

# Accepted Manuscript

An efficient multigrid strategy for large-scale molecular mechanics optimization

Jingrun Chen, Carlos J. García-Cervera

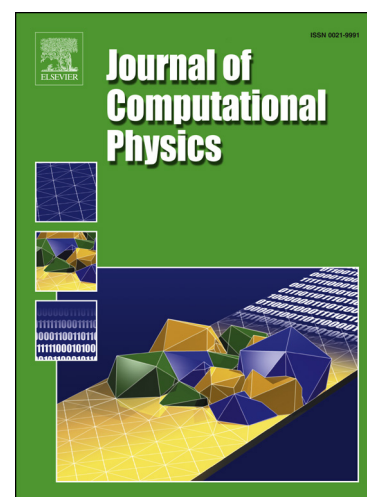
PII: S0021-9991(17)30306-6  
DOI: <http://dx.doi.org/10.1016/j.jcp.2017.04.035>  
Reference: YJCPH 7301

To appear in: *Journal of Computational Physics*

Received date: 16 January 2016  
Revised date: 25 January 2017  
Accepted date: 11 April 2017

Please cite this article in press as: J. Chen, C.J. García-Cervera, An efficient multigrid strategy for large-scale molecular mechanics optimization, *J. Comput. Phys.* (2017), <http://dx.doi.org/10.1016/j.jcp.2017.04.035>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



# AN EFFICIENT MULTIGRID STRATEGY FOR LARGE-SCALE MOLECULAR MECHANICS OPTIMIZATION

JINGRUN CHEN AND CARLOS J. GARCÍA-CERVERA

ABSTRACT. Static mechanical properties of materials require large-scale nonlinear optimization of the molecular mechanics model under various controls. This paper presents an efficient multigrid strategy to solve such problems. This strategy approximates solutions on grids in a *quasi-atomistic* and *inexact* manner, transfers solutions on grids following a coarse-to-fine (oneway) schedule, and finds physically relevant minimizers with linear scaling complexity. Compared to the full multigrid method which has the same complexity, the prefactor of this strategy is orders of magnitude smaller. Consequently, the required CPU time of this strategy is orders of magnitude smaller than that of the full multigrid method, and is smaller than that of the brute-force optimization for systems with more than 200,000 atoms. Considerable savings are found if the number of atoms becomes even larger due to the super-linear scaling complexity of the brute-force optimization. For systems with 1,000,000 atoms (over three million degrees of freedom), on average a more than 70% reduction of CPU time is observed regardless of the type of defects, including vacancies, dislocations, and cracks. In addition, linear scalability of the proposed strategy is tested in the presence of a dislocation pair for systems with more than 100 million atoms (over 400 million degrees of freedom).

## 1. INTRODUCTION

In the classical picture, atoms constitute matter and their interaction is described by a potential energy function. For a given system of atoms at zero (low) temperature, its equilibrium configuration is obtained by minimizing the potential energy with respect to atomic positions, known as the molecular mechanics (atomistic) model (see, e.g., [8]). The potential energy is highly nonlinear and the number of minimizers grows exponentially [46]

---

*Date:* April 12, 2017.

*2000 Mathematics Subject Classification.* 65K05, 65N55, 74G65, 90C06.

*Key words and phrases.* nonconvex optimization, molecular mechanics, multigrid, linear scaling, efficiency.

We thank Professor Weinan E for suggesting the topic studied here and Professor Pingbing Ming for helpful discussions. This work was supported by National Science Foundation grant DMS-1217315. JC also acknowledges support from National Natural Science Foundation of China via grant 21602149. CJGC also acknowledges support from the Bizkaia Talent program through the Basque Center for Applied Mathematics (BCAM).

Download English Version:

<https://daneshyari.com/en/article/4967320>

Download Persian Version:

<https://daneshyari.com/article/4967320>

[Daneshyari.com](https://daneshyari.com)