

## **Modeling bacteria flow from wildlife in the Leon basin, TX**

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### **I. Background**

Section 303(d) of the 1972 Federal Clean Water Act and EPA regulation 40 CFR 130.7 require states to identify water bodies that do not meet water quality standards. The compilation of subject water bodies is known as the 303(d) list. Each state must assign priorities to water bodies on the list, in order to schedule the development of TMDLs, the maximum amount of load that a water body can take each day and still meet applicable water quality standards.

Leon River, Segment 1221, was initially placed on the list of impaired waters in 1996 for elevated levels of bacterial indicators for pathogens. However, the Leon case was one that involved numerous stakeholders, including ranchers, dairymen, farmers, cities, counties, and EPA, whose interests diverge, making the effort to alleviate the water quality a complex negotiation process. A Watershed Protection Plan was written by Parsons Consulting in 2011, and management is ongoing. It was analyzed that between 41 and 55% of all bacteria in the Leon originated from wild animals, making it the most cost-effective reduction option.



water quality standards at each appropriate downstream outlet.

### III. Methods

#### Gathering key data:

Data was taken from the Leon TMDL final modeling report, derived from Texas Parks and Wildlife Department data (2004) and the EPA Fecal Tool (2000). The major wildlife species to be included in the analysis were determined by wildlife biologists for the composition of the modeling report, based on their site visits and consultation with Texas Parks and Wildlife Department staff. The key species included ducks, deer, raccoons, opossums, and feral hogs, based upon population and fecal production potential. Fecal production rates were derived from the EPA Fecal Tool. The 15 subwatersheds are named in multiples of 10.

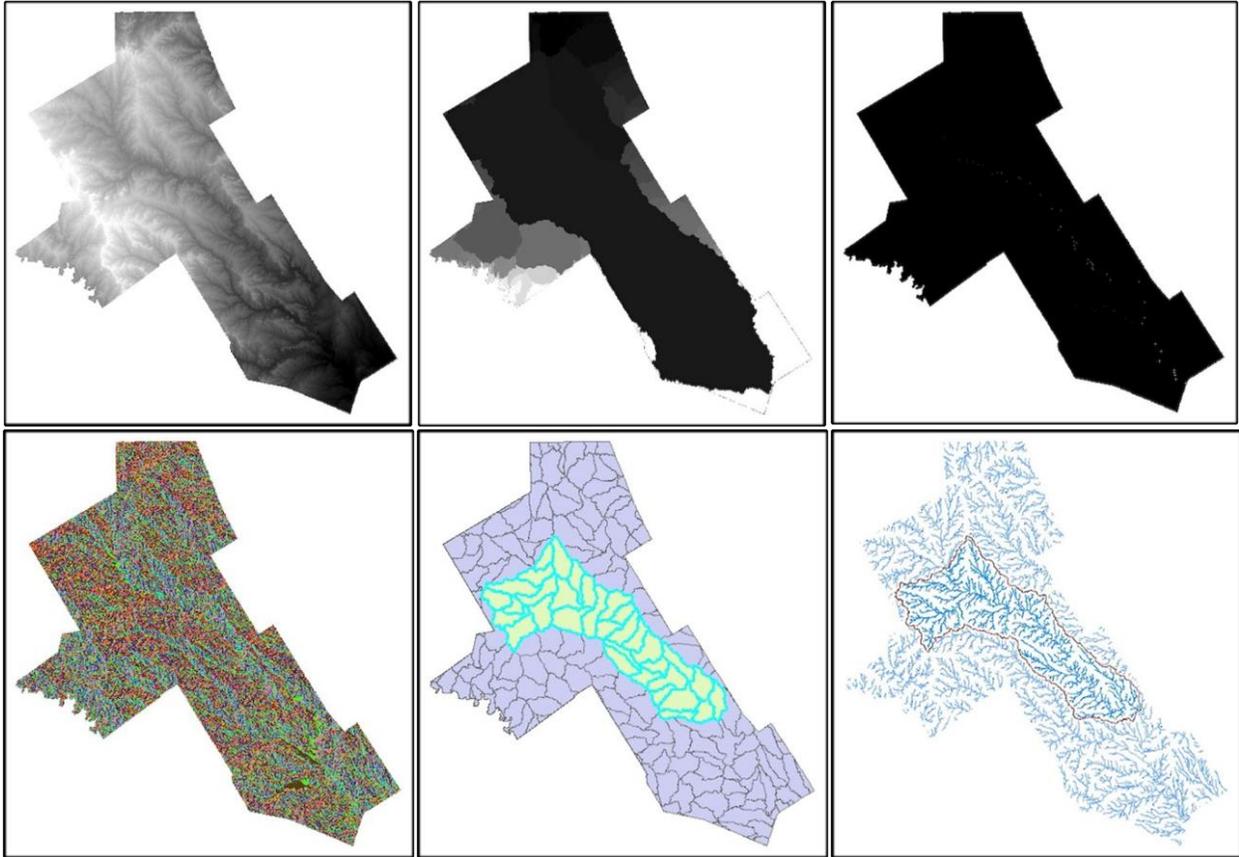
Subwatershed	Ducks	Deer	Raccoons	Opossums	Feral Hogs
10	4	327	261	1045	131
20	14	941	753	3011	376
30	39	7238	5790	23161	2895
40	53	10731	8585	34341	4293
50	20	2293	1834	7337	917
60	50	3790	3032	12128	1516
70	19	6903	5522	22088	2761
80	34	6636	5309	21234	2654
90	33	4148	3319	13275	1659
100	23	2193	1754	7017	877
110	35	4624	3699	14797	1850
120	38	4522	3618	14471	1809
130	22	2213	1771	7083	885
140	18	2418	1934	7737	967
150	48	8192	6554	26215	3277
<b>Total:</b>	<i>450</i>	<i>67169</i>	<i>53735</i>	<i>214940</i>	<i>26867</i>
<b>Bacteria count per animal</b>	<b>Duck</b>	<b>Deer</b>	<b>Raccoon</b>	<b>Opossum</b>	<b>Feral Hog</b>
	2.43E+09	5.00E+08	1.25E+08	1.25E+08	1.08E+10

Then, total daily bacteria load per subwatershed is calculated by multiplying the population estimate of wildlife in each subwatershed by the average bacteria produced by each species, which became the key data for the model.

Subwatershed	Ducks	Deer	Raccoons	Opossums	Feral Hogs	Total
10	9.72E+09	1.635E+11	3.263E+10	1.306E+11	1.415E+12	1.75127E+12
20	3.402E+10	4.705E+11	9.413E+10	3.764E+11	4.061E+12	5.03582E+12
30	9.477E+10	3.619E+12	7.238E+11	2.895E+12	3.127E+13	3.85986E+13
40	1.288E+11	5.366E+12	1.073E+12	4.293E+12	4.636E+13	5.72244E+13
50	4.86E+10	1.147E+12	2.293E+11	9.171E+11	9.904E+12	1.22451E+13
60	1.215E+11	1.895E+12	3.79E+11	1.516E+12	1.637E+13	2.02843E+13
70	4.617E+10	3.452E+12	6.903E+11	2.761E+12	2.982E+13	3.67677E+13
80	8.262E+10	3.318E+12	6.636E+11	2.654E+12	2.866E+13	3.53817E+13
90	8.019E+10	2.074E+12	4.149E+11	1.659E+12	1.792E+13	2.21456E+13
100	5.589E+10	1.097E+12	2.193E+11	8.771E+11	9.472E+12	1.17204E+13
110	8.505E+10	2.312E+12	4.624E+11	1.85E+12	1.998E+13	2.46891E+13
120	9.234E+10	2.261E+12	4.523E+11	1.809E+12	1.954E+13	2.41517E+13
130	5.346E+10	1.107E+12	2.214E+11	8.854E+11	9.558E+12	1.18247E+13
140	4.374E+10	1.209E+12	2.418E+11	9.671E+11	1.044E+13	1.29052E+13
150	1.166E+11	4.096E+12	8.193E+11	3.277E+12	3.539E+13	4.37004E+13

### **Making the base map:**

GIS data for the Leon basin was not publicly available. For watershed delineation, National Elevation Dataset 30m, Texas counties shapefile from exercise 1, and HUC-8 and HUC-12 boundary data from ArcGIS online were used. The following maps describe the chronological steps: filling sinks, creating a flow direction raster, creating a flow accumulation raster, creating a drainage basin raster, converting the basin raster to polygons with HUC-12 boundaries, and defining stream networks.



### Deriving the equation:

To model bacteria flow, I came up with the equation:

$$C_f = (C_u + C_i) * S / L * e^{-kt}$$

where  $C_f$  is concentration of bacteria in context of flow,  $C_u$  is the calculated upstream value,  $C_i$  is the initial concentration,  $S$  is the average percent slope for each subwatershed,  $L$  is the total length of streams in each subwatershed,  $k$  is the decay coefficient, and  $t$  is time in days.

The logic is that concentration in flow is affected by the initial load, the rate of decay, and the distance traveled, but also traveling a certain distance is not the same across the various

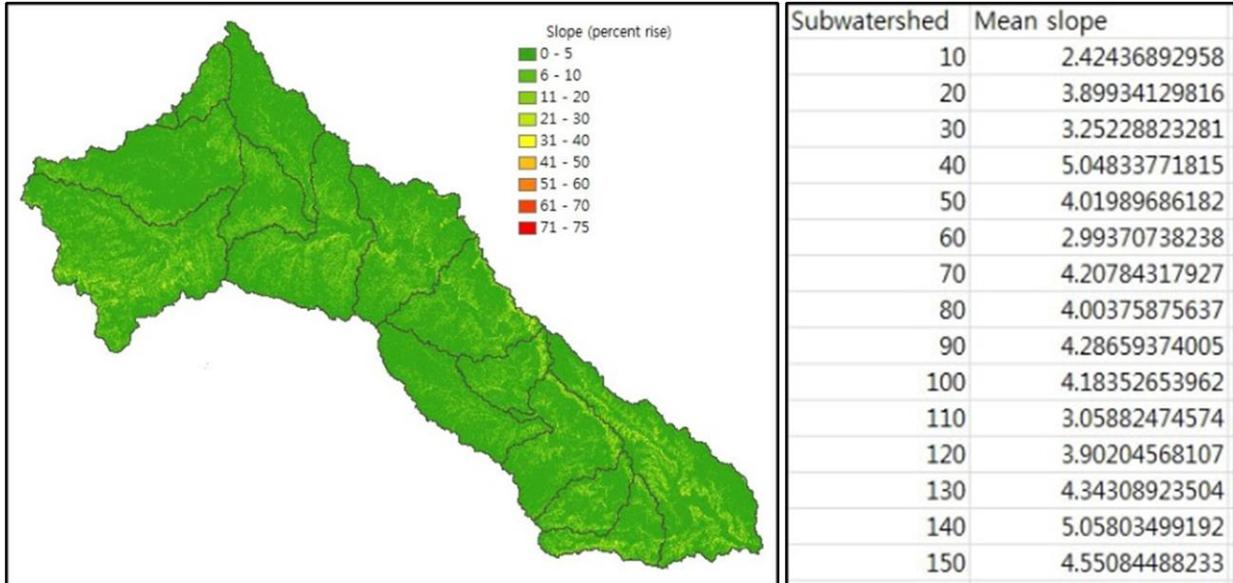
topographies—velocity will increase if slopes are steeper. Since the general upstream to downstream trend is known for the subwatersheds, small-scale negative slopes will be offset by using the average slope. I will arbitrarily use 0.5 for k, meaning half of the bacteria will die each day. Model parameters can be changed depending on the circumstances.

**Preparations for the model:**

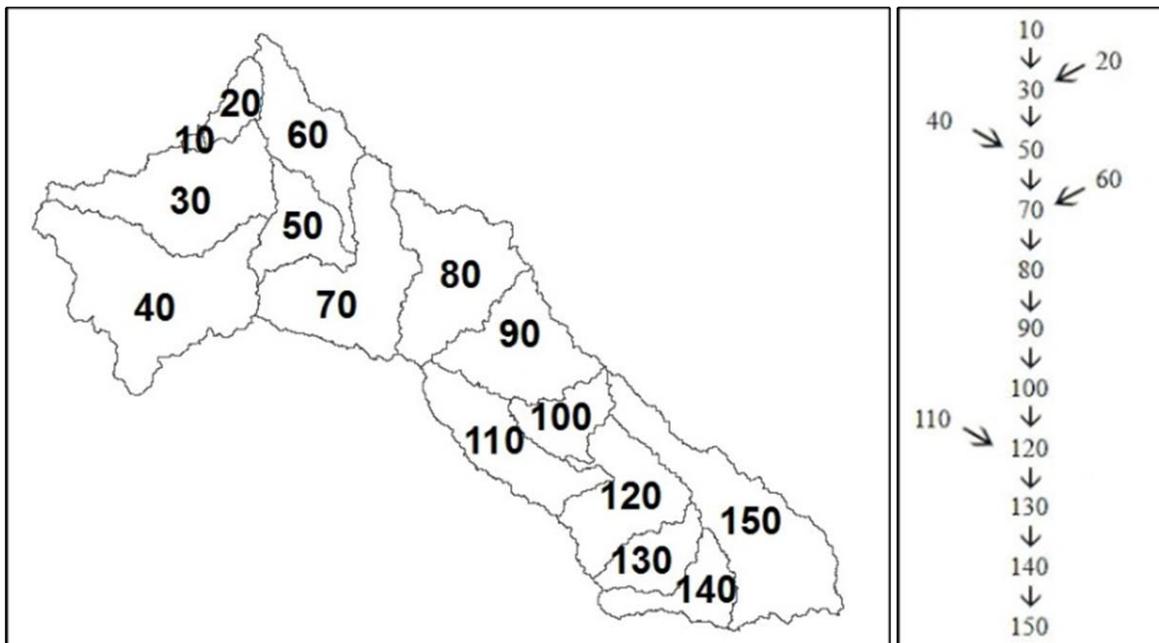
Streams were clipped using each of the subwatershed boundaries, in order to calculate the sum of stream lengths within each subwatershed. The statistics are as follows:

<b>Subwatershed</b>	<b>Total length of streams (m)</b>
<b>10</b>	21055
<b>20</b>	37324
<b>30</b>	211787
<b>40</b>	276001
<b>50</b>	113827
<b>60</b>	136883
<b>70</b>	183786
<b>80</b>	181250
<b>90</b>	117596
<b>100</b>	58028
<b>110</b>	119598
<b>120</b>	114253
<b>130</b>	77577
<b>140</b>	45712
<b>150</b>	200173

Slope was calculated for the elevation raster in the form of percent rise. Then Zonal Statistics as Table was performed to find the average slope for each subwatershed.

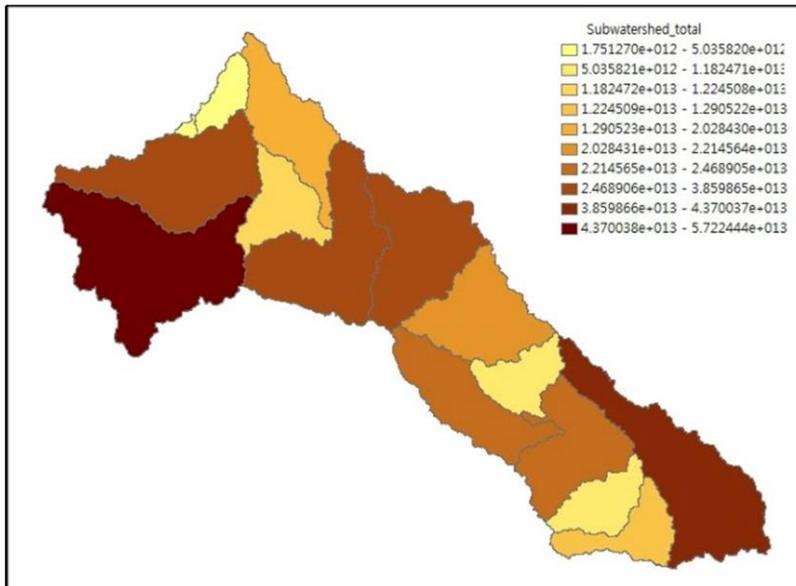


The naming scheme of the 15 subwatersheds and their order of flow are defined in the diagram below. Downstream subwatersheds must receive incoming value before processing a final output concentration. Accumulated concentration for each subwatershed is calculated by adding the calculated value(s) from its directly upstream neighbor(s) to its initial concentration, then multiplying by the decay coefficient. The process continues until the final outlet is reached.

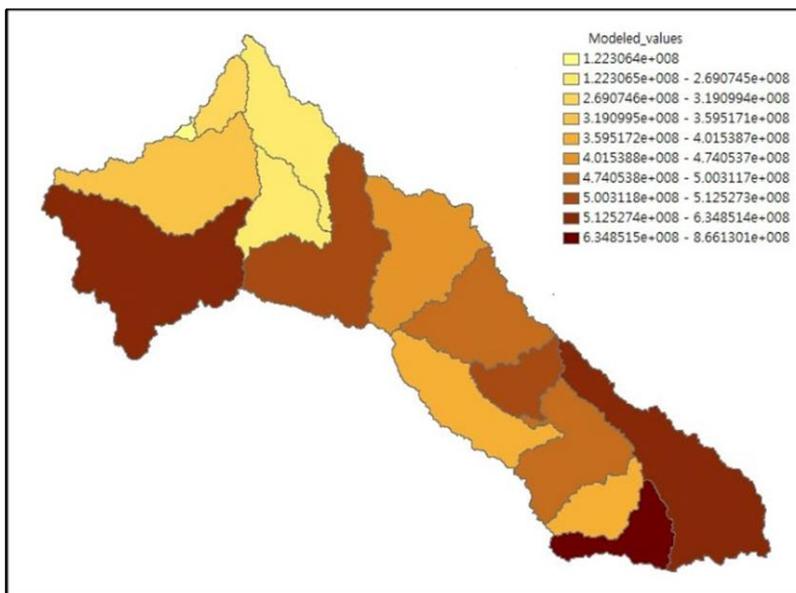


## Results of the model:

The values were calculated manually in a spreadsheet and entered into the attribute table for the subwatershed polygons. Two maps are displayed, first with raw load data and second with modeled flow results. The value figures are not very important, as the decay coefficient was arbitrarily chosen and model parameters can be changed. However, with both maps divided into 10 graduated categories, the differences in the relative concentrations are clearly visible. Unlike the raw data map, the modeled flow map shows higher values downstream, which is logical.



Raw data before modeling



Values after modeling

#### **IV. Conclusions and discussions**

GIS is useful for narrowing down information to be analyzed and visualizing the outcome, which is a useful tool in mediated modeling. GIS provided features and tools that were key to making the model for this study, which may be utilized in similar ways for a better model in the future.

The assumptions and possible shortcomings in the model must be addressed. Although the watershed follows upstream to downstream trend, slope may be negative for some areas within the subwatersheds. Also, average slope for the watershed may not necessarily be the average slope for the streams. The relationship between velocity and slope is not exactly one to one, as they are implied in my equation. Flow is assumed to be consistent throughout the whole basin. For a more accurate modeling, volume of water should also be considered. Temperature, pH, and other factors that may affect bacteria decay were kept as constants. It is unclear whether the bacteria are in growth, lag, or decline phase as they enter the water. Some bacteria can grow in water. For simplicity of the model, I have kept it constant as the exponential decay phase.

The data for wildlife populations is fairly old, and natural habitats may have changed, yet new extensive surveys are difficult to come by. Even if enough time and resources were put into the effort, estimations are inaccurate by definition.

For bacteria decay modeling, Schematic Processor in Arc Hydro tools could have been used. The Schematic Processor associates behavior to a network so that each node can receive and pass on values to other nodes through links, while taking into account decay coefficients and travel times. For the scope of this study, manual modeling was manageable, especially since the Schematic Processor requires a pre-designation of HydroIDs and JunctionIDs to construct a

network, which is not efficient if calculations can be easily done by hand. However, if the resolution of the study is to be higher (e.g., 30 subdivisions of the watershed instead of 15), manual calculation becomes complex and the utilization of the tool becomes a much more efficient option.

## **References**

James Miertschin & Associates Inc. 2006. Final modeling report for fecal coliform TMDL development for Leon River below Proctor Lake, Segment 1221.

Parsons Water & Infrastructure Inc. and the Brazos River Authority. 2011. Watershed Protection Plan for the Leon River below Proctor Lake and above Belton Lake.