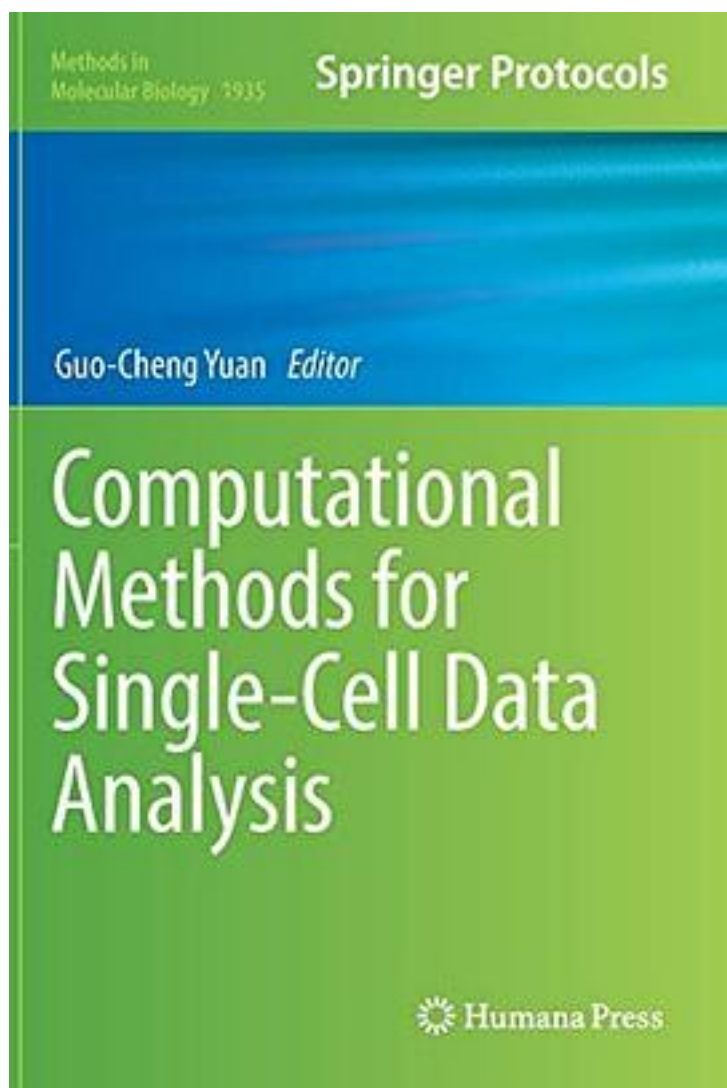# Computational Methods for Single-Cell Data Analysis

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著者:

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This detailed book provides state-of-art computational approaches to further explore the exciting opportunities presented by single-cell technologies. Chapters each detail a computational toolbox aimed to overcome a specific challenge in single-cell analysis, such as data normalization, rare cell-type identification, and spatial transcriptomics analysis, all with a focus on hands-on implementation of computational methods for analyzing experimental data. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls.Authoritative and cutting-edge, Computational Methods for Single-Cell Data Analysis aims to cover a wide range of tasks and serves as a vital handbook for single-cell data analysis.

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