

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

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## 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.

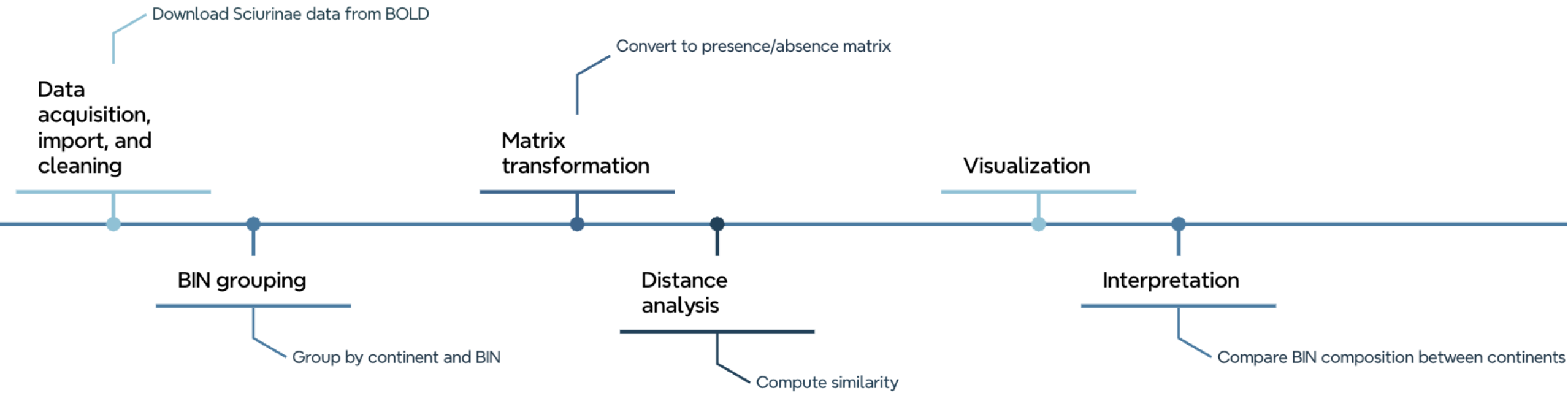
## Why study Sciurinae (tree and flying squirrels)?

- 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).

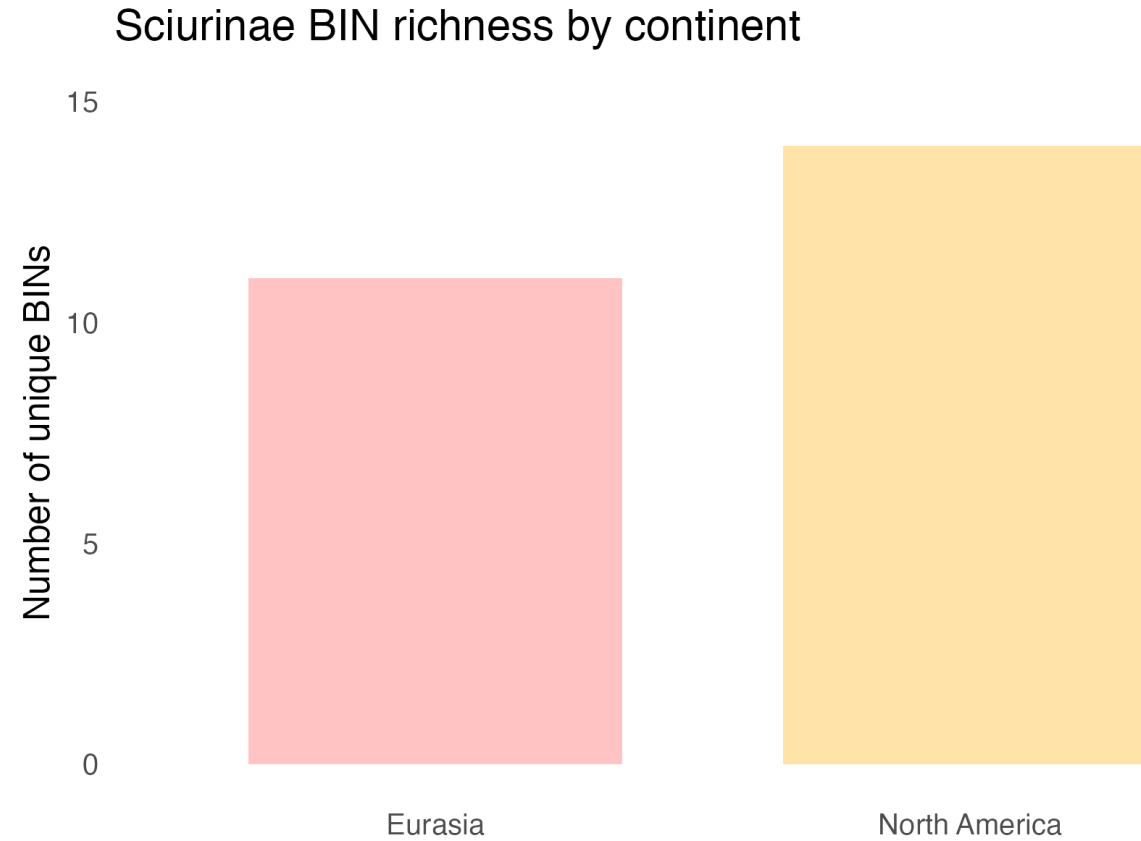
## Research goal and hypothesis

- 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.

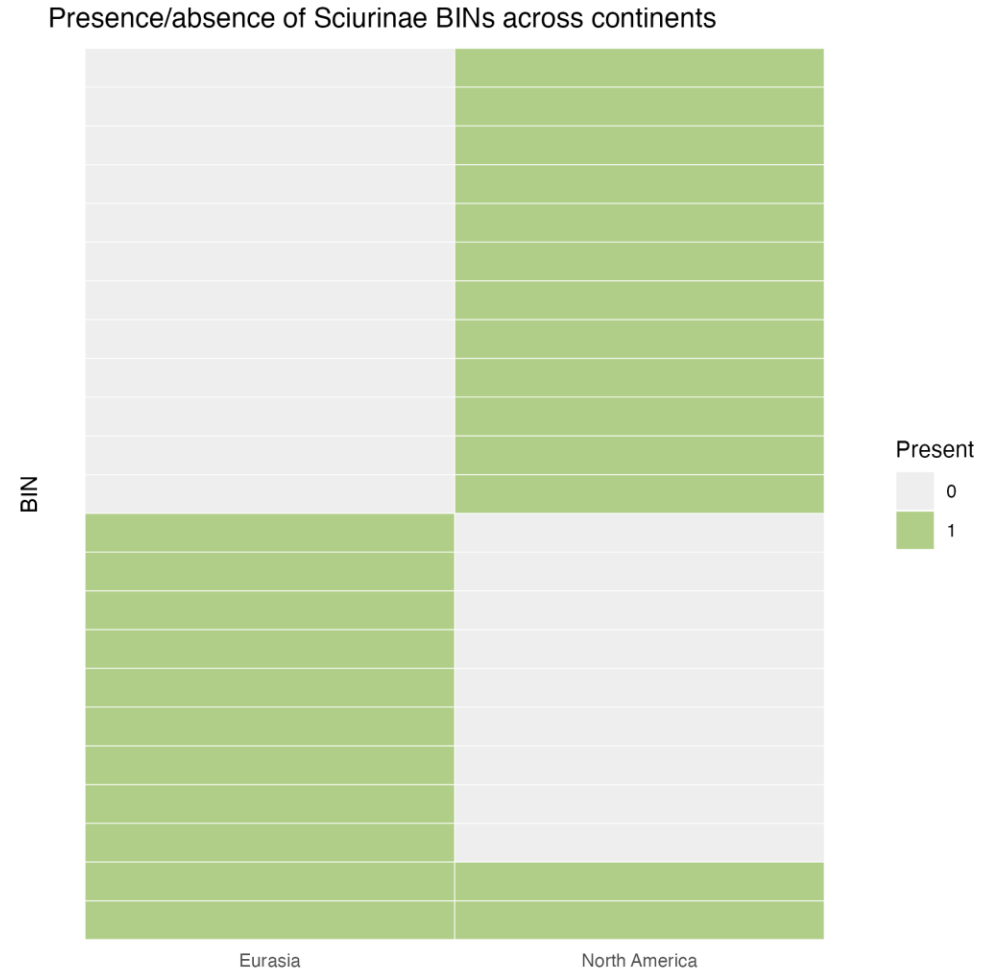
# Methods



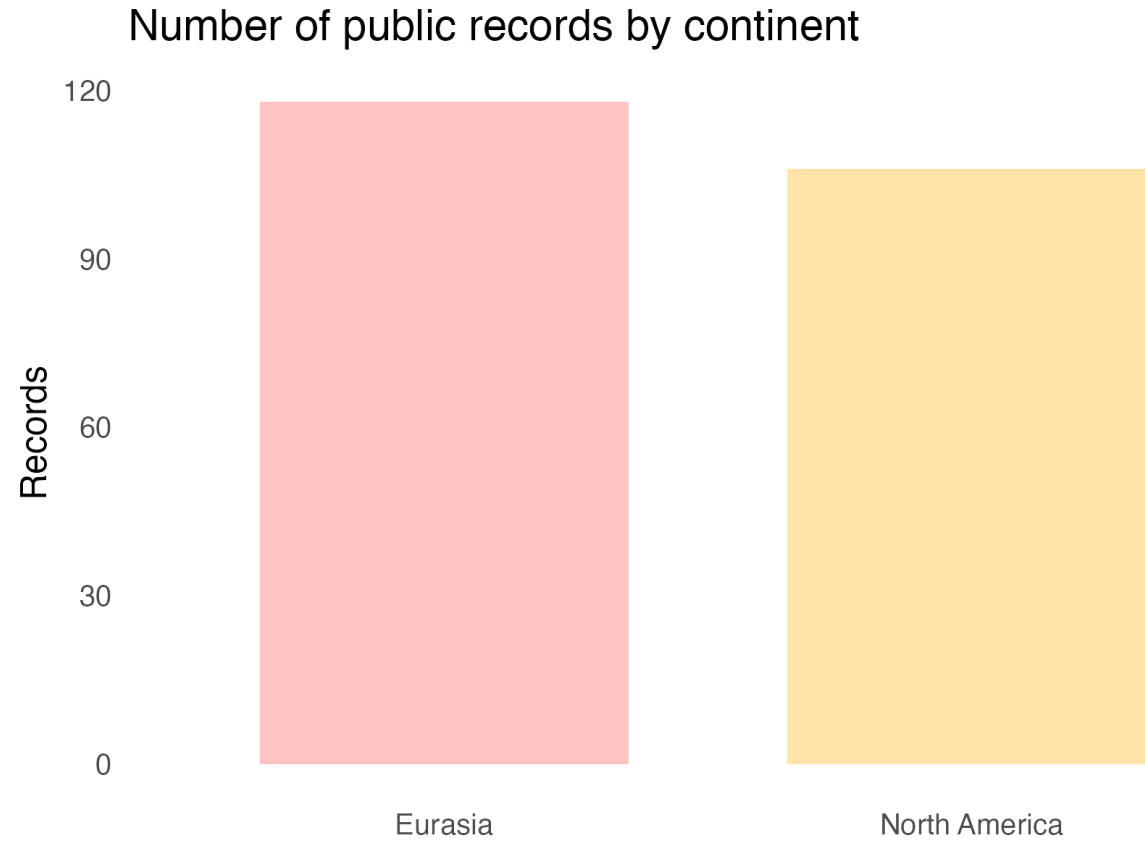
# North America shows slightly higher BIN richness than Eurasia



# 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

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