

# Development of a water state index to assess the severity of impacts on and changes in natural water resources

A. K. J. Suridge and A. C. Brent

## ABSTRACT

Lifecycle assessment (LCA) is a standardised methodology that is used to assess the impact of techno-economic systems on the natural environment. By compiling an inventory of energy and material inputs and environmental releases or outputs of a system, and evaluating the potential environmental impacts associated with the inventory, one can make an informed decision regarding the sustainability of a techno-economic system in question. However, the current lifecycle impact assessment (LCIA) methodologies that form part of LCA studies do not effectively consider the impacts of techno-economic systems on ground and surface water resources in South Africa (and elsewhere). It is proposed that a microbiology based index method, similar to methods proposed for terrestrial resources, can establish the states of water resources for six classes of current economic exploitation: protected, moderate use, degraded, cultivated, plantation, and urban. It is further suggested that changes in these classes (and states) can be used meaningfully in LCIA methodologies to quantify the extent to which techno-economic interventions may alter natural water resources. Research is recommended to further improve the accuracy and reliability of the water state index.

**Key words** | denaturing gradient gel electrophoresis (DGGE), environmental impact, lifecycle assessment (LCA), microbiology, polymerase chain reaction (PCR), 16S rDNA, water resources

### A. K. J. Suridge

Department of Plant Production and Soil Science,  
University of Pretoria,  
Pretoria,  
South Africa  
E-mail: karen.suridge@up.ac.za

### A. C. Brent

Natural Resources and the Environment,  
Council for Scientific and Industrial Research,  
Pretoria,  
South Africa

### A. C. Brent

Graduate School of Technology Management,  
University of Pretoria,  
Pretoria,  
South Africa

## INTRODUCTION

Lifecycle assessment (LCA) is a tool that is used to assess the impacts of techno-economic systems on the natural environment. It includes all processes from the harvest/mining of raw materials, through the manufacture of the product, until the return of the product-related materials and energy back to the environment (Brent 2003). By compiling an inventory of energy and material inputs and environmental releases/outputs of a techno-economic system, and evaluating the potential environmental impacts associated with the inventory, one can make an informed decision regarding the sustainability of a techno-economic system in question. LCAs that have been conducted on biofuel value chains, is an example (Kim & Dale 2005).

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In the LCA community, little is known about the impacts of techno-economic systems on ground and surface water resources in South Africa (and elsewhere). The Life Cycle Impact Assessment (LCIA) phase of LCAs, which has been standardised within the ISO 14000 family, quantifies environmental impacts on water and other natural resources. The quantification procedures of the LCIA phase takes into account regional and global, rather than site-specific, impacts. Table 1 describes the steps involved in the LCIA procedure. The need to develop factors to characterise the impacts of techno-economic systems on water resources, in the third step of the LCIA procedure, has been identified (Brent 2003; Landu & Brent 2006). Such

**Table 1** | Key steps of life cycle impact assessment (adapted from USEPA & SAIC 2001)

Category	Description
Selection and definition of impact categories	Identification of relevant environmental impact categories, e.g. global warming, acidification, terrestrial toxicity, etc
Classification	Assigning LCI results to the impact categories, e.g. classifying CO <sub>2</sub> emissions to global warming
Characterization	Modelling LCI impacts within impact categories using science-based conversion factors, e.g. modelling the potential impact of CO <sub>2</sub> and methane on global warming
Normalization	Expressing potential impacts in ways that can be compared, e.g. comparing the global warming and acidification potential impacts
Grouping	Sorting or ranking the indicators, e.g. sorting the indicators by location: local, regional, and global
Weighting	Emphasizing the most important potential impacts
Evaluating and reporting LCIA results	Gaining a better understanding of the reliability of the LCIA results

factors must consider the unique natural systems of South Africa with respect to comprehensiveness and modelling approaches (Brent 2003).

An impact or an environmental change is directly reflected in the microbiology of a water resource. For example, MacNaughton *et al.* (1999) monitored microbial community changes and pollution level reduction over time. Similarly, Wamberg *et al.* (2003) observed that chemical changes in the rhizosphere during plant growth were mirrored by concomitant changes within the bacterial community present. Thus it may be reasoned that a microbial community-monitoring index for both ground and surface water in South Africa could be beneficial to LCA practitioners in terms of paving the way towards generalised characterisation factors for LCIA.

Currently, there is no microbiological-oriented water state index in place that can be used directly in LCIA methodologies. However, Steyn *et al.* (2004) used a water-related quantitative microbial risk assessment (WRQMRA) process to determine probable levels of risk of pathogenic microbial infection from various water types in a local municipal area of the Free State Province of South Africa. The WRQMRA process either over- or under-estimated the risk of infection during single exposure events, indicating that, used on its own, WRQMRA could not reliably predict risk of infection. Steyn *et al.* (2004) recommended that the WRQMRA process be further developed to address predictive uncertainties. Several studies have been conducted using one indicator microorganism to infer a

particular aspect of water quality, e.g. the human pathogen *Cryptosporidium* has been genotyped in drinking water catchments and used in determining threats to public health (Ferguson *et al.* 2006). Therefore, an opportunity exists to develop a theoretical index by which water resources can be managed on the basis of microbiological indicators.

This paper proposes amalgamating all the published, available information on microbial diversity within both ground and surface water systems. The focus is on the probable microbial community variations within natural water resources when they are exposed to changes in water quality and quantity due to introduced techno-economic systems. The paper suggests a water state index that determines how quality and quantity changes in water resources can be assessed, based on changes in microbial diversity, and on specific predefined parameters obtainable from the information. Such a comprehensive microbial diversity index can then be applied to develop characterisation factors for the LCIA phase of LCAs, which, in turn, can aid in the decision making process regarding economic activities.

## THEORY AND LITERATURE REVIEW

By considering land use change and how it impacts water, there are several approaches that can be used in assessing water quality viz. physical, chemical and biological. For example, if land has changed from industrial to agricultural or vice versa the chemical changes that take place within

the soil first impact the microbial communities within the environment because they are the first to come into contact with these changes. Similarly, by monitoring the microbial community shifts within target aquatic ecosystems can prove to be an effective means of determining the impact a techno-economic system has on the aquatic environment.

In the case of exploring the impact of a system on either surface or ground water quality, certain indicators pertaining to the type of water usage can be established whereby baseline microbial communities can be monitored for changes that would indicate either detrimental or beneficial conditions prevailing in the environment being studied. However, it is important to note that only 1 to 10% of global bacterial species are culturable due to the selectivity of growth media and conditions making culture dependent ecological microbiological techniques increasingly obsolete (Kirk *et al.* 2004). Thus, the favoured approach for monitoring changes in microbial communities should be preferentially DNA/genome based. Several molecular techniques have been developed to identify and determine species diversity of microorganisms without their cultured isolation (Kawai *et al.* 2002). Polymerase chain reaction (PCR) based techniques are becoming increasingly popular for ecological research ranging from diagnostic work to genome fingerprinting and probing (Torsvik & Øvereås 2002). PCR is based on a series of thermal cycling steps that allow for exponential amplification of a precise selected portion of the cellular DNA, this is then used to yield specific information in this regarding microbial communities within the particular ecosystem being studied.

PCR is regularly applied to assay environmental samples due to the ability of the technique to detect relatively small numbers of microorganisms without requiring cell culture (Volossiuk *et al.* 1995). Thus, PCR can also be used to target certain types of genes expected within specific communities and performing specialised functions. Ribosomal RNA (rRNA) molecules, coded for by ribosomal genes within the cellular DNA (rDNA), are used as molecular chronometers due to their high degree of structural and functional evolutionary conservation. Consequently, domains within rDNA molecules harbour independent rates of sequence change (Kent & Triplett 2002) and therefore phylogenetic (relatedness) relationships can be determined by examining these changes over time (Kent & Triplett 2002).

Molecular methods used in ecological studies usually involve the separation of PCR product/amplicons on the basis of DNA nucleotide sequence differences, most often the 16S rRNA gene. However, taxonomic resolution of 16S rDNA sequences can be insufficient for discriminating between closely-related organisms in for example cyanobacteria, where the rRNA 16S to 23S internal transcribed spacer (rRNA-ITS) provided better distinction between species (Janse *et al.* 2003). Molecular methods used for these types of studies include denaturing gradient gel electrophoresis (DGGE), ribosomal intergenic spacer analysis (RISA), single strand conformation polymorphism (SSCP), amplified ribosomal DNA restriction analysis (ARDRA) and terminal restriction fragment length polymorphism (T-RFLP). Several of these methods, such as SSCP, ARDRA and T-RFLP, do not reveal diversity unless the community is very simple, due to only a very small number of species indicated in rehybridisation or sequence analysis being visualised on a gel (Nakatsu *et al.* 2000; Blackwood *et al.* 2003). Denaturing gradient gel electrophoresis (DGGE) is a most appropriate molecular method for monitoring microbial community ecology. It relies on variation in genetic sequence of a specific amplified region to differentiate between species within microbial communities (Banks & Alleman 2002; Koizumi *et al.* 2002). PCR product is electrophoresed through a polyacrylamide gel containing a linear DNA-denaturing gradient. The resulting band pattern on the gel forms a genetic fingerprint of the entire community being examined (Gillan 2004). Most commonly, 16S rRNA genes are used to give an overall indication of the species composition of a sample since they can easily be compared on gene databases. Partial sequence of this gene has been analysed from environments as complex as soil (Throbäck *et al.* 2004). Thus, global gene databases can yield invaluable information with regard to microbial organisms within communities that can be used as indicators in water impact assessments.

Much water-based data already produced using the above detailed methods are available. The National Centre for Biotechnology Information (NCBI) contains 15,472 genetic sequences for microorganisms found in ground water and 7 309 303 for those found in surface water; of these 56 are unique to polluted water in South Africa (NCBI 2007).

**Table 2** | Classes and data used to compile a water use index (adapted from Scholes & Biggs 2005)

Water/land use class	Description	Examples	Expected microbial community diversity
Protected	Minimal recent human impact on structure, composition or function of the ecosystem. Biotic populations inferred to be near their potential	Large protected areas, national, provincial and private nature reserves, 'wilderness' areas	Very diverse, containing many taxa and genera expected to be found in natural unstressed soils
Moderate use	Extractive use of populations and associated disturbance, but not enough to cause continuing or irreversible declines in populations. Processes, communities and populations largely intact	Forest areas used by indigenous peoples or under sustainable, low-impact forestry; grasslands grazed within their sustainable carrying capacity	Diverse, containing many taxa and genera expected to be found in natural unstressed soils, furthermore, taxa associated with human biology
Degraded	Extractive use at a rate exceeding replenishment and widespread disturbance. Often associated with high human population densities and poverty in rural areas. Productive capacity reduced to approximately 60% of 'natural' state	Clear-cut logging, areas subject to intense harvesting, hunting, fishing or overgrazing, areas invaded by alien vegetation	Low diversity containing most likely a high species richness in species that stress has selected for, e.g. microbes degrading wastes produced by human activities
Cultivated	Natural land cover replaced by planted crops. Most processes persist, but are significantly disrupted by ploughing and harvesting activities. Residual biodiversity persists in the landscape, mainly in set-asides and in strips between fields (matrix), assumed to constitute approximately 20% of class	Commercial and subsistence crop agriculture, both irrigated and dryland, including planted pastures and fallow, or recently abandoned cultivated areas. Orchards and vineyards	Fairly low species diversity as cultivation practices will select for taxa that grow under artificial conditions. Microbes will be more concentrated around root zones and may be existing symbiotically with specific plant species
Plantation	Natural land cover permanently replaced by dense plantations of trees. Unplanted areas assumed to constitute approximately 25% of class	Plantation forestry, typically Pinus and Eucalyptus species	Fairly low species diversity as forestry practices will select for taxa that grow under unnatural forest conditions. Microbes will be more concentrated around root zones and may be existing symbiotically with trees
Urban	Land cover replaced by hard surfaces such as roads and buildings. Dense populations of people. Most ecological processes are highly modified. Remnant semi-natural cover assumed to constitute 10% of class	Dense human settlements, industrial areas, transport infrastructure, mines and quarries	Very low diversity containing a high species richness in species that stress has selected for, e.g. microbes degrading structures and wastes produced by human activities

## SUGGESTED WATER STATE INDEX

The suggested water state index closely follows the biodiversity intactness index that has been introduced for terrestrial resources (Scholes & Biggs 2005). A number of classes have been proposed to define the economic exploitation of land resources. Similar classes for water resources are defined in Table 2. The following sections provide examples from the NCBI in terms of the potential quantified data associated with the expected microbial community diversity for the different classes.

## CONCLUSIONS

LCIA methodologies, that form part of LCA studies, rely on sound environmental modelled and empirical data to assess, in a quantitative manner, the potential impact of techno-economic systems on natural resources. With respect to water resources, this paper proposes that an amalgamation of microbiological information, indicating community change, as a result of techno-economic processes, is a possible means to develop appropriate characterisation factors for ground and surface water categories of LCIA.

Currently there is no microbiological index available that can be utilised directly in LCIA methodologies. The paper suggests such a water state index, based on land use classes, and available information in the NCBI. If a techno-economic system may cause a change in land use class in a region, then the extent of this impact can be determined by the degree to which the microbial states may change. Similarly, an influence on the water use class in a region can be evaluated by considering the states of microbial communities associated with different classes. The delta of the state changes can form the basis for LCIA characterisation factors.

To improve the accuracy and reliability of the water state index in the South African context the following further research activities are required:

- Collection of representative water samples of each defined area in South Africa.
- Microbial population diversity analyses.

- Tentative molecular identification of indicator microbial species.
- Classification of specific species into water/land use class.

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