

Using reciprocal best hit pack

Two tarballs are needed:

- 1) the database : refseq_genomes.tar.gz
- 2) the scripts for doing the search: rec_best_hit_pack.tar.gz

Other dependencies are muscle, blastall and fastacmd, the last two from the blast package.

To use it, everything needs to be unpacked and untarred, and afa_stats in rec_best_hit_pack directory compiled with

```
gcc -o afa_stats afa_stats.c
```

Next, the paths at the top of reciprocal_best_blast.pl and profile_almt.pl need to be changed to reflect your local setting.

In the work directory, type

```
$PATH_TO_REC_BEST/reciprocal_best_blast.pl <path_to_qry_seq> <name_of_species>
```

The query sequence must be in fasta format, and the name of the species it belongs to has to be one of the names in refseq_genomes directory. Typically, you will probably need to type "Homo_sapiens" as the <name_of_species> above.