

ANItools version 2.0

Name

ANItools – The bacterial species definition tool by calculating Average nucleotide identify (ANI) of pairs of genomes

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SYNOPSIS

```
perl Directory_ANItools/ANI_one_to_matrix_SpecialGene.pl -I  
<Query Genome(fasta format)> -O <Outputfile directory> -Genus  
<Genus Name> -Tag <Tag Name>
```

Or

```
perl Directory_ANItools/ANI_one_to_matrix_SpecialGene.pl -I  
<Query Genome(fasta format)> -O <Outputfile directory> -Species
```

<Species Name> -Tag <Tag Name>

Note: The Full path of Inputfile and Outputfile is necessary.

For example:

```
perl ANI_one_to_matrix_SpecialGene.pl -I genome.fa -O ./ -Genus  
Streptococcus -Tag 05ZYH33
```

or

```
perl ANI_one_to_matrix_SpecialGene.pl -I genome.fa -O ./ -Species  
Streptococcus_suis -Tag 05ZYH33
```

DESCRIPTION

ANIttools 1.0 is a tool for users to calculate ANI of two Bacteria genomes. The update version 2.0 support users to calculate ANI for a genome to a list of strains in a genus or a species. ANIttools version 2.0 only works in Linux system. ActivePerl and local blast are necessary for ANIttools. If you already installed these programs, you could directly install and use ANIttools.

COMMANDS AND OPTIONS

“Config.txt” is the file for users to set up parameters before first time using ANIttools.

Options:

ANIttools: Directory of program ANIttools .

Formatdb: Directory of a software tool to format protein or nucleotide databases for BLAST.

Blast: Directory of blast. The download link for blast is <ftp://ftp.ncbi.nlm.nih.gov/blast/executables/release/2.2.23/>.

INSTALLATION

This version could be only installed in Linux system. ActivePerl, and local blast are necessary for ANItools. If you already installed these programs, you could skip to the next step.

(1) Download Link:

Active Perl: <http://www.activestate.com/activeperl/downloads>

Local blast:

<ftp://ftp.ncbi.nlm.nih.gov/blast/executables/release/2.2.23/>

(2) install local blast

```
"gunzip blast-2.2.18-ia32-linux.tar.gz"
```

```
"tar -xpf blast-2.2.18-ia32-linux.tar"
```

(3) Downloading Bacterial Genome data from NCBI

Bacterial Genome Database:

<ftp://ftp.ncbi.nih.gov/genomes/Bacteria/>

(4) Install ANItools

Firstly, download ANItools.

Secondly, "tar -zxvf ANItools.tar.gz".

Then, Config.txt is the file for users to set up parameters before first

time using ANItools.

USAGE

(1) If users want to get ANI values of their query genome comparing with strains in a genus,

```
perl Directory_ANItools/ANI_one_to_matrix_SpecialGene.pl -I  
<Query Genome(fasta format)> -O <Outputfile directory> -Genus  
<Genus Name> -Tag <Tag Name>
```

“Query Genomes should be fasta file.

(2) If users want to get ANI values of their query genome comparing with strains in a genus,

```
perl Directory_ANItools/ANI_one_to_matrix_SpecialGene.pl -I  
<Query Genome(fasta format)> -O <Outputfile directory> -Species  
<Species Name> -Tag <Tag Name>
```

“Query Genomes should be fasta file.

(3) Output files

Output results will be shown in the screen and also saved in the file directory of “Outputdirectory”.

SEE ALSO

ANItools web site: <http://ani.bioinfo-icdc.org> or

<http://ani.mypathogen.cn/>

AUTHOR

Wen Zhang in the Bioinformatic Department of ICDC, China CDC wrote the key source codes.

LICENSE AND CITATION

If you use the ANItools, please cite the following papers:

Wen Z, Pengcheng D, Han Z, et al. Whole-genome sequence comparison as a method for improving bacterial species definition.[J]. Journal of General & Applied Microbiology, 2014, 60(2):75-78.

HISTORY

ANItools version 2.0 was released in December 2015.

ANItools version 1.0 was firstly released in December 2011.