Information geometry and entropy in a stochastic epidemic rate process

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Abstract

Epidemic models with inhomogeneous populations have been used to study major outbreaks and recently Britton and Lindenstrand [5] described the case when latency and infectivity have independent gamma distributions. They found that variability in these random variables had opposite effects on the epidemic growth rate. That rate increased with greater variability in latency but decreased with greater variability in infectivity. Here we extend their result by using the McKay bivariate gamma distribution for the joint distribution of latency and infectivity, recovering the above effects of variability but allowing possible correlation. We use methods of stochastic rate processes to obtain explicit solutions for the growth of the epidemic and the evolution of the inhomogeneity and information entropy. We obtain a closed analytic solution to the evolution of the distribution of the number of uninfected individuals as the epidemic proceeds, and a concomitant expression for the decay of entropy. The family of McKay bivariate gamma distributions has a tractable information geometry which provides a framework in which the evolution of distributions can be studied as the outbreak grows, with a natural distance structure for quantitative tracking of progress.

Keywords: Epidemic model, stochastic rate process, inhomogeneous, bivariate gamma, information geometry, entropy, distribution evolution.

1 Introduction

Epidemiology is a big subject with a long history and a large literature; standard texts on modeling include [4], [2], [11], note also the new volume on numerical methods [1].

The spreading of an infectious disease involves a (large) population in which an initially small number of individuals are infected. Each infected individual is for a period of latency L not yet infectious but at the end of the latent period the individual becomes infectious for a period I; models provide distributions for the random variables L and I. The rest of the population is susceptible to infection from infectious individuals; this susceptibility is often taken to be a constant but later we shall consider a population with an evolving inhomogeneous distribution of susceptibilities to infection. An infectious individual has random infectious contacts at a rate λ and contact with a susceptible individual results in infection and then the latent period of that individual commences. The so-called basic reproduction number is $R_0 = \lambda\mu_I$, the product of the rate of infectious contacts and the mean period of infectiousness μ_I.

[17] discussed the sensitivity of dynamical properties of an epidemic model to the choices of formulation and made use of a gamma distribution for the period of infectiousness and allowed for optional seasonality. [7] introduced a new approach to the analysis of epidemic time series data to take account of partial observation of latency and the temporal aggregation of observed data. They showed that homogeneous standard models can miss key features of epidemics in large populations. Also, [19] devised an estimate of reproduction number in terms of coarsely reported epidemic data, showing that an ideal reporting interval is the mean generation time rather than a fixed chronological interval. See also recent work by [13] for related results on partially observed data and by [18] on general distributions of generating intervals.

[8] have edited a new collection of articles on mathematical and statistical approaches to epidemic modelling and Chapter 2 there, by G. Chowell and F. Bauer, gives a detailed study of the basic reproduction rate in a variety of epidemic models. [20] addressed the sensitivity of the

reproduction number to the shape of the distribution of generation intervals and obtained upper bounds even in the situation of no information on shape.

Recently [5] described a model where the period of latency L and the period of infectiousness I have independent gamma distributions. They found that variability in these random variables had opposite effects on the epidemic growth rate. That rate increased with greater variability in L but decreased with greater variability in I. Here we extend their result by using the McKay bivariate gamma distribution for the joint distribution of L and I, recovering the above effects of variability but allowing in case it may be of relevance the possibility of correlation. One might imagine that in the case of a disease in which the physical changes during latency lead to longer future infectiousness if the period of their development is longer, then the random variables L and I may have a positive correlation. We use methods of stochastic rate processes to obtain explicit solutions for the growth of the epidemic and the evolution of the inhomogeneity and information entropy. This admits a closed analytic solution to the evolution of the distribution of the number of uninfected individuals as the epidemic proceeds, and a concomitant expression for the decay of entropy. The family of McKay bivariate gamma distributions has a tractable information geometry which provides a framework in which the evolution of distributions can be studied as the outbreak grows, with a natural distance structure for quantitative tracking of progress.

2 Inhomogeneous Malthusian epidemic models

In their discussion of epidemic modelling, [5] highlighted aspects when stochastic features are more important than deterministic ones. In particular, they described the importance of admitting random variables to represent the period of latency L and the period of infectiousness I, Their standard susceptible-exposed-infectious-removed (SEIR) epidemic model was elaborated using independent gamma distributions for L and I with means μ_L, μ_I and standard deviations σ_L, σ_I. The basic (mean) reproduction number is given by

$$R_0 = \lambda \mu_I \tag{1}$$

where λ is the rate of infectious contacts and μ_I is the mean length of infectious period. An epidemic becomes a major outbreak if $R_0 > 1$ and then the number infected increases exponentially,

$$n_I(t) \sim e^{rt} \tag{2}$$

where the Malthusian parameter r satisfies the equation

$$E\left(e^{-rt}\lambda \; Prob\{L < t < L + I\}\right) = 1. \tag{3}$$

Their independent bivariate model expresses $\frac{r}{R_0}$ in terms of the parameters of the two gamma distributions. They used means, μ_L, μ_I and coefficients of variation $\tau_L = \frac{\sigma_L}{\mu_L}, \tau_I = \frac{\sigma_I}{\mu_I}$ to deduce

$$r = \frac{R_0}{\mu_I}\left(1 + r\tau_L^2\mu_L\right)^{-1/\tau_L^2}\left(1 - \left(1 + r\tau_I^2\mu_I\right)^{-1/\tau_I^2}\right). \tag{4}$$

Then [5] found from numerical analysis of (4) that, at fixed R_0, the growth rate r is monotonically decreasing with μ_L, μ_I and τ_I, but it is increasing with τ_L. So increased variability in latency period increases the epidemic growth rate whereas increased variability in infectious period decreases the epidemic growth rate.

3 Bivariate gamma distribution of periods of latency and infectiousness

The model described here adds to the work of [5] in which they used *independent* univariate gamma distributions for the periods of latency and infectiousness in an epidemic model that they illustrated with data from the SARS outbreak [21]. They used numerical methods to obtain approximate solutions. Our contribution is to use a bivariate gamma distribution which allows positive correlation between the random variables representing the periods of latency and infectiousness. That could

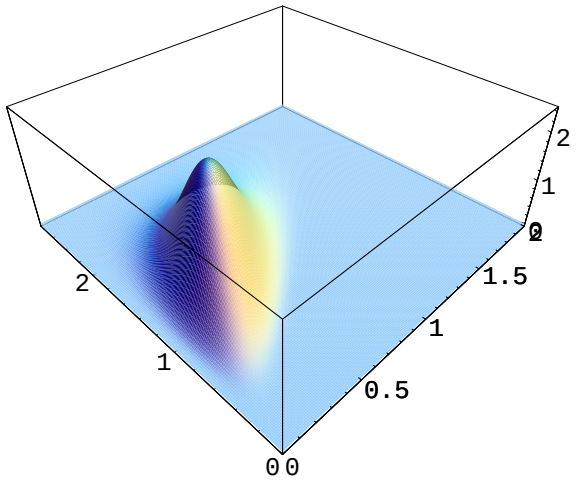

Figure 1: *Part of the family of McKay bivariate gamma probability density functions* $f(x,y)$ *with correlation coefficient* $\rho = 0.6$ *and* $\alpha_1 = 5$.

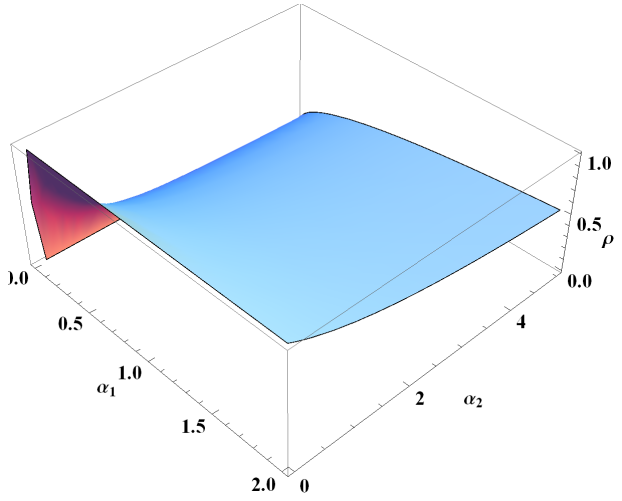

Figure 2: *Correlation coefficient* ρ *from equation (9) for McKay probablity density functions, in terms of* α_1, α_2. *This represents correlation between lengths of periods of latency and infectiousness.*

represent a situation where physical changes during the latency period lead to longer future infectiousness if the period of their development is longer. We obtain a closed analytic solution and show that the same qualitative features persist in the presence of such correlation. This makes available the analytic information geometry of the space of probability densities, allowing comparison of possible trajectories for the epidemic against, for example, exponential distributions for periods of infectiousness or of latency, corresponding to underlying Poisson processes.

Somewhat surprisingly, it is rather difficult to devise bivariate versions of Poisson, exponential distributions or more generally gamma distributions that have reasonably simple form, and indeed only Freund bivariate exponential and McKay bivariate gamma distributions seem to have tractable information geometry [3]. The family of McKay bivariate gamma density functions is defined on $0 < x < y < \infty$ with parameters $\alpha_1, \sigma_{12}, \alpha_2 > 0$ and probability density functions, Figure 1,

$$f(x,y;\alpha_1,\sigma_{12},\alpha_2) = \frac{(\frac{\alpha_1}{\sigma_{12}})^{\frac{(\alpha_1+\alpha_2)}{2}} x^{\alpha_1-1}(y-x)^{\alpha_2-1}e^{-\sqrt{\frac{\alpha_1}{\sigma_{12}}}y}}{\Gamma(\alpha_1)\Gamma(\alpha_2)} \ . \tag{5}$$

Here σ_{12}, which must be positive, is the covariance of x and y and $f(x,y)$ is the probability density for the two random variables x and $y = x + z$ where x and z both have gamma density functions.

We obtain the means, standard deviations and coefficients of variation by direct integration:

$$\text{Means}: \quad \mu_x = \sqrt{\alpha_1\sigma_{12}}, \quad \mu_y = \frac{(\alpha_1+\alpha_2)\sqrt{\sigma_{12}}}{\sqrt{\alpha_1}}, \quad \mu_z = \frac{\alpha_2\sqrt{\sigma_{12}}}{\sqrt{\alpha_1}} \tag{6}$$

$$\text{SDs}: \quad \sigma_x = \sqrt{\sigma_{12}}, \quad \sigma_y = \sqrt{\frac{\sigma_{12}(\alpha_1+\alpha_2)}{\alpha_1}}, \quad \sigma_z = \sqrt{\frac{\alpha_2\sigma_{12}}{\alpha_1}} \tag{7}$$

$$\text{CVs}: \quad \tau_x = \frac{1}{\sqrt{\alpha_1}}, \quad \tau_y = \frac{1}{\sqrt{\alpha_1+\alpha_2}}, \quad \tau_z = \frac{1}{\sqrt{\alpha_2}} \tag{8}$$

The correlation coefficient, and marginal probability density functions of x and y are given by

$$\rho = \sqrt{\frac{\alpha_1}{\alpha_1+\alpha_2}} > 0 \tag{9}$$

$$f_1(x) = \frac{(\frac{\alpha_1}{\sigma_{12}})^{\frac{\alpha_1}{2}} x^{\alpha_1-1} e^{-\sqrt{\frac{\alpha_1}{\sigma_{12}}}x}}{\Gamma(\alpha_1)}, \quad x>0 \tag{10}$$

$$f_2(y) = \frac{(\frac{\alpha_1}{\sigma_{12}})^{\frac{(\alpha_1+\alpha_2)}{2}} y^{(\alpha_1+\alpha_2)-1} e^{-\sqrt{\frac{\alpha_1}{\sigma_{12}}}y}}{\Gamma(\alpha_1+\alpha_2)}, \quad y>0 \tag{11}$$

Figure 2 shows a plot of the correlation coefficient from equation (9). The marginal probability density functions of latency period x and infectiousness period y are gamma with shape parameters α_1 and $\alpha_1+\alpha_2$, respectively. It is not possible to choose parameters such that both marginal functions are exponential, so the two random variables cannot both arise from Poisson processes in this model.

4 Stochastic rate processes

For a detailed monograph on stochastic epidemic models see [1]. We consider here a class of simple stochastic rate processes where a population N, of uninfected individuals, is classified by a smooth family of time-dependent probability density functions $\{P_t, t \geq 0\}$ with random variable $a > 0$, having at time t mean $E_t(a)$ and variance $\sigma^2(t)$. This situation was formulated by [14], [16] in the following way. Let $l_t(a)$ represent the frequency at the a-cohort, then we have

$$N(t) = \int_0^\infty l_t(a)\,da \quad \text{and} \quad P_t(a) = \frac{l_t(a)}{N(t)} \tag{12}$$

$$\frac{dl_t(a)}{dt} = -al_t(a) \quad \text{so} \quad l_t(a) = l_0(a)e^{-at} \tag{13}$$

General solutions for these equations were given in [14], from which we obtain

$$N(t) = N(0)L_0(t) \quad \text{where } L_0(t) = \int_0^\infty P_0(a)e^{-at}\,da \tag{14}$$

$$\frac{dN}{dt} = -E_t(a)\,N \quad \text{where } E_t(a) = \int_0^\infty a\,P_t(a)\,da = -\frac{d\log L_0}{dt} \tag{15}$$

$$\frac{dE_t(a)}{dt} = -\sigma_t^2(a) = (E_t(a))^2 - E_t(a^2) \tag{16}$$

$$P_t(a) = e^{-at}\frac{P_0(a)}{L_0(t)} \quad \text{and } l_t(a) = e^{-at}L_0(t) \tag{17}$$

$$\frac{dP_t(a)}{dt} = P_t(a)(E_t(a)-a). \tag{18}$$

Here $L_0(t)$ is the Laplace transform of the initial probability density function $P_0(a)$ and so conversely $P_0(a)$ is the inverse Laplace transform of the population (monotonic) decay solution $\frac{N(t)}{N(0)}$. See [12] for more discussion of the existence and uniqueness properties of the correspondence between probability densities and their Laplace transforms. In this section we shall use $N(t)$ to

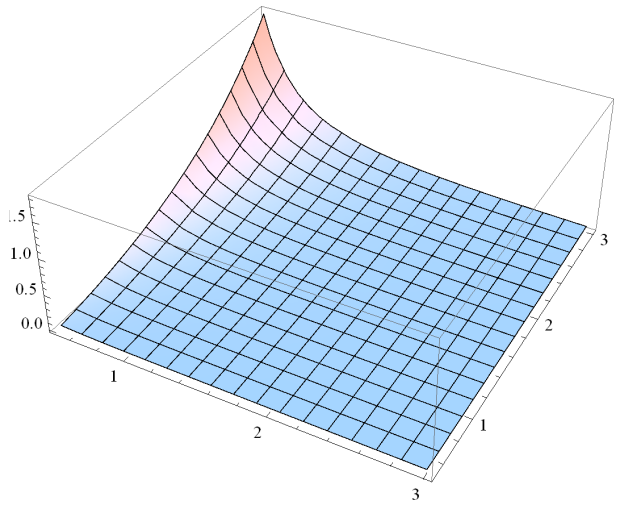

Figure 3: *Plot of the Malthusian parameter r against the coefficients of variation of periods of latency τ_x and infectiousness τ_y with means $\mu_x = 3$, $\mu_y = 2$ and $R_0 = 2.2$ from [5] for the SARS data [21]. So the exponential growth rate of infection decreases with variability in latency period (τ_x) but increases with variability in infectiousness period (τ_y).*

represent the decreasing population of *uninfected* individuals as an epidemic grows. In our context of an epidemic model we might view the random variable a as a feature representing susceptibility to infection in the population; in general this distribution will evolve during the epidemic. The model can be reformulated for a vector $(N^i(t))$ representing a composite population with a vector of distributions (P_t^i) and a matrix of variables $[a_{ij}]$.

It is easy to deduce the rate process for entropy from Karev's model. The Shannon entropy at time t is

$$S_t = -E_t\left(\log P_t(a)\right) = -E_t\left(\log \frac{P_0(a)e^{-at}}{L_0(t)}\right) \tag{19}$$

which reduces to

$$S_t = S_0 + \log L_0(t) + E_t(a)\, t. \tag{20}$$

By using $\dot{E}_t(a) = -\sigma^2(t)$, the decay rate is then

$$\frac{dS_t}{dt} = -t\ \sigma^2(t). \tag{21}$$

This result shows how the variance controls the entropy change during quite general inhomogeneous population processes. In fact equation (21) and further related results were given also in subsequent papers [15], [16]. We note that the reverse process of population growth may have applications in constrained disordering type situations [9].

4.1 Initial growth rate

We follow the method of [5] in their §3.2, to compute the initial exponential growth rate of the epidemic from equation (3) which we write for bivariate x, y in the form

$$\int_0^\infty \int_y^x e^{-r(y-x)}\, \lambda\, f(x,y)\ dy\, dx = 1 \tag{22}$$

Here, from [5], $R_0 = \lambda\mu_x$ for the average number of infections per infective, so λ is the contact rate; this gives the Malthusian parameter analytically in explicit form as

$$r = \frac{1}{\mu_x \tau_x^2}\left(\left(\frac{R_0}{\mu_y}\right)^{\tau_y^2} - 1\right). \tag{23}$$

Thus, r is monotonically decreasing with μ_x, μ_y and τ_x but increasing with τ_y; Figure 3 and Figure 4 plot typical values from the SARS epidemic [21] as used by [5]. Figure 5 and Figure 6

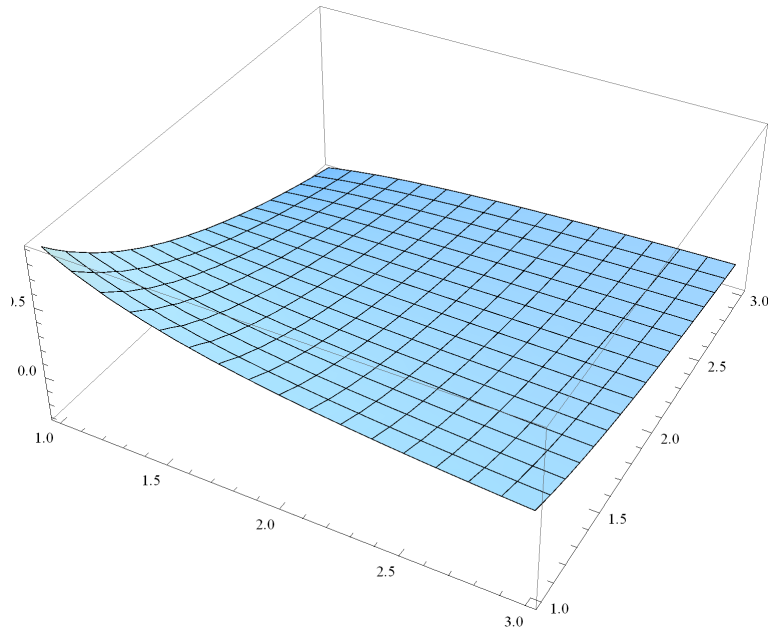

Figure 4: *Plot of the Malthusian parameter r against the means of periods of latency μ_x and infectiousness μ_y with coefficients of variation $\tau_x = \tau_y = 4/7$ and $R_0 = 2.2$ from [5] for the SARS data [21]. So the exponential growth rate of infection decreases with mean latency period (μ_x) and with mean infectiousness period (μ_y).*

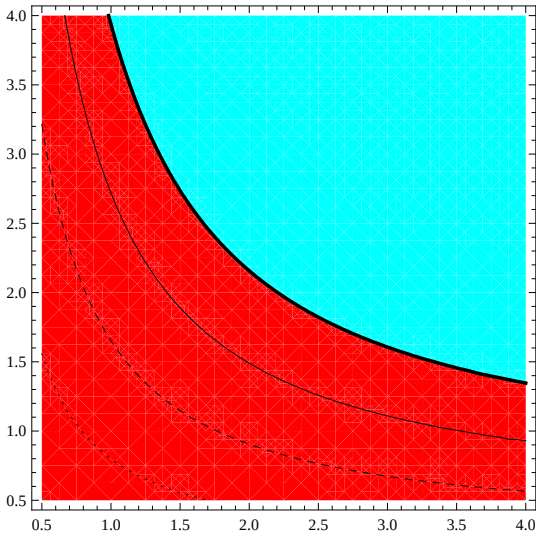

Figure 5: *Contour plot of the contact rate λ against the coefficients of variation of latency period τ_x and of infectiousness period τ_y with mean latency period $\mu_x = 3$ and $r = 0.053$ from [5] for the SARS data [21]. The levels are $\lambda = 1.1$ dotted, $\lambda = 1.5$ dashed, $\lambda = 3$ thin and $\lambda = 10$ thick.*

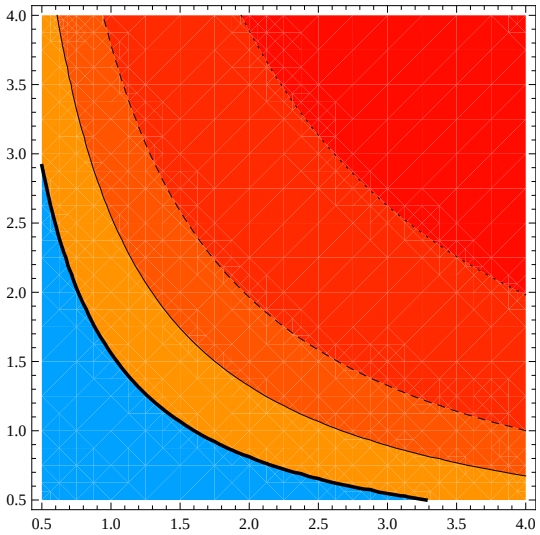

Figure 6: *Contour plot of the contact rate λ against the McKay parameters α_1 and α_2 with mean latency period $\mu_x = 3$ and $r = 0.053$ from [5] for the SARS data [21]. The levels are $\lambda = 1.02$ dotted, $\lambda = 1.04$ dashed, $\lambda = 1.06$ thin and $\lambda = 1.1$ thick.*

show corresponding contour plots of the infectivity rate λ. So the bivariate gamma model reveals that the result of [5] for the dependence of growth rate on variability in the periods of latency and infectiousness in the independent case persists also in the presence of correlation between these two random variables. Such a correlation may be relevant in particular applications, when physical changes evolve during the latent period and influence the length of the subsequent infectiousness period.

We can estimate also the evolution of an inhomogeneous distribution of susceptibility a, as the population $N(t)$ of uninfected individuals declines with time t. For example, the case when the initial distribution $P_0(a)$ is a gamma distribution with parameters s, k was solved in [14] giving the result

$$P_t(a) = \frac{P_0(a)}{L_0(t)} e^{-at} = \frac{(s+t)^k \, a^{k-1}}{\Gamma(k)} \, e^{-a(s+t)}, \quad \text{for time t} \geq 0. \tag{24}$$

Then the time dependences of mean, standard deviation and coefficient of variation are given by

$$\mu_a(t) = \frac{k}{s+t} \tag{25}$$

$$\sigma_a(t) = \frac{\sqrt{k}}{s+t} \tag{26}$$

$$\tau_a(t) = \frac{1}{\sqrt{k}}. \tag{27}$$

From (21), we can see that the *rate* of entropy decrease is greater for more variability in susceptibility.

5 Information geometry of the space of McKay bivariate gamma distributions

Information geometry of the smooth family M of McKay bivariate gamma probability density functions, which is of exponential type, has been studied in detail in [3] Chapter 4. This provides a Riemannian metric on M, yielding a curved 3-manifold so the affine immersion is a 3-dimensional object in $\mathbb{R}^4$, which we can only represent in $\mathbb{R}^3$ through its 2-dimensional submanifolds. Here we illustrate how the geometry may nevertheless be used to provide a natural distance structure on the space of the McKay distributions used in our epidemic model.

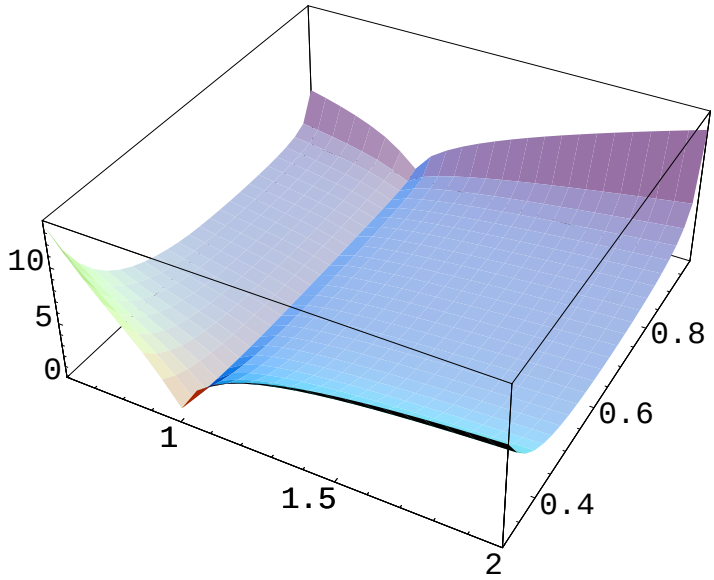

Figure 7: *Approximate information distances* $dE_M = \sqrt{E_M}$ *(equation (28)) in the McKay manifold, measured from distributions* T_0 *with exponential marginal distribution for* x *so* $\alpha_1 = 1$ *and* $\tau_x = 1$*. So the surface represents distances from an exponential process for periods of latency.*

First we measure distances from distributions with exponential marginal distributions—those for which $\alpha_1 = 1$, $\tau_x = 1$ when the latency periods are controlled by a Poisson event process. The derivation of a distance from distribution T_0 is given in [3], and yields in terms of τ_x and ρ

$$\begin{aligned} E_M(\tau_x,\rho)_{|[T_0:\alpha_1=1]} &= \frac{\left(\rho^2+1\right)^2}{16\rho^6}\left|\frac{1}{\tau_x^2}-1\right| \\ &+ \frac{1}{4}\left|\left(1-\frac{1}{\tau_x^2}\right)\left(1-\frac{1}{\rho^2}\right)+3\log\left(\tau_x^2\right)\right| \\ &+ \left|\psi\left(\frac{1}{\tau_x^2}\frac{1}{\rho^2}-1\right)-\psi\left(\frac{1}{\rho^2}-1\right)\right| \\ &+ \left|\psi\left(\frac{1}{\tau_x^2}\right)+\gamma\right| \end{aligned} \tag{28}$$

where $\psi(u) = \frac{d\log\Gamma(u)}{du}$ is the digamma function and γ is the Euler gamma constant—with numerical value about 0.577. Figure 7 shows a plot of $dE_M = \sqrt{E_M(\tau_x,\rho)}$ from equation (28). This is an approximation to the Riemannian distance but it represents the main features of the information distance of arbitrary latency period distributions T_1 from the curve of distributions T_0 with $\alpha_1 = 1$, $\tau_x = 1$.

Repeating the above procedure for the case when T_0 has $(\alpha_1 + \alpha_2) = 1$, which corresponds to an exponential infectiousness period distribution (and a Poisson process of infections) we obtain

$$\begin{aligned} E_M(\alpha_1,\alpha_2)_{|[T_0:\alpha_1+\alpha_2=1]} &= \left|\psi\left(\alpha_2\right)-\psi\left(1-\alpha_1\right)\right| \\ &+ \frac{1}{4}\left|\frac{\left(2\alpha_1+\alpha_2\right)^2}{4\alpha_1}-\frac{1}{2}\left(\alpha_1+1\right)\right|. \end{aligned} \tag{29}$$

This is plotted in Figure 8. The two graphics, Figures 7 and 8, show how we can depict the parameters in the joint distribution of periods of latency and infectiousness as surfaces of distance, measured from the two reference cases for the evolution of the epidemic starting from Poisson processes, respectively. On such surfaces could be represented data on the progress of epidemics under different intervention schemes, or simulations of such scenarios.

Geodesic curves in Riemannian manifolds give minimal arc length and examples are given in [9] for manifolds of Weibull, gamma and McKay bivariate gamma distributions, together with gradient

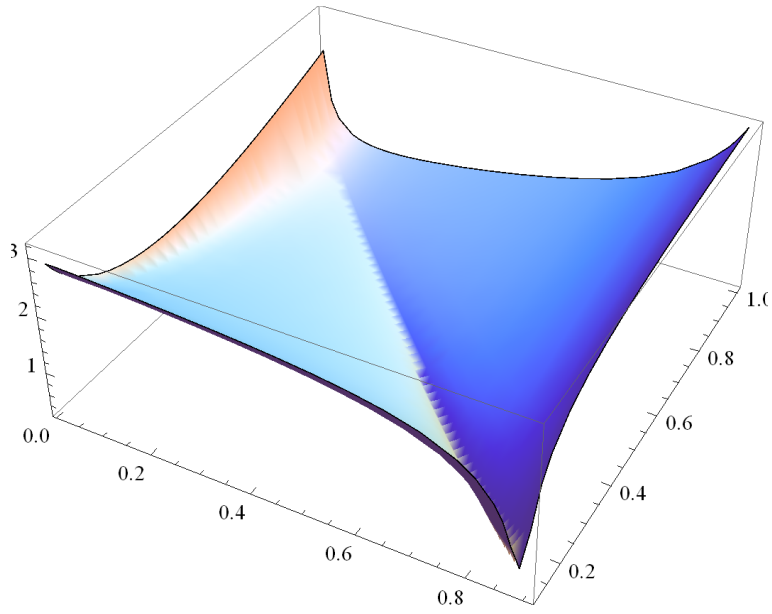

Figure 8: *Approximate information distances* $dE_M = \sqrt{E_M}$ *(equation (29)) in the McKay manifold, measured from distributions* T_0 *with exponential marginal distribution for* y*, so* $\alpha_1 + \alpha_2 = 1$ *and* $\tau_y = 1$*. So the surface represents distances from a Poisson process for infectivity.*

flow curves for entropy. More details of the information geometry of uniform, exponential, gamma, Gaussian, and bivariate versions with applications are provided in [3].

[5] highlighted aspects when stochastic features are important and used independent gamma random variables to represent inhomogeneity of latency and infectiousness periods. In this paper we have a bivariate inhomogeneous epidemic process, modeled by correlated gamma distributions and we can use similar methods to depict and quantify departures from exponential periods of latency and infectiousness. This shows that the result of [5] for the dependence of growth rate on variability in the periods of latency and infectiousness in the independent case persists also in the presence of correlation between the two random variables, Figures 3 and 4. Moreover, the information theoretic distance from the two reference scenarios of exponential distributions of periods latency and infectiousness, Figures 7 and 8, provide natural quantitative representations for comparing different parametric data.

[5] used independent gamma distributions for periods of latency and infectiousness, from which the reproduction rate can be estimated, with applications for example to the SARS outbreak [21]. Here we have used a bivariate gamma distribution which allows a corresponding reproduction rate to be computed. Also, we considered the case when the susceptibility to infection is not uniform and illustrated with the case when it begins as a gamma distribution then evolves as the epidemic proceeds. Other models could be used for the initial distribution of susceptibilities, including asymmetric distributions. A wide range of such other cases using log-gamma distributions is considered in [10] for a similar rate process applied to an evolutionary model when the random variable a represents unfitness (like susceptibility to infection) in a population.

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