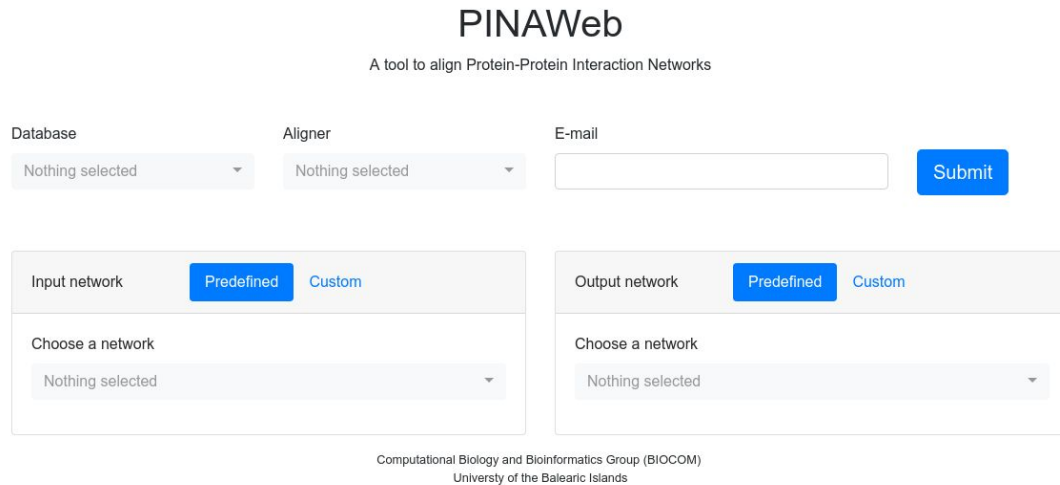


# How To Use PINAWeb

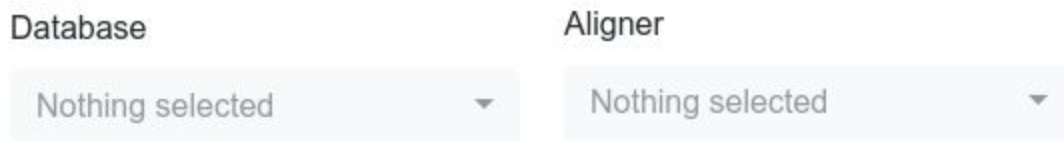
This is what the homepage looks like



The screenshot shows the PINAWeb homepage. At the top, the title "PINAWeb" is centered, with the subtitle "A tool to align Protein-Protein Interaction Networks" below it. The main form area contains three input fields: "Database" and "Aligner", both with dropdown menus showing "Nothing selected", and an "E-mail" text input field. A blue "Submit" button is to the right of the email field. Below these are two identical sections for "Input network" and "Output network". Each section has a "Predefined" button (highlighted in blue) and a "Custom" button. Under each button is a dropdown menu labeled "Choose a network" with "Nothing selected" as the current selection. At the bottom, the text "Computational Biology and Bioinformatics Group (BIOCOM) University of the Balearic Islands" is centered.

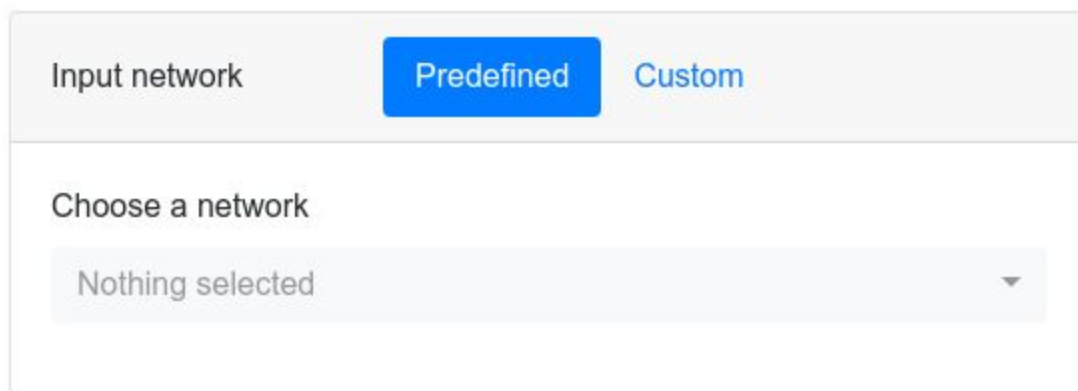
This home page has five sections:

- A section dedicated to select the database and another one to select the aligner



This block shows a close-up of the "Database" and "Aligner" selection fields. Both are dropdown menus with the text "Nothing selected" and a downward arrow icon.

- A section dedicated to select the input network



This block shows a close-up of the "Input network" section. It features a "Predefined" button (highlighted in blue) and a "Custom" button. Below the buttons is a dropdown menu labeled "Choose a network" with "Nothing selected" as the current selection.

- A section dedicated to select the output network

Output network

Predefined

Custom

Choose a network

Nothing selected

- You write your mail here and PINAWeb sends you the results

E-mail

Submit

## How to compute an alignment

1. Choose a database.

Database

StringDB

StringDB

2. Choose one or more aligners.

#### Aligner

Aligner

AlignNet, PINALOG

AlignNet

HubAlign

L-GRAAL

PINALOG

SPINAL

✓

✓

3. In case that you want to use a predefined network, write the first letters of the species.
  - (StringDB-specific) Then, you must choose the edge types (score types) from the full String DB network. You can set a threshold for each score (by default it is zero). An edge is included when at least one of your chosen score types is above the corresponding threshold.

Input network

Predefined

Custom

Choose a network

Nothing selected

Edge selection (2)

Choose which edge types should be considered. Additionally, you can specify thresholds for each edge score so that only edges with any of the chosen scores equal or above the given thresholds will be considered.

(All scores range from 0 to 1000.)

☒ Neighborhood score

500

☐ Neighborhood score from other species

☒ Fusion score

200

4. If you want to align your own network, click on custom button and upload the network.

Input network


Predefined


Custom

Upload a network

Choose File

No file chosen



Custom networks 

To introduce your own network upload a text file with two columns of proteins (separated by a tab character) such that each row will be an edge. Protein IDs must match those used for the selected database.

- [Generic example](#)
- [StringDB example](#)

Close

5. To select the output network proceed in the same way as for the input network.
6. Finally, write your email address and click submit.