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Analytical approximations for the phase plane trajectories of the SIR model with vital dynamics

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Abstract

We derive accurate, closed-form analytical approximations for the phase-plane trajectories of the standard susceptible-infectious-removed (SIR) epidemic model, including host births and deaths. Our approximations for the SIR ordinary differential equations also allow us to provide convenient, accurate analytical approximations for the associated Poincaré map, and the minimum and maximum susceptible and infected host densities in each epidemic wave. Our analysis involves matching asymptotic expansions across branch cuts of the Lambert W function.

1 Introduction

Infectious disease transmission dynamics have been modelled with a susceptible-infectious-removed (SIR) compartmental framework since the early 20th century [18, 3]. What has become the standard SIR ordinary differential equation (ODE) model [Equation (1) below] was first published by Kermack and McKendrick in 1927 [12] (hereafter KM).

An exact solution for the time course of the state variables in the standard SIR ODEs has never been found, though KM did find an approximate analytical solution that is reasonably accurate for weakly transmissible diseases, and has often been used to obtain (usually qualitative) insights (*e.g.*, [4, 24, 20]).

If we ignore the recruitment of new susceptible individuals—whether they result from births, immigration, or decay of immunity—then the SIR ODEs can be solved exactly in the susceptible-infectious phase plane. No such exact analytical solution in the phase plane is available for the more realistic situation in which susceptible recruitment is not negligible.

In this paper, we use multiple scale and singular perturbation methods [22, 13] to obtain accurate analytical approximations to the phase-plane trajectories of the standard SIR ODEs with vital dynamics (*i.e.*, with host births and deaths). A natural small parameter is the infectious period relative to host lifetime (denoted ε), but we find that substantially simpler expressions are obtained by expanding in the (even smaller) parameter $\epsilon = \varepsilon/\mathcal{R}_0$, where \mathcal{R}_0 is the basic reproduction number.

Our interest in approximating the phase-plane solutions of the SIR ODEs was motivated by a problem in stochastic epidemic theory, namely estimating the probability of persistence of a pathogen after an initial epidemic in a naïve population. Our solution to that problem [23] depends on an analytical estimate of the fraction susceptible near the end of a major outbreak [Equation (117) below], which is one of many expressions that we derive here.

Key words and phrases. epidemics, SIR model, matched asymptotics, Poincaré map.
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We are not the first to attempt to approximate solutions of the SIR ODEs in the phase plane. In particular, van Herwaarden [25]—who was also motivated by (a different approach to) the stochastic extinction problem—presented some closely related approximations that are valid in specific regions of the phase plane. Here, we provide approximations that are uniformly valid throughout the phase plane, and we derive approximate expressions for a number of epidemiologically important quantities (*e.g.*, the peak and minimum prevalence, and the minimum and maximum susceptible frequency, following initial disease invasion and following subsequent epidemics).

Our matching yields simple expressions that can, unlike previous results, be applied to an arbitrary number of epidemic cycles and allows us to find an accurate analytical approximation to the Poincaré map for the SIR model.

The related expressions that van Herwaarden [25] has presented previously—in addition to applying only to restricted subregions of the phase plane—depend on the numerical evaluation of integrals for which explicit analytical forms cannot be found. In contrast, our results are fully analytical closed-form expressions that are valid everywhere in phase space. We succeed by exploiting Lambert’s W function [7] to invert implicit relations, and by asymptotic matching across branch cuts of the W function. The asymptotic techniques that we use are non-trivial and not part of the standard technical toolbox employed in mathematical epidemiology. Consequently, we present our analyses without assuming any familiarity with matched asymptotics, and hope that in so doing we have made it easier for readers to apply the methods to other problems.

For convenience in using our approximations, all of our major results are summarized in Tables 2 and 3.

1.1 The SIR Model with Vital Dynamics

Writing the proportions of the host population that are susceptible, infective, and removed as X , Y , and Z , respectively, the standard SIR ordinary differential equations (ODEs) are [2]

$$\frac{dX}{dt} = \mu(1 - X) - \beta XY, \tag{1a}$$

$$\frac{dY}{dt} = (\beta X - \gamma - \mu)Y, \tag{1b}$$

$$\frac{dZ}{dt} = \gamma Y - \mu Z, \tag{1c}$$

where μ is the *per capita* rate of birth and death, β is the transmission rate, and γ is the recovery (or removal) rate. Our focus in this paper is on solutions of these deterministic equations (1), but elsewhere [23] we show how they can be used together with a branching process approximation to obtain accurate analytical results for the fully stochastic model (including the probability of pathogen extinction due to stochastic effects). In keeping with our stochastic analysis [23], we reserve S , I , and R for the *number* of individuals in each state. For the sake of clarity, we adopt the convention of using lower case letters to indicate independent variables and capitals to indicate dependent variables.

We henceforth work with dimensionless parameters. To that end, we first note that a natural timescale is the expected duration of an individual’s infectious period,

$$T_{\text{inf}} = \frac{1}{\gamma + \mu}. \tag{2}$$

Expressing the **expected infectious period** in units of the expected host lifetime ($1/\mu$), we define

$$\varepsilon = \frac{\mu}{\gamma + \mu}. \tag{3}$$

The **basic reproduction number** (\mathcal{R}_0) is the product of the transmission rate β and the mean infectious period,

$$\mathcal{R}_0 = \frac{\beta}{\gamma + \mu}, \tag{4}$$

70 which gives the expected total number of new infections caused by a single infective individual introduced
 71 into a naïve population. We define a new time variable, $\tau = t/(\gamma + \mu)$, so that one time unit corresponds to
 72 the expected duration of an individual's infectious period. The SIR model then becomes

$$73 \quad \frac{dX}{d\tau} = \varepsilon(1 - X) - \mathcal{R}_0XY, \quad (5a)$$

$$74 \quad \frac{dY}{d\tau} = (\mathcal{R}_0X - 1)Y. \quad (5b)$$

75 Since $X(\tau) + Y(\tau) + Z(\tau) = 1$ for all $\tau \geq 0$, the two equations above completely describe the dynamical system
 76 (1). The ratio of ε and \mathcal{R}_0 ,

$$77 \quad \epsilon = \frac{\varepsilon}{\mathcal{R}_0}, \quad (6)$$

78 turns out to be a better choice of small parameter to use in our analysis, because it leads to simpler asymptotic
 79 expressions.¹

80 Equations (5) have two nullclines. The y nullcline, $\frac{dY}{d\tau} = 0$, is the line

$$81 \quad x = \frac{1}{\mathcal{R}_0}, \quad (7a)$$

82 whereas the x nullcline, $\frac{dX}{d\tau} = 0$, is the curve

$$83 \quad y = \epsilon \left(\frac{1}{x} - 1 \right). \quad (7b)$$

84 When $\mathcal{R}_0 > 1$, these two nullclines intersect at (x_*, y_*) , where

$$85 \quad x_* = \frac{1}{\mathcal{R}_0}, \quad (8a)$$

$$86 \quad y_* = \epsilon \left(1 - \frac{1}{\mathcal{R}_0} \right) = \epsilon(1 - x_*). \quad (8b)$$

87 It is well known that any trajectory departing from an initial point (x_i, y_i) in the positive cone $\{(x, y) :$
 88 $x > 0, y > 0\}$ eventually converges on a globally asymptotically stable **endemic equilibrium** (EE) at
 89 (x_*, y_*) , whereas the **disease-free equilibrium** (DFE) at $(1, 0)$ is a saddle attracting the set $\{(x, y) : y = 0\}$.
 90 Approach to the EE occurs via damped oscillations provided [10, eq. 13]

$$\epsilon < \frac{4(\mathcal{R}_0 - 1)}{\mathcal{R}_0^2} = 4x_*(1 - x_*). \quad (9)$$

91 This condition is satisfied for most diseases of interest; we restrict our focus to this typical behaviour.

92 We will be primarily concerned with the phase-plane trajectories of (5), so rather than using those
 93 equations directly, we will make use of the phase-plane equations,

$$\frac{dY}{dx} = \frac{(\mathcal{R}_0x - 1)Y}{\varepsilon(1 - x) - \mathcal{R}_0xY} = \frac{(x - x_*)Y}{\epsilon(1 - x) - xY} \quad (10)$$

94 and

$$\frac{dX}{dy} = \frac{\varepsilon(1 - X) - \mathcal{R}_0Xy}{(\mathcal{R}_0X - 1)y} = \frac{\epsilon(1 - X) - Xy}{(X - x_*)y}. \quad (11)$$

95 Thus, $Y(x)$ and $X(y)$ indicate phase-plane solutions where x (resp. y) is the independent variable, whereas
 96 we use $X(\tau)$ and $Y(\tau)$ to indicate the solution to the time-parametrized equations (5). We shall need both

¹The biological meaning of ϵ is the time—in units of the mean infectious period—that can be expected to elapse before an infected individual that enters a fully susceptible population infects one other individual.

97 equations (10) and (11). Equation (10) [(11)] is singular where the susceptible [infected] hosts attain their
 98 minimum and maximum density, x and \bar{x} [y and \bar{y}], for a given cycle (these are points where nullclines, (7a)
 99 and (7b), are crossed). These singular points (see Figures 1 and 2) divide different branches of the multi-
 100 functions $Y(x)$ and $X(y)$, and we will need each equation to extend the solution beyond the singularities
 101 of the other. No exact analytical form is available for any of these turning points, but with our matched
 102 asymptotic expansions, we obtain asymptotic approximations to all of them (see Table 2 for a summary).
 103 We shall refer to the part of the trajectory above the x nullcline (7b) as the **epidemic phase** or simply as
 104 **epidemic** (e.g., we will speak of the **initial epidemic**, **second epidemic**, and so on) and the part below
 105 the x nullcline as the **trough**.

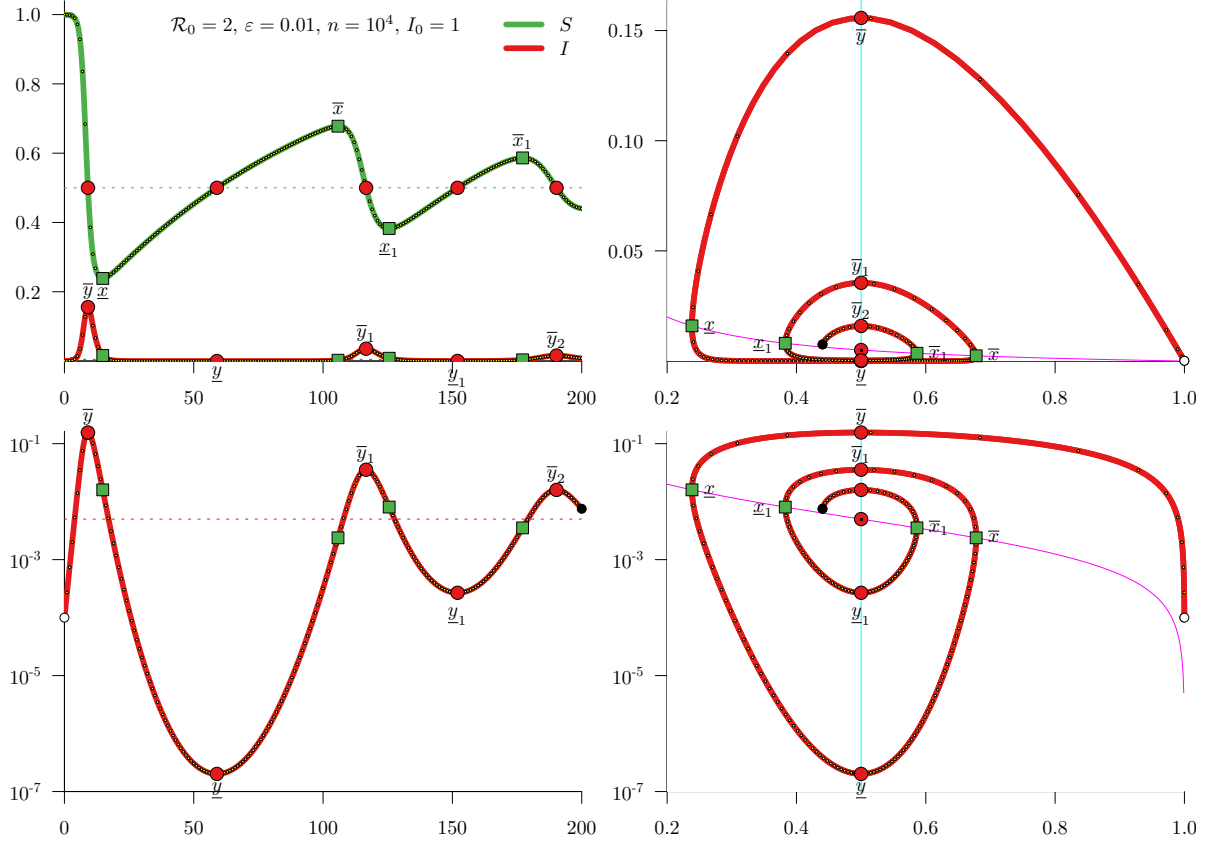


Figure 1: Sample solution of the SIR model Equation (1) for $\mathcal{R}_0 = 2$. *Top left*: the frequencies of susceptible and infected individuals. Symbols indicate the critical points of the curve of the corresponding colour. The j^{th} local minimum (maximum) of the susceptible [infective] frequency is labelled x_j (\bar{x}_j) [y_j (\bar{y}_j)]; we derive approximations to these optima and denote them $\underline{x}_{0,j}$, etc. (see Table 2). Dashed lines indicate the endemic equilibrium (8) of the model (1). *Bottom left*: the frequency of infected individuals (on a log scale) as a function of time. *Right*: trajectories in the susceptible-infected phase plane with the nullclines (*top right*: linear scale, *bottom right*: log scale).

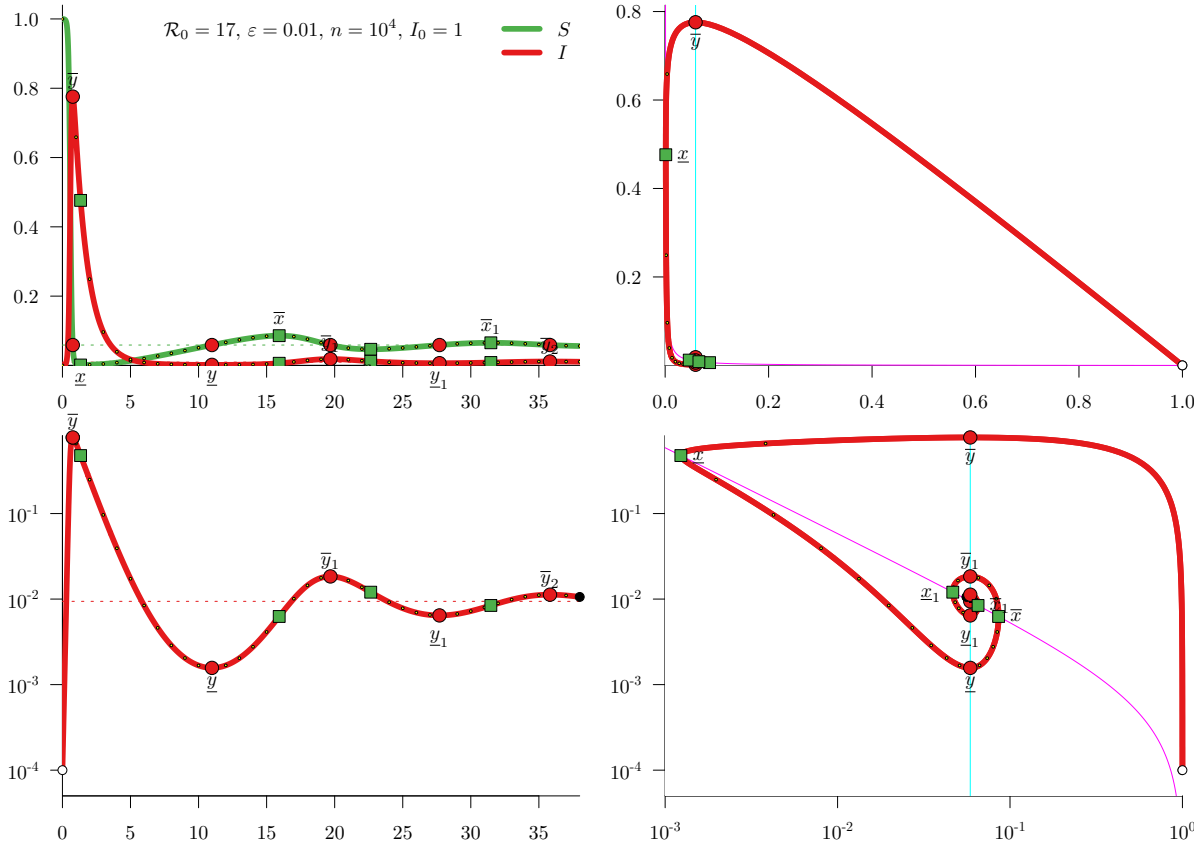


Figure 2: Sample solution of the SIR model Equation (1) for $\mathcal{R}_0 = 17$. See caption to Figure 1, but note that unlike Figure 1 both axes are logarithmic in the bottom right panel above.

1.2 The Method of Matched Asymptotic Expansions

Given a small parameter ϵ , an **asymptotic sequence** is a collection of functions²

$$\{\varphi_j(\epsilon), j = 1, 2, \dots\}, \quad \text{such that} \quad \varphi_{j+1}(\epsilon) \ll \varphi_j(\epsilon) \quad (12)$$

(a typical choice is $\varphi_j(\epsilon) = \epsilon^{j-1}$, but as we shall see below, other choices are often necessary). Given an equation—which may be an ordinary or partial differential equation—for an unknown function Y that depends on ϵ , we can look for a formal **asymptotic series** solution:

$$Y(x; \epsilon) = \sum_{j=0}^{\infty} Y_j(x) \varphi_j(\epsilon). \quad (13)$$

Note that we do not demand that the series converge; the infinite upper limit on the sum is to indicate that one could in principle compute an arbitrary number of terms.

Substituting the formal series into the exact equation (10) and equating terms of common order $\varphi_j(\epsilon)$, we obtain a hierarchy of equations that can be solved sequentially for the $Y_j(x)$. The first few terms of such a series solution often yield a good approximation to the exact solution. However, this approach may fail in regions of rapid change (*e.g.*, near boundaries or singularities) called **layers**³, especially in differential equations where one or more derivatives have coefficients depending on ϵ , which can make imposing all boundary (or initial or terminal) conditions impossible. The **method of matched asymptotic expansions** begins by identifying layers where different approximations better capture the correct quantitative and qualitative behaviour of the solution. These layers coincide with regions where some term in the equation is implicitly of size comparable to ϵ (*i.e.*, of order $\eta(\epsilon)$ for some function η), even when it doesn't explicitly contain ϵ , so that neglecting terms including ϵ fails to capture the correct dynamics. **Boundary layers** refer to subsets of the domain adjacent to the boundary (where one of the dependent variables is small compared to some function of ϵ) whereas **interior layers** occur away from the boundaries (*e.g.*, shear flow⁴ in a vector field could result in a region where one or more derivatives is small compared to a function of ϵ). **Corner layers** arise where boundary and/or interior layers intersect. (For the SIR model that we study here, there are boundary and corner layers, but no interior layers.)

Outside of such layers, the so-called **outer solution** provides a good approximation to the exact solution, but inside the layers it fails to capture the correct qualitative behaviour. Within a layer, rescaling of the independent and/or dependent variables by appropriately chosen factors $\eta(\epsilon)$ is used to amplify the local behaviour, and the resulting equation is then solved via another asymptotic series to obtain an **inner solution** that performs well in the layer, but typically is a poor approximation outside the layer. Inner and outer solutions are bridged by determining values for the constants of integration in the inner and outer solutions so that the various solutions intersect, and can thus be combined into a continuous approximation to the solution. When a combined solution is continuous, but not differentiable, a **corner layer (and corner layer solution)** near the point of intersection can be included in the matching to form a smooth approximation to the true trajectory that performs equally well across the entire domain (a **uniform asymptotic solution**). We discuss the matching procedure in greater detail in §3 below.

Table 1 lists estimates of natural history of infection parameters for a variety of common diseases. For the problem at hand, observing that infectious periods are typically of order days or weeks, whereas typical human lifetimes are longer than 50 years, we see that ϵ (6) will generally be quite small. Consequently, we anticipate that matched asymptotic solutions $Y(x; \epsilon)$ and $X(y; \epsilon)$ will provide good approximations to the exact solutions of (10) and (11). In subsequent sections, we derive and compare these asymptotic solutions to numerically computed trajectories for an illustrative parameter set (chosen with ϵ larger than for any acute infectious disease of humans so that discrepancies between the exact and asymptotic solutions are visible).

²We use the Hardy-Vinogradov notation: $f(\epsilon) \ll g(\epsilon)$ if and only if $\lim_{\epsilon \rightarrow 0} \frac{f(\epsilon)}{g(\epsilon)} = 0$. We also use Landau's "O" notation where convenient: $f(\epsilon) = o(g(\epsilon))$ if $f(\epsilon) \ll g(\epsilon)$, and $f(\epsilon) = \mathcal{O}(g(\epsilon))$ if there exists a positive constant C such that $|f(\epsilon)| \leq C|g(\epsilon)|$ as $\epsilon \rightarrow 0$.

³The terminology reflects the origins of the method in fluid mechanics [1].

⁴Shearing flow refers to adjacent regions where a vector field has substantially different magnitudes.

Disease	\mathcal{R}_0	x_*	T_{lat} [days]	T_{inf} [days]	$\varepsilon \times 10^3$	$\epsilon \times 10^3$	Source
measles	17	0.059	8	5	0.71	0.042	[2]
pertussis	17	0.059	8	14	1.2	0.071	[2]
mumps	12	0.08	15	6	1.1	0.092	[2]
chickenpox	11	0.091	10	5	0.82	0.075	[2]
COVID-19 (Delta)	6.8	0.15	5.8	14	1.1	0.16	[16]
rubella	6.5	0.15	10	7	0.93	0.14	[2]
scarlet fever	5.5	0.18	1.5	18	1	0.19	[2]
smallpox	4.5	0.22	15	7	1.2	0.27	[14]
COVID-19 (ancestral)	3	0.33	3.7	14	0.97	0.32	[16]
HIV	2.2	0.47	87	270	19	8.9	[11]
influenza (1918)	1.8	0.56	2	2.5	0.25	0.14	[19, 2]
Ebola	1.6	0.62	9.3	7	0.89	0.56	[26]
pneumonic plague	1.3	0.77	4.3	2.5	0.37	0.29	[9]

Table 1: Estimates of parameters associated with the natural history of infection for a variety of diseases. The observed parameters are the basic reproduction number (\mathcal{R}_0), the mean latent period (T_{lat}), and the mean infectious period (T_{inf}). The values of the other parameters were derived using Equations (2), (3), (6) and (8a). Note that the mean intrinsic generation interval in the SIR model (1) is $T_{\text{gen}} = 1/\gamma \simeq T_{\text{inf}}$, whereas in the SEIR model (which includes an exposed state in which individuals are not yet infectious), $T_{\text{gen}} \simeq T_{\text{lat}} + T_{\text{inf}}$ [15, 6]; consequently, SIR and SEIR dynamics correspond most closely if we set $1/\gamma$ in the SIR model to be the sum of the observed mean latent and infectious periods. We set $\mu = 0.02/\text{year}$ to mimic human birth and death rates, and compute $\varepsilon = \mu/(\gamma + \mu)$ [Equation (3)]. Where original sources present a range, we have listed the midpoint. Many of the estimates come from Anderson and May [2] (\mathcal{R}_0 from their Table 4.1 [2, p. 70]; the mean latent and infectious periods from their Table 3.1 [2, p. 31]).

2 Outer and Inner Solutions

As a first step in our analysis, in this section we derive solutions in the various subdomains where different approximations are natural. Then, in §3, we match local approximations to obtain a single global approximation that is uniformly valid throughout phase space.

2.1 Outer Solution

An outer solution is an asymptotic solution—obtained in the original variables—that captures the behaviour of the exact solution in the majority of phase space. Replacing Y in Equation (10) with

$$Y^{\text{out}}(x; \epsilon) = \sum_{j=0}^{\infty} Y_j^{\text{out}}(x) \epsilon^j, \quad (14)$$

and equating terms of similar order in ϵ , we obtain a hierarchy of equations that can be solved inductively for $Y_0^{\text{out}}(x)$, $Y_1^{\text{out}}(x)$, and so on. The lowest order equation is

$$\frac{dY_0^{\text{out}}}{dx} = \frac{x_*}{x} - 1, \quad (15)$$

which has generic solution

$$Y_0^{\text{out}}(x) = C_0^{\text{out}} - x + x_* \ln x, \quad (16)$$

159 where C_0^{out} is an arbitrary constant⁵. We can determine C_0^{out} by specifying initial conditions (x_i, y_i) , in which
 160 case Equation (16) gives the phase-plane trajectory of the SIR ODEs without vital dynamics, *i.e.*, for $\epsilon = 0$;
 161 see §3.1.1 below. In §3.1.2, we derive “effective initial conditions” that allow us to approximate subsequent
 162 epidemic waves.

163 2.2 x -axis Boundary Layer

164 The outer solution $\overset{\text{out}}{Y}(x; \epsilon)$ [Equation (14)] is a *function* of x , and cannot have the same qualitative behaviour
 165 as the exact trajectories, which have multiple branches as the fraction susceptible decreases to a minimum
 166 (\underline{x}) and then recovers (Figures 1 and 2). We thus seek a boundary layer solution along the x -axis that will
 167 capture the dynamics when the infected hosts are rare (*i.e.*, $y \ll 1$). Knowing that the equilibrium infective
 168 frequency y_* is $\mathcal{O}(\epsilon)$ [Equation (8b)], we might plausibly posit a solution

$$\overset{\text{xb}}{Y}(x; \epsilon) = \epsilon \Upsilon(x; \epsilon), \quad (17)$$

169 where $\Upsilon = \mathcal{O}(1)$. Substituting $\epsilon \Upsilon$ for Y in Equation (10) yields

$$\epsilon \left((1-x) - x \Upsilon(x; \epsilon) \right) \frac{d\Upsilon}{dx} = (x - x_*) \Upsilon(x; \epsilon). \quad (18)$$

170 Searching for a series solution,

$$\Upsilon(x; \epsilon) = \sum_{j=0}^{\infty} \Upsilon_j(x) \epsilon^j, \quad (19)$$

171 and collecting terms of common order ϵ^j yields, for $j = 0$,

$$0 = (x - x_*) \Upsilon_0(x), \quad (20a)$$

172 which implies that $\Upsilon_0(x) \equiv 0$. Now, suppose that $\Upsilon_0(x) \equiv \dots \equiv \Upsilon_{j-1}(x) \equiv 0$; then, for $j \geq 1$, collecting terms
 173 of order ϵ^j in Equation (18) yields

$$0 = (x - x_*) \Upsilon_j(x). \quad (20b)$$

174 By induction, it follows that $\Upsilon_j(x) \equiv 0$ for all j , and hence that $\overset{\text{xb}}{Y}(x; \epsilon) \equiv 0$, which is a contradiction. We
 175 must conclude that our assumption in Equation (19) that $\Upsilon(x; \epsilon)$ can be expanded in a series of powers of ϵ
 176 is incorrect. Instead, it must be that $\Upsilon(x; \epsilon)$ is **transcendentally small**, *i.e.*, vanishes more rapidly than
 177 any power ϵ^j as $\epsilon \rightarrow 0$ [13, p. 4].

178 As a means to guess the asymptotic dependence of $\Upsilon(x; \epsilon)$ on ϵ , we formally solve Equation (18) from
 179 the point of entry to the boundary layer (x_{in}) to an arbitrary point within it (x), which yields

$$\Upsilon(x; \epsilon) = \Upsilon(x_{\text{in}}; \epsilon) \exp \left(-\frac{1}{\epsilon} \int_{x_{\text{in}}}^x \frac{x_* - u}{(1-u) - u \Upsilon(u; \epsilon)} du \right). \quad (21)$$

180 We first note that $x < x_*$ in the x -axis boundary layer, so $1 - \xi > x_* - \xi > 0$ in the integrand above. Moreover,
 181 since $\xi \Upsilon(\xi; \epsilon)$ is transcendentally small we can expect that $\xi \Upsilon(\xi; \epsilon) \ll 1 - \xi$. Thus, the integrand can be
 182 expected to be positive throughout the layer, and the integral can be expected to be $\mathcal{O}(1)$ with respect to ϵ .
 183 Finally, the coefficient $\Upsilon(x_{\text{in}}; \epsilon)$ is evaluated at the edge of the boundary layer and can therefore be expected
 184 to be $\mathcal{O}(1)$. Putting these heuristic insights together, we hypothesize that $\Upsilon(x; \epsilon)$ is exponentially small in
 185 x with rate proportional to $\frac{1}{\epsilon}$. Consequently, we are led to what is known as a **WKB ansatz** [5, Chapter
 186 10], that is, we postulate a solution of the form

$$\overset{\text{xb}}{Y}(x; \epsilon) = e^{-\frac{\phi(x; \epsilon)}{\epsilon}} \quad (22)$$

⁵Throughout, we adopt the convention that C , with any combination of sub- and/or superscripts, indicates a constant of integration.

187 for some non-negative function $\phi(x; \epsilon)$ that can be expanded in an asymptotic series in ϵ . Substituting this
 188 ansatz (22) into Equation (10) gives us

$$\frac{1}{\epsilon} \frac{d\phi}{dx} = \frac{x_* - x}{\epsilon(1-x) - xe^{-\frac{\phi(x;\epsilon)}{\epsilon}}}, \quad (23)$$

189 for which we posit a series solution,

$$\phi(x; \epsilon) = \sum_{j=0}^{\infty} \phi_j(x) \epsilon^j, \quad (24)$$

190 so that

$$\begin{aligned} 191 \quad e^{-\frac{\phi(x;\epsilon)}{\epsilon}} &= e^{-\frac{\phi_0(x)}{\epsilon}} e^{-\phi_1(x)} e^{-\epsilon\phi_2(x) - \epsilon^2\phi_3(x) + \dots} \\ 192 \quad &= e^{-\frac{\phi_0(x)}{\epsilon}} e^{-\phi_1(x)} \left(1 - (\epsilon\phi_2(x) + \epsilon^2\phi_3(x) + \dots) + \frac{1}{2!} (\epsilon\phi_2(x) + \epsilon^2\phi_3(x) + \dots)^2 + \dots \right) \\ 193 \quad &= e^{-\frac{\phi_0(x)}{\epsilon}} e^{-\phi_1(x)} \left(1 - \epsilon\phi_2(x) + \epsilon^2 \left(\frac{\phi_2(x)^2}{2} - \phi_3(x) \right) + \dots \right), \end{aligned} \quad (25)$$

194 which is transcendentally small on any set where $\phi_0(x)$ is strictly positive (below we determine conditions
 195 under which $\phi_0(x) > 0$ on at least part of the interval $(0, 1)$). If $\phi_0(x) > 0$ then the term $e^{-\frac{\phi(x;\epsilon)}{\epsilon}}$ in
 196 Equation (23) is transcendentally small and we can omit it to obtain

$$\frac{d\phi_0}{dx} = \frac{x_* - x}{1 - x}, \quad (26)$$

197 and hence

$$\phi_0(x) = C_0^\phi - x - (1 - x_*) \ln(1 - x). \quad (27)$$

198 In contrast, we obtain $\frac{d\phi_1}{dx} = 0$, and hence

$$\phi_1(x) = C_1^\phi \quad (28)$$

199 (and similarly $\phi_j(x) = C_j^\phi$ for all $j > 1$). From the derivative (26), we see that $\phi_0(x)$ is increasing for $x < x_*$,
 200 decreasing for $x > x_*$, and has a vertical asymptote for $x = 1$. In particular, provided

$$C_0^\phi < x_* + (1 - x_*) \ln(1 - x_*), \quad (29)$$

201 $\phi_0(x)$ will be strictly positive on some subinterval of $(0, 1)$, as required. Inserting Equations (27) and (28)
 202 in Equation (25), we have an approximate solution in the x -axis boundary layer,

$$\overset{x_b}{Y}(x; \epsilon) = (1 - x)^{-\frac{1}{\epsilon}(1-x_*)} e^{\frac{1}{\epsilon}(C_0^\phi - x) + C_1^\phi}. \quad (30)$$

203 2.3 Corner layers

204 Close to the minimum susceptible frequency (\underline{x}), our outer (16) and inner (30) solutions have tangents of
 205 positive and negative slope respectively (see Figure 4), and thus meet in a non-differentiable corner, which
 206 we address by seeking a corner layer solution [13, p. 67]. The trajectories have vertical slope at \underline{x} , *i.e.*, $\frac{dY}{dx}$ is
 207 singular, so we will instead work with $\frac{dX}{dy}$. The increase from \underline{x} is caused by importation of new susceptible
 208 hosts at a rate proportional to ϵ [see Equation (11)], so we would expect the “turn-around” (change in sign of
 209 derivative) only when the frequency of infectives is sufficiently low that the first term dominates the second
 210 term in the numerator of Equation (11), *i.e.*, when y is $\mathcal{O}(\epsilon)$. We therefore amplify the behaviour near the
 211 x -axis, making a change of variable, $y = \epsilon v$, which converts Equation (11) to

$$\frac{dX}{dv} = \epsilon \frac{1 - X(v) - X(v)v}{(X(v) - x_*)v}. \quad (31)$$

212 Positing a series solution

$$\overset{\text{cor}}{X}(v; \epsilon) = \sum_{j=0}^{\infty} \overset{\text{cor}}{X}_j(v) \epsilon^j, \quad (32)$$

213 yields, to lowest order, $\frac{d\overset{\text{cor}}{X}_0}{dv} = 0$, so $\overset{\text{cor}}{X}_0$ is constant,

$$\overset{\text{cor}}{X}_0(v) = \overset{\text{cor}}{C}_0. \quad (33)$$

214 The next order term is

$$\frac{d\overset{\text{cor}}{X}_1}{dv} = -\left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) \frac{1}{v} + \left(\frac{\overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right), \quad (34)$$

215 with solution

$$\overset{\text{cor}}{X}_1(v) = -\left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) \ln v + \left(\frac{\overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) v + \overset{\text{cor}}{C}_1. \quad (35)$$

216 We now insert Equations (33) and (35) in Equation (32), and convert back to the original variable y .
217 Noting that $\ln v = \ln y + \ln \epsilon^{-1}$, we obtain

$$\overset{\text{cor}}{X}(y; \epsilon) = \overset{\text{cor}}{C}_0 + \left(\frac{\overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) y + \epsilon \ln \epsilon^{-1} \left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) - \epsilon \left[\left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) \ln y - \overset{\text{cor}}{C}_1 \right] + \mathcal{O}(\epsilon^2). \quad (36)$$

218 This solution contains a term of order $\epsilon \ln \epsilon^{-1}$, which is intermediate between $\mathcal{O}(1)$ and $\mathcal{O}(\epsilon)$, and which we
219 did not include in our proposed asymptotic series in v [Equation (32)]. The emergence of such a term when
220 switching back to original variables is known as “transcendental switchback” [22, p. 71], and experience has
221 shown that when this phenomenon occurs it is best to go back and include the intermediate order explicitly
222 in the asymptotic sequence at the outset. Thus, we replace our initial ansatz (32) with

$$\overset{\text{cor}}{X}(v; \epsilon) = \overset{\text{cor}}{X}_0(v) + \epsilon \ln \epsilon^{-1} \overset{\text{cor}}{X}_{\ln}(v) + \epsilon \overset{\text{cor}}{X}_1(v) + \mathcal{O}(\epsilon^2), \quad (37)$$

223 which includes a term of order $\epsilon \ln \epsilon^{-1}$ in addition to powers of ϵ . Inserting Equation (37) in Equation (31)
224 we obtain a new hierarchy of ODEs, with one new equation,

$$\frac{d\overset{\text{cor}}{X}_{\ln}}{dy} = 0, \quad (38)$$

225 which yields a new constant,

$$\overset{\text{cor}}{X}_{\ln}(y) = \overset{\text{cor}}{C}_{\ln}. \quad (39)$$

226 Our revised expansion is

$$\overset{\text{cor}}{X}(y; \epsilon) = \overset{\text{cor}}{C}_0 + \left(\frac{\overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) y + \epsilon \ln \epsilon^{-1} \left[\overset{\text{cor}}{C}_{\ln} + \left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) \right] - \epsilon \left[\left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0}\right) \ln y - \overset{\text{cor}}{C}_1 \right] + \mathcal{O}(\epsilon^2), \quad (40)$$

227 which differs from Equation (36) only in that it includes $\overset{\text{cor}}{C}_{\ln}$ in the $\mathcal{O}(\epsilon \ln \epsilon^{-1})$ term. Below, in §3.1.2, we
228 will see that the additional degree of freedom provided by the constant $\overset{\text{cor}}{C}_{\ln}$ is essential to successfully match
229 other asymptotic solutions.

230 **Remark 1** While this section concerns dynamics near \underline{x} , a virtually identical analysis provides a corner
231 solution near \bar{x} , where the fraction susceptible is at its maximum prior to a second epidemic wave. In
232 particular, we again have a solution of the form (40), albeit for different values of the constants $\overset{\text{cor}}{C}_0$ and $\overset{\text{cor}}{C}_1$.
233 We will refer to the corner solutions near \underline{x} and \bar{x} as the “left” and “right” corner solutions, $\overset{\text{lc}}{X}$ and $\overset{\text{rc}}{X}$,
234 respectively.

2.4 y -axis Boundary Layer

For large values of \mathcal{R}_0 , the trajectories of the SIR model approach the y -axis very closely, even when y is far from 0 (compare Figure 1 with $\mathcal{R}_0 = 2$ to Figure 2 with $\mathcal{R}_0 = 17$). Consequently, if \mathcal{R}_0 is large then there will be substantial periods during which x will be $\mathcal{O}(\epsilon)$ or smaller, and we can no longer assume that the effects of terms proportional to ϵ in Equation (10) can be safely neglected. Instead, we consider a boundary layer solution along the y -axis, making a change of variables $x = \epsilon\xi$ in Equation (10) to get

$$\frac{dY}{d\xi} = \frac{(\epsilon\xi - x_*)Y(\xi)}{1 - \epsilon\xi - \xi Y(\xi)}. \quad (41)$$

Positing a series solution,

$$Y(\xi; \epsilon) = \sum_{j=0}^{\infty} Y_j^{xb}(\xi) \epsilon^j, \quad (42)$$

we get, to lowest order,

$$\frac{dY_0^{xb}}{d\xi} = \frac{x_* Y_0^{xb}(\xi)}{\xi Y_0^{xb}(\xi) - 1}. \quad (43)$$

It is not immediately obvious how to solve this equation. However, if we invert the ODE, we have

$$\frac{d\xi}{dy} = \frac{\Xi_0(y)}{x_*} - \frac{1}{x_* y}, \quad (44)$$

and we can now find a solution, $\xi = \Xi_0(y)$, using the method of integrating factors, which yields

$$X_0^{yb}(y) = \epsilon \Xi_0(y) = \frac{\epsilon}{x_*} e^{\frac{y}{x_*}} \left(E_1\left(\frac{y}{x_*}\right) + c \right), \quad (45)$$

where $E_1(z) = \int_z^\infty \frac{e^{-u}}{u} du$ is the exponential integral function (see, *e.g.*, [21, §6.2(i)]).

2.5 Scaled exponential and Lambert W functions

To match our various solutions, some functions of x , some functions of y , we need to write all expressions as functions of the same variable. For our matching, the common variable will be y , which is facilitated by two functions that we introduce in this section.

The expression ze^z occurs frequently in our analysis, with u often being a non-trivial expression itself. Consequently, in order to reduce equation clutter and emphasize patterns in expressions more clearly, we define the **scaled exponential function**,

$$\mathcal{E}(z) = ze^z. \quad (46)$$

The second function is the **Lambert W function** [7], a transcendental multi-function defined by the implicit relation

$$\mathcal{E}(W(z)) = z. \quad (47)$$

Thus, W is a Lambert W function if \mathcal{E} is its left inverse. There are countably many such functions of a complex argument, leading to countably many branches $W_i(z)$. There are two branches that are real-valued for real arguments. We will need both real-valued branches, which are denoted W_{-1} and W_0 . They have overlapping domains, but non-overlapping ranges,

$$W_{-1} : \left[-\frac{1}{e}, 0\right) \rightarrow (-\infty, -1], \quad (48a)$$

$$W_0 : \left[-\frac{1}{e}, \infty\right) \rightarrow [-1, \infty). \quad (48b)$$

261 Thus, these two branches meet at -1 ,

$$W_{-1}(-1) = W_0(-1) = -\frac{1}{e} = \mathcal{E}(-1). \quad (49)$$

262 For any i , \mathcal{E} is also a *partial* right inverse of W_i , i.e., $W_i(\mathcal{E}(z)) = z$ on *part* of the domain of \mathcal{E} . The set on
263 which $W_i(\mathcal{E}(z)) = z$ depends on i ; for $i \in \{-1, 0\}$,

$$\begin{aligned} W_{-1}(\mathcal{E}(z)) &= z & \text{if } z \leq -1, \\ W_0(\mathcal{E}(z)) &= z & \text{if } z \geq -1. \end{aligned} \quad (50)$$

264 However, $W_i(\mathcal{E}(z))$ is well-defined outside the region on which \mathcal{E} is a right inverse, and it is on the domain
265 where $W_i(\mathcal{E}(z)) \neq z$ that we frequently need to evaluate it. Indeed, the explicit final size formula for the
266 SIR model (and many other models) is [17, Eq. (A.2)]

$$Z(\mathcal{R}_0) = 1 + \frac{1}{\mathcal{R}_0} W_0(\mathcal{E}(-\mathcal{R}_0)). \quad (51)$$

267 Graphs of $\mathcal{E}(z)$ and $W_i(\mathcal{E}(z))$ are shown in Figure 3.

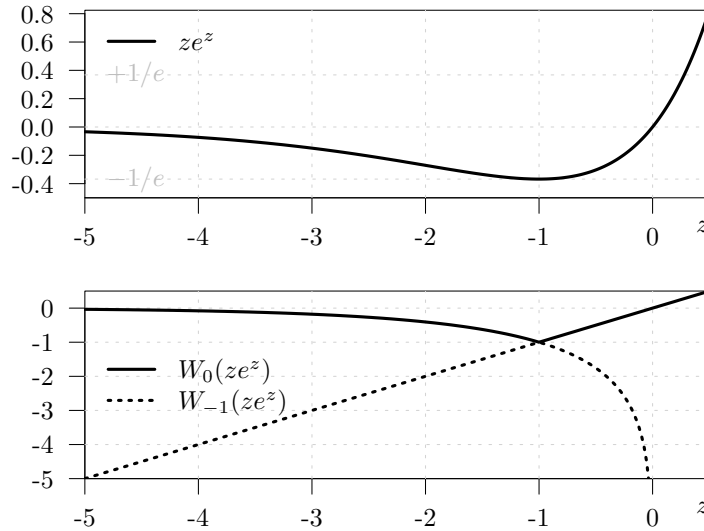


Figure 3: $\mathcal{E}(z) = ze^z$ (46) and Lambert W functions (47) evaluated at $\mathcal{E}(z)$.

268 We briefly recall some series and asymptotic expansions of the Lambert W function that we will need
269 below. See [7] for details and proofs.

270 (i) Implicitly differentiating the identity $\mathcal{E}(W_i(z)) = W_i(z)e^{W_i(z)} = z$ and solving for $\frac{dW_i}{dz}$ one finds that

$$\frac{dW_i}{dz} = \frac{W_i(z)}{z(1 + W_i(z))}. \quad (52)$$

271 (ii) Applying the Lagrange inversion theorem (see, e.g., [8, p. 180]) to the power series for $\mathcal{E}(x)$, one finds
272 that near 0,

$$W_0(z) = \sum_{n=1}^{\infty} \frac{(-n)^{n-1}}{n!} z^n = z + O(z^2), \quad (53)$$

273 with radius of convergence $\frac{1}{e}$.

274 (iii) For large z , there is a (convergent) asymptotic series representation,

$$W_0(z) = L_1 - L_2 + \sum_{m=0}^{\infty} \sum_{n=1}^{\infty} \frac{(-1)^m}{m!} \frac{L_2^n}{L_1^{m+n}}, \quad z \rightarrow \infty, \quad (54)$$

275 where $L_1 = \ln z$ and $L_2 = \ln(\ln z)$. The same expansion applies for $W_{-1}(z)$ as $z \rightarrow -0$ if one replaces L_1
 276 and L_2 with $\tilde{L}_1 = \ln(-z)$ and $\tilde{L}_2 = \ln(-\ln(-z))$.

277 (iv) We will also find it useful to expand

$$f_i(z) = W_i(-Ae^{-A+z}) = W_i(\mathcal{E}(-A)e^z) \quad (55)$$

278 in a series about $z = 0$ for various values of A . Using Equation (52), we find

$$f_i(z) = W_i(\mathcal{E}(-A)) + \frac{W_i(\mathcal{E}(-A))}{1 + W_i(\mathcal{E}(-A))} z + \mathcal{O}(z^2). \quad (56)$$

279 In particular, Equation (50) tells us that

$$f_i(z) = -A - \frac{A}{1-A} z + \mathcal{O}(z^2), \quad \text{if } i = 0 \text{ and } A \leq 1 \text{ or } i = -1 \text{ and } A \geq 1. \quad (57)$$

280 2.6 Inverting the outer and inner solutions

281 To facilitate matching, we now exploit the scaled exponential \mathcal{E} [Equation (46)] and Lambert's W [Equation
 282 (47)] to invert some of our asymptotic solutions.

283 Our outer solution (16) can be rearranged by setting $\overset{\text{out}}{Y}_0(x) = y$ and using Equation (46),

$$-\frac{1}{x_*} e^{-\frac{y-C_0}{x_*}} = \mathcal{E}\left(-\frac{x}{x_*}\right). \quad (58)$$

284 Next, using Equation (50), we have

$$W_i\left(-\frac{1}{x_*} e^{-\frac{y-C_0}{x_*}}\right) = W_i\left(\mathcal{E}\left(-\frac{x}{x_*}\right)\right) = -\frac{x}{x_*}, \quad (59)$$

285 where the $i = -1$ branch is to be used in the half-plane $x \geq x_*$ (since $W_{-1} \leq -1$, Equation (48a)), whereas the
 286 $i = 0$ branch is to be used in the half-plane $x \leq x_*$ (since $W_0 \geq -1$, Equation (48b)). From Equation (59), we
 287 obtain

$$\overset{\text{out}}{X}_0^i(y) = x = -x_* W_i\left(-\frac{1}{x_*} e^{-\frac{y-C_0}{x_*}}\right). \quad (60)$$

288 Thus, the inversion yields a multi-function $\overset{\text{out}}{X}_0^i(y)$ with two branches, both of which we need. These branches
 289 correspond to the growth ($i = -1$) and decline ($i = 0$) phases of the epidemic, which meet at $y = \overset{\text{out}}{Y}_0(x_*)$ (the
 290 maximum of $\overset{\text{out}}{Y}_0(x)$, and thus also the upper bound of the domain of its inverse, $\overset{\text{out}}{X}_0^i(y)$).

291 Similarly, we can invert our inner solution in the x -axis boundary layer [Equation (30)] to get

$$\overset{\text{xb}}{X}_0^i(y) = 1 + (1 - x_*) W_i\left(-\frac{1}{1-x_*} e^{-\frac{1-C_0^\phi}{1-x_*}} \left(\frac{e^{C_1^\phi}}{y}\right)^{\frac{\epsilon}{1-x_*}}\right), \quad (61)$$

292 where now the $i = -1$ and $i = 0$ branches give the solution for $x \leq x_*$ and $x \geq x_*$, respectively (the opposite of
 293 the situation for $\overset{\text{out}}{X}_0^i(y)$ in Equation (60), where $i = -1$ and $i = 0$ correspond to the right and left half-planes,
 294 respectively).

295 **Remark 2** *Once the constants have been determined by matching, we will be able to exploit the resulting*
 296 *symmetry (and the function \mathcal{E}) to simplify the inverted expressions considerably.*

3 Matched asymptotic solutions

We now turn to the task of identifying the unknown constants in the solutions above and combining these local approximations into a uniform approximation of the trajectory. Suppose we have two or more solutions defined at different asymptotic scales (*e.g.*, our outer (§2.1) and corner (§2.3) solutions). The local solutions are obtained by imposing a scale on dependent or independent variables (*e.g.*, we supposed x is $\mathcal{O}(1)$ to get the outer solution, and assumed y was $\mathcal{O}(\epsilon)$ to get the corner solution, whereas we obtained the y -axis boundary layer solution (§2.4) by assuming X is $\mathcal{O}(\epsilon)$). In practice, however, each local solution remains valid over some larger domain that can be characterized with another asymptotic scale. Matching (see, *e.g.*, [13, §2.1]) is achieved by considering an intermediate scale $\eta = \eta(\epsilon)$ on which all solutions remain valid. Solutions to be matched are evaluated at $x = \eta x_\eta$ (or $y = \eta y_\eta$) for some x_η (or y_η) independent of ϵ (for readability, we suppress the explicit dependence of η itself on ϵ). The constants of integration (*e.g.*, C_0^{cor} , C_1^ϕ , *etc.*) are then chosen so that the two solutions agree as well as possible (*i.e.*, so that they coincide on as many orders as possible when both are expanded as an asymptotic series). The **matched solution** is obtained by summing the component solutions—with the choice of constants of integration that maximizes their mutual agreement—and subtracting their common **overlap** (the sum of all terms occurring in both asymptotic series).

To illustrate the process without getting bogged down in details, suppose $F(x)$ and $G(x)$ are outer and inner (*e.g.*, boundary layer) asymptotic series approximations for a given (exact) function $E(x)$. Moreover, suppose we have

$$F(x) = f_0(x) + f_1(x)\varphi_1(\epsilon) + f_2(x)\varphi_2(\epsilon) + f_3(x)\varphi_3(\epsilon) + \mathcal{O}(\varphi_4(\epsilon)), \quad (62)$$

$$G(x) = g_0(x) + g_1(x)\varphi_1(\epsilon) + g_2(x)\varphi_2(\epsilon) + g_3(x)\varphi_3(\epsilon) + \mathcal{O}(\varphi_4(\epsilon)), \quad (63)$$

where the functions f_j and g_j contain arbitrary constants, and $\{\varphi_j\}$ is an asymptotic sequence [§1.2] (which typically refines the asymptotic sequences initially defined for the outer and inner solutions). If, say, the constants in $f_2(x)$ and $g_2(x)$ can be chosen so that these functions coincide exactly for all x , then $f_2(x)\varphi_2(\epsilon) = g_2(x)\varphi_2(\epsilon)$ is the overlap, and our matched approximation to $E(x)$ would be

$$F(x) + G(x) - f_2(x)\varphi_2(\epsilon). \quad (64)$$

If it were possible to choose the values of constants so that F and G agree in more than one order, so the overlap contains multiple orders (the more the better) then the resulting matched solution would be smoother (just as matching a function and its derivative at a single point leads to a smoother approximation at that point).

The matched solution has the virtue of being a valid approximation in both the inner and outer domains, so that one does not need to decide *a priori* which local solution (*e.g.*, outer, boundary, or corner) best approximates a given part of the trajectory.

In what follows, we will focus on matching the trajectory that escapes the DFE $[(x_i, y_i) = (1, 0)]$ along its unstable manifold, because that is the trajectory corresponding to disease invasion. We will give a detailed treatment of the first matching, and describe the second matching much more briefly. For easy reference, we summarize our results in Tables 2 and 3, while the matching constants are listed in Table 4.

3.1 Matching outer, corner and x -axis boundary layer solutions

3.1.1 Kermack and McKendrick's phase plane solution

Given an initial condition (x_i, y_i) , the constant of integration in Equation (16) is readily found to be

$$C_0^{\text{out}} = y_i + x_i - x_* \ln x_i, \quad (65)$$

$$\text{so that } Y_0^{\text{out}}(x, x_i, y_i) = y_i + x_i - x + x_* \ln\left(\frac{x}{x_i}\right), \quad (66)$$

336 which is the phase plane solution first discovered by KM. Equivalently, using Equation (60), we can express
 337 the solution as a function of y ,

$$\overset{\text{out.}}{X}_0^i(y, x_i, y_i) = -x_* W_i\left(-\left(x_i/x_*\right) e^{\frac{y-y_i-x_i}{x_*}}\right) = -x_* W_i\left(\mathcal{E}\left(-x_i/x_*\right) e^{\frac{y-y_i}{x_*}}\right). \quad (67)$$

338 Provided $x_i \geq x_*$ and $y_i \geq 0$, the solution (66) is non-negative and concave, with two positive roots [$x_f \in (0, x_*)$
 339 and another in $(x_*, 1)$], and a unique maximum \bar{y}_0 at x_* ,

$$\bar{y}_0(x_i, y_i) = \overset{\text{out.}}{Y}_0(x_*, x_i, y_i) = y_i + x_i - x_* \left(1 + \ln(x_i/x_*)\right). \quad (68)$$

340 Note that $\bar{y}_0(x_i, y_i)$ and $x_f(x_i, y_i)$ are the true peak prevalence and final size for the SIR model without
 341 vital dynamics ($\epsilon = 0$) started from (x_i, y_i) ; \bar{y}_0 only approximates the peak prevalence for the model with
 342 demography, and there is no “final” size if there is a continuous source of new susceptibles. Nevertheless, we
 343 informally refer to x_f as the “final size” for convenience (note that there *is* a minimum fraction susceptible,
 344 \underline{x} , near $x_f(x_i, y_i)$; see Equation (92) below).

345 Using the $i = 0$ branch to give the solution in the half-plane $x \leq x_*$, Equation (67) gives us an explicit
 346 expression for $x_f(x_i, y_i)$ [17],

$$x_f(x_i, y_i) = \overset{\text{out.}}{X}_0^0(0) = -x_* W_0\left(\mathcal{E}\left(-x_i/x_*\right) e^{-\frac{y_i}{x_*}}\right). \quad (69)$$

347 The series expansion for Lambert’s W function (53) then yields

$$x_f(x_i, y_i) = x_i e^{-(x_i+y_i)/x_*} + \mathcal{O}\left((x_{i,2}/x_*) e^{-2(x_i+y_i)/x_*}\right) = x_i e^{-\mathcal{R}_0(x_i+y_i)} + \mathcal{O}\left(\mathcal{R}_0(x_i) e^{-\mathcal{R}_0(x_i+y_i)}\right)^2, \quad (70)$$

348 so the final size is exponentially small in \mathcal{R}_0 , with a correction of exponentially smaller order.

349 When referring specifically to the focal solution emanating from the DFE [$(x_i, y_i) = (1, 0)$] we suppress the
 350 dependence on x_i and y_i and write $\overset{\text{out.}}{Y}_0(x)$, $\overset{\text{out.}}{X}_0^i(x)$, \bar{y}_0 , and x_f . While approximating this focal solution is our
 351 principal goal, in §3.1.3 below we will need to use solutions with $y_i = 0$ and $0 < x_i < 1$; for these solutions with
 352 infection-free endpoints, we write $\overset{\text{out.}}{Y}_0(x, x_i)$ or $\overset{\text{out.}}{X}_0^i(y, x_i)$, and refer to $\bar{y}_0(x_i)$ and $x_f(x_i)$. [$x_f(x_i, 0), x_i$] is the
 353 interval on which $\overset{\text{out.}}{Y}_0(x, x_i)$ is non-negative, and thus its domain for practical purposes; its range, $[0, \bar{y}_0(x_i)]$,
 354 is the domain for its inverse $\overset{\text{out.}}{X}_0^i(y, x_i)$.

355 3.1.2 Matching in the left half-plane ($x \leq x_*$)

356 Our next step is to match the outer solution $\overset{\text{out.}}{X}_0^0(y)$ [Equation (67) with $(x_i, y_i) = (1, 0)$] with the corner
 357 solution $\overset{\text{cor.}}{X}(y; \epsilon)$ [Equation (40)]. Note that the DFE lies in the right half-plane (since $x_* < 1$), but in the
 358 present subsection it is the $i = 0$ branch of the outer solution that we need because we are investigating only
 359 the part of the trajectory that lies in the left half-plane.

360 In order to consider the behaviour near $(x_f, 0)$ on scales intermediate between the outer solution (67)
 361 and the corner solution (40), we take $y = \eta y_\eta$ with

$$\epsilon \ll \eta \ll 1. \quad (71)$$

362 We haven’t yet identified an appropriate intermediate scale, but examples that satisfy Equation (71) include
 363 $\eta = \epsilon^{1/2}$ and $\eta = \epsilon \ln \epsilon^{-1}$.

364 Inserting $(x_i, y_i) = (1, 0)$ in the outer solution (67), and expanding it using Equation (56), we obtain

$$\overset{\text{out.}}{X}_0^0(\eta y_\eta) = -x_* W_i\left(\mathcal{E}\left(-1/x_*\right) e^{\frac{\eta y_\eta}{x_*}}\right) = x_f + \eta \frac{x_f}{x_* - x_f} y_\eta + \mathcal{O}(\eta^2). \quad (72)$$

365 On the other hand, inserting $y = \eta y_\eta$ in the corner solution (40) and expanding

$$\ln(\eta y_\eta) = -\ln \eta^{-1} + \ln y_\eta, \quad (73)$$

367 we can write

$$368 \quad \overset{\text{cor}}{X}(\eta y_\eta; \epsilon) = \overset{\text{cor}}{C}_0 + \eta \frac{\overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0} y_\eta + \epsilon \ln \epsilon^{-1} \left(\overset{\text{cor}}{C}_{\ln} + \frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0} \right) + \epsilon \ln \eta^{-1} \left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0} \right) - \epsilon \left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0} \ln(y_\eta) - \overset{\text{cor}}{C}_1 \right) + \mathcal{O}(\epsilon^2). \quad (74)$$

369 If we now refine our initial assumption (71) to

$$370 \quad \epsilon \ln \epsilon^{-1} \ll \eta \ll (\epsilon \ln \epsilon^{-1})^{1/2} \ll 1 \quad (75)$$

369 then in the expansions (72,74) each term has a distinct asymptotic order. Our scaling assumptions (75)
370 ensure that

$$371 \quad \epsilon \ll \epsilon \ln \eta^{-1} \ll \epsilon \ln \epsilon^{-1} \ll \eta \ll (\epsilon \ln \epsilon^{-1})^{1/2} \ll 1, \quad (76)$$

371 so if we take

$$372 \quad \overset{\text{cor}}{C}_0 = x_f \quad \text{and} \quad \overset{\text{cor}}{C}_{\ln} = - \left(\frac{1 - \overset{\text{cor}}{C}_0}{x_* - \overset{\text{cor}}{C}_0} \right) = - \frac{1 - x_f}{x_* - x_f} \quad (77)$$

373 then the two solutions (72,74) coincide to⁶ $\mathcal{O}(\epsilon \ln \epsilon^{-1})$. For the moment, $\overset{\text{cor}}{C}_1$ remains undetermined, but we
374 will use it to match with the inner solution.

375 To match the corner layer solution with the inner (x -axis boundary layer) solution we now let η denote
376 a different asymptotic order,

$$377 \quad e^{-\frac{C}{\epsilon}} \ll \eta \ll \epsilon \ll 1 \quad \text{for all } C > 0. \quad (78)$$

378 Since we are interested in $x \leq x_*$, as noted after Equation (61) we must use the $i = -1$ branch of the inner
379 solution $\overset{\text{xb}}{X}_0^i(y)$. (Once we have determined the constants C_0^ϕ and C_1^ϕ in Equation (61) by matching with
380 $i = -1$, the $i = 0$ branch will give the solution for $x \geq x_*$ without further work). We will use Equation (56) to
381 derive an asymptotic expansion, which motivates us—after some algebraic exploration—to set

$$382 \quad C_0^\phi = c_0^\phi - (1 - x_*) \ln(1 - c_0^\phi). \quad (79)$$

382 This choice for C_0^ϕ in Equation (61) leads to

$$383 \quad \overset{\text{xb}}{X}_0^i(\eta y_\eta) = 1 + (1 - x_*) W_i \left(- \frac{1 - c_0^\phi}{1 - x_*} e^{-\frac{1 - c_0^\phi}{1 - x_*}} \left(\frac{e^{C_1^\phi}}{\eta y_\eta} \right)^{\frac{\epsilon}{1 - x_*}} \right) = 1 + (1 - x_*) W_i \left(\mathcal{E} \left(- \frac{1 - c_0^\phi}{1 - x_*} \right) e^z \right), \quad (80a)$$

$$384 \quad \text{where} \quad z = \frac{\epsilon}{1 - x_*} \ln \left(\frac{e^{C_1^\phi}}{\eta y_\eta} \right) = \frac{\epsilon}{1 - x_*} (C_1^\phi - \ln \eta - \ln y_\eta). \quad (80b)$$

385 Because z contains a factor ϵ , it is guaranteed to be small, so we can apply Equations (55) and (57) to
386 Equation (80) to obtain

$$387 \quad \overset{\text{xb}}{X}_0^{-1}(\eta y_\eta) = c_0^\phi + \epsilon \left(\frac{1 - c_0^\phi}{x_* - c_0^\phi} \right) (C_1^\phi - \ln y_\eta) + \epsilon \ln \eta^{-1} \left(\frac{1 - c_0^\phi}{x_* - c_0^\phi} \right) + \mathcal{O}(\epsilon^2). \quad (81)$$

387 Our assumption that $\eta \ll \epsilon \ll 1$ [Equation (78)] implies that

$$388 \quad \eta \ll \epsilon \ll \epsilon \ln \epsilon^{-1} \ll \epsilon \ln \eta^{-1} \ll 1. \quad (82)$$

⁶The assumptions $\epsilon \ll \eta$ and $\eta \ll (\epsilon \ln \epsilon^{-1})^{1/2}$ [Equation (76)] together imply that $\epsilon^2 \ll \eta^2 \ll \epsilon \ln \epsilon^{-1}$, which is necessary to ensure that the $\mathcal{O}(\eta^2)$ terms in Equation (72) are negligible in comparison to $\epsilon \ln \epsilon^{-1}$.

388 Consequently, comparing Equations (74) and (81) to order $\mathcal{O}(\epsilon)$, we see that the overlap is maximized by
 389 taking

$$390 \quad c_0^\phi = \overset{\text{cor}}{C}_0 = x_f \quad (\text{see Equation (77)}), \quad \text{and} \quad \overset{\text{cor}}{C}_1 = \frac{1 - x_f}{x_* - x_f} C_1^\phi, \quad (83)$$

391 whereas C_1^ϕ is yet to be determined.

392 With the values of the constants determined above, the outer (72) and corner (74) solutions have a
 393 common overlap of

$$x_f + \eta \frac{x_f}{x_* - x_f} y_\eta, \quad (84)$$

394 whereas for the corner and inner (81) solutions, the overlap is

$$x_f - \epsilon \frac{1 - x_f}{x_* - x_f} (C_1^\phi - \ln y_\eta) + \epsilon \ln \eta^{-1} \frac{1 - x_f}{x_* - x_f}. \quad (85)$$

395 Summing the outer (72), inner (81) and corner (74) solutions and subtracting these two overlaps yields a
 396 matched solution to the left of x_* ,

$$\overleftarrow{X}(y; \epsilon) = \overset{\text{out}}{X}_0^0(y; \epsilon) + \overset{\text{xb}}{X}_0^{-1}(y; \epsilon) - x_f. \quad (86)$$

397 (Subtracting the overlaps (84,85) removes the corner solution (74) from the matched solution; the corner was
 398 nonetheless necessary to determine the matching constant c_0^ϕ .) For the matched solution to be continuous,
 399 \overleftarrow{X} must agree at (x_*, \bar{y}_0) with the outer solution (67) in the right half plane, *i.e.*, we need

$$\overleftarrow{X}(\bar{y}_0; \epsilon) = x_* = \overset{\text{out}}{X}_0^{-1}(\bar{y}_0). \quad (87)$$

400 This requirement is satisfied provided

$$C_1^\phi = \ln \bar{y}_0. \quad (88)$$

401 Substituting the values of the matching constants C_0^ϕ and C_1^ϕ into Equation (61), we find that the
 402 boundary layer inner solution expressed as a function of y is

$$\overset{\text{xb}}{X}_0^i(y; \epsilon) = 1 + (1 - x_*) W_i \left(\mathcal{E} \left(- \frac{1 - x_f}{1 - x_*} \right) \left(\frac{\bar{y}_0}{y} \right)^{\frac{\epsilon}{1 - x_*}} \right). \quad (89)$$

403 Substituting the values of C_0^ϕ and C_1^ϕ into Equation (30) gives us an alternative description of the boundary
 404 layer dynamics as a function of x ,

$$\overset{\text{xb}}{Y}(x; \epsilon) = \bar{y}_0 \left(\frac{1 - x_f}{1 - x} \right)^{\frac{1 - x_*}{\epsilon}} e^{-\frac{x - x_f}{\epsilon}}. \quad (90)$$

405 Inserting the values of $\overset{\text{cor}}{C}_0$, $\overset{\text{cor}}{C}_{\text{ln}}$, and $\overset{\text{cor}}{C}_1$, into Equation (40), we see that the corner solution near x_f is

$$\overset{\text{lc}}{X}(y; \epsilon) = x_f + \frac{x_f}{x_* - x_f} y + \epsilon \frac{x_f}{x_* - x_f} \ln \left(\frac{\bar{y}_0}{y} \right), \quad (91)$$

406 where, as noted in ?? 1, we use “lc” to emphasize that this is a “left corner” solution lying in the left
 407 half-plane. We will consider a right corner solution below.

408 **Minimum susceptible proportion** The left corner solution (91) approximately characterizes the trajec-
 409 tory near \underline{x} , the point where the fraction susceptible is minimized. Solving $\frac{dX}{dv} = 0$ [Equation (31)], we
 410 find that its minimum occurs at $v = \left(\frac{1}{x_f} - 1\right)$, whence the minimum fraction susceptible is approximately

$$411 \quad \underline{x}_0 = \underline{x}_0(x_f) = \overset{\text{ic}}{X}\left(\epsilon\left(\frac{1}{x_f} - 1\right); \epsilon\right) = x_f + \epsilon\left(\frac{1 - x_f}{x_* - x_f}\right)\left[1 + \ln\left(\frac{\epsilon\left(\frac{1}{x_f} - 1\right)}{\bar{y}_0}\right)\right] \quad (92)$$

$$412 \quad = x_f - \epsilon \ln \epsilon^{-1}\left(\frac{1 - x_f}{x_* - x_f}\right) + \epsilon\left(\frac{1 - x_f}{x_* - x_f}\right)\left[1 + \ln\left(\frac{\frac{1}{x_f} - 1}{\bar{y}_0}\right)\right].$$

413 **Prevalence trough** Substituting $x = x_*$ into Equation (90) gives us an approximation to \underline{y} , the minimum
 414 fraction infected after the initial epidemic,

$$\underline{y}_0 = \bar{y}_0 \left(\frac{1 - x_f}{1 - x_*}\right)^{\frac{1 - x_*}{\epsilon}} e^{-\frac{x_* - x_f}{\epsilon}}. \quad (93)$$

415 **Point of entry into the boundary layer** With the known values of the matching constants c_0^ϕ and C_0^ϕ ,
 416 we can write the leading term (27) in the asymptotic series (25) by which we obtained the inner solution as

$$\phi_0(x) = (x - x_f) - (1 - x_*) \ln\left(\frac{1 - x_f}{1 - x}\right). \quad (94)$$

417 The inner solution (22,30) is proportional to $e^{-\frac{\phi_0(x)}{\epsilon}}$ [see Equation (25)]. Consequently, as we observed in
 418 §2.2, the inner solution is transcendentally small in ϵ^{-1} on the set of x where $\phi_0(x) > 0$, whereas we see
 419 from Equation (94) that $\phi_0(x_f) = 0$. Thus, x_f is effectively the point of entry into the boundary layer:
 420 $e^{-\phi_0(x_f)/\epsilon} = 1 = \mathcal{O}(1)$, whereas for $x > x_f$ (near x_f), $e^{-\phi_0(x)/\epsilon}$ is transcendentally small.

421 **Point of exit from the boundary layer** In addition to x_f , $\phi_0(x)$ has a second root that we denote
 422 $x_{i,2}$ (for reasons that will become clear when we complete the matching). The point $x_{i,2}$ is where the
 423 trajectory exits the boundary layer: $\phi_0(x) > 0$ for $x \in (x_f, x_{i,2})$, and $\phi_0(x) < 0$ for $x > x_{i,2}$. Just as we used
 424 a corner solution at x_f to characterize the transition from the outer solution to the inner solution entering
 425 the boundary layer,⁷ a right corner solution at $x_{i,2}$ allows us to match the inner solution to a new outer
 426 solution corresponding to the second epidemic wave. To find an expression for $x_{i,2}$ we substitute $x = x_{i,2}$ into
 427 Equation (94) and obtain

$$(1 - x_*) \ln\left(\frac{1 - x_f}{1 - x_{i,2}}\right) - (x_{i,2} - x_f) = 0. \quad (95)$$

428 As in §(2.6), we solve this for $x_{i,2}$ using the Lambert W -function and find

$$x_{i,2} = 1 + (1 - x_*) W_0\left(\mathcal{E}\left(-\frac{1 - x_f}{1 - x_*}\right)\right). \quad (96)$$

429 3.1.3 Matching in the right half-plane ($x \geq x_*$)

430 Our matched inner layer solution (89) can be continued to the right of x_* by switching from the $i = -1$ to
 431 the $i = 0$ branch of Lambert's W . As we observed above, this boundary layer solution is transcendentally

⁷The pedantic reader (or author) might observe that the corner solution was obtained by assuming that $y = \mathcal{O}(\epsilon)$, whereas the outer and inner solutions correspond to $y = \mathcal{O}(1)$ and transcendentally small y , respectively. This apparent incongruity is reconciled by considering the solutions in a very small neighbourhood of x_f : for $C > 0$, $\exp\left(-\frac{\phi_0(x_f + C\epsilon \ln \epsilon^{-1})}{\epsilon}\right) = \mathcal{O}(\epsilon)$, and it is in this $\mathcal{O}(\epsilon \ln \epsilon^{-1})$ neighbourhood of x_f that the solutions match, which is reflected in the scaling (75) required when matching the solutions in §3.1.2.

432 small for $x < x_{i,2}$, *i.e.*, for all y such that $\overset{xb}{X}_0^0(y; \epsilon) < x_{i,2}$. As the trajectory leaves the boundary layer, the
 433 fraction infected goes from transcendentally small to $\mathcal{O}(1)$, until eventually the rate of infection exceeds the
 434 rate of replenishment of susceptible hosts by host demography, causing a second **turn-around**, where now
 435 the fraction susceptible starts to decrease. Our inner solution fails to capture this turn-around, which we
 436 now address, as in §3.1.2, with a (right) corner solution near $x_{i,2}$.

437 We begin by considering our solutions on a scale η that is intermediate between $\mathcal{O}(\epsilon)$ and transcendentally
 438 small [Equation (78)]. Expanding the inner solution $\overset{xb}{X}_0^0(\eta y_\eta)$ as in Equation (81), we find that

$$\overset{xb}{X}_0^0(\eta y_\eta) = x_{i,2} + \epsilon \frac{1 - x_{i,2}}{x_* - x_{i,2}} (\ln \bar{y}_0 - \ln y_\eta) + \epsilon \ln \eta^{-1} \frac{1 - x_{i,2}}{x_* - x_{i,2}} + \mathcal{O}(\epsilon^2). \quad (97)$$

439 Comparing this expansion to the corner series (74), we see that a maximal matching is obtained by taking

$$440 \quad \overset{cor}{C}_0 = x_{i,2}, \quad \overset{cor}{C}_{\ln} = -\frac{1 - x_{i,2}}{x_* - x_{i,2}}, \quad \text{and} \quad \overset{cor}{C}_1 = \frac{1 - x_{i,2}}{x_* - x_{i,2}} \ln \bar{y}_0. \quad (98)$$

441 Substituting these values in Equation (74) gives us the right corner solution,

$$\overset{rc}{X}(y; \epsilon) = x_{i,2} + \frac{x_{i,2}}{x_* - x_{i,2}} y + \epsilon \frac{1 - x_{i,2}}{x_* - x_{i,2}} \ln \left(\frac{\bar{y}_0}{y} \right) + \mathcal{O}(\epsilon^2). \quad (99)$$

442 Beyond the turn-around at the corner, we are again in the domain of validity of the outer solution $\overset{out}{X}_0^i(y)$
 443 [Equation (60)], where we now use the $i = -1$ branch as we are matching in the right half-plane. To match
 444 corner and outer solutions, we choose

$$\epsilon \ll \eta \ll 1 \quad (100)$$

445 and set $y = \eta y_\eta$. As we did for C_0^ϕ in the inner solution in §3.1.2 [Equation (79)], we make a change of
 446 constants,

$$\overset{out}{C}_0 = c_0^{\text{out}} - x_* \ln c_0^{\text{out}}, \quad (101)$$

447 in Equation (60) to get

$$\overset{out}{X}_0^{-1}(\eta y_\eta) = -x_* W_{-1} \left(-\left(c_0^{\text{out}} / x_* \right) e^{-\frac{c_0^{\text{out}} - \eta y_\eta}{x_*}} \right) = -x_* W_{-1} \left(\mathcal{E} \left(-\left(c_0^{\text{out}} / x_* \right) \right) e^{\frac{\eta y_\eta}{x_*}} \right). \quad (102)$$

448 Expanding this expression using Equations (55) and (57) then gives us

$$\overset{out}{X}_0^{-1}(\eta y_\eta) = c_0^{\text{out}} + \eta \frac{c_0^{\text{out}}}{x_* - c_0^{\text{out}}} y_\eta + \mathcal{O}(\eta^2). \quad (103)$$

449 Substituting $y = \eta y_\eta$ in Equation (99) and expanding exactly as in Equation (74), we find that Equations (99)
 450 and (103) agree to order $\mathcal{O}(\eta)$ provided

$$\overset{out}{c}_0 = x_{i,2}. \quad (104)$$

451 Thus, the matched solution is

$$\overset{out}{X}_0^{-1}(y, x_{i,2}) = -x_* W_{-1} \left(\mathcal{E} \left(-x_{i,2} / x_* \right) e^{\frac{y}{x_*}} \right). \quad (105)$$

452 As in our derivation of the left solution $\overleftarrow{X}(y; \epsilon)$ [Equation (86)], we now sum the outer (105), inner (89),
 453 and corner (99) solutions, and subtract their overlaps to obtain a uniform asymptotic solution to the right
 454 of x_* ,

$$\overrightarrow{X}(y; \epsilon) = \overset{out}{X}_0^{-1}(y, x_{i,2}) + \overset{xb}{X}_0^0(y; \epsilon) - x_{i,2}. \quad (106)$$

455 **Consistent approximations** We now have consistent approximations to the trajectory that starts from
 456 the DFE, $(x_i, y_i) = (1, 0)$. From the initial time until the peak prevalence is reached, the trajectory is in the
 457 right half-plane and we use the KM solution (66) for the model without vital dynamics ($\epsilon = 0$). We then
 458 continue into the left half-plane using $\overleftarrow{X}(y; \epsilon)$ [Equation (86)] until the first prevalence trough is reached at
 459 $x = x_*$, where we switch to $\overrightarrow{X}(y; \epsilon)$ [Equation (106)] to approximate the rising segment of the second epidemic.
 460 The switches from one approximation to another are differentiable and always occur when $x = x_*$, and the
 461 combined approximation is uniformly valid (*i.e.*, valid to the same order throughout the phase plane).

462 **Effective initial conditions** Comparing $\overleftarrow{X}_0^{-1}(y, x_{i,2})$ [(105)] to $\overleftarrow{X}_0^i(y, x_i, y_i)$ [(67)], we see that $(x_{i,2}, 0)$
 463 is an *effective initial condition* for the second epidemic: if $(x_{i,2}, 0)$ were used as the initial state in the KM
 464 ($\epsilon = 0$) solution, the resulting trajectory would meet the second rise of the actual solution as it curves up
 465 from the left in the phase plane at (approximately) \overline{x}_0 (see below). Thus, while $(x_{i,2}, 0)$ is not a point on
 466 the actual trajectory, it represents an “effective” initial condition that would give rise to the true dynamics
 467 after the end (*i.e.*, trough) of the first epidemic. This observation motivates our choice of notation $x_{i,2}$.

468 **Maximum fraction susceptible** Just as the minimum value of the left corner solution near x_f (91) gives
 469 an estimate of \underline{x} [Equation (92)], the maximum value for the right corner solution near $x_{i,2}$ (99) gives us an
 470 estimate of \overline{x} , the maximum fraction susceptible before a second epidemic wave,

$$\overline{x}_0 = \overline{x}_0(x_{i,2}) = x_{i,2} - \epsilon \frac{1 - x_{i,2}}{x_{i,2} - x_*} \left(1 + \ln \left(\epsilon \left(\frac{1}{x_{i,2}} - 1 \right) / \overline{y}_0 \right) \right), \quad (107)$$

471 which occurs at $y = \epsilon \left(\frac{1}{x_{i,2}} - 1 \right)$.

472 **Peak prevalence for the second wave** Writing Equation (105) as a function of x via KM’s formula
 473 (66),

$$\overleftarrow{Y}_0^{\text{out}}(x) = x_{i,2} - x + x_* \ln(x/x_{i,2}), \quad (108)$$

474 we can also obtain an approximation of the second epidemic’s prevalence peak,

$$\overline{y}_{0,2} \approx x_{i,2} - x_* (1 + \ln(x_{i,2}/x_*)). \quad (109)$$

475 3.1.4 Matching beyond the first epidemic wave

476 Our uniform matched asymptotic solutions, \overleftarrow{X} and \overrightarrow{X} (86,106), were derived starting from the DFE at
 477 $(x_i, y_i) = (1, 0)$. However, a straightforward observation allows us to use the formulae for \overleftarrow{X} and \overrightarrow{X} for the
 478 entire trajectory (*i.e.*, all epidemic waves). Other than x_* and ϵ (or the more fundamental parameters \mathcal{R}_0 and
 479 ε), the only parameters on which our approximations depend are the initial condition (x_i) , the approximate
 480 maximum size of the epidemic (\overline{y}_0) [(68)], the final size of the epidemic without vital dynamics (x_f) [(69)],
 481 and the effective initial condition for the next epidemic $(x_{i,2})$ [(96)].

482 **Epidemic iteration** Setting $x_{i,1} = x_i$, we iteratively obtain $x_{i,j+1}$ from $x_{i,j}$ by computing

$$x_{f,j} = x_f(x_{i,j}, 0) = -x_* W_0 \left(\mathcal{E}(-x_{i,j}/x_*) \right), \quad (110a)$$

$$\overline{y}_{0,j} = \overline{y}_0(x_{i,j}, 0) = x_{i,j} - x_* \left(1 + \ln(x_{i,j}/x_*) \right), \quad (110b)$$

$$x_{i,j+1} = 1 + (1 - x_*) W_0 \left(\mathcal{E} \left(-\frac{1 - x_{f,j}}{1 - x_*} \right) \right). \quad (110c)$$

486 The intermediate quantities in this recurrence relation, $x_{f,j}$ and $\overline{y}_{0,j}$, are the final fraction susceptible and
 487 maximal fraction infected, respectively, for the SIR model *without* vital dynamics ($\varepsilon = 0$) with initial condition
 488 $(x_{i,j}, 0)$.

489 Substituting these expressions (110) into our uniform matched asymptotic solutions (86,106) provides
 490 approximations to the full j^{th} epidemic wave for all $j \geq 1$, \overleftarrow{X} (\overrightarrow{X}) valid on $[\underline{x}_{0,j}, x_*]$ (resp., $[x_*, \overline{x}_{0,j}]$), where

$$491 \quad \underline{x}_{0,j} = \underline{x}_0(x_{f,j}, \overline{y}_{0,j}) = x_{f,j} + \epsilon \frac{1 - x_{f,j}}{x_* - x_{f,j}} \left(1 + \ln \left(\epsilon \left(\frac{1}{x_{f,j}} - 1 \right) / \overline{y}_{0,j} \right) \right), \quad (111a)$$

$$492 \quad \overline{x}_{0,j} = \overline{x}_0(x_{i,j+1}, \overline{y}_{0,j}) = x_{i,j+1} - \epsilon \frac{1 - x_{i,j+1}}{x_{i,j+1} - x_*} \left(1 + \ln \left(\epsilon \left(\frac{1}{x_{i,j+1}} - 1 \right) / \overline{y}_{0,j} \right) \right). \quad (111b)$$

493 **Poincaré map** If we think of the y nullcline ($x = x_*$) as a surface of section, we can use Equation (110) to
 494 explicitly write down the associated Poincaré map. Using Equation (93), we define

$$\underline{y}_{0,j} = \underline{y}_0(x_{f,j}, \overline{y}_{0,j}) = \overline{y}_{0,j} \left(\frac{1 - x_{f,j}}{1 - x_*} \right)^{\frac{1-x_*}{\epsilon}} e^{-\frac{x_* - x_{f,j}}{\epsilon}}. \quad (112)$$

495 We can then iteratively define the time-forward Poincaré map on the y nullcline via

$$\overline{y}_{0,1} \rightarrow \underline{y}_{0,1} \rightarrow \overline{y}_{0,2} \rightarrow \underline{y}_{0,2} \rightarrow \overline{y}_{0,3} \rightarrow \underline{y}_{0,3} \rightarrow \dots \quad (113)$$

496 3.2 Matching with the y -axis boundary layer solution

497 We conclude our analysis with a matching between the outer solution on the unstable manifold, $Y_0^{\text{out}}(x)$ (66),
 498 and the boundary layer solution along the y -axis, $X_0^{\text{yb}}(y)$ (45). For biologically relevant parameters, this new
 499 matching improves significantly upon our formulae for \overleftarrow{X} (86) and \overrightarrow{X} (106).

500 Having a boundary layer along the y -axis is sensible only for trajectories that approach the y -axis.
 501 Consequently, when studying this layer, we are assuming implicitly that $x_f = \mathcal{O}(\epsilon)$ (since $x_f < \underline{x}$ and no
 502 trajectory gets closer than \underline{x} to the y -axis). In particular, since

$$x_f = -x_* W_0 \left(\mathcal{E} \left(-\frac{1}{x_*} \right) \right) = -\frac{1}{\mathcal{R}_0} W_0(\mathcal{E}(-\mathcal{R}_0)) = e^{-\mathcal{R}_0} + \mathcal{O}(\mathcal{R}_0 e^{-2\mathcal{R}_0}), \quad (114)$$

503 we are implicitly assuming that $e^{-\mathcal{R}_0} = \mathcal{O}(\epsilon)$ or, equivalently, $\mathcal{R}_0 = \mathcal{O}(\ln \epsilon^{-1})$. For the diseases listed in
 504 Table 1, $\mathcal{R}_0 / \ln \epsilon^{-1}$ ranges from ~ 0.17 (for pneumonic plague and influenza) to ~ 1.7 (for measles and
 505 pertussis), suggesting it is not unreasonable to assume $\mathcal{R}_0 / \ln \epsilon^{-1}$. For the example in the top panels of
 506 Figures 4 and 5, $\mathcal{R}_0 / \ln \epsilon^{-1} \simeq 0.38$.

507 As with our original matching (§3.1), we use the outer solution expressed as a function of y , $X_0^{\text{out}}(y, x_i)$
 508 (67), and since we are matching in the left half-plane ($x \leq x_*$), we set $i = 0$. Matching $X_0^{\text{out}}(y, x_i)$ with the
 509 y -axis boundary layer solution $X_0^{\text{yb}}(y)$ (45) is uncharacteristically simple: the two are of different asymptotic
 510 orders ($\mathcal{O}(1)$ and $\mathcal{O}(\epsilon)$), and the solutions have no overlap. The matched solution is thus their sum, with
 511 the constant C_0^{yb} as yet undetermined.

512 We set

$$C_0^{\text{yb}} = -E_1 \left(\frac{\overline{y}_0(x_i)}{x_*} \right) \quad (115)$$

513 so that $X_0^{\text{yb}}(y)$ vanishes when evaluated at (x_*, \overline{y}_0) and consequently the sum $X_0^{\text{out}}(y, x_i) + X_0^{\text{yb}}(y)$ agrees at
 514 (x_*, \overline{y}_0) with $X_0^{\text{out}}(y)$ (67), the corresponding focal approximation in the right half-plane ($x \geq x_*$). Thus,
 515 $X_0^{\text{yb}}(y)$ becomes

$$X_0^{\text{yb}}(y) = \frac{\epsilon}{x_*} e^{-\frac{y}{x_*}} \left(E_1 \left(\frac{y}{x_*} \right) - E_1 \left(\frac{\overline{y}_0(x_i)}{x_*} \right) \right). \quad (116)$$

516 With the choice (115) for C_0^{yb} , the sum

$$517 \quad X_{\text{in}}(y; \epsilon) := \overset{\text{out}}{X}_0^0(y, x_i) + \overset{\text{yb}}{X}_0^0(y) = -x_* W_0 \left(\mathcal{E} \left(-\frac{x_i}{x_*} \right) e^{\frac{y}{x_*}} \right) + \epsilon \frac{e^{\frac{y}{x_*}}}{x_*} \left(E_1 \left(\frac{y}{x_*} \right) - E_1 \left(\frac{\bar{y}_0(x_i)}{x_*} \right) \right) \quad (117)$$

518 is a very good approximation to the trajectory, except in the x -axis boundary layer. Elsewhere [23], we use
 519 Equation (117) to approximate the fraction susceptible at the point of entry into the set $\{y \leq y_*\}$ (hence
 520 “in”).

521 We next match with the inner solution expressed as a function of y , $\overset{\text{yb}}{X}_0^{-1}(y)$ (61) (now the $i = -1$ branch
 522 gives the solution with $x \leq x_*$), for which we obtained the asymptotic expansion for $y = \eta y_\eta$ previously
 523 [Equation (81)].

524 To expand the matched outer and y -axis boundary layer solutions (117), we introduce the **complemen-**
 525 **tary exponential integral** ([21, 6.2.4]),

$$\text{Ein}(z) = \int_0^z \frac{1 - e^{-u}}{u} du, \quad (118)$$

526 an entire function that satisfies $\text{Ein}(z) = z + \mathcal{O}(z^2)$ and

$$E_1(z) = \text{Ein}(z) - \ln z - \gamma, \quad (119)$$

527 where $\gamma \simeq 0.57721$ is the Euler-Mascheroni constant [21, 5.9.18] (not the recovery rate in the SIR model (1)).
 528 Using Equation (119), Equation (117) becomes

$$X_{\text{in}}(y; \epsilon) = x_f + \eta \left(\frac{x_f}{x_* - x_f} \right) y_\eta + \epsilon \ln \eta^{-1} \frac{1}{x_*} + \epsilon \frac{1}{x_*} \left(\ln \bar{y}_0 - \ln y_\eta + \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right) \right) + \mathcal{O}(\epsilon \eta). \quad (120)$$

529 Comparing this expression with the asymptotic series expansion for the x -axis boundary layer solution (81),
 530 we see that the coefficient of $\ln y_\eta$ appears to be different in the two expansions ($\frac{\epsilon}{x_*}$ in (120) versus $\epsilon \frac{1-x_f}{x_*-x_f}$
 531 in (81)). This apparent difference is a consequence of the assumption implicit throughout this section that
 532 $x_f = \mathcal{O}(\epsilon)$, which implies that

$$\epsilon \frac{1-x_f}{x_*-x_f} = \frac{\epsilon}{x_*} + \mathcal{O}(\epsilon^2), \quad (121)$$

533 so the two coefficients are in fact *asymptotically* equal. With this in mind, we see that, as in the original
 534 matching,

$$c_0^\phi = x_f, \quad (122)$$

535 from which we obtain C_0^ϕ via Equation (79), whereas now

$$C_1^\phi = \ln \bar{y}_0 - \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right). \quad (123)$$

536 Substituting c_0^ϕ and c_1^ϕ into Equation (61) yields

$$\overset{\text{yb}}{X}_i^0(y) = 1 + (1-x_*) W_i \left(\mathcal{E} \left(-\frac{1-x_f}{1-x_*} \right) \left(\frac{\bar{y}_0}{y} \right)^{\frac{\epsilon}{1-x_*}} e^{-\frac{\epsilon}{1-x_*} \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right)} \right). \quad (124)$$

537 This expression differs from the matched boundary layer solution $\overset{\text{yb}}{X}_0^{-1}(y)$ (89) by an additional factor

$$e^{-\frac{\epsilon}{1-x_*} \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right)} = 1 - \frac{\epsilon}{1-x_*} \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right) + \mathcal{O}(\epsilon^2), \quad (125)$$

538 which multiplies the argument of the W -function, giving an $\mathcal{O}(\epsilon)$ refinement to $\bar{X}_0^{-1}(y)$.

539 Summing the outer and two inner solutions and subtracting the common overlap yields a solution uni-
 540 formly valid to the left of $x = x_*$,

$$\bar{X}(y; \epsilon) = \bar{X}_0^{\text{out}}(y) + \bar{X}_0^{\text{yb}}(y) + \bar{X}_0^{-1}(y) - x_f + \frac{\epsilon}{x_*} \left(\ln \left(\frac{y}{\bar{y}_0} \right) + \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right) \right). \quad (126)$$

541 This solution can be extended the right half-plane ($x \geq x_*$) using the $i = 0$ branch of Equation (61), with c_0^ϕ ,
 542 C_0^ϕ , and C_1^ϕ as determined above. The matching to the second epidemic wave then proceeds identically to
 543 §3.1.3 (except that the argument of the inner solution now has the additional factor $e^{-\frac{\epsilon}{1-x_*} \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right)}$), resulting
 544 in

$$\vec{X}(y; \epsilon) = \bar{X}_0^{-1}(y) + \bar{X}_0^{\text{yb}}(y) - x_{i,2}. \quad (127)$$

545 We summarize these results in Table 3 and compare them to the numerically evaluated trajectory in
 546 Figure 5.

547 **Subsequent epidemic waves** Just as before (§3.1.4), these solutions can be extended to subsequent
 548 epidemic waves, replacing \bar{y}_0 , x_f and $x_{i,2}$ by $\bar{y}_{0,j}$, $x_{f,j}$ and $x_{i,j+1}$ defined using the iterative scheme in Equa-
 549 tions (110a) to (110c).

Quantity		Expression	Equation
Equilibrium susceptible density	x_*	$\frac{1}{\mathcal{R}_0}$	(8a)
Peak prevalence (KM)	\bar{y}_0	$1 - x_* (1 - \ln(x_*))$	(68)
Final size (KM)	x_f	$-x_* W_0(\mathcal{E}(-1/x_*))$	(69)
Minimum prevalence	\underline{y}_0	$\bar{y}_0 \left(\frac{1-x_f}{1-x_*} \right)^{\frac{1-x_*}{\epsilon}} e^{-\frac{x_*-x_f}{\epsilon}} e^{-\text{Ein}\left(\frac{\bar{y}_0}{x_*}\right)}$	(93)
Minimum susceptible density	\underline{x}_0	$x_f + \epsilon \frac{1-x_f}{x_*-x_f} \left(1 + \ln\left(\epsilon\left(\frac{1}{x_f} - 1\right)/\bar{y}_0\right) \right)$	(92)
Effective initial condition	$x_{i,2}$	$1 + (1 - x_*) W_0\left(\mathcal{E}\left(-\frac{1-x_f}{1-x_*}\right)\right)$	(96)
Maximum susceptible density	\bar{x}_0	$x_{i,2} - \epsilon \frac{1-x_{i,2}}{x_{i,2}-x_*} \left(1 + \ln\left(\epsilon\left(\frac{1}{x_{i,2}} - 1\right)/\bar{y}_0\right) \right)$	(107)
Peak prevalence, second wave	$\bar{y}_{0,2}$	$x_{i,2} - x_* (1 + \ln(x_{i,2}/x_*))$	(109)

Table 2: Approximations of quantities of epidemiological interest for disease invasions, *i.e.*, on the trajectory that emanates from the disease-free equilibrium (DFE), $(x_i, y_i) = (1, 0)$. Each entry may depend upon entries above it in the table (but never on entries below). These quantities are used in our approximations to the full trajectories in Table 3. We use “(KM)” to indicate quantities that are exact for the Kermack-McKendrick SIR model *without* vital dynamics ($\epsilon = 0$). With vital dynamics ($\epsilon > 0$), the peak prevalence \bar{y}_0 is an approximation, and there is no “final” size, but the quantity x_f appears in the approximation to the minimum fraction susceptible (\underline{x}_0). Replacing x_i by $x_{i,j}$ as defined in Equation (110) gives asymptotic approximations for the j^{th} epidemic wave, given that the first wave starts on the trajectory emanating from the DFE. We discuss the effective initial condition (x_i^1) in §3.1.3. The expressions for the minimum and maximum susceptible densities ($\underline{x}_0, \bar{x}_0$) are identical except that \underline{x}_0 is evaluated at x_f and \bar{x}_0 is evaluated at $x_{i,2}$. In these expressions, note that $(x_f, \epsilon(\frac{1}{x_f} - 1))$ and $(x_{i,2}, \epsilon(\frac{1}{x_{i,2}} - 1))$ are points on the x nullcline $dX/d\tau = 0$. We write the formulae for \underline{x}_0 and \bar{x}_0 as compactly as possible here; see Equation (92) for the same expression written out with separate terms for each asymptotic order.

Solution	Notation	Expression	Branch	Domain	Equation
Outer	$\overset{\text{out}}{X}_0^i(y, x_i)$	$-x_* W_i \left(\mathcal{E}(-x_i/x_*) e^{\frac{y}{x_*}} \right)$	$i = \begin{cases} 0 & x \leq x_* \\ -1 & x \geq x_* \end{cases}$	$[0, \bar{y}_0]$	(60), (67)
y -axis bdry	$\overset{yb}{X}_0(y)$	$\frac{\epsilon}{x_*} e^{-\frac{y}{x_*}} \left(E_1 \left(\frac{y}{x_*} \right) - E_1 \left(\frac{\bar{y}_0}{x_*} \right) \right)$	–	$[\underline{y}_0, \bar{y}_0]$	(116)
Left corner	$\overset{lc}{X}(y; \epsilon)$	$x_f + \frac{x_f}{x_* - x_f} y + \epsilon \frac{1 - x_f}{x_* - x_f} \ln(\bar{y}_0/y)$	–	$[\underline{y}_0, \bar{y}_0]$	(36), (91)
x -axis bdry	$\overset{xb}{X}_0^i(y)$	$1 + (1 - x_*) W_i \left(\mathcal{E} \left(-\frac{1 - x_f}{1 - x_*} \right) \left(\frac{\bar{y}_0}{y} \right)^{\frac{\epsilon}{1 - x_*}} e^{-\frac{\epsilon}{1 - x_*} \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right)} \right)$	$i = \begin{cases} -1 & x \leq x_* \\ 0 & x \geq x_* \end{cases}$	$[\underline{y}_0, \bar{y}_0]$	(124)
Right corner	$\overset{rc}{X}(y; \epsilon)$	$x_{i,2} - \frac{x_{i,2}}{x_{i,2} - x_*} y - \epsilon \frac{1 - x_{i,2}}{x_{i,2} - x_*} \ln(\bar{y}_0/y)$	–	$[\underline{y}_0, \bar{y}_{0,2}]$	(36), (99)
Matched, left	$\vec{X}(y; \epsilon)$	$\overset{\text{out}}{X}_0^0(y, 1) + \overset{xb}{X}_0^{-1}(y) - x_f$ $+ \overset{yb}{X}_0(y) + \frac{\epsilon}{x_*} \left(\ln \left(\frac{y}{\bar{y}_0} \right) + \text{Ein} \left(\frac{\bar{y}_0}{x_*} \right) \right)$	–	$[\underline{y}_0, \bar{y}_0]$	(126)
Matched, right	$\vec{X}(y; \epsilon)$	$\overset{\text{out}}{X}_0^{-1}(y, x_{i,2}) + \overset{xb}{X}_0^0(y; \epsilon) - x_{i,2}$	–	$[\underline{y}_0, \bar{y}_{0,2}]$	(106)

Table 3: Matched solutions for disease invasions $[(x_i, y_i) = (1, 0)]$. The quantities x_* , x_f , \bar{y}_0 , $x_{i,2}$, and $\bar{y}_{0,2}$ are expressed in terms of the parameters \mathcal{R}_0 and ϵ in Table 2. Left and right corner solutions are valid in a neighbourhood of the points $(x_f, 0)$ and $(x_{i,2}, 0)$, respectively (and are identical up to swapping x_f and $x_{i,2}$). Left and right matched solutions are uniformly valid to the left and right of the y nullcline ($x = x_*$). Setting $x_i = 1$ gives the first epidemic wave emanating from the DFE. Asymptotic approximations for the j^{th} epidemic wave (for $j \geq 1$) are obtained by replacing x_i with $x_{i,j}$, x_f by x_f^j , $x_{i,2}$ by $x_{i,j+1}$, \bar{y}_0 by $\bar{y}_{0,j}$, and $\bar{y}_{0,2}$ and $\bar{y}_{0,j+1}$ in the expressions and domains [Equation (110)]. For each of the outer, inner, and left and right corner solutions, the equation reference first is the “raw” expression with undetermined matching constants (the matched values are listed in Table 4) and then the “matched” expression with the matched values of the constants inserted. Grey text is used to emphasize a factor in the x -axis boundary layer approximation and a term in the left matched solution that appear when we include the y -axis boundary layer approximation in the matching; Figure 4 shows results without the grey quantities, whereas Figure 5 shows the improvement obtained by including them.

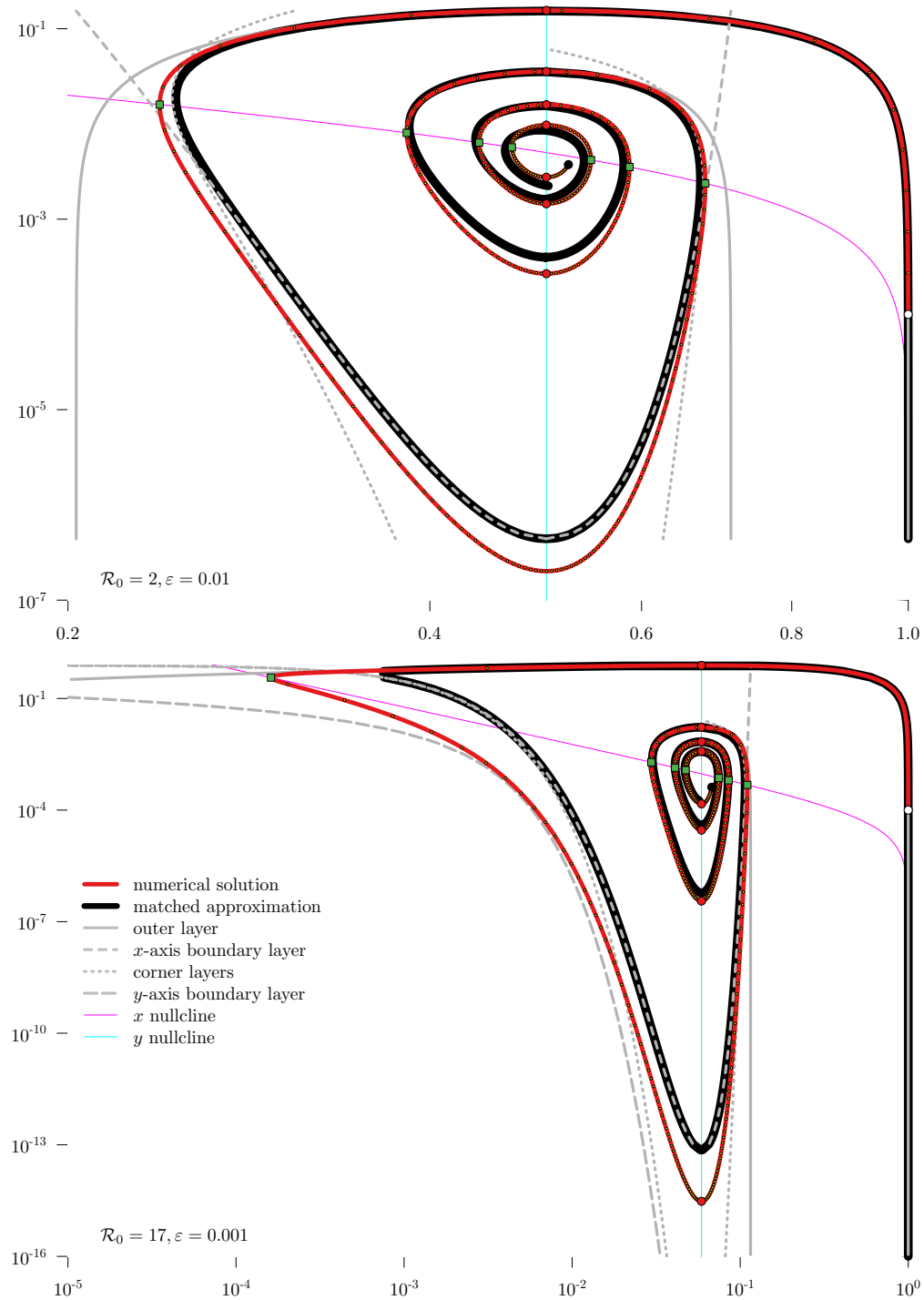


Figure 4: Solutions of the SIR ODEs Equation (1) and approximations (Table 3). *Top panel:* $\mathcal{R}_0 = 2$, $\varepsilon = 0.01$. *Bottom panel:* $\mathcal{R}_0 = 17$, $\varepsilon = 0.001$; similar to measles and whooping cough (Table 1). Various outer and inner approximations are shown in grey, and the matched approximation is in black. The numerically computed solutions are red, as in Figures 1 and 2.

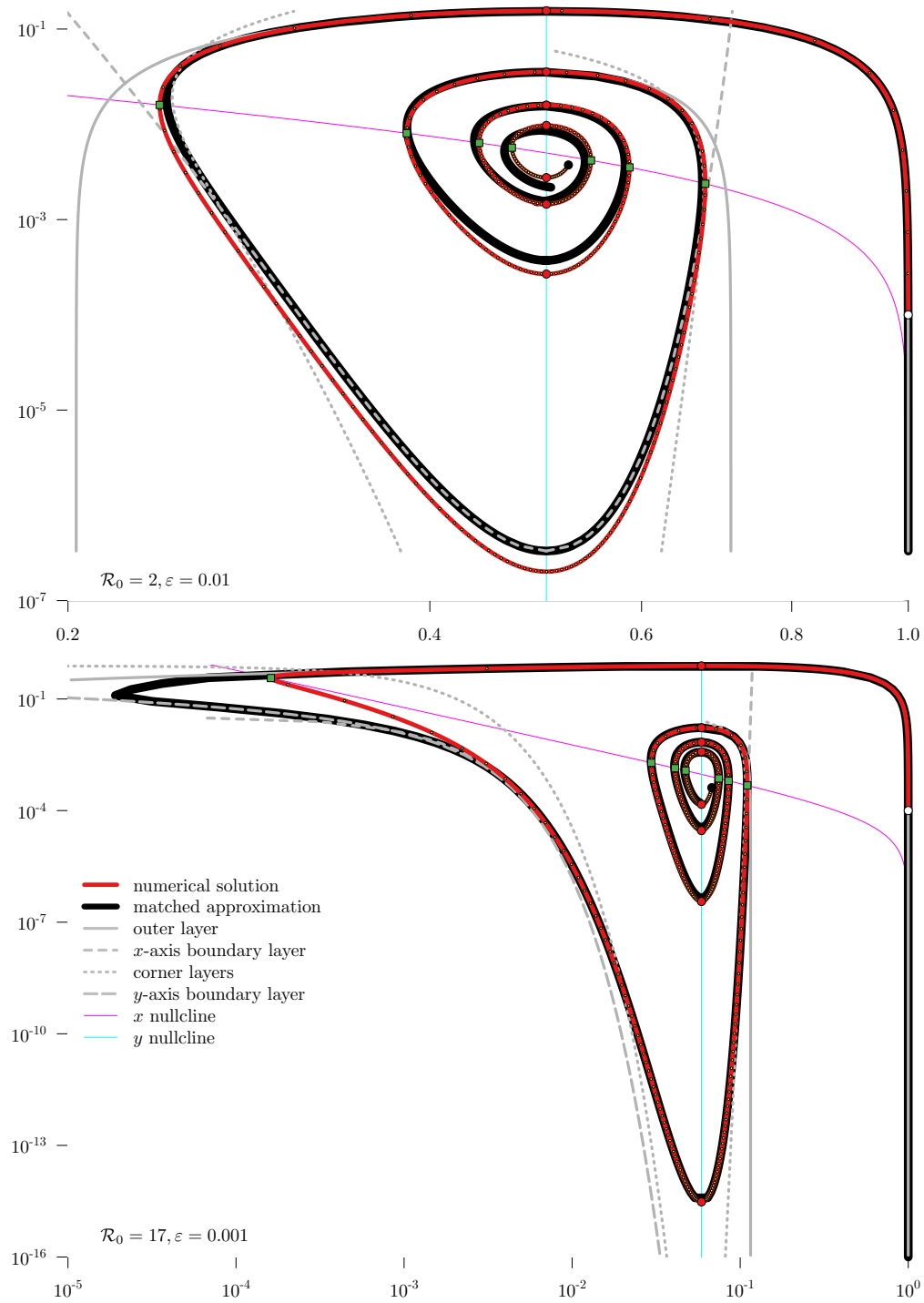


Figure 5: Similar to Figure 4, but including the y -axis boundary layer approximation (Y^b) in the matching.

4 Discussion

Nonlinear differential equations can rarely be solved exactly. Creative analyses leading to approximate analytical solutions were once the only way to study nonlinear systems (see [22, pp. 201–204] has a very concise history), but interest in such approximations has diminished as computers have become more powerful and software for efficient and accurate numerical solution of differential equations has become so easily accessible. However, closed-form analytical expressions can often lead to valuable insights, and can facilitate further analyses that would be impossible or exceedingly challenging to conduct numerically.

We have derived new, fully analytical approximations for the phase plane dynamics of the SIR model with vital dynamics. In Table 2, we list our expressions for key epidemiological quantities, including peaks and troughs of the susceptible and infectious proportions of the host population. We present a closed-form analytical approximation to the Poincaré map for the SIR model in §3.1.4. A highly accurate approximation to the susceptible proportion as the trajectory enters the x -axis boundary layer is given in Equation (117), and is a critical ingredient in a stochastic disease persistence analysis that we present elsewhere [23].

Our approach has involved matching asymptotic expansions across branch cuts of a special function (the Lambert W function, §2.5). To our knowledge, this is the first example of asymptotic matching across branch cuts.

We have focused on the most relevant case of the invasion of a novel pathogen into an epidemiologically naïve population *i.e.*, the trajectory escaping the DFE along its unstable manifold. Nonetheless, the solutions presented in §2 and the matching methodology remain valid for arbitrary initial conditions (x_i, y_i) . Obtaining approximations for any other initial condition would be a matter of determining new matching constants and modifying the expressions accordingly. We have considered only the standard SIR model, but the techniques we have presented can be adapted to other compartmental ODE models, which will explore in further work.

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A Summary Table of Matching Constants

Constant	Expression	Equations
$\overset{\text{out}}{C}_0$	$y_i + x_i - x_* \ln x_i$	(16), (60), (65)
$\overset{\text{cor}}{C}_0$ (left)	x_f	(33), (36), (77)
$\overset{\text{cor}}{C}_{\ln}$ (left)	$-\frac{1-x_f}{x_*-x_f}$	(36), (77)
$\overset{\text{cor}}{C}_1$ (left)	$\frac{1-x_f}{x_*-x_f} \ln \bar{y}_0$	(36), (83), (88),
c_0^ϕ	x_f	(83)
C_0^ϕ	$x_f - (1-x_*) \ln(1-x_f)$	(27), (30), (61), (79), (83)
C_1^ϕ	$\ln \bar{y}_0$	(28), (30), (61), (88)
$\overset{\text{cor}}{C}_0$ (right)	$x_{i,2}$	(33), (36), (98)
$\overset{\text{cor}}{C}_{\ln}$ (right)	$-\frac{1-x_{i,2}}{x_*-x_{i,2}}$	(36), (98)
$\overset{\text{cor}}{C}_1$ (right)	$\frac{1-x_{i,2}}{x_*-x_{i,2}} \ln \bar{y}_0$	(36), (98)
$\overset{\text{out}}{C}_0$ (2 nd)	$x_{i,2}$	(16), (60), (104)
$\overset{\text{out}}{c}_0$ (2 nd)	$x_{i,2} - x_* \ln x_{i,2}$	(102), (101), (104)
$\overset{y^b}{C}_0$	$-E_1\left(\frac{\bar{y}_0}{x_*}\right)$	(115), (45)
C_1^ϕ (y -axis matching)	$\ln \bar{y}_0 - \text{Ein}\left(\frac{\bar{y}_0}{x_*}\right)$	(28), (30), (61), (123)

Table 4: Matching constants for disease invasions $[(x_i, y_i) = (1, 0)]$. Left and right indicate constants appearing in the left and right corner solutions, while 2nd indicates constants for the second epidemic wave. See Table 2 for x_* , x_f , \bar{y}_0 , and $x_{i,2}$ expressed in terms of \mathcal{R}_0 and ϵ . The final expressions with these values for the matching constants are listed in Table 3.