




Interuniversity Cooperation Center Water & Health

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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

Derx J[1,6], Schijven J[2], Sommer R[3,6], Zoufal-Hruza CM[4], Reischer G[1,6], Kirschner A[3,6], Frick C[4], Farnleitner AH[1,5,6] & Blaschke AP[1,6]

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Overview

Background & Idea

QMRAcatch: the current modules

Case study: River Danube & Backwater

Conclusion & perspectives

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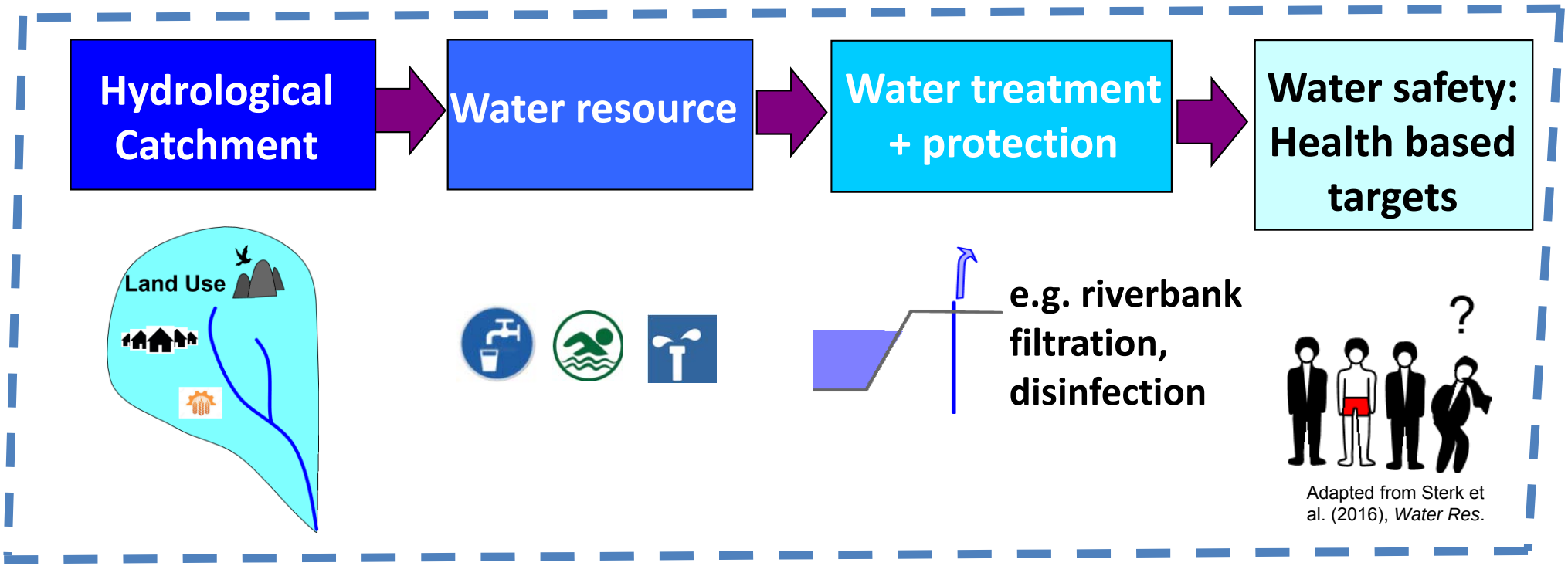
Ministry of Health, Welfare and Sport

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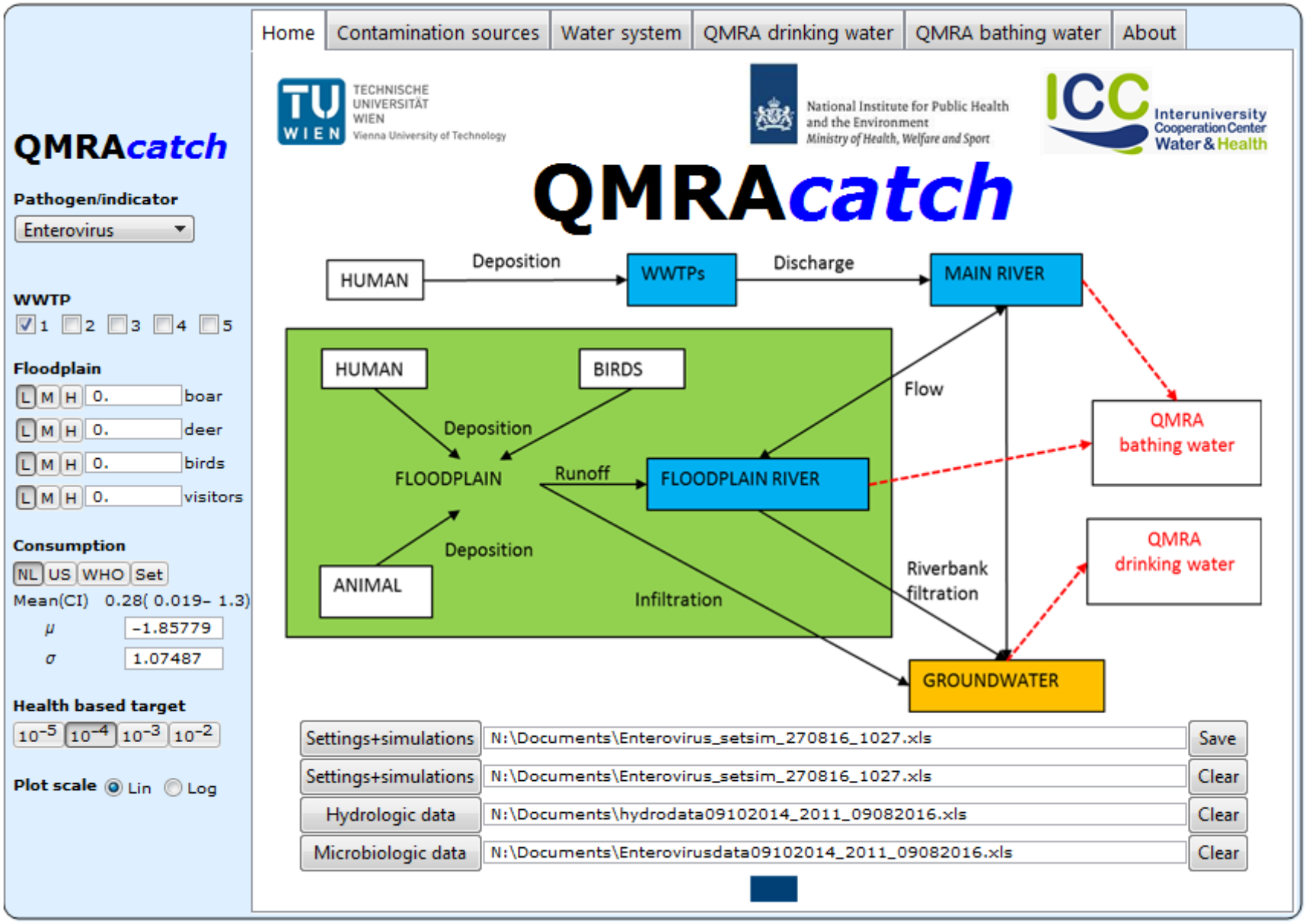
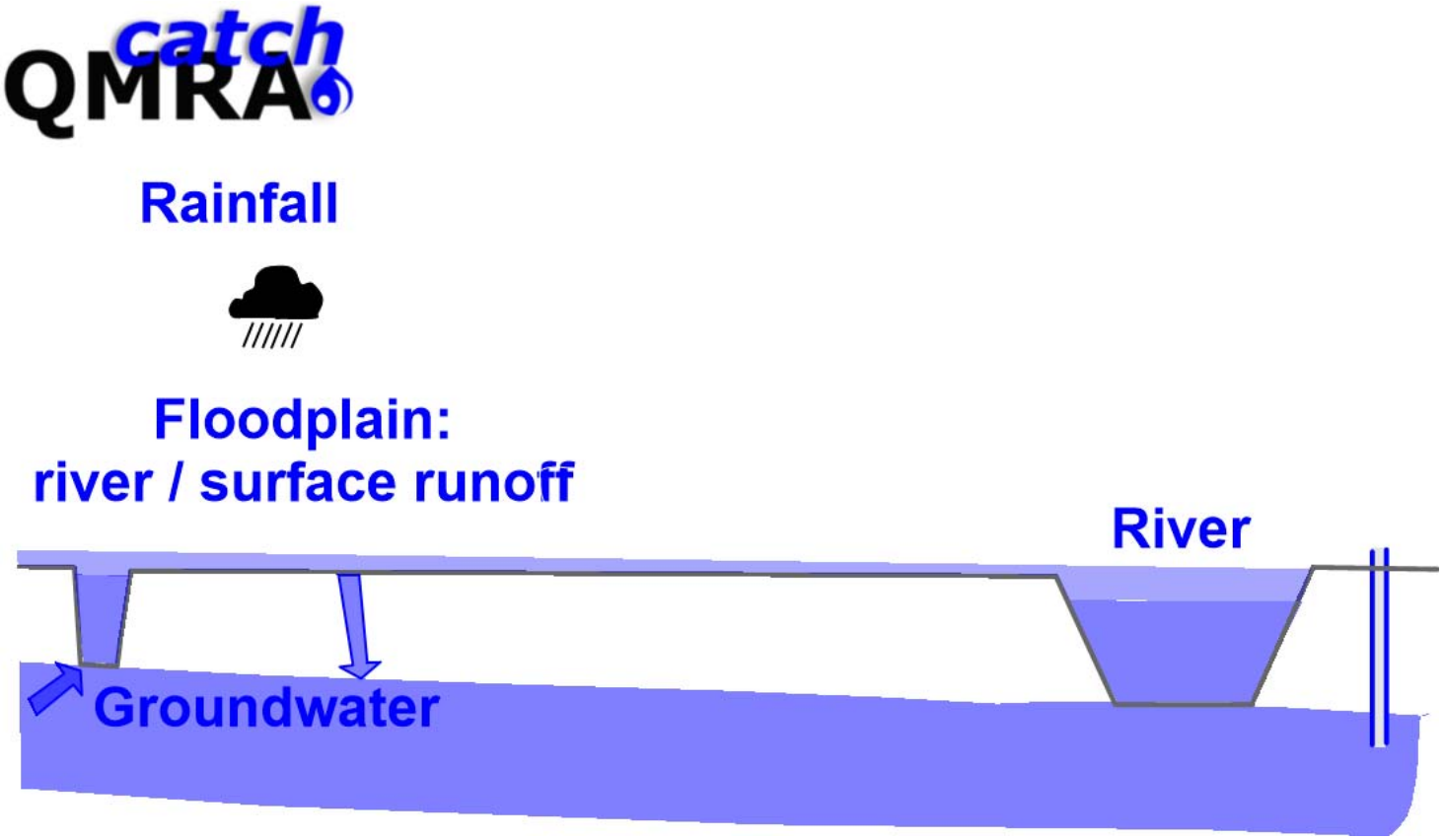
...a catchment-related microbial water quality simulation tool



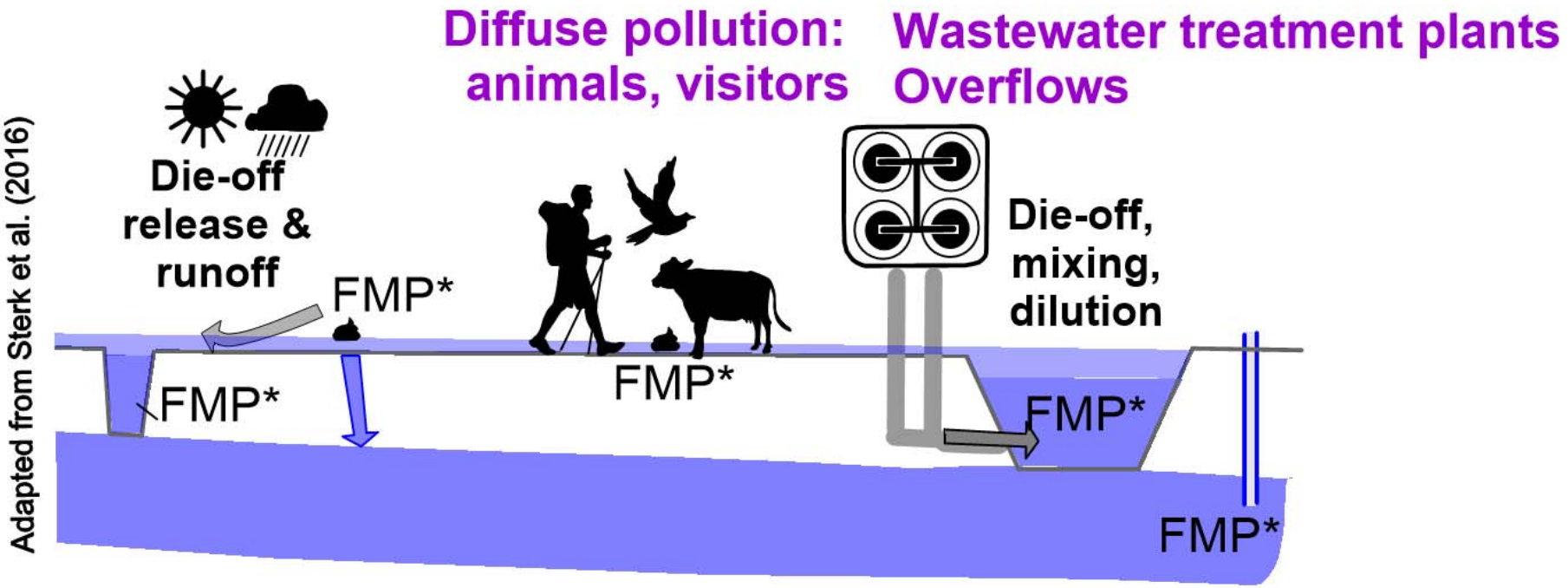
Schijven, J, Derx, J., De Roda Husman, A.M., Blaschke, A.P. & Farnleitner AH (2015) QMRAcatch - Microbial quality simulation of water resources including infection risk assessment. *J. Environ. Qual.* ***44(****5): 1491-1502*

Model components: Water system



- 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



FMP: Indicators & pathogens

- *E.coli*
- human-assoc. MST-marker
- Enterovirus
- Norovirus

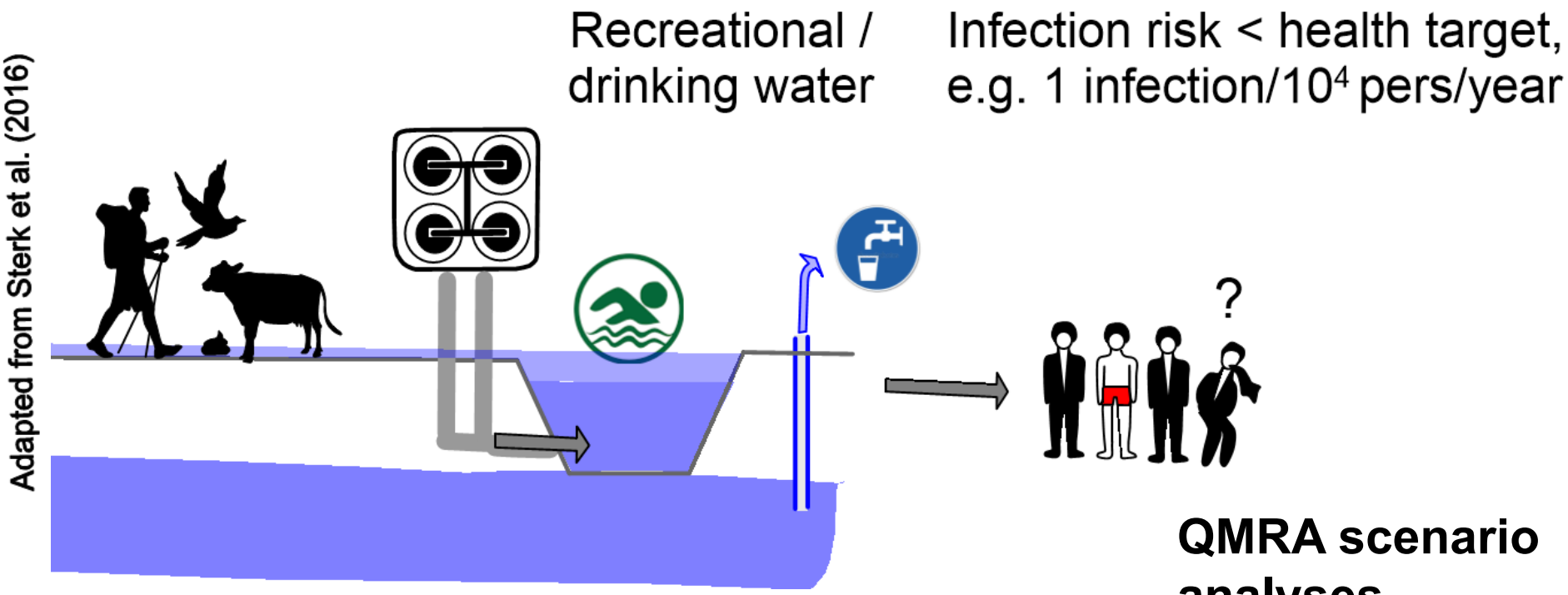
Human

- Campylobacter
- Cryptosporidium
- Giardia

Zoonotic

Model components:

Usage, quantitative microbial risk assessment (QMRA)



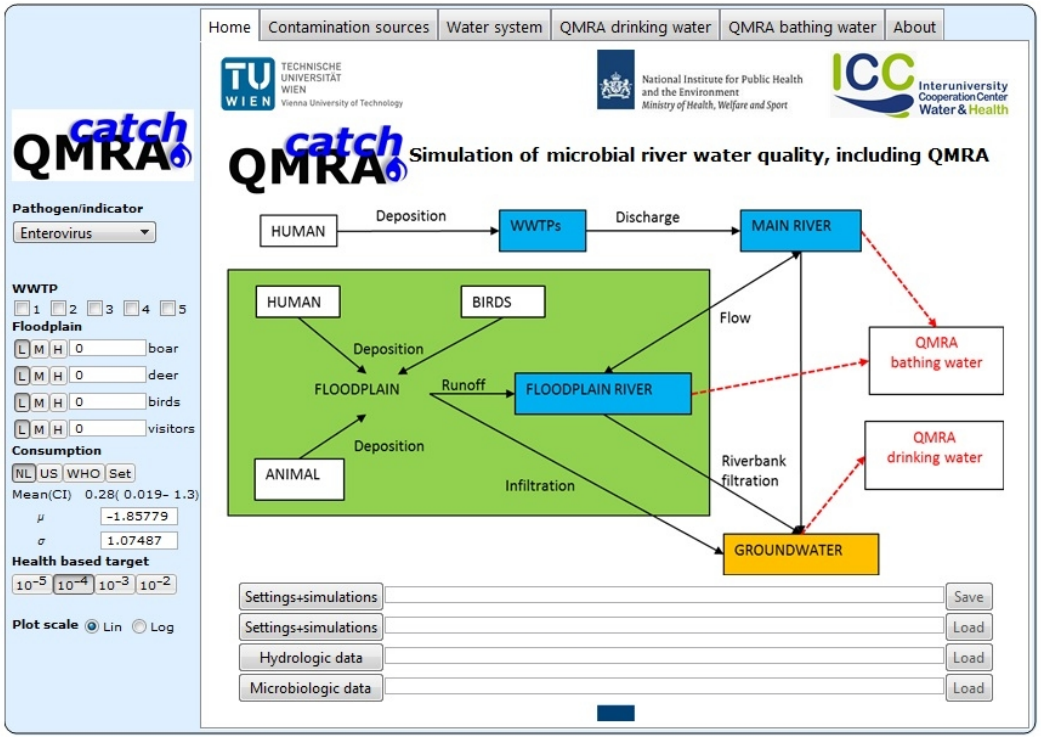
QMRA scenario analyses

- **guides catchment-management decisions**
- **to assess required final treatment (log_{10} reduction)**

- **to evaluate/guide catchment-management**

catch QMRA

Officially launched at the World Water Conference Brisbane, 2016



Free download links:

ICC Interuniversity Cooperation Center Water & Health 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

+ **Quick User Guide**
+ **Example spreadsheets** of settings, simulations, microbiological and hydrological data
+ Weblinks to Free CDF Player Download

Input variables and model use

status quo

scenarios

calibration (hydrological model) — **verification** (hydrological model) — **health-risk simulation** (exposure-dose-response model)

Multiple levels of microbial data

fecal indicator(s)

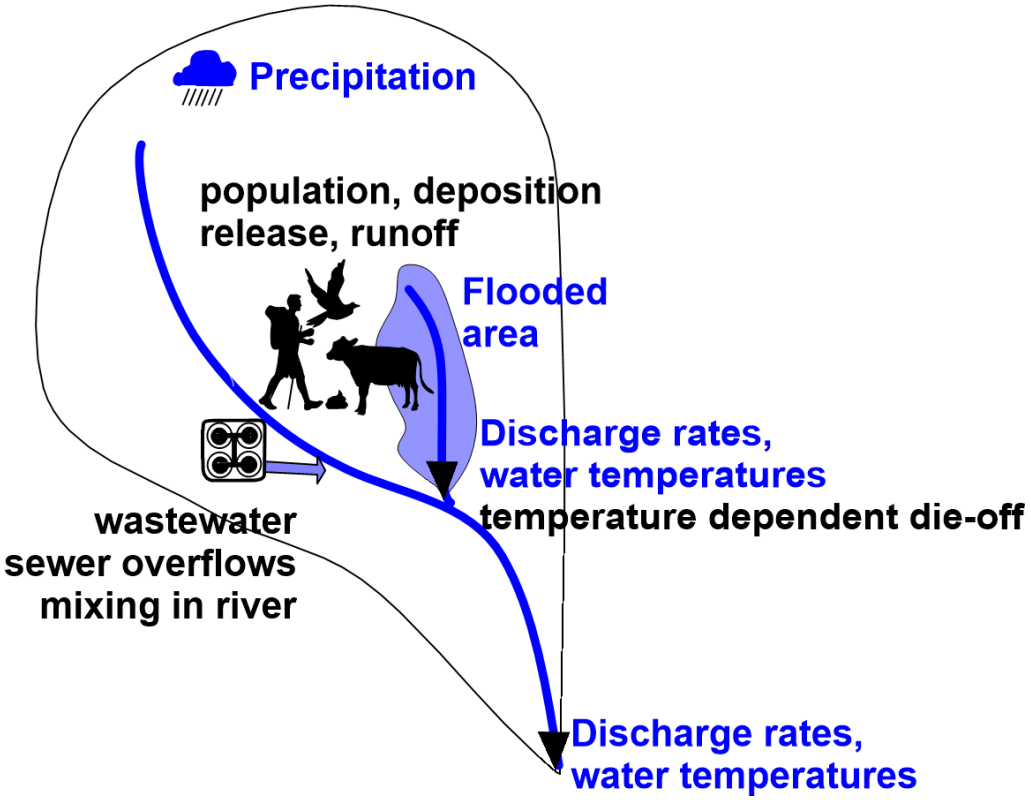
microbial source tracking marker(s)

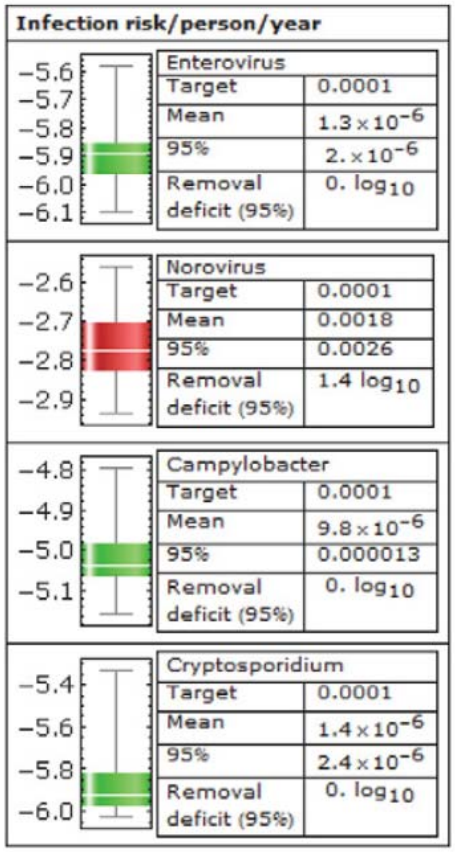
reference pathogens

measured

assumed (source-concentrations)

Hydrological model





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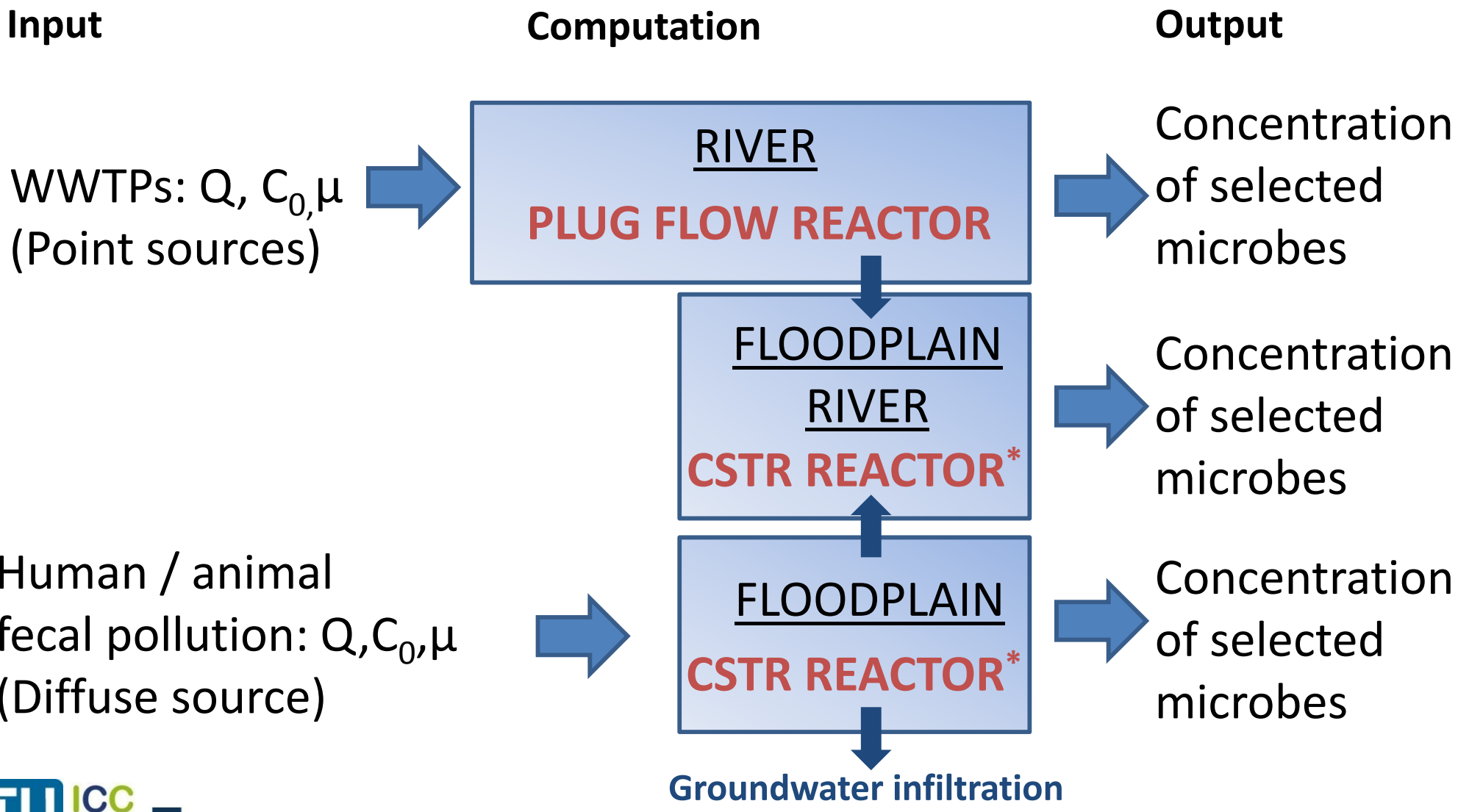
The concept

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



*continously stirred tank reactor

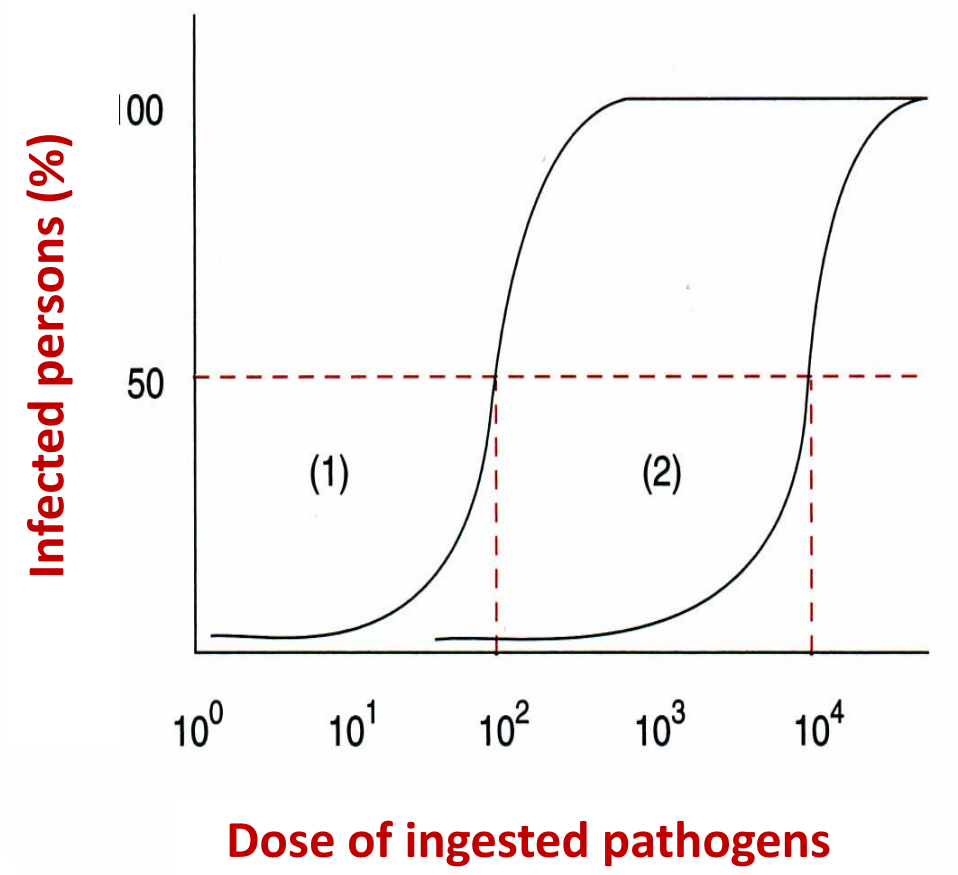
The concept

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

Input

Pathogen concentration (estimated in Step 1)

D-R model & defining a health-based target



Output

+ infection risks of reference pathogens
+ required log-reduction



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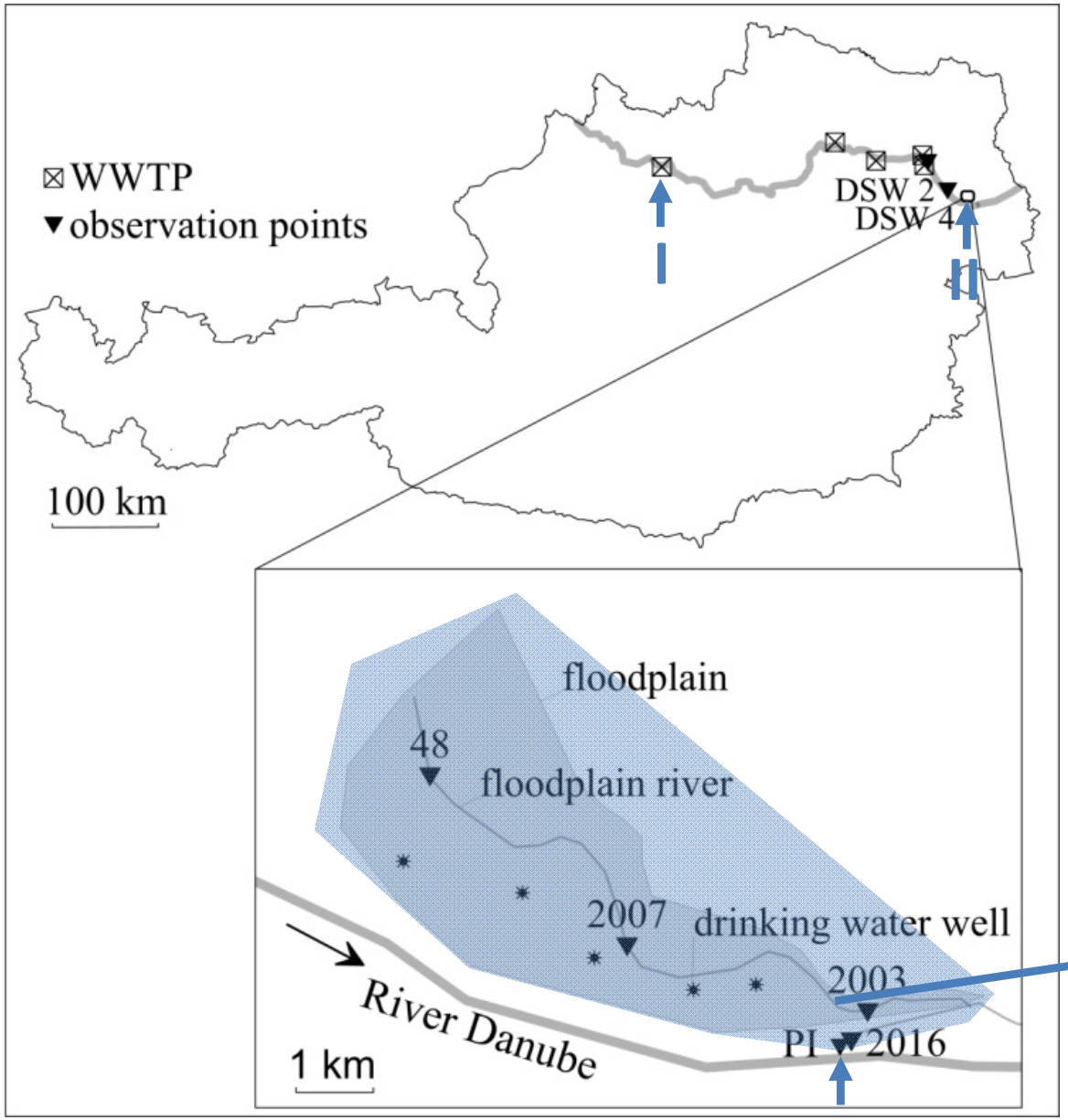
Study site & model domain



Extent of model domain:

I to II along the Danube

in the floodplain

PI Main River (= II)

Aims

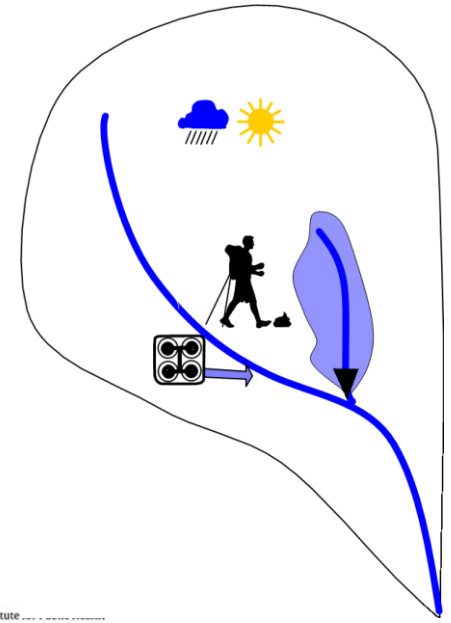
1) Simulate **human faecal pollution** in **a river-floodplain** area

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)

*Arnberger, 2006, Eder & Arnberger, 2006 ** Zhang 2013

Microbial data availability & use

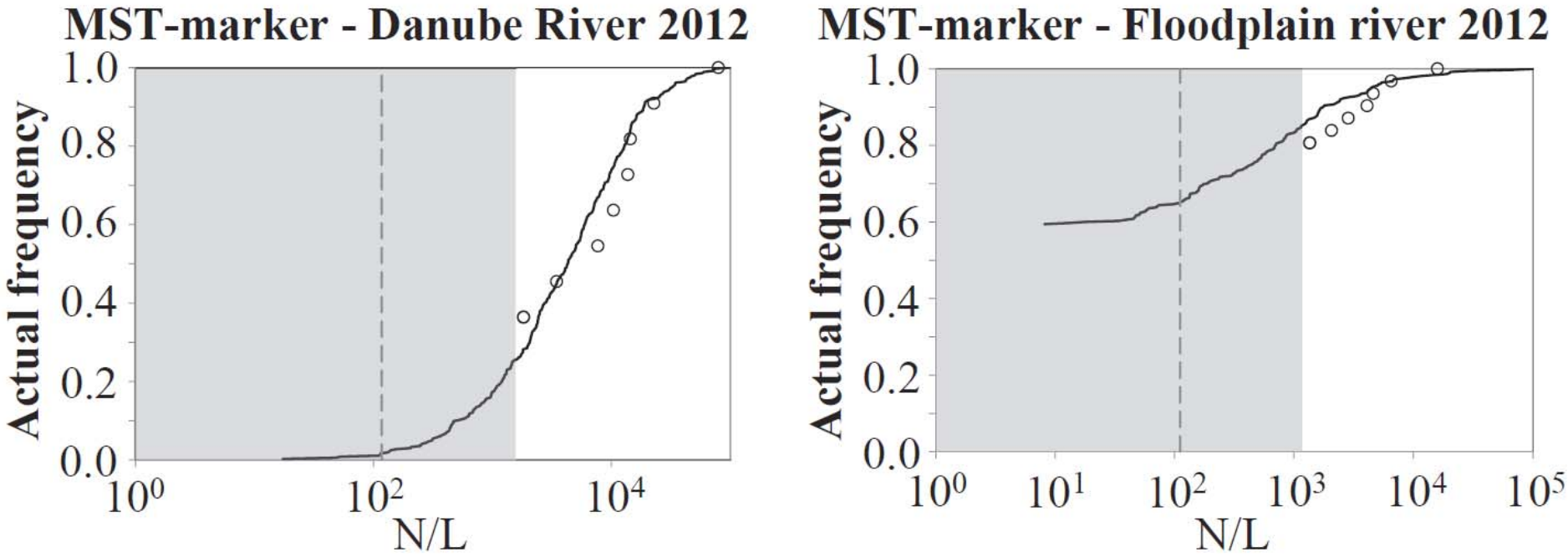
Microbial targets	Hydrological model calibration	Hydrological model verification	Risk assessment & log-reduction
E.coli	--	--	--
human-associated fecal marker*	**Yes 2012**	**Yes 2013**	
Enterovirus		**Yes, 2012+13**	**Yes 2010 - 2015**
Norovirus	--	--	**Yes, but source concentrations assumed from literature**

*HF183 II Taqman assay (Green et al 2014)

Hydrological model calibration

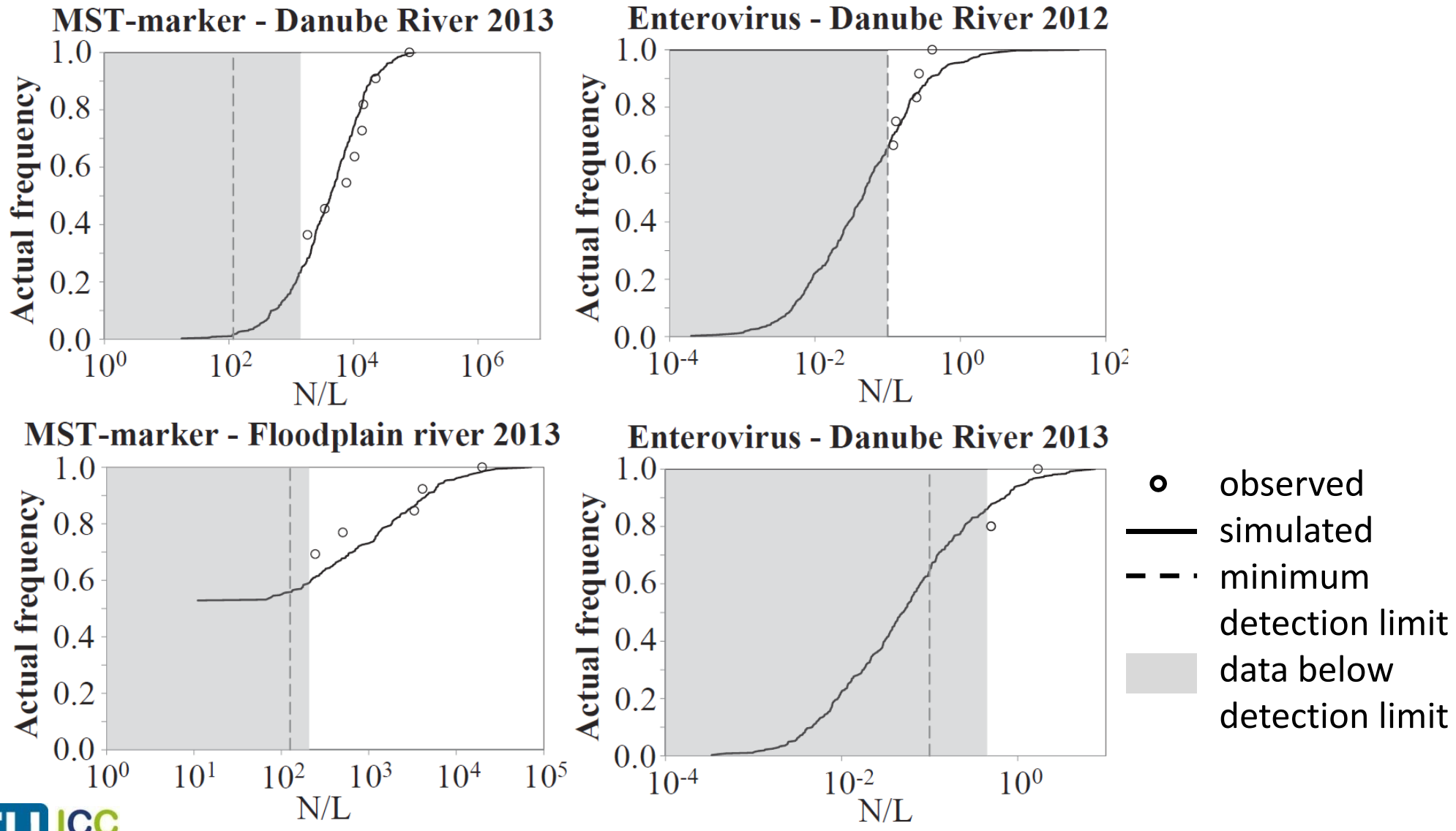
observed vs. **simulated** cummulated concentration frequencies (over one year)

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



Hydrological model verification

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



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 (≤ 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

*RBF = river bank filtration



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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

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