# “PATTERNS OF BIN AND SPECIES DIVERSITY IN *BRACHIOPODA*: MY INSIGHTS FROM BOLD DATA”

BY

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- The phylum *Brachiopoda* comprises a group of marine invertebrates that have persisted from the Paleozoic era to the present day. Although modern brachiopods are far less diverse than their fossil counterparts, they remain important indicators of marine biodiversity and biogeographic patterns (Emig *et al.,* (2019)

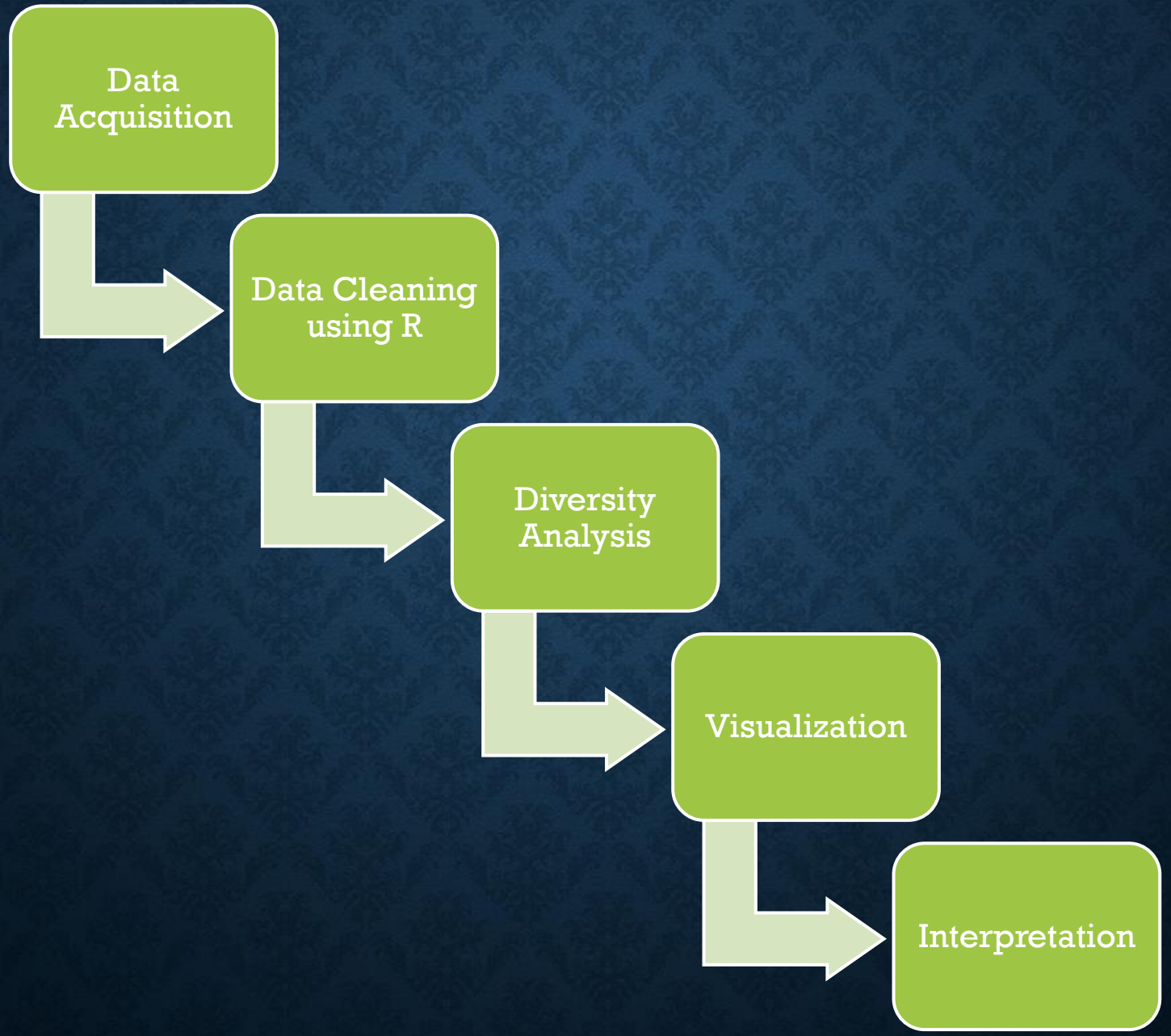
- The increasing availability of DNA barcode data has made it possible to assess genetic and species-level diversity across global datasets.

- The Barcode of Life Data System (BOLD) offers a standardized platform for storing and analyzing DNA barcode records, including Barcode Index Numbers (BINs), which serve as proxies for species-level genetic clusters (Ratnasingham & Hebert, 2007).

# OBJECTIVE:

- By analyzing BOLD data for *Brachiopoda*, this study investigates patterns of BIN richness, unique species representation, and spatial distribution of samples. Such analyses contribute to understanding the extent of taxonomic coverage in barcoding databases and highlight potential gaps or biases in global sampling efforts.

# METHODOLOGY



# DOES LATITUDE AFFECT BIN DIVERSITY ACROSS REGIONS?

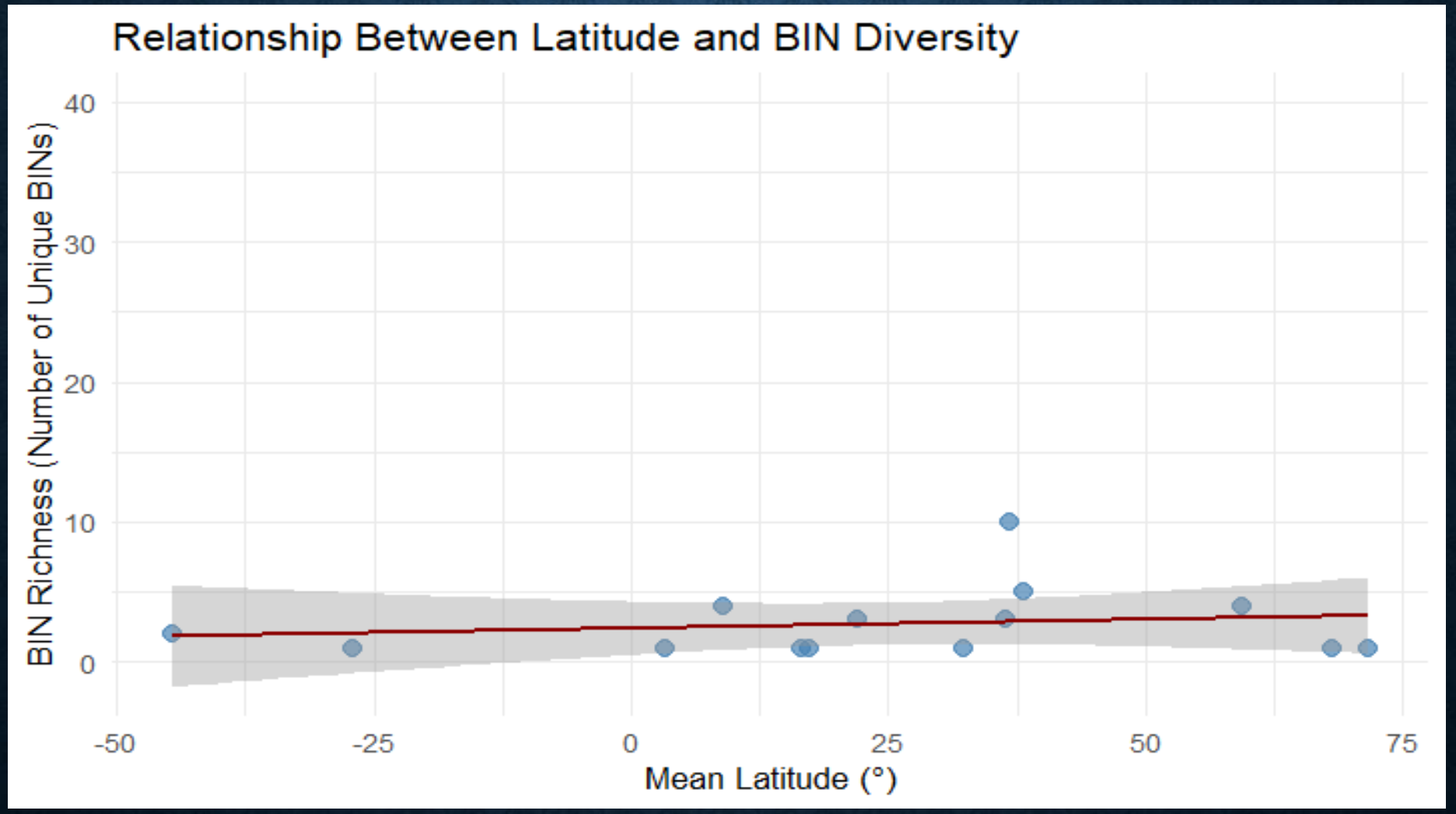



Fig 1

# HAS SAMPLE COMPLETENESS BEEN ATTAINED FOR THIS TAXA?

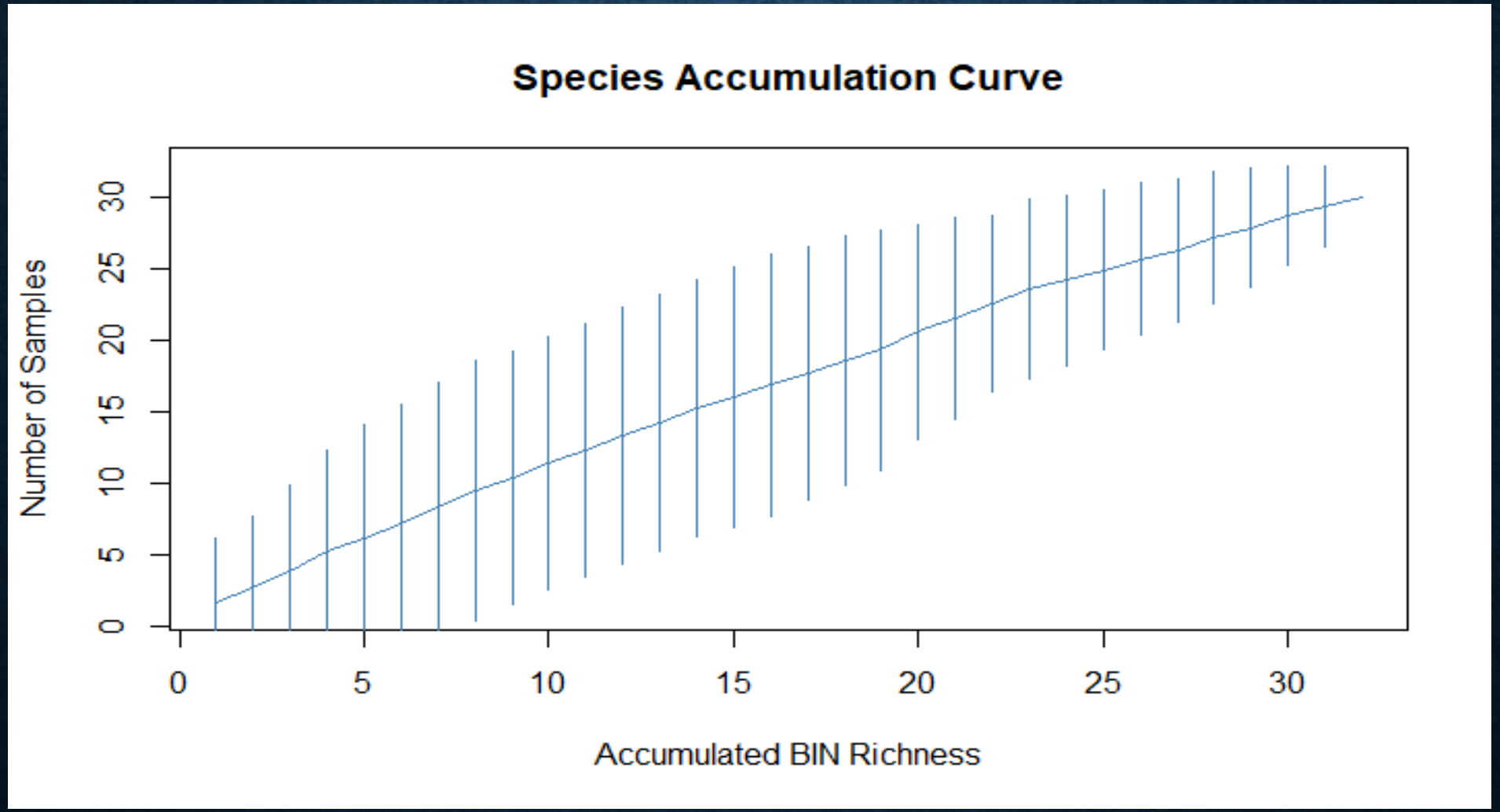



Fig 2

# WHAT DOES THE DISTRIBUTION OF BARCODE DIVERSITY ACROSS ORDERS REVEAL ABOUT BINS AND TAXA?

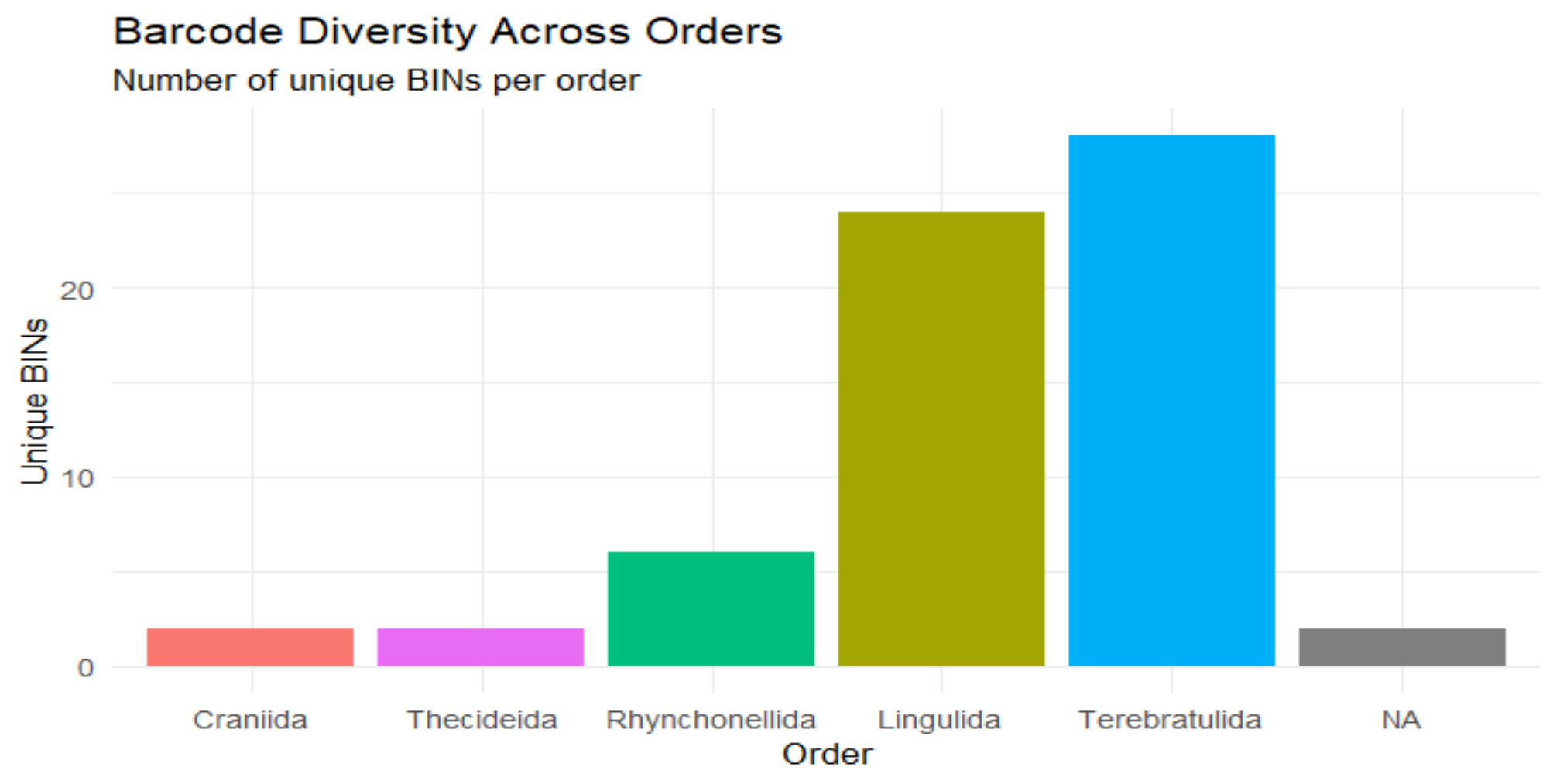



Fig 3

# RESULTS AND DISCUSSION

- Figure 1 shows the relationship between latitude and BIN diversity. Brachiopoda BIN diversity appears relatively constant across latitudes.
- This could mean the sampling effort may not be uniform as some latitudes may have fewer collections of the taxa
- Except for an outlier at 10 thereabouts which could mean some countries/ocean have better local species variation
- Figure 2 shows the species accumulation curve and this can be interpreted as a gradually flattening pattern, not a steep one.
- This actually means and suggests that the sampling is tending towards completeness i.e most of the species in this study area have already been captured.
- Even though it could be seen at the initial stage that it was somehow steepy.

# CONTD

- This bar chart shows the number of unique Barcode Index Numbers (BINs) for different taxonomic orders.
- *Terebratulida* has the highest barcode diversity up to 27 BINs), followed by *Lingulida* up to 24 BINs).
- These two groups represent the majority of barcoded diversity in this taxa *(Brachiopoda)*
- The dominance of *Terebratulida and Lingulida* suggests that these two orders make up the majority of molecular diversity in the dataset.
- Even though the other orders have lesser diversity, it could actually mean they were not well sampled not that maybe fewer species exist

# CONCLUSION

- One major thing I learnt from my data set is the importance of sampling, how it exposed me to locations in which some taxa are well sampled and giving room for chances to explore other regions.

- I think one thing I don’t agree with is the fact that some regions or taxa group maybe over documented maybe because of their location or their just easier to collect. This makes the other groups look under studied.

# ACKNOWLEDGEMENT


- I would like to appreciate the efforts of Yazan and Ayo, they made sure they were available to attend to my DMs especially in the last few hours to deadline as I suddenly encountered problem with my codes and I need a summary of what actually do we need to put in our slide
- Thanks to Fangyi, I started out the assignment on a badnote as I couldn't load my data despite following the class templates. She figured that my code just lacked a character.
- A major lesson I learnt was every input matters, from the semi colons, colons and other punctuations. A little mistake like "Longitude" instead of "longitude" could be a major factor in messing up one's efforts

# REFERENCES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