Figure S1. Relationship between $r \cdot f$ and $\tau$ when we limit the product $r \cdot f$ as opposed to $r$ and $f$ separately in SEIR, NYC simulation. We run our simulations limiting the product $r \cdot f$—for each location $r$ away from an agent’s home, we only allow $r \cdot f/r$ visits. We see a similar relationship as in the primary formulation of our paper, up to a certain $r \cdot f$ value. Focusing on limiting $r$ and $f$ separately, as we do in the main body of the paper, allows us to understand if the driver of this relationship is $r$ or $f$ individually or the product itself. Understanding this limit at which the scaling relation no longer holds—and whether it is a fundamental aspect of the relationship between $r \cdot f$ and disease or an artifact of our data—is an important point for future exploration.
Figure S2. Scaling collapse in SIR and SI model. Top row: scaling collapse for SIR model with 1% initial infected populations. $R^2$ values for best-fit lines are, from left to right, .962 and .843. Best-fit line parameters are $a = -0.16, b = 25.99$ (NYC) and $a = -0.04, b = 13.51$ (Dakar). Bottom row, scaling collapse for SI model with 1% initial infected populations. $R^2$ values for best-fit lines are, from left to right, .976 and .835. Best-fit line parameters are $a = -0.12, b = 10.02$ (NYC) and $a = -0.03, b = 9.71$ (Dakar).
Figure S3. Persistence across $i_0$ values. Scaling collapse for NYC simulations with $i_0 = .1\%, 1\%, 5\%$ (rows 1, 2, and 3, respectively). In these simulations, total infected population never reaches $1/e \approx 35\%$ of the population, so we instead choose as our threshold the minimum peak infection size across trials to ensure that it will be reached by all simulations. The relationship between $r \cdot f$ and $\tau$ holds across all $i_0$ and model types, though variation is higher in lower $i_0$ simulations (see row 1 of the Figure).
Figure S4. Relation limits in $r \cdot f$ for NYC data. In the main body of the paper, we show $r \cdot f$ collapse for $r, f < 7$. These thresholds were chosen so as to ensure that we have a reasonable number of observations for each $r, f$ pair. Top left shows, for each $r$ and $f$ pair, the number of individual-location observations within our dataset. For example, at $r = 5, f = 5$ there are 222 observations, each representing a given individual travelling to a given location that is 5 km away from their home 5 times. There are some $r, f$ pairs that never show up in our data: for example, there are no observations in our dataset where an individual travelled to a given location 16 km away from their home 16 times. For $r, f < 7$ (represented by box A on top left), all pairs of $r$ and $f$ are represented by at least 50 observations. If this threshold is lowered to 15 observations (which lets us expand our $r, f$ values to to $r < 12, f < 11$, represented by box B on top left) then the scaling relation still holds (see plot B). However, if all $r, f < 20$ are considered, there are several high-$r$, high-$f$ combinations which don’t contain any observations at all and many that contain < 15 observations (see box C on top left). Thus limiting $r$ and $f$ at these high values has little to no effect on the dataset and the relationship with $\tau$ no longer holds (see plot C). This is a limitation of our dataset, given that our data only contains 28 days of data—if we observed the individuals in our dataset for a full year, there would certainly be more people visiting locations 16 km from their house 16 times. However, it is unclear to what extent it is also a limitation of the relation itself. Additional research using data collected over a longer period of time would be required to understand the true limits of the scaling relation in $r \cdot f$. 
Figure S5. Characteristic times for SEIR simulations with lower $R_0 = 1.46$ (similar to the H1N1 epidemic) and higher $R_0 = 8.2$ (similar to the upper estimates of COVID-19 Delta variant contagion). $R^2$ of best-fit lines are .860 and .962, respectively. Simulations shown start with a 5% initial infected population. To calculate $\tau$ here, we used an infection threshold equal to the minimum peak infection size across $r \cdot f$ pairs in order to ensure that the threshold would be reached in the $R_0 = 1.46$ case. Note that, counterintuitively, characteristic time is lower in the $R_0 = 1.46$ case—this is because low-$R_0$ simulations have earlier peaks.

Figure S6. Collapse of spatial dispersion of infections for various $k$ in SEIR, NYC model. Spatial dispersion $M(k)$ shows a scaling relationship with $r \cdot f$ regardless of $k$. 95% confidence bands are shown in gray, indicating that the spatial clustering in infections remains significant across values of $r \cdot f$. 
Figure S7. PEPR simulation results, where $P_{\text{travel}} = .40$. When we run SEIR models across a set of trajectories $M_{\text{sim}}$ which have been created using the PEPR model with $P_{\text{travel}} = .40$, we see a similar relationship between $r \cdot f$ and $\tau$ to that in our real trajectories $M_{\text{real}}$. $R^2$ of best-fit lines are .869 and .955, respectively.