

SCREEN RECORDINGS

conda_init

- 2.3.1 (`conda init zsh`) 00:00 -- 00:09
- 2.3.2 (close and reopen) 00:16 -- 00:55

CreateMambaEnv

UNUSED

CreateSCRAPEnv

- 2.5.1 (mamba install) 02:44 -- 03:25
- 2.5.3 (env create) 05:08 -- 06:15

GitCloneInstallMamba

- 2.4.1 (`git clone`) 06:00 -- 06:45
- 2.5.1 (mamba install) 06:45 -- 07:15

InstallMiniconda

- 2.2.2 (`brew install miniconda`) 00:00 -- 00:50

InstallRefs

The instructions in 2.7-2.9 elaborate the parts of the command displayed in 2.6.

- 2.6
- 2.7
- 2.7.1 (SCRAP directory) 00:00:13 -- 00:00:27
- 2.8

- 2.9

Is_adapters

- 2.12.1 (adapter file directory) 00:00 -- 00:19
- 3.3.1 (adapter file directory) 00:00 -- 00:19

Is_annotation

- 2.9.1 (contents of annotation directory) 00:00 -- 00:15

Is_fasta

UNUSED

mirbase_abbr

- 2.8.1 (miRbase abbreviations) 00:16 -- 00:23

MoveBAMFiles

- 3.7.1 (files must be moved to the same folder prior to `samtools merge`) 00:00 -- 01:14

PeakAnnotation

- 3.6.1 & 3.6.2 (peak annotation) 00:00 -- 00:56

PeakCalling

The instructions in 3.3-3.5 elaborate parts of the command displayed in 3.2.

- 3.2
- 3.3.1 (sample directory and adapter file) 00:13 -- 00:45
- 3.3.2 (parameters) 00:45 -- 00:53
- 3.4.1 (family calling or not) 00:53 -- 00:55
- 3.5.1 (reference directory, miRbase abbr, and genome) 00:55 -- 01:10

samplendir_structure

- 2.11.1 (directory structure) 00:00 -- 00:21
- 2.11.2 (single sample dir structure) 00:21 -- 00:47

SamtoolsMergeSortIndex

- 3.7.1 (`samtools merge`) 00:12 -- 00:27
- 3.7.2 (`samtools sort`) 00:27 -- 00:36
- 3.8.1 (`samtools index`) 00:36 -- 00:49

SCRAP_1

The instructions in 2.11 - 2.13 elaborate parts of the command displayed in 2.10.

- 2.10

- 2.11

- 2.12.1 (adapter file path) 00:00:22 -- 00:00:39

- 2.12.2 (sample type and filters) 00:00:39 -- 00:00:50

- 2.13.1 (refdir, miRbase abbr, reference genome) 00:00:50 -- 00:01:21

SCRAP_2

UNUSED

scrap_platformsetup

- 2.2.1 (browser, platform setup) 00:00 -- 00:33

ucsc_genome

- 2.8.2 (browser, genome.ucsc.edu) 00:00 -- 00:15

ViewIGV

- 3.9.1 (view result in IGV) 00:00 -- 00:40

which_conda

- 2.1.3 (`which conda` when conda not installed) 00:00 -- 00:10

which_git

- 2.1.2 (`which git` when git is default with system) 00:00 -- 00:09