

Accelerating Numerical Simulation of Bone Remodeling Predictions with Vector Extrapolation Techniques

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Abstract

Bone modeling and remodeling were subjects of extensive studies in many fields of research. The process of adaptive bone remodeling can be described mathematically and simulated in a computer model, integrated with the finite element method (FEM). FEM can find out the long-term behavior of bone and the impact on bone biomechanics produced by any prosthetic models. As whole bone simulation is time consuming, the aim of this work is to accelerate the simulation of the process of bone remodelling. We combined FE simulation with numerical extrapolation techniques to accelerate the bone remodeling simulations. The two vector extrapolation methods, reduce ranked extrapolation (RRE) and minimal polynomial extrapolation (MPE), were used to reduce the simulation time. These extrapolation techniques are illustrated by the numerical example of the 2-D model based on a strain-adaptive bone remodeling model.

Keywords: bone remodeling, accelerating numerical simulation, finite element, extrapolation techniques, reduce ranked extrapolation, minimal polynomial extrapolation.

Several mathematical and computational theories have been developed to study the strain-adaptive bone remodeling problem [1]. Finite element (FE) simulation has proved to be specially suitable in the study of the behavior of any physiological unit, despite its complexity. Including all the difficulties for FE simulations of bone remodeling, such as geometric complexity which greatly complicates the generation of accurate simulation models, the whole procedure is very time consuming. Bone remodeling simulation normally starts assuming a uniform bone density distribution. As a consequence of the sequentially loads application, bone material properties changed, till a stable bone density distribution is predicted [2]. Therefore, we should run the FE solver for a large number of time increments to find out the final density distribution using bone remodeling algorithm. We run the FE solver for $t = n$ where n could be few hundreds and gather all the densities in matrix $X \in \mathbb{R}^{m \times n}$ where m is the total number of freedom degrees in the FE discretization and n is the number of time increments. By applying the singular value decomposition (SVD) on matrix X we recognize that the matrix has a huge potential for reduction, see Figure 1. The singular values show a significant and rapid decay and we can build up the left and right projection matrices by choosing the q largest singular values and the related columns in both matrices right and left singular vectors, which span the eigen space of the full density matrix X , where $q \ll (m, n)$. We can then project the matrix $X \in \mathbb{R}^{m \times n}$ to a reduced basis.

The main drawback for this classical approach remains on calculating the matrix X , the full final density distribution matrix. In some applications such as circuit simulations you need to re-simulate your problem many times so you only need to calculate the full problem once and then projecting the full system matrices to the reduced basis and re-simulate the reduced system which gives you a huge reduction in computational time [3]. This is out of interest in bone remodeling as we do not need to re-calculate the final density distribution for all time increments several times.

The main goal of this work is to use accelerate the convergence rate and use the reduction capability of the problem for the bone remodeling simulation. In fact, we study an approach based on vector extrapolation techniques [4, 5] to reduce the computational time for the numerical simulation of bone remodeling algorithms. In this work, we study two polynomial-type vector extrapolation methods that have proved to be very efficient convergence accelerators; namely, the minimal polynomial extrapolation (MPE) [4] and the reduced rank extrapolation (RRE) [5] to reduce the computational time and accelerating the bone remodeling algorithm. Finally, using the approach presented here we have demonstrated a reduction of the number of analyses by a factor of 10

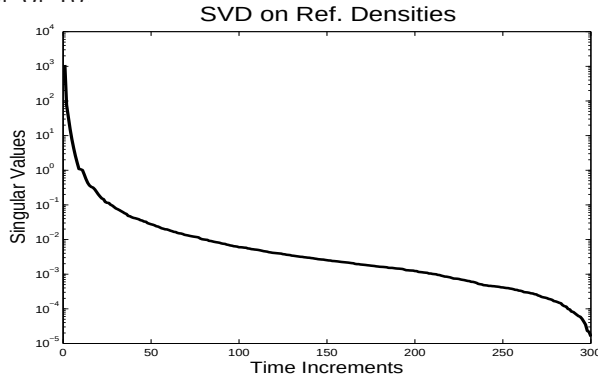


Figure 1: Singular Values for 2 – D model where $n = 300$, (semi-logarithmic scale).

Acknowledgements

The authors gratefully acknowledge the support through the (European Union) Seventh Framework Programme (FP7/2007-2013) under grant agreement Nu. 286179 (CAD-BONE project)"

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