

Quick User Guide to QMRACatch

General description

QMRACatch is a microbial water quality model for simulating target microbial concentrations in a river, a floodplain river and / or a floodplain compartment. Quantitative microbial risk assessment (QMRA) is performed based on predefined dose-response functions for Enterovirus, Norovirus, *Campylobacter jejuni*, *Cryptosporidium parvum*, *Giardia lamblia*, or based on user defined dose-response functions for any type of pathogen. QMRACatch simulates the required pathogen reductions from the compartments which have to be achieved by bank filtration and further disinfection steps to meet a defined infection risk target. Simulations are daily for a period of one year. Input parameters consist of river discharge (Q), source concentration (C_0) and microbial $\log_{10}$ removal of wastewater discharges (WWTPs), number of visitors and animals in the floodplain compartment, water temperature, rainfall depth, release rate, runoff rate, probability of defaecation of visitors and dimensions of each compartment. Mean and 95-percentiles of concentrations in wastewater and in faeces, $\log_{10}$ removal, quantity and weight of faecal droppings, and excretion probability of predefined statistical distributions have to be set by the user. The simulations are performed by the Monte Carlo method, i.e. random values are drawn from the statistical distributions.

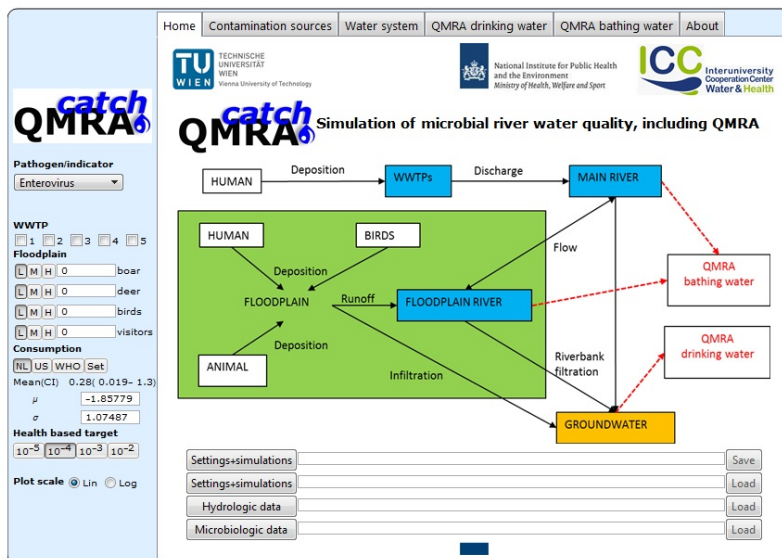


Figure 1 Home screen

1. Simulating microbial concentrations in the river, the floodplain river and the floodplain

Concentrations of the selected microorganism in the river are computed based on a plug flow reactor type model. At the point of interest (intake for drinking water production or recreational area), they vary depending on the up-stream distance of one to five wastewater treatment plants (WWTPs, Figure 1). Concentrations of the selected microorganism in the floodplain river and the floodplain are computed based on continuously stirred reactor type models assuming spatially uniform and completely mixed conditions over daily time intervals. Concentrations in all compartments are computed based on dilution, mixing and temperature-dependent die-off. Rainfall, infiltration, release

and runoff determine microbial concentrations in the floodplain and the floodplain river. During flood events (i.e. river discharges exceed a certain threshold) a part of the floodplain is flooded by inflow of river water. This area is computed based on a width of the floodplain river and a slope of the floodplain. All faecal deposits are assumed to be released in this area and animals are assumed to leave this area until the flood has receded.

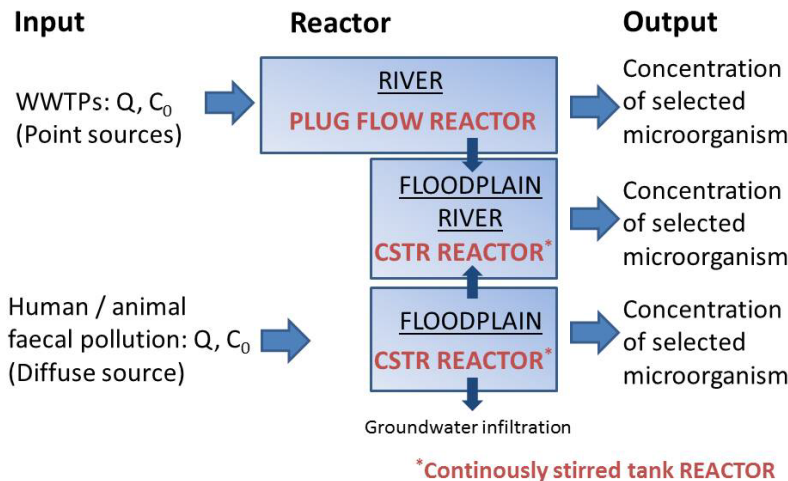


Figure 2 Conceptual model for 1) simulating daily microbial concentrations in the river, the floodplain river and the floodplain

2. QMRA: setting the required $\log_{10}$ reduction of target microbial pathogens to meet a certain health risk target (Figure 3)

The required reduction of pathogens by riverbank filtration, or other treatment methods for compliance with the selected infection risk target can be set. The Monte Carlo simulations can be repeated 10 000 to 1 000 000 times. Results include the 95-percentiles of the required $\log_{10}$ reductions, i.e. the reductions that have to be achieved by the respective treatment system over 95 % of the time. For the detailed model description including the model equations see Schijven et al. (2015).

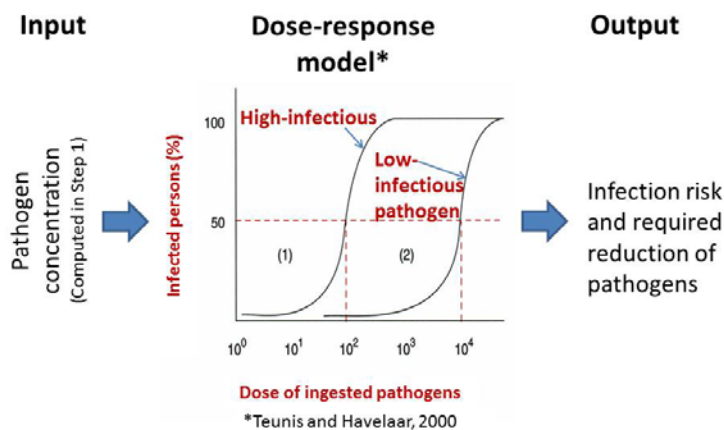


Figure 3 Conceptual model for 2) performing the QMRA. The output of QMRA is an infection risk estimate, and, in addition, the required $\log_{10}$ reduction of pathogens to comply with a set health risk target

Generating plots, saving and reading data in QMRACatch

Plots

All plots (i.e. concentration time series and logos) can be saved in QMRACatch as graphical images by right-clicking and then *Save Graphic As* in all common graphic formats. Plots of simulated concentrations can be displayed in linear and plot scale by checking either *Lin* or *Log* on the left panel of the QMRACatch screen.

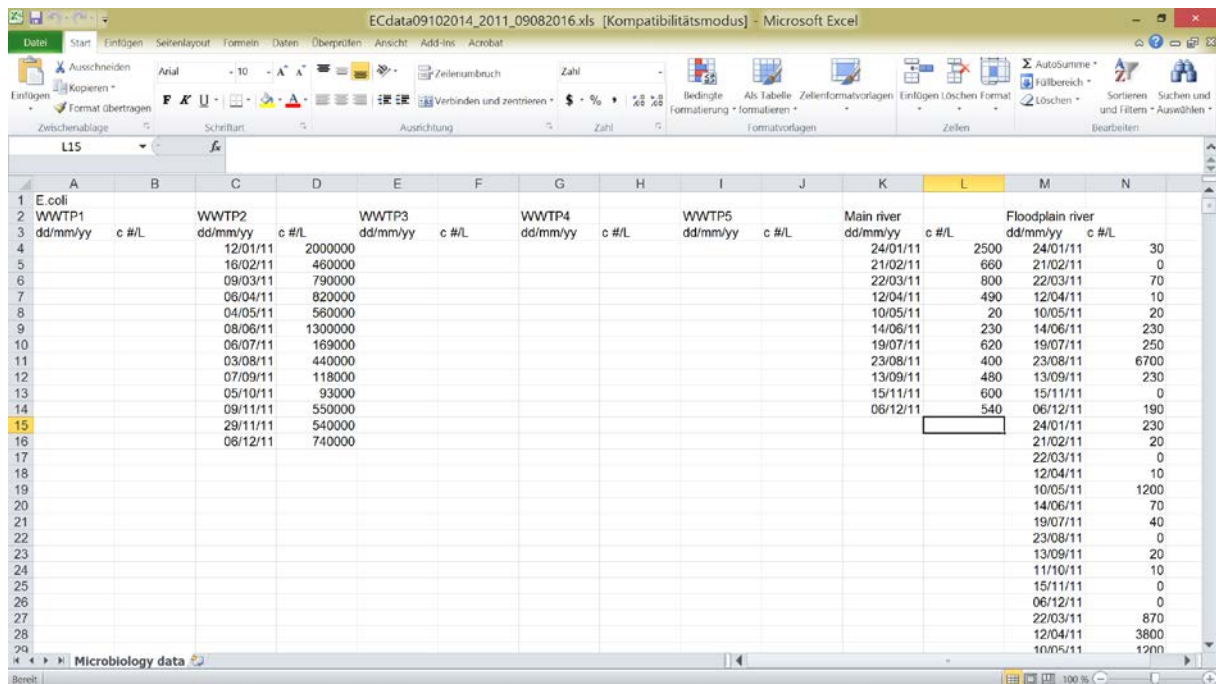
Save and read files

On the bottom of the home screen (Figure 1), there are options to save and load settings made by the user. Hydrologic and microbial data can be read from spreadsheet files with specific format rules (Figure 4 and 6). Examples spreadsheets are provided on the website.

- In the first row, all settings and simulated concentrations can be saved into a file by clicking on the button *Settings+simulations*, choosing the file directory and file name and pushing the *Save* button.
- In the second row, settings can be loaded from a previously saved file.
- In the third row, the hydrologic data can be loaded. The format of the data file is as shown in Figure 4. On each day in a year (1-365) have to be set: main river discharges, water temperatures, floodplain river discharges and water temperatures, floodplain river volumes, rainfall depth, flooded area and flooded volume. Derx et al. (2016) describes how floodplain river discharges can be determined if no observation data is available.
- In the fourth row, the microbiologic data can be loaded with format as shown in Figure 5. Dates and values of observed concentrations of the selected indicator can be set for: each WWTP, the Main river and the Floodplain river compartment. When plotting graphs of the simulated time series, the observed mean, 95-percentile, α and β parameters of the Gamma distribution (taking into account non-detects) are shown below the respective values of the simulated time series. The observed values are shown as circles in the graph (non-detects are not shown in plot-scale).

	A	B	C	D	E	F	G	H	I	J
1		Main river		Floodplain			Floodplain			
2	Day	q m3/s	oC	q m3/s(mr= oC		m3	mm prec	m2	m3	
3	1	1534	3.254167	0.25	5.254167	250000	1.080297	0	0	
4	2	1712	3.6	0.25	5.6	250000	0.111308	0	0	
5	3	1635	3.454167	0.25	5.454167	250000	0	0	0	
6	4	1537	3.391667	0.25	5.391667	250000	0	0	0	
7	5	1391	3.333333	0.25	5.333333	250000	0	0	0	

Figure 4 Spreadsheet format (.xlsx or .xls) for hydrologic data



	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	E. coli													
2	WWTP1		WWTP2		WWTP3		WWTP4		WWTP5		Main river		Floodplain river	
3	dd/mm/yy	c #/L	dd/mm/yy	c #/L	dd/mm/yy	c #/L	dd/mm/yy	c #/L	dd/mm/yy	c #/L	dd/mm/yy	c #/L	dd/mm/yy	c #/L
4			12/01/11	2000000							24/01/11	2500	24/01/11	30
5			16/02/11	460000							21/02/11	660	21/02/11	0
6			09/03/11	790000							22/03/11	800	22/03/11	70
7			06/04/11	820000							12/04/11	490	12/04/11	10
8			04/05/11	560000							10/05/11	20	10/05/11	20
9			08/06/11	1300000							14/06/11	230	14/06/11	230
10			06/07/11	169000							19/07/11	620	19/07/11	250
11			03/08/11	440000							23/08/11	400	23/08/11	6700
12			07/09/11	118000							13/09/11	480	13/09/11	230
13			05/10/11	93000							15/11/11	600	15/11/11	0
14			09/11/11	550000							06/12/11	540	06/12/11	190
15			29/11/11	540000									24/01/11	230
16			08/12/11	740000									21/02/11	20
17													22/03/11	0
18													12/04/11	10
19													10/05/11	1200
20													14/06/11	70
21													19/07/11	40
22													23/08/11	0
23													13/09/11	20
24													11/10/11	10
25													15/11/11	0
26													06/12/11	0
27													22/03/11	870
28													12/04/11	3800
29													10/05/11	1200

Figure 5 Spreadsheet format (.xlsx or .xls) for microbiologic data

Getting started

- Choose one type of microorganism (**pathogen/indicator**).

The following list of pathogens and indicators are available: Enterovirus, Norovirus, Campylobacter (jejuni), Cryptosporidium (parvum), Giardia (lamblia), E.coli, HF183, other (see below). For more information on HF183 see (Derx et al. 2016).

- Check the number of wastewater treatment plants (**WWTP**), 0 to 5, contributing to the simulated microbial concentrations in the river compartment.
- Enter the number of boar, deer, birds and visitors in the **floodplain** [per day].
- Drinking water **consumption**: choose mean and standard deviation values in L/d (predefined or set manually).

Other types of microorganisms

- For this case the parameters for the temperature dependent inactivation, a_0 and a_1 , have to be set manually, as explained by Schijven et al. (2015).
- Check if the microorganism is zoonotic. This will require setting contamination source concentrations of boar, deer and birds, if their numbers are set to a value greater than zero.
- Check if the microorganism is pathogenic. For a pathogenic microorganism, the dose-response relationship must be set. The user can choose either an exponential 1-parameter relationship, or, the hypergeometric model with model parameters α and β (Schijven et al. 2015, Teunis and Havelaar 2000).

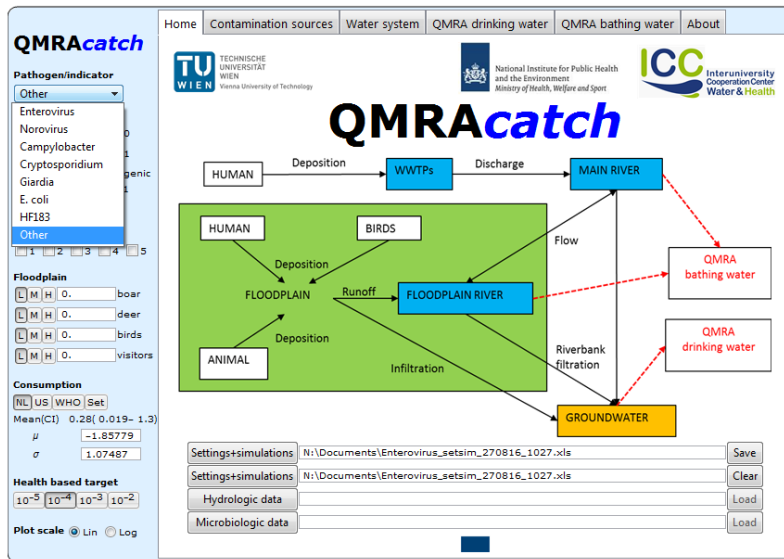


Figure 6 Choosing other types of microorganisms

Contamination sources

Wastewater treatment plants (WWTPs)

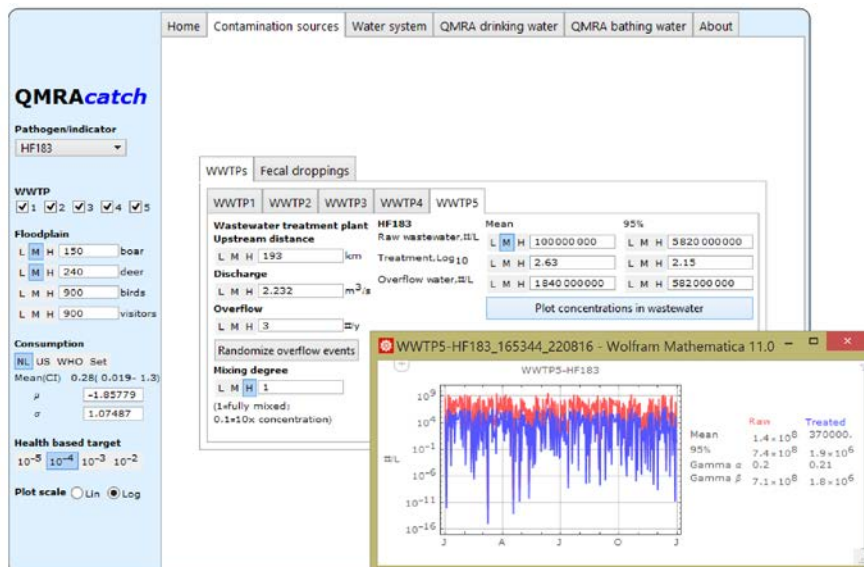


Figure 7 Contamination sources – Wastewater treatment plants (WWTPs)

- For each checked WWTP have to be set:

The upstream distance from the point of interest (PI)

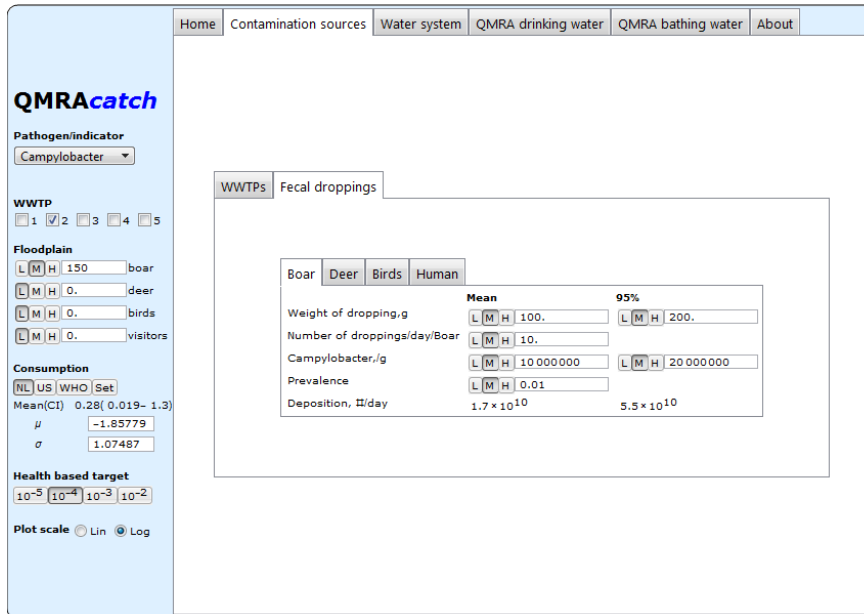
Mean discharge rates over a year

Number of overflows / year

Mixing degree; is the the fraction of the river width at the PI that the discharged wastewater of the WWTP has fully mixed with.

- For the selected target pathogen/indicator the respective raw wastewater concentrations, achieved $\log_{10}$ removal by wastewater treatment and overflow water concentrations have to be set (mean and 95-percentiles).
- The computed raw and treated target microbial concentrations in wastewater can be plotted (Figure 7).

Faecal droppings



QMRAcatch

Pathogen/indicator: Campylobacter

WWTPs: ☐ 1 ☒ 2 ☐ 3 ☐ 4 ☐ 5

Floodplain: ☐ boar ☐ deer ☐ birds ☐ visitors

Consumption: ☐ NL ☐ US ☐ WHO ☐ Set
Mean(CI) 0.28(0.019- 1.3)
 μ -1.85779
 σ 1.07487

Health based target: ☐ 10^{-5} ☐ 10^{-4} ☐ 10^{-3} ☐ 10^{-2}

Plot scale: ☐ Lin ☒ Log

WWTPs Fecal droppings

	Mean	95%
Weight of dropping, g	L M H 100.	L M H 200.
Number of droppings/day/Boar	L M H 10.	
Campylobacter, /g	L M H 10 000 000	L M H 20 000 000
Prevalence	L M H 0.01	
Deposition, II/day	1.7×10^{10}	5.5×10^{10}

Figure 8 Contamination sources – Faecal droppings

When boar, deer, or birds are considered, the weight of dropping (g), number of droppings / day / animal, the source concentrations (microbial particles/g) and the prevalence have to be set. Default values and references for some parameters are given in Schijven et al. (2015) and (Derx et al. 2016). The calculated total number of target microorganism per day is shown based on the set values.

When visitors are considered, a probability of defaecation replaces the number of droppings / day.

Water system - Main River + Floodplain River

The main river water system includes settings for the discharges (m^3/s), the average width (m), water depth (m) and slope (-) of the main river and Manning coefficient ($\text{s}/\text{m}^{1/3}$) of the river bed.

The floodplain river water system further includes settings for the discharges from the main to the floodplain river and the groundwater exfiltration into the floodplain river.

Water temperatures of the main river and floodplain river are calculated based on a triangular distribution over a year. The user has to set the date and values of the minimum and maximum water temperatures. Alternatively, daily values for water temperature can be used from hydrologic data by checking the option *Use data* (Figure 10, see Section on how to Save and read files).

River flow discharges

Discharges of the main river can be simulated based on ARMA processing (Schijven et al. 2015). Mean monthly discharge values have to be set. For setting a mean yearly discharge, use same values for all months. Set ARMA parameters α (-), β (-), ν (m^3/s)² and press *Randomize ARMAprocess*. The generated time series is shown on the top right of the screen. Alternatively, daily values for river discharges can be used from hydrologic data by checking the option *Use data* (Figure 10, see Section on how to Save and read files).

Discharges from the main river to the floodplain river

a) Use data

Daily values for floodplain river discharges can be used from hydrologic data by checking the option *Use data* (Figure 10, see Section on how to Save and read files).

b) Set

Fraction of the main river discharge (q_{mr}) minus a threshold discharge of the main river at which the main river connects to the floodplain river.

c) Advanced set

A polynomial regression function dependent on main river discharges can be entered.

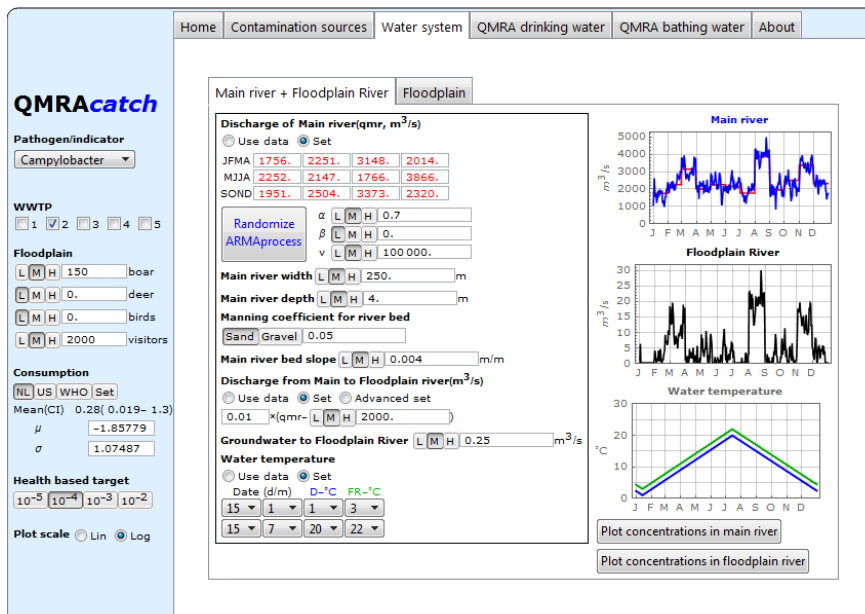


Figure 9 Water System: Main river + floodplain river

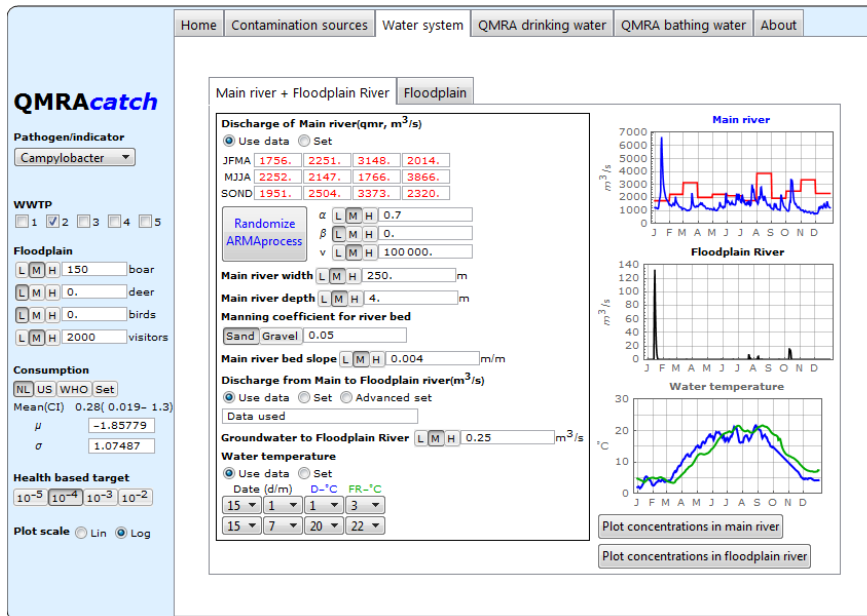


Figure 10 Water system: main river + floodplain river using loaded hydrologic data

Water system - Floodplain

The floodplain water system includes settings for daily precipitation, length, width, depth of the floodplain river, Manning coefficient and slope of the floodplain river bed, area, horizontal angle and area of the floodplain (Figure 11).

Daily precipitation values are calculated by means of a stochastic rainfall model, see Schijven et al. (2015) for details. The user has to set the mean rainfall rate (events per day) and mean rainfall depth (mm) and the month of maximum rainfall. Alternatively, daily values for precipitation can be used from hydrologic data by checking the option *Use data* (Figure 10, see Section on how to Save and read files).

The flooded area is calculated in QMRACatch based on set values of width, depth, length, the discharge and flow velocity of the floodplain river and the slope of the floodplain and floodplain river, see Schijven et al. (2015) for details.

Further settings are required for the release rates of microbial particles from faecal deposits per day, the evaporation and runoff (both fractions of precipitation). A sink term for the infiltration is calculated (also fraction of precipitation) by subtraction of the evaporation and runoff from precipitation (Figure 11).

When pushing the button on the bottom of the screen the simulated concentrations of the selected microorganisms in infiltration water are plotted.

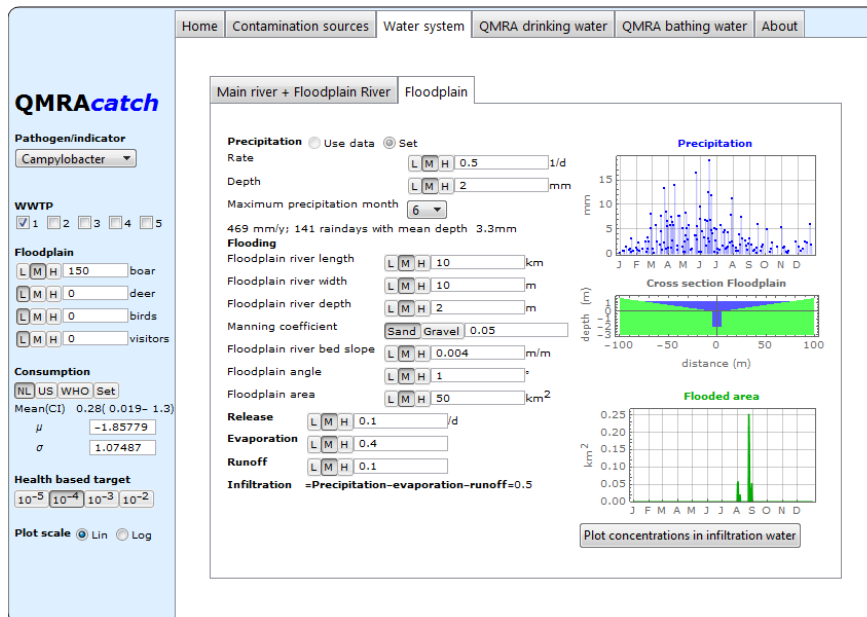


Figure 11 Water system: floodplain

QMRA drinking water

At this point the concentrations of a selected pathogen or indicator have been simulated in the *Water systems*, i.e. the Main River, the Floodplain River and the Floodplain.

Under this tab QMRA outcomes are shown. The simulated concentrations and set values for consumption (Section Getting Started) are fed into the dose-response models of the selected pathogen. The dose-response models are incorporated in the model program code for the listed pathogens (see Schijven et al. (2015) for details) or taken from the set model parameters as described in the Section Getting started – Other types of microorganisms.

For each compartment the user presses the respective button (*Main river*, *Floodplain river*, *Floodplain*). The required $\log_{10}$ treatment by bank filtration (+ further disinfection steps) are simulated for meeting the set health based target (Section Getting Started). Mean and 95-percentiles are simulated. The treatment systems are commonly designed based on 95-percentiles which have to be achieved over 95% of the time.

The next step is to calculate the infection risks from drinking water which was treated according to the previously simulated settings. The user can set ratios for each compartment that are contributing to the composition of well water.

For calculating the infection risks from drinking water, the number of Monte Carlo samples can be varied from low (L) to high (H) numbers. The simulations are repeated this number of times. If the results are sensitive to the number of samples, high values should be used.

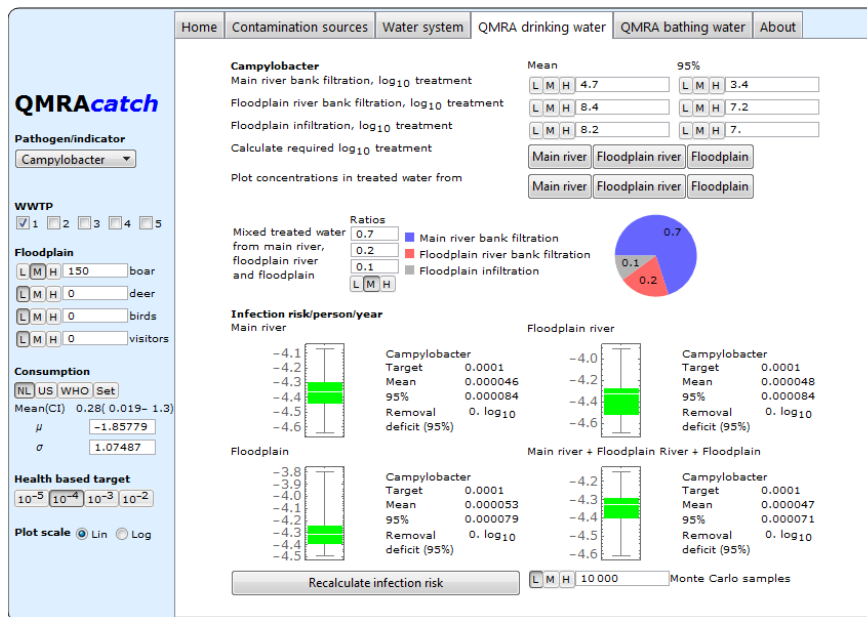


Figure 12 Quantitative microbial risk assessment (QMRA) for drinking water usage

QMRA bathing water

At this point the QMRA will be performed for bathing in the Main River and in the Floodplain River. The user can set the minimum bathing water temperature. Only the days are considered with water temperatures greater than this value. The user can further select *Man*, *Woman*, or *Child*, differing by their given volumes of swallowed water per event. An event is referred to an occasion that a person goes swimming. The simulated concentrations from the prior steps and set values for consumption are fed into the dose-response models of the selected pathogen. The models are integrated into the model program code for the list of pathogens (see Schijven et al. (2015) for details) or taken from the set model parameters as described in the Section Getting started – Other types of microorganisms.

By pushing *Recalculate infection risks* the mean and 94-percentile infection risks are calculated and displayed below the target value for the Main River (left) and the Floodplain River (right).

For calculating the infection risks, the number of Monte Carlo samples can be varied from low (L) to high (H) numbers. The simulations are repeated this number of times. If the results are sensitive to the number of samples, high values should be used.

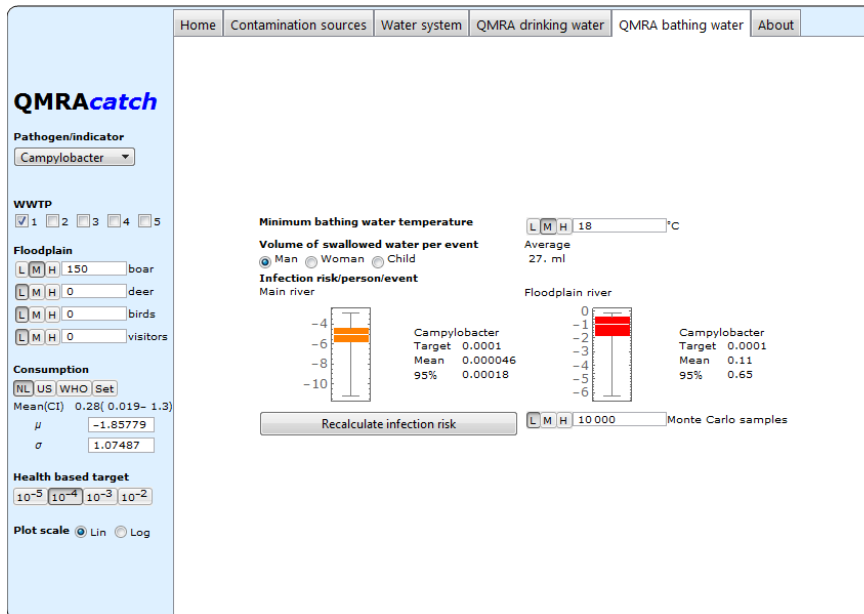


Figure 13 Quantitative microbial risk assessment (QMRA) for bathing water usage

Technical manual

The technical manual and other reference can be downloaded for free following the link in the *About* section.

References

Derx, J., Schijven, J., Sommer, R., Zoufal-Hruza, C.M., van Driezum, I.H., Reischer, G., Ixenmaier, S., Kirschner, A., Frick, C., Husman, A.M.D., Farnleitner, A.H. and Blaschke, A.P. (2016): **QMRACatch: Human-Associated Fecal Pollution and Infection Risk Modeling for a River/Floodplain Environment.** *Journal of Environmental Quality* 45(4), 1205-1214

Schijven, J., Derx, J., Husman, A.M.D., Blaschke, A.P. and Farnleitner, A.H. (2015): **QMRACatch: Microbial Quality Simulation of Water Resources including Infection Risk Assessment.** *Journal of Environmental Quality* 44(5), 1491-1502

Teunis, P.F.M. and Havelaar, A.H. (2000): **The Beta Poisson Dose-Response Model Is Not a Single-Hit Model.** *Risk Analysis* 20(4), 513-520