

The Challenges and Opportunities in Monitoring and Modeling Waterborne Pathogens in Water-  
and Resource-Restricted Africa:  
*Highlighting the critical need for multidisciplinary research and tool advancement*

Megan Kathleen Holcomb

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Kathleen A. Alexander  
Leigh-Anne H. Krometis  
Adil N. Godrej

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**ABSTRACT**

Water is a primary shared resource that connects all species across the landscape and can facilitate shared exposure to a community of waterborne pathogens. Despite remarkable global progress in sanitation and hygiene development in the past two decades, infectious diarrhea remains a prominent public health threat in sub-Saharan Africa. This thesis identifies and discusses persistent challenges limiting the success of current waterborne disease management strategies and several existing research hurdles that continue to impede characterization of microbial transmission and transport. In this work, the Chobe River watershed in Northern Botswana serves as a target study site for the application of hydrological modeling tools to quantify emergent water quality and health challenges in Southern Africa. A watershed model with extensive data requirements, the Hydrological Simulation Program – Fortran (HSPF), is used to identify primary data gaps and model assumptions that limit the progress of model development, and guide opportunities for data collection, tool development, and research direction. Environmental pathogen exposure risk and epidemiological outbreak dynamics are best described by interactions between the coupled human and environmental processes within a system. The challenge of reducing diarrheal disease incidence strengthens a call for research studies and management plans that join multiple disciplines and consider a range of spatiotemporal scales.

## Attribution

I would like to extend a gracious ‘thank you’ to my advisor and mentor, Kathleen A. Alexander, Ph.D, D.V.M., who is a co-author on chapters two and three of this thesis. Dr. Alexander is currently an associate professor of disease ecology in the Department of Fish and Wildlife Conservation at Virginia Polytechnic Institute and State University. Dr. Alexander manages the Alexander Wildlife Research Group at Virginia Tech and the CARACAL Biodiversity Center in Kasane, Botswana. CARACAL (Center for African Resources: Animals, Communities, and Land Use) is a field based non-governmental organization, which was started in 2001 in recognition of the need to integrate traditional and scientific understanding of natural resources and promote partnership between government and local communities in natural resource management. This work was inspired by her commitment, energy, and insight to advance our understanding of the extraordinary Chobe Region ecosystems.

Dr. Alexander can be reached through:

Department of Fish and Wildlife Conservation; *email*: kathyax@vt.edu;  
*address*: 100 Cheatham Hall Blacksburg, VA 24061; *phone*: +01 540 231 7580

CARACAL Biodiversity Center; *email*: caracal@caracal.info; *address*: PO Box 570, Kasane, Botswana; *phone*: +267 625 2392

# Table of Contents

<b>CHAPTER 1: INTRODUCTION.....</b>	<b>1</b>
1.1 THE MANAGEMENT OF LIMITED WATER RESOURCES AND DISEASE.....	1
1.2 REFERENCES .....	2
<b>CHAPTER 2: WATER AS A LIMITING RESOURCE TO DEVELOPMENT IN SOUTHERN AFRICA: CHALLENGES AND OPPORTUNITIES IN EVALUATING WATERBORNE DISEASE CAUSALITY, PATHOGEN TRANSMISSION, AND DISEASE PREDICTION .....</b>	<b>3</b>
2.1 ABSTRACT.....	3
2.2 INTRODUCTION .....	3
2.2.1 <i>Water – A limiting resource and complex management challenge</i> .....	3
2.2.2 <i>Infectious Diarrhea – A continued threat to human development and health</i> .....	4
2.2.3 <i>Resource Management – The dryland environments of southern Africa</i> .....	5
2.2.4 <i>The Complexities of Isolating Causality in Diarrheal Disease</i> .....	5
2.3 MAKING SENSE OF MULTIPLE TRANSMISSION PATHWAYS.....	7
2.3.1 <i>Where to direct intervention efforts in complex causation webs?</i> .....	7
2.3.2 <i>Waterborne pathogen transmission frameworks – moving beyond the F-Factors</i> .....	8
2.4 THE MISMATCH OF PREDICTIVE SCALES: UNCERTAINTIES IN DISEASE MONITORING, WATER QUALITY MODELING, AND CLIMATE CHANGE PREDICTIONS.....	10
2.4.1 <i>Monitoring waterborne pathogens</i> .....	11
2.4.2 <i>Modeling waterborne pathogen transport</i> .....	12
2.4.3 <i>Diarrhea prediction under changing climates</i> .....	13
2.5 RESEARCH AND MANAGEMENT OPPORTUNITIES: COMBINING TOOL APPLICATIONS ACROSS DISCIPLINES.....	13
2.6 CONCLUSION.....	15
2.7 REFERENCES .....	17
<b>CHAPTER 3: THE CHALLENGE OF MODELING WATERBORNE PATHOGENS IN DRYLAND RIVERINE FLOODPLAINS: A CRITICAL NEED FOR TOOL ADVANCEMENT IN WATER- AND RESOURCE-RESTRICTED AFRICA.....</b>	<b>24</b>
3.1 ABSTRACT.....	24
3.2 INTRODUCTION .....	24
3.2.1 <i>Water Quality Impacts on Human Health</i> .....	24
3.2.2 <i>Broad challenges for watershed modeling in Africa</i> .....	25
3.2.3 <i>Inventory of available pathogen transport models</i> .....	25
3.2.4 <i>Model selection</i> .....	28
3.3 METHODS AND RESULTS.....	28
3.3.1 <i>Study region</i> .....	28
3.3.2 <i>HSPF Model Structure and Development</i> .....	30
3.4 DISCUSSION.....	33
3.4.1 <i>HSPF Model application in semi-arid floodplain systems</i> .....	33
3.4.2 <i>Managing complex systems with watershed-scale water quality models</i> .....	36

3.4.3 <i>Recommendations for Tool Development</i> .....	36
3.5 CONCLUSION.....	40
3.6 APPENDIX A.....	41
3.7 REFERENCES .....	42

## List of Figures

<b>CHAPTER 2.....</b>	<b>3</b>
FIGURE 1.....	7
Factors contributing to a biased disease signal from which responsive health management decisions are to be made	
FIGURE 2.....	9
Possible routes of fecal transmission from source to human exposure	
FIGURE 3.....	15
While water quality models and epidemiological models are not currently designed to be used in tandem, these traditionally separate disciplines are highly connected in the venture of waterborne disease management	
<b>CHAPTER 3.....</b>	<b>24</b>
FIGURE 1.....	29
A multi-scale context of the research site	
FIGURE 2.....	32
A visual comparison of land use between computational processing and Landsat false color imagery.	
FIGURE 3.....	35
HSPF model development procedure with limitations to progress highlighted	

## List of Tables

<b>CHAPTER 3</b> .....	<b>24</b>
TABLE 1. ....	26
Pathogen transport models and hydrological-component program acronyms used in Chapter 3	
TABLE 2. ....	27
Comparison of pathogen transport models listed, roughly, in order of increasing compartmentalization and complexity	
TABLE 3. ....	30
Chobe River annual extent of flooding	
TABLE 4. ....	31
Watershed preprocessing programs	
TABLE 5. ....	32
Land use classification by sub-watershed	

## List of Abbreviations, Acronyms, and Definitions

ArcGIS	ArcGIS® and ArcMap™ software by Environmental Systems Research Institute (ESRI)
ArcHydro	ArcGIS® extension Version 2.0
ArcSWAT	ArcGIS® extension and graphical user input interface for SWAT
B.C.E.	Before the Common Era
BASINS4	Better Assessment Science Integrating point & Non-point Sources Version 4 (program)
COLI	Bacteria generation model
CREAMS	Chemicals, Runoff, and Erosion from Agricultural Management Systems (hydrology model)
disease triangle	conceptual model that shows the interactions between the environment, the host and an infectious (or abiotic) agent (Scholthof, 2006)
<i>E. coli</i>	<i>Escherichia coli</i>
eclecticism	conceptual approach that does not hold rigidly to a single paradigm or set of assumptions, but rather draws upon multiple theories, approaches, or ideas to gain complementary insights into a subject, or applies different theories in particular cases.
enteric disease	enteric infections enter the body through the mouth and intestinal tract and are usually spread through contaminated food and water or by contact with vomit or feces
ethnotheories	the ways people collectively recognize and explain disease etiology or causation, progression, prevention and treatment in terms of their own understandings of how the world works (Brewis et al., 2013)
FIB	fecal indicator bacteria
GIS	geographic information systems
GLEAMS	Groundwater Loading Effects of Agricultural Management Systems (hydrology model)
HECGeo-HMS	ArcGIS® Extension by Army Corps of Engineers
heuristic	experience-based techniques used for problem solving, learning, and discovery; heuristic methods are used to speed up the process of finding a “good enough” solution, where an exhaustive search is impractical.
HIV/AIDS	Human Immunodeficiency Virus / Acquired Immunodeficiency Syndrome
HSPF	Hydrological Simulation Program – Fortran (model)
hydrologic regimes	water distribution over time in a watershed, among precipitation, evaporation, soil moisture, groundwater storage, surface storage, and runoff
IHACRES-WQ	Identification of unit Hydrographs And Component flows from Rainfall, Evaporation and Streamflow data (model)
immunocompetence	ability to develop an immune response following exposure to an antigen
immunosuppression	partial or complete suppression of the immune response of an individual
km	kilometer
microbial modeling	mathematical descriptions of the physical, chemical, and biological processes governing microbial transport

mm	millimeter
MST	microbial source tracking
MWASTE	waste generation model
NPS	Non-Point Source (pollutant)
passive surveillance	Reports submitted from hospitals, clinics, public health units, or other sources to provide critical information for community health monitoring (Nsubuga et al., 2006)
PCB	Pathogen Catchment Budget (model)
prevalence	total number of cases of disease existing in a population
PROMISE	emission model
qPCR	quantitative Polymerase Chain Reaction
SADC	Southern African Development Community
SEDMOD	Spatially Explicit Delivery Model
STARS	Solute Transport with Advection, Resuspension and Settling (model)
SWAT	Soil and Water Assessment Tool (model)
TauDEM	Terrain Analysis Using Digital Elevation Models Version 5
UCI	User Control Input (HSPF core file)
WAMView	Watershed Assessment Model
WARMF	Watershed Analysis Risk Management Framework (model)
WASH	water, sanitation, and hygiene
WATFLOOD	University of Waterloo Flood Forecasting System (hydrology model)
WATNAT	dispersion (hydrology) model
WDM	Weather Data Management (HSPF core file)

# Chapter 1:

## Introduction

### 1.1 The management of limited water resources and disease

Concerns about the availability, accessibility, and quality of the world's freshwater resources are growing (Beck & Bernauer, 2011; Gleick, 1993; Ragab & Prudhomme, 2002; Sivapalan, 2003; Srebotnjak et al., 2012). As a life sustaining natural resource, water is one of the most basic components to human and animal survival and fundamental to the ecosystems on which we depend. Water resources also facilitate a shared exposure to communities of waterborne pathogens that contribute to high human mortality and morbidity associated with diarrheal disease around the world. Despite remarkable global progress in sanitation and hygiene development in the past two decades, infectious diarrhea remains a prominent concern in sub-Saharan Africa (Bandyopadhyay et al., 2011).

On many scales, water is the ultimate shared resource. Water-restricted environments under strong seasonal regimes are extremely vulnerable to natural and human-induced pollution across the landscape. Along with the cross-boundary nature of watersheds, this creates complex water-health management scenarios regardless of world region or national economic status. Successful water management strategies depend on "striking a balance between human resource use and ecosystem protection" (Vörösmarty et al., 2010).

Aspects of resource quality and quantity are strongly influenced by the linkages and coupled dynamics of human and natural environments. All life is subject to the variability of the water cycle, including the temporal and spatial heterogeneities in availability. Any imbalance between the local demand and availability of this resource is cause for public health concern and, depending on severity, is often referred to as water scarcity, -stress, or -vulnerability. The degree of water scarcity can be measured by the quantity of water in cubic meters available per person, per year, as defined by the Falkenmark Water Stress Index (Falkenmark, 1989). The term 'quantity' can, however, be misleading because scarcity is more than a physical volume of freshwater. Rather, it is the availability, accessibility, and quality of water resources, which may define scarcity in a region. Particularly in developing countries, water scarce regions include areas where rainfall is plentiful and freshwater is visually present across the landscape although unavailable for safe use.

It is critical that communities and governments prepare for changes in seasonality, population, and development in a region. Changes in any of these can affect the intensity of water scarcity and waterborne disease in a community, driving the need for resource abstraction planning, control, and treatment (Huntjens et al., 2011; Ragab & Prudhomme, 2002). Despite a broad research agenda to investigate social influences (e.g., hygiene, use, reuse, storage), institutional influences (e.g., sanitation, transport, technology, demand), and ecological influences (e.g., climate, land use, hydrology, environmental loading) on the microbial contamination of drinking water, few studies recommend holistic suggestions to improve infectious diarrhea monitoring

and mitigation strategies (Eisenberg et al., 2012). A comprehensive intervention approach should consider all intricacies and feedback loops of pathogen transmission, in context of the local culture and institutional system.

Substantial research hurdles remain that continue to impede a deeper understanding of microbial transmission, which could improve current disease intervention measures. Waterborne diseases do share fundamental environmental and social drivers, but the prevalence of disease is unique to the local landscape, local human impact, and dominant social and economic structure. The complex and integrated causes of diarrheal disease strengthen a call for research studies and management plans that cross multiple disciplines and span a range of scales.

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## CHAPTER 2:

# **Water as a limiting resource to development in southern Africa: *Challenges and opportunities in evaluating waterborne disease causality, pathogen transmission, and disease prediction***

Megan K. Holcomb and Dr. Kathleen A. Alexander

### **2.1 Abstract**

Water is a primary shared resource that connects all species across the landscape and can facilitate shared exposure to a community of waterborne pathogens. Despite remarkable global progress in sanitation and hygiene development in the past two decades, infectious diarrhea remains a prominent public health threat in sub-Saharan Africa. This paper identifies and discusses three persistent challenges limiting the success of current waterborne disease management strategies: (1) disease surveillance efforts can only describe a portion of the complex transmission web, and thus provide an incomplete or potentially biased picture of true disease prevalence; (2) disease causation is difficult to isolate as waterborne pathogen transmission arises from a complex array of organisms and interdependent exposure pathways involving social, institutional, ecological, and climatic factors; (3) our understanding of present disease and forecasts of future outbreaks are limited by our ability to relate and model system influences at multiple predictive scales. With a particular focus on Southern Africa, we review our current understanding of diarrheal disease dynamics and highlight future research and public health management needs.

### **2.2 Introduction**

#### **2.2.1 Water – A limiting resource and complex management challenge**

Water-restricted environments that experience strong seasonal regimes (dry and wet seasons) are extremely vulnerable to natural and human-induced pollution across the landscape. Dramatic seasonal changes in surface water availability can concentrate dependent animal and human communities around surface sources, intensifying pollution to already limited supplies. In these same water scarce regions, declines in water quality and quantity may not only impact the health of humans and animals but also economic or infrastructure development and political progress (Calder et al., 1995; Srebotnjak et al., 2012).

Endemic or episodic waterborne diarrheal disease is a persistent and global obstacle to health and development in resource-poor regions. Disease occurrence arises from the layered but interconnected effects of local climate, environmental dynamics, and socioeconomics occurring at the regional, community, household and individual levels. Aspects of water resource quality and quantity are strongly influenced by the linkages between humans and the natural environments. Aquatic environments facilitate a shared exposure to a community of pathogens

for all water-dependent species. Specifically, enteric pathogens that originate in humans or animals (zoonotic disease) and enter shared waterways effectively connect susceptible populations allowing pathogens to move between humans and animals. Even in the wild, open lands of Southern Africa, most individuals do not have direct contact with wildlife; pathogen transmission more commonly occurs though the shared landscape and, most directly, through shared water sources. Complex pathogen transmission and reservoir dynamics that involve humans, animals and the environment complicate the monitoring and management of waterborne disease. These dynamics are influenced by the density and distribution of humans and animals across a watershed, seasonal drivers, and physical landscape properties. Beyond environmental characteristics, human exposure risk is also affected by socioeconomics and individual and societal behavior influenced by local ethnotheories (Meays et al., 2004; Brewis et al., 2013). Enhanced predictive capacity and public health management of diarrheal disease requires that we identify a more detailed local understanding of the dynamic relationships between communities and the ecosystems to which they are connected.

### **2.2.2 Infectious Diarrhea – A continued threat to human development and health**

Diarrhea remains a prominent concern in developing countries due to frequent reliance on untreated drinking water, inconsistent sanitation standards and habits, and poor immunological health as compared to industrialized nations (e.g., malnutrition or HIV/AIDS (Human Immunodeficiency Virus / Acquired Immunodeficiency Syndrome)) (Snyder & Merson, 1982; Gleick, 1993; UNICEF & WHO, 2009; Wardlaw et al., 2010). Large-scale intervention efforts to improve water, sanitation, and hygiene (WASH) systems have been identified as a primary approach to reduce the global burden of diarrheal disease. While individual government and international programs have made progress in reducing diarrheal disease, this disease syndrome still remains the second leading cause of death in children under five years of age globally (Grabow, 1996; Eisenberg et al., 2012). Every year, there are 4 billion cases of diarrheal disease worldwide, which kill an estimated 1.8 million people (Tumwine et al., 2002; Cutler & Miller, 2004; Hutton et al., 2007; UNICEF & WHO, 2009). Of all global diarrheal-associated deaths, 41 percent occur in sub-Saharan Africa alone (Bandyopadhyay et al., 2011).

The impact on waterborne disease risk is further elevated in sub-Saharan Africa where it is estimated that 90% of HIV/AIDS patients suffer from chronic diarrheal disease with an unknown proportion being infectious in nature (Obi et al., 2006). Moreover, 9 of the 15 member countries in Southern African Development Community (SADC) are identified as having the highest HIV/AIDS prevalence rates in the world (CIA, 2013). These statistics make it readily apparent that diarrheal diseases impacts are likely to be compounded by the HIV epidemic (Obi et al., 2006). This epidemic has impacted population vulnerability to infectious disease: diarrheal disease is a particular threat in relation to direct immunosuppression as well as a heightened risk in children with altered immunocompetence (as a result of not being breast fed to reduce mother-to-child transmission of HIV) (Glass & Stoll, 1989). While diarrheal disease surveillance is still directed at the under-five age group as the primary population at risk, the elevated presence of immunologically compromised individuals in Southern Africa and elsewhere may require a reevaluation of this approach (Alexander & Blackburn, 2013).

### **2.2.3 Resource Management – The dryland environments of southern Africa**

In Southern Africa, public health programs are challenged with the complexity of managing both the quantity and quality of water resources, limiting human exposure to contaminant sources, and advising safe hygiene practices. Dominant factors governing limitations on water *quantity* can include: freshwater allocation (e.g., water rights, agricultural practices), climate variables (e.g., precipitation, seasonality), and the geological and ecological landscape (e.g., infiltration, storage, and transport). Factors which may degrade water *quality* include: non-point source pollution (related to wildlife populations or anthropogenic land use), point source pollution (e.g., waste effluent), and contamination at point-of-use (related to inappropriate hygiene practices and poor sanitation facilities).

Extreme wet-dry cycles in water scarce regions, like those in Southern Africa, have been shown to augment waterborne pathogen transmission. While vast stretches of Southern Africa are characterized by true- and semi-desert landscapes (i.e., Kalahari and Karoo deserts), water-scarce regions can include zones where rainfall is plentiful and freshwater is visually present across the landscape, though not appropriate for immediate potable use. Seasonal cycles and restricted surface water availability concentrates wildlife, livestock, and humans around critical regional resources (Alexander et al., 2012a). This density may increase pathogen concentrations in waterways and increase the potential for human exposure. Decreased availability of water resources may also result in significant sanitation and hygiene behavior modifications, such as wastewater reuse or decreased hand-washing, as well as the potential amplification of vector (i.e., fly) mediated pathogen transmission (Alexander et al., 2012b).

Limited or weak sanitation infrastructure in resource-poor settings remains a barrier to more rapid improvements of public health. Within sub-Saharan Africa, only 61% of the population has gained access to improved drinking water since 1990; this is in comparison to the 86% global average (WHO, 2012). Global or regional averages unfortunately fail to describe the large disparities between urban and rural development within the WASH sector. In 2004, it was estimated that only 31% of rural populations had access to improved sanitation – a strong contrast to the 73% of urban residents with improved systems (Obi et al., 2006).

Successful management of waterborne enteric disease is dependent on specific characteristics of the local landscape. Many of the traditional water quality management approaches (largely designed in industrialized nations) are grossly inefficient and ill fit for developing countries (Ongley, 1997). In poor to low economic environments, the maintenance and functionality of sanitation facilities (i.e., water treatment plants and sewage/waste disposal) are often below standards needed to protect communities against common waterborne disease (Carter et al., 1999). Even when sufficient water treatment facilities are in place, the degree of local dependence on untreated sources of household water (i.e., direct access) or household hygiene and storage habits may counteract any decrease in disease incidence related to sanitation system upgrades.

### **2.2.4 The Complexities of Isolating Causality in Diarrheal Disease**

Diarrheal disease is unusual among prominent global health issues because it is most often monitored and reported as one lumped, global disease syndrome rather than by specific etiological agent. Infectious diarrhea is a generic response to infections from bacteria such as *Escherichia coli* (*E. coli*), *Shigella*, *Salmonella*, and *Vibrio cholera*; protozoa such as *Cryptosporidium* and *Giardia*; or viruses such as measles or rotavirus (Prüss-Üstün et al., 2004; Fewtrell et al., 2007; Eisenberg et al., 2012; Tate et al., 2012). Due to the multitude of pathogenic agents responsible for infection and wide range of environmental sources and transmission mediums that can lead to exposure, health institutions rarely diagnose a specific cause of infectious diarrhea in both resource-sufficient and -limited settings (Pawlowski et al., 2009; Alexander & Blackburn, 2013). Diagnoses may be generalized for numerous reasons. For example, multiple pathogens (co-infection) could be responsible for the diarrhea syndrome, multiple health conditions may result in non-infectious diarrhea occurrence, a health facility may simply lack the necessary diagnostic equipment and reagents, or medical staff might lack the time and motivation to pursue diagnostic investigations (Alexander et al., 2013). Within these low-resource epidemiological settings, diarrheal disease causing pathogens require different diagnostic approaches making pathogen identification impractical and supportive care the primary medical response (Pawlowski et al., 2009).

Specific diagnoses become even more challenging in resource-poor settings where lack of human and economic resources limit outbreak investigations, long-term surveillance, and monitoring program scope and design (Alexander & Blackburn, 2013). Public health strategies aimed at reducing diarrheal disease are therefore limited by an incomplete understanding of specific disease drivers, the ability to distinguish infections among a broad spectrum of diarrhea-inducing agents, and the complex interactions between environmental transport and route of human exposure. Figure 1 provides an overview of the multitude of factors that shape observed trends in disease incidence or disease signal (e.g., the number of cases observed over a time). Interpretation of this often-biased signal can result in the application of public health interventions that do not adequately address underlying and often interdependent drivers of disease transmission. Outside of factors associated with the traditional assessment of host, pathogen, and environment interactions (e.g., the disease triangle), institutional, economic, and health policy frameworks will strongly influence disease exposure and risk (Figure 1). Further, reported case incidence of diarrheal disease from surveillance programs can be shaped by many local factors including education level, health seeking behavior, and the capacity of health facilities to track spatial and temporal outbreak patterns (Alexander et al., 2013).

Diarrheal case data reflect a composite data signal (unclear causality) and are often identified through passive, and potentially biased, surveillance systems. Case data reflects the *recorded* number of patients that present with diarrhea disease to a medical facility and this will not be equivalent to the true prevalence of the disease. For this reason, it is difficult for health management responders to interpret an outbreak's true magnitude and pattern of occurrence (Alexander & Blackburn, 2013). Despite the noise in this data signal reviewed here and elsewhere (Alexander et al., 2013) this will often be the only data source available.

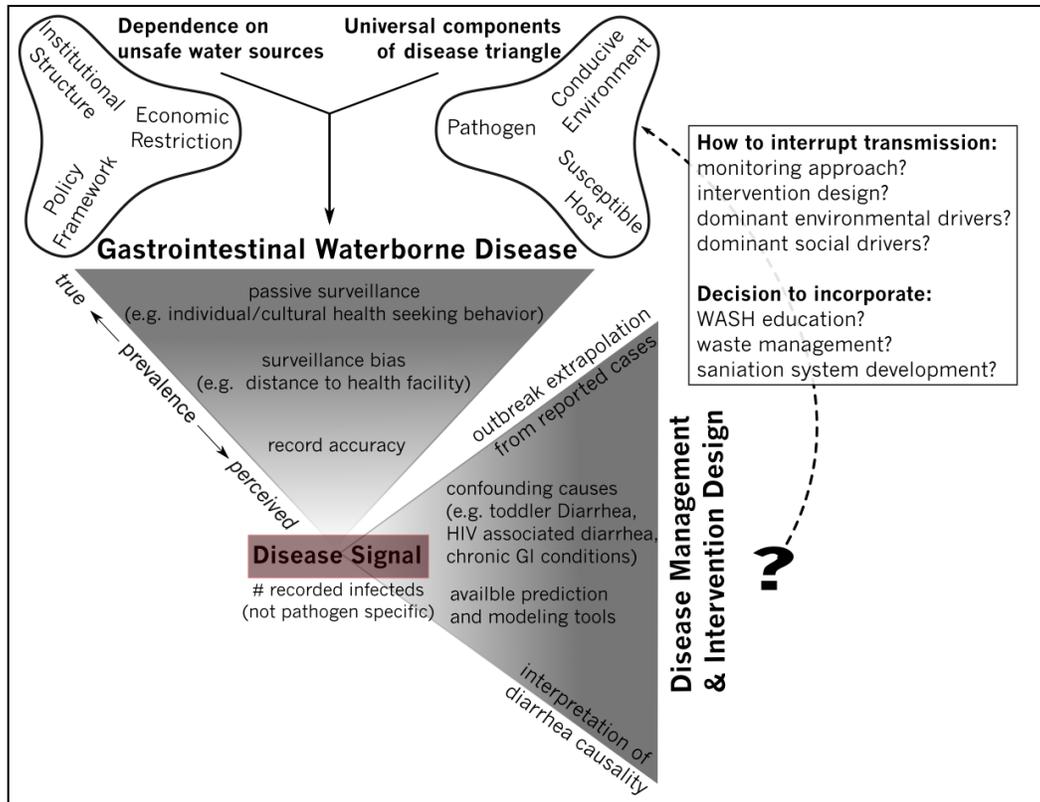


Figure 1. Factors contributing to a biased disease signal from which responsive health management decisions are to be made.

## 2.3 Making Sense of Multiple Transmission Pathways

### 2.3.1 Where to direct intervention efforts in complex causation webs?

Identifying and understanding the mechanisms in which interdependent driving forces influence waterborne pathogen transmission and diarrheal disease are fundamental to the design of effective and efficient public health interventions. The conclusion that multiple pathways influence fecal-oral pathogen transmission is long-standing, dating as far back to Hippocrates in 400 B.C.E (Before the Common Era) (Fewtrell et al., 2005; Halverson et al., 2010). However, much of the current literature acknowledges but does not directly address this challenge of understanding the full dynamics of enteric disease transmission (Eisenberg et al., 2012). Eisenberg et al. (2012) synthesize four decades of research on diarrheal disease epidemiology, noting a lack of emphasis on the interdependencies of enteric pathogen transmission. Of 415 articles reviewed, over half of the observational studies focused on only one transmission pathway. Even when studies included multiple transmission pathways, very few acknowledged the coupled systems and feedback loops can be created by sustained fecal-oral transmission as a result of seasonal water scarcity (e.g., increased animal density around reduced surface water, behavioral changes in water storage or hygiene habits, and wastewater disposal).

An extensive meta-analysis of WASH interventions by Fewtrell et al. (2005) found any intervention method implemented in a resource-poor community significantly reduced the risk of

diarrhea to some degree. While a possible publication bias for positive outcomes was noted, single-transmission pathway interventions had a similar degree of impact on disease risk, as did studies that addressed multiple-transmission pathways. The review supports the counterintuitive notion that multiple-transmission interventions may not actually have an additive effect – a phenomenon also noted by Esrey et al. (1991). A debate is ongoing over the relative effects of management interventions on the reduction of diarrheal disease and relative influence of source water quality compared to post-source contamination (Gundry et al., 2003).

Prüss-Üstün et al. (2004) hypothesized a log-linear relationship exists between fecal-oral pathogen dose and probability of infection for many infectious diarrheal diseases. Combined with the possibility that single- and multiple-transmission pathway interventions produce comparable results in developing countries supports an existing hypothesis that one transmission pathway may never fully dominate another until some tipping point in reduced exposure is achieved through WASH management efforts (Prüss-Üstün et al., 2004). Thus, these large and intricate waterborne pathogen transmission webs, characteristic of developing or resource-restricted communities, may obscure the direct effects of water quality interventions (watershed management), sanitation system interventions (source treatment), or hygiene interventions (post-source handling).

### **2.3.2 Waterborne pathogen transmission frameworks – moving beyond the F-Factors**

In the 1950s, the concept of transmission channels of disease from excreta was conceptually modeled and later termed the “F-diagram” (Wagner & Lanoix, 1958). The diagram, only slightly adapted over time, originally comprised several “F-factors” that influenced fecal-oral disease transmission: feces, fluids (drinking/storage/wash water), fingers (unclean hands), flies, food, fields (crops, soil, irrigation), and face (ingestion of contaminated water or food) (Eisenberg et al., 2007; Fewtrell et al., 2007; Prüss-Üstün et al., 2008). Conceptual maps such as the “F-diagram” help visualize pathogen pathways, but because they are very human-centric they can mask strong interdependencies, feedback loops, and connections across the human-animal interface.

Figure 2 illustrates significant components that influence pathogen loading, pathogen transport, and pathogen transmission that lead to exposure and disease incidence. Forcing factors external to the direct pathways of pathogen transmission, such as seasonality, population density, or intensity of human development, drive the spatiotemporal dynamics of exposure – influencing the density and spatial distribution of fecal loading across a watershed. Numerous climate and landscape factors can govern the likelihood that fecal matter is transported across the landscape and into waterways (e.g., land use, vegetation density and biodiversity, or the intensity of precipitation events). The magnitude and route of human exposure to contaminated “F-factors” in water-limited communities is largely dependent on local sanitary infrastructure, potable water supply, and human behavior.

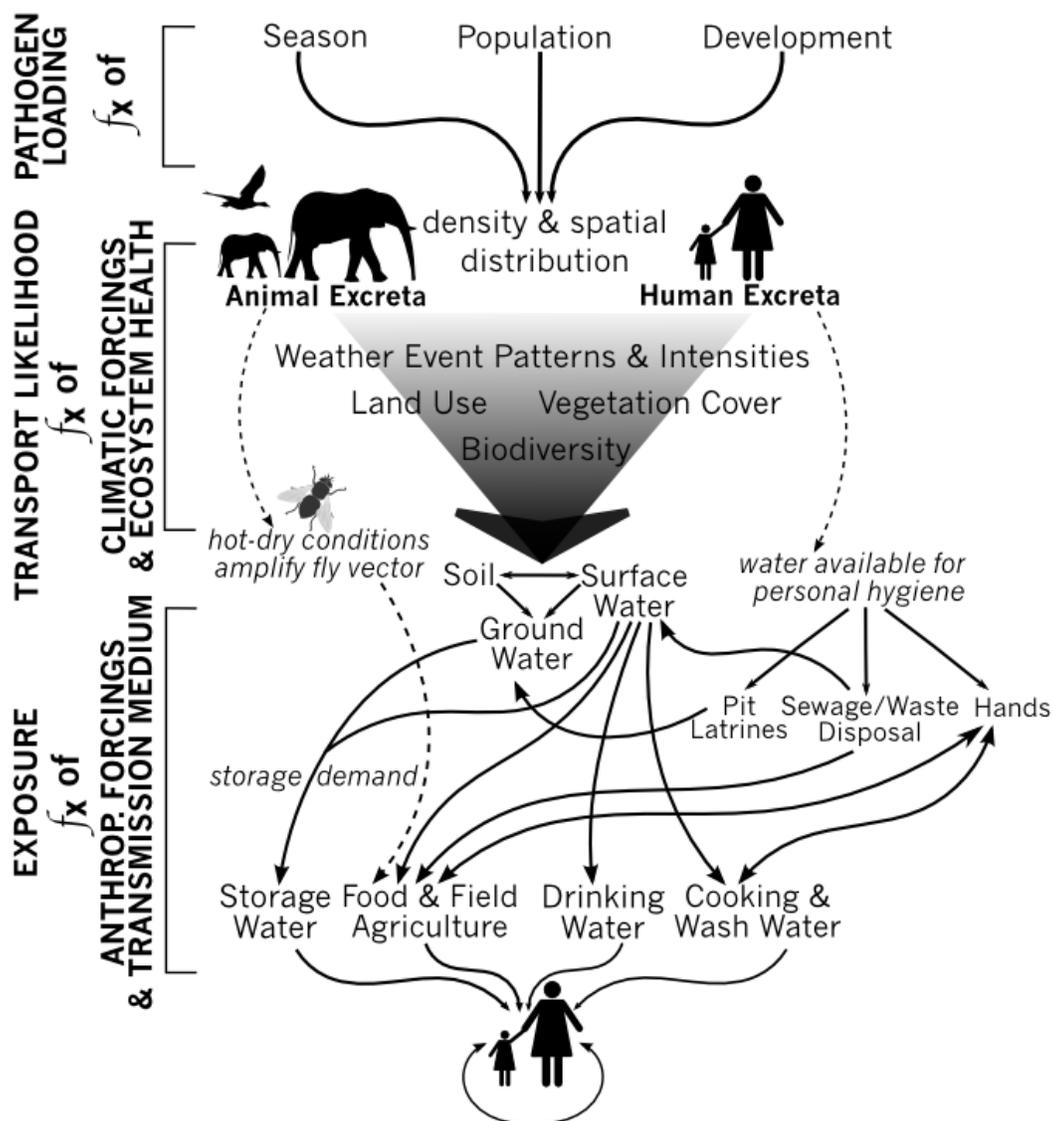


Figure 2. Possible routes of fecal transmission from source to human exposure. External forcings such as seasonality, population, and human development can drive the intensity of fecal loadings across the landscape. Dotted lines infer a transmission connection “is dependent on” some condition (*italicized*).

Eisenberg et al. (2007) modeled the effect of water quality improvements among five different transmission pathways: 1) between-households; 2) within-households; 3) household-to-water; 4) water-to-household; and 5) “external sources” which encompass upstream contamination, food, and infectious individuals exposed outside of the community (i.e., outside defined system boundaries). In this study, the effects of water quality improvements were ultimately dependent on the level of sanitation and hygiene within a household and not on the transmission mechanism. Shorter transmission routes within a household, also known as “domestic domain contamination” can override the impact of water quality improvements, which underscores the interdependent nature of diarrheal disease causation. These domestic domain contamination routes identify exposure and transmission risks that arise after acquisition of clean water (i.e., post source contamination) and can include water collection and storage practices, handling of

water used for drinking and cooking, laundering, washing, bathing, wastewater disposal, and personal hygiene (Tumwine et al., 2002; Prüss-Üstün et al., 2004; Eisenberg et al., 2012). Longer routes, characterized as “public domain transmission”, can include contamination through economic production schemes (e.g., food crop or industry), local waste and sanitation infrastructure, or environmental contamination (e.g., livestock, wildlife, or upstream pathogen introduction) to name a few.

Ezzati et al. (2005) used a “casual web” approach to explain diarrheal disease transmission that broadly describes environmental risk exposure in the developing world. While intentionally generalized, the framework recognizes that poor or marginalized communities bear a disproportionate exposure to multiple risk factors and are often more susceptible to those environmental hazards. The paper catalogs disease causality into distal (socioeconomic and demographic), proximal (technological, environmental, or behavioral), and physiological or pathophysiological causes. In itself, the framework does not provide deep insight into the causality of exposure and infection, but its representation of risk factors as a “linked network” is useful in guiding monitoring efforts and intervention evaluation across each “level” of causation (Ezzati et al., 2005). The authors note that certain feedbacks related to disease incidence exist can directly modify risk behavior (e.g., A child experiencing diarrhea may be bathed more frequently, either increasing the chance of infection through wastewater or decreasing disease risk through a conscious change in household hygiene habits).

These alternative frameworks offered by Eisenberg et al. (2007) and Ezzati et al. (2005) go beyond simplistic transmission webs; the integration of these with detailed “F-diagrams” may help depict a more complete system to direct future disease assessment or intervention efforts.

## **2.4 The Mismatch of Predictive Scales: Uncertainties in disease monitoring, water quality modeling, and climate change predictions**

Resource and health managers continually seek an improved understanding of local or regional factors that influence water supply demand and quality in order to design effective public health management strategies. This understanding requires insight into underlying hydrological processes, user demands, and the impact of changing climates (Daniel et al., 2011). An accurate assessment of hydrological regimes creates a foundation for water quality assessment to manage future development and climate change in a watershed (Simonovic, 2002).

Transparency in climate-, hydrological-, and disease-models is essential to best inform decision makers and encourage flexible management decisions. As predictive models are merely tools that help reveal trends for the purpose of informing resource management policies, researchers should always quantify uncertainties in data (historical and collected), calibrated parameters, and final predictions when appropriate (Wu et al., 2006). Uncertainty analysis is a means toward achieving transparency and a means of evaluating management alternatives based on the relative risks of violating water quality standards (Wu et al., 2006). Littell et al. (2011) advocates that “models incorporate imperfect information and are a simplified version of reality; by understanding these imperfections, we can use models to decrease the uncertainty associated with the future”. Uncertainty analysis is thus useful because a quantitative magnitude of

uncertainty provides a “measure of value of information” that can largely contribute to environmental management decisions (Reckhow, 1994).

### 2.4.1 Monitoring waterborne pathogens

In water resource management, water quality standards are often developed to identify measurable sanitation goals. Monitoring, defined as the long-term measurement and observation of the aquatic environment, is any systematic collection of data that describes the current water quality status in a riverway compared to long-term trends or set standards (Bartram, 1996). Only after standards are set can a governing body enforce compliance and regulation. In many developed countries, water quality models and regular monitoring programs are the dominant tools to define and, ideally, achieve these set standards. Unsafe freshwater sources or “impaired waters” are commonly flagged through monitoring activities where segments of waterways with excessive bacteria levels are deemed impaired if they violate some health standard, indicating remedial action is required (Kim et al., 2007).

Inherent uncertainty lies in the monitoring of waterborne pathogens for two main reasons. First, unlike other non-point source constituents (e.g., nitrogen, phosphorus, sediment), pathogens are subject to complex host dynamics (animal life cycles), host densities (animal movement), and independent life cycles (microorganism die-off or regrowth); this makes microbes “more transient in nature... in space and in time” (Dorner et al., 2006). Second, the organisms that can cause infectious diarrhea are numerous and vary in their particular mechanisms of fate and transport. Taylor et al. (2001) identified 348 water-associated pathogens that can cause over 115 different infectious diseases. *Waterborne* pathogens are typically enteric microbes transmitted by the fecal-oral route, whereas *water-associated* pathogens can include a broad array of viruses, bacteria, protozoan parasites, and vectored diseases (Grabow, 1996; Yang et al., 2012). To address the first concern, advances in water quality modeling are desperately needed to improve how we mathematically represent fecal pathogen movement. In respect to the second concern, progress has been made through recent advancements in how we quantify pathogenic organisms in the environment; however, these advances remain largely inaccessible to resource-poor regions as expanded upon below.

Many waterborne pathogens are either difficult to detect or the costs of assessment is prohibitively expensive. Combined with the breadth of diarrhea-syndrome inducing organisms, this creates challenges in testing and identifying the safety of drinking water. To date, water quality managers still primarily rely on fecal indicator bacteria (FIB) to link source contamination risk and disease burden (Dorner et al., 2006; Fewtrell et al., 2007; Field and Samadpour, 2007). FIB are used as a “proxy measure of recent fecal contamination events” (Levy et al., 2012). A truly ideal indicator organism for microbes causing infectious diarrhea should be one distributed in the gastrointestinal tract in high densities among both humans and animals, one that would not reproduce outside the animal host, and, ideally, the indicator species would have a similar “survival profile” to that of the pathogen being assessed (Field & Samadpour, 2007; Yost et al., 2011). However this is rarely obtainable. Although not the “ideal” metric, FIB such as fecal coliform, enterococci, and *E. coli* do serve as useful indicators of fecal contamination and often correlate well with gastrointestinal illness (Meays et al., 2004; Dick et al., 2010). Although these indicator bacteria are not generally pathogenic, they are easy to detect,

are representative of the presence of microorganisms that can be transmitted through the fecal-oral pathogen route, and are well established in the intestines and feces of warm-blooded animals (Meays et al., 2004; Benham et al., 2006; Dorevitch et al., 2010). As each indicator organism has strengths and limitations, selection should support the goal of each study or management objective with the use of multiple indicators providing a more ideal approach (Grabow, 1996).

The continued use of these common enteric organisms as *primary* indicators of waterborne enteric pathogens has been questioned in light of rapid progress in microbial source tracking (MST); however, related techniques targeting host-specific genetic markers in the *Bacteroides* genus via molecular approaches such as qPCR (quantitative Polymerase Chain Reaction) require far more sophisticated skills and resources than traditional fecal bacteria tests (Sinigalliano et al., 2010; USEPA, 2007). For these reasons, field studies employing *Bacteroides* and MST are still limited and applications in sub-Saharan Africa are rare (Schaper et al., 2002; Field & Samadpour, 2007; Santo Domingo et al., 2007; Stoeckel & Harwood, 2007; Jenkins et al., 2009; Dick et al., 2010; Dorevitch et al., 2010). Thus, while newer methods may be available, the low-cost and familiarity of *E. coli*-based approaches has supported its prolonged use as a primary measure of fecal contamination in water monitoring, especially in resource-poor laboratory environments.

#### **2.4.2 Modeling waterborne pathogen transport**

Model simulations of specific constituents in the aquatic environment have been used for decades to guide environmental decision-making and risk assessment; models provide the means to describe physical processes that are too complex to describe analytically (Mitsova-Boneva & Wang, 2007; Daniel et al., 2011). These tools provide a framework to help decision makers prioritize management options – both spatially and temporally. The reasons to model a hydrologic system can be abridged into three underlying research objectives: 1) analyze environmental impacts and design water treatment systems, 2) improve our understanding of complex, coupled systems, or 3) serve as a system to organize and interpret research (Barfield et al. 1991). Despite many challenges and unavoidable assumptions, water quality models remain a stand-by tool when researchers seek to evaluate linkages in climate and human health. As predictive models are merely tools that help reveal trends for the purpose of informing resource management policies, researchers should always quantify uncertainties in data (historical and collected), model parameters, and final predictions when appropriate. Uncertainty analysis is an extensive topic in relation to water quality modeling and can be reviewed elsewhere (Reckhow, 1994; Wu et al. 2006).

Freshwater allocations for human consumption and domestic use, as well as pollution control and natural resource protection, are commonly managed on the political boundary scale – a scale for which microbial fate and transport have no regard. Here we briefly review how water-health management challenges are magnified by the cross-boundary nature of watersheds. Despite their inclusive nature, “watersheds” have no defined scale of their own – ranging from hillslope catchments to continental cross-boundary river basins. Defining these physical boundaries is essential for the sake of hydrology and model calculations, but will always create policy challenges such as international watersheds, jurisdictional mismatch, unclear accountability and participation of private and public sectors, and the obvious but challenging facet of an open

system in which wildlife, humans, and groundwater easily transport pathogens across invisible surface hydrological boundaries (DePinto et al. 2004; Cohen & Davidson 2011). The benefits and challenges of watersheds as “common pool resources” must be acknowledged at face value: they remain useful hydrological units but not natural units of social organization (Kerr, 2007). It is increasingly evident that water monitoring, planning, and development must consider environmental connections and drivers that occur across national boundaries in order to effectively manage the persistent public health threat of waterborne disease.

### **2.4.3 Diarrhea prediction under changing climates**

Climate-health literature largely supports the conclusion that current climate projections are associated with increases in diarrhea prevalence in Southern Africa and semi-arid regions (Ragab & Prudhomme, 2002; Patz et al., 2005; DeWit & Stankiewicz, 2006; Bandyopadhyay et al., 2011; Kolstad & Johansson, 2011; Gaughan & Waylen, 2012). A large challenge in evaluating linkages in climate and human health is to relate the mismatch of predictive scales that impact disease prevalence (e.g., the influence of changing precipitation intensities, changes in household hygiene, or variations in microorganism transport). Future climate predictions originate from large-scale regional analyses, while the effects of climate and land use variables are explored at much smaller, sub-catchment scales. Most predictions are made at global or regional levels and not at scales useful for disease assessment or land managers (e.g., less than 250-1000 km<sup>2</sup> grid cells) (Patz et al., 2005; Tamerius et al., 2007; Littell et al., 2011). While it is expected that sub-Saharan Africa will be strongly impacted by climate change, it is not immediately obvious where climate patterns will differ across local landscapes and how these effects will influence community vulnerabilities (Parry et al., 2007).

Changes in precipitation patterns have great power in influencing interdependent ecological, hydrological, and socio-economic systems (Harley et al., 2011; Gaughan & Waylen, 2012). Specifically, climate variables such as temperature, rainfall intensity, and drought periods can influence a pathogen’s “viability, stability, and reproduction” (Semenza et al., 2012). Seasonal or long-term changes in climate can also strongly influence the behavior and movement of humans and wildlife. The climate-dependent variability in pathogen persistence and source loading is exaggerated in the extreme wet-dry climates of semi-arid Africa, where humans and wildlife settle in much higher densities around critical surface waters (Beck & Bernauer, 2010; Gaughan & Waylen, 2012). This phenomenon may exaggerate predicted impacts of decreased precipitation on disease prevalence and increase the effects of wildlife distribution on environmental contamination. Knowledgeable climate-health predictions at a catchment scale are thus largely contingent on specific local understandings of disease ecology and hydrology patterns (Tamerius et al., 2007).

## **2.5 Research and Management Opportunities: Combining tool applications across disciplines**

In addition to the challenge of understanding multiple pathway transmission at a community scale, numerous challenges remain in our ability to detect, monitor, and predict pathogen fate and transport on land and in water. Nowhere are these challenges more prevalent than in the data scarce, ungauged, or poorly gauged river basins that characterize much of Africa; these

widespread data limitations amplify inherent uncertainties in epidemiological-, water quality-, and climate-models (Sivapalan et al., 2003; Winsemius et al., 2009; Hughes et al., 2010). In a brief review of integrated water resource management in Southern Africa, Dent (2000) reminds us that while more empirical data are key in data-poor regions, we must wean ourselves off the common “data-led approach”. By suggesting a paradigm shift to use models as deliberate guides to data collection and monitoring, more robust predictions could be developed using data that are purposely compatible with a specific model’s underlying assumptions (Dent, 2000).

Prevention of waterborne disease requires an understanding of the complex hydrological and socioeconomic processes that influence water quality, quantity, and use. Environmental variables (e.g., animal source contamination, season, climate, land cover, erosion) jointly govern the transport likelihood of fecal pathogens; many predictive tools are available for decision-making that center on simulating watershed hydrology processes to explore the effect of these variables on exposure potential. Domestic variables (e.g., poor in-home hygiene, malnutrition, wastewater reuse, communal taps) have long been recognized as strong contributors to diarrheal disease transmission; many epidemiological models exist that focus on post-source transmission at the community or household level. The challenge of reducing global diarrhea status in water-limited regions calls for a systems biology approach and an integration of traditionally independent management tools (Figure 3). Especially in resource-restricted environments such as Southern Africa, we have a tendency to resist complex, eclectic, and heuristic approaches to ecological modeling (Alexander et al., 2011). Modeling tools and applications are needed at both the watershed and community scale in order to account for all contributing and interconnecting fecal transport and pathogen transmission pathways.

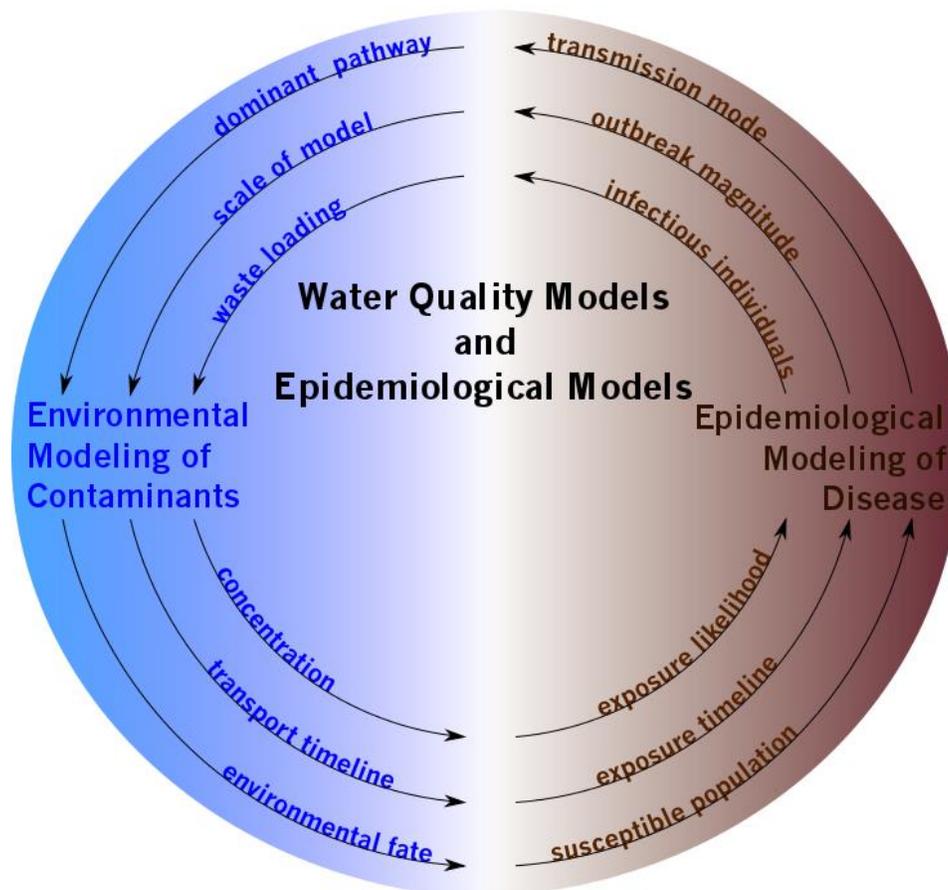


Figure 3. While water quality models and epidemiological models are not currently designed to be used in tandem, these traditionally separate disciplines are highly connected in the venture of waterborne disease management. Examples of idealized opportunities to link the outputs of one model as inputs to the other are illustrated above.

## 2.6 Conclusion

Diarrheal disease remains a persistent public health problem throughout Southern Africa and much of the world. Substantial research hurdles remain that continue to impede a deeper understanding of microbial transmission. Regardless of our current ability to better monitor and model microbial transport, efforts to understand the influence and relative strength of both ecological and social drivers are invaluable. Local ecological and anthropogenic drivers of transmission must be investigated to identify the most efficient and effective points for local public health interventions. Despite the “noise” of causation behind persistent diarrhea in a community, we must embrace uncertainties and act on what is known with the tools available. Large model assumptions and slow progress in this arena must not deter resource managers from acting in response to model predictions – given some description of predictive uncertainty is included when presenting management solutions to stakeholders.

The successes of health interventions will be limited by the extent to which management plans help disrupt the multiple and connected transmission pathways of enteric pathogens – climatic

and non-climatic – or explicitly consider uncertainties inherent in monitoring datasets. Because diarrhea causes are so integrated, research studies and management plans should span across traditional disciplines and warrant investigations at multiple scales. Lastly, waterborne infectious diseases share fundamental environmental and social drivers, but endemic and outbreak patterns are unique to the local landscape, local human-environmental interface, and dominant social and economic structure. Comprehensive intervention approaches should consider all intricacies and feedback loops in context of the local culture and institutional system.

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## CHAPTER 3:

### **The challenge of modeling waterborne pathogens in dryland riverine floodplains: *A critical need for tool advancement in water- and resource-restricted Africa***

Megan K. Holcomb and Dr. Kathleen A. Alexander

#### **3.1 Abstract**

Waterborne disease is a persistent public health threat across the globe, but particularly challenging in Africa where complex anthropogenic and environmental drivers increase community-vulnerabilities to impaired water resources. A limited variety of hydrological modeling tools exist to investigate microbial water quality and waterborne disease transmission dynamics and substantial research hurdles continue to impede characterization of transmission and waterborne pathogen transport. This limits improvements to public health intervention measures, particularly in Africa where microbial water quality assessments are infrequently utilized to address public health needs. Using the Chobe River watershed in northern Botswana, we assess the application of the Hydrological Simulation Program – Fortran (HSPF) to investigate microbial water quality and emergent health challenges in the region. We evaluate model application, identify data gaps, and provide recommendations for future research and tool development needs to address microbial water quality and health management in resource-poor dryland regions of southern Africa.

#### **3.2 Introduction**

##### **3.2.1 Water Quality Impacts on Human Health**

Globally, the burden of disease associated with water, sanitation, and hygiene remains high (Eisenberg et al. 2007; Fewtrell et al. 2007; Prüss-Üstün et al. 2008). Africa is particularly impacted by waterborne disease mortality and morbidity. Long-term climate and landscape changes in developing countries within this region create a need for increased adaptive capacity and rapid water-health improvements. Developing countries face exceptional challenges in dealing with traditional (e.g., fecal pathogens) and modern (e.g., toxic chemicals) water quality problems that result from, or are perpetuated by, severe resource and information limitations (Ongley 1997).

The challenges of waterborne disease management are heightened by the environmental vulnerabilities and social disparities inherent to the dryland environments of Africa. Dryland regions, including hyper-arid, arid, semi-arid, or dry-subhumid zones, cover almost half of the world's land surface; these areas are characterized by scarce water resources, wide temperature ranges, low precipitation and evapotranspiration ratios, and extreme variability in river discharge rates (Davies et al. 1994; Tooth 2000; Tooth and Nanson 2011). All management scales from

communities, to countries, or cross-boundary river basin units require public health interventions developed from a more extensive and specific understanding of system processes such as pathogen origin, social and environmental transmission, and hydrologically-governed transport to understand the coupled anthropogenic and natural systems driving pathogen exposure (Bridge et al. 2010a; Dufour et al. 2012; Sokolova et al. 2013). Microbial water quality dynamics and diarrheal disease transmission are influenced by site-specific social and environmental factors that must be understood in order to address community vulnerabilities.

Water, sanitation, and hygiene (WASH) system interventions, while necessary, are often reactive responses to immediate threats to human health rather than proactive, preventive strategies (see Fewtrell et al. (2005) for a review of common WASH interventions). Watershed-scale, water quality models are effective tools to help resource managers collect data, reveal gaps in system understanding, and communicate risk to decision makers. While water quality models remain common tools for non-point source (NPS) pollution management in temperate and developed regions, they remain scarcely utilized throughout Africa. Available models can provide researchers with a useful structure to understand dominant processes driving pathogen fate and transport.

### **3.2.2 Broad challenges for watershed modeling in Africa**

Sub-Saharan Africa is characterized by widespread poverty and resource limitations that have lead to weak institutional structures, limited technical capacities, and a widespread paucity of environmental data (Dent 2000; Hughes et al. 2010; Kusangaya et al. 2013; Ongley 1997). The region has been further impacted, both socially and economically, by the HIV/AIDS epidemic (Human Immunodeficiency Virus / Acquired Immunodeficiency Syndrome) (WHO 2012). Even without these barriers, monitoring and modeling complex hydrologic systems and waterborne disease transmission is “technologically and practically challenging” across the globe, making the challenge of water management an urgent problem facing Africa (Bridge et al. 2010b).

Pathogen pollution of surface water (NPS pollutants) is inherently difficult to quantify as microbes are diffuse within the watershed system and, by definition, cannot be monitored at a particular location (in contrast to point source contamination). Microorganisms are the most challenging of the NPS constituents to model mathematically. Rather than finite elemental or chemical NPS pollutants, fecal bacteria are living organisms with independent life cycles (variable die-off and regrowth rates) both within the animal gut and after excretion. Despite these challenges, it is essential that the water quality dynamics of microbial fate and transport be understood; most often this requires an application of watershed management tools, however imperfect (Brils et al. 2014; Rose and Grimes 2001).

### **3.2.3 Inventory of available pathogen transport models**

While mathematical characterization of microbial transport in receiving waters is notoriously limited, microbial watershed models are available and many existing programs have the potential for further development to include pathogen transport (Bridge et al. 2010b). Hydrological, watershed-scale models are numerous and well-summarized by Singh and Woolhiser (2002) and Quilbe et al. (2006). Several other reviews compare more prominently used hydrological models

in greater depth (Borah and Bera 2003; Migliaccio and Srivastava 2007; Moriasi et al. 2012). Only a small subset of watershed-scale models are equipped to simulate chemical or biological pollutants as well as landscape and in-stream processes; no single exhaustive review of these exists (Daniel et al. 2011; Wang et al. 2013). Haydon and Deletic (2006) even reason that a comprehensive pathogen transport watershed model has not yet been developed given the weaknesses of programs currently outfitted to model fecal bacteria (typically fecal coliform or *Escherichia coli* as indicators of pathogenic enteric organisms). Tables 1 and 2 summarize available pathogen transport models found in the literature to date.

Nearly all of the available tools summarized in Tables 1 and 2 were developed in industrialized countries and intended for application in temperate environments. Thus, many empirical and process based equations built into model components may be inappropriate for use in dissimilar landscapes or hydrologic regimes (Davies et al. 1994). While existing tools for water quality management were not developed for semi-arid landscapes with dramatic seasonal shifts, an attempt to apply them provides a first test-case, illuminating the most pressing model development needs (Bandurraga et al. 2011; Bouraoui et al. 2005; Dent 2000; Gericke et al. 2004; Gersberg et al. 2000; He and Hogue 2012; Johanson 1989).

Table 1. Pathogen transport models and hydrological-component program acronyms used in Chapter 3	
BASINS	Better Assessment Science Integrating point & Non-point Sources Version 4
COLI	Bacteria generation model
CREAMS	Chemicals, Runoff, and Erosion from Agricultural Management Systems
GLEAMS	Groundwater Loading Effects of Agricultural Management Systems
HSPF	Hydrological Simulation Program – Fortran
IHACRES-WQ	Identification of unit Hydrographs And Component flows from Rainfall, Evaporation and Streamflow data
MWASTE	Waste generation model
PCB	Pathogen Catchment Budget
PROMISE	Emission model
SEDMOD	Spatially Explicit Delivery Model
STARS	Solute Transport with Advection, Resuspension and Settling
SWAT	Soil and Water Assessment Tool
WAMView	Watershed Assessment Model
WARMF	Watershed Analysis Risk Management Framework
WATFLOOD	University of Waterloo Flood Forecasting System
WATNAT	Hydrological dispersion model

Table 2. Comparison of pathogen transport models listed, roughly, in order of increasing compartmentalization and complexity. Brief reviews of these models were found in Ferguson et al. (2003), Ferguson et al. (2007), Jamieson et al. (2004), and Moriasi et al. (2012).

Model	Reference	Scale	Model Type	Hydrological Component	Fecal Loading?		In Stream Processes?	GIS?	Designed for?
					Point	Nonpoint			
MWASTE	(Moore et al. 1988)	Field	Mechanistic	Event-based: CREAMS (Knisel 1980)	---	X	---	---	temperate
COLI	(Walker et al. 1990)	Watershed	Empirical	Rainfall-runoff: SCS curve number (Boughton 1989)	---	X	---	---	temperate
PROMISE	(Medema and Schijven 2001)	Only river network	Empirical	WATNAT (Schijven et al. 1995)	X	---	X	---	Netherlands Only
Unnamed	(Tian et al. 2002)	Watershed	Mechanistic	WAMView (Bottcher and Hiscock 2001)& GLEAMS (Knisel 1980)	X	X	X	X	New Zealand, pastureland
IHACRES-WQ	(Post and Jakeman 1999)	Watershed	Empirical, Conceptual (Proprietary)	Rainfall-runoff: IHACRES (Croke et al. 2005); In-stream: STARS (Green et al. 1999)	?	X	X	---	temperate, successful in Australia
Unnamed	(Dorner et al. 2006)	Watershed	Empirical, Probabilistic	WATFLOOD (Kouwen 2005)	---	X	X	X	temperate, rural only
SEDMOD	(Fraser et al. 1998)	Watershed	Mechanistic	Overland flow based on: hydraulic roughness, gradient, slope shape, stream proximity, normalized soil moisture index	?	X	---	X	temperate, pastureland only
PCB	(Ferguson et al. 2007)	Watershed	Mechanistic	IHACRES (Croke et al. 2005)	X	X	X	X	Australia
WARMF	(Goldstein 2001; Herr and Chen 2012)	Watershed	Mechanistic, Mixed (Proprietary)	Canopy interception, snow-pack accumulation, snowmelt, through-fall, evaporation, transpiration, infiltration, percolation, ground-water lateral flow, surface runoff	X	X	X	X	temperate, few international applications
SWAT	(Arnold et al. 1998)	Watershed	Mechanistic, Mixed	Canopy interception, snowmelt, irrigation, infiltration, evapotranspiration, lateral subsurface flow, shallow aquifer flow, surface runoff	X	X	X	X	temperate, many international applications
BASINS/HSPF	(Bicknell et al. 2001; Duda et al. 2012)	Watershed	Mechanistic, Mixed	Snow-pack depth, snowmelt, interception soil moisture, evapotranspiration, interflow, base flow, ground-water recharge, surface runoff	X	X	X	X	temperate, many international applications

### **3.2.4 Model selection**

Although arguments have been made for selecting the simplest model possible that suits one's objectives, the Hydrologic Simulation Program–FORTRAN (HSPF) was selected for the purpose of this study, chiefly for its flexibility and widespread use in North American microbial water quality management (Donigian et al. 1991). HSPF can simulate a large range of temporal scales, model system sizes, and various combinations of water quality constituents. HSPF is a continuous simulation, semi-lumped parameter, and mechanistic model with empirical features; it remains the industry standard for water quality modeling in the United States despite many limitations (Borah and Bera 2004; Johanson 1989; Skahill 2004). Its use extends internationally, while HSPF applications in Africa are rare.

A scarcity of previous applications of HSPF or similar models in resource-poor regions is likely due to the model's extensive data requirements, steep learning curve, labor-intensive set-up, and calibration requirements (and thus existing or collected calibration data) (Borah and Bera 2004; Quilbe et al. 2006). While these challenges are amplified for researchers in developing countries, the trade-off of simplifying complex problems, using simpler models, risks overlooking important landscape and in-river processes. As we aim to advance our understanding of the dynamic, coupled interactions of extreme wet-dry seasons, land use, human and wildlife fecal loading, and future climate on water quality in the Chobe River watershed, the exhaustive requirements of HSPF serve as an important guide to data collection.

We assess the model application, identify data gaps, and provide recommendations for future research and tool development needs to address microbial water quality and health management in resource-poor, dryland regions of southern Africa. We frame this examination by considering opportunities and barriers to the application of hydrological modeling tools specifically in dryland river systems found in southern Africa. We identify gaps and provide recommendations for future research and tool development to address the needs of these complex and vulnerable river floodplain systems.

## **3.3 Methods and Results**

### **3.3.1 Study region**

The Chobe River is representative of many dryland riverine floodplain systems where seasonal flood pulses drive ecosystem health and pathogen transmission dynamics. This transboundary watershed spans the border between Namibia and Botswana, supports multiple land uses that include wild, rural, and urban landscape overlaps, and is managed by disjointed institutional, policy, legal, and regulatory frameworks of the two nations. As the only surface water source in over 12,000 km<sup>2</sup> (square kilometers), this river system plays a vital role in both human and animal survival in the region. Climate change has already impacted this system with the 25-year median annual rainfall decreasing from 600 millimeters per year (mm/yr) (1950 to 1975) to 500 mm/yr (1980-2005); future climate change is expected to further impact this system and resident communities living in the region (Gaughan and Waylen 2012).

While 70% of Botswana is dominated by the Kalahari Desert and is sparsely populated by human settlements and wildlife, the Chobe National Park and surrounding northeast region of the country is host to an immense concentration of wildlife and an extensive ecotourism industry. As of 2011, approximately 15,000 people live in the watershed study region and are spread across two urban communities in Botswana, Kasane and Kazungula, and two rural communities in Namibia, Kasika and Impalila (Figure 1C). The Namibian side of the Chobe River remains mostly swampland (inundated floodplain) throughout the year and is heavily utilized by Namibian cattle farmers.

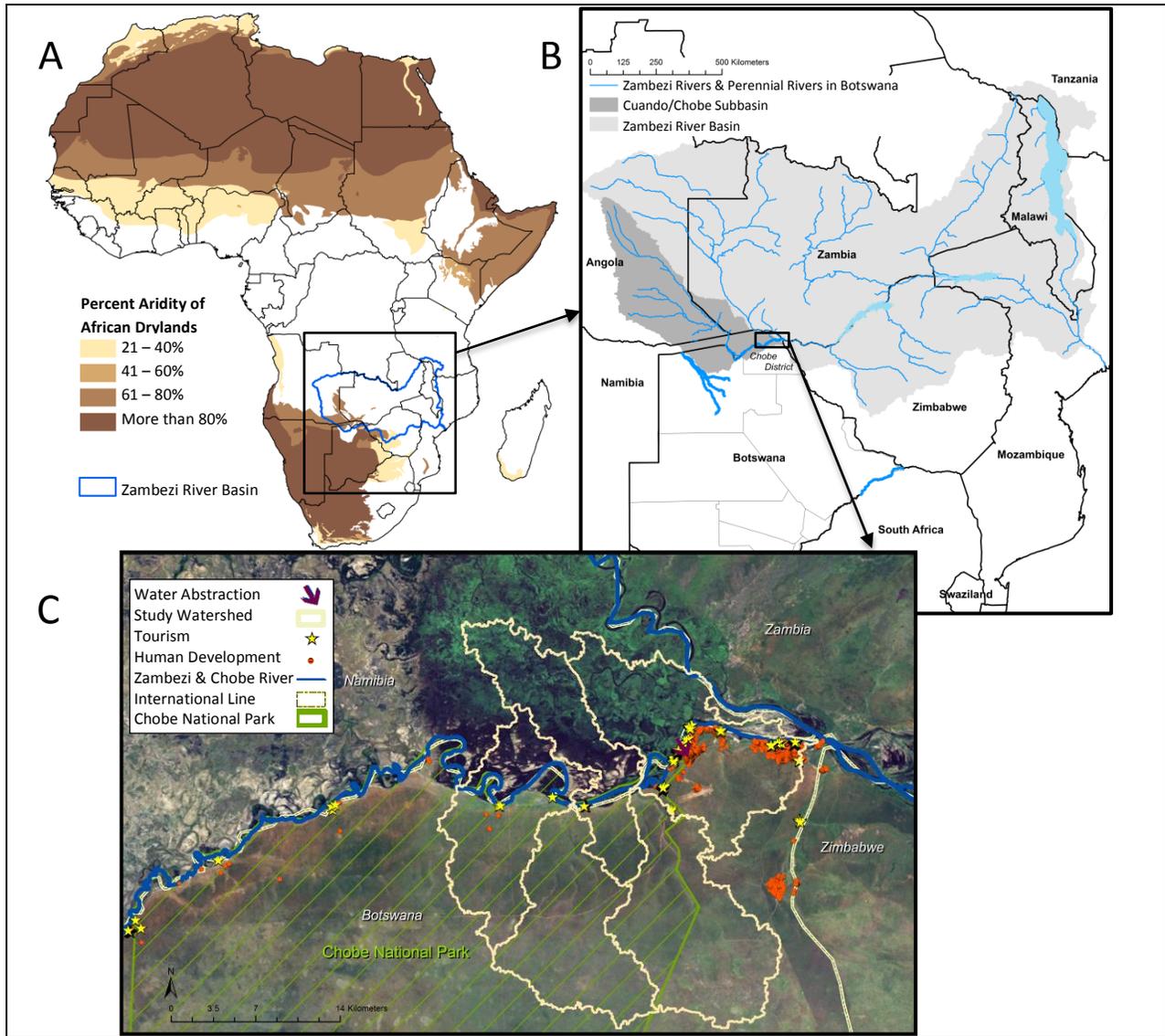


Figure 1. A multi-scale context of the research site. **A:** Map of African drylands by percent aridity with delineation of the Zambezi watershed (blue line in boxed region); **B:** Cuando/Chobe sub-basin (dark grey) within the Zambezi River Basin. In blue are the major water bodies of the ZBR and the only 3 perennial rivers in Botswana (Chobe River, Okavango Delta, Limpopo River); **C:** The Chobe-Linyanti River channel showing human infrastructure (orange and yellow stars), conservation areas, water abstraction, and watershed overlay of this model application

While the majority of people living or visiting the region will not have direct physical contact with wildlife, they do rely upon shared water resources, increasing the potential for pathogen transmission between humans and animals in the system. Immediately downstream of the Chobe National Park, water is abstracted for municipal use for all villages in the district. Piped water is available throughout the District. Rivers within the Cuando/Chobe sub-basin (Figure 1B) remain hydrologically undisturbed by dams or other primary water diverting structures (World Bank 2010). Analysis of reported diarrheal cases in the Chobe District reveals a bimodal peak of disease incidence that coincides with the biannual seasonal trends of heavy rainfall and flood recession (Alexander and Blackburn 2013).

This study’s water quality investigations are focused on the last 55 km stretch of the Chobe River before merging with the larger Zambezi River. The Chobe and Zambezi Rivers form a highly complex river-floodplain system with strong flood-pulse patterns across the Namibian floodplain (referred to by varying names in the literature and hereon as “Chobe Wetlands”) (Harrison et al. 2004; Pricope 2013). The flow of the Chobe River is governed by two dominant processes: 1) a rainfall-associated pulse from the Cuando that originates in the highlands of Angola and 2) backflow from the downstream Zambezi River when floods are strong. Pricope (2013) constructed the first complete assessment of the timing and magnitude of the Chobe’s annual flood regime, roughly summarized by month in Table 3.

Table 3. Chobe River Annual Extent of Flooding

	Month	Flooding Extent	Upstream Flow - Cuando	Downstream backflow - Zambezi	
<b>Wet Season</b>	Nov.	High: scattered storm-runoff associated pools	Low flows while stage builds in headwaters	-	
	Dec.			-	
	Jan.	Intermediate: mix of scattered pools & floodplain inundation		-	
	Feb.			Zambezi stage builds and floods across Chobe Wetlands	
	March			Floods peak pushing backflow waters into the Chobe (temporary river reversal)	
<b>Dry Season</b>	April	Very high: inundation concentrated in Chobe Wetlands	Average flows	Zambezi floods recede leaving southern Chobe Wetlands flooded	
	May			-	
	June	Low to Intermediate: largely limited to braided channel bed		A second delayed flood pulse from upper Cuando/Chobe subbasin enters Chobe-Linyanti channel	Chobe flow returns and flooding around the Linyanti-Chobe begins concentrating into main channel
	July				-
	Aug.	Low to none		Low flows	-
	Sept.				-
	Oct.				-
	-				

### 3.3.2 HSPF Model Structure and Development

The HSPF water quality model conceptually defines the true physical watershed landscape through the parameterization of three main modules: pervious land (areas where water can infiltrate the soil), impervious land (areas where water cannot infiltrate), and reaches or reservoirs (river segments or lakes). HSPF is designed to run many sub-modules that can be “turned on” or “off” as needed (i.e., just hydrology or any combination of hydrology, sediment, bacteria, nutrient, or other subroutine simulations). A Weather Data Management (WDM) file is the primary storage file for time series data (input and output) and the User Control Input (UCI)

file defines all modules, parameters, and contains the core “directions” for a complete simulation run (Ford 2000). Preliminary model set-up includes defining watershed boundaries, the river network, and dominant land use. Model development involves constructing a WDM, building a UCI skeleton, parameterizing the UCI, and debugging the UCI for model run errors. The focus of this work was to setup the model framework and assess its application to the system. Subsequent model steps of calibration, model validation, and uncertainty analysis will be undertaken together with modification of our modeling approach as identified from this work.

### **Watershed Definition**

The computational fallibility of automatic delineation for watersheds with extensive floodplain features proved a significant issue in this study and elsewhere (Al-Muqdad and Merkel 2011). Catchment delineation required over fifty trial runs to achieve a satisfactory delineation. Multiple Geographic Information System (GIS) preprocessing programs for watershed analyses were utilized (e.g., ArcMap, ArcHydro, HECGeo-HMS, TauDEM, ArcSWAT) (Table 4). These ArcGIS extensions, along with various combinations of raw or modified Digital Elevation Models (DEMs), produced highly variable and largely unrealistic watershed boundaries.

ArcGIS®	ArcGIS and ArcMap software by Environmental Systems Research Institute
ArcHydro	ArcGIS extension (Version 2)
ArcSWAT	ArcGIS extension and graphical user input interface for Soil and Water Assessment Tool
HECGeo-HMS	ArcGIS extension for Hydrologic Engineering Center’s Geospatial Hydrologic Modeling Extension
TauDEM	Terrain Analysis Using Digital Elevation Models (Version 5)

While imperfect, the ArcSWAT watershed delineation tool produced the most realistic and fine-scale catchment boundaries for the Chobe River. Prior to watershed analyses in ArcSWAT, a one arc second resolution DEM raster, produced by the Advanced Spaceborne Thermal Emission and Reflection Radiometer (ASTER), was hydrologically corrected to fill elevation sinks. During ArcSWAT processing, a satellite verified manual delineation of the Chobe River was “burned” into the DEM. The resulting sub-watersheds were limited to the last five watershed units (Figure 2B) and manually corrected as necessary against satellite and DEM data layers.

### **Land-Use Classification**

The semi-lumped parameter nature of HSPF allows each watershed to be divided into discrete areas with common geological and physical characteristics such as soil type, vegetation, and any user-defined land use. The five sub-watersheds were each classified into five land-use categories: “open water”, “wetland”, “barren land”, “shrubland”, and “developed” (Table 3). The study region soils were dominantly fluviosols (floodplain and river edge) and arenosols (Botswana plateau). A supervised land classification using Landsat imagery was run in ArcGIS (Figure 2A). The relative land-use percentages from this GIS classification were adjusted to account for the incorrect classification of bare sand as developed land (red in Figure 2A). Only tar roads, buildings, lodge areas, and villages were classified as “developed” (red in Figure 2B).

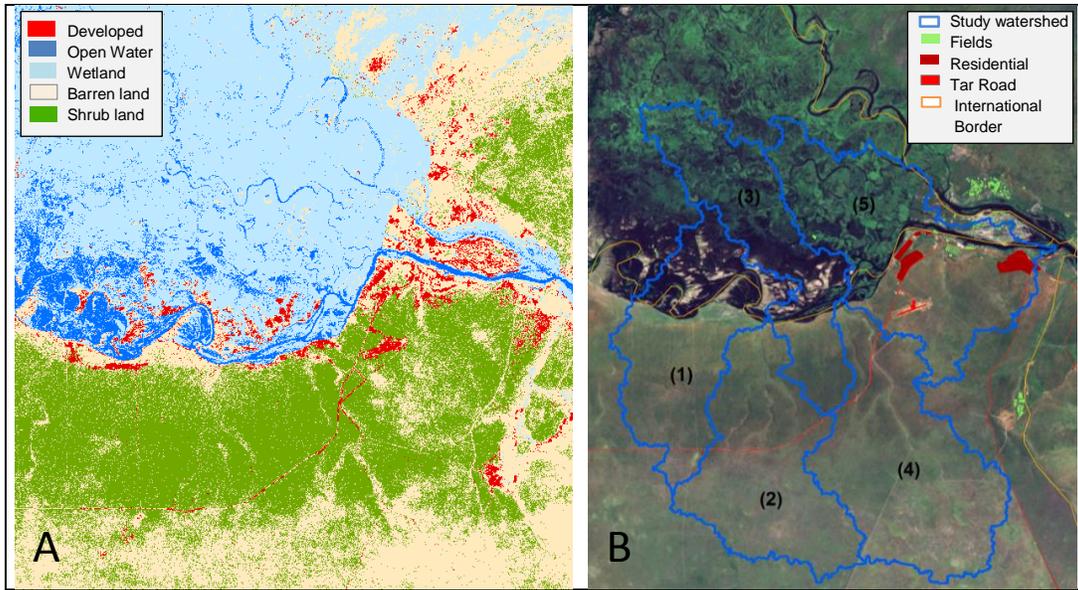


Figure 2. A visual comparison of land use between computational processing and Landsat false color imagery. **A:** ArcGIS supervised land use classification results; **B:** Manual classification of developed land, roads, and fields. Final delineation of five sub-watersheds

Table 5. Land Use Classifications by sub-watershed. See figure 2B for sub-watershed reference numbers.

Sub-watershed Description	Area (km <sup>2</sup> )	Reach Length (km)	Developed	Open Water	Wetland	Barren Land	Shrub Land
(1) Kabulabula to Puku Flats	113	24.3	2%	12%	17%	24%	45%
(2) Chobe National Park West	121	Negligible	0%	0%	0%	45%	55%
(3) Game Lodge Straight	102	5.72	1%	9%	64%	6%	20%
(4) Chobe National Park East	143	Negligible	0%	0%	0%	60%	40%
(5) Sedudu Is. to Kazungula	157	21.2	6%	6%	41%	23%	25%

### WMD File Construction

WMDUtil, while available through the BASINS program (Better Assessment Science Integrating point and Nonpoint Sources), works best in a Windows XP environment. Meteorological time series (precipitation, temperature, evaporation, flow) were formatted into a simple format (.csv) and imported individually into a blank WDM file.

### UCI File Construction

While the HSPF model interface is accessible as a standalone program (WinHSPF3.0), updated releases of HSPF (currently in version 12.2) are only accessible through the BASINS program. Model development within BASINS is built around numerous assumptions and highly specific data requirements that make building a new HSPF project problematic when a study site does not fit the BASINS mold. New HSPF applications commonly modify the UCI file of a previous project. In the data scarce watershed of the Chobe River, the requirements for BASINS could not be met and a comparable metric UCI file was unavailable for simple modification. An alternate, open-source method for HSPF model development was explored that utilized the Python

Programming Language (“HSPF.py” program script provided D. Lampert). Although further UCI development and parameter adjustment was required (especially for fecal loading modules), the Python application proved an efficient and flexible method to initial UCI file construction.

## **Data Sources & Parameterization**

A list of core data sources can be found in Appendix A. Initial parameterization values were selected from the few sources available that had application at some level to the Chobe system: a semi-arid HSPF application in Texas (LaWare and Rifai 2006), the BASINS parameter guide (United States EPA 2000b), GIS landscape values from HSPF.py output, and other semi-arid fecal coliform applications (Abdulla et al. 2009; Ferguson et al. 2007; He and Hogue 2012).

## **3.4 Discussion**

### **3.4.1 HSPF Model application in semi-arid floodplain systems**

While HSPF is a comprehensive model for water quality simulation, the assumptions it is built on prohibit the inclusion of the major hydrologic and landscape features particular to the Chobe River watershed (Figure 3 highlights the dominant obstacles identified). The extensive floodplains and flood pulse, features characteristic of many dryland river systems in the region, could not be represented in the HSPF modeling environment. These limitations exist in any of the currently available basin-scale water quality models capable of simulating pathogen transport. However, floodplain processes are essential to understanding runoff and discharge patterns as they significantly alter the duration, timing, and magnitude of flow regimes (Hughes et al. 2013). In the dryland regions of southern Africa, numerous moderate to large floodplain systems are associated with in-land rivers which exhibit characteristic seasonal flood-pulses and vegetation patterns (Noble and Hemens 1978; Taylor et al. 1995). The dynamics of these vital surface waters are complex and can be largely basin-specific; yet, the inclusion of at least some floodplain parameters can improve hydrological simulations and decrease model uncertainty (Noble and Hemens 1978; Taylor et al. 1995; Tooth and McCarthy 2007).

Existing support tools that help users develop fecal loading tables for HSPF are entirely geared toward temperate systems and largely lack the flexibility to quantify wildlife sources of bacterial loading data (Petersen et al. 2009; United States EPA 2000a; Zeckoski et al. 2005). In the open and wild landscapes of southern Africa, the contributions of fecal bacteria from wildlife, rather than livestock or domesticated companion animals, can be dominant system inputs (Alexander unpublished data). There remains inadequate literature on species-specific manure- and fecal coliform production rates for African wildlife, which is necessary to populate fecal loading tables independent of, or through the use of, HSPF-support programs. Available bacterial source load calculators also fail to account for direct human fecal contamination and require extensive assumptions and estimations to account for surface and subsurface contamination through pit latrine use, an important potential influence on subsurface and surface water (Alexander unpublished data).

Excluding important hydrologic features (e.g., floodplains) and crude estimations of wildlife fecal inputs significantly lessen the accuracy of a model’s system representation. Beyond these

water quality-related limitations, model development in an ungauged basin (i.e., poorly characterized hydrology/water quantity) may remain the largest barrier to acceptable water quality simulations (or rather opportunity for improved data monitoring). No flow gauge data exists within the study-site, at the Chobe-Zambezi confluence, or anywhere reasonably close upstream. The only flow data in the Cuando/Chobe sub-basin (used as input to the model) is located about 500 km upstream from the Chobe outlet at the Angola-Namibia border and the next downstream gauge station is not until Tete, Mozambique. Sporadic daily stage measurements exist for the Chobe River, however, crude river cross-section and velocity field measurements were not adequate enough to transform long-term stage data into a discharge time series for calibration. Daily flow data, daily evapotranspiration data, and African wildlife fecal coliform production rates remain the largest data gaps and opportunities to improve the parameterized HSPF model as it currently stands.

This study reveals some site-specific barriers and it illuminates the need for tool development general to pathogen transport modeling and specific to semi-arid environments. In the discussion below, we provide recommendations for a few of the most pressing model development needs and justify how these processes are critical considerations in semi-arid floodplain systems.

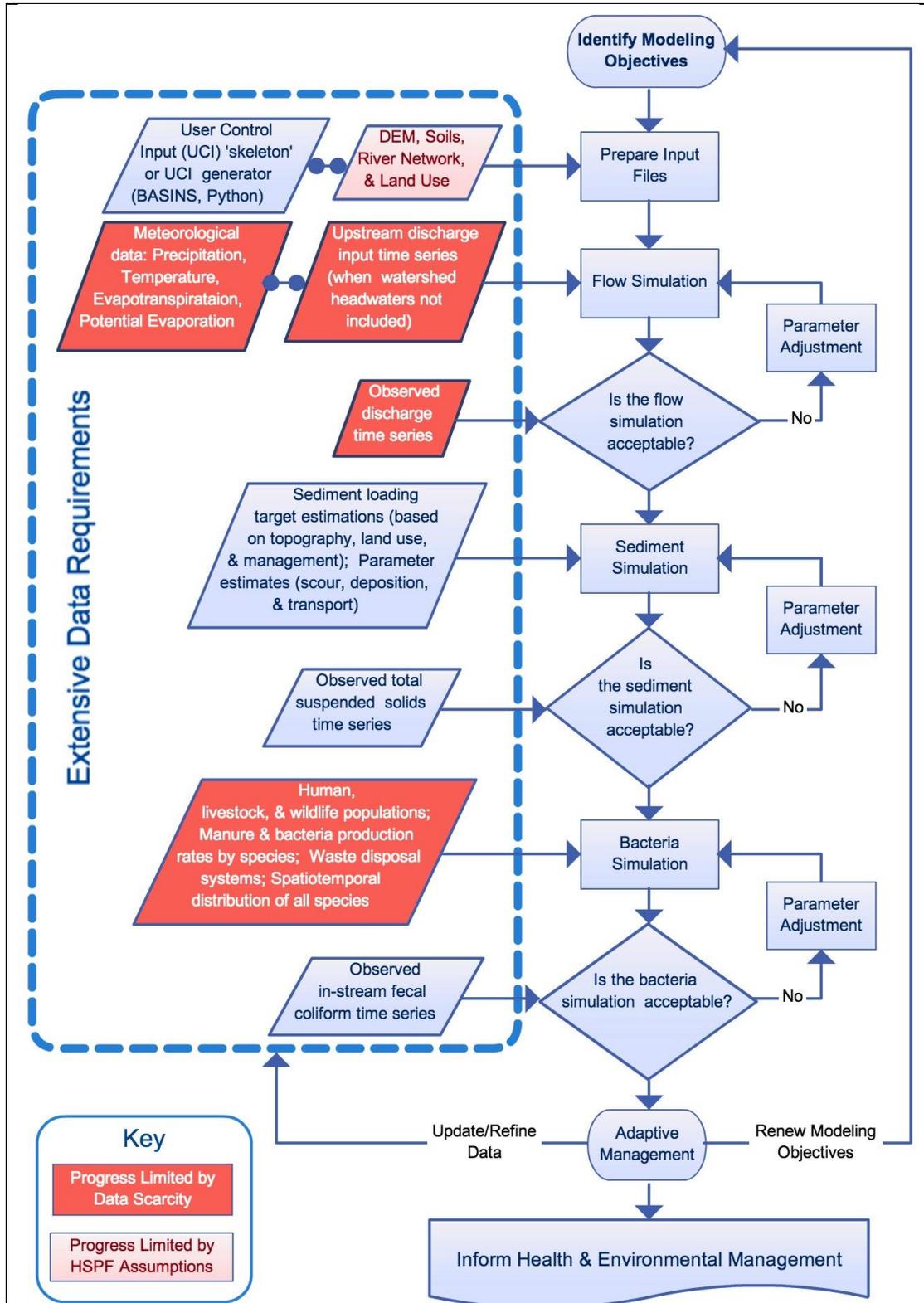


Figure 3. HSPF model development procedure with limitations to progress highlighted. Modeling issues are likely germane to other semi-arid, riverine floodplains in data-poor watersheds. Flow diagram adapted from Nasr and Bruen (2006).

### **3.4.2 Managing complex systems with watershed-scale water quality models**

Given the challenges presented in Figure 3, why would we still recommend more model applications in resource poor regions lacking data and trained personnel? Regardless of fine-scale data availability or the current state of model development, these tools allow us to identify system vulnerabilities and evaluate management response options rather than merely respond to negative health impacts.

These applications should not be accompanied by the same experimental expectations as the temperate, data-rich countries from which they originated. They can, however, contribute in significant and lasting ways by providing a framework in which data and management needs can be identified and prioritized. Known as “modeling-led monitoring,” data intensive watershed models can guide and incentivize environmental monitoring – data collection which otherwise may not be undertaken (Dent 2000). Under improved data conditions, these complex watershed models retain their potential to simulate complex system change and to predict climate- or land use change impacts (Migliaccio and Srivastava 2007). Engaging these tools help researchers untangle (simplify) complex realities (Daniel et al. 2011; Pappenberger and Beven 2006). Epstein (2008) lists many reasons to model pollutants in a hydrologic system, all of which are “informative” for the sake of “informed management” and thus satisfy a target for water and health research in developing countries.

### **3.4.3 Recommendations for Tool Development**

While a large body of experimental data exists on fecal pathogen fate and transport, only a small fraction is useful for the advancement of process-based modeling in sub-Saharan Africa (Pachepsky et al. 2006). In order to advance watershed management, four key limitations are identified: 1) scarcity of biome-specific (semi-arid) model development and reference data for parameterization; 2) exclusion of subsurface and floodplain processes; 3) poorly understood relationship between pathogens (or indicator bacteria) and sediments; and 4) data gaps in the contribution of fecal pathogens from wildlife and humans. Addressing these gaps in “catchment microbial dynamics” will contribute greatly to advancing watershed management and strengthening environmental health management planning (Bridge et al. 2010a).

Confidence in model predictions and interpretation of monitoring data will always be limited by the uncertainty that arises from natural systems where irregularities and extreme events commonly occur, measurement limitations persist, simplified mathematical representations of environmental processes are constructed, and data are of poor quality (Wu et al. 2006). These problems occur in even the most simplified watershed-scale models where ample and reliable data are available. Ferguson et al. (2003) provide a more comprehensive review of current knowledge gaps in conceptual watershed models and process-based model representations of pathogen movement in a watershed. Here, we highlight considerations in relation to dryland water systems found in sub-Saharan Africa.

#### **1) Consider Influence of Arid and Semi-arid Climate Patterns**

There are inherent differences between climate-driven hydrological dynamics in temperate and semi-arid regions. Few water quality model applications (none found in southern Africa) consider how a given model represents semi-arid specific landscape properties. Differences in regional soil composition, nutrient availability, and seasonal vegetation communities and distribution have important impacts on subsurface infiltration and microbial activity. Unlike more humid climates, biological activity is often limited by water availability in the desert and savanna biomes of southern Africa.

Microbial and botanical activity quickly responds to the rewetting of dry sediments, especially in parafluvial sediments (i.e., river channel regions) (Zeglin et al. 2011). When coupled with sedimentation or resuspension, flood pulse dynamics or rainfall can increase organism activity and growth, which may contribute to spikes in the detection of pathogens in the water column. A comprehensive paper by Belnap et al. (2005) emphasized that the amount, timing, and intensity of precipitation events in arid landscapes strongly influences microbial activity cycles. While high-mortality of both pathogenic and non-pathogenic organisms may occur in soils during dry periods, soil surface microbes can activate from even modest precipitation; this hydration may either increase competition with sediment-associate pathogens or supply a “flush of nutrients”, possibly beneficial for both pathogenic and non-pathogenic organisms (Belnap et al. 2005).

The authors emphasize that a critical “transfer of materials” (via infiltration or overland flow) governs pulses in microbial activity and feedback loops. Large precipitation events trigger overland flow to surface waters, with “flow” including sediment, excrement, and possibly bank/gully erosion that contains a rich soil crust community or microbial “reserve” (Belnap et al. 2005). In savannah landscapes, NPS fecal contamination in waterways may occur in dramatic storm pulses, especially after the dry season when wildlife excrement reserves have built up on dry lands. However, there exists evidence that short storms of high intensity can produce *localized* Hortonian overland flow, where high rates of runoff in semi-arid areas can infiltrate into fractured bedrock channels – contributing to subsurface flow rather than the watershed outlet (Hughes 1995). Especially in large dryland catchment areas with high rates of evaporation and high infiltration losses, overland flows may not actually reach surface waters unless rainfall events are widespread or recurrent (Tooth 2000); most hydrological models cannot incorporate such processes (Hughes 1995).

## **2) Develop Essential Subsurface Flow & Floodplain Dynamic Processes**

Although not limited to semi-arid regions, a large knowledge gap still exists regarding our understanding of the influence that subsurface hydrological processes have on pathogen fate and transport. Many hydrological models capable of including microbial contaminants do not consider subsurface flow even though overland flow occurs only when rainfall rates exceed the capacity of infiltration (Belnap et al. 2005; Jamieson et al. 2004). The rate of infiltration and subsurface transport are largely dependent on a catchment’s soils, vegetation type and distribution, and underlying geology. One hydrological model application in a temperate region identified that most pathogen loading from land occurred through subsurface drainage, although peak concentrations did occur during overland flow from storm surges (Dorner et al. 2006). The transport of microbes in subsurface flow has been fully reviewed, has shown to contribute

significantly to microbial contamination, yet it remains an entirely separate topic in current literature (Jamieson et al. 2004; Nevers et al. 2011).

Subsurface flow may be a critical factor influencing microbial loadings in receiving waters. There is a growing concern that pit latrines, the common waste disposal system of low-income countries, can contribute to widespread microbial contamination of groundwater (Graham and Polizzotto 2013; Nyenje et al. 2013; Tillett 2013). A review of studies that explored groundwater contamination from pit latrines used a variety of experimental techniques, reported highly variable ranges of microbial transport distances, yet frequently concluded that groundwater contamination occurred (Graham and Polizzotto 2013). As pit latrine use will remain a recommended improvement toward basic sanitation, the contribution of subsurface contamination should not be ignored in water quality modeling – particularly in low-lying riverine floodplains where the water table is, by definition, near surface-level. This disconnect between highly related physical processes (surface and subsurface water) maintains a significant barrier to true systems assessments of microbial transport.

### **3) Inclusion of Bacteria-Sediment Associations**

Past evidence strongly suggests that fecal indicator bacteria (FIB) are closely associated with sediments. Despite this, FIB are typically represented as neutrally buoyant, unattached “free” particles in common water quality models (Dorner et al. 2006; Gao et al. 2011; Russo et al. 2011). The free particle assumption may exaggerate microbial mobility and fail to describe important processes such as settling velocities (causing a large concentration gradient in the water column), resuspension (such as disturbance from wildlife or recreation), and lower decay rates in riverbed sediments compared to open waters. Water body sediment layers can function as reservoirs of viable indicator bacteria or enteric pathogens (Wu et al. 2009). This makes the exclusion of bacteria-sediment associations problematic, particularly in slow moving rivers with high levels of direct access for wild or domesticated animals (e.g., the Chobe River).

Russo et al. (2011) found that differences between sediment-associated models and free-phase models were significant but small, suggesting resuspension is dwarfed by increased microbe concentrations from runoff – contrary to a similar model by Dorner et al. (2006). Bai and Lung (2005) report highly variable findings in many field studies exploring bacteria and sediment associations: 1) attachment rates of fecal coliform and enterococci to sediment after rainfall in a creek and karst area can range from 5% to 100%; 2) bacteria concentrations in sediment beds can range between 10 to 10,000 times higher than concentrations found in the water column; 3) storms and wind turbulence can cause coliform spikes (via disturbance mediated resuspension) in streams, as can flooding, which results in concentrations 5–50 times higher than levels prior to flooding (see Bai and Lung (2005) for study citations). Central to sediment-bacteria transport modeling is the difference between the number of attached versus free-living bacteria; this estimation requires a subjective translation of micro-scale research theory into macro-scale modeling applications (Gao et al. 2011; Bai and Lung 2005).

Recommendations on which sediment processes to include in a watershed model application depend on the scale of the model and the confidence in all other variables. Including fine-scale sediment interactions (e.g., effects of particle size on settling velocities or effect of riverbed

bacteria concentrations on resuspension) can add an unnecessary layer of uncertainty to a model without significantly affecting the output. For the purposes of most rural watersheds in southern Africa, data uncertainties may often be large, but a process such as sediment resuspension from wildlife disturbance with direct stream access, should not be excluded from water quality simulations.

#### **4) Characterize Wildlife Fecal Loadings**

Significant uncertainty lies behind the estimation of microbial loading inputs for any water quality model. Humans, wildlife, and domestic animals (livestock and pets) are all potential sources of fecal bacteria, yet it is challenging to accurately quantify contributions from all of these potential polluters (Dufour et al. 2012; Teague et al. 2009). Watershed management of fecal loading, and thus pathogen release, is possible for controlled livestock and human populations but inherently unrealistic for wildlife. Assuming water quality targets are constant across multiple settings, this sets a high bar for water treatment plants in rural or wild environments where the background or “natural” levels of fecal contamination are high.

In southern Africa, vast regions with limited surface water sources experience dramatic changes in wildlife and domestic animal densities, largely based on seasonal changes in vegetation and access to surface water (Alexander et al. 2012; Redfern et al. 2003). The amount of time animals spend in and around surface water can have a significant impact on the concentration and mobility of fecal material and associated sediments in waterways. An investigation into surface water constraints on herbivores in savanna ecosystems indicated that herd distribution significantly correlates with distance to water during the dry season only (Redfern et al. 2003). This aggregation not only localizes fecal loading on stream banks and directly in river ways, but also affects local soil dynamics by eroding active floodplain sediments and accelerating vegetation loss which may amplify pathogen-sediment transport. Large animals or “ecosystem engineers” such as warthogs and hippopotamuses can significantly influence habitat creation, destruction, and maintenance (Ellery et al. 2003; Jones et al. 1994; Naiman and Rogers 1997). It remains unclear how an exclusion of wildlife-landscape modification such as these may affect model processes, especially sediment transport.

While animal population data and species-specific microbial shedding rates might be readily available for confined livestock, and crude estimates are available for wildlife in temperate regions, a massive data gap exists for native wildlife in southern Africa. In the literature, the range and rank of microbial concentrations by species are not consistent between microbial indicators and follow no apparent diet or body size trend. Direct components that affect pathogen shedding (the concentration and community of pathogens deposited) on land and in water by mammals and birds include: 1) animal age, diet, and seasonal distribution; 2) the amount of time each species spends in confinement, in pastures, or wading in streams; 3) the average mass of excrement per species; 3) the concentration of fecal indicator organisms (or pathogens) in a given mass of excreta (i.e., shedding); and 4) antibiotic treatment of livestock or human populations (Dufour et al. 2012; Jamieson et al. 2004; Oliver et al. 2010). A realistic estimation of enteric pathogen loading depends on the accuracy of quantification for these various factors.

Microbial shedding is variable for an individual from day to day, between individuals of a species, and between species. A very limited number of studies exist which quantify bacterial loading from animals and often use low sample numbers (Dufour et al. 2012). Interestingly, many studies reviewed cite previous summaries of species-specific bacterial densities rather than local empirical data, resulting in a long chain of citations dating back over fifty years (Geldreich et al. 1962; Jamieson et al. 2004; Reddy et al. 1981). Loading estimations of uncharacterized species (i.e., most wildlife) that rely on dissimilar empirical data are largely unsubstantiated or even inappropriate. Especially in the vast and undeveloped landscapes of southern Africa, where contact may be infrequent but shared landscapes are ubiquitous, wildlife and non-herded livestock excreta must not be ignored in microbial modeling

### 3.5 Conclusion

*"The problematic environments of developing countries must be accepted as givens and treated as challenges. These environmental preconditions are not in themselves problems because they are the norm for those populations. However, they are new to the technical assistance personnel from temperate countries that advise developing country governments. Often these personnel do not fully appreciate the consequences of hydroclimatic differences between the tropical and temperate zones." (Falkenmark and Widstrand 1992).*

Lessons from several decades of water and sanitation development in Africa indicate that reductions in waterborne disease burden will require sustainable interventions that do not break down in the absence of foreign aid (Batterman et al. 2009). A shift toward long-term solutions should include an assessment of the durability of predictive tools in addition to management actions. While many universal issues related to basin-scale pathogen transport models exist, the immediate applicability of these tools in dryland riverine-floodplain systems is exceptionally limited. Southern Africa and comparable resource-poor, dryland regions would hugely benefit from regionally developed tool adaptations.

Vulnerabilities to waterborne disease are inherently heightened when living organisms (wild, domestic, and human) are dependent on limited, shared water sources. The challenge of quantifying non-point sources contributing to enteric pathogen pollution remains a barrier to improved water quality modeling worldwide. However, the scarcity of biome-specific model development means critical landscape factors are not appropriately accounted for in international applications of temperate-based modeling programs (Levy et al. 2012). Most hydrological models include process-based mathematical components, which theoretically should apply to a large range of land uses and climates. It is not clear how our already limited, still largely empirical, understanding of microbial processes can transfer to semi-arid watersheds.

In rural watersheds with strong seasonal regimes, a complex web of ecological and socioeconomic processes drives waterborne disease. Climatic patterns and precipitation events play a major role in the intensity of fecal loading (animal concentration) near waterways, transport of pathogens and sediments, and the biological cycle of microbial activity in semi-arid lands. Despite the shortcomings of pathogen transport models, it is critical that vulnerable semi-arid communities worldwide employ preventative management tools sooner rather than later to guide data collection and illuminate core uncertainties for larger water-health research advancements.

### 3.6 Appendix A

<b>Data type</b>	<b>Data source &amp; Description</b>	<b>Date range, Time step</b>
Elevation	30m Advanced Spaceborne Thermal Emission and Reflection Radiometer (ASTER) 90 m Shuttle Radar Topography Mission (SRTM)	-
Land Use	Landsat file, supported by Mosugelo et al. (2002); Manual delineation of all buildings, roads, & fields	-
Soils	The influence of soil type in semiarid Botswana I and II (Farrar et al. 1994; Nicholson and Farrar 1994); Harmonized World Soil Database V1.21	-
Human Population	Botswana Water Statistics 2009 Published by Central Statistics Office, Gaborone, Botswana	-
Wildlife Population	Aerial wildlife census of the Caprivi River Systems (2007); Important Bird Areas in Africa and associated islands – Botswana (Tyler and Bishop 2001)	2007
Livestock Population	Aerial wildlife census of the Caprivi River Systems (Chase 2007)	2007
Discharge Data	GRDC station #1291200 in Kongola, Namibia Requested from Global Runoff Data Centre, 56068 Koblenz, Germany	April 19, 1980 – Sep. 29, 2003, <i>Daily</i>
Temperature	Francistown, Botswana; GHCN-D station #BC008948490 Extracted from Climate Research Unit TS 3.10 data set ( <a href="http://climexp.knmi.nl/">http://climexp.knmi.nl/</a> )	May 1, 1958 – Aug. 29, 2011, <i>Daily</i>
Precipitation	Kasane Airport, Botswana; Station #064-KASA Requested from Botswana Meteorological Services <i>Missing values replaced by Pandamatenga Data</i>	Jan. 1, 1960 – June 30, 2009, <i>Daily</i>
Evaporation	Kasane Airport, Botswana; Station #064-KASA Requested from Botswana Meteorological Services <i>Data disaggregated to daily time step; Interpolated missing values; Cloned data pattern back to 1980 to utilize full discharge data set.</i>	July 1992 – July 2006, <i>Monthly</i>

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