<div align="center">

LIANG XU
Groningen Institute for Evolutionary Life Sciences
University of Groningen
Groningen, The Netherlands

</div>

Personal Info

Phone   +31 0625190926

Email   xl0418@gmail.com /liang.xu@rug.nl

Birth date 18th, April, 1986

Birth place Chongqing, China

Web   xl0418.github.io

Education

2015 - 2020 UNIVERSITY OF GRONINGEN
  PhD candidate in Ecology and Evolution; Eco-evolutionary models on species assemblage
  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

Work Experience

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

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 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 combing 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.

Research Publications

2018   L. Xu & R. S. Etienne. Detecting local diversity-dependence in diversification. *Evolution,* 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. *Systematic Biology*. Under review.

2020   L. Xu, H. Hildenbrandt and R. S. Etienne. The spatially explicit phylogenetic Janzen-Connell effect predicts realistic macroecological and macroevolutionary patterns. *Ecology Letters*. Under review.
       doi: https://doi.org/10.22541/au.158152203.38129615

Grant

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

Academic Activities

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

R   Packages: SDDD; ggradar2.

Python   ABC-SMC algorithm; Deep learning algorithms.

Others   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