

ANIttools web Manual

Name

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

CONTENTS

DESCRIPTION

USAGE

SEE ALSO

AUTHOR

LICENSE AND CITATION

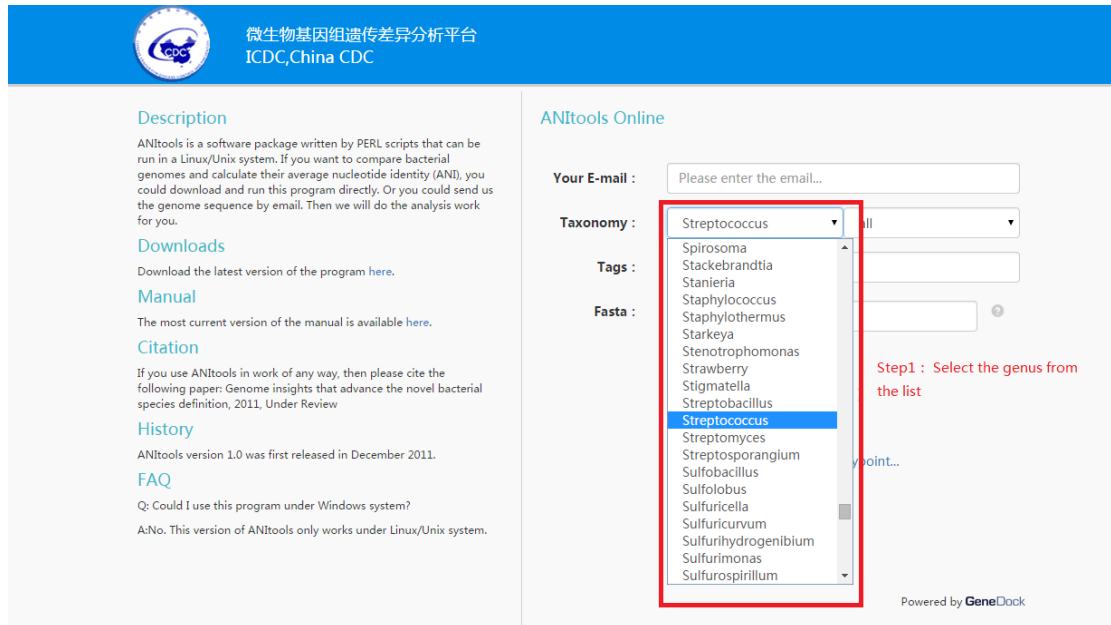
HISTORY

DESCRIPTION

The web version of ANIttools (<http://ANI.bioinfo-icdc.org>), which helps users directly get ANI values from online sources. A database covering ANI values of any two strains in a genus was also included (2773 strains, 1487 species and 668 genera). Importantly, ANIttools web can automatically run genome comparison between the input genomic sequence and data sequences (Genus and Species levels), and generate a graphical report for ANI calculation results.

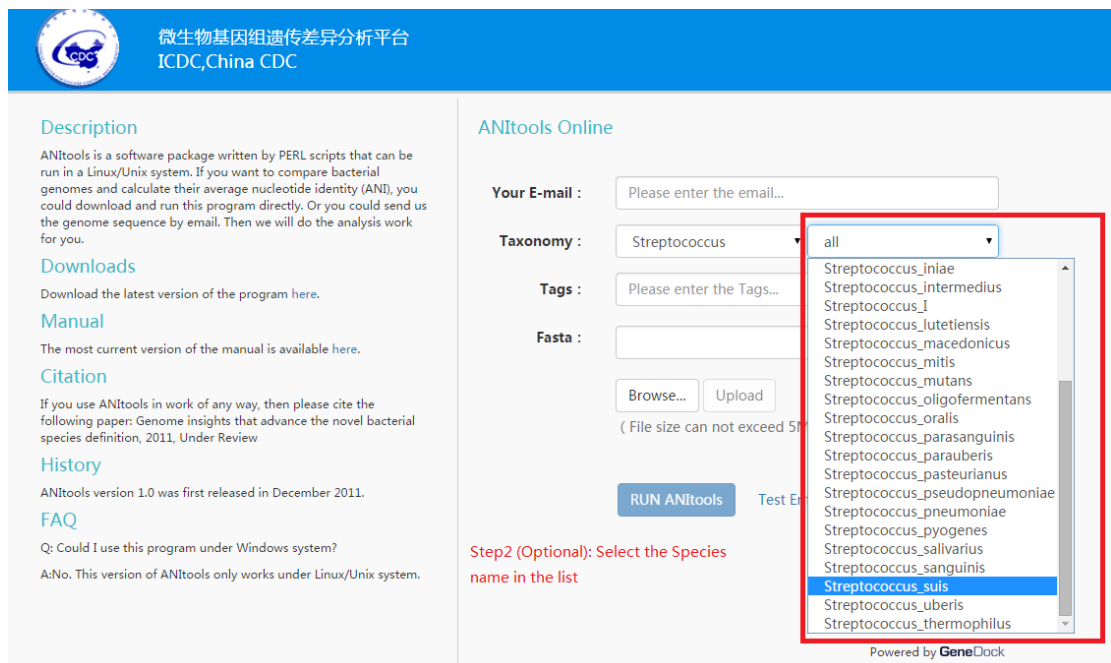
USAGE

Step 1: Select the Genus Name from the list




The screenshot shows the ANIttools Online web interface. The header includes the logo of the ICDC, China CDC and the text "微生物基因组遗传差异分析平台 ICDC,China CDC". The main content area is divided into two columns. The left column contains links for "Description", "Downloads", "Manual", "Citation", and "History". The right column, titled "ANIttools Online", contains a form with fields for "Your E-mail", "Taxonomy", "Tags", and "Fasta". The "Taxonomy" dropdown menu is open, showing a list of bacterial genera. "Streptococcus" is highlighted in blue. A red box highlights the dropdown menu, and a red text label "Step1 : Select the genus from the list" points to it. The interface is powered by GeneDock.

Step 2 (Optional): Select the Species Name from the list



The screenshot shows the ANIttools Online web interface. The header is the same as in Step 1. The "Taxonomy" dropdown menu is now set to "Streptococcus". The "Tags" dropdown menu is open, showing a list of species names under the genus Streptococcus. "Streptococcus_suis" is highlighted in blue. A red box highlights the dropdown menu, and a red text label "Step2 (Optional): Select the Species name in the list" points to it. The interface is powered by GeneDock.

Step 3: Fill in the name of the query sequence (for example, test, Sequence, 05ZYH33 and so on).

微生物基因组遗传差异分析平台
ICDC, China CDC

Description

ANIttools is a software package written by PERL scripts that can be run in a Linux/Unix system. If you want to compare bacterial genomes and calculate their average nucleotide identity (ANI), you could download and run this program directly. Or you could send us the genome sequence by email. Then we will do the analysis work for you.

Downloads

Download the latest version of the program [here](#).

Manual

The most current version of the manual is available [here](#).

Citation

If you use ANIttools in work of any way, then please cite the following paper: Genome insights that advance the novel bacterial species definition, 2011, Under Review

History

ANIttools version 1.0 was first released in December 2011.

FAQ

Q: Could I use this program under Windows system?
A:No. This version of ANIttools only works under Linux/Unix system.

ANIttools Online

Your E-mail :

Taxonomy : Streptococcus Streptococcus_suis

Tags :

Fasta :

(File size can not exceed 5MB)

Step 3: Fill in the name of query sequence (for example, test, Seqname, 05ZYH33 and so on).

Step 4: Prepare the query sequence in Fasta Format, just like that

```
>05ZYH33
atgaaccaagaacaacttttttggcaacgatttattgaattggcaaggttaaattttaagccatctatttatgattttaa
tgtcgtgatgcaaaattactcgggaatcaaccagcaagttgccaataatcttcttaaactcgtccatttaaaaaagatttct
gggaaaaaaactcgaagagttaattgattgcccgtagttttgaaagctacggagagcctcttaccatccaatatcaattt
acagaggatgaaacaggagattaggaatactacaaaacacaagaagttcaatagttcaccagggtacagacacttgagccggc
tactcctcaagaaaacttttaaacgggttcattctgatataaaaaaccagtacacctttgctaattttgtacaaggagaca
ataatcactgggcaaagggtgcagcttttagctgtatctgataacctaggtgagctctacaatccattattcatttttggg
ggctctggtcttggaaaaactcatattttaaatgcgattggaaataaggttctagccgataatccccaggcaaggataaa
atatgtctcatcggaaaacttcatcaatgaatttttagaacaacctcgtctcaatgatattgaaagtttcaaaaaaacct
atcgcaatctggacttacttaattgatgacatctcgtctcgttaataaagcaacaacacaggaagaatttttccat
acttttaatgctctcatgaaaaaaataagcagattgtactcacaagcgaccgtaatccccgatcaacttagacaatttgga
agaaagactagtaaacagcttcaaatgggggttaaacagtgaaatcactccacctgattttgaaacaggtatcgcaattt
tacgtaaacagtgcgagaaacctgccttacaactttacaatgagacgctatcctatctagctgggcaatttgattcgaa
gtacgtgacctgaaaggtgccttaaaagatataccatttgatagccactatgctgcaactgtctgagataagtgtcgaggt
tgctgctgaggctattcgatcaagaaaaaaaacaaatccacaaaacatggttatctctatggagaaaatccaaaccgaag
tgggaaatcttaccggtgtcagcttgaagaattaaaaggttctaagcgtggtcaacatctcgttcacgcgagacaaggt
gctatggttttagcacgtaaatgacagacaattcccttccaaaaattgggaaagaatttggtaatcgagaccatacaac
cgttatgcatgcatacaataaaaaactctcctcttgatgatgagaatttagaaaatagagattaccagtataaaaa
ataaactcgtttaacctgtgataacttttttaaaaaactcgtttttccacaagttgtgaacaagtttaattccgcag
ttttattggtcttccatcacttttccacagaatacacagagactactattactattaaccttatagataataaataaagg
aaaatccatgattcaattttctattaataaaaaataatattctacaagcacttagtattacttaaacgggcaatcagtaca
aaaatgctattccaattcttccaacagtaaaaaattacagtaactagtgaaggaatcactttaaactgggttcaaatggaca
atctcgatagaacatttttctattcaagatgaaaatgcagggcttttgatcagttctccagggttccattctcttaga
agctggtttctttattaatgtcgtatccagtatgcccgatttggctccttgacttcaatgaaattgaacaaaagcaaatcg
tttgacaagtggttaagtctgaaatcacattaagggaaaaagaagcagatcctcgtttacaggaagttccaact
tcaaaaccattggtgttagaaaccaaagtattaaaacaaacaaatgaacagcatttgagcttctacacaagaag
tcgtcctattcttaccgggtgtcattttgttttaacagaaaaataaaaactgtaaaactgttgcaacagattcacaccgta
tgagccaacggaaattggctccttgatccctctggtgatgttttaattgtgtcattccaagtcggttctcctcgtgaatt
actgcagtttttacagatgatattgaaacagtagaagttcttctttcaataatcaaatcctttttagaagcgagcatt
tagcttctatacacgcttattagaaggtacctaccctgataccgacgcttaattccaactgagtttaaaacaactgcaa
tttttgatactgcaaatctcgtcactcgtatggagcgtgctcgtcttcttcaaatgcaaccacaaaatgggtacagtaaaa
ctagaaattgctaataatggttatcggctcagtaaatctccagaagttggacgtgtgaaatgaggaatttagatactgt
agaagatcaggtgaagatttagtaatacagcttcaacccaacttacttgatagaagcattgaaagccacaactagtgaac
aagt.gaaatttagcttctctcctcctccatctacattgaatttcaaatgaaagggaaagattttattccaattt
```

Step 5: Click “Browse” button to select the query sequence in fasta

format (*.fasta or *.fa)

run in a Linux/Unix system. If you want to compare bacterial genomes and calculate their average nucleotide identity (ANI), you could download and run this program directly. Or you could send us the genome sequence by email. Then we will do the analysis work for you.

Downloads
Download the latest version of the program [here](#).

Manual
The most current version of the manual is available [here](#).

Citation
If you use ANIttools in work of any way, then please cite the following paper: Genome insights that advance the novel bacterial species definition, 2011, Under Review

History
ANIttools version 1.0 was first released in December 2011.

FAQ
Q: Could I use this program under Windows system?
A: No. This version of ANIttools only works under Linux/Unix system.

Your E-mail :

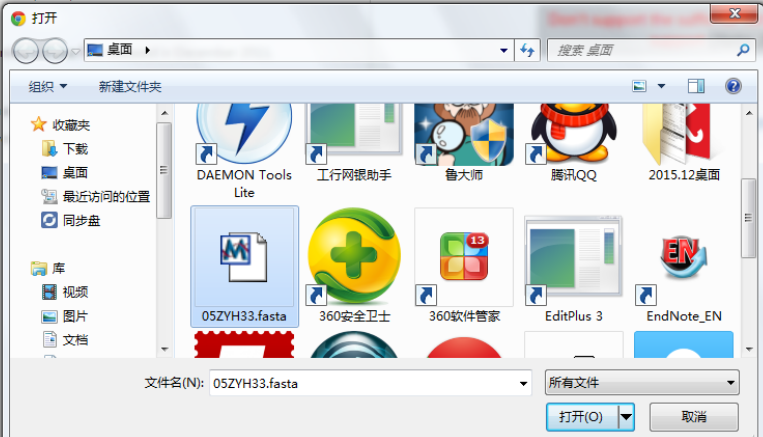
Taxonomy :

Tags :

Fasta :


(File size can not exceed 5MB)

Step 5: Click the "Browse" button to select the query sequence in fasta format



Powered by GeneDock

Step 6: Click the “Upload” button to upload the selected file.

 微生物基因组遗传差异分析平台
ICDC, China CDC

Description
ANIttools is a software package written by PERL scripts that can be run in a Linux/Unix system. If you want to compare bacterial genomes and calculate their average nucleotide identity (ANI), you could download and run this program directly. Or you could send us the genome sequence by email. Then we will do the analysis work for you.

Downloads
Download the latest version of the program [here](#).

Manual
The most current version of the manual is available [here](#).

Citation
If you use ANIttools in work of any way, then please cite the following paper: Genome insights that advance the novel bacterial species definition, 2011, Under Review

History
ANIttools version 1.0 was first released in December 2011.

FAQ
Q: Could I use this program under Windows system?
A: No. This version of ANIttools only works under Linux/Unix system.

ANIttools Online

Your E-mail :

Taxonomy :

Tags :


Fasta :

(File size can not exceed 5MB)

uploading :

Step 6: Click "Upload" button to upload the selected file

Step 7: When the status is “Uploaded successfully”, click the button “Run ANIttools”.



微生物基因组遗传差异分析平台
ICDC,China CDC

Description

ANIttools is a software package written by PERL scripts that can be run in a Linux/Unix system. If you want to compare bacterial genomes and calculate their average nucleotide identity (ANI), you could download and run this program directly. Or you could send us the genome sequence by email. Then we will do the analysis work for you.

Downloads

Download the latest version of the program [here](#).

Manual

The most current version of the manual is available [here](#).

Citation

If you use ANIttools in work of any way, then please cite the following paper: Genome insights that advance the novel bacterial species definition, 2011, Under Review

History

ANIttools version 1.0 was first released in December 2011.

FAQ

Q: Could I use this program under Windows system?
A:No. This version of ANIttools only works under Linux/Unix system.

ANIttools Online

Your E-mail :

Taxonomy :

Tags :


Fasta :

(File size can not exceed 5MB)

Uploaded successfully, please run...

Step 7: When the status is "Uploaded successfully", click the button "Run ANIttools"

Step 8: The waiting page. Several minutes later (5~20 min), a report page will be displayed automatically.



微生物基因组遗传差异分析平台
ICDC,China CDC

App Name	Start Time	End Time	State
-ANIttools	2016-01-14 13:34:06	---	running

Step 9: The report page



结果报告/ANItools Report

日期/Date: 2016/01/14 时间/Time: 13:41:28 用户/User: unknow

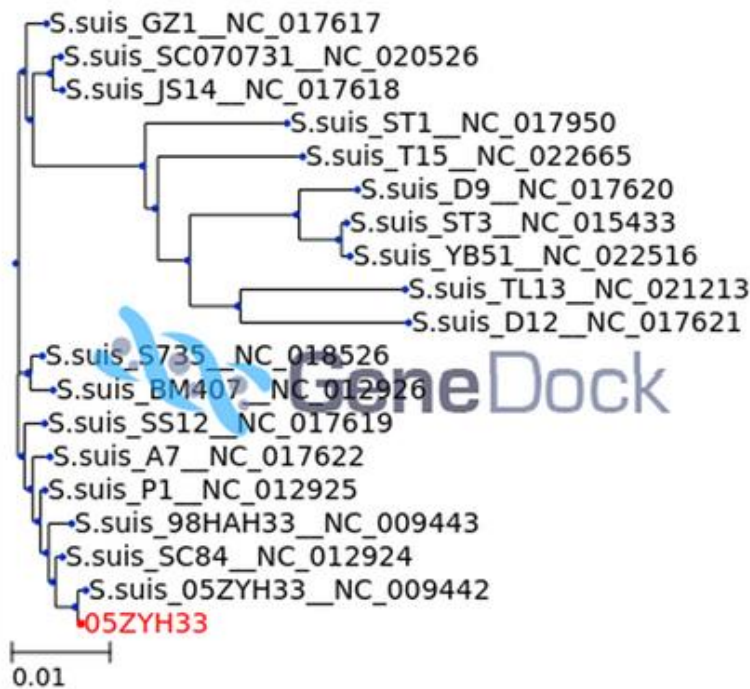
1. 基本信息/Basic Report

测试菌株名/Name of Query Strain: 05ZYH33 目标菌株数/Number of Target Strains: 18 目标菌株属名/Genus Name of Target Strains: Streptococcus 目标菌株种名/Species Name of Target Strains:

2. ANI值列表 (降序列表) /List of ANI values in a descending order

菌株名/Strain Name	菌株ID/Strain ID in NCBI	ANI value comparing with query strain
S.suis_05ZYH33	NC_009442	100.00%
S.suis_SC84	NC_012924	99.75%
S.suis_P1	NC_012925	99.71%
S.suis_A7	NC_017622	99.55%
S.suis_98HAH33	NC_009443	99.51%
S.suis_S735	NC_018526	99.51%
S.suis_GZ1	NC_017617	99.48%
S.suis_BM407	NC_012926	99.46%
S.suis_SS12	NC_017619	99.43%
S.suis_SC070731	NC_020526	99.40%
S.suis_JS14	NC_017618	99.34%
S.suis_ST1	NC_017950	96.72%
S.suis_T15	NC_022665	96.64%
S.suis_ST3	NC_015433	96.30%
S.suis_YB51	NC_022516	96.30%
S.suis_D9	NC_017620	96.10%
S.suis_TL13	NC_021213	95.51%
S.suis_D12	NC_017621	95.42%

3. 进化关系树/Phylogenetic tree based on ANI matrix



结果报告/ANItools Report

1. 基本信息/Basic Report

2. ANI值列表 (降序列表) /List of ANI values in a descending order

3. 进化关系树/Phylogenetic tree based on ANI matrix

SEE ALSO

ANIttools 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 ANIttools, 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

ANIttools version 2.0 was released in December 2015.

ANIttools version 1.0 was firstly released in December 2011.