

# *Phenotype-structured integro-differential models: derivation and qualitative analysis*

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## **Abstract**

In this work, we derive, analyse, and simulate several different integro-differential models, bridging the microscopic description of individual processes with mesoscopic and macroscopic representations of collective dynamics. The common thread running through the work is the use of a stochastic approach to connect individual-level mechanisms with emergent evolutionary dynamics at the population scale.

In the first chapter, we build upon and generalise kinetic theory approaches for multi-agent systems to develop a non-conservative modelling framework for phenotype-structured populations. We start from a stochastic agent-based formulation that describes individual dynamics driven by fundamental biological processes such as death, proliferation, and phenotype changes. Then, at the mesoscopic level, we formally derive the integro-differential equation governing the evolution of the population's phenotypic distribution. Subsequently, we consider a quasi-invariant regime of small and frequent phenotype changes and rigorously derive a non-local Fokker-Planck-type equation counterpart of this model.[1]

In the second chapter, we extend this modelling framework to multi-compartmental systems structured by continuous variables representing the levels of expression of compartment-specific traits. We contextualise our construction within an epidemiological framework and, following an analogous multi-scale procedure as in the previous chapter, derive a system of integro-differential equations at the mesoscopic level and a system of ordinary differential equations at the macroscopic level. We then obtain a general formula for the basic reproduction number  $\mathcal{R}_0$  for a reduced version of the previous system. This quantity is expressed directly in terms of key microscopic functions and parameters, thereby highlighting the connections between fundamental processes at the microscopic level and the resulting population-scale dynamics.[2]

In the third chapter, we introduce a model describing the co-evolutionary dynamics of two interacting and structurally heterogeneous subsystems: nutrients and consumers. Each subsystem features its own compartmental subdivision and is endowed with a specific structural variable that characterises its internal heterogeneity. Then, we consider a suitable quasi-stationary limit and, by exploiting the conservative properties of the system, reduce the dynamics to a coupled system of integro-differential equations. Thus, we prove a well-posedness theorem ensuring existence, uniqueness, and positivity of the solutions. Finally, we investigate the asymptotic regimes of the model, identifying the set of fittest traits and characterising the emergence of selection phenomena through both analytical and numerical results.

Finally, in the fourth chapter, we outline several future research perspectives, including, among others, the application of the techniques developed in this work to the context of non-convex optimisation. Preliminary numerical experiments suggest that the stochastic mechanisms underlying the models of the previous chapters may inspire new meta-heuristic algorithms, offering promising directions for future interdisciplinary research.

## References

- [1] Emanuele Bernardi, Tommaso Lorenzi, and Andrea Tosin. “Derivation and quasi-invariant asymptotics of phenotype-structured integro-differential models”. In: *arXiv preprint arXiv:2510.15646* (2025).
- [2] Emanuele Bernardi, Tommaso Lorenzi, Mattia Sensi, and Andrea Tosin. “Heterogeneously Structured Compartmental Models of Epidemiological Systems: From Individual-Level Processes to Population-Scale Dynamics”. In: *Studies in Applied Mathematics* 155.2 (2025), e70091.