

St. Petersburg Electrotechnical University "LETI"

St. Petersburg Department of Steklov Institute  
of Mathematics of the Russian Academy of Sciences

# Proceedings of Computer Assisted Mathematics 2025



Semjon Adlaj



Кафедра АМ - Поздняков



Soloviev



Косовская Татьяна



Artem Grebenschikov



Anna Telegina



Victoria Kazakevich



Даниил Гиршович



Alex Sakharov



Михаил Семенченко



Алексей Мегвегов



Aleksandr Spiridonov



Егор Малютин



Sergey Vakukenko



Хоганович Александр



Александр Ляцев



Николай Васильев



Victor Krug



Дмитрий Грошев



Иван Алейников



Anna Posova



Anastasija Dorogushina



Sergei Abramovich



Тараканова Александра



Alexei Semenov



Yuri Gurevich



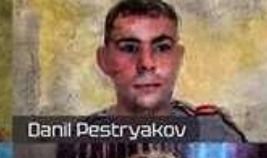
Komarenko Timofei



Тарасов Матвей



Serafim Ivanov



Danil Pestryakov



Vana Berlin



Roman Cherepanov



Кафедра АМ (Канал №2)



Dima Grigoriev



Беринов Максим

# CAM 2025

Extended Abstracts and Short Contributions  
Saint Petersburg 2025



ETU "LETI"  
SAINT PETERSBURG ELECTROTECHNICAL UNIVERSITY



St. Petersburg Electrotechnical University "LETI"

St. Petersburg Department of Steklov Mathematical Institute RAS

International Conference  
**Computer Assisted Mathematics**  
**CAM- 2025**  
July 15–17, 2025

ISBN 978-5-91406-100-2



9 785914 061002

St. Petersburg  
2025

International Conference

**Computer Assisted Mathematics CAM-2025**

St. Petersburg, Russia

July 15–17, 2025

St. Petersburg Electrotechnical University "LETI"

CAM-2025, Computer Assisted Mathematics: Proceedings of the International Conference / ed. by N. N. Vassiliev, S. N. Pozdniakov; org. by ETU "LETI", PDMI RAS. SPb: ANO "CTE" Center, 2025. 128 p.

**ISBN 978-5-91406-100-2**

The book contains short papers, extended abstracts and abstracts of reports presented at the International Conference Computer Assisted Mathematics CAM-2025.

Editor: A. Posova

Cover design: A. Vassilkova



**The book is published with the support  
of the  
Computer Tools in Education journal**

All rights reserved. No part of this publication may be reproduced in any form without the written permission of the publisher.

Editorial and publisher address:

197022 Russia, Saint Petersburg, str. Professor Popov, 5, lit. F.

URL: <http://cte.eltech.ru/ojs> E-mail: [info@kio.spb.ru](mailto:info@kio.spb.ru)

The Computer Assisted Mathematics conference is a forum for scientists and teachers developing the direction of algorithmic mathematics and interested in promoting of important discrete mathematics and theoretical informatics ideas into education in technical universities and schools, including through the development of computer tools for supporting research and productive thinking. The conference CAM'2025 is the 4th in the series.

**Organizing committee:**

Nicolai Vassiliev (St. Petersburg, co-Chair)  
Sergei Pozdnyakov (St. Petersburg, co-Chair)

**Program committee:**

Sergei Abramovich (State University of New York at Potsdam, USA)  
Semjon Adlaj (FRCIC of Russian Academy of Sciences, Russia)  
Alkiviadis Akritas (University of Thessaly, Greece)  
Vladimir Dubrovsky (Moscow State University, Russia)  
Viktor Freiman (Université de Moncton, Canada)  
Dima Grigoriev (CNRS, Lille, France)  
Alexander Liapzev (Herzen State Pedagogical University, Russia)  
Yuri Matiyasevich (PDMI of Russian Academy of Sciences, Russia)  
Tatiana Mylläri (St. George's University, Grenada, West Indies)  
Alexei Semenov (Federal Research Center Russian Academy of Sciences, Moscow, Russia)  
Sergei Soloviev (University of Toulouse, France)  
Alex Saharov (Principal of company Synstretch, Framingham, Massachusetts, USA)

**Sections:**

Section 1  
Computer Tools in Education  
Section 2  
Mathematics and Computer Science  
Section 3  
Young Scientists

**Topics of interest for CAM'2025 include but are not restricted to:**

Algorithmic mathematics; Mathematical modeling; Discrete analysis; Control theory; Theoretical computer science; Symbolic computations; Unsolved problems in theoretical and applied computer science; Software engineering; Computer aided education; Software in math education and research; Training in algorithmic mathematics and mathematical modeling; Computer tools and teaching technologies to support productive thinking in mathematics and computer science.

**Official languages:**

English, Russian.

# Imperfect Palindromes Depending on GC-content

Georgii Khaziev, Alexandr Seliverstov and Oleg Zverkov

**Abstract.** One can calculate the similarity of a given sequence to any perfect palindrome in quadratic time. We consider imperfect palindromes in DNA depending on the guanine-cytosine content. Our results are obtained with computer assisted simulation. They are useful for identifying conserved imperfect palindromes involved in genome regulation.

## Introduction

Let us consider nucleotide sequences. The nucleotides  $\{\mathbf{A}, \mathbf{C}, \mathbf{G}, \mathbf{T}\}$  form two complementary pairs:  $c(\mathbf{A}) = \mathbf{T}$ ,  $c(\mathbf{T}) = \mathbf{A}$ ,  $c(\mathbf{C}) = \mathbf{G}$ , and  $c(\mathbf{G}) = \mathbf{C}$ . Next,  $c(\cdot)$  denotes the reverse complement, i. e.,  $c(xy) = c(y)c(x)$  if  $x$  or  $y$  consists of one nucleotide. So, all perfect palindromes are of the type  $xc(x)$ , where  $x$  denotes a sequence. In particular, a sequence of odd length cannot be a perfect palindrome. There are many works devoted to the search for perfect as well as imperfect and degenerate palindromes, refer to [1, 2]. Direct repeats are also considered, refer to [3]. We consider imperfect palindromes, i. e., sequences with gaps and mismatches in some positions.

GC-content or guanine-cytosine content is the percentage of guanine (G) or cytosine (C) in a DNA sequence. For example, the average GC-content in human genomes equals 41 per cent. In regulatory DNA, a palindrome allows a transcription factor to bind as a homodimer. Regulatory palindromes are typically imperfect, refer to [4].

For two sequences  $x$  and  $y$ , let  $\text{dist}(x, y)$  denote the edit distance.

There is a quadratic-time algorithm that takes two sequences  $x$  and  $y$  as input and computes the optimal partition of sequence  $y$  as a concatenation  $y = wz$  that minimizes the edit distance between  $x$  and the palindrome  $wc(w)$ . The edit distance is also computed, refer to [5].

Let us denote by  $|x|$  the length of  $x$ . Let us denote by  $\text{imp}(x)$  the ratio of the minimum edit distance to the length of the sequence:

$$\text{imp}(x) = \frac{\min\{\text{dist}(x, wc(w)) \mid x = wz\}}{|x|}.$$

The ratio shows how imperfect the palindrome is. The correctness of the definition is based on the equality  $\text{imp}(x) = \text{imp}(c(x))$ .

## Results

For random nucleotide sequences of length 1000 with independent positions and set GC-content, the mean and standard deviation were estimated for the values of  $\text{imp}(x)$ , refer to Table 1. For lengths above 1000, the mean value is almost independent of the sequence length.

GC-content	Mean $\text{imp}(x)$	Standard deviation
0	0.147	0.0044
5	0.172	0.0054
10	0.193	0.0056
15	0.211	0.0056
20	0.225	0.0054
25	0.237	0.0052
30	0.246	0.0049
35	0.253	0.0048
40	0.258	0.0046
45	0.261	0.0044
50	0.262	0.0044

TABLE 1. The empirical estimation of the mean and standard deviation of  $\text{imp}(x)$  for long sequences with  $|x| = 1000$ .

The next series of empirical estimations are performed for random sequences of length 100. It can be seen that for almost all sequences the value of  $\text{imp}(x)$  is close to the median, refer to Table 2.

## Conclusion

We have improved known algorithms to solve some problems arising in bioinformatics. There are many examples of nucleotide sequences with perfect as well as imperfect palindromes. Our empirical estimations are useful for finding imperfect palindromes in DNA.

**Funding.** The research was carried out within the state assignment of Ministry of Science and Higher Education of the Russian Federation for IITP RAS.

GC-content	0.001%	0.01%	0.1%	1%	10%	50%
0	0.08	0.09	0.10	0.12	0.14	0.16
10	0.11	0.12	0.14	0.15	0.18	0.21
20	0.14	0.15	0.17	0.19	0.21	0.24
30	0.17	0.18	0.19	0.21	0.23	0.26
40	0.18	0.19	0.21	0.22	0.25	0.27
50	0.18	0.20	0.21	0.23	0.25	0.28

TABLE 2. The empirical estimates of quantiles of  $\text{imp}(x)$  for short sequences with  $|x| = 100$ .

## References

- [1] Alzamel M., Hampson C., Iliopoulos C.S., Lim Z., Pissis S., Vlachakis D., Watts S. Maximal degenerate palindromes with gaps and mismatches. *Theoretical Computer Science*. 2023, vol. 978, article no. 114182. <https://doi.org/10.1016/j.tcs.2023.114182>
- [2] Mieno T., Funakoshi M., Nakashima Y., Inenaga S., Bannai H., Takeda M. Computing maximal palindromes in non-standard matching models. *Information and Computation*. 2025, vol. 304, article no. 105283. <https://doi.org/10.1016/j.ic.2025.105283>
- [3] Lafond M., Lai W., Liyanage A., Zhu B. The longest subsequence-duplicated subsequence and related problems. *Information and Computation*. 2025, vol. 306, article no. 105313. <https://doi.org/10.1016/j.ic.2025.105313>
- [4] Datta R.R., Rister J. The power of the (imperfect) palindrome: sequence-specific roles of palindromic motifs in gene regulation. *Bioessays*. 2022, vol. 44, no. 4, article no. e2100191. <https://doi.org/10.1002/bies.202100191>
- [5] Zverkov O., Seliverstov A., Shilovsky G. Alignment of a hidden palindrome. *Mathematical Biology and Bioinformatics*. 2024, vol. 19, no. 2, pp. 427–438. (In Russian.) <https://doi.org/10.17537/2024.19.427>

Georgii Khaziev

Institute for Information Transmission Problems of the Russian Academy of Sciences (Kharkevich Institute), Moscow, Russia  
e-mail: [khaziev@iitp.ru](mailto:khaziev@iitp.ru)

Alexandr Seliverstov

Institute for Information Transmission Problems of the Russian Academy of Sciences (Kharkevich Institute), Moscow, Russia  
e-mail: [slvstv@iitp.ru](mailto:slvstv@iitp.ru)

Oleg Zverkov

Institute for Information Transmission Problems of the Russian Academy of Sciences (Kharkevich Institute), Moscow, Russia  
e-mail: [zverkov@iitp.ru](mailto:zverkov@iitp.ru)