

This Special Issue features Methods papers that were accepted for publication by Genome Research following selection and review in coordination with the 27th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2023).

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| Entropy predicts sensitivity of pseudorandom seeds Benjamin Dominik Maier and Kristoffer Sahlin | 1162 ^{OA} |
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| Efficient mapping of accurate long reads in minimizer space with mapquik Bariş Ekim, Kristoffer Sahlin, Paul Medvedev, Bonnie Berger, and Rayan Chikhi | 1188 ^{OA} |
| Extremely fast construction and querying of compacted and colored de Bruijn graphs with GGCAT Andrea Cracco and Alexandru I. Tomescu | 1198 ^{OA} |
| Aligning distant sequences to graphs using long seed sketches Amir Joudaki, Alexandru Meterez, Harun Mustafa, Ragnar Groot Koerkamp, André Kahles, and Gunnar Rätsch | 1208 |
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^{OA}Open Access paper



Cover “Moiré By the Sea.” A moiré pattern is an interference pattern that results from overlapping graphical elements, such as lines or dots. In the cover image, the overlapping lines in the ocean and overlapping dots in the clouds produce moiré patterns. In this issue, the PASTE2 algorithm to align spatial transcriptomics data from adjacent tissue slices is described. Spatial transcriptomics technologies measure gene expression at thousands of discrete locations, or spots, and thus images of aligned slices often yield moiré patterns (e.g., see Fig. 3 in Liu et al.). (Cover illustration by Lillian Raphael, www.lilyraphael.com. The cover art was generated using licensed versions of Procreate and Adobe Illustrator. Positions of points in clouds were computed in Mathematica using code from Stephen Wolfram, “Moiré Patterns,” <http://demonstrations.wolfram.com/MoirePatterns/>, Wolfram Demonstrations Project [published: March 7, 2011]. [For details, see Liu et al., pp. 1124–1132.]