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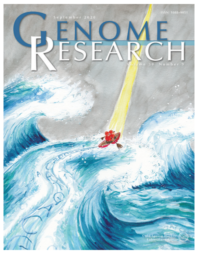

Cover Canoes are some of the oldest vessels used to traverse large bodies of water. Successfully navigating a canoe requires both the right knowledge and the right tools. Genome assembly is similar, benefiting both from experience of the user and tool developer as well as from the right algorithms and data. The cover depicts a new assembler, HiCanu, navigating the treacherous waters of genome assembly. In this issue, HiCanu combines previously described techniques (homopolymer compression, read correction, and simple repeat masking) with high-fidelity long reads to generate near-perfect data for genome assembly. This allows the resolution of segmental duplications, satellites, and allelic variants. The authors demonstrate that HiCanu accurately captures variants in a human genome and assembles multiple human centromeric regions, including Chromosome 16. These results will pave the way for routine telomere-to-telomere genome assembly in the future. (Cover artwork by Arang Rhie, arrhie@gmail.com. [For details, see Nurk et al., pp. 1291–1305.])