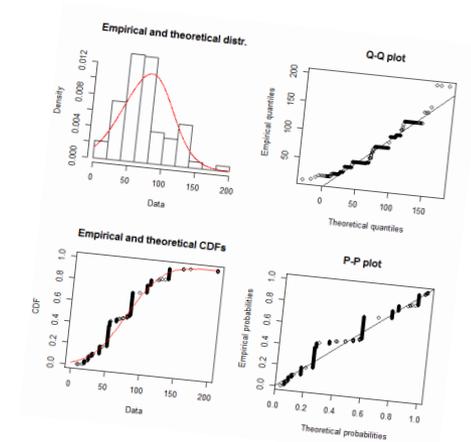


$$f(x) = \frac{\beta^{-\alpha} x^{\alpha-1} \exp(-x/\beta)}{\Gamma(\alpha)}$$



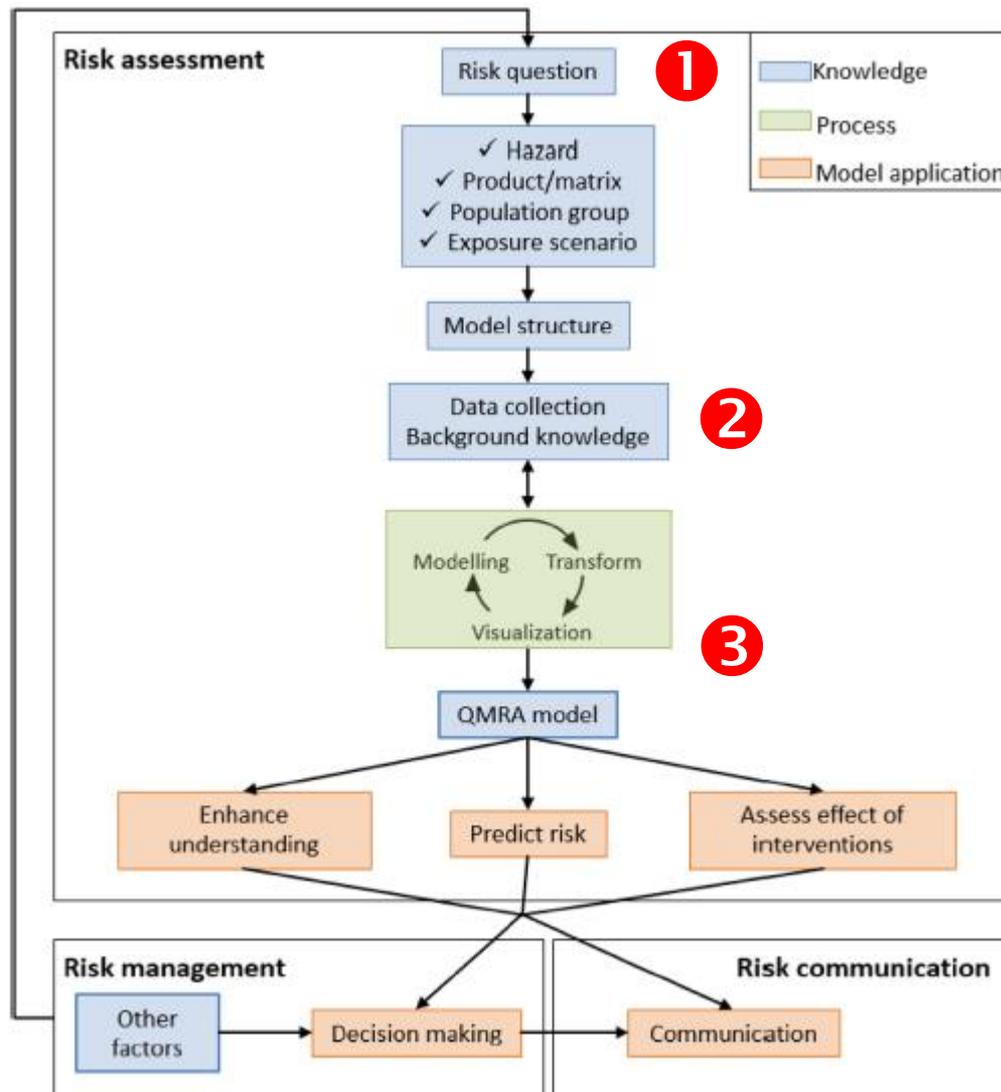
ARTISANE food - Workshop

Building a quantitative risk assessment

L. Guillier & F. Tenenhaus
21st November 2022



Quantitative risk assessment

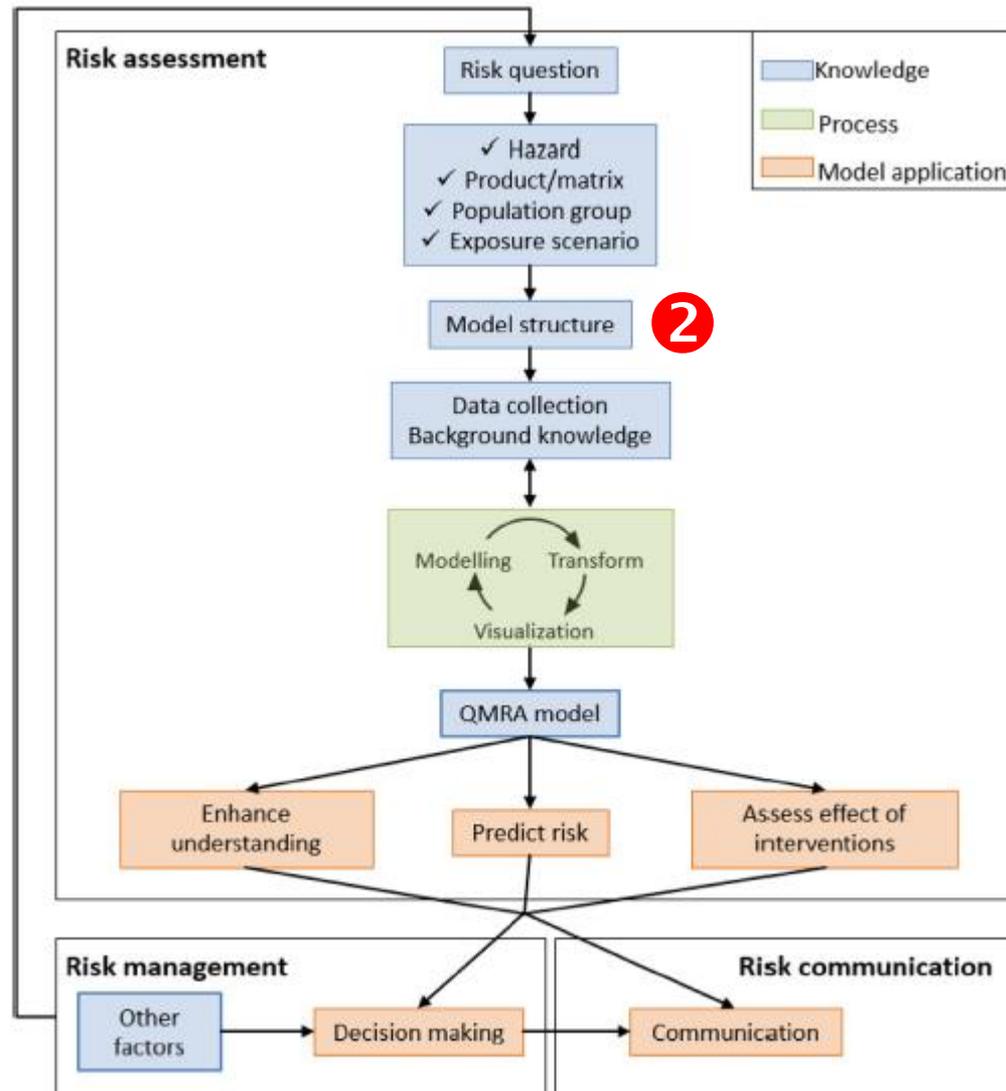


The different stages

1. Define the question to be answered
 - 1.1 Which hazard (*E. coli* stx+, *E. coli* O157, EHEC,...)
 - 1.2 Which food? (*fresh minced steak, 20% mg steak, ...*)
 - 1.3 Which population (*children <5 years, <15 years, ...*)
 - 1.4 What is the exposure scenario (*product consumed raw or rare,...*)
 - 1.5 What purpose(s)? Decision-making based on the response (*Determine the impact of the control measure₁, calculate the residual risk, ...*)



Quantitative risk assessment



The different stages (2)

2. Define the structure of the QMRA model

2.1 What is the starting point of the model?

2.2 Which stages of the manufacturing process, transport and storage, and consumer preparation should be included?

2.3 What data is available? What data do I need to acquire?

2.4 Processing of data before use in the QMRA

The different stages (2)

2. Define the structure of the QMRA model

2.1 What is the starting point of the model?

Must be upstream of the control measure

Often starts from the point where the most knowledge is available

2.2 Which stages of the manufacturing process, transport and storage, and consumer preparation should be included?

2.3 What data is available? What data do I need to acquire?

2.4 Processing of data before use in the QMRA

The different stages (2)

2. Define the structure of the QMRA model

2.1 What is the starting point of the model?

2.2 Which stages of the manufacturing process, transport and storage, and consumer preparation should be included?

Starting from the production diagram

Selecting the steps that have an assumed impact on the hazard

What basic phenomena (growth, destruction, mixing, partitioning, shrinkage, cross-contamination) come into consideration?

2.3 What data is available? What data do I need to acquire?

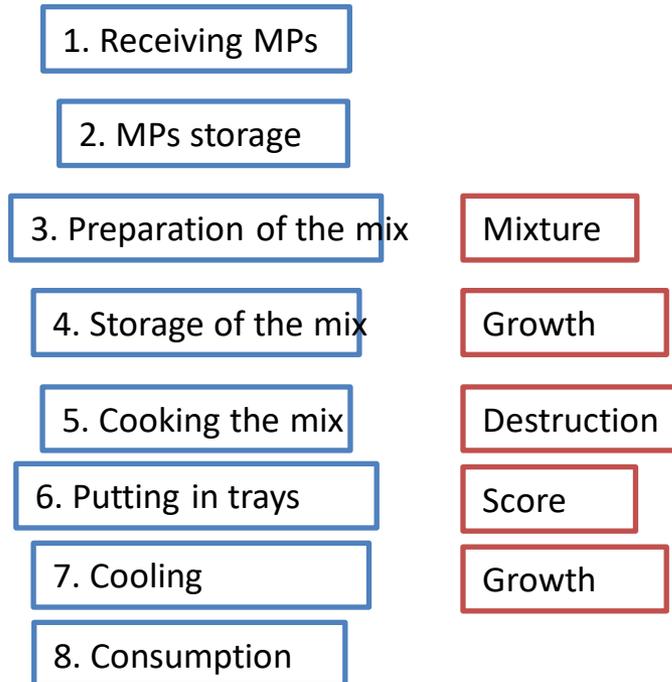
2.4 Processing of data before use in the QMRA

The different stages (2)

2. Define the structure of the QMRA model

2.1 What is the starting point of the model?

2.2 Which stages of the manufacturing process, transport and storage, and consumer preparation should be included?



This work is used to define the modelling assumptions.

- Storage of raw materials has no effect on contamination.
- There is no cross-contamination (everything comes from the raw materials)
- ...

The different stages (2)

2. Define the structure of the QMRA model

2.1 What is the starting point of the model?

2.2 Which stages of the manufacturing process, transport and storage, and consumer preparation should be included?

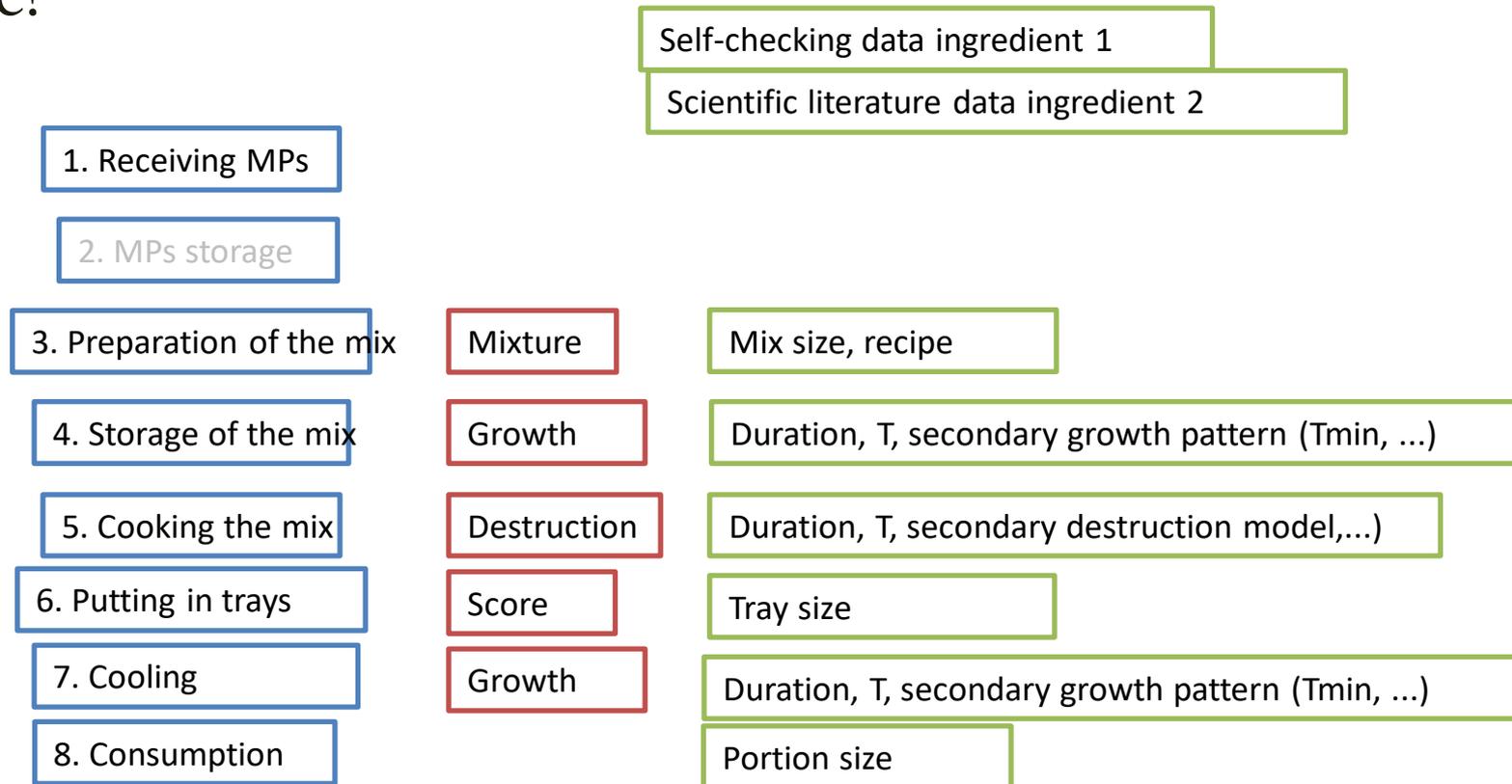
2.3 What data is available? What data do I need to acquire?

2.4 Processing of data before use in the QMRA

The different stages (2)

2. Define the structure of the QMRA model

2.3 What data is available? What data do I need to acquire?



The different stages (2)

2. Define the structure of the QMRA model

2.1 What is the starting point of the model?

2.2 Which stages of the manufacturing process, transport and storage, and consumer preparation should be included?

2.3 What data is available? What data do I need to acquire?

2.4 Processing of data before use in the QMRA

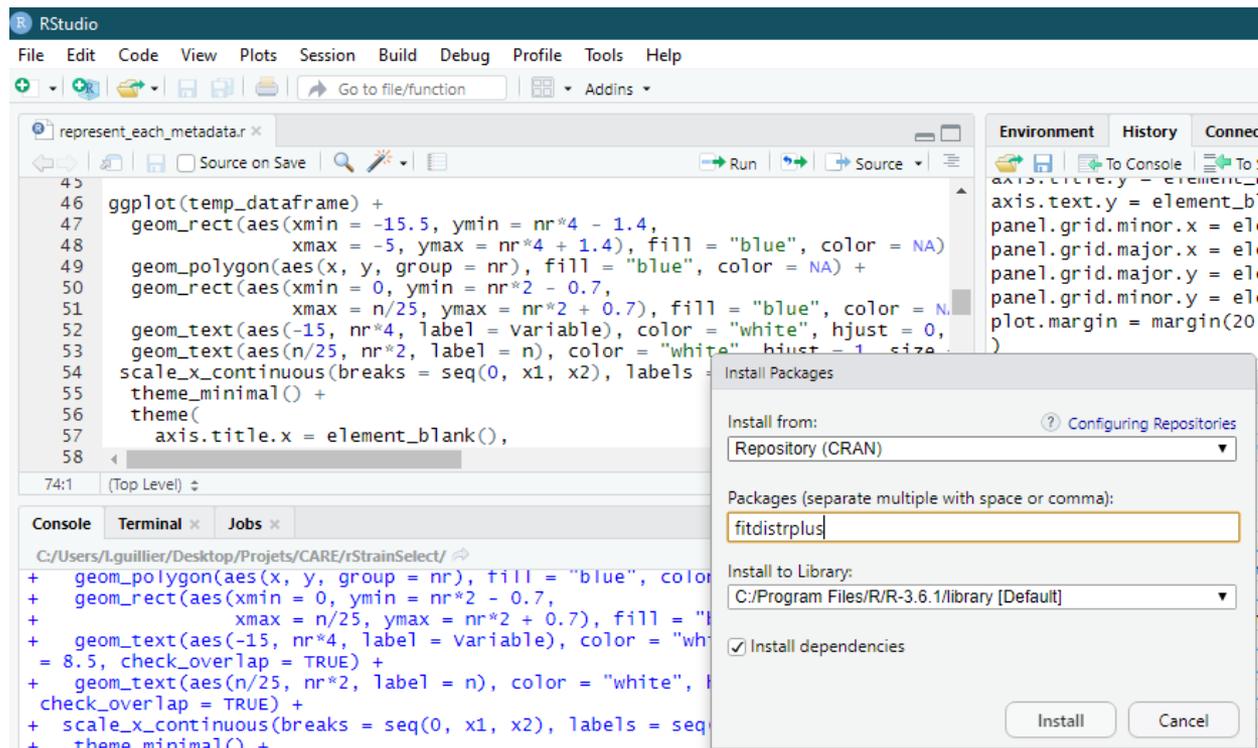
Workshop_AQR1.r (Variability characterisation work)

The tool used :

fitdistrplus: <http://cran.at.r-project.org/web/packages/fitdistrplus/index.html>

Pouillot, R., and M.-L. Delignette-Muller. 2010. Evaluating variability and uncertainty separately in microbial quantitative risk assessment using two R packages. *International Journal of Food Microbiology* 142:330-340.

Delignette-Muller, M. L., & Dutang, C. (2015). fitdistrplus: An R package for fitting distributions. *Journal of statistical software*, 64(4), 1-34.



The screenshot shows the RStudio interface. The main editor window contains the following R code:

```
45  
46 ggplot(temp_dataframe) +  
47   geom_rect(aes(xmin = -15.5, ymin = nr*4 - 1.4,  
48               xmax = -5, ymax = nr*4 + 1.4), fill = "blue", color = NA)  
49   geom_polygon(aes(x, y, group = nr), fill = "blue", color = NA) +  
50   geom_rect(aes(xmin = 0, ymin = nr*2 - 0.7,  
51               xmax = n/25, ymax = nr*2 + 0.7), fill = "blue", color = NA)  
52   geom_text(aes(-15, nr*4, label = variable), color = "white", hjust = 0,  
53             geom_text(aes(n/25, nr*2, label = n), color = "white", hjust = 1, size = 12))  
54   scale_x_continuous(breaks = seq(0, x1, x2), labels = seq(0, x1, x2))  
55   theme_minimal() +  
56   theme(  
57     axis.title.x = element_blank(),  
58   )
```

The console window shows the execution of the code, with the following output:

```
+ geom_polygon(aes(x, y, group = nr), fill = "blue", color = NA)  
+ geom_rect(aes(xmin = 0, ymin = nr*2 - 0.7,  
+             xmax = n/25, ymax = nr*2 + 0.7), fill = "blue", color = NA)  
+ geom_text(aes(-15, nr*4, label = variable), color = "white", hjust = 0,  
+             geom_text(aes(n/25, nr*2, label = n), color = "white", hjust = 1, size = 12))  
+ check_overlap = TRUE) +  
+ scale_x_continuous(breaks = seq(0, x1, x2), labels = seq(0, x1, x2))  
+ theme_minimal() +
```

An "Install Packages" dialog box is open in the foreground. It shows the following settings:

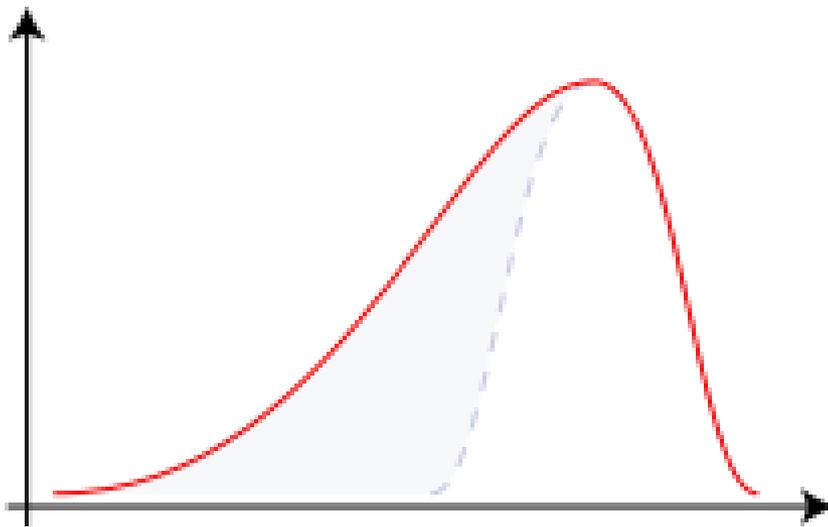
- Install from: Repository (CRAN)
- Packages (separate multiple with space or comma): fitdistrplus
- Install to Library: C:/Program Files/R/R-3.6.1/library [Default]
- Install dependencies

The "Install" button is highlighted.

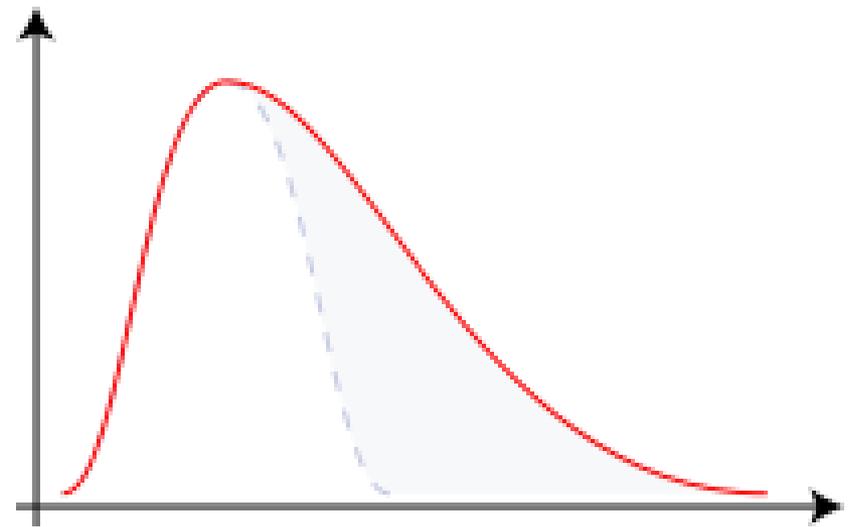
Asymmetry coefficient

Skewness

$$\text{skewness} = \frac{1/n \times \sum (x_i - \mu)^3}{\sigma^3}$$



Negative Skew



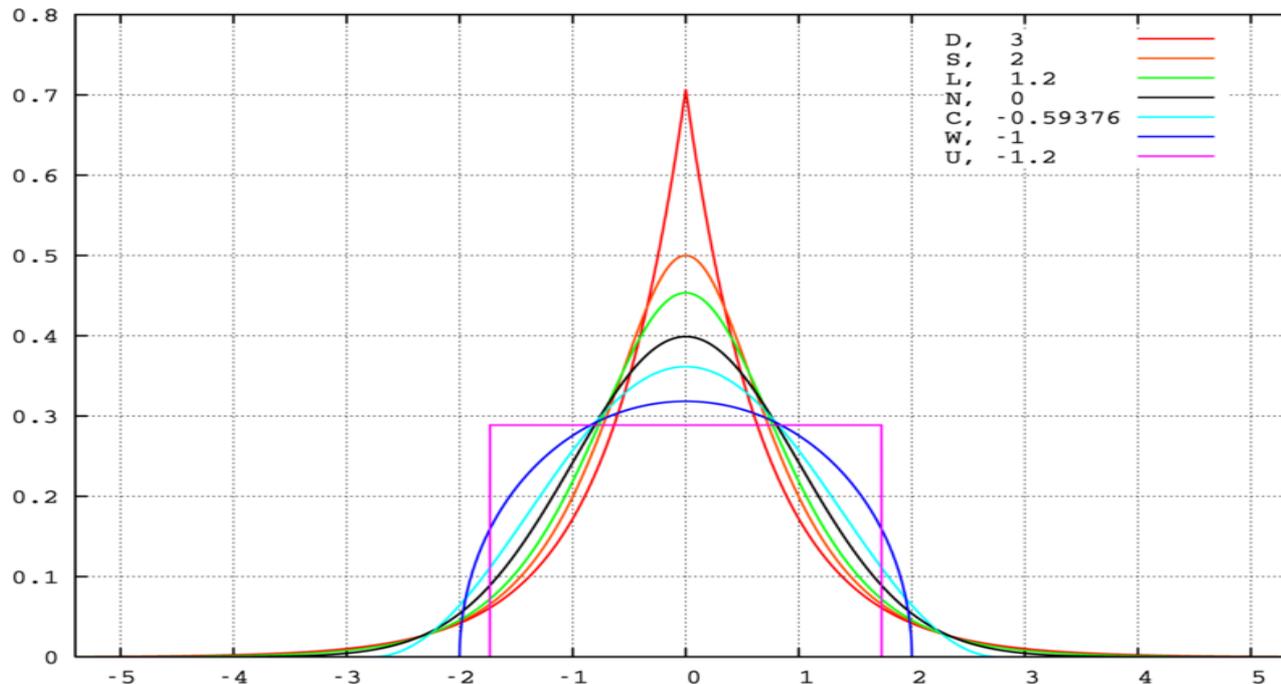
Positive Skew

Flattening coefficient

1. How to define a distribution?
2. How to identify candidate distributions?
3. How to fit a distribution?
4. How to characterize uncertainty?

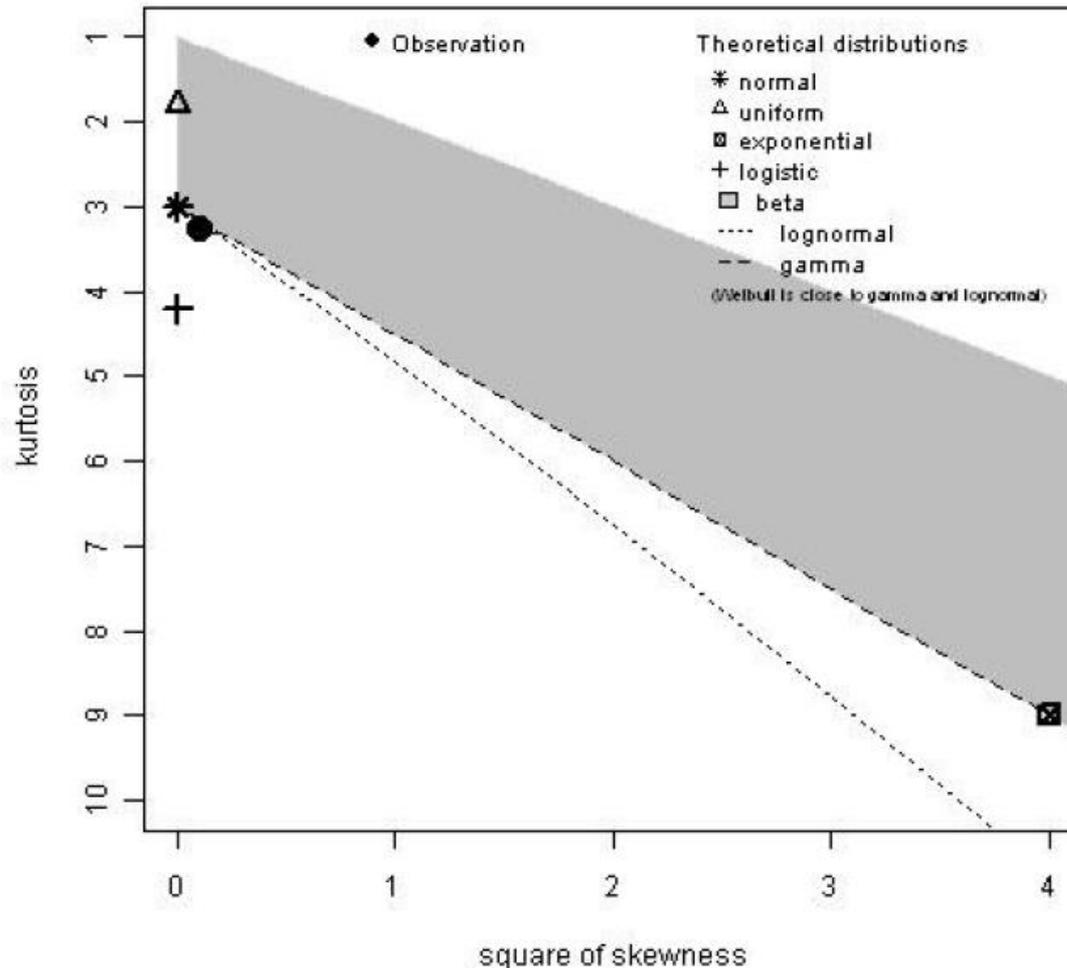
Kurtosis (measure of "peakedness")

$$kurtosis = \frac{1/n \times \sum (x_i - \mu)^4}{\sigma^4}$$



Skewness and kurtosis

Skewness and kurtosis plot for a **continuous** variable



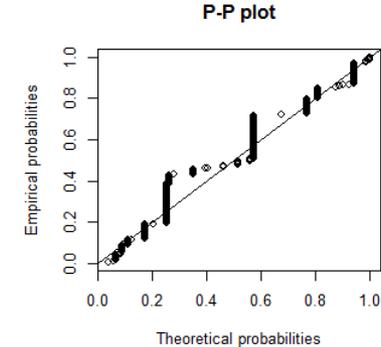
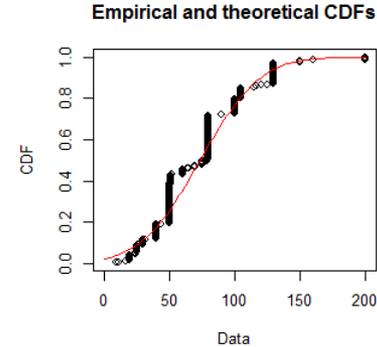
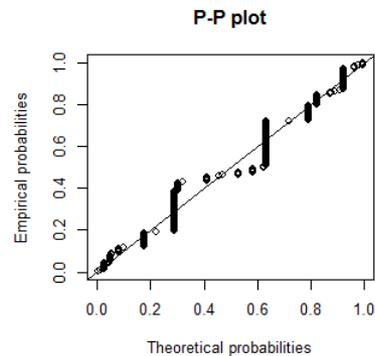
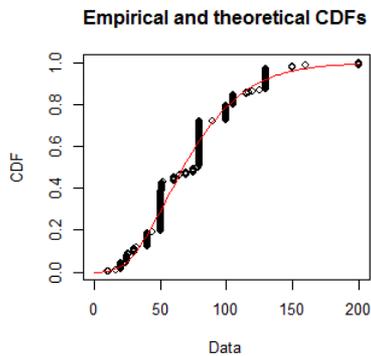
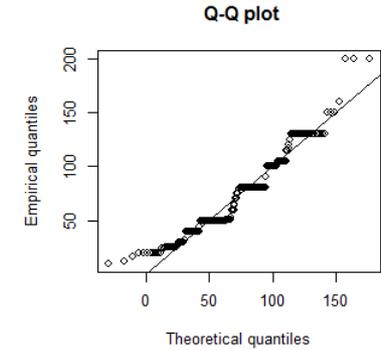
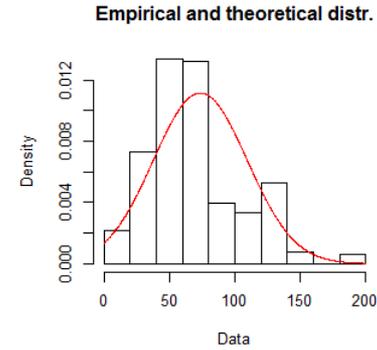
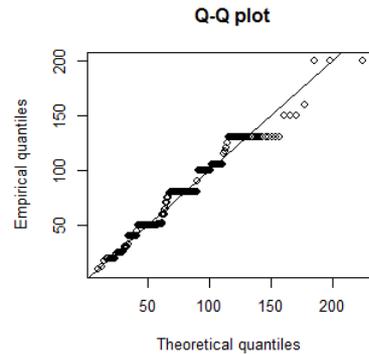
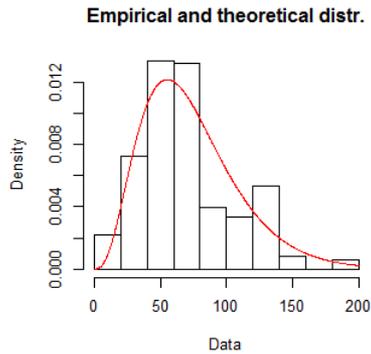
It's up to you!

```
#####  
# I Portion size  
#####  
  
# 1. importing data  
data<-read.csv("portions.csv",header=TRUE,sep=';')  
  
# 2. Which distribution laws?  
descdist(data$Portion) # Cullen & Frey graph  
  
# 3. Adjustment  
f_gamma<-fitdist(data$Portion, "gamma") # Gamma distribution adjustment  
f_Inorm<-fitdist(data$Portion, "lnorm") # Fit lognormal distribution  
  
plot(f_gamma)  
plot(f_Inorm)  
summary(f_gamma)  
summary(f_Inorm)  
  
hist(rgamma(1000,f_gamma$estimate[1],f_gamma$estimate[2]))  
  
#####  
# II Microbiological contamination data ingredient 1  
#####
```

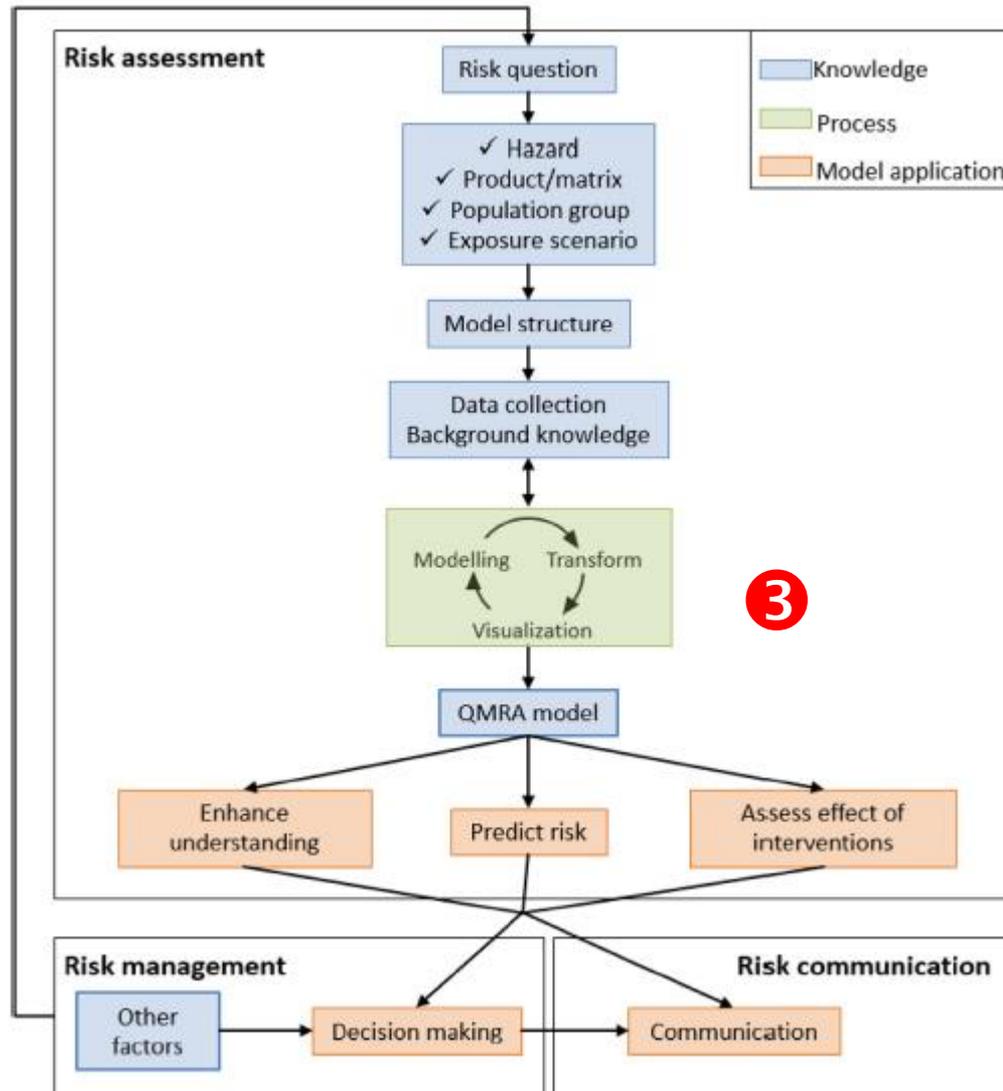
1. How to define a distribution?
2. How to identify candidate distributions?
3. How to fit a distribution?
4. How to characterize uncertainty?

Which distribution fit the best the data?

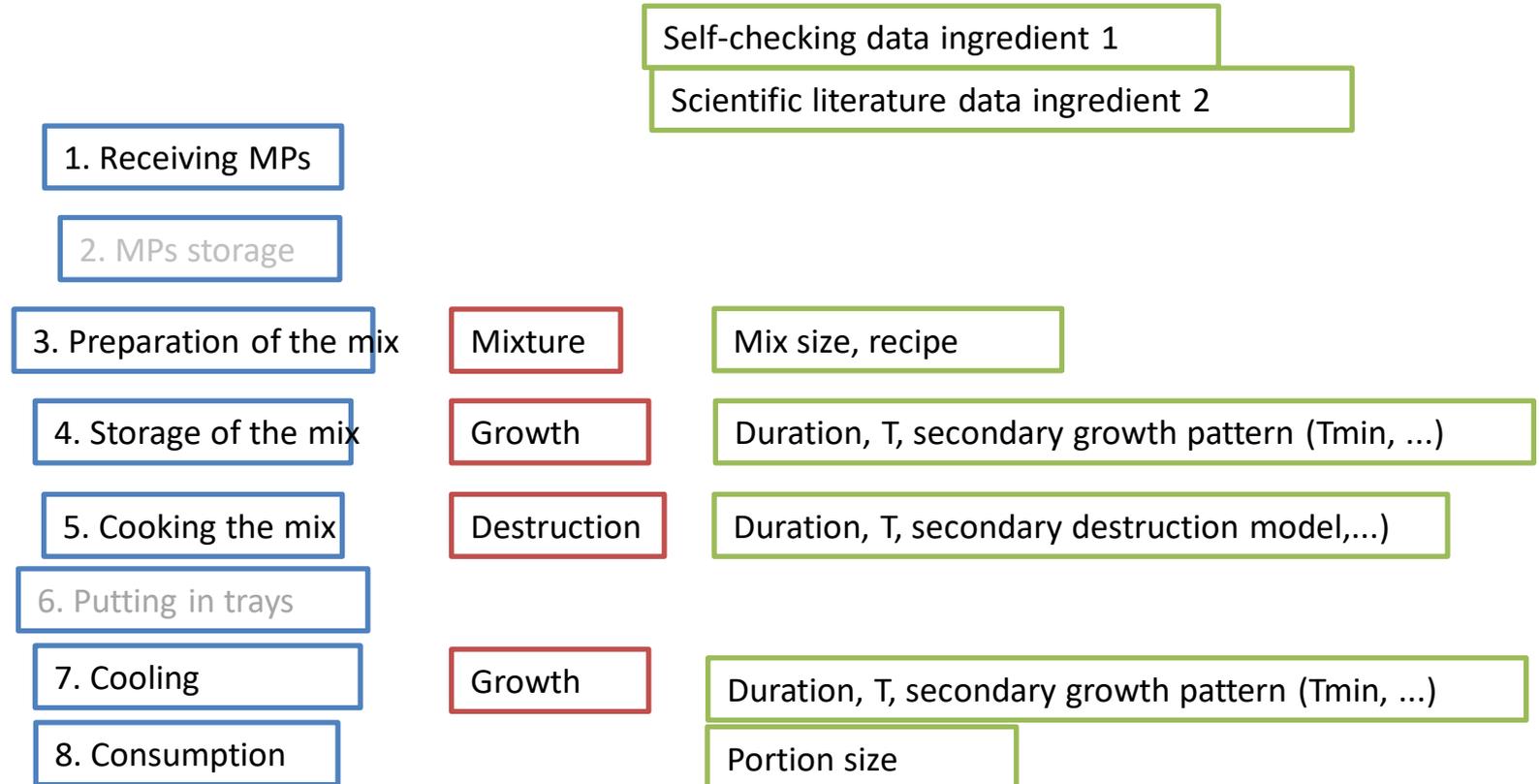
By graphic observation:
Distribution 1 Distribution 2



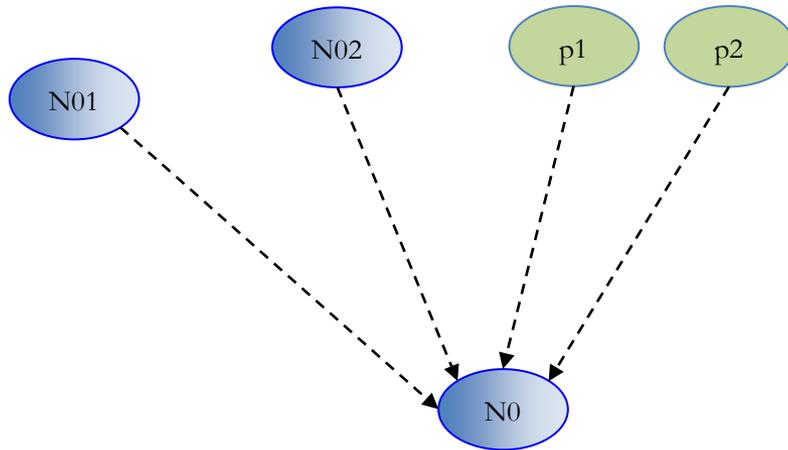
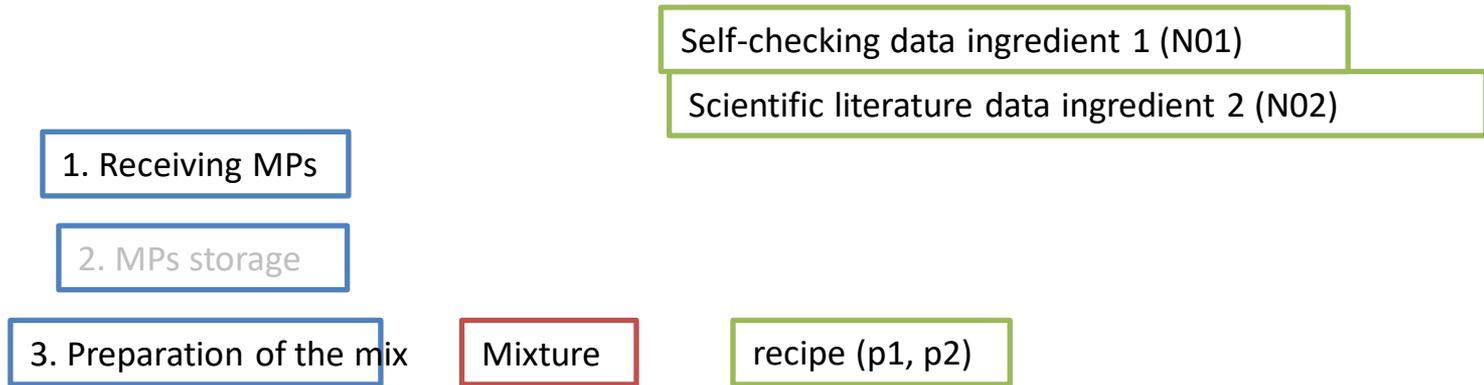
Quantitative risk assessment



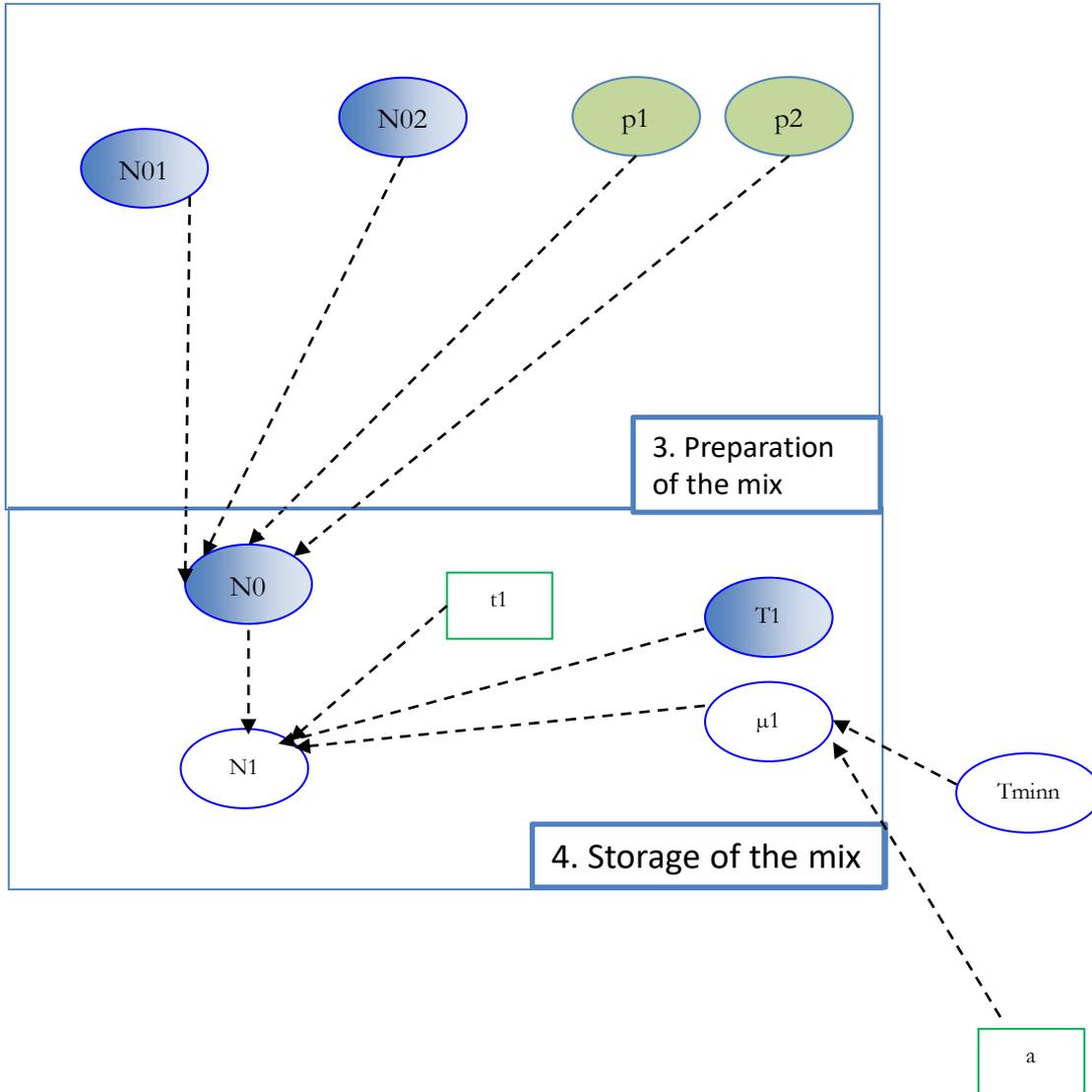
Make a representation of the model



Make a representation of the model



Make a representation of the model (cf. DAG_AQR.pdf)



Growth

Duration (t_1), T (T_1),
secondary growth pattern
(T_{min} , ...)

Describe the mathematical relationships of the nodes and between the nodes (see Variables and equations QMRA.pdf)

Model variables and equations	Abreviation	Definition	Unit
Initial contamination ingredient 1			
Average	M_{N01}	Estimated from self-checks (autocontroles_ing1.csv) and R script (formation_AQR1.r)	\log_{10} (cfu/g)
Standard deviation	S_{N01}	Estimated from self-checks (autocontroles_ing1.csv) and R script (formation_AQR1.r)	\log_{10} (cfu/g)
Concentration in ingredient 1	N_{01}	Normal (M_{N01}, S_{N01})	\log_{10} (cfu/g)
...			
Concentration in the mix	N_0	$\log_{10}((10^{N_{01}} p_1 + 10^{N_{02}} p_2))$	\log_{10} (cfu/g)
...			
Growth in the mix			
Average temperature of the cold room	M_{T1}	4	°C
SD of storage temperature of raw materials	S_{T1}	1	°C
Storage temperature of raw materials	T_1	Normal (M_{T1}, S_{T1})	°C
Storage time	t_1	10	hours
Ratkowski model constant	a	0.033	-

Your turn to play

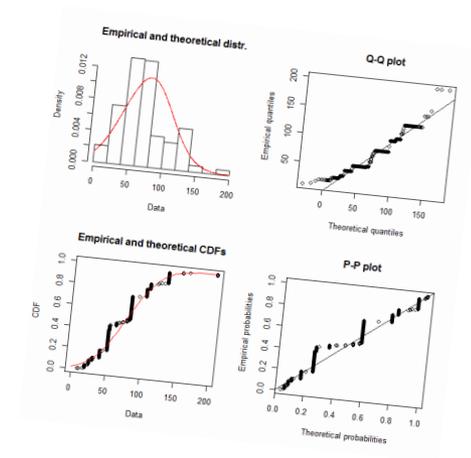
QMRA.xlsx

Measuring the impact on risk of different scenarios:

- Reduction of the initial average N01 contamination by $0.5 \log_{10}$
- Increase in heat treatment time (t2) from U(5-6) to U(6-7)
- Treatment temperature (T2): increase from 70 to 73°C
- Cooling temperature (T3) from 6°C to 4°C

What control measure do you retain?

$$f(x) = \frac{\beta^{-\alpha} x^{\alpha-1} \exp(-x/\beta)}{\Gamma(\alpha)}$$



Thank you!

Variables and equations of the AQR model	Abbreviation	Definition	Unit
Initial contamination ingredient 1			
Average	M_{N01}	Estimated from self-checks (autocontroles_ing1.csv) and R script (workshop_variability.r)	\log_{10} (cfu/g)
Standard deviation	S_{N01}	Estimated from self-checks (autocontroles_ing1.csv) and R script (workshop_variability.r)	\log_{10} (cfu/g)
Concentration in ingredient 1	N_{01}	Normal (M_{N01}, S_{N01})	\log_{10} (cfu/g)
Initial contamination ingredient 2			
Average	M_{N02}	-1,3	\log_{10} (cfu/g)
Standard deviation	S_{N02}	0,3	\log_{10} (cfu/g)
Concentration in ingredient 2	N_{02}	Normal (M_{N02}, S_{N02})	\log_{10} (cfu/g)
Preparation of the mix			
Share of ingredient 1	p1	Unif(0.7 - 0.8)	
Share of ingredient 2	p2	1-p1	
Concentration in the mix	NO	$\log_{10}((10^{N01} \cdot p1 + 10^{N02} \cdot p2))$	\log_{10} (cfu/g)
Storage of the mix			
Average temperature	M_{T1}	4	$^{\circ}\text{C}$
SD temperatures	S_{T1}	1	$^{\circ}\text{C}$
Storage temperature of the mix	T_1	Normal (M_{T1}, S_{T1})	$^{\circ}\text{C}$
Storage life of the mix	t_1	10	hours
Growth model parameter	a	0.033	-
Average Tmin	M_{Tmin}	-2	$^{\circ}\text{C}$
SD of Tmin	S_{Tmin}	0.25	$^{\circ}\text{C}$
Minimum growth temperature	T_{min}	Normal (M_{Tmin}, S_{Tmin})	$^{\circ}\text{C}$
Cooking			
Average cooking temperature	M_{T2}	65	$^{\circ}\text{C}$
SD of the cooking temperature	S_{T2}	2	$^{\circ}\text{C}$
Cooking temperature	T_2	Normal (M_{T2}, S_{T2})	$^{\circ}\text{C}$
Cooking time	t_2	Uniform(5,6)	minutes

Reference temperature	T_{ref}	70	°C
Mean reduction time at Tref	M_{Dref}	1	minutes
SDreduction time at Tref	S_{Dref}	0,01	
Decimal reduction time at Tref	D_{ref}	Normal (M_{Dref} , S_{Dref})	minutes
Value of z	z	8	°C

Cooling

Storage temperature of the cooked food	T_3	Normal (6,1.5)	°C
Shelf life	t_3	140	hours

Consumption

Parameter scale of the Gamma law	param1	Estimated from the survey (portions.csv) and R script (workshop_variability.r)	
Parameter rate of the Gamma law	Param2	Estimated from survey (portions.csv) and R script (workshop_variability.r)	
Quantity consumed in the tray	portion	Gamma (param1, param2)	g

Dose response

Dose-response parameter	r	1.10^{-10}	
-------------------------	-----	--------------	--

Equations

Growth rate during storage of the mix	μ_1	$(a \cdot (T_1 - T_{min}))^2$	h^{-1}
Contamination before cooking	N_1	$N_0 + \log_{10}(\exp(\mu_1 \cdot t_1))$	\log_{10} cfu/g
Contamination after cooking	N_2	$N_1 - (t \cdot 2.10^{(T_2 - T_{ref})/z}) / D_{ref}$	\log_{10} cfu/g
Growth rate during storage of cooked food	μ_3	$(a \cdot (T_3 - T_{min}))^2$	h^{-1}
Contamination after storage	N_3	$\min(9, N_2 + \log_{10}(\exp(\mu_3 \cdot t_3)))$	\log_{10} cfu/g
Dose ingested	dose	$10^{N_3} \cdot \text{portion}$	cfu
Risk for 1 batch	risk	$(1 - \exp(-r \cdot \text{dose}))$	Probability
Mean risk	mean_risk		

Connexion

Herramienta de Evaluación Cuantitativa del Riesgo Microbiano

microHibro

Autenticación

Usuario

Clave

Idioma ▼

[¿Ha olvidado su contraseña?](#)

[Regístrate aquí](#)

Limitación de responsabilidad

Optimizado para Mozilla Firefox 25, Internet Explorer 10 y Google Chrome 30 o superiores

Create a model

The screenshot shows the microlibro web application interface. At the top left, the logo "microlibro" is displayed. The user's name "Fanny Tenenhaus-Aziza" and a power icon are in the top right. Below the logo, there are navigation menus for "Ontologies", "Predictions", and "Sampling Plans". A search bar contains the text "arativelisteria saumon". A dropdown menu is open under "Risk Assessment", with "Microbial Models", "Shen-life models", and "Risk Assessment" visible. The "Risk Assessment" option is circled in red. Below the search bar, there are icons for settings, save, refresh, and delete. The main workspace has a tab bar with "L. monocytogenes o...(1)", "Listeria saumon(2)", "L. monocytogenes o...(1)", and "New(3)". The workspace itself is a grid with a green box labeled "Initial Model" and a blue dot. On the right side of the workspace, there are icons for edit, save, and delete, which are also circled in red. At the bottom, there are buttons for "Growth", "Transfer", "Inactivation", and "Dose Response". The "Dose Response" button is highlighted with a red border. To the right of these buttons, it says "Iterations: 100". At the bottom left, there are links for "Shared Models", "My comparisons", and "Instructions". At the bottom right, there is a "Contact Us" link and a footer with "Registro Propiedad Intelectual: RTA-99-12".

Initial prevalence and concentration

- Contamination prevalence = 6,29 %
- Initial conc at factory (log CFU/g)
 - Max = 5,7
 - Mean = - 0,28
 - SD = 0,9
 - Min = -1,4

The screenshot shows the 'Initial Model' dialog box in a software application. The interface is divided into two main sections: 'VARIABLES' and 'DISTRIBUTIONS'. The 'VARIABLES' section has three rows: 'M (g)' with a value of 100.00, 'N0 (log units/g)' with a value of 1.00, and 'Prevalence (%)' with a value of 6,29. The 'DISTRIBUTIONS' section has a 'Normal' distribution selected, with parameters: Minimum (-1.4), Maximum (5.7), Mu (-0.28), and Sigma (0.9). There are five red circles with numbers 1 through 5 highlighting specific elements: 1 points to the 'Initial Model' button, 2 points to the 'Prevalence' input field, 3 points to the 'M' input field, 4 points to the 'Mu' input field, and 5 points to the 'Apply' button.

Variable	Value	Range
M (g)	100.00	[0, 1000]
N0 (log units/g)	1.00	[-, -]
Prevalence (%)	6,29	[0, 100]

Parameter	Value
Distribution	Normal
Minimum	-1.4
Maximum	5.7
Mu	-0.28
Sigma	0.9

Modelling exposure and concentration

The image displays a software interface for modelling exposure and concentration, featuring a list of growth models, a distribution parameter table, and a metadata panel.

Growth Models List:

- Antunes et al. (2019) (Gilthead sea bream / *Shewanella putrefaciens*)
- Antunes et al. (2019) (Gilthead sea bream / *Lactic Acid Bacteria*)
- Chung et al. (2019) (Crab / *Vibrio parahaemolyticus*)
- Pérez-Rodríguez et al. (2017) (Heat-treated meat / *Listeria monocytogenes*)
- Pérez-Rodríguez et al. (2017); All (Cooked meat and sausage / *Listeria monocytogenes*)
- Pérez-Rodríguez et al. (2017); All (Smoked and gravad fish / *Listeria monocytogenes*)
- Chorin et al. (1997) (Brain-heart infusion broth / *Bacillus cereus*)
- Costa et al. (2020) (Brain-heart infusion broth / *Listeria monocytogenes*)
- Costa et al. (2020) (Brain-heart infusion broth / *Lactobacillus*)
- Fang et al. (2013) (Cantaloupe / *Listeria monocytogenes*)
- Gumudavelli et al. (2007) (Egg yolk / *Salmonella Enteritidis*)

DISTRIBUTION TABLE:

Variable	Value	Range
M (g)	100.00	[0, 100]
lag (h)	5.00	[0, 10000]
m (Dimensionless)	1.00	[0, 10]
t (h)	24.00	[0, 10000]
Temp (°C)	5.00	[-1.5, 30]

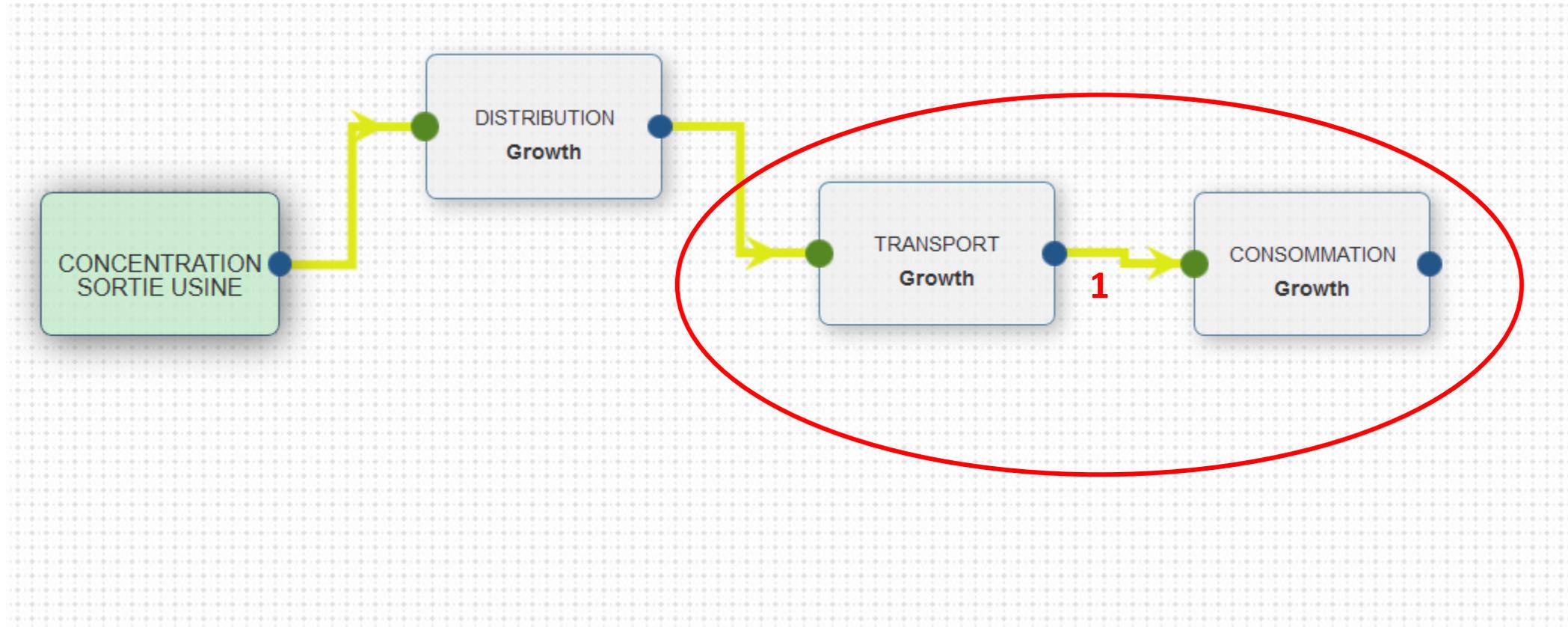
METADATA:

- Name:** DISTRIBUTION
- Category:** Growth Model
- Type:** Deterministic model
- Name:** Perez-Rodríguez et al. (2017); All
- Description:** Square-root model for growth rate of *Listeria monocytogenes* derived from literature and combase data for smoked fish
- Microorganism:** *Listeria monocytogenes*
- Foods:**
 - Smoked and gravad fish: it includes other fish species, under reduced oxygen packaging and normal atmosphere
- References:**
 - Baranyi & Roberts (1994)_log10(mu)
 - József Baranyi & Terry A. Roberts International Journal of Food Microbiology. 23, 277-294. (1994)
- Primary Function:**
 - Equation: $y_0 + (u_{max} / \ln(10)) * (t - lag + (\ln(1 - \exp(-u_{max} * t) + \exp(-u_{max} * (t - lag))) / u_{max}))) - (1 / (m * \ln(10))) * \ln(1 + ((\exp(m * u_{max} * (t - lag + (\ln(1 - \exp(-u_{max} * t) + \exp(-u_{max} * (t - lag))) / u_{max}))) - 1) / (\text{pow}(10, m * (y_{max} - y_0))))))$
- Secondary Function umax:**

Diagram:

The diagram shows a flow from "Initial Model" to "CONCENTRATION SORTIE USINE" and "DISTRIBUTION Growth".

Modelling exposure and concentration



Environmental parameters at each step

- Durations step (hours):

- Retail: max = 729 / min = 24 / Mean = 462 **-> TRIANGULAR**
- Transport: max = 4 / min = 0,5 **-> UNIFORM**
- Consumption: max = 720 / min = 24 / Mean = 153

- Temperature step (°C)

- Retail : max = 23 / min = 0 / Mean = 3,54 / SD = 1,72
- Transport: max = 9,5 / min = 4 / Mean = 7
- Consumption : max = 17 / min = 0 / Mean = 7 / SD = 2,7 **-> NORMAL**

M (g)	<input type="text" value="100.00"/>	Range: [0, 100]
lag (h)	<input type="text" value="x ∈ r"/>	Triangular[50;5,200]
m (Dimensionless)	<input type="text" value="1.00"/>	Range: [0,10]
t (h)	<input type="text" value="x ∈ r"/>	Triangular[462;24,729]
Temp (°C)	<input type="text" value="x ∈ r"/>	Normal[3.54,1.72;0,12]

Distribution

Minimum

Maximum

Mean

Apply

Triangular

24

729

1

462

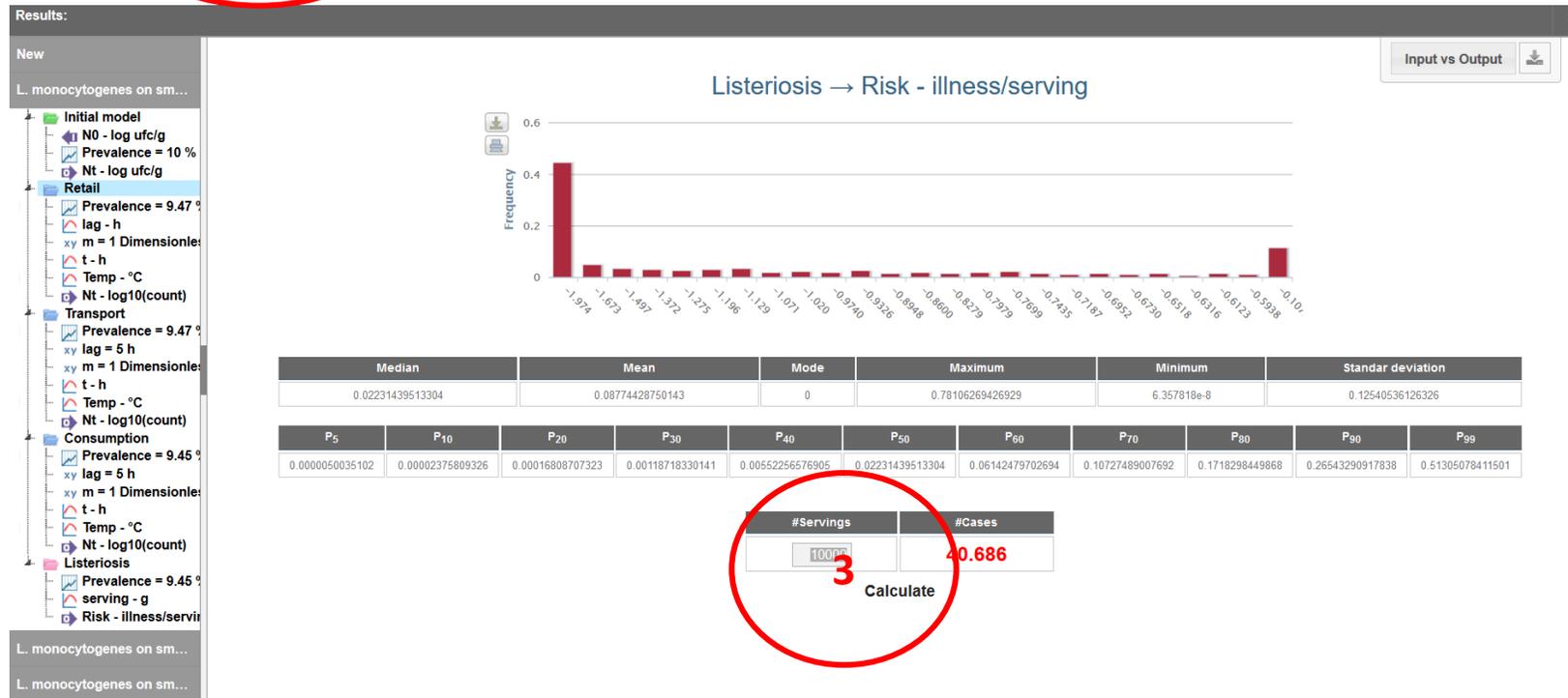
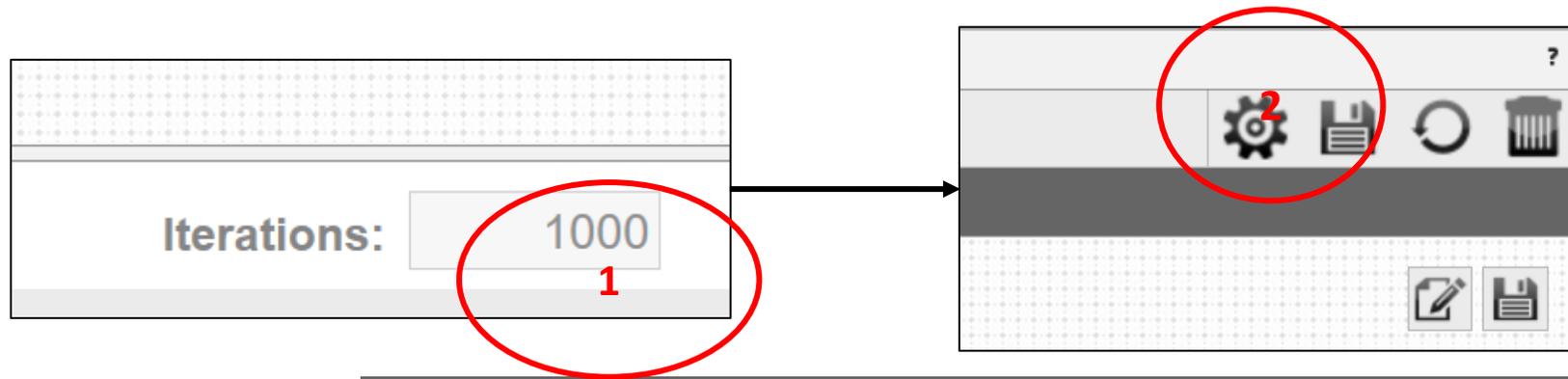
Cancel

Modèle dose réponse

The image shows a software interface for configuring a dose-response model. It consists of several panels:

- Dose-Response Models:** A list of three models. The second model, "Dose response model for Escherichia coli O157:H7 (Escherichia coli O157:H7)", is selected and circled in red with the number 2.
- Dose réponse:** A configuration panel with two main sections:
 - VARIABLES:** A variable named "serving (g)" is defined with a value of 10.00 and a range of [0,300].
 - DISTRIBUTIONS:** The distribution is set to "Uniform". The minimum value is 10 and the maximum value is 120. These values are circled in red with the number 3.
- Buttons:** At the bottom, there are buttons for "Transfer", "Inactivation", and "Dose Response". The "Dose Response" button is circled in red with the number 1.

Launching simulations / model outputs



Entrées vs sorties

Results:

L. monocytogenes on sm...

- Initial model
- Retail
- Transport
- Consumption
 - Prevalence = 9.5 %
 - xy lag = 5 h
 - xy m = 1 Dimensionless
 - t - h
 - Temp - °C**
 - Nt - log10(count)
 - Listeriosis
 - Prevalence = 9.5 %
 - serving - g
 - Risk - illness/serving

Consumption → Temp - °C

Input vs Output 1

Listeriosis → Nt - illness/serving vs. Consumption → Temp - °C

Frequency

Nt - illness/serving

Temp - °C

Contaminated s... Non-contaminat...

Median	Mean
7.343	7.25

P5	P10
2.676	3.464

num	Standar deviation
98	2.905

P70	P80	P90	P99
8.636	9.565	10.83	13.99

Case study : *Listeria* *monocytogenes* in sausages

Perez-Rodriguez et al. (2017) cooked meat and sausage

Initial contamination

Input variable	Description	Distribution/model/value	Unit
N_0	Initial concentration	Normal (1.05, 0.44)	Log_{10} CFU/g
P	Prevalence	7.5	%
W	Sausage weight	100	Grams

First storage

At the end of the first storage; in average the mean concentration increase of 0,43 log ufc/g

Second storage

Input variable	Description	Distribution/model/value	Unit
t_{st}	Storage at the factory duration	Uniform (0, 36)	h
T_{st}	Storage temperature at the factory	5	°C

Retail

Input variable	Description	Distribution/model/value	Unit
t_R	Storage time at retailing	Uniform (2, 6)	h
T_R	Temperature at retailing	Normal distribution (3.7, 1.78)	°C

Transport

Input variable	Description	Distribution/model/value	Unit
t_{TR}	Transport to home time	Uniform (0.25, 2)	h
T_{TR}	Transport to home temperature	Triangular distribution (10; 4; 25)	°C

Conservation

Input variable	Description	Distribution/model/value	Unit
t_H	Household storage time	Normal (103,2, 62,4)	h
T_H	Household temperature	Normal (6.62, 2.56)	°C

Consumption

Input variable	Description	Distribution/model/value	Unit
S_z	Serving size	Normal distribution (50, 5)	Grams

Dose Response model

Equation:
 $1 - \exp(-r \times \text{pow}(10, \text{dose}) \times \text{serving})$

Questions

- What is the distribution of the risk of listeriosis by portion (median, minimum, maximum) with 1000 iterations ? For sensitive population ? For population > 65 years old?
- If the temperature varies between 0°C et 3°C during transport between retailing and consumer home, what is the impact on the risk of listeriosis?