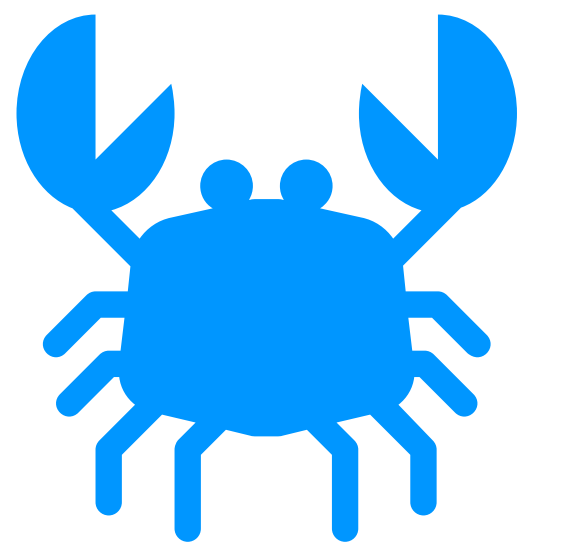


# Climatic and Geographic Influences on Cumacea Genetics in the Northern North Atlantic



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## ABSTRACT

- This study analyzes the **effect of environmental factors on the genetics** of Cumacea crustaceans in Icelandic North Atlantic waters, employing 16S rRNA mitochondrial gene sequences and *aPhyloGeo* software.
- Our analyses highlight significant spatial fluctuation of certain environmental parameters and Cumacea diversity across habitats, **with genetic sequences correlated** to wind speed (m/s) at the start of sampling and oxygen concentrations (mg/L), demonstrating potential local adaptations.
- These **preliminary results require further analysis** to elucidate the relationships between Cumacea genetics, and strongly support the hypothesis of natural selection contributing to the local acclimatization of Cumacea to environmental variations through climate change.
- The *aPhyloGeo* package is freely available to researchers and collaborators on GitHub and PyPi.

## DATA PRE-PROCESSING

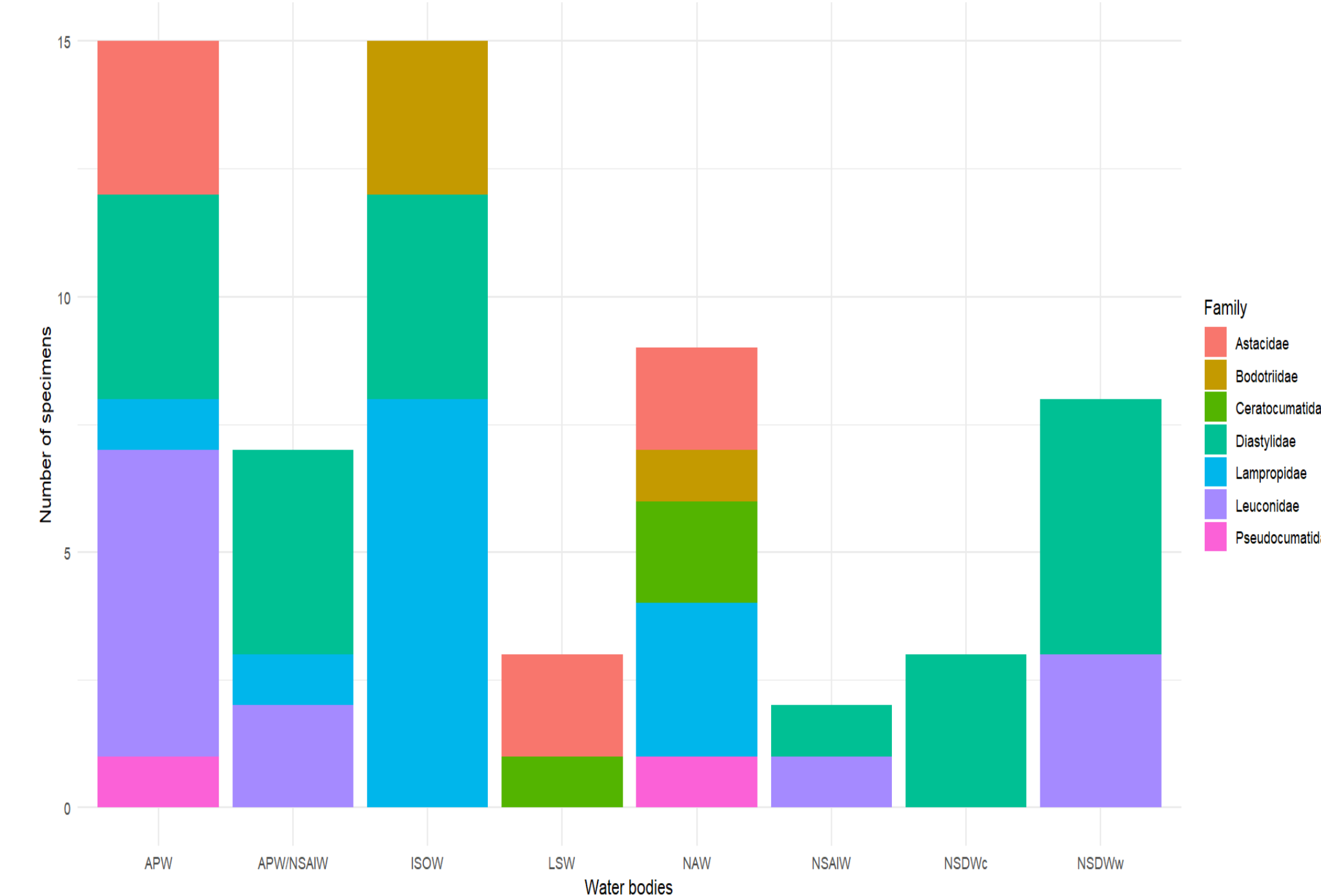


Figure 3: Distribution of Cumacea Families by Water Body

- Figure 3 shows the distribution of the different Cumacea families according to the variety of water bodies in which they were sampled
- Goal ->** Compare the diversity and potential preference of the different families in each body of water

- Figure 4 illustrates the distribution of the different Cumacea families according to the type of habitat they were collected during sampling
- Goal ->** Compare the diversity of the different families in each habitat type

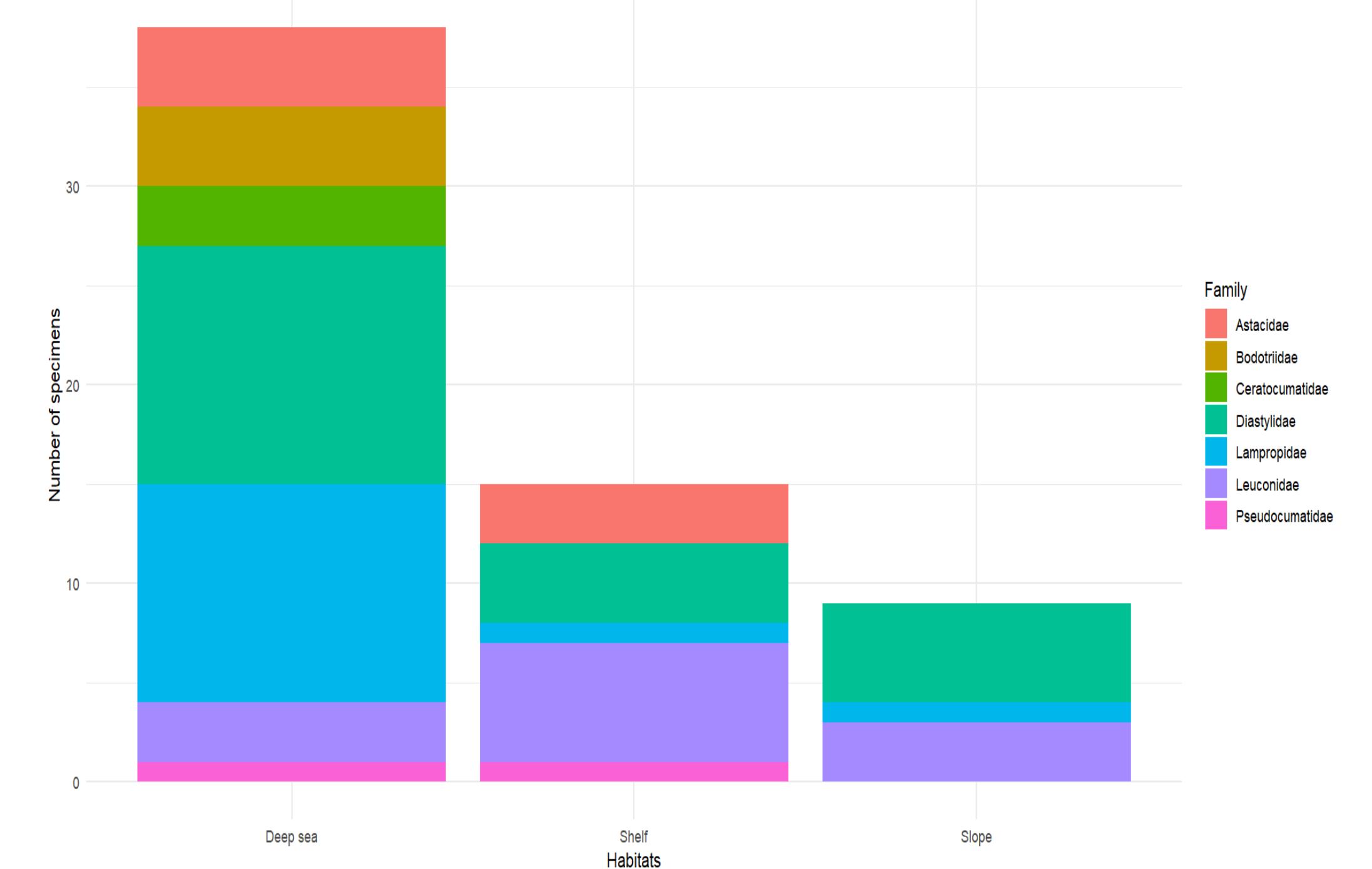


Figure 4: Distribution of Cumacea Families by habitat

## DATA DESCRIPTION

These diagrams and descriptive statistics are **essential** for :

- **Evaluate the conditions** of the habitats where the samples were collected
- **Highlighting unique habitats** that may have an effect on Cumacea genetics
- **Identify** general trends or irregularities in the data

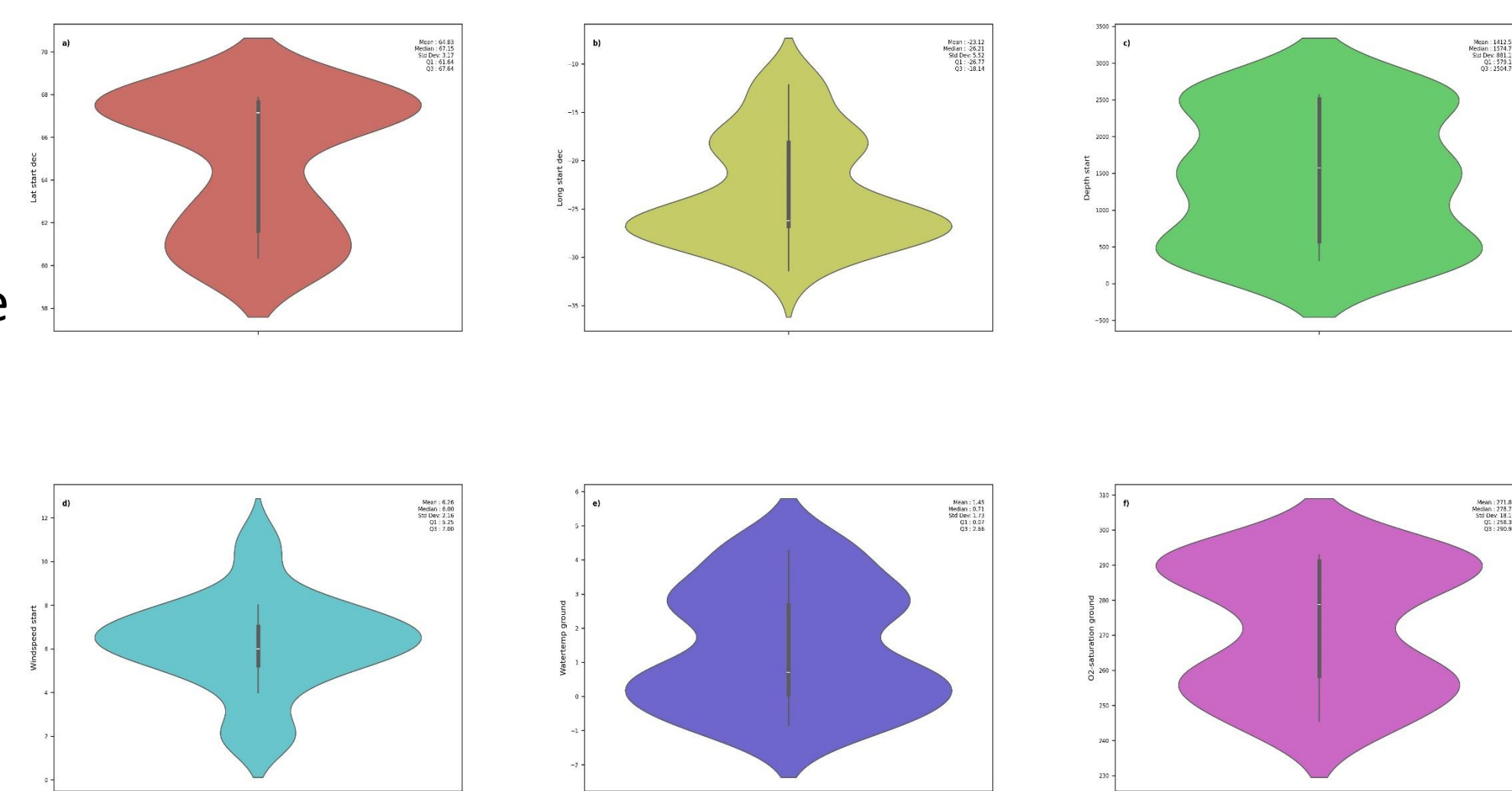


Figure 1: Violin diagrams of six geographical and environmental attributes in our sample

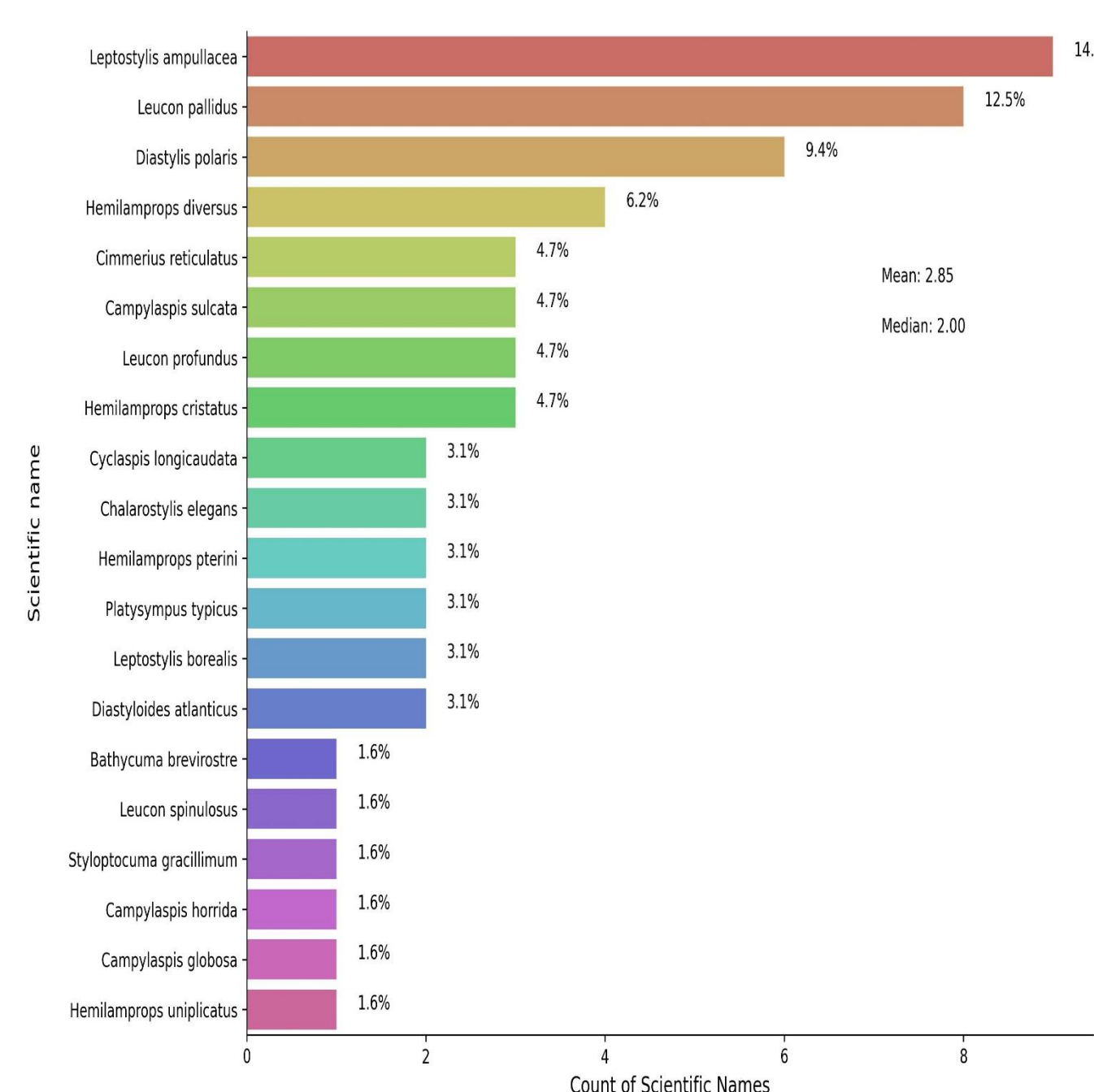


Figure 2: Distribution of Cumacea Species Frequency

Figure 2 shows the distribution and variety of the different Cumacea species in our sample

- The Figure **highlight the most and least represented species**, which is also supported by the average and median in the right corner
- It aims to **identify species that show genetic diversity** associated with their **geographical distribution**, as well as one or several local adaptations.

## PRELIMINARY RESULTS

- The **cross-platform software aPhyloGeo** was used for phylogeographic analyses, which is designed to analyse phylogenetic trees using climatic parameters.
- Four metrics were applied on our data : **Least-Squares distance**, **Robinson-Foulds (RF) distance**, **normalized Robinson-Foulds distance** and **Euclidean distance**.



Figure 5: Analysis of fluctuations in the four distances metrics using multiple sequence alignment (MSA) in correlation with wind speed (m/s) at the start of sampling

- The **Euclidean distance** presented in Figure 5d (between 520 aa to 529 aa) and 6d (between 1190 aa to 1199 aa) both shows the greatest sensitivity and heterogeneity from our data.
- These positions with the highest **Euclidean distance** demonstrate **significant dissimilarity between sequences** at these positions, which may point to a more fluctuating or evolutionarily unstable sites.

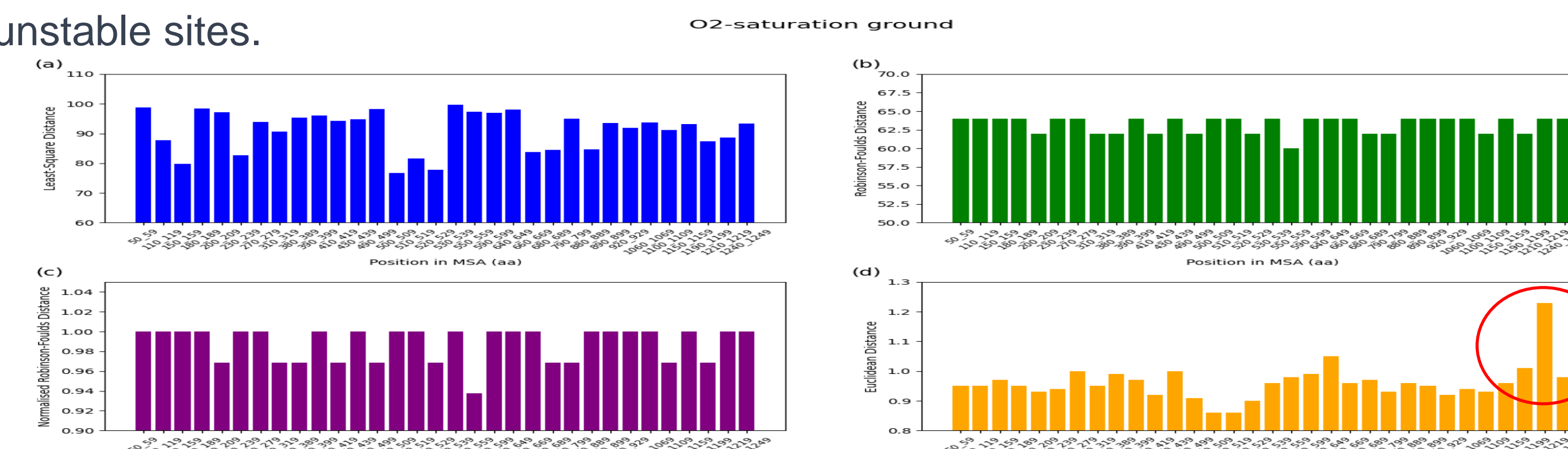


Figure 6: Analysis of fluctuations in the four distances metrics using multiple sequence alignment (MSA) in correlation with oxygen concentration (mg/L) where the samples were collected

## CONCLUSIONS

- This study investigates the influence of climatic and environmental variables on Cumacea around Iceland, attempting to correlate genetic information from the mitochondrial 16S rRNA gene with habitat properties using relevant data and phylogeographic analyses via *aPhyloGeo*.
- The results reveal a significant fluctuation in Cumacea environments linked to geographical and climatic variables, with DNA sequences showing specific genetic window with high mutation rates under the effect of climatic attributes such as wind speed (m/s) and water oxygen concentration (mg/L).
- This study highlights the value of investigating the relationship between environmental characteristics and genetics of Cumacea for predicting the future impact of environmental variations on marine biodiversity, although further analysis are required.

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## Source

GitHub Link

<https://github.com/tahiri-lab/aPhyloGeo>



Tahiri Lab website

<https://tahirinadia.github.io/>



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