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A Dynamic Transmission Model for Predicting Trends in *Helicobacter pylori* and Associated Diseases in the United States

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Appendix

The mathematical equations underlying our compartmental model of *Helicobacter pylori* are a system of partial differential equations:

$$\begin{split} &\frac{\partial I}{\partial t} + \frac{\partial I}{\partial a} = -\mu(a) \cdot I(a,t) \\ &\frac{\partial S}{\partial t} + \frac{\partial S}{\partial a} = -\left[\lambda_1(a,t) + \lambda_2(a,t) + \mu(a)\right] \cdot S(a,t) \\ &\frac{\partial AG}{\partial t} + \frac{\partial AG}{\partial a} = \lambda_1\left(a,t\right) \cdot S(a,t) - \left[\delta_1(a) + \delta_2\left(a\right) + \mu(a)\right] \cdot AG(a,t) \\ &\frac{\partial CG}{\partial t} + \frac{\partial CG}{\partial a} = \lambda_2\left(a,t\right) \cdot S(a,t) - \left[\delta_+\left(a\right) + \mu(a)\right] \cdot CG(a,t) \\ &\frac{\partial DU}{\partial t} + \frac{\partial DU}{\partial a} = \delta_2\left(a\right) \cdot AG\left(a,t\right) - \left[\delta_3\left(a\right) + \mu_{\mathrm{DV}} + \mu(a)\right] \cdot DU(a,t) \\ &\frac{\partial CAG}{\partial t} + \frac{\partial CAG}{\partial a} = \delta_3\left(a\right) \cdot DU(a,t) + \delta_+\left(a\right) \cdot CG(a,t) - \left[\delta_3\left(a\right) + \mu_{\mathrm{BV}} + \mu(a)\right] \cdot CAG(a,t) \\ &\frac{\partial GC}{\partial t} + \frac{\partial GG}{\partial a} = \delta_3\left(a\right) \cdot CAG(a,t) - \left[\mu_{\mathrm{BC}} + \mu(a)\right] \cdot GC(a,t) \end{split}$$

The mathematical equations underlying our compartmental model of *H. pylori* is a system of partial differential equations:

$$\begin{split} &\lambda_{1}\left(a,t\right)=p\left(a\right)\cdot\int\limits_{0}^{\infty}\beta(a',a)\cdot\left[AG(a',t)+CG(a',t)+DU\left(a',t\right)+\alpha\cdot CAG\left(a',t\right)+GC(a',t)\right]da'\\ &\lambda_{2}\left(a,t\right)=\left(1-p\left(a\right)\right)\cdot\int\limits_{0}^{\infty}\beta(a',a)\cdot\left[AG(a',t)+CG(a',t)+DU\left(a',t\right)+\alpha\cdot CAG\left(a',t\right)+GC(a',t)\right]da' \end{split}$$

where:

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\begin{split} &I(0,t) = p_{+} \cdot \Pi \\ &S(0,t) = (1-p_{+}) \cdot \Pi \\ &AG(0,t) = CG(0,t) = DU(0,t) = CAG(0,t) = GC(0,t) = 0 \end{split}
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Notation:

a, a'	age index
t	time index
П	birth rate per unit time
I(a,t)	number of isolated (not-susceptible) individuals of age a, at time t
S(a,t)	number of susceptible individuals of age a , at time t
AG(a,t) CG(a,t)	number of infected individuals of age <i>a</i> with antrum-predominant gastritis, at time <i>t</i> number of infected individuals of age <i>a</i> with corpus-predominant gastritis, at time <i>t</i>
DU(a,t)	number of individuals of age a with duodenal ulcer, at time t
CAG(a,t)	number of individuals of age a with chronic atrophic gastritis, at time t
GC(a,t)	number of individuals of age a with gastric cancer, at time t
p_I	proportion of population that is not-susceptible at birth
$\lambda_{I}(a,t)$	rate at which one susceptible of age <i>a</i> acquire infection and develop antrumpredominant gastritis
$\lambda_2(a,t)$	rate at which one susceptible of age a acquire infection and develop corpuspredominant gastritis
$\beta(a',a)$	transmission parameter; probability that an infective of age a ' will infect a susceptible of age a
p(a)	proportion of newly infected individuals of age a developing antrum (vs. corpus) predominant gastritis
$\delta_{1}(a)$	transition rate from antrum- to corpus-predominant gastritis in age group a
$\delta_2(a)$	progression rate from antrum-predominant gastritis to duodenal ulcer in age group a
$\delta_{\beta}(a)$	transition rate from duodenal ulcer to chronic atrophic gastritis in age group a
$\delta_4(a)\square$	progression rate from corpus-predominant gastritis to chronic atrophic gastritis in age group \boldsymbol{a}
$\delta_{5}(a)$	progression rate from chronic atrophic gastritis to gastric cancer in age group a
$\mu(a)$	age-specific background mortality rate due to all cases
$\mu_{\mathit{DU}}\square$	mortality rate due to duodenal ulcer
μ_{GU}	mortality rate due to gastric ulcer
μ_{GC}	mortality rate due to gastric cancer

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