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4.4 Performance of VGA on Simulated Data4.5 Performance of Existing Viral Assemblers on Simulated Consensus Error-Corrected Reads; 4.6 Performance of VGA on Real Hiv Data; 4.7 Comparison of Alignment on Error-Corrected Reads; 4.8 Evaluating of Error Correction Tools Based on High-Fidelity Sequencing Reads; Acknowledgment; References; Part II Genomics and Epigenomics; Chapter 5 Scaffolding Algorithms; 5.1 Scaffolding; 5.2 State-of-The-Art Scaffolding Tools; 5.3 Recent Scaffolding Tools; 5.4 Scaffolding Software Evaluation; References; Chapter 6 Genomic Variants Detection and Genotyping 6.1 Introduction6.2 Methods for Detection and Genotyping OF SNPs and Small Indels; 6.3 Methods for Detection and Genotyping of CNVs; 6.4 Putting Everything Together; References; Chapter 7 Discovering and Genotyping Twilight Zone Deletions; 7.1 Introduction; 7.2 Notation; 7.3 Non-Twilight-Zone Deletion Discovery; 7.4 Discovering ""Twilight Zone"" Deletions: New Solutions; 7.5 Genotyping ""Twilight Zone"" Deletions; 7.6 Results; 7.7 Discussion; 7.8 Availability; Acknowledgments; References; Chapter 8 Computational Approaches for Finding Long Insertions and Deletions with NGS Data 8.1 Background8.2 Methods; 8.3 Applications; 8.4 Conclusions and Future Directions; Acknowledgment; References; Chapter 9 Computational Approaches in Next-Generation Sequencing Data Analysis for Genome-Wide DNA Methylation Studies; 9.1 Introduction; 9.2 Enrichment-Based Approaches; 9.3 Bisulfite Treatment-Based Approaches; 9.4 Conclusion; References; Chapter 10 Bisulfite-Conversion-Based Methods for DNA Methylation Sequencing Data Analysis; 10.1 Introduction; 10.2 The Problem of Mapping BS-Treated Reads; 10.3 Algorithmic Approaches to the Problem Of Mapping BS-Treated Reads 10.4 Methylation Estimation

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