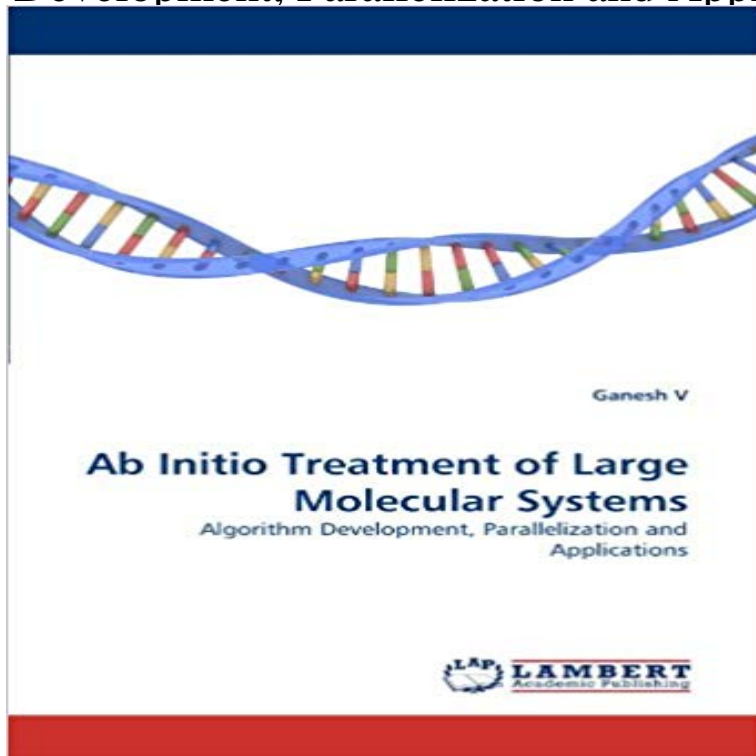


Ab Initio Treatment of Large Molecular Systems: Algorithm Development, Parallelization and Applications



The growth in computational power and storage driven by Moores law has enabled the scientific community to attempt solution of difficult problems in their areas of research. For example, it has become possible to routinely apply ab initio theories for attempting solutions of many challenging problems in chemistry, physics and biology. However, the formidable computational complexity of these methods is a major bottleneck towards applying them to larger chemical or biological systems. In consequence, even with huge computational resources, practical applications of conventionally coded ab initio methods are plausible only for the systems containing fewer than 100 atoms at a sufficiently reliable level of theory and basis. The main objective of this thesis is to develop reliable linear scaling algorithms and computer codes so as to extend the applicability of these accurate methods to larger systems including, but not restricted to protein fragments and molecular clusters.

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