Zerone tutorial

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1 Building instructions

Zerone is available as a Linux command line application and as an R package.

1.1 Downloading

We recommend that you use git to keep Zerone updated. You can clone the repository from Github with the following command on a standard terminal.

```
git clone git@github.com:gui11aume/zerone
```

Note that this requires that you already have a Github account and that the computer you are working on has an SSH key registered on GitHub. If this is not the case, follow the instructions from https://help.github.com/articles/generating-ssh-keys/.

Alternatively, if you prefer not to use git, you can download the source code from https://github.com/guillaume/zerone/archive/master.zip with the following commands.

```
wget https://github.com/guillaume/zerone/archive/master.zip
unzip zerone-master.zip
mv zerone-master zerone
```

This should create a directory named zerone.

1.2 Compiling

To build Zerone, execute the following from the zerone directory.

cd zerone

This should succeed on most Linux systems because make is available by default. If this is not the case, you can obtain it by typing sudo apt-get install make on the Ubuntu terminal.

Calling make should create an executable called zerone.

1.3 Testing

To check that the building was successful, test Zerone with the following commands.

make test -C src/test

If it passes the tests without any error message, then everything went fine and you are done with the build. If not, something went wrong. In this case, you can explain how to reproduce the problem on https://github.com/guillaume/zerone/issues.

Installing the Zerone R package

To install the Zerone R package, simply run this command from the zerone directory.

R CMD INSTALL ZeroneRPackage

Note that you need to have R installed on your computer. If this is not the case, run the command sudo apt-get install r-base on Ubuntu.

2 Zerone basics

2.1 Running Zerone

To run Zerone, you have to specify the files that contain the mapped reads of the ChIP-seq experiment you want to discretize. These can be in BED, SAM/BAM and GEM (.map) formats and can be gzipped. You can include as many mock control files and as many experimental replicates as you need, provided there is at least one mock control and one experimental replicate. Just enter mock controls after the -0 or --mock option, and targets after the -1 or --chip option.

For example, you can type in the following commands from the zerone directory.

./zerone --mock data/mock.sam --chip data/ctcf1.sam,data/ctcf2.sam

Where file1.bam and file2.bam are negative controls done without antibody, and file2.bam and file3.bam are two experimental replicates.

Note that path expansion will not work when using comma separated file names, so if you want to use path names starting with \sim , you can simply specify the mock and chip options as many times as needed, as shown below.

./zerone -0 data/mock.sam -1 data/ctcf1.sam -1 data/ctcf2.sam

Enter the option -h or --help for usage instructions and --version to print the version number.

2.2 Output

Running Zerone as shown above should produce an output like the following.

```
# QC score: 1.289
# advice: accept discretization.
chr1
         1
                   300
                            1
                                 0
                                      0
                                          0
                                 0
         301
                            1
                                      0
                                          0
chr1
                   600
         601
                   900
                            1
                                 0
                                      0
                                          0
chr1
                            1
                                 0
                                     0
                                          0
chr1
         901
                   1200
chr1
         998701
                  999000
                                 1
                                      11
                                          4
chr1
                            2
                                 2
         999001
                   999300
                                     72
                                          34
                            2
                                 2
chr1
         999301
                   999600
                                      128 69
         999601
                   999900
chr1
                                      10
                                          5
```

The first two lines contain the result of the **quality control**. It consists of a quality score followed by an advice to either **accept or reject** the discretization, if the score is positive or negative, respectively. If the score is higher than 1 (or lower than -1), the advice is extremely reliable.

The rest of the lines contain the discretization proper. The first three columns specify the chromosome, start and end positions of each window.

The fourth column represents the **enrichment**. Zerone classifies each window into one of three possible states. States 0 and 1 represent two types of background signal. State 2 represents an **enriched window**.

The fifth column contains the read count of all the control profiles summed together, and the rest of the columns contain the read count of each of the target profiles.

The -c or --confidence option adds an extra column with the probability that the given window is a target. This expresses the confidence that a target is real and can be used for post-processing. To test this feature, you can run this line.

./zerone -c -0 data/mock.sam -1 data/ctcf1.sam -1 data/ctcf2.sam
You should obtain the following output.

```
# QC score: 1.289
# advice: accept discretization.
chr1
         1
                  300
                                     0
                                         0
                                              0.300
chr1
         301
                  600
                            1
                                0
                                     0
                                         0
                                              0.162
         601
                            1
chr1
                  900
                                0
                                     0
                                          0
                                              0.096
                            1
                                     0
chr1
         901
                  1200
                                              0.064
                            2
chr1
         998701
                  999000
                                1
                                     11
                                         4
                                              0.979
                                2
chr1
         999001
                  999300
                           2
                                     72
                                         34
                                              1.000
                            2
                                2
         999301
                  999600
                                     128 69
                                              1.000
chr1
                  999900
                            2
chr1
         999601
                                0
                                     10
                                         5
                                              0.999
```

Looking at this output, we conclude that Zerone is 99.9% confident that CTCF is present on the last genomic window.

2.3 List output

With the -1 or --list-output option, Zerone produces an alternative output in which only enriched windows are shown. Also, all contiguous windows are merged together.

```
# QC score: 1.289
# advice: accept discretization.
chr1
        237601
                 238200
chr1
        521401
                 522000
chr1
        567301
                 567900
chr1
        714001
                 714900
chr1
        975901
                 976500
chr1
        990001
                 990600
        994201
chr1
                 995400
chr1
        998701
                 999900
```

The Zerone R package

You can load the package in R with this line.

library(zerone)

Type ?zerone from an R session to see the documentation.

3 Troubleshooting

In case Zerone crashes, start by recompiling it in debug mode. To do so, run the following commands from the zerone directory.

make clean
make debug

Then repeat the actions that triggered the crash and contact guillaume.filion@gmail.com attaching the debug information.