

## Chaste: Cancer, Heart and Soft Tissue Environment

Fergus R Cooper<sup>1</sup>, Ruth E Baker<sup>1</sup>, Miguel O Bernabeu<sup>2</sup>, Rafel Bordas<sup>3</sup>, Louise Bowler<sup>3</sup>, Alfonso Bueno-Orovio<sup>3</sup>, Helen M Byrne<sup>1</sup>, Valentina Carapella<sup>4</sup>, Louie Cardone-Noott<sup>3</sup>, Jonathan Cooper<sup>5</sup>, Sara Dutta<sup>3</sup>, Benjamin D Evans<sup>6, 7</sup>, Alexander G Fletcher<sup>8, 9</sup>, James A Grogan<sup>1</sup>, Wenxian Guo<sup>10</sup>, Daniel G Harvey<sup>3</sup>, Maurice Hendrix<sup>11,12</sup>, David Kay<sup>3</sup>, Jochen Kursawe<sup>13</sup>, Philip K Maini<sup>1</sup>, Beth McMillan<sup>3</sup>, Gary R Mirams<sup>11</sup>, James M Osborne<sup>14</sup>, Pras Pathmanathan<sup>15</sup>, Joe M Pitt-Francis<sup>3</sup>, Martin Robinson<sup>3</sup>, Blanca Rodriguez<sup>3</sup>, Raymond J Spiteri<sup>10</sup>, and David J Gavaghan<sup>3</sup>

**1** Wolfson Centre for Mathematical Biology, Mathematical Institute, University of Oxford, Oxford, UK **2** Centre for Medical Informatics, Usher Institute, University of Edinburgh, Edinburgh, United Kingdom **3** Department of Computer Science, University of Oxford, Oxford, UK **4** Division of Cardiovascular Medicine, Radcliffe Department of Medicine, University of Oxford, Oxford, UK **5** Research IT Services, University College London, London, UK **6** Centre for Biomedical Modelling and Analysis, Living Systems Institute, University of Exeter, Exeter, UK **7** School of Psychological Science, University of Bristol, Bristol, UK **8** School of Mathematics & Statistics, University of Sheffield, Sheffield, UK **9** Bateson Centre, University of Sheffield, Sheffield, UK **10** Department of Computer Science, University of Saskatchewan, Canada **11** Centre for Mathematical Medicine & Biology, School of Mathematical Sciences, University of Nottingham, Nottingham, UK **12** Digital Research Service, University of Nottingham, Nottingham, UK **13** Faculty of Biology, Medicine and Health, University of Manchester, Manchester, UK **14** School of Mathematics and Statistics, University of Melbourne, Victoria, Australia **15** Office of Science and Engineering Laboratories (OSEL), Center for Devices and Radiological Health (CDRH), U.S. Food and Drug Administration (FDA), Silver Spring, MD 20993, USA

DOI: [10.21105/joss.01848](https://doi.org/10.21105/joss.01848)

### Software

- [Review](#) ↗
- [Repository](#) ↗
- [Archive](#) ↗

**Editor:** [Marie E. Rognes](#) ↗

### Reviewers:

- [@finsberg](#)
- [@IgorBaratta](#)

**Submitted:** 13 September 2019

**Published:** 10 March 2020

### License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC-BY](#)).

## Summary

Chaste (Cancer, Heart And Soft Tissue Environment) is an open source simulation package for the numerical solution of mathematical models arising in physiology and biology.

To date, Chaste development has been driven primarily by applications that include continuum modelling of cardiac electrophysiology ('Cardiac Chaste'), discrete cell-based modelling of soft tissues ('Cell-based Chaste'), and modelling of ventilation in lungs ('Lung Chaste'). Cardiac Chaste addresses the need for a high-performance, generic, and verified simulation framework for cardiac electrophysiology that is freely available to the scientific community. Cardiac chaste provides a software package capable of realistic heart simulations that is efficient, rigorously tested, and runs on HPC platforms. Cell-based Chaste addresses the need for efficient and verified implementations of cell-based modelling frameworks, providing a set of extensible tools for simulating biological tissues. Computational modelling, along with live imaging techniques, plays an important role in understanding the processes of tissue growth and repair. A wide range of cell-based modelling frameworks have been developed that have each been successfully applied in a range of biological applications. Cell-based Chaste includes implementations of the cellular automaton model, the cellular Potts model, cell-centre models with cell representations as overlapping spheres or Voronoi tessellations, and the vertex model. Lung Chaste addresses the need for a novel, generic and efficient lung modelling software package that is both tested and verified. It aims to couple biophysically-detailed models of

airway mechanics with organ-scale ventilation models in a package that is freely available to the scientific community.

Chaste is designed to be modular and extensible, providing libraries for common scientific computing infrastructure such as linear algebra operations, finite element meshes, and ordinary and partial differential equation solvers. This infrastructure is used by libraries for specific applications, such as continuum mechanics, cardiac models, and cell-based models. The software engineering techniques used to develop Chaste are intended to ensure code quality, re-usability and reliability. Primary applications of the software include cardiac and respiratory physiology, cancer and developmental biology.

## The software

Chaste is available on GitHub <https://github.com/Chaste/Chaste>, and the current stable release is version 2019.1. Please see the Readme.md file on the Github repository for links to the Chaste wiki and install guides.

Previous publications about Chaste have detailed the rationale for, and design principles behind, Chaste (Pitt-Francis et al., 2009), as well as the main application areas of Chaste up to 2013 (Mirams et al., 2013).

Chaste places an emphasis on reproducibility and verification and, as such, extensive automated testing is used to ensure software quality and reliability. A series of test suites must all pass before any commit is considered a release-candidate. Most testing is performed on Long Term Support (LTS) versions of Ubuntu Linux, with unit tests additionally being run on macOS.

Testing includes compilation of all libraries with GCC, Clang and Intel C++ compilers; extensive unit testing; performance profiling to identify any slowdowns over time; memory testing with valgrind; verification of code coverage; and running unit tests with different combinations of dependencies to ensure portability. The output of these tests is available at <https://chaste.cs.ox.ac.uk/buildbot/>.

Since 2013, Chaste has substantially changed to modernise its infrastructure and to enable new science. In terms of infrastructure, Chaste now uses a modern CMake build system, the C++14 language standard, and makes extensive use of BuildBot for continuous integration. In terms of science, Lung Chaste is entirely new and allows the use of Chaste in a new scientific domain. In Cardiac Chaste, we can now create algebraic Jacobians for CellML ODE systems, which can improve speed of simulation for cardiac action potential and tissue simulations (Cooper, Spiteri, & Mirams, 2015), and metadata annotations of CellML files have replaced manual specification of variables in configuration files. Cell-based Chaste has been overhauled to improve flexibility. Changes include hierarchies of simulation modifiers, information writers, cell-cycle models, subcellular reaction network models, and numerical methods that allow new customisation points in almost every area of all cell-based simulations. In addition, simulation output has been standardised to use VTK, a standard and powerful visualisation framework, and some cell-centre simulations now run in parallel using MPI.

## Comparison with other software

Chaste provides substantial common infrastructure enabling a wide range of applications across multiple disciplines. Common elements include meshing, solving differential equations, input/output and continuum mechanics, and these form a platform for Cardiac, Cell-based and Lung Chaste.

A key goal of Chaste is to enable the implementation of many different modelling frameworks. This not only allows a user to select the most appropriate tool for their research but, importantly, enables the comparison of different modelling frameworks to better understand the

benefits and drawbacks of each (Osborne, Fletcher, Pitt-Francis, Maini, & Gavaghan, 2017). This is an explicit design goal of Chaste, which focusses on the flexibility of implementing multiple models rather than (for example) building a graphical user interface. See Table 1 for a comparison of alternatives to Chaste in specific domains, with all other software tools implementing a single modelling framework.

Software	Open Source	GUI	CA	CP	PM	VT	VM
Chaste	x		x	x	x	x	x
CompuCell3D	x	x		x			
Morpheus	x	x		x			
EPISIM		x			x		
CellSys		x			x		
PhysiCell	x				x		
Biocellion					x		
VirtualLeaf	x	x					x
EmbryoMaker	x	x			x		

**Table 1:** A comparison of software tools for cell-based modelling. GUI: graphical user interface. CA: cellular automata. CP: cellular Potts. PM: particle model, a cell-centre model. VT: Voronoi tessellation, a cell-centre model. VM: vertex model. References: CompuCell3D (Swat et al., 2012), Morpheus (Starruß, Back, Brusch, & Deutsch, 2014), EPISIM (Sutterlin, Kolb, Dickhaus, Jäger, & Grabe, 2013), CellSys (Hoehme & Drasdo, 2010), PhysiCell (Ghafarizadeh, Heiland, Friedman, Mumenthaler, & Macklin, 2018), Biocellion (Kang, Kahan, McDermott, Flann, & Shmulevich, 2014), VirtualLeaf (Merks, Guravage, Inzé, & Beemster, 2011), EmbryoMaker (Marin-Riera, Brun-Usan, Zimm, Välikangas, & Salazar-Ciudad, 2015).

## Installation

Installation of Chaste has been greatly simplified through the development of a Docker image <https://github.com/chaste/chaste-docker>. Docker is a lightweight, open-source virtualisation technology for running encapsulated applications ('containers') on all major operating systems at near-native speed. This enables Chaste (including all dependencies, environment settings, convenience scripts and the latest precompiled release) to be downloaded and installed with just a single command. Isolating Chaste within a container also means that its dependencies and those installed on the user's host system can coexist without interference or version conflicts.

In addition to simplifying the set-up and execution of Chaste, importantly this also enhances its reproducibility by providing a homogeneous computational environment regardless of the underlying operating system and hardware. Not only is the Chaste source code version-controlled, but so too are the dependencies, configuration settings and environment variables used to build and run it. This means that collaborators and reviewers can easily and consistently reproduce results (to within machine precision) on any platform while developers can seamlessly migrate and scale-up their simulations from a laptop to a workstation or HPC cluster.

## Example usage

Chaste has tutorials to walk users through basic functionality for each application area. Tutorial examples are bundled for each specific release version, and examples for this release are available at [https://chaste.cs.ox.ac.uk/chaste/tutorials/release\\_2019.1](https://chaste.cs.ox.ac.uk/chaste/tutorials/release_2019.1).

Tutorials take the form of C++ header files that each define 'tests' in the Chaste testing infrastructure. These tests must be compiled and run to produce an output, which can be visualised using [ParaView](#).

In the following sections we showcase a specific tutorial for each of cardiac, cell-based, and lung Chaste, with minimal commands necessary to reproduce the output shown.

### Cardiac example

Here we demonstrate how to run and visualise a three-dimensional monodomain cardiac simulation. This follows the tutorial `TestMonodomain3dRabbitHeartTutorial` which simulates the result of an electrical stimulus being applied to a realistic rabbit heart geometry. Assuming that

1. Chaste has been installed on Ubuntu Linux (or is running within a Docker container),
2. the Chaste source code exists at `$CHASTE_SOURCE_DIR`,
3. the environment variable `$CHASTE_TEST_OUTPUT` is set to a valid directory,

a minimal set of commands to build and run the tutorial is as follows:

```
mkdir build && cd build
cmake $CHASTE_SOURCE_DIR
make TestMonodomain3dRabbitHeartTutorial
ctest -R TestMonodomain3dRabbitHeartTutorial
```

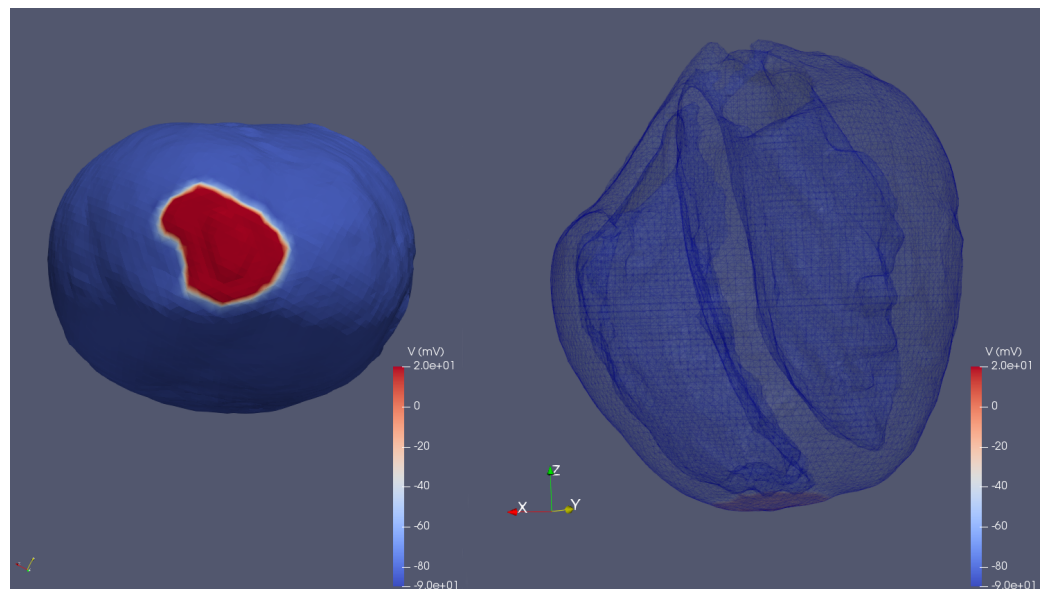
This will produce output in the following directory:

`$CHASTE_TEST_OUTPUT/Monodomain3dRabbitHeart`

To view the results evolving over time as an animation in ParaView it is necessary to post-process the results with the following command:

```
cd $CHASTE_TEST_OUTPUT/Monodomain3dRabbitHeart/vtk_output
python $CHASTE_SOURCE_DIR/python/Utils/AddVtuTimeAnnotations.py \
    results.vtu annotated_results.vtu
```

To visualise the output, open the file `annotated_results.vtu` in ParaView, and select to colour by V (voltage).



**Figure 1:** Trans-membrane voltage on the rabbit heart mesh at the end of the simulation. As viewed on the surface from the apex of the heart (left) and on a wireframe showing the ventricular cavities (right).

### Cell-based example

Here we demonstrate how to run and visualise a cell sorting simulation using Chaste's vertex model implementation. This follows the tutorial `TestRunningDifferentialAdhesionSimulationsTutorial`. Assuming that

1. Chaste has been installed on Ubuntu Linux (or is running within a Docker container),
2. the Chaste source code exists at `$CHASTE_SOURCE_DIR`,
3. the environment variable `$CHASTE_TEST_OUTPUT` is set to a valid directory,

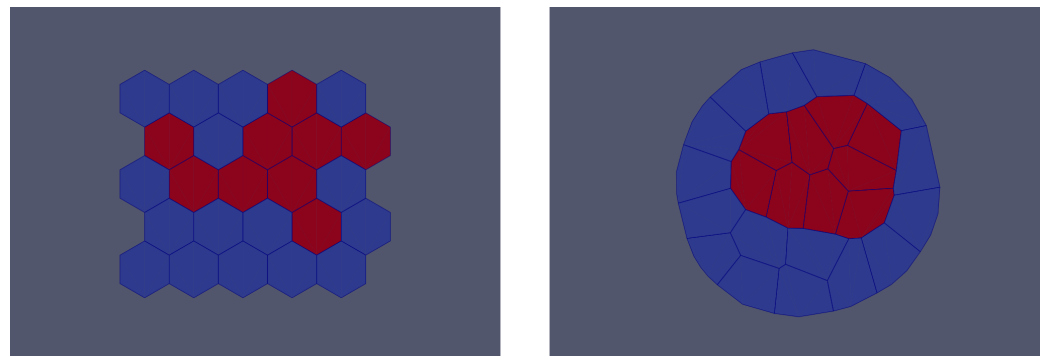
a minimal set of commands to build and run the tutorial is as follows:

```
mkdir build && cd build
cmake $CHASTE_SOURCE_DIR
make TestRunningDifferentialAdhesionSimulationsTutorial
ctest -R TestRunningDifferentialAdhesionSimulationsTutorial
```

This will produce output in the following directory:

`$CHASTE_TEST_OUTPUT/TestVertexBasedDifferentialAdhesionSimulation`

To visualise the simulation, open the file `results.pvd` in ParaView, choose to colour by 'Cell types', and display 'Surface With Edges'.



**Figure 2:** The initial configuration of cells (left), and the final configuration of cells after sorting has occurred (right).

### Lung example

Here we demonstrate how to run and visualise the lung airway generation tutorial. This follows the tutorial `TestAirwayGenerationTutorial` which statistically generates lung airways given initial geometry segmented from a CT scan. Assuming that

1. Chaste has been installed on Ubuntu Linux (or is running within a Docker container),
2. the Chaste source code exists at `$CHASTE_SOURCE_DIR`,

3. the environment variable `$CHASTE_TEST_OUTPUT` is set to a valid directory,

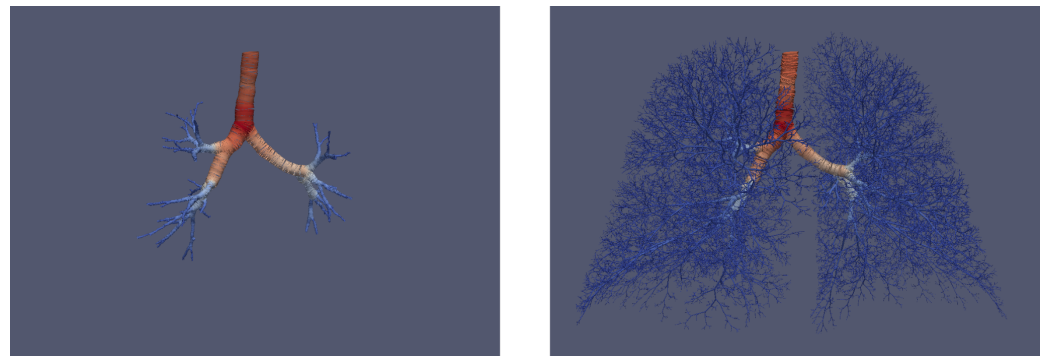
a minimal set of commands to build and run the tutorial is as follows:

```
mkdir build && cd build
cmake $CHASTE_SOURCE_DIR
make TestAirwayGenerationTutorial
ctest -R TestAirwayGenerationTutorial
```

This will produce output in the following directory:

`$CHASTE_TEST_OUTPUT/TestAirwayGenerationTutorial`

To visualise the generated airway geometry, open the file `example_complete_conducting_airway.vtu` in ParaView. Application of an 'Extract Surface' filter followed by a 'Tube' filter allows the centreline and radius information to be viewed as a series of tubes.



**Figure 3:** The initial geometry of major airways segmented from a CT scan (left), and an example of a complete generated airway tree (right).

## Recent publications enabled by Chaste

Since our last publication on Chaste (Mirams et al., 2013), over 70 peer-reviewed publications have been enabled, which we mention briefly below.

Publications using Cardiac Chaste have included scientific studies relating to: basic mechanisms of cardiac electrophysiology in healthy and diseased settings (Bartolucci et al., 2014; Cardone-Noott, Bueno-Orovio, Mincholé, Zemzemi, & Rodriguez, 2016; Corsi et al., 2017; Dutta, Mincholé, Quinn, & Rodriguez, 2017; Dutta et al., 2016; Lyon et al., 2018; Mahoney et al., 2016; Passini, Pellegrini, Caiani, & Severi, 2013; Pathmanathan & Gray, 2015; Reilly et al., 2016; Sadrieh et al., 2014; Samanta, Kar, Mirams, & Parekh, 2015; Walmsley, Rodriguez, et al., 2013; Zhou et al., 2016, 2019); the effects of realistic tissue structure on simulated cardiac electrical activity (Lekadir, Lange, Zimmer, Hoogendoorn, & Frangi, 2016; Lekadir et al., 2014; Walmsley et al., 2013; Zacur et al., 2017); the sources and consequences of inter-subject electrophysiological variability (Britton et al., 2013; Oliver J. Britton et al., 2017; Dutta, Mincholé, Walmsley, & Rodriguez, 2013; Elkins et al., 2013; Muszkiewicz et al., 2018; Walmsley, Mirams, Pitt-Francis, Rodriguez, & Burrage, 2015); predicting the effects of drugs on cardiac activity, including safety assessment (Beattie et al., 2013; Oliver J Britton et al., 2017; Cardone-Noott et al., 2014; Davies et al., 2016; Hill et al., 2016; Lim, Cun, Wang, Gray, & Glimm, 2018; McMillan, Gavaghan, & Mirams, 2017; Mirams et al., 2014; Moreno et al., 2015; Passini et al., 2017, 2016, 2014; Wallman, Smith, & Rodríguez, 2014;



Zemzemi et al., 2013; Zemzemi & Rodriguez, 2015); and the development of associated web-based tools (Cooper, Scharm, & Mirams, 2016; Daly et al., 2018; Williams & Mirams, 2015). Other studies enabled by Cardiac Chaste have advanced the methodologies for parameter identifiability and inference, model selection and uncertainty quantification for in cardiac electrophysiology models (Daly, Cooper, Gavaghan, & Holmes, 2017; Daly, Gavaghan, Holmes, & Cooper, 2015; Johnstone et al., 2016; Mirams, Pathmanathan, Gray, Challenor, & Clayton, 2016); and for the verification and efficient numerical simulation of such models (Agudelo-Toro & Neef, 2013; Campos, Oliveira, Santos, & Rocha, 2016; Cardone-Noott, Rodriguez, & Bueno-Orovio, 2018; Cervi & Spiteri, 2018; Corrado, Lassoued, Mahjoub, & Zemzemi, 2016; Green, Bohn, & Spiteri, 2019; Marsh, Ziaratgahi, & Spiteri, 2012; Pathmanathan & Gray, 2014; Spiteri & Torabi Ziaratgahi, 2016). The continuum-mechanics solvers in Chaste have been used for studies of dielectric elastomers (Langham, Bense, & Barkley, 2018); and our electro-mechanics code as used in (Carapella et al., 2014), has also been used to verify new numerical methods (Gurev et al., 2015).

Work using Cardiac Chaste has also been published on mesh generation and model simulation in the area of gastric electrophysiology, in particular focusing on interstitial cell of Cajal network structure and function (Gao, Sathar, O'Grady, Archer, & Cheng, 2015; Gao, Sathar, O'Grady, Han, & Cheng, 2014; Sathar et al., 2015a, 2015b, 2015c; Sathar, Trew, Du, O'Grady, & Cheng, 2014).

Publications enabled by Cell-based Chaste have focused on: the cellular mechanisms and dynamics of intestinal homeostasis and carcinogenesis (Almet, Hughes, Landman, Näthke, & Osborne, 2018; Baker et al., 2014; Carroll et al., 2017; Dunn, Näthke, & Osborne, 2013; Dunn, Osborne, Appleton, & Näthke, 2016; Hu & Cucinotta, 2014; Langlands et al., 2016; Muraro et al., 2018; Osborne, 2015); the mechanisms underlying vascular tumour growth and response to therapy in the Microvessel Chaste project (Grogan, Connor, et al., 2017; Grogan, Connor, Pitt-Francis, Maini, & Byrne, 2018; Grogan, Markelc, et al., 2017); the biomechanical characterization of skin lesions (Franzetti et al., 2015); the organisation and proliferation of stem and pluripotent cells in development (Atwell et al., 2015; Godwin et al., 2017; Koke, Kanesaki, Grosshans, Schwarz, & Dunlop, 2014); the dynamics of developing epithelial tissues (Abdullah et al., 2017; Finegan et al., 2018; Kursawe, Brodskiy, Zartman, Baker, & Fletcher, 2015; Tetley, Blanchard, Fletcher, Adams, & Sanson, 2016; Waites, Cavaliere, Cachat, Danos, & Davies, 2018); the spread of sexually-transmitted infections (Nelson et al., 2014); vascular remodelling (Osborne & Bernabeu, 2018); the similarities and differences between competing cell-based modelling approaches (Davit, Osborne, Byrne, Gavaghan, & Pitt-Francis, 2013; Figueredo, Joshi, Osborne, Byrne, & Owen, 2013; Fletcher, Osborne, Maini, & Gavaghan, 2013; Osborne et al., 2017); the calibration and parameterisation of such models (Cooper & Osborne, 2013; Kursawe, Baker, & Fletcher, 2018); and their efficient numerical solution (Cooper, Baker, & Fletcher, 2017; Harvey, Fletcher, Osborne, & Pitt-Francis, 2015; Kursawe, Baker, & Fletcher, 2017; Rubinacci et al., 2015).

Papers on Lung Chaste describe its use for patient-specific airway tree generation and flow modelling (Bordas et al., 2015; Burrowes et al., 2017; Soares, Owers-Bradley, Foy, Kay, & Siddiqui, 2017).

## Acknowledgements

F.R.C. was supported by the Engineering and Physical Sciences Research Council [grant number EP/G03706X/1]; R.E.B. is a Royal Society Wolfson Research Merit Award holder, would like to thank the Leverhulme Trust for a Research Fellowship, and also acknowledges the BBSRC for funding [grant number BB/R000816/1]; B.D.E. was generously supported by the Wellcome Trust Institutional Strategic Support Award [grant number 204909/Z/16/Z]; A.G.F. was supported by a University of Sheffield Vice-Chancellor's Fellowship and the Biotechnology and Biological Sciences Research Council [grant number BB/R016925/1]; J.K. was supported

by the Engineering and Physical Sciences Research Council [grant number EP/N509711/1]; G.R.M. was supported by a Sir Henry Dale Fellowship jointly funded by the Wellcome Trust and Royal Society [Wellcome Trust grant number 101222/Z/13/Z] and a Wellcome Trust Senior Research Fellowship [grant number 212203/Z/18/Z]; A.B.O. was supported by a British Heart Foundation Intermediate Basic Science Fellowship [grant number FS/17/22/32644]; B.R. was supported by a Wellcome Trust Senior Research Fellowship [grant numbers 100246/Z/12/Z and 214290/Z/18/Z]; creation of the virtual airway structures was funded partially through the EU FP 7 AirPROM project.

## References

- Abdullah, A., Avraam, D., Chepizhko, O., Vaccari, T., Zapperi, S., La Porta, C. A. M., & Vasiev, B. (2017). Universal statistics of epithelial tissue topology. *arXiv preprint arXiv:1710.08527*. Retrieved from <https://arxiv.org/abs/1710.08527>
- Agudelo-Toro, A., & Neef, A. (2013). Computationally efficient simulation of electrical activity at cell membranes interacting with self-generated and externally imposed electric fields. *J. Neural Eng.*, 10(2), 026019. doi:[10.1088/1741-2560/10/2/026019](https://doi.org/10.1088/1741-2560/10/2/026019)
- Almet, A. A., Hughes, B. D., Landman, K. A., Näthke, I. S., & Osborne, J. M. (2018). A multicellular model of intestinal crypt buckling and fission. *Bull. Math. Biol.*, 80(2), 335–359. doi:[10.1007/s11538-017-0377-z](https://doi.org/10.1007/s11538-017-0377-z)
- Atwell, K., Qin, Z., Gavaghan, D., Kugler, H., Hubbard, E. J. A., & Osborne, J. M. (2015). Mechano-logical model of *C. elegans* germ line suggests feedback on the cell cycle. *Development*, 142(22), 3902–3911. doi:[10.1242/dev.126359](https://doi.org/10.1242/dev.126359)
- Baker, A.-M., Cereser, B., Melton, S., Fletcher, A. G., Rodriguez-Justo, M., Tadrous, P. J., Humphries, A., et al. (2014). Quantification of crypt and stem cell evolution in the normal and neoplastic human colon. *Cell Rep*, 8(4), 940–947. doi:[10.1016/j.celrep.2014.07.019](https://doi.org/10.1016/j.celrep.2014.07.019)
- Bartolucci, C., Moreno, C., Cruz, A. de la, Lambiase, P., Severi, S., & Valenzuela, C. (2014). Linking a novel mutation to its short QT phenotype through multiscale computational modelling. In *Computing in cardiology 2014* (pp. 1017–1020). IEEE.
- Beattie, K. A., Luscombe, C., Williams, G., Munoz-Muriedas, J., Gavaghan, D. J., Cui, Y., & Mirams, G. R. (2013). Evaluation of an in silico cardiac safety assay: using ion channel screening data to predict QT interval changes in the rabbit ventricular wedge. *J Pharmacol Toxicol Methods*, 68(1), 88–96. doi:[10.1016/j.vascn.2013.04.004](https://doi.org/10.1016/j.vascn.2013.04.004)
- Bordas, R., Lefevre, C., Veeckmans, B., Pitt-Francis, J., Fetita, C., Brightling, C. E., Kay, D., et al. (2015). Development and analysis of patient-based complete conducting airways models. *PloS one*, 10(12), e0144105. doi:[10.1371/journal.pone.0144105](https://doi.org/10.1371/journal.pone.0144105)
- Britton, O. J., Abi-Gerges, N., Page, G., Ghetti, A., Miller, P. E., & Rodriguez, B. (2017). Quantitative comparison of effects of dofetilide, sotalol, quinidine, and verapamil between human ex vivo trabeculae and in silico ventricular models incorporating inter-individual action potential variability. *Frontiers in physiology*, 8, 597. doi:[10.3389/fphys.2017.00597](https://doi.org/10.3389/fphys.2017.00597)
- Britton, O. J., Bueno-Orovio, A., Van Ammel, K., Lu, H. R., Towart, R., Gallacher, D. J., & Rodriguez, B. (2013). Experimentally calibrated population of models predicts and explains intersubject variability in cardiac cellular electrophysiology. *Proc Natl Acad Sci USA*, 110(23), E2098–E2105. doi:[10.1073/pnas.1304382110](https://doi.org/10.1073/pnas.1304382110)
- Britton, O. J., Bueno-Orovio, A., Virág, L., Varró, A., & Rodriguez, B. (2017). The electrogenic Na<sup>+</sup>/K<sup>+</sup> pump is a key determinant of repolarization abnormality susceptibility in human ventricular cardiomyocytes: A population-based simulation study. *Frontiers in Physiology*, 8, 278. doi:[10.3389/fphys.2017.00278](https://doi.org/10.3389/fphys.2017.00278)



- Burrowes, K., Doel, T., Kim, M., Vargas, C., Roca, J., Grau, V., & Kay, D. (2017). A combined image-modelling approach assessing the impact of hyperinflation due to emphysema on regional ventilation-perfusion matching. *Computer Methods in Biomechanics and Biomedical Engineering: Imaging & Visualization*, 5(2), 110–126. doi:[10.1080/21681163.2015.1023358](https://doi.org/10.1080/21681163.2015.1023358)
- Campos, J. O., Oliveira, R. S., Santos, R. W. dos, & Rocha, B. M. (2016). Lattice Boltzmann method for parallel simulations of cardiac electrophysiology using GPUs. *J Comput Appl Math*, 295, 70–82. doi:[10.1016/j.cam.2015.02.008](https://doi.org/10.1016/j.cam.2015.02.008)
- Carapella, V., Bordas, R., Pathmanathan, P., Lohezic, M., Schneider, J. E., Kohl, P., Burrage, K., et al. (2014). Quantitative study of the effect of tissue microstructure on contraction in a computational model of rat left ventricle. *PLOS ONE*, 9(4), e92792. doi:[10.1371/journal.pone.0092792](https://doi.org/10.1371/journal.pone.0092792)
- Cardone-Noott, L., Bueno-Orovio, A., Mincholé, A., Zemzemi, N., & Rodriguez, B. (2016). Human ventricular activation sequence and the simulation of the electrocardiographic QRS complex and its variability in healthy and intraventricular block conditions. *EP Europace*, 18(suppl\_4), iv4–iv15. doi:[10.1093/europace/euw346](https://doi.org/10.1093/europace/euw346)
- Cardone-Noott, L., Bueno-Orovio, A., Mincholé, A., Burrage, K., Wallman, M., Zemzemi, N., Dall'Armellina, E., et al. (2014). A computational investigation into the effect of infarction on clinical human electrophysiology biomarkers. In *Computing in cardiology* (pp. 673–676). IEEE.
- Cardone-Noott, L., Rodriguez, B., & Bueno-Orovio, A. (2018). Strategies of data layout and cache writing for input-output optimization in high performance scientific computing: Applications to the forward electrocardiographic problem. (R. S. Oliveira, Ed.) *PLOS ONE*, 13(8), e0202410. doi:[10.1371/journal.pone.0202410](https://doi.org/10.1371/journal.pone.0202410)
- Carroll, T. D., Langlands, A. J., Osborne, J. M., Newton, I. P., Appleton, P. L., & Näthke, I. (2017). Interkinetic nuclear migration and basal tethering facilitates post-mitotic daughter separation in intestinal organoids. *J Cell Sci*, 130(22), 3862–3877. doi:[10.1242/jcs.211656](https://doi.org/10.1242/jcs.211656)
- Cervi, J., & Spiteri, R. J. (2018). High-order operator splitting for the bidomain and monodomain models. *SIAM J. Sci. Comput*, 40(2), A769–A786. doi:[10.1137/17M1137061](https://doi.org/10.1137/17M1137061)
- Cooper, F. R., Baker, R. E., & Fletcher, A. G. (2017). Numerical analysis of the Immersed Boundary Method for cell-based simulation. *SIAM J. Sci. Comput*, 39(5), 943–967. doi:[10.1137/16M1092246](https://doi.org/10.1137/16M1092246)
- Cooper, J., & Osborne, J. (2013). Connecting models to data in multiscale multicellular tissue simulations. *Procedia Comput Sci*, 18, 712–721. doi:[10.1016/j.procs.2013.05.235](https://doi.org/10.1016/j.procs.2013.05.235)
- Cooper, J., Scharm, M., & Mirams, G. R. (2016). The cardiac electrophysiology web lab. *Biophys J*, 110(2), 292–300. doi:[10.1016/j.bpj.2015.12.012](https://doi.org/10.1016/j.bpj.2015.12.012)
- Cooper, J., Spiteri, R. J., & Mirams, G. R. (2015). Cellular cardiac electrophysiology modeling with Chaste and CellML. *Front Physiol*, 5, 511. doi:[10.3389/fphys.2014.00511](https://doi.org/10.3389/fphys.2014.00511)
- Corrado, C., Lassoued, J., Mahjoub, M., & Zemzemi, N. (2016). Stability analysis of the POD reduced order method for solving the bidomain model in cardiac electrophysiology. *Math Biosci*, 272, 81–91. doi:[10.1016/j.mbs.2015.12.005](https://doi.org/10.1016/j.mbs.2015.12.005)
- Corsi, C., Cortesi, M., Callisesi, G., De Bie, J., Napolitano, C., Santoro, A., Mortara, D., et al. (2017). Noninvasive quantification of blood potassium concentration from ECG in hemodialysis patients. *Sci Rep*, 7, 42492. doi:[10.1038/srep42492](https://doi.org/10.1038/srep42492)
- Daly, A. C., Clerx, M., Beattie, K. A., Cooper, J., Gavaghan, D. J., & Mirams, G. R. (2018). Reproducible model development in the cardiac electrophysiology Web Lab. *Progress in Biophysics and Molecular Biology*, 139, 3–14. doi:[10.1016/j.pbiomolbio.2018.05.011](https://doi.org/10.1016/j.pbiomolbio.2018.05.011)

- Daly, A. C., Cooper, J., Gavaghan, D. J., & Holmes, C. (2017). Comparing two sequential Monte Carlo samplers for exact and approximate Bayesian inference on biological models. *JR Soc Interface*, 14(134), 20170340. doi:[10.1098/rsif.2017.0340](https://doi.org/10.1098/rsif.2017.0340)
- Daly, A. C., Gavaghan, D. J., Holmes, C., & Cooper, J. (2015). Hodgkin-Huxley revisited: reparametrization and identifiability analysis of the classic action potential model with approximate Bayesian methods. *R Soc Open Sci*, 2(12), 150499. doi:[10.1098/rsos.150499](https://doi.org/10.1098/rsos.150499)
- Davies, M. R., Wang, K., Mirams, G. R., Caruso, A., Noble, D., Walz, A., Lavé, T., et al. (2016). Recent developments in using mechanistic cardiac modelling for drug safety evaluation. *Drug Discovery Today*, 21(6), 924–938. doi:[10.1016/j.drudis.2016.02.003](https://doi.org/10.1016/j.drudis.2016.02.003)
- Davit, Y., Osborne, J. M., Byrne, H. M., Gavaghan, D. J., & Pitt-Francis, J. M. (2013). Validity of the Cauchy-Born rule applied to discrete cellular-scale models of biological tissues. *Phys Rev E*, 87, 042724. doi:[10.1103/PhysRevE.87.042724](https://doi.org/10.1103/PhysRevE.87.042724)
- Dunn, S.-J., Näthke, I. S., & Osborne, J. M. (2013). Computational models reveal a passive mechanism for cell migration in the crypt. *PLOS ONE*, 8(11), e80516. doi:[10.1371/journal.pone.0080516](https://doi.org/10.1371/journal.pone.0080516)
- Dunn, S.-J., Osborne, J. M., Appleton, P. L., & Näthke, I. (2016). Combined changes in Wnt signaling response and contact inhibition induce altered proliferation in radiation-treated intestinal crypts. *Mol Biol Cell*, 27(11), 1863–1874. doi:[10.1091/mbc.E15-12-0854](https://doi.org/10.1091/mbc.E15-12-0854)
- Dutta, S., Mincholé, A., Quinn, T. A., & Rodriguez, B. (2017). Electrophysiological properties of computational human ventricular cell action potential models under acute ischemic conditions. *Progress in Biophysics and Molecular Biology*, 129, 40–52. doi:[10.1016/j.pbiomolbio.2017.02.007](https://doi.org/10.1016/j.pbiomolbio.2017.02.007)
- Dutta, S., Mincholé, A., Walmsley, J., & Rodriguez, B. (2013). Ionic mechanisms of variability in electrophysiological properties in ischemia: A population-based study. In *Computing in cardiology* (pp. 691–694). IEEE.
- Dutta, S., Mincholé, A., Zacur, E., Quinn, T. A., Taggart, P., & Rodriguez, B. (2016). Early afterdepolarizations promote transmural reentry in ischemic human ventricles with reduced repolarization reserve. *Progress in Biophysics and Molecular Biology*, 120(1-3), 236–248. doi:[10.1016/j.pbiomolbio.2016.01.008](https://doi.org/10.1016/j.pbiomolbio.2016.01.008)
- Elkins, R. C., Davies, M. R., Brough, S. J., Gavaghan, D. J., Cui, Y., Abi-Gerges, N., & Mirams, G. R. (2013). Variability in high-throughput ion-channel screening data and consequences for cardiac safety assessment. *J Pharmacol Toxicol Methods*, 68(1), 112–122. doi:[10.1016/j.vascn.2013.04.007](https://doi.org/10.1016/j.vascn.2013.04.007)
- Figueredo, G. P., Joshi, T. V., Osborne, J. M., Byrne, H. M., & Owen, M. R. (2013). On-lattice agent-based simulation of populations of cells within the open-source Chaste framework. *Interface focus*, 3(2), 20120081. doi:[10.1098/rsfs.2012.0081](https://doi.org/10.1098/rsfs.2012.0081)
- Finegan, T. M., Na, D., Skeeters, A. V., Cammarota, C., Nadasi, T. J., Dawney, N. S., Fletcher, A. G., et al. (2018). Tissue tension and not interphase cell shape determines cell division orientation in the *Drosophila* follicular epithelium. *EMBO Journal*, 38, e100072. doi:[10.15252/embj.2018100072](https://doi.org/10.15252/embj.2018100072)
- Fletcher, A. G., Osborne, J. M., Maini, P. K., & Gavaghan, D. J. (2013). Implementing vertex dynamics models of cell populations in biology within a consistent computational framework. *Prog Biophys Mol Biol*, 113, 299–326. doi:[10.1016/j.pbiomolbio.2013.09.003](https://doi.org/10.1016/j.pbiomolbio.2013.09.003)
- Franzetti, G., Crippa, F., Cutrì, E., Spatafora, G., Montin, E., Mainardi, L., Spadola, G., et al. (2015). Combined approach for the biomechanical characterization of skin lesions. In *37th annual international conference of the ieee engineering in medicine and biology society (embc)* (pp. 913–916). doi:[10.1109/EMBC.2015.7318511](https://doi.org/10.1109/EMBC.2015.7318511)

- Gao, J., Sathar, S., O'Grady, G., Archer, R., & Cheng, L. K. (2015). A stochastic algorithm for generating realistic virtual interstitial cell of Cajal networks. *IEEE Trans Biomed Eng*, 62(8), 2070–2078. doi:[10.1109/TBME.2015.2412533](https://doi.org/10.1109/TBME.2015.2412533)
- Gao, J., Sathar, S., O'Grady, G., Han, J., & Cheng, L. K. (2014). Developmental changes in postnatal murine intestinal interstitial cell of Cajal network structure and function. *Ann Biomed Eng*, 42(8), 1729–1739. doi:[10.1007/s10439-014-1021-9](https://doi.org/10.1007/s10439-014-1021-9)
- Ghaffarizadeh, A., Heiland, R., Friedman, S. H., Mumenthaler, S. M., & Macklin, P. (2018). PhysiCell: An open source physics-based cell simulator for 3-D multicellular systems. *PLoS Comput. Biol.*, 14(2), e1005991. doi:[10.1371/journal.pcbi.1005991](https://doi.org/10.1371/journal.pcbi.1005991)
- Godwin, S., Ward, D., Pedone, E., Homer, M., Fletcher, A. G., & Marucci, L. (2017). An extended model for culture-dependent heterogenous gene expression and proliferation dynamics in mouse embryonic stem cells. *NPJ Syst Biol Appl*, 3(1), 19. doi:[10.1038/s41540-017-0020-5](https://doi.org/10.1038/s41540-017-0020-5)
- Green, K. R., Bohn, T. A., & Spiteri, R. J. (2019). Direct function evaluation versus lookup tables: When to use which? *SIAM J. Sci. Comput.*, 41(3), C194–C218. doi:[10.1137/18M1201421](https://doi.org/10.1137/18M1201421)
- Grogan, J. A., Connor, A. J., Markelc, B., Muschel, R. J., Maini, P. K., Byrne, H. M., & Pitt-Francis, J. M. (2017). Microvessel chaste: an open library for spatial modeling of vascularized tissues. *Biophys J*, 112(9), 1767–1772. doi:[10.1016/j.bpj.2017.03.036](https://doi.org/10.1016/j.bpj.2017.03.036)
- Grogan, J. A., Connor, A. J., Pitt-Francis, J. M., Maini, P. K., & Byrne, H. M. (2018). The importance of geometry in the corneal micropocket angiogenesis assay. *PLoS Comput Biol*, 14(3), e1006049. doi:[10.1371/journal.pcbi.1006049](https://doi.org/10.1371/journal.pcbi.1006049)
- Grogan, J. A., Markelc, B., Connor, A. J., Muschel, R. J., Pitt-Francis, J. M., Maini, P. K., & Byrne, H. M. (2017). Predicting the influence of microvascular structure on tumor response to radiotherapy. *IEEE Trans Biomed Eng*, 64(3), 504–511. doi:[10.1109/TBME.2016.2606563](https://doi.org/10.1109/TBME.2016.2606563)
- Gurev, V., Pathmanathan, P., Fattebert, J.-L., Wen, H.-F., Magerlein, J., Gray, R. A., Richards, D. F., et al. (2015). A high-resolution computational model of the deforming human heart. *Biomechanics and modeling in mechanobiology*, 14(4), 829–849. doi:[10.1007/s10237-014-0639-8](https://doi.org/10.1007/s10237-014-0639-8)
- Harvey, D. G., Fletcher, A. G., Osborne, J. M., & Pitt-Francis, J. (2015). A parallel implementation of an off-lattice individual-based model of multicellular populations. *Comput Phys Commun*, 192, 130–137. doi:[10.1016/j.cpc.2015.03.005](https://doi.org/10.1016/j.cpc.2015.03.005)
- Hill, A. P., Perry, M. D., Abi-Gerges, N., Couderc, J.-P., Fermini, B., Hancox, J. C., Knollmann, B. C., et al. (2016). Computational cardiology and risk stratification for sudden cardiac death: one of the grand challenges for cardiology in the 21st century. *J Physiol*. doi:[10.1113/JP272015](https://doi.org/10.1113/JP272015)
- Hoehme, S., & Drasdo, D. (2010). A cell-based simulation software for multi-cellular systems. *Bioinformatics*, 26(20), 2641–2. doi:[10.1093/bioinformatics/btq437](https://doi.org/10.1093/bioinformatics/btq437)
- Hu, S., & Cucinotta, F. A. (2014). Epidermal homeostasis and radiation responses in a multiscale tissue modeling framework. *Integr Biol*, 6(1), 76–89. doi:[10.1039/C3IB40141C](https://doi.org/10.1039/C3IB40141C)
- Johnstone, R. H., Chang, E. T. Y., Bardenet, R., De Boer, T. P., Gavaghan, D. J., Pathmanathan, P., Clayton, R. H., et al. (2016). Uncertainty and variability in models of the cardiac action potential: Can we build trustworthy models? *J Mol Cell Cardiol*, 96, 49–62. doi:[10.1016/j.yjmcc.2015.11.018](https://doi.org/10.1016/j.yjmcc.2015.11.018)
- Kang, S., Kahan, S., McDermott, J., Flann, N., & Shmulevich, I. (2014). Biocellion: accelerating computer simulation of multicellular biological system models. *Bioinformatics*, 30(21), 3101–3108. doi:[10.1093/bioinformatics/btu498](https://doi.org/10.1093/bioinformatics/btu498)

- Koke, C., Kanesaki, T., Grosshans, J., Schwarz, U. S., & Dunlop, C. M. (2014). A computational model of nuclear self-organisation in syncytial embryos. *J Theor Biol*, 359, 92–100. doi:[10.1016/j.jtbi.2014.06.001](https://doi.org/10.1016/j.jtbi.2014.06.001)
- Kursawe, J., Baker, R. E., & Fletcher, A. G. (2017). Impact of implementation choices on quantitative predictions of cell-based computational models. *J Comput Phys*, 345, 752–767. doi:[10.1016/j.jcp.2017.05.048](https://doi.org/10.1016/j.jcp.2017.05.048)
- Kursawe, J., Baker, R. E., & Fletcher, A. G. (2018). Approximate Bayesian computation reveals the importance of repeated measurements for parameterising cell-based models of growing tissues. *J Theor Biol*, 443, 66–81. doi:[10.1016/j.jtbi.2018.01.020](https://doi.org/10.1016/j.jtbi.2018.01.020)
- Kursawe, J., Brodskiy, P. A., Zartman, J. J., Baker, R. E., & Fletcher, A. G. (2015). Capabilities and limitations of tissue size control through passive mechanical forces. *PLoS Comput Biol*, 11(12), e1004679. doi:[10.1371/journal.pcbi.1004679](https://doi.org/10.1371/journal.pcbi.1004679)
- Langham, J., Bense, H., & Barkley, D. (2018). Modeling shape selection of buckled dielectric elastomers. *J Appl Phys*, 123(6), 065102. doi:[10.1063/1.5012848](https://doi.org/10.1063/1.5012848)
- Langlands, A. J., Almet, A. A., Appleton, P. L., Newton, I. P., Osborne, J. M., & Näthke, I. S. (2016). Paneth cell-rich regions separated by a cluster of lgr5+ cells initiate crypt fission in the intestinal stem cell niche. *PLOS Biology*, 14(6), 1–31. doi:[10.1371/journal.pbio.1002491](https://doi.org/10.1371/journal.pbio.1002491)
- Lekadir, K., Lange, M., Zimmer, V. A., Hoogendoorn, C., & Frangi, A. F. (2016). Statistically-driven 3D fiber reconstruction and denoising from multi-slice cardiac DTI using a Markov random field model. *Med Image Anal*, 27, 105–116. doi:[10.1016/j.media.2015.03.006](https://doi.org/10.1016/j.media.2015.03.006)
- Lekadir, K., Pashaei, A., Hoogendoorn, C., Pereanez, M., Albà, X., & Frangi, A. F. (2014). Effect of statistically derived fiber models on the estimation of cardiac electrical activation. *IEEE Trans Biomed Eng*, 61(11), 2740–2748. doi:[10.1109/TBME.2014.2327025](https://doi.org/10.1109/TBME.2014.2327025)
- Lim, H., Cun, W., Wang, Y., Gray, R. A., & Glimm, J. (2018). The role of conductivity discontinuities in design of cardiac defibrillation. *Chaos*, 28(1), 013106. doi:[10.1063/1.5019367](https://doi.org/10.1063/1.5019367)
- Lyon, A., Bueno-Orovio, A., Zacur, E., Ariga, R., Grau, V., Neubauer, S., Watkins, H., et al. (2018). Electrocardiogram phenotypes in hypertrophic cardiomyopathy caused by distinct mechanisms: apico-basal repolarization gradients vs. Purkinje-myocardial coupling abnormalities. *EP Europace*, 20(suppl\_3), iii102–iii112. doi:[10.1093/europace/euy226](https://doi.org/10.1093/europace/euy226)
- Mahoney, V. M., Mezzano, V., Mirams, G. R., Maass, K., Li, Z., Cerrone, M., Vasquez, C., et al. (2016). Connexin43 contributes to electrotonic conduction across scar tissue in the intact heart. *Sci Rep*, 6, 26744. doi:[10.1038/srep26744](https://doi.org/10.1038/srep26744)
- Marin-Riera, M., Brun-Usan, M., Zimm, R., Välikangas, T., & Salazar-Ciudad, I. (2015). Computational modeling of development by epithelia, mesenchyme and their interactions: a unified model. *Bioinformatics*, 32(2). doi:[10.1093/bioinformatics/btv527](https://doi.org/10.1093/bioinformatics/btv527)
- Marsh, M. E., Ziaratgahi, S. T., & Spiteri, R. J. (2012). The secrets to the success of the rush–larsen method and its generalizations. *IEEE Transactions on Biomedical Engineering*, 59(9), 2506–2515. doi:[10.1109/TBME.2012.2205575](https://doi.org/10.1109/TBME.2012.2205575)
- McMillan, B., Gavaghan, D. J., & Mirams, G. R. (2017). Early afterdepolarisation tendency as a simulated pro-arrhythmic risk indicator. *Toxicology Research*, 6(6), 912–921. doi:[10.1039/C7TX00141J](https://doi.org/10.1039/C7TX00141J)
- Merks, R. M. H., Guravage, M., Inzé, D., & Beemster, G. T. S. (2011). VirtualLeaf: an open-source framework for cell-based modeling of plant tissue growth and development. *Plant Physiol*, 155(2), 656–66. doi:[10.1104/pp.110.167619](https://doi.org/10.1104/pp.110.167619)

- Mirams, G. R., Arthurs, C. J., Bernabeu, M. O., Bordas, R., Cooper, J., Corrias, A., Davit, Y., et al. (2013). Chaste: an open source C++ library for computational physiology and biology. *PLoS Comput Biol*, 9, e1002970. doi:[10.1371/journal.pcbi.1002970](https://doi.org/10.1371/journal.pcbi.1002970)
- Mirams, G. R., Davies, M. R., Brough, S. J., Bridgland-Taylor, M. H., Cui, Y., Gavaghan, D. J., & Abi-Gerges, N. (2014). Prediction of thorough QT study results using action potential simulations based on ion channel screens. *J Pharmacol Toxicol Methods*, 70(3), 246–254. doi:[10.1016/j.vascn.2014.07.002](https://doi.org/10.1016/j.vascn.2014.07.002)
- Mirams, G. R., Pathmanathan, P., Gray, R. A., Challenor, P., & Clayton, R. H. (2016). Uncertainty and variability in computational and mathematical models of cardiac physiology. *J Physiol*. doi:[10.1113/JP271671](https://doi.org/10.1113/JP271671)
- Moreno, C., Oliveras, A., Cruz, A. de la, Bartolucci, C., Muñoz, C., Salar, E., Gimeno, J. R., et al. (2015). A new KCNQ1 mutation at the S5 segment that impairs its association with KCNE1 is responsible for short QT syndrome. *Cardiovasc Res*, cvv196. doi:[10.1093/cvr/cvv196](https://doi.org/10.1093/cvr/cvv196)
- Muraro, D., Parker, A., Vaux, L., Filippi, S., Almet, A. A., Fletcher, A. G., Watson, A. J. M., et al. (2018). Chronic TNF $\alpha$ -driven injury delays cell migration to villi in the intestinal epithelium. *J R Soc Interface*, 15(145), 20180037. doi:[10.1098/rsif.2018.0037](https://doi.org/10.1098/rsif.2018.0037)
- Muszkiewicz, A., Liu, X., Bueno-Orovio, A., Lawson, B. A. J., Burrage, K., Casadei, B., & Rodriguez, B. (2018). From ionic to cellular variability in human atrial myocytes: an integrative computational and experimental study. *American Journal of Physiology-Heart and Circulatory Physiology*, 314(5), H895–H916. doi:[10.1152/ajpheart.00477.2017](https://doi.org/10.1152/ajpheart.00477.2017)
- Nelson, M. R., Sutton, K. J., Brook, B. S., Mallet, D. G., Simpson, D. P., & Rank, R. G. (2014). STI-GMaS: an open-source environment for simulation of sexually-transmitted infections. *BMC Syst Biol*, 8(1), 1. doi:[10.1186/1752-0509-8-66](https://doi.org/10.1186/1752-0509-8-66)
- Osborne, J. M. (2015). Multiscale model of colorectal cancer using the cellular Potts framework. *Cancer Inform*, 14(Suppl 4), 83. doi:[10.4137/CIN.S19332](https://doi.org/10.4137/CIN.S19332)
- Osborne, J. M., & Bernabeu, M. O. (2018). A fully discrete open source framework for the simulation of vascular remodelling. In *2018 40th annual international conference of the IEEE engineering in medicine and biology society (EMBC)* (pp. 4552–4555). doi:[10.1109/EMBC.2018.8513223](https://doi.org/10.1109/EMBC.2018.8513223)
- Osborne, J. M., Fletcher, A. G., Pitt-Francis, J. M., Maini, P. K., & Gavaghan, D. J. (2017). Comparing individual-based approaches to modelling the self-organization of multicellular tissues. *PLoS Comput Biol*, 13(2), 1–34. doi:[10.1371/journal.pcbi.1005387](https://doi.org/10.1371/journal.pcbi.1005387)
- Passini, E., Britton, O. J., Lu, H. R., Rohrbacher, J., Hermans, A. N., Gallacher, D. J., Greig, R. J., et al. (2017). Human in silico drug trials demonstrate higher accuracy than animal models in predicting clinical pro-arrhythmic cardiotoxicity. *Frontiers in physiology*, 8, 668. doi:[10.3389/fphys.2017.00668](https://doi.org/10.3389/fphys.2017.00668)
- Passini, E., Mincholé, A., Coppini, R., Cerbai, E., Rodriguez, B., Severi, S., & Bueno-Orovio, A. (2016). Mechanisms of pro-arrhythmic abnormalities in ventricular repolarisation and anti-arrhythmic therapies in human hypertrophic cardiomyopathy. *Journal of Molecular and Cellular Cardiology*, 96, 72–81. doi:[10.1016/j.yjmcc.2015.09.003](https://doi.org/10.1016/j.yjmcc.2015.09.003)
- Passini, E., Pellegrini, A., Caiani, E., & Severi, S. (2013). Computational analysis of head-down bed rest effects on cardiac action potential duration. In *Computing in cardiology* (pp. 357–360). IEEE.
- Passini, E., Rodriguez, B., Mincholé, A., Coppini, R., Cerbai, E., Severi, S., & Bueno-Orovio, A. (2014). Late sodium current inhibition counteracts pro-arrhythmic mechanisms in human hypertrophic cardiomyopathy. In *Computing in cardiology* (pp. 861–864). IEEE.



- Pathmanathan, P., & Gray, R. A. (2014). Verification of computational models of cardiac electro-physiology. *Int J Numer Meth Biomed Eng*, 30(5), 525–544. doi:[10.1002/cnm.2615](https://doi.org/10.1002/cnm.2615)
- Pathmanathan, P., & Gray, R. A. (2015). Filament Dynamics during Simulated Ventricular Fibrillation in a High-Resolution Rabbit Heart. *BioMed Research International*, 2015, 720575. doi:[10.1155/2015/720575](https://doi.org/10.1155/2015/720575)
- Pitt-Francis, J., Pathmanathan, P., Bernabeu, M. O., Bordas, R., Cooper, J., Fletcher, A. G., Mirams, G. R., et al. (2009). Chaste: A test-driven approach to software development for biological modelling. *Comput Phys Commun*, 180(12), 2452–2471. doi:[10.1016/j.cpc.2009.07.019](https://doi.org/10.1016/j.cpc.2009.07.019)
- Reilly, S. N., Liu, X., Carnicer, R., Recalde, A., Muszkiewicz, A., Jayaram, R., Carena, M. C., et al. (2016). Up-regulation of miR-31 in human atrial fibrillation begets the arrhythmia by depleting dystrophin and neuronal nitric oxide synthase. *Science Translational Medicine*, 8(340), 340ra74–340ra74. doi:[10.1126/scitranslmed.aac4296](https://doi.org/10.1126/scitranslmed.aac4296)
- Rubinacci, S., Graudenzi, A., Caravagna, G., Mauri, G., Osborne, J., Pitt-Francis, J., & Antoniotti, M. (2015). CoGNAC: a Chaste plugin for the multiscale simulation of gene regulatory networks driving the spatial dynamics of tissues and cancer. *Cancer Inform*, 14(Suppl 4), 53. doi:[10.4137/CIN.S19965](https://doi.org/10.4137/CIN.S19965)
- Sadrieh, A., Domanski, L., Pitt-Francis, J., Mann, S. A., Hodgkinson, E. C., Ng, C.-A., Perry, M. D., et al. (2014). Multiscale cardiac modelling reveals the origins of notched T waves in long QT syndrome type 2. *Nat Commun*, 5. doi:[10.1038/ncomms6069](https://doi.org/10.1038/ncomms6069)
- Samanta, K., Kar, P., Mirams, G. R., & Parekh, A. B. (2015). Ca<sup>2+</sup> channel re-localization to plasma-membrane microdomains strengthens activation of Ca<sup>2+</sup>-dependent nuclear gene expression. *Cell Rep*, 12(2), 203–216. doi:[10.1016/j.celrep.2015.06.018](https://doi.org/10.1016/j.celrep.2015.06.018)
- Sathar, S., Cheng, L. K., & Trew, M. L. (2015a). A comparison of solver performance for complex gastric electrophysiology models. In *37th annual international conference of the IEEE engineering in medicine and biology society (EMBC)* (pp. 1452–1455). IEEE. doi:[10.1109/EMBC.2015.7318643](https://doi.org/10.1109/EMBC.2015.7318643)
- Sathar, S., Trew, M. L., & Cheng, L. K. (2015b). Tissue specific simulations of interstitial cells of cajal networks using unstructured meshes. In *37th annual international conference of the IEEE engineering in medicine and biology society (EMBC)* (pp. 8062–8065). doi:[10.1109/EMBC.2015.7320264](https://doi.org/10.1109/EMBC.2015.7320264)
- Sathar, S., Trew, M. L., Du, P., O'Grady, G., & Cheng, L. K. (2014). A biophysically based finite-state machine model for analyzing gastric experimental entrainment and pacing recordings. *Ann Biomed Eng*, 42(4), 858–870. doi:[10.1007/s10439-013-0949-5](https://doi.org/10.1007/s10439-013-0949-5)
- Sathar, S., Trew, M. L., O'Grady, G., & Cheng, L. K. (2015c). A multiscale tridomain model for simulating bioelectric gastric pacing. *IEEE Trans Biomed Eng*, 62(11), 2685–2692. doi:[10.1109/TBME.2015.2444384](https://doi.org/10.1109/TBME.2015.2444384)
- Soares, M., Owers-Bradley, J., Foy, B., Kay, D., & Siddiqui, S. (2017). The evaluation of frequency dependence of resistance using a patient-specific 3D physical model and a computational model, 50, PA2476. doi:[10.1183/1393003.congress-2017.PA2476](https://doi.org/10.1183/1393003.congress-2017.PA2476)
- Spiteri, R. J., & Torabi Ziaratgahi, S. (2016). Operator splitting for the bidomain model revisited. *J. Comput. Appl. Math.*, 296, 550–563. doi:[10.1016/j.cam.2015.09.015](https://doi.org/10.1016/j.cam.2015.09.015)
- Starruß, J., Back, W. de, Brusch, L., & Deutsch, A. (2014). Morpheus: a user-friendly modeling environment for multiscale and multicellular systems biology. *Bioinformatics*, 30(9), 1331–1332. doi:[10.1093/bioinformatics/btt772](https://doi.org/10.1093/bioinformatics/btt772)
- Sutterlin, T., Kolb, C., Dickhaus, H., Jager, D., & Grabe, N. (2013). Bridging the scales: semantic integration of quantitative SBML in graphical multi-cellular models and simulations



- with EPISIM and COPASI. *Bioinformatics*, 29(2), 223–229. doi:[10.1093/bioinformatics/bts659](https://doi.org/10.1093/bioinformatics/bts659)
- Swat, M. H., Thomas, G. L., Belmonte, J. M., Shirinifard, A., Hmeljak, D., & Glazier, J. A. (2012). Multi-scale modeling of tissues using CompuCell3D. *Methods Cell Biol.*, 110, 325–366. doi:[10.1016/B978-0-12-388403-9.00013-8](https://doi.org/10.1016/B978-0-12-388403-9.00013-8)
- Tetley, R. J., Blanchard, G. B., Fletcher, A. G., Adams, R. J., & Sanson, B. (2016). Unipolar distributions of junctional Myosin II identify cell stripe boundaries that drive cell intercalation throughout *Drosophila* axis extension. *eLife*, 5, e12094. doi:[10.7554/eLife.12094](https://doi.org/10.7554/eLife.12094)
- Waites, W., Cavaliere, M., Cachat, É., Danos, V., & Davies, J. A. (2018). An information-theoretic measure for patterning in epithelial tissues. *IEEE Access*, 6, 40302–40312. doi:[10.1109/ACCESS.2018.2853624](https://doi.org/10.1109/ACCESS.2018.2853624)
- Wallman, M., Smith, N. P., & Rodríguez, B. (2014). Computational methods to reduce uncertainty in the estimation of cardiac conduction properties from electroanatomical recordings. *Med Image Anal*, 18, 228–240. doi:[10.1016/j.media.2013.10.006](https://doi.org/10.1016/j.media.2013.10.006)
- Walmsley, J., Mirams, G. R., Efimov, I. R., Burrage, K., & Rodriguez, B. (2013). Estimation of conductivity tensors from human ventricular optical mapping recordings. In *International conference on functional imaging and modeling of the heart* (pp. 224–231). Springer. doi:[10.1007/978-3-642-38899-6\\_27](https://doi.org/10.1007/978-3-642-38899-6_27)
- Walmsley, J., Mirams, G. R., Pitt-Francis, J., Rodriguez, B., & Burrage, K. (2015). Application of stochastic phenomenological modelling to cell-to-cell and beat-to-beat electrophysiological variability in cardiac tissue. *J Theor Biol*, 365, 325–336. doi:[10.1016/j.jtbi.2014.10.029](https://doi.org/10.1016/j.jtbi.2014.10.029)
- Walmsley, J., Rodriguez, J. F., Mirams, G. R., Burrage, K., Efimov, I. R., & Rodriguez, B. (2013). mRNA expression levels in failing human hearts predict cellular electrophysiological remodelling: A population- based simulation study. *PLOS ONE*, 8(2). doi:[10.1371/journal.pone.0056359](https://doi.org/10.1371/journal.pone.0056359)
- Williams, G., & Mirams, G. R. (2015). A web portal for in-silico action potential predictions. *J Pharmacol Toxicol Methods*, 75, 10–16. doi:[10.1016/j.vascn.2015.05.002](https://doi.org/10.1016/j.vascn.2015.05.002)
- Zacur, E., Mincholé, A., Villard, B., Carapella, V., Ariga, R., Rodriguez, B., & Grau, V. (2017). MRI-Based Heart and Torso Personalization for Computer Modeling and Simulation of Cardiac Electrophysiology. In (pp. 61–70). Springer, Cham. doi:[10.1007/978-3-319-67552-7\\_8](https://doi.org/10.1007/978-3-319-67552-7_8)
- Zemzemi, N., Bernabeu, M. O., Saiz, J., Cooper, J., Pathmanathan, P., Mirams, G. R., Pitt-Francis, J., et al. (2013). Computational assessment of drug-induced effects on the electrocardiogram: from ion channel to body surface potentials. *Br J Pharmacol*, 168(3), 718–733. doi:[10.1111/j.1476-5381.2012.02200.x](https://doi.org/10.1111/j.1476-5381.2012.02200.x)
- Zemzemi, N., & Rodriguez, B. (2015). Effects of L-type calcium channel and human ether-a-go-go related gene blockers on the electrical activity of the human heart: a simulation study. *Europace*, 17(2), 326–333. doi:[10.1093/europace/euu122](https://doi.org/10.1093/europace/euu122)
- Zhou, X., Bueno-Orovio, A., Orini, M., Hanson, B., Hayward, M., Taggart, P., Lambiase, P. D., et al. (2016). In Vivo and In Silico Investigation Into Mechanisms of Frequency Dependence of Repolarization Alternans in Human Ventricular Cardiomyocytes. *Circulation Research*, 118(2), 266–278. doi:[10.1161/CIRCRESAHA.115.307836](https://doi.org/10.1161/CIRCRESAHA.115.307836)
- Zhou, X., Bueno-Orovio, A., Schilling, R. J., Kirkby, C., Denning, C., Rajamohan, D., Burrage, K., et al. (2019). Investigating the complex arrhythmic phenotype caused by the gain-of-function mutation *kcnq1-g229d*. *Frontiers in Physiology*, 10, 259. doi:[10.3389/fphys.2019.00259](https://doi.org/10.3389/fphys.2019.00259)