

JAMES RENNIE BEQUEST

REPORT ON EXPEDITION / PROJECT / CONFERENCE

**Expedition/Project/
Conference Title:** Workshop on “Integrative Taxonomy in the Big Data Era”

Travel Dates: 9th to 15th June 2024

Location: Institut de Systématique, Evolution, Biodiversité (ISYEB) at the
Museum National D'histoire Naturelle (Paris)

Group member(s): _____

Aims: Study the concepts and methods of integrative taxonomy in the 21st
century and the practical tools for phylogenomics, species
delimitation, and analysis of NGS data.

Photography consent form attached: Yes
(please refer to your award letter) No

OUTCOME (a minimum of 500 words):-

I would like to thank the James Rennie Bequest Committee for their financial support, which allowed me to attend the “Integrative Taxonomy in the Big Data Era” workshop, organized by the Institut de Systématique, Evolution, Biodiversité (ISYEB) at the Museum National d'Histoire Naturelle (Paris). Although not a mandatory part of my PhD at the University of Edinburgh, this workshop significantly enhanced my knowledge and skills in plant systematics and taxonomy, specifically for my research on the evolution of Begonias.

Workshop Overview

The workshop addressed the evolving field of integrative taxonomy, focusing on how to combine morphological, molecular, and bioinformatic data to improve species delimitation. The growth of Next-Generation Sequencing (NGS) technologies has drastically increased the amount of genomic data available for analysis, making it crucial for researchers to adopt new methods for managing and interpreting this information.

Each day began with theoretical lectures covering broad topics such as genomics, sequencing technologies, and NGS data analysis. The afternoons were devoted to practical sessions, where we had the opportunity to apply what we had learned. This combination of theory and hands-on practice was highly beneficial in reinforcing complex concepts and methods.

Tools and Methodologies

Throughout the workshop, I was introduced to several new tools that will be instrumental for my research. One of these was the software MEGA, which I used to generate pairwise distance matrices. These matrices were later applied to the ASAP (Assemble Species by Automatic Partitioning) method, a useful tool for species delimitation from single-locus data. Using ASAP provided a fresh perspective on how to refine species boundaries with molecular data, offering more precision than traditional morphological approaches.

Another critical tool we explored was the Galaxy project interface (<https://usegalaxy.eu/>), a graphical platform designed for processing and analyzing NGS data. For someone like me, with limited programming experience, Galaxy made it easier to understand the logic behind

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data cleaning and processing workflows. This tool will be invaluable as I incorporate genomic data into my ongoing research.

We also worked with the General Mixed Yule Coalescent (GMYC) method, which helps delineate species by analyzing the phylogenetic tree's branching patterns. This method is particularly useful in distinguishing between intraspecies and interspecies variations. Additionally, the BPP (Bayesian Phylogenetics and Phylogeography) software introduced us to Bayesian approaches for analyzing DNA sequence data. BPP can simultaneously estimate species trees and divergence times, while accounting for incomplete lineage sorting, which is common in plants that hybridize frequently, such as Begonias.

Practical Applications and Learning Outcomes

The workshop helped me gain a better understanding of how to process and clean raw genomic data, ensuring the accuracy of my analyses. Learning the importance of reproducibility in bioinformatics was especially helpful, and I now feel more confident in integrating these techniques into my own research.

Beyond computational tools, we had the chance to work with specimens in the herbarium. This provided a great opportunity to link molecular data to physical plant characteristics, making it easier to connect theoretical knowledge to practical taxonomy. Engaging in discussions with peers and instructors during these sessions was extremely beneficial, as it allowed me to contribute my own expertise in plant systematics and to learn from others who specialize in different organisms and methodologies.

Networking and Collaboration Opportunities

One of the most valuable aspects of the workshop was the opportunity to network with professionals and peers. Discussions with other participants and instructors opened up potential collaboration opportunities, particularly in using some of the methods we explored, such as GMYC and BPP, in joint research projects. The workshop brought together researchers from diverse backgrounds, and this exchange of ideas not only broadened my perspective on taxonomy but also laid the groundwork for future collaborative work.

Conclusion

The "Integrative Taxonomy in the Big Data Era" workshop was an exceptional learning experience that significantly enhanced both my theoretical knowledge and practical skills. The tools and methods I acquired will directly contribute to my PhD research on the taxonomy and evolution of Begonias. Furthermore, the networking opportunities and discussions with fellow researchers have opened new possibilities for collaboration and knowledge exchange. I am immensely grateful to the James Rennie Bequest Committee for their support, which made this enriching experience possible. I look forward to applying what I learned to my future research endeavors and to continuing to grow in this dynamic and evolving field.

Some photos taken at the Museum National d'Histoire Naturelle (Paris)

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