HELMINTH DYNAMICS: MEAN NUMBER OF WORMS

FULL TITLE: HELMINTH DYNAMICS: MEAN NUMBER OF WORMS, REPRODUCTIVE RATES

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Abstract. Understanding the mean number of worms and burden of soil transmitted helminth infections are considered as important parameters in formulating treatment strategies to eliminate worms among children who are effected by helminth infections [3]. We derive mean number of worms in a newly helminth infected population before secondary infections are started (population is closed). Further we bring analytical solutions. We also theoretically demonstrate computing net reproductive rates within and outside a human host.

Key words: worm density, measurable functions, disease modeling, chemotherapy, treatment MSC: 92D30.

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1. Mean number of worms

Infection of helminthiasis or simply helminth can cause severe damage to health of children and their childhood behaviour, for example poor attendance in schools, etc [2]. A general description of infectious disease epidemiology of helminths for example for hookworms, and density-dependent fecundity and mortality models are described in [1]. Mean worm burden is one of the key epidemiological parameter in treatment formulations among children suffering with helminth infections [3, 5, 4, 6]. Moreover, mean worm burden is often considered as an important parameters in treatment and control of parasites in wild life [7, 8, 9]. In this paper, we treat worm burden as a function of worm reproductive rates and mean number of worms. For computation of mean number of worms within a host there are no directly available mathematical functions, and we try to theoretically understand the mean number and reproduction of worms within a host and present a theoretical analysis. In this section we derive formulae for the mean number of worms at the host level and at the population level. We obtain mean number of worms in the host population by treating population aging over the period, i.e. treating both time and age as dynamic. We assume no chemotherapy scenario at first and then introduce chemotherapy for studying disease dynamics. Populations means are derived from the individual host worm densities.

1.1. Cross sectional mean. Let $M(t)$ be the mean number of worms present in the host population at time $t$. We compute, $M(t)$ as below:
Where \( H_i(x,t) \) is the number of worms in a host who is of age \( x \) at time \( t \) in the \( i^{th} \) sub-population \((H(x,t)dx\) is differential number of hosts between \( x \) and \( x + dx \) at time \( t \)); \( \Lambda_i(x,t) \) is net growth of worms in \( i^{th} \) sub-population of age \( x \) at time \( t \); \( k_i(x,t) \) are weights for age \( x \) at time \( t \); \( N \) is size of the human population sub-types, \( \omega \) is age of humans until they are at risk of keeping helminth worms. \( \int_0^\omega H_i(x,t)dx \) is total number of hosts and \( \int_0^\omega H_i(x,t)\Lambda_i(x,t)dx \) is net worms present in \( i^{th} \) sub-population at time \( t \). When we divide age range \([0, \omega)\) into smaller age intervals at lengths, \( a_1, a_2 - a_1, ..., \omega - a_k \), the mean number of worms in the equation (1.1) is written as follows:

\[
M(t) = \sum_{i=1}^{N} \frac{\int_0^\omega [k_i(x,t)H_i(x,t)\Lambda_i(x,t)] \, dx}{\int_0^\omega k_i(x,t) \, dx}
\]

(1.1)

We define \( H_i(x,t) = \begin{cases} 
P_i(t-x)\pi(0,x) & \text{for } x < t \\
H_i(x-t,0)\pi(x-t,x) & \text{for } x \geq t 
\end{cases} \)
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Here $P_i(x-t)$ is births to hosts in the age $x-t$, $\pi(0, x)$ is probability that a newly born individual will survive up to age $x$, $\pi(x-t, x)$ is probability that a individual of age $x-t$ will survive up to age $x$. By this definition, equation (1.2) will become

\[ M(t) = \sum_{i=1}^{N} \left[ \frac{\int_{0}^{a_1} \left[ k_i(x, t)P_i(a_1 - x) \pi(0, a_1)\Lambda_i(x, t) \right] dx}{\int_{0}^{a_1} k_i(x, t) dx} + \right. \]

\[ \left. \frac{\int_{a_1}^{a_2} \left[ k_i(x, t)P_i((a_2 - a_1 + x) \pi(0, a_2 - a_1)\Lambda_i(x, t) \right] dx}{\int_{a_1}^{a_2} k_i(x, t) dx} + \right. \]

\[ \left. \cdots + \frac{\int_{a_{k-1}}^{a_k} \left[ k_i(x, t)P_i(a_k - a_{k-1} + x) \pi(0, a_k - a_{k-1})\Lambda_i(x, t) \right] dx}{\int_{a_{k-1}}^{a_k} k_i(x, t) dx} \right] \]

(1.3)

We have obtained equation (1.3) by assuming

\[ \frac{\int_{a_k}^{\omega} \left[ k_i(x, t)H_i(x, t)\Lambda_i(x, t) \right] dx}{\int_{a_k}^{\omega} k_i(x, t) dx} = 0. \]

1.2. Cohort mean. Suppose we are following helminth infected hosts at time $t$ in $i^{th}$ sub-population, (say, $P_i$). Denote by $M_i^*(t)$ for net number of worms produced by $i^{th}$ sub-population, which is expressed by the integral, $\int_{t}^{\omega} H_i(x, t)\Lambda_i(x, t) dx$. Then the net number of worms produced during $t$ to $t + h_1$, $t + h_1$ to $t + h_2$, ..., $t + h_N$ to $\omega$ are

\[ \int_{t}^{t+h_1} \int_{0}^{\omega} H_i(x, t)\Lambda_i(x, t) dx ds, \]

\[ \int_{t+h_1}^{t+h_2} \int_{0}^{\omega} H_i(x, t)\Lambda_i(x, t) dx ds , \cdots, \]

\[ \int_{t+h_N}^{t+N+\delta} \int_{0}^{\omega} H_i(x, t)\Lambda_i(x, t) dx ds. \]

Each double integral indicates net worms observed during a time interval indicated. The last double integral is where maximum possible net worms produced as in a logistic growth model with a variable
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$M^*$ and with carrying capacity $\int_{t+h}^{\omega} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds$, then the growth rate, $r^*_i$ of worms for the entire period for $i^{th}$ sub-population is

$$r^*_i = \frac{1}{t_N + \delta - t} \log \left[ \frac{M^* \left( \int_0^t \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds - \int_0^{t_N+\delta} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds \right)}{\int_0^t \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds \left( M^* - \int_0^{t_N+\delta} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds \right)} \right]$$

(1.4)

Under the Lyapunov stability set-up, we explain carrying capacity as, for each time interval $0$ to $t_n + \delta$ for $n = 1, 2, 3, \ldots$, we define

(1.5) $$\int_0^{t_n+\delta} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds$$

as cumulative number of net worms present in the $i^{th}$ sub-population during $0$ to $t_n + \delta$ for some $\delta > 0$ and $n = 1, 2, 3, \ldots$. For some positive integer $N$, we will have condition,

$$\left| \int_0^{t_n+\delta} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds - \int_0^{t_N+\delta} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds \right| < g$$

(1.6)

$$\Rightarrow \int_0^{t_n+\delta} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds \to \int_0^{t_N+\delta} \int_0^\omega H_i(x, t) \Lambda_i(x, t) dxds$$

whenever $n \geq N$ and for every $g > 0$. For the population weights $k(P_i)$, the mean number of worms present in the population is
\[ M(t) = \sum_{i=1}^{N} \frac{\int_0^{t+hN} \int_0^\omega k(P_i)H_i(x,t)\Lambda_i(x,t)dxds}{\int_0^N k(P_i)di} \]

(1.7)

1.3. Theorems on worm growth potential in hosts.

**Theorem 1.** \( F_1 \) is a measurable function, where \( F_1 \) is defined as,

\[ F_1 : (-\infty, t_x + \delta) \to \int_0^{t_x+\delta} \int_0^\omega H_i(x,t)\Lambda_i(x,t)dxds \]

for \( x = 1, 2, 3, \ldots \) and \( \delta > 0 \).

**Proof.** Observe that \( F_1 \) maps each interval from the set

\[ \{ (-\infty, t_x + \delta) : x = 1, 2, 3, \ldots \text{ and } \delta > 0 \} \]

to a function in the set

\[ \left\{ \left( \int_0^{t_x+\delta} \int_0^\omega H_i(x,t)\Lambda_i(x,t)dxds \right) : x = 1, 2, 3, \ldots \text{ and } \delta > 0 \right\} . \]

Note that for some arbitrary \( k \),

\[
\lim_{(-\infty,t_x+\delta)\to(-\infty,t_k+\delta)} F_1 = \lim_{(-\infty,t_x+\delta)\to(-\infty,t_k+\delta)} \left[ \left( \int_0^{t_x+\delta} \int_0^\omega H_i(x,t)\Lambda_i(x,t)dxds \right) \right] \\
= \left( \int_0^{t_k+\delta} \int_0^\omega H_i(x,t)\Lambda_i(x,t)dxds \right).
\]

Hence, \( F_1 \) is continuous and \( F_1 \) is a measurable. \( \square \)
Remark 2. \( F_1 \left\{ \bigcup_{x=1}^{\infty} (0, t_x + \delta) \right\} = F_1 (0, t_N + \delta) \) for the description of \( N \) in section 1.2.

Remark 3. Suppose \( M^* \) be the worms observed during time intervals \((0, t_x + \delta)\) for \( x = 1, 2, 3, \ldots \), then a class \( G \) by the below notation

\[
\begin{align*}
G_1 &= \bigcup_{x=1}^{1} F_1 (0, t_x + \delta) \\
G_2 &= \bigcup_{x=1}^{2} F_1 (0, t_x + \delta) \\
&\quad \vdots \\
G_N &= \bigcup_{x=1}^{N} F_1 (0, t_x + \delta) \\
&\quad \vdots 
\end{align*}
\]

is \( \sigma \)-algebra.

**Theorem 4.**

\[
\lim_{x \to \infty} \left( \int_0^{t_x + \delta} \int_0^{\omega} H_i(x, t) \Lambda_i(x, t) dx ds \right) = \left( \int_0^{t_N + \delta} \int_0^{\omega} H_i(x, t) \Lambda_i(x, t) dx ds \right)
\]

**Proof.** By using Lebesgue monotonic convergence theorem, we can prove this result because, \( F_1 \) is monotonic function and measurable. \( \square \)
2. Net Production Rates within and outside human host

We define net productive rates for helminth in this section. We assume that there are two sets of counting we do here, one is growth in the number of helminth population within human host and second is contribution of this human host to outside environment in the life time. We also assume that initial age distribution of helminths in human host is known. Suppose, \( M^1(t) \) be the population of helminth within a human host at time \( t \), \( M^1_0 \) be the initial population, \( K \) is carrying capacity, and \( r \) is growth rate, then under the logistic growth rate, we can express, \( M^1(t) \), as

\[
M^1(t) = \frac{M^1_0 Ke^{rt}}{K + M^1_0(e^{rt} - 1)}
\]

solving for growth rate, \( r \), we get,

\[
r = \frac{1}{t} \log \left[ \frac{M^1(t)(M^1_0 - K)}{M^1_0(M^1(t) - K)} \right]
\]

Suppose, \( M^1(a, 0) \) is initial helminth population at age \( a \) within an host is known, then using \( \rho(a + da, 0) \), the survival probability that a group of worms at age \( a \) will survive until age \( a + da \), we can obtain age distribution of worms at age \( a + da \) and at time \( da \) by,

\[
M^1(a, 0)\rho(a + da, 0) = M^1(a + da, da)
\]
Note that, \( \int_0^\infty M^1(a, 0)da = M_0^1 \). Let \( s \) is the time at point of inflection of logistic growth or we assume at \( s \), we will have \( M^1 = K/2 \). We obtain \( M^1(a, s) \) and \( M^1(a, T^*) \) for some \( T^* > s \) using growth rate in equation (2.1). Using these two population age structures at times \( s \) and \( T^* \), we obtain effective worm population, \( M^*(a, T) \) in the life time of human host (where \( s < T < T^* \)). We define net rate of production, \( \mathcal{R} \) within a human host as,

\[
(2.3) \quad \mathcal{R} = \int_0^\infty \left\{ \frac{L(a, T)}{M^*(a, T)} \right\} \rho(a, T)da
\]

In the equation (2.3) \( L(a, T) \) denotes number of eggs produced by worms of age \( a \) at \( T \). In case of direct availability of rate of egg bearing at age \( a \) by a female worm, say, \( f(a, T) \) then we can replace it for the ratio \( L(a, T)/M^*(a, T) \) in the equation (2.3) and modify it as

\[
(2.4) \quad \mathcal{R} = \int_0^\infty f(a, T)\rho(a, T)da
\]

3. IMPACT OF CHEMOTHERAPY

We establish few results when chemotherapy is introduced into the host population suffering with helminth and capture the dynamics. Suppose the chemotherapy is introduced at \( t_N + \delta \) and \( \epsilon_i(x, t) \) be the net production rate of worms in the host population in age \( x \) at time \( t \) (due to chemotherapy it is assumed that the net number of worms produced per host is negative because there are less number of worms produced than they are removed), then the worm numbers in the \( i \)th sub-population during \( (t_N + \delta, t_{N+1} + \delta) \) i.e. \( \int_{t_N+\delta}^{t_{N+1}+\delta} \int_0^\infty H_i(x, s) \epsilon(x, s) dx ds \)
starts reducing until they eliminated. The exponential growth rate, \( r_{c(N)} \) until the time \( t \) can be computed as,

\[
\begin{align*}
\tag{3.1}
 r_{c(N)} (t_N + \delta - t) \int_0^t \int_0^\omega H_i(x,s) \epsilon(x,s) \, dx \, ds &= \\
\tag{3.2}
- \int_0^{t_{N+1} + \delta} \int_0^\omega H_i(x,s) \epsilon(x,s) \, dx \, ds
\end{align*}
\]

It is not necessary to introduce chemotherapy at time stability time point i.e at \( t_N + \delta \) and chemotherapy could be introduced at time \( t_j + \delta \) for \( j = 1, 2, \ldots, N \) after the initial phase of detection of worms during \((0, t)\). By taking all such populations and population weights \( k_j(x, t) \), we obtain below equation, which we call equation for the nested growth of the worm population.

\[
\sum_{j=1}^N \left[ \frac{r_{j(c)}(t_j + \delta - t)}{k_j(x, t)} \left\{ \int_0^t \int_0^\omega H_i(x,s) \epsilon(x,s) \, dx \, ds \right\} \right] + \\
\sum_{j=1}^N \int_0^{t_j + \delta - t} \int_0^\omega H_i(x,s) \epsilon(x,s) \, dx \, ds = 0
\]

\[
\tag{3.3}
\]

**Theorem 5.** \( F_2 \) is a measurable function, where \( F_2 \) is defined as,

\[
\tag{3.4}
F_2 : (-\infty, t_x + \delta) \rightarrow \sum_{j=1}^N \int_0^{t_j + \delta - t} \int_0^\omega H_i(x,s) \epsilon(x,s) \, dx \, ds
\]

for \( x = 1, 2, 3, \ldots \) and \( \delta > 0 \).
**Proof.** We can prove this theorem with similar arguments as in the proof of theorem [1].

4. Discussion

We have derived formulae which can be used to compute the worm densities within a host and within the affected community. We have proved theoretical results of the functional forms derived for the net reproduction rates. Theoretical results derived indicates that the carrying capacities of worms within a host are measurable functions, which will help to understand bounds of the worm densities.

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