DEEP SEA CTENOPHORE DATA EXPLORATION

Background

The deep sea is the largest habitat on Earth, with over 90% of the available living space on the planet being in waters below 200 meters (Haddock & Choy, 2024). Despite this, scientists know very little about the biology of organisms that live there. How do deep sea animals survive at near-freezing temperatures and crushing hydrostatic pressures?

Ctenophores ("comb jellies") are great for studying deep-sea survival (Figure 1). With over 200 species living from tropical surface waters to the deep-sea floor (and everywhere in between), they show us how organisms can adapt to different environments. Although diverse in shape, size, color, diet, and habitat, all ctenophores have a mouth, sticky tentacles to catch food, and eight rows of comb-like hairs (called ctenes) for swimming.

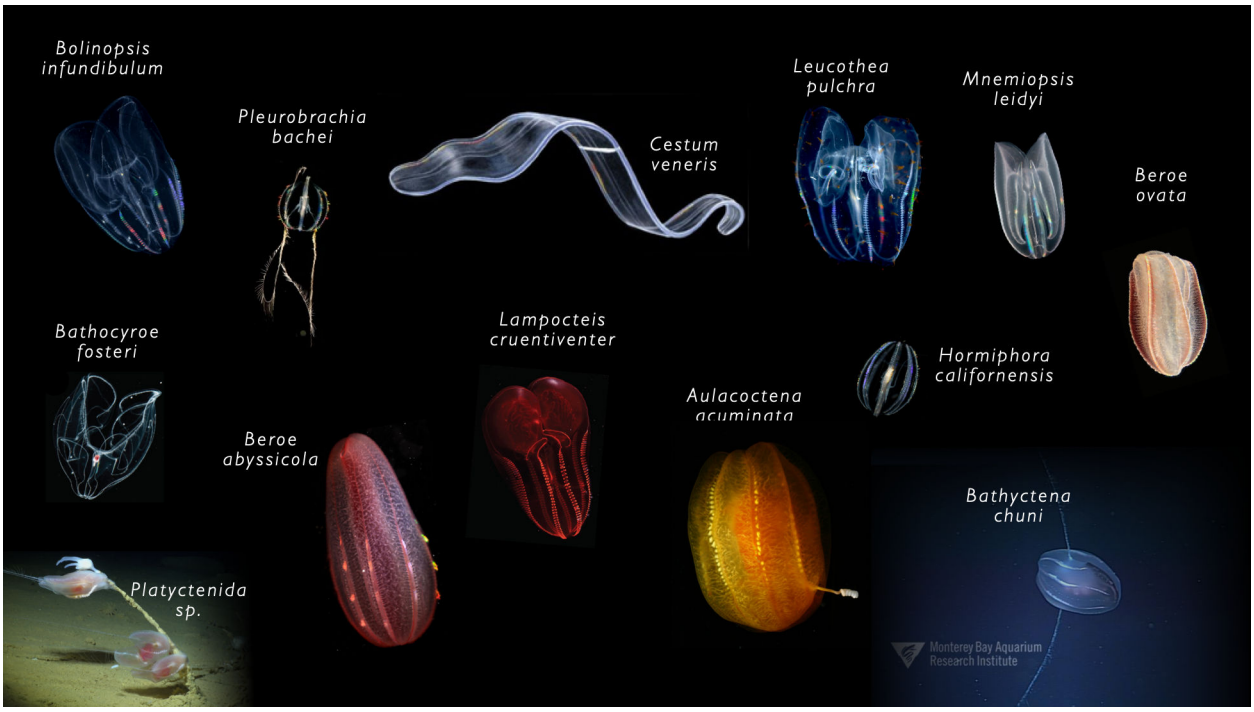
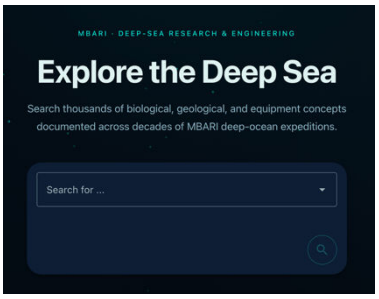


Figure 1. Ctenophores are diverse group of marine invertebrates. You will be examining some real and some simulated datasets including all of the species in this image. Photos: William Browne (*Mnemiopsis leidyi*), Anik Grearson (*Beroe abyssicola*), Shannon Johnson (*Hormiphora californensis*), MBARI (*Platyctenida sp.* and *Bathyctena chuni*), Leonid Moroz (*Pleurobrachia bachei*), Kevin Raskoff (*Aulacoctena acuminata*), Joseph Trumpey (*Cestum veneris*), and Steven Haddock (all others).

At MBARI's Biodiversity and Biooptics lab we tackle one big question from multiple angles: **how do deep-sea ctenophores survive extreme conditions?**

1. Ecology: What is the deep-sea environment like? Where do ctenophores live?
2. Genetics: What genes show signs of adaptation to deep-sea conditions?
3. Biochemistry: What specific molecular changes do ctenophores make to keep their cells working under extreme pressure?
4. Physiology: Do these molecular changes maintain cellular function in the deep sea?

I. ECOLOGY DATA EXPLORATION: Explore MBARI's Deep Sea Guide



MBARI has tracked thousands of deep-sea observations over decades. We can use this data to see where animals live and how populations may change over time.

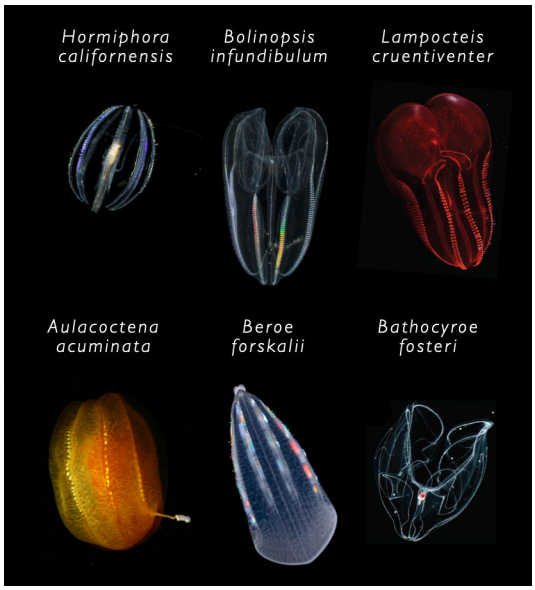
In this activity, we use MBARI's Deep Sea Guide to learn more about where ctenophores live in the water column.

How to explore

1. Visit MBARI's Deep Sea Guide and search for an animal
    - If this link doesn't work, go here, then scroll to the bottom and click "Visit Deep Sea Guide"
    - Make sure pop-ups aren't blocked, which might prevent the page from loading.
2. Go to its page, scroll down, and click "Data plots"
3. Leave settings as default, and click "Generate plots"
4. You'll see a depth histogram (how deep they're found) and a time histogram (how observations have changed over years)

Questions for discussion: (Hint: Try looking for these ctenophore species, and a few others from Figure 1) →

- Which species live in shallow waters?
- Which live deep?
- Do you notice any patterns over time?



Expected results for a few species

- *Hormiphora californensis*: ~0-500m
- *Bolinopsis infundibulum*: ~0-2000m
- *Lampocteis cruentiventer*: ~400-300m
- *Aulacoctena acuminata*: ~900-1200m
- *Beroe forskali*: ~0-700m
- *Bathocyroe fosteri*: ~300-3000m

Takeaway: Ctenophores live across a wide range of depths, from surface waters to several thousand meters below. This wide range is what makes understanding their adaptations so fascinating.

II. GENETICS DATA EXPLORATION: Build a DNA alignment & tree

DNA is the instruction manual for life. It's made of four building blocks called nucleotides: A, T, G, and C. These letters are arranged in a specific order that codes for proteins (the molecules that do the actual work in cells). When organisms are closely related, their DNA is more similar (they inherited it from a common ancestor). When they are more distantly related, their DNA has accumulated more differences. By comparing DNA sequences, we can build a "family tree" showing how species are related to one another.

Using DNA sequences, we can answer questions like:

- Which species are more closely related?
- Which genes are most important for survival in certain habitats?
- Do different genes tell the same evolutionary story?

In this activity, we will compare two hypothetical genes in ctenophores and ask: do they tell the same story about how deep-sea and shallow-sea ctenophores are related?

***About the dataset*:** Below are simulated DNA sequences for two hypothetical genes from 10 ctenophore species (5 deep, 5 shallow). Note: DNA data aren't real, but are *simulated* to illustrate plausible evolutionary scenarios and patterns you might observe in actual phylogenetic trees. For resources on how to find real DNA sequences to align, see the Resources & Links section on page 9 of this document.

- Piezotolerin: A hypothetical "pressure-response" gene
- Ancestrin: A hypothetical "housekeeping" gene with basic cellular function

How to compare: We will be using an online tool to line up DNA sequences, count up how different each pair of sequences is, and build a family tree based on those differences.

1. Go to Clustal Omega
2. Copy all piezotolerin sequences and paste them in the box
3. Select "DNA" as the sequence type, and leave all parameters as default
4. Click "Submit" and wait a few seconds
5. Go to "Tool Output" to view the alignment
    a. Optional: Go to "Alignments" for a more interactive view of the alignment, where you can visualize it using different color schemes.
6. Go to "Phylogenetic Tree" to see the tree (use the arrows to adjust viewing settings)
7. Repeat for ancestrin sequences (click on "Input Form" to submit another run)

Questions for discussion

- Where do deep and shallow species differ most consistently in the alignment?
- How do the trees look different for each gene?
- Why might piezotolerin cluster by depth while ancestrin doesn't?
- Which gene might be more important for deep-sea survival?

Sequences – Piezotolerin (copy and paste these into Clustal Omega)

```
>piezotolerin_Mnemiopsis_leidyi_SHALLOW
ATCGGGACCACCGAGTTAGTCTAGACCCGCCCGGTCAACCCCACCAAGGGGCCAATCTCAGAAGTCGGTCTGTCTTGATCTGCTCTGATA
>piezotolerin_Bolinopsis_infundibulum_SHALLOW
ATCGGGACCACCGAGTTAGTCTAGACCCGCCCGGTCAACCCCACCGAGGGGCCAATCTTAGAAGTCGGTCTACCTTGATCTGCTCTGATA
>piezotolerin_Leucothea_pulchra_SHALLOW
ATCGGGACCACCGAGTTAGTCTAGACCCGCCCGGTCAACCCCACCGAGGGGTCAACCTTAGAAGTCGGTCTGTCTGGATCTGCTCTGCGA
>piezotolerin_Beroe_ovata_SHALLOW
ATCGGGACCACCGAGTTAGTCTAGACCCGCTCGGTCAACCCCACCGAGGGGCCAATCTTAGAAGACGGTCTGTCTGGATCTACTCTGCGT
>piezotolerin_Pleurobrachia_bachei_SHALLOW
ATCGGGACCACCGAGTTAGTCTAGACCCGCTCGGTCAACCCCACCGAGGGGCCAACCTTAGAAGAAGGTCTGTCTGGTTCTGCTCTGCGT
>piezotolerin_Lampocteis_cruentiventer_DEEP
GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCTTCTGAAGCTGTAAAACTGGTTCTGCATGAAGGTTGGT
GAGGTTTAGTGTCGCGT
>piezotolerin_Bathocyroe_fosteri_DEEP
GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCTTCTGAAGCTATAAAACTGGTTCTGCATGAAAGTCGGT
GAGGTTTAGTGCCGCGT
>piezotolerin_Beroe_abyssicola_DEEP
GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCTTCTGAAGCTGTAAAATTGGTTCTGGATGAAGGTTTGT
GAGGTTCTGTGCCGCGT
>piezotolerin_Bathyctena_chuni_DEEP
GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCTTCTGAAGCTGTAAAATTGGCTCTGGATGAAGGTCTGT
CAGGTTCTGCGCCGCGT
>piezotolerin_Aulacoctena_acuminata_DEEP
GCTAAAGTTGTTAGACCGACTCGAGTTCATTTGACTGGTTTTGATGGTGATGAAGAACCTTCTGAAGCTGTAAAACTGGCTCTGGAAGAAGGTCTGT
CTGGTTCTGCGCTGCGT
```

Sequences – Ancestrin (copy and paste these into Clustal Omega)

```
>ancestrin_Mnemiopsis_leidyi_SHALLOW
CCTGTTTCTATGATGGCTTGGAAAACTGCTGAACAATTTGAACTGTCTTCTGATAAAATTATTACTTTTGAACTGGATGCTACTTCTGATCGTCAAG
GTAATTCTTTTAAAGCT
>ancestrin_Pleurobrachia_bachei_SHALLOW
CAAGCTTCTCTGATGTCTTGGGAACCTGCTATTAATTATGAAGTTTCTCTGGATCAACTGATTACTATTGGTATTGATGCTACTGGTGATCGTAAAT
ATAAATCTCTGAAAGCT
>ancestrin_Beroe_ovata_SHALLOW
CCTGCTGGTACTCTGGCTTGGGATACTGCTATTCAATATAAAGTTTCTTCTAATCAACTGGTTACTTTTGATCTGGATGCTACTTCTGATCGTCAAT
ATAATGTTCTGAAATCT
>ancestrin_Bolinopsis_infundibulum_SHALLOW
CCTGCTGCTATGATGGCTTGGAAAACTGCTGCTCAATTTGAACTGTCTTCTAAAAAAATTATTGCTTTTGAACTGGAACTGACTTCTGATCGTCAAG
GTAATACTTTTAAAGCT
>ancestrin_Leucothea_pulchra_SHALLOW
CCTGCTTCTATGATGGCTTGGAAAACTGCTGCTCAATTTGAACTGTCTTCTAAAAAAATTGCTACTTTTGAACTGGATCTGACTTCTGATAAACAAG
GTAATACTTTTAAAGCT
>ancestrin_Lampocteis_cruentiventer_DEEP
CCTGCTTCTATGATGGCTTGGAAAACTGCTATTCAATATGAAGTTTCTTCTGATAAAATTGTTGGTTTTGAACTGGATGCTACTTCTGATCGTCAAT
ATAATTCTTTTCTGGCT
>ancestrin_Aulacoctena_acuminata_DEEP
CCTGGTTCTCTGATGGCTGAAGGTCAAGCTATTCAATATGAAGATTCTTCTGAACAAATTCTGTATATTGAACTGGATGCTACTTCTGATAAAAAAT
TTAATGAACTGAAAGCT
>ancestrin_Beroe_abyssicola_DEEP
CCTGCTGGTATGATGGCTTGGGAAACTGCTATTCAATATGAAGTTTCTTCTGATCAAATTATTAAATTTTATCTGGATGCTACTTCTGATCGTCAAT
ATAATGTTCTGAAATCT
>ancestrin_Bathyctena_chuni_DEEP
CCTGGTTCTCAAATGGCTTGGAAAACTGCTTTTAAATATGAAGCTTCTTGGGATCATATTCTGACTGTTGAACTGGATGCTACTTCTGATCGTAAAT
ATAATGCTCTGAAAGTT
>ancestrin_Bathocyroe_fosteri_DEEP
CCTGCTTCTATGATGGCTTGGAAAACTGCTATTCAATTTGCTGTTTCTTCTGAACAAATTATTTCTTTTGAACTGGATGCTACTTCTGATCGTCAAT
ATGATTCTTTTAAATCT
```

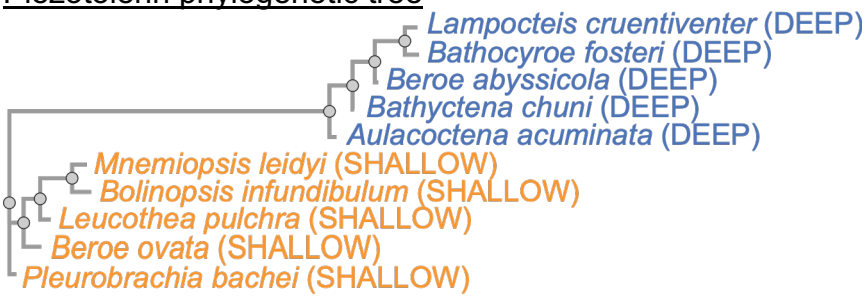
Expected results: Different genes don't always tell the same story!

- Piezotolerin: Deep and shallow species form separate clusters in the tree (notice the **bold/underlined** sections present only in deep species in the DNA alignment)
- Ancestrin: Species mix together regardless of depth in the tree.

Below are the outputs you will see from Clustal Omega. Here's how to read them:

- **Colors:** Blue for deep species, orange for shallow (we colored them for you!)
- **Asterisks (*):** Mark positions where all species share the exact same nucleotide
- **Dashes (-):** Gaps in the alignment. Pay special attention to where shallow species have long stretches of dashes while deep species have nucleotides!
- **Numbers on the right:** Position numbers showing where you are in the sequence

Piezotolerin phylogenetic tree

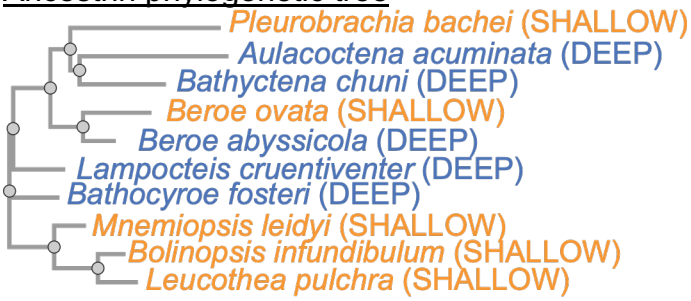


Piezotolerin alignment

```
Lampocteis_cruentiventer_DEEP      GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCT    60
Bathocyroe_fosteri_DEEP            GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCT    60
Aulacoctena_acuminata_DEEP         GCTAAAGTTGTTAGACCGACTCGAGTTCATTTGACTGGTTTTGATGGTGATGAAGAACCT    60
Beroe_abyssicola_DEEP              GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCT    60
Bathyctena_chuni_DEEP              GCTAAAGTTGTTAGACCGACTCGAGTTCATCTGACTGGTTTTGATGGTGATGAAGAACCT    60
Mnemiopsis_leidyi_SHALLOW          --------------------ATCGGGACCACCGAGTTAGTCTAGACCCGCCCGGTCAACCC    41
Bolinopsis_infundibulum_SHALLOW    --------------------ATCGGGACCACCGAGTTAGTCTAGACCCGCCCGGTCAACCC    41
Leucothea_pulchra_SHALLOW          --------------------ATCGGGACCACCGAGTTAGTCTAGACCCGCCCGGTCAACCC    41
Beroe_ovata_SHALLOW                --------------------ATCGGGACCACCGAGTTAGTCTAGACCCGCTCGGTCAACCC    41
Pleurobrachia_bachei_SHALLOW       --------------------ATCGGGACCACCGAGTTAGTCTAGACCCGCTCGGTCAACCC    41
                                                        *** *  **      * ** * **       *   ****

Lampocteis_cruentiventer_DEEP      TCTGAAGCTGTAAAACTGGTTCTGCATGAAGGTTGGTGAGGTTTAGTGTCGCGT    114
Bathocyroe_fosteri_DEEP            TCTGAAGCTATAAAACTGGTTCTGCATGAAAGTCGGTGAGGTTTAGTGCCGCGT    114
Aulacoctena_acuminata_DEEP         TCTGAAGCTGTAAAACTGGCTCTGGAAGAAGGTCTGTCTGGTTCTGCGCTGCGT    114
Beroe_abyssicola_DEEP              TCTGAAGCTGTAAAATTGGTTCTGGATGAAGGTTTGTGAGGTTCTGTGCCGCGT    114
Bathyctena_chuni_DEEP              TCTGAAGCTGTAAAATTGGCTCTGGATGAAGGTCTGTCAGGTTCTGCGCCGCGT    114
Mnemiopsis_leidyi_SHALLOW          CACCAAGGGGCC-----AATCTCAGAAGTCGGTCTGTCTTGATCTGCTCTGATA    90
Bolinopsis_infundibulum_SHALLOW    CACCGAGGGGCC-----AATCTTAGAAGTCGGTCTACCTTGATCTGCTCTGATA    90
Leucothea_pulchra_SHALLOW          CACCGAGGGGTC-----AACCTTAGAAGTCGGTCTGTCTGGATCTGCTCTGCGA    90
Beroe_ovata_SHALLOW                CACCGAGGGGCC-----AATCTTAGAAGACGGTCTGTCTGGATCTACTCTGCGT    90
Pleurobrachia_bachei_SHALLOW       CACCGAGGGGCC-----AACCTTAGAAGAAGGTCTGTCTGGTTCTGCTCTGCGT    90
                                        **                * *   **       * *       *
```

Ancestrin phylogenetic tree



Ancestrin alignment

```
Pleurobrachia_bachei_SHALLOW          CAAGCTTCTCTGATGTCTTGGGAACCTGCTATTAATTATGAAGTTTCTCTGGATCAACTG    60
Aulacoctena_acuminata_DEEP            CCTGGTTCTCTGATGGCTGAAGGTCAAGCTATTCAATATGAAGATTCTTCTGAACAAATT    60
Bathyctena_chuni_DEEP                 CCTGGTTCTCAAATGGCTTGGAAAACTGCTTTTAAATATGAAGCTTCTTGGGATCATATT    60
Beroe_ovata_SHALLOW                   CCTGCTGGTACTCTGGCTTGGGATACTGCTATTCAATATAAAGTTTCTTCTAATCAACTG    60
Beroe_abyssicola_DEEP                 CCTGCTGGTATGATGGCTTGGGAAACTGCTATTCAATATGAAGTTTCTTCTGATCAAATT    60
Lampocteis_cruentiventer_DEEP         CCTGCTTCTATGATGGCTTGGAAAACTGCTATTCAATATGAAGTTTCTTCTGATAAAATT    60
Bathocyroe_fosteri_DEEP               CCTGCTTCTATGATGGCTTGGAAAACTGCTATTCAATTTGCTGTTTCTTCTGAACAAATT    60
Mnemiopsis_leidyi_SHALLOW             CCTGTTTCTATGATGGCTTGGAAAACTGCTGAACAATTTGAACTGTCTTCTGATAAAATT    60
Bolinopsis_infundibulum_SHALLOW       CCTGCTGCTATGATGGCTTGGAAAACTGCTGCTCAATTTGAACTGTCTTCTAAAAAAATT    60
Leucothea_pulchra_SHALLOW             CCTGCTTCTATGATGGCTTGGAAAACTGCTGCTCAATTTGAACTGTCTTCTAAAAAAATT    60
                                      *  * *  *    ** **         ***    * * *      ***    *  *  *

Pleurobrachia_bachei_SHALLOW          ATTACTATTGGTATTGATGCTACTGGTGATCGTAAATATAAATCTCTGAAAGCT   114
Aulacoctena_acuminata_DEEP            CTGTATATTGAACTGGATGCTACTTCTGATAAAAAATTTAATGAACTGAAAGCT   114
Bathyctena_chuni_DEEP                 CTGACTGTTGAACTGGATGCTACTTCTGATCGTAAATATAATGCTCTGAAAGTT   114
Beroe_ovata_SHALLOW                   GTTACTTTTGATCTGGATGCTACTTCTGATCGTCAATATAATGTTCTGAAATCT   114
Beroe_abyssicola_DEEP                 ATTAAATTTTATCTGGATGCTACTTCTGATCGTCAATATAATGTTCTGAAATCT   114
Lampocteis_cruentiventer_DEEP         GTTGGTTTTGAACTGGATGCTACTTCTGATCGTCAATATAATTCTTTTCTGGCT   114
Bathocyroe_fosteri_DEEP               ATTTCTTTTGAACTGGATGCTACTTCTGATCGTCAATATGATTCTTTTAAATCT   114
Mnemiopsis_leidyi_SHALLOW             ATTACTTTTGAACTGGATGCTACTTCTGATCGTCAAGGTAATTCTTTTAAAGCT   114
Bolinopsis_infundibulum_SHALLOW       ATTGCTTTTGAACTGGAACTGACTTCTGATCGTCAAGGTAATACTTTTAAAGCT   114
Leucothea_pulchra_SHALLOW             GCTACTTTTGAACTGGATCTGACTTCTGATAAACAAGGTAATACTTTTAAAGCT   114
                                             **    * **    ***  ****    **  * *     *      *
```

Takeaway: Different genes tell different stories! Piezotolerin shows clear adaptation to depth (deep and shallow species have very different sequences). Ancestrin looks more similar across all species, which whose function may remain the same across depth. This shows us that genes can have different evolutionary histories *even within the same organism*. This is why geneticists study many genes because different ones reveal different parts of animals' evolutionary story.

Note: Another possibility to explain the "ancestrin" gene pattern is that the different deep species modified their protein in *different* ways to function in the deep sea! They all independently reached a similar solution to solve the same challenge. This could be an example of **convergent evolution**. Although we didn't cover it in this activity, we have linked a page that briefly covers how convergent evolution works in the "Resources & Links" section on page 9.

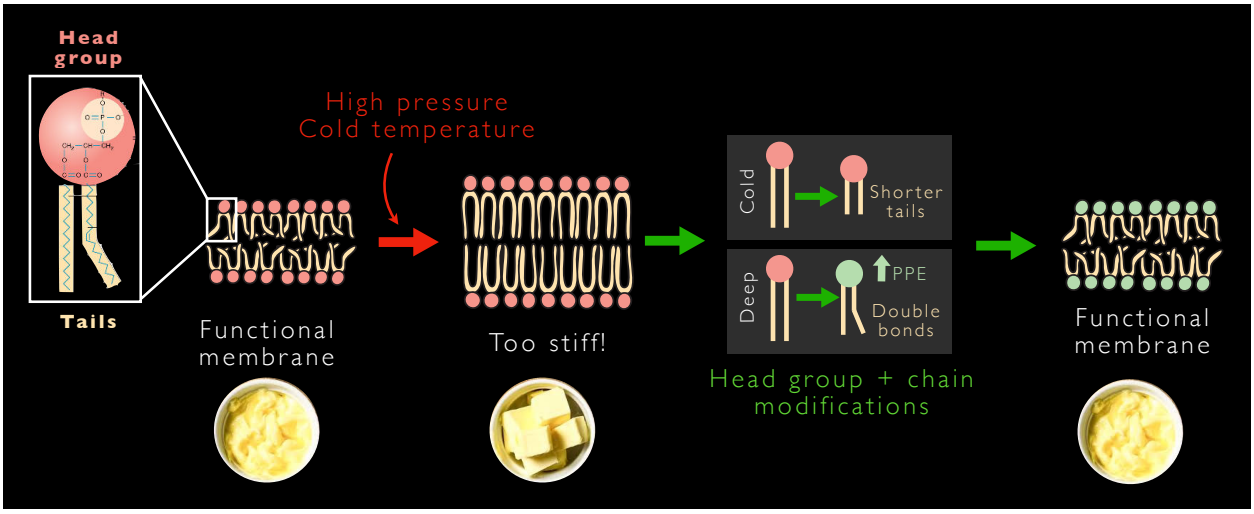
III. BIOCHEMISTRY & PHYSIOLOGY DATA EXPLORATION: Explore how cell membrane traits change with habitat

Every cell is wrapped in a **membrane** that controls what gets in and out of the cell. These membranes need to be flexible enough to let the cell work, but no so fluid that things leak out. Think of it like finding the perfect spreadable butter: too cold, and it is brittle and cracks; too warm and it becomes runny. Cell membranes are made of special fat molecules, each having two parts: a **headgroup**, and **two carbon tails** (made of a chain of carbons). If the tails are straight, they pack tightly together and make a stiff membrane. If the tails are kinked, they pack loosely and make a more flexible membrane.

Cold temperatures and crushing pressures both make membranes stiff and brittle. Animals in the deep sea must deal with both cold temperatures *and* high pressure, so, how do deep-sea ctenophores keep their membranes flexible? They have evolved to modify their cell membranes in response to their environment.

- In cold, shallow seas ctenophores make their carbon tails *shorter* and pack less tightly, so their membranes stay flexible even when cold.

- In the deep sea, ctenophores have carbon tails with more double bonds between carbons, making them more kinked so they don't pack as tightly. They also use more of a special head group called plasmenyl PE (PPE) that helps space out the fat molecules and keeps membranes flexible even under pressure.



In this activity, we will compare how different cell membrane properties in ctenophores change with habitat depth and temperature.

About the dataset

We've simulated cell membrane properties in 65 ctenophore specimens (5 individuals from each of 9 species) in the ***cteno_biochem_physio.csv*** file. Note: membrane data are *simulated* but based on real patterns documented in actual ctenophores (Winnikoff et al., 2021, Winnikoff et al., 2024). Each row is one specimen with these measurements:

Column	What it means	Why it matters
`species`	Latin name (e.g., *Beroe abyssicola*)	Identifies the species
`number`	Which of the 5 animals from that species (1-5)	What individual
`depth_m`	How deep the ctenophore was living (meters)	Deep = high pressure = stiffens membranes
`temp_c`	Water temperature where it lived (°C)	Cold = stiffens membranes
`chain_length_c`	Average number of carbons in the membrane fat molecule tails (15-20)	*Lower = more flexible*
`double_bonds`	Average # of double bonds per tail (~1-3)	*Higher = more flexible*
`ppe_fraction_pct`	Percent of membrane fat molecules made with PPE headgroups (0-100%)	*Higher = more flexible*
`fluidity`	How flexible the membrane actually is (0-10 scale)	*Higher = more flexible*

How to visualize trends

1. Go to CODAP and launch the tool by clicking "Launch CODAP"
2. Click "Create new document"
3. Copy the biochemistry data table from the CSV file
4. In CODAP, click "Tables > New from clipboard" to import the data
5. Click "Graph" to create a new plot
6. Drag variables from the table to the X and Y axes to explore relationships

Try plotting:

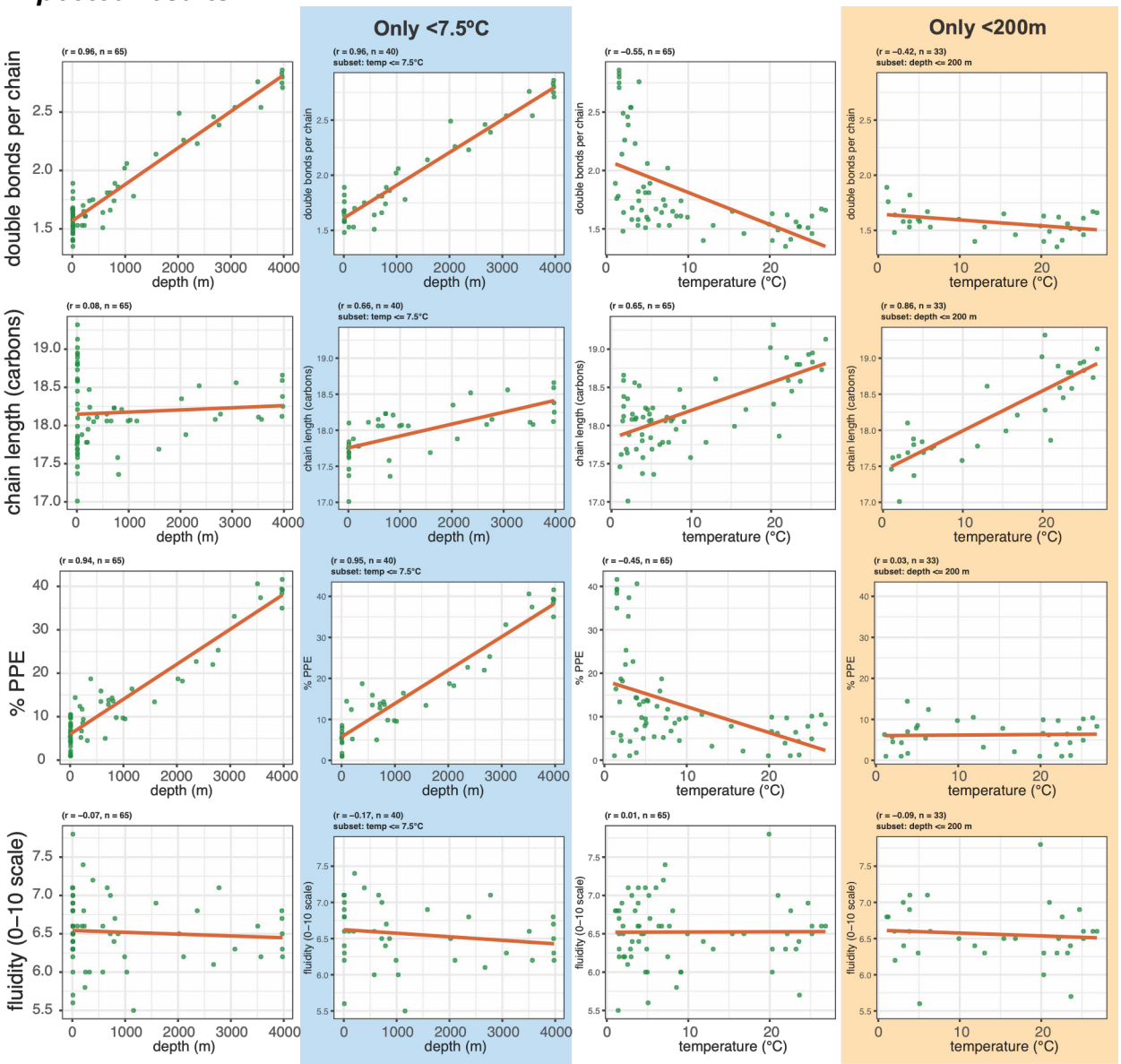
- Depth vs. temperature
- Each trait (double bonds, chain length, PPE, fluidity) (on Y) vs. depth or temperature (on X)

7. To see temperature effects alone (with temp_c on X axis), filter to shallow species only by clicking “Measure > Add Filter Formula > Type “depth_m<200” > Apply”
8. To see depth effects alone (with depth_m on X axis), filter to cold species only by clicking “Measure > Add Filter Formula > Type “temp_c<7.5” > Apply”
9. To see a linear trend line, click “Measure” and check “Least squares line”

Questions to discuss

- What patterns do you see? How does each trait change with depth/temperature?
- How do the trends differ between shallow/cold species and deep/cold species?

Expected results



Takeaway: Ctenophores modify the composition of fatty molecules in their membranes to maintain similar cell membrane flexibility and function under different depths and temperatures.

KEY TAKEAWAYS

Deep sea animals face a problem: survive under conditions that would kill most surface animals. In this activity, we looked at how deep-sea ctenophores can do this in three ways:

- Ecology: We looked at where ctenophores actually live. Some live in the deep sea, while others life in shallow waters.
- Genetics: We compared DNA sequences from deep and shallow species. Different genes tell different stories about how they are related.
- Biochemistry & physiology: We looked at how cell membranes remain flexible in the deep sea. Chemical changes in the fatty molecules in these membranes help maintain flexibility under different extreme pressure and cold temperatures.

RESOURCES & LINKS

Ecology

- Some cool photos of deep-sea animals (courtesy of Steve)
- All about ctenophores!
- Marine Biological Laboratory video about ctenophore swimming
- MBARI pages about abyssal comb jellies and bloody belly comb jellies

Genetics (you can use Clustal Omega for DNA, RNA or protein sequence alignment!)

- Where to find real DNA sequences: NCBI (type a particular group of animals, species, or gene of interest in the search box)
    - If you click on it, each entry contains:
        - The source species
        - The DNA sequence (“Origin”)
        - The protein sequence (“translation”)
        - What paper it was published in (authors, title, journal, etc.)
    - For all published ctenophore sequences on NCBI
        - “Nucleotide” for DNA and RNA sequences, “Protein” for protein sequences
- Where to find real protein sequences: UniProt
    - Search for a specific protein (e.g., “COI ctenophores”)
    - If you want to download these sequences, use the check boxes to select which ones to download > Download > “Fasta (canonical)” > Download
- Evolution and phylogenetics 101 and convergent evolution resources from UC Berkeley (scroll to bottom for teaching resources)
- Convergent evolution article from the London Natural History Museum

Biochemistry/Physiology

- How ctenophores handle the pressure YouTube video
- Cell membrane fluidity overview by Khan Academy

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These materials were prepared by Anik Grearson and Steven Haddock for the EARTH Workshop 2026. They're designed to let teachers explore the types of data we use in deep-sea research and develop their own lesson plans around real scientific questions. This research is supported by the National Science Foundation. If you have any questions, feel free to reach out to us via email at agrearson@mbari.org and haddock@mbari.org.