Bayesian modelling of *Escherichia coli* O157:H7 dose response incorporating age as a covariable

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NCSC 2010, 09/28/2010



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## Escherichia coli O157 :H7

- a Shiga toxin-producing Escherichia coli
- linked to a large number of human infections due to consumption of contaminated food products (especially ground beef)
- potential severe clinical manifestations : hemolytic uremic syndrome (HUS)
- most common cause of acute renal failure in children, preferentially among children under 10 years

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### Dose-response characterization

From which data?

- experimental data
  - on animals? Difficult to extrapolate
  - on human volunteers? Low susceptibility and ethically not reasonable
  - on children (higher susceptibility)? Ethically not reasonable
- outbreak data and surveillance data disparate data with much uncertainty
  ⇒ appropriate methods need to be developed bayesian methods may be of interesting in such a case

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### Recent works

• Teunis et al., 2008

A meta-analysis on 8 outbreaks :

hierarchical model linking the risk of illness (diarrhea cases) to the ingested dose

(estimation of parameters by bayesian inference)

• Delignette-Muller and Cornu, 2008

An analysis of one well-documented french outbreak : two models linking the risk of severe complication (HUS cases) to the ingested dose for two age classes ("< 5 years" and "5-10 years")

(estimation of parameters by bayesian inference).

Greater susceptibility in the class "< 5 years".

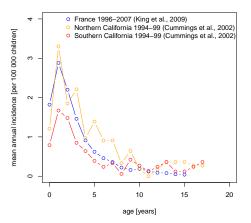
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## Objective

To build a unique *E. coli* O157 :H7 dose-response model for children under 16 years incorporating age as a covariable, from outbreak data used in our previous work and surveillance data.

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## Surveillance data



Incidence of HUS cases

Decrease of susceptibility with age with a lower value for babies certainly due to a lower exposure before food diversification.

## Outbreak data

Largest community-wide outbreak of *E. coli* O157 :H7 in France, associated with consumption of contaminated frozen beef burgers in households.

• Estimated total number of contaminated consumed patties : N = 2155

(information from the distributor)

• Estimation of ingested dose : depends on the initial contamination level (*C*[*cfu*.*g*<sup>-1</sup>]) and of the consumption preference (*CP*) and the serving size (*S*)

A challenge : to incorporate age as a covariable in the estimation of all parameters of the exposure model ( $N_{age}$ ,  $CP_{age}$ ,  $S_{age}$ ).

### Exposure model

#### Ingested dose D for one consumer

$$D_{age} \sim \textit{Poisson}(\textit{C} imes \textit{S}_{age} imes 10^{-R_{age}})$$

 $R_{age}$  depending on  $CP_{age}$ 

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- C : initial mean contamination level on frozen ground beef (*cfu.g*<sup>-1</sup>)
- S<sub>age</sub> : serving size (g)
- R<sub>age</sub> : number of decimal reduction due to cooking
- *CP<sub>age</sub>* : consumption preference (raw, rare, medium or well-done)

## Initial mean contamination level C

Estimated from microbial detection and counts performed on 22 frozen patties sampled from the contaminated batch Bayesian estimation :  $5.8 \ cfu.g^{-1}$ 95% credibility interval : [3.2; 9.4]

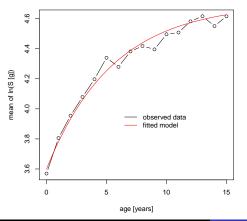
Modelling of the initial mean contamination level

 $C = 5.8 \ cfu.g^{-1}$ 

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# Serving size $S_{age}$ (1)

Consumption data (890 ground beef intakes by children under 16 years old) : strong effect of age on mean of ln(S) distribution and no significant effect on standard deviation



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# Serving size $S_{age}$ (2)

Modelling of the serving size distribution by a lognormal distribution,

with the mean described as a function of age.

Estimation of parameters from consumption data, using bayesian inference with non-informative priors.

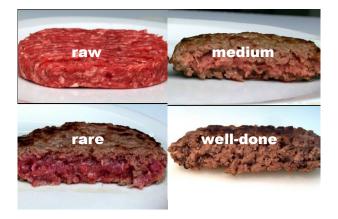
#### Modelling of the serving size

$$ln(S_{age}) \sim N(\mu_{age}, \sigma)$$
  
with  $\mu_{age} = \mu_0 + \Delta \mu \times (1 - e^{-\beta \times age})$   
with  $\mu_0 = 3.6$ ,  $\Delta \mu = 1.1$ ,  $\beta = 0.18$  and  $\sigma = 0.40$ 

A (1) > A (2) > A (2) > (1)

## Consumption preference $CP_{age}(1)$

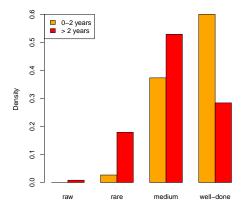
Estimation of the *CP* distribution from a consumer survey (on 589 children under 16 years old) based on 4 photos of ground beef patties illustrating different consumption preferences.



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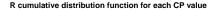
## Consumption preference $CP_{age}$ (2)

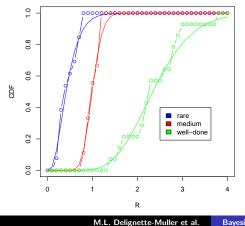
Two distributions : one for children between 0 and 2 years old and one for children over 2 years old.



## Number of decimal reduction due to cooking $R(CP_{age})$

Characterization of R distribution for each cooking preference from experimental data by gamma distributions (36 ground beef patties experimentally contaminated and cooked)





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# Number of patties consumed in each age group : $N_{age}$

**Proportions**  $p_{age}$  of total ground beef servings consumed in each age group (length 1 year) estimated from **mean numbers of patties consumed per year** and **demographic data** From consumer surveys (890 ground beef intakes by children under 16 years old and 1288 on adults and children over 16 years), **Mean ground beef consumption** :

- under one year old : 13.6 patties per year,
- from one year old to 15 years old : 35.8 patties per year.
- over 15 years old : 23.3 patties per year.

#### Estimated numbers of intakes per age class during the outbreak

$$\begin{split} N_{age} &= p_{age} \times N \text{ with } N = 2155 \\ N_{age} &= [7; 38; 38; 39; 39; 37; 37; 36; 37; 36; 36; 36; 37; 38; 39] \\ \text{for } age &= 0 \text{ to } 15 \text{ years old} \\ \text{and } N_{>15years} &= 1587 \end{split}$$

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#### Dose response model

#### Simple choice of a single-hit model,

characterized by the parameter r (probability of HUS from a single ingested cell), here defined as an exponential function of age (from the trend observed on surveillance data)

#### Modelling of the HUS outcome (HUS or not) for chidren

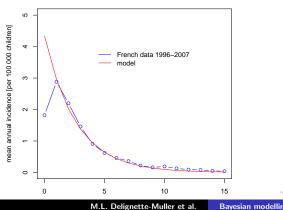
 $HUS_{age} \sim Bernouilli(HUSrisk_{age})$  $HUSrisk_{age} = 1 - (1 - r_{age})^{D_{age}}$  $D_{age}$  defined in exposure model and  $r_{age} = r_0 \times e^{-k \times age}$  for age from 0 to 15 years old

Two parameters to estimate :  $r_0$  and k.

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## Preliminar estimation of k from surveillance data

Estimation of the parameter of the exponential trend from french surveillance data excluding babies (< 1 year), and assuming a common exposition on other age groups : k = 0.38 (95% credibility interval [0.33; 0.43])



Incidence of HUS cases

et al. Bayesian modelling of E. coli O157:H7 dose response

## Estimation of k and $r_0$ from outbreak data

Bayesian estimation from outbreak data using the previously developped exposure model to describe the dose D as a function of age, with

- informative prior for k : the posterior distribution from the previous bayesian estimation
- non-informative prior for  $r_0$

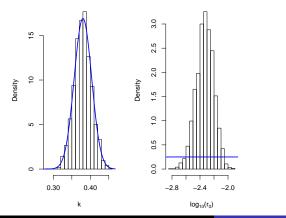
#### Estimated parameters

k = 0.38 (95% credibility interval [0.33; 0.43]) $log_{10}(r_0) = -2.33 (95\% \text{ credibility interval } [-2.58; -2.09])$ 

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### Posterior distributions of parameters

Comparison of posterior distributions (histograms) to prior ones No more information on k, but its ponctual estimation is robust to prior : unchanged using a uniform non-informative prior for k



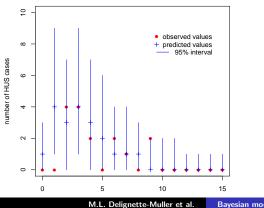
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## Goodness-of-fit of the model

Comparison between observed numbers of HUS cases and predicted ones with credibility intervals :

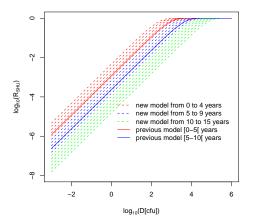
One observed value outside the 95% credibility interval (the consumption of ground beef may be overestimated in our model for children of one year old).





### Comparison with previously proposed models for HUS risk

Agreement between the HUS new model and previous ones. The new model describes a larger variability due to age and a greater risk for younger children in each age group.



HUS risk as a function dose in log-log scale

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## Conclusion

- The proposed model was built on only one dataset and with some oversimplified hypotheses and should thus be validated under other data (but HUS data are scarce).
- It is the first attempt to incorporate age as a covariable in a dose-response model for microbial risk assessment in food.
- Bayesian inference was performed using JAGS (developed by Martyn Plummer).

The great flexibility offered by bayesian tools such as JAGS and WinBUGS is very interesting in dose-response modelling using outbreak data, especially to incorporate non trivial models for the dose.

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