Adaptation of the fish to depth

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Introduction

Living in the depth claims specific adaptations.

There is a correlation between the light wavelength the fish eye can catch and the depth.

The vast majority of deep-sea fish have only a single visual pigment **(rhodopsin)** with the maximum wavelength around **468–492 nm**, whereas other fish have more than one rhodopsin with different wavelengths.

Deep water fish

Anoplogaster cornuta (Beryciformes)

Malacosteus niger (Stomiiformes)


Synaphobranchus kaupii (Anguilliformes)

Lestrolepis japonica (Aulopiformes)

Goal

To analyse the **rhodopsin gene and protein (rh1)** in the deep water fish and compare the nucleotide and amino acid changes to find out if there are any specific changes that occur in the non-related deep water fishes.

The identical changes in the non-related species are, most probably, connected with the adaptation to the depth.
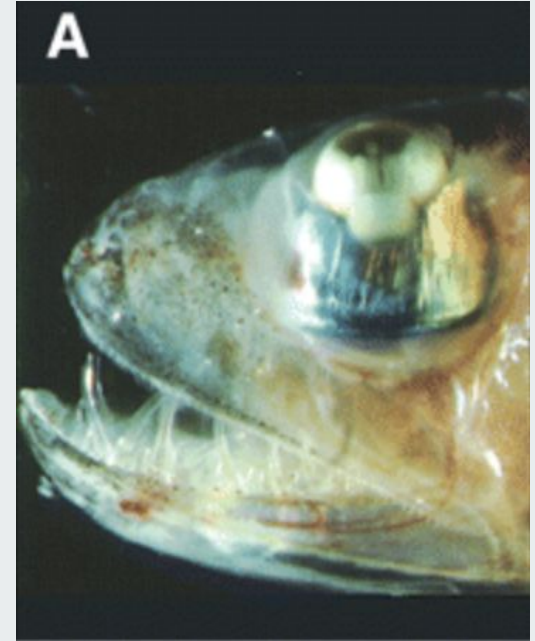
Objectives

1. To find the **rhodopsin gene (rh1)** of the fish species in Genbank, that includes the deep water fishes and shallow water fishes for comparison

2. To download the sequences from Genbank

3. To align the sequences

4. To write and apply the Python script to estimate the percent of the nucleotide and amino acid changes in the alignment

5. To draw conclusions on the most often changes in the deep water fishes dataset sequences.

Searching for the fish species

The species were found from the papers, as well as internet sources

Each species were checked through Genbank to check if the rhodopsin gene was uploaded for it. Other genes uploaded for those species also were recorded.
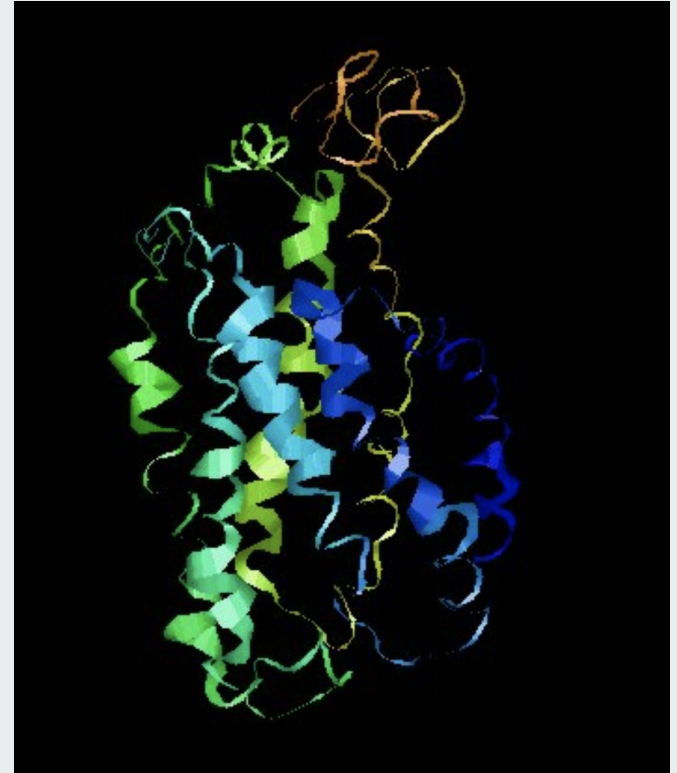
Searching for the fish species

We found the data on **35 species** from seven orders of **deep water fishes**, which live on the depth from up to 3000m to up to 5610m from seven orders

For comparison, we also used **28 species** living in relatively **shallow** (<1000 m) water from the same orders
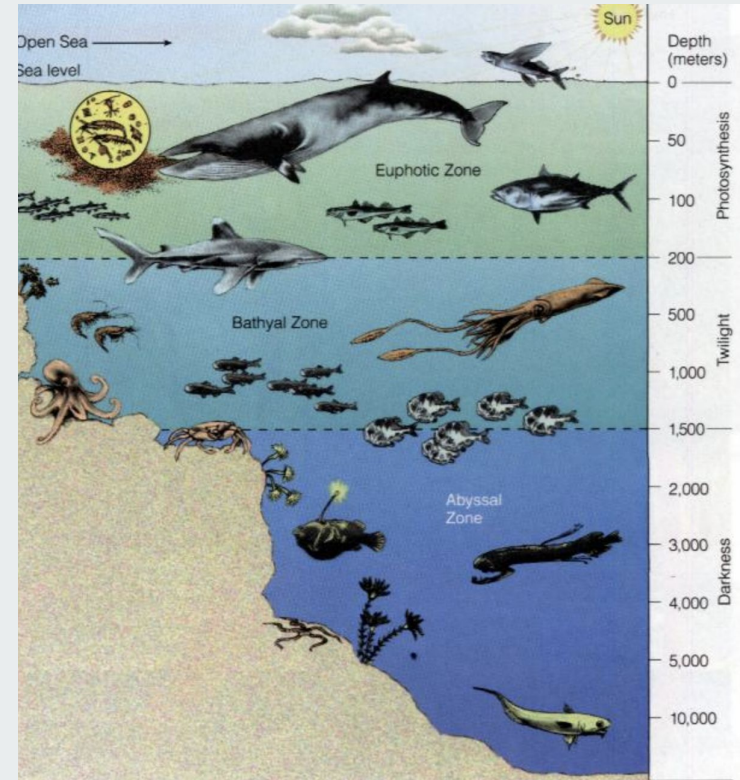
Gene download and alignment

Genes were downloaded using **Batch Entrez** separately for deep water and shallow water fish in .fasta format

The alignments were made using **Geneious** with the **Muscle** algorithm. The gene appeared to be conserved, there were not gaps in the alignments.
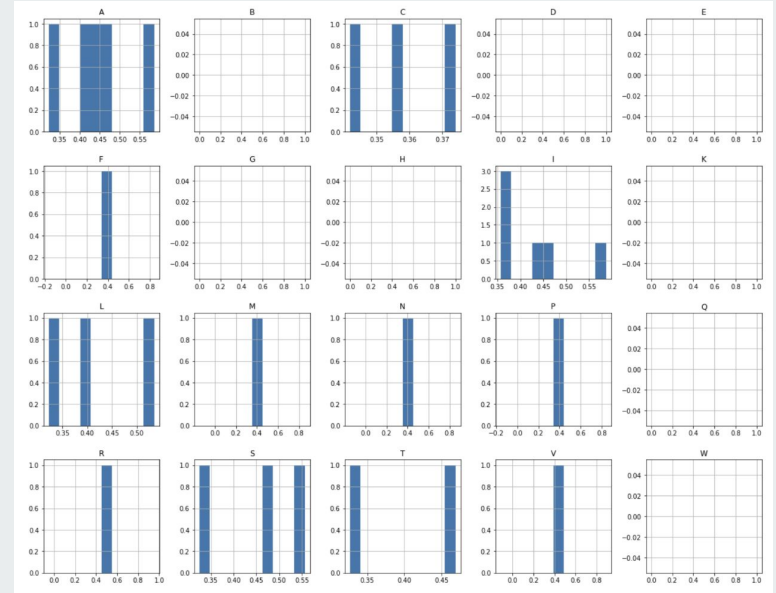

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Gene download and alignment

Alignment of rh1 for deep water fish species

Amino acid frequency counting

$$|P(A)^2 - P(B)^2|$$

P(A) - amino acid frequency in deep sea fish

P(B) - amino acid frequency in shallow fish

Choosing significant changes

The changes with differences of square frequencies >0.3 have been selected

Overall the significant changes have been found in 18 positions

To further sort the changes, we used the following criteria:

- *More changes in the deep water fish dataset in comparison to shallow water dataset*

- *The identical change should occur in >2 fish orders*

Changes potentially connected with living in the depth

Change	Number of changes in deep water dataset	Number of changes in shallow water dataset	Number of families with this changes in deep water dataset	Number of families with this changes in shallow water dataset	Grantham's score
Pro > Ala	22	7	3	1	27
Thr > Ser	19	6	4	2	58
Thr > Leu	22	7	4	3	92
Ala > Ser	15	3	4	1	99
Ile > Val	20	7	6	3	29
Ser > Gly	18	5	4	3	56

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Sources

[Git repo](#)

PILOT FISH
Naucrates ductor