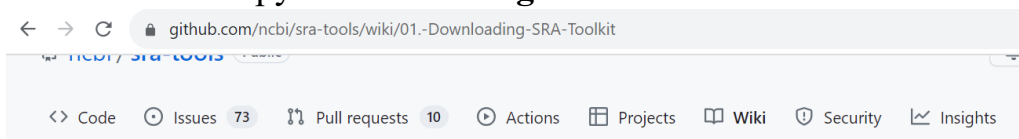


SRA TOOLKIT INSTALLATION

1) From this site copy the link and **wget** in commandline



01. Downloading SRA Toolkit

Andrew Klymenko edited this page on Aug 29 · 31 revisions

NCBI SRA Toolkit

Below are the latest releases of various tools and release checksum file.

SRA Toolkit

Compiled binaries/install scripts of August 29, 2023, version 3.0.7:

- [CentOS Linux 64 bit architecture](#) - non-sudo tar archive
- [Ubuntu Linux 64 bit architecture](#) - non-sudo tar archive
- [Cloud - apt-get install script](#) - for Debian and Ubuntu - requires sudo permissions

2) Then do decompressed the file by

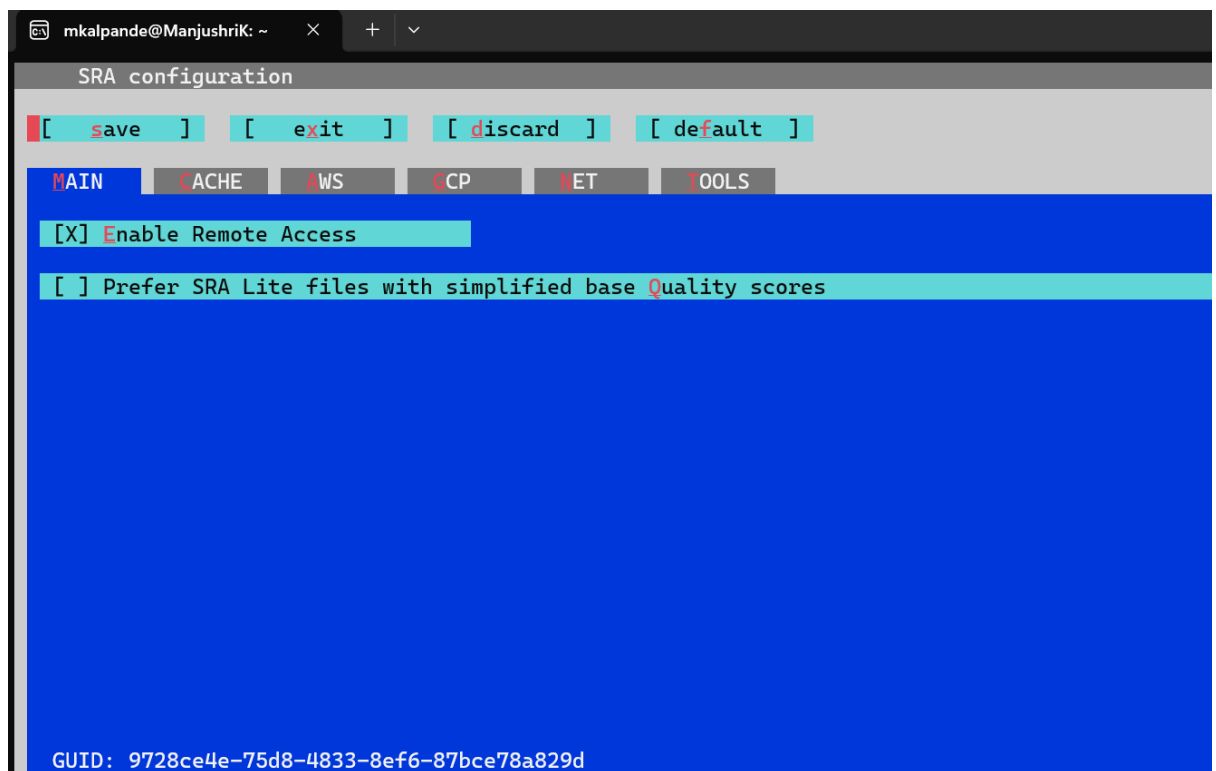
tar -xvf sra...

```
mikalpande@Manjushrik:~$ ls
FastQC                               bwa-0.7.17.tar.bz2                htlib-1.18
HTSeq-2.0.4                         bwa-0.7.17.tar.bz2:Zone.Identifier htlib-1.18.tar.bz2
HTSeq-2.0.4.tar.gz                 fastqc_v0.12.1.zip                samtools-1.18
HTSeq-2.0.4.tar.gz:Zone.Identifier hisat2                             samtools-1.18.tar.bz2
bcftools-1.18                      hisat2-2.2.1                      sratoolkit.3.0.7-ubuntu64
bcftools-1.18.tar.bz2              hisat2-2.2.1-Linux_x86_64.zip      sratoolkit.3.0.7-ubuntu64.tar.gz
bwa-0.7.17                         hisat2-2.2.1-Linux_x86_64.zip:Zone.Identifier
mikalpande@Manjushrik:~$ ls sratoolkit.3.0.7-ubuntu64
CHANGES  README-blastn  README-vdb-config  README.md  bin  example  schema
```

3)

```
mikalpande@Manjushrik:~$ ls sratoolkit.3.0.7-ubuntu64
CHANGES  README-blastn  README-vdb-config  README.md  bin  example  schema
mikalpande@Manjushrik:~$ ls sratoolkit.3.0.7-ubuntu64/bin/
abi-dump          fastq-dump          ncbi                sra-search          vdb-config.3.0.7
abi-dump.3       fastq-dump-orig.3.0.7 pacbio-load         sra-search.3        vdb-copy
abi-dump.3.0.7   fastq-dump.3       pacbio-load.3       sra-search.3.0.7    vdb-copy.3
abi-load         fastq-dump.3.0.7   pacbio-load.3.0.7   sra-sort            vdb-copy.3.0.7
abi-load.3       fastq-load          prefetch            sra-sort-cg         vdb-decrypt
abi-load.3.0.7   fastq-load.3       prefetch-orig.3.0.7 sra-sort-cg.3       vdb-decrypt.3
align-info       fastq-load.3.0.7   prefetch.3          sra-sort-cg.3.0.7   vdb-decrypt.3.0.7
align-info.3     helicob-load        prefetch.3.0.7      sra-sort.3          vdb-dump
align-info.3.0.7 helicob-load.3      rcexplain.3         sra-sort.3.0.7      vdb-dump-orig.3.0.7
bam-load         helicob-load.3.0.7 rcexplain.3.0.7     sra-stat            vdb-dump.3
bam-load.3       illumina-dump       rcexplain.3.0.7     sra-stat.3          vdb-dump.3.0.7
bam-load.3.0.7   illumina-dump.3    sam-dump            sra-stat.3.0.7      vdb-encrypt
cache-mgr        illumina-dump.3.0.7 sam-dump-orig.3.0.7 srapiath            vdb-encrypt.3
cache-mgr.3      illumina-load       sam-dump.3          srapiath-orig.3.0.7 vdb-encrypt.3.0.7
cache-mgr.3.0.7 illumina-load.3     sam-dump.3.0.7      srapiath.3          vdb-lock
cg-load          illumina-load.3.0.7 sff-dump            sra-tools.3.0.7     vdb-lock.3
cg-load.3        kar                 sff-dump.3         sra-tools.3.0.7     vdb-lock.3.0.7
cg-load.3.0.7   kar.3              sff-dump.3.0.7     srf-load            vdb-unlock
dump-ref-fasta   kar.3.0.7          sff-load           srf-load.3          vdb-unlock.3
dump-ref-fasta.3 kdbmeta            sff-load.3         srf-load.3.0.7     vdb-unlock.3.0.7
dump-ref-fasta.3.0.7 kdbmeta.3         sff-load.3.0.7     test-sra            vdb-validate
fasterq-dump     kdbmeta.3.0.7     sff-load.3.0.7     test-sra.3          vdb-validate.3
fasterq-dump-orig.3.0.7 latf-load          sra-pileup-orig.3.0.7 test-sra.3.0.7     vdb-validate.3.0.7
fasterq-dump.3   latf-load.3        sra-pileup.3        vdb-config          vdb-validate.3.0.7
fasterq-dump.3.0.7 latf-load.3.0.7   sra-pileup.3.0.7   vdb-config.3
mikalpande@Manjushrik:~$
```

- 4) now to set the configurations we are going to use- sratoolkit.3.0.7-ubuntu64/bin/vdb-config -interactive
to activate the tool we have to do this just exit and do nothing.



- 5) next we move the sratoolkit in a new folder

```
mkalpande@ManjushriK:~$ mkdir apps
mkalpande@ManjushriK:~$ ls
FastQC                               bwa-0.7.17                               hisat2-2.2.1-Linux_x86_64.zip:Zone.Identifier
HTSeq-2.0.4                         bwa-0.7.17.tar.bz2                      htlib-1.18
HTSeq-2.0.4.tar.gz                 bwa-0.7.17.tar.bz2:Zone.Identifier      htlib-1.18.tar.bz2
HTSeq-2.0.4.tar.gz:Zone.Identifier fastqc_v0.12.1.zip                      samtools-1.18
apps                               hisat2                                   samtools-1.18.tar.bz2
bcftools-1.18                     hisat2-2.2.1                             sratoolkit.3.0.7-ubuntu64
bcftools-1.18.tar.bz2             hisat2-2.2.1-Linux_x86_64.zip            sratoolkit.3.0.7-ubuntu64.tar.gz
mkalpande@ManjushriK:~$ mv -v sratoolkit.3.0.7-ubuntu64 sratoolkit
renamed 'sratoolkit.3.0.7-ubuntu64' -> 'sratoolkit'
mkalpande@ManjushriK:~$ ls
FastQC                               bwa-0.7.17                               hisat2-2.2.1-Linux_x86_64.zip:Zone.Identifier
HTSeq-2.0.4                         bwa-0.7.17.tar.bz2                      htlib-1.18
HTSeq-2.0.4.tar.gz                 bwa-0.7.17.tar.bz2:Zone.Identifier      htlib-1.18.tar.bz2
HTSeq-2.0.4.tar.gz:Zone.Identifier fastqc_v0.12.1.zip                      samtools-1.18
apps                               hisat2                                   samtools-1.18.tar.bz2
bcftools-1.18                     hisat2-2.2.1                             sratoolkit
bcftools-1.18.tar.bz2             hisat2-2.2.1-Linux_x86_64.zip            sratoolkit.3.0.7-ubuntu64.tar.gz
mkalpande@ManjushriK:~$ mv -v sratoolkit apps
renamed 'sratoolkit' -> 'apps/sratoolkit'
```

```
mkalpande@ManjushriK:~$ ls apps
sratoolkit
```

6) next is to set path in .bashrc file

```
PATH=${PATH}:/home/mkarpande/.local/bin
export PATH=${PATH}:/home/mkarpande/FastQC
export PATH=${PATH}:/home/mkarpande/hisat2-2.2.1
export PATH=${PATH}:/home/mkarpande/htslib-1.18
export PATH=${PATH}:/home/mkarpande/samtools-1.18
export PATH=${PATH}:/home/mkarpande/bcftools-1.18
export PATH=${PATH}:/home/mkarpande/apps/sratoolkit/bin
```

7) its done properly

```
mkarpande@ManjushriK:~$ fastq-dump

Usage:
  fastq-dump [options] <path> [<path>...]
  fastq-dump [options] <accession>

Use option --help for more information

fastq-dump : 3.0.7

mkarpande@ManjushriK:~$ |
```

Steps to download data using sra toolkit-

Commands first - vdb-config --prefetch-to-cwd

Explanation-

- 1) vdb-config: This is the name of the configuration tool for the SRA Toolkit.
- 2) prefetch-to-cwd: This is an option for the vdb-config tool. It tells the SRA Toolkit to prefetch SRA data directly to the current working directory (cwd).
- 3) To download the file use command – prefetch SRR

Sample download of other file:

```
mkarpande@ManjushriK:~/sra_data$ prefetch SRR16235266

2023-12-11T08:17:46 prefetch.3.0.7: Current preference is set to retrieve SRA Normalized Format files with full base quality scores.
2023-12-11T08:17:47 prefetch.3.0.7: 1) Downloading 'SRR16235266'...
2023-12-11T08:17:47 prefetch.3.0.7: SRA Normalized Format file is being retrieved, if this is different from your preference, it may
be due to current file availability.
2023-12-11T08:17:47 prefetch.3.0.7: Downloading via HTTPS...
2023-12-11T08:18:00 prefetch.3.0.7: HTTPS download succeed
2023-12-11T08:18:00 prefetch.3.0.7: 'SRR16235266' is valid
2023-12-11T08:18:00 prefetch.3.0.7: 1) 'SRR16235266' was downloaded successfully
2023-12-11T08:18:00 prefetch.3.0.7: 'SRR16235266' has 0 unresolved dependencies
mkarpande@ManjushriK:~/sra_data$ ls
```

```
mkalpande@Manjushrik:~/sra_data$ ls SRR16235266
SRR16235266.sra
mkalpande@Manjushrik:~/sra_data$ fasterq-dump SRR16235266
spots read      : 23,011
reads read      : 46,022
reads written    : 23,011
reads 0-length  : 23,011
mkalpande@Manjushrik:~/sra_data$ |
```