SPORTS1.0

Small non-coding RNA annotation Pipeline Optimized for rRNA- and tRNA-Derived Small RNAs

Requirements

Linux system, enough disk space and Ram depending on the size of RNA deep sequencing data. (Tested system: ubuntu 12.04 LTS, ubuntu 16.04 LTS)

Installation

1. Download SPORTS1.0 pipeline package.`wget https://github.com/junchaoshi/sports1.0/archive/master.zip`
2. Download necessary software, packages and reference databases as listed below:
   1. Perl 5 (https://www.perl.org) (Tested version: v5.14.2, v5.22.1); Perl 5 might be already installed in the linux system.
   2. Bowtie [1] (http://bowtie-bio.sourceforge.net/index.shtml) (Tested version: 1.1.2, 1.2.1.1)
   3. SRA Toolkit (https://ncbi.github.io/sra-tools/) (Tested version: 2.8.2)
   4. cutadapt [2] (http://cutadapt.readthedocs.io/en/stable/index.html) (Tested version: 1.11)
   5. R (https://www.r-project.org/) (Tested version: 3.2.3, 3.2.5)
   6. Reference database (See lists and download link of all pre-compiled species' databases in appendix)
3. Installation tutorial for software and packages.
   1. Install SPORTS1.0
      1. Unpack SPORTS1.0 package.`unzip sports1.0-master.zip`
      2. Attach the SPORTS directory to your PATH:`echo 'export PATH=$PATH:your_path_to_sports1.0-master/source' >> ~/.bashrcchmod 755 your_path_to_sports1.0-master/source/sports.pl`
   2. Install Bowtie
      1. Unpack bowtie-1.x.x-linux-x86_64.zip.`unzip bowtie-1.x.x-linux-x86_64.zip`
      2. Attach the bowtie directory to your PATH:`echo 'export`

    `PATH=$PATH:your_path_to_bowtie' >> ~/.bashrc`

3. If you are administrator user, type the following command and password to easily install bowtie:

    `sudo apt-get install bowtie`

4. Install SRA Toolkit
   1. Unpack SRA toolkit files.
   2. Attach the SRA Toolkit executable path to your PATH: `echo 'export PATH=$PATH:your_path_to_sra-toolkit/bin' >> ~/.bashrc`
5. Install cutadapt
   1. Use pip on the command line to install latest version of cutadapt: `pip install --user --upgrade cutadapt`
   2. Attach the cutadapt directory to your PATH: `echo 'export PATH=$PATH:$HOME/.local/bin' >> ~/.bashrc`
6. Install R and R package
   1. Unpack R-x.y.z.tar.gz with: `tar -xf R-x.y.z.tar.gz`
   2. Enter into the R-x.y.z directory: `cd R-x.y.z`
   3. Type following command in terminal: `./configure`

      `make`

      `make check`

      `make install`
   4. Install R packages by typing following command in terminal: `R`

      `install.packages('ggplot2', dependencies=TRUE, repos='http://cran.rstudio.com/')`

      `install.packages('data.table', dependencies=TRUE, repos='http://cran.rstudio.com/')`

      `install.packages('stringr', dependencies=TRUE, repos='http://cran.rstudio.com/')`

      `q()`

      `n`

4. Start a new shell session to apply changes to environment variables: `source ~/.bashrc`
5. Test if everything is installed properly: `perl -v`

   `sports.pl -h`

   `bowtie`

   `fastq-dump`

   `cutadapt -h`

   `R --version`
   `If you get any error messages you should install the software once again.`

Script description

sports.pl

1. Input query format:
   1. .sra files.
   2. .fastq/.fq, .fasta/.fa files of deep sequencing reads.
2. `Attention: compressed files need to be unpacked before input!`
3. Options: --Input: `-i <file> Input could be:`

   `a .sra, .fastq/.fq or .fasta/.fa file;`

   `a directory (will run all qualified files in the directory recursively);`

   `a text document with absolute path information for each file/folder (when` processing multiple data, input each file/folder path per line)
   --Output: `-o <str> output address of annotation results (default: input address)`

   `-k keep all the intermediate files generated during the running progress`
   --Alignment: `-l <int> the minimal length of the output sequences (default = 15)`

   `-L <int> the maximal length of the output sequences (default = 45)`

   `-M <int> the total number of mismatches in the entire alignment (default = 0)`

   `-a  Remove 5' / 3' adapters`

   `-x <str> (if -a applied) 5' adapter sequence. Default =` `"GTTCAGAGTTCTACAGTCCGACGATC"`

   `-y <str> (if -a applied) 3' adapter sequence. Default = "TGGAATTCTCGGGTGCCAAGG"`
   --Others: `-v print version information`

   `-h print this usage message`
4. Example
   ◦ Example use 1:
5. The user wants to map a single fasta file against rat reference genome to get the mapping genome annotation only. (No output figures) Type following command in terminal: `sports.pl -i` `reads.fa -g /foo/bar/Rattus_norvegicus/UCSC/rn6/Sequence/BowtieIndex/genome`
   ◦ Example use 2:
6. The user wants to map several already trimed human sequencing files to human reference genome, miRNA database, tRNA database, rRNA database and piRNA database by using 4 CPU threads, then to output the result to the address: '/foo/bar/output/'. Write all the fastq files' addresses into a text document, e.g.: `seq_address.txt`
   ```
   --------------------------
   /foo/bar/fold_1/seq_1.fastq
   /foo/bar/fold_2/seq_2.fq
   /foo/bar/fold_2/seq_3.fq
   /foo/bar/fold_3/seq_4.fasta
   /foo/bar/fold_4/seq_5.fa
   --------------------------
   ```
   Type following command in terminal: `sports.pl -i seq_address.txt -p 4 -g` `/foo/bar/Homo_sapiens/UCSC/hg38/Sequence/BowtieIndex/genome -m` `/Homo_sapiens/miRBase_21/miRBase_21-has -r /foo/bar/Homo_sapiens/rRNA_db/human_rRNA` `-t /foo/bar/Homo_sapiens/GtRNAdb/hg19-tRNAs -w` `/foo/bar/Homo_sapiens/piRBase/piR_human -o /foo/bar/output/`

○ Example use 3:

7. The user wants to map several untrimmed mouse sequencing files downloaded from NCBI or somewhere else to mouse reference genome, miRNA database, tRNA database, rRNA database, piRNA database, ensembl noncoding RNA database and Rfam database by using 4 CPU threads, then to output the result to the address: '/foo/bar/output/' and keep all the intermediate files generated during the running progress. `Put all the sequencing files into a folder, e.g.:`

```
folder structure:

-----------------------
download_seq
    |
    ├─fold_1
    |   |
    |   ├─seq_1.sra
    |   |
    |   └─seq_2.sra
    |
    ├─fold_2
    |   |
    |   ├─fold_3
    |   |   |
    |   |   ├─seq_3.fastq
    |   |   |
    |   |   └─seq_4.fq
    |   |
    |   └─seq_5.fasta
    |
    └─seq_6.fa
-----------------------
```

Type following command in terminal: `sports.pl -i /foo/bar/download_seq/ -p 4 -a -x GTTCAGAGTTCTACAGTCCGACGATC -y TGGAATTCTCGGGTGCCAAGG -g /foo/bar/Mus_musculus/UCSC/mm10/Sequence/BowtieIndex/Genome -m /foo/bar/Mus_musculus/miRBase_21/miRbase_21-mmu -r /foo/bar/Mus_musculus/rRNA_db/mouse_rRNA -t /foo/bar/Mus_musculus/GtRNAdb/mm10-tRNAs -w /foo/bar/Mus_musculus/piRBase/piR_mouse -e /foo/bar/Mus_musculus/Ensembl/Mus_musculus.GRCm38.ncrna -f /foo/bar/Mus_musculus/Rfam_12.3/Rfam-12.3-mouse -o /foo/bar/output/ -k`

8. Example output file structure for 1 query file input (e.g. SeqFile):

```
    Output folder structure
        |
        ├─1_SeqFile
        |   |
        |   ├─SeqFile_fa (if -k applied)
        |   |   |
        |   |   ├─SeqFile.fa                    ---unique seqs with reads number
        |   |   |
        |   |   ├─SeqFile_disgarded_reads.fa        ---seqs that cannot pass
adapter removing process
        |   |   |
        |   |   ├─SeqFile_too_short_reads.fa        ---seqs that are lower than
required minimal length threshold
        |   |   |
```

```
|   |       ├SeqFile_too_long_reads.fa           ---seqs that are higher than
required maximal length threshold
|   |   |   |
|   |       ├SeqFile_match_genome.fa             ---seqs that can match to
reference genome
|   |   |   |
|   |       ├SeqFile_unmatch_genome.fa           ---seqs that cannot match to
reference genome
|   |   |   |
|   |       ├SeqFile_match_<X>_match_genome.fa       ---seqs that can match to
both <X> database and reference genome
|   |   |   |
|   |       ├SeqFile_match_<X>_unmatch_genome.fa     ---seqs that can match to
<X> database but not reference genome
|   |   |   |
|   |       ├SeqFile_unmatch_<X>_match_genome.fa     ---seqs that cannot match
to <X> database but can match to reference genome
|   |   |   |
|   |       └SeqFile_unmatch_<X>_unmatch_genome.fa      ---seqs that match to
<X> rfam database nor reference genome
|   |   |
|       ├SeqFile_processed (if -k applied)
|   |   |   |
|   |       ├SeqFile_output_match_genome        ---seqs that match to reference
genome in BOWTIE format
|   |   |   |
|   |       ├SeqFile_output_<X>_match_genome        ---seqs that match to both
miRNA database and reference genome in BOWTIE format
|   |   |   |
|   |       └SeqFile_output_<X>_unmatch_genome      ---seqs that match to miRNA
database but not reference genome in BOWTIE format
|   |   |
|       └SeqFile_result
|   |   |
|           ├SeqFile_output.txt                 ---6 column table file including
annotation information for every unique sequence
|   |   |
|           ├SeqFile_summary.txt                ---3 column table file including
reads number of each major- (e.g. rRNA) and sub- (e.g. 5S rRNA) classes
|   |   |
|           ├SeqFile_length_distribution.txt        ---3 column table file
including reads number of each length distribution of each major class
|   |   |
|           ├SeqFile_mismatch_summary.txt          ---11 column table file
including mismatch statistics information for each mismatch loci (if -M >0)
|   |   |
|           ├SeqFile_sncRNA_distribution.pdf       ---figure of length
distribution of miRNA, rsRNA, tsRNA, piRNA and other RNAs, if sequence matches
existed
|   |   |
|           ├SeqFile_rRNA_distribution.pdf         ---figure of length
distribution of different types of rRNAs, if sequence matches existed
|   |   |
|           ├SeqFile_rRNA_mapping.pdf              ---figure of rsRNAs mapping
against different types of rRNAs, if sequence matches existed
|   |   |
|           └SeqFile_tRNA_mapping.pdf              ---figure of length
```

```
distribution of different types of tRNAs, if sequence matches existed
        |
      ├─processing_report (if -k applied)
      |   |
      |   └1_SeqFile.txt                    ---processing log file
      |
      └─sh_file (if -k applied)
          |
          └1__SeqFile.sh                    ---rocessing script file
```

```
    Some output folders only exist when '-k' parameter is applied in sports.pl;

    SeqFile_mismatch_summary.txt only exist when '-M' parameter is lager than 0 in
sports.pl;

    Some output files might not exist if the file size is zero.
```

fastq2fasta.pl

Extracted from miRDeep2 [3] (https://github.com/rajewsky-lab/mirdeep2)

1. Description:Parses fastq format files into fasta format.
2. Input:A fastq file.
3. Output:A fasta file, one sequence per line (the sequences are expanded).
4. options:-
5. Example usage:`fastq2fasta.pl reads.fq > reads.fa`

fastaparse.pl

Extracted from miRDeep2 [3] (https://github.com/rajewsky-lab/mirdeep2)

1. Description:Performs simple filtering of entries in a fasta file.
2. Input:A fasta file
3. Output:A filtered fasta file
4. Options:-a only output entries where the sequence is minimum int nts long-b remove all entries that have a sequence that contains letters other than a,c,g,t,u,n,A,C,G,T,U,N.-s output progress
5. Example usage:`fastaparse.pl reads.fa -a 15 -s > reads_no_short.fa 2> reads_discarded.fa`

combine_reads.pl

1. Description:Combine reads in the fasta file to get unique sequence and its read number.
2. Input:A fasta file
3. Output:

```
    A filtered fasta file.
    ------------------------------
    >t00000001 1234567
    TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC
    ------------------------------
    't00000001' is the unique ID of the sequence, representing the abundance
ranking among all the sequences. In this case, the abundance of this sequence is
```

```
   the highest.
      '1234567' represents the reads number of sequence
'TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC'
```

1. Options:-
2. Example usage:`combine_reads.pl reads.fa > combined_reads.fa`

tRNA_db_processing.pl

1. Description:This script adds CCA end to original genomic tRNA 3' end and add G to Histidine tRNA 5' end.
2. Input:The reference tRNA database file in .fa formatA fasta file
3. Options: -
4. Example usage:`tRNA_db_processing.pl input_tRNA_file.fa`

annotation.pl

1. Description:Combine the annotation information generated from sports.pl
2. Input:sports.pl output folder address:
3. Output:
   1. _output.txt: A 6 column table file including annotation information for every unique sequence.
4.
```
-----------------------------------------------------------------------------
------------------------
    ID          Sequence                              Length    Reads
Match_Genome    Annotation
    t00000001   TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC      32        1234567    Yes
tRNA-Glu-CTC_5_end

-----------------------------------------------------------------------------
------------------------

    -ID: t00000001                               --Represents the unique ID of the
sequence, represents the abundance ranking among all the sequences. In this case,
the abundance of this sequence is the highest.

    -Sequence: TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC    --Represents the sequence.

    -Length: 32                                  --Length of the sequence.

    -Reads: 1234567                              --Reads number of the sequence.

    -Match_Genome: Yes                           --If the sequence can match the
reference genome.

    -Annotation: tRNA-Glu-CTC_5_end              --The annotation of the sequence.
This sequence mapped against the 5' end of tRNA-Glu-CTC sequence.
```
   1. \<seq_fold>_summary.txt: A 3 column table file including reads number of each major- and sub- classes.
5.
```
-----------------------------------------------------------------------------
------------------------
    Class                            Sub_Class          Reads
    tRNAdb-tRNA_5_end_Match_Genome   -                  123456
    -                                tRNA-Glu-CTC_5_end 78910
```

```
--------------------------------------------------------------------------------
------------------------

    -Class: tRNAdb-tRNA_5_end_Match_Genome     --The major class name.
    -Sub_Class: tRNA-Glu-CTC_5_end              --The sub class name.
    -Reads: 123456                              --The reads number of the class.
```
   1. \<seq_fold>_length_distribution.txt: A 3 column table file including reads number of each length distribution of each major class.
6.
```
--------------------------------------------------------------------------------
------------------------

    Class                              Length    Reads
    tRNAdb-tRNA_5_end_Match_Genome     30        1234
    tRNAdb-tRNA_5_end_Match_Genome     31        23456
    tRNAdb-tRNA_5_end_Match_Genome     32        34567
    tRNAdb-tRNA_5_end_Match_Genome     33        4567

    ......


--------------------------------------------------------------------------------
------------------------

    -Class: tRNAdb-tRNA_5_end_Match_Genome     --The major class name.
    -Length: 30                                --Length of the sequence.
    -Reads: 1234                               --The reads number of the class.
```
7. Options: -
8. Example usage: `annotation.pl <SPORTS_output_fold_address>`

tRNA_mapping.pl

1. Description: Perl script calculates expression level of genomic loci by bowtie 1 output information.
2. Input: bowtie 1 output file
3. Output: expression summary file
4. Options: -
5. Example usage: `tRNA_mapping.pl bowtie_output_file summary_file`

mismatch_summary.pl

1. Description: Perl script summarizes mismatch information generated by Bowtie 1 if parameter '-M' >0 applied in sports.pl
2. Input: bowtie 1 output file and threshold of reads number.
3. Output: mismatch summary file
4. Options: -
5. Example usage: `mismatch_summary.pl bowtie_output_file 10 > mismatch_summary.txt`

overall_RNA_length_distribution.R

1. Description: Generate figure of length distribution of miRNA, rsRNA, tsRNA, piRNA and other RNAs, if sequence matches exists.

2. Input: Files generated by annotation.pl
3. Output: \<seq_fold>_sncRNA_distribution.pdf Generate figure of length distribution of different types of rRNAs, if sequence matches exists.
4. Options: -
5. Example usage: `Rscript --vanilla overall_RNA_length_distribution.R <SPORTS_output_fold_address> <dataset_name>`

rRNA_length_distribution.R

1. Description: Generate figure of length distribution of different types of rRNAs, if sequence matches exists. (e.g. 4.5S, 5S, 5.3S, 5.8S, 12S, 16S, 18S, 28S, 45S ...)
2. Input: Files generated by annotation.pl
3. Output: \<seq_fold>_rRNA_distribution.pdf
4. Options: -
5. Example usage: `Rscript --vanilla r_RNA_length_distribution.R <SPORTS_output_fold_address> <dataset_name>`

rRNA_mapping.R

1. Description: Generate figure of rsRNAs mapping against different types of rRNAs if sequence matches existed. (e.g. 4.5S, 5S, 5.3S, 5.8S, 12S, 16S, 18S, 28S, 45S ...)
2. Input: Files generated by annotation.pl
3. Output: \<seq_fold>_rRNA_mapping.pdf
4. Options: -
5. Example usage: `Rscript --vanilla rRNA_mapping.R <SPORTS_output_fold_address> <dataset_name>`

tRNA_mapping.R

1. Description: Generate figure of rsRNAs mapping against different types of tRNAs if sequence matches existed.
2. Input: Files generated by tRNA_mapping.pl
3. Output: \<seq_fold>_tRNA_mapping.pdf
4. Options: -
5. Example usage: `Rscript --vanilla tRNA_mapping.R <SPORTS_output_fold_address>_tRNA_mapping.txt <dataset_name>_tRNA_mapping.pdf`

mismatch_stat.R

1. Description: Generate statistics result for mismatch information generated from mismatch_summary.pl
2. Input: File generated by mismatch_summary.pl and base-calling error
3. Output: \<seq_fold>_mismatch_summary.txt
4. Options: -
5. Example usage: `Rscript --vanilla mismatch_stat.R <SPORTS_output_fold_address>_mismatch_summary.txt 0.01`

Appendix

Available species lists of bowtie-index based reference database

```
    To build bowtie-index of your own:
        cd /foo/bar/your_reference_database/
        bowtie-build <your_reference_database_name>.fa
<your_reference_database_name>
    The built bowtie index will be:
/foo/bar/your_reference_database/your_reference_database_name

    Unpack reference genome (e.g. human genome):
        tar zxvf Homo_sapiens_UCSC_hg38.tar.gz
```

Main database source:

```
-mirbase 21 database [4] (Original source: http://www.mirbase.org/index.shtml)

-rRNA database (Original source: https://www.ncbi.nlm.nih.gov/nuccore)

-GtRNAdb 2.0 database [5] (Original source: http://gtrnadb.ucsc.edu/)

-piRBase database [6] (Original source:
http://www.regulatoryrna.org/database/piRNA/)

-piRNABank [7] (Original source: http://pirnabank.ibab.ac.in/index.shtml)

-ensembl ncRNA database [8] (Original source: http://www.ensembl.org/index.html)

-rfam 12.3 database [9] (Original source: http://rfam.xfam.org/)
```

1. Homo sapiens (Human)
   1. annotation databases: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0773ed3d5f6b74f35bbd643e1af221c31&authkey=AcRxf8walnGUIEhgI--8CDc)
2.
```
    -genome with bowtie-index (UCSC hg38) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Homo_sapiens_U
CSC_hg38.tar.gz)
    -mirbase 21 with bowtie-index (Original source:
http://www.mirbase.org/ftp.shtml)
    -rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
    -tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/genomes/eukaryota/Hsapi19/hg19-tRNAs.fa)
    -piRNA database with bowtie-index (Original source:
http://www.regulatoryrna.org/database/piRNA/ &&
http://pirnabank.ibab.ac.in/request.html)
```

```
        -ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/homo_sapiens/ncrna/)
        -rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

1. SPORTS1.0 related parameters if you download recommended reference database:

3.
```
     -g /<your_defined_address>/Homo_sapiens/UCSC/hg38/Sequence/BowtieIndex/genome
    -m /<your_defined_address>/Homo_sapiens/miRBase_21/miRBase_21-hsa
    -r /<your_defined_address>/Homo_sapiens/rRNA_db/human_rRNA
    -t /<your_defined_address>/Homo_sapiens/GtRNAdb/hg19-tRNAs
    -w /<your_defined_address>/Homo_sapiens/piRBase/piR_human
    -e /<your_defined_address>/Homo_sapiens/Ensembl/Homo_sapiens.GRCh38.ncrna
    -f /<your_defined_address>/Homo_sapiens/Rfam_12.3/Rfam-12.3-human
```

4. Gorilla gorilla gorilla (Gorilla)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=03a9a8d26cca14b458007e9c6ee4541f7&authkey=Aag33OX-IjvagRWePhYNF3k)
   ```
   -genome with bowtie-index (UCSC gorGor5) (Original source:
   http://hgdownload.soe.ucsc.edu/goldenPath/gorGor5/bigZips/gorGor5.fa.gz)
   -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
   -tRNA database with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Acaro2/anoCar2-tRNAs.fa)
   -rfam 12.3 database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   ```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
   ```
   /<your_defined_address>/Gorilla_gorilla/UCSC/gorGor5/Sequence/BowtieIndex/genome
   -m /<your_defined_address>/Gorilla_gorilla/miRBase_21/miRBase_21-ggo
   -t /<your_defined_address>/Gorilla_gorilla/GtRNAdb/gorGor3-tRNAs
   -f /<your_defined_address>/Gorilla_gorilla/Rfam_12.3/Rfam-12.3-gorilla
   ```

5. Pan paniscus (Bonobo)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=03a74e9f6c2594f1e86a31acd8e554621&authkey=AYrgOm8rrAY7hrFYQ03gmTA)
   ```
   -genome with bowtie-index (UCSC panPan1) (Original source:
   http://hgdownload.soe.ucsc.edu/goldenPath/panPan1/bigZips/panPan1.fa.gz)
   -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
   -rfam 12.3 database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   ```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
   ```
   /<your_defined_address>/Pan_paniscus/UCSC/panPan1/Sequence/BowtieIndex/genome
   -m /<your_defined_address>/Pan_paniscus/miRBase_21/miRBase_21-ppa
   -f /<your_defined_address>/Pan_paniscus/Rfam_12.3/Rfam-12.3-Bonobo
   ```

6. Pan troglodytes (Chimp)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=09c13507ee7414365843de3450aa9ad3e&authkey=AdsLOHA5q2--SbiP2C6Qjpc)
   ```
   -genome with bowtie-index (Ensembl CHIMP2.1.4)
   (ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Pan_troglodytes/UCSC/panTro4/Pan_tr
   oglodytes_UCSC_panTro4.tar.gz)
   -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
   -tRNA database with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ptrog4/panTro4-tRNAs.fa)
   -ensembl ncRNA database with bowtie-index (Original source:
   ftp://ftp.ensembl.org/pub/release-89/fasta/pan_troglodytes/ncrna/)
   -rfam 12.3 database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   ```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g /<your_defined_address>/Pan_troglodytes/UCSC/panTro4/Sequence/BowtieIndex/genome -m /<your_defined_address>/Pan_troglodytes/miRBase_21/miRBase_21-ptr -t /<your_defined_address>/Pan_troglodytes/GtRNAdb/panTro4-tRNAs -e /<your_defined_address>/Pan_troglodytes/Ensembl/Pan_troglodytes.CHIMP2.1.4.ncrna -f /<your_defined_address>/Pan_troglodytes/Rfam_12.3/Rfam-12.3-chimp`

7. Pongo abelii (Orangutan)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=037168296877942ecb9735f26afcb450a&authkey=AZkU5ib3A0KOiT4KxrhgTGQ)

   ```
   -genome with bowtie-index (UCSC ponAbe2) (Original source:
   http://hgdownload.soe.ucsc.edu/goldenPath/ponAbe2/bigZips/chromFa.tar.gz)
   -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
   -tRNA database with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ppygm2/ponAbe2-tRNAs.fa)
   -ensembl ncRNA database with bowtie-index (Original source:
   ftp://ftp.ensembl.org/pub/release-89/fasta/pongo_abelii/ncrna/)
   -rfam 12.3 database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   ```

   2. SPORTS1.0 related parameters if you download recommended reference database: `-g /<your_defined_address>/Pongo_abelii/UCSC/ponAbe2/Sequence/BowtieIndex/genome -m /<your_defined_address>/Pongo_abelii/miRBase_21/miRBase_21-ppy -t /<your_defined_address>/Pongo_abelii/GtRNAdb/ponAbe2-tRNAs -e /<your_defined_address>/Pongo_abelii/Ensembl/Pongo_abelii.PPYG2.ncrna -f /<your_defined_address>/Pongo_abelii/Rfam_12.3/Rfam-12.3-orangutan`

8. Nomascus leucogenys (Gibbon) 6.1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=068ef6629d31b4fb28100f667050be1d1&authkey=AWEPi3HUmOVD_PPPnkMhdvs) ```

   ```
   -genome with bowtie-index (UCSC nomLeu3) (Original source:
   http://hgdownload.soe.ucsc.edu/goldenPath/nomLeu3/bigZips/nomLeu3.fa.gz)
   -tRNA database with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Nleuc3/nomLeu3-tRNAs.fa)
   -rfam 12.3 database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   ```

   6.2 SPORTS1.0 related parameters if you download recommended reference database: ```
   ```
   -g /<your_defined_address>/Nomascus_leucogenys/UCSC/nomLeu3/Sequence/BowtieIndex/genome
   -t /<your_defined_address>/Nomascus_leucogenys/GtRNAdb/nomLeu3-tRNAs
   -f /<your_defined_address>/Nomascus_leucogenys/Rfam_12.3/Rfam-12.3-gibbon
   ```

9. Macaca mulatta (Rhesus)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=07fededf7468444ba9b863b74316b8504&authkey=Aa6X06J4ExLvKtH8mJ-CESs)

   ```
   -genome with bowtie-index (UCSC rheMac8) (Original source:
   http://hgdownload.soe.ucsc.edu/goldenPath/rheMac8/bigZips/rheMac8.fa.gz)
   -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
   -tRNA database with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mmula3/rheMac3-tRNAs.fa)
   -rRNA database with bowtie-index (Original source:
   https://www.ncbi.nlm.nih.gov/nuccore)
   ```

```
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
  2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Macaca_mulatta/UCSC/rheMac8/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Macaca_mulatta/miRBase_21/miRBase_21-mml
-r /<your_defined_address>/Macaca_mulatta/rRNA_db/rhesus_rRNA
-t /<your_defined_address>/Macaca_mulatta/GtRNAdb/rheMac3-tRNAs
-f /<your_defined_address>/Macaca_mulatta/Rfam_12.3/Rfam-12.3-rhesus
```
10. Papio anubis (Baboon)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=03a22a2092c7b46fb93a8fc49cf234720&authkey=Ad_hzH3MUIMh0-9BLoH_Vmw)
```
-genome with bowtie-index (UCSC papAnu2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/papAnu2/bigZips/papAnu2.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Panub2/papAnu2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Papio_anubis/UCSC/papAnu2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Papio_anubis/GtRNAdb/papAnu2-tRNAs
-f /<your_defined_address>/Papio_anubis/Rfam_12.3/Rfam-12.3-baboon
```
11. Callithrix jacchus (Marmoset)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=077698888fa8d40408df8c979e91146e4&authkey=AeoDYl5a3lKyF-CWgupu6IA)
```
-genome with bowtie-index (UCSC calJac3) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/calJac3/bigZips/calJac3.fa.gz)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Cjacc3/calJac3-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Callithrix_jacchus/UCSC/calJac3/Sequence/BowtieIndex/genom
e
-m /<your_defined_address>/Callithrix_jacchus/rRNAdb/marmoset_rRNA
-t /<your_defined_address>/Callithrix_jacchus/GtRNAdb/calJac3-tRNAs
-f /<your_defined_address>/Callithrix_jacchus/Rfam_12.3/Rfam-12.3-marmoset
```
12. Carlito syrichta (Tarsier)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0c761313792b64396b87a66a6e04101be&authkey=AZBsjTA5-hXdASOIimxNL4I)
```
-genome with bowtie-index (UCSC tarSyr2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/tarSyr2/bigZips/tarSyr2.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Tsyri2/tarSyr2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Carlito_syrichta/UCSC/tarSyr2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Carlito_syrichta/GtRNAdb/tarSyr2-tRNAs
-f /<your_defined_address>/Carlito_syrichta/Rfam_12.3/Rfam-12.3-tarsier
```
13. Rattus norvegicus (rat)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0b2cacd8453104b2abb60298863fc4c16&authkey=AZAYeCOsLKuc_ml-QMqBJoQ)

```
-genome with bowtie-index (UCSC rn6) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Rattus_norvegicus/UCSC/rn6/Rattus_no
rvegicus_UCSC_rn6.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Rnorv5/rn5-tRNAs.fa)
-piRNA database with bowtie-index (Original source:
http://www.regulatoryrna.org/database/piRNA/ &&
http://pirnabank.ibab.ac.in/request.html)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/rattus_norvegicus/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Rattus_norvegicus/UCSC/rn6/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Rattus_norvegicus/miRBase_21/miRBase_21-rno
-r /<your_defined_address>/Rattus_norvegicus/rRNA_db/mouse_rRNA
-t /<your_defined_address>/Rattus_norvegicus/GtRNAdb/rn5-tRNAs
-w /<your_defined_address>/Rattus_norvegicus/piRBase/piR_rat
-e
/<your_defined_address>/Rattus_norvegicus/Ensembl/Rattus_norvegicus.Rnor_6.0.ncrna
-f /<your_defined_address>/Rattus_norvegicus/Rfam_12.3/Rfam-12.3-rat
```

14. Mus musculus (mouse)
    1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0833653a140eb47f098267d7a23d3b63c&authkey=Ab8aoYC8paqFl2yRabIo7Ok)

```
-genome with bowtie-index (UCSC mm10) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Mus_musculus/UCSC/mm10/Mus_musculus_
UCSC_mm10.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/genomes/eukaryota/Mmusc10/mm10-tRNAs.fa)
-piRNA database with bowtie-index (Original source:
http://www.regulatoryrna.org/database/piRNA/ &&
http://pirnabank.ibab.ac.in/request.html)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/mus_musculus/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Mus_musculus/UCSC/mm10/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Mus_musculus/miRBase_21/miRBase_21-mmu
-r /<your_defined_address>/Mus_musculus/rRNA_db/mouse_rRNA
-t /<your_defined_address>/Mus_musculus/GtRNAdb/mm10-tRNAs
-w /<your_defined_address>/Mus_musculus/piRBase/piR_mouse
-e /<your_defined_address>/Mus_musculus/Ensembl/Mus_musculus.GRCm38.ncrna
-f /<your_defined_address>/Mus_musculus/Rfam_12.3/Rfam-12.3-mouse
```

15. Cricetulus griseus (Hamster)
    1. annotation database: (We provide a download link for all databases listed below:

https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
px?docid=0b0ac3830026f4007958774cbdb421632&authkey=AZnURBxU1PYzUO1yyrcoZ_M)

```
-genome with bowtie-index (UCSC criGri1) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/criGri1/bigZips/criGri1.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Cgris1/criGri1-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Cricetulus_griseus/UCSC/criGri1/Sequence/BowtieIndex/genom
e
-m /<your_defined_address>/Cricetulus_griseus/miRBase_21/miRBase_21-cgr
-r /<your_defined_address>/Cricetulus_griseus/rRNA_db/hamster_rRNA
-t /<your_defined_address>/Cricetulus_griseus/GtRNAdb/criGri1-tRNAs
-f /<your_defined_address>/Cricetulus_griseus/Rfam_12.3/Rfam-12.3-hamster
```
16. Cavia porcellus (Guinea pig)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0d27261e6ae9c4402bbc9465addb544de&authkey=Ad1xlk56DNm0StozUWDqCYw)
```
-genome with bowtie-index (UCSC cavPor3) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/cavPor3/bigZips/cavPor3.fa.gz)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Cporc3/cavPor3-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Cavia_porcellus/UCSC/cavPor3/Sequence/BowtieIndex/genome
-r /<your_defined_address>/Cavia_porcellus/rRNA_db/guinea_rRNA
-t /<your_defined_address>/Cavia_porcellus/GtRNAdb/cavPor3-tRNAs
-f /<your_defined_address>/Cavia_porcellus/Rfam_12.3/Rfam-12.3-guinea
```
17. Heterocephalus glaber (Naked mole-rat)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0ceff76c620884395899bcd385bfaa098&authkey=ATiBTnSjWKqY0zPKQOmM6kU)
```
-genome with bowtie-index (UCSC hetGla2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/hetGla2/bigZips/hetGla2.fa.gz)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Hglab2/hetGla2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Heterocephalus_glaber/UCSC/hetGla2/Sequence/BowtieIndex/ge
nome
-r /<your_defined_address>/Heterocephalus_glaber/rRNA_db/mole_rRNA
-t /<your_defined_address>/Heterocephalus_glaber/GtRNAdb/hetGla2-tRNAs
-f /<your_defined_address>/Heterocephalus_glaber/Rfam_12.3/Rfam-12.3-mole
```
18. Ictidomys tridecemlineatus (Squirrel)
   1. annotation database: (We provide a download link for all databases listed below:

https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0419ea57bd00548cc94574d8ce9717fcd&authkey=Aa1pkb9R7850Ss3GFmB6GzM)

```
-genome with bowtie-index (UCSC speTri2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/speTri2/bigZips/speTri2.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Strid2/speTri2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Ictidomys_tridecemlineatus/UCSC/speTri2/Sequence/BowtieInd
ex/genome
-t /<your_defined_address>/Ictidomys_tridecemlineatus/GtRNAdb/speTri2-tRNAs
-f /<your_defined_address>/Ictidomys_tridecemlineatus/Rfam_12.3/Rfam-12.3-squirrel
```

19. Ochotona princeps (Pika)
   1. annotation database: (We provide a download link for all databases listed below:
   https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=068d8da8388b74c38943e50237a259a88&authkey=AemP73yDCDiObexIk-DcRVQ)
   ``` -genome with bowtie-index (UCSC ochPri3) (Original source:
   http://hgdownload.soe.ucsc.edu/goldenPath/ochPri3/bigZips/ochPri3.fa.gz) -tRNA database
   with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Oprin3/ochPri3-tRNAs.fa) -rfam 12.3
   database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Ochotona_princeps/UCSC/ochPri3/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Ochotona_princeps/GtRNAdb/ochPri3-tRNAs
-f /<your_defined_address>/Ochotona_princeps/Rfam_12.3/Rfam-12.3-pika
```

20. Oryctolagus cuniculus (Rabbit)
   1. annotation database: (We provide a download link for all databases listed below:
   https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=01b2d69333c97448196cc69b212e92fc9&authkey=ARbwyo0-WJX10nDdXwvNygc)
```
-genome with bowtie-index (UCSC oryCun2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/oryCun2/bigZips/oryCun2.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ocuni2/oryCun2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Oryctolagus_cuniculus/UCSC/oryCun2/Sequence/BowtieIndex/ge
nome
-m /<your_defined_address>/Oryctolagus_cuniculus/miRBase_21/miRBase_21-ocu
-r /<your_defined_address>/Oryctolagus_cuniculus/rRNA_db/rabbit_rRNA
-t /<your_defined_address>/Oryctolagus_cuniculus/GtRNAdb/oryCun2-tRNAs
-f /<your_defined_address>/Oryctolagus_cuniculus/Rfam_12.3/Rfam-12.3-rabbit
```
21. Ovis aries (Sheep)
   1. annotation database: (We provide a download link for all databases listed below:
   https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e880ae29a16747bebf5b9afdb5956921&authkey=AYIP0UkTwtVuiuI45XA7mYE)
```
-genome with bowtie-index (UCSC oviAri3) (Original source:
http://hgdownload.cse.ucsc.edu/goldenPath/oviAri3/bigZips/oviAri3.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
```

```
     -tRNA database with bowtie-index (Original source:
     http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Zmays5/zeaMay5-tRNAs.fa)
     -rfam 12.3 database with bowtie-index (Original source:
     ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
     /<your_defined_address>/Ovis_aries/UCSC/oviAri3/Sequence/BowtieIndex/genome
     -m /<your_defined_address>/Ovis_aries/miRBase_21/miRBase_21-oar
     -t /<your_defined_address>/Ovis_aries/GtRNAdb/oviAri1-tRNAs
     -f /<your_defined_address>/Ovis_aries/Rfam_12.3/Rfam-12.3-sheep
```
22. Bos taurus (Cow)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0a58e56dc7cb743299631fec15b72e69d&authkey=AeosGslpVMdvtZa6qtKJBCE)
```
     -genome with bowtie-index (UCSC bosTau8) (Original source:
     ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Bos_taurus/UCSC/bosTau8/Bos_taurus_U
     CSC_bosTau8.tar.gz)
     -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
     -tRNA database with bowtie-index (Original source:
     http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Btaur8/bosTau8-tRNAs.fa)
     -rRNA database with bowtie-index (Original source:
     https://www.ncbi.nlm.nih.gov/nuccore)
     -ensembl ncRNA database with bowtie-index (Original source:
     ftp://ftp.ensembl.org/pub/release-89/fasta/bos_taurus/ncrna/)
     -rfam 12.3 database with bowtie-index (Original source:
     ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
     /<your_defined_address>/Bos_taurus/UCSC/bosTau8/Sequence/BowtieIndex/genome
     -m /<your_defined_address>/Bos_taurus/miRBase_21/miRBase_21-bta
     -r /<your_defined_address>/Bos_taurus/rRNA_db/cow_rRNA
     -t /<your_defined_address>/Bos_taurus/GtRNAdb/bosTau8-tRNAs
     -e /<your_defined_address>/Bos_taurus/Ensembl/Bos_taurus.UMD3.1.ncrna
     -f /<your_defined_address>/Bos_taurus/Rfam_12.3/Rfam-12.3-cow
```
23. Sus scrofa (Pig)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0e15d39ac05b24a9b899e7a9dfcf96773&authkey=AYaNWQ9KLlkqq7f2qbWzchc)
```
     -genome with bowtie-index (UCSC susScr3) (Original source:
     ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Sus_scrofa/UCSC/susScr3/Sus_scrofa_U
     CSC_susScr3.tar.gz)
     -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
     -rRNA database with bowtie-index (Original source:
     https://www.ncbi.nlm.nih.gov/nuccore)
     -tRNA database with bowtie-index (Original source:
     http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Sscro3/susScr3-tRNAs.fa)
     -rfam 12.3 database with bowtie-index (Original source:
     ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
     /<your_defined_address>/Sus_scrofa/UCSC/susScr3/Sequence/BowtieIndex/genome
     -m /<your_defined_address>/Sus_scrofa/miRBase_21/miRBase_21-ssc
     -r /<your_defined_address>/Sus_scrofa/rRNA_db/pig_rRNA
     -t /<your_defined_address>/Sus_scrofa/GtRNAdb/susScr3-tRNAs
     -f /<your_defined_address>/Sus_scrofa/Rfam_12.3/Rfam-12.3-pig
```
24. Tursiops truncatus (Dolphin)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=08396ad3619a247d695508aee771e3991&authkey=AVKuiimDuoOGVKfGvZcK_ik)

```
-genome with bowtie-index (UCSC turTru2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/turTru2/bigZips/turTru2.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ttrun2/turTru2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
   ```
   /<your_defined_address>/Tursiops_truncatus/UCSC/turTru2/Sequence/BowtieIndex/genom
   e
   -t /<your_defined_address>/Tursiops_truncatus/GtRNAdb/turTru2-tRNAs
   -f /<your_defined_address>/Tursiops_truncatus/Rfam_12.3/Rfam-12.3-dolphin
   ```

25. Balaenoptera acutorostrata (Minke whale)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0d27ad173ffdb4dcc8a4954f9ba5426eb&authkey=AUdYvbA-_q0lzVEEBlth8V8)
       ```
       -genome with bowtie-index (UCSC balAcu1) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/balAcu1/bigZips/balAcu1.fa.gz)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Bacut1/balAcu1-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Balaenoptera_acutorostrata/UCSC/balAcu1/Sequence/BowtieInd
       ex/genome
       -t /<your_defined_address>/Balaenoptera_acutorostrata/GtRNAdb/balAcu1-tRNAs
       -f /<your_defined_address>/Balaenoptera_acutorostrata/Rfam_12.3/Rfam-12.3-whale
       ```

26. Erinaceus europaeus (Hedgehog)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0633e2d7781ab4aefb59fc03f1347657b&authkey=AXrP4XnyiHQqkC5WOUhhS5w)
       ```
       -genome with bowtie-index (UCSC eriEur2) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/eriEur2/bigZips/eriEur2.fa.gz)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Eeuro2/eriEur2-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Erinaceus_europaeus/UCSC/eriEur2/Sequence/BowtieIndex/geno
       me
       -t /<your_defined_address>/Erinaceus_europaeus/GtRNAdb/eriEur2-tRNAs
       -f /<your_defined_address>/Erinaceus_europaeus/Rfam_12.3/Rfam-12.3-hedgehog
       ```

27. Sorex araneus (Shrew)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0399046c56fb246c39630c84db61a23ad&authkey=AWE7pAlGt1TAAUylD4qoE9A)
       ```
       -genome with bowtie-index (UCSC sorAra2) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/sorAra2/bigZips/sorAra2.fa.gz)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Saran2/sorAra2-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Sorex_araneus/UCSC/sorAra2/Sequence/BowtieIndex/genome
       -t /<your_defined_address>/Sorex_araneus/GtRNAdb/sorAra2-tRNAs
       -f /<your_defined_address>/Sorex_araneus/Rfam_12.3/Rfam-12.3-shrew
       ```

28. Canis familiaris (Dog)
    1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06a45d60105a04796b5e96a9417d86f4c&authkey=AY37yxKX-C5u9DG71tzrFEI)

    ```
    -genome with bowtie-index (UCSC canFam3) (Original source:
    ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Canis_familiaris/UCSC/canFam3/Canis_
    familiaris_UCSC_canFam3.tar.gz)
    -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
    -tRNA database with bowtie-index (Original source:
    http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Cfami3/canFam3-tRNAs.fa)
    -rfam 12.3 database with bowtie-index (Original source:
    ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
    ```

    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

    ```
    /<your_defined_address>/Canis_familiaris/UCSC/canFam3/Sequence/BowtieIndex/genome
    -m /<your_defined_address>/Canis_familiaris/miRBase_21/miRBase_21-cfa
    -t /<your_defined_address>/Canis_familiaris/GtRNAdb/canFam3-tRNAs
    -f /<your_defined_address>/Canis_familiaris/Rfam_12.3/Rfam-12.3-dog
    ```

29. Mustela putorius furo (Ferret)
    1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0ef4e067d42f241359e2e606b14e0d8f9&authkey=AUW2yr7SM356KpD5uhBNOeM)

    ```
    -genome with bowtie-index (UCSC musFur1) (Original source:
    http://hgdownload.soe.ucsc.edu/goldenPath/musFur1/bigZips/musFur1.fa.gz)
    -tRNA database with bowtie-index (Original source:
    http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mputo1/musFur1-tRNAs.fa)
    -rfam 12.3 database with bowtie-index (Original source:
    ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
    ```

    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

    ```
    /<your_defined_address>/Mustela_furo/UCSC/musFur1/Sequence/BowtieIndex/genome
    -t /<your_defined_address>/Mustela_furo/GtRNAdb/musFur1-tRNAs
    -f /<your_defined_address>/Mustela_furo/Rfam_12.3-ferret
    ```

30. Ailuropoda melanoleuca (Panda)
    1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0215799b172f94c909c5251061e317540&authkey=AdE82hkEi1MHl3OL1vY92b8)

    ```
    -genome with bowtie-index (UCSC ailMel1) (Original source:
    http://hgdownload.soe.ucsc.edu/goldenPath/ailMel1/bigZips/ailMel1.fa.gz)
    -tRNA database with bowtie-index (Original source:
    http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Amela1/ailMel1-tRNAs.fa)
    -rfam 12.3 database with bowtie-index (Original source:
    ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
    ```

    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

    ```
    /<your_defined_address>/Ailuropoda_melanoleuca/UCSC/ailMel1/Sequence/BowtieIndex/g
    enome
    -t /<your_defined_address>/Ailuropoda_melanoleuca/GtRNAdb/ailMel1-tRNAs
    -f /<your_defined_address>/Ailuropoda_melanoleuca/Rfam-12.3-panda
    ```

31. Felis catus (Cat)
    1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0203fe1a0c8954879878ef8cabcfe37cf&authkey=AZ32jdZI7FoFU_t8_NFb9o0)

    ```
    -genome with bowtie-index (UCSC felCat8) (Original source:
    http://hgdownload.soe.ucsc.edu/goldenPath/felCat8/bigZips/felCat8.fa.gz)
    -rRNA database with bowtie-index (Original source:
    https://www.ncbi.nlm.nih.gov/nuccore)
    -tRNA database with bowtie-index (Original source:
    ```

```
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ocuni2/oryCun2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
     2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
/<your_defined_address>/Felis_catus/UCSC/felCat8/Sequence/BowtieIndex/genome
-r /<your_defined_address>/Felis_catus/rRNA_db/cat_rRNA
-t /<your_defined_address>/Felis_catus/GtRNAdb/felCat5-tRNAs
-f /<your_defined_address>/Felis_catus/Rfam_12.3/Rfam-12.3-cat
```
32. Equus caballus (Horse)
     1. annotation database: (We provide a download link for all databases listed below:
        https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
        px?docid=0e7011a73d57545ea8be3c71335b3cf4c&authkey=AWHkBfbzVmwz_HjmQXo8lJU)
```
-genome with bowtie-index (UCSC equCab2) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Equus_caballus/UCSC/equCab2/Equus_ca
ballus_UCSC_equCab2.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ecaba2/equCab2-tRNAs.fa)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
     2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
/<your_defined_address>/Equus_caballus/UCSC/equCab2/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Equus_caballus/miRBase_21/miRBase_21-eca
-r /<your_defined_address>/Equus_caballus/rRNA_db/horse_rRNA
-t /<your_defined_address>/Equus_caballus/GtRNAdb/equCab2-tRNAs
-f /<your_defined_address>/Equus_caballus/Rfam_12.3/Rfam-12.3-horse
```
33. Ceratotherium simum (White rhinoceros)
     1. annotation database: (We provide a download link for all databases listed below:
        https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
        px?docid=0f836e7106664459bacda6f94dc15e22d&authkey=AVSh1b1dr84q53sLTqD9sRA)
```
-genome with bowtie-index (UCSC cerSim1) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/cerSim1/bigZips/cerSim1.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Csimu1/cerSim1-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
     2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
/<your_defined_address>/Ceratotherium_simum/UCSC/cerSim1/Sequence/BowtieIndex/geno
me
-t /<your_defined_address>/Ceratotherium_simum/GtRNAdb/cerSim1-tRNAs
-f /<your_defined_address>/Ceratotherium_simum/Rfam_12.3/Rfam-12.3-rhinoceros
```
34. Myotis lucifugus (Microbat)
     1. annotation database: (We provide a download link for all databases listed below:
        https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
        px?docid=03dcc351bbc274cfc8692e5f2b1f5d0f3&authkey=AbjlxSozqu1c-2sRUrTGn7k)
```
-genome with bowtie-index (UCSC myoLuc2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/myoLuc2/bigZips/myoLuc2.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mluci2/myoLuc2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
     2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
/<your_defined_address>/Myotis_lucifugus/UCSC/myoLuc2/Sequence/BowtieIndex/genome
```

```
    -t /<your_defined_address>/Myotis_lucifugus/GtRNAdb/myoLuc2-tRNAs
    -f /<your_defined_address>/Myotis_lucifugus/Rfam_12.3/Rfam-12.3-bat
```

35. Trichechus manatus (Manatee)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06448172c574b4b9cbe0d906cf75bc68b&authkey=AX_fEuPmr18NZPEFbcg9nEQ)
```
      -genome with bowtie-index (UCSC triMan1) (Original source:
      http://hgdownload.soe.ucsc.edu/goldenPath/triMan1/bigZips/triMan1.fa.gz)
      -tRNA database with bowtie-index (Original source:
      http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Tmana1/triMan1-tRNAs.fa)
      -rfam 12.3 database with bowtie-index (Original source:
      ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
      /<your_defined_address>/Trichechus_manatus/UCSC/triMan1/Sequence/BowtieIndex/genom
      e
      -t /<your_defined_address>/Trichechus_manatus/GtRNAdb/triMan1-tRNAs
      -f /<your_defined_address>/Trichechus_manatus/Rfam_12.3/Rfam-12.3-manatee
```
36. Loxodonta africana (Elephant)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e0146e32fe4745bba50bbede409efddc&authkey=AT8bNP2DhjKysDaGD4Qy-7s)
```
      -genome with bowtie-index (UCSC loxAfr3) (Original source:
      http://hgdownload.soe.ucsc.edu/goldenPath/loxAfr3/bigZips/loxAfr3.fa.gz)
      -tRNA database with bowtie-index (Original source:
      http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Lafri3/loxAfr3-tRNAs.fa)
      -rfam 12.3 database with bowtie-index (Original source:
      ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
      /<your_defined_address>/Loxodonta_africana/UCSC/loxAfr3/Sequence/BowtieIndex/genom
      e
      -t /<your_defined_address>/Loxodonta_africana/GtRNAdb/loxAfr3-tRNAs
      -f /<your_defined_address>/Loxodonta_africana/Rfam_12.3/Rfam-12.3-elephant
```
37. Dasypus novemcinctus (Armadillo)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0c68adc6b2afc447a9dfe45a1a5eedd49&authkey=AUPTS51dr88E3AMvcZtljrk)
```
      -genome with bowtie-index (UCSC dasNov3) (Original source:
      http://hgdownload.soe.ucsc.edu/goldenPath/dasNov3/bigZips/dasNov3.fa.gz)
      -tRNA database with bowtie-index (Original source:
      http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Dnove3/dasNov3-tRNAs.fa)
      -rfam 12.3 database with bowtie-index (Original source:
      ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
      /<your_defined_address>/Dasypus_novemcinctus/UCSC/dasNov3/Sequence/BowtieIndex/gen
      ome
      -t /<your_defined_address>/Dasypus_novemcinctus/GtRNAdb/dasNov3-tRNAs
      -f /<your_defined_address>/Dasypus_novemcinctus/Rfam_12.3/Rfam-12.3-armadillo
```
38. Notamacropus eugenii (Wallaby)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=076db8740d2e34caabb25669fd6297e36&authkey=AWv-dFi1Mm7C0QH9K00WHH4)
```
      -genome with bowtie-index (UCSC macEug2) (Original source:
      http://hgdownload.soe.ucsc.edu/goldenPath/macEug2/bigZips/macEug2.fa.gz)
      -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
      -tRNA database with bowtie-index (Original source:
```

```
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Meuge2/macEug2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Notamacropus_eugenii/UCSC/macEug2/Sequence/BowtieIndex/gen
ome
-m /<your_defined_address>/Notamacropus_eugenii/miRBase_21/miRBase_21-meu
-t /<your_defined_address>/Notamacropus_eugenii/GtRNAdb/macEug2-tRNAs
-f /<your_defined_address>/Notamacropus_eugenii/Rfam_12.3/Rfam-12.3-wallaby
```
39. Sarcophilus harrisii (Tasmanian devil)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0469dc3788cbb40bab7472ee70a230dc0&authkey=AXA1nDb4QpYeuIJFC-D6mL0)
```
-genome with bowtie-index (UCSC sarHar1) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/sarHar1/bigZips/sarHar1.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Sharr1/sarHar1-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Sarcophilus_harrisii/UCSC/sarHar1/Sequence/BowtieIndex/gen
ome
-m /<your_defined_address>/Sarcophilus_harrisii/miRBase_21/miRBase_21-sha
-t /<your_defined_address>/Sarcophilus_harrisii/GtRNAdb/sarHar1-tRNAs
-f /<your_defined_address>/Sarcophilus_harrisii/Rfam_12.3/Rfam-12.3-tasmanian
```
40. Monodelphis domestica (Opossum)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=05e9cd2f3891a4761ade95d98aa3ebc78&authkey=Ae_jBKIdBC7HypVTN7S98Rw)
```
-genome with bowtie-index (UCSC monDom5) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/monDom5/bigZips/chromFa.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mdome5/monDom5-tRNAs.fa)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/monodelphis_domestica/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Monodelphis_domestica/UCSC/monDom5/Sequence/BowtieIndex/ge
nome
-m /<your_defined_address>/Monodelphis_domestica/miRBase_21/miRBase_21-mdo
-t /<your_defined_address>/Monodelphis_domestica/GtRNAdb/monDom5-tRNAs
-e
/<your_defined_address>/Monodelphis_domestica/Ensembl/Monodelphis_domestica.BROADO
5.ncrna
-f /<your_defined_address>/Monodelphis_domestica/Rfam_12.3/Rfam-12.3-opossum
```
41. Ornithorhynchus anatinus (Platypus)
   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=07f0f4ed088844a86afa5db763407699c&authkey=AUFx9yWXHtg1CQc-wfpJ81M)
```
-genome with bowtie-index (UCSC ornAna2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/ornAna2/bigZips/ornAna2.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
```

```
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Oanat1/ornAna1-tRNAs.fa)
-piRNA database with bowtie-index (Original source:
http://pirnabank.ibab.ac.in/request.html)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/ornithorhynchus_anatinus/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Ornithorhynchus_anatinus/UCSC/ornAna2/Sequence/BowtieIndex
/genome
-m /<your_defined_address>/Ornithorhynchus_anatinus/miRBase_21/miRBase_21-oan
-t /<your_defined_address>/Ornithorhynchus_anatinus/GtRNAdb/ornAna1-tRNAs
-w /<your_defined_address>/Ornithorhynchus_anatinus/piRBase/piR_platypus
-e
/<your_defined_address>/Ornithorhynchus_anatinus/Ensembl/Ornithorhynchus_anatinus.
OANA5.ncrna
-f /<your_defined_address>/Ornithorhynchus_anatinus/Rfam_12.3/Rfam-12.3-platypus
```
42. Taeniopygia guttata (Zebra finch)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0defbf712045f4e7f85b373b0eba4cd1b&authkey=AbieXkq6akbsD8tY1oGctDI)
```
-genome with bowtie-index (UCSC taeGut2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/taeGut2/bigZips/taeGut2.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Tgutt2/taeGut2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Taeniopygia_guttata/UCSC/taeGut2/Sequence/BowtieIndex/geno
me
-m /<your_defined_address>/Taeniopygia_guttata/miRBase_21/miRBase_21-tgu
-t /<your_defined_address>/Taeniopygia_guttata/GtRNAdb/taeGut2-tRNAs
-f /<your_defined_address>/Taeniopygia_guttata/Rfam_12.3/Rfam-12.3-finch
```
43. Melopsittacus undulatus (Budgerigar)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0e0046ab3b1a9458a9a183b45507ea0c3&authkey=AWiCroVnVDQcPENZDX_76VM)
```
-genome with bowtie-index (UCSC melUnd1) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/melUnd1/bigZips/melUnd1.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mundu1/melUnd1-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Melopsittacus_undulatus/UCSC/melUnd1/Sequence/BowtieIndex/
genome
-t /<your_defined_address>/Melopsittacus_undulatus/GtRNAdb/melUnd1-tRNAs
-f /<your_defined_address>/Melopsittacus_undulatus/Rfam_12.3/Rfam-12.3-budgerigar
```
44. Gallus gallus (Chicken)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0abafb326c4074fe9971d60a26497126c&authkey=AcRw_9ltjRXbdNAfmLRl_gg)
```
-genome with bowtie-index (UCSC galGal5) (Original source:
```

```
ftp://igenome2:u7NMwVkm@ftp.illumina.com/Gallus_gallus/UCSC/galGal5/Gallus_gallus_
UCSC_galGal5.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ggall4/galGal4-tRNAs.fa)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-piRNA database with bowtie-index (Original source:
http://www.regulatoryrna.org/database/piRNA/)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/gallus_gallus/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. PORTS1.0 related parameters if you download recommended reference database: `-g`
   ```
   /<your_defined_address>/Gallus_gallus/UCSC/galGal5/Sequence/BowtieIndex/genome
   -m /<your_defined_address>/Gallus_gallus/miRBase_21/miRBase_21-gga
   -r /<your_defined_address>/Gallus_gallus/rRNA_db/chicken_rRNA
   -t /<your_defined_address>/Gallus_gallus/GtRNAdb/galGal4-tRNAs
   -w /<your_defined_address>/Gallus_gallus/piRBase/piR_gga_v1.0
   -e
   /<your_defined_address>/Gallus_gallus/Ensembl/Gallus_gallus.Gallus_gallus-5.0.ncrn
   a
   -f /<your_defined_address>/Gallus_gallus/Rfam_12.3/Rfam-12.3-chicken
   ```

45. Meleagris gallopavo (Turkey)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0c88e1661f08e4b6d945d87e8120bdf07&authkey=AWlCjj414nXNuNbrNM7mbE4)
       ```
       -genome with bowtie-index (UCSC melGal1) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/melGal1/bigZips/melGal1.fa.gz)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mgall1/melGal1-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Meleagris_gallopavo/UCSC/melGal1/Sequence/BowtieIndex/geno
       me
       -t /<your_defined_address>/Meleagris_gallopavo/GtRNAdb/melGal1-tRNAs
       -f /<your_defined_address>/Meleagris_gallopavo/Rfam_12.3/Rfam-12.3-turkey
       ```

46. Chrysemys picta (Painted Turtle)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0fbd62d91eb4442a88525f89684a74242&authkey=AY3fgBdvPRzWpqqD4yd_Sqw)
       ```
       -genome with bowtie-index (UCSC chrPic1) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/chrPic1/bigZips/chrPic1.fa.gz)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ocuni2/oryCun2-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Chrysemys_picta/UCSC/chrPic1/Sequence/BowtieIndex/genome
       -t /<your_defined_address>/Chrysemys_picta/GtRNAdb/chrPic1-tRNAs
       -f /<your_defined_address>/Chrysemys_picta/Rfam_12.3/Rfam-12.3-turtle
       ```

47. Anolis carolinensis (Lizard)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=06986df31c45c4a00a6a2b47ce4ee7af2&authkey=AaE-i58-1fjJeqcDHZUpLLo)

```
-genome with bowtie-index (UCSC anoCar2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/anoCar2/bigZips/anoCar2.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Acaro2/anoCar2-tRNAs.fa)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/anolis_carolinensis/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
/<your_defined_address>/Anolis_carolinensis/UCSC/anoCar2/Sequence/BowtieIndex/geno
me
-m /<your_defined_address>/Anolis_carolinensis/miRBase_21/miRBase_21-aca
-t /<your_defined_address>/Anolis_carolinensis/GtRNAdb/anoCar2-tRNAs
-e
/<your_defined_address>/Anolis_carolinensis/Ensembl/Anolis_carolinensis.AnoCar2.0.
ncrna
-f /<your_defined_address>/Anolis_carolinensis/Rfam_12.3/Rfam-12.3-lizard
```

48. Xenopus laevis (Frog)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0d9b3d45b3bf3483c826c36d2b340f0fd&authkey=AdGZ969RHd1lpwBpm7lsGEQ)
       ```
       -genome with bowtie-index (UCSC xenTro7) (Original source:
       ftp://hgdownload.soe.ucsc.edu/goldenPath/xenTro7/bigZips/xenTro7.fa.gz)
       -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Xtrop3/xenTro3-tRNAs.fa)
       -rRNA database with bowtie-index (Original source:
       https://www.ncbi.nlm.nih.gov/nuccore)
       -piRNA database with bowtie-index (Original source:
       http://www.regulatoryrna.org/database/piRNA/)
       -ensembl ncRNA database with bowtie-index (Original source:
       ftp://ftp.ensembl.org/pub/release-89/fasta/xenopus_tropicalis/ncrna/)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: -g
       ```
       /<your_defined_address>/Xenopus_laevis/UCSC/xenTro7/Sequence/BowtieIndex/genome
       -m /<your_defined_address>/Xenopus_laevis/miRBase_21/miRBase_21-xtr
       -r /<your_defined_address>/Xenopus_laevis/rRNA_db/frog_rRNA
       -t /<your_defined_address>/Xenopus_laevis/GtRNAdb/xenTro3-tRNAs
       -w /<your_defined_address>/Xenopus_laevis/piRBase/piR_xtr_v1.0
       -e /<your_defined_address>/Xenopus_laevis/Ensembl/Xenopus_tropicalis.JGI_4.2.ncrna
       -f /<your_defined_address>/Xenopus_laevis/Rfam_12.3/Rfam-12.3-frog
       ```
49. Latimeria chalumnae (Coelacanth)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0be8104aeb59d4ff89909d0c62d0a2f4e&authkey=AasK4DZcbB12a8wB8CNz6Ak)
       ```
       -genome with bowtie-index (UCSC latCha1) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/latCha1/bigZips/latCha1.fa.gz)
       -rRNA database with bowtie-index (Original source:
       https://www.ncbi.nlm.nih.gov/nuccore)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Lchal1/latCha1-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: -g

```
/<your_defined_address>/Latimeria_chalumnae/UCSC/latCha1/Sequence/BowtieIndex/geno
me
-r /<your_defined_address>/Latimeria_chalumnae/rRNA_db/coelacanth_rRNA
-t /<your_defined_address>/Latimeria_chalumnae/GtRNAdb/latCha1-tRNAs
-f /<your_defined_address>/Latimeria_chalumnae/Rfam_12.3/Rfam-12.3-coelacanth
```

50. Tetraodon nigroviridis (Tetraodon)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=06252eaadd5894a3795afce052716fd17&authkey=AWZ9FVt-iphiQFRDzuKoJtA)
       ```
       -genome with bowtie-index (UCSC tetNig2) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/tetNig2/bigZips/chromFa.tar.gz)
       -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Tnigr2/tetNig2-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Tetraodon_nigroviridis/UCSC/tetNig2/Sequence/BowtieIndex/g
       enome
       -m /<your_defined_address>/Tetraodon_nigroviridis/miRBase_21/miRBase_21-tni
       -t /<your_defined_address>/Tetraodon_nigroviridis/GtRNAdb/tetNig2-tRNAs
       -f /<your_defined_address>/Tetraodon_nigroviridis/Rfam_12.3/Rfam-12.3-tetraodon
       ```
51. Takifugu rubripes (Fugu)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=026501a5c4aa54930a00289acf9691f5f&authkey=AWUaDYW0_VZx-1dy5wnCfdQ)
       ```
       -genome with bowtie-index (UCSC fr3) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/fr3/bigZips/fr3.fa.gz)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Trubr3/fr3-tRNAs.fa)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Takifugu_rubripes/UCSC/fr3/Sequence/BowtieIndex/genome
       -t /<your_defined_address>/Takifugu_rubripes/GtRNAdb/fr3-tRNAs
       -f /<your_defined_address>/Takifugu_rubripes/Rfam_12.3/Rfam-12.3-fugu
       ```
52. Gasterosteus aculeatus (Stickleback)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=0268db779d3654712b39d5450bac55894&authkey=AQwh0wJeAcvF78JRu4RHddM)
       ```
       -genome with bowtie-index (UCSC gasAcu1) (Original source:
       http://hgdownload.soe.ucsc.edu/goldenPath/gasAcu1/bigZips/chromFa.tar.gz)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Gacul1/gasAcu1-tRNAs.fa)
       -ensembl ncRNA database with bowtie-index (Original source:
       ftp://ftp.ensembl.org/pub/release-89/fasta/gasterosteus_aculeatus/ncrna/)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Gasterosteus_aculeatus/UCSC/gasAcu1/Sequence/BowtieIndex/g
       enome
       -t /<your_defined_address>/Gasterosteus_aculeatus/GtRNAdb/gasAcu1-tRNAs
       -e
       /<your_defined_address>/Gasterosteus_aculeatus/Ensembl/Gasterosteus_aculeatus.BROA
       DS1.ncrna
       ```

```
    -f /<your_defined_address>/Gasterosteus_aculeatus/Rfam_12.3/Rfam-12.3-stickleback
```
53. Oryzias latipes (Medaka)
1. annotation database: (We provide a download link for all databases listed below:
   https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
   px?docid=0f5089e2cc47245f28dca1a3f8f75343c&authkey=AV8N2wRviWth_LjhJqpB0zk)
```
    -genome with bowtie-index (UCSC oryLat2)
    (http://hgdownload.soe.ucsc.edu/goldenPath/oryLat2/bigZips/oryLat2.fa.gz)
    -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
    -tRNA database with bowtie-index (Original source:
    http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Olati2/oryLat2-tRNAs.fa)
    -rfam 12.3 database with bowtie-index (Original source:
    ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
    /<your_defined_address>/Oryzias_latipes/UCSC/oryLat2/Sequence/BowtieIndex/genome
    -m /<your_defined_address>/Oryzias_latipes/miRBase_21/miRBase_21-ola
    -t /<your_defined_address>/Oryzias_latipes/GtRNAdb/oryLat2-tRNAs
    -f /<your_defined_address>/Oryzias_latipes/Rfam_12.3/Rfam-12.3-medaka
```
54. Oreochromis niloticus (Nile tilapia)
1. annotation database: (We provide a download link for all databases listed below:
   https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
   px?docid=0cf791d1d99de4f4c8ed7f8de6d5694f8&authkey=AZZgbe3d1aKb7GDuCDlv81w)
```
    -genome with bowtie-index (UCSC oreNil2) (Original source:
    http://hgdownload.soe.ucsc.edu/goldenPath/oreNil2/bigZips/oreNil2.fa.gz)
    -tRNA database with bowtie-index (Original source:
    http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Onilo2/oreNil2-tRNAs.fa)
    -rfam 12.3 database with bowtie-index (Original source:
    ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
    /<your_defined_address>/Oreochromis_niloticus/UCSC/oreNil2/Sequence/BowtieIndex/ge
    nome
    -t /<your_defined_address>/Oreochromis_niloticus/GtRNAdb/oreNil2-tRNAs
    -f /<your_defined_address>/Oreochromis_niloticus/Rfam_12.3/Rfam-12.3-tilapia
```
55. Gadus morhua (Atlantic cod)
1. annotation database: (We provide a download link for all databases listed below:
   https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
   px?docid=08f5a65a279f34d518cc4017cb04fe469&authkey=ASMQLlwmWReD_bVW922N0Io)
```
    -genome with bowtie-index (UCSC gadMor1) (Original source:
    http://hgdownload.soe.ucsc.edu/goldenPath/gadMor1/bigZips/gadMor1.fa.gz)
    -rRNA database with bowtie-index (Original source:
    https://www.ncbi.nlm.nih.gov/nuccore)
    -tRNA database with bowtie-index (Original source:
    http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Gmorh1/gadMor1-tRNAs.fa)
    -rfam 12.3 database with bowtie-index (Original source:
    ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
2. SPORTS1.0 related parameters if you download recommended reference database: -g
```
    /<your_defined_address>/Gadus_morhua/UCSC/gadMor1/Sequence/BowtieIndex/genome
    -r /<your_defined_address>/Gadus_morhua/rRNA_db/cod_rRNA
    -t /<your_defined_address>/Gadus_morhua/GtRNAdb/gadMor1-tRNAs
    -f /<your_defined_address>/Gadus_morhua/Rfam_12.3/Rfam-12.3-cod
```
56. Danio rerio (Zebrafish)
1. annotation database: (We provide a download link for all databases listed below:
   https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
   px?docid=07d3448d6cd29485498e70f8f067a619d&authkey=Aa1-VjshX-GKLZI7limHFIo)
```
    -genome with bowtie-index (UCSC danRer10) (Original source:
    ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Danio_rerio/UCSC/danRer10/Danio_reri
```

```
o_UCSC_danRer10.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Dreri_v8/danRer6-tRNAs.fa)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-piRNA database with bowtie-index (Original source:
http://www.regulatoryrna.org/database/piRNA/)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensembl.org/pub/release-89/fasta/danio_rerio/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Danio_rerio/UCSC/danRer10/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Danio_rerio/miRBase_21/miRBase_21-dre
-r /<your_defined_address>/Danio_rerio/rRNA_db/zebrafish_rRNA
-t /<your_defined_address>/Danio_rerio/GtRNAdb/danRer6-tRNAs
-w /<your_defined_address>/Danio_rerio/piRBase/piR_dre_v1.0
-e /<your_defined_address>/Danio_rerio/Ensembl/Danio_rerio.GRCz10.ncrna
-f /<your_defined_address>/Danio_rerio/Rfam_12.3/Rfam-12.3-zebrafish
```

57. Callorhinchus milii (Elephant shark)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=053976e5c17b9435982d22223b9389eba&authkey=ASL1VUPU4Ol2PskRXpj94t4)

```
-genome with bowtie-index (UCSC calMil1) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/calMil1/bigZips/calMil1.fa.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Cmili1/calMil1-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Callorhinchus_milii/UCSC/calMil1/Sequence/BowtieIndex/geno
me
-t /<your_defined_address>/Callorhinchus_milii/GtRNAdb/calMil1-tRNAs
-f /<your_defined_address>/Callorhinchus_milii/Rfam_12.3/Rfam-12.3-shark
```

58. Petromyzon marinus (Lamprey)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=013a1f7a5585b462b801f1cfe3faf2cdd&authkey=AVN94xcHd1_Aa2ofYovsw8Q)

```
-genome with bowtie-index (UCSC petMar2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/petMar2/bigZips/petMar2.fa.gz)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Pmari2/petMar2-tRNAs.fa)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Petromyzon_marinus/UCSC/petMar2/Sequence/BowtieIndex/genom
e
-r /<your_defined_address>/Petromyzon_marinus/rRNA_db/lamprey_rRNA
-t /<your_defined_address>/Petromyzon_marinus/GtRNAdb/petMar2-tRNAs
-f /<your_defined_address>/Petromyzon_marinus/Rfam_12.3/Rfam-12.3-lamprey
```

59. Strongylocentrotus purpuratus (Sea urchin)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as

px?docid=0840567689dbe4ff49852c8744056f172&authkey=AWhmaQmPgN5fuB1RXlKc69U)

```
-genome with bowtie-index (UCSC strPur2) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/strPur2/bigZips/strPur2.fa.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Spurp/Spurp-tRNAs.fa)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/strongylocentrotus_purpu
ratus/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Strongylocentrotus_purpuratus/UCSC/strPur2/Sequence/Bowtie
Index/genome
-m /<your_defined_address>/Strongylocentrotus_purpuratus/miRBase_21/miRBase_21-spu
-r /<your_defined_address>/Strongylocentrotus_purpuratus/rRNA_db/urchin_rRNA
-t /<your_defined_address>/Strongylocentrotus_purpuratus/GtRNAdb/Spurp-tRNAs
-e
/<your_defined_address>/Strongylocentrotus_purpuratus/Ensembl/Strongylocentrotus_p
urpuratus.GCA_000002235.2.ncrna
-f
/<your_defined_address>/Strongylocentrotus_purpuratus/Rfam_12.3/Rfam-12.3-urchin
```

60. Drosophila melanogaster (Drosophila)
    1. annotation database: (We provide a download link for all databases listed below:
       https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
       px?docid=06d15ec2032e141648ce4eedd413b0e0c&authkey=ARejQLC8ofAhQq9IwwoB0Pw)
       ```
       -genome with bowtie-index (UCSC dm6) (Original source:
       ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Drosophila_melanogaster/UCSC/dm6/Dro
       sophila_melanogaster_UCSC_dm6.tar.gz)
       -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
       -tRNA database with bowtie-index (Original source:
       http://gtrnadb.ucsc.edu/genomes/eukaryota/Dmela6/dm6-tRNAs.fa)
       -rRNA database with bowtie-index (Original source:
       https://www.ncbi.nlm.nih.gov/nuccore)
       -piRNA database with bowtie-index (Original source:
       http://www.regulatoryrna.org/database/piRNA/)
       -ensembl ncRNA database with bowtie-index (Original source:
       ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/drosophila_melanogaster/
       ncrna/)
       -rfam 12.3 database with bowtie-index (Original source:
       ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
       ```
    2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
       ```
       /<your_defined_address>/Drosophila_melanogaster/UCSC/dm6/Sequence/BowtieIndex/geno
       me
       -m /<your_defined_address>/Drosophila_melanogaster/miRBase_21/miRBase_21-dme
       -r /<your_defined_address>/Drosophila_melanogaster/rRNA_db/drosophila_rRNA
       -t /<your_defined_address>/Drosophila_melanogaster/GtRNAdb/dm6-tRNAs
       -w /<your_defined_address>/Drosophila_melanogaster/piRBase/piR_dme
       -e
       /<your_defined_address>/Drosophila_melanogaster/Ensembl/Drosophila_melanogaster.BD
       GP6.ncrna
       -f /<your_defined_address>/Drosophila_melanogaster/Rfam_12.3/Rfam-12.3-drosophila
       ```
61. Anopheles gambiae (Mosquito)
    1. annotation database: (We provide a download link for all databases listed below:

https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
px?docid=003bfc542d06b42edb24a94969bb12b36&authkey=AdgdWQ5emWRWTYvXcgPT0Fo)

```
-genome with bowtie-index (UCSC anoGam1) (Original source:
http://hgdownload.soe.ucsc.edu/goldenPath/anoGam1/bigZips/chromFa.zip)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Agamb/Agamb-tRNAs.fa)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/anopheles_gambiae/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Anopheles_gambiae/UCSC/anoGam1/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Anopheles_gambiae/miRBase_21/miRBase_21-aga
-t /<your_defined_address>/Anopheles_gambiae/GtRNAdb/Agamb-tRNAs
-e
/<your_defined_address>/Anopheles_gambiae/Ensembl/Anopheles_gambiae.AgamP4.ncrna
-f /<your_defined_address>/Anopheles_gambiae/Rfam_12.3/Rfam-12.3-mosquito
```

62. Pristionchus pacificus (Roundworm)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0877c09c8493b47e9b9fb6c2c0bdc6015&authkey=AQJrbZlyZz9MDnPB9uYxMYE)
      ```
      -genome with bowtie-index (UCSC priPac1) (Original source:
      http://hgdownload.soe.ucsc.edu/goldenPath/priPac1/bigZips/chromFa.tar.gz)
      -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
      -tRNA database with bowtie-index (Original source:
      http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ppaci1/priPac1-tRNAs.fa)
      -rfam 12.3 database with bowtie-index (Original source:
      ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
      ```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
      ```
      /<your_defined_address>/Pristionchus_pacificus/UCSC/priPac1/Sequence/BowtieIndex/g
      enome
      -m /<your_defined_address>/Pristionchus_pacificus/miRBase_21/miRBase_21-ppc
      -r /<your_defined_address>/Pristionchus_pacificus/rRNA_db/roundworm_rRNA
      -t /<your_defined_address>/Pristionchus_pacificus/GtRNAdb/priPac1-tRNAs
      -f /<your_defined_address>/Pristionchus_pacificus/Rfam_12.3/Rfam-12.3-roundworm
      ```

63. Caenorhabditis elegans (Nematode):
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0cffdc7d5a3844567bc5303adca47fb81&authkey=AdA1jCVLRJkz2k8oSVU-pCl)
      ```
      -genome with bowtie-index (UCSC ce10) (Original source:
      ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Caenorhabditis_elegans/UCSC/ce10/Cae
      norhabditis_elegans_UCSC_ce10.tar.gz)
      -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
      -tRNA database with bowtie-index (Original source:
      http://gtrnadb.ucsc.edu/genomes/eukaryota/Celeg_WS220/ce10-tRNAs.fa)
      -rRNA database with bowtie-index (Original source:
      https://www.ncbi.nlm.nih.gov/nuccore)
      -piRNA database with bowtie-index (Original source:
      http://www.regulatoryrna.org/database/piRNA/)
      -ensembl ncRNA database with bowtie-index (Original source:
      ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/caenorhabditis_elegans/n
      crna/)
      -rfam 12.3 database with bowtie-index (Original source:
      ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
      ```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Caenorhabditis_elegans/UCSC/ce10/Sequence/BowtieIndex/geno
me
-m /<your_defined_address>/Caenorhabditis_elegans/miRBase_21/miRBase_21-cel
-r /<your_defined_address>/Caenorhabditis_elegans/rRNA_db/cel_rRNA
-t /<your_defined_address>/Caenorhabditis_elegans/GtRNAdb/ce10-tRNAs
-w /<your_defined_address>/Caenorhabditis_elegans/piRBase/piR_cel_v1.0
-e
/<your_defined_address>/Caenorhabditis_elegans/Ensembl/Caenorhabditis_elegans.WBce
l235.ncrna
-f /<your_defined_address>/Caenorhabditis_elegans/Rfam_12.3/Rfam-12.3-nematode
```

64. Saccharomyces cerevisiae (Yeast)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as px?docid=0a974d08ffcb842dea8d18462dcfaf2f4&authkey=AQ6wsr9hNwVfCfqvuScKStE)

```
-genome with bowtie-index UCSC sacCer3) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Saccharomyces_cerevisiae/UCSC/sacCer
3/Saccharomyces_cerevisiae_UCSC_sacCer3.tar.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Scere3/sacCer3-tRNAs.fa)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensemblgenomes.org/pub/fungi/release-36/fasta/saccharomyces_cerevisiae/n
crna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Saccharomyces_cerevisiae/UCSC/sacCer3/Sequence/BowtieIndex
/genome
-r /<your_defined_address>/Saccharomyces_cerevisiae/rRNA_db/yeast_rRNA
-t /<your_defined_address>/Saccharomyces_cerevisiae/GtRNAdb/sacCer3-tRNAs
-e
/<your_defined_address>/Saccharomyces_cerevisiae/Ensembl/Saccharomyces_cerevisiae.
R64-1-1.ncrna
-f /<your_defined_address>/Saccharomyces_cerevisiae/Rfam_12.3/Rfam-12.3-yeast
```

65. Zea mays (Corn)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as px?docid=0abdce07adf9449e89bdcb89d4d4609a4&authkey=AViNEp3y6Y4hNBYSEuW_sYg)

```
-genome with bowtie-index (Ensembl AGPv4) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Zea_mays/Ensembl/AGPv4/Zea_mays_Ense
mbl_AGPv4.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Zmays5/zeaMay5-tRNAs.fa)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/zea_mays/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

2. SPORTS1.0 related parameters if you download recommended reference database: `-g`

```
/<your_defined_address>/Zea_mays/Ensembl/AGPv4/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Zea_mays/miRBase_21/miRBase_21-zma
-r /<your_defined_address>/Zea_mays/rRNA_db/corn_rRNA
-t /<your_defined_address>/Zea_mays/GtRNAdb/zeaMay5-tRNAs
```

```
-e /<your_defined_address>/Zea_mays/Ensembl/Zea_mays.AGPv4.ncrna
-f /<your_defined_address>/Zea_mays/Rfam_12.3/Rfam-12.3-corn
```

66. Sorghum bicolor (Sorghum)

   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as px?docid=0335fb9b05a024e61819c04db7ffd2a51&authkey=AdMT31NWtny7F1NzJNn3zZI)

   ```
   -genome with bowtie-index (Ensembl Sbi1) (Original source:
   ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Sorghum_bicolor/Ensembl/Sbi1/Sorghum
   _bicolor_Ensembl_Sbi1.tar.gz)
   -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
   -tRNA database with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Sbico/Sbico-tRNAs.fa)
   -rRNA database with bowtie-index (Original source:
   https://www.ncbi.nlm.nih.gov/nuccore)
   -ensembl ncRNA database with bowtie-index (Original source:
   ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/sorghum_bicolor/ncrna/)
   -rfam 12.3 database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   ```

   2. SPORTS1.0 related parameters if you download recommended reference database: `-g` `/<your_defined_address>/Sorghum_bicolor/Ensembl/Sbi1/Sequence/BowtieIndex/genome`

   ```
   -m /<your_defined_address>/Sorghum_bicolor/miRBase_21/miRBase_21-sbi
   -r /<your_defined_address>/Sorghum_bicolor/rRNA_db/sorghum_rRNA
   -t /<your_defined_address>/Sorghum_bicolor/GtRNAdb/Sbico-tRNAs
   -e
   /<your_defined_address>/Sorghum_bicolor/Ensembl/Sorghum_bicolor.Sorghum_bicolor_v2.
   ncrna
   -f /<your_defined_address>/Sorghum_bicolor/Rfam_12.3/Rfam-12.3-sorghum
   ```

67. Oryza sativa (Rice)

   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as px?docid=0510818bde4a342868928f982420dd07c&authkey=ASfslUL0BX2HYew7xrw2x1A)

   ```
   -genome with bowtie-index (Ensembl IRGSP-1.0) (Original source:
   ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Oryza_sativa_japonica/Ensembl/IRGSP-
   1.0/Oryza_sativa_japonica_Ensembl_IRGSP-1.0.tar.gz)
   -mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
   -tRNA database with bowtie-index (Original source:
   http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Osati/Osati-tRNAs.fa)
   -rRNA database with bowtie-index (Original source:
   https://www.ncbi.nlm.nih.gov/nuccore)
   -ensembl ncRNA database with bowtie-index (Original source:
   ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/oryza_sativa/ncrna/)
   -rfam 12.3 database with bowtie-index (Original source:
   ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
   ```

   2. SPORTS1.0 related parameters if you download recommend reference database: `-g` `/<your_defined_address>/Oryza_sativa/Ensembl/IRGSP-1.0/Sequence/BowtieIndex/genome`

   ```
   -m /<your_defined_address>/Oryza_sativa/miRBase_21/miRBase_21-osa
   -r /<your_defined_address>/Oryza_sativa/rRNA_db/rice_rRNA
   -t /<your_defined_address>/Oryza_sativa/GtRNAdb/Osati-tRNAs
   -e /<your_defined_address>/Oryza_sativa/Ensembl/Oryza_sativa.IRGSP-1.0.ncrna
   -f /<your_defined_address>/Oryza_sativa/Rfam_12.3/Rfam-12.3-rice
   ```

68. Arabidopsis thaliana (Arabidopsis)

   1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as px?docid=08ec312d8fc7d4211952170468dfbb202&authkey=AeVag9p4ifZJG58C5UbXstE)

   ```
   -genome with bowtie-index (Ensembl TAIR10) (Original source:
   ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Arabidopsis_thaliana/Ensembl/TAIR10/
   ```

```
Arabidopsis_thaliana_Ensembl_TAIR10.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Athal10/araTha1-tRNAs.fa)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/arabidopsis_thaliana/ncrn
a/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```

   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Arabidopsis_thaliana/Ensembl/TAIR10/Sequence/BowtieIndex/g
enome
-m /<your_defined_address>/Arabidopsis_thaliana/miRBase_21/miRBase_21-ath
-r /<your_defined_address>/Arabidopsis_thaliana/rRNA_db/Arabidopsis_rRNA
-t /<your_defined_address>/Arabidopsis_thaliana/GtRNAdb/araTha1-tRNAs
-e
/<your_defined_address>/Arabidopsis_thaliana/Ensembl/Arabidopsis_thaliana.TAIR10.n
crna
-f /<your_defined_address>/Arabidopsis_thaliana/Rfam_12.3/Rfam-12.3-arabidopsis
```
69. Glycine max (Soybean)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=079974655bb2e4f62b669c3d1701fffeb&authkey=AWVriz_LNaTMDsBjbMXDS60)
```
-genome with bowtie-index (Ensembl Gm01) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Glycine_max/Ensembl/Gm01/Glycine_max
_Ensembl_Gm01.tar.gz)
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Gmax2/glyMax2-tRNAs.fa)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
   2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
```
/<your_defined_address>/Glycine_max/Ensembl/Gm01/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Glycine_max/miRBase_21/miRBase_21-gma
-r /<your_defined_address>/Glycine_max/rRNA_db/soybean_rRNA
-t /<your_defined_address>/Glycine_max/GtRNAdb/glyMax2-tRNAs
-f /<your_defined_address>/Glycine_max/Rfam_12.3/Rfam-12.3-soybean
```
70. Escherichia coli (E.coli)
   1. annotation database: (We provide a download link for all databases listed below:
      https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.as
      px?docid=0645cc2a0024d41fdba5be31a17bd5374&authkey=AaR4ui2QEXqh2-SpOIxaUik)
```
-genome with bowtie-index (Ensembl EB1) (Original source:
ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Escherichia_coli_K_12_DH10B/Ensembl/
EB1/Escherichia_coli_K_12_DH10B_Ensembl_EB1.tar.gz)
-tRNA database with bowtie-index (Original source:
http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/bacteria/Esch_coli/eschColi-tRNAs.fa)
-rRNA database with bowtie-index (Original source:
https://www.ncbi.nlm.nih.gov/nuccore)
-ensembl ncRNA database with bowtie-index (Original source:
ftp://ftp.ensemblgenomes.org/pub/bacteria/release-36/fasta/bacteria_91_collection/
escherichia_coli/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
```

```
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
```
2. SPORTS1.0 related parameters if you download recommended reference database: `-g`
   ```
   /<your_defined_address>/Escherichia_coli/Ensembl/EB1/Sequence/BowtieIndex/genome
   -r /<your_defined_address>/Escherichia_coli/rRNA_db/e_coli_rRNA
   -t /<your_defined_address>/Escherichia_coli/GtRNAdb/eschColi-tRNAs
   -e
   /<your_defined_address>/Escherichia_coli/Ensembl/Escherichia_coli.HUSEC2011CHR1.nc
   rna
   -f /<your_defined_address>/Escherichia_coli/Rfam_12.3/Rfam-12.3-e_coli
   ```

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History

1.0.4 - 03/25/2018 1. New function added: if '-M > 0' applied in sports.pl, statistics of mismatch information will generated to predict potential nucleic acid modification loci; 2. Figure of tRNA mapping information will generated if tRNA database is defined; 3. A sample output result of dataset GSM2304822 (mouse sperm) is uploaded with the parameters '-M 1'.

1.0.3 - 01/27/2018 1. Changed the mapping order to make the mapping results more accurate

according to the paper " Juan Pablo Tosar, Carlos Rovira, Alfonso Cayota. Non-coding RNA fragments account for the majority of annotated piRNAs expressed in somatic non-gonadal tissues. Communications Biology. 2018;1, Article number: 2. doi: 10.1038/s42003-017-0001-7 ".

1.0.2 - 01/22/2018 1. Fixed bugs to generate more accurate mature tRNA database.

1.0.1 - 01/13/2018 1. Fixed bugs that caused unexpected exit. 2. Optimized script to speed up tRNA annotation process.

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Contact information

Contact author: Junchao Shi

E-mail: sports.rna@gmail.com; junchao.shi@yahoo.com