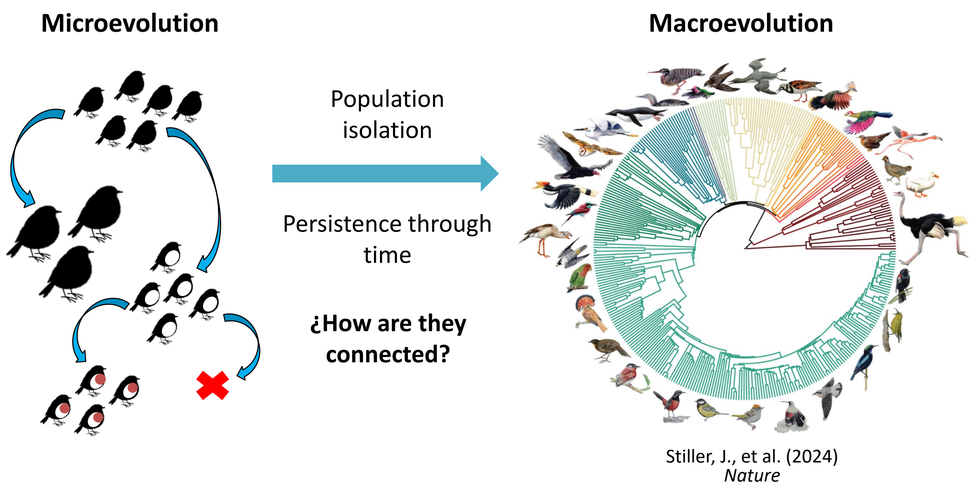
Understanding the link between population-level processes and broad-scale biodiversity patterns in birds

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Introduction

- Speciation rates vary dramatically across lineages and regions.
- While most speciation studies focus on reproductive barriers and ecological differentiation, the **isolation and persistence** of diverging populations through time remain comparatively understudied.[1]
- Understanding how these population-level processes shape speciation rates and species richness is crucial for uncovering the poorly understood link between **microevolution** and **macroevolution.** [2]



Central hypothesis: Lineages with a greater propensity to form isolated and persistent populations are more likely to give rise to new species and, consequently, exhibit higher long-term speciation rates.

Objectives

- To investigate how variation in population isolation and persistence is **connected** to **patterns of speciation and biodiversity** in birds.
- **To characterize population isolation and persistence** across bird species at a global scale.

Methods

- To characterize population isolation, we used **genetic and geographic distances** to calculate **βIBD**, the **isolation-by-distance** slope describing the relationship between these distances.
- We obtained data from **published studies for 5 bird species** and performed a **preliminary analysis** to test the **sensitivity of βIBD** to:

- Different genomic filtering schemes
- Proportion of the genome sequenced and number of markers (SNPs)
- Different individual sample sizes

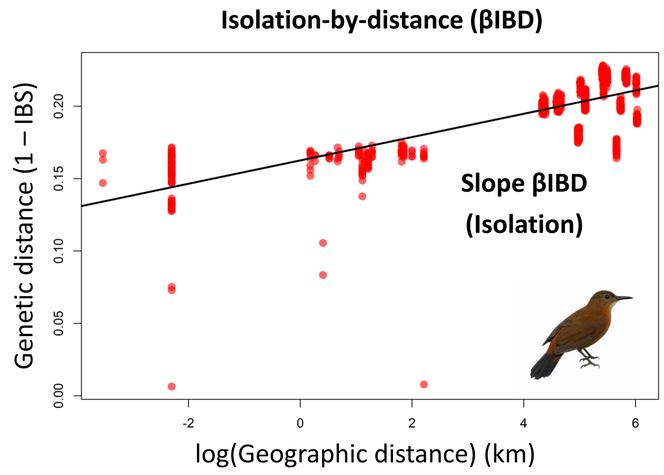
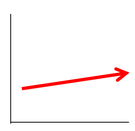


Fig. 1. Representative example of the isolation-by-distance pattern (βIBD) observed in one of the study species (*Sclerurus cearensis*).



Steeper slope = greater isolation (less gene flow)



Shallower slope = lower isolation (greater gene flow)

Validating βIBD (isolation): key results

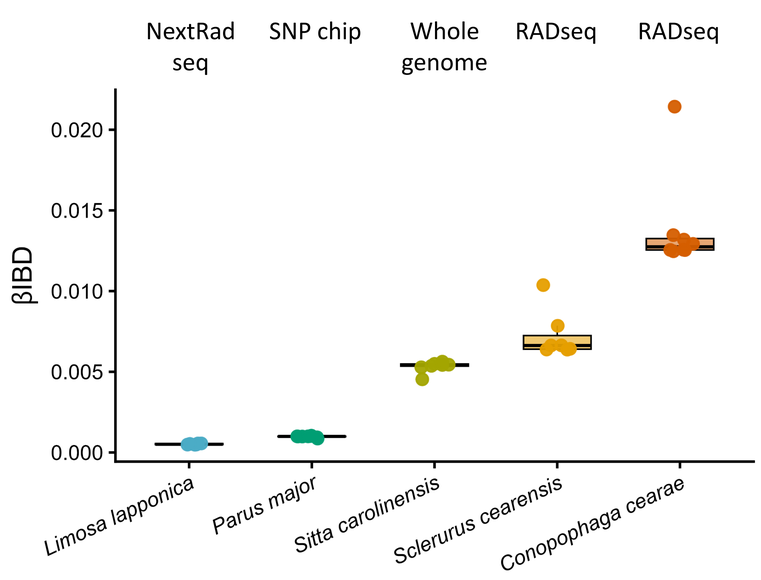
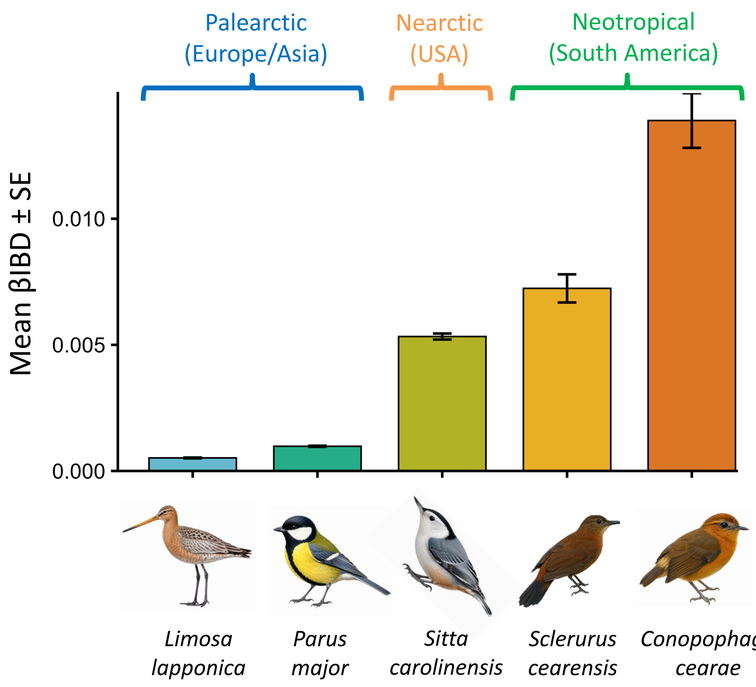
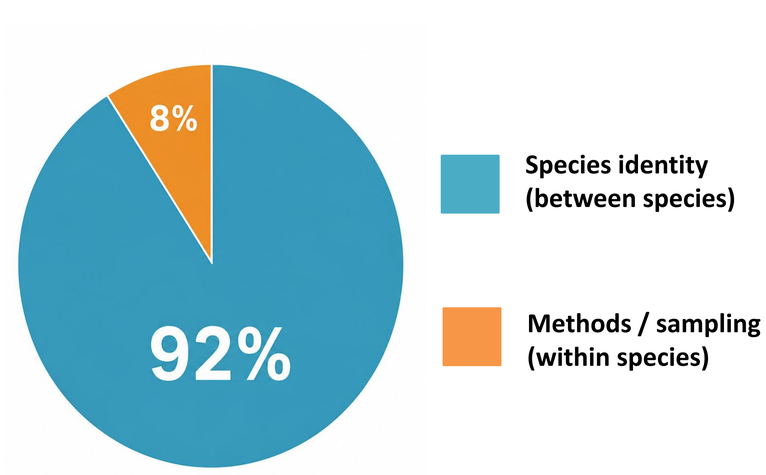


Fig. 2. (A) Within-species robustness of βIBD across different genomic data configurations. (B) Comparison of mean βIBD values among species. (C) Partitioning of βIBD variance attributable to species identity and methodological effects.

- Coefficient of variation (CV) < 0.3 across all species and their modified subdatasets. 3 of 5 species showed CV < 0.1 (**high stability**).



- **Macroecological pattern: tropical** species (Neotropics) exhibit greater isolation than **temperate** species (Palearctic).
- Pairwise comparisons showed **significant differences** among almost all species ($p < 0.05$).
- Exceptions: Limosa–Parus and Sitta–Sclerurus.



- **92%** of the total variation in **βIBD** is attributable to **species identity**, rather than methodological artefacts or differences in genomic sampling design.
- **βIBD is a robust metric** for comparing population isolation across species.

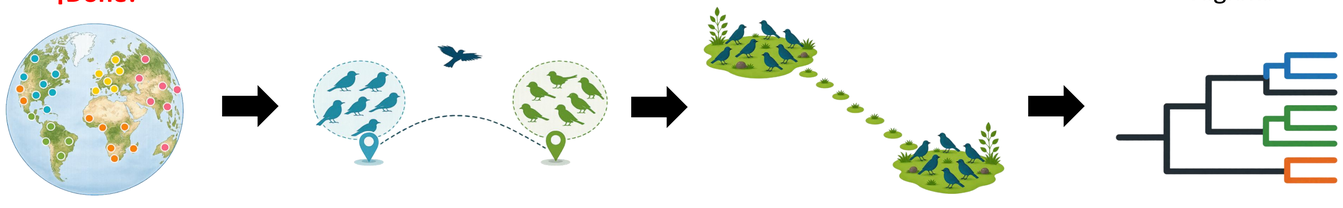
More info

Conclusions

- **βIBD is robust**: insensitive to different filtering schemes, SNP densities, and sample sizes.
- **Captures real biological differences** in population isolation among species.
- **The preliminary study reveals consistent macroecological patterns**: greater isolation in **tropical species**.
- Provides a **strong foundation** for a **broader analysis linking population-level** processes to large-scale **biodiversity patterns.**

Next steps

Compile global genomic datasets (+100 bird species) **¡Done!** → Estimate population isolation (βIBD) → Estimate population persistence → Investigate links with speciation rates and climatic regions



References

[1] Harvey, M. G., Singhal, S. and Rabosky, D. L. (2019) 'Beyond Reproductive Isolation: Demographic Controls on the Speciation Process.' Annual Review of Ecology, Evolution, and Systematics, 50(1) pp. 75–95.

[2] Rabosky, D. L. (2016) 'Reproductive isolation and the causes of speciation rate variation in nature.' Biological Journal of the Linnean Society, 118(1) pp. 13–25.

Acknowledgements

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