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The program HubAlign finds a global alignment between a pair of networks. Given two networks with N and M nodes, it returns min(N,M) pairs, which each pair indicates two aligned nodes from two networks.

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How to run HubAlign:

- Suppose two input networks are named 'Test1.tab' and 'Test2.tab', which are tab separated files where each line contains an interaction. Number of nodes in the first network must be smaller than the Number of nodes in the second Network.
- Run the HubAlign. Here is a sample invocation:

```
./HubAlign Test1.tab Test2.tab -l 0.1 -a 0.7 -d 10 -b similarityFile.txt
```

The options are as follows:

-l : The parameter λ that controls the importance of the edge weight relative to the node weight. Usually $\lambda=0.1$ yields a biologically more meaningful alignment. Default value is equal to 0.1.

-a : the parameter α that controls the contribution of sequence information relative to topological similarity. Default value for this parameter is equal to 0.7. $\alpha=1$ implies that only topological information is used.

-d : the parameter d that controls the number of nodes removed from network in the process of making the skeleton.

-b : similarity file that includes the sequence information of proteins. Here, we used Blast bitscores. The similarity file is a tab-separated file with three columns where each line is in form:

<id1>	<id2>	<bitscore>
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<bitscore> is the bitscore between two proteins <id1> and <id2> . You don't need this file if $\alpha=1$. Here is a sample invocation when $\alpha=1$:

```
./HubAlign Test1.tab Test2.tab -l 0.1 -a 1
```

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Analyze the output

For two input networks 'Test1.tab' and 'Test2.tab', HubAlign produces two output files:

1. Test1-Test2.alignment
2. Test1-Test2.eval

File '*.alignment' is a tab separated file in which each line indicates the matching pair of nodes from two networks. File '*.eval' includes EC, S3 and LCCS (both node and edge) of the alignment.

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If you have any questions or if you have found any problem in the software, please email Hashemifar@ttic.edu. For the latest updates, please visit <http://ttic.uchicago.edu/~hashemifar/>