SLIR*: Calculating prevalence of latent individuals

- Prevalence of latent individuals will be the number of latent cases that occurred in the last *x* time periods, where *x* is the number of periods that latency lasts

Time	*Latent incidence*	*Latent prevalence*	*Cases*	*Immune*	*Susceptible*
0	0	0	1	0	100
1	2	2	0	1	98
2	0	2	0	1	98
3	0	0	2	1	98
4	4	4	0	3	94
5	0	4	0	3	94
6	0	0	4	3	94
7	7	7	0	7	87
8	0	7	0	7	87
9	0	0	7	7	87

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Latency lasts for 2 time periods

Reed-Frost *SLIR*: Calculating the number of new cases

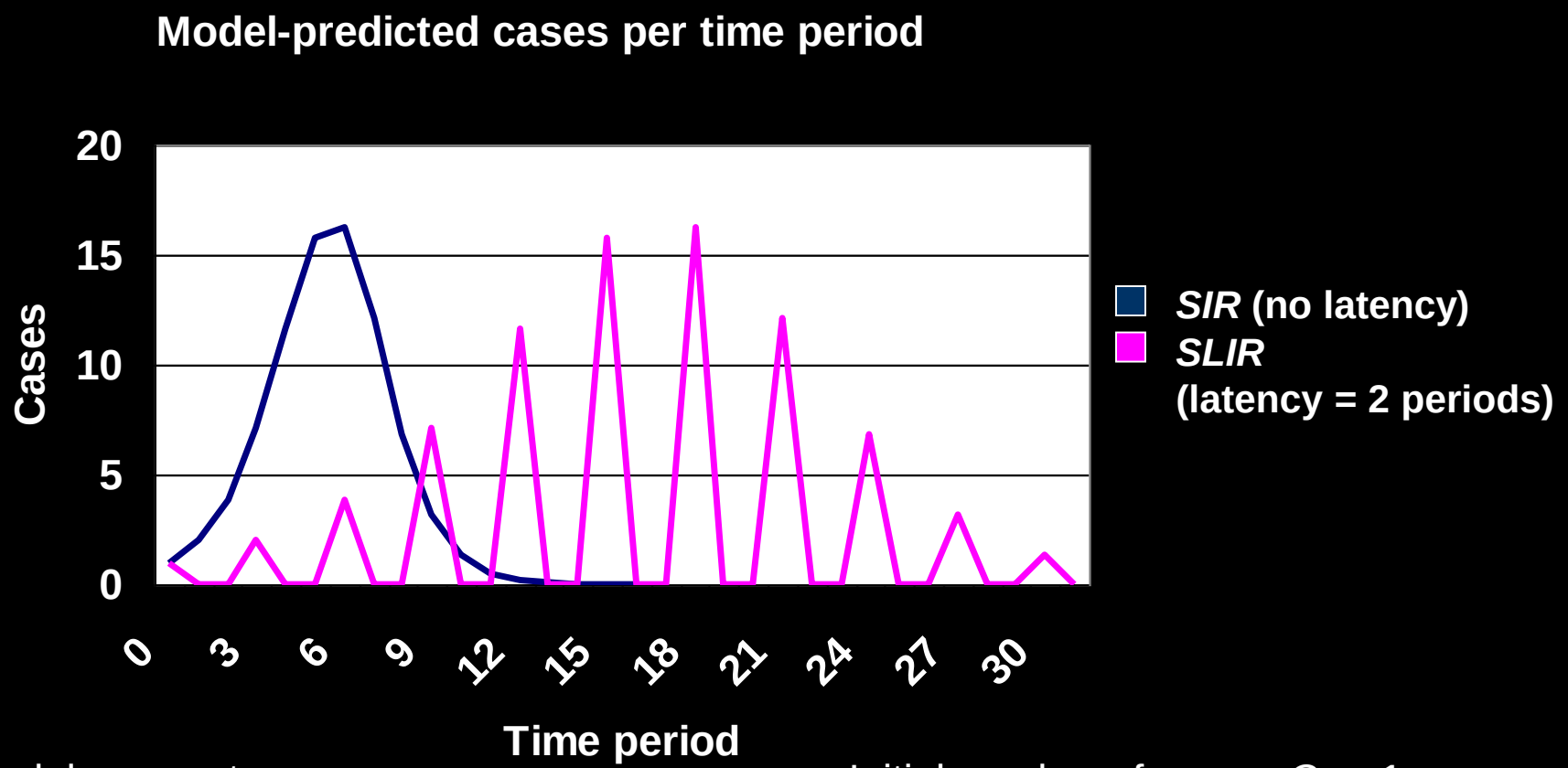
- Individuals that become latent in time period *t* will become infectious cases in time period *t* + *x* where *x* is the duration of latency

Time	*Latent incidence*	*Latent prevalence*	*Cases*	*Immune*	*Susceptible*
0	0	0	1	0	100
1	2	2	0	1	98
2	0	2	0	1	98
3	0	0	2	1	98
4	4	4	0	3	94
5	0	4	0	3	94
6	0	0	4	3	94
7	7	7	0	7	87
8	0	7	0	7	87
9	0	0	7	7	87

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Latency lasts for 2 time periods

Modified Reed-Frost models: *SLIR* (III)



Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Latency lasts for 2 time periods

Modified Reed-Frost models: *SIR* with extended infectiousness (I)

- We'll keep track of new cases (case incidence) as well as the accumulated cases (case prevalence)

Time	*Case incidence*	*Case prevalence*	*Immune*	*Susceptible*
0	1	1	0	100
1	2	3	0	98
2	6	8	1	92
3	13	19	3	79
4	25	39	9	54
5	29	54	22	25
6	16	45	47	8
7	5	21	76	3
8	1	6	93	2
9	0	1	98	2
10	0	0	99	2

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Infectiousness lasts for 2 time periods

Reed-Frost *SIR* with extended infectiousness: Calculating case incidence

- New cases continue to be calculated as before

Time	*Case incidence*	*Case prevalence*	*Immune*	*Susceptible*
0	1	1	0	100
1	2	3	0	98
2	6	8	1	92
3	13	19	3	79
4	25	39	9	54
5	29	54	22	25
6	16	45	47	8
7	5	21	76	3
8	1	6	93	2
9	0	1	98	2
10	0	0	99	2

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Infectiousness lasts for 2 time periods

Reed-Frost *SIR* with extended infectiousness: Calculating case prevalence

- Case prevalence will be the number of cases that occurred in the last *x* time periods, where *x* is the number of periods that infectiousness lasts

Time	*Case incidence*	*Case prevalence*	*Immune*	*Susceptible*
0	1	1	0	100
1	2	3	0	98
2	6	8	1	92
3	13	19	3	79
4	25	39	9	54
5	29	54	22	25
6	16	45	47	8
7	5	21	76	3
8	1	6	93	2
9	0	1	98	2
10	0	0	99	2

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Infectiousness lasts for 2 time periods

Reed-Frost *SIR* with extended infectiousness: Calculating number of immune individuals

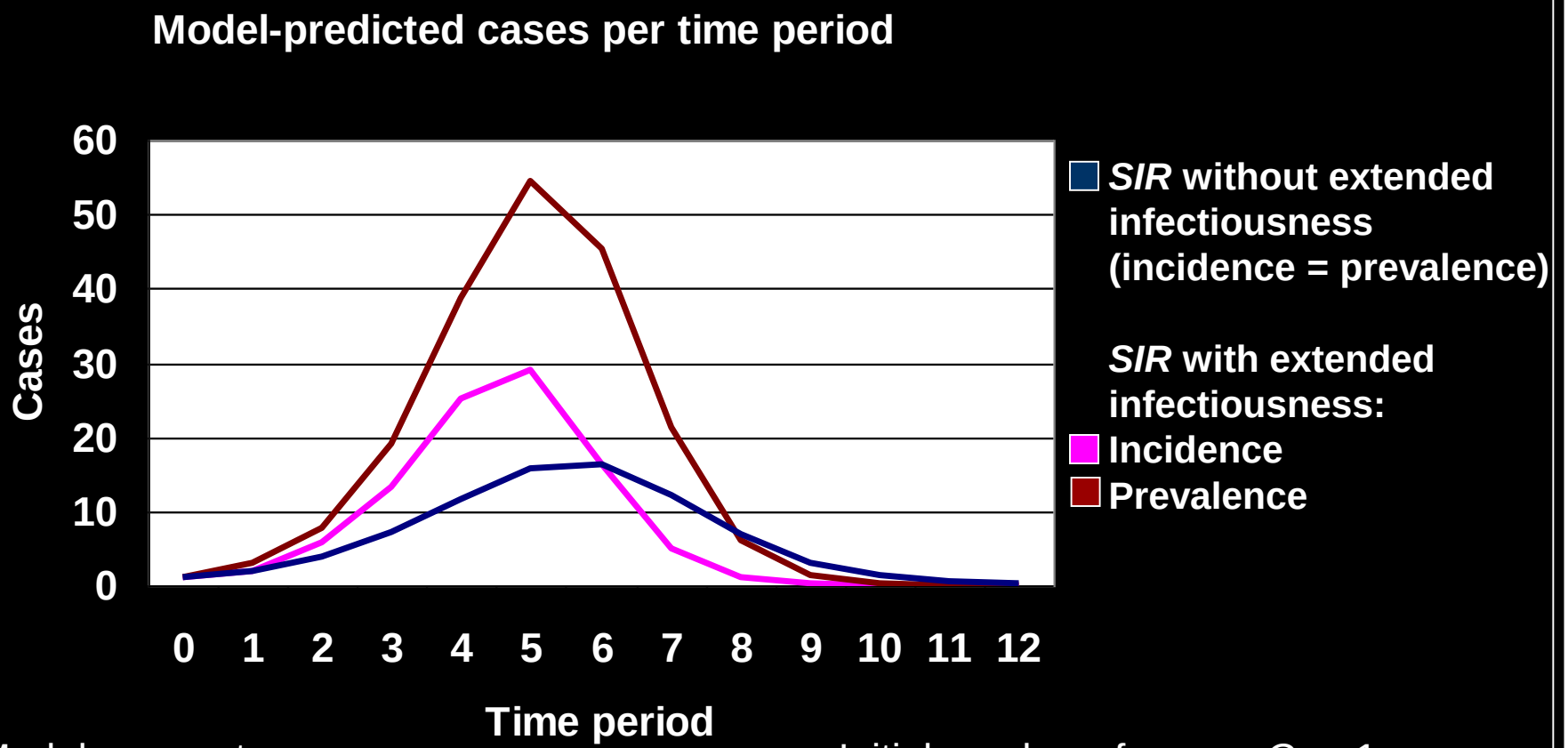
- Number of immune individuals will depend on the number of cases that occurred *x* time periods ago

Time	*Case incidence*	*Case prevalence*	*Immune*	*Susceptible*
0	1	1	0	100
1	2	3	0	98
2	6	8	1	92
3	13	19	3	79
4	25	39	9	54
5	29	54	22	25
6	16	45	47	8
7	5	21	76	3
8	1	6	93	2
9	0	1	98	2
10	0	0	99	2

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Infectiousness lasts for 2 time periods

Modified Reed-Frost models: *SIR* with extended infectiousness (II)



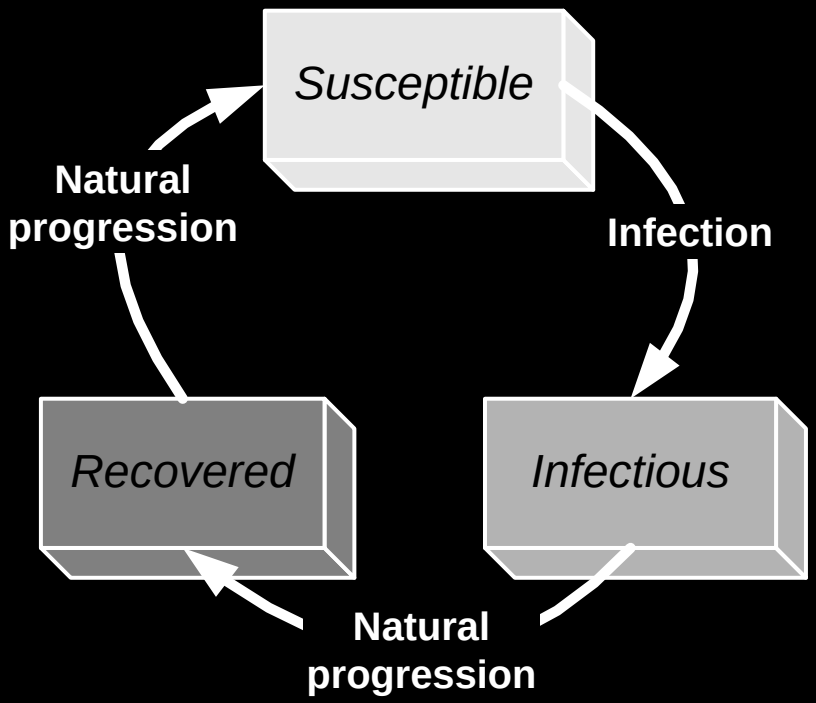
Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Infectiousness lasts for 2 time periods

Modified Reed-Frost models: *SIR* with extended infectiousness (III)

- We've seen that, for a basic Reed-Frost model: $k = R_0$
- In this modified Reed-Frost model:
  - Population size: $N = 101$
  - Prob. of adequate contact: $p = 0.02$
  - $k = 2$
  - Infectiousness lasts for 2 time periods
- What is R_0?
  - In this case, $R_0 = 4$
- In general:
  - $R_0 = k \times$ (# of time periods that an individual is infectious)

Modified Reed-Frost models: *SIRS* (I)



- For diseases that have a temporary immune period, a *Susceptible-Immune-Recovered-Susceptible* model might be appropriate
- In the context of a Reed-Frost model, individuals may be immune for one or more time periods before returning to a susceptible state
- As we've done before, we'll follow the incidence and prevalence of immune individuals

Reed-Frost *SIRS*: Calculating incidence of immune individuals

- Individuals become infectious just as in the basic *SIR* model

Time	Cases	Immune Incidence	Immune prevalence	Susceptible
0	1	0	0	100
1	2	1	1	98
2	4	2	3	94
3	7	4	6	88
4	12	7	11	78
5	17	12	19	66
6	19	17	28	54
7	17	19	35	49
8	14	17	36	51
9	13	14	31	57
10	13	13	27	61

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Immunity lasts for only 2 time periods

Reed-Frost *SIRS*: Calculating prevalence of immune individuals

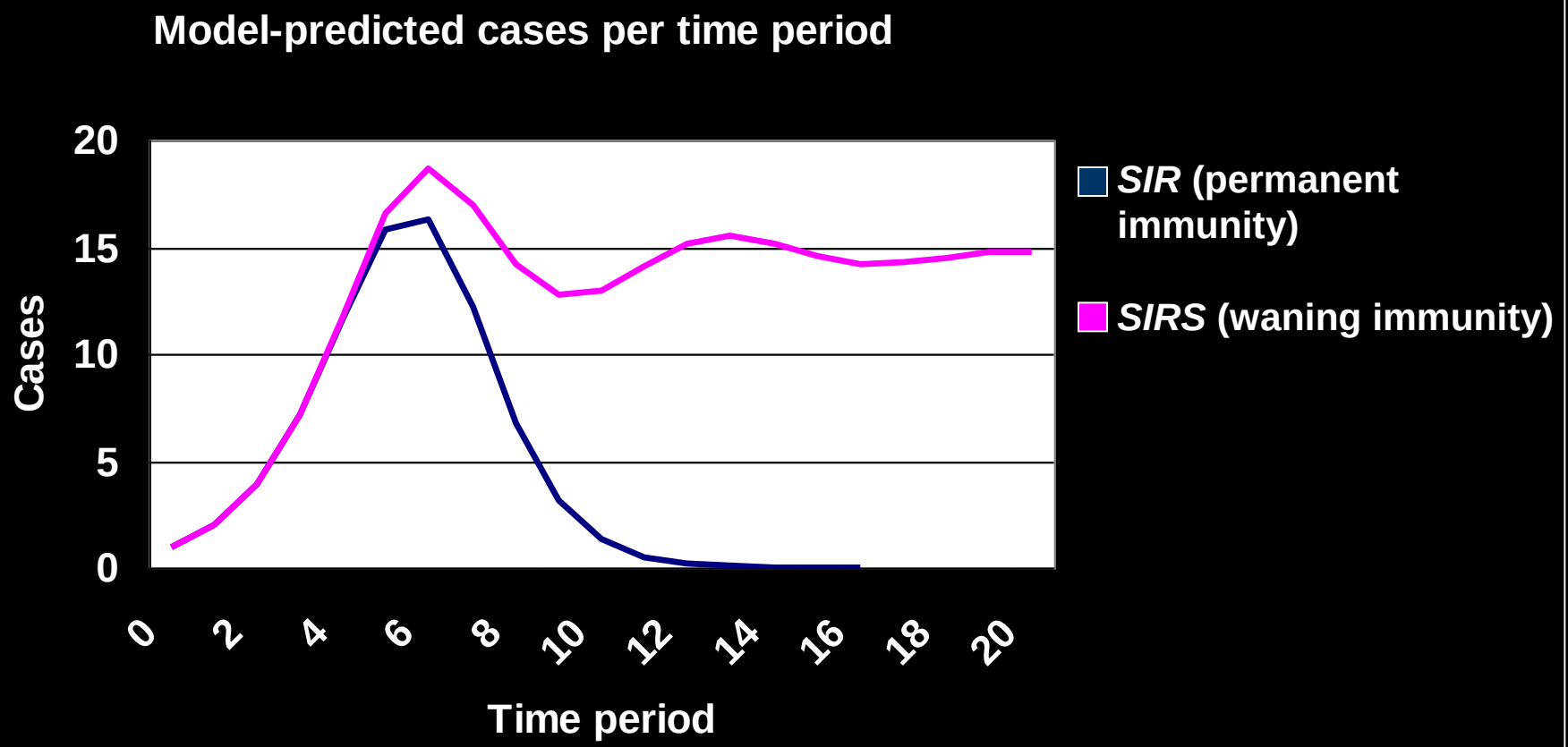
- Prevalence will be the number of newly immune individuals from the last *x* time periods, where *x* is the number of periods that immunity lasts

Time	Cases	Immune Incidence	Immune prevalence	Susceptible
0	1	0	0	100
1	2	1	1	98
2	4	2	3	94
3	7	4	6	88
4	12	7	11	78
5	17	12	19	66
6	19	17	28	54
7	17	19	35	49
8	14	17	36	51
9	13	14	31	57
10	13	13	27	61

Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Immunity lasts for only 2 time periods

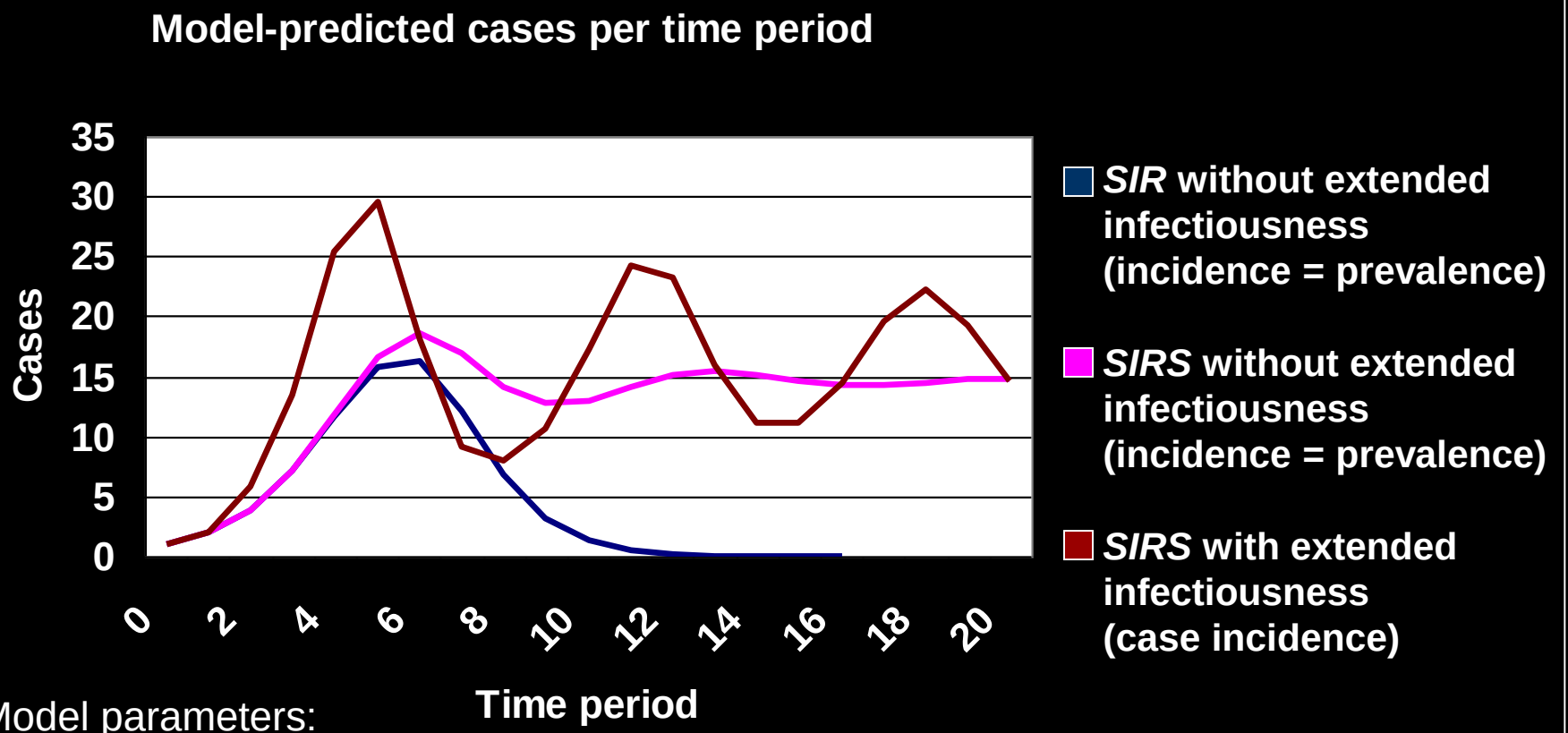
Modified Reed-Frost models: *SIRS* (III)



Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Immunity lasts for only 2 time periods

Modified Reed-Frost models: *SIRS* with extended infectiousness



Model parameters:

- Population size: $N = 101$
- Initial number of susceptibles: $S_0 = 100$
- Initial number of cases: $C_0 = 1$
- Prob. of adequate contact: $p = 0.02$
- Infectiousness lasts 2 time periods
- Immunity lasts for only 2 time periods

Summary

- The concept of disease state is common to many disease models, regardless of their form (differential calculus, Reed-Frost-type, Markov chain, *etc*.)
- The basic Reed-Frost model provides a framework in which the number of new cases can be predicted based on the number of cases in the previous time period: $C_{t+1} = S_t(1 - q^{C_t})$
- Some of the assumptions of the basic Reed-Frost model can be modified to model more complex situations
- The goodness of fit of model predictions to actual data can be assessed with statistical techniques
- This afternoon, we will build several Reed-Frost-type models, and observe their behavior under a variety of conditions

Questions?

Recommended reading

- Abbey, H., 1952. An examination of the Reed-Frost theory of epidemics. *Human Biology* 24: 201–233. *(One of two early papers describing the basic Reed-Frost model)*
- Carpenter, T.E., 1984. Epidemiologic modeling using a microcomputer spreadsheet package. *American Journal of Epidemiology* 120: 943–951. *(While the hardware and software used now seem quaint, the description of Reed-Frost modeling with a spreadsheet is still applicable, as are the model assumptions)*
- Daley, D.J., and Gani, J. 1999. Epidemic Modelling: An Introduction. Cambridge, UK: Cambridge University Press. *(Chapter 6 discusses fitting models to observed data from a more mathematical perspective)*
- Maia, J.O.C., 1952. Some mathematical developments on the epidemic theory formulated by Reed and Frost. *Human Biology* 24: 167–200. *(The second of two early papers describing the basic Reed-Frost model: discusses the role of k)*
- Thrusfield, M. 2005. Veterinary Epidemiology, 3rd ed. Oxford: Blackwell Science Ltd. *(Chapter 8 describes the basic Reed-Frost model)*

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- Sokal, R. R., and Rohlf, F. J. 1994. Biometry: The Principles and Practice of Statistics in Biological Research, 3rd ed. New York: Freeman.
- Miller, W.M. 1976. A state-transition model of epidemic foot-and-mouth disease. In Ellis, P.R., Shaw, A.P.M., and Stephens, A.J., eds. New Techniques in Veterinary Epidemiology and Economics, Proceedings of a Symposium, University of Reading, England: ISVEE I. *http://www.sciquest.org.nz*