USING GIS TO CALCULATE BACTERIAL LOADINGS ALONG THE TEXAS GULF COAST

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ABSTRACT: The purpose of this project is to evaluate bacterial loadings to six bays along the Texas Gulf Coast that currently do not meet state water quality standards. Our specific objectives are to calculate the overall bacterial loading to the bays and to identify the portions of the watersheds having the greatest impact on bacteria concentrations within the bays. These areas can then be targeted for pollution control measures. Arc Hydro was used to create a Schematic Network for the study area. Additional nodes and links were added to the network to connect bay processes with the watershed. Due to the nature of water quality regulations, two additional networks were created: a point source network introducing a fourth node/link definition and a combined point/non-point source network. The Schematic Processor can now be used to model bacterial movement throughout the watershed. Methods also included using the Network Analyst with the NHDPlus data to trace out catchments within a one to three day travel time of the bay. This exercise highlights those catchments that are most likely to contribute viable bacteria to the bays. To the extent possible, the methodologies of this project were developed with national data sources to ensure transferability of these methods to other systems across the country.

KEY TERMS: water quality, total maximum daily loads (TMDLs), Network Analyst, Schematic Network, NHDPlus

INTRODUCTION

Numerous bays along the Texas Gulf Coast are listed on the US Environmental Protection Agency’s (EPA) Section 303(d) List for bacterial impairments. Due to their inclusion on the list, the Clean Water Act requires a Total Maximum Daily Load (TMDL) study be prepared for each of these waterbodies. The Texas Commission on Environmental Quality (TCEQ) is interested in developing a general approach for performing bacterial TMDLs for these bays and the watersheds that drain into them. Our work focuses on developing this approach for a six bay study area extending from Copano Bay north to East Matagorda Bay (see Figure 1).
TMDLs are a national issue and apply to a variety of pollutants. A main goal is, therefore, to develop an approach that is general enough to be transferred to other parts of the country and to pollutants other than bacteria. To accomplish this we rely heavily upon the National Hydrologic Dataset Plus (NHDPlus). NHDPlus is a suite of datasets related to the hydrologic resources of the United States; it includes flowlines, catchments, monitoring station locations, and various attributes related to each (Horizon Systems 2007). Developing a methodology within the NHDPlus framework saves the vast effort required to create this information and allows for the transfer of our methodologies to other areas of the country where NHDPlus coverage is available.

CREATING A SCHEMATIC NETWORK

Using Arc Hydro, a schematic network was built for the study area. The schematic network indicates connectivity between hydrologic features by assigning nodes to each hydrologic feature and links to connect the nodes. This network provides the information necessary to account for the movement of water within a watershed. The schematic network defaults to creating two types of nodes: watershed nodes and river junction nodes. To account for the interaction of the watershed and the bay, a third node/link combination was added to the bays and connected to the original watershed network. Figure 2 shows the schematic network for the Copano Bay watershed. Bay node (Type 3) locations are based on the location of the NHDPlus catchments and previous work that segmented the bays of the Texas Gulf Coast for modeling purposes (Ward and Armstrong 1997).
The TMDL program considers point and non-point sources both separately and in a combined fashion. To account for the bacterial contribution of each, two additional networks were constructed: a point source network and a combined point/non-point source network. Creation of these networks required the addition of a fourth node/link combination to account for point sources in the watershed. Type 4 nodes were placed at the outlet of the point source and connected to the network through a link to the nearest stream junction (node Type 2).

Using these networks we can now utilize the Schematic Processor tool. Schematic processor was developed at the Center for Research in Water Resources (University of Texas at Austin) by Dr. Timothy Whiteaker. This tool uses the node/link structure of the schematic network to model hydrologic and/or water quality processes within a watershed (Whiteaker et al. 2006). It allows for receiving and passing functions at nodes to model the movement of water or contaminants from one node to the next. It also allows for data manipulation, such as decay processes, along the schematic links. Future steps will use the Schematic Processor to model the movement of bacteria through the study area. Though applications within this project use NHDPlus data, the schematic network and processor will work on a variety of hydrologic data sources.

CALCULATING CONTRIBUTING AREA

Previous studies in the Copano Bay watershed indicate that the first-order decay rate of a bacterial cell in this watershed is approximately 2 days$^{-1}$ (Gibson et al. 2006). Based on this decay rate, 99% of a bacterial load will decay within 2.3 days of entering the system. This information can be used to determine the areas of the watershed where bacterial contribution to the bay is of the most concern. By delineating the areas of the watershed that are within 2 days +/- travel time to the bay (via the stream network), we can determine the areas that are most likely to contribute viable bacteria to the bay system. These areas will then be the primary focus of pollution control efforts.

Network Analyst was used to trace the stream segments within 1, 2, and 3 days travel time to the bay. Travel times were calculated as a sum of residence times (Res_Time) within each river segment of the NHDPlus data. These calculations were based upon the segment’s recorded length and the mean annual velocity as given in the MAVELU field of the value added attribute table “flowlineattributesflow”. Two new fields were added to the flowline attribute table: LENGTH_FT and Res_Time. Calculations of these fields are shown below.
In preparation for using the Network Analyst, a new network dataset was created on the NHDPlus flowlines with Res_Time set as a Cost.

To calculate the segments within the desired travel time, the “New Service Area” command within Network Analyst was used. This command is often used in traffic studies for calculating areas within a certain driving distance of a landmark, such as a store or facility. For our purposes, the “facilities” layer was modeled as the intersections of rivers and bays with barriers set around the facilities to prevent the tracing of bay edges. The analysis was then set to trace back the stream network within a 1 day residence time of the facilities. Results of this analysis are shown in Figure 3.

Similar analyses were completed for 1, 2, and 3 day residence times for all six bays in the study area. Results are shown in Figure 4.
This information can now be used to highlight the NHDPlus catchments that are of the highest concern for contributing non-point source bacteria to the bay segments. It will also be used to highlight point sources whose outlets are within the segments of concern.

REFERENCES