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# An Adaptive Rectangular Mesh Management and Refining Method with Applications to Models of Cancer Invasion

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## Abstract

For the administration of adaptive mesh refinement on (hyper-)rectangular meshes, we provide a method. Our method is an efficient, easy-to-use method for h-refinement on 1-, 2-, and 3-D domains that does not need navigating the connectivity graph of the ancestry of mesh cells. The use of a rectangular mesh structure substantially facilitates the detection of siblings and nearby cells [1-15]. The administration method is especially made for meshes that are smooth since matrix operations use smoothness on an as-needed basis. It is inexpensive for a variety of mesh resolutions over a broad class of issues thanks to its modest memory footprint. We provide three uses for this method, one of which discusses the advantages of h-refinement in a 2D setting.

Adaptive mesh refinement (AMR) has frequently been used to increase the precision of numerical techniques and lessen their computing weight. AMR is frequently used in the domains of engineering, astronomy, and fluid dynamics, where the related techniques have become an essential part of the total numerical inquiry. Mathematical biology, on the other hand, has not yet seen much of their use. Examples are available.

## Introduction

AMR has established itself as a standard for which specific and complex numerical techniques have been created. Even still, mesh administration is still a challenging task that most scientific computing initiatives prefer to avoid. The purpose of this work is to offer a "do-it-yourself" recipe for AMR and mesh administration that places an emphasis on its ease of use and implementation while allowing for the management of circumstances that span the majority of the scientific computing spectrum.

According to this viewpoint, one of the objectives of our research is to apply AMR to models that depict the invasion of the extracellular matrix (ECM), the first stage in the spread of cancer and one of its defining characteristics. The models that we take into account in our work are typically advection-reaction-diffusion (ARD) systems, where the macroscopic densities of the related variables serve as a representation of those quantities. AMR is regarded as a key technique since the dynamics that their solutions exhibit can be complex and difficult to treat numerically. In our earlier work we investigated a 1D application of AMR specifically h-refinement—in a Finite Volume (FV) technique for such a system. There, we showed that the use of AMR significantly increased accuracy and productivity. However, a number of extra numerical challenges appear for examples in 2D (or higher dimensional) space. For instance, the structure of these specific cancer invasion models encourages the use of FV approaches rather than rectangular cell meshes, which when used in conjunction with h-refinement techniques result in hanging nodes. This makes it very difficult to calculate the system's advection and, most crucially, diffusion components. 2D convection-diffusion problems have been handled in the past using FV approaches and AMR techniques; for examples, see and the references therein.

## Subjective Heading

The application of AMR techniques raises a lot of technical challenges as well. The identification of sibling and neighbour cells required for the computation of the numerical fluxes and for the refinement/coarsening procedures, as well as traversing the connectivity network between children, parents, and ancestor mesh cells, are some examples of typical tasks. Other problems, such as model peculiarities

that might impose extra requirements on the structure and mesh handling, are less frequent. To name a few, the "smoothness" of the mesh is a manifestation of the fast dynamics of the solutions and the diffusion of the model; see, for example, for a detailed discussion of the topology of mesh generation. The application of AMR techniques raises a lot of technical challenges as well. The identification of sibling and neighbour cells required for the computation of the numerical fluxes and for the refinement/coarsening procedures, as well as traversing the connectivity network between children, parents, and ancestor mesh cells, are some examples of typical tasks. Other problems, such as model peculiarities that might impose extra requirements on the structure and mesh handling, are less frequent. To name a few, the "smoothness" of the mesh is a manifestation of the fast dynamics of the solutions and the diffusion of the model; see, for example, for a detailed discussion of the topology of mesh generation

To address the above numerical and technical issues, we develop our own AMR and mesh administration techniques. There are several reasons for that: first, we aim for simplicity, flexibility, and portability of our algorithms. Secondly, we want complete control of all the stages of the numerical treatment of the models. This includes various components of the implementation: the numerical methods for the solution of the partial differential equation (PDE) systems, the AMR techniques for the refinement/coarsening process, as well as the grid administration and bookkeeping algorithms for the handling of the data on the mesh.

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## Discussion

The whole effort is significant, as we have previously discussed in our discussions of the 1D h-refinement methodology and the creation of numerical algorithms to solve the relevant models and The administration and handling of the grid are the main topics of the current paper. A real example of the application of h-refinement to a 2D cancer invasion system is also presented. Cell bisection in 2, 4, or 8 equivalent rectangle cells in 1D, 2D, or 3D, respectively, is used in the h-refinement method that we use. This strategy has been applied to AMR techniques frequently. The most typical method is to employ mesh data structures that are pointer-based. This method explicitly represents the fundamental objects under consideration, such as vertices, using their physical coordinates. Using a series of pointers or handles, the edges, faces, or cells are defined with reference to the vertices; see, for example, These references are saved for the three vertices and the three neighbouring triangles of each triangle in the specific instance of a 2D triangulation. This method is intuitive and rather simple to use, but it has a large memory footprint and adds additional computational effort at each stage technique. The references referring to a discretization cell and the other cells it points to need to be modified as the cell is refined; this can be a difficult operation, especially in 3D volumes. We cite and the references therein for more details on the implementation and applications of this technique. Alternative strategies have been developed primarily to improve the methods' efficiency; see, for example, for implementations of half-edge and half-facet array-based mesh data structures. These methods have mostly been used to the 3D computer graphics representation of surface objects, as seen, for instance,

In the present study, we suggest a problem-specific methodology that focuses on rectangular meshes in 1, 2, and 3D. Unlike the pointer-based approach, we store the entire mesh tree data structure as a matrix and refer to various mesh cells via the associated matrix lines. Every cell points to its children and parent cells. Instead of storing the physical coordinates of each cell's vertices, we instead store the indices of the mesh cells, which represent the refinement level and an intra-level identifier for each cell. More specifically, we pre-compile a matrix in which we store details about each cell of the discretization tree for given minimum and maximum refinement levels.

Our technique shows both similarities and differences when compared to the software library p4est .On the one hand, both methods presuppose a cell hierarchy based on a tree that extends from a root cell to the leaf cells. Every cell identifies its parent and child cells. In contrast, our method characterises the computational cells in the mesh tree by a single integer (in one-, two-, and three-D), whereas in p4est each 3-dimensional mesh cell is characterised by 3 (real number) coordinates: x, y, and z. Furthermore, whereas the lower left corner is represented in p4est, our representation relates to the centre of the computational cell. Since no two distinct cells in a binary-, quad-, or octree share the same information, this creates some ambiguity functioning. Additionally, we mention its use in the deal. II computational framework. The comparison between our suggested method and alugrid is less straightforward since alugrid stores information that is more diversified and contains vertices, edges, faces, and other types of information. However, for a detailed description of this strategy and its application inside the DUNE computational we direct the interested reader to the mesh data structure we propose in this work can manage mesh resolutions that are enough for a variety of academic research in 1-, 2-, and 3-D, and it is simple to comprehend, construct, and utilise. We demonstrate this adaptability by outlining three distinct applications and investigations, with a focus on a cancer invasion issue.

The remainder of the study is organised as follows: in Section we explain the mesh administration technique, examine memory use and computing costs, and cover fundamental operations like refinement/ coarsening and the identification of neighbours and siblings. We give three numerical experiments in Section a general one that displays the mesh's characteristics administration technique, as well as applications in a Euler system and a cancer invasion model. We discuss the basic ingredients of the numerical methods and the AMR technique we use.

## Conclusion

We developed a simple method that avoids traversing the connectedness graph to determine a cell's ancestry, and because of the mesh's topology, it makes it much easier to identify neighbouring cells. It is simple to use and may be applied to a variety of issues in 1-, 2-, and higher dimensional areas. It is especially made for smooth meshes and dynamically utilises their smoothness in matrix computations. On coarse to extremely fine mesh resolutions, the approach is cost-effective due to its small memory footprint. Furthermore, our method offers a wide range of monitor functions and threshold parameters, as well as adaptive minimum and maximum refinement levels. Despite the fact that the current paper does not analyse these qualities.

## Acknowledgement

## Conflict of Interest

The authors declare that they are no conflict of interest.

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