

A BioInstaller

Name of item

Version of item

Buildver version (Database needed, e.g. hg19, hg38)

Download directory (Hints)

Download directory

Github Configuration File

Other Configuration File

License

Logical Values

Download only

Save the installation info

Overwrite the installation dir

Extra parameters

E Spack

Sub command of spack

Parameters

F

```

@CMD:@@ BioInstaller::spack
@Params:@@
$suffix_params
[1] "install zlib"

==> Installing zlib
==> Fetching http://zlib.net/fossils/zlib-1.2.11.tar.gz
==> Staging archive: /Users/ljff/Bioinfo/spack/var/spack/stage/zlib-1.2.11-caosjr5fcruvzyoctnqqkpackpwyzp/zlib-1.2.11.tar.gz
==> Created stage in /Users/ljff/Bioinfo/spack/var/spack/stage/zlib-1.2.11-caosjr5fcruvzyoctnqqkpackpwyzp
==> No patches needed for zlib
==> Building zlib [Package]
==> Executing phase: 'install'
==> Successfully installed zlib
Fetch: 21.75s. Build: 3.81s. Total: 25.57s.
[+] /Users/ljff/spack/opt/darwin-highsierra-x86_64/clang-10.0.0-apple/zlib-1.2.11-caosjr5fcruvzyoctnqqkpackpwyzp

```

B Status of system

Disk capacity

Memory capacity

Running tasks

```

Loading required package: BioInstaller
INFO [2018-08-03 22:07:11] Debug:rawe@_ucsc_refgene
INFO [2018-08-03 22:07:11] Debug:destdir:
INFO [2018-08-03 22:07:11] Debug:db:/usr/local/Cellar/ucsc_refgene/3.5.0/Resources/Library/BioInstaller/extdata/config/github/github.toml
INFO [2018-08-03 22:07:11] Debug:github.cfg:/Library/Frameworks/R.framework/Versions/3.5/Resources/Library/BioInstaller/extdata/config/nongithub/nongithub.toml
INFO [2018-08-03 22:07:11] Debug:nongithub.cfg:/Library/Frameworks/R.framework/Versions/3.5/Resources/Library/BioInstaller/extdata/config/db/db_main.toml
INFO [2018-08-03 22:07:11] Debug:nongithub.cfg:/Library/Frameworks/R.framework/Versions/3.5/Resources/Library/BioInstaller/extdata/config/db/db_annovar.toml
INFO [2018-08-03 22:07:11] Debug:nongithub.cfg:/Library/Frameworks/R.framework/Versions/3.5/Resources/Library/BioInstaller/extdata/config/db/db_annot.toml
INFO [2018-08-03 22:07:12] Fetching @_ucsc_refgene versions...
INFO [2018-08-03 22:07:12] Install version:refgene
INFO [2018-08-03 22:07:12] Now start to install @_ucsc_refgene in /Users/ljff/BioInstaller/download.
INFO [2018-08-03 22:07:12] Running before install steps.
INFO [2018-08-03 22:07:12] Now start to download @_ucsc_refgene in /Users/ljff/BioInstaller/download.
trying URL 'http://hgdownload.cse.ucsc.edu/goldenPath/hg19/database/refgene.txt.gz'
Content type 'application/gzip' length 699829 bytes (6.7 MB)

```

C Conda

Conda subcommands

Conda environment

Conda parameters

D

```

----- ~/BioInstaller/log/3BzNcg1Jda0901EzHVuHlevs06rhZL7CgBMj0geHo6a1FW6u.log
-----
@Task start at:@@ 2018-08-16 17:38:04
@Worker nodename:@@ macos
@Worker user:@@ ljff
@Worker locale:@@ C/UTF-8/C/C/C/C
@Worker PID:@@ 79667
2018 08-16 17:38:04 Running R command for key 3BzNcg1Jda0901EzHVuHlevs06rhZL7CgBMj0geHo6a1FW6u
@CMD:@@ $apply(req_pkgs, function(x){require(x, character.only = TRUE)})
Loading Required package: BioInstaller
@CMD:@@ BioInstaller::conda
@Params:@@
$prefix_params
[1] "source activate base;"

$suffix_params
[1] "create -n test_env_from_BioInstaller -y"

Solving environment: ...working... done

## Package Plan ##

environment location: /Users/ljff/Bioinfo/miniconda3/envs/test_env_from_BioInstaller

Preparing transaction: ...working... done
Verifying transaction: ...working... done
Executing transaction: ...working... done
#
# To activate this environment, use
#
# $ conda activate test_env_from_BioInstaller
#
# To deactivate an active environment, use
#
# $ conda deactivate

```