Note S1. Methods

## Note S1 Methods

The schema of the proposed method is illustrated in Fig. S1. There are five major stages in this method, including

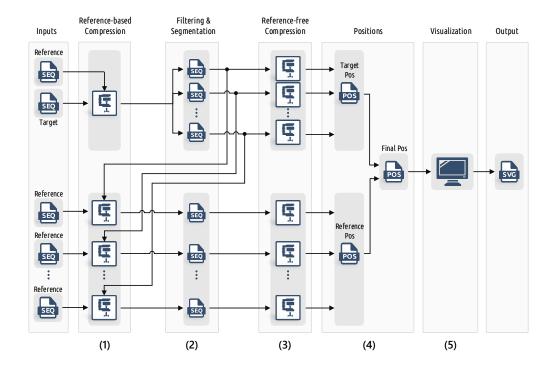


Fig. S1. The schema of Smash++.

## S1.1 Building models of the data

## S1.2 finding similar regions

In order to smooth the profile information, we use Hann window [1], which is a discrete window function given by

$$w[n] = 0.5 - 0.5 \cos\left(\frac{2\pi n}{N}\right) = \sin^2\left(\frac{\pi n}{N}\right),$$
 (Eq. S1)

in which,  $0 \leq n \leq N$  and length of the window is N+1 (Fig. S2).

### S1.3 Computing complexities

## S1.4 The software

Besides Hann window, that is used as default to filter the profile information obtained by the reference-based compression, we have implemented several other window functions (Fig. S3), including Blackman [1], Hamming [2], Nuttall [3], rectangular [4], sine [5], triangular [6] and Welch [7]

S1.4. The software

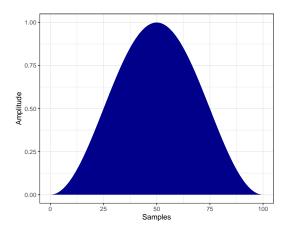


Fig. S2. Hann window for 101 samples.

windows. These functions are given by

$$\begin{split} w[n] &= 1, & \text{(rectangular)} \\ w[n] &= 1 - \left| \frac{n - N/2}{L/2} \right|, \quad L = N, & \text{(triangular/Bartlett)} \\ w[n] &= 1 - \left( \frac{n - N/2}{N/2} \right)^2, & \text{(Welch)} \\ w[n] &= \sin\left(\frac{\pi n}{N}\right), & \text{(sine)} \\ w[n] &= 0.54348 - 0.45652 \cos\left(\frac{2\pi n}{N}\right), & \text{(Hamming)} \\ w[n] &= 0.42659 - 0.49656 \cos\left(\frac{2\pi n}{N}\right) + 0.07685 \cos\left(\frac{4\pi n}{N}\right), & \text{(Blackman)} \\ w[n] &= 0.35577 - 0.48740 \cos\left(\frac{2\pi n}{N}\right) + 0.14423 \cos\left(\frac{4\pi n}{N}\right) - 0.01260 \cos\left(\frac{6\pi n}{N}\right). & \text{(Nuttall)} \\ &\text{(Eq. S2)} \end{split}$$

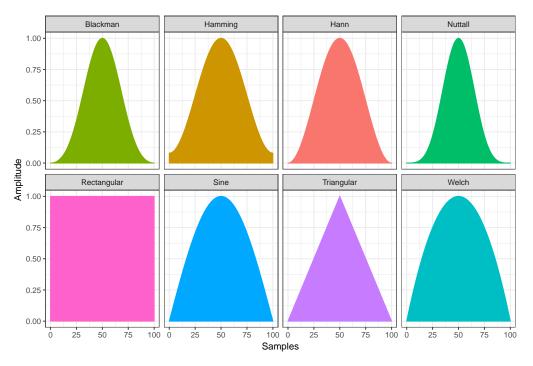


Fig. S3. Window functions.

# Note S2 Experiment setup

## S2.1 Datasets

Table S1. Datasets used in the experiments.

Category	Reference	Length (base)	Target	Length (base)	Description
Synthetic	RefS	1,000	TarS	1,000	
Synthetic	RefM	100,000	$\operatorname{TarM}$	100,000	
Synthetic	RefL	5,000,000	TarL	5,000,000	
Synthetic	RefXL	100,000,000	TarXL	100,000,000	

Note S3. Results 4

## 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 [8]. This tool is able to find and visualize rearrangements in sequences, FASTA and FASTQ files; although, it is highly recommended to use sequences as input. In the following sections, we describe installing and running Smash++.

#### S4.1 Install

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

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

#### S4.2 Run

A reference file and a target file are clearly mandatory to run Smash++ (without visualization). Running

```
1 ./smashpp
```

provides the following guide:

```
SYNOPSIS
2
     ./smashpp OPTIONS... -r REF-FILE -t TAR-FILE
3
4
   SAMPLE
5
   DESCRIPTION
6
7
     Mandatory arguments
     -r, --ref FILE
8
                                 reference file (Seq/Fasta/Fastq)
     -t, --tar FILE
                                                (Seq/Fasta/Fastq)
9
                                 target file
10
11
     Options
     -v, --verbose
                                 more information
12
     -1, --level INT
                                 level of compression: [0, 5]
13
     -m, --min INT
                                 min segment size: [1, 4294967295]
14
15
     -nr, --no-redun
                                 do NOT compute self complexity
                                 Entropy of 'N's: [0.0, 100.0]
     -e, --ent-n FLOAT
16
     -n, --nthr INT
                                 number of threads: [1, 8]
17
     -fs, --filter-scale S\,|\,M\,|\,L\, scale of the filter:
18
19
                                 {S|small, M|medium, L|large}
                                 window size: [1, 4294967295]
     -w. --wsize INT
20
     -wt, --wtype INT/STRING
                                 type of windowing function:
21
22
                                 {O|rectangular, 1|hamming, 2|hann,
23
                                 3|blackman, 4|triangular, 5|welch,
24
                                 6|sine, 7|nuttall}
     -d, --step
25
                    INT
                                 sampling steps
26
     -th, --thresh FLOAT
                                 threshold: [0.0, 20.0]
27
     -sb, --save-seq
                                 save sequence (input: Fasta/Fastq)
28
     -sp, --save-profile
                                 save profile (*.prf)
     -sf, --save-filter
                                 save filtered file (*.fil)
29
30
     -ss, --save-segment
                                 save segmented files (*-s_i)
     -sa, --save-all
                                 save profile, filetered and
31
32
                                 segmented files
     -h, --help
                                 usage guide
33
34
     -rm, --ref-model k,[w,d,] ir, a,g/t, ir, a,g:...
35
     -tm, --tar-model k, [w,d,]ir,a,g/t,ir,a,g:...
                                 parameters of models
36
                           (INT) k: context size
37
38
                           (INT) w: width of sketch in log2 form,
                                     e.g., set 10 for w=2^{-1}0=1024
39
                           (INT) d: depth of sketch
40
41
                           (INT) ir: inverted repeat: {0, 1, 2}
```

S4.3. Example 6

```
42
                                        0: regular (not inverted)
43
                                        1: inverted, solely
44
                                        2: both regular and inverted
                           (FLOAT) a:
45
                                        estimator
46
                           (FLOAT)
                                        forgetting factor: [0.0, 1.0)
                                   g:
47
                             (INT) t:
                                       threshold (no. substitutions)
```

The arguments "-r" and "-t" are used to specify the reference and the target, respectively, which are highly recommended to have short names. Level of compression, that is an integer between 0 and 5, can be determined with "-l". By setting "-m" to an integer value, only those regions in the reference file that are greater than that value can be considered for the compression. Triggering "-nr" makes the tool not to perform the reference-free compression (self-complexity computation) part.

In implementation of the reference-based compression, we have replaced 'N' bases in the references and the targets with 'A's and 'T's, respectively. On reference-free compression, they are replaced with 'A's, in both references and targets. If a user tends to replace 'N' bases in a sequence with a normal distribution of 'A', 'C', 'G' and 'T's, he/she can employ GOOSE toolkit [9]. Note that we have set the entropy of 'N's to 2.0, by default, but it is possible for the user to set them to another value of interest, by "-e" option.

Building different finite-context models can be done in the multi-threaded fashion, setting "-n" to an integer. To find similar regions in the reference and the target, information profile (obtained by compression) needs to be filtered, of which the scale can be set as S (small), M (medium) or L (large). Size of the window and type of the windowing function, described in S1.4, can be set by "-w" and "-wt" options, respectively. Instead of considering the complete profile information, the user is able to make samples of it by steps of which size can be determined by "-d". For the purpose of segmenting the filtered information profile, the average entropy of reference-based compression is used as the threshold, by default. However, this threshold can be altered by "-th" option.

Smash++ accepts FASTA and FASTQ files as input, in addition to sequences. In these cases, the input files are converted to sequences and then processed further. It is possible to save these sequences by "-sb" option.

After obtaining the information profile, Smash++ filters it and then removes it, by default. However, it is possible to save the profile by "-sp" option. The same thing happens to the filtered file, i.e., it is segmented and then is removed. But, the user can use "-sf" to save the filtered file. Also, the segmented files can be saved using "-ss". The user can save all the information profile, filtered and segmented files, by triggering "-sa" option.

For the purpose of compression, either reference-based or reference-free, it is recommended to use "-l" option, since it configures the models automatically. However, using "-rm" and "-tm", the user would be able to manually configure the reference model, for reference-based compression, and the target model, for reference-free compression. Parameters of the models are described in detail in section S1.

## 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 7

#### References

[1] R. Blackman and J. Tukey, "Particular pairs of windows," The measurement of power spectra, from the point of view of communications engineering, pp. 95–101, 1959.

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- [9] D. Pratas. Goose. [Online]. Available: https://github.com/pratas/goose