Repo: https://github.com/waynebhayes/BLANT

git clone https://github.com/waynebhayes/BLANT.git

To start with one seed pair:

First, load module:
> load module python/3.7.1

Then run with options:
> python3.7 dijkstra/run_recursive_seed.py -g1 [graph1] -g2 [graph2] -g1s [seed1] -g2s [seed2] -sn [seednum that chooses which seed to start with]
-s [sim file] -pk [pickle file for sim file]
-d [delta for choosing a “worse” pair] -ed [lower edge density bound] -ec1 [lower ec1 bound] -sb [similarity lower bound]
-t [timestop that stop the program after specified time] -at [alignstop that stop the program after a specified number of alignments generated]

example:
python3.7 dijkstra/run_recursive_seed.py -g1 /home/sana/networks/MMusculus-3.5.174.el -g2 /home/sana/networks/HSapiens-3.5.174.el -g1s /home/hanweny/BLANT/alignment_seeds_unambig/MMusculus_8_25_150000_uDMAX_e0.3.txt -g2s /home/hanweny/BLANT/alignment_seeds_unambig/HSapiens_8_25_150000_uDMAX_e0.3.txt -g1sline 1985 -g2sline 3264 -s /home/sana/sims/Importance/MMusculus-3.5.174--HSapiens-3.5.174.sim.xz -d 0.0 -ec1 1.0 -ec2 1.0 -ed 0.3 -sb 1.0 -sn 4999 -pk /extra/wayne0/preserve/utsavj/SANA/dijkstra/alignments/pickles/MMusculus-3.5.174HSapiens-3.5.174.sim.pickle

To run many seeds with sge:

example:
>load module sge
>python3.7 /extra/wayne0/preserve/utsavj/SANA/dijkstra/run_recursive_sge.py -g1 /home/sana/networks/MMusculus-3.5.174.el -g2 /home/sana/networks/HSapiens-3.5.174.el -g1s /home/hanweny/BLANT/alignment_seeds_unambig/MMusculus_8_25_150000_uDMAX_e0.3.txt -g2s /home/hanweny/BLANT/alignment_seeds_unambig/HSapiens_8_25_150000_uDMAX_e0.3.txt -s /home/sana/sims/Importance/MMusculus-3.5.174--HSapiens-3.5.174.sim.xz -d 0.0 -ec1 1.0 -ec2 1.0 -ed 0.3 -sb 1.0 -pk /extra/wayne0/preserve/utsavj/SANA/dijkstra/alignments/pickles/MMusculus-3.5.174HSapiens-3.5.174.sim.pickle