# Modeling and simulation of mechano-chemical pattern formation processes MORE 2017

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- Motivation
- Modeling
- Numerics & Results





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### Theories explaining pattern formation processes

- 1. A sequence of successive chemical patterns form. This would rule out spontaneous self-organized processes, as they are observed in dissociated and re-aggregated cells.
- 2. Chemical patterns can form spontaneously by an interplay of mutual interaction of diffusing morphogens by the Turing mechanism. While the Turing mechanism creates many relevant patterns, experiments usually do not find morphogens with requires diffusion and reaction rates.

Turing: The chemical basis of morphogenesis, Phil. Trans. R. Soc. London, 1953 Meinhardt & Gierer: Pattern formation by local self-activation and lateral inhibition, Bioessays, 2000

• Both theories say, that mechanical patterns are *blind end results* of chemical pre-patterns. Recent studies however show, that mechanical patterns play an active role.

**Brouzes & Farge:** Interplay of mechanical deformation and patterned gene expression in developing embryos, Curr. Opin. Genet. Dev., 2004

 $-\operatorname{div} (\mathbf{F} \mathbf{\Sigma}) = 0$  in V,

assuming a St. Venant Kirchhoff material

$$
\Sigma = 2\mu \mathbf{E} + \lambda \operatorname{tr}(\mathbf{E})I
$$
,  $\mathbf{E} = \frac{1}{2}(\mathbf{F}^T \mathbf{F} - I)$ ,  $\mathbf{F} = I + \nabla \mathbf{u}$ 

With

 $\mathbf{u} = 0$  on  $\Gamma_D$ ,  $\mathbf{F\Sigma n} = g$  on  $\Gamma_N$ 

We assume, that growth is very slow compared to elastic dynamics such that the mechanical system is always in a stationary limit

#### (Bio-)Chemistry

System of reaction diffusion equations (in Lagrangian coordinates)

$$
J\partial_t c_i - \text{div} \left( J \mathbf{F}^{-1} D \mathbf{F}^{-T} \nabla c_i \right) - J R_i(c_1, \dots, c_n) = 0 \text{ in } V \text{ for } i = 1, \dots, n
$$

with initial and boundary conditions

$$
c_i = c_i^0
$$
 for  $t = 0$  and  $J\mathbf{F}^{-1}D\mathbf{F}^{-T}\nabla c_i \mathbf{n} = 0$  on  $\Gamma$ 

• Intermediate configuration

 $\hat{V} \xrightarrow{\hat{T}_a} \hat{V}_a \xrightarrow{\hat{T}_e} V$ 

• Active deformation  $\hat{T}_a$  and elastic deformation  $\hat{T}_e$ 



Elasticity takes place between  $V_a$  and V

$$
\boldsymbol{\Sigma} = \boldsymbol{\Sigma}(\mathbf{F}_e) = \boldsymbol{\Sigma}(\mathbf{F}\mathbf{F}_a^{-1})
$$

For the St. Venant Kirchhoff material

$$
\mathbf{\Sigma} = J_a \mathbf{F}_a^{-1} \mathbf{\Sigma}_e \mathbf{F}_a^{-T}, \quad \mathbf{\Sigma}_e = 2\mu \mathbf{E}_e + \lambda \operatorname{tr}(\mathbf{E}_e) I, \quad \mathbf{E}_a = \frac{1}{2} (\mathbf{F}_e^T \mathbf{F}_e - I) = \frac{1}{2} (\mathbf{F}_a^{-T} \mathbf{F}^T \mathbf{F} \mathbf{F}_a^{-1} - I).
$$

Rodriguez, Hoger & McCulloch: Stress-depedent finite growth in soft elastic tissues, J. BioMech. 1994 Ambrosi & Mollica: On the mechanics of a growing tumor, IJ Eng. Science 2002



• Active deformation (here apical constriction) depends on one chemical concentration  $c$ 

$$
\hat{\mathbf{F}}_a(x, y, z, c)\Big|_M = \begin{pmatrix} 1 + \kappa c\hat{z} & 0 & \kappa c\hat{x} \\ 0 & 1 + \kappa c\hat{z} & \kappa c\hat{y} \\ 0 & 0 & 1 \end{pmatrix}, \quad \begin{pmatrix} \hat{x} \\ \hat{y} \\ \hat{z} \end{pmatrix} = \begin{pmatrix} x - x_M \\ y - y_M \\ z - z_M \end{pmatrix}
$$
rel. to midpoint of cell M

• (Simplified, as we first have to rotate every biological cell to a reference orientation)



- High morphogen level causes apical constriction  $\mathbf{F}_a = \mathbf{F}_a(c)$
- Apical constriction causes elastic feedback with local compression  $\Sigma_e = \Sigma(\mathbf{FF}_a^{-1})$
- Local compression triggers morphogen production (Michaelis-Menten kinetics)

$$
R(c, \mathbf{F}) = \kappa_1 \frac{\max\{\det \mathbf{F}, 0\}}{\kappa_3 + \max\{\det \mathbf{F}, 0\}} - \kappa_2 c, \quad \kappa_1, \kappa_2, \kappa_3 > 0
$$

- We consider a layer of biological cells. The (adaptive) finite element discretization is much finer
- Overall very large active and elastic deformation appears



reference configuration

### **Numerical Tools** 5 - 1

#### Monolithic Model

$$
U = {\mathbf{u}, c} \in \mathcal{X} : A(U)(\Phi) = 0 \quad \forall \Phi \in \mathcal{X}
$$

The variational formulation is given by

$$
A(U)(\Phi) = (\mathbf{F}J_a \mathbf{F}_a^{-1} \Sigma_e \mathbf{F}_a^{-T}, \nabla \phi)
$$
  
+  $(J\partial_t c, \psi) + (J\mathbf{F}^{-1}D\mathbf{F}^{-T} \nabla c, \nabla \psi) - (JR(c, \mathbf{F}), \psi)$ 

with

• Growth model

$$
\hat{\mathbf{F}}_a \Big|_M = \begin{pmatrix} 1 + \kappa c\hat{z} & 0 & \kappa c\hat{x} \\ 0 & 1 + \kappa c\hat{z} & \kappa c\hat{y} \\ 0 & 0 & 1 \end{pmatrix}
$$

• Reaction feedback

$$
R(c, \mathbf{F}) = \kappa_1 \frac{\max\{\det \mathbf{F}, 0\}}{\kappa_3 + \max\{\det \mathbf{F}, 0\}} - \kappa_2 c
$$

• Stress model with growth-splitting

$$
\Sigma_e = 2\mu \mathbf{E}_e + \lambda \operatorname{tr}(\mathbf{E}_e), \quad \mathbf{E}_e = \frac{1}{2} (\mathbf{F}_a^{-T} \mathbf{F}^T \mathbf{F} \mathbf{F}_a^{-1} - I),
$$

$$
\mathbf{F} = I + \nabla \mathbf{u}
$$

• Quadratic finite elements (3 deformation variables  $+1$  concentration)

$$
X_h \subset \mathcal{X}, \quad X_h := \{ \phi \in C(\bar{\Omega})^{3+1}, \phi \big|_K \in Q^2(K)^4 \,\forall K \in \Omega_h \}
$$

- Adaptive Meshes to efficiently resolve biological cells (there are jumps in the active growth model  $\mathbf{F}_a$  at the biological cell boundaries)
- Monolithic coupled approach

Find  $U_h = (\mathbf{u}_h, c_h) \in X_h : A(U_h)(\Phi_h) = 0 \quad \forall \Phi_h \in X_h$ 

• Time stepping with the implicit Euler method. We found, that temporal accuracy is of lesser important (compared to spatial accuracy and stability problems)

#### Nonlinear Solver

Linearization with Newton's method

$$
A'(U_h^{(i)})(W_h^{(i)}, \Phi_h) = F(\Phi_h) - A(U_h^{(i)})(\Phi_h) \quad \forall \Phi_h \in X_h, \quad U_h^{(i+1)} = U_h^{(i)} + \omega W_h^{(i)}
$$

Analytic computation of the monolithic Jacobian





## Numerical Tools **Solution** 5 - 3

• Large and ill-structure linear system of equations (couplings to elasticity **A** to growth  $\mathbf{A}_G$  chemistry transport M, diffusion  $A_d$ , reaction  $A_R$  and mapping to Lagrangian coordinates  $A_E$ 

$$
\begin{pmatrix} \mathbf{A} & \mathbf{A}_G \\ \mathbf{A}_R + \mathbf{A}_E & k^{-1}M + \mathbf{A}_d \end{pmatrix} \begin{pmatrix} \delta \mathbf{u} \\ \delta c \end{pmatrix} = \begin{pmatrix} \mathbf{b}_\mathbf{u} \\ \mathbf{b}_c \end{pmatrix}
$$

• Multigrid solver for the linear systems

 $Ax = b$ 

• Parallelization of the multigrid solver by a *domain decomposition smoother* 

- Highly complex simulations (nonlinearity and ill-structured linear systems)
- Fine meshes are required
- About 20 seconds per time-step
- Total simulation time in 3d about 10 days





## Feedback Mechanism:

- Apical constriction
- Morphogen production by compression

## morphogen Results:

- The process is stable in the following sense: different initial morphogen concentrations give the same stationary mechanical pattern
- Similar patterns are observed in Hydra development





## Feedback Mechanism:

- Basal constriction
- Morphogen production by compression

## Results:

- Again, stable process
- Similar results are found in Nematostella and Xenopus gastrulation.



### • Numerical Simulation

We identify possible feedback-loops and mechanisms

- What is the trigger for morphogen production? Cell-size or shape **F**, elastic stress  $\Sigma_e$ , strain **E**<sub>e</sub> or **E**?
- How does the biological cell react? Compression, apical or basal constriction, shear, ...

## • Biological verification

Currently, experimentalists run experiments that are based on our simulations:

- Can we trigger morphogen-production by a mechanical stimulus?
- Can we produce a mechanical reaction by a injecting morphogens?

## • Mathematical Analysis

Is the coupled mechano-chemical system of partial differential equations well-posed?

- Stability estimates for the long-term simulations. Control of the chemical concentration and elastic stresses
- Design of robust and efficient solvers

#### Summary

- Novel numerical model that is able to show spontaneous pattern formation processes based on an interplay of mechanics and bio-chemistry
- Robust high-performance framework for mechano-chemical coupled simulations

All computations done with Gascoigne 3D

Upcoming thesis:

Felix Brinkmann: Mathematical models and numerical simulation of mechanochemical pattern formation in biological tissues, Dissertation, University of Heidelberg, 2017





Y. Yang & T.R. & W. Jäger & M. Neuss-Radu: An ALE approach to mechano-chemical processes in fluid-structure interactions, Int. J. Numer. Meth. Fluids, 2017 M. Mercker & F. Brinkmann & A. Marcinbia-Czochra & T.R.: Beyond Turing: Mechano-

chemical pattern formation in biological tissues, Biology Direct, 2016

**T.R.:** Fluid-structure Interactions.. Lecture Notes in Computational Science and Engineering 118, November 2017