

# Reconstructing evolutionary history



Can I infer the past from present day observations?



**Assumption 1:** Genes are passed on vertically from ancestor to offspring



**Assumption 2:** A gene is not invented twice

## Analysis

In this exercise, we will extract the sequences of a subset of orthologs for two PCD gene families from [our interactive webtool](#). We will align these sequences and calculate a phylogenetic tree. This tree will then help us to better understand the evolutionary history of the gene family

### Task 1: GH27\_QRW17738.1

1. Extract the sequences of GH27\_QRW17738.1 orthologs for the following taxa:

[GH27\\_QRW17738.1\\_taxa.txt](#)

```
Rhizoctonia solani
Aspergillus oryzae
Trichomonas vaginalis
Cordyceps militaris
Bradysia coprophila
Hydra vulgaris
Notolabrus celidotus
Homo sapiens
```

2. **To get the sequences** click on the dot in the columns of the respective species in the GH27\_QRW17738.1 row (use the search boxes on the left to find them!).
  - In the bottom left corner, you can click on “Detailed plot”, opening up a window with more information that also contains the sequence.
  - If no sequence is shown, look at the barcharts on the top of the page. Click on the highest barchart to select one gene from the available options. This will give you the sequence
  - Save the sequences in a [FASTA file](#) (use the species name in the FASTA header!)

3. Align the sequences using [ClustalOmega](#)
4. Inspect the distance tree generated by ClustalOmega. What can you learn?

## Shortcut to Sequence file

[GH27\\_QRW17738.fa](#)

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```

## Task 2: GH28\_QRW23661.1

1. Repeat the analysis using GH28\_QRW23661.1 and the following taxon set:

[GH28\\_QRW23661.1\\_taxa.txt](#)

```
Spodoptera litura
Rhizoctonia solani
Rhagoletis zephyria
Bradysia coprophila (XP_037032572.1)
Protomyces lactucae-debilis
Pyricularia oryzae 70-15
Arcicella rosea (WP_367284634.1)
```

## Shortcut to Sequence file

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```

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```

## Summary and Discussion

- Why are there plant cell wall degrading enzymes in animals?
- Why is GH28 of *Spodoptera litura* identical to a bacterial sequence? What are the consequences given the assumptions stated above?

## Supplementary Data

all\_cellulase\_sequences.fa.gz

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