



Computational and Evolutionary Analysis of HIV Molecular Sequences

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Computational and Evolutionary Analysis of HIV Molecular Sequences is for all researchers interested in HIV research, even those who only have a nodding acquaintance with computational biology (or those who are familiar with some, but not all, aspects of the field). HIV research is unusual in that it brings together scientists from a wide range of disciplines: clinicians, pathologists, immunologists, epidemiologists, virologists, computational biologists, structural biologists, evolutionary biologists, statisticians and mathematicians. This book seeks to bridge the gap between these groups, in both subject matter and terminology. Focused largely on HIV genetic variation, *Computational and Evolutionary Analysis of HIV Molecular Sequences* covers such issues as sampling and processing sequences, population genetics, phylogenetics and drug targets.

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