## STAZIONE ZOOLOGICA ANTON DOHRN

## WITHIN THE SZN-OPEN UNIVERSITY PH.D. PROGRAM PH.D. THESIS

## Modeling Macroecological Patterns in Marine Ecosystems: From Community Structures to Gene Expressions

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Academic Year 2024/2025

## ABSTRACT

ARINE ECOSYSTEMS, CHARACTERIZED BY EXTRAORDINARY SPECIES DIVERSITY, RELY HEAVILY ON MICROBIAL COMMUNITIES THAT DRIVE KEY ECOLOGICAL AND BIOGEOCHEMICAL PROCESSES. Although high-throughput molecular techniques have substantially expanded our knowledge of microbial communities, many open questions persist regarding the processes shaping their composition, diversity, and function.

This thesis addresses these gaps through two complementary lines of research. First, it investigates how temporal delays influence the stability and collective dynamics of large ecological systems. Delays arise naturally from spatial diffusion or interactions with environmental variables, and we show that they alter classical stability criteria in ways that generalize May's complexity–stability result. By examining near-equilibrium and generalized Lotka–Volterra dynamics, we find that delayed self-interactions can trigger not only instability regimes, but also chaotic states and collective oscillations, offering alternative explanations for synchronization in real-world ecosystems, beyond traditional predator–prey cycles.

Second, we adopt a macroecological lens to study marine phytoplankton, focusing on diatoms. We revisit Hutchinson's paradox of the plankton and a proposed inverted paradox, which predicts unrealistically high biodiversity under neutral assumptions. Our analytical approach reveals that extinction timescales depend critically on initial conditions, and incorporating a realistic rare-biosphere distribution resolves the paradox without invoking non-neutral processes. Building on this insight, we analyze diatom community data from the *Tara Oceans* expeditions, finding that neutral models capture the majority of rare species but fail for hyper-dominant taxa. This suggests that while neu-

trality is helpful in describing much of the community, additional selective or historical factors underlie the rise of dominant diatoms. Finally, to explore the functional dimension of diatom communities, we propose a null model coupling metagenomic and metatranscriptomic abundances, which we successfully fit to empirical data, offering a possible new way to normalize unigene abundances across samples. We quantify gene-expression patterns, proposing a temperature-dependent transcription efficiency, that is able to reproduce a universal sublinear scaling in the number of expressed genes.

Taken together, these findings highlight the value of integrating advanced theoretical models with empirical datasets to illuminate how microbial communities assemble, persist, and function—ultimately contributing to a deeper understanding of Earth's remarkable biodiversity.