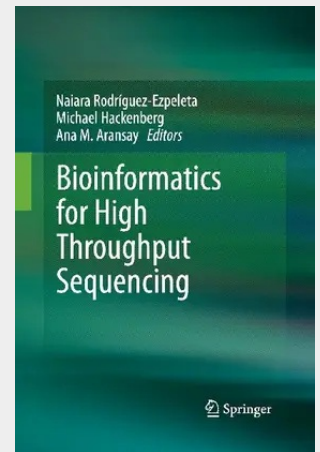


Bioinformatics for High Throughput Sequencing

Next generation sequencing is revolutionizing molecular biology. Owing to this new technology it is now possible to carry out a panoply of experiments at an unprecedented low cost and high speed. These go from sequencing whole genomes, transcriptomes and small non-coding RNAs to description of methylated regions, identification protein – DNA interaction sites and detection of structural variation. The generation of gigabases of sequence information for each of this huge bandwidth of applications in just a few days makes the development of bioinformatics applications for next generation sequencing data analysis as urgent as challenging.

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160,49 €

149,99 € (zzgl. MwSt.)

Lieferfrist: bis zu 10 Tage

Artikelnummer: 9781489998767

Medium: Buch

ISBN: 978-1-4899-9876-7

Verlag: Springer

Erscheinungstermin: 25.10.2014

Sprache(n): Englisch

Auflage: 2012

Produktform: Kartoniert

Gewicht: 411 g

Seiten: 255

Format (B x H): 155 x 235 mm

