Supplementary information

A  The single hit model for infection

A.1  Exposure

Simplest we can assume for exposure is a Poisson sample from a suspension of strength $C$, sample volume $V$

$$\text{Prob}(n|C, V) = \frac{(CV)^n}{n!}e^{-CV} \quad (A.1)$$

Where $CV$ is the (expected) dose, the probability of exposure

$$\text{Prob}(n \geq 1|C, V) = 1 - \text{Prob}(n = 0|C, V) = 1 - e^{-CV} \quad (A.2)$$

A.2  Infection: fixed $p_m$

Suppose we have a host who has ingested $n$ pathogens, and all pathogens have equal survival probabilities $p_m$, then the probability that $k$ pathogens survive is

$$\text{Prob}(k|n, p_m) = \binom{n}{k} p_m^k (1 - p_m)^n \quad (A.3)$$

if survival is independent.

Infection corresponds to survival of at least 1 pathogen (a ‘single hit’) with probability

$$\text{Prob}(k \geq 1|n, p_m) = 1 - \text{Prob}(k = 0|n, p_m) = 1 - (1 - p_m)^n \quad (A.4)$$

The marginal probability of infection therefore is

$$\text{Prob}(k \geq 1|C, V, p_m) = \sum_{n=1}^{\infty} \frac{e^{-CV}(CV)^n}{n!} [1 - (1 - p_m)^n] \quad (A.5)$$

which can be simplified, by first taking the sum from $n = 0$

$$P_{inf}(C, V, p_m) = 1 - \sum_{n=0}^{\infty} \frac{e^{-CV}(CV)^n}{n!}(1 - p_m)^n \quad (A.6)$$

and noting that

$$\sum_{n=0}^{\infty} \frac{e^{-CV(1-p_m)}(CV(1 - p_m))^n}{n!} = 1 \quad (A.7)$$
so that
\[ P_{\text{inf}}(C, V, p_m) = 1 - e^{-CV} e^{CV(1-p_m)} = 1 - e^{-p_m CV} \quad \text{(A.8)} \]

### A.3 Infection: heterogeneous \( p_m \)

In case of heterogeneity in \( p_m \), described by a Beta pdf
\[ f(p_m|\alpha, \beta) = \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha)\Gamma(\beta)} p_m^{\alpha-1}(1-p_m)^{\beta-1} \quad \text{(A.9)} \]

the marginal dose response relation for infection becomes
\[ P_{\text{inf}}(C, V|\alpha, \beta) = \int_{p_m=0}^{\infty} f(p_m|\alpha, \beta) \left(1 - e^{-p_m CV}\right) \]
\[ \text{which can be written as a (Kummer) confluent hypergeometric function} \]
\[ P_{\text{inf}}(C, V|\alpha, \beta) = {}_1F_1(\alpha, \alpha + \beta; -CV) \quad \text{(A.11)} \]

Furumoto and Mickey [23] have shown how this relation can be simplified into
\[ P_{\text{inf}}(C, V|\alpha, \beta) = 1 - \left(1 + \frac{CV}{\beta}\right)^{-\alpha} \quad (\beta \gg 1; \alpha \ll \beta) \quad \text{(A.12)} \]

### B Heterogeneity in the dose

#### B.1 Exposure, dose variable

In outbreak situations the dose often is inappropriately characterized by a simple Poisson model. Instead, we may use a Poisson-Gamma mixture to model extra-Poisson variation. The observed number is again a Poisson sample
\[ \text{Prob}(n|C, V) = \frac{(C \cdot V)^n}{n!} e^{-C \cdot V} \quad \text{(A.13)} \]

Where \( C \cdot V \) is the (expected) dose. The concentration \( C \) now is assumed to have a Gamma density
\[ g(C|\rho, \lambda) = \frac{\lambda^{-\rho}}{\Gamma(\rho)} C^{\rho-1} e^{-C/\lambda} \quad \text{(A.14)} \]
with shape parameter $\rho$ and scale parameter $\lambda$. The marginal distribution of the counts then is negative binomial

$$\text{Prob}(n|\rho, \lambda, V) = \frac{\Gamma(n + \rho)}{n!\Gamma(\rho)} \left( \frac{1}{1 + \lambda V} \right)^{\rho} \left( 1 - \frac{1}{1 + \lambda V} \right)^n$$  \hspace{1cm} (A.15)

And the probability of exposure is

$$\text{Prob}(n \geq 1|\rho, \lambda, V) = 1 - \text{Prob}(n = 0|\rho, \lambda, V) = 1 - (1 + \lambda V)^{-\rho} \hspace{1cm} (A.16)$$

which may be written as

$$\text{Prob}(n \geq 1|\rho, \tilde{c}, V) = 1 - \left( 1 + \frac{\tilde{c} V}{\rho} \right)^{-\rho} \hspace{1cm} (A.17)$$

where $\tilde{c} = \lambda \rho$ is the mean concentration.

## B.2 Infection, dose variable, fixed $p_m$

The marginal probability of infection can be found as above

$$\text{Prob}(k \geq 1|\rho, u, p_m) = \sum_{n=1}^{\infty} \frac{\Gamma(n + \rho)}{n!\Gamma(\rho)} u^{\rho} (1-u)^n \left[ 1 - (1 - p_m)^n \right]$$  \hspace{1cm} (A.18)

substituting $u = 1/(1 + \lambda V)$.

This can be simplified by first taking the sum from $n = 0$

$$P_{\text{inf}}(\rho, u, p_m) = 1 - \sum_{n=0}^{\infty} \frac{\Gamma(n + \rho)}{n!\Gamma(\rho)} u^{\rho} (1-u)^n (1-p_m)^n \hspace{1cm} (A.19)$$

If we note that

$$\sum_{n=0}^{\infty} \frac{\Gamma(n + \rho)}{n!\Gamma(\rho)} [1 - (1 - u)(1 - p_m)]^{\rho} [(1-u)(1-p_m)]^n = 1 \hspace{1cm} (A.20)$$

then

$$P_{\text{inf}}(\rho, u, p_m) = 1 - \left( \frac{1 - (1 - u)(1 - p_m)}{u} \right)^{-\rho} \hspace{1cm} (A.21)$$

or

$$P_{\text{inf}}(\rho, \lambda, V, p_m) = 1 - (1 + \lambda V p_m)^{-\rho} \hspace{1cm} (A.22)$$

$$P_{\text{inf}}(\rho, \tilde{c}, V, p_m) = 1 - \left( 1 + \frac{\tilde{c} V}{\rho} p_m \right)^{-\rho} \hspace{1cm} (A.23)$$
B.3 Infection: heterogeneous pm

In case of heterogeneity in pm, described by a Beta pdf the marginal dose response relation for infection becomes

\[ P_{\text{inf}}(\rho, \tilde{c}, V|\alpha, \beta) = \int_{p_m=0}^{\infty} f(p_m|\alpha, \beta) \left( 1 - \left( 1 + \frac{\tilde{c}V}{\rho p_m} \right)^{-\rho} \right) \]  \hspace{1cm} (A.24)

which can be written as another hypergeometric function

\[ P_{\text{inf}}(\rho, \tilde{c}, V|\alpha, \beta) = _2F_1(\alpha, \rho, \alpha + \beta; -\tilde{c}V/\rho) \]  \hspace{1cm} (A.25)

C Sexual reproduction and infection

Suppose we have a host who has ingested of n pathogens, of whom k females (♀) and n – k males (♂).

Infection can occur if and only if 1 or more ♀ pathogens and 1 or more ♂ pathogens survive. Suppose ♀ and ♂ pathogens have equal survival probabilities pm, then the probability that 1 or more ♀ pathogens survive is

\[ p_\text{♀} = 1 - (1 - p_m)^k \]  \hspace{1cm} (A.26)

and the probability that 1 or more ♂ pathogens survive

\[ p_\text{♂} = 1 - (1 - p_m)^{n-k} \]  \hspace{1cm} (A.27)

Suppose ♀ and ♂ pathogens are present in proportions r and 1 – r (r is the sex ratio: the fraction ♀). Then the numbers of ♀ and ♂ pathogens are binomial

\[ \text{Prob}(k\text{♀}, n - k\text{♂}|r) = \binom{n}{k} r^k (1 - r)^{n-k} \]  \hspace{1cm} (A.28)

and the probability of infection is

\[ P_{\text{inf}}(n|r) = \sum_{k=0}^{n} \binom{n}{k} r^k (1 - r)^{n-k} \left[ 1 - (1 - p_m)^k \right] \left[ 1 - (1 - p_m)^{n-k} \right] \]  \hspace{1cm} (A.29)

which can be shown to equal

\[ P_{\text{inf}}(n|r) = 1 + (1 - p_m)^n - [1 - p_m(1 - r)]^n - (1 - p_m r)^n \]  \hspace{1cm} (A.30)

C.1 Exposure

Simplest we can assume for exposure is Poisson sample, from a suspension of strength C, sample volume V. The exposure dose response relation (de-
scribing the probability of having ingested at least 1 ♀ and 1 ♂ organism can be written as a linear combination of three terms

\[ \text{Prob}(\varphi \geq 1, \sigma \geq 1|r, C, V) = 1 - e^{-(1-r)CV} - e^{-rCV} \] (A.31)

simply by taking the terms of equation (A.30) for \( p_m = 1 \).

For heterogeneous exposure we can again assume a Poisson–Gamma mixture, leading to an exposure dose response

\[ \text{Prob}(\varphi \geq 1, \sigma \geq 1|r, \rho, \tilde{c}, V) = 1 - \left(1 + \frac{\tilde{c}V}{\rho} (1 - r)\right)^{-\rho} - \left(1 + \frac{\tilde{c}V}{\rho} r\right)^{-\rho} \] (A.32)

C.2 Infection, fixed \( p_m \)

For Poisson exposure and fixed “hit” probability \( p_m \) we get

\[ P_{\text{inf}}(C \cdot V|p_m, r) = 1 + e^{-C \cdot V p_m} - e^{-C \cdot V p_m(1-r)} - e^{-C \cdot V p_m r} \] (A.33)

analogous to the exponential dose response relation for asexually reproducing pathogens.

For Poisson–Gamma exposure the relation is

\[ P_{\text{inf}}(\rho, \tilde{c}, V|p_m, r) = 1 + \left(1 + \frac{\tilde{c}V}{\rho} p_m\right)^{-\rho} - \left(1 + \frac{\tilde{c}V}{\rho} p_m(1 - r)\right)^{-\rho} - \left(1 + \frac{\tilde{c}V}{\rho} p_m r\right)^{-\rho} \] (A.34)

C.3 Infection, variable \( p_m \)

The model for heterogeneous \( p_m \) can again be written as a linear combination of hypergeometric relations (see equation (A.11)).

\[ P_{\text{inf}}(C \cdot V|\alpha, \beta, r) = 1 + \text{1} F_1 [\alpha, \alpha + \beta; -C \cdot V] \]
\[ - \text{1} F_1 [\alpha, \alpha + \beta; -C \cdot V(1 - r)] - \text{1} F_1 [\alpha, \alpha + \beta; -C \cdot V r] \] (A.35)

In case the dose also has extra–Poisson variation, the resulting dose response relation is a combination of the functions in equation (A.25)

\[ P_{\text{inf}}(\rho, \tilde{c}, V|\alpha, \beta, r) = 1 + 2 \text{1} F_1 (\alpha, \rho, \alpha + \beta; -\tilde{c}V/\rho) \]
\[ - 2 \text{1} F_1 (\alpha, \rho, \alpha + \beta; -\tilde{c}V(1 - r)/\rho) - 2 \text{1} F_1 (\alpha, \rho, \alpha + \beta; -\tilde{c}V r/\rho) \] (A.36)
D Hierarchical dose response model

The likelihood is binomial: for each incident $K$ out of $N$ subjects exposed to a dose $D = g(\rho, \tilde{c}, V)$ have been observed to be affected.

Given the hit theory dose response function a single observed attack rate may allow prediction of the dose response relation [2]. We want to incorporate multiple attack rates at various doses. However, such an approach inevitably involves an additional level of biological variation. While a different human population similar in age and health status might have similar susceptibility, a different isolate of the pathogen is likely to have completely different infectivity, if only because of a different history (different food vehicle, different previous host, . . . ). Therefore, analysis of data from different outbreaks requires a hierarchical model (Figure A1).

Figure A1: Two-level model for dose response assessment of several outbreaks, each with their separate pathogen isolates and possibly susceptibility distributions ($N_{\text{outbreaks}}$ = number of outbreaks; $n_{\text{doses}}(j) = 1$ for all outbreaks except the first [5], where $n_{\text{doses}}(1) = 2$).

If there are $j$ observations in group $i$ and the dose response model

$$f(d|\theta)$$

with parameter vector $\theta$ the contribution of group $i$ to the likelihood is

$$\ell_i(\theta) = \prod_j [f(d_{i,j}|\theta)]^{k_{i,j}} [1 - f(d_{i,j}|\theta)]^{n_{i,j} - k_{i,j}}$$

all observations in group $i$ share the same parameter set $\theta$

When the joint distribution of $\theta$ over all groups is

$$h(\theta|\Xi)$$

A6
with hyperparameter vector $\Xi$, the marginal likelihood can be written

$$
\ell_i(\Xi) = \int_{\theta} \ell_i(\theta) h(\theta|\Xi) d\theta \\
= \int_{\theta} [f(d_{i,j}|\theta)]^{k_{i,j}} [1 - f(d_{i,j}|\theta)]^{n_{i,j} - k_{i,j}} h(\theta|\Xi) d\theta \quad (A.40)
$$

and the hierarchical likelihood, to be evaluated, is

$$
L(\Xi) = \prod_i \ell_i(\Xi) \quad (A.41)
$$

The dose is characterized by the expected concentration of pathogens, and their variation, characterized by the Gamma shape parameter $\rho$. These two parameters are estimated separately using whatever information was available in the outbreak reports, usually quantiles characterizing location and spread of intake of contaminated unheated (or inadequately heated) meat.

Infectivity parameters are transformed as in [2]: since we have only one data point per outbreak, the parameters $(\alpha, \beta)$ of the Beta Poisson model are highly correlated: parameter estimation is improved by transformation to

$$
u = \frac{\alpha}{\alpha + \beta} \\
v = 10 \log(\alpha + \beta) \quad (A.42)
$$

so that we are estimating the mean value ($u$) of the Beta distribution for $p_{mn}$ and a quantity that is inversely related to its variance (for very large positive values of $v$ the variance tends to zero). Further $u$ is logit–transformed and $v$ is log–transformed

$$
w = \log[u/(1 - u)] \\
z = \log(v) \quad (A.43)
$$

We use normal priors for $w$ and $z$ (mean $\rho$, standard deviation $\lambda$). Uncorrelated non–informative normal (-8,8) hyperpriors were taken for the means of $w$ and $z$ ($\rho$), gamma (0.001,1000) priors were taken for the standard deviations of $w$ and $z$ ($\lambda$).

Posterior parameter samples have been obtained using the Metropolis-Hastings algorithm, implemented in Mathematica [2].
### Additional outbreak information

<table>
<thead>
<tr>
<th>City/village name</th>
<th>year</th>
<th>nr. cases</th>
<th>parasite strain</th>
<th>asympt. cases</th>
<th>type of meat</th>
<th>cons. g/pers.</th>
<th>cons. larv/g</th>
<th>cons. abroad</th>
<th>meat import</th>
<th>animal import</th>
<th>local</th>
<th>reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Perpignan</td>
<td>2001</td>
<td>1</td>
<td>NA</td>
<td>NA</td>
<td>pork</td>
<td>NA</td>
<td>NA</td>
<td>yes</td>
<td></td>
<td></td>
<td>CNR</td>
<td>Trichinella</td>
</tr>
<tr>
<td>Paris</td>
<td>2001</td>
<td>1</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>yes</td>
<td></td>
<td></td>
<td>CNR</td>
<td>Trichinella</td>
</tr>
<tr>
<td>Quillan (Aude)</td>
<td>2002</td>
<td>4</td>
<td>NA</td>
<td>NA</td>
<td>Wild Boar</td>
<td>NA</td>
<td>NA</td>
<td>yes</td>
<td></td>
<td></td>
<td></td>
<td>CNR Trichinella</td>
</tr>
<tr>
<td>Villeneuve d’Entraunes (Alpes Maritimes)</td>
<td>2003</td>
<td>6</td>
<td>T. britovi</td>
<td>1</td>
<td>Wild Boar</td>
<td>150</td>
<td>3</td>
<td>yes</td>
<td></td>
<td></td>
<td>yes</td>
<td>7</td>
</tr>
<tr>
<td>Rouen (Seine Maritime)</td>
<td>2004</td>
<td>1</td>
<td>T. nativa</td>
<td>0</td>
<td>Black Bear</td>
<td>300</td>
<td>250</td>
<td>yes</td>
<td></td>
<td></td>
<td>CNR Trichinella</td>
<td></td>
</tr>
<tr>
<td>Martigues (Bouches du Rhône)</td>
<td>2004</td>
<td>1</td>
<td>T. britovi</td>
<td>0</td>
<td>Jackal</td>
<td>NA</td>
<td>NA</td>
<td>yes</td>
<td></td>
<td></td>
<td>[24]</td>
<td></td>
</tr>
<tr>
<td>Rouen (Seine maritime)</td>
<td>2005</td>
<td>3</td>
<td>NA</td>
<td>6</td>
<td>pork</td>
<td>NA</td>
<td>NA</td>
<td>yes</td>
<td></td>
<td></td>
<td>CNR Trichinella</td>
<td></td>
</tr>
<tr>
<td>Orléans (Loiret), Narbonne (Aude)</td>
<td>2005</td>
<td>17</td>
<td>T. nativa</td>
<td>8</td>
<td>Black Bear</td>
<td>150</td>
<td>300</td>
<td>yes</td>
<td>yes</td>
<td></td>
<td>[25]</td>
<td></td>
</tr>
<tr>
<td>Orel (31)</td>
<td>2006</td>
<td>2</td>
<td>NA</td>
<td>NA</td>
<td>Wild Boar</td>
<td>NA</td>
<td>NA</td>
<td>yes</td>
<td></td>
<td></td>
<td>CNR</td>
<td>Trichinella</td>
</tr>
<tr>
<td>Nans les Pins (Var)</td>
<td>2006</td>
<td>3</td>
<td>T. spiralis</td>
<td>NA</td>
<td>Wild Boar</td>
<td>200</td>
<td>40</td>
<td>yes</td>
<td></td>
<td></td>
<td>CNR Trichinella</td>
<td></td>
</tr>
<tr>
<td>Collobrières (Var)</td>
<td>2006</td>
<td>4</td>
<td>T. britovi</td>
<td>6</td>
<td>Wild Boar</td>
<td>150</td>
<td>5–10</td>
<td>yes</td>
<td></td>
<td></td>
<td>CNR Trichinella</td>
<td></td>
</tr>
</tbody>
</table>

Table A1: Data from France provided by J. Dupouy–Camet (May 2007).