Note S1. Methods

# Note S1 Methods

# Note S2 Experiment setup

## S2.1 Datasets

Note S3. Results 3

## Note S3 Results

Smash++ and several other methods have been carried out on a collection of synthetic and real sequences. The machine used for the tests had an 8-core 3.40 GHz Intel<sup>®</sup> Core<sup>™</sup> i7-6700 CPU with 32 GB RAM.

### Note S4 Tool availability and implementation

Smash++ is implemented in C++ language and is available at [1]. This tool is able to find rearrangements in sequences, Fasta and Fastq files; although, it is highly recommended to use sequences as input. To work with Smash++, it should be first installed. In the following sections, we describe installing and running Smash++.

#### S4.1 Install

In order to install Smash++, we run the following commands:

```
git clone https://github.com/smortezah/smashpp.git
cd smashpp
cmake .
make
```

#### S4.2 Run

Running

```
1 ./smashpp
```

provides the following guide:

```
SYNOPSIS
     ./smashpp [OPTIONS]... -r [REF-FILE] -t [TAR-FILE]
2
3
4
   SAMPLE
5
6
   DESCRIPTION
7
     Mandatory arguments:
     -r, --ref FILE
                                 reference file (Seq/Fasta/Fastq)
8
     -t, --tar FILE
9
                                target file
                                               (Seq/Fasta/Fastq)
10
11
     Options:
12
     -v, --verbose
                                 more information
     -1, --level INT
13
                                 level of compression [0;4]
                                                                 COMPRESS
14
     -e, --ent-n FLOAT
                                Entropy of 'N's [0.0;100.0]
                                                                 COMPRESS
15
          --nthr INT
                                 number of threads [1;8]
     -n,
     -fs, --filter-scale S|M|L scale of the filter {S|small,
16
                                                                   FILTER
17
                                 M|medium, L|large}
18
     -w, --wsize INT
                                 window size [1;100000]
                                                                   FILTER
19
     -wt, --wtype [0;7]
                                 type of windowing function
                                                                   FILTER
                                 {O|rectangular, 1|hamming, 2|hann,
20
                                 3| blackman, 4| triangular, 5| welch,
21
22
                                 6|sine, 7|nuttall}
     -d, --step
23
                                 sampling steps
                                                                   FILTER
                   INT
     -th, --thresh FLOAT
24
                                 threshold [0.0;20.0]
                                                                   FILTER
     -sp, --save-profile
25
                                 save profile (*.prf)
                                                                     SAVE
26
     -sf, --save-filter
                                 save filtered file (*.fil)
                                                                     SAVE
27
                                 save sequence (input: Fasta/Fastq) SAVE
     -sb, --save-seq
28
     -ss, --save-segment
                                 save segmented files (*-s )
                                                                      SAVE
     -sa, --save-all
29
                                 save profile, filetered and
                                                                     SAVE
                                 segmented files
30
     -h, --help
31
                                 usage guide
     -rm, --ref-model [
32
                            , [
                                       ,]ir,\alpha,
                                                  /
                                                        ,ir, ,
   MODEI.
     -tm, --tar-model [
                            , [
                                      ,]ir, ,
33
                                                           ir,
   MODEL
34
                                 parameters of models
                           (INT)
                                    : context size
35
36
                           (INT)
                                     : width of sketch in log2 form,
37
                                     e.g., set 10 for w=2^10=1024
38
                                     : depth of sketch
39
                                 ir: inverted repeat {0, 1, 2}
```

S4.3. Example 5

```
0: regular (not inverted)
1: inverted, solely
2: both regular and inverted
43 (FLOAT) : estimator
44 (FLOAT) : forgetting factor [0.0;1.0)
45 (INT) : threshold (no. substitutions)
```

The arguments "-r" and "-t" are used to specify the reference and the target files. It is highly recommended to choose short names for these files. Note that if a user tends to replace 'N' bases in a sequence with a normal distribution of 'A', 'C', 'G' and 'T' bases, he/she can employ GOOSE toolkit [2].

### S4.3 Example

This section guides, step-by-step, employing Smash++ to find rearrangements.

### Install Smash++ and provide the required files

First, we install Smash++:

```
git clone https://github.com/smortezah/smashpp.git
cd smashpp
cmake .
make
```

Then, we copy Smash++'s binary file into example/ directory and go to that directory:

```
cp smashpp example/
cd example/
```

References 6

## References

[1] M. Hosseini, D. Pratas, and A. J. Pinho. Smash++. [Online]. Available: https://github.com/smortezah/smashpp

 $[2]\,$  D. Pratas. Goose. [Online]. Available: https://github.com/pratas/goose