Because PISwap is implemented as a python library, we need to install python and networkx package to run PISwap.

1. Install python2.6 (http://www.python.org or http://www.activestate.com/activepython/downloads)

2. Install networkX (http://networkx.github.io/download.html) and numpy (http://www.numpy.org).

3. Copy PSB2009_3opt_2.py and matching.py to the "Lib" folder of python.

4. Write a python script to call and run PISwap as follow:

```
from __future__ import print_function
import PSB2009_3opt_2 as psb09
import matching as match

G = psb09.getGraph("network1.tab") #input network1
G2 = psb09.getGraph("network2.tab")#input network2
GS =
psb09.graphScores("pairwise_sequence_similarity_of_network1_and_2.evals")
#input pairwise sequence similarity of network1 and 2.

M0 = match.max_weight_matching(GS) #run hungorian algorithm to produce initial
alignment

(S, M) = psb09.processOnce(G, G2, GS, M0, 0.6, 200) #run PISwap

#output the alignment result
F = open("match_output.txt","w")
for node in M:
    print(node+" "+M[node], file = F)
F.close()
```

5. Network files:
You'll need A.tab and B.tab , tab-separated files
where each line contains an interaction. For example, the first 5 lines of
A.tab are:

```
====== BEGIN ========
INTERACTOR_A INTERACTOR_B
a0 a1
a0 a2
a0 a3
a0 a4
====== END ========
```

Columns are separated by tabs. The first line is a header line of the

form as shown above (the '_A' and '_B' in the header has nothing to do with species names). All other lines describe an interaction, one perline.

6. Sequence similarity file:

The first 5 lines of the A-B.evals file are:

```
====== BEGIN ========
a0      b0      1
a1      b1      1
a2      b2      1
a3      b3      1
a4      b4      1
====== END ========
```

Each line is of the form:
<id1> <id2> <Bit-Score>