

SIR Model Modes of Computation - Agent & Equation

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Abstract

We describe how an SIR model can be transformed from agent-base to equation-based and vice versa. Different assumptions about the nature of the equations in the SIR model or the agents are considered.

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1 ODE: Well Mixed SIR

We describe how a first-order ODE, an SIR model, can be translated into an agent-based model in discrete time with quantized agents. First, the SIR model as ODE:

$$\dot{S} = \frac{-\beta SI}{N}, \dot{I} = \frac{\beta SI}{N} - rI, \dot{R} = rI \quad (1)$$

where: N =population size in units of *individual*, β =transition rate from sick to infected in units of $1/s$, r =recovery rate in units of $1/s$

The population is assumed to be "well-mixed." This assumption is observable in the $\frac{\beta SI}{N}$ term. The product $S \cdot I$ counts the number of individual interactions that can take place while the β/N scales how many of these interactions produce an infection. It is interesting that the SIR model *does not* imply any specific location of the agents. Rather it is only required that they are dispersed such that at every instant all susceptible individuals are exposed to all infectious individuals.

The interpretation of rI is obvious.

1.1 Agent-Based Model

We need several items to define an agent based model:

1. Types of individuals
2. Number of individuals by type in population at $t = 0$
3. Definition of individuals: what makes their state?
4. The rules for how individuals state changes, if any.

One might think that defining *types* of individuals and state is redundant. Why not avoid type of individual and use the type as a state variable? Here we can encode the idea that some state variables are *immutable*. Consider a cancer cell model of tumor cells and effector cells. These types of cells never transition in the model.

1.2 Given State Transition Graph

We now assume from the TA1 artifacts we have derived:

1. There is one type of individual.
2. The number of individuals is N .
3. The individuals are characterized by three possible states: S, I, R . Critically, we assume the *state transition* have been defined: $S \rightarrow I \rightarrow R$.

With these, we can derive the rules for state transitions.

Let us consider state transition: $S \rightarrow I$. Given any ODE, we can claim that a single equation can be found for \dot{S} . If there are two equations provided for \dot{S} either they are in different spatial domains which is not the case here since we have no spatial domains; or the case is that the equations must be identical under some algebraic manipulation. For our SIR case, we have:

$$\dot{S} = \frac{-\beta SI}{N} \rightarrow \frac{dS}{dt} = \frac{-\beta SI}{N} \rightarrow dS = -\beta S \frac{I}{N} dt \quad (2)$$

Our goal then is to determine how to calculate dS for individual agents.

We know that on average at every time step, dt , the number of transitions $S \rightarrow I$ is $\beta S \frac{I}{N} dt$; therefore:

$$E[dS] = -\beta S \frac{I}{N} dt = \sum_m^N -1 \cdot P(S \rightarrow I|m) + 1 \cdot P(I \rightarrow S|m) + P(S \rightarrow S|m) \cdot 0 \quad (3)$$

Where $P(A \rightarrow B|m)$ means for the probability of the m th individual the transitioning from state A to B .

Given the transition graph: $S \rightarrow I \rightarrow R$, we can derive $P(I \rightarrow S|m) = 0 \forall m$. We are left with:

$$-\beta S \frac{I}{N} dt = \sum_m^N -P(S \rightarrow I|m) \quad (4)$$

given that for all individuals which are not in state S $P(S \rightarrow I|m) = 0$, we can reduce the sum:

$$-\beta S \frac{I}{N} dt = \sum_m^S -P(S \rightarrow I|m) \quad (5)$$

The "well-mixed" assumption indicates that all these probabilities are identical:

$$-\beta S \frac{I}{N} dt = -SP(S \rightarrow I|m) \quad (6)$$

$$\beta \frac{I}{N} dt = P(S \rightarrow I|m) \quad (7)$$

We thus have the probability that at each time-step an agent that is in state S will transition to state I . Next let us derive the probability of transitioning $I \rightarrow R$. We follow the same approach:

$$E[dR] = rI \cdot dt = \sum_m^N P(I \rightarrow R|m) * 1 + P(R \rightarrow I|m) * -1 \quad (8)$$

Given the state transition network: $\forall m \rightarrow P(R \rightarrow I|m) = 0$

$$E[dR] = rI \cdot dt = \sum_m^N P(I \rightarrow R|m) * 1 \quad (9)$$

For all individual agents A_m where state $A_m \neq I \rightarrow P(I \rightarrow R|m) = 0$

Thus we reduce the upperbound of the sum:

$$E[dR] = rI \cdot dt = \sum_m^I P(I \rightarrow R|m) * 1 \quad (10)$$

Given the well-mixed assumption all these probabilities are equal:

$$rI \cdot dt = I \cdot P(I \rightarrow R|m) \quad (11)$$

$$r \cdot dt = P(I \rightarrow R|m) \quad (12)$$

We now have the probability that agent in state I will transition to state R at each time step.

We can now write the transition equations in probabilistic form:

$$A_{j,t+1} = A_{j,t} + \begin{cases} 1 & \text{if } A_{j,t} = 0 \text{ and } u \leq \beta \frac{I}{N} dt \\ 1 & \text{if } A_{j,t} = 1 \text{ and } u \leq r dt \\ 0 & \text{otherwise} \end{cases} \quad (13)$$

Where u is a number drawn from the uniform distribution $U(0, 1)$ at each step for each individual.

Critical assumptions we must draw from the user or the TA1 artifacts:

- There is **one** population.
- There are **three** states and they transition $S \rightarrow I \rightarrow R$
- Aggregate transitions between states is governed by the ODE equations.
- Agents are **equally mixed**.

2 ABM: Well Mixed

We provide a general method for translating from an agent-based model of viral transmission to an ODE: the traditional SIR model.

2.1 ABM Artifacts

First, we state the model as the state transition function for any agent at any time step:

$$A_{j,t+1} = A_{j,t} + \begin{cases} 1 & \text{if } A_{j,t} = 0 \text{ and } u \leq \beta \frac{I}{N} \Delta t \\ 1 & \text{if } A_{j,t} = 1 \text{ and } u \leq r \Delta t \\ 0 & \text{otherwise} \end{cases} \quad (14)$$

where u is a random number in the $U(0,1)$ drawn at each time step. β is the transmission rate, N is the number of individuals in the model, I is the number of individuals in the infected state ($A_j = 1$) in the population. r is the recovery rate.

Second, have the initial condition (some portion of the agents are infected at the start):

- We have the set of agent indices $\mathbf{W} \in \mathbb{Z}$ where $|\mathbf{W}| = N$. We also have a subset of infected agents at $t = 0$: $\mathbf{I}_0 \subset \mathbf{W}$
- We set $A_{i,0} = 1 \ \forall i \in \mathbf{I}_0$
- We set $A_{i,0} = 0 \ \forall i \in \mathbf{W} - \mathbf{I}_0$

2.2 General Approach

We can automatically derive three states, and label them in the obvious manner S, I, R where states correspond to numeric value:

$$0 \rightarrow S, 1 \rightarrow I, 2 \rightarrow R \quad (15)$$

The labeling and the piecewise function enables us to derive some probability statements. These will be key to transitioning to an ODE that describes the average evolution of the number of agents within each state through time.

We define a specific notation:

$$P(H_s \rightarrow H_v | j)$$

is the probability of agent j transitioning from state H_s to state H_v at the given time step. We will abuse the notation of S, I, R such that when we use one of these labels in a probability definition, we mean the probability

of transitioning between the labeled states: $P(S \rightarrow I|j)$ means the probability of the j th agent transitioning from susceptible to infected.

With this notation, we can easily derive some probability statements:

$$P(I \rightarrow S|j) = P(R \rightarrow I|j) = P(R \rightarrow S|j) = P(S \rightarrow R|j) = 0 \quad \forall j \in \mathbf{W} \quad (16)$$

$$P(S \rightarrow I|A_j = 0) = \beta \frac{I}{N} \Delta t \quad (17)$$

$$P(I \rightarrow R|A_j = 1) = r \Delta t \quad (18)$$

$$P(S \rightarrow I|A_j \neq 0) = P(I \rightarrow R|A_j \neq 1) = 0 \quad (19)$$

We now lay out the statistical background for deriving $\dot{S}, \dot{I}, \dot{R}$.

Our probabilistic statements above enable us to compute the average number of agents in a given state at some point in time:

$$E[H_k(t)] = E\left[H_k(0) + \sum_i^t \Delta H_k(i)\right] = E[H_k(0)] + E\left[\sum_i^t \Delta H_k(i)\right] \quad (20)$$

$$= H_k(0) + E\left[\sum_i^t \Delta H_k(i)\right] \quad (21)$$

$$= H_k(0) + \sum_i^t E[\Delta H_k(i)] \quad (22)$$

where $H_k(t)$ is the number of agents in state H_k at time t . $k \in [0, 1, 2]$ and maps to the S, I, R states.

We concentrate on: $E[\Delta H_k(i)]$. Using the definition of expected values we can write this in terms of probability of each possible type of transition:

$$E[\Delta H_k(i)] = \sum_m^N \sum_g^{g \neq k} P(H_g \rightarrow H_k | A_m) - P(H_k \rightarrow H_g | m) \quad (23)$$

Where $P(H_g \rightarrow H_k | m)$ is the probability of agent m transitioning from state H_g to state H_k . Since the agent is transitioning to the state of interest, the contribution to the expected value is positive. The contribution when transitioning away from H_k is negative.

Our approach for each state is to expand the right-hand-side and then see if we can find a dH_k .

Our agent-based model as defined earlier, provides all of these probabilities. To generalize this method for “any” probability transition functions, we restate our earlier non-zero transition probabilities:

$$P(S \rightarrow I|A_j = 0) = f(S, I, \beta, N, r) \Delta t = f(\dots) \Delta t = \beta \frac{I}{N} \Delta t \quad (24)$$

$$P(I \rightarrow R|A_j = 1) = g(S, I, \beta, N, r) \Delta t = g(\dots) \Delta t = r \Delta t \quad (25)$$

We wrote “any” because we realize that we have removed the Δt from the definition. Further development is necessary here for complete generalization.

2.3 Expand: $E[\Delta S(i)]$

$$E[\Delta S(i)] = \sum_m^N P(I \rightarrow S|m) - P(S \rightarrow I|m) + P(R \rightarrow S|m) - P(S \rightarrow R|m) \quad (26)$$

Recall:

$$P(I \rightarrow S|m) = P(R \rightarrow S|m) = P(S \rightarrow R|m) = 0 \quad \forall m \in \mathbf{W} \quad (27)$$

$$E[\Delta S(i)] = \sum_m^N -P(S \rightarrow I|m) \quad (28)$$

We recall that $P(S \rightarrow I|A_j \neq 0) = 0$. We can use this in our sum above to zero many elements. The interpretation is straightforward: agents that are not in the S *cannot* possibly transition to the I state. The remaining $P(\dots)$ terms that are non-zero are precisely S in quantity.

$$E[\Delta S(i)] = -S \cdot P(S \rightarrow I|m) = -Sf(\dots)\Delta t \quad (29)$$

As $\Delta t \rightarrow 0$, our differences become differentials:

$$E[dS] = -Sf(\dots)dt \quad (30)$$

We have dropped the i from the S since it does not depend on it on the RHS.

$$\frac{E[dS]}{dt} = -Sf(\dots) \quad (31)$$

This is *almost* the original \dot{S} equation. We have an expected value here though. We loosely drop the expected value as there are no remaining probability statements on the RHS:

$$\frac{dS}{dt} = -\beta \frac{SI}{N} \Delta t \quad (32)$$

What is this differential equation about? It describes how the *expected value* of the total number of susceptible agents changes through time.

2.4 Expand: $E[\Delta I(i)]$

$$E[\Delta I(i)] = \sum_m^N P(S \rightarrow I|m) - P(I \rightarrow S|m) + P(R \rightarrow I|m) - P(I \rightarrow R|m) \quad (33)$$

Recall:

$$P(I \rightarrow S|m) = P(R \rightarrow I|m) = 0 \quad \forall m \in \mathbf{W} \quad (34)$$

$$E[\Delta I(i)] = \sum_m^N P(S \rightarrow I|m) - P(I \rightarrow R|m) \quad (35)$$

We recall that $P(S \rightarrow I|A_j \neq 0) = 0$ and $P(I \rightarrow R|A_j \neq 1) = 0$ which allows us to zero many of these elements. The remaining elements of transition $S \rightarrow I$ are S in count while the remaining $I \rightarrow R$ elements are I in count:

$$E[\Delta I(i)] = S \cdot P(S \rightarrow I|m) - I \cdot P(I \rightarrow R|m) \quad (36)$$

Using our generalized transition probabilities:

$$E[\Delta I(i)] = Sf(\dots)\Delta t - Ig(\dots)\Delta t \quad (37)$$

We take the limit $\Delta t \rightarrow 0$ to get differentials:

$$E[dI] = Sf(\dots)dt - Ig(\dots)dt = (Sf(\dots) - Ig(\dots))dt \quad (38)$$

$$\frac{E[dI]}{dt} = Sf - Ig \quad (39)$$

Dropping the expected value and substituting in f, g :

$$\frac{dI}{dt} = S\beta \frac{I}{N} - rI \quad (40)$$

2.5 Expand $E[\Delta R(i)]$

$$E[\Delta R(i)] = \sum_m^N P(S \rightarrow R|m) - P(R \rightarrow S|m) + P(I \rightarrow R|m) - P(R \rightarrow I|m) \quad (41)$$

Recall:

$$P(S \rightarrow R|m) = P(R \rightarrow S|m) = P(R \rightarrow I|m) = 0 \quad \forall m \in \mathbf{W} \quad (42)$$

$$E[\Delta R(i)] = \sum_m^N P(I \rightarrow R|m) \quad (43)$$

We recall that $P(I \rightarrow R|A_m \neq 0) = 0$. We zero many elements. The non-zero elements are I in quantity.

$$E[\Delta R(i)] = I \cdot P(I \rightarrow R|m) \quad (44)$$

$$E[\Delta R(i)] = I \cdot g(\dots)\Delta t \quad (45)$$

Taking $\Delta \rightarrow 0$

$$E[dR] = Ig(\dots)dt \quad (46)$$

$$\frac{E[dR]}{dt} = Ig(\dots) \quad (47)$$

Drop the expected value and substitute in g :

$$\frac{dR}{dt} = rI \quad (48)$$

2.6 Boundary Conditions

Recall our earlier statement:

$$E[H_k(t)] = H_k(0) + \sum_i^t E[\Delta H_k(i)] \quad (49)$$

The boundary condition $S(0), I(0), R(0)$ is obvious: we simply count the agents in each state.

2.7 Caveats

- We slyly went from discrete S, I, R to continuous versions. How can we do this more rigorously?
- Can we actually say that $E[dH_k] = dH_k$ if the RHS contains no probability expressions?
- A critical step is recognizing the zero and non-zero probability elements in a statement like: $E[\Delta R(i)] = \sum_m^N P(I \rightarrow R|m)$. How would we do this automatically in software?
- The translation process isn't *trivial*, but it is certainly enabled by the *form* of our state transition function. Namely, the state transition is *probabilistic* and conveniently has a dt in it. It seems to me that any ABM could be massaged into the form we have. Is that true?

3 ABM: Agents on Static Graph

Consider an agent-based model of agents on a static graph: nodes and edges are neither added to or removed from the graph as the simulation progresses. Agents have two properties:

- Location - An agent exists on a specific node on the graph. Agents may not move to other nodes. A node may not have more than one agent on it.
- Health Status - An agent is Susceptible, Infected, or Recovered.

Given this definition of an agent, we can define some functions:

$$A_i(t) = \text{The state of the } i\text{th agent} = \{0, 1, 2\} \text{ (Susceptible, Infected, Recovered)} \quad (50)$$

$$B_i(t) = \text{The index of the node at which the } i\text{th agent resides.} \quad (51)$$

At time=0, no agents are in the Recovered state. Some are in the Susceptible state while others (usually far fewer) are in the Infected state. The state transition rule follows (Below δ is the amount of time that passes between each time step):

- If $A_i(t) = 0$, then the probability that $A_i(t+1) = 1$ is $aI_n\delta$ where a is some constant and I_n is the number of neighbors that are infected. Neighbor here means agents that are one hop away from B_i .
- If $A_i(t) = 1$, then the probability that $A_i(t+1) = 2$ is $\gamma\delta$ where γ is some constant.
- If $A_i(t) = 2$, then the $P(A_i(t+j) = 2) = 1 \forall j$. (Agents once recovered remain recovered.)

Given these transition rules, we can define a unique agent-based model with the following:

- N is the total number of agents and thus graph nodes throughout the simulation.
- G is the graph on which these agents reside. This defines edges which determines neighbors.
- S_0 is the number of susceptible agents at $t = 0$.
- I_0 is the number of infected agents at $t = 0$.
- R_0 is the number of recovered agents at $t = 0$.

Our goal is to show how this agent based model can be transformed into a system of differential equations that tracks the expected counts of susceptible, infected, and recovered agents through time.

3.1 General Graph

We derive here general expressions for the expected value of the change of the counts of agents at each time step given a general graph. We make no assumption over the structure of the graph. Subsequent sections take these equations and add further assumptions to arrive at a differential equation for \dot{S} .

Let $S(t), I(t), R(t)$ be the total number of agents in the susceptible, infected, and recovered states at time t . Our intent is to write expressions for $E[\Delta S]$, $E[\Delta I]$, and $E[\Delta R]$: the expected value of the change of each count of states. For now, we have derived $E[\Delta S]$.

3.1.1 Derivation: $E[\Delta S]$

We begin with deriving the expected value for how susceptible agents transition to being infected. Considering our transition rule from susceptible to infectious, the expected value of ΔS is straightforward to write in terms of probabilities:

$$E[\Delta S] = \sum_i^N -1 \cdot P(\text{Agent } i \text{ becomes infected}) = \sum_i^N -1 \cdot P(A_i = 0 \cap \text{Neighbors transmit infection}) \quad (52)$$

Recall that N is the total number of agents. For an agent to contribute to the decrease in S , the agent must be both susceptible and have infectious neighbors. Notice the -1 , this causes the contribution to decrease the count of susceptible.

We now turn to the definition of conditional probability to expand. Given

$$P(B)P(A|B) = P(A \cap B) \quad (53)$$

we can write:

$$E[\Delta S] = \sum_i^N -1 \cdot P(A_i = 0) \cdot P(\text{Neighbors transmit infection} | A_i = 0) \quad (54)$$

One might be tempted to assume independence of being susceptible and having the infection transmitted to agent i ; but it turns out this is not necessarily true. We will comment on this when we define the conditional probability in equation 54. The probability of agent i being susceptible is trivial:

$$P(A_i = 0) = S/N \quad (55)$$

given $S(t)$ susceptible agents at time t

The probability $P(\text{Neighbors transmit infection} | A_i = 0)$ is not so straightforward. The $S \rightarrow I$ transition rule states that the probability of becoming infected depends on the *number* of infected neighbors. Given a static graph and immobile agents, we can define a constant k_i for each agent: the number of neighbors of the i th agent. Given this constant, we can write a probabilistic expression of infection that depends on the number of infected neighbors. We don't know how many infected neighbors there are; but we do know that it cannot be more than $L = \min(I, k_i)$. Note here this statement depends on the condition that agent i is susceptible. If the agent were in any state, the upper bound on the number of infected neighbors is not $\min(I, k_i)$ as the agent itself could be infected! We know the agent is infected; therefore, we can define an upper bound. Given the discrete number of infected neighbors gives us a partition of the probability space, we use the law of total probability:

$$P(\text{Neighbors transmit infection} | A_i = 0) = \sum_j^L P(\text{Infection} | j \text{ infected neighbors}) P(j \text{ infected neighbors}) \quad (56)$$

The first probability factor can be derived directly from the transition rule:

$$P(\text{Infection} | j \text{ infected neighbors}) = aj\delta \quad (57)$$

The second factor we will state and then explain:

$$P(j \text{ infected neighbors}) = \left[\binom{k_i}{j} \binom{N - k_i - 1}{I - j} \right] / \binom{N - 1}{I} \quad (58)$$

where $\binom{A}{B}$ is the binomial coefficient or commonly known in combinatorics as *n choose k*. We now explain equation 58. Given some graph and I infected agents, there are $\binom{N-1}{I}$ total combinations of agents *besides agent i* (thus the $N - 1$) being infected. Of these, we are interested in the total combination of ways that j of the I agents can be neighbors of agent i . Assuming there are j infected neighbors, then $\binom{k_i}{j}$ gives us the number of ways that the neighbors could be infected. Finally, for every combination of infected neighbors, there are a multitude of combinations of infected agents who *are not* neighbors of agent i . In fact, there are $\binom{N - k_i - 1}{I - j}$ ways: $N - k_i - 1$ agents that could possibly be infected and $I - j$ agents who are not neighbors to be infected. We thus have a complete definition for the expected change of S .

$$E[\Delta S] = \sum_i^N -1 \cdot P(\text{Agent } i \text{ becomes infected}) = \sum_i^N -\frac{S}{N} \left[\sum_j^{\min(I, k_i)} aj\delta \cdot \left(\binom{k_i}{j} \binom{N - k_i - 1}{I - j} \right) / \binom{N - 1}{I} \right] \quad (59)$$

This is hardly a differential equation. It is a rather complex difference equation given the unfortunate $\min(I, k_i)$

3.1.2 When $I = N$

We note a caveat to equation 59: $I = N$. What happens if the entire population is infected? If so, then $S = 0$. We might be tempted to say that $S/N \rightarrow 0/N \rightarrow 0$; therefore, the entire sum collapses to zero. The expected change in S is zero, as expected once all agents have become infected. The difficulty lies in the term in brackets. In this case, the coefficient

$$\binom{N - 1}{I} = \binom{N - 1}{N} = 0 \quad (60)$$

by convention whenever $n < k$ $\binom{n}{k} = 0$. What we would like to have is some expression in the brackets that when $I = N$ evaluates to 1 for $j = k_i$ and 0 otherwise. With a fully infected population, the only possibility of infected neighbors is that they are all infected. There is no possibility of having less than k_i infected neighbors. Our expression in brackets though was derived from a conditional probability which is the expansion of the probability of the union of the two events of interest: agent i being susceptible and the infection being transmitted to agent i . One could claim that at point, our probability is immediately zero since when $S = 0$, that probability of unions is zero simply by definition. The question is how to be rigorous about this in the expansion. All we can say for now is that equation 59 holds when $I < N$.

3.2 Complete Graph

Assume that G is a complete graph: an edge exists between every pair of nodes. Such a graph mimics "perfect mixing" which is an assumption of the basic SIR system of differential equations: any susceptible agent is exposed to all infected agents at each time step. We might be encouraged that the eyesore that is equation 59 is useful *if* given a complete graph, the equation reduces to the familiar differential equation for S :

$$\frac{dS}{dt} = -aSI \quad (61)$$

We first note that given a complete graph the upper bound $\min(I, k_i)$ in equation 59 can be simplified to just I . As noted in section 3.1.2, equation 59 holds when $I < N$: the entire graph is not infected. The maximum number of agents that can be infected then is $N - 1$. The number of neighbors in a complete graph is $N - 1$ which in this case is just I . Our inner sum becomes:

$$\sum_j^I aj\delta \cdot \left(\binom{N-1}{j} \binom{N-(N-1)-1}{I-j} \right) / \binom{N-1}{I} \quad (62)$$

$$\sum_j^I aj\delta \cdot \left(\binom{N-1}{j} \binom{0}{I-j} \right) / \binom{N-1}{I} \quad (63)$$

We note the curious term $\binom{0}{I-j}$. Recall that $\binom{N-k_i-1}{I-j}$ signified the number of ways of arranging $I - j$ infected agents on the nodes *not including* agent i and its neighbors. With a complete graph, there are exactly zero nodes that are not neighbors of agent i ; therefore, there are zero to choose from. By convention, the binomial coefficient is taken to be zero whenever $n < k$ for $\binom{n}{k}$. For all $I - j > 0$, the terms become zero in the sum. What about when $I = j$? Again by convention, the binomial coefficient is taken to one when both terms are zero: there is one way of choosing zero elements. This has an intuitive interpretation here for us. We expect there is some number of ways of arranging the I infected agents on the neighboring nodes; therefore all the terms should not be zero! The single term that survives then is when $I = j$. Again this is intuitive. The only surviving possibility is when the number of infected neighbors, j , is equal to the number of infected agents on the graph. Dropping all terms except the surviving one ($I = j$):

$$aI\delta \cdot \binom{N-1}{I} / \binom{N-1}{I} \quad (64)$$

The binomial coefficients cancel, substituting into equation 59, and simplifying the sum gives:

$$E[\Delta S] = \sum_i^N -\frac{S}{N} aI\delta = -aSI\delta \quad (65)$$

Now δ was the length of the time step. Let us be more explicit as to what exactly ΔS is:

$$E[S(t + \delta) - S(t)] = \sum_i^N -\frac{S}{N} aI\delta = -aSI\delta \quad (66)$$

We divide by δ and take the limit $\delta \rightarrow 0$.

$$\frac{E[dS]}{dt} = -aSI \quad (67)$$

We have now a differential equation that tells how the expected value of S changes in time. By definition, the SIR model tracks the average (expected) value of the number of agents in each state. We claim this is equivalent in meaning to equation 61. Possibly, equation 59 is not so unruly after all.