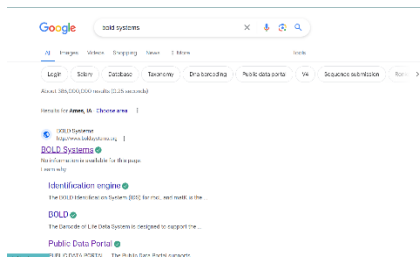


Reproducing Figure 2 to using BOLD system

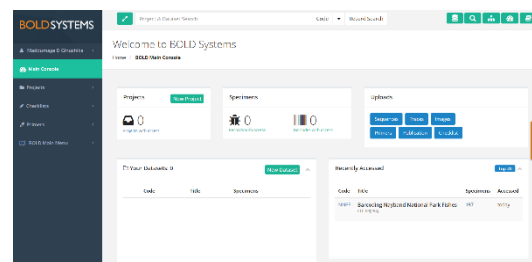
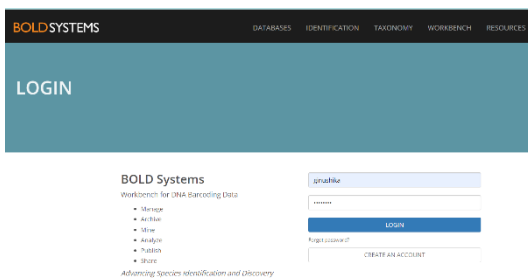
Search and Open BOLD Systems in the browser



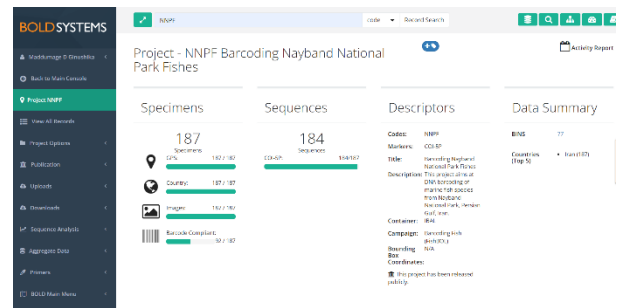
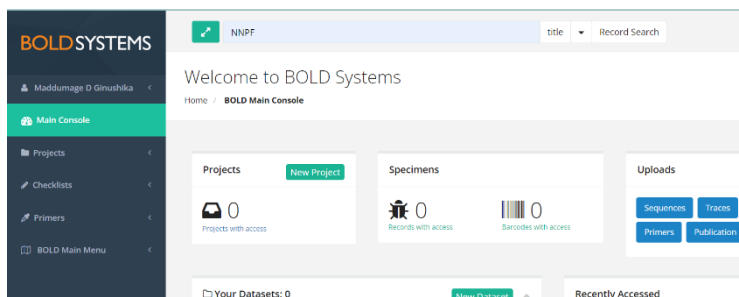
DESIGNED TO SUPPORT THE GENERATION & APPLICATION OF DNA BARCODE DATA

BOLD is a cloud-based data storage and analysis platform developed at the Centre for Biodiversity Genomics in Canada. It consists of four main modules, a data portal, an educational portal, a registry of BINs (putative species), and a data collection and analysis workbench.

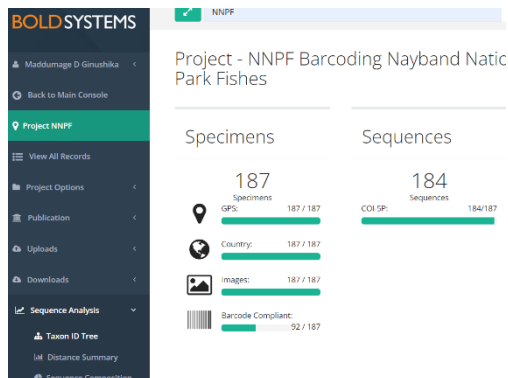
Login to the system or create an account if you are a first-time user



Search for the NNPF project as the code



Then select sequence analysis and select Taxon ID tree



In the pop-up window select parameters;

Tree type – multipage classic

Align sequences – None (use the submitted alignment)

Select preferred labels, in this case Sequence/Process ID, Species and order

Ambiguous base/Gap handling – Pairwise deletion

Codon positions include – 1st 2nd 3rd

Click build tree

Taxon ID Tree - NNPF

The Taxon ID Tree functionality allows for the visualization of phylogenetic trees from selected sequences using the neighbor joining algorithm. The different types of trees that can be generated are Circular Phylogram, Circular Cladogram, Cladogram, Phylogram and Unrooted tree types.

Required fields are marked in red.

Tree Type: Multipage Classic

Sequence Data: Nucleotide

Distance Model: Kimura 2 Parameter

Tree Building Method: Neighbor joining

Marker: COI-5P - Cytochrome Oxidase Subunit 1 5' Region (184)

Align Sequences*: None (use submitted alignment)
* When using MUSCLE or KALIGN, analysis is limited to 500 & 800 sequences respectively.

Select Branch Labels: Voucher

☐ Sample ID ☒ Sequence/Process ID ☐ Field ID ☐ Museum ID
☐ Collection Code ☐ Institution Storing

Matching Data: ☐ Matching specimen photographs and spreadsheet (Only available with Tree Type Multipage Classic)

Apply Filters: Nucleotide Sequence Length ≥ 400 bp
The length filter should be set at a value above 50% the length of the selected marker
☐ Exclude Contaminants
☐ Exclude Records with Stop Codons
☐ Exclude Records Flagged as Misidentifications or Errors

Colorize Tree Based on: Problematic Sequences

Ambiguous Base/Gap Handling: ☒ Pairwise Deletion ☐ Complete Deletion

Minimum Complete Overlap: 0 bp

Codon Positions Included: ☒ 1st ☒ 2nd ☒ 3rd

Result Options: View the results immediately

Build Tree

Analysis ID: DATA-62704839A242METADATA-51C5N756A6B6CUSTOMFIELDS-4595C932D1C-37565325-4B39-41ee-84f4-84240e248807

From the next pop-up window download the tree file and record the analysis description file

Tree Result - NNPF

Tree File:

PDFNewick FormatPostscript

* Note: Postscript files are very large, but are the most editable


Taxonomy Report:

ExcelText

Summary of taxonomic assignments

Data Summary

Analysis description



The Taxon ID Tree functionality allows for the visualization of phylogenetic trees from selected sequences using the neighbor joining algorithm. The different types of trees that can be generated are Circular Phylogram, Circular Cladogram, Cladogram, Phylogram and Unrooted tree types.

Distance Model:

Kimura 2 Parameter

Marker:

COI-5P

Labels:

Process ID, Taxon

Codon:

1, 2, 3

Deletion Method:

Pairwise Deletion

Colourization:

Problematic Sequences

Minimum Complete Columns:

0

Tree Type:

multipage

Alignment:

None (use submitted alignment)

Filters Applied:

> 400bp only

Filter Summary