



Functional Biodiversity Modelling for Agricultural Systems: Lessons from Environmental Risk Assessment

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Functional biodiversity modelling aims to understand how species traits and ecological processes sustain agricultural productivity through pollination, pest control, and ecosystem resilience. Yet translating these models into management decisions reveals a fundamental challenge exemplified by environmental risk assessment (ERA): the reductionist trap. Current ERA illustrates this problem starkly. We have developed sophisticated assessments for individual chemicals with great precision, yet real agricultural systems face multiple interacting stressors that do not conform to these isolated evaluations. The current ERA takes over 10 years and can cost €100,000 in administrative costs per product, yet still produces ecological surprises such as delayed neonicotinoid bans and ongoing pollinator declines. We assess chemicals individually with detailed precision but miss landscape-scale cumulative effects because we optimise for single-chemical safety rather than ecosystem stress capacity. Precise isolated assessments created false confidence while missing the emergent properties and system-level thresholds that drive real-world biodiversity outcomes.

This talk advocates reversing traditional workflows: instead of building isolated models and connecting them later, we must define agricultural systems first, establish ecosystem-level thresholds for functional biodiversity analogous to carbon budgets, then assess interventions within this integrated context. We can demonstrate this is feasible, enabling questions impossible with siloed approaches such as “Can we establish chemical stress budgets maintaining biodiversity services while enabling sustainable agriculture?”. The path forward requires functional biodiversity modellers to embrace interoperability from the start, building tools interoperable across ecological, agronomic, and chemical domains. Agricultural systems do not respect disciplinary boundaries, and our models should not either.