



PAPER

# Smash++: finding rearrangements

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### Some Mathematics Sample

Let  $X_1, X_2, \dots, X_n$  be a sequence of independent and identically distributed random variables with  $E[X_i] = \mu$  and  $\text{Var}[X_i] = \sigma^2 < \infty$ , and let

$$S_n = \frac{X_1 + X_2 + \dots + X_n}{n} = \frac{1}{n} \sum_i X_i \quad (1)$$

denote their mean. Then as  $n$  approaches infinity, the random variables  $\sqrt{n}(S_n - \mu)$  converge in distribution to a normal

$\mathcal{N}(0, \sigma^2)$ .

## Background

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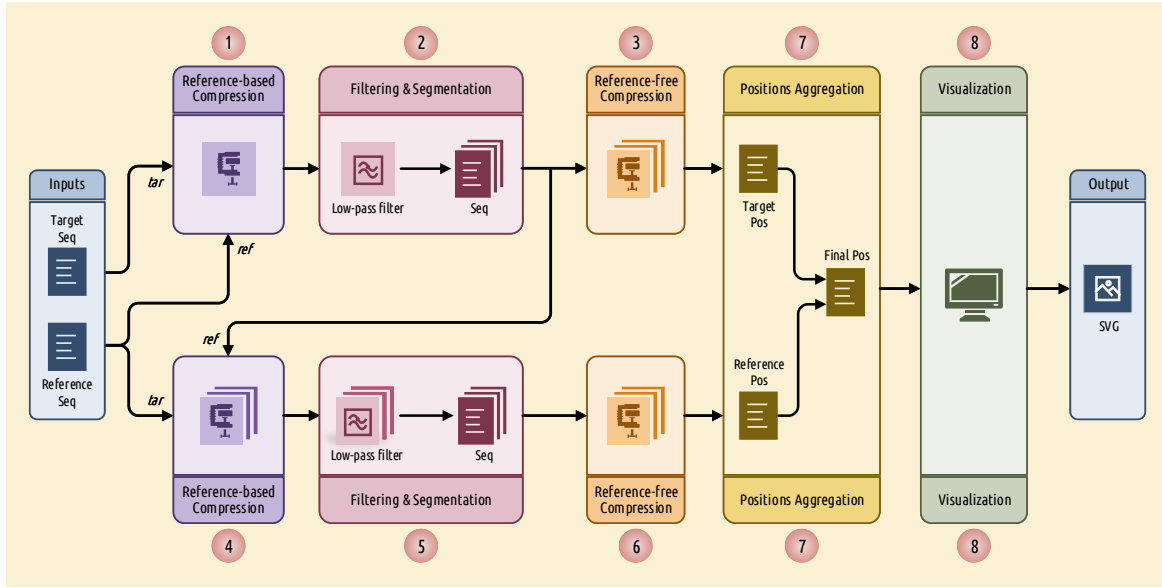
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**Figure 1.** The schema of Smash++. The process of finding similar regions in reference and target sequences and also, computing redundancy in each region includes eight stages. Finally, Smash++ outputs a \*.pos file that includes the positions of the similar regions, and can be then visualized, resulting in an SVG image.

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## Methods

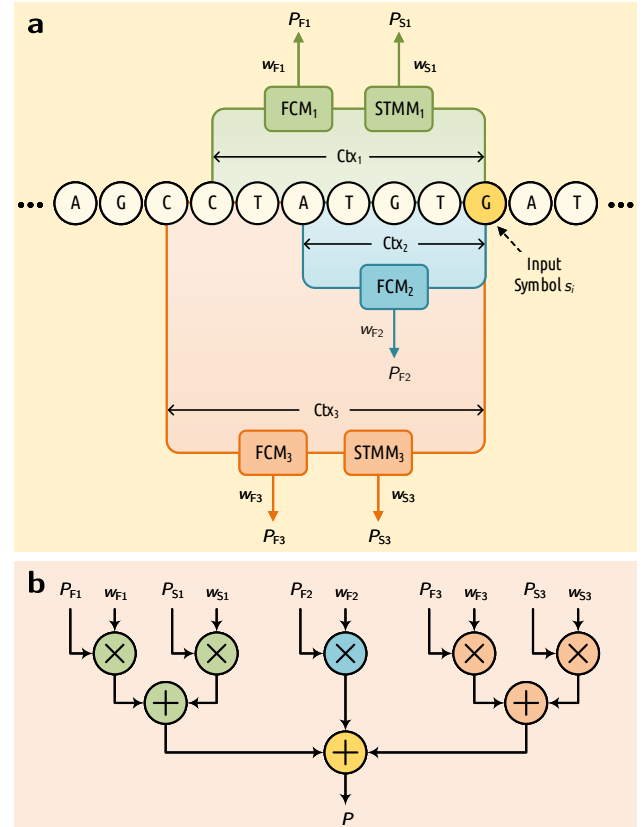
The schema of the proposed method is illustrated in Figure 1. Smash++ takes as inputs a reference and a target file and produces as output a position file, which is then fed to the Smash++ visualizer to produce an SVG image. This process has eight major stages: (1) compression of the original target file, based on the model of original reference file, (2) filtering and segmentation of the compressed file, (3) reference-free compression of the segmented files, obtained by the previous stage, (4) compression of the original reference file, based on the model of segmented files obtained by stage 2, (5) filtering and segmentation of the compressed files, (6) reference-free compression of the segmented files, that are obtained by the stage 5, (7) aggregating positions, generated by stages 3 and 6, and (8) visualizing the positions. The following sections describe the process in detail.

## Data modeling

Smash++ works on the basis of cooperation between finite-context models (FCMs) and substitutional tolerant Markov models (STMMs). Applying these models on various contexts provides probability and weight values, illustrated in Figure 2a, which are then mixed (by multiplication and addition, shown in Figure 2b) to provide the final probability ( $P$ ) of occurring an input symbol. The following subsections describe FCMs and STMMs in detail.

### Finite-context model (FCM)

A finite-context model considers Markov property to estimate the probability of the next symbol in an information source, based on the past  $k$  symbols (a context of size  $k$ ) [? 4? ]. Denoting the context as  $c_{k,i} = s_{i-k}s_{i-k+1} \dots s_{i-2}s_{i-1}$ , the probability of the next symbol  $s_i$  in an information source  $S$ , which is posed



**Figure 2.** Data modelling by Smash++. (a) cooperation between finite-context models (FCMs) and substitutional-tolerant Markov models (STMMs). Note that each STMM needs to be associated with an FCM. (b) probability of an input symbol is estimated by employing the probability and weight values that have been obtained from processing previous symbols.

at  $i$ , can be estimated as

$$P_m(s_i|c_{k,i}) = \frac{N(s_i|c_{k,i}) + \alpha}{N(c_{k,i}) + \alpha|\Theta|}, \quad (2)$$

in which  $m$  stands for model (FCM in this case),  $N(s_i|c_{k,i})$  shows the number of times that the information source has generated symbol  $s_i$  in the past,  $|\Theta|$  denotes size of the alphabet  $\Theta$ ,  $N(c_{k,i}) = \sum_{b \in \Theta} N(b|c_{k,i})$  represents the total number of events occurred for the context  $c_{k,i}$  and  $\alpha$  allows to keep a balance between the maximum likelihood estimator and the uniform distribution. Eq. 2 turns to the Laplace estimator, for  $\alpha = 1$ , and also behaves as a maximum likelihood estimator, for large number of events  $i$  [5].

#### Substitutional tolerant Markov model (STMM)

A substitutional tolerant Markov model [6] is a probabilistic-algorithmic model that assumes at each position, the next symbol in the information source is the symbol which has had the highest probability of occurrence in the past. This way, an STMM ignores the real next symbol in the source. Denoting the past  $k$  symbols as  $c_{k,i} = s_{i-k} s_{i-k+1} \dots s_{i-2} s_{i-1}$ , the probability of the next symbol  $s_i$ , can be estimated as

$$P_m(s_i|c'_{k,i}) = \frac{N(s_i|c'_{k,i}) + \alpha}{N(c'_{k,i}) + \alpha|\Theta|}, \quad (3)$$

where  $N$  represents the number of occurrences of symbols, that is saved in memory, and  $c'_{k,i}$  is a copy of the context  $c_{k,i}$  which is modified as

$$c'_{k,i} = \arg \max_{b \in \Theta} P_m(b|c'_{k,i}). \quad (4)$$

STMMs can be used along with FCMs to modify the behavior of Smash++ in confronting with nucleotide substitutions in genomic sequences. These models have the potential to be disabled, to reduce the number of mathematical calculations and consequently, increase the performance of the proposed method. Such operation is automatically performed using an array of size  $k$  (the context size), named history, which preserves the past  $k$  hits/misses. Seeing a symbol in the information source, the memory is checked for the symbol with the highest number of occurrences. If they are equal, a hit is saved in the history array; otherwise, a miss is inserted into the array. Before getting to store a hit/miss in the array, it is checked for the number of misses and in the case they are more than a predefined threshold  $t$ , the STMM will be disabled and also the history array will be reset. This process is performed for each symbol in the sequence.

This example shows the distinction between a finite-context model and a substitutional tolerant Markov model. Assume, the current context at position  $i$  is  $c_{11,i} = \text{GGCTAACGTAC}$ , and the number of occurrences of symbols saved in memory is  $A = 10$ ,  $C = 12$ ,  $G = 13$  and  $T = 11$ . Also, the symbol to appear in the sequence is  $T$ . An FCM would consider the next context as  $c_{11,i+1} = \text{GCTAACGTACT}$ , while an STMM would consider it as  $c'_{11,i+1} = \text{GCTAACGTACG}$ , since the base  $G$  is the most probable symbol, based on the number of occurrences stored in memory.

### Availability of source code and requirements (optional, if code is present)

Lists the following:

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- Project home page: e.g. <http://sourceforge.net/projects/mged>
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### Declarations

#### List of abbreviations

CPU: central processing unit; FCM: finite-context model; RAM: random access memory; STMM: substitutional-tolerant Markov model;

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The authors declare that they have no competing interests.

### Funding

This work was supported by Programa Operacional Factores de Competitividade – COMPETE (FEDER); and by national funds through the Foundation for Science and Technology (FCT), in the context of the projects [UID/CEC/00127/2013, PTCD/EEI-SII/6608/2014] and the grant [PD/BD/113969/2015].

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### References

1. Fan J, Peng H. Nonconcave penalized likelihood with a diverging number of parameters. *Ann Statist* 2004;32:928–61.
2. Cox DR. Regression models and life tables (with Discussion). *J R Statist Soc B* 1972;34:187–220.
3. Heard NA, Holmes CC, Stephens DA. A Quantitative Study of Gene Regulation Involved in the Immune Response of Anopheline Mosquitoes: An Application of Bayesian Hierarchical Clustering of Curves. *J Am Statist Assoc* 2006;101:18–29.
4. Hosseini M, Pratas D, Pinho AJ. AC: A Compression Tool for Amino Acid Sequences. *Interdisciplinary Sciences: Computational Life Sciences* 2019;11(1):68–76.
5. Pratas D, Silva RM, Pinho AJ, Ferreira PJ. An alignment-free method to find and visualise rearrangements between pairs of DNA sequences. *Scientific reports* 2015;5:10203.
6. Pratas D, Hosseini M, Pinho AJ. Substitutional tolerant Markov models for relative compression of DNA sequences. In: *International Conference on Practical Applications of Computational Biology & Bioinformatics (PACBB)* Springer; 2017. p. 265–272.