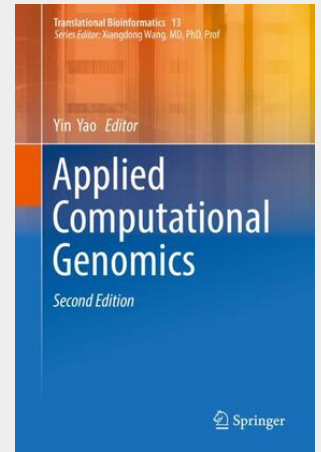Yao

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The volume provides a review of statistical development and application in the area of human genomics, including candidate gene mapping, linkage analysis, population-based genome-wide association, exon sequencing, and whole genome sequencing analysis. The authors are extremely experienced in the field of statistical genomics and will give a detailed introduction to the evolution of the field, as well as critical comments on the advantages and disadvantages of the proposed statistical models. The future directions of translational biology will also be described.

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