

# *L. monocytogenes* in cold-smoked salmon

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The objective of this case study is to assess the risk of invasive listeriosis from consumption of cold-smoked salmon in France.

The process of interest lays from the end of the production line in the factory, when the cold-smoked salmon is vacuum-packed, to the consumption.

The data and the model are adapted to illustrate the use of ‘mc2d’: the results will not and *should not* be interpreted as an assessment of the actual risk of listeriosis from consumption of cold-smoked salmon.

Interested readers could refer to \cite{POUILLLOT-2007} and \cite{POUILLLOT-2009} for a complete risk assessment on that issue.

The model will be developed in a first section, without considering variability or uncertainty (deterministic model). Variability will then be introduced in a second section, and a last section will consider variability and a part of the data uncertainty.

### # The Model

In this section, no variability nor uncertainty is considered.

We assess the final level of *L. monocytogenes* in the product, the exposure and the risk of invasive listeriosis for an "average" individual of the "healthy" French population.^[It makes little sense, but it will help us introducing smoothly the model.]

During the logistic, the retail and the home step, a bacterial growth is modeled considering *i*) the fluctuating temperature during the various stages and; *ii*) the bacterial competition with the food flora.

We use the models developed and/or used in \cite{POUILLLOT-2007}. The data are adapted from

\cite{POUILLOT-2007} and \cite{DELIGNETTE-2006}:

- The DMS model predicts the bacterial growth during a stage of duration  $d$ , when the temperature is fluctuating, with an intra-stage average temperature  $m_T$  and an intra-stage standard deviation of the temperature  $s_T$ . It is written:  

$$N_1 = \min\left(N_0 + \frac{\mu_{ref}}{\ln(10)} \times d \times \frac{\left(s_T^2 + (m_T - T_{min})^2\right)}{\left(T_{ref} - T_{min}\right)^2}, N_{max}\right)$$
\label{DMS}
- if  $m_T > T_{min}$ , with  $N_1$  the  $\log_{10}$  concentration of bacteria ( $\log_{10}$  CFU/g) at the end of the stage,  $N_0$  the  $\log_{10}$  concentration at the beginning,  $\mu_{ref}$  the specific growth rate ( $\text{day}^{-1}$ ) at a reference temperature  $T_{ref}$  ( $^{\circ}\text{C}$ ),  $T_{min}$  the minimal growth temperature ( $^{\circ}\text{C}$ ), and  $N_{max}$  the maximum achievable concentration ( $\log_{10}$  CFU/g). If  $m_T \leq T_{min}$ ,  $N_1 = N_0$ .
- We will use  $T_{ref} = 25^{\circ}\text{C}$ . In this section  $N_{max} = 7.27 \log_{10}$  CFU/g.
- The model for *L. monocytogenes* uses  $\mu_{ref,Lm} = 6.2 \text{ day}^{-1}$  and  $T_{min,Lm} = -2.9^{\circ}\text{C}$ .
- The same model is used for the food flora, with  $\mu_{ref,ff} = 4.1 \text{ day}^{-1}$  and  $T_{min,ff} = -4.5^{\circ}\text{C}$ .
- The growth model for bacterial competition considers the Jameson effect, i.e., the growth of *L. monocytogenes* and the food flora are stopped as soon as one population reaches  $N_{max}$ .

In practice, one evaluates  $d_{Lm}$  and  $d_{ff}$ , the time needed for *L. monocytogenes* or the food flora to reach  $N_{max}$ , and models growth during an effective duration of  $\min(d, d_{Lm}, d_{ff})$ .

The time needed to reach  $N_{max}$  is evaluated by inverting \eqref{DMS}:

$$d_{\left(N_1=N_{max}\right)} = \frac{\left(N_{max}-N_0\right) \times \frac{\ln(10)}{\mu_{ref}} \times \frac{\left(T_{ref}-T_{min}\right)^2}{\left(s_T^2+\left(m_T-T_{min}\right)^2\right)}}$$

The other assumptions are:

- A cold-smoked salmon package is homogeneously contaminated with *L. monocytogenes* at the end of production at a level of  $0.1$  CFU/g.
- The food flora level at the end of production is  $10^{2.78}$  CFU/g.
- The time-temperature profile is:
  - 1.1 days at an average temperature of  $3.2^{\circ}\text{C}$  (logistic step), with an intra-stage SD of  $2.1^{\circ}\text{C}$ .
  - 4.7 days at  $5.5^{\circ}\text{C}$  at retail, with intra-stage SD of  $1.0^{\circ}\text{C}$ .
  - 4.3 days at  $8.2^{\circ}\text{C}$  in the consumer's home, with intra-stage SD of  $2.0^{\circ}\text{C}$ .
- A healthy, non-elderly, non-pregnant individual eats 35 g of this product.
- The individual dose-response model is a one-hit model  
 $\Pr(\text{Illness} \mid D) = 1 - (1-r)^D$   
with  $r = 4.7 \times 10^{-14}$  for this healthy sub-population. The mean-population dose-response (Poisson-distributed dose with mean  $D$ ) is  
 $\Pr(\text{Illness} \mid D) = 1 - \exp(-r \times D)$ .

The question is: \*What is the risk for this "average" individual?\*

```
''' r
Nmax <- 7.3
murefLm <- 6.2; TminLm <- -2.9
murefFF <- 4.1; TminFF <- -4.5
Lm0 <- log10(1); FF0 <- 2.78
d1 <- 1.1; mT1 <- 3.2; sdT1 <- 2.1
d2 <- 4.7; mT2 <- 5.5; sdT2 <- 1.0
d3 <- 4.3; mT3 <- 8.2; sdT3 <- 2.0
conso <- 35
r <- 4.7e-14

modGrowth <- function(duration, mTemp, sdTemp,
                        NOLm, murefLm, TminLm,
                        NOFF, murefFF, TminFF,
                        Nmax, Tref = 25) {
  NOLm <- pmin(NOLm, Nmax)
  NOFF <- pmin(NOFF, Nmax)
  dLm <- (Nmax - NOLm) * log(10) / murefLm * (Tref - TminLm)^2 /
    (sdTemp^2 + (mTemp - TminLm)^2)
  dLm <- ifelse(mTemp < TminLm & NOLm != Nmax, Inf, dLm)
  dFF <- (Nmax - NOFF) * log(10) / murefFF * (Tref - TminFF)^2 /
    (sdTemp^2 + (mTemp - TminFF)^2)
  dFF <- ifelse(mTemp < TminFF & NOFF != Nmax, Inf, dFF)
  realDuration <- pmin(duration, dLm, dFF)
  xLm <- NOLm + (mTemp > TminLm) * murefLm / log(10) *
    (sdTemp^2 + (mTemp - TminLm)^2) / (Tref - TminLm)^2 * realDuration
  xFF <- NOFF + (mTemp > TminFF) * murefFF / log(10) *
    (sdTemp^2 + (mTemp - TminFF)^2) / (Tref - TminFF)^2 * realDuration
  return(list(xLm = xLm, xFF = xFF))
}

x1 <- modGrowth(d1, mT1, sdT1, Lm0, murefLm, TminLm, FF0, murefFF, TminFF, Nmax)
x2 <- modGrowth(d2, mT2, sdT2, x1$xLm, murefLm, TminLm, x1$xFF, murefFF, TminFF, Nmax)
x3 <- modGrowth(d3, mT3, sdT3, x2$xLm, murefLm, TminLm, x2$xFF, murefFF, TminFF, Nmax)
x3

## $xLm
## [1] 3.21
##
## $xFF
## [1] 5.35

conta <- 10^x3$xLm; conta

## [1] 1637
```

```
expo <- conso * conta; expo
```

```
## [1] 57281
```

```
risk <- 1 - (1 - r)^expo; risk
```

```
## [1] 2.69e-09
```

`modGrowth` is a convenient function for the growth model. Within this function `dLm` is the time needed for *L. monocytogenes* to reach `Nmax`, `dFF` for the food flora, and `realDuration` is the effective duration of growth during the stage. Note that:

- This function is “vectorized” — it can take vectors for any parameter and returns a vector. `pmin` (parallel minimum) is used instead of `min` (which returns the minimum of *all* values), and `ifelse` instead of `if`.
- It handles *all* edge cases that can occur in a Monte-Carlo simulation, such as  $N_0 \geq N_{max}$  or  $m_T \leq T_{min}$ , for either bacterial population.

`x1`, `x2` and `x3` are the bacterial concentrations at the end of the logistic, retail and home steps, respectively.

## 1 Including Variability

We now specify variability distributions for some inputs, following [1] and [3].

```
library(fitdistrplus)
library(mc2d)
ndvar(10001)
```

```
## [1] 10001
```

### 1.1 Specifying Variability Distributions

#### 1.1.1 Initial Contamination

For the initial contamination levels in *L. monocytogenes*, we have 62 enumeration data from a representative sample of positive packages of cold-smoked salmon: 43 samples < 0.2 CFU/g, 7 at 0.2 CFU/g, 4 at 0.4 CFU/g, 2 at 0.6 CFU/g, and values of 0.3, 1.0, 1.6, 2.4, 5.4 and 7.0 CFU/g [3]. We use `fitdistrplus` to fit a normal distribution to the  $\log_{10}$  values, accounting for censoring. The initial concentrations are then modelled through a truncated normal<sup>1</sup> on  $[-2, \infty)$   $\log_{10}$  CFU/g.

For the food flora, we use the distribution from [1]:  $N_{0ff} \sim N(2.78, 1.14)$ .

```
dataC <- data.frame(
  left = c(rep(NA, 43), rep(.2, 7), .3, rep(.4, 4), 1, 1.6, .6, .6, 2.4, 5.4, 7),
  right = c(rep(0.2, 43), rep(.2, 7), .3, rep(.4, 4), 1, 1.6, .6, .6, 2.4, 5.4, 7)
)
fit <- fitdistcens(log10(dataC), "norm")
fit
```

---

<sup>1</sup>so that at least one CFU is included in one 100 g package

Table 1: Time-Temperature Profiles

Stage	Mean Temperature (°C)	Intra-Stage SD of T (°C)	Time (days)
logistic	$N(3.2, 2.2)$ trunc. on $[-3; 25]$	$\Gamma(1.16, 4.61)$	Exp(1.1)
retail	$N(5.5, 2.2)$ trunc. on $[-3; 25]$	$\Gamma(0.65, 2.09)$	Exp(4.7)
consumer	$N(8.2, 3.8)$ trunc. on $[-3; 25]$	$\Gamma(0.35, 19.7)$	Exp(4.3)

```
## Fitting of the distribution ' norm ' on censored data by maximum likelihood
## Parameters:
##      estimate
## mean    -1.117
## sd      0.764
```

```
LmOV <- mcstoc(rnorm, mean = fit$est["mean"], sd = fit$est["sd"], rtrunc = TRUE, linf = -2)
FFOV <- mcstoc(rnorm, mean = 2.78, sd = 1.14)
```

By default, the type of variability modelled is "V" (variability).

### 1.1.2 Growth Parameters

Distributions derived from [1]:

- $N_{max} \sim N(7.27, 0.86) \log_{10} \text{ CFU/g.}$
- $\mu_{ref,Lm} \sim N(6.24, 0.75) \text{ day}^{-1}$ , truncated on  $[0, \infty)$ .  $T_{min,Lm} \sim N(-2.86, 1.93)^\circ\text{C.}$
- $\mu_{ref,ff} \sim N(4.12, 1.97) \text{ day}^{-1}$ , truncated on  $[0, \infty)$ .  $T_{min,ff} \sim N(-4.52, 7.6)^\circ\text{C.}$

```
NmaxV <- mcstoc(rnorm, mean = 7.27, sd = 0.86)
murefLmV <- mcstoc(rnorm, mean = 6.24, sd = 0.75, rtrunc = TRUE, linf = 0)
TminLmV <- mcstoc(rnorm, mean = -2.86, sd = 1.93)
murefFFV <- mcstoc(rnorm, mean = 4.12, sd = 1.97, rtrunc = TRUE, linf = 0)
TminFFV <- mcstoc(rnorm, mean = -4.52, sd = 7.66)
```

### 1.1.3 Time-Temperature Profiles

The time-temperature profiles are modelled using Table 1 (adapted from [3]).<sup>2</sup> We assume a shelf life of 28 days with  $d_1 + d_2 + d_3 \leq 28$ .<sup>3</sup>

```
d1V <- mcstoc(rexp, rate = 1/1.1)
mT1V <- mcstoc(rnorm, mean = 3.2, sd = 2.2, rtrunc = TRUE, linf = -3, lsup = 25)
sdT1V <- sqrt(mcstoc(rgamma, shape = 1.16, scale = 4.61))

d2V <- mcstoc(rexp, rate = 1/4.7, rtrunc = TRUE, lsup = 28 - d1V)
mT2V <- mcstoc(rnorm, mean = 5.5, sd = 2.2, rtrunc = TRUE, linf = -3, lsup = 25)
sdT2V <- sqrt(mcstoc(rgamma, shape = 0.65, scale = 2.09))

d3V <- mcstoc(rexp, rate = 1/4.3, rtrunc = TRUE, lsup = 28 - (d1V + d2V))
mT3V <- mcstoc(rnorm, mean = 8.2, sd = 3.8, rtrunc = TRUE, linf = -3, lsup = 25)
sdT3V <- sqrt(mcstoc(rgamma, shape = 0.35, scale = 19.7))
```

<sup>2</sup> $\Gamma$  denotes the Gamma distribution parameterized as  $\Gamma(\text{shape}, \text{scale})$ .  $\text{Exponential}(x)$  denotes the exponential distribution with mean  $x$ .

<sup>3</sup>See the code for how to model this using truncated distributions.

### 1.1.4 Serving Size

From observed data, a discrete empirical distribution is used [3]: values  $V = \{10, 12, 19, 20, 30, 34, 40, 50, 60, 67.5, 80, 100, 250\}$  g, observed  $F = \{11, 1, 1, 29, 12, 1, 41, 4, 4, 1, 4, 1, 1\}$  times.

```
consoV <- mcstoc(rempiricalD,
  values = c(10, 12, 19, 20, 30, 34, 40, 50, 60, 67.5, 80, 100, 250),
  prob = c(11, 1, 1, 29, 12, 1, 41, 4, 4, 1, 4, 1, 1))
```

## 1.2 Applying the Model

```
r <- mcdata(4.7e-14, type = "0")
x1V <- modGrowth(d1V, mT1V, sdT1V, Lm0V, murefLmV, TminLmV, FFOV, murefFFV, TminFFV, NmaxV)
x2V <- modGrowth(d2V, mT2V, sdT2V,
  x1V$xLm, murefLmV, TminLmV, x1V$xFF, murefFFV, TminFFV, NmaxV)
x3V <- modGrowth(d3V, mT3V, sdT3V,
  x2V$xLm, murefLmV, TminLmV, x2V$xFF, murefFFV, TminFFV, NmaxV)

contaV <- 10^x3V$xLm
expoV <- consoV * contaV
riskV <- 1 - exp(-r * expoV)
Lm1 <- mc(Lm0V, FFOV, NmaxV, murefLmV, TminLmV, murefFFV, TminFFV,
  d1V, mT1V, sdT1V, d2V, mT2V, sdT2V, d3V, mT3V, sdT3V,
  consoV, r, contaV, expoV, riskV)

Lm1
```

##	node	mode	nsv	nsu	nva	variate	min	mean	median	max	Nas	type	outm
## 1	Lm0V	numeric	10001	1	1	1	-2.00e+00	-9.30e-01	-9.88e-01	1.76e+00	0	V	each
## 2	FFOV	numeric	10001	1	1	1	-1.28e+00	2.78e+00	2.78e+00	6.85e+00	0	V	each
## 3	NmaxV	numeric	10001	1	1	1	3.97e+00	7.26e+00	7.27e+00	1.06e+01	0	V	each
## 4	murefLmV	numeric	10001	1	1	1	2.85e+00	6.24e+00	6.25e+00	9.25e+00	0	V	each
## 5	TminLmV	numeric	10001	1	1	1	-1.01e+01	-2.83e+00	-2.85e+00	3.69e+00	0	V	each
## 6	murefFFV	numeric	10001	1	1	1	1.31e-02	4.19e+00	4.17e+00	1.13e+01	0	V	each
## 7	TminFFV	numeric	10001	1	1	1	-3.51e+01	-4.52e+00	-4.46e+00	2.66e+01	0	V	each
## 8	d1V	numeric	10001	1	1	1	5.36e-05	1.10e+00	7.69e-01	9.69e+00	0	V	each
## 9	mT1V	numeric	10001	1	1	1	-2.98e+00	3.20e+00	3.15e+00	1.14e+01	0	V	each
## 10	sdT1V	numeric	10001	1	1	1	3.37e-02	2.08e+00	1.96e+00	6.57e+00	0	V	each
## 11	d2V	numeric	10001	1	1	1	1.70e-03	4.69e+00	3.29e+00	2.67e+01	0	V	each
## 12	mT2V	numeric	10001	1	1	1	-2.53e+00	5.53e+00	5.50e+00	1.35e+01	0	V	each
## 13	sdT2V	numeric	10001	1	1	1	1.60e-03	9.66e-01	8.63e-01	4.76e+00	0	V	each
## 14	d3V	numeric	10001	1	1	1	3.84e-04	4.09e+00	2.89e+00	2.53e+01	0	V	each
## 15	mT3V	numeric	10001	1	1	1	-2.98e+00	8.24e+00	8.21e+00	2.26e+01	0	V	each
## 16	sdT3V	numeric	10001	1	1	1	1.31e-06	1.91e+00	1.41e+00	1.16e+01	0	V	each
## 17	consoV	numeric	10001	1	1	1	1.00e+01	3.55e+01	4.00e+01	2.50e+02	0	V	each
## 18	r	numeric	1	1	1	1	4.70e-14	4.70e-14	4.70e-14	4.70e-14	0	0	each
## 19	contaV	numeric	10001	1	1	1	1.16e-02	4.09e+06	2.22e+01	5.04e+09	0	V	each
## 20	expoV	numeric	10001	1	1	1	1.70e-01	1.18e+08	6.85e+02	1.01e+11	0	V	each
## 21	riskV	numeric	10001	1	1	1	7.99e-15	5.55e-06	3.22e-11	4.73e-03	0	V	each

```
sLm1 <- mc(contaV = Lm1$contaV, expoV = Lm1$expoV, riskV = Lm1$riskV)
summary(sLm1, probs = c(0, 0.5, 0.75, 0.95, 1))
```

```
## contaV :
##          mean          sd      Min 50% 75%      95%      Max      nsv Na's
## NoUnc 4092015 76520808 0.0116 22.2 867 1962680 5.04e+09 10001      0
##
## expoV :
##          mean          sd      Min 50% 75%      95%      Max      nsv Na's
## NoUnc 1.18e+08 1.88e+09 0.17 685 27251 60077024 1.01e+11 10001      0
##
## riskV :
##          mean          sd      Min      50%      75%      95%      Max      nsv Na's
## NoUnc 5.55e-06 8.82e-05 7.99e-15 3.22e-11 1.28e-09 2.82e-06 0.00473 10001      0
```

Lm1 contains all parameters and outputs. sLm1 extracts a short summary.

### 1.3 Final Estimate

If 6.5% of cold-smoked salmon packages are contaminated, 49,090,000 French people are in the “non-susceptible” population, and they consume smoked salmon 6.4 times per year on average, the expected number of listeriosis cases is:

```
meanRisk <- mcappl(riskV, "var", mean)
expectedN <- round(0.065 * unmc(meanRisk) * 6.4 * 49090000)
expectedN
```

```
## [1] 113
```

## 2 Including (a Part of the) Uncertainty

We include both variability and uncertainty, focusing on the uncertainty in initial contamination, growth parameters, and prevalence.

### 2.1 Specifying Uncertainty

#### 2.1.1 Initial Contamination

The uncertainty around initial *L. monocytogenes* contamination is modelled using a bootstrap procedure with `bootdistcens` from `fitdistrplus`.

```
ndunc(101)
```

```
## [1] 101
```

```

bootLm0 <- bootdistcens(fit, niter = ndunc())
MLm0 <- mcdata(bootLm0$est$mean, type = "U")
SLm0 <- mcdata(bootLm0$est$sd, type = "U")
LmOVU <- mcstoc(rnorm, type = "VU", mean = MLm0, sd = SLm0, rtrunc = TRUE, linf = -2)

```

For the food flora, uncertain hyperparameters  $M_{N0ff}$  and  $\sigma_{N0ff}$  govern the variable parameter  $N_{0ff}$  [1]:

$$N_{0ff} \sim N(M_{N0ff}, \sigma_{N0ff}), \quad M_{N0ff} \sim N(2.78, 0.265), \quad \ln(\sigma_{N0ff}) \sim N(0.114, 0.172)$$

```

MLmOFF <- mcstoc(rnorm, type = "U", mean = 2.78, sd = 0.265)
SLmOFF <- mcstoc(rlnorm, type = "U", meanlog = 0.114, sdlog = 0.172)
FFOVU <- mcstoc(rnorm, type = "VU", mean = MLmOFF, sd = SLmOFF)

```

### 2.1.2 Growth Parameters

Uncertainty around  $\mu_{ref,Lm}$ ,  $T_{min,Lm}$ ,  $\mu_{ref,ff}$ ,  $T_{min,ff}$  and  $N_{max}$  is modelled via hyperparameters [1].<sup>4</sup>

$$\begin{aligned}
\mu_{ref,Lm} &\sim N(M_{\mu_{ref,Lm}}, \sigma_{\mu_{ref,Lm}}), & M_{\mu_{ref,Lm}} &\sim \Gamma(69.7, 0.0896), & \ln(\sigma_{\mu_{ref,Lm}}) &\sim N(1.03, 0.191) \\
T_{min,Lm} &\sim N(M_{T_{min,Lm}}, \sigma_{T_{min,Lm}}), & M_{T_{min,Lm}} &\sim N(-2.86, 0.459), & \ln(\sigma_{T_{min,Lm}}) &\sim N(0.638, 0.208) \\
\mu_{ref,ff} &\sim N(M_{\mu_{ref,ff}}, \sigma_{\mu_{ref,ff}}), & M_{\mu_{ref,ff}} &\sim \Gamma(32.5, 0.127), & \ln(\sigma_{\mu_{ref,ff}}) &\sim N(-0.656, 0.221) \\
T_{min,ff} &\sim N(M_{T_{min,ff}}, \sigma_{T_{min,ff}}), & M_{T_{min,ff}} &\sim N(-4.52, 1.23), & \ln(\sigma_{T_{min,ff}}) &\sim N(2.00, 0.257) \\
N_{max} &\sim N(M_{N_{max}}, \sigma_{N_{max}}), & M_{N_{max}} &\sim N(7.27, 0.276), & \ln(\sigma_{N_{max}}) &\sim N(-0.172, 0.218)
\end{aligned}$$

with  $\mu_{ref} > 0$  and  $T_{min} < 25$ .

```

MmurefLm <- mcstoc(rgamma, type = "U", shape = 69.7, scale = 0.0896)
SmurefLm <- mcstoc(rlnorm, type = "U", meanlog = 1.03, sdlog = 0.191)
murefLmVU <- mcstoc(rnorm, type = "VU", mean = MmurefLm, sd = SmurefLm, rtrunc = TRUE, linf = 0)

MTminLm <- mcstoc(rnorm, type = "U", mean = -2.86, sd = 0.459)
STminLm <- mcstoc(rlnorm, type = "U", meanlog = 0.638, sdlog = 0.208)
TminLmVU <- mcstoc(rnorm, type = "VU", mean = MTminLm, sd = STminLm, rtrunc = TRUE, lsup = 25)

MmurefFF <- mcstoc(rgamma, type = "U", shape = 32.5, scale = 0.127)
SmurefFF <- mcstoc(rlnorm, type = "U", meanlog = -0.656, sdlog = 0.221)
murefFFVU <- mcstoc(rnorm, type = "VU", mean = MmurefFF, sd = SmurefFF, rtrunc = TRUE, linf = 0)

MTminFF <- mcstoc(rnorm, type = "U", mean = -4.52, sd = 1.23)
STminFF <- mcstoc(rlnorm, type = "U", meanlog = 2.00, sdlog = 0.257)
TminFFVU <- mcstoc(rnorm, type = "VU", mean = MTminFF, sd = STminFF, rtrunc = TRUE, lsup = 25)

MNmax <- mcstoc(rnorm, type = "U", mean = 7.27, sd = 0.276)
SNmax <- mcstoc(rlnorm, type = "U", meanlog = -0.172, sdlog = 0.218)
NmaxVU <- mcstoc(rnorm, type = "VU", mean = MNmax, sd = SNmax)

```

<sup>4</sup>Note: there was a typo in [1] that led to an error in [3]: the standard-error for  $\ln(\sigma_{\mu_{ref,Lm}})$  is 1.03, not  $-1.03$ . We use the correct value here.



### 2.1.3 Prevalence

The prevalence (6.5%) was estimated from 41 positive packages out of 626 tested [3]. Assuming 100% sensitivity and specificity, uncertainty around the true prevalence is modelled with a Beta(1,1) prior:

```
prevU <- mcstoc(rbeta, type = "U", shape1 = 41 + 1, shape2 = 626 - 41 + 1)
```

## 2.2 Applying the Model

```
x1VU <- modGrowth(d1V, mT1V, sdT1V,
                  LmOVU, murefLmVU, TminLmVU, FF0VU, murefFFVU, TminFFVU, NmaxVU)
x2VU <- modGrowth(d2V, mT2V, sdT2V,
                  x1VU$xLm, murefLmVU, TminLmVU, x1VU$xFF, murefFFVU, TminFFVU, NmaxVU)
x3VU <- modGrowth(d3V, mT3V, sdT3V,
                  x2VU$xLm, murefLmVU, TminLmVU, x2VU$xFF, murefFFVU, TminFFVU, NmaxVU)

contaVU <- 10^x3VU$xLm
expoVU <- consoV * contaVU
riskVU <- 1 - exp(-r * expoVU)
Lm2 <- mc(LmOVU, FF0VU, NmaxVU, murefLmVU, TminLmVU, murefFFVU, TminFFVU,
          d1V, mT1V, sdT1V, d2V, mT2V, sdT2V, d3V, mT3V, sdT3V,
          consoV, r, contaVU, expoVU, riskVU)

Lm2
```

##	node	mode	nsv	nsu	nva	variate	min	mean	median	max	Nas	type	outm
## 1	LmOVU	numeric	10001	101	1	1	-2.00e+00	-9.29e-01	-9.90e-01	4.71e+00	0	VU	each
## 2	FF0VU	numeric	10001	101	1	1	-3.90e+00	2.81e+00	2.81e+00	9.30e+00	0	VU	each
## 3	NmaxVU	numeric	10001	101	1	1	1.02e+00	7.30e+00	7.31e+00	1.32e+01	0	VU	each
## 4	murefLmVU	numeric	10001	101	1	1	6.55e-05	6.48e+00	6.40e+00	2.43e+01	0	VU	each
## 5	TminLmVU	numeric	10001	101	1	1	-1.58e+01	-2.86e+00	-2.86e+00	8.90e+00	0	VU	each
## 6	murefFFVU	numeric	10001	101	1	1	2.58e-01	4.15e+00	4.12e+00	9.05e+00	0	VU	each
## 7	TminFFVU	numeric	10001	101	1	1	-5.67e+01	-4.51e+00	-4.51e+00	2.50e+01	0	VU	each
## 8	d1V	numeric	10001	1	1	1	5.36e-05	1.10e+00	7.69e-01	9.69e+00	0	V	each
## 9	mT1V	numeric	10001	1	1	1	-2.98e+00	3.20e+00	3.15e+00	1.14e+01	0	V	each
## 10	sdT1V	numeric	10001	1	1	1	3.37e-02	2.08e+00	1.96e+00	6.57e+00	0	V	each
## 11	d2V	numeric	10001	1	1	1	1.70e-03	4.69e+00	3.29e+00	2.67e+01	0	V	each
## 12	mT2V	numeric	10001	1	1	1	-2.53e+00	5.53e+00	5.50e+00	1.35e+01	0	V	each
## 13	sdT2V	numeric	10001	1	1	1	1.60e-03	9.66e-01	8.63e-01	4.76e+00	0	V	each
## 14	d3V	numeric	10001	1	1	1	3.84e-04	4.09e+00	2.89e+00	2.53e+01	0	V	each
## 15	mT3V	numeric	10001	1	1	1	-2.98e+00	8.24e+00	8.21e+00	2.26e+01	0	V	each
## 16	sdT3V	numeric	10001	1	1	1	1.31e-06	1.91e+00	1.41e+00	1.16e+01	0	V	each
## 17	consoV	numeric	10001	1	1	1	1.00e+01	3.55e+01	4.00e+01	2.50e+02	0	V	each
## 18	r	numeric	1	1	1	1	4.70e-14	4.70e-14	4.70e-14	4.70e-14	0	0	each
## 19	contaVU	numeric	10001	101	1	1	1.00e-02	1.00e+07	1.90e+01	4.20e+11	0	VU	each
## 20	expoVU	numeric	10001	101	1	1	1.00e-01	3.70e+08	5.79e+02	2.10e+13	0	VU	each
## 21	riskVU	numeric	10001	101	1	1	4.66e-15	1.67e-05	2.72e-11	6.27e-01	0	VU	each

```
sLm2 <- mc(contaVU = Lm2$contaVU, expoVU = Lm2$expoVU, riskVU = Lm2$riskVU)
summary(sLm2, probs = c(0, 0.5, 0.75, 0.95, 1))
```

```
## contaVU :
##          mean      sd    Min  50%   75%   95%    Max   nsv Na's
## median  6299495 9.57e+07 0.0114 18.36 1244.5 5485146 6.12e+09 10001 0
## mean    10025362 2.54e+08 0.0120 26.79 2893.2 8564635 2.02e+10 10001 0
## 2.5%    1486775 2.06e+07 0.0101 3.86  97.4  202346 8.85e+08 10001 0
## 97.5%   53421962 1.94e+09 0.0174 82.67 14469.4 31267142 1.62e+11 10001 0
##
## expoVU :
##          mean      sd    Min  50%   75%   95%    Max   nsv Na's
## median  2.35e+08 4.07e+09 0.153 566 37475 1.64e+08 2.59e+11 10001 0
## mean    3.70e+08 1.09e+10 0.162 814 90618 2.66e+08 9.07e+11 10001 0
## 2.5%    5.39e+07 7.65e+08 0.105 117 2946 6.30e+06 2.85e+10 10001 0
## 97.5%   1.96e+09 8.21e+10 0.233 2505 491756 1.00e+09 6.68e+12 10001 0
##
## riskVU :
##          mean      sd    Min  50%   75%   95%    Max   nsv Na's
## median  1.09e-05 0.000191 7.22e-15 2.66e-11 1.76e-09 7.69e-06 0.01209 10001 0
## mean    1.67e-05 0.000452 7.60e-15 3.83e-11 4.26e-09 1.25e-05 0.03642 10001 0
## 2.5%    2.53e-06 0.000036 4.94e-15 5.48e-12 1.38e-10 2.96e-07 0.00134 10001 0
## 97.5%   8.22e-05 0.003279 1.09e-14 1.18e-10 2.31e-08 4.71e-05 0.26748 10001 0
```

The summary provides the mean, SD, minimum, median ... and a 95% credible interval. The point estimate is the median of the 101 values in the uncertainty dimension; the credible interval runs between the 2.5th and 97.5th percentiles of the uncertainty dimension.

## 2.3 Final Estimate

```
meanRiskU <- mapply(riskVU, "var", mean)
expectedNU <- round(prevU * meanRiskU * 6.4 * 49090000)
summary(expectedNU)
```

```
## node :
##      NoVar
## median 223.0
## mean   342.3
## 2.5%   48.5
## 97.5%  1586.5
```

This estimate reflects uncertainty from initial contamination, bacterial growth parameters, and sampling of positive packages. Many other uncertainties (notably around the dose-response model) are not considered here; see [3, 2] for a complete analysis.

The tornado chart in the variability dimension suggests a large impact from the growth rate of *L. monocytogenes*, the storage duration during the consumer step, and the initial contamination level. The tornado in the uncertainty dimension highlights the impact of uncertainty around  $N_{max}$  on the mean risk.

```
torn <- tornado(Lm2); torn
```

```
## Spearman's rho statistic
## Output: riskVU
```

```
## $riskVU
##      Lm0VU  FF0VU NmaxVU murefLmVU TminLmVU murefFFVU TminFFVU  d1V  mT1V  sdT1V  d2V
## median 0.301 -0.0796 0.0690 0.452 -0.241 -0.03035 0.115 0.0437 0.0329 0.00669 0.281
## mean 0.303 -0.0845 0.0726 0.446 -0.240 -0.03230 0.123 0.0433 0.0332 0.00628 0.282
## 2.5% 0.191 -0.1568 0.0301 0.324 -0.337 -0.06209 0.033 0.0226 0.0181 -0.00653 0.207
## 97.5% 0.402 -0.0286 0.1377 0.557 -0.159 -0.00414 0.229 0.0613 0.0482 0.02273 0.347
##      mT2V  sdT2V  d3V  mT3V  sdT3V  consoV  contaVU expoVU
## median 0.158 0.00511 0.409 0.260 0.0292 0.125 0.991 1
## mean 0.160 0.00539 0.411 0.261 0.0288 0.126 0.991 1
## 2.5% 0.129 -0.00727 0.319 0.212 0.0146 0.101 0.986 1
## 97.5% 0.185 0.01854 0.495 0.308 0.0446 0.155 0.994 1
```

```
tornunc <- tornadounc(Lm2, quant = .975); tornunc
```

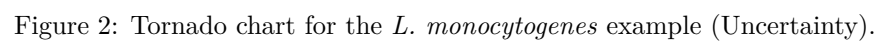
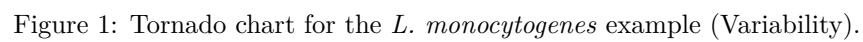
```
## Tornado on uncertainty
## Spearman's rho statistic
## Output: riskVU
## $riskVU
##      mean Lm0VU sd Lm0VU 97.5% Lm0VU mean FF0VU sd FF0VU 97.5% FF0VU mean NmaxVU sd NmaxVU
## mean riskVU -0.0087 -0.0347 -0.0527 -0.0404 -0.0322 -0.08867 0.401 0.550
## sd riskVU -0.0572 -0.0808 -0.0985 -0.0366 -0.0909 -0.12235 0.162 0.684
## 97.5% riskVU 0.0507 -0.0159 -0.0191 -0.0331 0.0659 -0.00686 0.545 -0.075
##      97.5% NmaxVU mean murefLmVU sd murefLmVU 97.5% murefLmVU mean TminLmVU sd TminLmVU
## mean riskVU 0.823 0.415 0.348 0.493 0.0298 0.0923
## sd riskVU 0.755 0.235 0.303 0.353 0.1061 0.0785
## 97.5% riskVU 0.346 0.667 0.358 0.625 -0.1985 0.0646
##      97.5% TminLmVU mean murefFFVU sd murefFFVU 97.5% murefFFVU mean TminFFVU sd TminFFVU
## mean riskVU 0.0846 -0.0801 -0.0872 -0.102 0.1059 -0.0897
## sd riskVU 0.1139 -0.0135 -0.0120 -0.011 0.0843 -0.1136
## 97.5% riskVU -0.0470 -0.3539 -0.2595 -0.421 0.1261 -0.0200
##      97.5% TminFFVU mean contaVU sd contaVU 97.5% contaVU mean expoVU sd expoVU
## mean riskVU -0.0331 0.988 0.892 0.636 1.000 0.896
## sd riskVU -0.0644 0.857 0.939 0.325 0.897 1.000
## 97.5% riskVU 0.0278 0.649 0.317 0.996 0.637 0.330
##      97.5% expoVU
## mean riskVU 0.638
## sd riskVU 0.330
## 97.5% riskVU 1.000
```

```
plot(torn)
plot(tornunc, stat = "mean risk")
```

As a conclusion, this example illustrates how predictive growth models can be implemented within `mc2d`...

## References

- [1] M.-L. Delignette-Muller, M. Cornu, R. Pouillot, and J.-B. Denis. Use of bayesian modelling in risk assessment: application to growth of *Listeria monocytogenes* and food flora in cold-smoked salmon. *International Journal of Food Microbiology*, 106(2):195–208, 2006.
- [2] R. Pouillot, V. Goulet, M. L. Delignette-Muller, A. Mahe, and M. Cornu. Quantitative risk assessment of *listeria monocytogenes* in french cold-salmon : Ii. risk characterization. *Risk Analysis*, 29(6):806–819, 2009.



- [3] R. Pouillot, N. Miconnet, A.-L. Afchain, M.-L. Delignette-Muller, A. Beaufort, L. Rosso, J.-B. Denis, and M. Cornu. Quantitative risk assessment of listeria monocytogenes in french cold-salmon : I. quantitative exposure assessment. *Risk Analysis*, 27(3):683–700, 2007.