

# Computer visualisation and modelling of plant morphogenesis: In-vivo segmentation and tracking of cells using confocal microscopy

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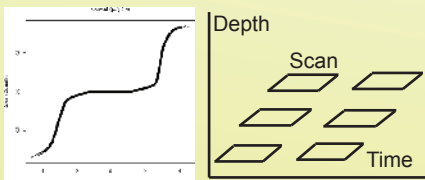
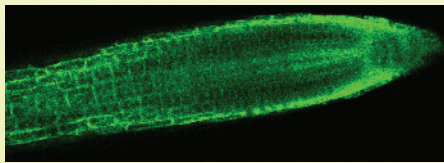
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## 3D, Hierarchical, Groupwise Probabilistic Registration

**Introduction:** Confocal Microscopy produces large amounts of data that is challenging to visualise and analyse. Some key limitations of the current PIV method (Poster #1) are:

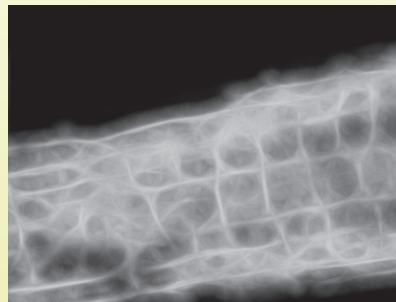
- Sparse, pairwise, 2D motion estimates only
- No estimates of uncertainty
- Motion is not rigid in large patches
- Incorrect noise model (Gaussian)
- Results presented in image co-ordinates
- Multiple motions are present



Top: A scan from a GFP-ER dataset. Bottom Left: A QQ-normal plot shows the distribution of the noise from two successive images to be clearly non-Gaussian. Bottom Right: 3D motion estimation is complicated by the lack of instantaneous volume acquisition because of significant inter-scan motion.

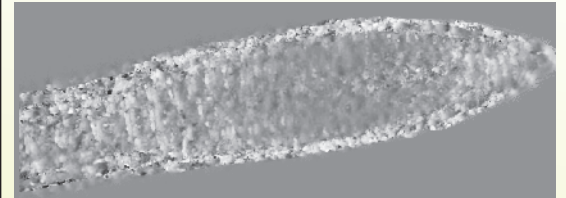
### Proposed Solution:

A 3D, hierarchical, probabilistic model of the joint appearance and motion. Representing the motion in the root co-ordinate system gives a more compact description and eases interpretation. A mixture model is used to describe the noise.

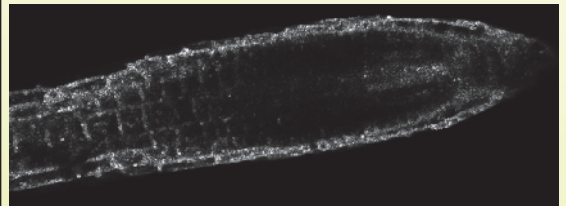


Above: The projection of the log posterior for the cell wall. Detecting separate structures based upon motion and appearance provides results that are more accurate and easier to interpret. For example, cell walls and cell nucleus can be identified and associated with different but coupled motion models and their relative motion can be investigated.

### Preliminary Results:



Dense estimate of expected horizontal motion based upon probabilistic grouping over locally consistent structures.

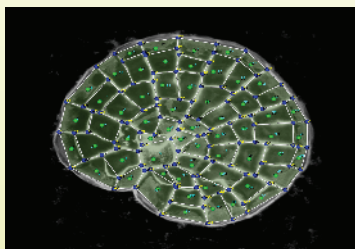


Estimate of the certainty in the estimate of motion. Clearly in many parts of the root local motion estimation is ill posed.

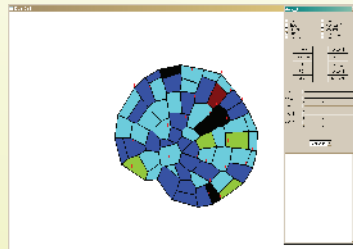
Currently, many ad-hoc prior constraints are applied to the model and its parameters. Future work will focus upon learning a hierarchical appearance-motion model in a Bayesian model selection framework to enable generic motion estimation. A key challenge is computational efficiency and a trans-dimensional sampling scheme is being developed.

## Mechanistic Modelling and Simulation of Morphogenesis

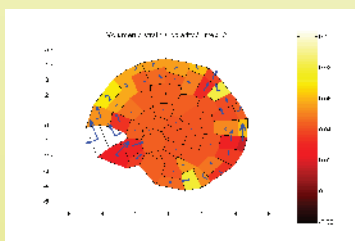
**Objectives:** numerical computer simulations are being investigated to help understanding the biological and physical processes occurring during plant morphogenesis. Various approaches are being developed in the project:



A simplified representation of the plant tissue is derived using a watershed segmentation algorithm. This hierarchical cellular data is coded as XML and used in other analysis tools.

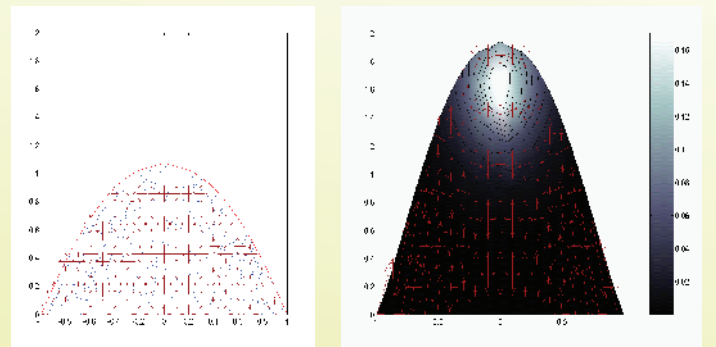


A cell simulation environment, called Evocell, is being developed to model cells and cell interactions (e.g. GRN, auxin flux) and study the complex emergent behaviour of cellular networks.



Left: In order to understand the root growth a viscoelastic mechanical cell model has been investigated. The finite element method is used to compute deformation of the structure, in relation to both turgor pressure and changes in cell wall material properties.

An alternative to explicitly modelling single cells is to considering plant tissues as a continuum associated with a microstructure. As the tissue expands and cells divide, various pattern are to observed.



Here, an initial uniform configuration of microstructure (left), shows a particular re-distribution after division (grey level on right) and expansion process.

Future work will investigate incorporating more physically realistic models and comparing the predictions from these models, such as turgor pressure, to experimental observations.