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Deliverable 7.1: MARS suite of tools 1

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D7.1-1: MARS suite of tools 1: Freshwater Information System (FIS)

D7.1-2: MARS Diagnostic Tools to diagnose the causes of deterioration of water bodies

Non-technical summary

D7.1-1

This deliverable gives an overview of the functionality of the Freshwater Information System (FIS) through a number of screenshots and a short explanatory text. FIS is one of the tools that are developed within the MARS project. It is the web-based information system providing access to information and practical tools generated in MARS. FIS contains informative factsheets for DPSIR, stressors, ecosystem services and MARS case studies on the impact of multiple stressors for ecological status as well as a model selection tool for river basin management. The design and functionality has been discussed internally with MARS partners (Deltares, UDE, IGB) and with end-users during workshops in Delft (September 2015) and Den Helder (October 2016). FIS will be integrated in the Freshwater Information Platform, which aims at bringing together the results of many projects dealing with freshwater ecosystems in one a single platform.

D7.1-2

While the assessment of the ecological status of surface water bodies has become quite straightforward nowadays, almost two decades after the WFD has been launched, the inference of appropriate management options from the assessment is still challenging. More precisely, water body managers face the ecological status assessment of a given water body that usually integrates over several or numerous (multiple) stressors impacting the water body. The challenge is to identify the most-impacting stressor(s) and to distinguish them from the minor ones. Such stressor hierarchies are required to infer the appropriate hierarchy of management options to address the relevant stressors. This report presents tools to assist water body managers in the inference of management options to address the impact of multiple stressors on surface water bodies.

The first chapter presents a conceptual model to visualise the published evidence of the impacts of combined stressors (here: nutrient enrichment and fine sediment pollution) on river organisms. The structured evaluation of published evidence can help identify potential interactions of stressors, which then require consideration in water body management.

The second chapter presents an approach to diagnose the causes of deterioration of lowland rivers based on the causes' (stressors') effects on selected diagnostic metrics derived from the macrozoobenthos community. The approach uses a Bayesian (Belief) Network (BN) to statistically infer the probabilities of the causes to be causal for the detected effects at the water body.

In the third chapter, we present an interactive online tool that builds upon the BN as presented in Chapter 2. The tool provides a graphical interface that allows the user to easily enter evidence (i.e. the states of selected effect variables) to the BN. The results are graphically displayed and accompanied by helpful background information and web links to relevant sources of information.

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Deliverable 7.1

MARS suite of tools 1: Freshwater Information System (FIS)

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SUMMARY

This deliverable gives an overview of the functionality of the Freshwater Information System (FIS) through a number of screenshots and a short explanatory text. FIS is one of the tools that are developed within the MARS project. It is the web-based information system providing access to information and practical tools generated in MARS. FIS contains informative factsheets for DPSIR, stressors, ecosystem services and MARS case studies on the impact of multiple stressors for ecological status as well as a model selection tool for river basin management. The design and functionality has been discussed internally with MARS partners (Deltares, UDE, IGB) and with end-users during workshops in Delft (September 2015) and Den Helder (October 2016). FIS will be integrated in the [Freshwater Information Platform](#), which aims at bringing together the results of many projects dealing with freshwater ecosystems in one a single platform.

1. INTRODUCTION

Within MARS several tools are being developed: an information system, which is described in this report (Task 7.1), a diagnostic tool (Task 7.2), an application of Bayesian Belief Networks (BBN) to a selection of case studies and a model selection tool, which is incorporated in the information system (Task 7.3), and a scenario analysis tool (Task 7.4).

The impact of multiple stressor combinations is highly diverse and complex. The MARS project has addressed this at various spatial scales (Europe, individual basins down to experiments aiming at enlarged insight into the causal mechanisms) for the present state and through scenarios based on contrasting storylines for future environment conditions. The information system is designed to serve as an introductory gateway to this complex world and to the results of the MARS project (Figure 1). It has three components: i) an information library, ii) case studies on the impact of multiple stressors on ecological status under present conditions and future scenarios and iii) a model selection tool for river basin management.

For the information library and case studies the information is supplied through to-the-point factsheets with reference or links to background information.

FIS will be expanded and updated during the remainder of the MARS project with additional factsheets. After MARS has ended, it will be hosted by and integrated in the [Freshwater Information Platform](#) which allows expanding and updating its content.



Figure 1. Home page of the Freshwater Information System (FIS)

2. INFORMATION LIBRARY

The first component of the Freshwater Information Systems (FIS) is the information library (Figure 2). The information library is structured around the building blocks of driver-pressure-state-impact-response framework (DPSIR), which is commonly applied in river basin management with links to ecosystem services, future scenarios and stressors. It comprises factsheets that introduce the main features with links to background information. These factsheets form an informative reference for stakeholders and also illustrate impacts of multiple stressors on the provision of ecosystem services from freshwater ecosystems under different climatic and land-use scenarios.

Within the DPSIR component six different driver- and eight different pressure-categories are distinguished. Ecosystem services follow the categorisation of the Millennium Assessment and address three main groups: regulating, provisioning and cultural services. Future scenarios comprise three storylines, which the MARS project used to group the various directions for environmental changes in Europe: a ‘techno world’, a ‘consensus world’ and a ‘fragmented world’. Stressors address five individual categories: chemical, morphological, hydrological, thermal, biological and the complex world of multiple stressor combinations, which is the core topic of MARS.

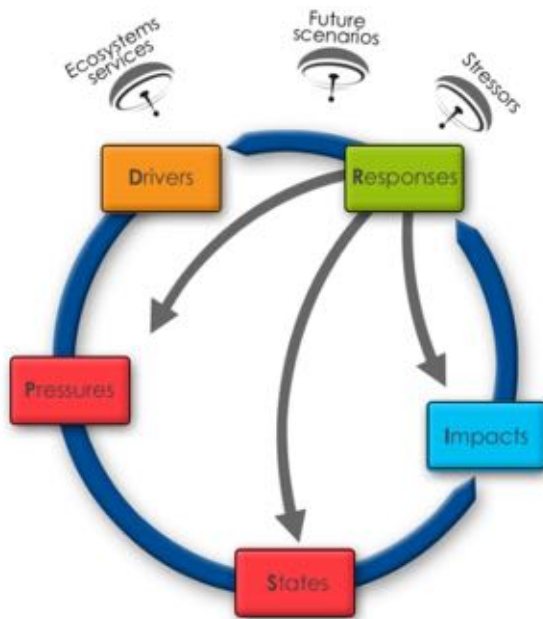


Figure 2. The information library is structured according to the DPSIR, ecosystem services, future scenarios and stressors.

3. CASE STUDIES

As part of the MARS project, 16 catchments (rivers, lakes and transitional) throughout Europe have investigated the relationships between pressures, water quantity and quality, ecological responses, ecological functioning and ecosystem services under a wide range of multi-stressor scenarios (Figure 3). The detailed results are documented in MARS deliverable 4.1¹. In the FIS each of these case studies is synthesized from a water management perspective: What issues are at stake? Which future scenarios have been considered? What can be concluded and how is this of concern for water management?

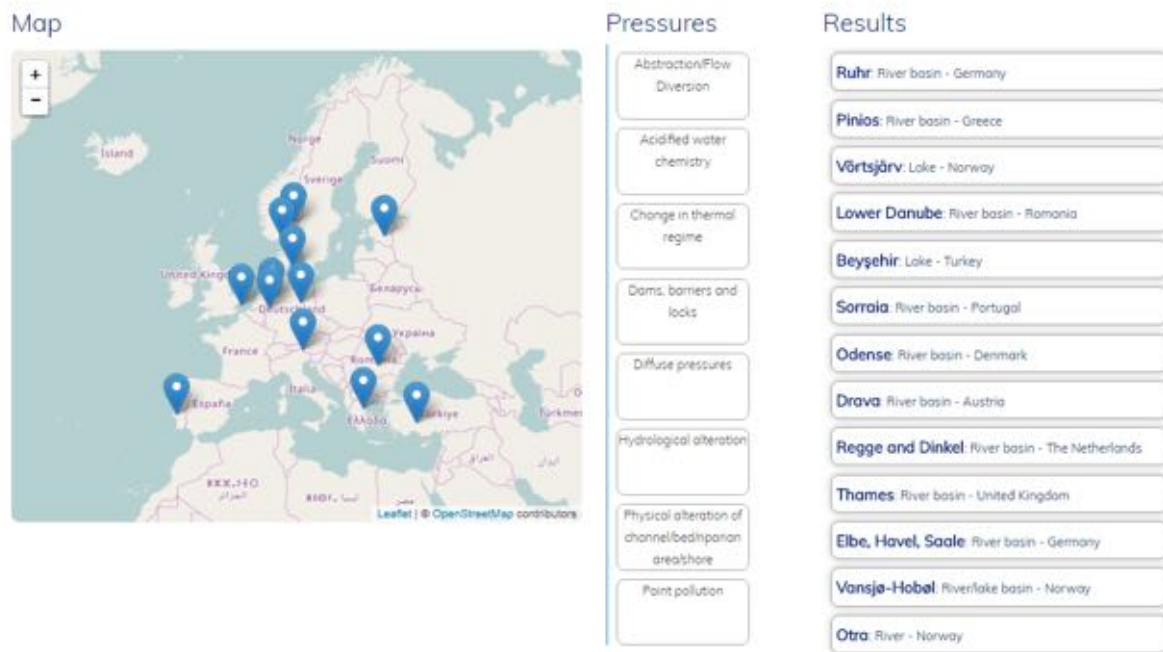


Figure 3. MARS case studies where catchments have been modelled for multi-stressor scenarios.

¹ MARS Deliverable 4.1 Case study synthesis - Final Report

4. MODEL SELECTION TOOL

Models are widely used in water management. Quite often models are chosen which people are familiar with or have heard of. There was, however, no simple tool presenting an overview of the applicability of widely used models for river basin management². Therefore MARS developed a model selection tool (Figure 4). At present the tool comprises > 20 models.

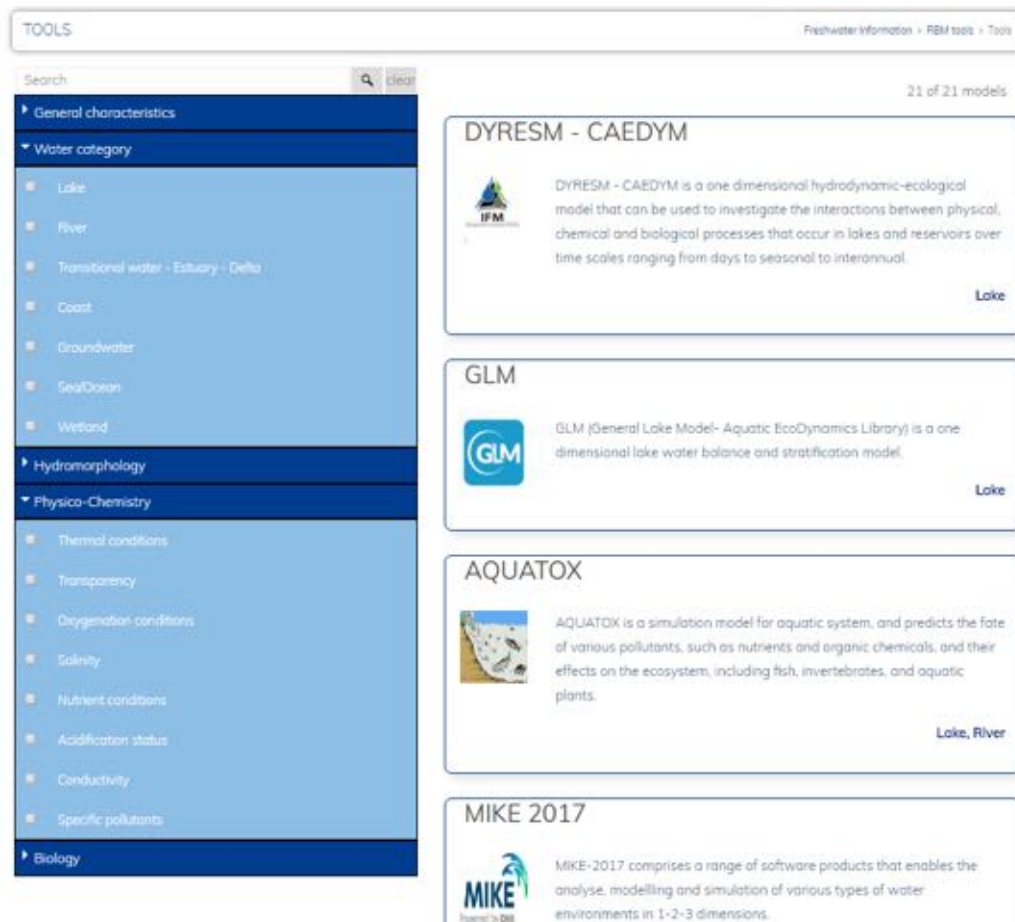


Figure 4. Model selection tool for river basin management: filtering models in the left panels instantly lists the model meeting the criteria on the right.

For each model general characteristics (e.g. open source, domain, space and time resolution), applicability for the various water categories (e.g. lakes, rivers), hydromorphology, physico-chemistry and biology are given, which is summarised in a factsheet including contact information and links to websites. Models can be filtered either through tick boxes or pull down menus whereby the selection of relevant models is immediately shown to the right.

² There has been a previous FP5 project 'Benchmark Models for the Water Framework Directive' (BMW) with advice regarding selection and use of models in the context of implementation of the EU Water Framework Directive (2000/60/EC), but the tool is no longer available online (Hutchins et al. 2006). The criteria used in BMW have been revisited, simplified and adapted from a water management perspective.

Reference: Hutchins, M., Urama, K., Penning, E., Icke, J., Dilks, C., Bakken, T., Perrin, C., Saloranta, T., Candela L. & Kämäri, J. (2006). The model evaluation tool: guidance for applying benchmark criteria for models to be used in river basin management. Archiv für Hydrobiologie. Supplementband. Large rivers, 17(1-2), 23-48.

Factsheet overview for each model:

Short model description

Water category

- Lake, River, Transitional water - Estuary – Delta, Coast, Sea/Ocean

Hydromorphology

- H - Quantity and dynamics of water flow, H - Residence time, T - Freshwater flow, T - Direction of dominant currents, T - Wave exposure, River continuity, M - Structure and substrate of the bed, M - Width variation, M - Depth variation

Physico-Chemistry

- Thermal conditions, Transparency, Oxygenation conditions, Salinity, Nutrient conditions, Acidification status, Conductivity, Specific pollutants

Biology

- PH – Composition, PH – Abundance, PH – Biomass, AF – Abundance, FI - Age structure

General characteristics

- Software License, Graphical User Interface, Number of model dimensions, Space and time resolution, Model domain – (Hydromorphology, Physico-Chemistry, Biology)

Contact information

- Acronym/abbreviation, Website, Country of origin, Contact details, Language

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Deliverable D7.1-Task 7.2: MARS Diagnostic Tools to diagnose the causes of deterioration of water bodies

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Non-technical summary

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The first chapter presents a conceptual model to visualise the published evidence of the impacts of combined stressors (here: nutrient enrichment and fine sediment pollution) on river organisms. The structured evaluation of published evidence can help identify potential interactions of stressors, which then require consideration in water body management.

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Conceptual cause-effect tools, based on ecological evidence data for multiple stressor impacts on riverine ecosystems



Contribution to MARS WP7.1 Deliverable

Harmonisation of international conceptual cause-effect tools,
based on ecological evidence data for multiple stressor impacts
on riverine ecosystems

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Summary

European rivers are impacted by multiple stressors, which alone and in combination cause changes in riverine ecosystems. The cause-effect chains leading to ecological impairments should be critically diagnosed in order to plan effective restoration measures to improve the biological condition. Methods for ecological causal assessment, as well as associated tools have been developed simultaneously in different parts of the world. These methods use scientific evidence in ecological literature to support causal assessments in environmental investigations. The objective of this thesis is to support the development of diagnostic and predictive tools in the EU-funded project MARS (Managing Aquatic ecosystems and water Resources under Multiple Stress), by studying existing methods and creating conceptual ecological models with their assistance.

The results of this work contain literature-based evidence on causes and ecological effects of excess fine sediment and nutrients in rivers. The results are visualised in conceptual diagrams, which organise and combine the evidence on cause-effect associations. The diagrams demonstrate how fine sediment and nutrients affect the ecological functioning of rivers by changing benthic invertebrate and fish community structures. The combined effects of the stressors are mainly additive multi-stressor relationships, but the reference

literature also evidenced synergistic and antagonistic effects between the stressors. Additionally, the study revealed a research gap concerning joint effects of the stressors on fish indicators. The main challenges for the future development of cause-effect tools are effective extraction of cause-effect associations from the primary studies and visualisation of complex multi-stress relationships in conceptual models.

Introduction

Rivers and streams are sensitive ecosystems, which are impacted by host of stressors caused by agriculture, hydropower production, flood protection, urban development, deforestation, industry and transport, to mention few. The impacts of the stressors individually or in combination typically lead to a decrease in biodiversity because of degraded habitat, reduced water quality, biologically unsuitable flow regimes, dispersal barriers, altered inputs of organic matter or sunlight, etc. (Palmer et al. 2010). Managers should critically diagnose the causes of the impairments and invest resources first in repairing those problems most likely to limit restoration (Palmer et al. 2010). For conservation to be effective, decision-makers should base their decisions on effectiveness, which is demonstrated by scientific evidence. But rather than evidence provided by scientific research, environmental conservation practise is largely based on traditional land management practises (Pullin et al. 2004) or expert opinions (Webb et al. 2012). Additionally, very little evidence is collected on the consequences of current practice so that future decisions cannot be based upon the experience of what does or does not work (Sutherland et al. 2004). Evidence-based frameworks have become effective tools in medicine, incorporating the results of medical research into medical practice (Roberts et al. 2006). In environmental policy and practice, available science is still not widely used (Pullin & Knight 2003; Sutherland et al. 2004; Dicks et al. 2014). The limited use of scientific information in environmental decisions might be caused by difficulties to access relevant scientific literature (Pullin & Knight 2003; Pullin et al. 2004), lack of effort to incorporate the growing evidence base into decision frameworks (Dicks et al. 2014), lack of scientific studies addressing the right questions (Dicks et al. 2014), and limited collection of information from individual practitioners in a form that could be used by others (Sutherland et al. 2004). Many management interventions remain unevaluated (Pullin et al. 2004; Sutherland et al. 2004). The result is that decisions are often made without access to the best quality evidence thus increasing the probability that inappropriate management options will be adopted (Pullin & Knight 2003). Review articles are often the only source of evidence used by decision makers in conservation and environmental management to assess effectiveness and impact of actions (Roberts et al. 2006). When ecological reviews (reviews from the disciplines of conservation, ecology and environmental management) were compared to medical systematic reviews, ecological reviews were more likely to be prone to bias, lacking details in the methods used to search for studies, and were less likely to assess the relevance of studies, quality of the original experiments and to quantitatively synthesise the evidence (Roberts et al. 2006). Review updates and amendment is standard practice in medicine, and the search infrastructure and information databases

available to the medical community are better integrated than those in ecology (Stewart et al. 2005).

There is a growing interest in integrating evidence-based approaches to conservation practises as well (Pullin & Knight 2003; Pullin et al. 2004; Sutherland et al. 2004; Roberts et al. 2006; Pullin & Knight 2009). Sutherland et al. (2004) believe that a greater shift to evidence-based conservation would be highly effective, and additionally likely to result in enhanced funding by actively demonstrating this effectiveness to funders and policy formers.

Evidence syntheses that review and combine the findings from primary research articles to assess the effectiveness of an environmental intervention or the impact of an exposure are important for consolidating research, as the evidence provided by primary studies is expanding rapidly (Woodcock et al. 2014). Scientific evidence should be easily accessible, quantified, and in usable format to be used effectively by water managers. Ecological cause-effect evidence databases and conceptual models can offer useful tools to gather, store, organize, visualise and share the expanding evidence base. Conceptual models, which are based on ecological evidence data extracted from scientific peer reviewed literature offer highly repeatable, transparent, and structured method for causal assessment. They can be used as support in conservation and environmental management, helping in shifting to more evidence-based decision making in environmental issues. The diagnostic tool should be able to diagnose linkages between multiple stressors affecting water bodies, and their biological responses, as well as offer management options to cope with the problems. The ultimate goal is to improve the conditions of European water bodies to meet the objectives of the WFD. The first step is to create literature-based conceptual models visualising the linkages between stressors and their responses in the ecosystems. In this task conceptual models on causal chains leading to ecological impairments in riverine ecosystems will be created with help of existing international cause-effect modelling tools. These models support the creation of diagnostic tools within the MARS project.

What are conceptual cause-effect models and why do we need them

Conceptual ecological models are qualitative models which are based on causal linkages among sources, stressors and biological effects. In this thesis, the models will be based on quantitative evidence supporting the given cause-effect associations. The work will examine existing international cause-effect tools, which can be used for gathering, storing and visualising causal ecological relationships. Understanding such relationships is required in sound decision making in environmental research and management (e.g. Norris et al. 2012; Webb et al. 2012). The cause-effect tools can be used to gather together several studies supporting given ecological causal linkage. In this means many individually weak studies are accumulated to strengthen the evidence, which helps in identifying the causes of impairments and the necessary steps for management actions. Conceptual cause-effect models also help indicating knowledge gaps where more research would be needed in order to have sufficient evidence to reach a conclusion.

Causal relations are difficult to demonstrate in natural environments because of the difficulty of performing experiments, natural variability, lack of replication, and the presence of confounding influences. Partly because of this, most environmental management decisions are made using expert opinion (Webb et al. 2012). Such decisions can lack transparency. Literature-based cause-effect models yield scientifically defensible results by transparent and reproducible evaluation. The method can identify causal relationships that are not immediately apparent and prevent biases. All evidence supporting given causal relationship increase confidence that restoration effects can improve biological condition.

International methods of evidence synthesis and conceptual models

CADDIS

CADDIS (The Causal Analysis/Diagnosis Decision Information System) is a website developed by US-EPA, to help scientists and engineers conduct causal assessments in aquatic systems. It provides a process for identifying stressor or combination of stressors that cause biological impairment. The approach is an example of causal pluralism, in that multiple concepts of causation are accepted as well as all relevant evidence and methods for turning data into evidence. Although a cause can never be proven and can seldom be disproven, the method can determine which causal hypothesis is best supported by the evidence (U.S. EPA 2010).

In the Stressor Identification Guidance Document provided by CADDIS is stated that biological assessments have become increasingly important tools for managing water quality. These methods, which use measurements of aquatic biological communities, are particularly important for evaluating the impacts of chemicals for which there are no water quality standards, and for non-chemical stressors such as flow alteration, siltation, and invasive species. However, although biological assessments are critical tools for detecting impairment, they do not identify the cause or causes of the impairment. The Stressor Identification Guidance Document is intended to lead water resource managers through a process that identifies stressors causing biological impairment in aquatic systems, and provides a structure for organizing the scientific evidence supporting the conclusions (U.S. EPA 2000). The essence of the CADDIS approach to causal inference is the comparison of alternate candidate causes by determining which is the best supported by the totality of evidence. Its standard process provides transparency and reduces inferential errors without restricting the types of evidence used (U.S EPA 2010). CADDIS method is organized into five volumes:

1. Stressor identification – provides a step-by-step guide for identifying probable causes of impairment in a particular system, based on the U.S. EPA's Stressor Identification process.
2. Sources, Stressors & Responses – provides background information on many common sources, stressors, and biotic responses in stream ecosystems
3. Examples & Applications – provides examples illustrating different steps of causal assessments

4. Data analysis – provides guidance on the use of statistical analysis to support causal assessments

5. Causal Databases – provides access to literature databases and associated tools for use in causal assessments

The fifth volume, Causal Databases, provides two tools to help users access and apply literature-based evidence in causal assessments. The Interactive Conceptual Diagram (ICD) application uses conceptual diagrams as an organizing framework to provide supporting literature for linkages among different sources, stressors and responses. Users can view existing diagrams and the literature supporting the linkages of the causal pathways. The application can as well be used in creating own diagrams and saving the literature references supporting the linkages. The other tool provided by this section is the CADDIS Literature Resource (CADLit), which contains information on stressor-response associations reported in the peer-reviewed scientific literature. The CADLit database can be used to search for information by keywords, or by location, habitat, exposure parameter or taxa. The search results can be further downloaded to an Excel spreadsheet (U.S. EPA 2007).

Eco Evidence

Eco Evidence is another method that uses evidence in the extensive published ecological literature to assess support for cause-effect hypotheses in environmental investigations. Eco Evidence is provided by eWater Cooperative Research Centre, a publicly owned not-for-profit organisation, which is committed to ecologically sustainable water management in Australia and around the world. Eco Evidence provides an 8-step process (figure 1) in which the user conducts a systematic review of the evidence for one or more cause-effect hypotheses to assess the level of support for an overall question. Eco Evidence is based partly upon the epidemiological method of causal criteria analysis (Susser 1991). It uses a subset of ‘causal criteria’ most relevant to environmental investigations, and weights each piece of evidence according to its study design such that stronger studies contribute more to the assessment of causality, but weaker evidence is not discarded. The outputs of the analysis are a guide to the strength of evidence for or against the cause-effect hypotheses. It strengthens confidence in the conclusions drawn from the evidence, but cannot ever prove causality (eWater website).

The method is supported by the freely available Eco Evidence software package, which produces a standard report, maximizing the transparency and repeatability of the assessment. Using the Eco Evidence method, environmental scientists can better use the extensive published literature to guide evidence-based decisions and undertake transparent assessments of ecological cause and effect hypotheses (Norris et al. 2012). Eco Evidence helps answer cause-effect questions, make assessments, plan for restorations, and carry out critical reviews on a specific topic of interest.

The Eco Evidence software also provides an online database (Webb et al. 2015), which stores information about causal relationships extracted from environmental science stud-

ies. This information is specifically geared to support cause and effect assessments. The online database can be used in searching evidence supporting causal relationships between the parameters of specific interest. The other software tool provided by Eco Evidence is the Eco Evidence Analyses software, which guides users through the 8-step framework gathering and weighting the evidence and produces a concluding report. The method has been described e.g. by Norris et al. (2012) and Webb et al. (2012).

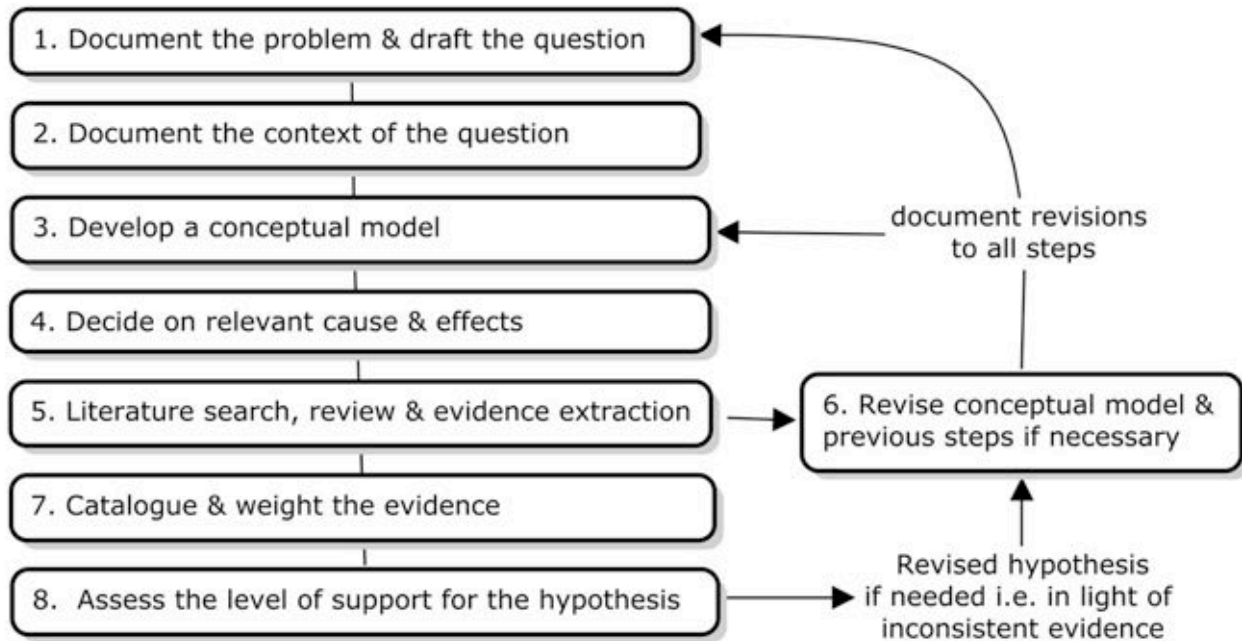


Figure 1: The 8-step framework provided by the Eco Evidence analyser software (<http://www.toolkit.net.au/tools/eco-evidence>).

WISER

The WISER (Water bodies in Europe: Integrative Systems to assess Ecological status and Recovery) was an EU project, which ended in 2012. The WISER aimed to support the implementation of the WFD by developing tools for the integrated assessment of the ecological status of European surface waters. In module five of the project (management and restoration – impacts of pressure reduction and climate change on the ecological status), methods for assessing and restoring aquatic ecosystems were developed. The results include conceptual models illustrating the relationships between restoration measures, their effects on instream environmental key variables, and eventually the impact of changing variables on benthic algae, macrophytes, benthic invertebrates and fish (WISER website).

DPSIR framework

The diagrams, which will be created in this study, will follow *Driver-Pressure-State-Impact-Response* categories, which are used slightly differently as introduced by European Environment Agency (EEA 1999). In the MARS project, the terminology defined by CIS Guidance

IMPRESS (2002) is followed, except for the definition of the *Impact* category. The drivers lead to pressures, which in turn lead to changes in the abiotic and biotic states of the water body. The altered states cause impacts on human beings. Finally, the responses can be addressed to any of the other DPSIR categories in order to improve the state of the water body. The DPSIR indicator categories used in the MARS are defined as follows:

Driver is an anthropogenic activity that may have an environmental effect (e.g. agriculture, industry).

Pressure is the direct effect of the driver (for example, an effect that causes a change in flow or a change in the water chemistry).

State is the condition of the system under study (e.g. water body) resulting from both natural and anthropogenic factors (i.e. physical, chemical and biological characteristics).

Impacts are effects on human beings, ecosystems and man-made capital resulting from changes in environmental quality with relevance for ecosystem processes and/or components actively or passively required, demanded or used by man (e.g. ecosystem services), triggering social *Response*.

Responses are the measures taken to improve the state of the water body (e.g. restricting abstraction, limiting point source discharges, developing best practise guidance for agriculture).

Multiple stressors and stressor interactions MARS prototype

European rivers are affected by alterations of water quality, hydrology and morphology (Schinegger et al. 2012). Most European water bodies are affected by multiple stressors, yet little is known about their combined effects (Hering et al. 2015). Human pressure often alter more than one environmental factor, and also pressures from several sources often coincide (Ormerod et al. 2010). This means that most human activities create impacts on the environment via multiple, prospective pathways of cause and effect (Downes 2010). Stressors often interact with each other, and sometimes the effects of these interactions are synergistic or antagonistic in character, rather than simply additive. When combined effect of multiple stressors is greater than the sum of effects by individual stressors, the interaction is called synergistic. In antagonism, the effect is less than the sum of individual stressors. This is the most common scientific usage of these terms (Folt et al. 1999). The complexity of multiple stressor interactions makes it difficult to identify their combined effects to the ecosystems. Also identifying and prioritising the management issues is challenging (Ormerod et al. 2010). Freshwaters appear to be at particular risk of multiple-stressor effects, which might be caused by conflicts between multiple uses of water and the protection of freshwater environments (Ormerod et al. 2010). It is difficult to sort out which stressors are the direct causes of an unacceptable change and which are just correlates (Downes 2010). Nevertheless, the exact cause-effect relationships should be identified in order to understand the various pathways how stressors alone and in combination affect river ecosystems. This is crucial for the restoration measures to be effective.

In this task a prototype of a causal conceptual diagram visualising the cause-effect pathways leading to ecological impairments in river ecosystems was created for the MARS project. Two international methods (CADDIS and Eco Evidence), and the tools that they offer, have been tested by searching and evaluating causal ecological data, and harmonized as a MARS eco-evidence based conceptual prototype model. The model will address stressors, their causes and ecological effects on running water ecosystems. The cause-effect linkages will be gathered from several sources.

Nõges et al. (2016) reviewed publications concerning multiple stressor impacts in rivers, lakes, transitional and coastal waters, as well as groundwaters. The part of the review, which consists data of multiple stressor impacts on riverine ecosystems (reviewed by Florian Pletterbauer), acts as a starting point to this work. The most common stressor combination in numbers of evidence items (cause-effect relationships) in this part of the review, is excess in fine sediment and nutrients. The conceptual diagrams will be constructed based on these data, and more evidence will be gathered concerning the common and individual effects of these stressors on biological indicators in rivers. According to the DPSIR categories used in the MARS project, increased fine sediment and nutrient concentrations represent the altered abiotic states of the water bodies. Their causes (drivers and pressures) and ecological responses (biotic state variables) will be extracted from scientific literature and visualised in form of conceptual diagrams. The ecological indicators of the impairments selected to be used in this study are fish and benthic invertebrates.

Methods

Evidence search

Nõges et al. (2016) quantified biotic and abiotic responses to multiple stress in freshwater, marine and groundwater ecosystems. The part of this literature review concerning rivers forms a basis to this study. The cause-effect relationships will be gathered from these scientific references, and used in the diagrams. Additional literature search on single stressor effects will be performed. This search will focus on fine sediment or nutrients as stressors affecting riverine ecosystems, and fish and benthic invertebrates as ecological indicators of the impairments. The causes for altered abiotic states (increase in nutrients and/or fine sediment content) of the waterbodies will be searched from the same references where the relationships between abiotic and biotic state variables will be gathered. These causes will be divided in drivers and pressures according to the DPSIR categories used in the MARS project. Only quantitative evidence will be regarded in this study. Furthermore evidence on causal ecological linkages will be searched from the CADDIS Literature Resource (CADLit, <http://cfpub.epa.gov/cadlit/index.cfm>) and Eco Evidence online database of the eWater toolkit (<http://www.toolkit.net.au/tools/Online/EE/>). The biotic response variables will be harmonised by dividing them into broad variable categories which were introduced in WISER project by Feld et al. (2011): composition and abundance, sensitive and tolerant taxa, diversity, age structure, biomass, processes and functions.

Eco Evidence database

The Eco Evidence online database can be used for storing and sharing evidence items. It provides a permanent repository for causal evidence items and allows users to access and re-use evidence items entered by other users (Webb et al. 2011). The information in the database is organized such that a citation can have one or more evidence items, which is a summary of the findings contained in a study assessing a cause-effect linkage (Webb et al. 2012).

The cause-effect data in Eco Evidence online database describes study's location or environment, methods and study design, results and citation details. The evidence can be searched by citation details or by selecting cause or causes and effect or effects in evidence fields. The users can search for evidence items using the following criteria (from Webb et al. 2012) like bibliographic information, multiple causes, or if study characteristics restrict to the scope of search.

The causes and effects are identified by typing key words into the cause or effect fields, or by selecting them from the standard terms list. The search in this study was conducted by selecting cause parameters in evidence fields. The selected causes were: bedload, substrate, nutrients, suspended sediment and turbidity. Fish and invertebrates were selected in effect fields. Selecting fish in general includes the following sub-categories: abundance, age structure, assemblage, behaviour, competition, condition, deformities, disease, dispersal, diversity, exotic invasion, fish kills, gasping, growth, mortality, recruitment, reproduction and tissue toxicant concentration. The sub-categories in invertebrates' field are: abundance, age structure, assemblage, behaviour, competition, condition, deformities, disease, dispersal, diversity, exotic invasion, growth, mortality, recruitment and reproduction. A similar search was conducted to find possible drivers eventually leading to eutrophication and increase in fine sediment content. In this search the following parameters were selected to the cause fields: agriculture, floodplain, flow regulation, industry and land use. The causes of the previous search (bedload, substrate, nutrients, suspended sediment and turbidity) were selected in effect fields.

Strength of the evidence

The quality of the evidence can be evaluated with the Eco Evidence tool in terms of three study quality attributes, which are: study design type, number of independent sampling units used as controls, and numbers of (potentially) impacted independent sampling units.

Studies in which the error terms are well controlled (e.g. BACI designs) attract greater weighing than less rigorously controlled designs. Also studies with more than one impact location have more weight, as well as increasing numbers of control locations (Greet et al. 2011). The overall study weight is given by summing the weights of each of these three attributes. The default weightings are listed in table 1. They can also be adjusted to suit the particular circumstances of a review, but any changes made by the user should be documented and justified (Greet et al. 2011).

In this study the strength of the evidence was calculated according to the Eco Evidence Analysis (Nichols et al. 2011). Instead of calculating the strength of different cause-effect relationships, each reference paper received a weight according to the study design and number of control and impact locations (Humer 2015).

Table 1 The default weightings in Eco Evidence Analysis (modified after Nichols et al. 2011).

Study design type	Weight
After impact only	1
Reference/Control vs. impact (no before)	2
Before vs. after (no reference/control)	2
Gradient response model	3
BACI or BARI MBACI or Beyond MBACI	4
Number of control/reference locations	
0	0
1	2
≥2	3
Number of impact locations	
1	0
2	2
>2	3
Number of impact locations in gradient-based designs	
3	0
4	2
5	4
≥6	6

Model construction

The conceptual diagrams have been constructed with CADDIS ICD application (see Humer 2015) and MARS conceptual model based on Microsoft Visio diagramming platform (below), as the Eco Evidence tool is missing this function. The diagrams visualise the causal linkages gathered from the literature, and the literature references supporting the given linkages are stored in the CADDIS model for future applications.

Results

Evidence search

The results of the literature search are listed in appendix A. In the table each row consists one evidence item, which besides the citation details includes information about at least the abiotic state (nutrients or fine sediment or both) and the biotic state which is impacted by it. Same citation might have multiple evidence items, which are listed on separate rows of the table. Details on the results of the CADDID CADLit search contained 95 citations and Eco

Eco Evidence online database contained 39 evidence items are listed by Humer (2015) and can be found in the appendix (A). Full citations can be found in the reference list of this study.

Harmonisation of the biotic response variables

One of the original variable categories, which were introduced in WISER project by Feld et al. (2011) is absent in the results of this work (age structure). In the reference literature used in this study, no metrics concerning the age structure of fish or invertebrate communities were found. On the other hand one additional variable category, *disease and deformities*, is introduced here. The categories describing ecological impacts in this work are:

1. composition and abundance (e.g. relative abundance of specific taxa, total community abundance, indices of biotic integrity),
2. sensitive and tolerant taxa (e.g. metrics concerning salmonid fish species or benthic invertebrates belonging to Ephemeroptera-Plecoptera-Trichoptera [EPT] taxa),
3. diversity (e.g. diversity indices, taxon richness),
4. biomass and density (e.g. fish biomass, invertebrate dry mass, density of specific taxa, total density),
5. processes and functions (e.g. species traits such as feeding types or body size),
6. disease and deformities (e.g. percentage of fish with disease or deformities).

Each biological response variable has been placed to only one of these categories. Therefore e.g. EPT diversity indices are grouped in the *sensitive and tolerant taxa* even though they could also be placed in *diversity* or *composition and abundance*. Also *processes and functions* overrides the other categories despite the fact that changes in the species traits also affect the total community composition.

Drivers and pressures causing increased fine sediment and nutrient concentrations in rivers

Many references list common causes for elevated nutrient and fine sediment concentrations, but only part of the studies (e.g. Lange et al. 2014; Mondy & Usseglio-Polatera 2013; Scruton et al. 2008; Robertson et al. 2008; Sutherland et al. 2002; Townsend et al. 2008; Wagenhoff et al. 2011; Wang et al. 2007) link them statistically to the abiotic state variables. Many of the studies (e.g. Piggott et al. 2012; Wagenhoff et al. 2012; Matthaei et al. 2010) were experimental in character, where drivers usually do not exist. Research papers often do not contain the complete cause-effect chain, but in a conceptual diagram the data from different sources can be united to form complete causal pathways. The causes for changes in abiotic states can therefore be searched separately and brought into the diagrams. According to the reviewed literature, the most common driver causing elevated nutrient as well as fine sediment concentrations in the waterbodies was agriculture (e.g. Lange et al. 2014;

Mondy & Usseglio-Polatera 2013; Robertson et al. 2008). The two stressors were also linked to absence of forest (e.g. Robertson et al. 2008), which nevertheless is often related to agriculture. As the same causes lead to an increase in both abiotic state variables, it is not surprising that these stressors often occur together. Better management results are gained if their ecological impacts are also quantified together.

Only two of the identified causes belong to the pressure category. These are reduced high flows (Osmundson et al. 2002) and water abstraction (Lange et al. 2014a). Diffuse pressure from agriculture was not quantified in the literature and therefore the link between agriculture and the abiotic states is missing in the diagrams as well. This might be caused by difficulties to measure the diffuse pressure quantitatively. The conceptual diagrams are also weaker in presenting the possible drivers and pressures, as the primary focus of the literature search was to find evidence supporting the cause-effect linkages between the abiotic and biotic state variables.

Cause-effect linkages between the stressors and their ecological responses in rivers

Fine sediment

Fine sediment is a natural and essential component in running waters, but excess input of fine sediment affects the biological functioning in rivers by altering habitat quality and quantity (Owens et al. 2005). In the reviewed literature an increase in fine sediment caused mostly negative effects on stream invertebrate metrics. Most uniform responses, which were also supported by several scientific references were e.g. decrease in total taxon richness (e.g. Rabení et al. 2005; Bo et al. 2007; Robertson et al. 2008; Larsen et al. 2009; Matthaei et al. 2010; Clapcott et al. 2012; Wagenhoff et al. 2012; Buendia et al. 2013), decrease in EPT richness (e.g. Zweig & Rabení 2001; Townsend et al. 2008; Larsen et al. 2009; Wagenhoff et al. 2012, Buendia et al. 2013) and decrease in total invertebrate density (Osmundson et al. 2002; Matthaei et al. 2010; Buendia et al. 2013). Investigated fish metrics were less, but they were without exceptions negative concerning fish abundance (Richardson & Jowett 2002; Robertson et al. 2008), diversity (Richardson & Jowett 2002), sensitive fish species (Argent & Flebbe 1999; Robertson et al. 2008; Bryce et al. 2010; Lange et al. 2014b), and several functional groups, e.g. spawning types (Sutherland et al. 2002; Robertson et al. 2008) and feeding types (Robertson et al. 2008).

Nutrients

There has been a significant reduction in the levels of nutrients in European freshwaters over the past two decades (EEA 2015). However, nutrient enrichment is still widespread and diffuse pollution from agriculture remains a significant pressure in more than 40% of Europe's rivers (EEA 2015). In the reference studies nutrient enrichment caused diverse responses in invertebrate metrics. Increase in nitrogen and/or phosphorus had both positive and negative effects to the indicator metrics in all but one (disease and deformities) response categories. Common type of response curve was hump-shaped, indicating a subsidy-stress response. Many indicator metrics first benefit from increasing nutrient concentration, but after reach-

ing a threshold level the direction of the response curve changes to negative. At modest levels, nutrient enrichment can stimulate primary production, which in turn can increase production of invertebrates and fish. Further eutrophication, however, can lead to algal blooms that are stressful to most animals by causing low dissolved oxygen and poor habitat quality (Niyogi et al. 2007). Subsidy-stress relationships might lead to the situation, where the type of response in the studies differ depending on the background level of the nutrients (if the threshold is already reached), and the enriched nutrient concentration (if the threshold will be reached during the study). This makes it important to quantify these threshold values, and recognize the critical concentrations. In the study by Piggot et al. (2012) nutrient enrichment generally acted as a subsidy, increasing both pollution-tolerant (e.g. Chironomidae) and sensitive taxa (EPT), indicating that enriched levels were still within the range providing subsidy effects. Enriched nutrient concentrations corresponded to moderate levels in New Zealand dairy farming streams, but higher anthropogenic levels occur elsewhere in the world (Piggot et al. 2012).

Concerning fish the impacts of nutrients were mostly negative. Fish IBI decreased by the impact of nitrogen (Miltner & Rankin 1998; Wang et al. 2007; Robertson et al. 2008) and by phosphorus (Miltner & Rankin 1998; Wang et al. 2007). Salmonids and other sensitive species were affected negatively as well (Wang et al. 2007; Robertson et al. 2008; Lange et al. 2014b). Some positive effects were also found (e.g. increasing fish biomass), following the increase in nitrogen concentration (Wang et al. 2007). Increase in nutrients also increased the percentage of fish having disease or deformities (Robertson et al. 2008).

Multi-stressor relationships

Fine sediment and nutrients had additive, synergistic, as well as antagonistic multi-stressor impacts on benthic invertebrates. Three references supported synergistic interactions affecting negatively on invertebrate diversity indices (Townsend et al. 2008; García Molinos & Donohue 2010; Lange et al. 2014a). Synergistic interaction is harmful for the ecosystem, but important to recognise for planning appropriate management actions. By eliminating one stressor, the state of the ecosystem can improve more than expected based on single stressor impacts. On the contrary, in case of antagonistic interaction both stressors may need to be removed or moderated to produce any substantial recovery (Jackson et al. 2016). Concerning sensitive EPT taxa, the effects were negative, but all possible interaction types were reported. Trait-based responses to multiple stressors were mainly additive (e.g. Wagenhoff et al. 2012; Lange et al. 2014a). The collected evidence items contain altogether 69 biological responses to multi-stressor impacts, where nutrients (N or P or both) and fine sediment are interacting. Approximately 60% of the effects were additive, 30% were synergistic and 10% antagonistic. In recent meta-analysis of the effects of multiple stressors in freshwater ecosystems, net effects of stressor pairs were frequently more antagonistic (41%) than synergistic (28%), additive (16%) or reversed (15%, Jackson et al. 2016). Nevertheless, the effects for nitrification paired with habitat alteration (including sedimentation) were additive (Jackson et al. 2016), supporting the results of this study.

Only one multi-stressor relationship was found, which affects the fish communities. This relationship was additive in character, causing decrease in trout density (Lange et al. 2014b). Synergistic or antagonistic effects between the stressors were not observed (Lange et al. 2014b). It could be, that these stressors differ more fundamentally in their mode of action for fish as opposed to invertebrates and therefore act independently when affecting fish populations (Lange et al. 2014b).

Stressor comparison

The effects of fine sediment were generally more negative than the effects of nutrient enrichment. Also many references indicate that fine sediment is more pervasive stressor (Wagenhoff et al. 2011; Piggot et al. 2012; Wagenhoff et al. 2012), counteracting and overwhelming initial subsidy effects of increased nutrients. Macroinvertebrate responses to sediment seemed to be more common and more often negative. Effect sizes were considerably larger and effects were predicted with greater certainty than those of nutrients (Wagenhoff et al. 2012). The effects of high nutrient concentrations were weaker and modelled with less certainty, probably reflecting the indirect modes of action of nutrients (Wagenhoff et al. 2011). The indirect influences of anthropogenic nutrient enrichment on fish and macroinvertebrates might result from overgrowing primary producers that create low oxygen-associated conditions (Wang et al. 2007). In the study by Lange et al. (2014a) the nutrients showed more marked effects via food availability. Nevertheless, nutrients also interacted synergistically (e.g. Townsend et al. 2008; Matthaei et al. 2010; Wagenhoff et al. 2011; Lange et al. 2014a) and antagonistically (Lange et al. 2014a) with fine sediment, and the best restoration outcomes would be achieved by addressing both stressors (Wagenhoff et al. 2011).

Strength of the evidence

A simple type of weighing the evidence is used in the diagrams, as the line thickness indicates the number of reference papers supporting the given relationship. Additionally, the strength of the evidence was calculated according to the Eco Evidence Analysis (Nichols et al. 2011) for each reference paper (except a review) that was used in the diagrams. The average study design weight of the reviewed papers was relatively high, being 7.2. Many of the studies followed gradient-response model, which usually provides evidence on the dose-response relationships. This was not a coincidence, because the reference literature was chosen in a way that it provides quantified evidence on cause-effect relationships. This already excludes very weak pieces of evidence. Nevertheless, it should be taken into account that information about the strength of the correlation or the coefficient of determination is not provided in the diagrams. Every statistically significant relationship was considered even if the relationship was weak.

Conceptual models

The following flowcharts were made without customised cause-effect diagramming tools, using Microsoft Visio for drawing. The pattern is following the approach, which was used in the EU project WISER (see Feld et al. 2011). Figure 2 shows a general conceptual framework presenting the outlines of the model construction. In the final models (figures 3 and Appendix B4) the linkages between abiotic and biotic state variables are divided into two diagrams.

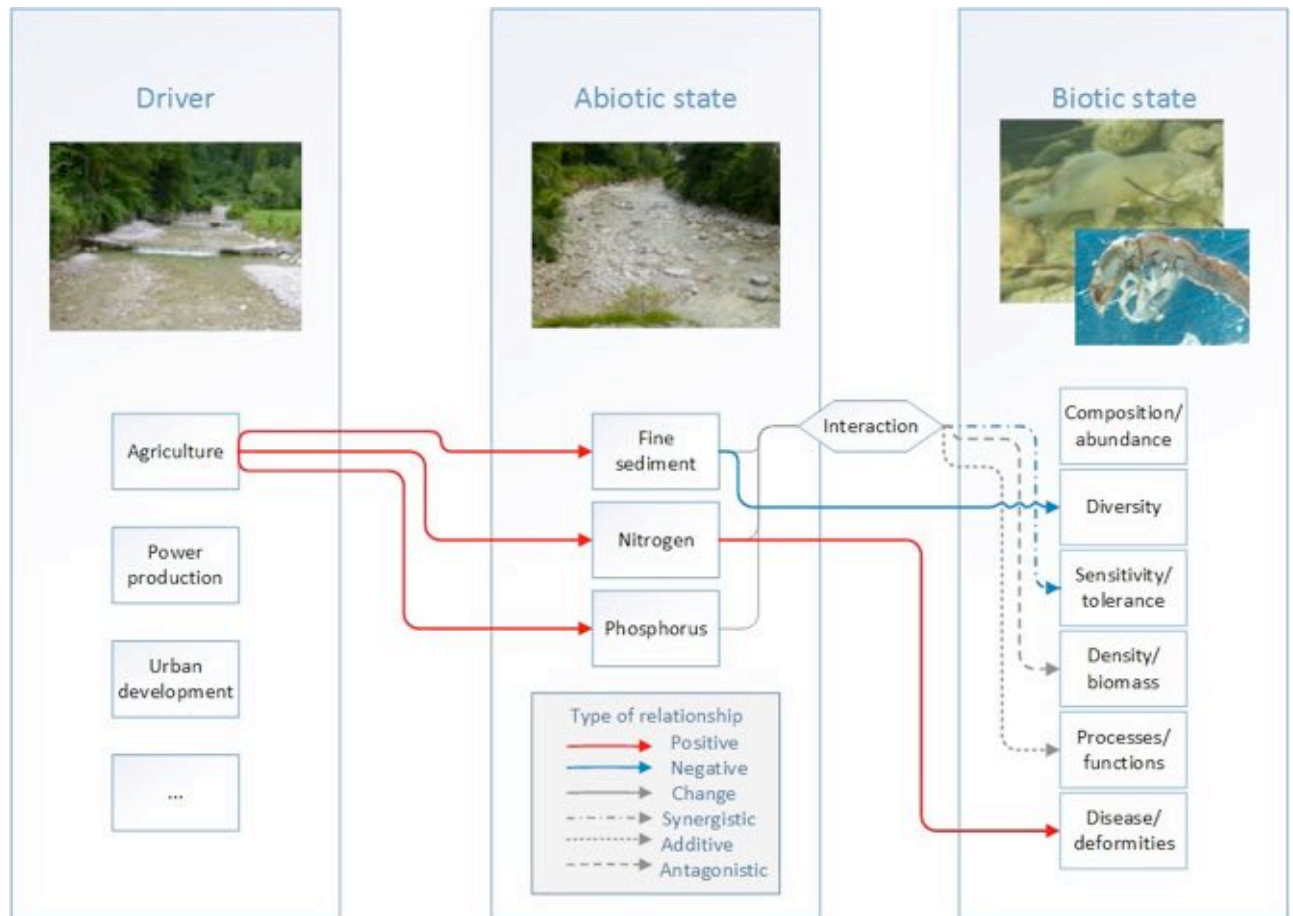


Figure 2: General conceptual model presenting the structure of the diagrams and the types of interaction between the variables (pictures: Hans Rund [*Thymallus thymallus*] & Günther Jans-Danzer [*Polycentropus excisus*]).

The lines between abiotic and biotic state variables are based on 591 quantified relationships, which were extracted from the reference literature. Fish variables were indicators of the impairments in 192 relationships, and macroinvertebrates in 399 relationships. *Processes and functions* category contains the biggest share of the effects, 34% (211 cause-effect relationships) respectively. The number of cause-effect relationships per variable category, as well as the share of the total number of evidence items per variable category, are presented in table 2. The share of the effects caused by the different abiotic stressors (fine sediment, nutrients and multi-stress) on response variable categories is calculated as well, more about negative and positive effects see Humer (2015).

Table 2 The share of all effects and effects caused by different abiotic stressors on different response variable groups. The number of all effects per variable category in brackets.

Variable category	% all effects	% fine sediment effect	% nutrient effect	% multi-stress effect
Biomass/density (29)	5 %	9 %	3 %	1 %
Composition/abundance	23 %	18 %	28 %	13 %
Disease and deformities (2)	0 %	0 %	1 %	0 %
Diversity (42)	7 %	11 %	5 %	4 %
Processes/functions (211)	34 %	34 %	30 %	56 %
Sensitivity/tolerance (179)	31 %	29 %	33 %	25 %
Grand Total (591)	100 %	100 %	100 %	100 %

Figure 3 visualises the MARS multi-stressor relationships and the second one figure 4 Appendix B shows the single-stressor relationships. This division was made to make the diagrams readable, otherwise the flowcharts are identical. On the left side of the diagrams the drivers, which were identified (and quantified) in the reference literature, are presented. The drivers are followed by pressures, abiotic state variables and biotic state variables, which are harmonised by dividing them into the six metric groups. The cause-effect linkages between the variables are presented by lines, showing the type of relationship (positive, negative, neutral) by colour, and number of supporting reference papers by thickness. The lines are numbered, and the numbers are linked to the reference literature in Appendix table 4 Appendix B. The relationship is marked as positive, when majority of the cause-effect linkages between the variables are positive. This does not mean that there would not be any evidence supporting the opposite direction. The relationship is marked as neutral when both positive and negative relationships are more or less equally dominant or the majority of the biotic effects are subsidy-stress responses. Individual biotic indicator metrics within one variable group can have strong positive or negative responses caused by the stressor, regardless of the mean response type. Special interaction shapes are placed between the abiotic state variables, indicating interactions between the stressors. The type of interaction is visualised by different dashed line types, uniting the interaction shapes with biotic response variables.

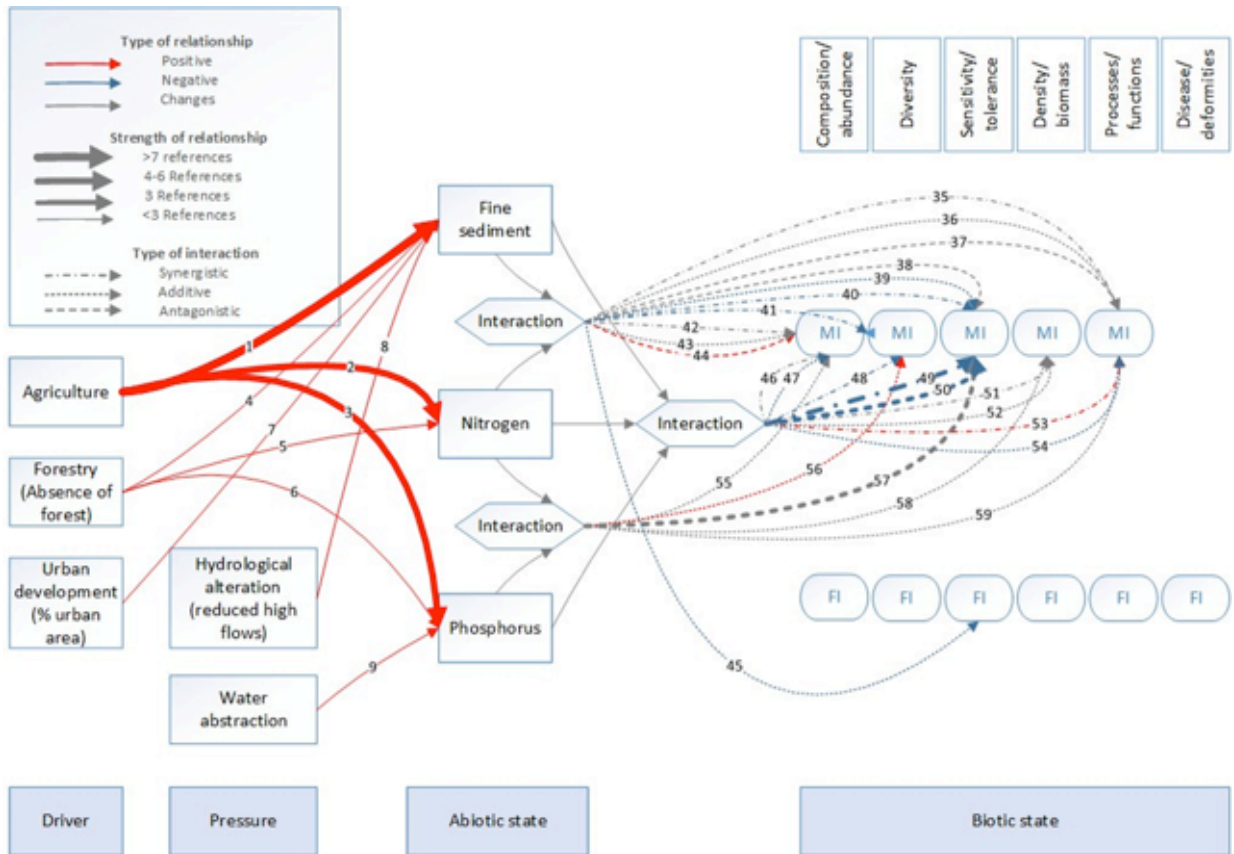


Figure 3: Conceptual diagram visualising the multi-stress relationships and their effects on biotic state variables. The variable group Sensitivity/tolerance shows negative responses when sensitive taxa are affected negatively or tolerant taxa positively. MI – macroinvertebrates, FI – fish.

Discussion and Conclusion

The main objective of this work was to find evidence of Causal Relationships by collecting quantified cause-effect associations data and possible thresholds of fine sediment and nutrients and their ecological effects in rivers to be used in the conceptual diagrams and further used in the MARS project. Finding literature, where the evidence is quantified, was challenging. The same was realised by Nõges et al. (2016), who state that many of the cause-effect linkages seem to be accepted as common knowledge. The reference list which is used in this study is not comprehensive, but rather a starting point on which the further evidence can be built on.

The Second objective was to give an overview of existing methods of standardized evidence based conceptual models and to find out the suitability of their components to the European purposes (MARS project). The methods, which were tested in this work, are CADDIS and Eco Evidence. These methods have been shortly described in the introduction chapter, and further presented in the methods. My subjective view and discussion about the suitability of their functions to the purposes of the MARS project will be given in the next sub-chapters.

CADDIS Literature resource

CADLit literature database contains vast amount of citations, especially concerning sediment and nutrients. The database contains detailed information on study design and context, exposure parameters and response parameters, but it does not provide specific cause-effect linkages between them. Therefore the database did not offer direct help in identifying causal relationships. At the moment an update of the CADDIS Literature Database is under development. The new release targets to explicitly capture information on specific cause-effect relationships, which can then be linked directly to ICD diagrams (Kate Schofield, personal communication, February 17, 2016). CADLit database was originally conceived as a centralized storage place for detailed stressor-response information, which could be used by the scientists working in the Office of Research and Development (ORD) of the U.S. EPA. One objective of the new release is broaden the community of users that would help to populate the database by simplifying data entry process. The new literature resource will also allow data exchange between the CADLit and similar databases developed by the collaborators of the U.S. EPA (e.g., Eco Evidence). The new CADDIS database, called “CADLink” is foreseen to be released in fall 2016 (Kate Schofield, personal communication, September 2017, MARS eco evidence workshop Vienna).

ICD application

The ICD application was easy to use and it offers a great tool for storing and visualising ecological evidence on causal pathways. The application does not produce diagrams automatically, but the user has to place the shapes and other features on the canvas and feed the information about the linkages and citations. The strength is in organising the evidence supporting different cause-effect relationships. From the ready diagram it is easy to see where the evidence is strong or where it is insufficient for a robust conclusion. In such cases the need for future research can be identified. The advantage of such an approach is also that it collects together evidence from different sources to form complete causal pathways and strengthen the evidence. The chain of causal relationships can therefore be followed from the driving forces until the ecological effects thus providing a better understanding of the linkages between the biological indicators and their physical environment (Norton & Schofield 2017).

The possibility to connect literature citations with cause-effect linkages is the best feature of the application. Finding the relevant references from CADDIS diagrams is fast and easy, as the citations can be viewed linkage by linkage. The second big advantage is the practical and convenient interactive operation of the application, which unfortunately is difficult to demonstrate without the possibility to online usage. A nice feature is also, that the user can not only create diagrams, but also view and edit diagrams made by other users (with their allowance).

The diagrams (e.g. the ones which were made for this study) cannot be used interactively without registering and logging into the application. The interactive use is the key to use the diagrams in an effective way, especially when larger or more complex diagrams are in ques-

tion. The diagrams can be exported from the application as pictures, but then arrows or other visual linkages are required in order to see the relationships between the entities. In large diagrams this is not easy to visualise with the functions of the application. It would be a good addition if there would be a way to view the diagrams online without the registration process (e.g. with a link provided by the creator of the diagram).

The linkages in the diagrams can be created between two shapes only. Visualising multi-stressor relationships is challenging. It is possible to select multiple shapes and create a linkage between all the possible combinations of two shapes between them. But even by this mean the result is always considering only two shapes, and the user can view and search references between two shapes only.

In the application it is not possible to add attributes to the linkages. Positive and negative effects on indicator biota cannot be indicated by different colours or by adding this information in the reference list. Instead the information on the direction of the ecological impact has to be incorporated in the shapes, which increases the amount of shapes that are used in the diagrams. In case of multi-stressor impacts the type of the interaction cannot be visualised with the current functions of the application.

Eco Evidence

Eco Evidence literature database offered genuine help in searching for references supporting the ecological linkages in the diagrams. The structure of the database is clear and good, and the possibility to search for the evidence according to causes and effects, and to weigh the evidence makes it an excellent tool for causal assessments. Eco Evidence is easy to use, and the data is clearly structured. Registration is simple and searching for evidence is fast and convenient. The disadvantage is that concerning many topics the database is not comprehensive. A diagramming application would be a useful addition, as in the 8 step process user is asked to draw a conceptual model (in step 3).

MARS conceptual model diagrams

The final objective of this thesis was to create a causal conceptual model visualising the causes and ecological effects of excess nutrients and fine sediment in riverine ecosystems using fish and benthic invertebrates as indicators of the impairments. The Eco Evidence and CADDIS tools offered help in searching and evaluating cause-effect data and perceiving the structure of causal conceptual diagrams, but the final models were made with MS Visio diagramming platform. The advantage compared to the CADDIS ICD application is that the possibilities to visualise the information are more versatile. The disadvantage is that there are no pre-designed patterns, but the model construction has to be done from the beginning on by selecting the appropriate shapes and linkage types for the model. Also the reference list has to be created separately and cannot be automatically linked to the cause-effect relationships as in the ICD application. Therefore updating the models is more complicated than with the CADDIS tool.

The structure of the flowcharts largely follow the approach of the past EU project WISER. The important change compared to the previous methods is the central role of multiple stressor impacts, and the need to visualise the stressor interactions. Diverse ways of interaction and effect types necessarily increase the complexity of the final diagrams. The functions of the CADDIS ICD application were not applicable to the MARS approach, but the ideas and structures are converted to the MS Visio diagrams (Melcher et al. 2017).

Challenges

Finding research papers where the effect is quantitatively linked to the given cause (stressor) with statistically significant results was not easy and required lots of time. Also comparing the data from multiple studies is always challenging because of different study designs, diverse measurement units and unprecise expressions as well as natural variability in abiotic and biotic conditions. The first step is to harmonise and merge existing information in a way that it can be effectively used. These challenges highlight the importance of evidence databases and conceptual models. Ideally the harmonised information would already be found in an open access database, in such format that it would be ready to be used in analyses. This would save time and resources, and make evidence synthesis easier to conduct. Eco Evidence and CADDIS are good examples of such methods. Both methods and associated tools are continuously under development, and they are also collaborating, aiming to link existing databases and allowing data exchange between the projects (Ziegler et al. 2015). The challenge is to make the cause-effect tools used by the scientific community in a way, that the databases are up to date and include all the relevant evidence information. The Eco Evidence also aims to become a peer-produced and user-moderated resource (Webb et al. 2012). In ideal case authors themselves would enter the evidence into the database, and thus increase the probability that their studies are cited (Webb et al. 2012, Webb et al. 2017).

The effectiveness of such tools depends not only on the commitment of the scientific community, but also on the willingness of environmental managers to adopt new methods and change their habits and beliefs. According to the study by Pullin et al. (2004) management plan compilers are not making full or systematic use of the available information to support their decision-making. Additionally, when the beliefs of conservation managers were investigated in UK, only small minority (5%) considered evidence-based information more influential than experience-based information (Pullin et al. 2004). Evidence-based findings might not result in managers learning and updating their beliefs, even if presented and explained to managers (McConnachie & Cowling 2013).

Future recommendations

The main objective of this study was to create conceptual ecological models to be used in the MARS project. Existing international methods and tools (CADDIS and Eco Evidence) offered great help, but could not alone fulfil the needs of the MARS approach. The main challenge was the central role of multiple stressor effects and the need to visualise these linkages in the models.

More evidence on the ecological effects of fine sediment as well as nutrients would be available, and could be extracted from the primary research papers. On the other hand, studies combining the effects of these stressors are rare, especially the ones that quantify their effects simultaneously along both stressor gradients. Existing studies are also conducted mainly by the same group of researchers, and cover small geographic area. More multiple stressor studies would be needed in order to gain strong evidence on the joint effects of the stressors. Especially distinct research gap exists concerning the joint effects of fine sediment and nutrients on fish indicators. This knowledge gap is also visible in the created conceptual diagram (figure 19).

In future models it should be considered if spatial and temporal scales, river type, geographical and geological parameters or other characteristics should be taken into account in creating the models. Also in the studies reviewed for this work the scale and location impacted the ecological effects of fine sediment (e.g. Larsen et al. 2009) as well as nutrients (e.g. Miltner & Rankin 1998). The biological quality elements, which should be considered according to the WFD, include also composition and abundance of aquatic flora (EC, 2000). Therefore, the models could be expanded to include macrophyte and diatom indicators as well.

The evidence search conducted in this work focused on finding quantified relationships between abiotic and biotic state variables. The models could be completed with more evidence linking other DPSIR categories to the causal pathways (Melcher et al. 2017, Webb et al. 2017).

Most importantly, the causal databases should be completed with associations concerning larger scope of topics. The challenge remains how to extract causal relationships effectively from the primary studies to complete the online databases. Ziegler et al. (2015) suggest that some combination of mark-up, text-mining and crowdsourcing may offer the best hope for widespread cataloguing of associations. It may also be useful to work with scientific journals to encourage authors to more clearly summarize evidence of cause-effect relationships, for example, by reporting associations and effect sizes in tables, so that this information is more easily extracted. In addition, evidence databases and visualization tools such as CADLit, ICDs, and EcoEvidence would need enhancement to efficiently capture and display evidence of interactions (Melcher et al. 2017, Nichols et al. 2017, Norton & Schofield 2017, Webb et al. 2017).

Evidence-based frameworks could, if becoming a standard procedure help in shifting from expert-based decision making to evidence-based environmental management. The growing interest to the topic appears in the projects aiming to synthesise the evidence with cause-effect tools by working groups from several continents. By working together and sharing data and information effective tools for causal assessment can be further developed. An international data standard for evidence, suggested by Webb et al. (2017) would allow evidence databases to communicate, greatly increasing the store of evidence available to users and strengthening global collaborations. This interoperability would reduce the amount of new evidence that would have to be extracted for any new assessment, thereby further reducing the

effort and time required for evidence assessment—the principal goal of rapid assessment methods. The prototype Ecological Exchange Language (EEL; Ziegler et al. 2015) is a first step in this direction. It defines standard information fields for an evidence item and allows data exchange between the Eco Evidence Database and the EPA's CADDIS Literature database.

Evidence assessment in ecology and environmental science is a rapidly evolving field (Dicks et al. 2014, Haddaway et al. 2015). The need is great for methods that will enable users to synthesize the growing body of evidence available in the literature and in monitoring data sets to help inform management of human-affected environments. Methods used in medicine have informed development of evidence-synthesis methods for environmental science, but natural environments and management plans differ from patients and medical treatments. Webb et al. further concluded in 2017, that the heterogeneity of both observational and experimental study designs, the influence of geographic context on response, and the frequent need to consider multiple species and levels of biological organization pose formidable challenges. The first international conference of the Collaboration for Environmental Evidence was held in September 2016, and rapid evidence synthesis featured prominently in the program. A working group was established to develop rapid evidence synthesis methods further and to demonstrate better their relation to full systematic reviews, which was also part of the EU Mars Project WP 7.1 task. Thus, considerable momentum exists for further development and refinement, and contributions from research groups around the world will contribute to this advancement.

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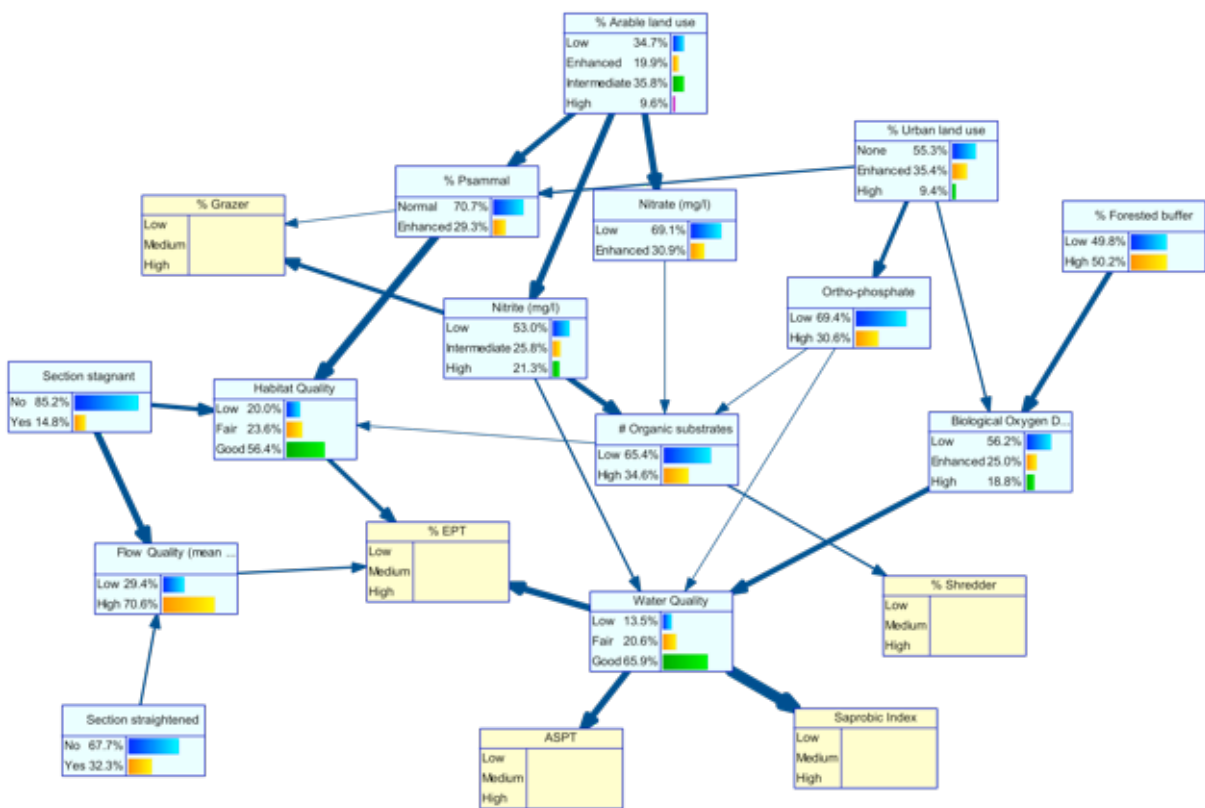
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Probability-based diagnosis of the causes of deterioration using Bayesian (Belief) Networks



Summary

Since 2000, water body management in Europe is based on biological assessment and monitoring. In lotic systems, for example, fish, macrozoobenthos, aquatic plants and algae are to be used to determine the ecological status. At present, numerous structural and functional metrics can be easily calculated from taxalists, to inform water body managers about the ecological status of any water body. While biological assessment has become quite straightforward, however, the inference of appropriate management options to achieve good ecological status is still challenging because of several reasons. One reason is the lack of knowledge to interpret the biological assessment results.

Here, we present an approach to combine the knowledge of the causes of biological deterioration with their effects on several biological response metrics. Conceptualised as cause-effect chains, they provide the basis for the development of a Bayesian (Belief) Network (BN). Using environmental and biological data from mid-sized sand-bottom rivers of central Europe, the BN is trained. Cause-effect relationships that are statistically derived from the data are translated to conditional probabilities, i.e. a kind of knowledge rules to statistically infer the probabilities of the causes to be causal for the effects. The resulting BN allows to diagnose the causes of deterioration based on the states of selected (biological) effect variables. This procedure is equivalent to the inference of potential diseases (causes) based on a series of symptoms (effects) in clinical diagnosis. The outcome is a list of probabilities of the causes that allows the user to distinguish likely from less likely causes.

The development of the BN is presented as a stepwise procedure, covering all steps from the initial BN conceptualisation until the validation of the BN using external (new) data. All data analysis is performed using the open-source statistical environment R. This allows others to use the BN presented here as a template for the development of other BNs, for example, for different river types, for lakes or for different biological quality elements.

In addition to the data-driven BN on river macrozoobenthos, a second case study is presented that is purely based on expert knowledge. The BN structure was developed during a workshop with an expert on phytoplankton assessment in large lowland rivers. The BN allows the user to identify, whether a moderate or worse phytoplankton ecological assessment is located within a water body of interest, or whether it is located further upstream in the continuum and is just "imported" into the water body of interest.

Introduction

Diagnosing the causes of deterioration in multiple-stressors environments is complex, because the stressors may interact and thus reveal ecological and biological effects that differ from single stressor's effects (Townsend, Uhlmann & Matthaei 2008). There is tremendous evidence from experimental studies that underpins the synergistic or antagonistic interaction of stressors under controlled conditions (Folt *et al.* 1999), Matthaei, Piggott & Townsend 2010, Wagenhoff *et al.* 2011, Piggott *et al.* 2012, Lange, Townsend & Matthaei 2014, Elbrecht *et al.* 2016). In contrast, the evidence of multiple-stressors effects from survey data (e.g., Lange *et al.* 2014, Gieswein, Hering & Feld 2017), although comparatively rare, suggests that complex stressors interactions are less common or less pronounced under uncontrolled "survey" conditions. (Gieswein, Hering & Feld 2017) showed that complex interactions are less common with composite indicators based on community metrics (e.g., % EPT taxa), for such community-based metrics usually lack a mechanistic relationship to single environmental stressor variables.

In order to derive generalisable cause-effect chains from single and multiple stressors effects, it is necessary to synthesise the evidence. A conceptual approach has already been presented in the previous chapter. While this evidence-based approach is useful to visualise and communicate multiple-stressors effects, the conceptual models do not allow for a quantification of the stressors effects. This quantification, however, is required to develop stressor hierarchies, as a prerequisite for the management of multiple stressors operating simultaneously within a water body. Practitioners are in need of three basic tiers of information: first, they need to know *which* stressors impact ecological status within a water body. Second, they need to know in which *order* of importance the stressors operate. And third, information is required of potential stressors *interactions*, i.e. the potential stressors mutual enhancement or attenuation.

This chapter presents an approach to quantify the individual stressor's effects in a multiple-stressors environment. The approach is based on a Bayesian (Belief) Network (BN) and allows to assign probabilities on classified effect variables (e.g., low, intermediate and high effect) within a complex cause-effect network. While the approach itself is not capable of identifying stressors interactions, it can help distinguish important from less important stressors and thus guide practitioners towards a stressor hierarchy, as a prerequisite to derive appropriate management options and its order of implementation.

In brief, the approach allows to diagnose the causes (stressors) of deterioration based on biological/ecological symptoms (i.e. biological assessment metrics or indices). As such, Bayesian diagnosis is similar to medical diagnosis, where the causes of a disease (i.e. the stressors) are diagnosed based on various symptoms (i.e. the biological 'metrics'). In fact, BNs are widely applied within medical diagnosis for a long time, which is why the approach is putatively suitable also for the diagnosis of the causes of deterioration of water bodies.

In the following, we present the development of two case studies that mainly differ in the set-up of the initial cause-effect relationship underlying each BN. The first case addresses the catchment-scale causes of deterioration in sand-bottom lowland rivers of Central Europe, di-

agnosed by the benthic invertebrate community. It is based on survey data taken from (Feld & Hering 2007) and presents a step-wise process to explore the data, to conceptualise the BN, to identify cause-effect thresholds, to derive conditional probabilities, to train the BN and eventually to validate the BN using external data. This approach has been applied also to reach-scale and site-scale stressor variables of the same data set (results not shown here; the BNs will be implemented online until the termination of MARS in January 2018). Check the MARS website (www.mars-project.eu) for updates.

The second case addresses another approach, where the initial conceptual cause-effect relationships are not driven by survey data, but by expertise. The BN uses river phytoplankton symptoms and some additional environmental variables to further specify the potential causes of deterioration and its location in the river continuum upstream. This approach allows to develop a diagnostic BN purely based on knowledge rules, which then can be tested using survey data at a later stage. The expert's approach is particularly beneficial, if data for sound statistical analyses of stressor-response relationships and ecological thresholds is sparse.

The spatial unit of diagnosis is the water body, i.e. a particular stretch of a river or a (part of a) lake, estuary or coastal water. As such, the approach is limited to the type of water body for which it is developed, i.e. mid-sized sand-bottom lowland rivers of Central Europe (case 1) and large/very large rivers (case 2). This is basically due to the selection of biological/ecological metrics (symptoms) and their relationships to the environmental stressor variables, both of which are likely to differ among water body types. Therefore, the two case studies are meant to exemplify the development of BNs to diagnose the causes of deterioration of water bodies. They provide detailed "cook books" on how to develop diagnostic BNs. The approach itself is generic and can be applied to all types of water bodies, provided that there is data/knowledge, to set-up the relevant cause-effect relationships and to derive the probabilities of particular effect classes.

Case 1: Diagnosing catchment-scale causes of deterioration using macroinvertebrates in mid-sized sand-bottom rivers of Central Europe

Data

The development of the Bayesian (Belief) Network (referred to as 'BN' in the following) of this case study is data driven, i.e. data analysis informed all steps of the development of the BN. The data comprises 144 macroinvertebrate samples and accompanying environmental variables, taken at 75 mid-sized sand bottom rivers of the Central European lowlands (Feld & Hering 2007, Lemm and Feld 2017). All data was gathered between 2000 and 2003. Macroinvertebrates were sampled from multiple habitats (multi-habitat sampling) of the stream bottom to ensure that the whole variety of representative (Hering *et al.* 2004) habitats was covered. Environmental variables were recorded in parallel to sampling (e.g., microhabitat distribution, riparian integrity, floodplain land use) or derived from maps using GIS (e.g., land use in the catchment).

The taxalists were entered the calculation software 'ASTERICS' (<http://www.fliessgewaesserbewertung.de/en/download/berechnung/>), to calculate numerous biological and ecological metrics (traits), which then provided the candidate 'symptom' variables for the BNs. Similar to medical diagnosis, the symptoms provide the starting point to investigate the potential causes (= 'diseases' in clinical diagnosis).

Bayesian Network development

The BN was developed during a step-wise process and started with the conceptualisation of the relevant cause-effect relationships for diagnosis. Environmental variables that reflect potential causes of deterioration were contrasted biological symptoms (metrics, traits) that reflect potential responses to these causes. Both environmental variables and biological metrics are referred to as 'nodes' in context of BNs. The eight steps of the development process are described in the following.

(1) Conceptualise cause-effect relationships between variables (i.e. from causes to symptoms) (Jensen 1996; Jensen & Nielsen 2007); this graphical approach visualises expected and data-derived causal relations between variables. The outcome is also known as a Directed Acyclic Graph (DAG), where acyclic refers to the absence of cyclic relationships from nodes to other nodes and back to the BNs.

(2) Learn the BN structure based on data and using R's package `bnlearn` (Scutari et al. 2010; Nagarajan et al. 2013). This procedure helps identify certain relationships between variables, to refine the expert-based initial model developed in step 1. This step may be restricted to the variables (nodes) contained in the initial structure (step 1). Alternatively, one may start with this step and continue drafting the initial BBN based already on the outcome of the R package `bnlearn`.

(3) Refine the initial model and enter the causal structure to a BN software. This may be implemented in R too, but here, the BN software GENIE (v2.1, for academic use, a free-ware version of GeNie is available at:

<https://download.bayesfusion.com/files.html?category=Academia>) is used because of its capability to visualise the BNs. It is also easier to apply for the user untrained with R.

(4) Verify the causal structure between variables (nodes) and each variable's strength as a descriptor of other variables. Therefore, variables are grouped into i) catchment-scale causes of deterioration, ii) natural covariates, iii) corresponding environmental effect variables that respond to the causes of deterioration and iv) biological response variables (traits, metrics, indices). This procedure is similar to that developed by Trigg et al. (2000).

(5) Apply a cluster analysis to the response metrics, to define potential groups of response variables and to test their (potentially) specific response to individual groups of environmental causes as defined under step 3.

(6) Analyse the distribution of the data behind each node (variable), to identify the required number of states (discrete classes) for the variable. This step is done using density plots, histograms, and Conditional Inference Trees (CIT). CITs belong to the family of tree-based analysis methods and are implemented with R's packages `party` and `partykit`. The more recent `partykit` contains a function (`ctree`), which is similar to regression tree analysis. It handles all kinds of covariates and response variables (binary, ordinal, continuous, censored) and also multivariate response variables, such as abundances of various species (see `ctree`'s vignette at

<https://www.rdocumentation.org/packages/partykit/versions/1.1-1/topics/ctree> for details).

(7) Populate the Conditional Probability Tables (CPT) for each node of the BN. This is the most difficult step in the development process, because probabilities need to be defined for each state of an effect variable, conditional on all possible combinations of states of the causes that are linked to the effect variable. With three causes, each of which has three states, for example, there are already 27 combinations to be translated into individual probabilities of certain effects.

The causality of relationships between node states can be checked using conditional inference trees (CIT). The method allows of predictions and calculates a confusion matrix of true and false predictions.

Another approach follows experts judgement (Allan et al. 2011): the cause variable is divided into groups of impact strength covering the entire impact gradient. For instance, thresholds are set for % agricultural land use at 10, 20, 30, 50, 80 and 100% (this is similar to Fig. 4 in Allan et al. 2011). Then experts are requested to estimate the value of an effect (response, symptom) variable for each of the stressor values defined before. More specifically, they are requested to estimate the minimum, maximum and median values, and the

quartiles (25th and 75th).

The third approach is also described in Allan et al. (2011): thresholds (or intervals thereof) are identified for each variable that separate the states. Then, if plotted in a scatter plot, the thresholds mark intervals as 2-D areas along both axes, of which all data points within each of the areas can be expressed as a "probability". That is the number of data points in comparison to all data points. The selection of states can be informed by Frequency Distribution Diagrams (FDD) and Density Diagrams (DD), to identify a reasonable number of states (Allan et al. 2011), while this approach may also aim to achieve a more balanced number of data points within each of the states (i.e. a trade-off between statistically-derived thresholds and a more subjective desire to evenly distribute data points among states to increase statistical rigour).

(8) Validate the BN. This step is crucial to estimate the reliability of the cause-effect relationships defined for the BN and of the conditional probabilities underlying the relationships. Validation is feasible by using standard model statistics (sensitivity, value of information) or preferably external (new) data. Based on new data, GENIE v.2.1 allows to calculate accuracy values (%) for each node in the model and for the overall model performance. The values are somehow alike R^2 that indicate the resemblance between the modelled inference based on the training and validation data.

Understanding all background behind BNs requires some basic understanding of the concept behind Bayesian inference, in particular of Bayes' rule. This knowledge is already available with numerous well-structured textbooks, to which we would like to refer the interested reader. Here, we focus on the application of BNs, to develop diagnostic models for water bodies. A good overview of BNs is given by Jensen (1996) and Jensen & Nielsen (2007). Also, part I of Kruschke (2015) provides a good introduction to Bayesian data analysis. The implementation of BNs using R is described in Scutari et al. (2010) and Nagarajan et al. (2013).

Step 1: Graphical representation of causal relationships

An initial conceptual flowchart of putative cause-effect relationships of catchment-scale influences in mid-sized sand-bottom lowland rivers of Central Europe is given in Fig. 1. The marginal nodes mark the entry points, while the terminal nodes mark the endpoints, i.e. the biological metrics. The conditional nodes represent mediating variables that link the marginal with the terminal nodes. Diagnosis operates opposite to the arrows direction, i.e. from the terminal to the marginal nodes.

This initial concept may be developed purely on expert's knowledge; data is not required to conceptualise the cause-effect relationships, which is beneficial if such data is sparse, or even completely lacking.

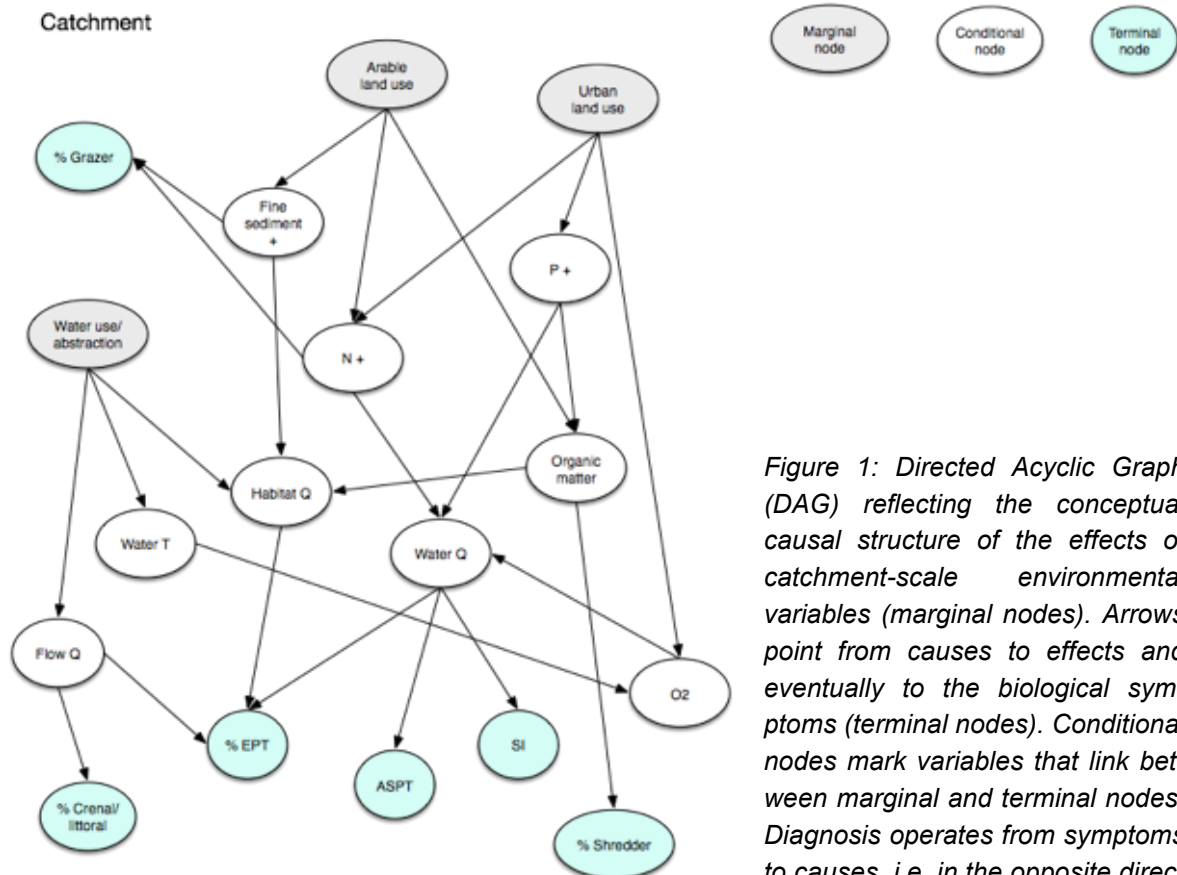


Figure 1: Directed Acyclic Graph (DAG) reflecting the conceptual causal structure of the effects of catchment-scale environmental variables (marginal nodes). Arrows point from causes to effects and eventually to the biological symptoms (terminal nodes). Conditional nodes mark variables that link between marginal and terminal nodes. Diagnosis operates from symptoms to causes, i.e. in the opposite direction.

Alternatively, it may be useful to develop BNs separately for different causal groups (e.g. water quality, habitat quality, flow quality). This is up to the specific requirements a user has to the BN. The initial causal relationships defined for sand-bottom lowland rivers (Fig. 1) were drafted based on expertise. The causal structure, however, includes some nodes (e.g. Habitat Quality, Water Quality), that represent 'intermediate' nodes (aka 'mediating' nodes acc. to Jensen 2001 or 'latent' nodes acc. to Marcot et al. 2006). Intermediate nodes help simplify the structure in that they help reduce the number of parent nodes pointing at the same child node. Many parents render the definition of conditional probabilities (step 7) difficult. As a rule of thumb, a child node should not have more than three parent nodes.

Step 2: Learn the directed causal structure from data using `bnlearn`

`bnlearn` helps identify the causal structure of a BN from data. It allows to generate a Directed Acyclic Graph (DAG), which is equivalent to the graphical cause-effect structure underlying the BN (Fig. 1). Directed means that causes point to effects; the opposite direction is not meaningful. Acyclic refers to the convention, that arrows must not constitute a cyclic connection, from a given node via other nodes and back to the given node. Two algorithms are available: grow-shrink (`gs`) and hill-climbing (`hc`). Both algorithms were applied to the original (continuous, but not discretised) data. Both algorithms revealed some useful information of

the causal structure in the data (Fig. 2a and 2b), which already reflects some elements of the conceptual cause-effect relationships (Fig. 1). This data-driven analysis thus can help identify cause-effect relationships inherent to the data that might have been omitted in step 1. The analysis helps estimate too, which initially-drafted conceptual cause-effect relationships are actually represented by the data.

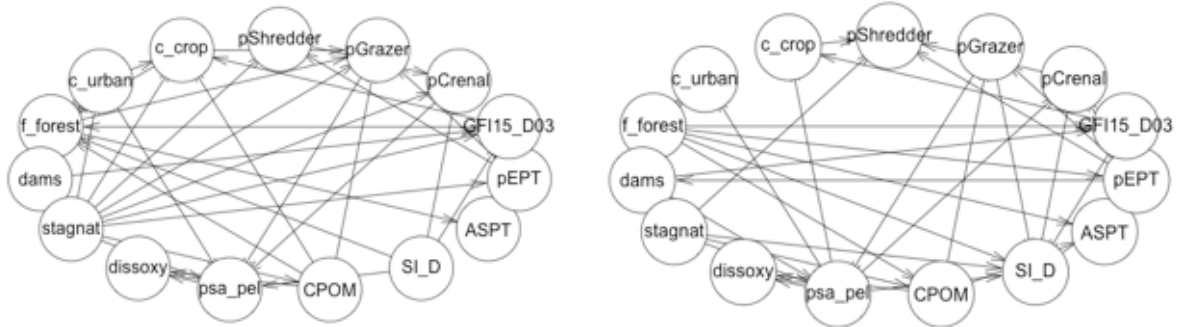


Figure 2a: DAG derived from catchment-scale data using the grow-shrink (*gs*) algorithm in *bnlearn*.

Figure 2a: DAG derived from catchment-scale data using the hill-climbing (*hc*) algorithm in *bnlearn*.

For instance, the percentage of forested floodplain (*f_forest*) is related to the amount of CPOM (coarse particulate organic matter) on the river bottom, akin to percent catchment arable land (*c_crop*), which is linked to percent sand and silt (*psa_pel*) on the bottom (Fig. 2a and 2b; note that the direction does not always follow the cause-effect direction and that both algorithms result in slightly different cause-effect diagrams).

Step 3: Refine the BN structure using a graphical software

Based on the conceptual work of step 1 and the data-driven cause-effect analysis of step 2, the cause-effect network is refined. For instance, relationships that were revealed by the data analysis might be incorporated in the flow chart. The refined causal structure is then entered a BN software, to graphically visualise BN structure and to implement the BN itself. Here, we do not use R's comprehensive capabilities, but recommend using a software with a graphical user interface (GUI). The BN software GENIE v2.1 (free for academic use: <https://download.bayesfusion.com/files.html?category=Academia>), for example, does provide such a GUI, which is more intuitive to apply than related BN packages of R. The resulting initial BN is shown in Fig. 3.

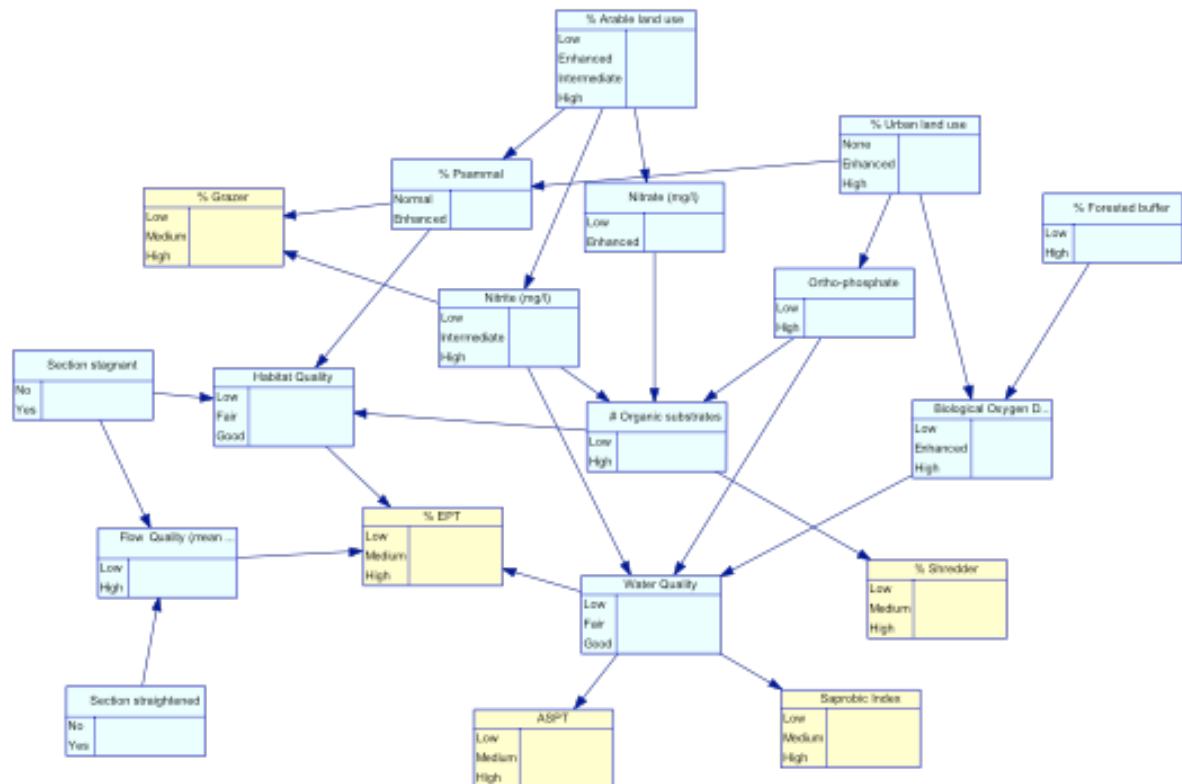


Figure 3: Initial BN structure for the catchment-scale cause-effect relationships implemented in GENIE v2.1. The BN structure already includes different states for each node (variable), which will be subjected in more detail in step 6. Symptom nodes are yellow, cause and intermediate nodes are blue.

The a priori classification of node states is most straightforward for binary variables, such as 'stagnation', which has only two states: present (yes) and absent (no). Three states were set a priori in case a distinction of 'high', 'intermediate' and 'low' was deemed necessary. Four states might be drafted, if the state 'none' is added. Five states might be useful in case the WFD-related classification is followed: 'high-good-moderate-poor-bad'. In general, a user may wish to keep the number of states handy, because later on, conditional probabilities need to be defined for each possible combination of states of (parent) variables that point to the same (child) node (step 7).

The number of states per node can be revised at a later stage, for example, during the tree-based analysis (Trigg et al. 2000). Based on real data, split points can be identified. The number of split points identified for a descriptor (and its frequency distribution along a gradient, Allan et al. 2011) inform the decision about the best suitable number of states for the particular variable.

Both GeNie and NETICA provide different file formats to store a BN. Here, we recommend using the .net ("dot-net") format, which later on allows to directly import the GeNie/NETICA BNs into the Diagnostic Tool (see Chapter 3).

Step 4: Verify the causal structure of the BN

The causal structure of the BN (Fig. 3) can be expressed as different groups of nodes. The first group contains the catchment-scale causes, i.e. the broad-scale pressures that ultimately cause deterioration, environmental as well as biological deterioration. The second group of variables contains environmental effect variables, i.e. abiotic variables that change due to the causes. This second group can be divided into i) physical habitat and structure, ii) substrates, iii) water quality and iv) flow. In addition, natural environmental co-variables (e.g., altitude, stream size) might be assigned this second group of variables. The third group of variables contains all biological metrics, which respond to the deterioration (i.e. the 'symptom variables').

Each of these variables can be defined as a (dependent) response variable and subjected to a univariate analysis, where all other variables can be defined (independent) predictors of the response variable. Such an analysis helps identify important abiotic and biotic descriptors in the dataset. The results of such an analysis are given in Tab. 1. In brief, a Boosted Regression Tree (BRT) analysis was run for each variable, and cause variables (pressures) and/or biological metrics (symptoms) were used as descriptor variables. For example, row one of Tab. 1 lists the three biological metrics that determine best the altitude of a sample site. Similarly, row 11 (Effect habitat) lists the top-3 causal and biological predictors of the proportion of shade (f_shade) at a sampling site.

Table 1: Grouping of environmental variables into environmental causes (pressures), effects (environmental states) and biological responses (biological states). The three strongest cause variables (Cause 1–3) are given for each environmental effect variable (env. state). 'Biol 1–3' refer to the three strongest biological response variables (biol. states). Number in brackets mark the variable's column in the data matrix (not relevant here).

Group	Variable	Cause 1	Cause 2	Cause 3	Biol 1	Biol 2	Biol 3
Cause natural	alt (6)				SI_D (39)	pCrenal (51)	pGrazer (60)
	catchm (9)				GF114 (46)	pFiltP (65)	pShredder (62)
	wid_str (23)				pCrenal (51)	GF114 (46)	r_K (48)
Cause pressure	c_crop (10)				SI_D (39)	pFiltA (64)	GF114 (46)
	c_urban (11)				GF114 (46)	pFiltP (65)	pPelal (56)
	f_forest (12)				GF115 (47)	GF114 (46)	SI_D (39)

Group	Variable	Cause 1	Cause 2	Cause 3	Biol 1	Biol 2	Biol 3
	f_crop (13)				SI_D (39)	GFI_D01 (44)	pAkal (55)
	dams (18)				pAkal (55)	pShredder (62)	pPelal (56)
	bafi_sto (19)				GFI_D01 (44)	pPhytal (58)	pCrenal (51)
	straight (21)				GFI_D01 (44)	pEPT (43)	SI_D (39)
Effect habitat (env. state)	f_shade (14)	f_forest (12)	straight (21)	alt (6)	GFI15_D03 (45)	pPsammal (57)	pXylo (61)
	wid_rip (15)	f_forest (12)	catchm (9)	c_crop (10)	pCrenal (51)	pShredder (62)	GFI_D01 (44)
	dens_rip (17)	f_forest (12)	catchm (9)	alt (6)	GFI15_D03 (45)	ASPT (40)	pShredder (62)
	logs (16)	catchm (9)	f_forest (12)	c_urban (11)	pGatherer (63)	GFI15_D03 (45)	pFiltP (65)
Effect substrate (env. state)	macrolit (25)	f_crop (13)	catchm (9)	bafi_sto (19)	pPsammal (57)	pGrazer (60)	pFiltP (65)
	mesolit (26)	wid_str (23)	bafi_sto (19)	alt (6)	pCrenal (51)	GFI15_D03 (45)	pAkal (55)
	microlit (27)	catchm (9)	alt (6)	wid_str (23)	pGrazer (60)	pPhytal (58)	pAkal (55)
	akal (28)	wid_rip (15)	wid_str (23)	f_shade (14)	GFI_D01 (44)	pPelal (56)	pAkal (55)
	psa_pel (29)	c_crop (10)	catchm (9)	logs (16)	SI_D (39)	pFiltA (64)	pCrenal (51)
	sub.mac (30)	catchm (9)	wid_str (23)	f_shade (14)	pFiltA (64)	pCrenal (51)	pPhytal (58)
	em_mac (31)	alt (6)	catchm (9)	c_crop (10)	NA	NA	NA
	xylal (32)	logs (16)	wid_rip (15)	wid_str (23)	pXylo (61)	pGatherer (63)	GFI15_D03 (45)

Group	Variable	Cause 1	Cause 2	Cause 3	Biol 1	Biol 2	Biol 3
	CPOM (33)	wid_str (23)	f_forest (12)	logs (16)	pGrazer (60)	GFI15_D03 (45)	pGatherer (63)
	FPOM (34)	catchm (9)	wid_str (23)	wid_rip (15)	pXylo (61)	pShredder (62)	pFiltP (65)
	NoOrgSub (35)	logs (16)	catchm (9)	wid_str (23)	pGatherer (63)	pXylo (61)	pFiltP (65)
	NoAllSub (36)	f_forest (12)	logs (16)	wid_str (23)	pPelal (56)	pPsammal (57)	pGatherer (63)
Effect water quality (env. state)	dissoxy (22)	psa_pel (29)	logs (16)	CPOM (33)	pPelal (56)	pFiltA (64)	r_K (48)
	conduct (24)	c_crop (10)	c_urban (11)	alt (6)	pGrazer (60)	GFI15 (47)	pFiltP (65)

Group	Variable	Cause 1	Cause 2	Cause 3	Biol 1	Biol 2	Biol 3
Effect flow (env. state)	stagnat (20)	dams (18)	f_shade (14)	catchm (9)	pAkal (55)	GFI14 (46)	r_K (48)
Response indices (biol. state)	SI_D (39)	f_forest (12)	c_crop (10)	psa_pel (29)	pFiltA (64)	pCrenal (51)	pPhytal (58)
	ASPT (40)	f_forest (12)	wid_rip (15)	f_crop (13)	pGrazer (60)	pXylo (61)	r_K (48)
	pEPT (43)	wid_rip (15)	f_forest (12)	psa_pel (29)	pGrazer (60)	pPsammal (57)	pPhytal (58)
	GFI_D01 (44)	f_forest (12)	straight (21)	bafi_sto (19)	pPelal (56)	pPhytal (58)	pGatherer (63)
	GFI14 (46)	f_forest (12)	bafi_sto (19)	f_crop (13)	pPhytal (58)	pAkal (55)	pPelal (56)
	GFI15_D03 (45)	f_forest (12)	bafi_sto (19)	wid_rip (15)	pPelal (56)	pGatherer (63)	pXylo (61)
	GFI15 (47)	bafi_sto (19)	wid_rip (15)	f_forest (12)	pPelal (56)	pAkal (55)	pXylo (61)
Response traits (biol. state)	r_K (48)	catchm (9)	psa_pel (29)	logs (16)			
	pCrenal (51)	catchm (9)	alt (6)	psa_pel (29)			
	pAkal (55)	wid_str (23)	psa_pel (29)	logs (16)			
	pPelal (56)	bafi_sto (19)	psa_pel (29)	logs (16)			
	pPsammal (57)	catchm (9)	wid_str (23)	psa_pel (29)			
	pPhytal (58)	wid_str (23)	bafi_sto (19)	f_crop (13)			
	pGrazer (60)	macrolit (25)	alt (6)	psa_pel (29)			
	pXylo (61)	logs (16)	wid_rip (15)	xylal (32)			
	pShredder (62)	catchm (9)	wid_rip (15)	dens_rip (17)			
	pGatherer (63)	logs (16)	catchm (9)	bafi_sto (19)			
	pFiltA (64)	psa_pel (29)	c_crop (10)	bafi_sto (19)			

Group	Variable	Cause 1	Cause 2	Cause 3	Biol 1	Biol 2	Biol 3
	pFiltP (65)	logs (16)	catchm (9)	wid_rip (15)			

Step 5: Cluster analysis of response metrics

Although this step is not a key part of the analysis, it may help inform the selection of non-redundant biological state variables (symptoms). In general, biological states can be highly correlated and then do not provide independent symptoms for diagnosis.

Cluster analysis can easily identify groups of similar variables based on their Euclidean Distance (ED) or other measures of (dis)similarity and illustrate the groups in a dendrogram (Fig. 4). For diagnostic purposes, we recommend using up to two biological symptom variables of each group.

Different groups of response variables, however may reflect different aspects of environmental deterioration, such as water quality, habitat or flow alteration. If this is the case, members of each groups should be included in the final BBN, to ensure that these different aspects are being addressed.

The results of the cluster analysis reveal several distinct groups of biological response metrics that obviously show different distributions in the dataset and thus might reflect different community aspects (Fig 4). The first group is quite homogeneous and represents biological metrics of habitat structure and quality (e.g., German Fauna Indices, ASPT, percent xylophagous taxa). The second group reflects the influence of fine material (psammal, pelal) and the feeding types active and passive filterers, which suggests that this group is linked to flow. The third group consists of percent akal (gravel) dwellers, which seem to constitute an own habitat group in sand-dominated rivers. The fourth sensitive taxa group consists of pEPT (% Ephemeroptera-Plecoptera-Trichoptera) only. The fifth group is a feeding type group related to organic matter.

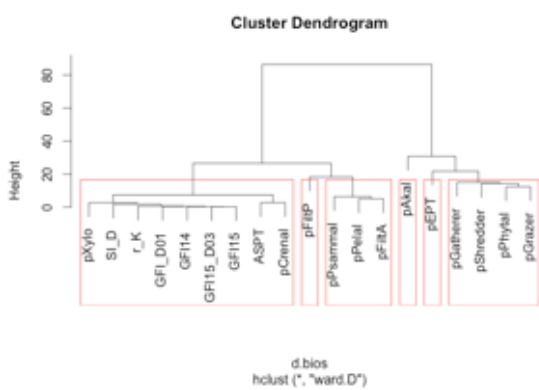


Figure 4: Cluster analysis (distance measure: Euclidean Distance, linkage method: Ward) of biological symptom variables. Six groups are separated in this example (see Tab. 2 for other possible groupings): i) general habitat and structure indices/metrics, ii) flow-related and fine sediment-related metrics, iii) akal preferences, iv) sensitive (EPT) taxa and v) feeding types related to organic material/primary production. (Height is equivalent to the distance between metrics and groups of metrics.)

The interpretation of different groups according to the cluster dendrogram is artificial; it is possible to assign less groups, for instance only two groups at the height (distance) of 50 in Fig. 4. Table 2 shows the group members conditional on different numbers of groups. In general, it seems that the ecological aspects behind the groupings do not change much.

Table 2: Biological symptom variables and cluster group allocation (Fig. 4). The 5-group classification is reflected by the colour coding of metric names (see text for the interpretation of groups).

Metric name	3 groups	4 groups	5 groups	6 groups
pXylo	1	1	1	1
SI_D	1	1	1	1
r_K	1	1	1	1
GFI_D01	1	1	1	1
GFI14	1	1	1	1
GFI15_D03	1	1	1	1
GFI15	1	1	1	1
ASPT	1	1	1	1
pCrenal	1	1	1	1
pFiltP	1	2	2	2
pPsammal	1	2	2	3
pPelal	1	2	2	3
pFiltA	1	2	2	3
pAkal	2	3	3	4
pEPT	3	4	4	5
pGatherer	3	4	5	6

Metric name	3 groups	4 groups	5 groups	6 groups
pShredder	3	4	5	6
pPhytal	3	4	5	6
pGrazer	3	4	5	6

Step 6: Inferring node states using histograms and conditional inference trees

This step is crucial, to analyse the distribution of the values of each variable, and to subsequently derive the appropriate number of states (classes) for each variable. Thereby, different univariate statistical tools can help identify splits in the data, i.e. change points along gradients of values, at which an effect variable shows a notable change. Such change points, for example, could mark values of riparian shade, at which a biological symptom variables (e.g., % EPT taxa) abruptly increases or decreases. It is also possible that change points occur repeatedly along a variable's gradient.

The statistical tools suitable to graphically interpret the data and to numerically analyse splits in the data are manifold. Here, we suggest using simple histograms (frequency plots) to visualise the variable's distribution. In addition, we apply conditional inference trees (CITs) to statistically identify split points. CITs can be run using the function `ctree` of R's package `partykit` (Hothorn et al. 2006).

Although this step of the BN development is presented based on the analysis of survey data in the following, the definition of split points and thus of variable (node) states might also be based on or additionally informed by expert knowledge.

% Arable land use in the catchment

The histogram of % arable land use (Fig. 5a) suggests splits at 10%, 20% and 40% arable land use based on the frequency distribution of values in the dataset. The candidate split point at 20% may be omitted, because it is less pronounced in the overall distribution. Here, we apply the three splits, which results in four states for % arable land use: <10%, 10–20%, 21–40%, >40%.

The candidate splits are confirmed by `ctree` analysis using nitrate, ortho-phosphate and % psammal (sand) on the river bottom as descriptors of % arable land use (results not shown here).

% Urban area in the catchment

The histogram of the proportion of urbanised areas in the catchment suggests two splits at 0% and 10%. An additional split point might be set by 20%, yet the frequency of this high values

is quite low, which renders this candidate split less useful based on the given data. This results in three states for % urban area in the catchment: none (0%), enhanced (<10%) and high ($\geq 10\%$).

The splits are supported by CITs (`ctree`) based on nitrate, ortho-phosphate and BOD₅, whereas the 10%-split is only weakly confirmed by the `ctree` analysis (Fig. 5b; note the location of medians in both bar plots).

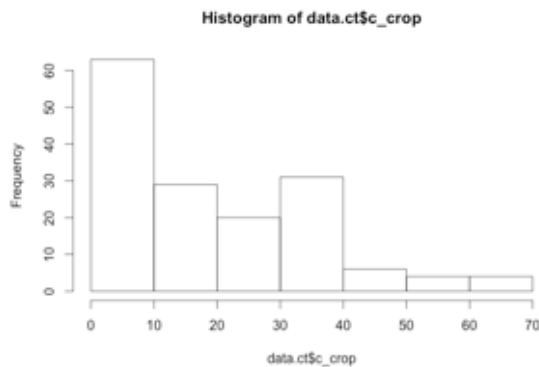


Figure 5a: Histogram of % arable land use in the catchment (`c_crop`).

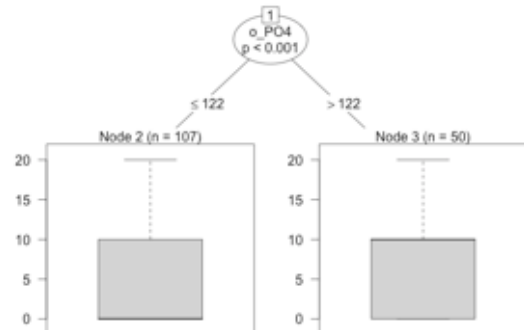
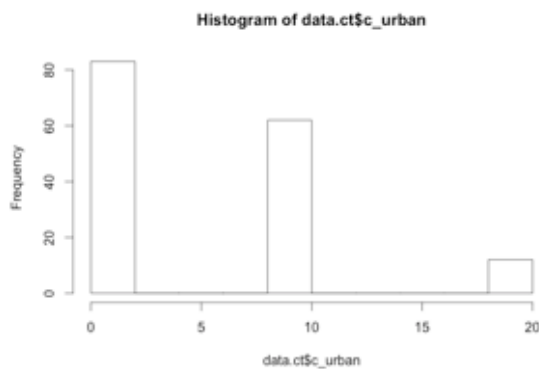


Figure 5b: Histogram and `ctree` plot of % urban area in the catchment (`c_urban`).

Nitrite concentration

The analysis of nitrite (Fig. 5c) suggests two splits at 0.05 and 0.10 mg/l based on its relationship to % arable land use (`c_crop`). This results in three states for nitrite: low (0–0.05), intermediate (>0.05–0.1) and high (>0.1 mg/l).

Nitrate concentration

The histogram of nitrate suggests one split at 20 mg/l (Fig. 5d). This is weakly confirmed by the `ctree` analysis based on the relationship of nitrate to % arable land use and % urbanised area (plots not shown here). This results in two states for nitrate concentration: low (0–20) and enhanced (>20 mg/l).

ortho-Phosphate concentration

The analysis of ortho-phosphate (o-PO₄) suggests only one split at 100 µg/l (Fig. 5e), based on its relationship to % urbanised area in the catchment (`c_urban`). This results in two states for ortho-phosphate: low (0–100) and high (>100 µg/l).

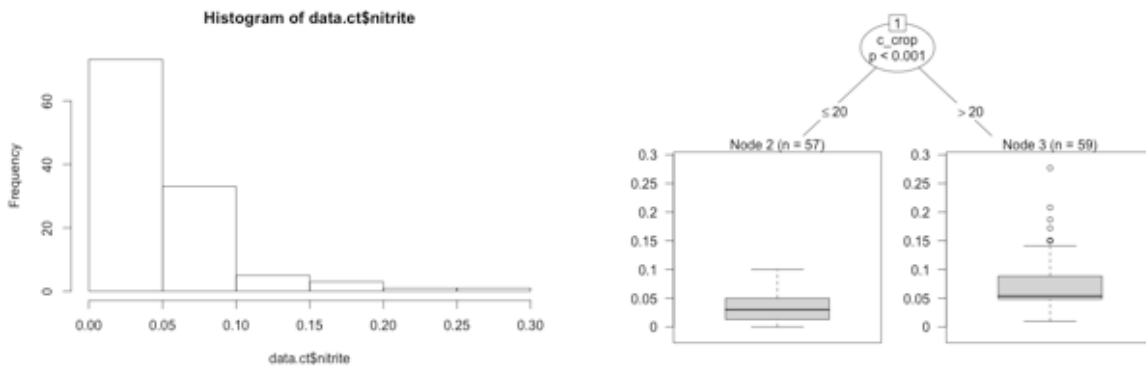


Figure 5c: Histogram and `ctree` plot of nitrite.

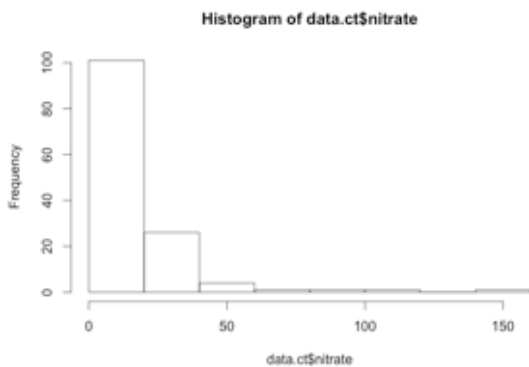


Figure 5d: Histogram of nitrate.

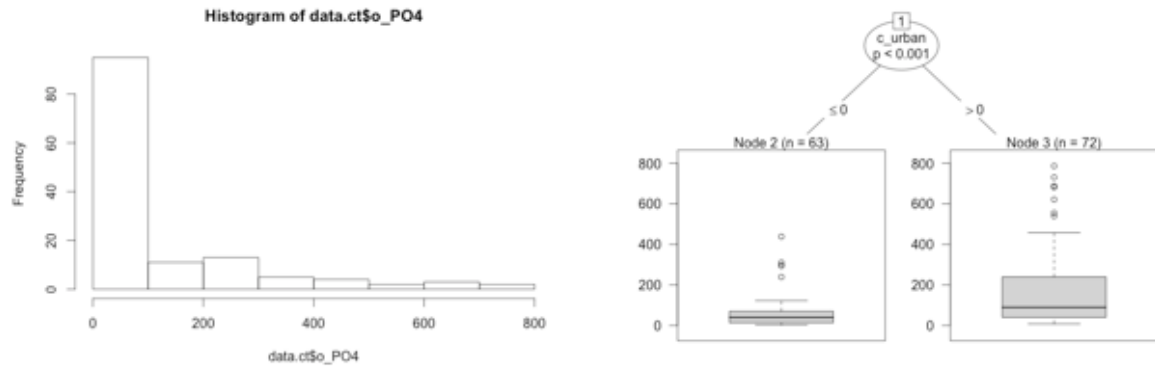


Figure 5e: Histogram and `ctree` plot of ortho-phosphate (`o_PO4`).

% Psammal (sand) on the river bottom

The proportion of sand (<2 mm grain size) on the river bottom suggests one split at 90% (Fig. 5f), based on the relationship of sand to % urbanised area in the catchment (`c_urban`). This results in two states for `% psammal`: normal (0–90) and enhanced (>90%). Due to inconsistent results, the `ctree` results are not shown here.

Number of organic substrates on the river bottom

The analysis of the number of organic substrates (`no_orgsub`) on the stream bottom suggests one split at three organic substrates (Fig. 5g). This results in two states: low (0–3) and enhanced (>3). The `ctree` results are not shown.

Biological oxygen demand in five days (BOD₅)

The histogram of BOD₅ values suggests a split at 3 mg/l, whereas the `ctree` plot reveals a split at 2 mg/l to be more suited (Fig. 5h). Two splits were finally introduced, resulting in three states for BOD₅: low (0–2), enhanced (>2–3) and high (>3 mg/l).

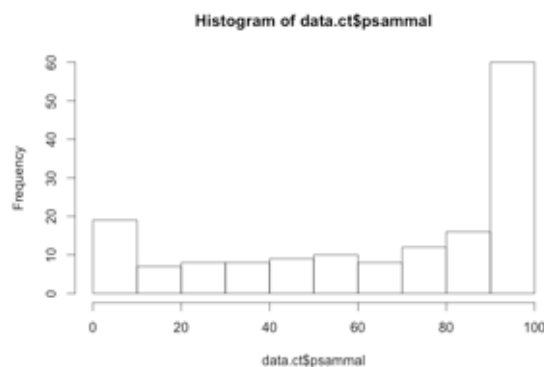


Figure 5f: Histogram of % Psammal (sand) on the river bottom

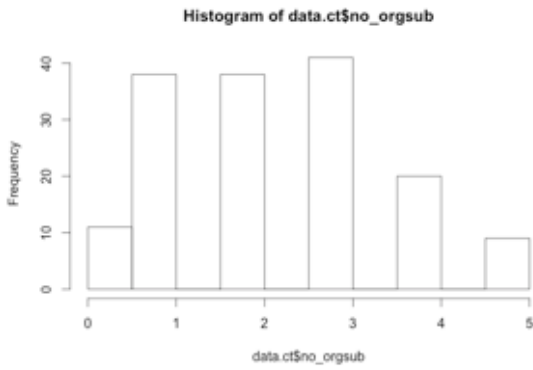


Figure 5g: Histogram of the number of organic substrates indicating the variability of organic matter available on the stream bottom.

Mean current velocity

The histogram of mean current velocity suggests a split at 0.15 or 0.2 m/s, which is confirmed by the `ctree` plot (Fig. 5h). Among the covariates water body straightened (y/n), water body stagnant (y/n) and % bank fixation with stones at water body (bafi_sto), only the latter is linked to the mean current velocity. This link, however, reflects a coincidence of both variables, rather than a causal relationship. Bank fixation, thus turns out to be a proxy of current velocity, with lower velocity in modified (enforced) stream sections. The threshold is at 40% bank fixation with stones (bafi_sto). Thus, one split is introduced, resulting in two states for the mean current velocity: low (≤ 0.2) and high (> 0.2 m/s).

% Ephemeroptera-Plecoptera-Trichoptera (% EPT)

The histogram of % EPT taxa (Fig. 5j) suggests two splits at 20 and 60%, resulting in three states for % EPT: low (< 20), medium (20–60) and high ($> 60\%$).

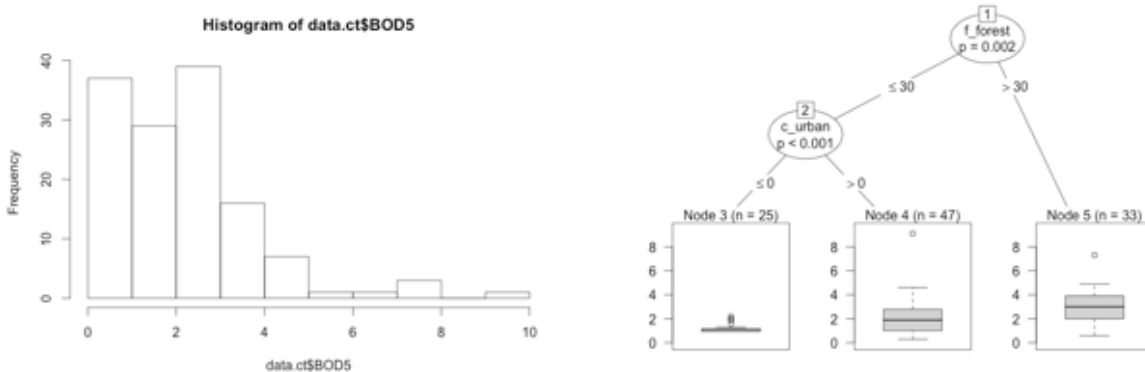


Figure 5h: Histogram of biological oxygen demand in 5 days.

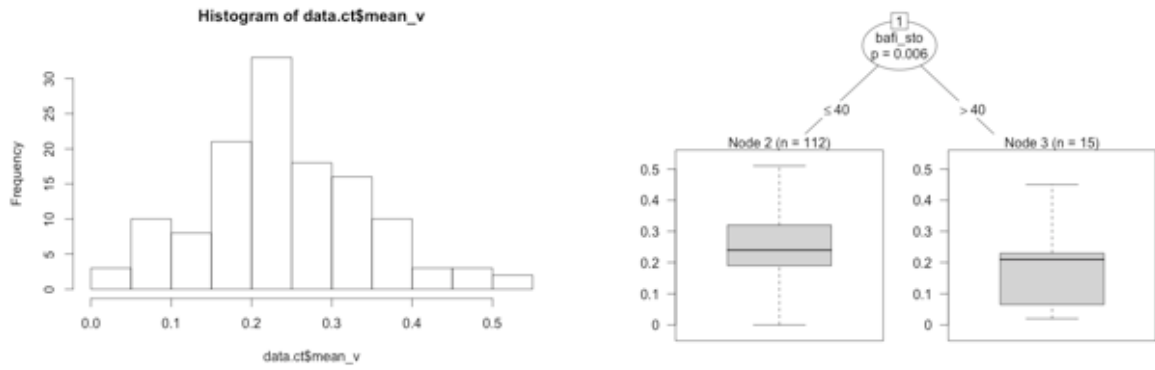


Figure 5i: Histogram of mean current velocity (*mean_v*).

Average Score Per Taxon (ASPT)

The histogram of ASPT suggests two splits at 5 and 6.5 (Fig. 5k), resulting in three states for ASPT: low (<5), medium (5–6.5) and high (>6.5). The *ctree* plot is not shown because of inconsistent results.

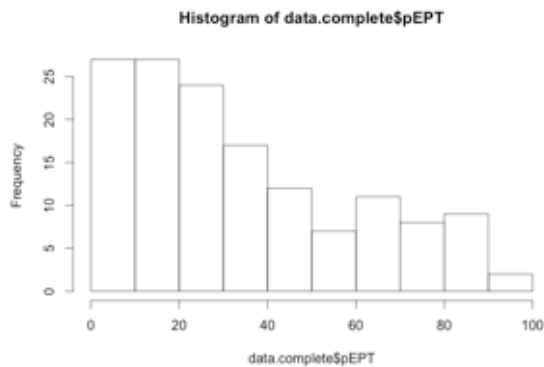


Figure 5j: Histogram of % EPT taxa (*pEPT*).

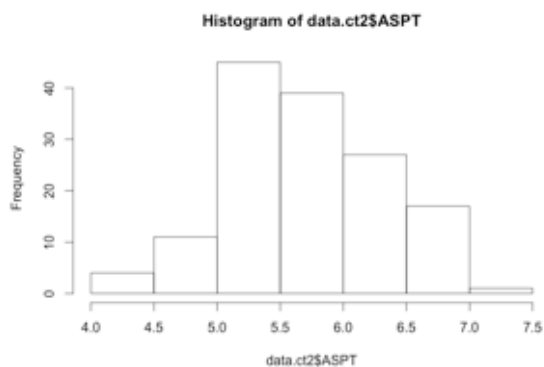


Figure 5k: Histogram of ASPT.

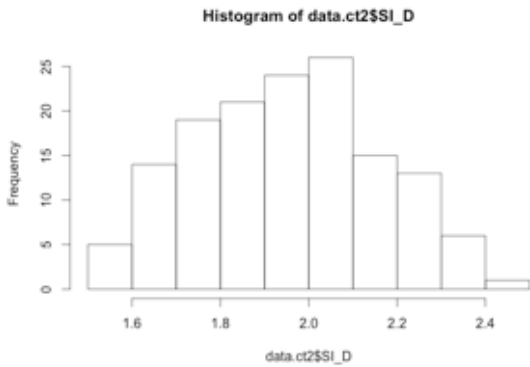


Figure 6l: Histogram of the Saprobic Index (SI).

Saprobic index (SI)

The histogram of the Saprobic Index (SI) suggests two splits at 1.8 and 2.1 (Fig. 6l), based on the frequency distribution of values. However, a clear separation of classes is not possible, which is why the final classification also considered the quality targets set for this stream type in Germany. Accordingly, three states were defined for SI: low (>2.5), medium (2.5–2.0) and high (<2). The `ctree` plot is not shown because of inconsistent results.

% Shredder

The histogram of % shredder in the macroinvertebrate community, i.e. the specimens that feed on coarse particulate organic matter, suggests two splits at 20 and 40% (Fig. 5m), resulting in three states for % shredder: low (<20), medium (20–40) and high (>40%). The `ctree` plot is not shown because of inconsistent results.

% Grazers

The histogram of % grazers suggests two splits at 5 and 20% (Fig. 5n), however, the second split was set to 15%, because this was deemed more appropriate for the targeted stream type. This results in three states for % grazers: low (<5), medium (5–15) and high (>15%). The `ctree` plot is not shown because of inconsistent results.

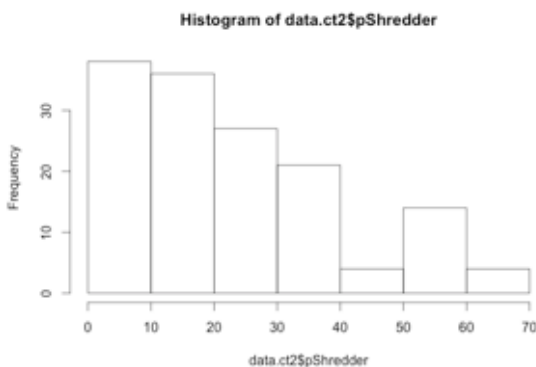


Figure 5m: Histogram of % shredder.

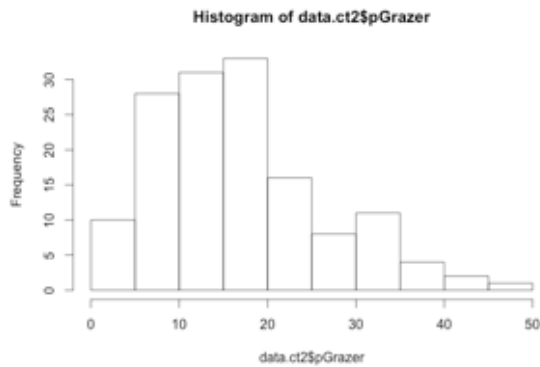


Figure 5n: Histogram of % grazer.

Summary of node states

All node states of the catchment-scale macrozoobenthos model are listed in Tab. 3.

Table 3: Summary of node states of the diagnostic BN for catchment-scale causes.

Variable (node) name	Split points (range of values)			
	State 1 (low impact)	State 2 (enhanced impact)	State 3 (high impact)	State 4 (very high impact)
% Arable land use	<10	10–20	21–40	>40
% Urban land use	0	>0–<10	>10	
Nitrite [mg/l]	≤0.05	>0.05–0.1	>0.1	
Nitrate [mg/l]	≤20	>20		
ortho-Phosphate [μg/l]	≤100	>100		
% Psammal (sand)	≤90	>90		
No. of organic substrates	≤3	>3		
BOD ₅ [mg/l]	≤2	>2–3	>3	

Variable (node) name	Split points (range of values)			
	State 1 (low impact)	State 2 (enhanced impact)	State 3 (high impact)	State 4 (very high impact)
Mean current velocity [m/s]	≤0.2	>0.2		
% EPT taxa	<20	20–60	>60	
Average Score Per Taxon (ASPT)	<5	5–6.5	>6.5	
Saprobic Index	>2.5	2.5–2.0	<2.0	
% Shredder	<20	20–40	>40	
% Grazer	<5	5–15	>15	

Step 7: Populate Conditional Probability Tables (CPT)

This step sets the probabilities of the occurrence of states and state combinations for each node in the BBN, conditional on the states of the parents of that node. For instance, consider two parent nodes A and B, each with two states A1, A2 and B1, B2, respectively. The child of both nodes thus has four states (2^2), which are equivalent to all possible combinations of the parent states: A1-B1, A1-B2, A2-B1 and A2-B2. With three two-state nodes (A, B and C), the number of possible combinations would be 8 (2^3) already: A1-B1-C1, A2-B1-C1, A1-B2-C1, A1-B1-C2, A2-B2-C1, A1-B2-C2, A2-B1-C2 and A2-B2-C2.

Assigning conditional probabilities to all state combinations is the major task during the development of a BN, because the developer has to assign values to each child node state, i.e. he/she has to indicate, how probable each child node states are, based on the combinations of parent nodes. With four states (i.e. based on two two-state parents), this might be straightforward. With eight states, however, assigning reliable and meaningful probabilities might already turn into guessing, if sufficient data is missing to inform the decision. With three three-state nodes (i.e. $3^3 = 27$ possible combinations), probability assignment quickly turns into a major challenge, unlikely to be driven by data alone. This is the reason why the developer may wish to keep the number of parent nodes directing at a given child as well as the number of parent nodes states as high as necessary, but first and foremost, as low as possible.

For nodes equivalent to parameters in the explored dataset (e.g., nitrate concentration, % arable land use), it is straightforward to use the data in order to estimate appropriate probabilities for each state combination. If mediating (i.e. latent) nodes are included, the CPTs would

be based on expertise rather than on data analysis. This was the case, for example, with the nodes Habitat Quality and Water Quality (Fig. 6). The underlying CPTs are listed in Tab. 4.

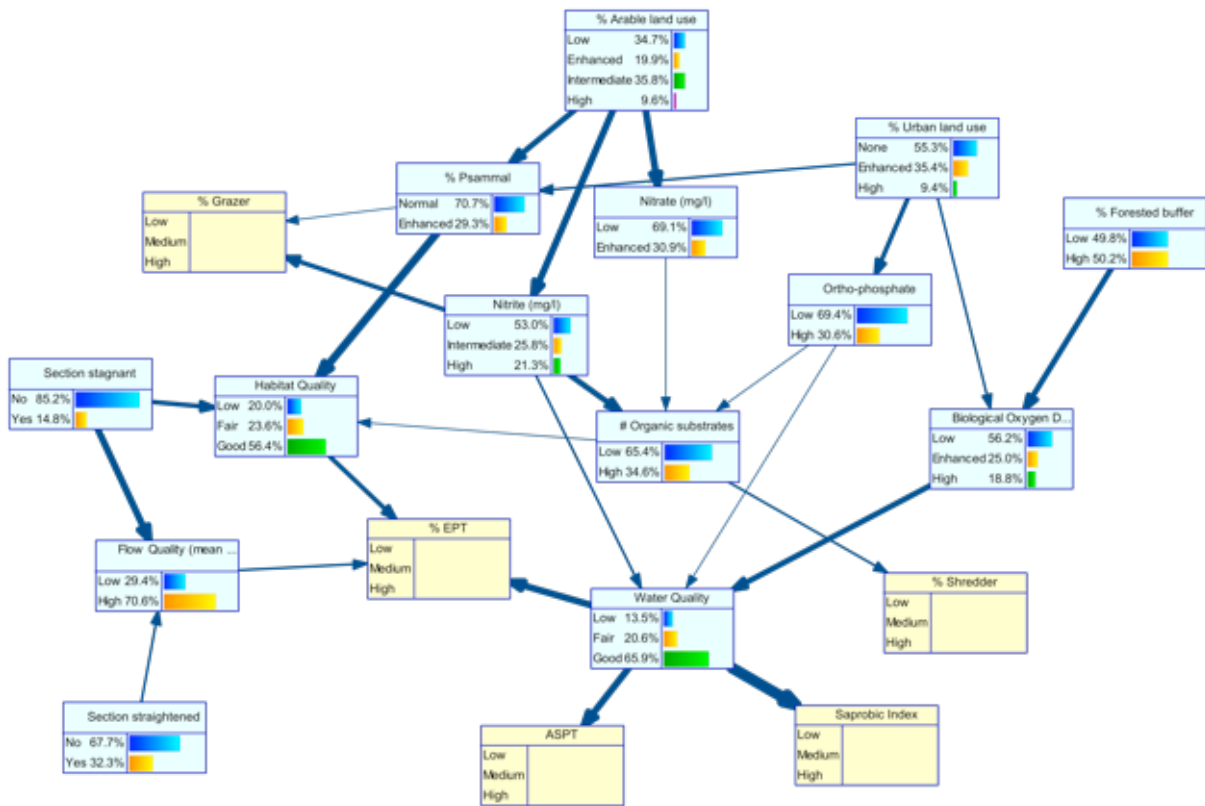


Figure 6: Bayesian Network of catchment-scale causes of deterioration in sand-bottom lowland rivers based on macrozoobenthos metrics (symptom variables, yellow nodes). Because the biological symptoms constitute the entry-nodes for diagnosis, conditional probabilities are not provided for the symptom nodes in the BN. The probabilities of node states in the BN reflect the initial (null) model state based on the underlying dataset of 144 samples of this stream type. For example, % arable land use was low in 34.7 % of the data, enhanced in 19.9 % and so on. Based on the user's entry of biological symptoms (= metric states, yellow nodes), the probabilities of the nodes states change, and it is these changes (compared to the null model) that indicate the changes in the probability of each individual cause variable (e.g., land uses, nutrient variables) to be responsible for the biological symptoms.

Table 4: Conditional probabilities of nodes of the catchment-scale BN of deterioration in sand-bottom lowland rivers based on macrozoobenthos metrics (symptoms).

Flow Quality

Stagnant	Straightened	Low Quality	High Quality
No	No	16	84
No	Yes	35	65

Stagnant	Straightened	Low Quality	High Quality
Yes	No	75	25
Yes	Yes	75	25

% Psammal (sand)

% Urban land use	% Arable land use	Normal ($\leq 90\%$)	Enhanced ($> 90\%$)
No (0)	Low (< 10)	95	5
No (0)	Enhanced (10–20)	75	25
No (0)	Intermediate ($> 20-40$)	65	35
No (0)	High (> 40)	60	40
Enhanced ($> 0-10$)	Low (< 10)	90	10
Enhanced ($> 0-10$)	Enhanced (10–20)	60	40
Enhanced ($> 0-10$)	Intermediate ($> 20-40$)	50	50
Enhanced ($> 0-10$)	High (> 40)	30	70
High (≥ 10)	Low (< 10)	80	20
High (≥ 10)	Enhanced (10–20)	50	50
High (≥ 10)	Intermediate ($> 20-40$)	40	60
High (≥ 10)	High (> 40)	20	80

Habitat Quality

No. Org. Subst.	% Psammal	Stagnant	Low	Fair	Good
Low (≤ 3)	Normal (≤ 90)	No	10	20	70

No. Org. Subst.	% Psammal	Stagnant	Low	Fair	Good
Low (≤ 3)	Normal (≤ 90)	Yes	20	30	50
Low (≤ 3)	Enhanced (> 90)	No	30	40	30
Low (≤ 3)	Enhanced (> 90)	Yes	70	20	10
High (> 3)	Normal (≤ 90)	No	5	5	90
High (> 3)	Normal (≤ 90)	Yes	50	30	20
High (> 3)	Enhanced (> 90)	No	50	40	10
High (> 3)	Enhanced (> 90)	Yes	60	30	10

Nitrate concentration

% Arable land use	Low (≤ 20 mg/l)	Enhanced (> 20 mg/l)
Low (≤ 10)	90	10
Enhanced ($> 10-20$)	75	25
Intermediate ($> 20-40$)	60	40
High (> 40)	20	80

Nitrite concentration

% Arable land use	Low (≤ 0.05 mg/l)	Intermediate ($> 0.05-0.1$ mg/l)	High (> 0.1 mg/l)
Low (≤ 10)	75	20	5
Enhanced ($> 10-20$)	50	30	20
Intermediate ($> 20-40$)	40	30	30

% Arable land use	Low (≤ 0.05 mg/l)	Intermediate ($>0.05-0.1$ mg/l)	High (>0.1 mg/l)
High (>40)	25	45	30

ortho-Phosphate concentration

%Urban	Low (≤ 100 μ g/l)	High (>100 μ g/l)
Non (0)	80	20
Enhanced ($>0- <10$)	60	40
High (≥ 10)	40	60

BOD₅

% Urban land use	% Forest buffer	Low (<2 mg/l)	Slight ($2-3$ mg/l)	Severe (>3 mg/l)
Non (0)	Low (<30)	75	20	5
Non (0)	High (≥ 30)	50	25	25
Enhanced ($>0- <10$)	Low (<30)	70	20	10
Enhanced ($>0- <10$)	High (≥ 30)	30	30	40
High (>10)	Low (<30)	50	30	20
High (>10)	High (≥ 30)	30	50	20

Number of organic substrates

o-PO ₄	Nitrite	Nitrate	# org. Subst. (≤ 3)	# org. Subst. (>3)
Low (≤ 100)	Low (≤ 0.05)	Low (≤ 20)	60	40
Low (≤ 100)	Low (≤ 0.05)	Enhanced (>20)	10	90
Low (≤ 100)	Intermediate ($>0.05-0.1$)	Low (≤ 20)	50	50

o-PO ₄	Nitrite	Nitrate	# org. Subst. (≤ 3)	# org. Subst. (> 3)
Low (≤ 100)	Intermediate ($> 0.05-0.1$)	Enhanced (> 20)	75	25
Low (≤ 100)	High (> 0.1)	Low (≤ 20)	95	5
Low (≤ 100)	High (> 0.1)	Enhanced (> 20)	95	5
High (> 100)	Low (≤ 0.05)	Low (≤ 20)	60	40
High (> 100)	Low (≤ 0.05)	Enhanced (> 20)	95	5
High (> 100)	Intermediate ($> 0.05-0.1$)	Low (≤ 20)	70	30
High (> 100)	Intermediate ($> 0.05-0.1$)	Enhanced (> 20)	90	10
High (> 100)	High (> 0.1)	Low (≤ 20)	90	10
High (> 100)	High (> 0.1)	Enhanced (> 20)	95	5

Water Quality

Nitrite	o-PO ₄	BOD ₅	Low	Fair	Good
Low (≤ 0.05)	Low (≤ 100)	Low (≤ 2)	5	5	90
Low (≤ 0.05)	Low (≤ 100)	Slight ($> 2-3$)	10	30	60
Low (≤ 0.05)	Low (≤ 100)	Severe (> 3)	15	25	60
Low (≤ 0.05)	High (> 100)	Low (≤ 2)	10	10	80
Low (≤ 0.05)	High (> 100)	Slight ($> 2-3$)	15	35	50
Low (≤ 0.05)	High (> 100)	Severe (> 3)	20	40	40
Intermediate ($> 0.05-0.1$)	Low (≤ 100)	Low (≤ 2)	10	10	80
Intermediate ($> 0.05-0.1$)	Low (≤ 100)	Slight ($> 2-3$)	15	35	50

Nitrite	o-PO ₄	BOD ₅	Low	Fair	Good
Intermediate (>0.05–0.1)	Low (≤100)	Severe (>3)	20	40	40
Intermediate (>0.05–0.1)	High (>100)	Low (≤2)	15	15	70
Intermediate (>0.05–0.1)	High (>100)	Slight (>2–3)	20	40	40
Intermediate (>0.05–0.1)	High (>100)	Severe (>3)	25	45	30
High (>0.1)	Low (≤100)	Low (≤2)	15	15	70
High (>0.1)	Low (≤100)	Slight (>2–3)	20	40	40
High (>0.1)	Low (≤100)	Severe (>3)	25	45	30
High (>0.1)	High (>100)	Low (≤2)	20	20	60
High (>0.1)	High (>100)	Slight (>2–3)	25	45	30
High (>0.1)	High (>100)	Severe (>3)	30	50	20

% EPT taxa

Water Quality	Habitat Quality	Flow Quality	Low (<20%)	Medium (20–60%)	High (>60%)
Low	Low	Low (≤0.2)	90	5	5
Low	Low	High (>0.2)	85	10	5
Low	Fair	Low (≤0.2)	80	15	5
Low	Fair	High (>0.2)	75	15	10
Low	Good	Low (≤0.2)	75	15	10
Low	Good	High (>0.2)	70	20	10
Fair	Low	Low (≤0.2)	60	30	10

Water Quality	Habitat Quality	Flow Quality	Low (<20%)	Medium (20–60%)	High (>60%)
Fair	Low	High (>0.2)	50	30	20
Fair	Fair	Low (<=0.2)	40	30	30
Fair	Fair	High (>0.2)	30	40	30
Fair	Good	Low (<=0.2)	30	40	30
Fair	Good	High (>0.2)	20	40	40
Good	Low	Low (<=0.2)	40	30	30
Good	Low	High (>0.2)	30	40	30
Good	Fair	Low (<=0.2)	30	50	20
Good	Fair	High (>0.2)	20	40	40
Good	Good	Low (<=0.2)	20	30	50
Good	Good	High (>0.2)	5	15	80

ASPT

Water Quality	Low (<5)	Medium (5–6.5)	High (>6.5)
Low	80	20	0
Fair	60	40	10
Good	20	30	50

Saprobic Index

Water Quality	Low (>2.5)	Medium (2–2.5)	High (<2)
Low	90	10	0
Fair	50	40	10

Water Quality	Low (>2.5)	Medium (2–2.5)	High (<2)
Good	5	15	80

% Shredder

# Organic Substrates	Low (<20%)	Medium (20–40%)	High (>40%)
Low (≤ 3)	60	20	20
High (>3)	40	30	30

% Grazer

% Psammal	Nitrite (mg/l)	Low (<5)	Medium (5–15)	High (>15)
Normal (≤ 90)	Low (≤ 0.05)	15	30	55
Normal (≤ 90)	Intermediate (>0.05–0.1)	20	50	30
Normal (≤ 90)	High (>0.1)	25	70	5
Enhanced (>90)	Low (≤ 0.05)	20	50	30
Enhanced (>90)	Intermediate (>0.05–0.1)	25	60	15
Enhanced (>90)	High (>0.1)	25	50	25

Step 8: Validation

Model validation is considered a crucial step towards the finalisation of Bayesian Networks (BN). Model validation aims to estimate the reliability of a BN. The validation of BNs is usually based on real datasets (e.g., generated through field sampling) that provide values (= evidence) of all variables (nodes) included in the model. This procedure is referred to as evidence-based validation in the following.

BN validation procedures also allow of data gaps, i.e. the values of one or several variables may lack completely in the data or one or several variable's values may lack for a certain case (sample). While case-wise (or complete variable's) deletion would be required for multivariate analysis, BNs can handle these data gaps. It should be noted, however, that the level of uncertainty in the model cannot be accurately estimated with significant data gaps in the validation data.

Another validation approach refers to the use of validation statistics. This approach does not require evidence cases (i.e. samples with real data), but uses internal model statistics to estimate, for example, the sensitivity of each node. In the following, the results of both validation approaches are provided. The validation was deployed using Genie 2.1 and Netica 5.23.

- For evidence-based validation, a dataset of 47 streams of the same stream type was used. The dataset contains the same variables as were used for the BN development, which allowed to simply import the data into the software and then run the validation. This procedure checks to what degree the conditional probabilities of the BN are reflected by the validation data. More specifically, each node's state is checked for the current assignment to all other related node's states. The degree of mismatch between the change of conditional probabilities of all nodes in the null BN model and in the validation data is then used to estimate the concordance between both. Evidence-based validation is probably the most powerful (and also honest) way to validate a BN. This procedure is available with both Genie (Diagnosis > Validate) and Netica (Cases > Test With Cases), but in the following the Genie procedure is used because of its more advanced user menu that provides more options to generate validation statistics. Here, evidence-based validation was performed using GeNie v2.1.
- Sensitivity-based validation: Sensitivity refers to the degree of case-wise influences of each node on each other node in the BN. In other words, sensitivity (in %) describes, how much a given node is influenced by a change of any other related node in the model. The more sensitive a node is, the more is its inference sensitive to a single state (i.e. an evidence case) of another node. This step allows to identify highly influential nodes in the model. Influential nodes determine the outcome more than less-influential nodes, which is why a developer may wish to revise highly influential nodes as to the number of state and state thresholds of such nodes. Here, sensitivity-based validation was performed using NETICA v5.23.

Evidence-based validation

Altogether, data from 47 stream sites (i.e. evidence cases) were available for validation. The dataset originates from the STAR project (www.eu-star.ac.at) and comprises macroinvertebrate metrics and environmental parameters from Germany, Denmark, UK and Sweden (Furse *et al.* 2006). While the Swedish sites are deemed most comparable to the lowland stream type considered, the Danish and UK sites might be slightly different as to the dominant mineral substrates on the stream bottom (sand in DE and SE, gravel in DK and UK). In particular the UK sites are characterised by more pebbles and cobbles on the stream bottom.

Validation is quite straightforward if using Genie v2.1. The tabular matrix of sites/samples (in rows) and environmental parameters (= node variables, in columns) is converted into a .txt/.csv file and opened within the GeNie project containing the BN. The validation procedure requires the allocation of variables in the BN to those in the validation dataset. In case there is a mismatch of variable names and/or state names/state numbers, GeNie asks for cor-

rection. Allocations are possible during the validation procedure. The output of this procedure contains an estimate of the accuracy of the whole BN (expressed as % matching node states) as well as of individual nodes and states. This accuracy estimate is based on the confusion matrix of correctly modelled states against actual validation states. The confusion matrix compares the correct and incorrect allocations as true and false positives, and true and false negatives.

Overall, the catchment-scale BN's accuracy was modest, with two thirds of the nodes states (67.8% = 446 out of 658 states correctly allocated. Yet, the accuracy of individual nodes was much better, as shown for selected nodes in Tab. 5.

Table 5: BN nodes with an accuracy >75% in the BN model. Accuracy was generated through Genie's validation procedure.

Node name	Accuracy (%)
Nitrate	77
Psammal	83
Straightened	81
Stagnant	87
Dams	87
Shredder	85
Saprobic Index	79

The confusion matrix underlying the accuracy calculation suggests merging states in some cases, for example, if two states refer to "very low" and "low", which cannot be sufficiently distinguished by the model. Merging both states into "low" thus might help significantly increase the accuracy of a node. Candidates for mergers are shown in Tab. 6.

Table 6: Candidate nodes and states for merging, to increase accuracy.

Node name	Suggested merger
% Arable land use	Combine states enhanced & Intermediate

Sensitivity-based validation

For this step, no evidence was defined in the BN, so that all calculations are based on the "null" BN. The results are listed in Tab. 7 and should read as follows: Each row's node is sensitive to a single evidence case of a node in the columns. The % value indicates, how sensitive the row nodes are to the column nodes. In other words, an evidence item for a column node does influence the row node's posterior belief by x%. With regard to the metrics, the sensitivity analysis reveals several metrics (symptoms) to be fairly sensitive to a particular environmental variable (cause), which may help identify stressor-specific (or stressor group-specific) metrics.

Table 7: Sensitivity matrix of nodes in the catchment-scale BN. Sensitivity values indicate the degree to which a row node is influenced by a change of the nodes in the columns. For instance, the influence of percent sand on the stream bottom (%Psammal) on the habitat quality (HabitatQ) is 18%.

	#OrgSub	%Arable	%Forest	%Psammal	%Urban	BOD5	FlowQ	HabitatQ	Nitrate	Nitrite	P	Stagnant	Straight	WaterQ
# Organic substrates	100	0	0	0	0	0	0	1	0	6	2	0	0	0
% Arable land use	1	100	0	12	0	0	0	2	17	8	0	0	0	0
% Forested buffer	0	0	100	0	0	6	0	0	0	0	0	0	0	1
% Psammal	0	6	0	100	2	0	0	11	2	1	0	0	0	0
% Urban land use	0	0	0	3	100	2	0	0	0	0	7	0	0	0
Biological Oxygen Demand	0	0	8	0	2	100	0	0	0	0	0	0	0	8
Flow Quality (mean veloc)	0	0	0	0	0	0	100	1	0	0	0	18	2	0
Habitat Quality	1	1	0	18	0	0	1	100	0	0	0	7	0	0
Nitrate (mg/l)	0	8	0	2	0	0	0	0	100	1	0	0	0	0
Nitrite (mg/l)	10	6	0	1	0	0	0	0	2	100	0	0	0	2
P	2	0	0	0	4	0	0	0	0	0	100	0	0	1
Section stagnant	0	0	0	0	0	0	13	3	0	0	0	100	0	0
Section straightened	0	0	0	0	0	0	2	0	0	0	0	0	100	0
Water Quality	0	0	1	0	0	7	0	0	0	2	1	0	0	100
% EPT	0	0	0	2	0	1	3	5	0	0	0	2	0	12
% Grazer	1	1	0	2	0	0	0	0	0	5	0	0	0	0
% Shredder	3	0	0	0	0	0	0	0	0	0	0	0	0	0
ASPT	0	0	0	0	0	2	0	0	0	0	0	0	0	19
Saprobic Index	0	0	0	0	0	3	0	0	0	1	1	0	0	41

The sensitivity analysis revealed a number of important inferential relationships in the models, however, the majority of sensitivity values are below 5%. At the catchment scale, % sand, nitrate (and nitrite) content and flow (stagnation) are the three most influential nodes in the network (Tab. 8). These nodes also refer the flow, habitat and water quality. The most responsive metrics in the model are % EPT taxa, Average Score Per Taxon and Saprobic Index (Tab. 7 and 8), which may point at the capability of the catchment-scale model to diagnose water quality deterioration due to point-source and diffuse-source pollutions in course of urban and arable land use. Besides, % EPT is known to respond to hydromorphological deterioration, for example, in course of habitat and flow modifications.

Table 8: Most influential environmental variables in the BN.

Variable name	Influential
Nitrate	x

Nitrite	x
Stagnation	x
Fine sediment content	x
Most responsive metrics	% EPT, ASPT, SI

Macrozoobenthos diagnostic examples

A fully-functional interactive tool of the macrozoobenthos diagnostic BN will be made available online soon. The tool will be implemented based on R (R Core Team 2017) and Shiny (R Studio Inc. 2017). Its description and technical implementation is given in Chapter 3 "Diagnostic Tool". Additional diagnostic prototypes will be developed by the end of the MARS project and will be made available through the Freshwater Information Platform (FIP) at <http://www.freshwaterplatform.eu> under "Freshwater Multi-Stressor Tools".

Case 2: Diagnosing the origin of phytoplankton deterioration in large sand-bottom lowland rivers—an example from River Elbe

Eutrophication through diffuse sources (e.g., agriculture) constitutes a major pressure of lowland river basins in central Europe. The surplus of nitrogen and phosphorous provided by intensive agriculture imposes a major threat on lotic ecosystem's ecological quality. While eutrophication impacts on lotic biology are usually assessed and monitored with aquatic macrophytes and benthic diatoms, these biological quality elements are replaced by phytoplankton in large rivers. Because of the depth and increasing turbidity (also caused by phytoplankton) of large rivers, the availability of light for plants attached to the river bottom is limited.

In contrast to benthic macrophytes and diatoms, however, river phytoplankton is constantly moving downstream. Hence, the presence of a phytoplankton problem, for example, indicated by a moderate or worse phytoplankton ecological quality at a given water body, does not necessarily translate to a cause of the problem situated in that water body. The phytoplankton may be "imported" from a water body situated further above in the catchment.

In the following, we present a tool to diagnose the location of the cause of a phytoplankton problem in large sand-bottom lowland rivers of central Europe. More specifically, the diagnostic Bayesian Network (BN) attempts to identify, whether nutrient and other environmental conditions at a given water body do promote a phytoplankton problem or not. If not, the model indicates the problem is likely to be originated further above in the river continuum.

As opposed to the previously described Case 1, this example of the development of a Bayesian Network for diagnostic purposes is not driven by data, but by knowledge from river phytoplankton experts. This knowledge was obtained during an expert workshop and further translated into knowledge rules, to build the basis of the BN.

Data

The "data" used for the development of the phytoplankton diagnostic BN comprises a set of knowledge rules. These knowledge rules are based on the results of phytoplankton monitoring in large rivers (Mischke *et al.* 2011). More specifically, the following rules were defined:

- Stagnant water bodies: reduced flow and stagnant flow conditions promote phytoplankton growth in general, through various influences on nutrient concentrations and water temperature. Hence, stagnant and non-stagnant water bodies must be diagnosed separately.
- Total phosphorous (TP) concentration: TP can limit phytoplankton growth, if the concentration falls below a threshold. This threshold is different for stagnant and non-stagnant water bodies.
- Alike, dissolved inorganic nitrogen (DIN) can limit phytoplankton growth, if the concentration falls below a threshold. Again, this threshold is different for stagnant and non-stagnant water bodies.

- A high specific runoff rate for a given water body can limit phytoplankton growth through dilution. The threshold for limiting conditions does not differ between stagnant and non-stagnant water bodies.
- Flood events during the phytoplankton reproduction period (April–October) can limit phytoplankton growth, through enhanced flow conditions, increasing turbidity and dilution. The threshold for limiting conditions does not differ between stagnant and non-stagnant water bodies.
- Phytoplankton growth is enhanced in warm water and reduced in cold water. The threshold for limiting conditions does not differ between stagnant and non-stagnant water bodies.
- Riparian shade can limit phytoplankton growth. The threshold for limiting conditions does not differ between stagnant and non-stagnant water bodies.
- Phytoplankton growth can be limited by river channel width. The threshold for limiting conditions does not differ between stagnant and non-stagnant water bodies.

Bayesian Network development

The development of the phytoplankton diagnostic BN started with the draft of a conceptual model, to structure the knowledge rules and to visualise the cause-effect relationships between the phytoplankton assessment (symptom) and the environmental variables (cause nodes). The structure was then implemented in NETICA v.5.23, to visualise the BN and to prepare the population of the network with conditional probabilities. This step was followed by the definition of thresholds for each knowledge rule. After translating the thresholds into node states for each environmental variable, the node's conditional probability tables (CPTs) were populated. Finally, the resulting diagnostic BN was checked for validity by experts. No data was used to further validate the BN.

Step 1: Conceptual model

The conceptual model contains eight causal nodes and one symptom (phytoplankton) node (Fig. 1).



Figure 1: Conceptual model of the phytoplankton diagnostic BN. Nodes are coloured according to their relevance for eutrophication (red), dilution effects (dark blue), and accompanying environmental parameters (light blue).

The nodes for TP and DIN are connected to stagnant flow conditions, because nutrient thresholds are deemed to differ between stagnant and free-flowing river sections. The same applies to channel width, which is related to the maximum amount of riparian shade reaching the river channel. Although the BN looks simple, there is a challenge to populate the conditional probabilities for the phytoplankton node. There are seven arrows already pointing at that node, which would already translate to $2^7 = 128$ combinations of states, with only two-state nodes. This is already way too much for a sound and reliable BN. Therefore, the model was further simplified by the inclusion of intermediate nodes (Fig. 2). The nutrient-relevant nodes are linked to a node "N/P limitation", which summarises the probability that DIN and/or TP conditions are limiting and thus cannot cause phytoplankton growth in the water body. The hydrological (dark-blue nodes in Fig. 1) are linked to a node "Hydrological limitation" that summarises the probability of hydrological dilution effects to be present in the water body and thus limit phytoplankton growth. Eventually, the accompanying parameters (light-blue nodes in Fig. 1) are linked to the intermediate node "Water body type sensitive", to summarise the probability of these parameters to promote phytoplankton growth at a given water body.

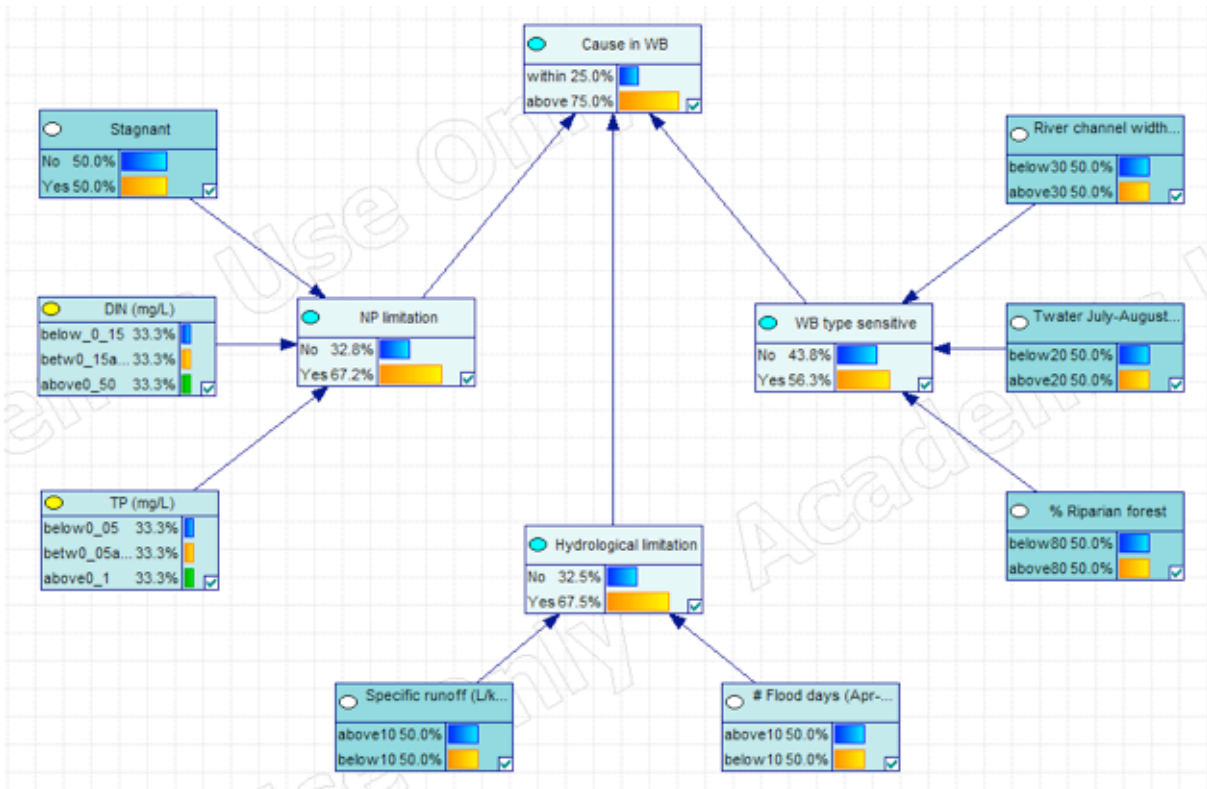


Figure 2: Simplified phytoplankton diagnostic BN with three intermediate variables, implemented in GeNie v2.1. The diagram already contains the node states and the thresholds defined for each state. Causal nodes are coloured dark-blue, while intermediate and terminal nodes are light-blue. The introduction of intermediate nodes keeps the number of conditional probabilities handy. The terminal node gives the probability of the phytoplankton problem's cause being located in the given water body.

Step 2: Defining thresholds for node states

Except for the two nutrient nodes, all other nodes are two-state nodes (Tab. 1). The thresholds were set based on the values that were reported during the expert workshop. These expert's estimates in turn are based on their individual data sets and long-term monitoring results.

Table 1: Thresholds to defined node states for the phytoplankton diagnostic BN.

Node name	State 1 (low)	State 2 (intermediate)	State 3 (high)
Water body stagnant	No	Yes	
Dissolved Inorganic Nitrogen (DIN) (mg/l)	<0.15	0.15–0.5	>0.5
Total Phosphorous (TP) ($\mu\text{g/l}$)	<0.05	0.05–0.1	>0.1
Specific runoff rate ($\text{l/km}^2 \cdot \text{s}$)	≤ 10	>10	
No. of flood days (Apr–Oct)	≤ 10	>10	
Channel width (m)	≤ 30	>30	
Maximum Water temperature (Jul–Aug) ($^{\circ}\text{C}$)	≤ 20	>20	
Riparian forest (shade) (%)	≤ 80	>80	

Step 3: Defining conditional probabilities

Due to the inclusion of intermediate nodes, it was possible to keep the CPTs handy (Tab. 2). At the same time, it was possible to develop a single model for both stagnant and free-flowing conditions.

N or P limitation

Table 2: Conditional Probability Tables (CPTs) of the phytoplankton diagnostic BN.

WB stagnant	DIN (mg/l)	TP ($\mu\text{g/l}$)	No	Yes

WB stagnant	DIN (mg/l)	TP ($\mu\text{g/l}$)	No	Yes
No	<0.15	<0.05	1	99
No	<0.15	0.05–0.1	5	95
No	<0.15	>0.1	10	90
No	0.15–0.5	<0.05	5	95
No	0.15–0.5	0.05–0.1	10	90
No	0.15–0.5	>0.1	20	80
No	>0.5	<0.05	10	90
No	>0.5	0.05–0.1	20	80
No	>0.5	>0.1	90	10
Yes	<0.15	<0.05	1	99
Yes	<0.15	0.05–0.1	5	95
Yes	<0.15	>0.1	10	90
Yes	0.15–0.5	<0.05	5	95
Yes	0.15–0.5	0.05–0.1	90	10
Yes	0.15–0.5	>0.1	95	5
Yes	>0.5	<0.05	20	80
Yes	>0.5	0.05–0.1	95	5
Yes	>0.5	>0.1	99	1

Hydrological limitation

Specific runoff	No. of flood days (Apr–Oct)	No	Yes
-----------------	-----------------------------	----	-----

Specific runoff	No. of flood days (Apr–Oct)	No	Yes
≤10	≤10	1	99
>10	>10	10	90
No	≤10	20	80
No	>10	99	1

WB type sensitive

River channel width (m)	Max. water temperature (Jul–Aug) (°C)	% Riparian forest	No	Yes
≤30	≤20	≤80	90	10
≤30	≤20	>80	95	5
≤30	>20	≤80	40	60
≤30	>20	>80	30	70
>30	≤20	≤80	30	70
>30	≤20	>80	40	60
>30	>20	≤80	5	95
>30	>20	>80	20	80

Cause in water body

WB type sensitive	N/P limitation	Hydrological limitation	Within WB	Above WB
No	No	No	90	10
No	No	Yes	20	80
No	Yes	No	5	95

WB type sensitive	N/P limitation	Hydrological limitation	Within WB	Above WB
No	Yes	Yes	1	99
Yes	No	No	95	5
Yes	No	Yes	80	20
Yes	Yes	No	10	90
Yes	Yes	Yes	5	95

Phytoplankton diagnostic examples

A draft online diagnostic tool is available at https://www.hed.cc/?s=MARSpp&t=BN_PP2. The tool (Fig. 3) allows the user to enter the states of several potentially causal variables (radio buttons in Fig. 3) based on his/her observations at a water body. Based on the user's entries, the underlying BN calculates the probability of a cause being located in the water body. The probability is displayed by a blue bar on top of a grey bar, the latter of which indicates the initial probability of the null model. The difference between both bars shows the changes in the probability based on the user's indications (Fig. 4).

Figure 4 shows an example with indications only for TP, DIN and stagnant flow conditions.

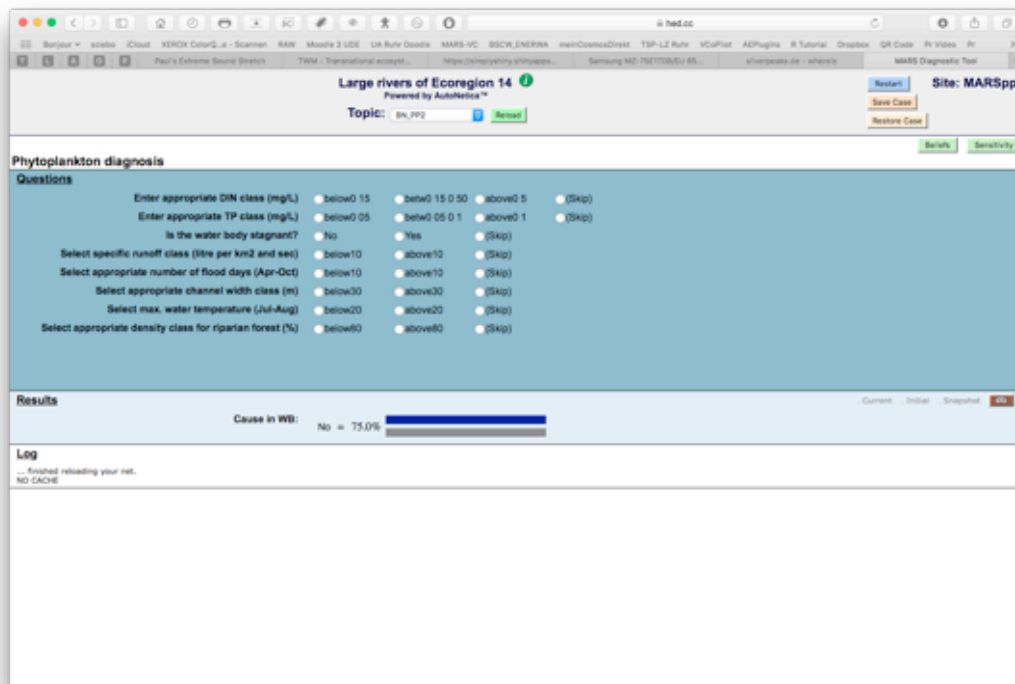


Figure 3: Screenshot of the draft diagnostic tool implemented in Auto NETICA. A more user-friendly version of the tool with information on causes and effects will be made available by the end of the MARS project. The screenshot shows the null model, without any indication by the user. Based on the null model, the initial probability of the problem to be located within the water body is 25%.

Figure 4: Screenshot of the draft phytoplankton BN, with indications for intermediate TN and DIN concentrations and of stagnant flow conditions. This results in a 60.3% probability (i.e. 35.3% increase from the initial null value of 25%) of the problem located within the given water body.

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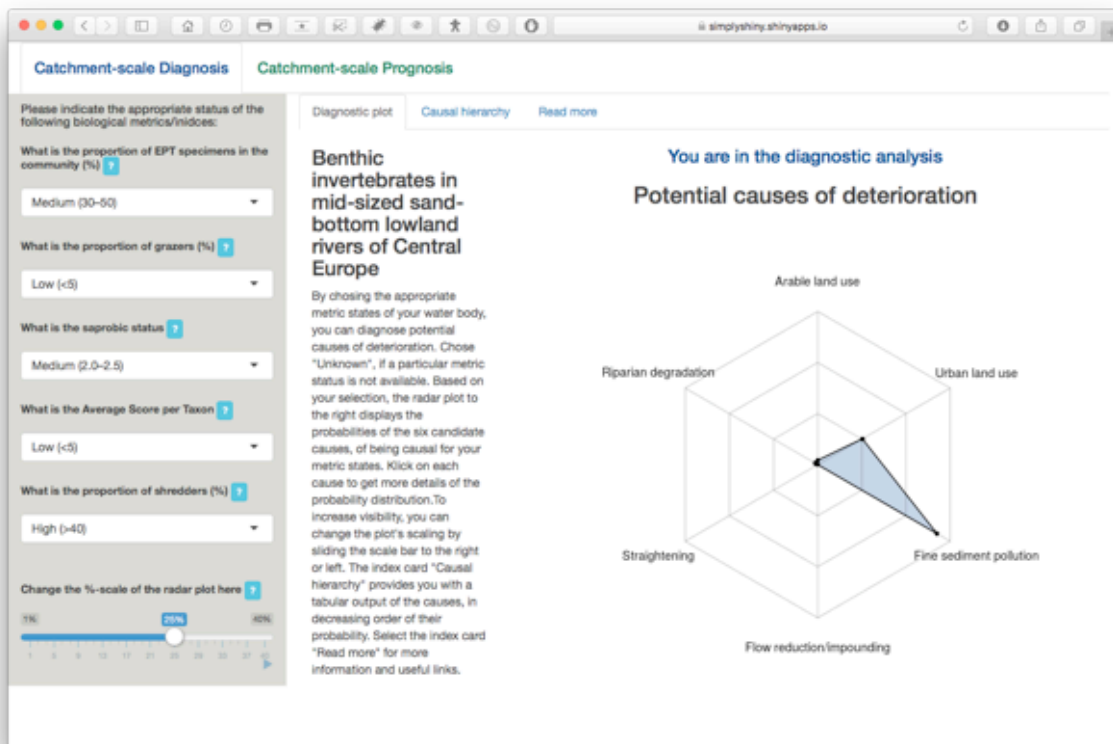
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Helpful online documentations

- NETICA online tutorial: http://www.norsys.com/tutorials/netica/nt_toc_A.htm
- NETICA user guide: https://norsys.com/downloads/old_versions/NeticaMan_Win_105.pdf
- NETICA online help: http://www.norsys.com/WebHelp/NETICA/X_Welcome.htm
- Genie online help: <http://support.bayesfusion.com/docs/genie/hello.html>
- GeNie documentation: <http://support.bayesfusion.com/docs/>

The MARS Diagnostic Tool (DTool)

A tool to diagnose the causes of deterioration of water bodies



Note: The Help buttons (?) and weblinks provided by the Diagnostic Tool are not fully functional on Apple's Macintosh computers running OS10.9 or higher in combination with Safari and Firefox. Using Google's Chrome instead on Macs seems to be a suitable workaround for this problem.

Summary

Bayesian (Belief) Networks (BNs) provide the statistical foundation to infer the probability of a particular variable's state conditional on the states of other variables. This renders BNs useful for the diagnosis of causes of deterioration based on the states of selected response (symptom) variables.

Here, we present a web-based interactive tool, to diagnose the causes of deterioration of a particular river water body. The Diagnostic Tool (DTool) builds upon a BN that was developed to diagnose the probability with which catchment-scale causes of deterioration (e.g., land use) are responsible for the deterioration of selected biological (symptom) metrics. The BN was developed using environmental and macrozoobenthos data sampled at mid-sized sand-bottom lowland rivers in central Europe.

The DTool is implemented in Shiny, a freeware graphical user interface that interactively links to the freeware statistical software program R. While R provides the core to calculate the posterior probabilities of the BN, Shiny provides the interface to enter data (evidence) and to display the results. Although the example DTool is applicable only for the river type mentioned above, the general framework of the implementation is transferable to other cases.

Introduction

An approach to diagnose the causes of deterioration of lotic water bodies is presented in Chapter 2. The approach is based on Bayesian (Belief) Networks and allows to diagnose the causes of deterioration based on a selection of biological (symptom) variables. As such, the approach is similar to clinical (medical) diagnosis: a doctor comes up with a diagnosis of the causes of a disease based on the patient's symptoms.

Here, the patient is the water body of interest, which suffers from multiple pressures (causes of deterioration). The symptoms are equivalent to the biological (assessment) metrics obtained for the water body (e.g., biological and ecological traits, community structural and functional indices). Hence, the approach to diagnose surface water bodies is similar to clinical diagnosis; based on the values of several diagnostic (symptom) metrics, the Bayesian Network (BN) generates the probabilities of potential causes (pressure variables) to be ultimately causal for the combinations symptoms.

The advantage of BNs is that they can build the basis for web-based queries, where a user is asked to indicate the status of several symptom variables (e.g., results of the biological quality assessment) and the underlying BN then allows to calculate the probability of a set of causes. Thus, it is possible to implement BNs as web doctors, i.e. Diagnostic Tools to help identify the causes of deterioration of water bodies.

Here, we present such a Diagnostic Tool (DTool). The DTool is based on the macrozoobenthos example (Case 1) presented in Chapter 2 and allows to diagnose a selection of catchment-scale causes of deterioration of mid-sized sand-bottom lowland rivers in central Europe. The application of this specific DTool example is restricted to the given water body type, because both causes and symptoms are water body type-specific; they are likely to change from sand-bottom to gravel-bottom streams, from lowland to upland lakes or from Scandinavian to alpine rivers. However, the framework of implementation that is presented in the following allows a user to tailor the DTool based on his/her own specific requirements for and conditions at the water body (type) of interest. As such, Chapter 2 and 3 of this report present a kind of guidance to "cook" your own DTool based on Bayesian Networks.

To support the general applicability of the DTool, it is implemented using free software applications and open-source software, namely GeNie (<https://download.bayesfusion.com/files.html?category=Academia>; free for academic use only), R (R Core Team 2017) and Shiny (R Studio Inc. 2017). GeNie is a graphical user interface (GUI) that allows a user to graphically develop a BN, which is a much more straightforward approach for beginners. However, BNs can also be developed in R, without the use of other software tools.

The BN software application NETICA (<https://www.norsys.com/netica.html>) provides another tool to graphically develop BNs, but this would require the user to purchase the application. Both GeNie and NETICA allow the user to store BNs as .net files, which then can be imported and further processed in R. Our implementation of the DTool builds upon .net files,

generated either using GeNie or NETICA, or any other BN software application that allows to store the BNs as .net files.

Technical implementation of the Diagnostic Tool in R and Shiny

The framework for the implementation of a web-based DTool presented in the following is based on Bayesian Networks (BNs) available as .net files. Details on how to graphically develop a BN using GeNie or NETICA and store the results as .net file are provided in Chapter 2 (Case 1, Step 3).

The implementation consists of three steps:

1. Import the BN into R.
2. Compute posterior probabilities of causes based on the user entries of symptoms (evidence).
3. Develop a graphical user interface in Shiny, to support the user's data entry and to display the results as well as related background information, necessary to understand and interpret the results.

Import the Bayesian Network into R

This step allows to directly import a .net file into R. This step is required to allow the calculation of posterior probabilities in R, which is a prerequisite for the following steps. During the development process, BNs are populated with conditional probabilities (see Chapter 2, Case 1, Step 7). These probabilities are to be estimated separately for each child node by the developer. The result is a null model, i.e. the "empty" BN without any state selected for any (biological) symptom variable. This null model provides the basis to calculate the prior probabilities (short: priors) of the cause variables, i.e. the initial probability of all nodes in the BN without any evidence of a specific symptom. If evidence of symptom is indicated, the BN recalculates the probabilities, which results in posterior probabilities, i.e. the probabilities after the indication of evidence.

R's package `bnlearn` (Scutari 2010) is able to read BNs created, for example, using GeNie as .net files.

```
library(bnlearn)
## Attaching package: 'bnlearn'
## Loading network into R
bnlearn_net <- bnlearn::read.net(file = your_path_to_network_file_with_.net_format)
## Check bnlearn_network
# Call node names
names (bnlearn_net) # Example: Chapter 2, Case 1

 [1] "Arable"      "N"           "Urban"       "Fines"       "Nitrate"
 [6] "Grazer"      "oPO4"        "BufForest"   "BOD5"        "WaterQ"
[11] "OrgMatter"   "Stagnant"    "HabitatQ"    "Straight"     "FlowQ"
[16] "EPT"         "ASPT"        "SI"          "Shredder"
```

Now, the BN has been imported into R. The call of node names allows to check, if all variables have been imported correctly.

Compute posterior probabilities of causes

Once the network is available in the `bnlearn` format, the user may directly compute posterior probabilities by querying the network in `bnlearn` with the use of the `cpquery` function. Although this step is fairly time consuming, it does not lead to the exact posterior probabilities. In order to compute the exact values, we thus recommend using the package `gRain` (Højsgaard 2012) (via package '`gRbase`', Dethlefsen and Højsgaard 2005). Thus, we need to convert the BN into the appropriate format.

```
library(gRbase)
## Attaching package: 'gRbase'
library(gRain)
## Attaching package: 'gRbain'
# Re-format BN as grain format
grain_net <- bnlearn::as.grain(x = bnlearn_net) # re-formats BN
# Compile network
grain_net <- gRbase::compile(object = grain_net) # compiles BN
```

Having the network in the correct format now, we can compute priors and posteriors with the function `querygrain` from package `gRain`. Priors are simply calculated by querying the network without any evidence entered.

```
## Compute prior of '% Fines' (coverage of sand on the stream bottom)
priors <- gRain::querygrain (object = grain_net, nodes = c("Fines", "Grazer"),
type = "marginal")
priors

## $Fines
## Fines
## Normal      Enhanced
## 0.6612729 0.3387271
## $Grazer
## Grazer
## Low          Medium      High
## 0.08563417 0.47169971 0.44266612
```

By setting evidence on the symptom nodes, we can compute the posteriors of the BN.

```
## Compute posterior of 'Straight' (straightening yes/no) considering the fact that
we already know the proportion of 'Grazer' is low
posteriors <- gRain::querygrain (object = grain_net, nodes = c("Fines", "Grazer"),
type = "marginal", evidence = list (Grazer = "Low"), exclude = FALSE)
posteriors # here, the code chunk '(Grazer = "Low")' sets the evidence

## $Fines
## Fines
## Normal      Enhanced
## 0.4351154 0.5648846
```

```
## $Grazer  
## Grazer  
## Low Medium High  
## 1 0 0
```

Hence, by indicating evidence on the % Grazer within the macrozoobenthos community, the prior probabilities of '% Fines' (sand) change from:

```
## Normal Enhanced  
## 0.6612729 0.3387271
```

to:

```
## Normal Enhanced  
## 0.4351154 0.5648846
```

Thus, the evidence of a low proportion of grazers found at a given river site increases the probability that the proportion of sand on the river bottom is enhanced as compared to the reference conditions of the appropriate river type. The causal relationship between the variables is detailed in Chapter 2.

Although R provides a very handy environment to quickly compute the posteriors for all cause variables of a BN, R by no means could be called 'user-friendly' to the untrained person. Therefore, we implemented the BN using Shiny, to provide a user-friendly graphical interface. This Shiny application builds upon the calculations of posteriors as described above, but lets the user set the evidence more intuitively. The posteriors are visualised, so that no further statistical background knowledge is required from the user to apply the application and to understand the outcome. The Shiny application constitutes the core framework for the MARS Diagnostic Tool.

The MARS Diagnostic Tool

Figure 1 shows the entry page of the MARS Diagnostic Tool (DTool), when loaded for the first time. The different sections of the page are highlighted in Fig. 1 and will be explained in the following. The DTool is available at: https://simplyshiny.shinyapps.io/catch_2_spider_plot/.

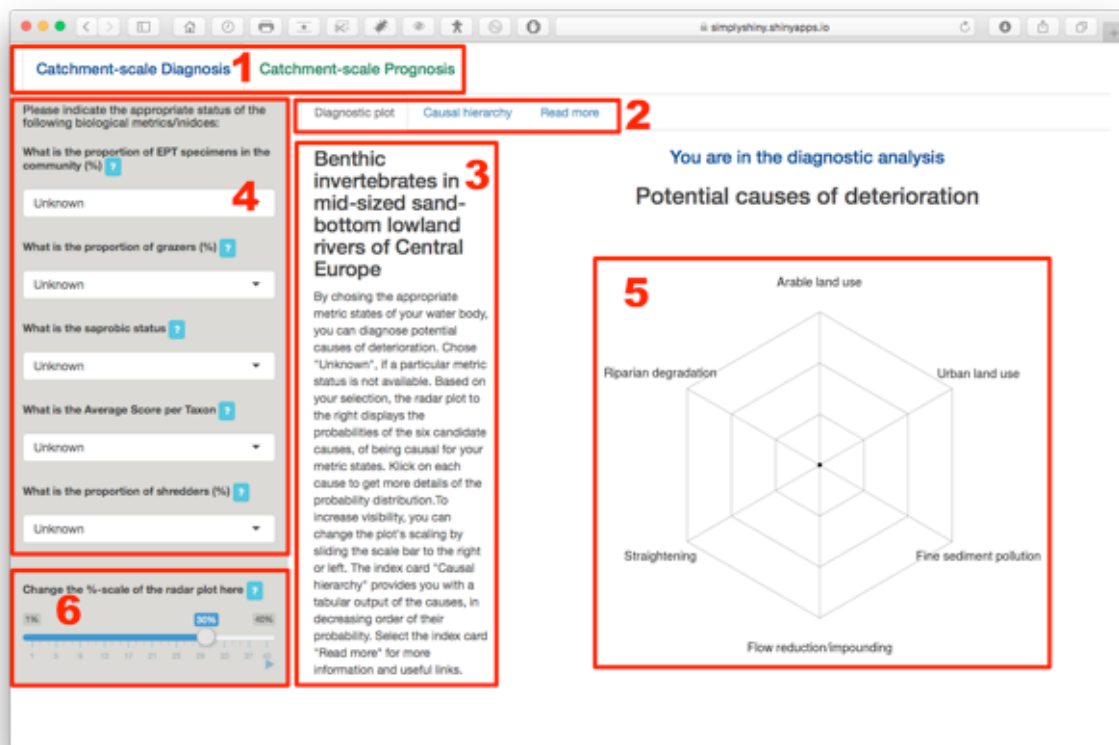


Figure 1: Screenshot of the DTool when loaded from https://simplyshiny.shinyapps.io/catch_2_spider_plot/. By default, the diagnostic page is loaded. See text for the description of the six section marked red.

DTool Section 1

Chose the tabs to switch between the diagnostic and prognostic directions of the tool. While the (default) diagnostic part of the DTool allows to evaluate the causes of deterioration, the prognostic part allows to estimate potential biological deteriorations based on the evidence of catchment-scale pressures. Thus, the prognostic tool constitutes a kind of inverse version of the diagnostic tool.

DTool Section 2

Here, the user can select between the graphical (Diagnostic plot) and tabular display (Causal hierarchy) of the results. The tab 'Read more' provides additional background information on diagnosis and useful links.

DTool Section 3

This column provides general information of the application of the DTool.

DTool Section 4

This section is the major entry section, where the user is asked to set the evidence on selected nodes. The nodes represent the biological symptoms, i.e. the diagnostic metrics and indices of the BN. Each node is introduced by a question, which can be answered using the pull-down menu of the node. If a node's state is unknown, chose 'Unknown' from the list. If a question is unclear, click on the small blue boxes (containing a question mark) on the right, to obtain helpful comments.

Please note that the posterior probabilities become more uncertain, the more nodes are answered 'Unknown'.

DTool Section 5

This radar plot marks the main output area of the DTool. Based on the evidence a user provided, the radar plot summarises the posterior probabilities of all cause variables (Fig. 2). This allows the user to easily identify the potential causes of deterioration of the water body.

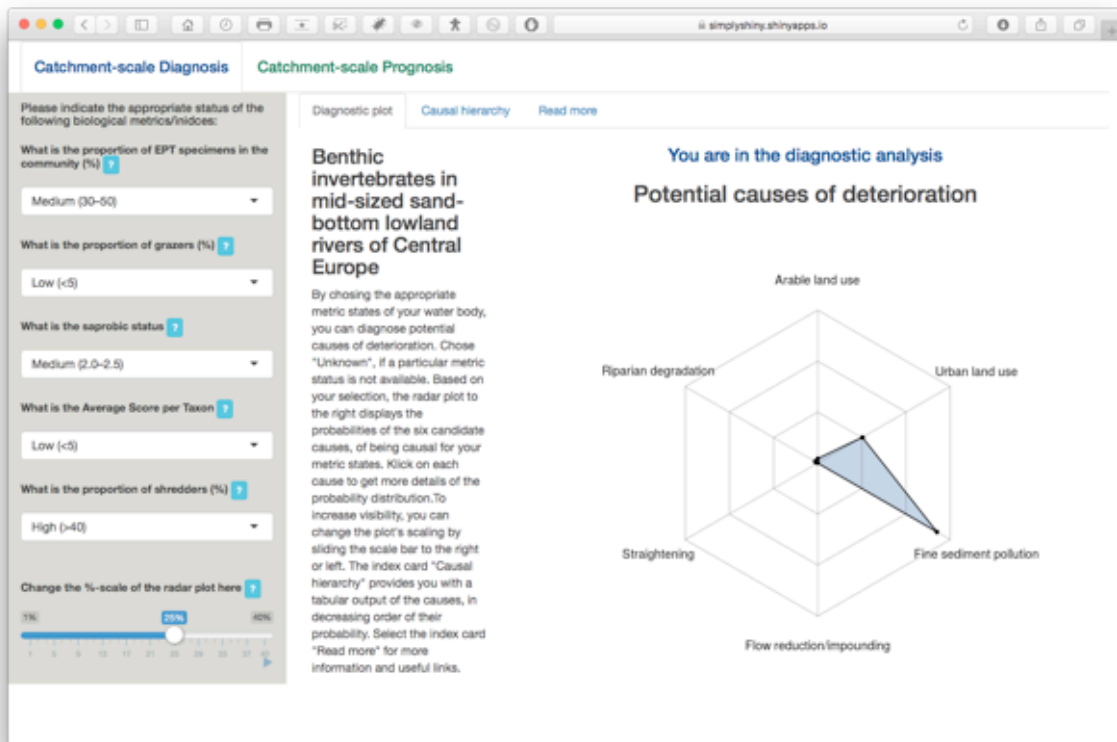


Figure 2: DTool with evidence set for all symptom nodes of the BN. The radar plot summarises the posterior probabilities of the six cause variables in the BN. Accordingly, based on the evidence, there is a high probability of deterioration through an increased coverage of fine sediments (sand) on the river bottom. Also, the probability of deterioration through urban land use increased, although to a lesser degree. The other pressure variables seem not to be causal in this example. The scaling of the radar plot can be adjusted using the slider on the left-bottom side of the window (Section 6 in Fig. 1).

Please note that the posterior probabilities are based on a complex network of causes and effects. As such, they help estimate potential effects of deterioration, but do not provide the user with exact values of the actual impacts that cause the biological deterioration of the water body.

Rather, the user is recommended to continue diagnosis based on the outcome of the DTool. For example, additional data queries of the actual fine sediment coverage on the river bottom or of the influences through urban areas within (and upstream of) the water body can help narrow down the causes of deterioration.

A detailed explanation of the six potential causes as displayed in the radar plot (Fig. 2) can be obtained by clicking on the cause's names. The pop-up window for 'Fine sediment pollution' is exemplarily shown in Fig. 3. Besides potential sources of the problem, management options are given to reduce fine sediment pollution or to mitigate its biological implications. At the bottom, there is a bar plot showing the posterior probabilities for all states of the cause variable. This is redundant with two states only (the value of state 1 is equivalent to the negative value of state 2), but provides additional information for cause variables with >2 states.

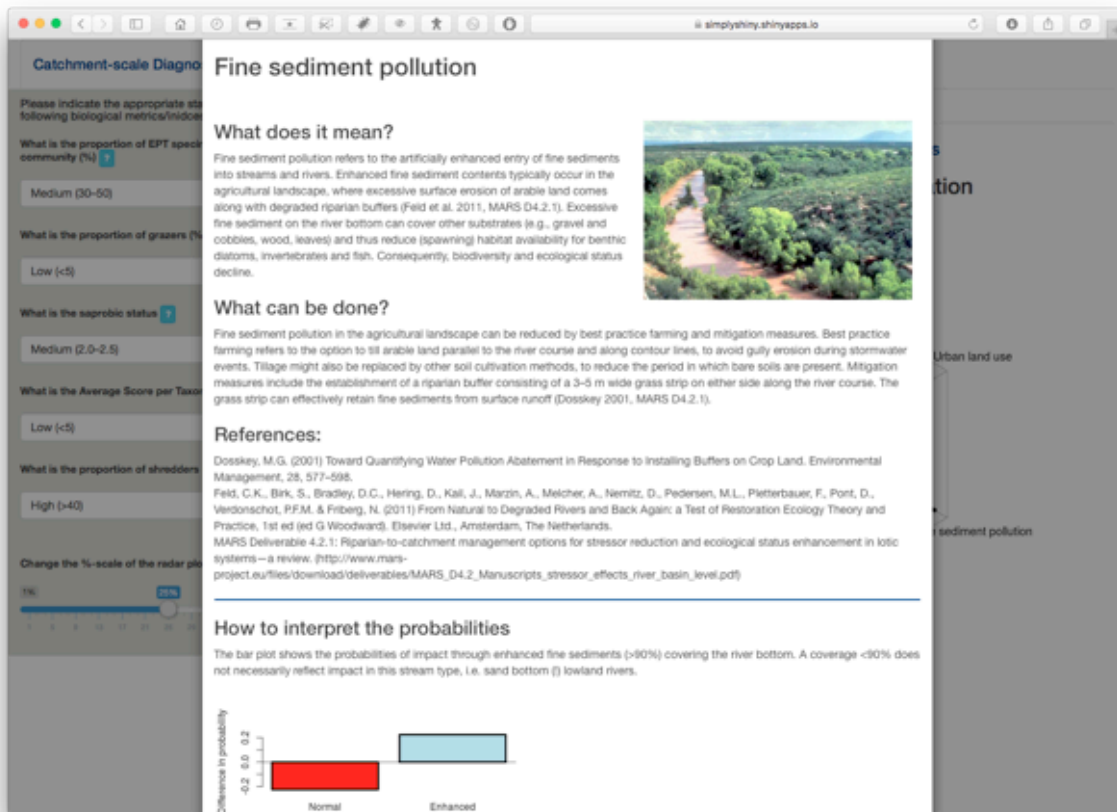


Figure 3: Additional background information and useful references provided for the potential causes of deterioration. The information can be obtained by clicking on the cause's names in the radar plot (Fig. 2).

DTool Section 6

The slider allows the user to adjust the scaling of the radar plot, to better fit the posterior probabilities. By default, the slider is set to 30%, which impedes the visualisation of much smaller values. Slide to the left, in order to display small posteriors.

Causal hierarchy (Section 2)

By choosing this tab, the user can access a tabular output of the posterior probabilities, listed in descending order (Fig. 4).

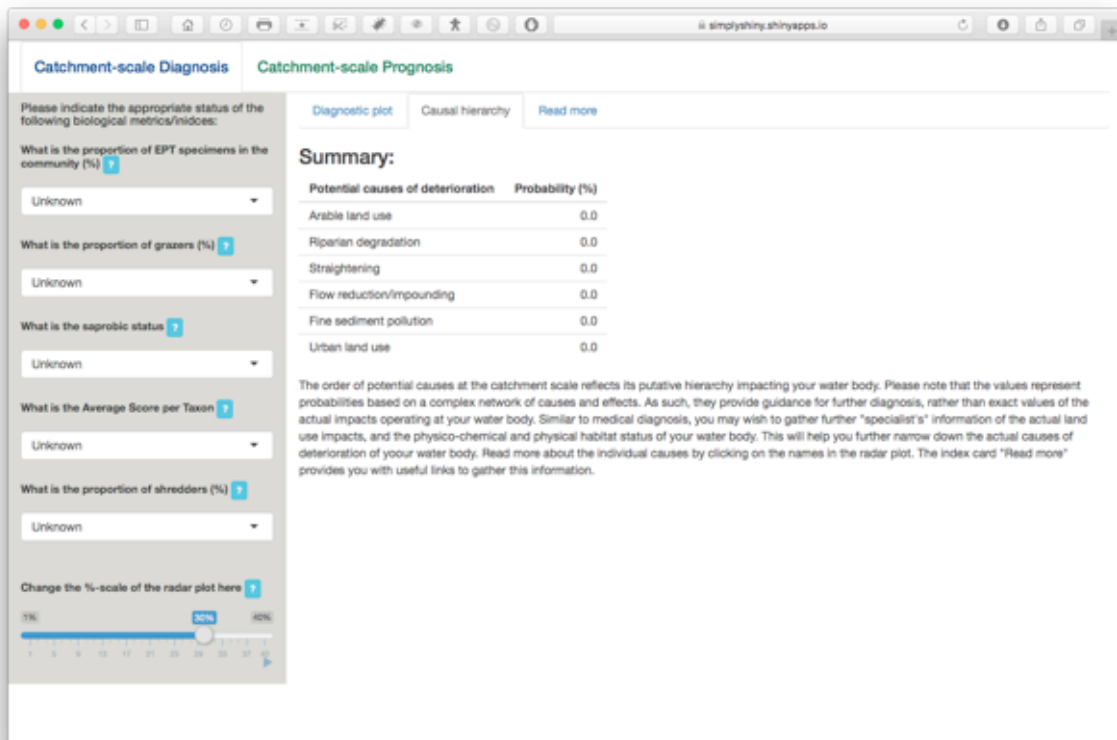


Figure 4: Causal hierarchy tab showing the posterior probabilities in a tabular form, in descending order of probabilities.

Read more (Section 2)

Here, the user can access useful information of how to obtain the evidence required by the DTool (Fig. 5). For instance, a user may lack information of the states of the diagnostic metrics, but hold a taxa list. Then, by using additional software tools (links also provided), it is possible to calculate the diagnostic metrics and eventually select the appropriate evidence in the DTool. Further links can help obtain broad-scale information, for example, of the land use and riparian conditions in the catchment above a water body of interest. This section also provides links to relevant MARS' outcome, reports, publications and the MARS Information Tool (ITool). The MARS ITool provides a comprehensive knowledge base of multiple-stressor effects on and management options for the surface waters of Europe.

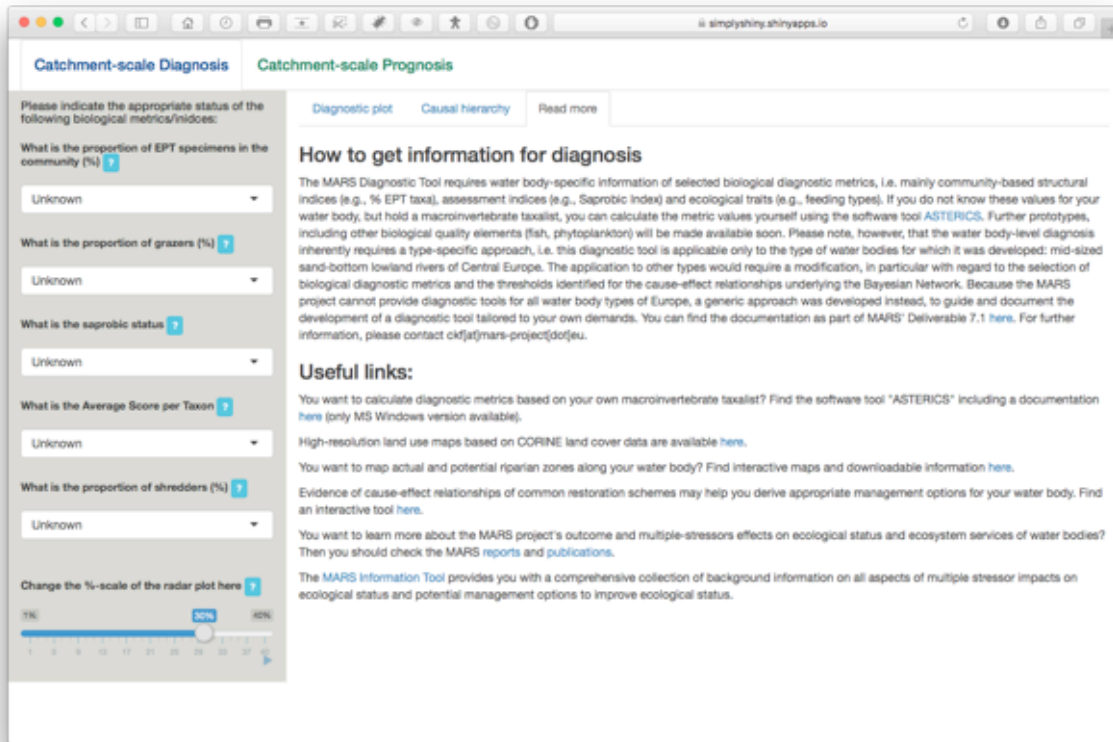


Figure 5: The tab 'Read more' provides the user of the DTool with useful information and links that help derive the evidence (diagnostic metrics) required to use the DTool. Further links point at available broad-scale information and relevant publications of the MARS consortium.

Prognosis (Section 1)

The prognostic part of the DTool inverts the direction of diagnosis, i.e. causes and symptoms are swapped in this application. Hence, the tool helps estimate potential biological effects (not causes) of deterioration based on the evidence that a user sets for a selection of causes (pressure variables). The sections of the prognostic application are similar to those of the diagnostic application (Fig. 1).

Figure 6 shows an example with evidence set for the six pressure variables. Accordingly, based there is a high probability for the % EPT taxa (Ephemeroptera-Plecoptera and Trichoptera) to be impacted by the pressure states selected by the user. Alike diagnosis, the prognostic application is equipped with additional (blue) help buttons and pop-up windows (Fig. 7). By clicking on a biological metric's names in the radar plot, detailed information on the metric is provided that may help interpret the results. Also links to relevant MARS publications are provided here.

Finally, alike in the diagnostic application, there are two additional tabs also available for prognosis: 'Biological impact hierarchy' and 'Read more'. While the former provides a tabular

output of posterior probabilities for the five diagnostic metrics, the latter further explains the meaning of prognosis and provides useful links.

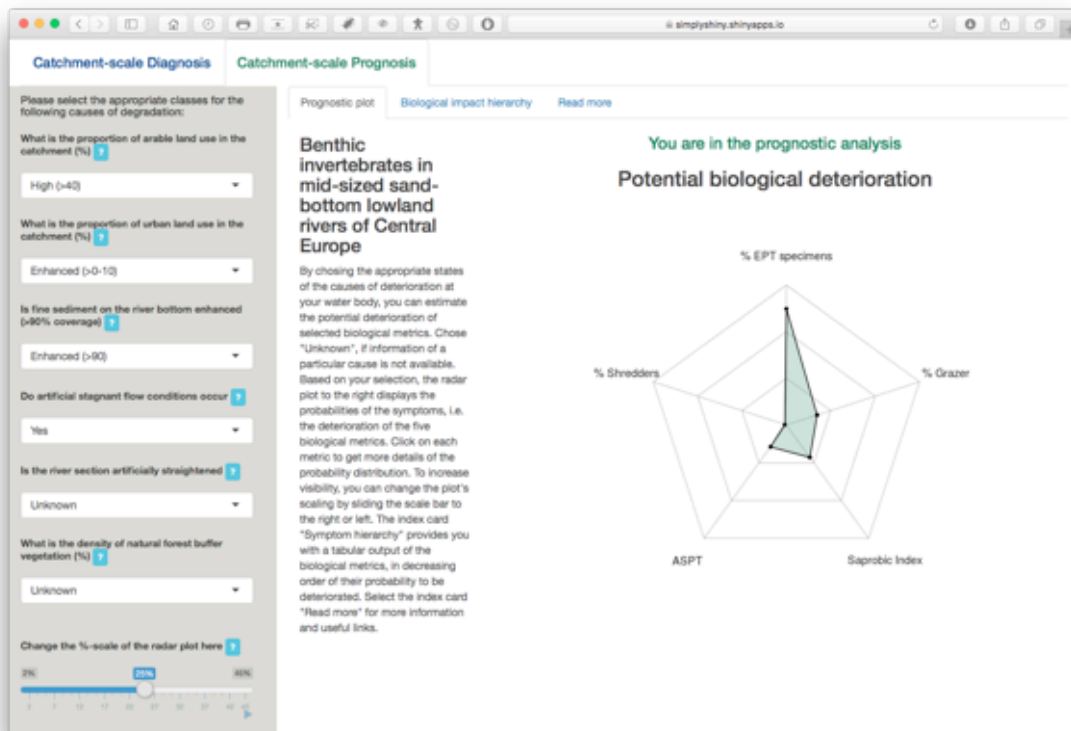


Figure 6: Prognostic application of the DTool with evidence (pressure variables) set for the six variables listed in the grey column on the left-hand side.

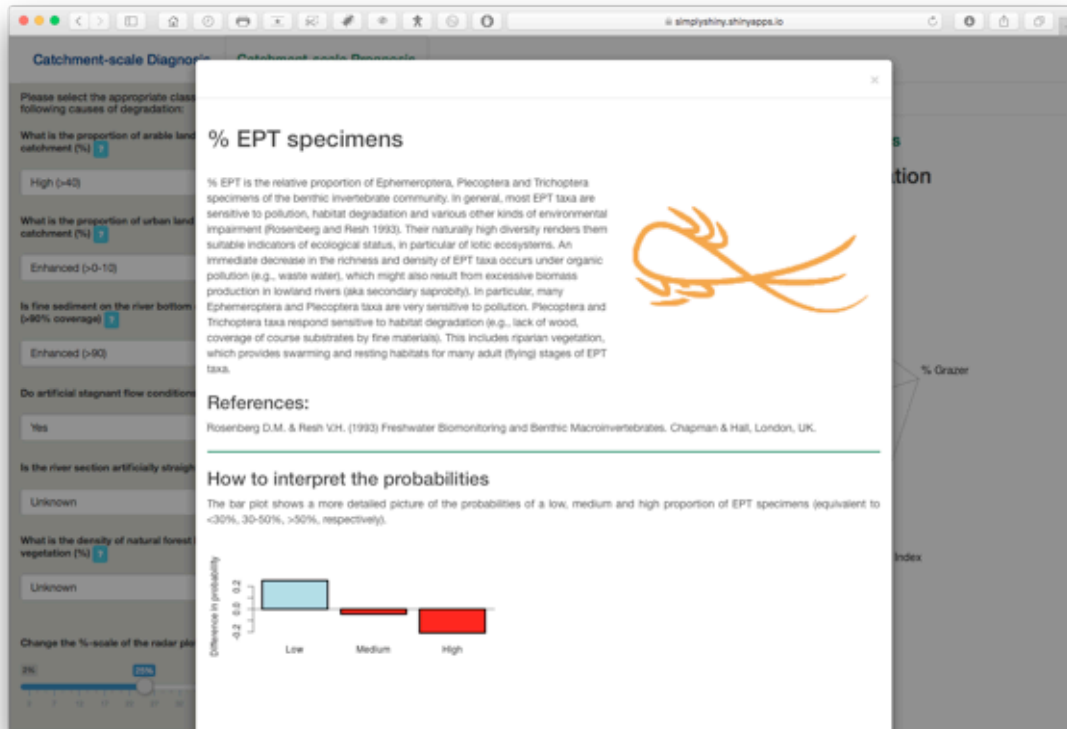


Figure 7: Pop-up window providing detailed information of the diagnostic metrics. The pop-up window can be obtained by clicking on a metric's name in the radar plot (Fig. 6).

References

- Dethlefsen, C. & Højsgaard, S. (2005). A Common Platform for Graphical Models in R: The gRbase Package. *Journal of Statistical Software*, **14(17)**, 1–12. <http://www.jstatsoft.org/v14/i17/>
- Højsgaard, S. (2012). Graphical Independence Networks with the gRain Package for R. *Journal of Statistical Software*, **46(10)**, 1–26. <http://www.jstatsoft.org/v46/i10/>.
- R Core Team (2017). R: a language and environment for statistical computing. R Foundation for Statistical Computing. Austria. URL, Vienna <https://www.R-project.org>.
- R Studio Inc. (2017). Shiny: easy web applications in R. <http://www.rstudio.com/shiny/>.
- Scutari M. (2010). Learning Bayesian Networks with the bnlearn R Package. *Journal of Statistical Software*, **35(3)**, 1–22. URL <http://www.jstatsoft.org/v35/i03/>.

Appendix A

The original evidence search information, which was collected to the excel table database includes the following details are referring to chapter 3.1 evidence search:

- Number of evidence item
- **First author**
- **Year of publication**
- Full reference
- Country
- Study type (survey or experiment)
- Drivers and pressures causing increased fine sediment (fs), nitrogen (N) and/or phosphorus (P) levels
- **Stressor(s) and type of interaction (synergistic [syn], additive [add] or antagonistic [ant])**
- Fine sediment compartment and unit
- Fine sediment minimum value
- Fine sediment maximum value
- Nitrogen compartment
- Nitrogen minimum value ($\mu\text{g/l}$)
- Nitrogen maximum value ($\mu\text{g/l}$)
- Phosphorus compartment
- Phosphorus minimum value ($\mu\text{g/l}$)
- Phosphorus maximum value ($\mu\text{g/l}$)
- Indicator group, macroinvertebrates (MI) or fish (FI)
- **Indicator metric**
- **Sign of the response of the indicator metric (+, - or +/- [subsidy-stress response])**
- Remarks
- Nitrogen threshold
- Phosphorus threshold
- Fine sediment threshold
- Other thresholds
- Variable category

Table 3A Relationships between the stressors and their biological effects, extracted from scientific reference literature (*No* – Number of evidence item, *Author* – first author, *Year* – year of publication, *Drivers/pressures* – drivers and pressures causing increased fine sediment/nutrient levels, *Stressor(s)* – fs (fine sediment), N (nitrogen), P (phosphorus), *add* (additive relationship), *ant* (antagonistic relationship), *syn* (synergistic relationship), *Ind* – Indicator group [MI- macroinvertebrates, FI – fish], *Metric* – indicator metric, *sign* – direction of the ecological response to increased stressor[s])

No	Author	Year	Drivers/pressures	Stressor(s)	Ind	Metric	sign	variable category
1	Bo	2007		fs	MI	invertebrate abundance	-	composition/ abundance
2	Bo	2007		fs	MI	taxa richness	-	diversity
3	Bo	2007		fs	MI	density of filterers	-	process/ functions
4	Bryce	2010		fs	MI	IBI	-	composition/ abundance
5	Bryce	2010		fs	MI	IBI	-	composition/ abundance
6	Bryce	2010		fs	MI	8 sensitive species	-	sensitivity/ tolerance
7	Bryce	2010		fs	MI	8 sensitive species	-	sensitivity/ tolerance
8	Buendia	2013		fs	MI	density	-	biomass/ density
9	Buendia	2013		fs	MI	taxon richness	-	diversity
10	Buendia	2013		fs	MI	Shannon index	-	diversity
11	Buendia	2013		fs	MI	max size 0.25-0.5mm	-	process/ functions
12	Buendia	2013		fs	MI	max size 0.5-1mm	+	process/ functions
13	Buendia	2013		fs	MI	max size 1-2mm	+	process/ functions
14	Buendia	2013		fs	MI	max size 2-4mm	-	process/ functions
15	Buendia	2013		fs	MI	max size 4-8mm	-	process/ functions
16	Buendia	2013		fs	MI	life-cycle duration <1 year	+	process/ functions
17	Buendia	2013		fs	MI	life-cycle duration >1 year	-	process/ functions
18	Buendia	2013		fs	MI	potential generations per year <1	-	process/ functions
19	Buendia	2013		fs	MI	potential generations per year = 1	-	process/ functions
20	Buendia	2013		fs	MI	potential generations per year >1	+	process/ functions
21	Buendia	2013		fs	MI	shredders	-	process/ functions
22	Buendia	2013		fs	MI	scrapers	+	process/ functions
23	Buendia	2013		fs	MI	filter feeders	-	process/ functions
24	Buendia	2013		fs	MI	deposit feeders	+	process/ functions
25	Buendia	2013		fs	MI	respiration with gills	+	process/ functions
26	Buendia	2013		fs	MI	swimmers	-	process/ functions
27	Buendia	2013		fs	MI	crawlers	-	process/ functions
28	Buendia	2013		fs	MI	burrowers	-	process/ functions
29	Buendia	2013		fs	MI	EPT density	-	sensitivity/ tolerance
30	Buendia	2013		fs	MI	EPT richness	-	sensitivity/ tolerance
31	Buendia	2013		fs	MI	%EPT	+	sensitivity/ tolerance
32	Clapcott	2011		fs	MI	Biodiversity	-	diversity
33	Clapcott	2011		fs	MI	Biodiversity	-	diversity
34	Lange	2014a	farming (fS, N, P), water abstraction (P)	ant TN & SIS	MI	% <i>Corynoneura</i> spp.	+/-	sensitivity/ tolerance
35	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	% <i>Deleatidium</i> spp.	-	sensitivity/ tolerance
36	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	EPT richness	-	sensitivity/ tolerance

37	Lange	2014a	farming (fS, N, P), water abstraction (P)	ant TN & SIS	MI	% EPT	-	sensitivity/ tolerance
38	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	% Oligochaeta	+	composition/ abundance
39	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	% <i>Potamopyrgus</i> spp.	+	composition/ abundance
40	Lange	2014a	farming (fS, N, P), water abstraction (P)	ant TN & SIS	MI	% Nematoda	+	composition/ abundance
41	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	% Copepoda	+/-	composition/ abundance
42	Lange	2014a	farming (fS, N, P), water abstraction (P)	syn TN & SIS	MI	% <i>Sphaerium</i> spp.	+/-	composition/ abundance
43	Lange	2014a	farming (fS, N, P), water abstraction (P)	syn TN & SIS	MI	% Orthocladinae	-	sensitivity/ tolerance
44	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	MCI	-	composition/ abundance
45	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	% Ostracoda	+	composition/ abundance
46	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	% <i>Gyraulus</i> spp.	+	composition/ abundance
47	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	% <i>Physella</i> spp.	+	composition/ abundance
48	Lange	2014a	farming (fS, N, P), water abstraction (P)	syn TN & SIS	MI	taxon richness	-	diversity
49	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	evenness	+	diversity
50	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	functional diversity	-	diversity
51	Lange	2014a	farming (fS, N, P), water abstraction (P)	syn TN & SIS	MI	max pot size ≤ 5 mm	+	process/ functions
52	Lange	2014a	farming (fS, N, P), water abstraction (P)	ant TN & SIS	MI	max pot size 5-10 mm	-	process/ functions
53	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	max pot size 10-20 mm	+	process/ functions
54	Lange	2014a	farming (fS, N, P), water abstraction (P)	ant TN & SIS	MI	max pot size 20-40 mm	+/-	process/ functions
55	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	semivoltine	+/-	process/ functions
56	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	1 reprod. cycle per individual	-	process/ functions
57	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	>2 reprod. cycle per individual	+/-	process/ functions
58	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	life duration of adults 1-10 days	+/-	process/ functions
59	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	life duration of adults 10-30 days	+/-	process/ functions
60	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	life duration of adults 30-365 days	+/-	process/ functions
61	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	asexual reprod.	+/-	process/ functions
62	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	hermaphroditism	+/-	process/ functions
63	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	sexual reprod.	-	process/ functions
64	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	oviposition water surface	-	process/ functions
65	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	oviposition beneath surface	+/-	process/ functions
66	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	oviposition terrestrial	+/-	process/ functions
67	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	eggs free	-	process/ functions
68	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	female bears eggs	+/-	process/ functions
69	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	dissemination potential low (10m)	+/-	process/ functions
70	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	dissemination potential high (>1km)	-	process/ functions
71	Lange	2014a	farming (fS, N, P), water abstraction (P)	syn TN & SIS	MI	swimmers	+/-	process/ functions
72	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	attached to substrate	-	process/ functions
73	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	no body flexibility	+	process/ functions

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74	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	low body flexibility	-	process/ functions
75	Lange	2014a	farming (fS, N, P), water abstraction (P)	ant TN & SIS	MI	flattened body form	-	process/ functions
76	Lange	2014a	farming (fS, N, P), water abstraction (P)	ant TN & SIS	MI	cylindrical body form	+	process/ functions
77	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	spherical body form	+/-	process/ functions
78	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	aquatic stages: adult, larva	+/-	process/ functions
79	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	aquatic stages: adult or larva	-	process/ functions
80	Lange	2014a	farming (fS, N, P), water abstraction (P)	syn TN & SIS	MI	aquatic stages: larva, pupa	+/-	process/ functions
81	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	plurivoltine	-	process/ functions
82	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	life duration of adults >365 days	+/-	process/ functions
83	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	shredders	+/-	process/ functions
84	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	filter feeders	+	process/ functions
85	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	eggs cemented	-	process/ functions
86	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	respiration: tegument	+/-	process/ functions
87	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	burrowers	+	process/ functions
88	Lange	2014a	farming (fS, N, P), water abstraction (P)	fs	MI	high body flexibility	-	process/ functions
89	Lange	2014a	farming (fS, N, P), water abstraction (P)	add TN & SIS	MI	respiration: gills	+/-	process/ functions
90	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	crawlers	-	process/ functions
91	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	scrapers	-	process/ functions
92	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	deposit feeders	+	process/ functions
93	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	predators	+	process/ functions
94	Lange	2014a	farming (fS, N, P), water abstraction (P)	N	MI	respiration: atmospheric O2	-	process/ functions
95	Larsen	2009		fs	MI	Oligochaeta relative abundance (%)	+	composition/ abundance
96	Larsen	2009		fs	MI	total abundance	+	composition/ abundance
97	Larsen	2009		fs	MI	% Chironomidae	-	sensitivity/ tolerance
98	Larsen	2009		fs	MI	% Coleoptera	-	composition/ abundance
99	Larsen	2009		fs	MI	total abundance	-	composition/ abundance
100	Larsen	2009		fs	MI	taxon richness	-	diversity
101	Larsen	2009		fs	MI	taxon richness	-	diversity
102	Larsen	2009		fs	MI	Shannon index	+	diversity
103	Larsen	2009		fs	MI	taxon richness	-	diversity
104	Larsen	2009		fs	MI	EPT richness	-	sensitivity/ tolerance
105	Larsen	2009		fs	MI	EPT richness	-	sensitivity/ tolerance
106	Larsen	2009		fs	MI	% EPT	+	sensitivity/ tolerance
107	Larsen	2009		fs	MI	total abundance	+	composition/ abundance
108	Larsen	2009		fs	MI	% Chironomidae	-	sensitivity/ tolerance
109	Larsen	2009		fs	MI	% Coleoptera	-	composition/ abundance
110	Larsen	2009		fs	MI	total abundance	-	composition/ abundance
111	Larsen	2009		fs	MI	taxon richness	-	diversity
112	Larsen	2009		fs	MI	Shannon index	-	diversity
113	Larsen	2009		fs	MI	EPT richness	-	sensitivity/ tolerance
114	Larsen	2009		fs	MI	% EPT	+	sensitivity/ tolerance

115	Matthaei	2010		fs	MI	Total invertebrate density	-	biomass/ density
116	Matthaei	2010		NP	MI	total density	+	biomass/ density
117	Matthaei	2010		syn	MI	total density	+/-	biomass/ density
118	Matthaei	2010		fs	MI	community composition		composition/ abundance
119	Matthaei	2010		fs	MI	Deleatidium spp.		sensitivity/ tolerance
120	Matthaei	2010		fs	MI	<i>Pycnocentroides</i> spp.		sensitivity/ tolerance
121	Matthaei	2010		fs	MI	<i>Austrosimulium</i> spp.		composition/ abundance
122	Matthaei	2010		fs	MI	Deleatidium spp.		sensitivity/ tolerance
123	Matthaei	2010		fs	MI	Potamopyrgus antipodarum		composition/ abundance
124	Matthaei	2010		fs	MI	<i>Austrosimulium</i> spp.		composition/ abundance
125	Matthaei	2010		fs	MI	Copepoda		composition/ abundance
126	Matthaei	2010		fs	MI	community composition		composition/ abundance
127	Matthaei	2010		syn	MI	<i>Austrosimulium</i> spp.	+/-	composition/ abundance
128	Matthaei	2010		NP	MI	Potamopyrgus antipodarum		composition/ abundance
129	Matthaei	2010		NP	MI	community composition		composition/ abundance
130	Matthaei	2010		fs	MI	taxon richness	-	diversity
131	Matthaei	2010		NP	MI	Tanypodinae		sensitivity/ tolerance
132	Matthaei	2010		fs	MI	EPT richness	-	sensitivity/ tolerance
133	Matthaei	2010		fs	MI	EPT richness	-	sensitivity/ tolerance
134	Matthaei	2010		NP	MI	Chironomidae		sensitivity/ tolerance
135	Matthaei	2010		NP	MI	Deleatidium spp.		sensitivity/ tolerance
136	Matthaei	2010		syn	MI	Deleatidium spp.	+/-	sensitivity/ tolerance
137	Miltner	1998		N	MI	ICI	-	composition/ abundance
138	Miltner	1998		N	MI	ICI	-	composition/ abundance
139	Miltner	1998		P	MI	ICI	-	composition/ abundance
140	Miltner	1998		P	MI	ICI	-	composition/ abundance
141	Molinos	2010		syn	MI	Shannon	-	diversity
142	Mondy	2013	agriculture	fs	MI	% filter feeder	+	process/ functions
143	Mondy	2013	agriculture	fs	MI	ovoviviparity	+	process/ functions
144	Mondy	2013	agriculture	fs	MI	isolated cemented eggs	-	process/ functions
145	Mondy	2013	agriculture	fs	MI	crawlers	-	process/ functions
146	Mondy	2013	agriculture	fs	MI	burrowers	+	process/ functions
147	Mondy	2013	agriculture	fs	MI	% scraper	-	process/ functions
148	Osmundson	2002	river regulation (reduced high flows)	fs	MI	Invertebrate dry mass	-	biomass/ density
149	Osmundson	2002	river regulation (reduced high flows)	fs	MI	Invertebrate dry mass	-	biomass/ density
150	Piggot	2012		fs	MI	total invertebrate abundance	+	composition/ abundance
151	Piggot	2012		fs	MI	community composition		composition/ abundance
152	Piggot	2012		NP	MI	total invertebrate abundance	+	composition/ abundance
153	Piggot	2012		fs	MI	Cladocera abundance		composition/ abundance
154	Piggot	2012		NP	MI	community composition		composition/ abundance
155	Piggot	2012		NP	MI	<i>P. antipodarum</i> abundance		composition/ abundance
156	Piggot	2012		fs	MI	Copepoda abundance		composition/ abundance

157	Piggot	2012		fs	MI	Deleatidium spp. Abundance	-	sensitivity/ tolerance
158	Piggot	2012		fs	MI	Hydora spp. Abundance		composition/ abundance
159	Piggot	2012		fs	MI	Nematoda abundance	+	composition/ abundance
160	Piggot	2012		fs	MI	<i>P. antipodarum</i> abundance		composition/ abundance
161	Piggot	2012		fs	MI	Conoescidae abundance	-	sensitivity/ tolerance
162	Piggot	2012		fs	MI	taxon richness	+/-	diversity
163	Piggot	2012		NP	MI	Hydrobiosidae abundance		sensitivity/ tolerance
164	Piggot	2012		NP	MI	<i>Oxyethira</i> spp. Abundance		sensitivity/ tolerance
165	Piggot	2012		NP	MI	Conoescidae abundance	+	sensitivity/ tolerance
166	Piggot	2012		fs	MI	sensitive EPT density	-	sensitivity/ tolerance
167	Piggot	2012		fs	MI	total EPT abundance		sensitivity/ tolerance
168	Piggot	2012		fs	MI	EPT richness		sensitivity/ tolerance
169	Piggot	2012		add	MI	Conoescidae abundance	+/-	sensitivity/ tolerance
170	Piggot	2012		NP	MI	Chironomidae abundance	+	sensitivity/ tolerance
171	Piggot	2012		NP	MI	total EPT abundance	+	sensitivity/ tolerance
172	Piggot	2012		add	MI	total EPT abundance	+/-	sensitivity/ tolerance
173	Piggot	2012		add	MI	EPT richness		sensitivity/ tolerance
174	Rabeni	2005		fs	MI	taxa richness	-	diversity
175	Rabeni	2005		fs	MI	% gatherers (taxa)	+	process/ functions
176	Rabeni	2005		fs	MI	% shredders (taxa)	+	process/ functions
177	Rabeni	2005		fs	MI	scrapers (richness)	-	process/ functions
178	Rabeni	2005		fs	MI	gatherers (richness)	-	process/ functions
179	Rabeni	2005		fs	MI	filterers (richness)	-	process/ functions
180	Rabeni	2005		fs	MI	predators (richness)	-	process/ functions
181	Rabeni	2005		fs	MI	% filteres	-	process/ functions
182	Rabeni	2005		fs	MI	% scrapers	-	process/ functions
183	Rabeni	2005		fs	MI	clingers (richness)	-	process/ functions
184	Rabeni	2005		fs	MI	swimmers (richness)	-	process/ functions
185	Rabeni	2005		fs	MI	sprawlers (richness)	-	process/ functions
186	Rabeni	2005		fs	MI	% clingers (taxa)	-	process/ functions
187	Rabeni	2005		fs	MI	% climbers (taxa)	+	process/ functions
188	Robertson	2008	agriculture, absence of forest, urban area (%)	fs	MI	hbi	+	composition/ abundance
189	Robertson	2008	agriculture, absence of forest, urban area (%)	fs	MI	species richness	-	diversity
190	Robertson	2008	agriculture, absence of forest, urban area (%)	fs	MI	%ephem	-	sensitivity/ tolerance
191	Robertson	2008	agriculture, absence of forest, urban area (%)	fs	MI	mean pollution tolerance value	+	sensitivity/ tolerance
192	Robertson	2008	agriculture, absence of forest	N	MI	hbi	+	composition/ abundance
193	Robertson	2008		P	MI	hbi	+	composition/ abundance
194	Robertson	2008		P	MI	hbi	+	composition/ abundance
195	Robertson	2008	agriculture	N	MI	species richness	-	diversity
196	Robertson	2008		P	MI	species richness	-	diversity
197	Robertson	2008		P	MI	species richness	-	diversity
198	Robertson	2008		P	MI	species richness	-	diversity
199	Robertson	2008	agriculture	N	MI	species richness	-	diversity
200	Robertson	2008	agriculture	N	MI	%scrap	-	process/ functions
201	Robertson	2008	agriculture	N	MI	%scrap	-	process/ functions
202	Robertson	2008	agriculture	N	MI	%shred	+	process/ functions

203	Robertson	2008	agriculture	P	MI	%ephem	-	sensitivity/ tolerance
204	Robertson	2008	agriculture	P	MI	%plec	-	sensitivity/ tolerance
205	Robertson	2008	agriculture	P	MI	mean pollution tolerance value	+	sensitivity/ tolerance
206	Robertson	2008	agriculture	P	MI	%ephem	-	sensitivity/ tolerance
207	Robertson	2008	agriculture	P	MI	%plec	-	sensitivity/ tolerance
208	Robertson	2008	agriculture	P	MI	mean pollution tolerance value	+	sensitivity/ tolerance
209	Robertson	2008	agriculture	N	MI	%ephem	-	sensitivity/ tolerance
210	Robertson	2008	agriculture	N	MI	%plec	-	sensitivity/ tolerance
211	Robertson	2008	agriculture	N	MI	%trichop	+	sensitivity/ tolerance
212	Robertson	2008	agriculture	N	MI	mean pollution tolerance value	+	sensitivity/ tolerance
213	Robertson	2008	agriculture	N	MI	%trichop	+	sensitivity/ tolerance
214	Robertson	2008	agriculture	N	MI	%plec	-	sensitivity/ tolerance
215	Robertson	2008	agriculture	N	MI	%ephem	-	sensitivity/ tolerance
216	Robertson	2008	agriculture	N	MI	%plec	-	sensitivity/ tolerance
217	Robertson	2008	agriculture	N	MI	%eptx	-	sensitivity/ tolerance
218	Robertson	2008	agriculture	N	MI	%depositional habitat tolerant individuals	-	sensitivity/ tolerance
219	Robertson	2008	agriculture	N	MI	mean pollution tolerance value	+	sensitivity/ tolerance
220	Townsend	2008	agriculture	fs	MI	Oligochaeta density	+	biomass/ density
221	Townsend	2008		syn	MI	total taxon richness	-	diversity
222	Townsend	2008		syn	MI	% 2+ cycles/ind.	+	process/ functions
223	Townsend	2008		syn	MI	single individual reproduction	+	process/ functions
224	Townsend	2008	agriculture	fs	MI	% burrowers	+	process/ functions
225	Townsend	2008	agriculture	fs	MI	% respiration gills	-	process/ functions
226	Townsend	2008	agriculture	fs	MI	% surface egg laying	-	process/ functions
227	Townsend	2008	agriculture	fs	MI	EPT richness	-	sensitivity/ tolerance
228	Townsend	2008	agriculture	fs	MI	EPT density	+	sensitivity/ tolerance
229	Townsend	2008		syn	MI	EPT richness	-	sensitivity/ tolerance
230	Wagenhoff	2011	agriculture (fS, N)	add	MI	surface eggs %	-	process/ functions
231	Wagenhoff	2011	agriculture (fS, N)	syn	MI	% more than two reproductive cycles per ind.	+	process/ functions
232	Wagenhoff	2011	agriculture (fS, N)	fs	MI	% single indiv. Reprod.	+	process/ functions
233	Wagenhoff	2011	agriculture (fS, N)	add	MI	EPT richness	-	sensitivity/ tolerance
234	Wagenhoff	2011	agriculture (fS, N)	syn	MI	% Deleatidium	-	sensitivity/ tolerance
235	Wagenhoff	2011	agriculture (fS, N)	syn	MI	% EPT	-	sensitivity/ tolerance
236	Wagenhoff	2011	agriculture (fS, N)	add	MI	% <i>Pycnocentroides</i>	-	sensitivity/ tolerance
237	Wagenhoff	2011	agriculture (fS, N)	add	MI	MCI (macroinv. Community index)	-	composition/ abundance
238	Wagenhoff	2011	agriculture (fS, N)	syn	MI	% Oligochaetes	+	composition/ abundance
239	Wagenhoff	2011	agriculture (fS, N)	syn	MI	% Elmidae	+/-	composition/ abundance
240	Wagenhoff	2011	agriculture (fS, N)	fs	MI	% <i>P. antipodarum</i>	+	composition/ abundance
241	Wagenhoff	2012		fs	MI	cladocera density	-	biomass/ density
242	Wagenhoff	2012		fs	MI	Hydora density	-	biomass/ density
243	Wagenhoff	2012		fs	MI	Temnocephalus density	-	biomass/ density
244	Wagenhoff	2012		fs	MI	Psilochorema density	-	biomass/ density
245	Wagenhoff	2012		fs	MI	Oligochaeta density	+/-	biomass/ density
246	Wagenhoff	2012		fs	MI	nematoda density	+/-	biomass/ density
247	Wagenhoff	2012		fs	MI	copepoda density	+/-	biomass/ density
248	Wagenhoff	2012		fs	MI	ostracoda density	+/-	biomass/ density
249	Wagenhoff	2012		fs	MI	total density	+/-	biomass/ density
250	Wagenhoff	2012		NP	MI	Oligochaeta density	-	biomass/ density
251	Wagenhoff	2012		NP	MI	cladocera density	-	biomass/ density

Appendix

252	Wagenhoff	2012		NP	MI	ostracoda density	-	biomass/ density
253	Wagenhoff	2012		NP	MI	Psilochorema density	+/-	biomass/ density
254	Wagenhoff	2012		NP	MI	total density	+/-	biomass/ density
255	Wagenhoff	2012		NP	MI	evenness	+	diversity
256	Wagenhoff	2012		NP	MI	total taxon richness	+/-	diversity
257	Wagenhoff	2012		fs	MI	total taxon richness	-	diversity
258	Wagenhoff	2012		fs	MI	evenness	+/-	diversity
259	Wagenhoff	2012		add	MI	19 variables (e.g. cladocera density, % spherical body shape, total EPT)	all	biomass/ density, processes, sensitive taxa
260	Wagenhoff	2012		fs	MI	surface eggs %	-	process/ functions
261	Wagenhoff	2012		fs	MI	clingers %	-	process/ functions
262	Wagenhoff	2012		fs	MI	low body flexibility %	-	process/ functions
263	Wagenhoff	2012		fs	MI	spherical body shape %	-	process/ functions
264	Wagenhoff	2012		fs	MI	grazers %	-	process/ functions
265	Wagenhoff	2012		fs	MI	filterers %	-	process/ functions
266	Wagenhoff	2012		fs	MI	% single indiv. Reprod.	+	process/ functions
267	Wagenhoff	2012		NP	MI	>2 reprod. Cycles/ind %	-	process/ functions
268	Wagenhoff	2012		fs	MI	% burrowers	+	process/ functions
269	Wagenhoff	2012		fs	MI	% deposit feeders	+	process/ functions
270	Wagenhoff	2012		fs	MI	% predators	+	process/ functions
271	Wagenhoff	2012		NP	MI	single individual reproduction %	-	process/ functions
272	Wagenhoff	2012		NP	MI	spherical body shape %	-	process/ functions
273	Wagenhoff	2012		fs	MI	% respire using gills	+	process/ functions
274	Wagenhoff	2012		fs	MI	Average body size	+	process/ functions
275	Wagenhoff	2012		NP	MI	% filterers	-	process/ functions
276	Wagenhoff	2012		NP	MI	% surface eggs	+	process/ functions
277	Wagenhoff	2012		NP	MI	% low body flexibility	+	process/ functions
278	Wagenhoff	2012		fs	MI	>2 reprod. Cycles/ind %	+/-	process/ functions
279	Wagenhoff	2012		NP	MI	% respire using gills	+	process/ functions
280	Wagenhoff	2012		NP	MI	Average body size	+	process/ functions
281	Wagenhoff	2012		fs	MI	Chironomidae density	-	sensitivity/ tolerance
282	Wagenhoff	2012		fs	MI	Deleatidium density	-	sensitivity/ tolerance
283	Wagenhoff	2012		fs	MI	Tanypodinae density	-	sensitivity/ tolerance
284	Wagenhoff	2012		fs	MI	Oxyethira density	-	sensitivity/ tolerance
285	Wagenhoff	2012		fs	MI	EPT density	-	sensitivity/ tolerance
286	Wagenhoff	2012		fs	MI	% EPT	-	sensitivity/ tolerance
287	Wagenhoff	2012		fs	MI	EPT richness	-	sensitivity/ tolerance
288	Wagenhoff	2012		NP	MI	% EPT	+	sensitivity/ tolerance
289	Wagenhoff	2012		NP	MI	Chironomidae density	+/-	sensitivity/ tolerance
290	Wagenhoff	2012		NP	MI	Deleatidium density	+/-	sensitivity/ tolerance
291	Wagenhoff	2012		NP	MI	Tanypodinae density	+/-	sensitivity/ tolerance
292	Wagenhoff	2012		NP	MI	EPT density	+/-	sensitivity/ tolerance
293	Wagenhoff	2012		NP	MI	EPT richness	+/-	sensitivity/ tolerance
294	Wagenhoff	2012		syn	MI	EPT richness	-	sensitivity/ tolerance
295	Wagenhoff	2012		syn	MI	Chironomidae density	-	sensitivity/ tolerance
296	Wang	2007	agriculture, absence of forest	NO3	MI	MIBI	-	composition/ abundance
297	Wang	2007	agriculture, absence of forest	NH4	MI	HBI	+	composition/ abundance
298	Wang	2007	agriculture, absence of forest	NH4	MI	ISOPONB%	+	composition/ abundance

299	Wang	2007	agriculture, absence of forest	NH4	MI	ISOPOTX%	+	composition/abundance
300	Wang	2007	agriculture, absence of forest	NH4	MI	TOP2NB%	+	composition/abundance
301	Wang	2007	agriculture, absence of forest	TP	MI	HBI	+	composition/abundance
302	Wang	2007	agriculture, absence of forest	TP	MI	ISOPONB%	+	composition/abundance
303	Wang	2007	agriculture, absence of forest	TP	MI	ISOPOTX%	+	composition/abundance
304	Wang	2007	agriculture, absence of forest	NH4J	MI	HBI	+	composition/abundance
305	Wang	2007	agriculture, absence of forest	NH4J	MI	MIDGENB%	+	composition/abundance
306	Wang	2007	agriculture, absence of forest	TKN	MI	HBI	+	composition/abundance
307	Wang	2007	agriculture, absence of forest	TKN	MI	ISOPONB%	+	composition/abundance
308	Wang	2007	agriculture, absence of forest	TKN	MI	ISOPOTX%	+	composition/abundance
309	Wang	2007	agriculture, absence of forest	TP	MI	MIDGETX%	+	composition/abundance
310	Wang	2007	agriculture, absence of forest	TP	MI	TOP2NB%	+	composition/abundance
311	Wang	2007	agriculture, absence of forest	TPJ	MI	HBI	+	composition/abundance
312	Wang	2007	agriculture, absence of forest	TPJ	MI	ISOPOTX%	+	composition/abundance
313	Wang	2007	agriculture, absence of forest	TPA	MI	HBI	+	composition/abundance
314	Wang	2007	agriculture, absence of forest	TPA	MI	ISOPONB%	+	composition/abundance
315	Wang	2007	agriculture, absence of forest	TKN	MI	MIDGENB%	+	composition/abundance
316	Wang	2007	agriculture, absence of forest	TKNJ	MI	HBI	+	composition/abundance
317	Wang	2007	agriculture, absence of forest	TKNJ	MI	MIDGENB%	+	composition/abundance
318	Wang	2007	agriculture, absence of forest	TN	MI	HBI	+	composition/abundance
319	Wang	2007	agriculture, absence of forest	TN	MI	MIBI	-	composition/abundance
320	Wang	2007	agriculture, absence of forest	TN	MI	MIDGENB%	+	composition/abundance
321	Wang	2007	agriculture, absence of forest	TN	MI	TOP2NB%	+	composition/abundance
322	Wang	2007	agriculture, absence of forest	TNJ	MI	HBI	+	composition/abundance
323	Wang	2007	agriculture, absence of forest	TNJ	MI	MIBI	-	composition/abundance
324	Wang	2007	agriculture, absence of forest	TNA	MI	HBI	+	composition/abundance
325	Wang	2007	agriculture, absence of forest	TNA	MI	MIBI	-	composition/abundance
326	Wang	2007	agriculture, absence of forest	TNA	MI	MIDGENB%	+	composition/abundance
327	Wang	2007	agriculture, absence of forest	TNA	MI	TOP2NB%	+	composition/abundance
328	Wang	2007	agriculture, absence of forest	TPA	MI	ISOPOTX%	+	composition/abundance
329	Wang	2007	agriculture, absence of forest	TPA	MI	MIDGETX%	+	composition/abundance
330	Wang	2007	agriculture, absence of forest	DP	MI	HBI	+	composition/abundance
331	Wang	2007	agriculture, absence of forest	DP	MI	ISOPONB%	+	composition/abundance
332	Wang	2007	agriculture, absence of forest	DP	MI	ISOPOTX%	+	composition/abundance
333	Wang	2007	agriculture, absence of forest	DPJ	MI	HBI	+	composition/abundance
334	Wang	2007	agriculture, absence of forest	DPJ	MI	MIDGENB%	+	composition/abundance
335	Wang	2007	agriculture, absence of forest	NO3	MI	SDIVERSI	-	diversity

336	Wang	2007	agriculture, absence of forest	NO3	MI	TAXANB	-	diversity
337	Wang	2007	agriculture, absence of forest	NH4	MI	SDIVERSI	-	diversity
338	Wang	2007	agriculture, absence of forest	NH4	MI	TAXANB	-	diversity
339	Wang	2007	agriculture, absence of forest	TN	MI	SDIVERSI	-	diversity
340	Wang	2007	agriculture, absence of forest	TN	MI	TAXANB	-	diversity
341	Wang	2007	agriculture, absence of forest	TNJ	MI	SDIVERSI	-	diversity
342	Wang	2007	agriculture, absence of forest	TNJ	MI	TAXANB	-	diversity
343	Wang	2007	agriculture, absence of forest	TNA	MI	SDIVERSI	-	diversity
344	Wang	2007	agriculture, absence of forest	TNA	MI	TAXANB	-	diversity
345	Wang	2007	agriculture, absence of forest	NO3	MI	GATHETX%	+	process/ functions
346	Wang	2007	agriculture, absence of forest	NO3	MI	PREDANB%	-	process/ functions
347	Wang	2007	agriculture, absence of forest	NO3	MI	PREDATX%	-	process/ functions
348	Wang	2007	agriculture, absence of forest	NO3J	MI	PREDANB%	-	process/ functions
349	Wang	2007	agriculture, absence of forest	NO3J	MI	PREDATX%	-	process/ functions
350	Wang	2007	agriculture, absence of forest	TKN	MI	FILTETX%	-	process/ functions
351	Wang	2007	agriculture, absence of forest	TKN	MI	SCRAPNB%	+	process/ functions
352	Wang	2007	agriculture, absence of forest	TKN	MI	SHREDNB%	+	process/ functions
353	Wang	2007	agriculture, absence of forest	TKN	MI	SHREDTX%	+	process/ functions
354	Wang	2007	agriculture, absence of forest	TN	MI	PREDANB%	-	process/ functions
355	Wang	2007	agriculture, absence of forest	TN	MI	PREDATX%	-	process/ functions
356	Wang	2007	agriculture, absence of forest	TNJ	MI	PREDANB%	-	process/ functions
357	Wang	2007	agriculture, absence of forest	TNA	MI	PREDANB%	-	process/ functions
358	Wang	2007	agriculture, absence of forest	TNA	MI	PREDATX%	-	process/ functions
359	Wang	2007	agriculture, absence of forest	TP	MI	EPTNB%	-	sensitivity/ tolerance
360	Wang	2007	agriculture, absence of forest	TP	MI	EPTTX%	-	sensitivity/ tolerance
361	Wang	2007	agriculture, absence of forest	TP	MI	TOLVALUE	+	sensitivity/ tolerance
362	Wang	2007	agriculture, absence of forest	TPJ	MI	EPTNB%	-	sensitivity/ tolerance
363	Wang	2007	agriculture, absence of forest	TPJ	MI	EPTTX%	-	sensitivity/ tolerance
364	Wang	2007	agriculture, absence of forest	TPJ	MI	TOLVALUE	+	sensitivity/ tolerance
365	Wang	2007	agriculture, absence of forest	TPA	MI	EPTNB%	-	sensitivity/ tolerance
366	Wang	2007	agriculture, absence of forest	TPA	MI	EPTTX%	-	sensitivity/ tolerance
367	Wang	2007	agriculture, absence of forest	TPA	MI	TOLVALUE	+	sensitivity/ tolerance
368	Wang	2007	agriculture, absence of forest	DP	MI	EPTNB%	-	sensitivity/ tolerance
369	Wang	2007	agriculture, absence of forest	DP	MI	EPTTX%	-	sensitivity/ tolerance
370	Wang	2007	agriculture, absence of forest	DP	MI	TOLVALUE	+	sensitivity/ tolerance
371	Wang	2007	agriculture, absence of forest	DPJ	MI	EPTNB%	-	sensitivity/ tolerance
372	Wang	2007	agriculture, absence of forest	DPJ	MI	EPTTX%	-	sensitivity/ tolerance

373	Wang	2007	agriculture, absence of forest	DPJ	MI	TOLVALUE	+	sensitivity/ tolerance
374	Wang	2007	agriculture, absence of forest	NH4	MI	EPTNB%	-	sensitivity/ tolerance
375	Wang	2007	agriculture, absence of forest	NH4	MI	EPTTX%	-	sensitivity/ tolerance
376	Wang	2007	agriculture, absence of forest	NH4	MI	TOLVALUE	+	sensitivity/ tolerance
377	Wang	2007	agriculture, absence of forest	NH4J	MI	EPTNB%	-	sensitivity/ tolerance
378	Wang	2007	agriculture, absence of forest	NH4J	MI	EPTTX%	-	sensitivity/ tolerance
379	Wang	2007	agriculture, absence of forest	NH4J	MI	TOLVALUE	+	sensitivity/ tolerance
380	Wang	2007	agriculture, absence of forest	TKN	MI	EPTNB%	-	sensitivity/ tolerance
381	Wang	2007	agriculture, absence of forest	TKN	MI	EPTTX%	-	sensitivity/ tolerance
382	Wang	2007	agriculture, absence of forest	TKN	MI	TOLVALUE	+	sensitivity/ tolerance
383	Wang	2007	agriculture, absence of forest	TKNJ	MI	EPTTX%	-	sensitivity/ tolerance
384	Wang	2007	agriculture, absence of forest	TKNJ	MI	TOLVALUE	+	sensitivity/ tolerance
385	Wang	2007	agriculture, absence of forest	TN	MI	EPTNB%	-	sensitivity/ tolerance
386	Wang	2007	agriculture, absence of forest	TN	MI	EPTTX%	-	sensitivity/ tolerance
387	Wang	2007	agriculture, absence of forest	TN	MI	TOLVALUE	+	sensitivity/ tolerance
388	Wang	2007	agriculture, absence of forest	TNJ	MI	EPTNB%	-	sensitivity/ tolerance
389	Wang	2007	agriculture, absence of forest	TNJ	MI	EPTTX%	-	sensitivity/ tolerance
390	Wang	2007	agriculture, absence of forest	TNJ	MI	TOLVALUE	+	sensitivity/ tolerance
391	Wang	2007	agriculture, absence of forest	TNA	MI	EPTNB%	-	sensitivity/ tolerance
392	Wang	2007	agriculture, absence of forest	TNA	MI	EPTTX%	-	sensitivity/ tolerance
393	Wang	2007	agriculture, absence of forest	TNA	MI	TOLVALUE	+	sensitivity/ tolerance
394	Zweig	2001	no access!	fs cover %	MI	EPT density	-	sensitivity/ tolerance
395	Zweig	2001		fs cover %	MI	EPT richness	-	sensitivity/ tolerance
396	Zweig	2001		fs cover %	MI	EPT/Chironomidae richness	-	sensitivity/ tolerance
397	Argent	1999		fS weight %	FI	incubating Brook trout survival	-	sensitivity/ tolerance
398	Bryce	2010		fS cover %	FI	4 sensitive species	-	sensitivity/ tolerance
399	Bryce	2010		fS cover %	FI	4 sensitive species	-	sensitivity/ tolerance
400	Lange	2014b	farming	add TN & fs	FI	trout density	-	sensitivity/ tolerance
401	Lange	2014b	farming	TN	FI	Bully presence	+/-	biomass/ density
402	Lange	2014b	farming	TN	FI	Bully density	+/-	biomass/ density
403	Lange	2014b	farming	fSdepth mm	FI	trout presence	-	sensitivity/ tolerance
404	Lange	2014b	farming	fSdepth mm	FI	trout density	-	sensitivity/ tolerance
405	Lange	2014b	farming	TN	FI	trout density	-	sensitivity/ tolerance
406	Miltner	1998		TIN	FI	IBI	-	composition/ abundance
407	Miltner	1998		TIN	FI	IBI	-	composition/ abundance
408	Miltner	1998		TP	FI	IBI	-	composition/ abundance
409	Miltner	1998		TP	FI	IBI	-	composition/ abundance
410	Miltner	1998		TIN	FI	IBI	-	composition/ abundance
411	Richardson	2002	natural exacerbated by forest clearance (agriculture)	SSC g/m3	FI	fish abundance	-	composition/ abundance

412	Richardson	2002	natural exacerbated by forest clearance (agriculture)	SSC g/m3	FI	fish diversity	-	diversity
413	Robertson	2008	agriculture, absence of forest, urban area (%)	SSC	FI	riverine species (nr)	-	composition/ abundance
414	Robertson	2008	agriculture, absence of forest, urban area (%)	SSC	FI	%riversp	-	composition/ abundance
415	Robertson	2008	agriculture, absence of forest, urban area (%)	SSC	FI	IBI	-	composition/ abundance
416	Robertson	2008	agriculture, absence of forest, urban area (%)	SSC	FI	%litspawn	-	process/ functions
417	Robertson	2008	agriculture, absence of forest, urban area (%)	SSC	FI	%sucker	-	process/ functions
418	Robertson	2008	agriculture	TP	FI	riverine species (nr)	-	composition/ abundance
419	Robertson	2008	agriculture, absence of forest, urban area (%)	SSC	FI	%insect	-	process/ functions
420	Robertson	2008	agriculture	TP	FI	%riversp	-	composition/ abundance
421	Robertson	2008	agriculture	TP	FI	IBI	-	composition/ abundance
422	Robertson	2008	agriculture	DP	FI	nativesp	-	composition/ abundance
423	Robertson	2008	agriculture	DP	FI	riverine species (nr)	-	composition/ abundance
424	Robertson	2008	agriculture	DP	FI	%riversp	-	composition/ abundance
425	Robertson	2008	agriculture	TN	FI	riverine species (nr)	-	composition/ abundance
426	Robertson	2008	agriculture	TN	FI	%riversp	-	composition/ abundance
427	Robertson	2008	agriculture	TN	FI	IBI	-	composition/ abundance
428	Robertson	2008	agriculture	NH4	FI	nativesp	-	composition/ abundance
429	Robertson	2008	agriculture	NH4	FI	riverine species (nr)	-	composition/ abundance
430	Robertson	2008	agriculture	NH4	FI	%riversp	-	composition/ abundance
431	Robertson	2008	agriculture	NH4	FI	IBI	-	composition/ abundance
432	Robertson	2008	agriculture	TKN	FI	riverine species (nr)	-	composition/ abundance
433	Robertson	2008	agriculture	TKN	FI	%riversp	-	composition/ abundance
434	Robertson	2008	agriculture	TKN	FI	IBI	-	composition/ abundance
435	Robertson	2008	agriculture	TP	FI	%disease	+	Disease and deformities
436	Robertson	2008	agriculture	TP	FI	sucker	-	process/ functions
437	Robertson	2008	agriculture	TP	FI	%litspawn	-	process/ functions
438	Robertson	2008	agriculture	TP	FI	%sucker	-	process/ functions
439	Robertson	2008	agriculture	TP	FI	%insect	-	process/ functions
440	Robertson	2008	agriculture, absence of forest, urban area (%)	SSC	FI	intol	-	sensitivity/ tolerance
441	Robertson	2008	agriculture, absence of forest	NO3	FI	disease	+	Disease and deformities
442	Robertson	2008	agriculture	TN	FI	%litspawn	-	process/ functions
443	Robertson	2008	agriculture	TN	FI	%sucker	-	process/ functions
444	Robertson	2008	agriculture	TN	FI	%insect	-	process/ functions
445	Robertson	2008	agriculture	NO3	FI	%litspawn	-	process/ functions
446	Robertson	2008	agriculture	NO3	FI	%sucker	-	process/ functions
447	Robertson	2008	agriculture	NO3	FI	%insect	-	process/ functions
448	Robertson	2008	agriculture	NH4	FI	sucker	-	process/ functions
449	Robertson	2008	agriculture	NH4	FI	%litspawn	-	process/ functions
450	Robertson	2008	agriculture	NH4	FI	%sucker	-	process/ functions
451	Robertson	2008	agriculture	DP	FI	sucker	-	process/ functions
452	Robertson	2008	agriculture	DP	FI	%litspawn	-	process/ functions
453	Robertson	2008	agriculture	DP	FI	%sucker	-	process/ functions

454	Robertson	2008	agriculture	NH4	FI	%insect	-	process/ functions
455	Robertson	2008	agriculture	TKN	FI	sucker	-	process/ functions
456	Robertson	2008	agriculture	TKN	FI	%litspawn	-	process/ functions
457	Robertson	2008	agriculture	TKN	FI	%sucker	-	process/ functions
458	Robertson	2008	agriculture	TKN	FI	%insect	-	process/ functions
459	Robertson	2008	agriculture	TP	FI	intol	-	sensitivity/ tolerance
460	Robertson	2008	agriculture	DP	FI	intol	-	sensitivity/ tolerance
461	Robertson	2008	agriculture	TN	FI	intol	-	sensitivity/ tolerance
462	Robertson	2008	agriculture	NO3	FI	intol	-	sensitivity/ tolerance
463	Robertson	2008	agriculture	TKN	FI	intol	-	sensitivity/ tolerance
464	Sutherland	2002	agriculture	baseflow turbidity (NTU)	FI	benthic crevice and gravel spawners (rel. Abundance of adult fishes)	-	process/ functions
465	Sutherland	2002	agriculture	baseflow turbidity (NTU)	FI	benthic excavators (rel. Abundance of adult fishes)	ns	process/ functions
466	Sutherland	2002	agriculture	baseflow turbidity (NTU)	FI	benthic nest builders and benthic nest associates (rel. Abundance of adult fishes)	-	process/ functions
467	Sutherland	2002	agriculture	Embeddedness %	FI	benthic crevice and gravel spawners (rel. Abundance of adult fishes)	-	process/ functions
468	Sutherland	2002	agriculture	Embeddedness %	FI	benthic excavators (rel. Abundance of adult fishes)	+	process/ functions
469	Sutherland	2002	agriculture	Embeddedness %	FI	benthic nest builders and benthic nest associates (rel. Abundance of adult fishes)	ns	process/ functions
470	Wang	2007	agriculture, absence of forest	NO3	FI	FISBIOMA	+	biomass/ density
471	Wang	2007	agriculture, absence of forest	NO3J	FI	FISBIOMA	+	biomass/ density
472	Wang	2007	agriculture, absence of forest	TP	FI	FISIBI	-	composition/ abundance
473	Wang	2007	agriculture, absence of forest	TPJ	FI	FISIBI	-	composition/ abundance
474	Wang	2007	agriculture, absence of forest	TPA	FI	FISIBI	-	composition/ abundance
475	Wang	2007	agriculture, absence of forest	DP	FI	FISIBI	-	composition/ abundance
476	Wang	2007	agriculture, absence of forest	DPJ	FI	FISIBI	-	composition/ abundance
477	Wang	2007	agriculture, absence of forest	NH4	FI	FISIBI	-	composition/ abundance
478	Wang	2007	agriculture, absence of forest	NH4	FI	NATINB	-	composition/ abundance
479	Wang	2007	agriculture, absence of forest	NH4	FI	NATINB%	-	composition/ abundance
480	Wang	2007	agriculture, absence of forest	NH4	FI	NATISP%	-	composition/ abundance
481	Wang	2007	agriculture, absence of forest	NH4	FI	SUNFNB	+	composition/ abundance
482	Wang	2007	agriculture, absence of forest	TKN	FI	FISIBI	-	composition/ abundance
483	Wang	2007	agriculture, absence of forest	TKN	FI	NATINB	-	composition/ abundance
484	Wang	2007	agriculture, absence of forest	TKN	FI	NATINB%	-	composition/ abundance
485	Wang	2007	agriculture, absence of forest	TKN	FI	NATISP%	-	composition/ abundance
486	Wang	2007	agriculture, absence of forest	TKN	FI	SUNFNB	+	composition/ abundance
487	Wang	2007	agriculture, absence of forest	TKN	FI	SUNFNB%	+	composition/ abundance

488	Wang	2007	agriculture, absence of forest	TKN	FI	SUNFSP%	+	composition/ abundance
489	Wang	2007	agriculture, absence of forest	TKNJ	FI	SUNFNB	+	composition/ abundance
490	Wang	2007	agriculture, absence of forest	TKNJ	FI	SUNFNB%	+	composition/ abundance
491	Wang	2007	agriculture, absence of forest	TN	FI	FISIBI	-	composition/ abundance
492	Wang	2007	agriculture, absence of forest	TNJ	FI	FISIBI	-	composition/ abundance
493	Wang	2007	agriculture, absence of forest	TNA	FI	FISIBI	-	composition/ abundance
494	Wang	2007	agriculture, absence of forest	TP	FI	CARNNB	-	process/ functions
495	Wang	2007	agriculture, absence of forest	NO3	FI	OMNINB%	+	process/ functions
496	Wang	2007	agriculture, absence of forest	NO3	FI	OMNISP%	+	process/ functions
497	Wang	2007	agriculture, absence of forest	NO3J	FI	OMNINB%	+	process/ functions
498	Wang	2007	agriculture, absence of forest	NH4	FI	CARNNB	-	process/ functions
499	Wang	2007	agriculture, absence of forest	TP	FI	CARNNB%	-	process/ functions
500	Wang	2007	agriculture, absence of forest	TP	FI	CARNSP%	-	process/ functions
501	Wang	2007	agriculture, absence of forest	TP	FI	OMNISP%	+	process/ functions
502	Wang	2007	agriculture, absence of forest	TPJ	FI	CARNNB	-	process/ functions
503	Wang	2007	agriculture, absence of forest	TPJ	FI	CARNNB%	-	process/ functions
504	Wang	2007	agriculture, absence of forest	TPJ	FI	CARNSP%	-	process/ functions
505	Wang	2007	agriculture, absence of forest	TPJ	FI	OMNISP%	+	process/ functions
506	Wang	2007	agriculture, absence of forest	TPA	FI	CARNNB	-	process/ functions
507	Wang	2007	agriculture, absence of forest	TPA	FI	CARNNB%	-	process/ functions
508	Wang	2007	agriculture, absence of forest	TPA	FI	CARNSP%	-	process/ functions
509	Wang	2007	agriculture, absence of forest	TPA	FI	OMNISP%	+	process/ functions
510	Wang	2007	agriculture, absence of forest	DP	FI	CARNNB	-	process/ functions
511	Wang	2007	agriculture, absence of forest	DP	FI	CARNNB%	-	process/ functions
512	Wang	2007	agriculture, absence of forest	DP	FI	CARNSP%	-	process/ functions
513	Wang	2007	agriculture, absence of forest	DP	FI	OMNINB	+	process/ functions
514	Wang	2007	agriculture, absence of forest	DP	FI	OMNISP%	+	process/ functions
515	Wang	2007	agriculture, absence of forest	DPJ	FI	CARNNB	-	process/ functions
516	Wang	2007	agriculture, absence of forest	DPJ	FI	CARNNB%	-	process/ functions
517	Wang	2007	agriculture, absence of forest	DPJ	FI	CARNSP%	-	process/ functions
518	Wang	2007	agriculture, absence of forest	DPJ	FI	OMNISP%	+	process/ functions
519	Wang	2007	agriculture, absence of forest	NH4	FI	CARNNB%	-	process/ functions
520	Wang	2007	agriculture, absence of forest	NH4	FI	CARNSP%	-	process/ functions
521	Wang	2007	agriculture, absence of forest	NH4	FI	INSECSP%	+	process/ functions
522	Wang	2007	agriculture, absence of forest	NH4	FI	OMNINB	+	process/ functions
523	Wang	2007	agriculture, absence of forest	NH4	FI	OMNISP%	+	process/ functions
524	Wang	2007	agriculture, absence of forest	NH4J	FI	CARNNB	-	process/ functions

525	Wang	2007	agriculture, absence of forest	NH4J	FI	CARNNB%	-	process/ functions
526	Wang	2007	agriculture, absence of forest	NH4J	FI	INSECNB%	+	process/ functions
527	Wang	2007	agriculture, absence of forest	NH4J	FI	INSECSP%	+	process/ functions
528	Wang	2007	agriculture, absence of forest	TKN	FI	CARNNB	-	process/ functions
529	Wang	2007	agriculture, absence of forest	TKN	FI	CARNNB%	-	process/ functions
530	Wang	2007	agriculture, absence of forest	TKN	FI	CARNSP%	-	process/ functions
531	Wang	2007	agriculture, absence of forest	TKN	FI	INSECNB%	+	process/ functions
532	Wang	2007	agriculture, absence of forest	TKN	FI	OMNISP%	+	process/ functions
533	Wang	2007	agriculture, absence of forest	TKNJ	FI	CARNNB	-	process/ functions
534	Wang	2007	agriculture, absence of forest	TKNJ	FI	CARNNB%	-	process/ functions
535	Wang	2007	agriculture, absence of forest	TKNJ	FI	INSECNB%	+	process/ functions
536	Wang	2007	agriculture, absence of forest	TN	FI	CARNNB	-	process/ functions
537	Wang	2007	agriculture, absence of forest	TN	FI	CARNNB%	-	process/ functions
538	Wang	2007	agriculture, absence of forest	TN	FI	CARNSP%	-	process/ functions
539	Wang	2007	agriculture, absence of forest	TN	FI	OMNINB%	+	process/ functions
540	Wang	2007	agriculture, absence of forest	TN	FI	OMNISP%	+	process/ functions
541	Wang	2007	agriculture, absence of forest	TNJ	FI	OMNINB%	+	process/ functions
542	Wang	2007	agriculture, absence of forest	TNJ	FI	OMNISP%	+	process/ functions
543	Wang	2007	agriculture, absence of forest	TNA	FI	CARNNB%	-	process/ functions
544	Wang	2007	agriculture, absence of forest	TNA	FI	OMNINB%	+	process/ functions
545	Wang	2007	agriculture, absence of forest	TNA	FI	OMNISP%	+	process/ functions
546	Wang	2007	agriculture, absence of forest	TP	FI	INTONB	-	sensitivity/ tolerance
547	Wang	2007	agriculture, absence of forest	TP	FI	INTONB%	-	sensitivity/ tolerance
548	Wang	2007	agriculture, absence of forest	TP	FI	INTOSP%	-	sensitivity/ tolerance
549	Wang	2007	agriculture, absence of forest	TP	FI	SALMONNB	-	sensitivity/ tolerance
550	Wang	2007	agriculture, absence of forest	TPJ	FI	INTONB	-	sensitivity/ tolerance
551	Wang	2007	agriculture, absence of forest	TPJ	FI	INTONB%	-	sensitivity/ tolerance
552	Wang	2007	agriculture, absence of forest	TPJ	FI	INTOSP%	-	sensitivity/ tolerance
553	Wang	2007	agriculture, absence of forest	TPJ	FI	SALMONNB	-	sensitivity/ tolerance
554	Wang	2007	agriculture, absence of forest	TPA	FI	INTONB	-	sensitivity/ tolerance
555	Wang	2007	agriculture, absence of forest	TPA	FI	INTONB%	-	sensitivity/ tolerance
556	Wang	2007	agriculture, absence of forest	TPA	FI	INTOSP%	-	sensitivity/ tolerance
557	Wang	2007	agriculture, absence of forest	TPA	FI	SALMONNB	-	sensitivity/ tolerance
558	Wang	2007	agriculture, absence of forest	DP	FI	INTONB	-	sensitivity/ tolerance
559	Wang	2007	agriculture, absence of forest	DP	FI	INTONB%	-	sensitivity/ tolerance
560	Wang	2007	agriculture, absence of forest	DP	FI	INTOSP%	-	sensitivity/ tolerance
561	Wang	2007	agriculture, absence of forest	DP	FI	SALMONNB	-	sensitivity/ tolerance

Appendix

562	Wang	2007	agriculture, absence of forest	DPJ	FI	INTONB%	-	sensitivity/ tolerance
563	Wang	2007	agriculture, absence of forest	DPJ	FI	INTOSP%	-	sensitivity/ tolerance
564	Wang	2007	agriculture, absence of forest	DPJ	FI	SALMONNB	-	sensitivity/ tolerance
565	Wang	2007	agriculture, absence of forest	NH4	FI	INTONB	-	sensitivity/ tolerance
566	Wang	2007	agriculture, absence of forest	NH4	FI	INTONB%	-	sensitivity/ tolerance
567	Wang	2007	agriculture, absence of forest	NH4	FI	INTOSP%	-	sensitivity/ tolerance
568	Wang	2007	agriculture, absence of forest	NH4	FI	SALMONNB	-	sensitivity/ tolerance
569	Wang	2007	agriculture, absence of forest	NH4	FI	TOLENB	+	sensitivity/ tolerance
570	Wang	2007	agriculture, absence of forest	NH4	FI	TOLENB%	+	sensitivity/ tolerance
571	Wang	2007	agriculture, absence of forest	NH4	FI	TOLESP%	+	sensitivity/ tolerance
572	Wang	2007	agriculture, absence of forest	NH4J	FI	SALMONNB	-	sensitivity/ tolerance
573	Wang	2007	agriculture, absence of forest	TKN	FI	INTONB	-	sensitivity/ tolerance
574	Wang	2007	agriculture, absence of forest	TKN	FI	INTONB%	-	sensitivity/ tolerance
575	Wang	2007	agriculture, absence of forest	TKN	FI	INTOSP%	-	sensitivity/ tolerance
576	Wang	2007	agriculture, absence of forest	TKN	FI	SALMONNB	-	sensitivity/ tolerance
577	Wang	2007	agriculture, absence of forest	TKN	FI	TOLENB%	+	sensitivity/ tolerance
578	Wang	2007	agriculture, absence of forest	TKN	FI	TOLESP%	+	sensitivity/ tolerance
579	Wang	2007	agriculture, absence of forest	TKNJ	FI	SALMONNB	-	sensitivity/ tolerance
580	Wang	2007	agriculture, absence of forest	TN	FI	INTONB	-	sensitivity/ tolerance
581	Wang	2007	agriculture, absence of forest	TN	FI	INTONB%	-	sensitivity/ tolerance
582	Wang	2007	agriculture, absence of forest	TN	FI	INTOSP%	-	sensitivity/ tolerance
583	Wang	2007	agriculture, absence of forest	TN	FI	SALMONNB	-	sensitivity/ tolerance
584	Wang	2007	agriculture, absence of forest	TNJ	FI	INTOSP%	-	sensitivity/ tolerance
585	Wang	2007	agriculture, absence of forest	TNA	FI	INTONB	-	sensitivity/ tolerance
586	Wang	2007	agriculture, absence of forest	TNA	FI	INTONB%	-	sensitivity/ tolerance
587	Wang	2007	agriculture, absence of forest	TNA	FI	INTOSP%	-	sensitivity/ tolerance

Appendix B

The evidence based model prototypes B1 and B2 for the MARS project

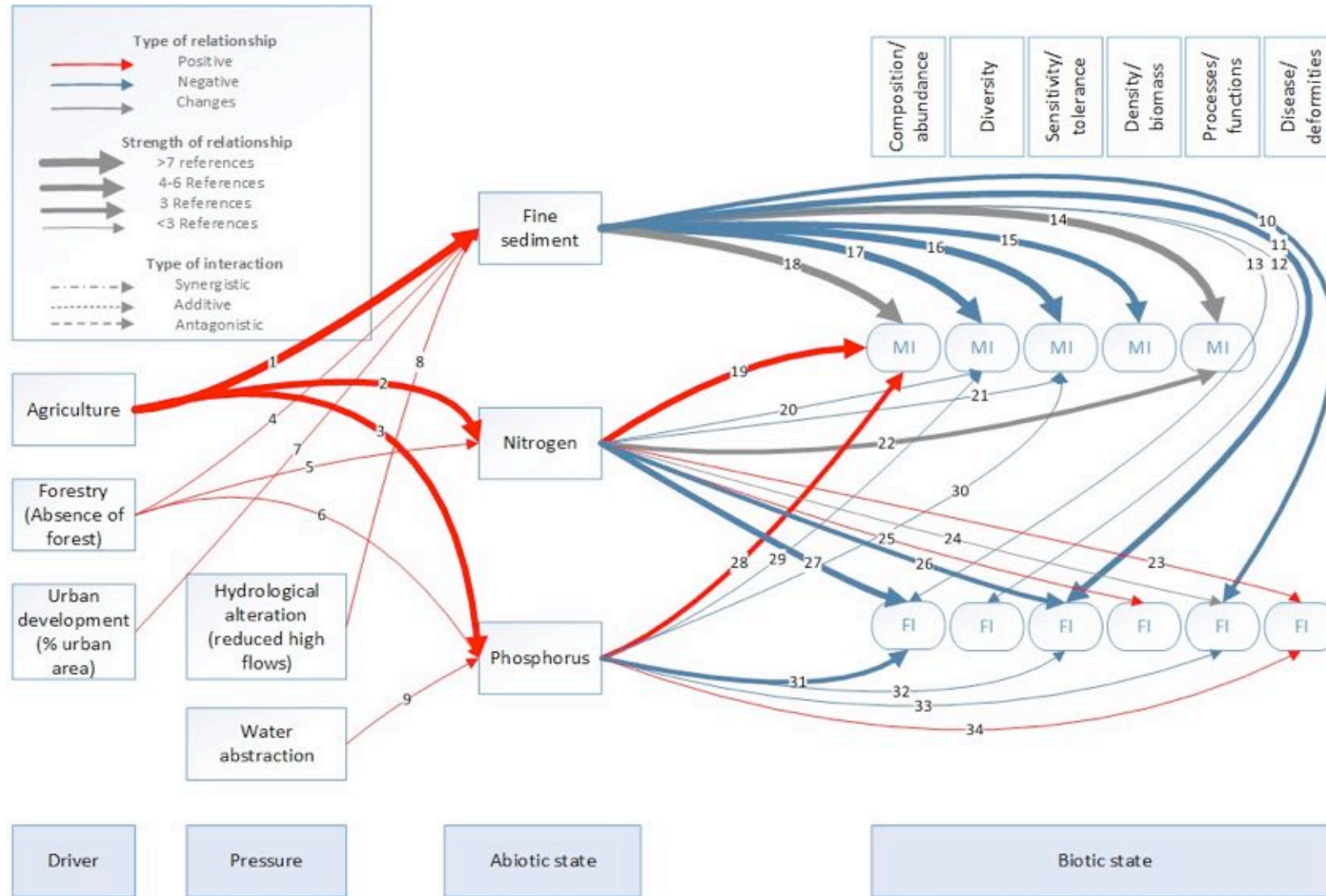


Fig 4 B1 Conceptual diagram visualising the causes and ecological effects of fine sediment and nutrients in rivers. The variable group Sensitivity/tolerance shows negative responses when sensitive taxa are affected negatively or tolerant taxa positively. MI – macroinvertebrates, FI – fish.

Table 9 The articles supporting the cause-effect linkages in the diagrams (fig. 18 & 19). Study weight is calculated according to the Eco Evidence analysis (Nichols et al. 2011). Full citation information in the reference list

Serial No.	Model link No.																														Serial No.	First author	Year	Study weight						
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30					31	32	33			
1																																		1	Angradi	1999	8			
2																																			2	Argent	1999	3		
3																																			3	Bjornn	1977	3		
4																																			4	Bo	2007	3		
5																																				5	Bryce	2010	9	
6																																				6	Buendia	2013	9	
7																																				7	Clapcott	2011	review	
8																																				8	Cover	2008	4	
9																																				9	Harrison	2010	8	
10																																				10	Kaller	2001	8	
11																																				11	Kaller	2004	4	
12	x	x	x																																	12	Lange	2014a	9	
13	x	x	x																																	13	Lange	2014b	9	
14																																					14	Larsen	2009	9
15																																					15	Larsen	2010	9
16																																					16	Larsen	2011	8
17																																					17	Lintermans	1998	5
18																																					18	Matthaei	2010	9
19																																					19	Miltner	1998	9
20																																					20	Molinos	2010	9
21	x	x	x																																		21	Mondy	2013	9
22																																					22	Osmundson	2002	3
23																																					23	Piggot	2012	9
24																																					24	Rabeni	2005	5
25																																					25	Richardson	2002	9
26	x	x	x	x	x	x																															26	Robertson	2008	9
27	x																																				27	Sutherland	2002	7
28	x																																				28	Townsend	2008	9
29	x	x																																			29	Wagenhoff	2011	9
30																																					30	Wagenhoff	2012	9
31	x	x																																			31	Wang	2007	9
32																																					32	Wood	2005	4
33																																					33	Zweig	2001	5