Genes of Ecological Networks

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An ecological network [1] consists of flow rates of conserved quantities (biomass, energy, Carbon) among a set of compartments (species). While this data is relatively small in size, its collection from field experiments can be extremely challenging. Mathematical and computational methods used to model and analyze ecological networks need to cope with (partial) lack of data and low quality data (due to experimental errors and external factors.) This situation is in contrast to other branches of life sciences, having the privilage to mine the abundant data afforded by high throughput experimental techniques such as microarrays. Ecosystem ecology has to make the most of its hard earned little data available. Therefore we ask the following question: Is there a transform that maps the available data to a much larger data set that we can mine using advanced machine learning techniques? Are there any hidden smaller constituents that make up a flow rate between two compartments?

We identify these constituents that are analogous to genes in living organisms. It is possible to use machine learning to extract useful information by identifying which constituents (genes) of the ecosystem model are responsible of a specific trait, such as response to an environmental impact, climate change, or species extinctions. We demonstrate our methodology on a model of the Neuse River Estuary [2], which has only seven compartments and 34 flows, but 640 constituents (genes). While the seasonal variations are not clearly apparent in the collected experiemtal data, we were able to identify only 3 constituents (out of the 640) that determines the seasonal variations with 100% accuracy.

References

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