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Personal Info

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Education

2015 - 2020 UNIVERSITY OF GRONINGEN
PhD candidate in Ecology and Evolution; Modelling species interactions in macroevolution and macro ecology
Defense on 5th of June, 2020

2008 - 2010 HONG KONG UNIVERSITY
Master of Philosophy in Mathematics; Epidemic models of HIV infection

2004 - 2008 BEIJING NORMAL UNIVERSITY
Bachelor in Mathematics and Applied Mathematics

Grant

2015 - 2019 PhD project is funded by China Scholarship Committee (CSC).

Work Experience

2015 - 2020 UNIVERSITY OF GRONINGEN
PhD student

Research: Modelling species interactions in macroevolution and macroecology

2010 - 2015 CHONGQING UNIVERSITY OF TECHNOLOGY & SCIENCES
Lecturer in Department of Mathematics and Physics

Responsibility: Bachelor students teaching.

Teaching courses: Calculus; Linear algebra; Differential equations; Mathematical modeling.

Research Interests

Eco-evolution A major challenge in ecology is the need for a better theoretical framework to understand how species assemblages (ecological communities) arise, why some are species-rich and others species-poor, and why some species are present or dominant whereas others are not. My interest is to construct theoretical models of stochastic differential equations to model species interactions in macroecology and macroevolution.

Algorithms Due to the complex system of nonlinearity and high dimension, I invent efficient computational tools like process-based simulations, individual-based simulations, and likelihood-free algorithms to reveal underlying mechanisms from ecological and evolutionary patterns. I am interested in approximate Bayesian computation algorithms that rely on biological process-based simulations. Besides, I am into machine learning algorithms that show advantage on speed and large scale data processing.

Research Projects

- 1 **INFERRING LOCAL DIVERSITY-DEPENDENCE**
Biology: It is still hotly debated that whether there exists ecological limit to diversity. A diversity-dependent diversification model has been developed to infer diversity-dependent signal. However, the model ignores local information. In this project, we aim to model the evolutionary processes incorporating the local details and explore that if we can still detect the local diversity-dependence.
Modeling: A hidden Markov model is constructed to describe changes of evolutionary states.
Algorithm: *R* is used to do processes simulation, parameter inference and data analysis. A bootstrapping approach is exploited to assess statistical power of detecting diversity-dependent signal.

- 2 **INFERRING THE EFFECT OF SPECIES INTERACTIONS ON TRAIT EVOLUTION**
Biology: Ecology and evolution jointly help to form the pattern of traits of species. We construct an eco-evolutionary framework combining both ecological interaction and evolutionary history to describe how traits of species evolve under environmental stabilizing selection and species interactions.
Modeling: A system of stochastic differential equations is developed to describe the trait evolution and population dynamics.
Algorithm: *Python* is the main language used in this project for simulation, evolutionary algorithm development and data analysis. Approximate Bayesian computation algorithms are exploited to infer the parameters of interest and do model selection. A deep learning algorithm is used to distinguish trait patterns among variety of models.

- 3 **A SPATIAL PHYLOGENETIC JANCEN-CONNELL EXTENSION TO THE NEUTRAL THEORY OF SPECIES DIVERSITY**
Biology: The neutral theory of species diversity opens a new window to explain species assembly. However, the neutral assumption that all changes in distribution and abundance occur because of purely random variation in births, deaths, migration and speciation violates the recognition of the importance in species differences. Here, we focus on tree species and develop a spatial phylogenetic Jansen-Connell extension to the neutral theory. We aim to explore to what extent the additional mechanism indeed affects species assembly.
Modeling: A spatially explicit probability model is defined to account for the probability of individual colonization.
Algorithm: This project comprises an intensive simulation study and large scale data analysis. Around 30 thousands of simulations were deployed on a cluster of high performance

computers. *Bash* scripts were used to split data into parts of the same categories. *R* is used to do data analysis.

Mini Projects

- 1 THE GOVERNMENT SHOULD TAKE A FAST REACTION TO PREVENT COVID-19 DEVELOPMENT
An one-week Kaggle competition on COVID-19 pandemic: The outbreak of the COVID-19 virus has given the world a heavy punch in 2020. Flooded by the daily news of how serious the pandemic becomes, I am wondering whether and to what extent the government can stop the pandemic. Specifically, if the government takes a fast response to restrict social activities, will the pandemic be stopped at an early stage? Thus, I took part in the one-week competition and built an individual-based virus spread model in which I considered how the speed of the government reaction affects pandemic development.
Website: https://xl0418.github.io/Kaggle_corona/
- 2 DATA VISUALIZATION: DEVELOP A SHINY APP TO TRACK COVID-19 SPREAD
Data visualization: Using the data from Johns Hopkins University, I developed a shiny app to show the worldwide pandemic situation. In addition, a model is under construction to make predictions on the future trend of the pandemic.
Modeling: A system of stochastic differential equations is developed to describe how the number of different classes of people (like the infected cases, the asymptomatic cases, the severely symptomatic cases, etc.) changes through time.
Website: https://liangxu-groningen.shinyapps.io/corona_shiny/

Research Publications

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| 2018 | L. Xu & R. S. Etienne. Detecting local diversity-dependence in diversification. <i>Evolution</i> , 2018 Jun;72(6):1294-1305. doi: 10.1111/evo.13482. |
| 2020 | L. Xu, S. van Doorn, H. Hildenbrandt and R. S. Etienne. Inferring the effect of species interactions on trait evolution. <i>Systematic Biology</i> . Accepted. |
| 2020 | L. Xu, H. Hildenbrandt and R. S. Etienne. The phylogenetic Janzen-Connell effect can explain multiple macroecological and macroevolutionary patterns. <i>Global Ecology and Biogeography</i> . Under review. |

Academic Activities

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| Nov, 2017 | The 2017 Congress of the European Society for Evolutionary Biology: Poster presentation |
| Mar, 2018 | The First Conference of the Netherlands Society for Evolutionary Biology (NLSEB): Poster presentation |
| Aug, 2018 | Joint Congress on Evolutionary Biology: Poster presentation |

Programming Skills

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| R | Proficiency. Packages: SDDD; ggradar2. Data visualization via Shiny apps. Model simulations. |
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Python **Proficiency**. ABC-SMC algorithm; Deep learning algorithms; Model simulations.

Others **Bash scripting** used for large-scale data processing; **High performance computer cluster usage**. More programming details can be found on my website: xl0418.github.io

References

Rampal S. Etienne Professor in theoretical and evolutionary community ecology,
the University of Groningen. r.s.etienne@rug.nl

Sander van. Doorn Assistant Professor, the University of Groningen. g.s.van.doorn@rug.nl

Hanno Hildenbrandt Programming technician, the University of Groningen. h.hildenbrandt@rug.nl