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{POUILLOT-2007} and \cite{POUILLOT-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{POUILLOT-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:
  \begin{equation}
  N_{1}=
  \min\left(
    N_{0} +
    \frac{\mu_{ref}}{\ln(10)} \times d \times
    \frac{\left(s_{T}^{2}+\left(m_{T}-T_{min}\right)^{2}\right)}{\left(T_{ref}-T_{min}\right)^{2}},
    \: N_{max}\right) \label{DMS}
  \end{equation}
  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,
  μ_{ref} the specific growth rate (day^{-1}) at a reference temperature T_{ref} (°C),
  T_{min} the minimal growth temperature (°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 $T_{ref}=25$°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
  $T_{min,Lm}=-2.9$°C.
- The same model is used for the food flora, with $\mu_{ref,ff}=4.1\ \text{day}^{-1}$ and
  $T_{min,ff}=-4.5$°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}:
$$
d_{\left(N_{1}=N_{max}\right)}=
\left(N_{max}-N_{0}\right)\times
\frac{\ln(10)}{\mu_{ref}} \times
\frac{\left(T_{ref}-T_{min}\right)^{2}}{\left(s_{T}^{2}+\left(m_{T}-T_{min}\right)^{2}\right)}
$$

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°C (logistic step), with an intra-stage
      SD of 2.1°C.
    - 4.7 days at 5.5°C at retail, with intra-stage SD of 1.0°C.
    - 4.3 days at 8.2°C in the consumer's home, with intra-stage SD of 2.0°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 $r=4.7\times10^{-14}$ 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,
                      N0Lm, murefLm, TminLm,
                      N0FF, murefFF, TminFF,
                      Nmax, Tref = 25) {
  N0Lm <- pmin(N0Lm, Nmax)
  N0FF <- pmin(N0FF, Nmax)
  dLm <- (Nmax - N0Lm) * log(10) / murefLm * (Tref - TminLm)^2 /
         (sdTemp^2 + (mTemp - TminLm)^2)
  dLm <- ifelse(mTemp < TminLm & N0Lm != Nmax, Inf, dLm)
  dFF <- (Nmax - N0FF) * log(10) / murefFF * (Tref - TminFF)^2 /
         (sdTemp^2 + (mTemp - TminFF)^2)
  dFF <- ifelse(mTemp < TminFF & N0FF != Nmax, Inf, dFF)
  realDuration <- pmin(duration, dLm, dFF)
  xLm <- N0Lm + (mTemp > TminLm) * murefLm / log(10) *
         (sdTemp^2 + (mTemp - TminLm)^2) / (Tref - TminLm)^2 * realDuration
  xFF <- N0FF + (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
```

```r
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[1] 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
```

[1] 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
```

```
Lm0V <- mcstoc(rnorm, mean = fit$est["mean"], sd = fit$est["sd"], rtrunc = TRUE, linf = -2)
FF0V <- 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]:

- $N_{max} \sim N(7.27,\ 0.86)$ $\log_{10}$ CFU/g.
- $\mu_{ref,Lm} \sim N(6.24,\ 0.75)$ day^{-1}, truncated on $[0, \infty)$. $T_{min,Lm} \sim N(-2.86,\ 1.93)$°C.
- $\mu_{ref,ff} \sim N(4.12,\ 1.97)$ day^{-1}, truncated on $[0, \infty)$. $T_{min,ff} \sim N(-4.52,\ 7.6)$°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]).[2] We assume a shelf life of 28 days with $d_1 + d_2 + d_3 \leq 28$.[3]

```
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))
```

[2] Γ denotes the Gamma distribution parameterized as $\Gamma(shape,\ scale)$. Exponential(x) denotes the exponential distribution with mean x.

[3] 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, FF0V, 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, FF0V, 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      FF0V 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  <- mcapply(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")
Lm0VU   <- mcstoc(rnorm, type = "VU", mean = MLm0, sd = SLm0, rtrunc = TRUE, linf = -2)
```

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

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

```
MLm0FF <- mcstoc(rnorm,  type = "U", mean = 2.78,  sd = 0.265)
SLm0FF <- mcstoc(rlnorm, type = "U", meanlog = 0.114, sdlog = 0.172)
FF0VU  <- mcstoc(rnorm,  type = "VU", mean = MLm0FF, sd = SLm0FF)
```

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].[4]

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

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)
```

[4]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,
                  Lm0VU, 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(Lm0VU, 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      Lm0VU 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  <- mcapply(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.

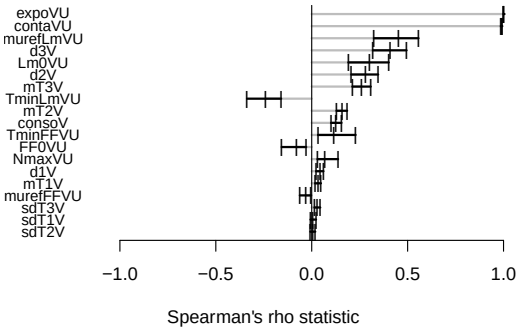

Figure 1: Tornado chart for the *L. monocytogenes* example (Variability).

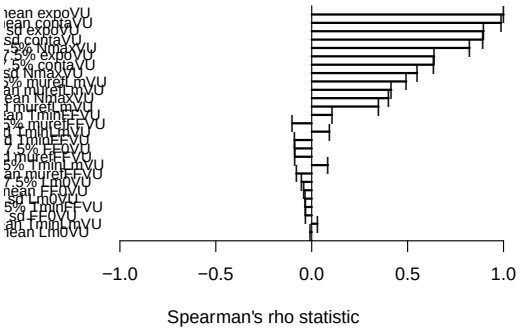

Figure 2: Tornado chart for the *L. monocytogenes* example (Uncertainty).

[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.