

## Parametrization and Model Fitting

### *Population genetic model of antimicrobial resistance evolution*

To model the evolutionary trajectory and temporal dynamics of antimicrobial resistance in the context of inappropriate antibiotic prescription, we developed a spatially-averaged (US national scale) population genetic model. For a given pathogen, the resistance frequency at time  $t$ ,  $r(t)$ , starting at initial frequency  $r_0$  can be modeled as

$$r(t) = \frac{r_0 e^{mt}}{1 - r_0 + r_0 e^{mt}}, \quad (1)$$

where  $m$  is the Malthusian selection coefficient ([Hartl and Clark 2007](#); [Johnsen et al. 2011](#)). Selective pressure from inappropriate antibiotic prescription increases the relative fitness of resistant bacteria ([Austin, Kristinsson, and Anderson 1999](#)), therefore we assume that the constant  $m$  is time dependent:

$$m = \rho^* a^* r t + (\theta - 1), \quad (2)$$

where  $\rho$  is a fitted parameter that conveys the degree to which selection is affected by counter-productive prescription,  $a_y$  quantifies the amount of counter-productive prescription for the year  $y$ , and  $\theta$  is the difference between the exponential growth of susceptible bacteria and the exponential growth of resistant bacteria in the absence of antibiotics. Equation (1) can then be determined step-wise:

$$r(t) = \frac{r(y) e^{m_y t}}{1 - r(y) + r(y) e^{m_y t}}, \quad (3)$$

for  $y \leq t < y + 1$ , where the time unit

By taking the reciprocal of both sides and simplifying Eq. 1 to

$$\frac{1}{r_t} - 1 = \frac{\frac{1}{r_0} - 1}{e^{m * t}}, \quad (4)$$

the model can be further transformed into a generalized linear regression,

$$\ln\left(\frac{1}{r_t} - 1\right) = \ln\left(\frac{1}{r_0} - 1\right) - m * t. \quad (5)$$

### *Parameterization*

To parameterize  $\theta$ , we calculated the average relative fitness of five strains of *E. coli* harboring newly acquired resistance plasmids ([Di Luca et al. 2017](#)). To account for variability among strains and uncertainty for each strain associated with this dataset, we iteratively sampled a fitness from each of the five strain-specific best-fit Normal error distributions, and then calculated the mean. One thousand stochastic iterations of probabilistic sensitivity were conducted and the 25th and 97.5th quantiles were taken to describe the 95% sensitivity interval.

Taking the carbapenem consumption over the time frame of the collected historical surveillance data over the 12 years from 2000–2011, the counter-productive carbapenem prescription used in the Malthusian selection coefficient equation (**Eq 2**) for estimating the parameters  $\rho$  and  $\theta$  was obtained using the fitted values of consumption onto the time variables

$$at = \beta_0 + \beta_1 * t + \epsilon_t$$

Annual carbapenem consumption from 2000–2011 were obtained from the Center For Disease Dynamics, Economics & Policy (CDDEP) as  $at$  with a unit of daily doses per 1,000 individuals (DDD/1000). To obtain the annual inappropriate carbapenem consumption, we take the product of  $at$  and the proportion of prescription given inappropriately,  $x$ , where  $x$  is calculated as the percentage of the inappropriate empiric treatment (IET) out of the total treatment number (both non-IET and IET) ([Zilberberg et al. 2017](#)).

We estimated the number of patients with bacteremia that are given inappropriate empiric treatment with a carbapenem,

$$y = N_t \times e \times x \times q \times p,$$

where  $N_t$  is the population size each year ([US Census Bureau n.d.](#));  $e$  represents the incidence rate for bacteremia ([Angus DC n.d.](#); [Nielsen n.d.](#); [Simmering et al. 2017](#));  $p$  is the proportion of bacteremia attributed to *P. aeruginosa*, obtained from proportional breakdowns from hospital and national databases;  $q$  is the proportion of bacteremia patients prescribed carbapenems; and  $x$  is the proportion given inappropriate empiric treatment, defined as first-line antibiotic prescribed to a resistant pathogen, with failure to initiate appropriate treatment within two days of a positive culture ([Zilberberg et al. 2017](#); **Table 1**).

US carbapenem consumption during 2000–2011 was previously quantified from national surveys of pharmaceutical sales ([ResistanceMap - Antibiotic Use](#)). The surveillance approach shifted between 2012 and 2013, restricting our ability to draw on data beyond this time frame ([“ResistanceMap - Antibiotic Resistance” n.d.](#)).

### Data

The number of resistant cases among bacteremia patients as a function of inappropriate carbapenem prescription at given year is computed as

$$kt = dtrt,$$

where  $r_t$  is the resistance frequency at a given year, and  $t$  is the year, indexed as  $t = 1$  in 2000. By the end of the five-year antibiotic stewardship program, we project a reduction in inappropriate prescription of carbapenems of 51.7% ([Van Hollebeke et al. 2016](#)), with a yearly proportional decreasing trend. The number of inappropriately prescribed cases at the  $j$ th year ( $j = 1 \dots 5$ ) during the widespread implementation of stewardship was specified as

$$bt = b_0(1 - 0.2^j \cdot 51.7\%).$$

**Table 1.** Dynamic model parameters, definitions, constraints, priors, and sources of data.

Parameter	Definition	Constraints	Prior distribution	Source
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$c_y$	Carbapenem prescription (in a given year)	—	annual point value specified	CDDEP <sup>a</sup>
$x$	Proportion of inappropriate prescription <i>Bacteremia</i> <i>Pneumonia</i> <i>UTI</i>	—	point value specified	Zilberberg et al. 2017
$q$	Proportion of cases treated by prescription of carbapenems <i>Bacteremia</i> <i>Pneumonia</i> <i>UTI</i>	—	point value specified	Merck
$p$	Proportion of bacteremia (pneumonia and UTI) attributed to <i>P. aeruginosa</i>	—	point value specified	Gaynes et al. 2005 (NHSN <sup>b</sup> )
$e$	Incidence rate for bacteremia (pneumonia and UTI)		point value specified	(Angus DC n.d.; Nielsen n.d.; Simmering et al. 2017)
$a$	Inappropriate carbapenem prescription averaged t=1nat		average value from historical data	
$a_t$	Inappropriate carbapenem prescription after the 5-yr stewardship program complete		point value estimated	
$\theta$	Relative fitness of the resistant strain compared to the susceptible strain	$\theta < 1$	point value specified	Di Luca et al. 2016
$\rho$	Scaling factor for the susceptible fitness constant	—	no prior specification	
$r_0$	Initial resistance frequency	$0 < r_0 < 1$	no prior specification	
$\mu_i$	Mean value of the relative fitness for transformant $i$	$i$ in [1, 5]	Point value	Zilberberg et al. 2017
$\sigma_i$	Standard deviation of the relative fitness for a given transformant	$i$ in [1, 5]	Point value	Zilberberg et al. 2017
$N_y$	US population at year $y$		annual point value specified	US Census Bureau

<sup>a</sup>Center for Disease Dynamics Economics & Policy (<http://resistancemap.cddep.org/>)

<sup>b</sup>National Healthcare Safety Network (<https://www.cdc.gov/nhsn/index.html>)

### Model fitting

Data from 2000–2011 on the pathogen *P. aeruginosa* and diagnosis-specific US carbapenem resistance from Merck were combined with a larger CDDEP dataset, which included pathogen-specific carbapenem resistance data in the US.

the least square estimates of which were used for expressing the unknown parameters. The initial resistance frequency  $r_0$  can be assessed from the intercept,  $1r_0-1$ , and the slope corresponds to  $-m$ . From **Eq 2**, we calculated

$$\rho = \frac{-m - (\theta - 1)}{a_t}, \quad (7)$$

with  $a_t$  obtained by linearly fitting the annual carbapenem consumption on the time variable  $t$  and further projected into the future years.

To account for uncertainty within the resistance data, 1,000 trials were conducted and the 95% confidence interval was estimated.