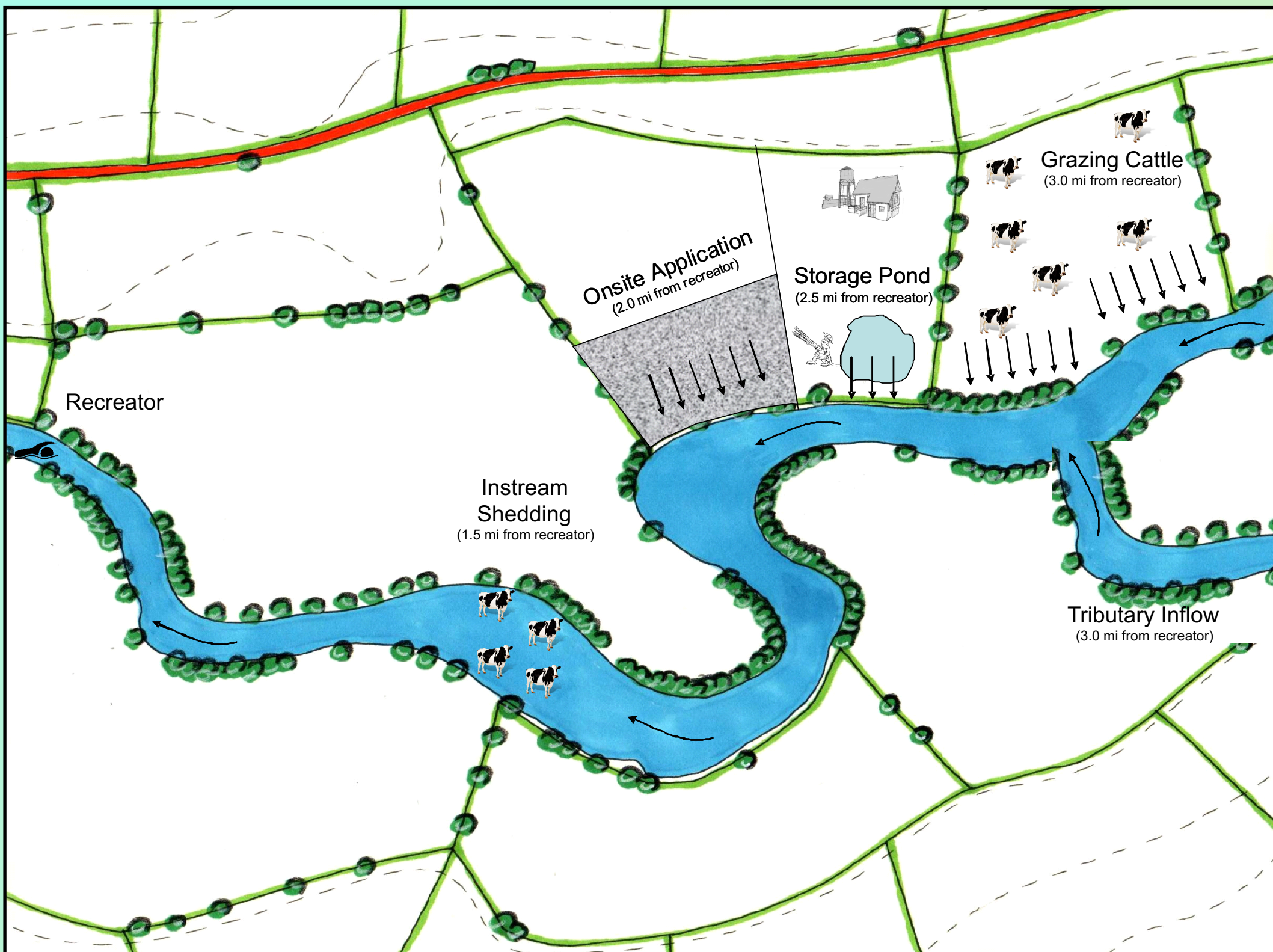


Abstract

Pathogen contamination is the number one cause of impaired recreational waters. Traditionally pathogen exposure risks are measured directly via an epidemiological study. A Quantitative Microbial Risk Assessment (QMRA) is a modeling based approach that integrates interdisciplinary fate/transport, exposure, and impact models and databases to characterize potential health impacts/risks due to pathogens. Here we present an example QMRA, leveraging and combining disparate models in a unified framework for model integration. Source-to-outcome microbial exposure and risk modeling is demonstrated for an agricultural contaminated runoff scenario in a conceptual watershed.

- Motivation
 - Integrate QMRA methodology with pathogen fate and transport modeling to develop exposure risk estimates
 - Develop a conceptual example illustrating our integrated approach
 - Present Agency multimedia integrated modeling capabilities and vision

Conceptual Example



Stream segment with agricultural operations impacting a recreational facility

To motivate the QMRA analysis, a conceptual example has been developed. The example is typical of watersheds influenced by agricultural sources of fecal contamination. The example consists of multiple fecal contamination sources located within a watershed adjacent to each other. These sources include:

- Inflow from upstream tributary - 1-day lag time
- Grazing cattle - 360 cows on 180 acres, 24 kg/d/cow shedding rate
- Leakage to aquifer from a manure slurry storage pond
- Overflow of storage pond during storm events
- Periodic land application of storage pond contents, 4 times/year
- Cattle shedding directly in stream - 10% of cows, 24 kg/d/cow shedding rate

Periodic rainfall events drive contamination from runoff related sources to an area of the stream where recreation occurs. Other sources are influenced by agricultural operations and practices. Fecal contamination enters the stream segment and flows downstream to a recreational facility. A QMRA analysis of the conceptual watershed is performed using modeling tools described in the next section.

- Model Assumptions:
 - Overland transport calculated via kinematic wave equation
 - Groundwater transport calculated using advection, dispersion reaction equation with dilution and attenuation
 - Instream transport calculated using the advection, dispersion, reaction equation with diffusion
 - Periodic rainfall events, intensity 1-yr return frequency, duration 24 hours
 - Transport delay for sources ranges from 1 to 3 days

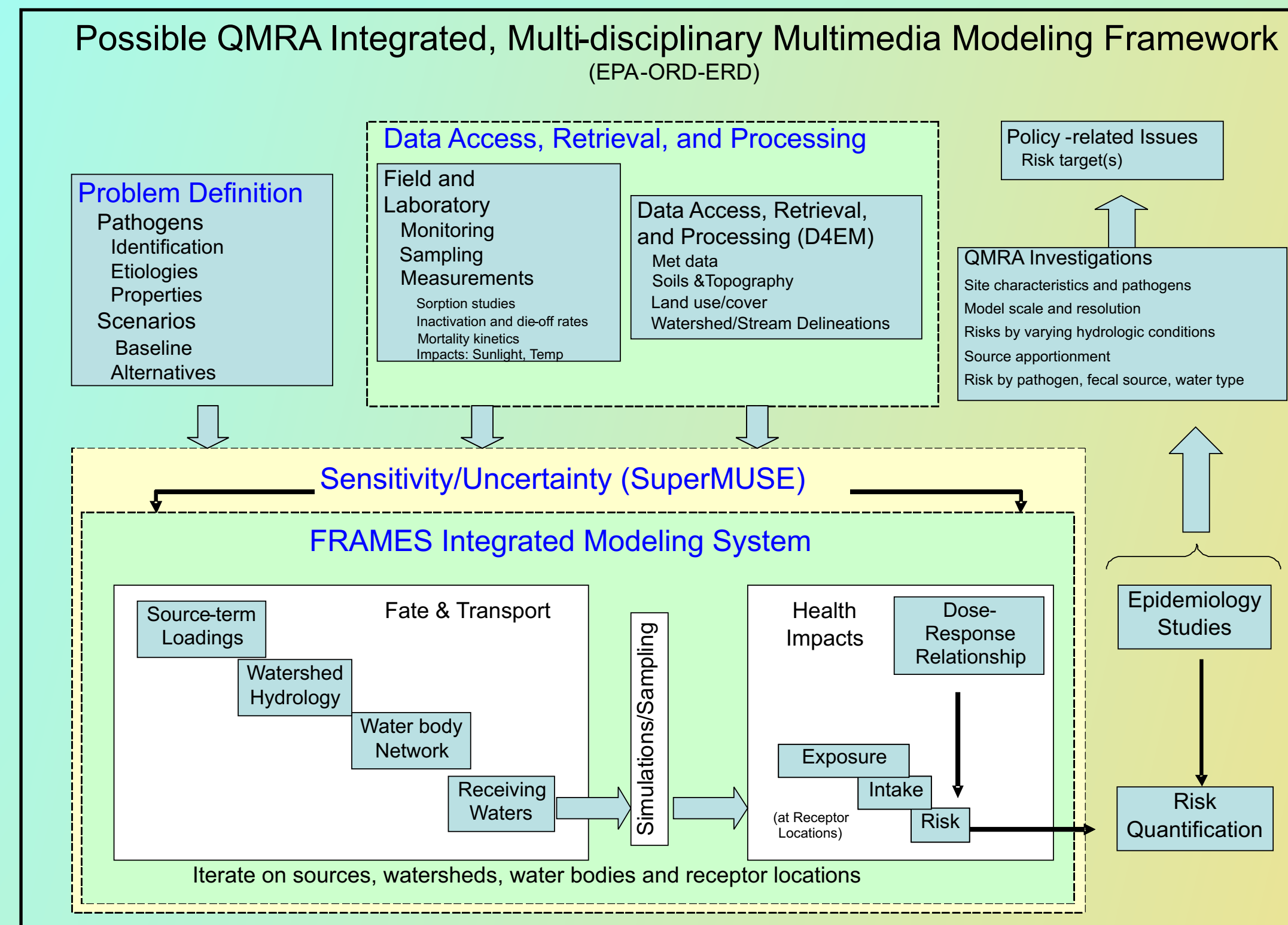


Credit: Photo by Keith Waller, USDA, ARS

Modeling Approach

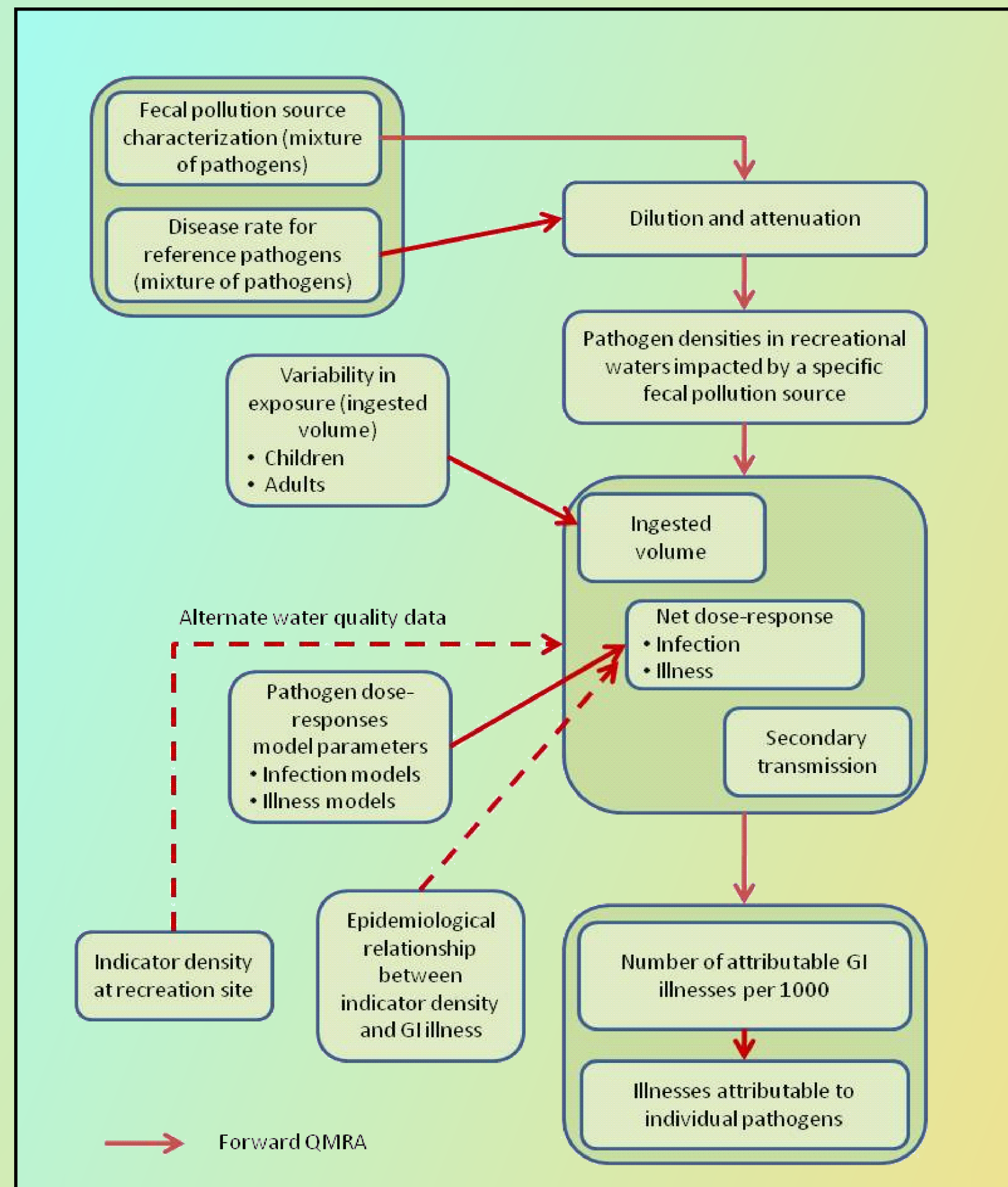
The Microbial risk modeling framework leverages the following integrated modeling technologies:

- **FRAMES** - facilitates linkage and execution of framework components
- **D4EM** - access, retrieves, and processes data for integrated modeling systems
- **SuperMUSe** - Facilitates execution of modeling systems across cluster resources for uncertainty and sensitivity analysis
- **MRA-IT** - characterizes risks associated with exposure to waterborne pathogens and/or infection dynamics in exposed populations



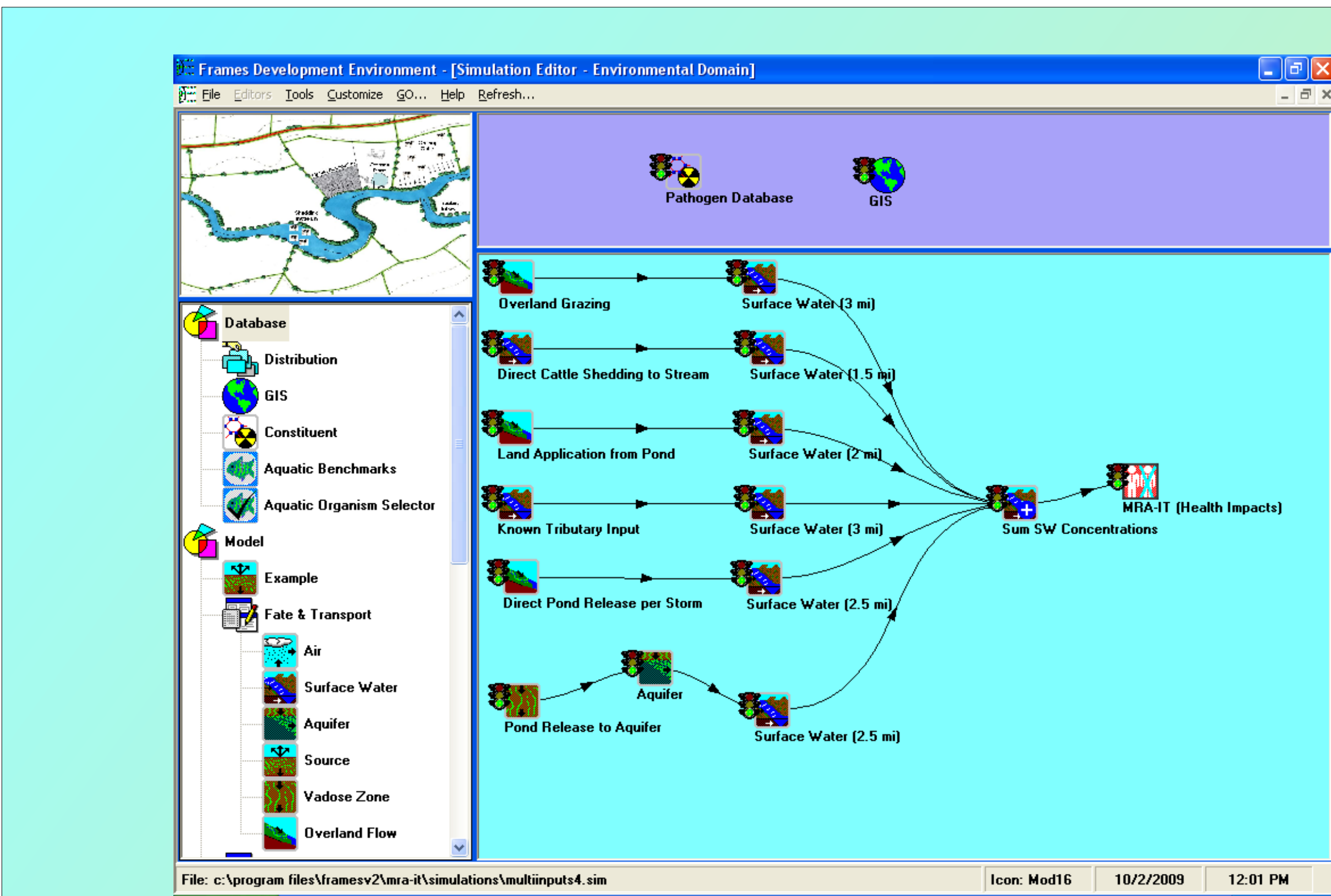
FRAMES microbial risk modeling framework configuration

QMRA fits well with multimedia modeling paradigms that have been widely exercised in the chemical and radionuclide communities, using software system architectures, like the Framework for Risk Analysis in Multimedia Environmental Systems (FRAMES). FRAMES provides the infrastructure to seamlessly link disparate models and databases, providing an assessor with the ability to construct an appropriate conceptual site model from a host of modeling choices, so a myriad number of QMRA analyses can be supported and reproduced.



MRA-IT risk quantification problem formulation

QMRA is analogous to the chemical risk paradigm, but developed for assessing risks stemming from microbial exposures. Microbial Risk Assessment Interface Tool (MRA-IT) is an open-source, integrated software tool for characterizing human health risk based on the pathogen of interest, exposure, intake, and dose. The program contains several key components, including, but not limited to, pathogen specification, exposure scenario identification, and dose-response relationships. MRA-IT includes individual (static) and population (dynamic) risk models and was developed for reclaimed waters. The current version of MRA-IT lacks upstream fate and transport components that produce pathogen and indicator concentrations in the water column prior to exposure. Linking an integrated pathogen transport model with MRA-IT enables the quantification of exposure risk as a function of fecal pollution source characteristics.



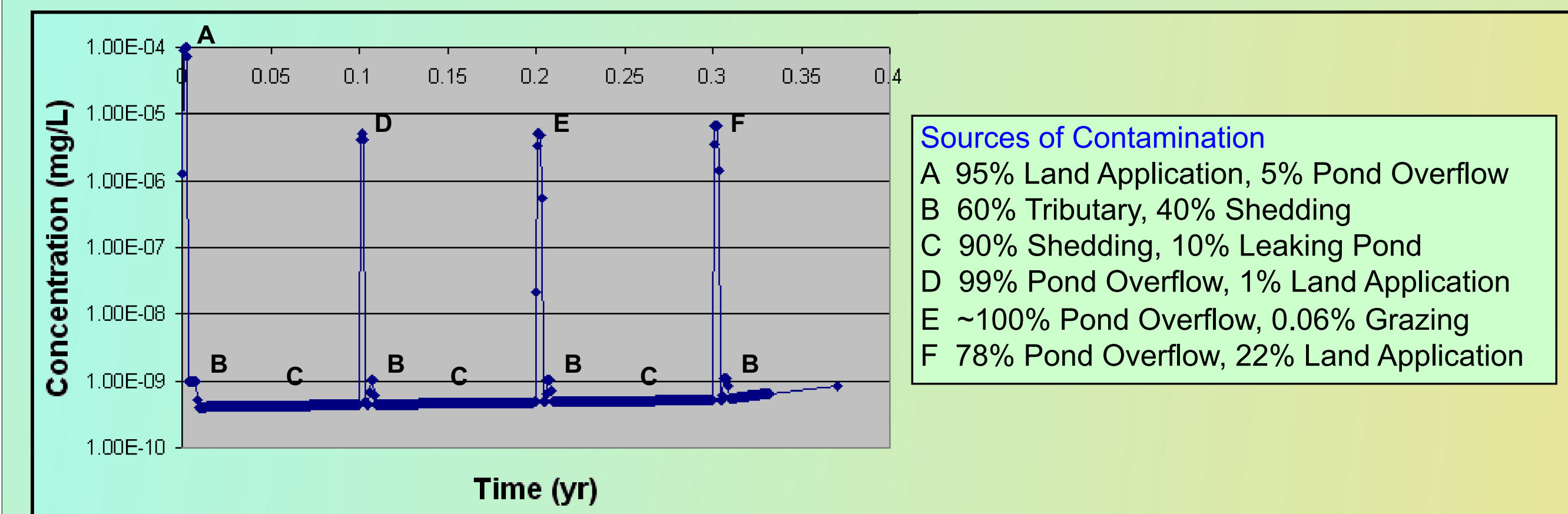
FRAMES model constructed for conceptual example

The MRA-IT is seamlessly linked, using FRAMES, with upstream fate and transport models. The final package is a software technology framework that focuses on linkages across the source-to-outcome continuum and provides an illustrative demonstration of microbial fate and transport, exposure routes and scenarios, intake volumes, dose, and risk computations.

The conceptual example was assembled accordingly:

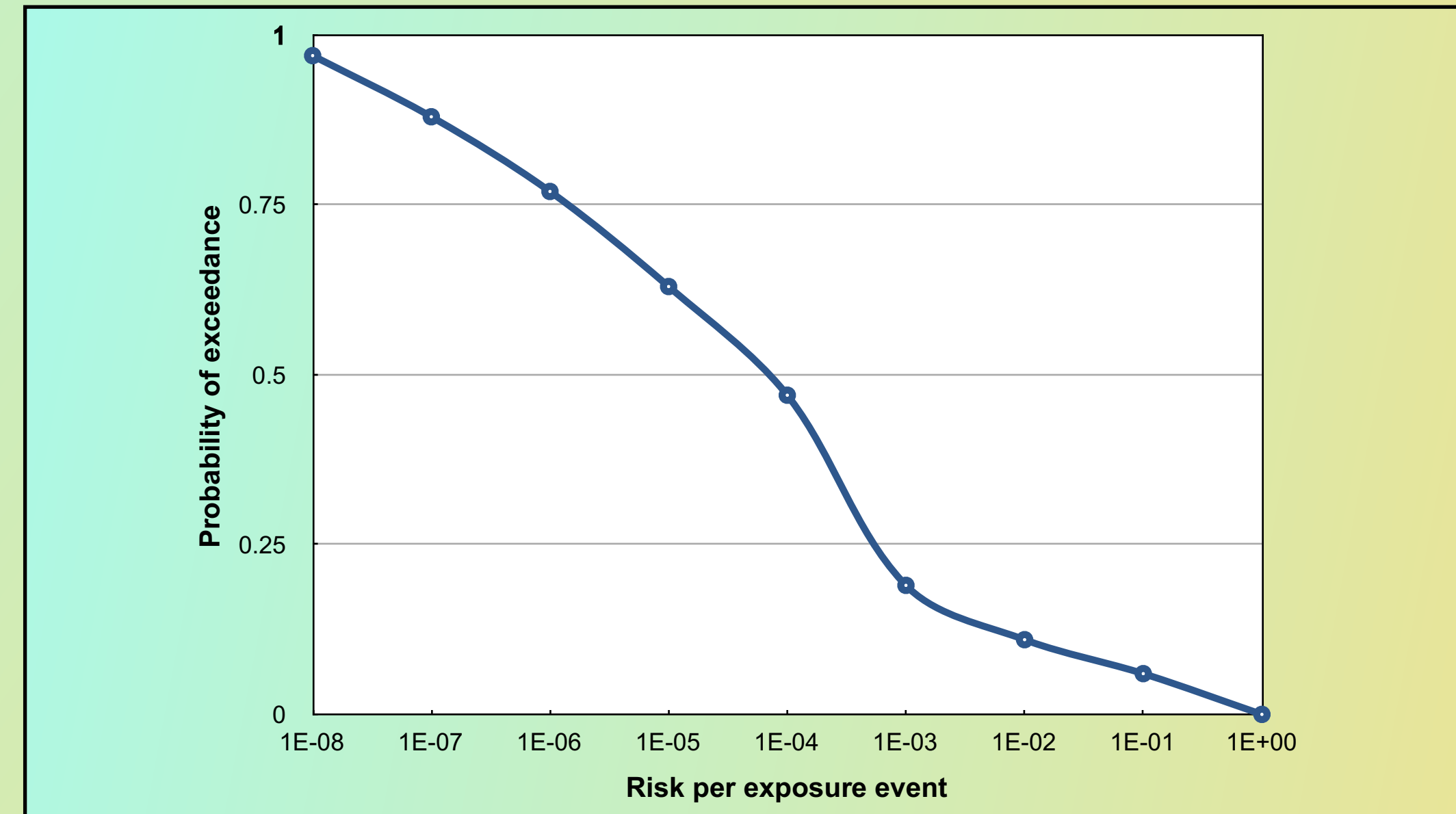
- Source and transport components are linked for each of the six source types
- Concentrations for individual sources are superimposed at the point of exposure
- Concentrations are transferred to MRA-IT and combined with exposure estimates and dose response relationship to compute exposure risk

Results



Time series of pathogen (*Cryptosporidium*) concentrations observed at recreation facility

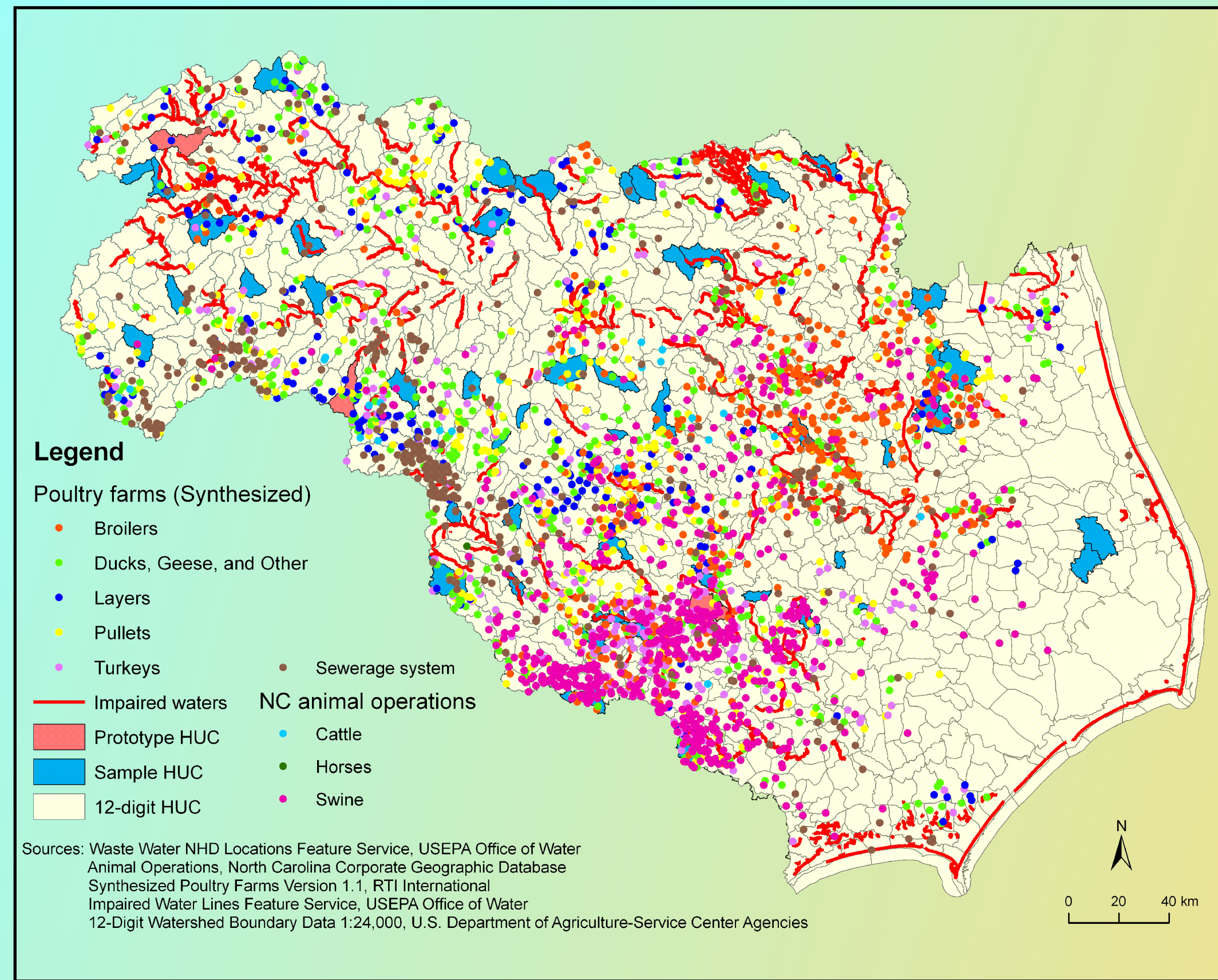
Peaks A, D, E, and F correspond with rainfall runoff events. Peak A coincides with land application activities that subsequently dominate as a source of contaminated runoff. The remaining peaks are predominately pond overflow. Pond leakage and direct shedding influence pathogen concentrations under conditions where steam base flow predominates. The results indicate that pathogen concentrations at a receptor can be a complex function of runoff drivers and the spatiotemporal characteristics of the watershed and sources in question.



Probability of exposure risk over the event window

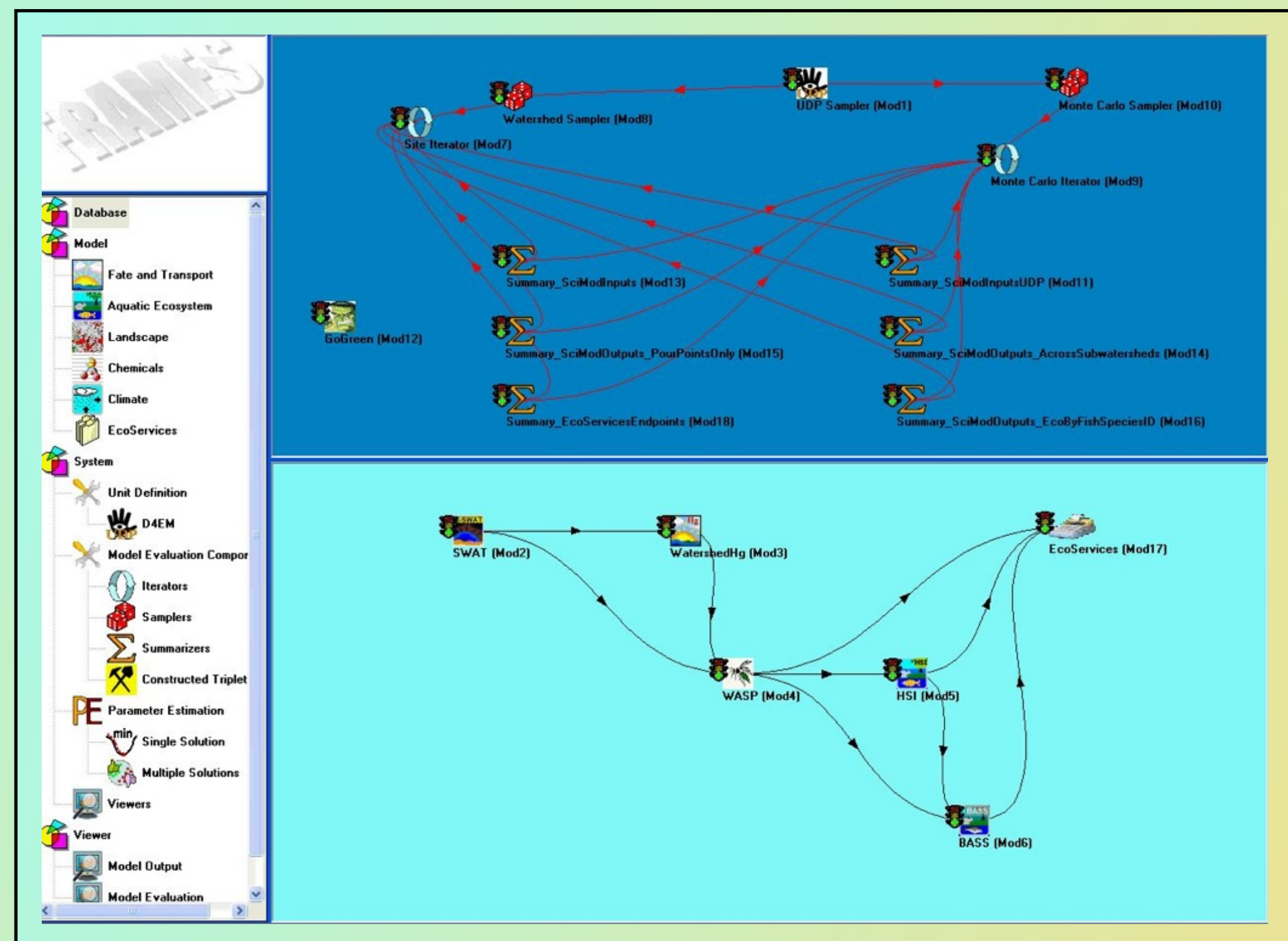
MRA-IT accepts pathogen concentration as its input and produces a probability of exposure risks. Using MRA-IT the probability of exposure risks was calculated for a 1.5 day period of time occurring immediately after peak D in the previous figure. Pathogen concentrations simulated during this period were lognormally distributed. The results suggest a 10% probability of exceedance for exposure risk equal to 32 infections / 1000 exposures.

Vision



APES regional map showing agricultural operations and impaired stream reaches

The Albemarle and Pamlico Estuaries (APES) region spanning Virginia and North Carolina has a high density of agricultural operations that may be contributing to stream impairment. An integrated assessment tool capable of estimating exposure risks due to agricultural and other pathogen sources is envisioned. Such a tool would be capable of the analysis demonstrated in the conceptual example rolled up to a regional scale.



Frames editor view for APES model

By leveraging readily available modeling technologies we envision a modeling framework that :

- Automates the tedious repetitive portions of an assessment
- Allows flexible definition of assessment region and modeling components
- Automates download and population of model components with data
- Controls execution of the integrated model
- Enhances quality control of data and analysis of results

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