LadderpathCalculator Manual

http://8.138.85.255/#/

Input

Accepts two formats:
One is the Python list of strings format, such as:

```
['ABDEDBED', 'ABDED', 'ABDABD', 'CAB', 'ED']
```

The other is fasta format, such as:

```
>Chrysosplenium_lanuginosum
TTGTAACCTGCCTAGCAGTGCAACTCGTGAACATGTATATAAAATGTG
>S._epiphylla_123
TCGCCGCTTGCTTAAAGCAAAACAACTTGTGAACATGTAATCGCAACT
```

Both formats of data can be directly entered into the input box or uploaded via a file (use Upload file).

The total length of the data can be on the order of 10,000 and can be quickly calculated, for example, within 5 minutes.

Results Display

Left Side: Laddergraph

Laddergraph is a type of diagram that represents the hierarchical and nested relationship between repeated substructures (for details, please refer to the references at the end [1,2,3]).
The node pointed to by the arrow represents the parent node, which contains the substructure represented by the node at the other end of the arrow, such as AB (child node) pointing to ABC (parent node).

- Users can drag nodes to adjust their positions (this function is still under development)
- Users can color nodes: by coloring any node, all its parent nodes can be colored the same color (select the color you want under Change ladderon color)

- Users can download all data (Download all data and figures): this will download all ladderpath-related files obtained from the calculation

Further down is the list of Ladderons: displaying all ladderons, their IDs corresponding to the labels in the Laddergraph. On the right are calculated metrics: Ladderpath-index, Order-index, Size-index, and the *partially ordered multiset* representing the ladderpath.

Right Side: Dendrogram (Phylogenetic tree)

They are used to analyze the distances between input objects (species, molecules, gene sequences, protein sequences, etc.)

- We provide two ways to calculate distances:
  - One is `laddergraph_diff` : This is a distance defined based on the structure of the laddergraph, essentially the sum of the lengths from the individual roots to the leaves of two objects minus their shared length in the laddergraph (this will be specifically explained in our subsequent articles). We recommend always using this type of distance;
  - The other is `ladderon_basis` : This is a distance calculated using ladderons as bases. We are currently experimenting with this (thus not as well-defined as the former), so it is not recommended for use at the moment.
- The colors of the species in the phylogenetic tree will change according to the color changes in the laddergraph on the left, making it easier to identify which species have common modules.
- Users can download the color-adjusted phylogenetic tree (`Download this figure`).

At the bottom right is the minimum spanning tree calculated based on the distance selected by the user above, which can also represent the closeness or distance between species.