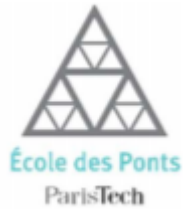


QMRA of alternative urban water resources



Research project
Intern: Caroline Kimie Miyazaki
Supervisor: Martin Seidl



BACKGROUND INFORMATION



Environmental Engineering (bachelor degree)



2 years of work experience in water and sanitation projects



UNICAMP

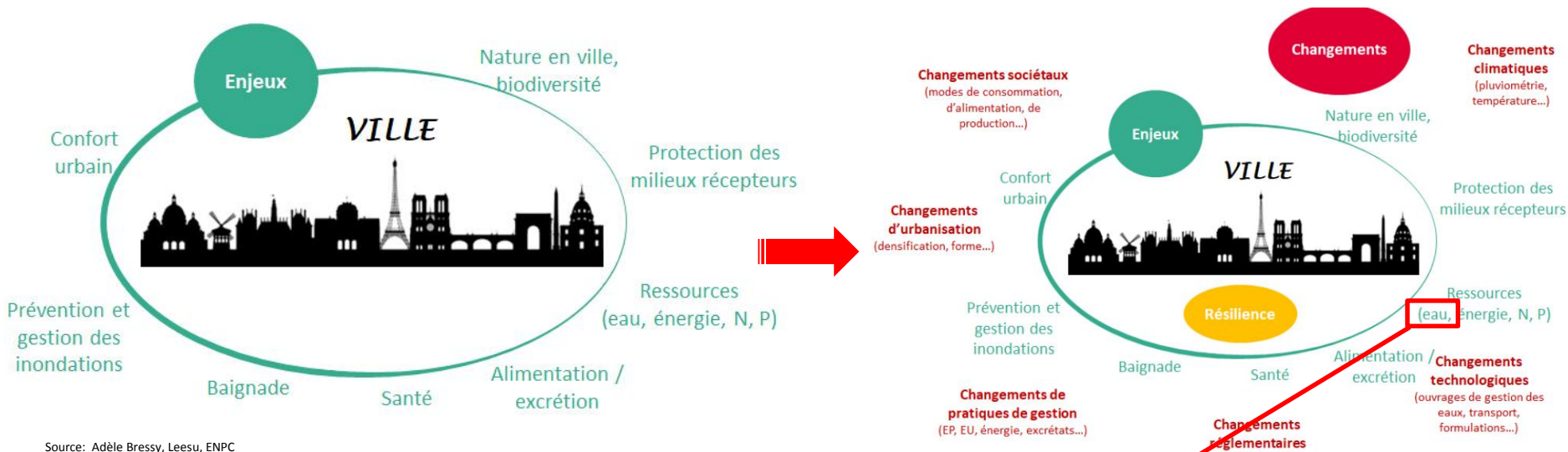
Civil Engineering (masters degree)

Research intern: Urban Risk lab (2021), LEESU (Martin SEIDL) and EDP (Laurent Moulin)



CONTEXT

RESILIENCE



Source: Adèle Bressy, Leesu, ENPC

Source: Adèle Bressy, Leesu, ENPC

Water sector: demands resilient infrastructure and strategic management

WATER RESOURCES – NON POTABLE USE



Piscine municipale - Ville de Rennes

Source: Ville de Rennes



Cuve de réutilisation des eaux pluviales du Parc du Quartier des Bords de Seine à Asnières-sur-Seine

Source: Composante urbaine



Poste d'épuisement de la RATP

Source: RATP



Rivière Meguro au Japon

Source: A. Tajima, M. Yoshizawa, K. sakurai, M. Minamiyama, establishment of guidelines for the reuse of treated wastewater

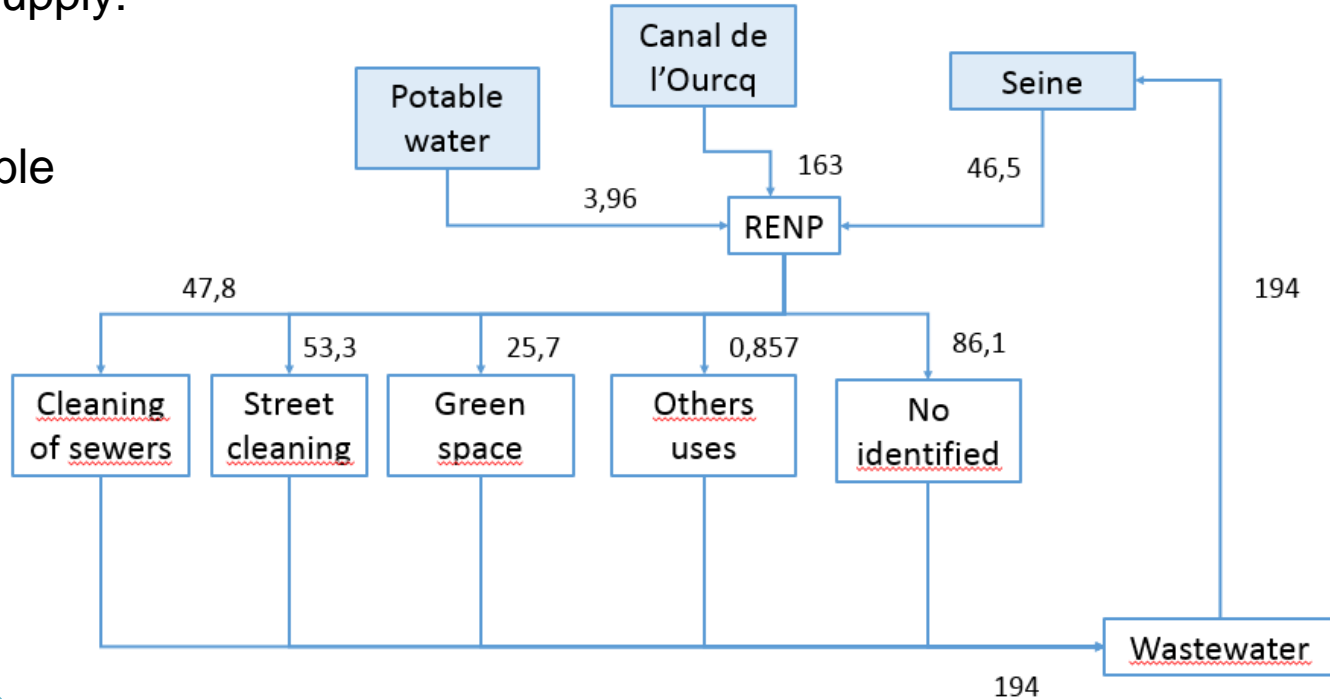
Source	Pool water	Rainwater	Mine water	Reclaimed wastewater
Median volume (m ³ /year)	698*10 ³	2,94*10 ⁶	9,83*10 ⁶	352*10 ⁶
Percentage in relation to the volume of non-potable water distributed	< 1%	4% (discontinuos)	12%	448%
Quality constraints	Chlore	Bacteria	Conductivity, sulfate	Pathogen

Source: Adapted from (Trinh 2017)

RENp

Dual water supply:

- Potable network
- Non-potable network



Source: Adapted from (Trinh 2017)

OBJECTIVE

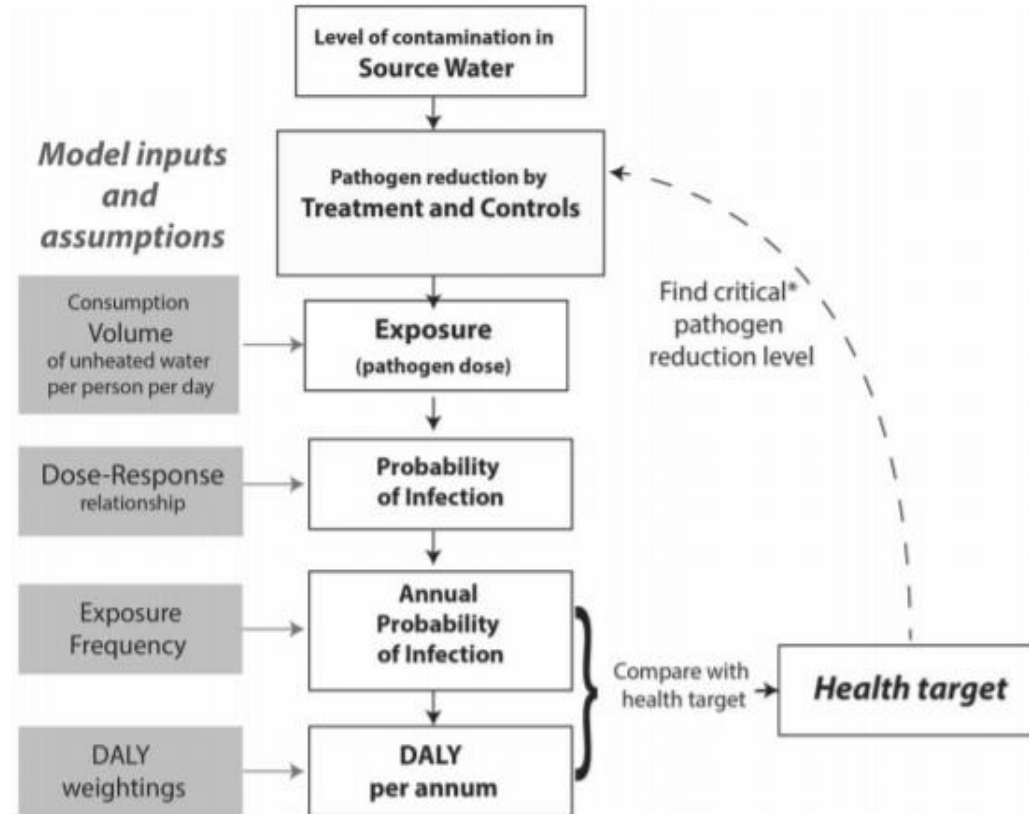
The aims of the present study are to compare the health risk for the rainwater and Paris non-potable network, through the application of QMRA tool. The specific objectives are:

- Identify scenarios exposures for each use;
- Calculate the risk through QMRA steps;
- Compare the scenario for each alternative water resource.

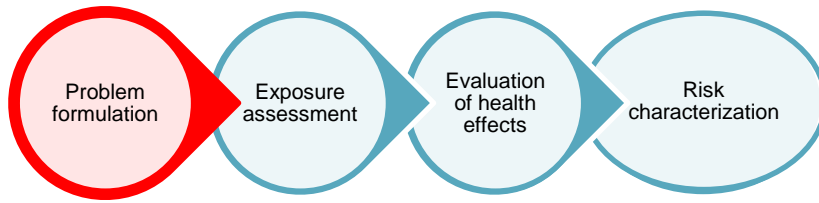
METHOD

QMRA

Quantitative microbial risk assessment:



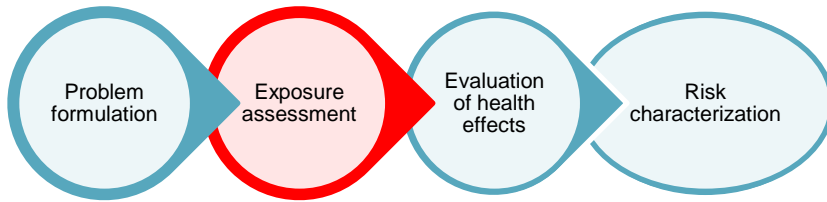
*The critical pathogen reduction level is the Log_{10} reduction that yields a measure of risk equal to the health target



QMRA

Pathogen	Greywater	Rainwater	Stormwater	Seepage	Wastewater reuse
Norovirus	Yellow	Light Blue	Yellow	Yellow	Yellow
Rotavirus	Yellow	Light Blue	Yellow	Yellow	Yellow
Adenovirus	Yellow	Light Blue	Yellow	Light Blue	Yellow
Enterovirus	Yellow	Light Blue	Yellow	Light Blue	Yellow
Cryptosporidium	Yellow	Yellow	Yellow	Yellow	Yellow
Giardia lamblia	Yellow	Yellow	Yellow	Yellow	Yellow
Campylobacter	Yellow	Yellow	Yellow	Yellow	Yellow
Salmonella spp	Yellow	Yellow	Yellow	Light Blue	Light Blue
E.Coli	Yellow	Yellow	Light Blue	Yellow	Yellow
L. pneumophila	Light Blue	Yellow	Yellow	minewater	Light Blue
Mycobacterium avium complex (MAC)	Light Blue	Yellow	Light Blue	Light Blue	Light Blue

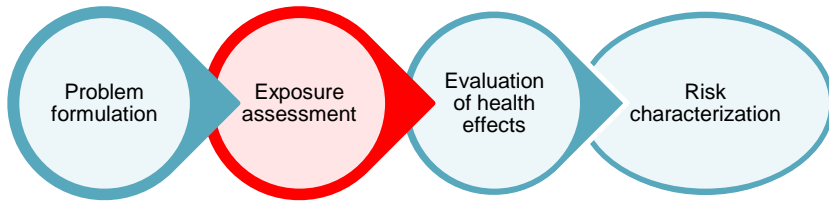
Fonte: a- (Shi et al. 2018); b- (Gonçalves et al. 2020) ; c- (Ottoson and Stenström 2003); d- (Fiona Barker et al. 2013); e- (Schoen et al. 2017); f- (Schoen and Garland 2017), g- (Hora et al. 2017), h- (Hamilton et al. 2017); i- (Ahmed et al. 2010); j- (Fewtrell and Kay 2007) ; k- (Madera-García et al. 2019); l- (Petterson and Ashbolt 2016); m- (McBride et al. 2013); n- (NRMCC 2006); o- (National Academies of Sciences 2015); p- (Zhiteneva et al. 2020) ;q- (Schoen et al. 2014)



QMRA

Use	Greywater	Rainwater	Stormwater	Seepage	Wastewater reuse
Toilet flushing	Yellow	Yellow	Yellow	Yellow	Yellow
Food-crop irrigation	Yellow	Yellow	Yellow	Yellow	Yellow
Drinking	Yellow	Yellow	Yellow	Yellow	Yellow
Showering	Yellow	Yellow	Yellow	Yellow	Yellow
Food washing	Yellow	Yellow	Yellow	Yellow	Yellow
Municipal irrigation	Yellow	Yellow	Yellow	Yellow	Yellow
Garden hosing	Yellow	Yellow	Yellow	Yellow	Yellow
Car washing	Yellow	Yellow	Yellow	Yellow	Yellow
Produce consumption	Yellow	Yellow	Yellow	Yellow	Yellow
Clothes washing	Yellow	Yellow	Yellow	Yellow	Yellow
Accidental ingestion	Yellow	Yellow	Yellow	Yellow	Yellow
Playing	Yellow	Yellow	Yellow	Yellow	minewater
Fire fighting	Yellow	Yellow	Yellow	Yellow	Yellow
Inhalation of water contaminated	Yellow	Yellow	Yellow	Yellow	minewater

Fonte: a- (Shi et al. 2018); b-(Goçalves et al. 2020); c- (Ottoson and Stenström 2003); d- (Fiona Barker et al. 2013); e- (Schoen et al. 2017); f- (Schoen and Garland 2017); g- (Hora et al. 2017); h- (Hamilton et al. 2017); i-(Ahmed et al. 2010); j-(Fewtrell and Kay 2007);k- (Madera-Garcia et al. 2019); l- (Pettersson and Ashbolt 2016); m- (McBride et al. 2013); n-(NRRMMC 2006); o- (National Academies of Sciences 2015); p- (Zhiteneva et al. 2020)



QMRA

Routes of contamination:

- Ingestion route

$$D_{ij} = C_{ij} * V_{ing,j}$$

D_{ij} = daily dose of pathogen i for water source j
(where j = non-potable network or rainwater)

C_{ij} = concentration of pathogen i for water source j

$V_{ing,j}$ = the volume ingested per exposure per event.

- Inhalation route

$$D_{ij} = \frac{1}{R} * C_{ij} * B * t * \sum_{d=1}^n (C_{aer,d} * V_{aer,d} * DE_d)$$

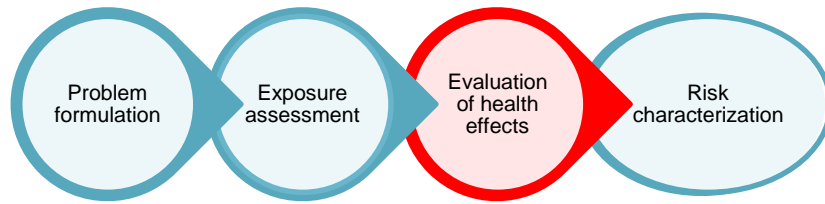
B = breathing rate (m³/min)

t = exposure duration (min)

$C_{aer,d}$ = concentration of aerosols of diameter d

$V_{aer,d}$ = volume of each aerosol size ($4/3\pi r^3$)

DE = alveolar deposition efficiency of size d .



QMRA

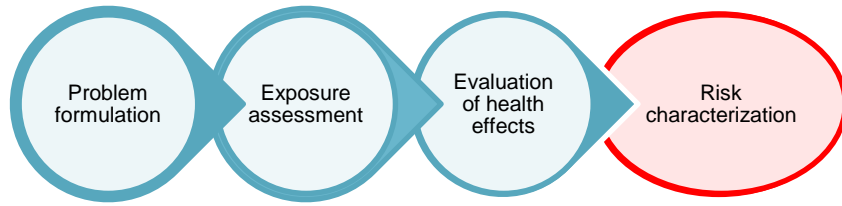
Established dose-response models

- Exponential model:

$$Pe = 1 - exp(-r * dose)$$

- Beta-Poisson model:

$$Pb = 1 - \left(1 + \frac{dose}{\beta}\right)^{-\alpha}$$



QMRA

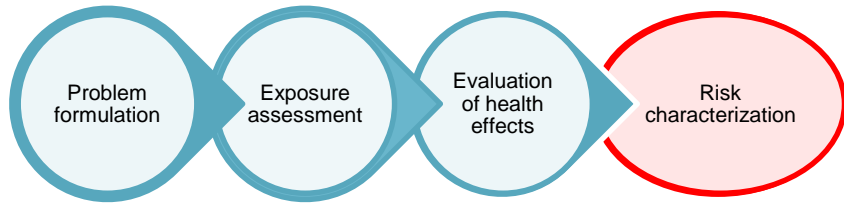
Two end-point in the literature to measure the impact:

- Probability of infection
- Disease burden in **DALYs**



Mortality is not enough to measure the burden of disease.

Disability-adjusted life year (DALY): combine the years-lost due to premature mortality (YLL) and years of life lost due to disability (YLD)



QMRA

$$P_{inf_y} = 1 - \left(1 - P_{inf}\right)^{365*f}$$

$$P_{ill_y} = P_{inf_y} * P_{ill|inf}$$

$$D = DALYh * P_{ill_y} * s$$

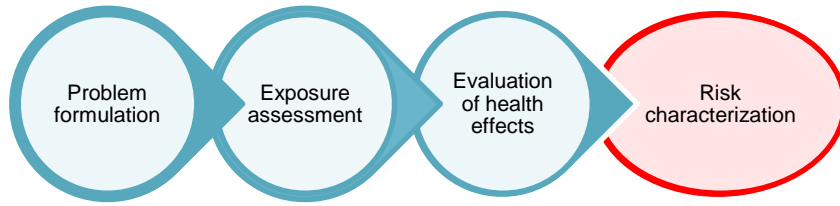
$$Total\ DALYs = \sum_0^h Dh$$

- P_{inf_y} is the annual risk of infection
- f is the frequency of exposure in per person per year.

- P_{ill_y} is the annual risk of illness
- $P_{ill|inf}$ is the risk of illness given infection

- D is the disease burden in DALYs
- $DALYh$ (DALYs/case) is pathogen-specific burden of disease
- “ s ” is fraction of population susceptible to be exposed

- h is the reference pathogen



QMRA

Risk characterization:

- Benchmark: $P_{inf} < 10^{-4}$ pppy or $D < 10^{-6}$ DALY pppy
- Tool - R programme

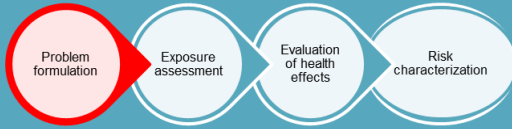
Uncertainty and variability:

- Uncertainty: lack of information
- Variability: elements changing over time and space



Monte Carlo simulation (10 000 runs)
 Sensitivity analysis (spearman correlation)

RESULTS AND DISCUSSION

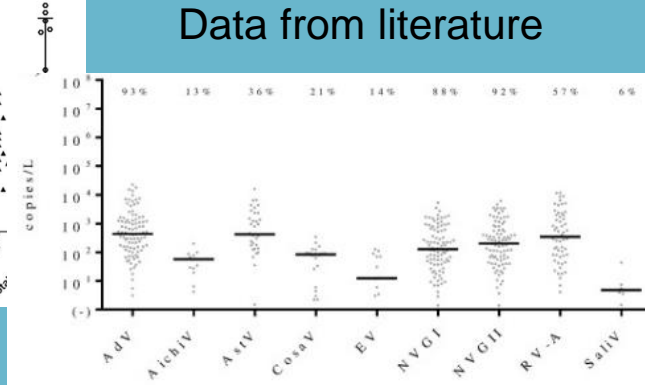
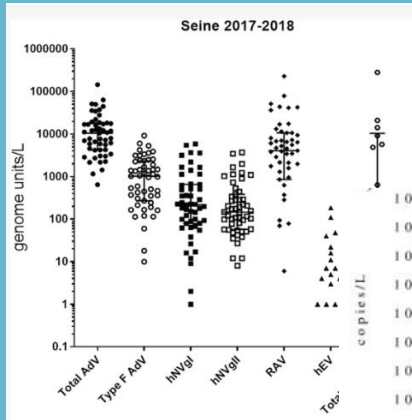


PROBLEM FORMULATION

Target pathogen:

Adenovirus, human norovirus I and II, rotavirus, cryptosporidium, giardia, campylobacter, salmonella, E.Coli (O157:H7), Legionella pneumophila

Pathogen concentration:



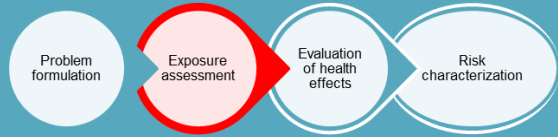
Wan's method (assuming normal distribution)

$$\bar{X} \approx \frac{a + 2m + b}{4}$$

b = maximum value
a = minimum value
m = median concentration

$$S \approx \frac{b - a}{2\Phi^{-1}\left(\frac{n - 0.375}{n + 0.25}\right)}$$

n = sample size
 Φ^{-1} = inverse function of the upper zth percentile of the standard normal distribution



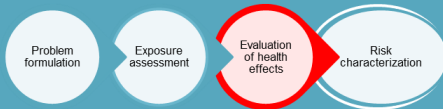
EXPOSURE ASSESSMENT

Use: Municipal irrigation



Scenario	Exposed group	Volume ingested (mL)	Contact exposure (min)	Events per year
A	Pedestrian ingestion/inhalation from spray irrigation	0.1 ^a	10 ^b	50 ^{a,b}
B	Ingestion via casual contact with children playing on irrigated grass (frequent hand-to-mouth activity)	4 ^a	10 ^b	50 ^{a,b}
C	Municipal irrigation worker	1 ^a	60 ^c	80 ^c

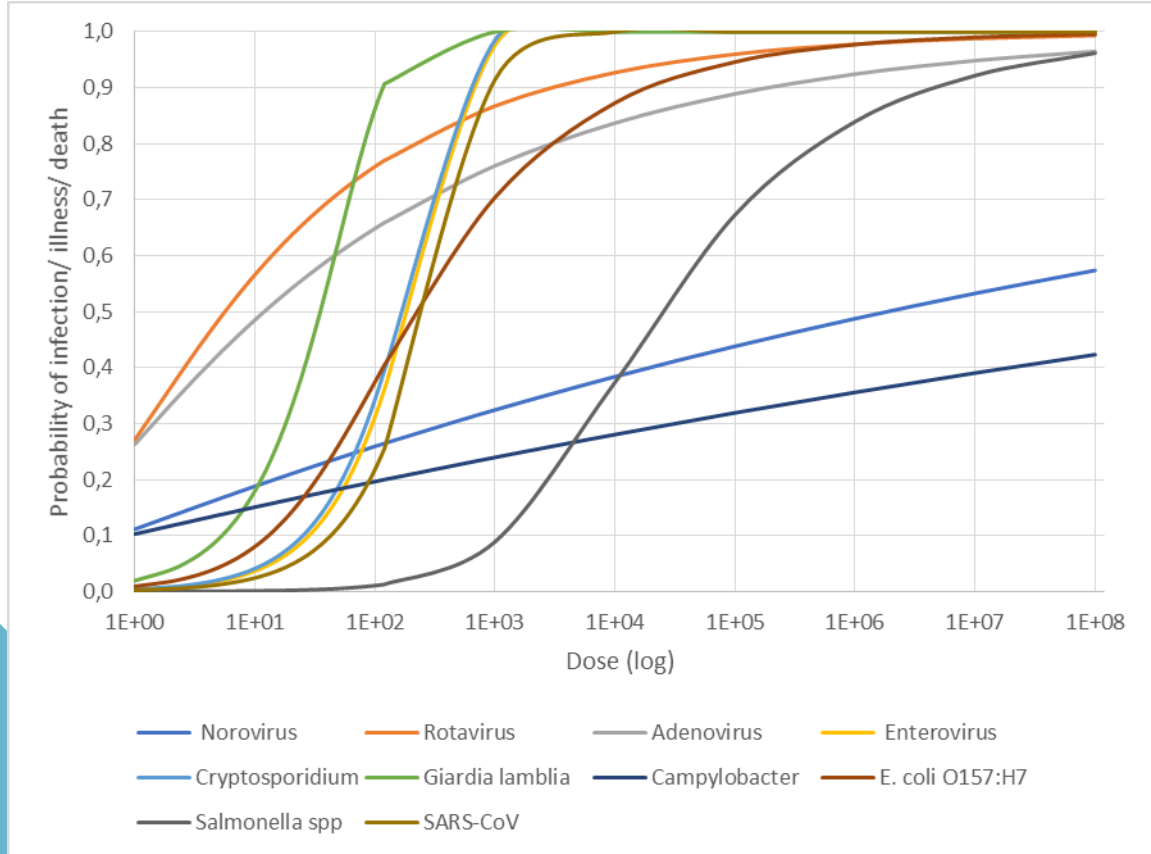
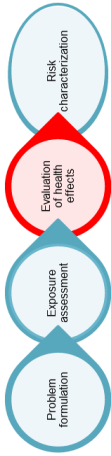
Sources: a- (NRMCC 2006; Ahmed et al. 2011; Schoen et al. 2017; Hamilton et al. 2017); b- Assumed in the summer time, 4 months (2-3 days of working per week), 10 min per day. ; c-Assumed in the summer time, 4 months (5 days of working per week), 1 hour per day.



HEALTH EFFECTS ASSESSMENT

Reference pathogen	Representative	Model	Parameter	Values	Units	Reference	Mobidity ratio ^c	Reference
Adenovirus	Adenovirus 4	Exponential ^d	r	0.4172		Haas et al., 1999	0.5	Haas et al., 1999
Human norovirus	Norwalk virus (GI)	Hypergeometric ^a	Alpha	0.04	Genome copies	(Teunis et al. 2008a)	0.6	(Soller et al. 2017)
			Beta	0.055				
Human norovirus	(GI & GII.4)	Fractional poisson ^b	P	0.722	Genome copies	(Messner et al. 2014)	0.6	(Soller et al. 2017)
			μ	1106				
Rotavirus	Rotavirus (CJN strain)	Beta-Poisson	Alpha	0.2531	FFU	(Mitchell et al. 2015)	0.35	(Gerba et al. 1996; McBride et al. 2013)
			Beta	0.4265				
Human enteroviruses	Echovirus 12	Beta-Poisson	Alpha	0.401	PFU	(Teunis et al. 1996)	0.5	(Teunis et al. 1996)
			Beta	227.2				
Cryptosporidium	Cryptosporidium spp .	Fractional poisson ^f	P	0.737	oocytys	(Messner and Berger 2016)	0.39	(DuPont et al. 1995, p. 199)
Giardia	Giardia lamblia	Exponential	r	0.0199	cytys	(RENDTORF 1954)	0.5	(Rose et al. 1991)
Campylobacter	Campylobacter jejuni	Beta-Poisson	Alpha	0.145	CFU	Haas et al., 1999	0.16	(Haas et al. 1996)
			Beta	7,589				
Salmonella	Non-typhoid	Beta-Poisson	Alpha	0.3126	CFU	Haas et al., 1999	1 ^e	Haas et al., 1999
			Beta	2884				
E.Coli	E.Coli O157 :H7	Beta-Poisson	Alpha	0.373	CFU	(Teunis et al. 2008b)	1 ^e	(Teunis et al. 2008b)
			Beta	39.71				
Legionella pneumophila		Exponential ^d	r	0.000107	CFU	(Armstrong and Haas 2008)	1 ^e	(Armstrong and Haas 2008)

HEALTH EFFECTS ASSESSMENT



Established dose-response models

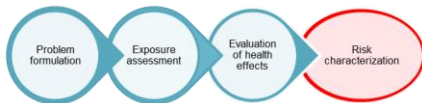
- Exponential model:

$$P = 1 - \exp(-r * dose)$$
- Beta-Poisson model:

$$P = 1 - \left(1 + \frac{dose}{\beta}\right)^{-\alpha}$$
- Hypergeometric:

$$P(c * V; \alpha, \beta) = 1 - 1F1(\alpha, \alpha + \beta; -c * V)$$
- Fractional poisson:

$$P(Dose, P) = P * (1 - e(-dose / \mu))$$



RISK CHARACTERIZATION

Variable	Abbreviation	Value
Number of interactions	n	10000
Ingestion volume	v	0.0001
Frequency of exposure	f	50
Concentration Human Norovirus I (RENP)	C_n1_rp	rlnorm(n, meanlog = 4.76, sdlog = 1.52)
Concentration Human Norovirus I (rainwater)	C_n1_rw	0
Model dose-response Human Norovirus I	alfa_n1	0.04
Model dose-response Human Norovirus I	beta_n1	0.055
DALY per Human Norovirus I	DALYS_n1	0.00101
Illness per infection Human Norovirus I	Pinf_ill_n1	0.6
Concentration Human Norovirus II (RENP)	C_n2_rp	rlnorm(n, meanlog = 5.17, sdlog = 1.22)
Concentration Human Norovirus II (rainwater)	C_n2_rw	0
Model dose-response Human Norovirus II	P_n2	0.722
Model dose-response Human Norovirus II	u_n2	1106
DALY per Human Norovirus II	DALYS_n2	0.00101
Illness per infection Human Norovirus II	Pinf_ill_n2	0.6
Concentration Rotavirus (RENP)	C_r_rp	rlnorm(n, meanlog = 6.34, sdlog = 1.59)
Concentration Rotavirus (rainwater)	C_r_rw	0
Model dose-response Rotavirus	alfa_r	0.2531
Model dose-response Rotavirus	beta_r	0.4265
DALY per Rotavirus	DALYS_r	0.014
Illness per infection Rotavirus	Pinf_ill_r	0.35
Concentration Human enterovirus (RENP)	C_he_rp	rlnorm(n, meanlog = 2.55, sdlog = 1.19)
Concentration Human enterovirus (rainwater)	C_he_rw	0
Model dose-response Human enterovirus	alfa_he	0.41
Model dose-response Human enterovirus	beta_he	2272
DALY per Human enterovirus	DALYS_he	0.01
Illness per infection Human enterovirus	Pinf_ill_he	0.5
Concentration cryptosporidium (RENP)	C_c_rp	rlnorm(n, meanlog = 0.32, sdlog = 1.40)
Concentration cryptosporidium (rainwater)	C_c_rw	unif(n, 2,240)
Model dose-response cryptosporidium	P_c	

DATA INPUT (Excel)

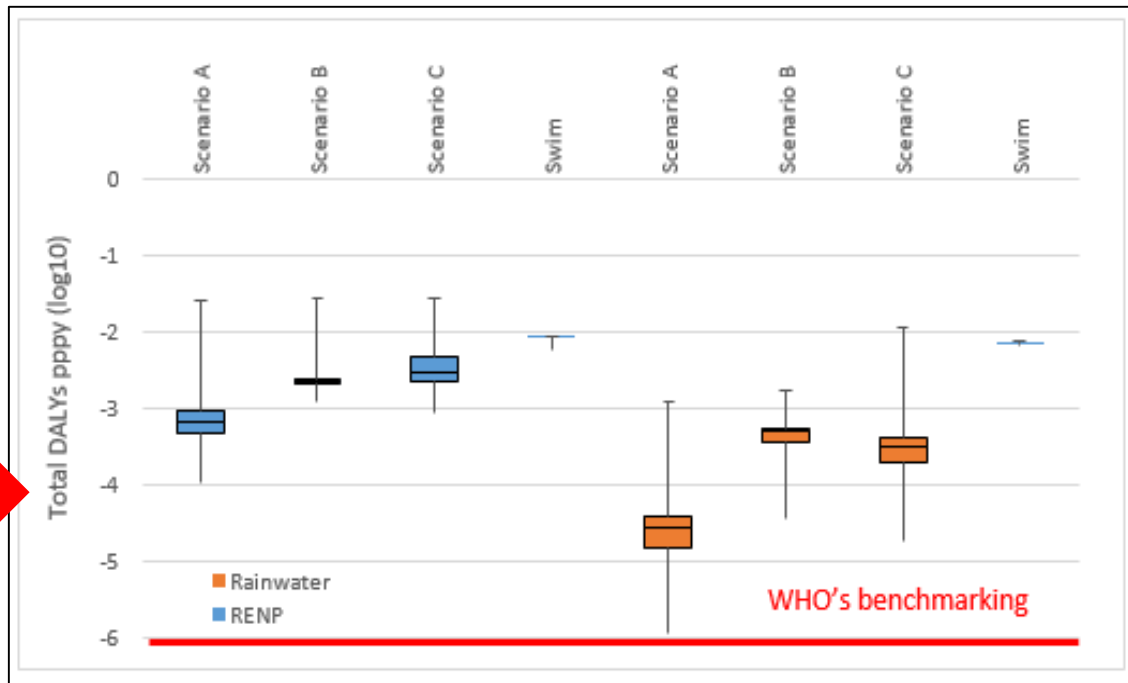
Simulation (R)

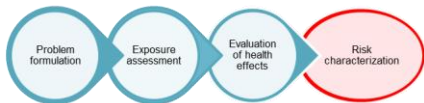
```

#####
### Human norovirus I#####
x_n1 <- alfa_n1+beta_n1 #general data
y_n1_rp <- (-1*C_n1_rp*v) #RENP
output_rp <- sapply(y_n1_rp, function(i) { #RENP
  hypergeometricF1(alfa_n1, beta_n1, i, FALSE) #RENP
})
Pinf_n1_rp = 1-output_rp #RENP
Pinf.y_n1_rp = 1-(1-Pinf_n1_rp)^f #RENP
Pill.y_n1_rp = Pinf_ill_n1*Pinf.y_n1_rp #RENP
D_n1_rp=DALYS_n1 * Pill.y_n1_rp #RENP

y_n1_rw <- (-1*C_n1_rw*v) #rainwater
output_rw <- sapply(y_n1_rw, function(i) { #rainwater
  hypergeometricF1(alfa_n1, x_n1, i, log = FALSE) #rainwater
})
Pinf_n1_rw = 1-output_rw #rainwater
Pinf.y_n1_rw = 1-(1-Pinf_n1_rw)^f #rainwater
Pill.y_n1_rw = Pinf_ill_n1*Pinf.y_n1_rw #rainwater
D_n1_rw=DALYS_n1 * Pill.y_n1_rw #rainwater

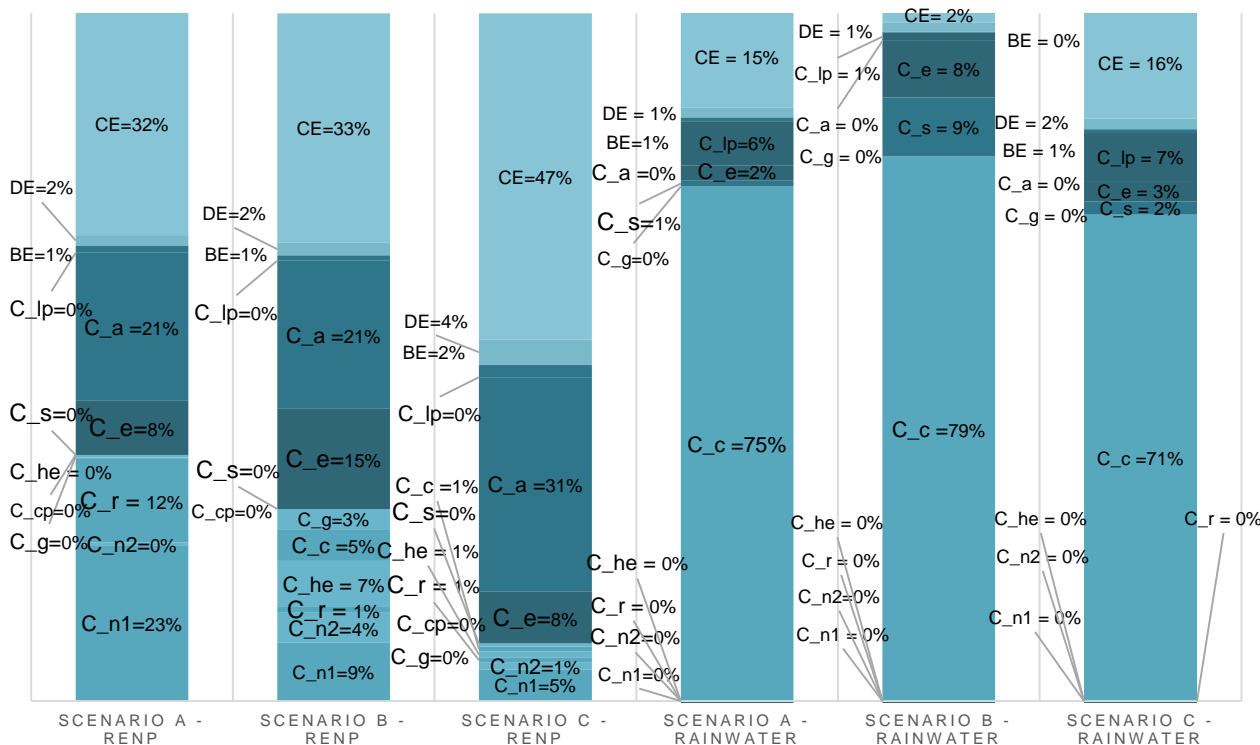
## Human norovirus II ##
Dose_n2_rp=C_n2_rp*v #RENP
Pinf_n2_rp = F_n2*(1-exp(-dose_n2_rp/u_n2)) #RENP
Pinf.y_n2_rp = 1-(1-Pinf_n2_rp)^f #RENP
Pill.y_n2_rp = Pinf_ill_n2*Pinf.y_n2_rp #RENP
D_n2_rp=DALYS_n2 * Pill.y_n2_rp #RENP
  
```





SENSITIVITY ANALYSIS

Total disease burden in DALYs for each source



Predictor factor:

- RENP: concentration of aerosols diameters
- Rainwater: the concentration of cryptosporidium



UNCERTAINTY ANALYSIS

- Pathogen target (concentration of pathogen in Seine river, survival and persistence of microorganism, personal hygiene behavior and personal protective equipment)
- Exposure evaluation based on literature
- Model dose-response (not considered susceptible populations, secondary transmission)

CONCLUSION

CONCLUSION

Internship hopes to give the field actor some preliminary knowledge for better decision-making.

Further studies in the field could improve the model

Rainwater source pose less risk than the water from non-potable network

Children exposure is similar to municipal irrigation workers

THANKS!
MERCI!

[caroline.kimie-miyazaki@enpc.fr/](mailto:caroline.kimie-miyazaki@enpc.fr)

cahckm@gmail.com