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The Role of Import and Increasing Mosquito Abundance in Vector-borne Disease Invasion Scenarios

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Abstract. We investigate invasion scenarios of vector-borne diseases in yet non-endemic areas of the world, where imported human cases from endemic countries can trigger outbreaks of autochtonous cases. We focus mainly on vector-borne diseases like dengue fever, chikungunya and Zika, transmitted by mosquitoes. For increasing mosquito abundance due to changing environmental conditions the epidemiological system approaches from below a critical epidemiological threshold, at which large critical fluctuations appear, and power law scaling can be observed, like previously described e.g. in the COVID-19 pandemic after the lockdown lifting in mid 2020.

Key words. Critical Fluctuations, Power Laws, COVID-19, Dengue Fever, Zika, Chikungunya

1 Introduction

The epidemiological threshold between exponential growth and exponential decline has to be redefined in systems with import which originates from external reservoirs. Here still we have supercritically an exponential increase, but subcritically a stationary state can be reached via imported infected disease cases in abundance of susceptibles.

During the COVID-19 pandemic many countries experienced a harsh lockdown which could not be sustained for long time. However, the lifting of the lockdown should avoid a new exponential explosion of cases, such that we approached from below the above described epidemic threshold including import. Close to the threshold, as in many critical phenomena and especially in percolation known for long time, large fluctuations occur. Hence the system was regulated close to such a state with large fluctuations and power law scaling [1]. We investigate in the example of the Basque Country with very good data on COVID-19 cases, hospitalizations and ICU admissions this scenario in the second half of 2020, which also gives a good basis for the analysis of the subsequent introduction of vaccines and its impact in 2021 [6].

In the present case study, well in line with the recent climatic changes, in areas where vector-borne diseases like dengue fever, chikungunya and Zika e.g. are not established but tropical mosquito invasion started to be observed in recent years, we are again in a subcritical regime approaching from below the epidemic threshold, where now in the Basque Country we have good data on imported cases, returning travelers from endemic countries infected, and proxy data for mosquito abundance, in this case egg counts, modulating the infectivity to eventual autochthonous cases. Hence risk maps are desired, again in an epidemiological scenario of approaching an epidemiological threshold from below.

In both case studies concepts from dynamical isotropic percolation (dyIP) come to place, with import as a conjugated external field in technical terms of phase transitions. Data analysis and stochastic process analytics and simulations give insight into the role of import causing eventual

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large isolated outbreaks, far from the usually considered mean field approximation of simple ODE epidemic models.

2 COVID-19 and Subcritical Fluctuation Scaling

As a first qualitative model we now will investigate the SIRS model, and later extend to a fully developed COVID-19 model, used to give management advices to the Basque government during the COVID-19 pandemic crisis. These models caught especial attention during the initial phase of exponential growth in spring 2020, when we were involved by the Basque government to advice on the basis of their day to day notfication data on reported cases, hospitalized and intensive care unit admited (ICU) and deceased cases, and continued into the lockdown lifting phase in summer 2020 and the vaccination intorduction phase in 2021. Here we concentrate on the phase after the lockdown had to be lifted, but still keeping the system away from a new exponential explosion.

As a first model to understand the essential dynamics we consider an SIRS model with import, since travel restrictions were lifted at the same time of lockdown relaxations, i.e. a susceptible, infected, recovered model, SIR, with infection rate β, recovery rate γ, and an at the time less important waning immunity rate α and total population size N

$$\begin{aligned} \frac{d}{dt}S &= \alpha R - \frac{\beta}{N}S(I+\varrho N) \\ \frac{d}{dt}I &= \frac{\beta}{N}S(I+\varrho N) - \gamma I \\ \frac{d}{dt}R &= \gamma I - \alpha R \end{aligned} \tag{1}$$

including imported disease cases from outside the study area $Y = \varrho N$. This captures e.g. Basque people traveling out and come back infected, or non-Basque people traveling to the Basque country and infecting local people.

In the initial spreading regime, when nearly everybody is still susceptibles or susceptibles are present in abundance, i.e. $S/N \approx 1$, we have

$$\frac{d}{dt}I = \beta\frac{S}{N}(I+\varrho N) - \gamma I \approx (\beta-\gamma)I + \beta\varrho N \tag{2}$$

with the system under community spreading control, i.e. $\varepsilon := \beta - \gamma < 0$ due to still some sanitary restrictions in place, but allowing for people to travel, hence possible imported cases igniting new cases in the study area.

A simple stochastic version of such an epidemiological situation with import and long immunity $\alpha \to 0$

$$\begin{aligned} \frac{d}{dt}p(S,I,t) &= \beta\frac{S+1}{N}((I-1)+\varrho N)\, p(S+1,I-1,t) \\ &\quad +\gamma(I+1)\, p(S,I+1,t) \\ &\quad -\left(\beta\frac{S}{N}(I+\varrho N)+\gamma I\right)\, p(S,I,t) \end{aligned} \tag{3}$$

shows already large fluctuations and highly non-Gaussian distributions of disease cases, see e.g. [1] for the qualitative behaviour observed in stochastic simulations.

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Further, it has in mean field approximation the solution, using $S/N = 1$, for the expected number of infected cases $\langle I\rangle(t) := \sum_{I=0}^{N} Ip(I,t)$ as

$$\langle I\rangle(t) = I(t_0)\cdot e^{-(\gamma-\beta)(t-t_0)} + \frac{\beta\varrho N}{\gamma-\beta}\left(1-e^{-(\gamma-\beta)(t-t_0)}\right) \tag{4}$$

which gives some insight into the qualitative behaviour of such subcritical epidemiological systems subject to imported cases, as the information of initial conditions gets faded away and a stationary solution is being approached, stabilized by imported cases, though local transmission cannot be keeping the disease spreading in the population of investigation.

Interestingly, at criticality $\varepsilon = \beta - \beta_c = 0$, i.e. here $\beta_c = \gamma$, the solution of the dynamic mean field equation is given by

$$\langle I\rangle_c(t) = I(t_0) + \beta_c\varrho N\cdot(t-t_0) \tag{5}$$

signaling here a linear, and in spatially extended systems a general power law behaviour with an exponent different from unit for small spatial dimensions, e.g. in two-dimensional systems.

Hence we have asymptotically a homogeneous function relation [5], here in our epidemiological application given by

$$\langle I\rangle(t,\varepsilon,\varrho) = t^{\hat{\theta}}\cdot F(\varepsilon\cdot t^{1/\hat{\nu}_\parallel}, \varrho\cdot t^{\hat{\mu}/\nu_\parallel}) \tag{6}$$

and for the SIR as a representative of the dynamical isotropic percolation univeersality class giving known critical exponents in 2 dimensional spreading and in mean field approximation

$$\hat{\theta}_{d=2} = 0.5844 \qquad , \qquad \hat{\theta}_{m.f.} = 0 \tag{7}$$

and

$$\hat{\nu}_{d=2} = 1.5078 \qquad , \qquad \hat{\nu}_{m.f.} = 1 \tag{8}$$

and $\hat{\mu}$ as a new exponent with $\mu_{m.f.} = 1$. The explicit for of the scaling function F is most of the time unimportant, but the feature of a homogeneous function indicates self-similarity at criticality with power law behaviour, also for cluster distributions.

The same qualitative behaviour, as we just decribed in the simple SIR system, was also found in COVID-19 model after lockdown lifting as given in a SHARUCD modelling framework

$$\begin{aligned}
\frac{d}{dt}S &= -\beta(t)\frac{S}{N}(H+\phi A+(1-\eta)\varrho(t)N)\\
\frac{d}{dt}H &= \eta(1-\nu)\beta(t)\frac{S}{N}(H+\phi A)-(\gamma+\mu)H\\
\frac{d}{dt}A &= (1-\eta)\beta(t)\frac{S}{N}(H+\phi A+\varrho(t)N)-\gamma A\\
\frac{d}{dt}R &= \gamma(H+U+A)\\
\frac{d}{dt}U &= \nu\eta\beta(t)\frac{S}{N}(H+\phi A)-(\gamma+\mu)U\\
\frac{d}{dt}C_H &= \eta(1-\nu)\beta(t)\frac{S}{N}(H+\phi A)\\
\frac{d}{dt}C_A &= \xi(t)(1-\eta)\beta(t)\frac{S}{N}(H+\phi A+\varrho(t)N)\\
\frac{d}{dt}C_R &= \gamma(H+U+\xi A)\\
\frac{d}{dt}C_U &= \nu\eta\beta(t)\frac{S}{N}(H+\phi A)\\
\frac{d}{dt}D &= \mu(H+U)
\end{aligned} \tag{9}$$

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describing additional features of COVID-19 epidemiology like distinguishing the infected as mild or asymptomatic cases A and severe or hospitalised cases H, ICU cases U, deceases D and its cumulative cases C, as empirical data were always reported as cumulative cases, never as indicences or prevalences of infected, see [1] for more details. In brief, besides the usual SIR-parameters of infection rate β, recovery γ and disease induced death rate μ, we have the hospitalization ratio η and the ICU admission ratio ν and as a new and quite important parameter ϕ as the contribution of infection of asymptomatic cases to the force of infection. Finally, ξ is the detection rate of asymptomatic/mild cases, which increased during the year of 2020 due to increasing testing capacity. This analysis helped then also in investigating the subsequent impact of vaccination introduction from January 2021 on when vaccines developed in 2020 became accessible [6].

3 The SIRUV Model in Invasion Scenario Area, Including Imported Cases and Reduced Mosquito Abundance

We now investigate our main application of epidemiological systems below and eventually close to the epidemiological threshold of self-sustained transmission, and in its initial phase exponential growth, versus import sustained subcritical clustered outbreaks. Basic parameters of vector-borne disease models can be obtained fro endemic areas, and only minor alterations of the basic models already give substantially different qualitative behaviour, especially in stochastic processes versions of the models. Here we consider basic vector-borne disease models of SIRUV type, hence besides the human disease compartments SIR also disease vectors V, i.e. infected mosquitoes, and unifected disease models U, see [3, 4, 2] for further description of the modelling framework and its dynamical behaviour.

In an area with no sustained transmission, but imported cases $Y = \varrho N$ and mosquitoes present, with reduced supply rate (due to e.g. environmental constraints) of $\psi(k) = \nu k m N$ with mosquito abundance $k < 1$ as opposed to the one in endemic areas with $k = 1$ we have the following model, introducing imported cases in the infection term for uninfected mosquitoes

$$\begin{aligned} \frac{d}{dt}S &= \alpha R - \frac{\beta}{mN}SV \\ \frac{d}{dt}I &= \frac{\beta}{mN}SV - \gamma I \\ \frac{d}{dt}R &= \gamma I - \alpha R \\ \frac{d}{dt}U &= \psi(k) - \frac{\vartheta}{N}U(I + \varrho N) - \nu U \\ \frac{d}{dt}V &= \frac{\vartheta}{N}U(I + \varrho N) - \nu V \end{aligned} \tag{10}$$

with the mosquito supply rate reduced. In endemic countries the same models hold, just for $k = 1$ and import close to negligible, i.e. $\varrho \approx 0$. Hence the model describes an epidemiological scenario with reduced mosquito abundance, via $k < 1$ and imported cases $Y = \varrho N$, from which we can infer the risk of outbreaks of autochthonous cases I in the invasion scenario areas as opposed to the endemic areas.

Since it is difficult to monitor adult mosquitoes contributing directly to the infection process, the relative mosquito abundance k could be measured via surrogate data like the ovitrap counts giving information about the related adult mosquitoes, as available in the case of the Basque Country, Euskadi. Hence we can use

$$k = \frac{\text{ovitrap counts in invasion area}}{\text{ovitrap counts in endemic areas}} \tag{11}$$

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in case of comparable traps in the different regions. The human imported cases Y are reported in Euskadi, giving information about the import ϱ via $Y = \varrho N$ with $N \approx 2.2 \cdot 10^6$ the population size of Euskadi. To get a grip on eventual outbreaks of autochthonous infected cases I originating from mosquito abundance k and import ϱ we will now investigate the stochastic process of the SIRUV dynamics.

4 Stochastic SIRUV Model in Invasion Scenario Areas

The stochastic SIRUV model is given by the dynamics of the probability $p(\underline{X}, t)$ of any realization of the state vector $\underline{X} := (S, I, R, U, V)^{tr}$, of all dynamical variables of the SIRUV model, via a discrete state and continuous time Markov process with master equation, see e.g. [8] with many further references therein. Hence the dynamics of the probabilities is given by

$$\frac{d}{dt}\, p(\underline{X}, t) \quad = \quad \sum_{j=1}^{n} \Big(\, w_j(\underline{X} + \Delta\underline{X}_j) \cdot p(\underline{X} + \Delta\underline{X}_j, t) \quad - w_j(\underline{X}) \cdot p(\underline{X}, t) \Big) \tag{12}$$

with $n = 7$ different transitions and deviation from state $\underline{X}$ as $\Delta\underline{X}_j := \underline{r}_j$. For the basic SIRUV model for endemic area scenarios we have explicitly the following transitions $w_j(\underline{X})$ and its shift vectors $\underline{r}_j$ given by

$$\begin{array}{lll} w_1(\underline{X}) = \alpha R & , & \underline{r}_1 = (-1, 0, 1, 0, 0)^{tr} \\ w_2(\underline{X}) = \frac{\beta}{mN} SV & , & \underline{r}_2 = (1, -1, 0, 0, 0)^{tr} \\ w_3(\underline{X}) = \gamma I & , & \underline{r}_3 = (0, 1, -1, 0, 0)^{tr} \\ w_4(\underline{X}) = \psi & , & \underline{r}_4 = (0, 0, 0, -1, 0)^{tr} \\ w_5(\underline{X}) = \frac{\vartheta}{N} UI & , & \underline{r}_5 = (0, 0, 0, 1, -1)^{tr} \\ w_6(\underline{X}) = \nu U & , & \underline{r}_6 = (0, 0, 0, 1, 0)^{tr} \\ w_7(\underline{X}) = \nu V & , & \underline{r}_7 = (0, 0, 0, 0, 1)^{tr} \quad . \end{array} \tag{13}$$

With these $w_j(\underline{X})$ and $\underline{r}_j$ specified we can calculate stochastic realization of the process via the Gillespie algorithm, see e.g. for a recent account of the process [1] with further references.

In case of a well defined system size, we also can express the stochastic process in terms of densities of the state variables, hence $x_1 := S/N$, $x_2 := I/N$, $x_3 := R/N$, $x_4 := U/N$ and $x_5 := V/N$, hence state vector $\underline{x} := (x_1, ..., x_5)^{tr}$ and its deviations now being small $\Delta\underline{x}_j := \frac{1}{N} \cdot \underline{r}_j$. Hence we can obtain the mean field ODE system and in Kramers-Moyal approximation of the master equation to a Fokker-Planck equation a stochastic differential equation system, see e.g. [7] for a more detailed description.

In areas with the invasion scenario we have the inclusion of import in the transition $j = 5$ given by

$$w_5(\underline{X}) = \tfrac{\vartheta}{N} U(I + \varrho N) \quad , \quad \underline{r}_5 = (0, 0, 0, 1, -1)^{tr} \quad . \tag{14}$$

and reduced $\psi = \nu \cdot k \cdot mN$ with $k < 1$. Now we are interested in the expected number of autochthonous infected case, the expectation value or mean value defined by

$$\langle I \rangle := \sum_{\underline{X}} I \; p(\underline{X}, t) = \langle I(t) \rangle \tag{15}$$

which is due to temporally changing probabilities $p(\underline{X}, t)$ of the state $\underline{X}$ itself a time dependent quantity $\langle I \rangle(t)$, with its dynamics given by the dynamics of the probabilities $p(\underline{X}, t)$. This gives after some calculations, see e.g. [8],

$$\frac{d}{dt}\langle I \rangle = \sum_{\underline{X}} I \; \frac{d}{dt} p(\underline{X}, t) = \frac{\beta}{mN} \langle SV \rangle - \gamma \langle I \rangle \tag{16}$$

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and in mean field approximation (neglecting variances and covariances), we obtain the ODE term of the deterministic ODE system given above as

$$\frac{d}{dt}\langle I\rangle = \frac{\beta}{mN}\langle S\rangle\langle V\rangle - \gamma\langle I\rangle \tag{17}$$

hence the ODE system describes the stochastic process in terms of expectation values in mean field approximation. Then the risk of autochthonous infected cases in expectation value is given via the full stochastic process as function of imported cases, and mosquito abundance

$$\langle I\rangle = f(k,\varrho) \tag{18}$$

which we will tackle below. In an invasion scenario driven by imported cases we can derive under certain conditions an analytical expression for $\langle I\rangle = f(k,\varrho)$ in good numerical agreement with the full dynamical system.

5 Analytic Results For Expected Risk of Autochthonous Cases

In an area with no sustained transmission, but imported cases $Y = \varrho N$ and mosquitoes present, gives below the epidemiological threshold of exponentially growing autochthonous outbreaks the expected number of autochthonous cases as

$$\langle I\rangle^* = \frac{k\beta\frac{\vartheta}{\nu}\frac{S_0}{N}}{\gamma - k\beta\frac{\vartheta}{\nu}\frac{S_0}{N}} \cdot \varrho N \tag{19}$$

and in approximation of few or none autonomous cases I after a short transient of increasing expectation of cases, hence in $V(I)$ given, from time scale separation arguments [3, 2], by

$$V(I) = \frac{\frac{\vartheta}{\nu}\frac{I}{N}}{1 + \frac{\vartheta}{\nu}\frac{I}{N}} \cdot kmN \tag{20}$$

the approximation $\frac{\vartheta}{\nu}\frac{I}{N} \ll 1$ can be used

$$V(I) = \frac{\vartheta}{\nu}\frac{I}{N} \cdot kmN \quad . \tag{21}$$

This approximation is in good agreement with the exact expression from Eq. (20) with nonlinear dependence of V on I, with solution in form of $\langle I\rangle^* = (\frac{1}{2}q + \sqrt{\frac{1}{4}q^2 + r})N$ with parameter dependent constants q and r. Hence the expected risk of autochthonous cases I with relative mosquito abundance k and imported cases $Y = \varrho N$ is given by the following multiplicative factors

$$\langle I\rangle^* = k \cdot \beta_{eff} \cdot \frac{1}{\varepsilon} \cdot \varrho N \quad = f(k,\varrho) \tag{22}$$

with effective infectivity $\beta_{eff} = \beta\frac{\vartheta}{\nu}\frac{S_0}{N}$, import ϱN and $1/\varepsilon$, with ε the distance towards criticality, the epidemiological threshold above which exponential growth of autochthonous cases appears. The approximation, Eq. (22) compares well numerically with the stationary state of the full SIRUV system. The value of the approximation well below one autochthonous infected in expectation, still can generate smaller or larger clustered outbreaks.

The exact stationary state expression, approximated in good numerical accuracy by $\langle I\rangle^* = k \cdot \beta_{eff} \cdot \frac{1}{\varepsilon} \cdot \varrho N$, is explicitly given as

$$\langle I\rangle^* = \left(-\frac{1}{2}q + \sqrt{\frac{1}{4}q^2 + r}\right) N \tag{23}$$

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with $b := k\beta\frac{\vartheta}{\nu}\frac{S_0}{N}$, $g := \gamma\frac{\vartheta}{\nu}$, giving $q = \frac{1}{g}(\gamma - b + g\varrho)$ and $r = \frac{b}{g}\varrho$, initially evaluated for $S_0 = N$ the whole population being susceptible. The stationary state equation Eq. (19) indicates that we have in this application to invasion scenarios of vector-borne diseases we have a similar scaling close to the epidemiological threshold as in the COVID-19 case, see Eq. (6), since this implies for the stationary state the relation $\langle I\rangle^* = \varepsilon^{-\hat{\theta}\hat{\nu}_\parallel} \cdot \tilde{F}(\varepsilon \cdot \varrho^{-\hat{\mu}})$. The scaling relation holds for non-linear as well as for linear $V(I)$, since we are in the regime of low numbers of infected I close to the critical threshold. In conclusion, we have shown that epidemiological systems operating close to critical thresholds are now more important to be considered than previously expected, and especially the subcritical regime stabilized by external import is of increasing research importance.

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