Liang Xu

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Education

- **University of Groningen** — Groningen, The Netherlands
  PhD — *2015 - 2020*
  Ecology and Evolution: Modelling species interactions in macroevolution and macroecology
- **University of Hong Kong** — Hong Kong, P.R.China
  Master of Philosophy — *2008 - 2010*
  Mathematics: Epidemic models of HIV infection
- **Beijing Normal University** — Beijing, P.R.China
  Bachelor — *2004 - 2008*
  Mathematics: Mathematics and Applied Mathematics

Experience

- **Carnegie Institution for Science at Stanford University** — California, USA
  Postdoctoral Research Assistant — *Aug 2022 - now*
  Project: The mutual impact of biodiversity of microorganisms and carbon cycling in the ocean
- **Department of Biology at University of Oxford** — Oxford, UK
  Postdoctoral Research Assistant — *Jan 2021 - Jul 2022*
  Project: Competition in crisis: Investigating bias when building models of plant communities
- **Groningen Institute for Life Sciences at University of Groningen** — Groningen, NL
  PhD student — *Oct 2015 - Jun 2020*
  Project: Modelling species interactions in macroevolution and macroecology
- **Chongqing University of Science & Technology** — Chongqing, P.R.China
  Lecturer in Department of Mathematics and Physics — *Jul 2010 - Sep 2015*
  Teaching courses: Calculus; Linear algebra; Differential equations; Mathematical modeling; etc.

Projects

- **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.
- **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.
- **A spatial phylogenetic Janzen-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.
- **Estimating competition in metacommunities: accounting for biases caused by dispersal**:

- **Biology**: Estimating the strength of interactions among species in natural communities has always been a challenge for empirical ecologists. Sessile organisms, like plants or corals, often occur in metacommunities where they compete only with their immediate neighbours but disperse propagules over a wider area. Ignoring dispersal in population models often leads to bias in estimation of the strength of competition. To determine the impact of ignoring dispersal, we derived the bias that would arise if such regression methods were applied to a metacommunity in which a fraction of seeds disperse beyond their natal cells.
- **Modeling**: We present results from a range of population models that make different assumptions about the nature of competition and assess the performance of our bias formulae by analysing data from simulated metacommunities.
- **Algorithm**: Analytical solution has been developed and contrasted with simulation results. R is used to do data analysis.

Publications

- **L. Xu**, A. Clark, M. Rees and L. Turnbull. Dispersal causes bias in estimating the strength of competition in plant communities. Methods in Ecology and Evolution . **2022**. DOI: 10.1111/2041-210X.14022
- **L. Xu**, S.Van Doorn, H. Hildenbrandt, R.S. Etienne, Inferring the Effect of Species Interactions on Trait Evolution, ***Systematic Biology***, **2020** Sep; doi: 10.1093/sysbio/syaa072
- **L. Xu** & R. S. Etienne. Detecting local diversity-dependence in diversification. ***Evolution***, **2018** Jun;72(6):1294-1305. doi: 10.1111/evo.13482
- **L. Xu**, H. Hildenbrandt and R. S. Etienne. The phylogenetic Janzen-Connell effect can explain multiple macroecological and macroevolutionary patterns. In preparation
- **L. Xu**."A Functional Analytic Approach to the Power Series Solutions of an Nonlinear Differential Equations," **Asia-Pacific Power and Energy Engineering Conference**, **2012**, pp. 1-4, doi: 10.1109/APPEEC.2012.63 07563.

Mini Projects

- **The government should respond quickly 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/
- **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-shinyapps.shinyapps.io/corona_shiny/
- **Plant communities simulation Shiny app**:
  - **Biology:**: Simulation and parameter inference visualization of the project "Estimating competition in metacommunities" at the department of Plant Sciences, Oxford University.
  - **Website:**: https://liangxu-shinyapps.shinyapps.io/PlantSimShiny/
- **Coral DNA data analysis**:
  - **Meta analysis:**: Analyze a single file of 80G Coral DNA data of over 241 individuals.

Academic activities

- **Dec, 2022**: Talk at Complex Systems Colloquium, University of Oldenburg, Germany
- **Jun, 2021**: Talk at German Centre for Integrative Biodiversity Research (iDiv)), Halle-Jena-Leipzig, Germany
- **Aug, 2018**: Joint Congress on Evolutionary Biology: Poster presentation, Montpellier, France
- **Mar, 2018**: The First Conference of the Netherlands Society for Evolutionary Biology (NLSEB): Poster presentation, Lunteren (Akoesticum), Netherlands
- **Nov, 2017**: The 2017 Congress of the European Society for Evolutionary Biology: Poster presentation, Groningen, Netherlands

Teaching

- **Jan, 2021 - Jan, 2022 Oxford University**: Active leader; Teaching assistant: Research skills (4th year undergraduates); Computer skills; Advanced ecology and evolution - Stability, stationarity and perturbation in ecological and evolutionary systems (3rd year undergraduates); Ecology and Evolution (2nd year undergraduates).
- **Oct, 2015 - Jun, 2020 Groningen University**: Teaching assistant: Ecological interactions – Competition & response; Models in Life Sciences
- **Jul, 2010 - Jun, 2015 Chongqing University of Science & Technology**: Lecturer: Advanced Calculus; Matrix; Linear Algebra; Differential equations; Mathematical modeling, etc.

Programming Skills

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

Honors and Awards

- PhD project is funded by China Scholarship Committee (CSC) - May, 2015