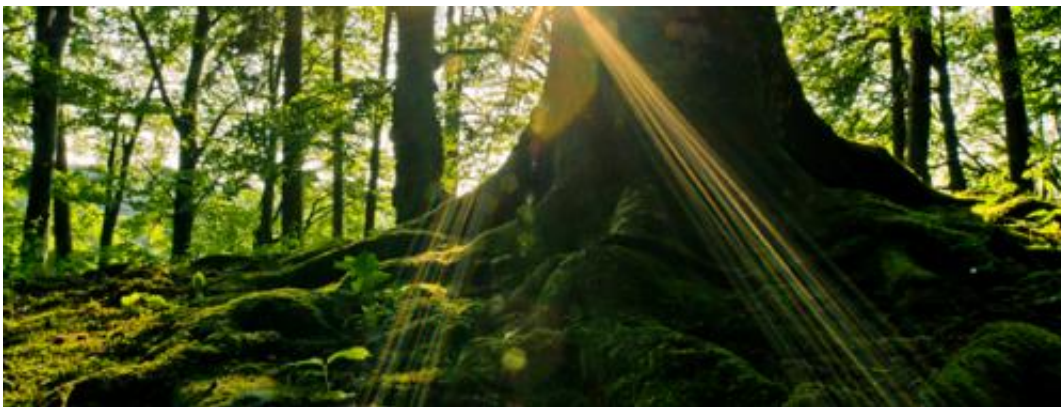# Estimating 'regions of attraction' should improve computer models of biological systems

September 18 2012, by Matt Shipman

(Phys.org)—Researchers have found an effective means of estimating the "regions of attraction" (ROA) when developing computer models of biological systems – improving the ability of these models to predict how a system will respond to changing conditions. But to talk about that, we probably need to explain what an ROA is – and why it matters.

When developing computer models to predict the behavior of [biological systems](link), an enormous number of variables come into play – ranging from nutrient concentrations to the presence (or absence) of specific environmental stressors.

In most cases, the value of these variables leads to a specific phenotype, or observable characteristic. For example, a tree growing in a damp environment is less likely to drive its roots deep into the soil. A tree growing in a dry environment is more likely to drive its roots deep into the soil, in search of water. The variable in this example is the presence of environmental water. The amount of water affects which phenotype is expressed – deep roots or shallow ones.

The range of possible values for a given variable that result in a specific phenotype is called an ROA. Using the previous example, the point at which the soil becomes so dry that a tree begins to send its roots deeper into the ground is the point at which it passes from the "shallow roots" ROA to the "deep roots" ROA.

And being able to accurately estimate the ROA, or range of values that lead to a given physical characteristic, for all of a system's possible phenotypes is an important part of the modeling process for biological systems.

"Accurate estimates of the regions of attraction of biological systems allow us to assess how systematic changes in control variables, and even changes in environmental stressors, can change the relative size of the ROA – making them larger or smaller," says Dr. Cranos Williams, a researcher at NC State who co-authored a paper on the research. "Changes in ROAs associated with plant metabolism, for example, can have a potential impact on the plant's ability to survive or adapt to changing conditions such as climate, drought, or pollution.

"Furthermore, if we understand what changes these ROAs, we may be able to determine how the relevant variables can be manipulated to minimize the likelihood of unwanted phenotypes – such as characteristics linked to premature cell death."

Most existing tools that estimate ROAs were developed for use in models that aren't designed to capture the dynamic nature of biological systems. And while a few, more sophisticated, estimation techniques have been developed, it remained unclear whether they could be used in conjunction with biological systems.

But now we're back where we started. Researchers from NC State have identified an ROA estimation technique that is compatible with at least some complex biological models – and may be applicable to many more.

Williams and Megan Matthews, a Ph.D. student at NC State, applied this technique – developed by Sascha Warthenpfuhl, et al., at the University of Wuppertal – to two biological models, and found the approach was able to successfully estimate ROAs associated with these systems.

Matthews is currently leading an effort to modify the technique to improve its accuracy, as well as determine how broadly the technique may be applied.

The paper, "Region of attraction estimation of biological continuous Boolean models," will be presented at the 2012 IEEE International Conference on Systems, Man and Cybernetics, being held Oct. 14-17 in Seoul, Korea.

Provided by North Carolina State University