

## Computational Framework

We use a parallel finite element library called `hiperlife` (High Performance Library for Finite Elements) [1], which serves as the core numerical engine for the simulations presented in this study. This library depends on other open-source libraries. The library is openly distributed to the community and is available online at <https://gitlab.com/hiperlife/hiperlife>. The aim of this library is to provide a computational framework to address problems of cell and tissue mechanobiology for a wide range of cases and users, with special focus on curved surfaces. The `hiperlife` is written in C++, uses the Message Passing Interface (MPI) paradigm for parallelism, and is built on top of several packages of the Trilinos Project. The installation of the `hiperlife` libraries can be carried out by following the guidelines provided at: <https://gitlab.com/hiperlife/hiperlife/-/blob/dev/INSTALL.md>. Prior to following the instructions for installation, it is necessary to clone the libraries via Linux command `git clone git@gitlab.com:hiperlife/hiperlife.git` or download from <https://gitlab.com/hiperlife/hiperlife>.

## Code Organization and Project Setup

For the present work, we implemented the problem-specific code within the `hiperlife` ecosystem by creating a top-level project folder named `wrinkling_epithelial_continuum`. This project folder contains a global `CMakeLists.txt` file, which controls the compilation, and one or more subprojects (applications), each corresponding to a specific simulation setup. For example, the application `inflate_hold_deflate` implements the model of interest here and resides in its own folder with a local `CMakeLists.txt`. The code used in this study is openly available at [https://github.com/pradeep927/mechanics\\_of\\_epithelial\\_domes](https://github.com/pradeep927/mechanics_of_epithelial_domes).

The build system relies on CMake to configure and manage the compilation. Two additional files are kept in the project root: `cmake.project.ubuntu.20.04.sh`, a shell script to automate the configuration process on Ubuntu systems; and `userConfig.cmake`, a configuration file where paths to `hiperlife`, Trilinos, and other dependencies are specified. The typical installation procedure is as follows: Install `hiperlife` following the instructions at <https://hiperlife.gitlab.io/hiperlife/Installation/index.html>. For our simulations, the libraries were installed on a workstation running Ubuntu 22.04. Place the two files inside the top-level project folder `wrinkling_epithelial_continuum`. From the terminal, make the script executable and launch the build configuration:

```
chmod 777 cmake.project.ubuntu.20.04.sh
./cmake.project.ubuntu.20.04.sh
```

Enter the build directory and compile:

```
cd build
make -j4 install
```

This process generates the executable binary at:

```
/home/ubuntu/wrinkling_epithelial_continuum/source_compiled/bin/hlinflate_hold_deflate
```

## Running Simulations

To execute a simulation, we create a dedicated folder `run_simulation` that contains the mesh files and the configuration files. Meshes are provided in VTK format and typically correspond to epithelial footprints with prescribed geometries. For example, a mesh named `aspect_26` corresponds to a circular domain with aspect ratio 26. Boundary conditions are imposed by carefully fixing the exterior nodes of the domain using elastic springs, which mimic physical anchoring constraints.

The simulation parameters, including references to the mesh files, are specified in a configuration file named `config.cfg`. This file allows the user to set model parameters, time-stepping controls, solver tolerances, and material constants.

A simulation is launched in parallel using MPI as:

```
mpirun -n 4 /home/ubuntu/wrinkling_epithelial_continuum/  
source_compiled/bin/hlinflate_hold_deflate config.cfg
```

Here, the option `-n 4` specifies the number of processors. This value can be adjusted according to the available computational resources and the problem size.

## Postprocessing and Visualization

During execution, the code generates output files in VTK format (e.g., `sol_dis.vtk`), which store the displacement and other field variables at different time steps. These files can be directly visualized and post-processed using ParaView. To streamline postprocessing, we provide a ParaView state file (`paraview_state.pvsm`), which loads the output files, applies predefined visualization settings, and enables rapid analysis of simulation results, including deformation fields, wrinkling patterns, and stress distributions.

## Code Availability

The code is openly available at [https://github.com/pradeep927/mechanics\\_of\\_epithelial\\_domes](https://github.com/pradeep927/mechanics_of_epithelial_domes).

## References

- [1] Santos-Olivan, D., Vilanova, G., & Torres-Sanchez, A. (2025). hiperlife (release-5.0.0-alpha). Zenodo. <https://zenodo.org/doi/10.5281/zenodo.14927572>