RESEARCH ARTICLE

Figures and figure supplements

Emerging dynamics from high-resolution spatial numerical epidemics

Olivier Thomine *et al*

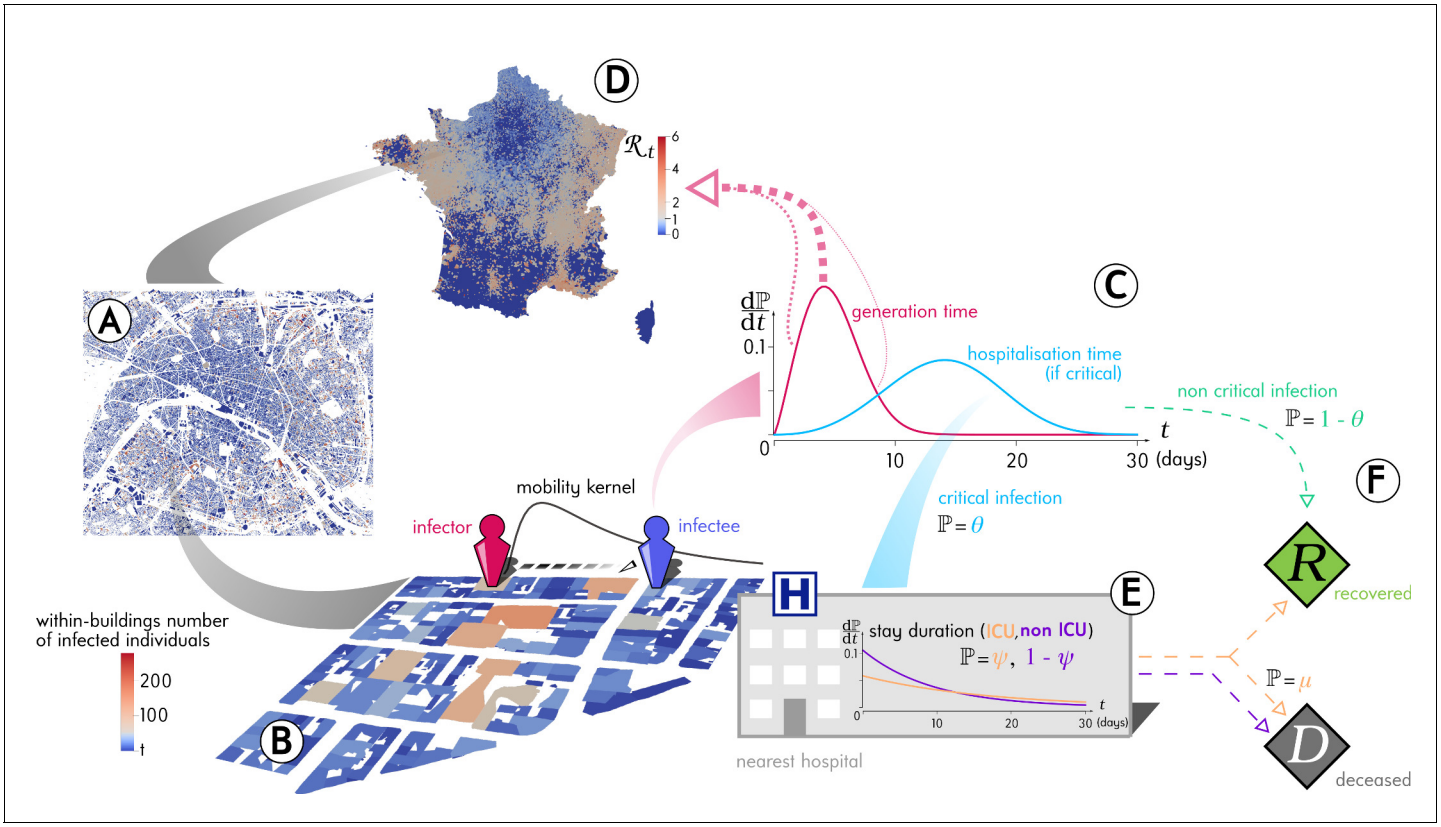

Figure 1. Outline of the Epidemap simulation framework. (**A**) The 66 millions inhabitants of metropolitan France are explicitly mapped to housing buildings following cartographic and demographic data. (**B**) At each time point of the simulation, the number of infected individuals in each building of the country is recorded, as well as the time past since each got infected (the panel shows the Paris area). (**C**) Every day, individuals can randomly move from their home to other buildings according to a mobility kernel and meet other people. If an infected individual encounters a susceptible host, a transmission event can occur. (**D**) The contagiousness of a infected individual varies depending on the time since infection. (**E**) A small fraction θ of infected individuals develop a critical form of the disease that requires their hospitalisation to the nearest facility. Clinical dynamics can be assumed not to affect transmission dynamics because more than 95% of the secondary transmission events occur before hospital admission.

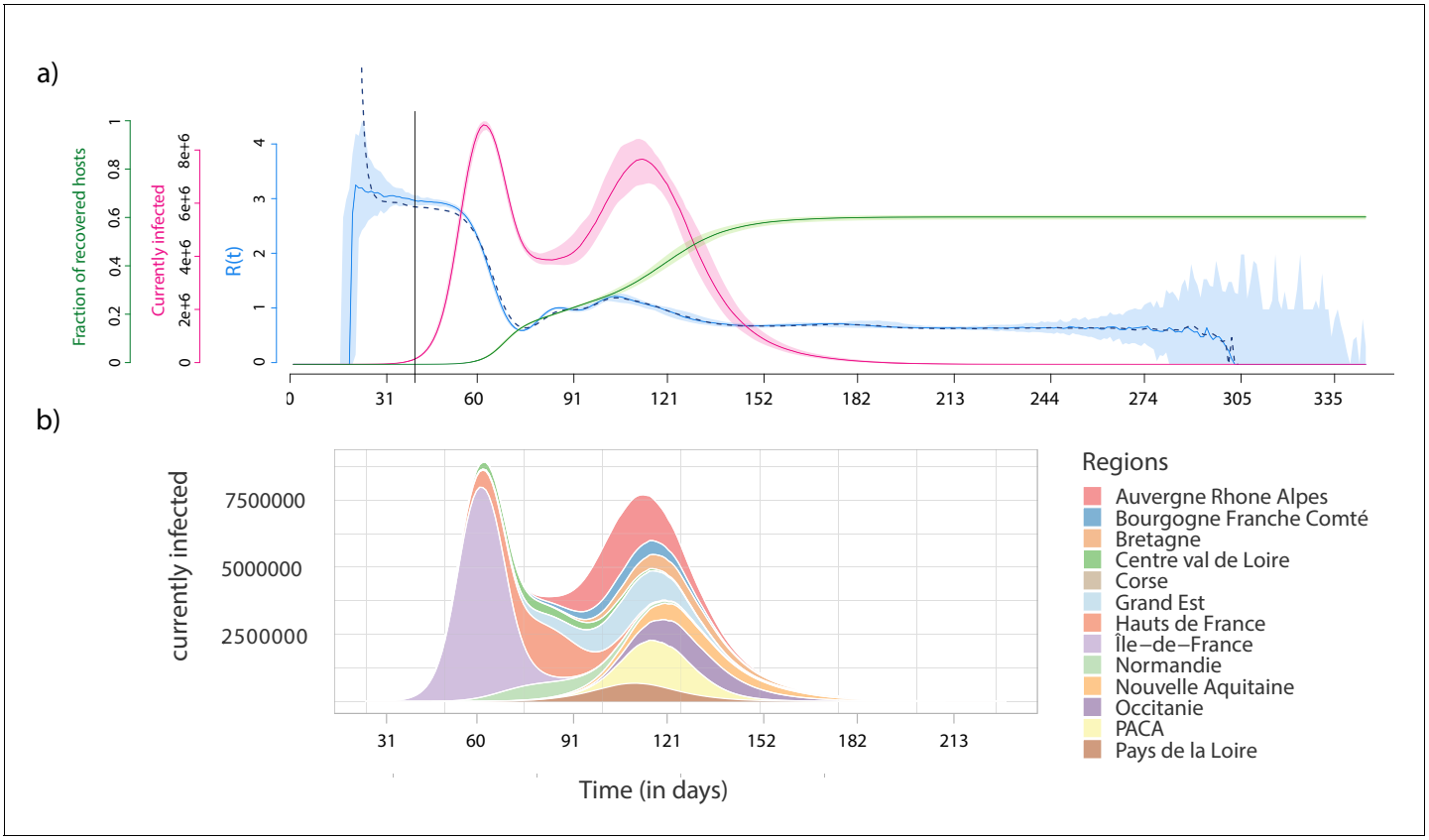

Figure 2. Epidemiological dynamics at the national (**a**) and regional (**b**) level. (**a**) The daily prevalence (the number of infected individuals) is in red, the temporal reproduction number (R_t) in blue, and the cumulative number of recovered individuals in green. Shaded areas show the 95% sample quantiles of 100 stochastic simulations. The dashed line shows the median R_t calculated on the case incidence data. (**b**) Each colour shows the prevalence in a French region.

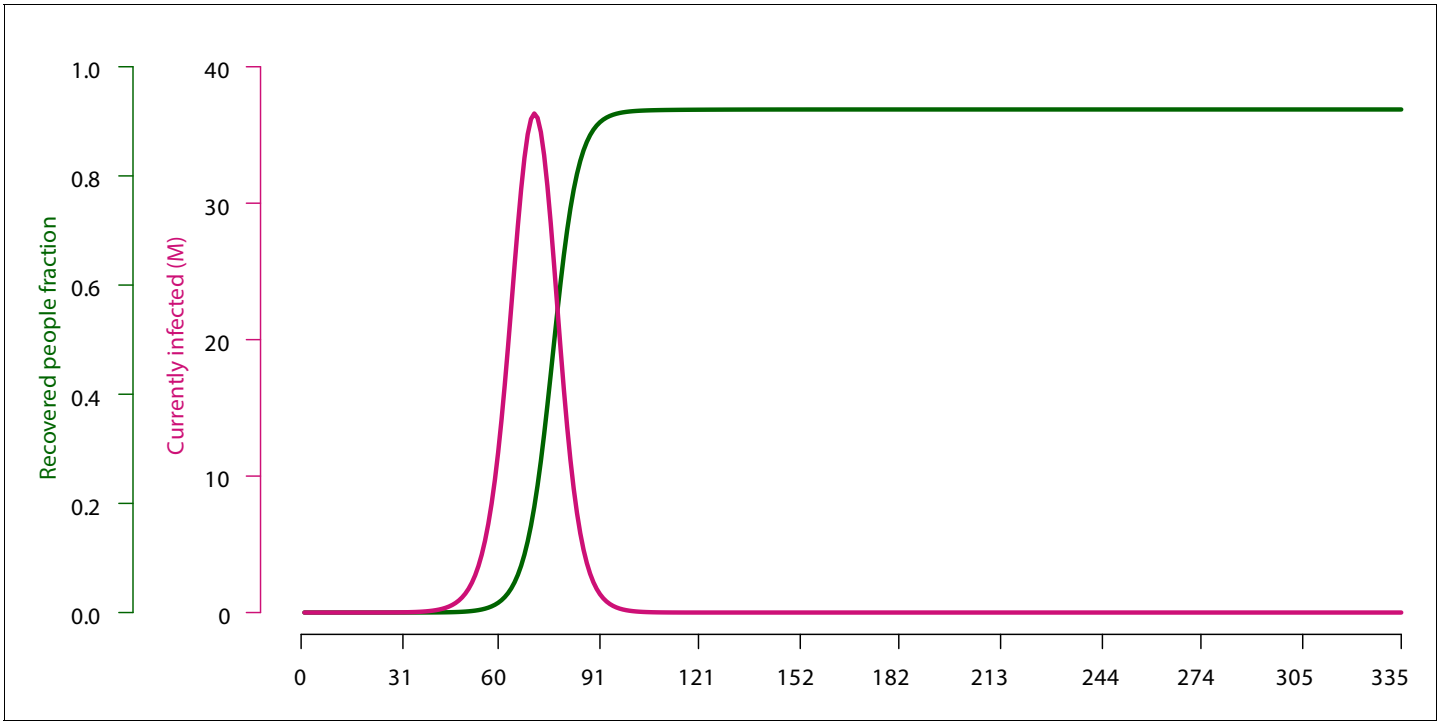

Figure 2—figure supplement 1. Mean field epidemiological dynamics. The transmission model is identical to that in ***Figure 2*** of the main text and the R0 is set to 3. The dynamics of the number of currently infected individuals (in millions in pink) does not exhibit a two-peaks dynamics. See ***Figure 2*** for additional details.

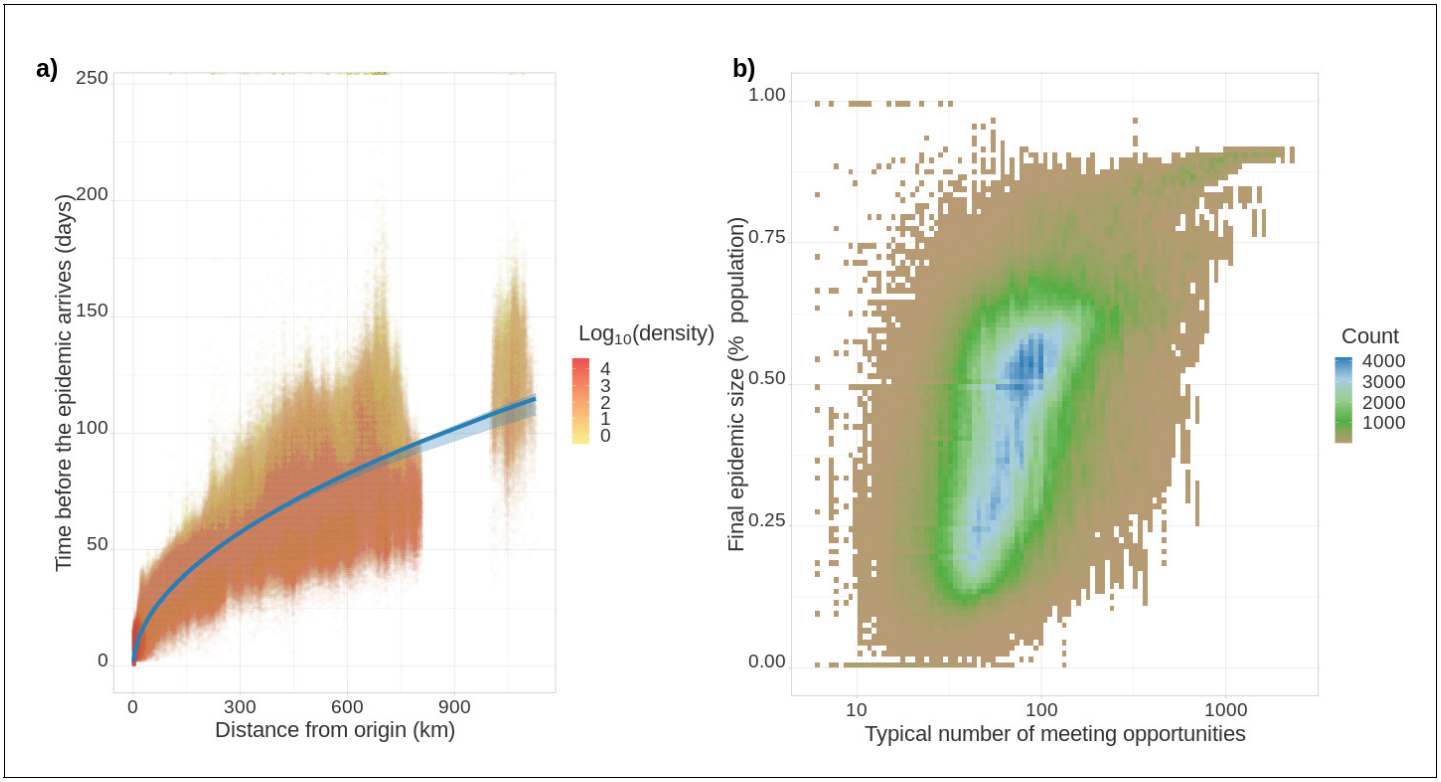

Figure 3. Epidemic arrival date and size at the district level. (**a**) Effect of the distance from the epicentre on the number of days until the epidemic begins in a district. The colour indicates the population density in the district (number of inhabitants divided by the district's surface). (**b**) District final epidemic size as a function of the characteristic distance between two individuals normalised by the average dispersal distance. The latter is computed as $2E[X]\sqrt{\text{density}}$, where X is the log-normal distribution of daily individual covered distance. Both panels show the value for 35,234 French districts and 100 stochastic simulations.

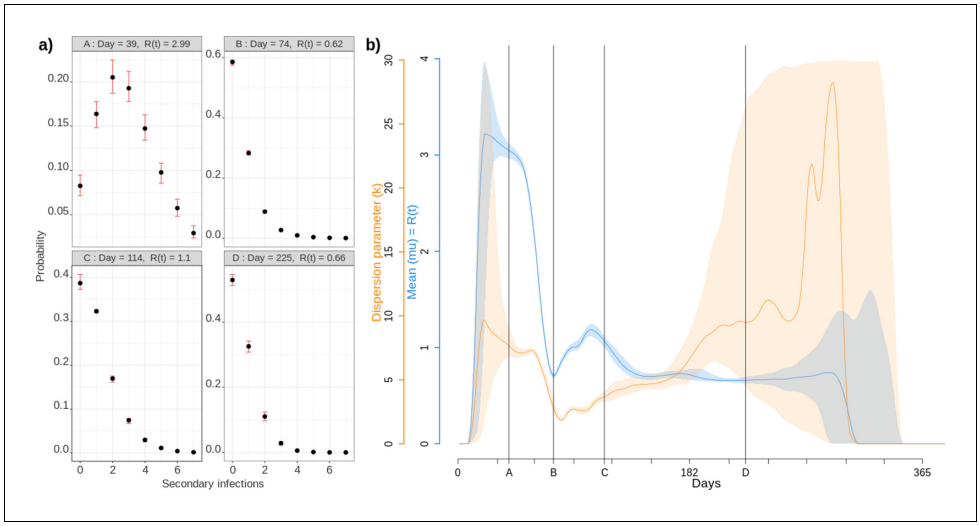

Figure 4. Individual reproduction number dynamics. (**a**) Distribution obtained over the whole population on 4 different days post outbreak. (**b**) Daily variation of the mean (in blue) and dispersion (in orange) of the distribution of individual reproduction numbers, which is assumed to follow a Negative Binomial distribution (***Lloyd-Smith et al., 2005***). Shaded areas show the 95% CI.

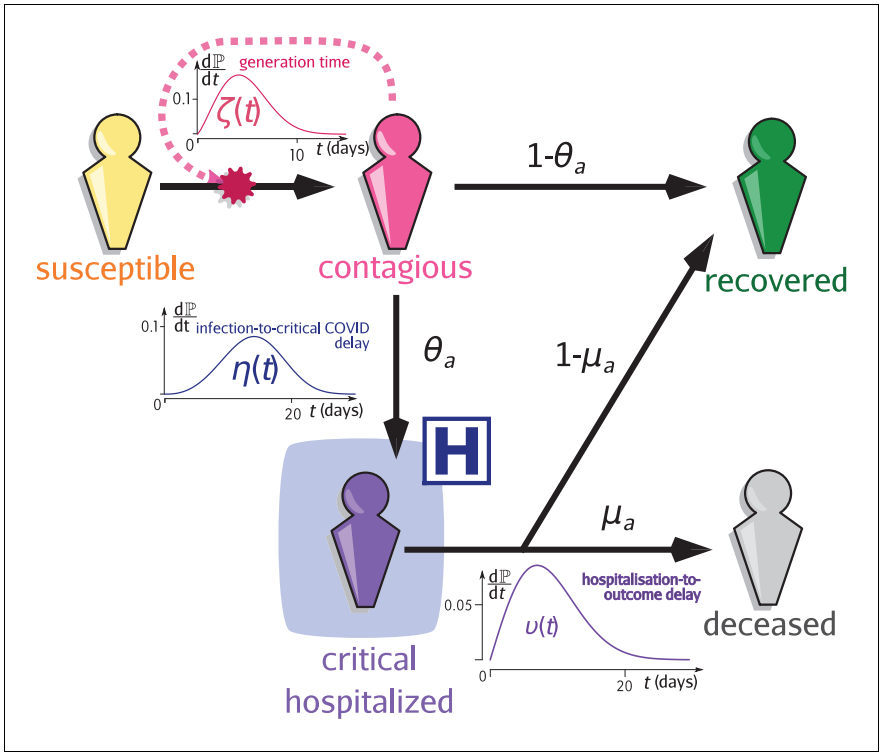

Figure 5. Infection model flow chart. Susceptible individuals (yellow figurine), are exposed to viral transmission from contagious individuals (pink figurine). Once infected, a host is more or less contagious depending on the time since contamination according to distribution ζ called the generation time (and usually parameterised using the empiric serial interval). A fraction θ_a, the value of which depends on the age of the host a, will develop a critical infection and be admitted to a hospital (purple figurine) according to the complication delay distribution η. The complementary fraction $1-\theta_a$ is assumed to recover with perfect and long-lasting immunity (green figurine). This compartment is also reachable after hospitalisation with the age-dependent probability $1-\mu_a$, after the discharge delay distribution υ. The complementary fraction μ_a eventually dies from COVID-19. See ***Sofonea et al., 2021*** for additional details.