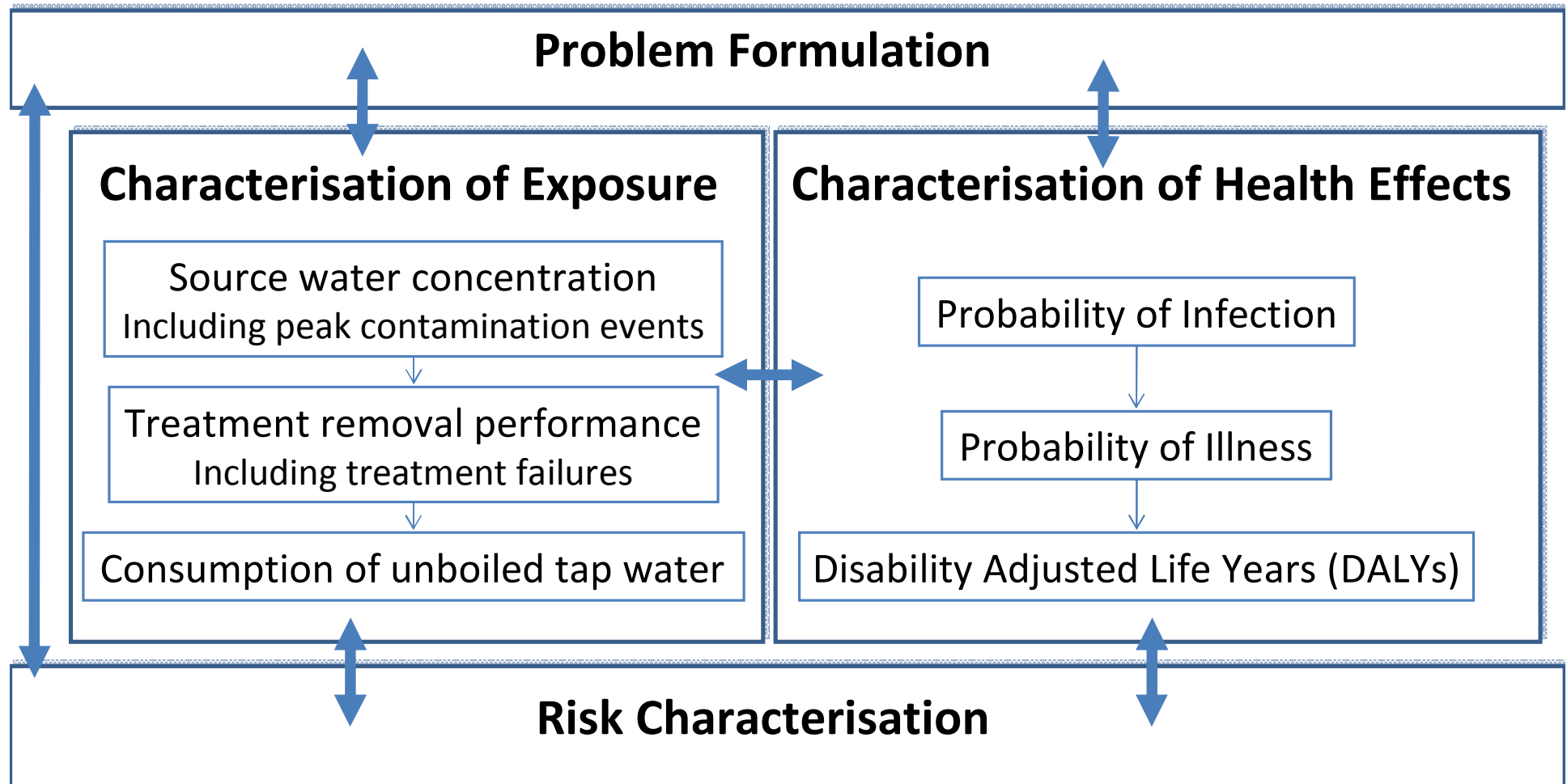


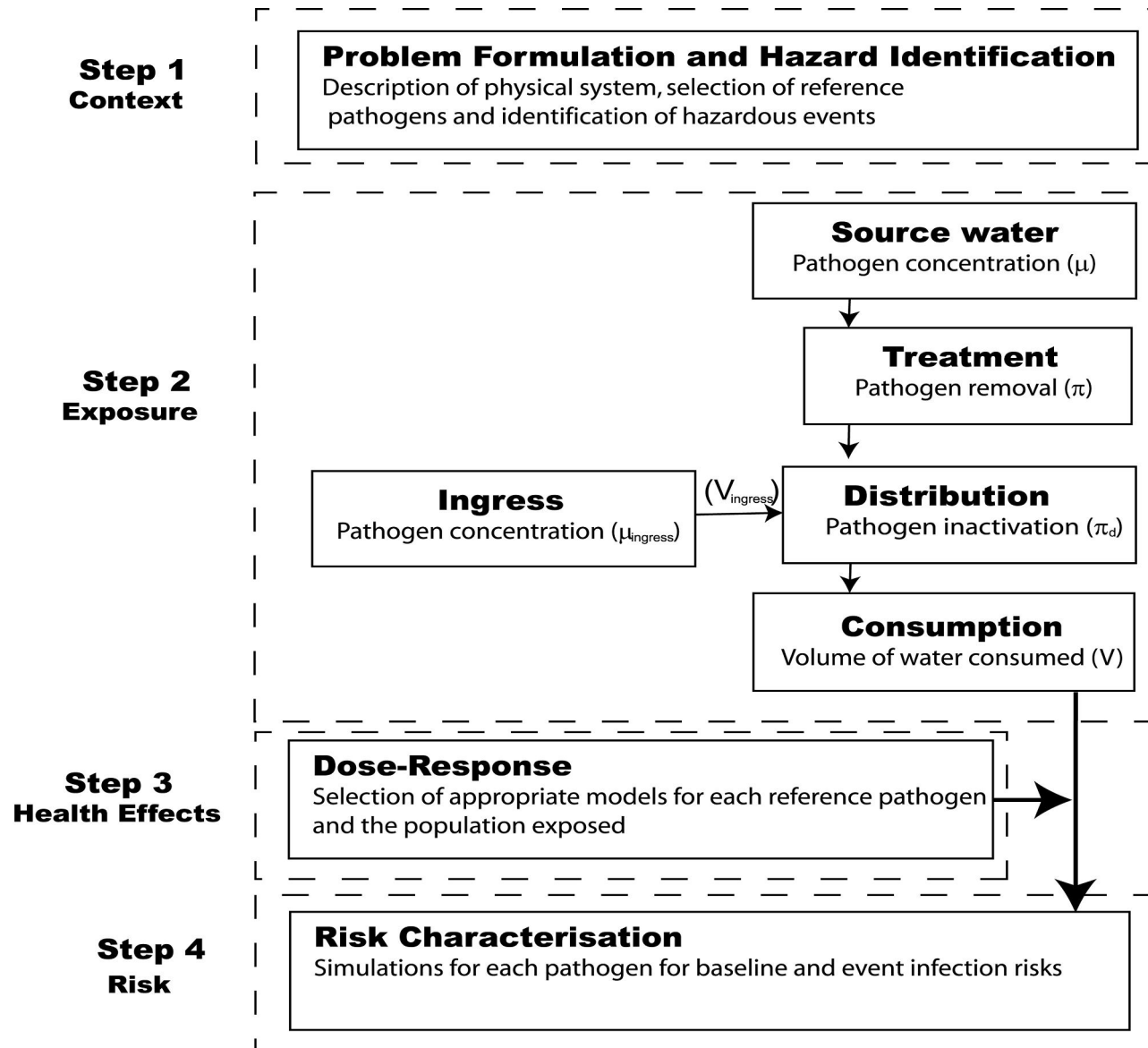
Model tools for prediction of probabilities of infection

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Quantitative Microbial Risk Assessment



Quantitative Microbial Risk Assessment



Objectives of the tool

- Centralise QMRA assumptions
- Simplify repeat calculations
- Facilitate scenario modelling by water companies – hence a user-friendly interface is essential

Model Application 1: Drinking water treatment in Sweden

GENERIC MODEL: Drinking Water QMRA

Read me first!

Läs mig först!

Version: Beta - October 27, 2008.
For testing purposes only

Indices

1. Choose Reference Pathogens for QMRA Choose one reference pathogen from each group

Bacterial Pathogen: Campylobacter

Viral Pathogen: Norovirus

Protozoan Pathogen: Cryptosporidium

2. Characterise the source water

Choose approach for quantifying source water pathogen concentration:

Occurrence

Enter concentration
(org. per litre):

Bacteria concentration: Directly enter bacteria concentration (org. per litre) Lognorma

Virus concentration: Directly enter virus concentration (virus units per litre) Lognorma

Protozoan concentration: Directly enter protozoan concentration ([oo]cysts per litre) Lognorm

In the absence of pathogen estimates in raw water, select "Model concentration assuming source is raw sewage" and then enter the contribution from a specific point source.

3. Drinking Water Treatment Processes Select "Yes" to include process in your treatment train

No Additional Process 1: user input

Additional Process Barrier 1

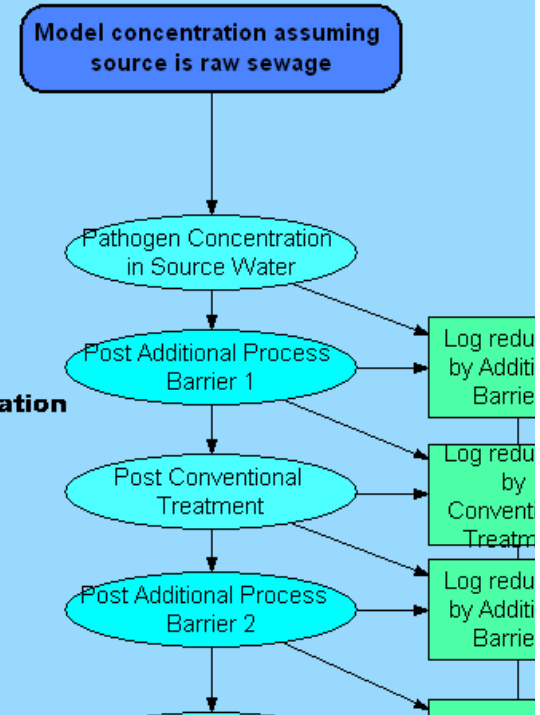
No Conventional Treatment: Coagulation/Flocculation/Sedimentation/Rapid Filtration

Conventional Treatment Performance

No Additional Process 2: user input

Additional Process Barrier 2

No Slow Sand Filtration / Biological Filtration



Slow Sand Filtration / Biological Filtration

Number of parallel filtration lines

user inp

Slow Sand Filtration

Removal performance under nominal conditions across an individual filter

Removal Performance Data

Is Local Data Available?

Type of local input

Bacteria

No

Conc. In and

Viruses

No

Conc. In and

Protozoa

No

Conc. In and Out

Conc. In and Out

Arithmetic Mean
concentration IN

Arithmetic Mean
concentration OUT

Log 10 reduction

user input

user input

Calc

mid

user input

user input

Calc

mid

user input

user input

Calc

mid

Log 10 reduction

Bacteria

Triangula

Viruses

Triangula

Protozoa

Triangula

OR

Reliability Data

Type of reliability analysis:

Random

Reliability

Are historical performance data available for SSF?

No

Time under sub-optimal filtration (hours)

user input

Total length of record (hours)

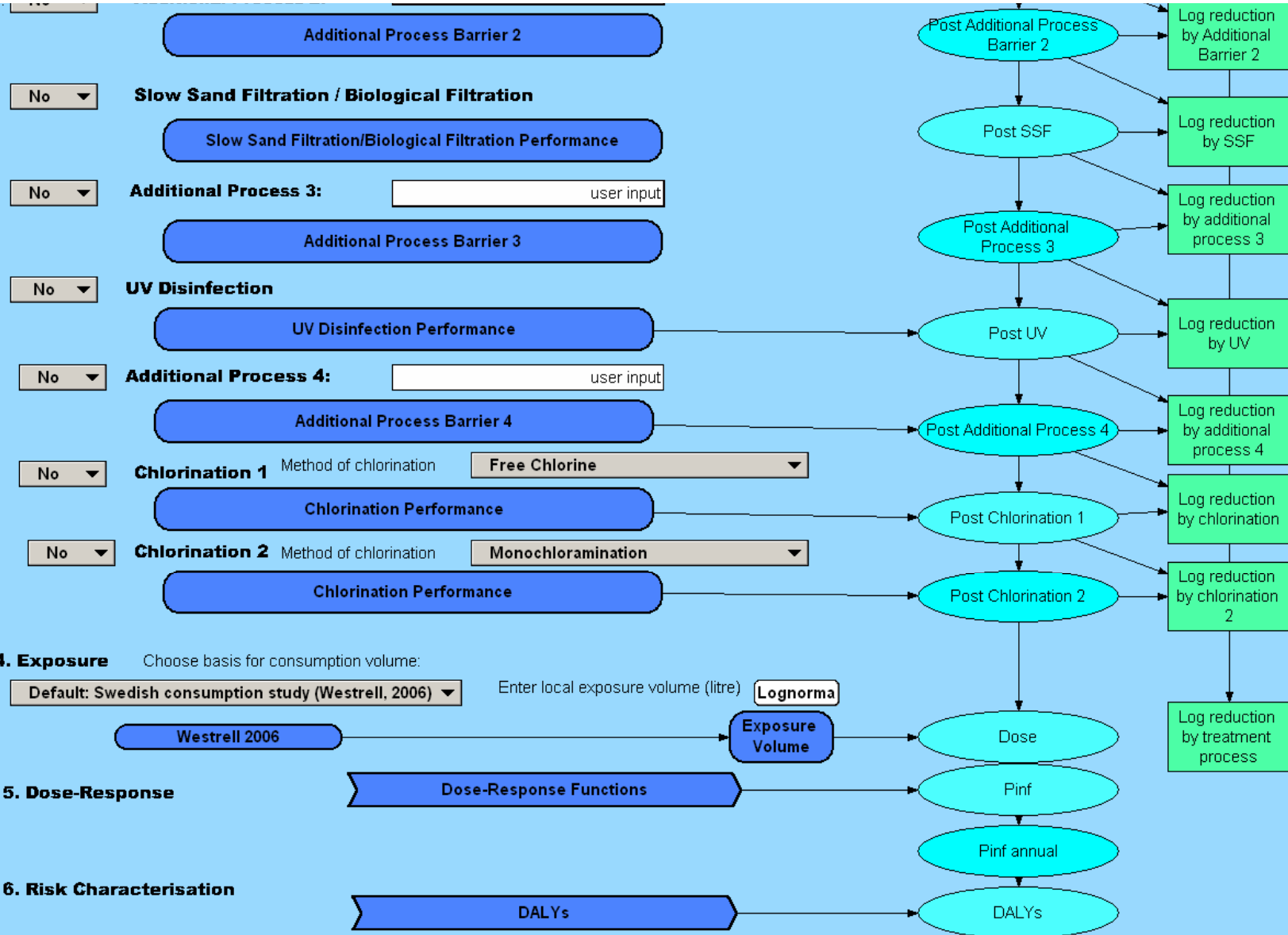
user input

Scenario Analysis

Number of Filters failing?

user

SSF Nodes

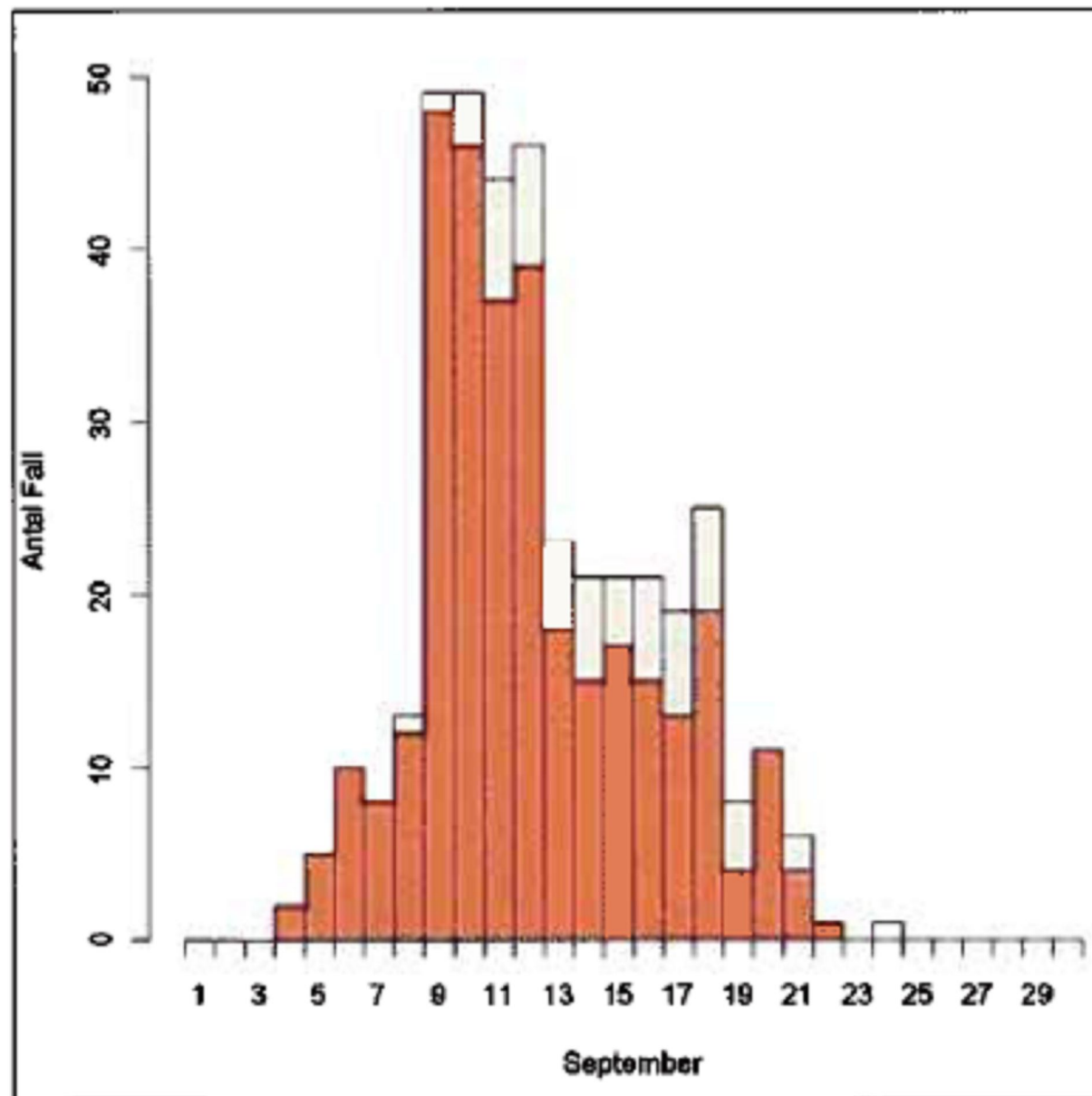


Results

Log 10 reduction by treatment process	Probability of Infection (daily)	Probability of Infection (annual)	DALYs
Calc mid	Pinf	Calc μ± Pinf annual	Calc μ

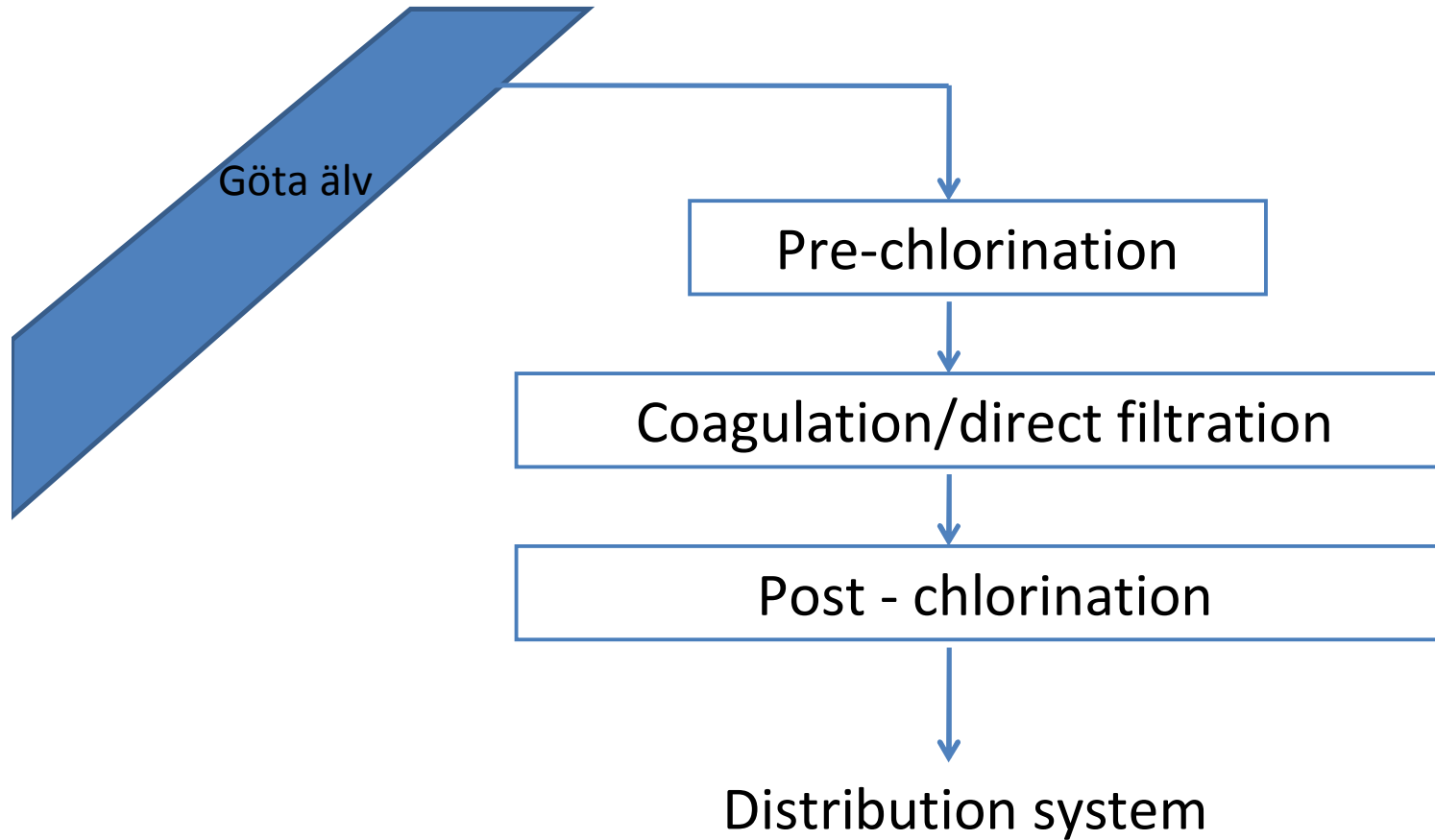
Case study: Lilla Edet

- Norovirus outbreak in September, 2008
- 32% inhabitants estimated to have fallen ill
- Most likely cause identified as drinking water
- Three microbial discharge events, in the period prior to the outbreak, upstream of the Lilla Edet offtake were identified



Insjukningskurva för de 379 personer som i enkäten svarat att de varit magsjuka. Röda staplar representerar de som bor i hushåll med vatten från vattenverket i centrala Lilla Edet, gula staplar representerar de som bor i hushåll med annat vatten.

Case study: Lilla Edet



Application of the QMRA tool

The QMRA modelling tool was applied to investigate the likely norovirus infection rates resulting from the reported upstream discharge events.

For each of three reported events:

- The QMRA tool was combined with hydraulic modelling of the river to estimate norovirus concentration at the offtake
- Nominal treatment performance of the WTP was assumed
- Probability of infection with norovirus (per day) was estimated

Results

Daily probability of infection with norovirus (expressed as a %) for the three discharge events.

Discharge event	5%-perc.	median	mean	95%-perc.
CSOs in Trollhättan	0.3	17	24	69
CSOs in Lilla Edet	0.03	3.1	15	48
Emergency discharge	0.01	0.9	5.6	31

Calculated with default conditions for norovirus incidence, treatment efficiency and water consumption

Model Application 2: HiWATE

Comparison between DBPs and disinfection efficacy

Objectives of the HiWATE tool:

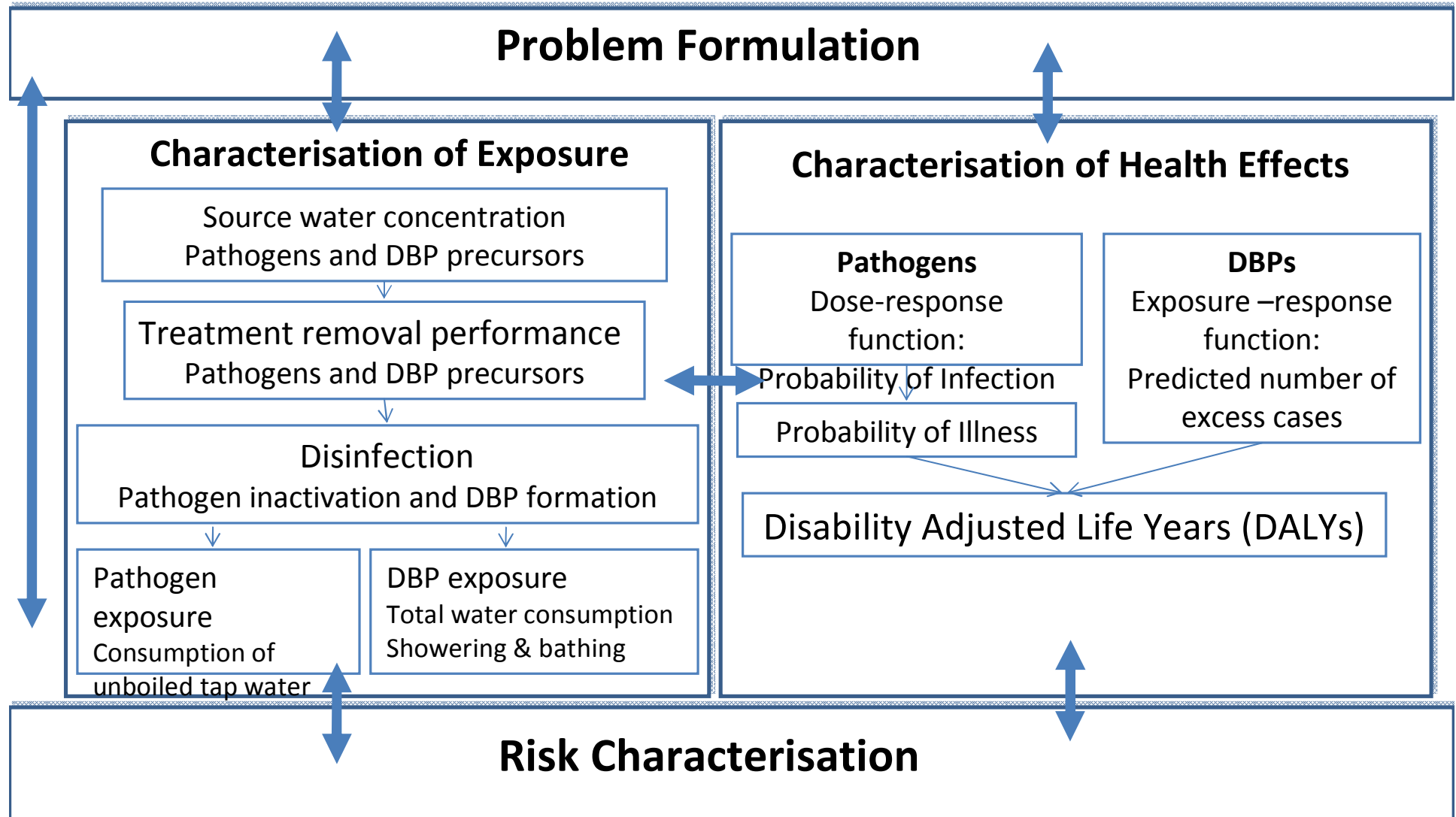
- Generally applicable for WTP in Europe
- Apply DALYs as a common metric for comparison between DBP and pathogen risks
- Facilitate overall drinking water quality management to meet health-based targets

Water management scenario investigation

QMRA tool applied to predict overall health outcomes associated with:

- Change in water source
 - Surface, groundwater, desalination
- Change in disinfection dose
 - Overall increase in dose
 - Short term super-chlorination during events
- Change in disinfectant
 - Free chlorine, chlorine dioxide, monochloramine

Comparative Quantitative Risk Assessment DBPs and Pathogens



HiWATE risk-benefit model

Source Water Concentration

Select approach for quantifying pathogen concentration in raw water

Estimate Campylobacter concentration based on:	Modelled based on faecal indicator values ▼
Estimate Rotavirus concentration based on:	Modelled based on faecal indicator values ▼
Estimate Giardia concentration based on:	Enter concentration ▼
Estimate Cryptosporidium concentration based on:	Enter concentration ▼

Enter concentration (microorganisms.L-1)

Campylobacter concentration	<input type="button" value="Edit Table"/>
Rotavirus concentration	<input type="button" value="Edit Table"/>
Giardia concentration	<input type="button" value="Edit Table"/>
Cryptosporidium concentration	<input type="button" value="Edit Table"/>

Select typical source concentration from literature

Water Source

Model concentration using indicator data

Measured E. coli concentration in surface water .L-1

Measured Clostridium perfringens concentration in surface water.L-1

Drinking Water Treatment

Physical treatment processes

Is Coagulation/Flocculation included in treatment train?	<input style="border: 1px solid black; padding: 2px;" type="button" value="Yes"/>	Is Coagulation OPTIMAL?	<input style="border: 1px solid black; padding: 2px;" type="button" value="Yes"/>
Is Rapid Sand Filtration included in treatment train?	<input style="border: 1px solid black; padding: 2px;" type="button" value="Yes"/>		
Is Slow Sand Filtration included in the treatment train?	<input style="border: 1px solid black; padding: 2px;" type="button" value="No"/>		
Is GAC Filtration included in treatment train?	<input style="border: 1px solid black; padding: 2px;" type="button" value="Yes"/>		

Total Microbial Log-reduction

Disinfection

	Disinfectant dose (mg.L-1)	TOC	Temperature Degrees C	Reaction time (minutes)	Bromide conc. mg.L-1	pH
Is Free Chlorine used?	<input style="border: 1px solid black; padding: 2px;" type="button" value="Yes"/>	<input type="text" value="Toc_mg_l"/>	<input type="text" value="15.8"/>	<input type="text" value="30"/>	<input type="text" value="1.3"/>	<input type="text" value="7.1"/>
Is Chlorine dioxide used?	<input style="border: 1px solid black; padding: 2px;" type="button" value="No"/>	<input type="text" value="0"/>				
Is Ozone used?	<input style="border: 1px solid black; padding: 2px;" type="button" value="No"/>	<input type="text" value="3.5"/>		<input type="text" value="5"/>	<input type="text" value="86"/>	<input type="text" value="7.5"/>

Total Microbial Log-reduction by disinfection

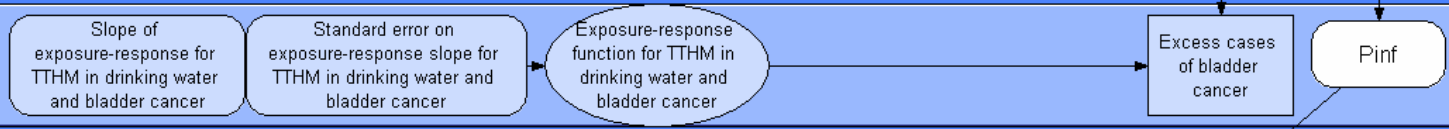
TTHM concentration

Exposure

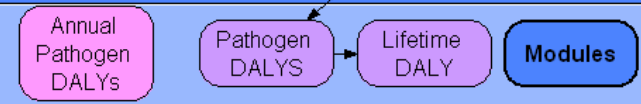
Total water consumption (mL)	<input type="text" value="1153"/>	Number of showers per day	<input type="text" value="1"/>
Consumption unboiled drinking water (mL)(mL)	<input type="text" value="0.67*115"/>	Number of baths per day	<input type="text" value="0"/>

TTHM exposure Pathogen exposure

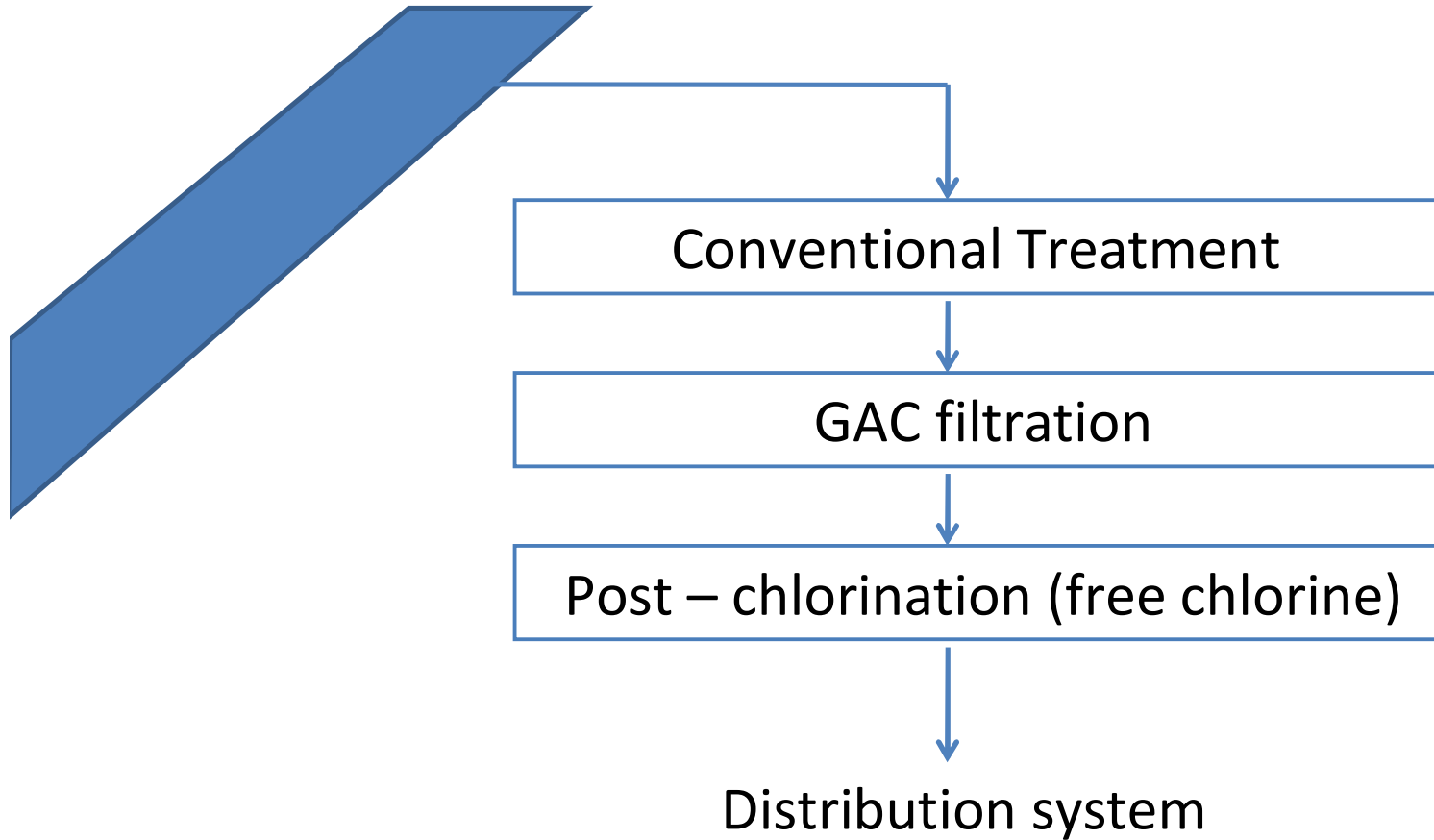
Dose-response

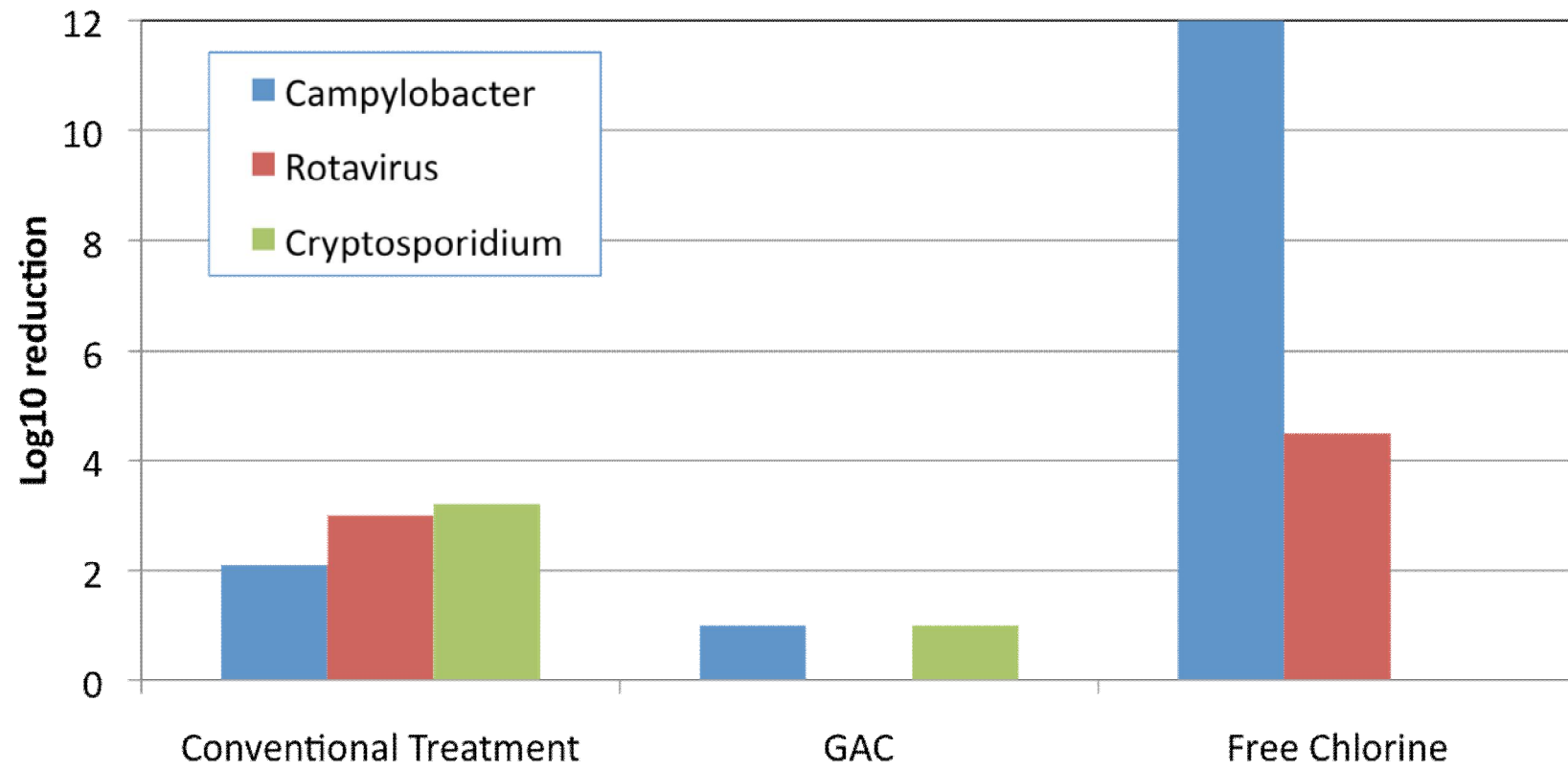


DALYs

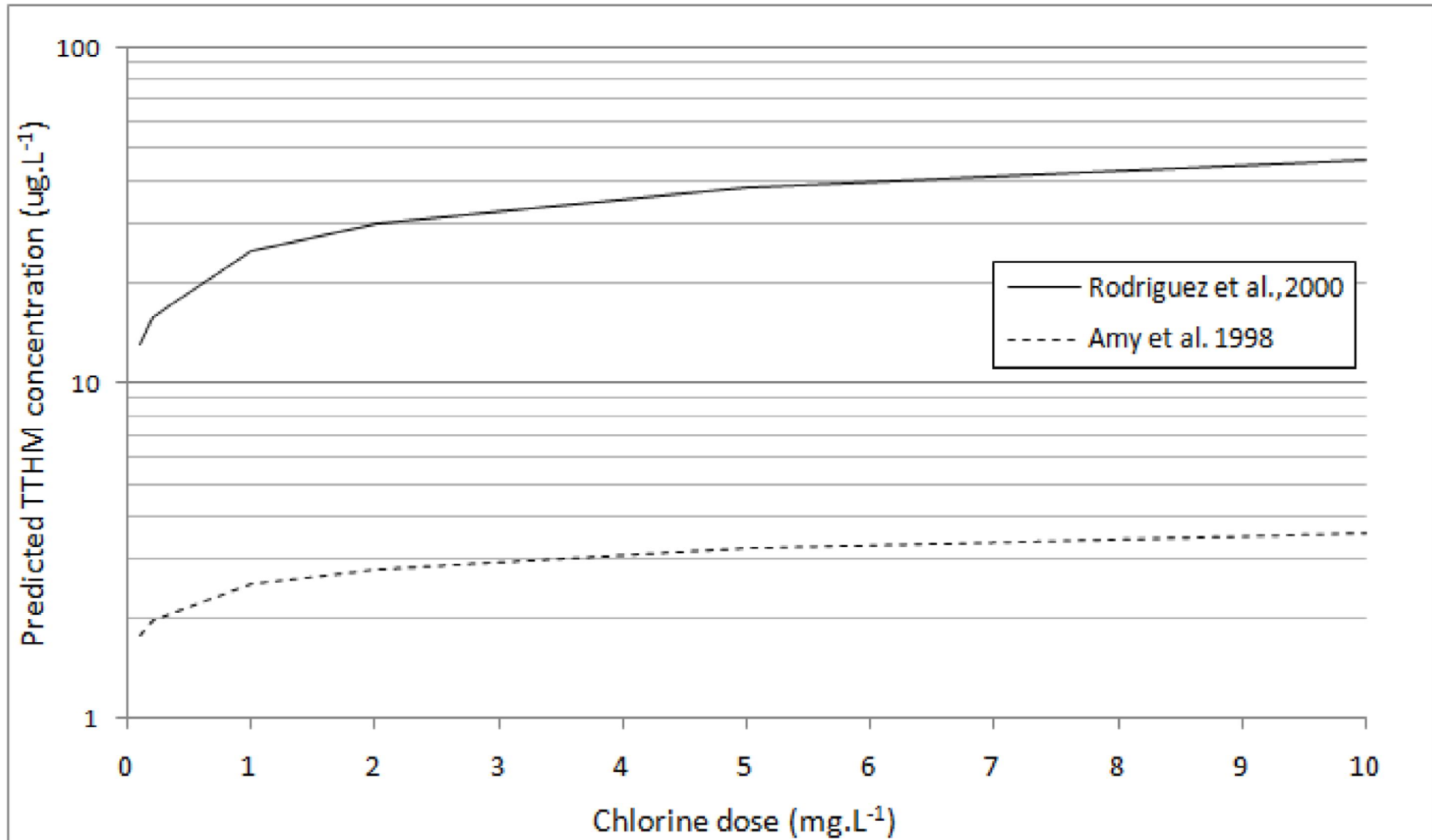


Case Study : Surface water source

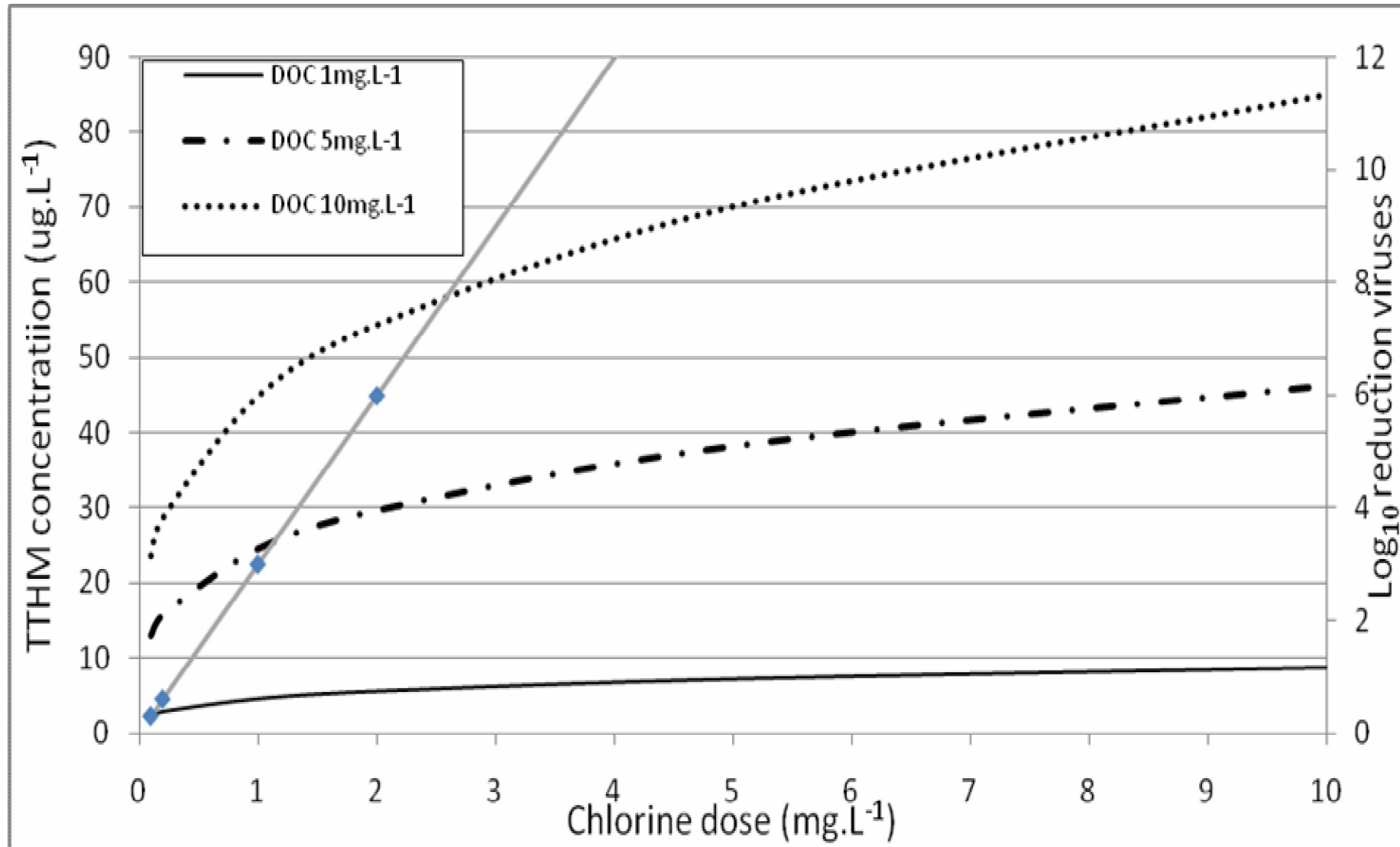




Predicted TTHM concentration with change in chlorine dose for two predictive models



Change in predicted TTHM concentration and Log_{10} reduction of viruses with chlorine dose



SUMMARY

- A modelling tool has been developed and adapted as a predictive instrument
- The tool is flexible and input data from different treatment train configuration can be done
- The tool has been tested in relation to outbreaks
- The tool is currently adapted to account for both microbial data and DBP data within the EU project HIWATE
- The tool is never better than the input values that it is based on. The current lack of full-scale data for the reduction of different pathogens is a limitation