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Author(s)	GALBRAITH, Elroy Louis Matthias
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## 学 位 論 文 内 容 の 要 旨

博士の専攻分野の名称 博士（情報科学） 氏名 Elroy Louise Matthias Galbraith

### 学 位 論 文 題 名

Whispers in Murky Waters: Bacterioplankton Interaction Networks Underpinning Ecosystem Health  
(澱んだ水の中のささやき: 生態系の健全性を支えるバクテリアプランクトンの相互作用ネットワーク)

Accurate monitoring and prediction of aquatic ecosystems at multiple scales are crucial to maintaining the biosphere, especially given the role of rivers, estuaries, and oceans in species habitat provision and biogeochemical cycling in the land-atmosphere continuum. Communities of aquatic bacterioplankton – the bacteriome – perform many ecosystems regulating functions, emitting informative signals of environmental pressure via patterns in their collective structure and function. Current approaches to eco-health assessment using the bacteriome miss global and habitat-specific signals informative of ecosystem state by ignoring the collective dynamics of these complex systems, choosing instead to focus on individual indicator taxa or functions, and biogeochemical thresholds. In response, this work aims to improve ecohealth assessment and ecoengineering by utilizing phylogenetic, structural, and functional patterns within the collective dynamics of the bacteriome; and to identify biogeochemical management priorities after similarly analyzing the environment as a complex assemblage of interacting elements – the Envirome – whose destabilizing impact likely emerges from patterns within that network.

In Chapter 3, patterns in community phylogenetic relatedness, population abundance distributions, and species interactions within the Bacteriome network (inferred from information fluxes) are shown to be informative of ecosystem state. Two novel patterns are presented: the info-theoretic Kleiber’s Law between bacterioplankton phylum co-predictability (directed interactions) and population and community abundance uncertainty, with an average exponent strikingly similar to theoretical expectations; and the Phylogenetic Separation Rate describing how communities accrue new functional groups much slower than new species.

In Chapter 4, the novel Eco-Evo Mandala is presented: it is a multiscale map of the Bacteriome considering habitat-defined distributions, species interactions, and phylogeny, which signals community (and likely ecological) departures from relative theoretical optimality. The Mandala confirmed that these departures were habitat-specific, mostly considering the structural and functional traits related to bacterioplankton abundance and interaction distributions (reflected by power law and exponential distribution parameters, respectively), which were not linearly associated with each other.

In Chapter 5, the Envirome factors responsible for community disorganization, such as temperature, salinity, and nutrient loads, are pinpointed, and the means by which the Envirome destabilizes the Bac-

terioime is elucidated. Disorganization within the Envirome meant environmental impacts rearranged the Bacteriome into more disorganized, random interaction topologies.

In Chapter 6, conclusions are shown. The perspectives underlying this work are used to inspire a possible future for ecological research and practice. Emphasis is placed on how functional diversity regulating community optimality is different from taxonomic richness and must be combined with probabilistic bacterio-environmental covariations to create a fulsome picture of ecosystem state, especially because full biological knowledge is presently too cumbersome to obtain. Such an approach is applicable in multiple scales and contexts, enabling the coordination of local and global environmental interventions. Consequently, eco-engineering policies, research, and technologies should focus less on moderating the individual whispers from populations or environmental drivers, and more on orchestrating all components into a symphony of order and health.