NSF NRT Meeting

Supplement for poster: "Modeling age-targeted interventions for TB in India"

We modify the model in Blower et al. (1995) and Arregui et al. (2018) to include discretized age-classes and additional transitions representing disease reinfection. Since capturing realistic contact patterns among different age groups is crucial for modeling incidence among different age groups (Arregui et al. 2018), we use projected contact data for India published by Prem, Cook, and Jit (2017) which includes contact between 16 different age classes (0-4, 5-10.., up to 75-80). To focus on TB dynamics, and allow us to ignore potential impacts of coinfection with HIV, we will focus on modeling TB in India where the most recently published WHO report estimates there were 2.7 million new cases in 2016 (WHO).

The corresponding model equations represent individuals each infection state and age-class *i* with model parameters given in Table 1. As in Blower et al. (1995), $\lambda = \beta \mathrm{I}_i$ and in this model, $\beta = bC$ where C is the projected contact matrix from Prem, Cook, Jit (2017). The parameter *a* represents the aging matrix.

$$\frac{d\mathrm{S}_i}{dt} = \pi_i - \lambda \mathrm{S}_i - \mu \mathrm{S} - a\mathrm{S}_i + a\mathrm{S}_{i-1}$$
$$\frac{d\mathrm{L}_i}{dt} = (1-\rho_i)\lambda \mathrm{S} - (v_i + \mu)\mathrm{L}_i + \psi_i \mathrm{R} - a\mathrm{L}_i + a\mathrm{L}_{i-1}$$
$$\frac{d\mathrm{I}_i}{dt} = \rho_i q_i \lambda \mathrm{S} + q_i v_i \mathrm{L} + \omega q_i \mathrm{R} - (\mu + \mu_t + c_i)\mathrm{N}_i - a\mathrm{N}_i + a\mathrm{N}_{i-1}$$
$$\frac{d\mathrm{N}_i}{dt} = \rho_i (1-q_i)\lambda \mathrm{S} + (1-q_i)v_i \mathrm{L} + \omega(1-q_i)\mathrm{R} - (\mu + \mu_t + c_i)\mathrm{N}_i - a\mathrm{N}_i + a\mathrm{N}_{i-1}$$

$$\frac{d\mathrm{R}_i}{dt} = c_i(\mathrm{I} + \mathrm{N}) - (2\omega + \mu)\mathrm{R}_i - \psi_i \mathrm{R}_i - a\mathrm{R}_i + a\mathrm{R}_{i-1}$$

Table 1. Model parameters.

	Biological Interpretation	**Units**	**Value**	**Source**
S_0, L_0, I_0, N_0, R_0	Initial values of model compartments	people		Fitted
b	Transmission coefficient	/person/year	3×10^{-4}	Fitted
c_i	Treatment rate	/person/year	0.5, varies	Upper bound from Arregui et al. (2018)
v_i	Progression rate to TB from latent infection	/person/year	0.100	Fitted
q_i	Probability of developing infectious TB		0.80 (0-15 years), 0.9 (16+ years)	Arregui et al. (2018)
μ_r	Mortality rate due to TB	/person/year	0.1	Arregui et al. (2018)
ω	Rate of relapse to active TB	/person/year	0 (0-4 years), 0.005 (5-9 years), 0.02	

			(10+ years)	
ψ_i	Rate of reinfection	/person/year	0.001 (0-4 years), 0.005 (5-9 years), 0.02 (10+ years)	
μ	Natural mortality	people/year	0 (0-65), 0.1 (75+)	Constant mortality function as in (Brooks-Polluck et al. 2010)
ρ_i	Proportion of new infections that develop TB within a year		0.1 (0-9 years), 0.15 (10-54 years), 0.1 (55+ years)	Arregui et al. (2018)
π_i	Birth rate into age class *i*	people/year	26,000,000	India census

References:

Arregui, Sergio, María José Iglesias, Sofía Samper, Dessislava Marinova, Carlos Martin, Joaquín Sanz, and Yamir Moreno. 2018. "Data-Driven Model for the Assessment ofMycobacterium Tuberculosistransmission in Evolving Demographic Structures.." *Proceedings of the National Academy of Sciences of the United States of America* 115 (14). National Academy of Sciences: E3238–45. doi:10.1073/pnas.1720606115.

Blower, Sally M, Angela R McLean, Travis C Porco, Peter M Small, Philip C Hopewell, Melissa A Sanchez, and Andrew R Moss. 1995. "The Intrinsic Transmission Dynamics of Tuberculosis Epidemics." *Nature Medicine* 1 (8). Nature Publishing Group: 815–21. doi:10.1038/nm0895-815.

Prem, Kiesha, Alex R Cook, and Mark Jit. 2017. "Projecting Social Contact Matrices in 152 Countries Using Contact Surveys and Demographic Data.." Edited by Betz Halloran. *PLoS Computational Biology* 13 (9). Public Library of Science: e1005697. doi:10.1371/journal.pcbi.1005697.