Forward and inverse modelling of eco-evolutionary dynamics

in biological and economic systems

Victor BOUSSANGE

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Summary

Biological and economic systems are complex adaptive systems, composed of heterogeneous organisms and entities that interact in nonlinear ways and experience evolutionary processes. The processes of interaction and evolution act at different organizational scales, from genes to ecosystems and from organizational routines to economies, generating complex couplings across scales. Yet despite this complexity, biological and economic systems often show organized structural properties and invariant patterns. These invariant patterns must originate from general organizational principles, which we need to identify in order to advance our understanding.

Recently, studies have shown that evolutionary processes can occur on similar time scales as ecological processes, generating eco-evolutionary feedbacks which may play an important role on the dynamics of biological systems. In economic systems, studies are suggesting that economic change is determined by analogous eco-evolutionary processes. Yet, our understanding of eco-evolutionary processes and feedback mechanisms in empirical systems is limited, because of the over simplicity of current eco-evolutionary models and the lack of confrontation with empirical data. Aiming at advancing our understanding of general eco-evolutionary processes and mechanisms shaping the dynamics of biological and economic systems, this thesis develops novel modelling approaches to integrate realism and empirical data into eco-evolutionary models.

?? develops and analyses an eco-evolutionary model on spatial graphs to understand how eco-evolutionary processes, in combination with complex habitat structures, influence the phenotypic distribution of biological populations. **??** develops an inverse modelling method to estimate the parameters of eco-evolutionary models from empirical data, and discriminate between competing eco-evolutionary hypotheses. **??** uses the inverse modelling method, together with 59 years of economic data, to investigate whether processes involving positive and negative interactions between economic activities, spatial transfers, and economic activity transformations, can explain the dynamics of economic systems at the country level. **??** finally develops two numerical methods to efficiently simulate eco-evolutionary models capturing the evolution of high dimensional spatial and phenotypic distribution.

Together, this thesis develops novel forward and inverse modelling methods to improve the ability of eco-evolutionary models to describe real-world features, and to use them in combination with empirical data to infer knowledge. These

methods allow to establish a map of causal pathways involved in local adaptation and phenotypic differentiation in spatially structured biological populations, and highlights that processes akin to those in biological systems shape the dynamics of economic systems. In the face of the climate and biodiversity crisis ahead of us, it is of utmost urgency to quickly advance our general understanding of the mechanisms shaping the dynamics of life on Earth. Bridging biology, mathematical modelling, machine learning and economics can massively accelerate this understanding.

Résumé

Contents

1 Introduction

> *Nature loves to hide.*
>
> — **Heraclitus (c.6th-5th century BCE)**

1.1 Context

1.1.1 Biological and economic systems as complex adaptive systems

What are the similarities between the dynamics of biological and economic systems? Think of a biological system as a community of interacting biological organisms (Chapin et al., 2002), and think of an economic system as a community of interacting economic agents (Dopfer and Potts, 2007). The dynamics of a biological system depends on fluxes of matter and energy between organisms, and the dynamics of an economic system depends on fluxes of capital between economic agents. *A priori*, the underlying processes strongly differ, because the behavior of economic agents is motivated by rationality, where economic agents maximize utility (Lawson, 2013). Nonetheless, economic agents are faced with uncertainty (Foster and Metcalfe, 2012) and their rationality is bounded (Veblen, 1898; Nelson, 1985). As a result, economic agents adopt a variety of behavioral rules (e.g. technological, organizational, institutional, Foster and Metcalfe, 2012) through trial-and-errors, which are subject to natural selection through competition processes (Schumpeter, 2017). In this perspective, both biological and economic systems are complex adaptive systems (Levin, 2002), composed of heterogeneous entities that interact in nonlinear ways and experience evolutionary processes. The processes of interaction and evolution involved take many forms and operate at different organizational level (Levin, 1998), from genes to ecosystems, and from organizational routines to economies, with feedback mechanisms between the organizational levels (see Fig. 1.1). Interestingly, the stochasticity of the processes involved, and their couplings, do not necessarily lead to unpredictable structures and dynamics, but rather induce organized structural properties and invariant patterns (Olff et al., 2009; Mitchell, 2009). In biological systems, invariant patterns include patterns of species richness, where for instance montane regions are often associated with a disproportionately high number of species (Rahbek et al., 2019b). In economic systems, invariant patterns include the bimodal shape of the distribution of international income, where some countries have systematically developed much more rapidly than others (Acemoglu et al., 2001). A common direction on the research agenda in biology and economics is to understand general organizational principles, i.e. to underpin the fundamental processes and feedbacks that generate invariant patterns (Levin, 2002; Olff et al., 2009; Veldhuis et al., 2018). In biological systems, the fundamental processes resulting in patterns of species richness are identified (Rahbek et al., 2019a; Rangel et al., 2018; Hagen, 2022), and the current challenge is to underpin the mechanisms resulting from their couplings (Hagen, 2022). In economic systems, we still do not exactly understand the fundamental processes at stake.

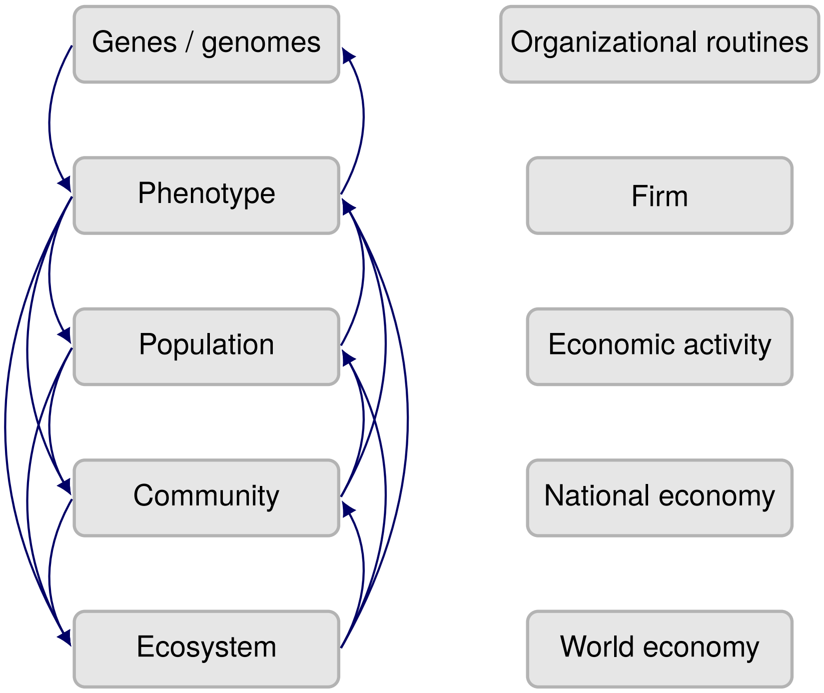

Fig. 1.1: Graphical representation of organizational levels and their interactions in biological and economic systems. An arrow indicates that the organizational level at its tail can influence the organizational level at its head. No arrow is represented in the right diagram, because how organizational levels influence each other is unclear in economic systems. Left diagram is inspired from Hendry, 2016.

1.1.2 Ecological and evolutionary processes drive the dynamics of biological systems

In biological systems, interaction processes are more commonly designated as ecological processes, and encompass the processes of interaction between organisms (biotic interactions) and between organisms and their environment (abiotic interactions), as well as dispersal processes (movement of individual across space) (Vellend, 2010, see Fig. 1.2 for a graphical representation). Evolutionary processes designate those processes responsible for the change of heritable characteristics (DNA, genes, phenotypes) over successive generations ((Hall, 2013), Fig. 1.2). The coupling between ecological and evolutionary processes is acknowledged since the very birth of the theory of evolution. During his voyage on the Beagle, Darwin documented a link between the different ecological opportunities across the Galápagos Islands and the different beak shapes in the finches he found on each island (Darwin, 1859). He reasoned that the variations in ecological opportunities lead to a differential in survival for certain phenotypes, which over time resulted in the evolution of different beak shapes. Since then, we know that ecological processes interact with evolutionary processes, and they together shape the long term dynamics of biological systems (Rahbek et al., 2019a; Rangel et al., 2018; Hagen, 2022). Empirical studies have now demonstrated that evolution can be rapid and occur on similar time scales as ecology (Hairston et al., 2005; Pelletier et al., 2009) and have quantifiable effects on ecological dynamics (Ezard et al., 2009), leading to feedbacks between ecological and evolutionary processes, so-called eco-evolutionary feedbacks (Pelletier et al., 2009; Schoener, 2011; Govaert et al., 2019). Eco-evolutionary feedbacks involve situations where an ecological process (e.g., replication, competition, dispersal) influences an evolutionary process (e.g. phenotypic change), which then feeds back to an ecological process, or vice versa (Govaert et al., 2019, Fig. 1.2). Examples are feedbacks between population dynamics (replication and competition) and phenotypic change, which can lead to evolutionary branching through the effect of competition (Dieckmann and Doebeli, 1999). In spatially structured populations, another classical example of eco-evolutionary feedbacks is the mechanism of local adaptation (Savolainen et al., 2007), where feedbacks between population dynamics, dispersal and trait evolution can facilitate or prevent populations to adapt to local environmental conditions (Meszéna et al., 1997; Doebeli and Dieckmann, 2003). Importantly, the eco-evolutionary feedbacks involved in adaptation mechanisms are expected to affect the dynamics of ecosystems in the coming decades (Norberg et al., 2012; Urban et al., 2016), because of the expected rapid changes in environmental conditions due to anthropogenic pressure and climate change (Ellis, 2011; Midgley and Hannah, 2019). Nevertheless, our understanding of eco-evolutionary feedbacks in realistic biological scenarios is limited (Lion et al., 2022).

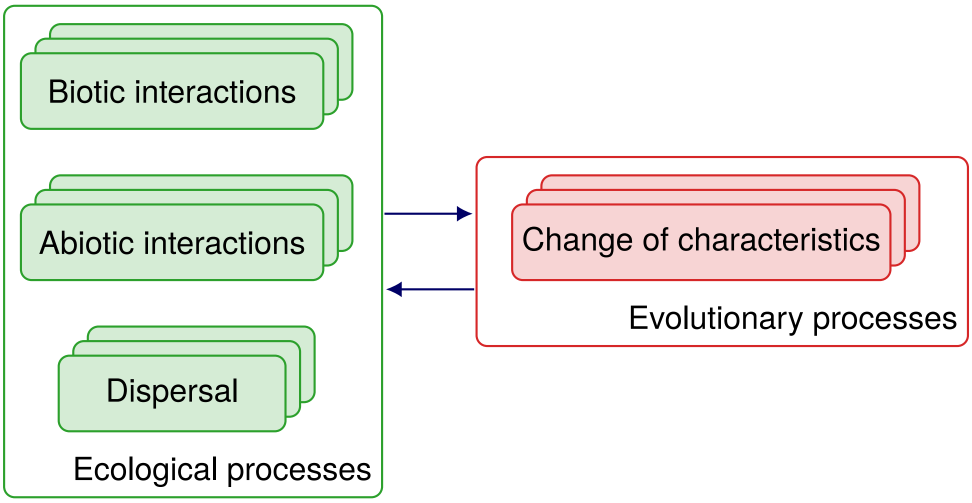

Fig. 1.2: Graphical representation of the eco-evolutionary processes determining eco-evolutionary dynamics in biological. By extension, I use this terminology to designate interaction and evolutionary processes in economic systems.

1.1.3 Drivers of economic change

In economic systems, the fundamental processes determining economic change are controversial (Dopfer and Potts, 2007; Nelson et al., 2014; Hodgson, 2019). To explain economic development, the neoclassical theory (Lawson, 2013) assumes that economic systems are in equilibrium, in the sense that the demand and supply of goods and services are balanced on all relevant markets. Firms are rational in maximizing profits by adapting to demand and supply, and the observed economic change is driven by exogenous forces, such as technological change (Romer, 1986). Evolutionary economics, promoted by the seminal work of Nelson et al., 2014, criticizes this view and seeks to explain economic change by focusing on endogenous forces. Evolutionary economics suggests that interactions between economic agents, firms and economic activities, and evolutionary processes acting upon them, are major processes contributing to economic change (Hodgson, 2019). These interactions may consist in facilitation processes through supply chains (Ozman, 2009; Saavedra et al., 2009; Van Der Panne, 2004) or competition within markets (Wernerfelt, 1989). What determine these interactions, and firm and economic activities' behavior in general, are organizational routines (Fig. 1.1), which spread across space and adapt (Cordes, 2006), affecting economic development at the local, regional, national, and international scale. Because these proposed processes are analogous to eco-evolutionary processes driving the dynamics of biological systems (which motivates the use of this terminology for designating economic processes in the following), a number of modelling approaches have borrowed concepts and methods from biology, aiming at underpinning the fundamental processes underlying invariant patterns in economic systems (Tacchella et al., 2018; Saavedra et al., 2009; Scholl et al., 2021; Zhang et al., 2018; Modis, 1997; Saavedra et al., 2014; Farmer and Lo, 1999; Michalakelis et al., 2011; Marasco et al., 2016; Gatabazi et al., 2019; Cauwels and Sornette, 2012; Applegate and Lampert, 2021; Suweis et al., 2015). For instance, (Saavedra et al., 2009) has successfully used a model of mutualistic interaction to explain structural patterns in industrial cooperation. Also, Scholl et al., 2021 uses the concepts of food webs and density dependence to explain market malfunctions and excess volatility in financial markets. However, those studies did not seek to understand how eco-evolutionary processes may affect economic development at the national scale. Biologically inspired eco-evolutionary models may help to disentangle the effect of eco-evolutionary processes on the dynamics of national economic systems, and could explain differences in economic development across countries.

1.2 Modeling eco-evolutionary dynamics

1.2.1 Forward modelling of eco-evolutionary processes

The complex interplay between ecological and evolutionary processes can hardly be studied with experimental approaches (Pontarp et al., 2019; Hagen, 2022). As such, a deductive approach, relying on forward modelling, has traditionally been put forward to underpin the mechanisms underlying invariant patterns in biological systems (Brummitt et al., 2020). Along this approach, hypotheses about causal processes are embedded in a model, whose forward integration generates emergent (non-anticipated) properties (see Fig. 1.3). Emergent properties may be seen as predictions from the consideration of the processes considered (May, 2004), and the role of the modeler is to underpin the underlying mechanisms, i.e. to disentangle how the interplay between the processes generate the observed behavior. In the early 1930s to 1940s, by formulating tractable mathematical models implementing the processes of reproduction, dispersal and mutations, the work of Fisher, Wright and Haldane has greatly contributed to the modern synthesis of evolutionary biology (Huxley and Others, 1942), generally accepted as the basis of our current understanding of evolutionary dynamics. Yet in order to obtain tractable mathematical model, Fisher, Wright and Haldane have neglected eco-evolutionary feedbacks (Govaert et al., 2019). In particular, ecological processes have been strongly simplified, and the effect of evolutionary processes on population dynamics has been neglected (Lion et al., 2022).

With the increase in computational capacity, novel modelling approaches relying on individual based models (IBMs) have appeared (DeAngelis and Mooij, 2005). These models require less simplifying assumptions than traditional mathematical models (DeAngelis and Mooij, 2005), and can unveil more realistic mechanisms by allowing to capture processes acting at the individual level. However, the lack of analytical tractability of IBMs is a shortcoming, because it challenges the ability of the modeler to underpin general principles from the simulations (Lion, 2016; May, 2004). The recent development of mathematical techniques, such as moment closure approximations (Law and Dieckmann, 1999; Gandhi et al., 2000; Nordbotten et al., 2020; Lion, 2016), adaptive dynamics theory (Metz et al., 1995), and probability theory (Champagnat et al., 2006), are generating novel pathways by filling the gap between IBMs and mathematical models. Analogous to renormalization group analysis developed in quantum and statistical physics (Sayama, n.d.), they form a toolbox to rigorously derive how emergent properties are influenced by processes operating at different organizational levels. As such, these mathematical techniques allow an analytical underpinning to IBM simulations, and can generate a general understanding of the key mechanisms at stake (Lion, 2016).

The combination of numerical simulations and, e.g., adaptive dynamics theory, has successfully shed new lights on the emergence of evolutionary branching under feedbacks between population dynamics and phenotypic change (Dieckmann and Doebeli, 1999; Doebeli and Dieckmann, 2003). An other example is the work of Meszéna et al., 1997; Débarre et al., 2013; Mirrahimi and Gandon, 2020, that has provided new insights on the effect of habitat heterogeneity on local adaptation. However, our current understanding of eco-evolutionary feedbacks neglects specificities of real biological populations that may significantly alter the resulting mechanisms, such as the structuration of populations over complex spatial structures (Nowak and Komarova, 2001) and highly dimensional phenotypic space (Doebeli and Ispolatov, 2010).

The consideration of such factors is important to advance our understanding, but raises challenging methodological issues. In particular, adding complexity in eco-evolutionary models may hinder the fundament mechanisms underlying the emergence of a pattern. Also, the consideration of multiple traits leads to an increase in the dimensionality of the model, which in turn leads to an exponential increase in the computational cost associated to the numerical simulations (Bellman, 2010). In order to better understand eco-evolutionary dynamics, we need to investigate more realistic scenarios, which in turn require methodological developments, in order to cope with the extra complexity and computational cost.

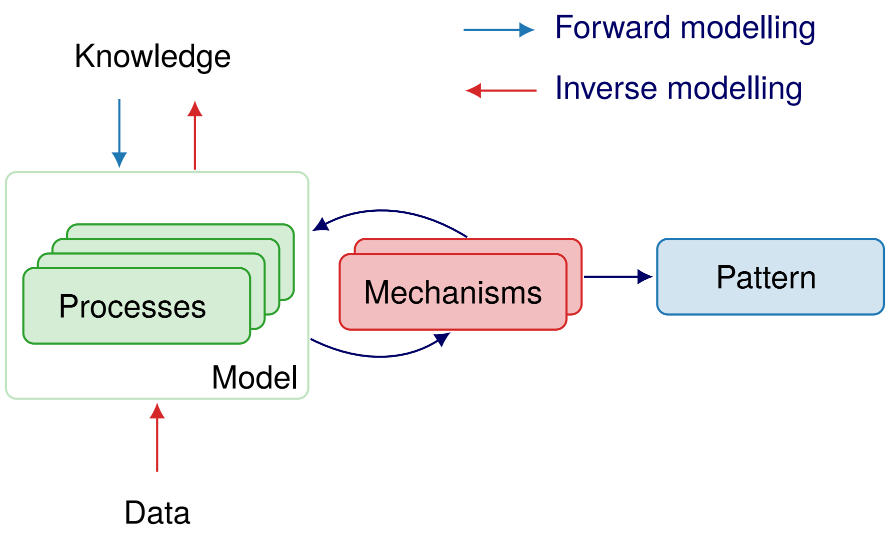

Fig. 1.3: Forward and inverse modelling approaches for the understanding of complex adaptive systems. A forward modelling approach consists in deriving a model, embedding a set of processes inspired from prior knowledge. The objective is to understand how the interplay between the processes considered transforms in (feedback) mechanisms that are associated with an invariant pattern. An inverse modelling approach integrates empirical observation within the modelling process. The data constrains the processes within the model, generating new knowledge.

1.2.2 Inverse modelling

Another approach to underpin processes and mechanisms in biological systems consists in inverse modelling, where empirical data is used to constrain the model (Clermont and Zenker, 2015, see Fig. 1.3 for a graphical illustration). Inverse modelling can take the form of parameter estimation (Schartau et al., 2017) or model selection (Johnson and Omland, 2004), both involving the use of inference methods to estimate, respectively, the most probable model parameter value, or the most probable model among candidates, given empirical data. In parameter estimation, provided that they are inferred together with uncertainties, parameters can be interpreted to better understand the strengths and effects of the processes considered (Pontarp et al., 2019). For instance, Higgins et al., 2010; Curtsdotter et al., 2019 infer the parameters of population dynamic models to understand the processes involved in ecosystem functions. In model selection, candidate models embedding competing hypotheses about causal processes are derived, and the relative support of each model given the data is computed to discriminate between the hypotheses (Johnson and Omland, 2004). For instance, using inverse modelling and alternative eco-evolutionary models, (Skeels et al., 2022) shows that temperature-dependent evolutionary speed most likely explains variations in biodiversity patterns, among alternative evolutionary speed hypotheses.

The computation of the most probable model parameter values, or the computation of the different model supports, critically involves inference methods. Inference methods commonly demand many forward integration of the model, resulting in a computational cost that can be prohibitively expensive (Schneider et al., 2017). The number of forward integration required may dramatically increase with the number of model parameters (Csilléry et al., 2010), and the number of model parameters, together with the model nonlinearities, can eventually lead to false estimates of the most probable model parameter values (Gábor and Banga, 2015). Consequently, inverse modelling methods have mostly been used with simple evolutionary models (Csilléry et al., 2010). Eco-evolutionary models are dependent on numerous parameters (Boyd, 2012), are strongly nonlinear (Hastings et al., 1993; Huisman and Weissing, 1999; Benincà et al., 2008), and their integration is computationally expensive (Fisher et al., 2018), challenging the use of inverse modelling to underpin eco-evolutionary processes. Advances in the field of artificial intelligence could circumvent these issues, allowing to advance our knowledge of eco-evolutionary dynamics in empirical systems.

1.2.3 Artificial intelligence to leverage forward and inverse modelling

In the recent years, the field of artificial intelligence (AI) has made enormous progresses in computer vision (Voulodimos et al., 2018) and natural language processing (Young et al., 2018). At the backbone of this success are key computational techniques that could leverage the forward and inverse modelling of eco-evolutionary dynamics. Advances in computer vision and natural language processing rely on deep learning methods, that allow neural networks to learn abstract representation of mechanisms from large datasets (LeCun et al., 2015). These abstractions can hardly be interpreted to generate scientific theories (Karpatne et al., 2017), and their prediction ability is limited by the information contained in the training datasets. As such, neural networks cannot be used *per se* to gain scientific insights and extrapolate beyond observed trends (Barnosky et al., 2012; Urban et al., 2016). Nevertheless, their traditional applications and associated methods have been successfully derived in other scientific fields for this purpose (Kashinath et al., 2021; Schneider et al., 2017; Yazdani et al., 2020; Rolnick et al., 2022). Neural networks have been used to reduce the cost of the forward integration of climate models, learning more efficient representations of physical mechanisms (Kashinath et al., 2021). They have also been used to approximate the solution of partial differential equation (PDE) models (Sirignano and Spiliopoulos, 2018; Han et al., 2018), with the major advantage of approximating high dimensional problems at a lower computational cost than traditional methods. Underlying the training of neural network is the technique of backpropgation (LeCun et al., 2015). This technique can be generalised to train any scientific model against data (Rackauckas et al., 2020a), with the potential to leverage inverse modelling techniques (Frank, 2022). Consequently, AI techniques offer unique opportunities for advancing our understanding of eco-evolutionary dynamics.

1.2.4 Programming languages

Combining AI techniques with scientific models requires a computational environment that allows to easily develop scientific models, while ensuring simulation performance, and providing composability between AI and other scientific libraries (Rackauckas et al., 2020a). Unfortunately, performance and composability are features that are poorly represented in mainstream programming languages used by the scientific community, such as Python, Matlab or R. Those languages are naturally attractive because they are dynamically typed (Bezanson et al., 2017), allowing convenient development iterations. Nonetheless, prototypes written in Python, Matlab or R need to be rewritten in low level, compiled languages such as C, C++ or Fortran for speed and predictable mapping to hardware (Perkel, 2019; Bezanson et al., 2017). This conversion requires significant efforts, leading to a problem commonly designated as the "two-language problem" (Bezanson et al., 2017). In order to circumvent performance issues, most libraries in Python, Matlab or R rely on bindings with low level languages. For instance, the most used deep learning libraries in Python, TensorFlow and PyTorch, are internally written in C++ (see *Tensorflow* 2015; Foundation, 2016). However, bindings with low level languages come with major negative externalities. First, they restrict the understandability of their source code to computer scientists – prohibiting potential development contributions from the scientific community. Second, they prevent the composability of, e.g., traditional scientific computing libraries and deep learning libraries (Innes et al., 2019). This absence of composability arises because deep learning libraries must differentiate the numerical models to be trained. Yet, TensorFlow or PyTorch are only able to differentiate models written in their own internal source code (Innes et al., 2019).

Julia is a recently developed programming language that addresses the issue of the two-language problem (Bezanson et al., 2017; Bezanson et al., 2018). Julia was built over a type-specializing, just-in-time compiler, which makes it easy to generate performant programs in pure Julia, while preserving the essential features of Python, Matlab or R, such as dynamic typing and automatic memory management

(Perkel, 2019). The source code of most Julia libraries is consequently written in pure Julia, guaranteeing understandability and composability. In particular, Julia is an automatic differentiation pervasive language (Innes et al., 2019), which allows to differentiate any model written in pure Julia without any modification. As a result, deep learning libraries can be used on any scientific model written in Julia (Rackauckas et al., 2020b). Solving the two-language problem, Julia permits scientists to prototype a program which is readily generic and performant, benefitting not only the development process but also the entire research community (Bezanson et al., 2017). Overall, the composability and productivity granted by Julia makes it an ideal computational environment to accelerate research.

1.3 Thesis outline

In summary, while it is increasingly acknowledged that feedbacks between ecological and evolutionary processes play an important role in biological systems (Pelletier et al., 2009; Urban et al., 2016), our understanding of eco-evolutationary dynamics in realistic scenarios is limited. Under increasing anthropogenic pressure, advancing this understanding is essential (Urban et al., 2016) but raises challenging methodological issues. Further, while analogous processes to eco-evolutionary processes have been suggested to influence the dynamics of economic systems (Hodgson, 2019), we do not know their effect on economic dynamics at the scale of a country. Here, I present novel forward and inverse modelling approaches to advance our understanding of eco-evolutionary dynamics, and utilize them to shed light on the eco-evolutionary processes and feedbacks in biological and economic systems.

In **??**, I investigate how eco-evolutionary processes, in combination with complex habitat structures, influence the phenotypic distribution of biological populations. I proceed using a forward modelling approach: I derive a stochastic eco-evolutionary IBM where individuals are structured over a spatial graph, and experience the fundamental processes of reproduction, competition, mutation and migration. Seeking to understand how those processes result in phenotypic differentiation at the population level, I derive analytical approximations of the IBM. Together with extensive numerical simulations, they provide insights into how the graph properties affect the population size and phenotypic differentiation. In particular, I show that three main graph properties, relating to landscape connectivity, heterogeneity in connectivity, and habitat spatial auto-correlation, shape phenotypic differentiation. These results establish mechanistic links between landscape features and the eco-evolutionary dynamics of biological populations.

In **??**, I develop an inverse modelling method to estimate the parameters of eco-evolutionary models and perform model selection. The method is based on a machine learning framework and involves the combination of state-of-the-art AI techniques and a novel learning strategy. The learning strategy consists in training the model against mini-batches of data with short time horizon, which I analytically show to bypass problems arising from model nonlinearities. I implement the ML framework in the Julia library **MiniBatchInference.jl**, and demonstrate through numerical experiments that it can efficiently and accurately estimate model parameters and provide model support from noisy, incomplete and independent time series. Altogether, the proposed ML framework is a workhorse for inverse modelling and can elucidate mechanistic pathways in biological and economic systems.

In **??**, I quantify the effect of eco-evolutionary processes on the dynamics of economic systems. I employ the ML framework developed in **??** to investigate how alternative eco-evolutionary population models can explain the dynamics of economic activities in 74 of the world's richest countries, relying on 59 year of economic data. The models embed the processes of ecological interactions between economic activities, spatial transfers, and economic activity transformations, which statistical support is compared to a simple logistic growth model, taken as a null model. I find strong statistical evidence for positive interactions between national economic activities, and spatial transfers across countries. To my knowledge, this is the first study providing quantitative evidences that eco-evolutionary processes shape the dynamics of economic systems.

In **??**, I extend two recent methods to solve high dimensional non-local nonlinear PDEs. This class of PDEs can be used to construct generic eco-evolutionary models capturing the evolution of complex phenotypic populations, but up to now, could only be simulated in low dimensions. The first method presented relies on Picard iterations, while the second is based on deep learning and involves neural networks to approximate the PDE model output. I implement both methods in the Julia library **HighDimPDE.jl**, and evaluate their performance on high dimensional eco-evolutionary models, and on PDE models arising in physics. The methods yield good results with short run times, opening up new venues to further our understanding of eco-evolutionary dynamics.

CV

2

Personal Information

Residence	Zürich, Switzerland
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Github	github.com/vboussange
Age	Born 1995 (age 27)
Citizenship	France citizen

Personal skills

Languages	English (fluent)
	French (native)
	Spanish (B2)
	German (B1)
Programming languages	Julia
	Python
	C++
	Java
	Matlab
	R
	Bash
	VBA
Sports	Ski mountaineering
	Alpinism
	Rock climbing
	Enduro mountainbiking
	Surfing
Alpine CV	[vboussange.github.io/pages/alpine_cv/]

Education

10.2022 09.2018 **Ph.D in Environmental Sciences,** Swiss Federal Institute for Forest, Snow and Landscape (WSL | Swiss Federal Institute of Technology Zurich, ETH), Switzerland
Forward and inverse modelling of eco-evolutionary processes in biological and economic systems. Under the guidance of Prof. Dr. Loïc Pellissier.

06.2017 09.2016 **Full year academic exchange,** University of New South Wales (UNSW Sydney), Australia

06.2017 02.2017 **Master thesis in theoretical geomechanics,** UNSW Sydney | CSIRO, Australia
Numerical continuation and bifurcation analysis for unconventional geomechanics. Under the guidance of Dr. Thomas Poulet.

08.2018 09.2013 **M.S. in Energy and Environmental Engineering,** Institut National Des Sciences Appliquées de Lyon (INSA Lyon), France
Three-year undergraduate engineering course in Energy and Environmental Systems, focused on Advanced Energy Systems and Efficiency.

08.2018 09.2013 **B.S. in Mathematics and Physics,** Institut National Des Sciences Appliquées de Lyon (INSA Lyon), France
Ranking : 21/650 students.

Professional appointments

08.2018 03.2018 **R&D intern,** Compagnie National du Rhône (CNR), France
Development of an Energy Management System based on various optimisation techniques for optimal production of renewable resources. Applications to EU sponsored projects: Jupiter1000 (power-to-gas), Move in pure (vehicle-to-grid), Marie-Galante island (micro-grid)

Publications

Peer-reviewed

1. **Boussange, V.** & Pellissier, L., *Eco-evolutionary model on spatial graphs reveals how habitat structure affects phenotypic differentiation*. Commun Biol 5, 668 (2022). [bioRxiv]

Preprints

1. **Boussange, V.**, Vilimelis-Aceituno, P., Pellissier, L., *Mini-batching ecological data to improve ecosystem models with machine learning* [bioRxiv] (2022), 46 pages. In review.

2. **Boussange, V.**, Becker, S., Jentzen, A., Kuckuck, B., Pellissier, L., *Deep learning approximations for non-local nonlinear PDEs with Neumann boundary conditions*. [arXiv] (2022), 59 pages. Revision requested from Partial Differential Equations and Applications.

Proceedings

1. Poulet, T., Alevizos, S., Veveakis, M., **Boussange, V.**, Regenauer-Lieb, K., *Episodic mineralising fluid injection through chemical shear zones*, ASEG Extended Abstracts (2018), 5 pages.

In preparation

1. **Boussange, V.**, Sornette, D., Lischke, H., Pellissier, L., *Analogous forces to ecological interactions, dispersal and mutations shape the dynamics of economic activities*.

Talks

07.2022 **Speaker,** HighDimPDE.jl: A Julia package for solving high-dimensional PDEs, JuliaCon2022, online. youtube.com/watch?v=4sXqGhhknT4

06.2022 **Speaker,** Interpretable machine learning for forecasting dynamical processes in ecosystems, World Biodiversity Forum, Davos, Switzerland.

06.2022 **Invited speaker,** Investigating empirical patterns of biodiversity with mechanistic eco-evolutionary models, Seminar at the Theoretical Ecology and Evolution group, Universität Bern.

11.2021 **Invited speaker,** Numerical approximations of solutions of highly dimensional, non-local nonlinear PDEs, StAMBio seminar, St Andrews, UK.

10.2021 **Speaker,** Graph topology and habitat assortativity drive phenotypic differentiation in an eco-evolutionary model, Conference on Complex Systems, Lyon, France.

10.2021 **Speaker,** Using graph-based metrics to assess the effect of landscape topography on diversification, ECBC, Amsterdam, Netherlands.

09.2021 **Speaker,** Solving non-local nonlinear Partial Differential Equations in high dimensions with HighDimPDE.jl, International Conference on Computational Methods in Systems Biology, Bordeaux, France.

04.2021 **Speaker,** Responses of neutral and adaptive diversity to complex geographic population structure, Mathematical Population Dynamics, Ecology and Evolution, CIRM Marseille, France.

Softwares

2022 **MiniBatchInference.jl** Julia
github.com/vboussange/MiniBatchInference.jl
A Julia package for maximum likelihood estimation and model selection of strongly nonlinear dynamical models.

2021 **HighDimPDE.jl** Julia
github.com/vboussange/HighDimPDE.jl
A Julia package that breaks down the curse of dimensionality in solving non local, non linear PDEs.

2021 **EvoId.jl** Julia
2019 github.com/vboussange/EvoId.jl

Evolutionary individual based modelling, mathematically grounded.

2018 **OptiVPP** Python, GAMS
confidential
Energy Management System for Virtual Power Plants.

Open source software contributions

SciML
DiffEqFlux.jl
CUDA.jl
Flux.jl
LightGraphs.jl

Teaching and supervision

12.2020 – 09.2020 **701-3001-00L Environmental Systems Data Science,** ETH Zürich, D-USYS, Switzerland

06.2020 – 04.2020 **262-0100-00L Lab rotation,** ETH Zürich, D-BSSE, Switzerland

12.2020 – 09.2020 **Taste of research internship,** Polytech Nice-Sophia, France

Reviews

2022 **Journal of Open Source Software**
2019 **Journal of Theoretical Biology**

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List of Figures