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Uncertainty and variability in Bayesian inference for dietary risk: Listeria in RTE fish

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Listeria in Ready To Eat (RTE) Fish:
Cold Smoked Salmon & Salt Cured Salmon, (CSS/SCS).

(1) Concentration data & growth model

(2) Consumption data

(3) Bayesian inference

(4) Dose-response model

(5) Epidemiologic data: reported cases & population data, age groups.

(1) Variation between products μ_0
+ growth: μ_t = growth(μ_0), t days

…

https://www.cookipedia.co.uk/recipes_wiki/File:Ikea_Gravadllax.jpg

q = prevalence of positive CSS/SCS ≈ 22%

$\mu_0^1 \quad \mu_0^2 \quad \mu_0^3$ Log-concentrations μ_0^n

~ N(μ,σ^2)
43 values,
179 were <LOQ

$$\mu_0^1 \to \mu_t^1 \qquad \mu_0^2 \to \mu_t^2 \qquad \mu_0^3 \to \mu_t^3 \qquad \mu_0^n \to \mu_t^n$$

$\mu_t^1 \quad \mu_t^2 \quad \mu_t^3 \quad \mu_t^n$ Logistic growth model

(2) Variation between consumptions: 48h food diaries

- Log-serving sizes $\sim N(\eta,\delta^2)$.
- Consumption on a day, given consumption on previous day:

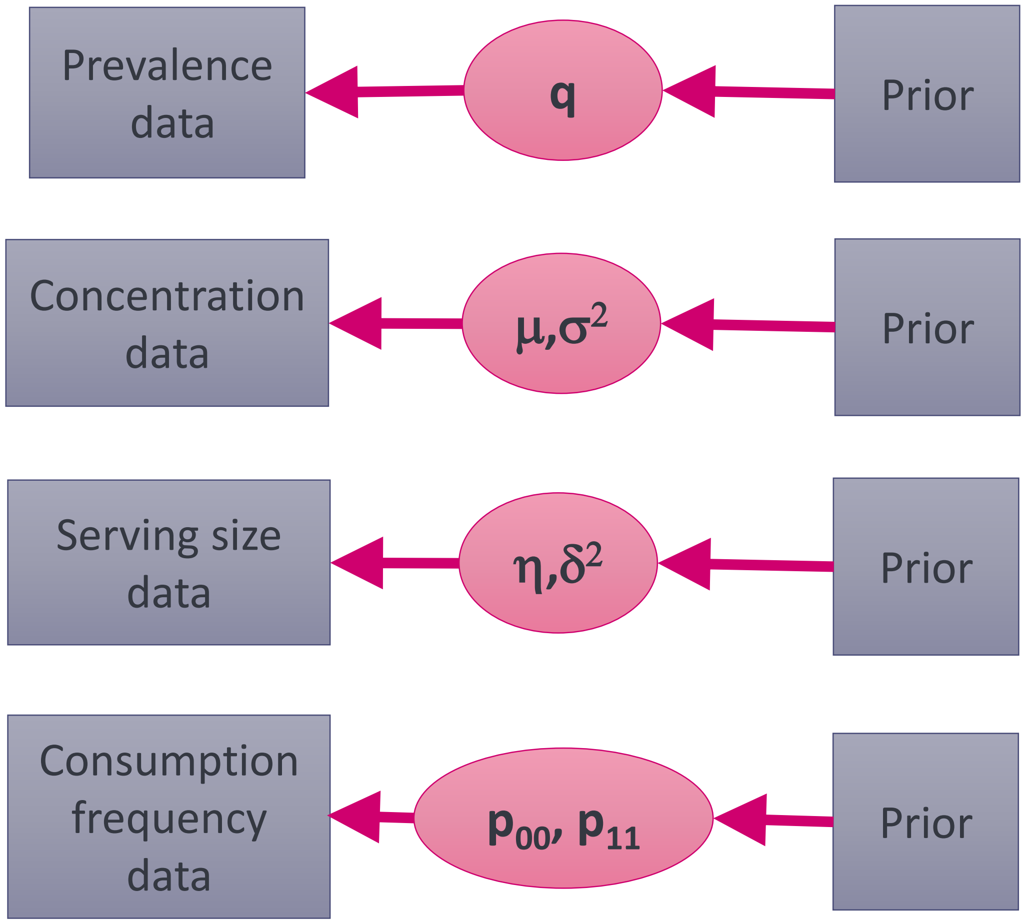
  $P(\text{yes}|\text{yes})=p_{11}$. Likewise p_{00}.
- Consumption on a day: two-state Markov chain stationary probability p_1.

Each of the above have uncertain parameters:

- Core population parameters: $\theta = (q,\mu,\sigma^2,\eta,\delta^2,p_{00},p_{11})$.

(3) Bayesian inference: P(θ|data) uncertainty of population parameters

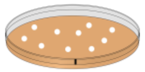
- Listeria prevalence in CSS/SCS   (q)
  - Uncertain due to sample size, method accuracy.
- Concentration distribution: (μ,σ^2)
  - Uncertain due to sample size, and many values <LOQ.
- Serving size distribution: (η,δ^2)
  - Uncertain due to sample size, stratification by age.
- Consumption frequencies: transition probabilities (p_{00}, p_{11})
  - Uncertain due to rare occasions, stratification by age.



(4) Conditional dose-response probability, given consumption of contaminated CSS/SCS & parameter **r**

- $P(\text{illness} \mid \boldsymbol{r}, E(d)) = 1 - \exp\big(-\boldsymbol{r}E(d)\big)$ $\{d \sim \text{Poisson}\big(E(d)\big)\}$
- $E(d) = \exp(\mu_t^* + s^*) = \exp(g_t(\mu_0^*) + s^*)$

- μ_t^* = predicted log-concentration on day t, $\mu_t^* = g_t(\mu_0^*)$, predicted initial value μ_0^*.



- s^* = predicted log-consumption amount, if consuming.

- μ_0^*, s^* predicted from the distributions: $f(\mu_0^* \mid \mu, \sigma^2)$, $f(s^* \mid \eta, \delta^2)$,
  conditional on the uncertain $\mu, \sigma^2, \eta, \delta^2$

(4) Conditional probability to acquire illness, allowing repeated consumptions

- Probability to start consuming, purchase of CSS/SCS.
- Probability to continue next day, same product.
- Chance of acquiring illness conditionally on ’still at risk’ & exposure on a day.
- **Total probability of illness**, over several days, allowing repeated use:

$$P(\text{illness }|r,\theta) =$$

$$(1-p_1)p_{01}q\left[P_1(\text{ill}|r,\mu,\sigma,\eta,\delta)+\sum_{t=2}^{7}\prod_{i=1}^{t-1}(1-P_i(\text{ill}|r,\mu,\sigma,\eta,\delta))p_{11}^{t-1}\,P_t(\text{ill}|r,\mu,\sigma,\eta,\delta)\right]$$

- (Age group specific).

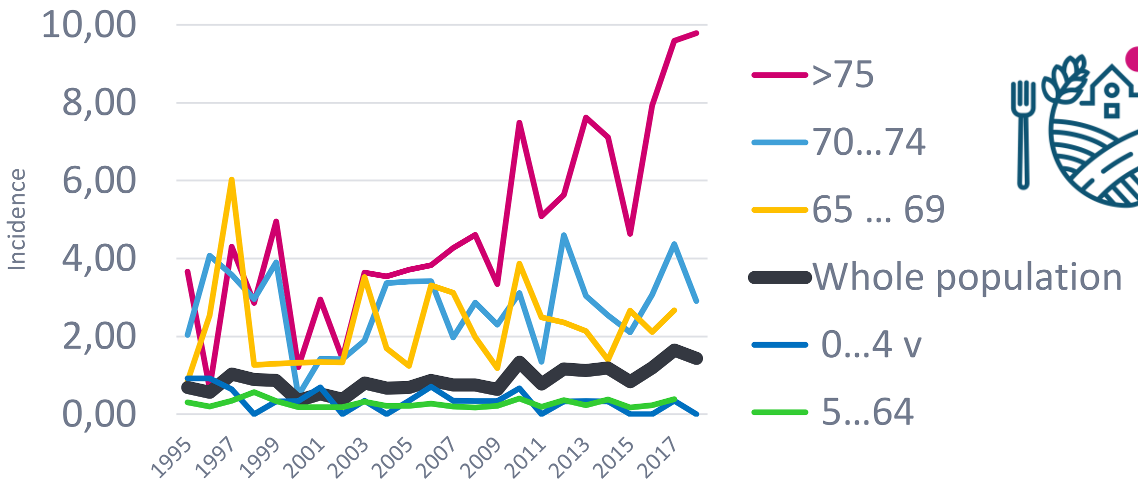
(4) Population illness probability (risk), individual variability integrated

- Accounting for individual variability in μ_t^*, s^* requires integration:
- $P_t(\text{illness} \mid r, \mu, \sigma, \eta, \delta) = E(P_t(\text{illness} \mid r, g_t(\mu_0^*), s^*)) =$
  $\iint_{-\infty,-\infty}^{\infty,\infty} (1 - \exp(-r \exp(g_t(\mu_0^*) + s^*)))\, f(\mu_0^* \mid \mu, \sigma) f(s^* \mid \eta, \delta)\, d\mu_0^*\, ds^*$

- This may have no analytic solution, but a Monte Carlo approximation:

- $\hat{P}_t(\text{illness} \mid r, \mu, \sigma, \eta, \delta) \approx \sum_{k=1}^{K} (1 - \exp(-r \exp(g_t(\mu_0^{*k}) + s^{*k})))/K$
  where μ_0^{*k}, s^{*k} are sampled from $f(\mu_0^* \mid \mu, \sigma)$ and $f(s^* \mid \eta, \delta)$.

(5) Epidemiologic data



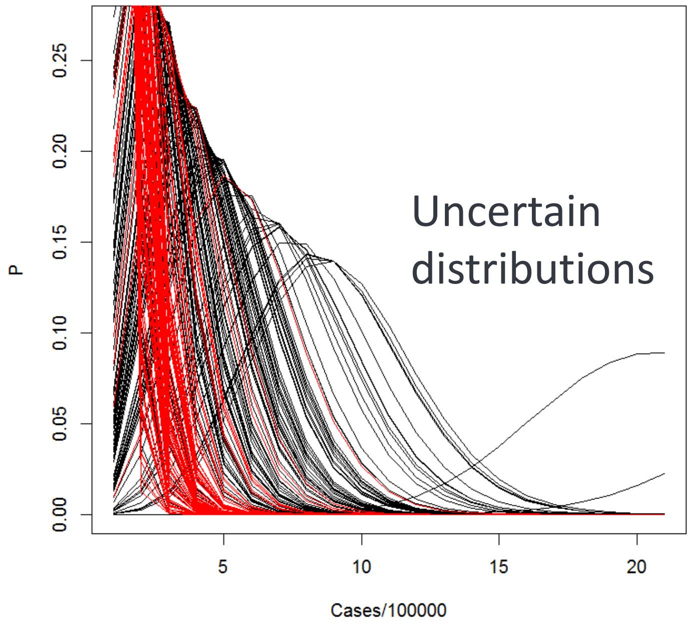
- Unknown dose-response parameter **r** for specific age groups.
  - Uncertain due to lack of detailed epidemiological data, stratification by age.
- Using the reported cases as epidemiological data in the model.
  - Proportion of cases due to CSS/SCS? $0 \leq \text{cases}_{\text{age}} \leq \text{total}_{\text{age}}$.
  - Could use source attribution modelling, expert opinion, scenario assumption.
    - Reported cases around **12** in both 65-74 and 25-64 year olds, annually.
    - Population sizes about **470,000** vs **2,900,000.**
    - So we know *something* about incidence. → Use this in the model.
  - Actually, published estimates of r rely on some back-calculations, or 'adjusting' predictions with reported incidence.

(5) Full model Bayesian inference

- Full posterior density from the model, all parameters r, θ, formally:

$$P(r, \theta | \text{concentration \& consumption data, cases, popula}) \propto$$
$$\hat{P}(\text{cases}|r, \theta, \text{popula}) P(\text{concentration \& consumption data}|\theta) P(r, \theta)$$

- Where $\hat{P}(\text{cases}|r, \theta, \text{popula})$=Poisson() is based on Monte Carlo approximation of the population risk within each MCMC iteration.
  - Intractable likelihood function.
  - Also denoted ”2D” Monte Carlo, or MC within MCMC.
  - Increases computational burden.



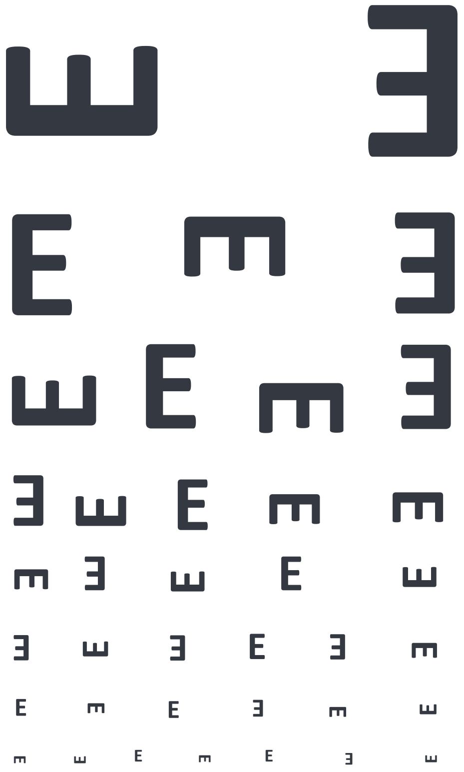
Unquantified uncertainty

- Growth model with fixed parameters?
  - No home storage data.
  - Assumed temperatures as scenarios.
- Unevenly distributed, clustered microbes, mixing?
  - No data.
- Variable susceptibility among consumers?
  - Can only relate exposure and incidence data by main age-groups.
- Unknown size of purchased packages?
  - Total number of servings?
- Majority of consumptions were at home, but not all.
- Not all cases due to CSS/SCS, although major risk. Source attribution, under reporting.

Quantify as much uncertainty & variability as you can!

(while keeping it simple, feasible, evidence based…)

- This was easy →
- This was possible →
- It gets harder here →
- … …Uhhhh →



← but some of these *could still be* important.

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Thank you!

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