

HERITABILITY CALCULATOR

(INPUT SPECIFICATIONS)

This document specifies the needed user input for the heritability calculator program.

It is important to provide the correct data in order for the core algorithm to work properly.

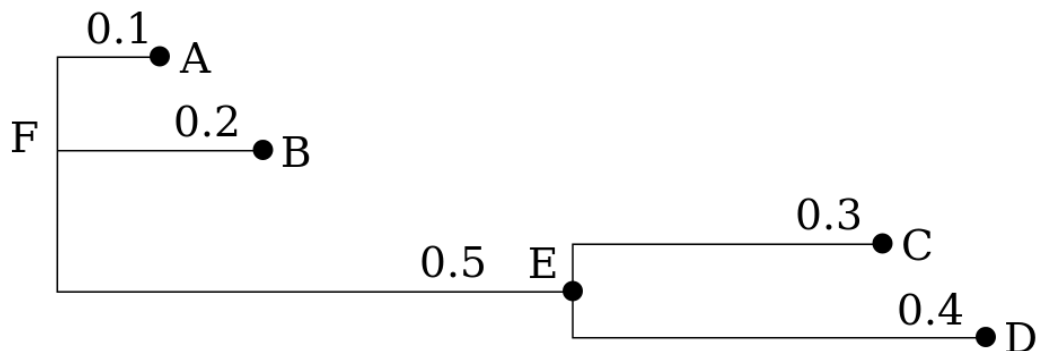
Using this calculator in order to calculate Heritability, you must provide the program with the following input:

1. Newick Formatted Phylogenetic Tree:

Newick tree format is a way of representing graph-theoretical trees with edge lengths using parentheses and commas.

- *Input format:* One text file (.txt extension).
- *Content:* A string representation of a tree using Newick format.

For example, the following tree:



Will be represented (using newick format with distances and leaf names) as: **(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);**

For more information regarding newick format:

[Http://evolution.genetics.washington.edu/phylip/newicktree.html](http://evolution.genetics.washington.edu/phylip/newicktree.html)

2. The following data set:

- Emission matrix
 - Distance matrix
 - Observed traits
 - Order of traits notation
-
- *Input format:* Json file (.json)
 - *Content:* See example ahead.

The algorithm uses Emission Matrix in order to calculate transition rates of phenotypic values. It is also uses a Distance Matrix that is actually a description of the biological distances of phenotypic values between each other. Observed traits are also being given as they are representing the phenotypic values of the leaf nodes. The algorithm also needs to have a knowledge of the order the phenotypic values are stored in the matrices.

The following is an example of a .json file content, describing the data above for a researched phenotype that is Eye Color of species:

```
{
  "DistanceMatrix": [
    [
      0,
      0.2,
      0.7
    ],
    [
      0.2,
      0,
      0.5
    ],
    [
      0.7,
      0.5,
      0
    ]
  ],
  "EmissionMatrix": [
    [
      -1,
      0.75,
      0.25
    ],
    [
      0.5,
      -1,
      0.5
    ],
    [
      0.6,
      0.4,
      -1
    ]
  ],
  "ObservedTraits": [
    {
```

```

        "Name": "A",
        "Value": "red"
    },
    {
        "Name": "B",
        "Value": "red"
    },
    {
        "Name": "C",
        "Value": "green"
    },
    {
        "Name": "D",
        "Value": "red"
    },
    {
        "Name": "E",
        "Value": "blue"
    },
    {
        "Name": "F",
        "Value": "red"
    },
    {
        "Name": "G",
        "Value": "blue"
    },
    {
        "Name": "B",
        "Value": "red"
    },
    {
        "Name": "C",
        "Value": "green"
    },
    {
        "Name": "D",
        "Value": "red"
    },
    {
        "Name": "E",
        "Value": "blue"
    },
    {
        "Name": "F",
        "Value": "red"
    },
    {
        "Name": "G",
        "Value": "blue"
    }
    ],
    "Traits": [
        "red", "green", "blue"
    ]
}

```

This is an example of 3 valued phenotypic trait matrices format:

Distances:

	Val1	Val2	Val3
Val1	θ	α	β
Val2	α	θ	γ
Val3	β	γ	θ

Emission:

	Val1	Val2	Val3
Val1	$-(\alpha+\beta)$	α	β
Val2	ε	$-(\varepsilon+\delta)$	δ
Val3	λ	μ	$-(\lambda+\mu)$

For more information regarding Json format: <https://www.json.org>