

Comparing the BIN Composition of Subfamily Sciurinae between North America and Eurasia

Kexin Gong

DNA barcoding as a tool for studying biodiversity

- DNA barcoding uses short standardized gene regions (e.g., COI in animals) to identify and compare species.
- Each unique genetic cluster corresponds to a Barcode Index Number (BIN), which serves as a proxy for a species.
- The Barcode of Life Data System (BOLD) is a global open-access database containing millions of DNA barcode records from around the world.
- BOLD data allow researchers to explore species distributions, diversity, and biogeographic patterns at large scales.

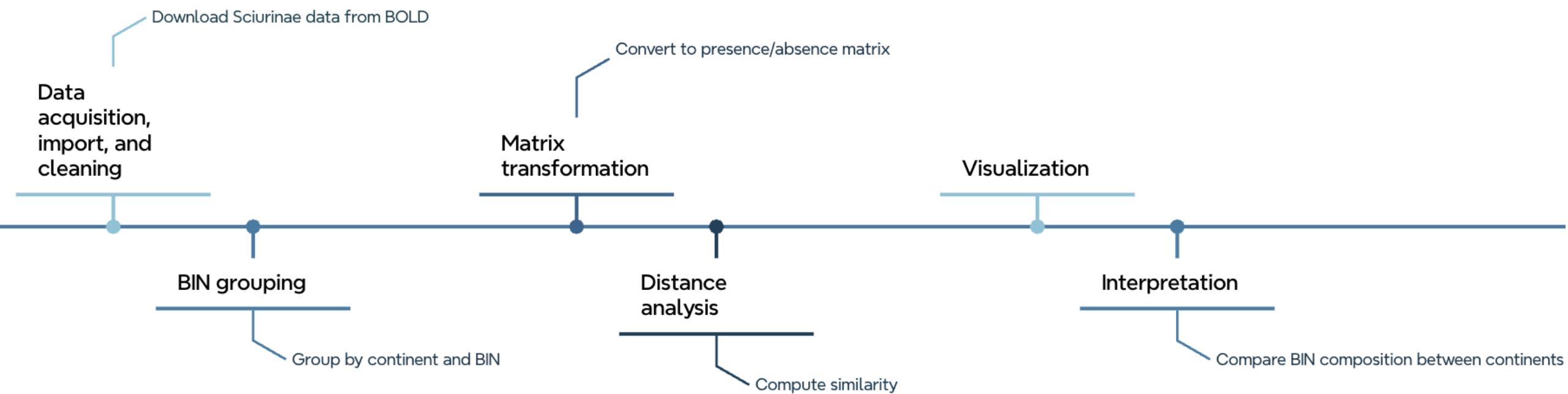
Why study Sciurinae (tree and flying squirrels)?

- The subfamily Sciurinae includes both tree squirrels and flying squirrels, distributed across North America, Eurasia, and other regions (Black, 1972).
- These mammals are ecologically important seed dispersers and indicators of forest ecosystem health (Steele & Yi, 2020).
- Despite their wide range, genetic data on continental-scale diversity remain limited.
- Comparing their BIN composition between continents can reveal biogeographic differentiation and potential historical connections (e.g., Bering Land Bridge).

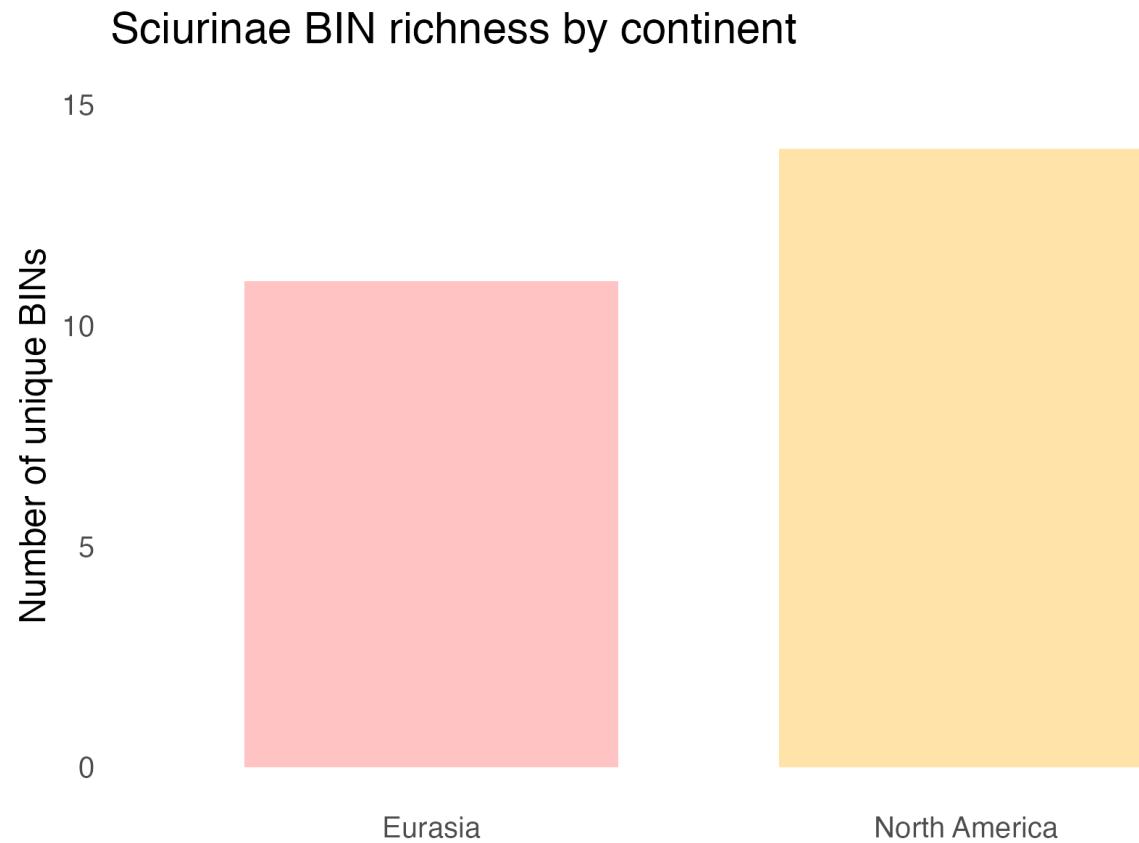
Research goal and hypothesis

- Research question: How similar is the BIN composition of subfamily Sciurinae between North America and Eurasia?
- Hypothesis: Because of long-term geographic isolation, Sciurinae populations in North America and Eurasia will show distinct BIN assemblages with limited overlap.

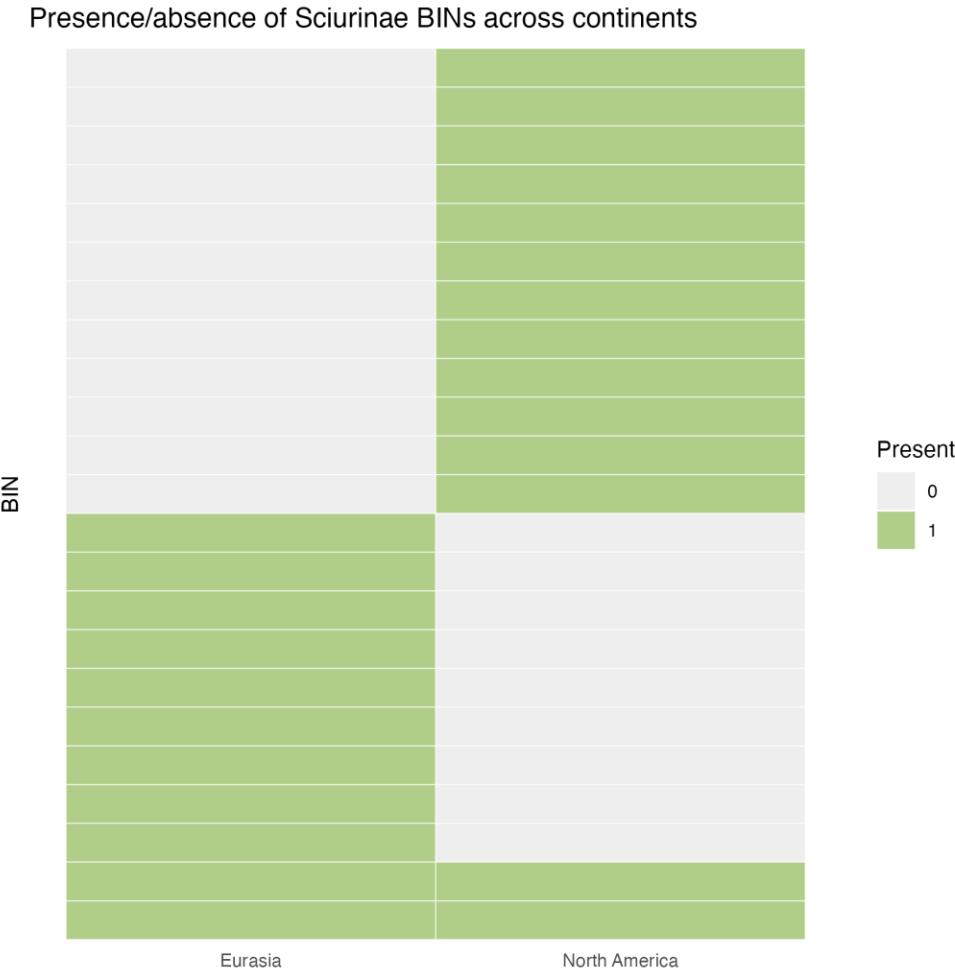
Methods



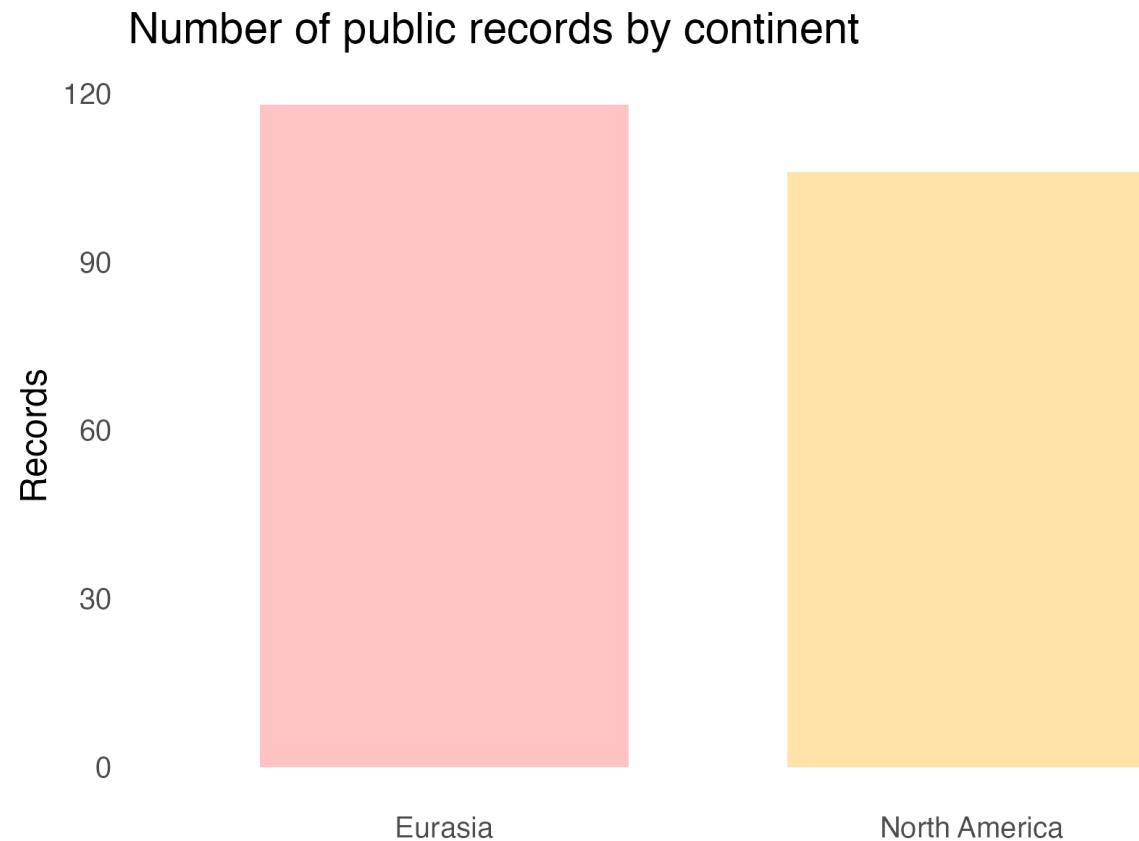
North America shows slightly higher BIN richness than Eurasia



Most BINs are continent-specific, with very limited overlap between regions



Eurasia has slightly more public records, suggesting minor sampling imbalance



Results: BIN composition differs strongly between continents

- Our analysis of Sciurinae barcode data from BOLD revealed clear genetic separation between North America and Eurasia.
- North America contained 12 unique BINs, whereas Eurasia contained 11.
- Although BIN richness was similar, the calculated Jaccard distance (0.913) and Bray–Curtis dissimilarity (0.929) show that the two regions share very few BINs.
- This strong dissimilarity supports the hypothesis that Sciurinae populations on the two continents have evolved largely in isolation, consistent with limited historical dispersal across the Bering region.

Discussion: Drivers of continental divergence

- The near-absence of shared BINs indicates independent diversification of Sciurinae within each continent.
- Long-term climatic and geological barriers, particularly intermittent closure of the Bering Land Bridge, likely limited gene flow and promoted allopatric speciation (Winker et al., 2023).
- This pattern mirrors previous findings of pronounced biogeographic breaks among North American and Eurasian small mammals (Bofarull et al., 2008).
- DNA barcoding thus effectively detects large-scale evolutionary structure even when morphological variation appears subtle.

Caveats and future directions

- The dataset (~220 records) is moderate but sufficient for exploratory analysis.
- Sampling density was slightly higher in Eurasia (\approx 118 records) than in North America (\approx 106), producing a minor potential bias in observed richness.
- However, both similarity indices (Jaccard = 0.913; Bray–Curtis = 0.929) confirm that continental separation is robust.
- To strengthen these results, future work should: incorporate additional regions (e.g., South America and Africa) to test global patterns; conduct sequence-level or phylogenetic analyses to evaluate the depth of BIN divergence; link BIN distributions with ecological and climatic variables to identify drivers of diversification.
- Together, these findings generate a clear, testable hypothesis: Sciurinae lineages diversified independently following the late Miocene closure of intercontinental corridors, leading to enduring continental-scale genetic partitions.

References

- Black, C. C. (1972). Holarctic Evolution and Dispersal of Squirrels (Rodentia: Sciuridae). In T. Dobzhansky, M. K. Hecht, & W. C. Steere (Eds.), *Evolutionary Biology: Volume 6* (pp. 305–322). Springer US. https://doi.org/10.1007/978-1-4684-9063-3_10
- Bofarull, A. M., Royo, A. A., Fernández, M. H., Ortiz-Jaureguizar, E., & Morales, J. (2008). Influence of continental history on the ecological specialization and macroevolutionary processes in the mammalian assemblage of South America: Differences between small and large mammals. *BMC Evolutionary Biology*, 8(1), 97. <https://doi.org/10.1186/1471-2148-8-97>
- Steele, M. A., & Yi, X. (2020). Squirrel-Seed Interactions: The Evolutionary Strategies and Impact of Squirrels as Both Seed Predators and Seed Dispersers. *Frontiers in Ecology and Evolution*, 8. <https://doi.org/10.3389/fevo.2020.00259>
- Winker, K., Withrow, J. J., Gibson, D. D., & Pruett, C. L. (2023). Beringia as a high-latitude engine of avian speciation. *Biological Reviews*, 98(4), 1081–1099. <https://doi.org/10.1111/brv.12945>