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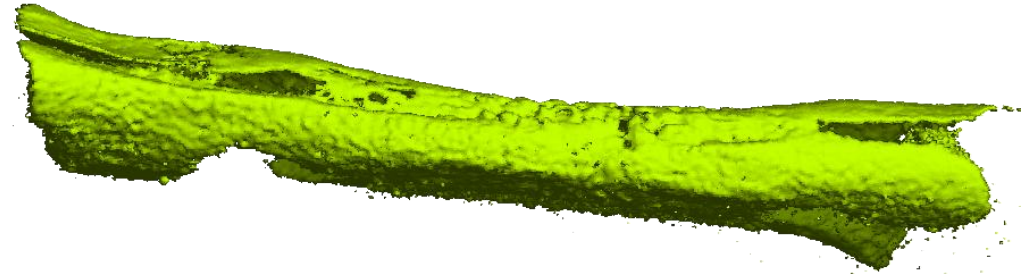
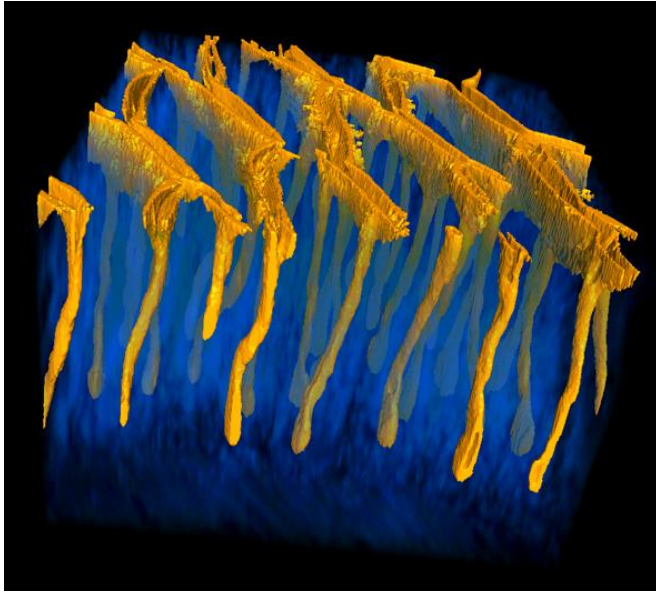


Motivation and framework

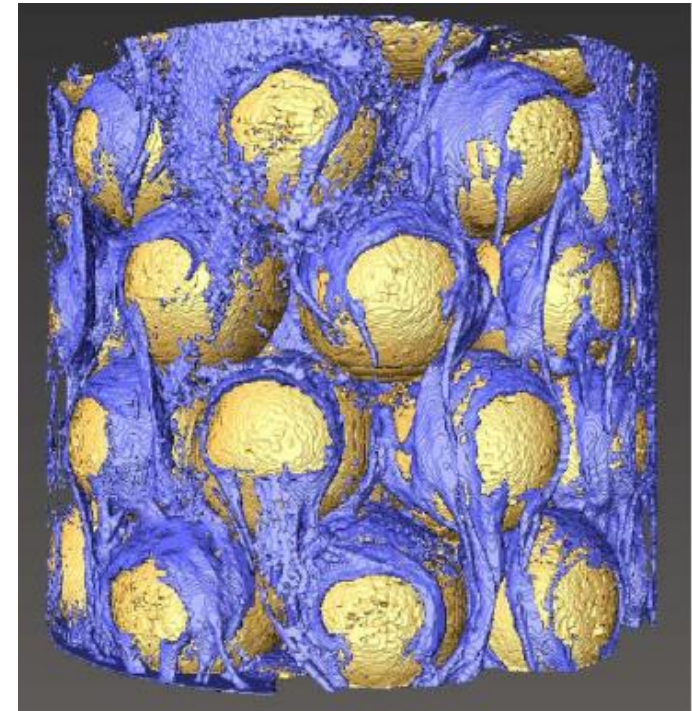


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Modelling/ simulation interests



- Tissues and collections of cells:
- How cells move, divide and die
- Interact with each other and the environment
- How cellular level properties influence tissue level behaviour



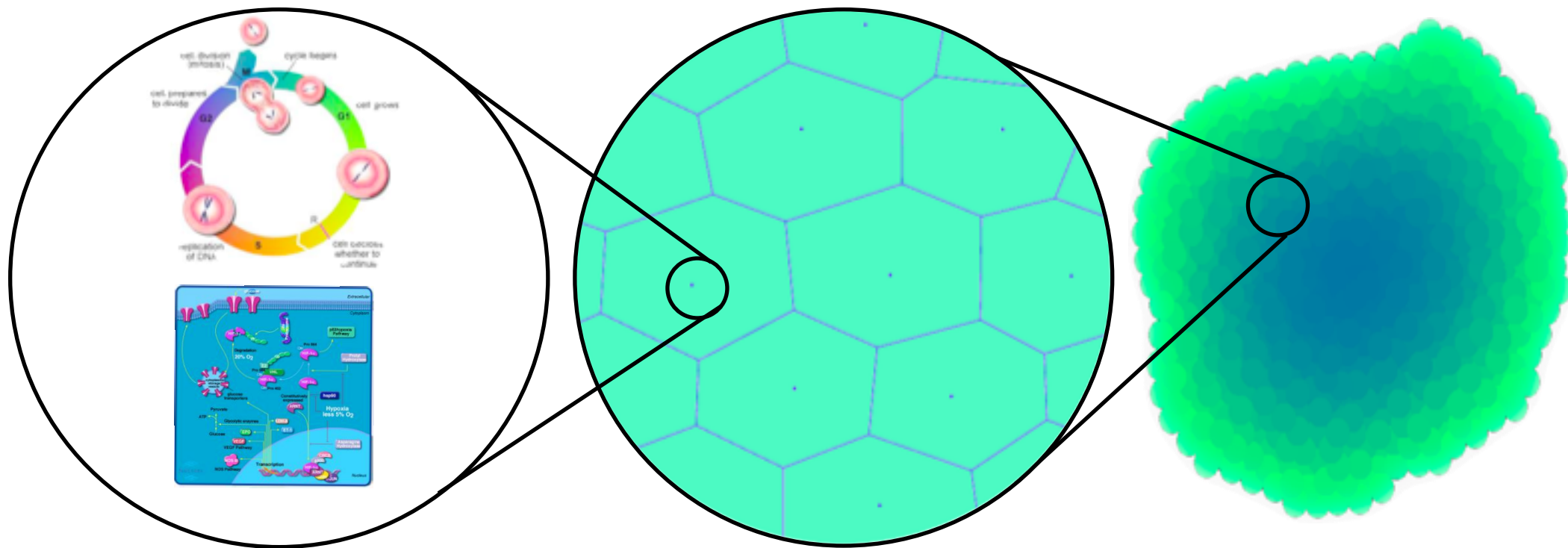


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Multiscale cell centric framework



“Fundamental unit of biology
would seem to be the cell”



Multiple possible models at each scale



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Modelling populations of cells

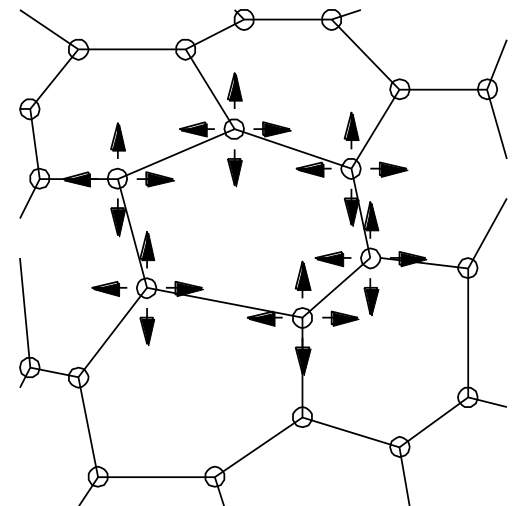
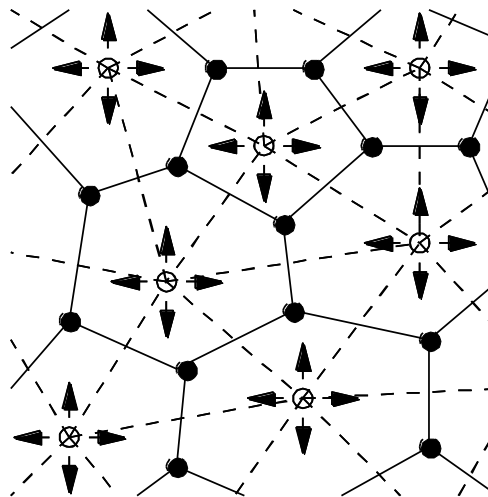
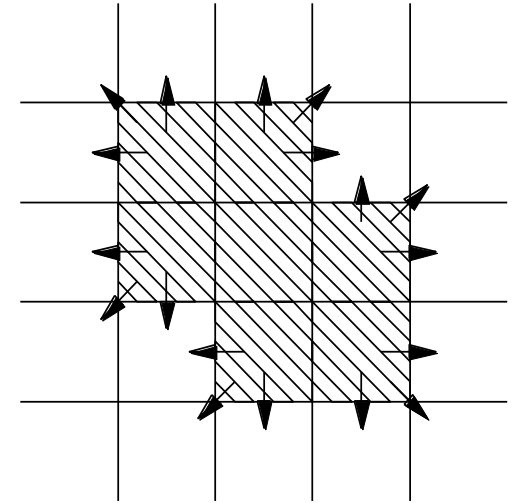
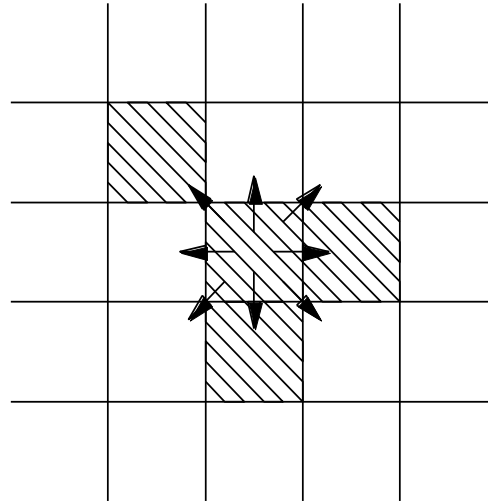


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Cell-level models



- Here we explicitly consider individual cells
- Track cell movement, size, shape
- Influences from 'above' and 'below'
- Cellular automata, cellular potts, cell-centre based models, vertex models



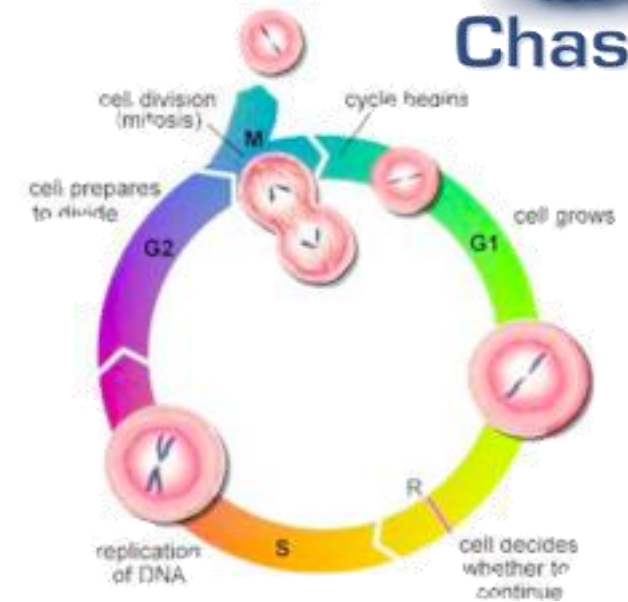


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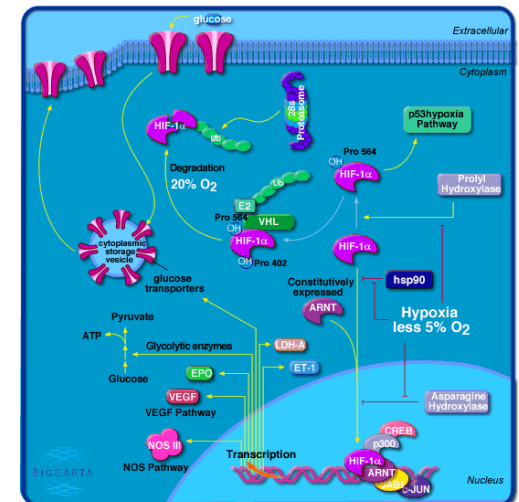
Modelling sub-cellular processes



- Simple agent based models
- Cell cycle
- Other metabolic pathways
 - Reaction networks
 - Typically a system of non-linear ODEs
- Coupled to extracellular concentrations
- Influence cell division, cell size/shape, cell-stromal and cell-cell adhesion, cell fate



<http://teachline.ls.huji.ac.il>



www.biocarta.com

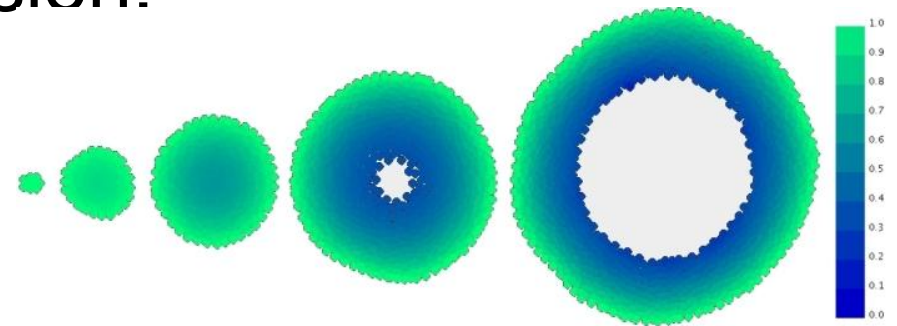
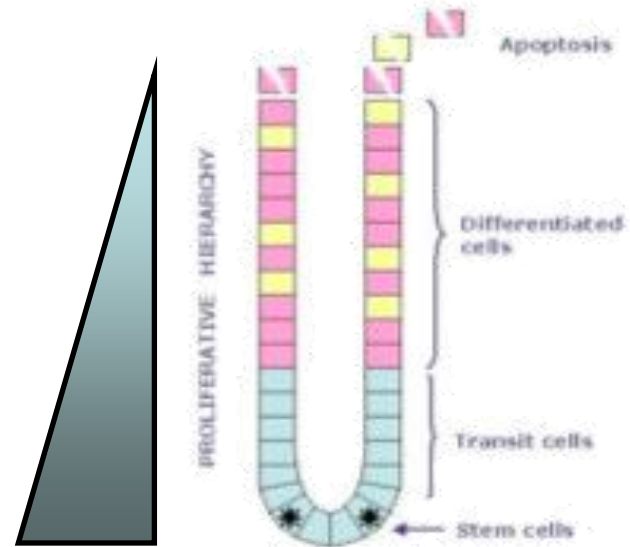


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Modelling tissue-level processes



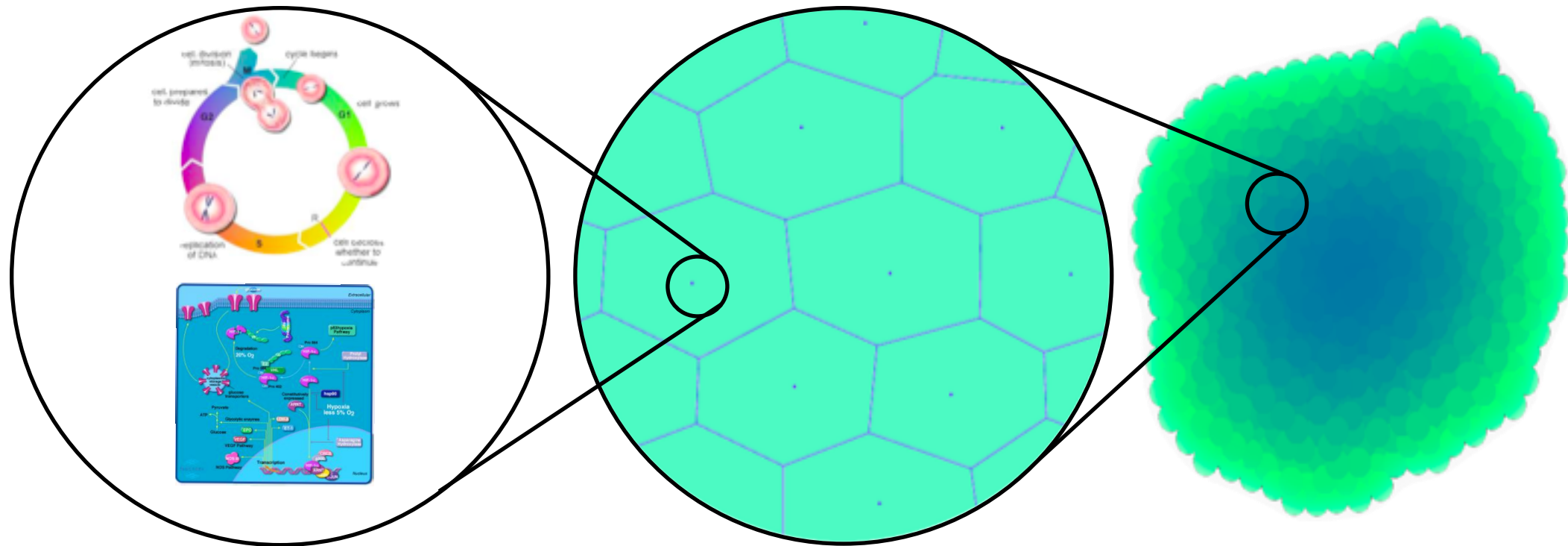
- Geometrical constraints
- Imposed gradients
- Vascular networks
- Juxtacrine signalling
- Field equations:
 - nutrient or inhibitor diffusion.
 - cells as sinks/sources,
 - on a growing domain
- Fluid flow
 - Mechano-transduction





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Putting it all together



Multiple possible models at each scale.
Also need to specify interactions between scales.



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Cell Based Chaste: running multicellular simulations



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What is Chaste?



- Library of numerical code, for solving problems in computational biology
- Started in 2005
- 2 main components: Cardiac and Cell Based
- Aim: to produce a robust, easily extensible, reliable, re-usable and well documented code base
 - XP - Test driven development
 - Tested continuously/nightly/weekly
 - Over 250,000 lines of source code and over 200,000 lines of tests (C++)
 - Open source - BSD Licence

“Cancer Heart
and Soft Tissue
Environment”]

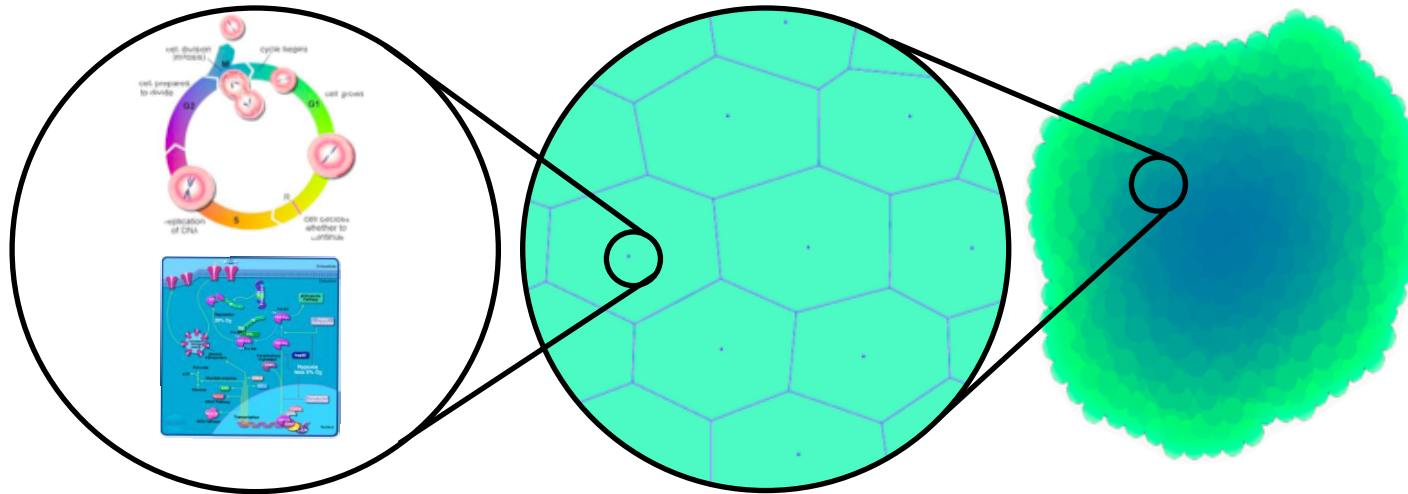


<http://www.cs.ox.ac.uk/chaste/>



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Cell-base functionality



Sub-cellular level:

- rule based;
- stochastic;
- ODE based cell cycles models/ other networks

Cell level:

- cell centre;
- OS,
- voronoi
- vertex based;
- cellular Potts;
- cellular automata

Tissue level:

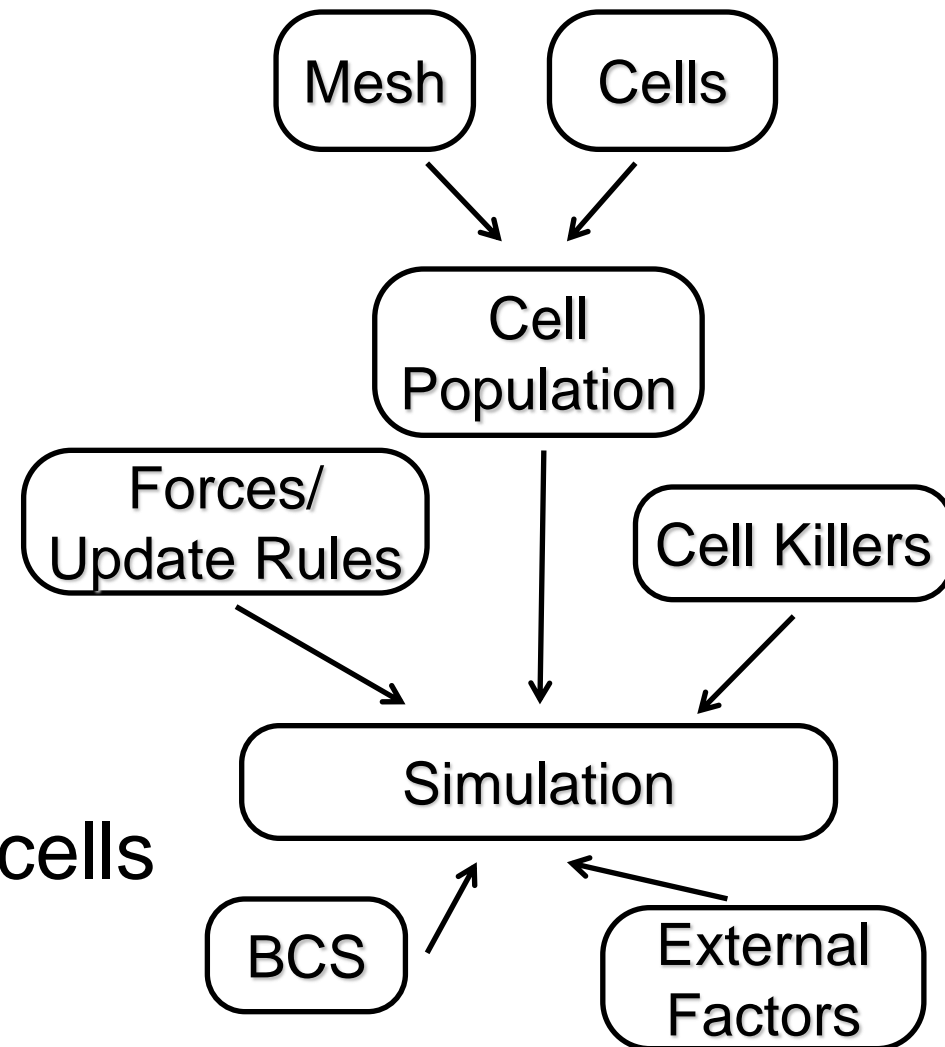
- external factors;
- juxtacrine signalling;
- PDEs: reaction diffusion, etc, on growing domain

Setting up a simulation



Going from Biological Model to simulation

- Type of cell level model
 - interaction forces/rules
 - boundary forces/rules
- Sub cellular model
 - proliferation,
 - growth, death .etc.
- Diffusible species
 - how these interact with cells
 - How they diffuse
 - boundary conditions





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Example Simulations



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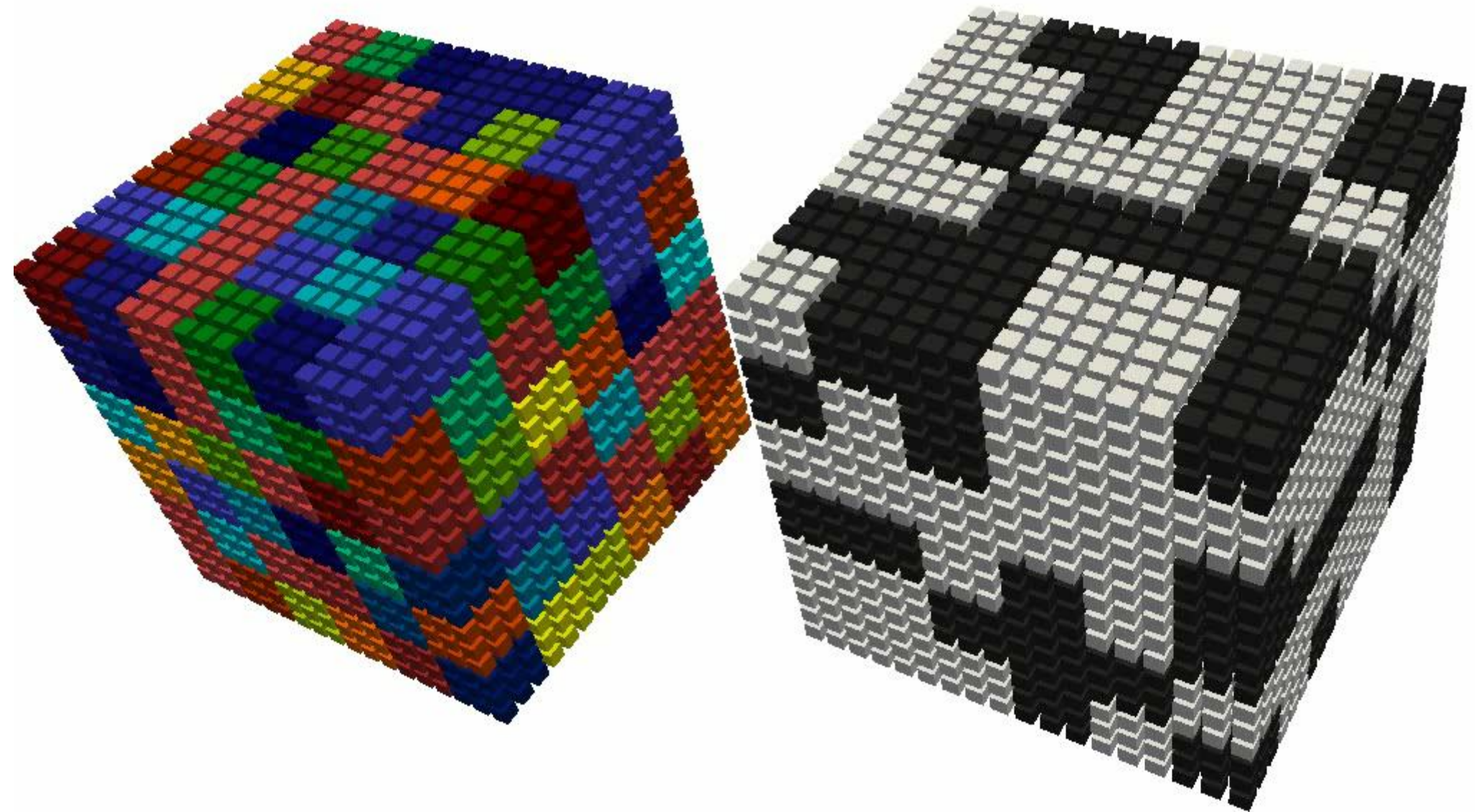
Tracking cell lineages





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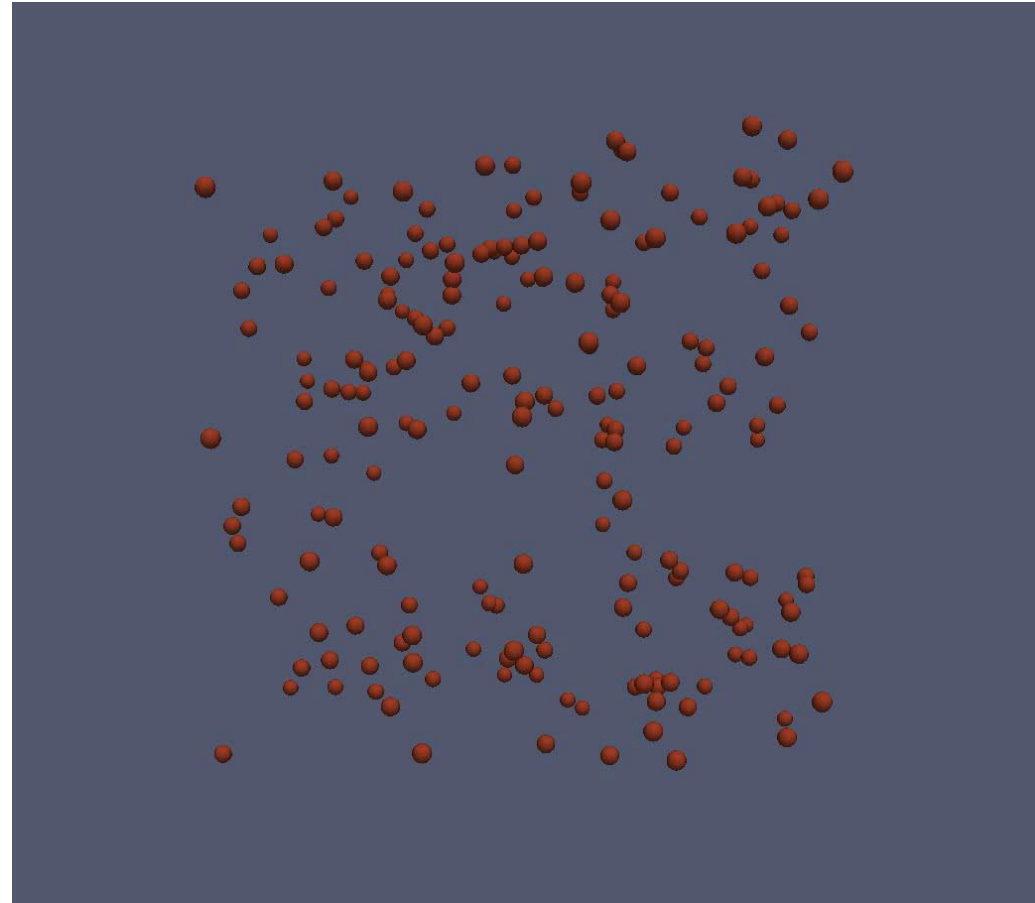
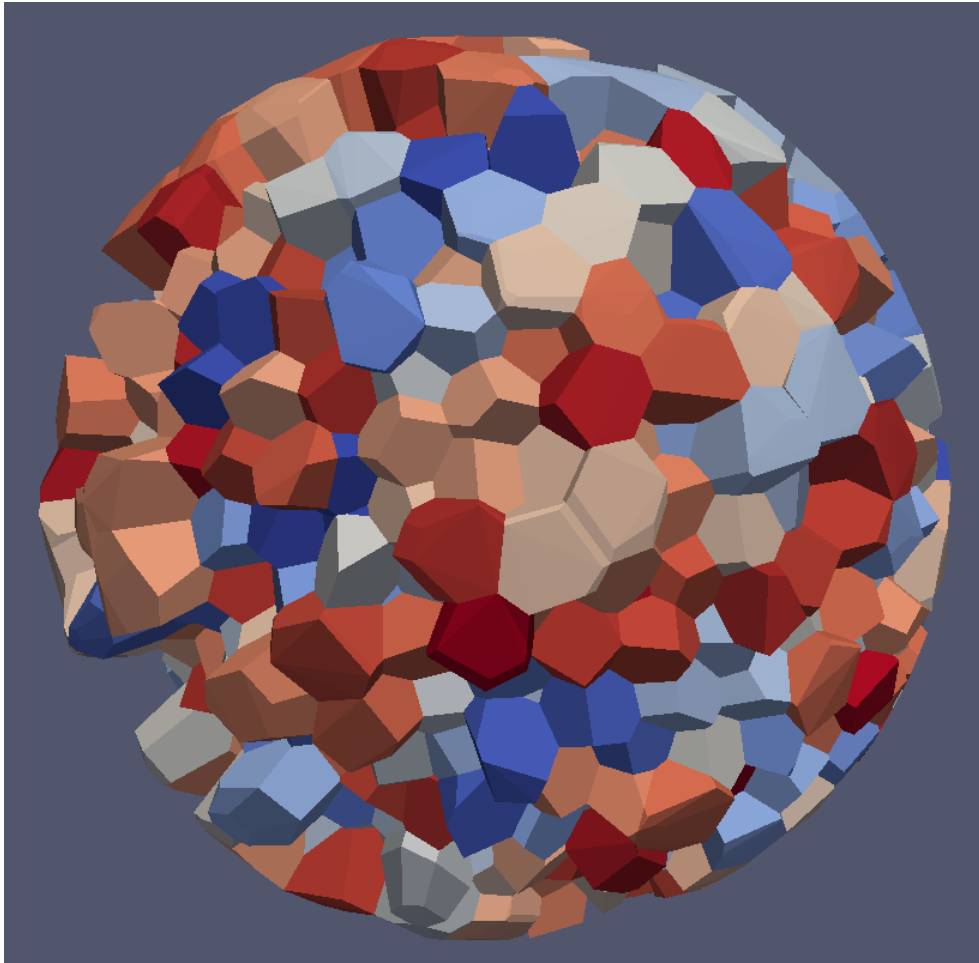
Cell sorting





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Other examples





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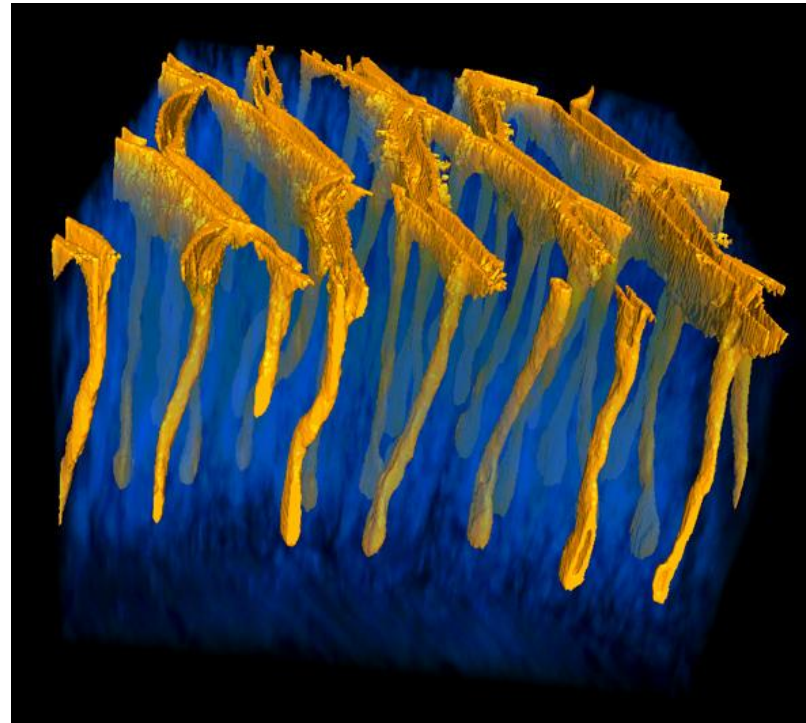
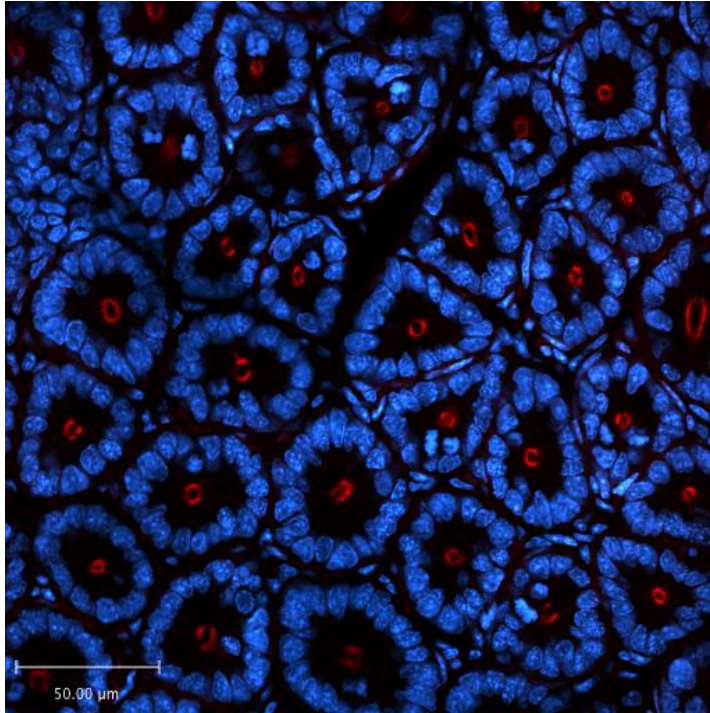


Simple model comparison



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Colorectal crypt



Paul Appleton, Dundee

- Crypts of Lieberkühn in the gut ~5 million in adults
- About 700 cells and renewal every 3-5 days
- 20-50 million cells per minute lost into gut, 10 per crypt
- Mutations in crypt lead to onset of CRC



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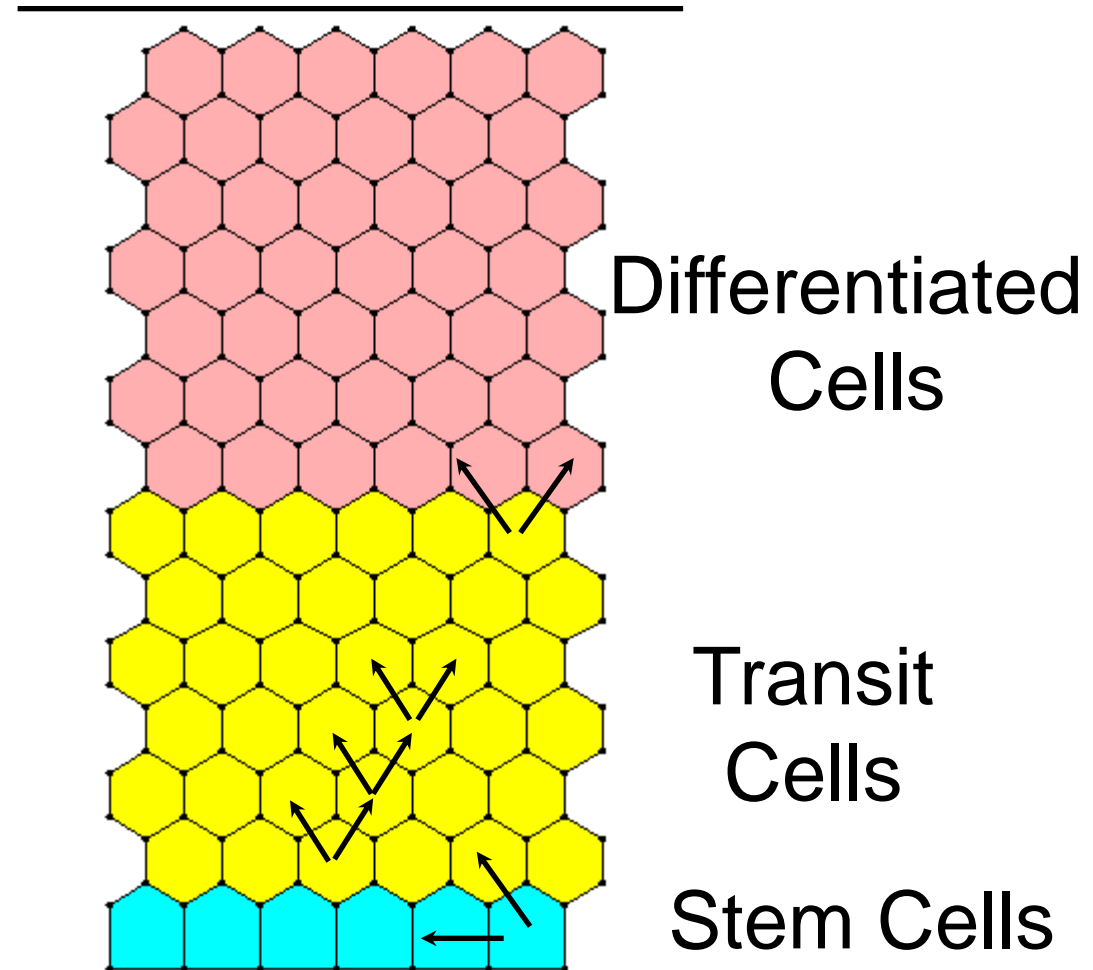
Model comparison



Simplified Crypt model

- Small periodic domain
- Solid base
- Simple stochastic generation based model for cell birth
- Cell sloughing
- Cell centre; vertex and cellular Potts model
- Parameterised by number leaving per hour

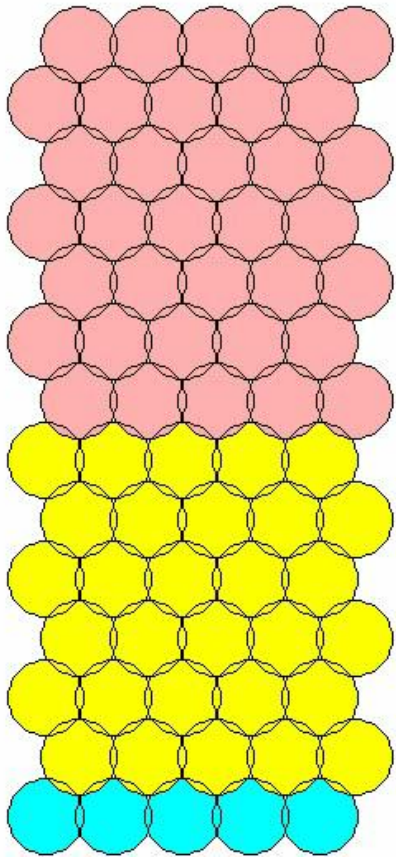
Cells Sloughed



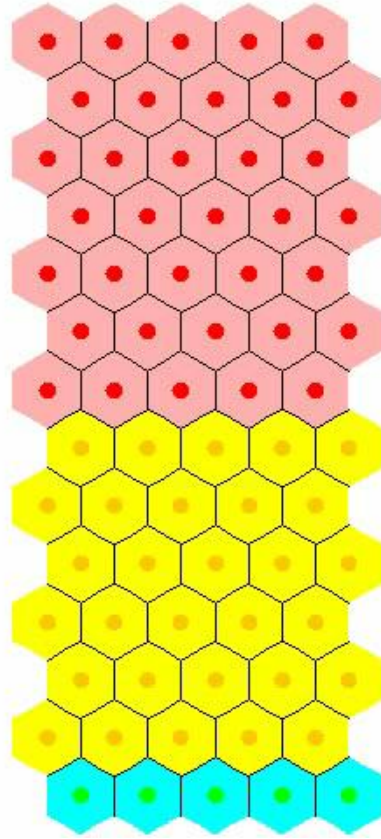


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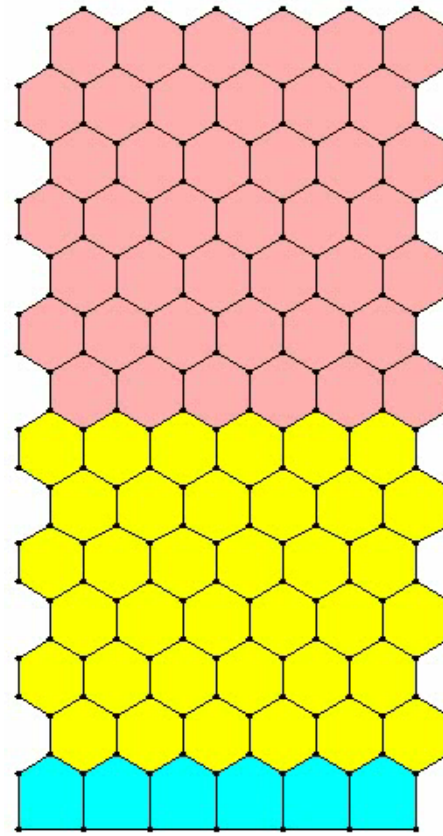
Comparison of cell level models



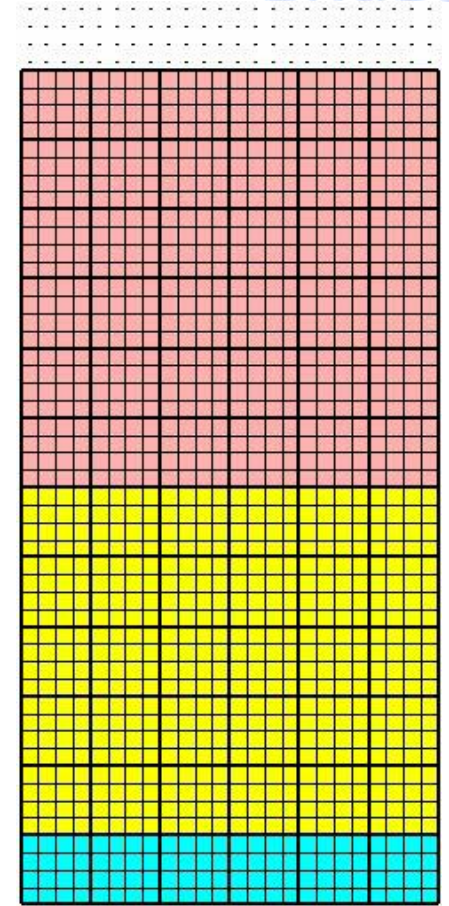
OS based



Tessellation
based



Vertex based



Cellular Potts

Compare: numbers of types of cells; distribution of cell types; time spent in crypt.



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Where we're going



Specifying simulations:

- Ways to specify models at each scale effectively
- Specify connections between scales
- Equate parameters between modelling paradigms: force vs probability

Running simulations:

- Tools/ languages to build simulations from descriptions of system
- Protocol specification – Functional Curation: Jon Cooper
- Writing simulations - Matlab interface

Acknowledgements

- David Gavaghan
- Philip Maini
- Helen Byrne
- Alex Fletcher
- Sara-Jane Dunn
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- Dan Harvey



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- Philip Murray

