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Predicting levels of microorganisms and viruses in river Danube water resources with a lumped hydrological water quality and infection risk model

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Overview

Background & Idea

QMRAcatch: the current modules

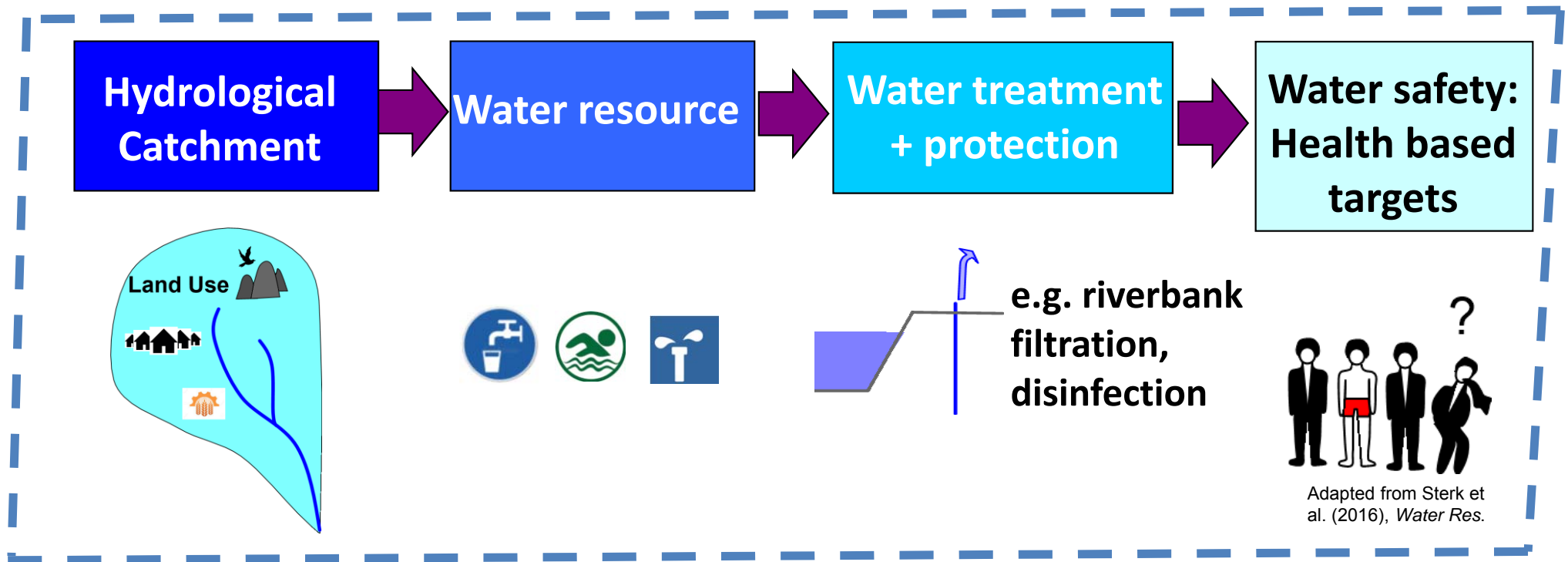
Case study: River Danube & Backwater

Conclusion & perspectives

Challenges of Water Safety Management in the 21st century

“Whole system approach”

e.g. “water safety plan principle”



→ System Assessment/System Design

- Integrated use of **best available information/techniques**
- Need for **modelling tools of catchment microbial transport**

→ Sanitation safety plans, Water Wise Cities, etc..

The idea of the QMRACatch modelling tool:



- Catchment-based microbial **water quality** & **health risk simulations**
“from the fecal pollution source(s) to the exposed human population”
- **Status quo** & (future) scenarios
 - understand the system
 - sustainable decision making & risk management
- Integrated use of best-available quantitative information
 - **site- & habitat-specific** field data
 - data from **online data basis** and literature (e.g. GWPP)



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...a catchment-related microbial water quality simulation tool

The screenshot displays the QMRACatch web application interface. The top navigation bar includes links: Home, Contamination sources, Water system, QMRA drinking water, QMRA bathing water, and About. Logos for TU WIEN, National Institute for Public Health and the Environment, and ICC are present. The main title 'QMRAcatch' is prominently displayed.

Pathogen/indicator: Enterovirus (selected from a dropdown menu).

WWTP: Checkboxes for 1, 2, 3, 4, and 5. Checkboxes 1 and 2 are selected.

Floodplain: Input fields for boar, deer, birds, and visitors, each with L, M, H, and 0.0 options.

Consumption: Buttons for NL, US, WHO, and Set. Mean(CI) is 0.28(0.019– 1.3). μ is -1.85779 and σ is 1.07487.

Health based target: Radio buttons for 10^{-5} , 10^{-4} , 10^{-3} , and 10^{-2} . 10^{-4} is selected.

Plot scale: Radio buttons for Lin and Log. Lin is selected.

Flow Diagram: A central diagram showing the flow of contamination. It includes boxes for HUMAN, BIRDS, FLOODPLAIN, FLOODPLAIN RIVER, MAIN RIVER, and GROUNDWATER. Arrows indicate processes: Deposition (HUMAN to FLOODPLAIN), Runoff (FLOODPLAIN to FLOODPLAIN RIVER), Infiltration (FLOODPLAIN to GROUNDWATER), Discharge (WWTPs to MAIN RIVER), and Flow (MAIN RIVER to FLOODPLAIN RIVER). Red dashed arrows point from the FLOODPLAIN RIVER and GROUNDWATER to boxes labeled 'QMRA bathing water' and 'QMRA drinking water'.

Settings and Data: A table at the bottom lists settings and data files with corresponding Save or Clear buttons.

Settings+simulations	File Path	Action
Settings+simulations	N:\Documents\Enterovirus_setsim_270816_1027.xls	Save
Settings+simulations	N:\Documents\Enterovirus_setsim_270816_1027.xls	Clear
Hydrologic data	N:\Documents\hydrodata09102014_2011_09082016.xls	Clear
Microbiologic data	N:\Documents\Enterovirusdata09102014_2011_09082016.xls	Clear

Schijven, J., Derx, J., De Roda Husman, A.M., Blaschke, A.P. & Farnleitner AH (2015) QMRACatch - Microbial quality simulation of water resources including infection risk assessment. *J. Environ. Qual.* **44**(5): 1491-1502 ⁵

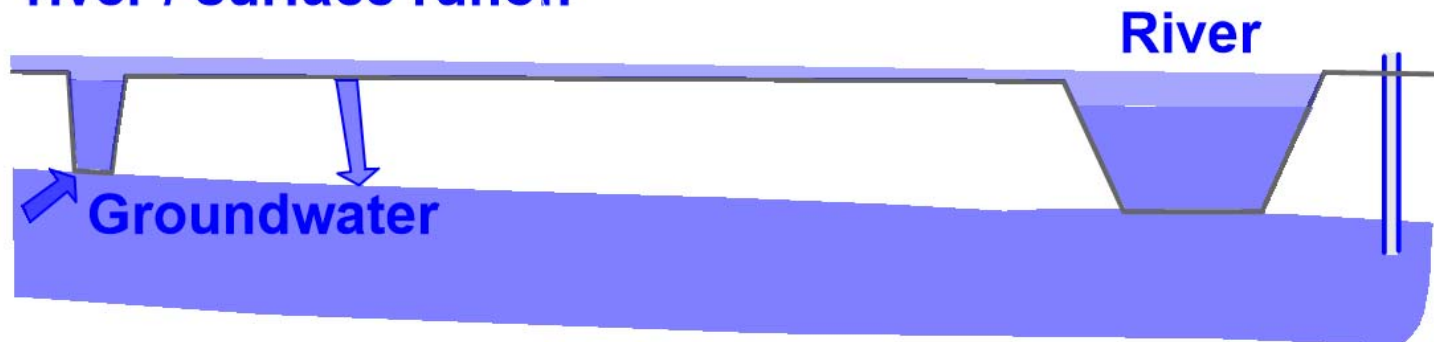
Model components: **Water system**

QMRA *catch*

Rainfall



Floodplain:
river / surface runoff



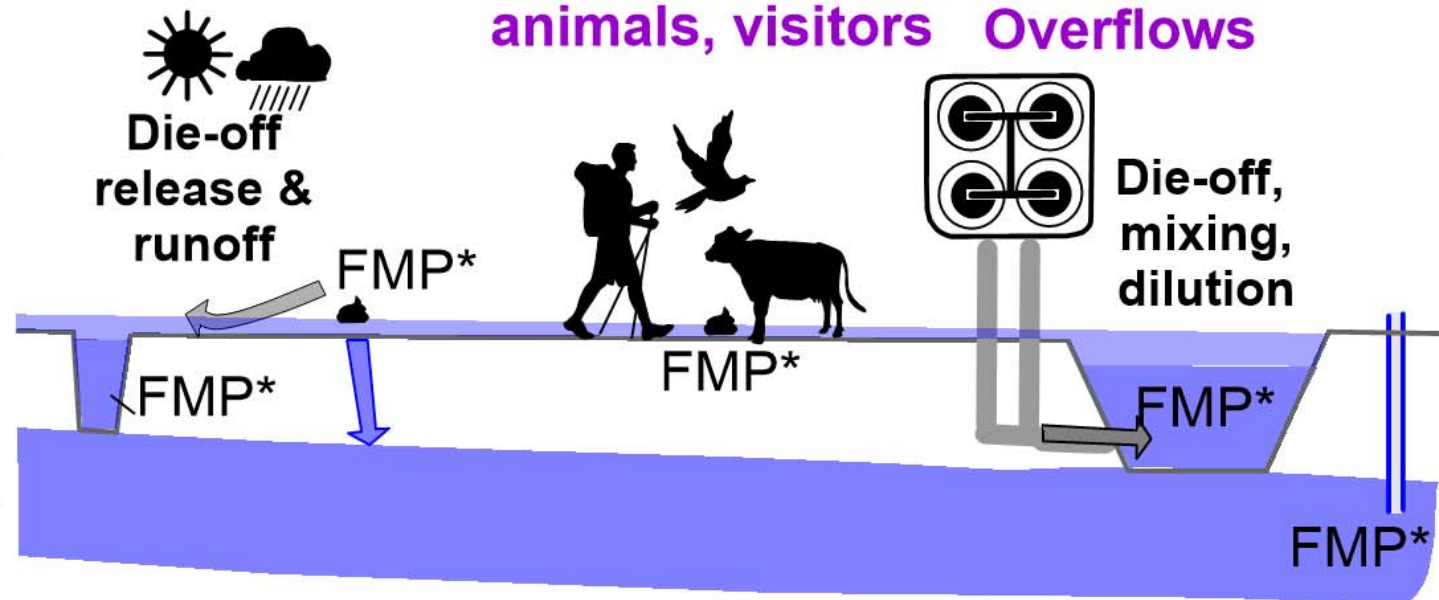
- Size of water system compartments is set by user
- Water system components treated as homogeneous systems
- Time step: 1 day, simulation time: 1 year

Model components: Contamination system, process variables

catch
QMRA

Diffuse pollution: Wastewater treatment plants
animals, visitors Overflows

Adapted from Sterk et al. (2016)

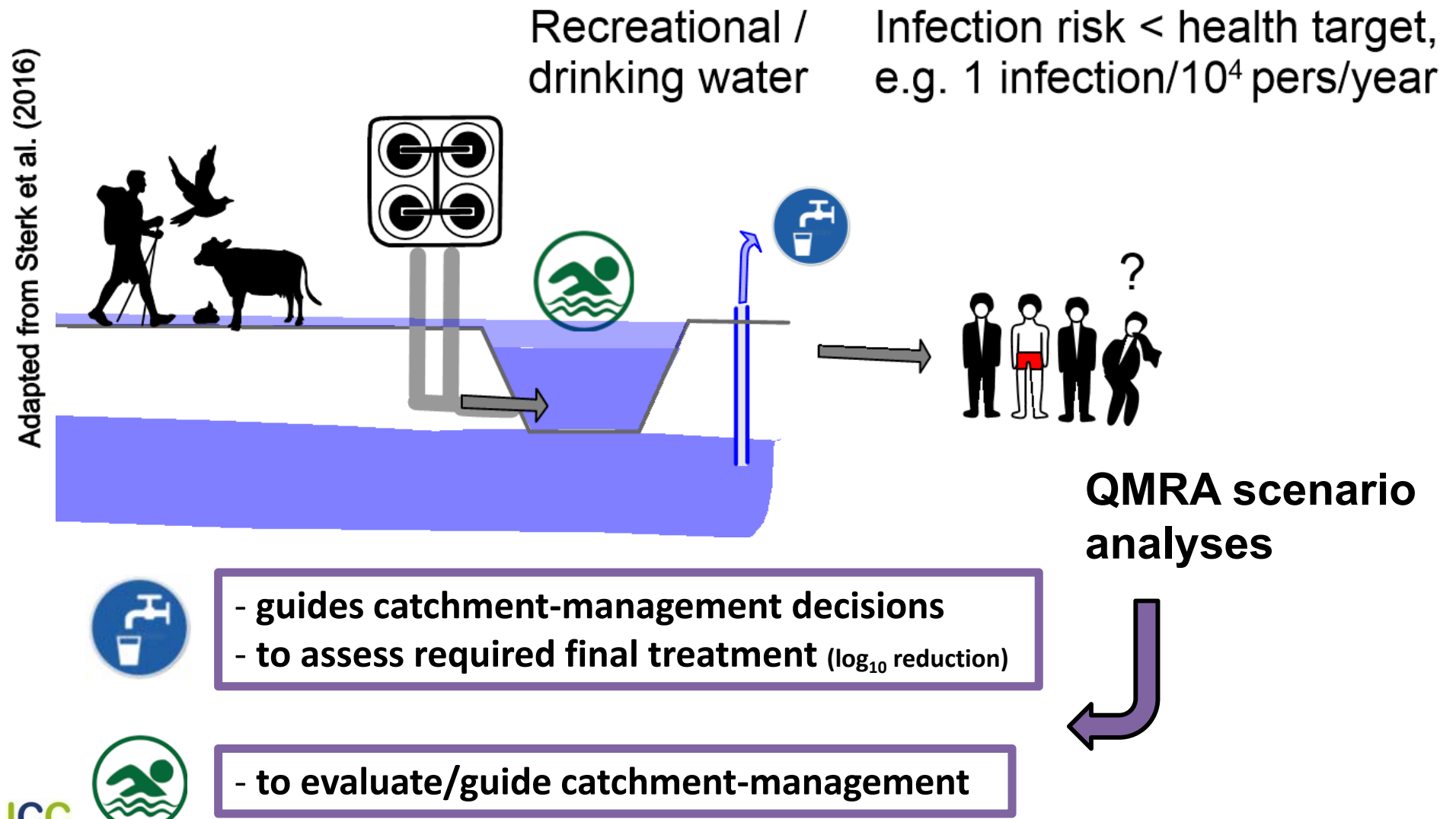


FMP: Indicators & pathogens

- *E.coli*
 - human-assoc. MST-marker
 - Enterovirus
 - Norovirus
 - Campylobacter
 - Cryptosporidium
 - Giardia
- Human
- Zoonotic

Model components:

Usage, quantitative microbial risk assessment (QMRA)



catch QMRA

Officially launched at the
World Water Conference
Brisbane, 2016

Free download links:



www.waterandhealth.at



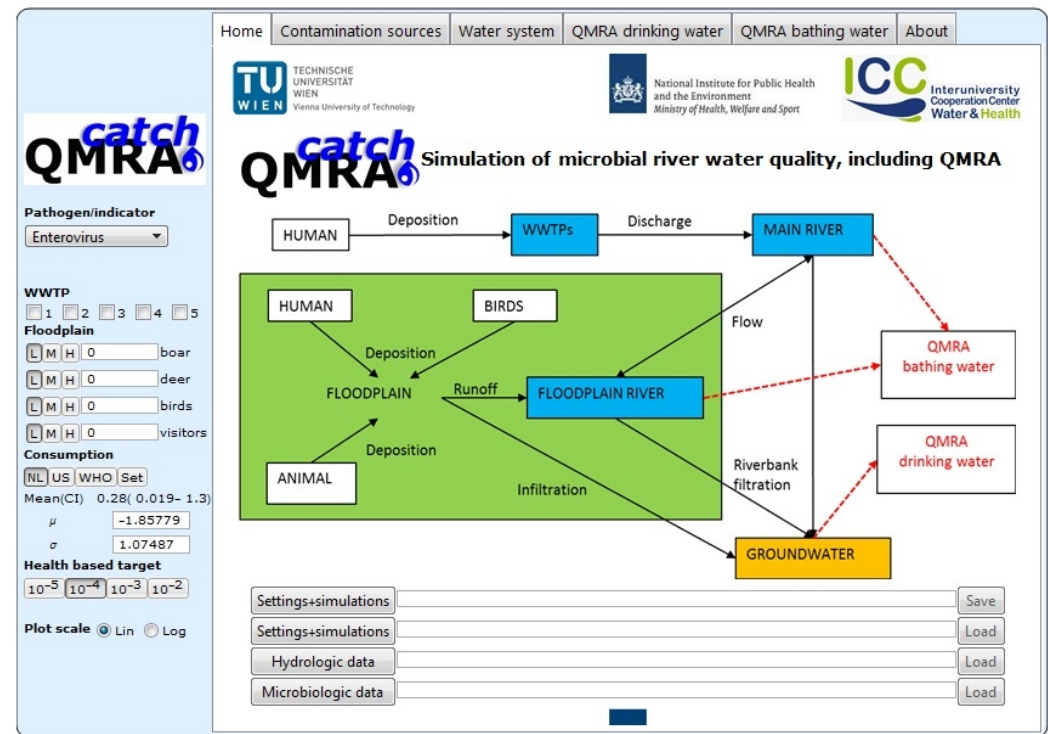
National Institute for Public Health
and the Environment
Ministry of Health, Welfare and Sport

[www.rivm.nl/en/Topics/W/
WHO_Collaborating_Centre_
Risk_Assessment_of_Pathogens
_in_Food_and_Water/Tools](http://www.rivm.nl/en/Topics/W/WHO_Collaborating_Centre_Risk_Assessment_of_Pathogens_in_Food_and_Water/Tools)

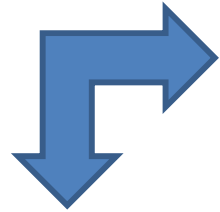
+ Quick User Guide

+ **Example spreadsheets** of settings, simulations, microbiological and hydrological data

+ Weblinks to Free CDF Player Download



Input variables and model use



Multiple levels of
microbial data

fecal indicator(s)

microbial source
tracking marker(s)

reference
pathogens

measured

assumed
(source-
concentrations)

calibration

(hydrological model)

verification

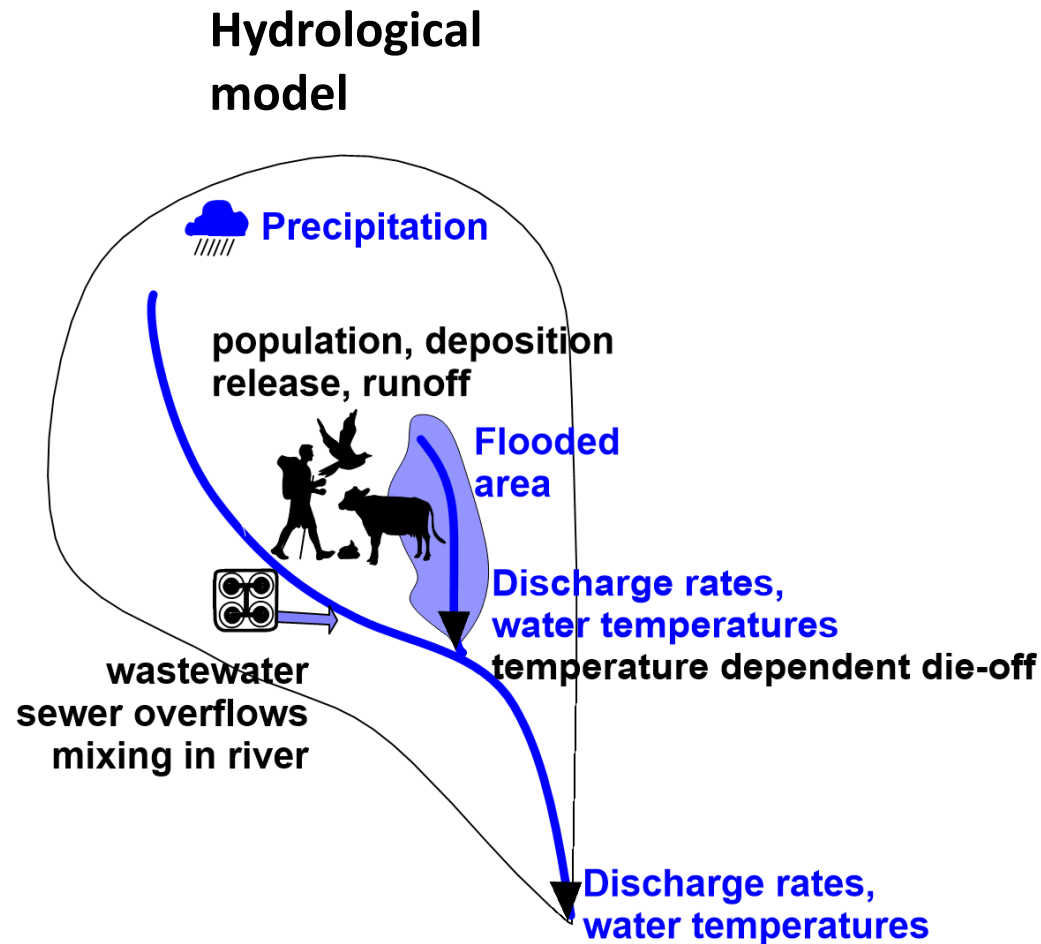
(hydrological model)

**health-risk
simulation**

(exposure-dose-
response model)

status quo

scenarios



Infection risk/person/year		
	Enterovirus	
	Target	0.0001
	Mean	1.3×10^{-6}
	95%	$2. \times 10^{-6}$
	Removal deficit (95%)	0. log ₁₀
	Norovirus	
	Target	0.0001
	Mean	0.0018
	95%	0.0026
	Removal deficit (95%)	1.4 log ₁₀
	Campylobacter	
	Target	0.0001
	Mean	9.8×10^{-6}
	95%	0.000013
	Removal deficit (95%)	0. log ₁₀
	Cryptosporidium	
	Target	0.0001
	Mean	1.4×10^{-6}
	95%	2.4×10^{-6}
	Removal deficit (95%)	0. log ₁₀

The concept

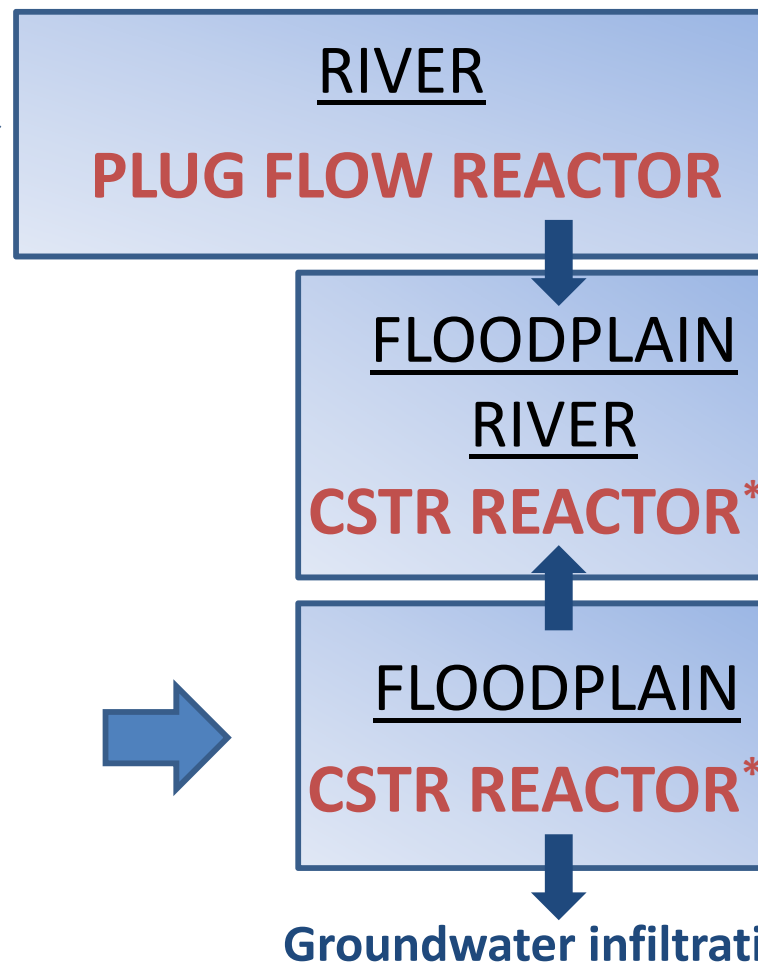
Step 1: Simulate concentrations in surface water (raw water) from source concentrations (hydrological model)

Input

WWTPs: Q, C_0, μ
(Point sources)

Human / animal
fecal pollution: Q, C_0, μ
(Diffuse source)

Computation



Output

Concentration
of selected
microbes

Concentration
of selected
microbes

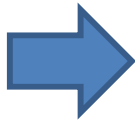
Concentration
of selected
microbes

The concept

Step 2: exposure assessment, dose-response modelling,
risk characterisation & required treatment

Input

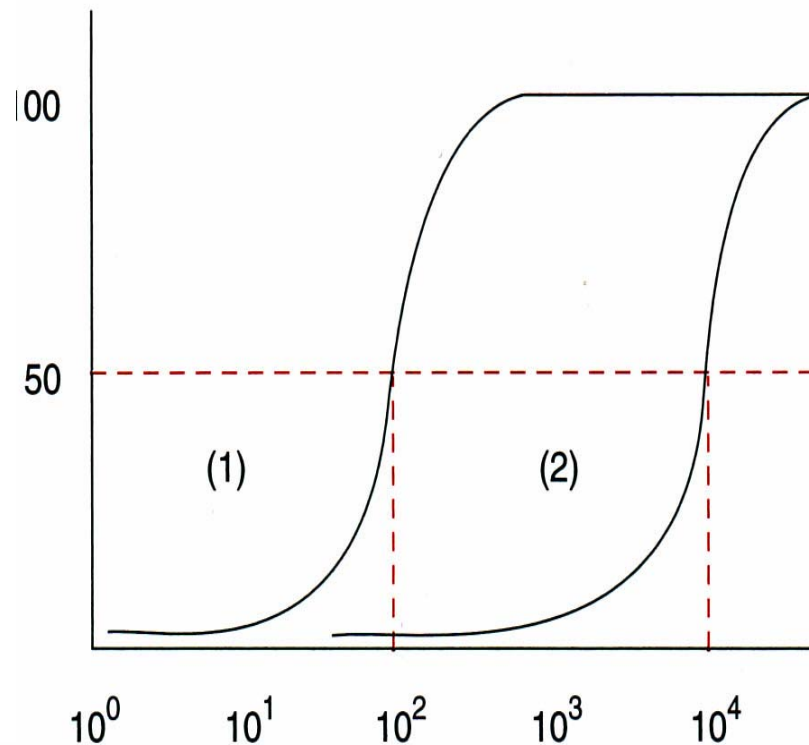
Pathogen
concentration
(estimated in Step 1)



Infected persons (%)

D-R model &

defining a health-based target



Output



+ infection risks
of reference
pathogens
+ required log-
reduction



Overview

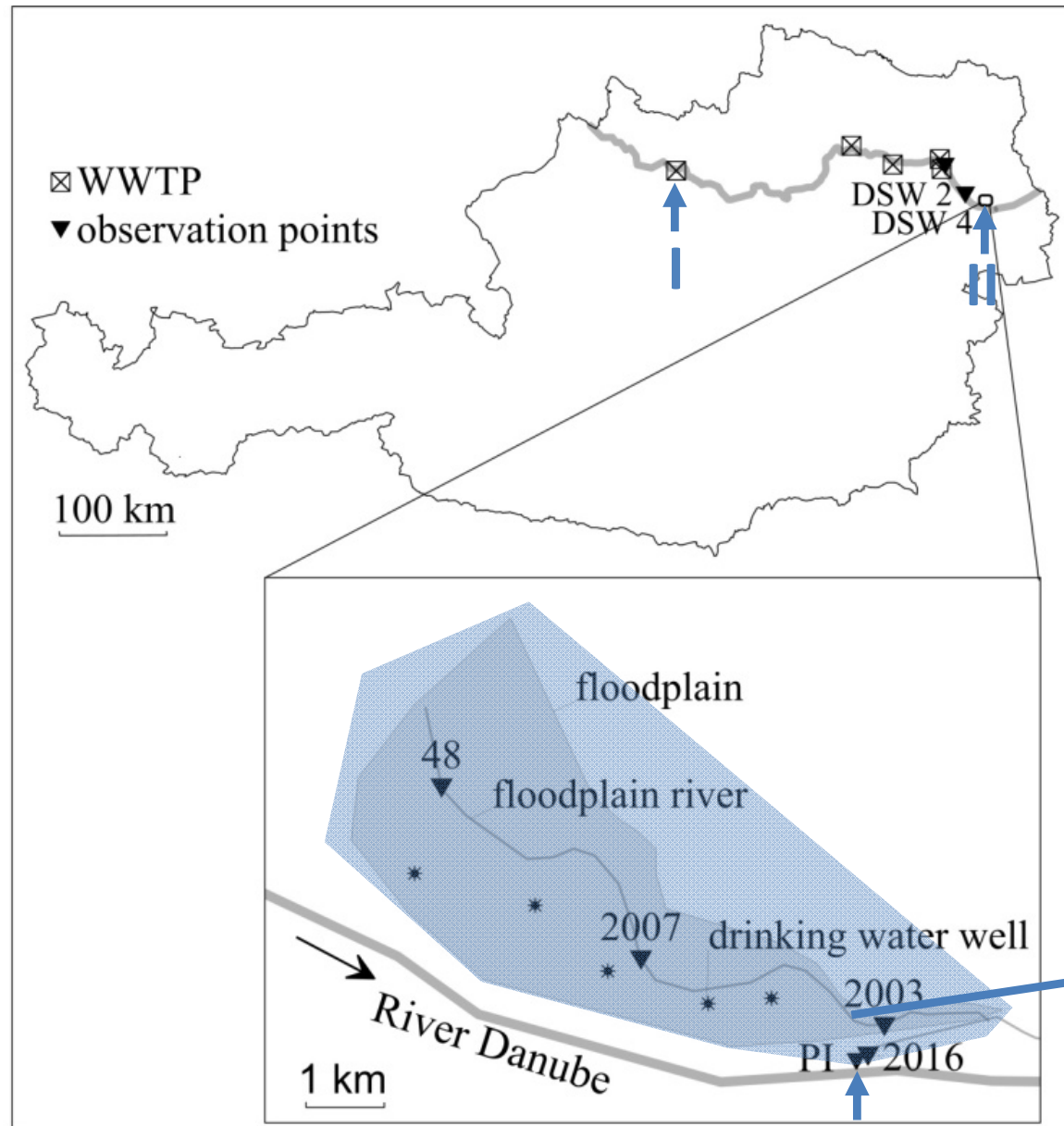
Background & Idea


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Conclusion & perspectives

Study site & model domain



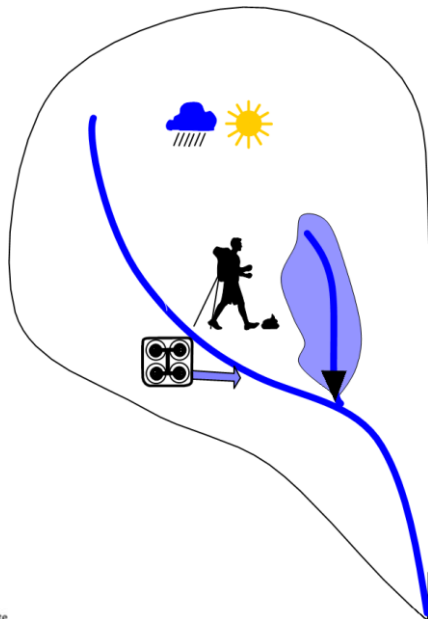
Extent of model domain:
I to II along the Danube
 in the floodplain



PI Main River (= II)

Aims

- 1) Simulate **human faecal pollution** in a **river-floodplain** area
- 2) Use **human-associated MST marker** to support **source-specific** model calibration
- 3) Evaluate sustainable **virus-reduction targets** required for **riverbank filtration & disinfection** (10^{-4} infec. person⁻¹ year⁻¹)
 - different **future scenarios** in the catchment
 - hydrology, wastewater disposal, epidemiology



Considered “fecal pollution” scenarios

1) current situation, 2) good case, 3) bad case

Hydrology & Waste Water Treatment Variables (Main River)

- wettest & driest hydrological years (since 1996)
- virus removal by WWTP (5 to 0 \log_{10} reduction)

Floodplain Variables

- visitor numbers to floodplain (650 persons to 1700 person /d*)
- excretion probability of visitors (10^{-4} – 1 per person)

Viral Epidemiology and Release

- viral prevalence (0.01 – 0.15 per person**)
- viral release rate from faecal products (0.005 – 0.5 per d)

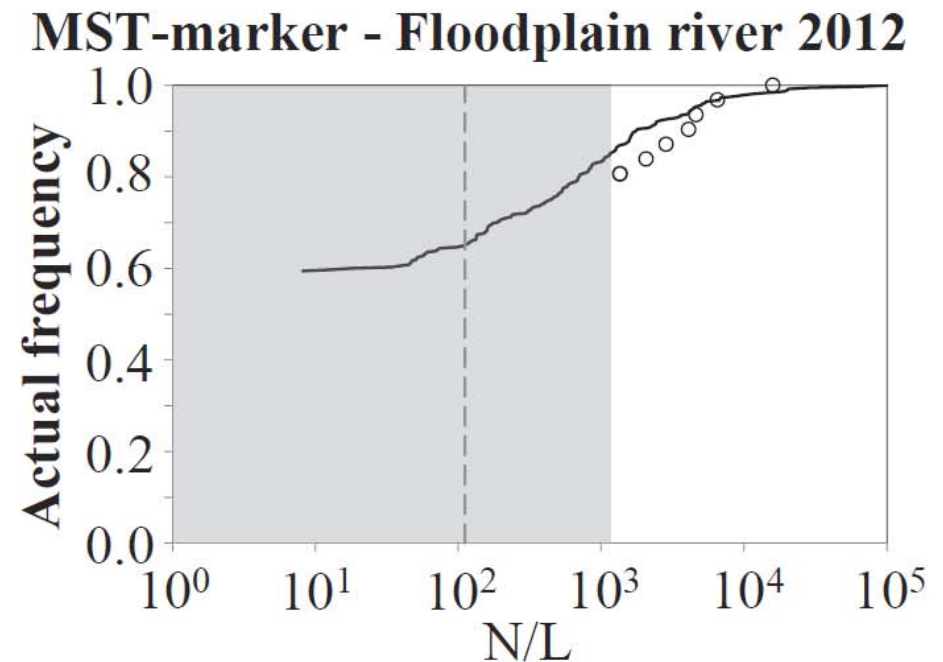
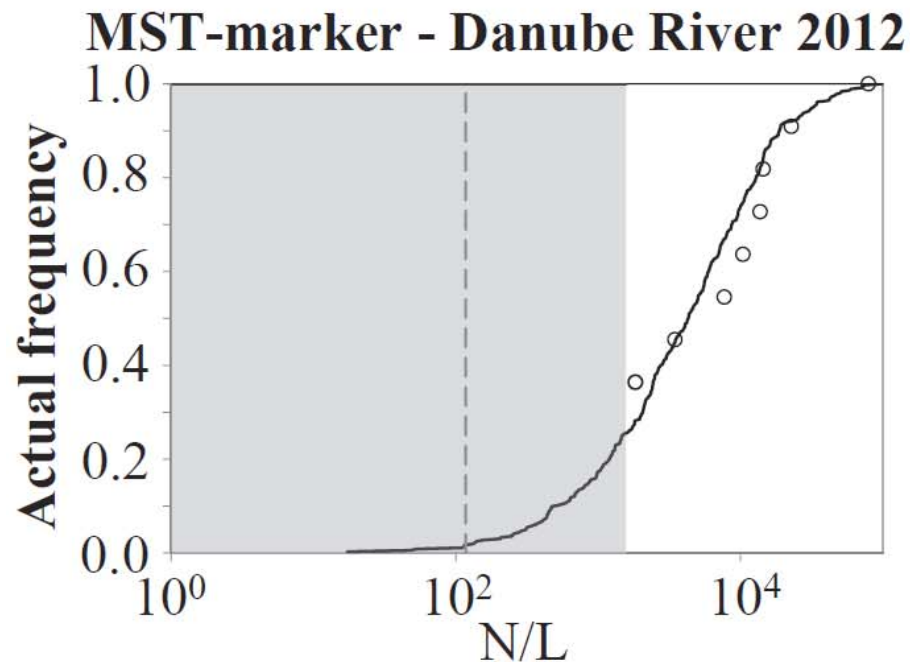
Microbial data availability & use

Microbial targets	Hydrological model calibration	Hydrological model verification	Risk assessment & log-reduction
<i>E.coli</i>	--	--	--
human-associated fecal marker*	Yes 2012	Yes 2013	
Enterovirus		Yes, 2012+13	Yes 2010 - 2015
Norovirus	--	--	Yes, but source concentrations assumed from literature

Hydrological model calibration

observed vs. simulated cumulated concentration frequencies (over one year)

maximum deviation of $0.4 \log_{10}$ (simulated minus observed)

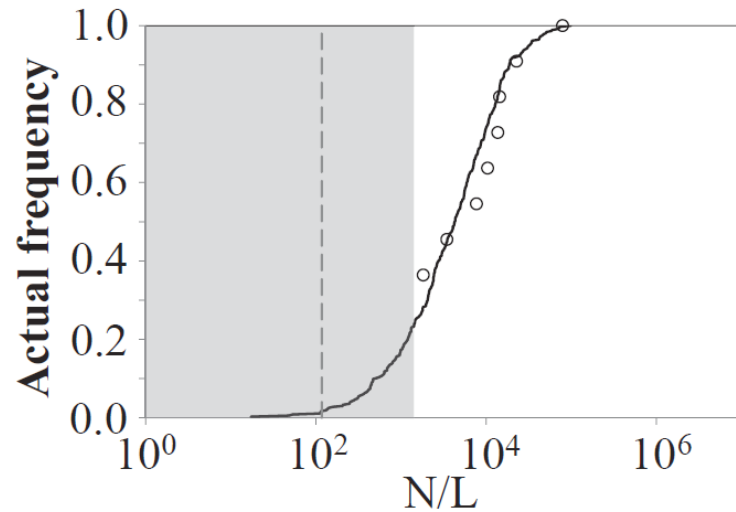


- observed
- simulated
- - - Minimum detection limit
- data below detection limit

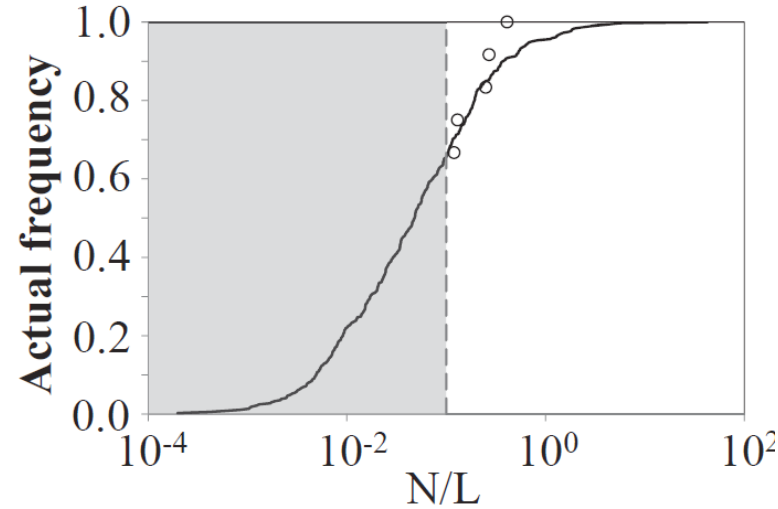
Hydrological model verification

maximum deviation of $0.6 \log_{10}$ (simulated-observed)

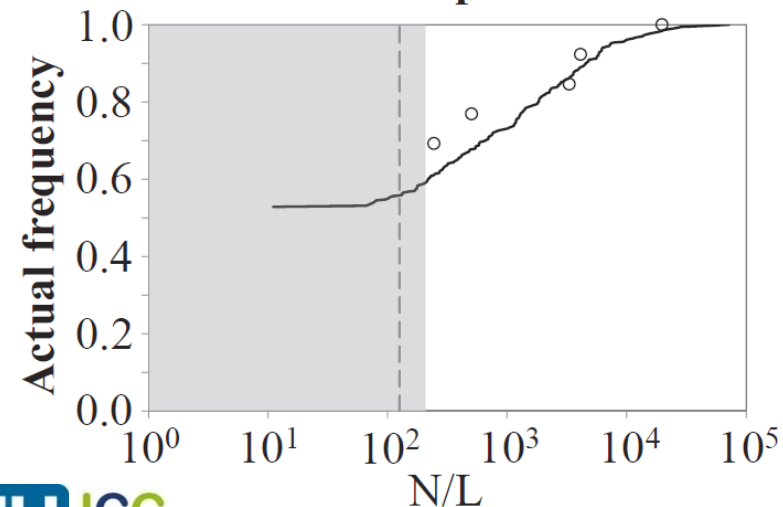
MST-marker - Danube River 2013



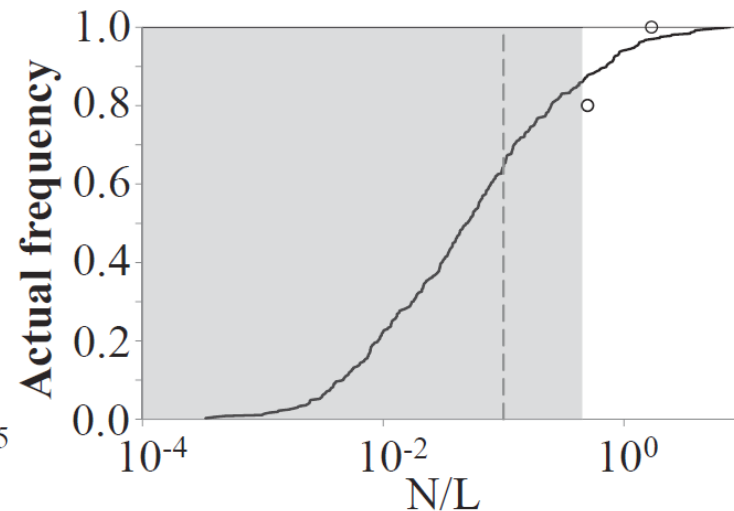
Enterovirus - Danube River 2012



MST-marker - Floodplain river 2013



Enterovirus - Danube River 2013



- observed
- simulated
- - - minimum detection limit
- data below detection limit

Simulated pathogen concentrations in the Danube and the floodplain river (95% percentiles) – Step 1

N/L	Current	Good	Bad
Danube PI			
Enterovirus	1	1×10^{-4}	11
Norovirus	51	5×10^{-3}	500
Floodplain-river PI			
Enterovirus	0.1	1×10^{-6}	630
Norovirus	14	1×10^{-4}	720

Estimated numbers of pathogens per litre

Simulated \log_{10} -reduction requirements by RBF* and disinfection (95% percentiles) to reach drinking water quality ($\leq 10^{-4}$ infections $p^{-1} y^{-1}$) – Step 2

Log ₁₀	Current	Good	Bad
Danube PI			
Enterovirus	4.5	2.1 	5.7
Norovirus	6.6	4.3 	8.2
Floodplain river PI			
Enterovirus	3.6	0.0 	7.7
Norovirus	5.7	1.1 	7.8





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Conclusion: „River Danube PI“



- ✓ Successful **calibration/verification** of the hydrological model based on **human-associated MST marker** & enterovirus data
- ✓ Successful combination of **microbial source tracking (MST)** & **microbial risk assessment (QMRA)**
- ✓ **Sustainable reduction targets** for **human viruses** during
 - river bank filtration and subsequent disinfection
(**bad case** and **good case** scenarios)

Perspective & Outlook



Extend to other compartments

- karst module
- urban module, etc.

Include other MST-markers & pathogens

- host-associated & specific MST-marker
- other zoonotic pathogens, etc.

Expand to other exposure scenarios

- recreation (not only swimming)
- irrigation
- wastewater reuse

Thank you!



References:

Schijven, J. F., J. Derx, A. M. de Roda Husman, A. P. Blaschke, A. H. Farnleitner. 2015. **QMRAcatch: Microbial quality simulation of water resources including infection risk assessment.** *J. Env. Qual.* **44(5): 1491-1502**

Derx, J., J. Schijven, R. Sommer, C. M. Zoufal-Hruza, Inge v. Driezum, G. Reischer, S. Ixenmaier, A. Kirschner, C. Frick, A. H. Farnleitner, A. P. Blaschke. 2016: **QMRAcatch: human-associated faecal pollution and infection risk modeling of water resources in a river-floodplain environment** *J. Env. Qual.* **45(4):1205-14**



Der Wissenschaftsfonds.



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