How to run ASFinder program

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Please do not redistribute the program withou getting permission from Dr. Min

Note: for big genomes and large number of ESTs, it may take several days to generate the final output.

ASFinder standalone program contains several programs for use.

1) users need to install SIM4 program (here I have included a pre-compiled sim4 in the package for Linux. However, if it does not work properly, please got to the following site to get source code for installing on your system:
http://globin.bx.psu.edu/html/docs/sim4.html).
2) using a text editor to revise ASFinder.pl program - line 6 - replace the sim4 path with SIM4 path on your system. save.
3) run ASFinder in the directory where you have all the programs, using the following command: perl ./ASFinder.pl genome_input est_input identity len.
      identity: 85 - 97;
      len: aligned length (80 or above)
4) three directories will be created -
      /tmp/: contains splited genome files.
      /out/: alignment files and exon files.
      /save/: this is an important directory containing 4 final output files -
            AS_clusters.txt - all potential AS clusters;
            AS.gtf - AS pairs in gtf format - this file can be used to upload into astalavista server (http://genome.crg.es/astalavista/)
                  for AS events analysis.
            est2genome_align.txt: all alignment information;
            est2genome.gtf: all aligned data in gtf format.
5) AS.gtf can be uploaded to astalavista server, then download landscape.gtf file (for more informaiton: please go to http://proteomics.ysu.edu/tools/docs/ASFinder_faq.html .
6) Run "gtf2events.pl" to get a summary file (summary.events) and conver codes to events
      - usage: gtf2events.pl landscape.gtf output.tab

After each run, please move (or remove all directory includign tmp, out, save) to other locations for next run.

Questions - contact Dr. Min (xmin@ysu.edu).