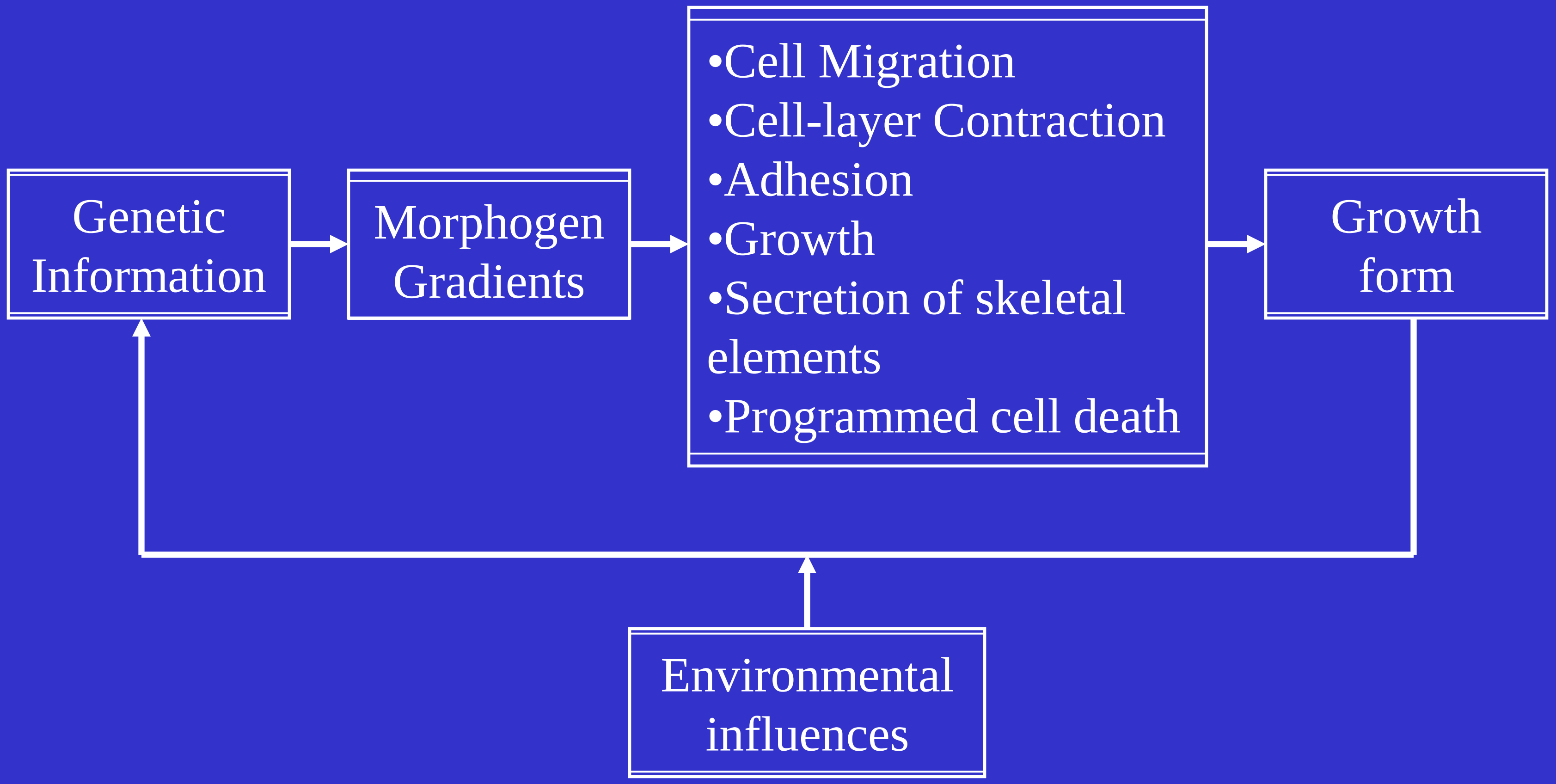
Models of embryogenesis and biomineralization

Jaap A. Kaandorp
Computational Science Lab
Faculty of Science
University of Amsterdam
Science Park 904, 1098 XH Amsterdam
The Netherlands
E-mail: J.A.Kaandorp@uva.nl
http://www.science.uva.nl/~jaapk

Essay biomineralization

- Biomineralization in scleractinian corals or molluscs or fishes etc (you can decide which group you select)
- Summarize what is know about this biomineralization process (physiology, gene regulation, etc.)
- Discuss the of role scientific visualization, quantitative modelling and morphometrics in studying biomineralization
- maximum of 4 pages. The essay must include a section for bibliographic references listing the sources cited in the main text. The deadline for submission would be May 9th, 2025. (email: j.a.kaandorp@uva.nl)
-

From DNA to Form



Genetic Information

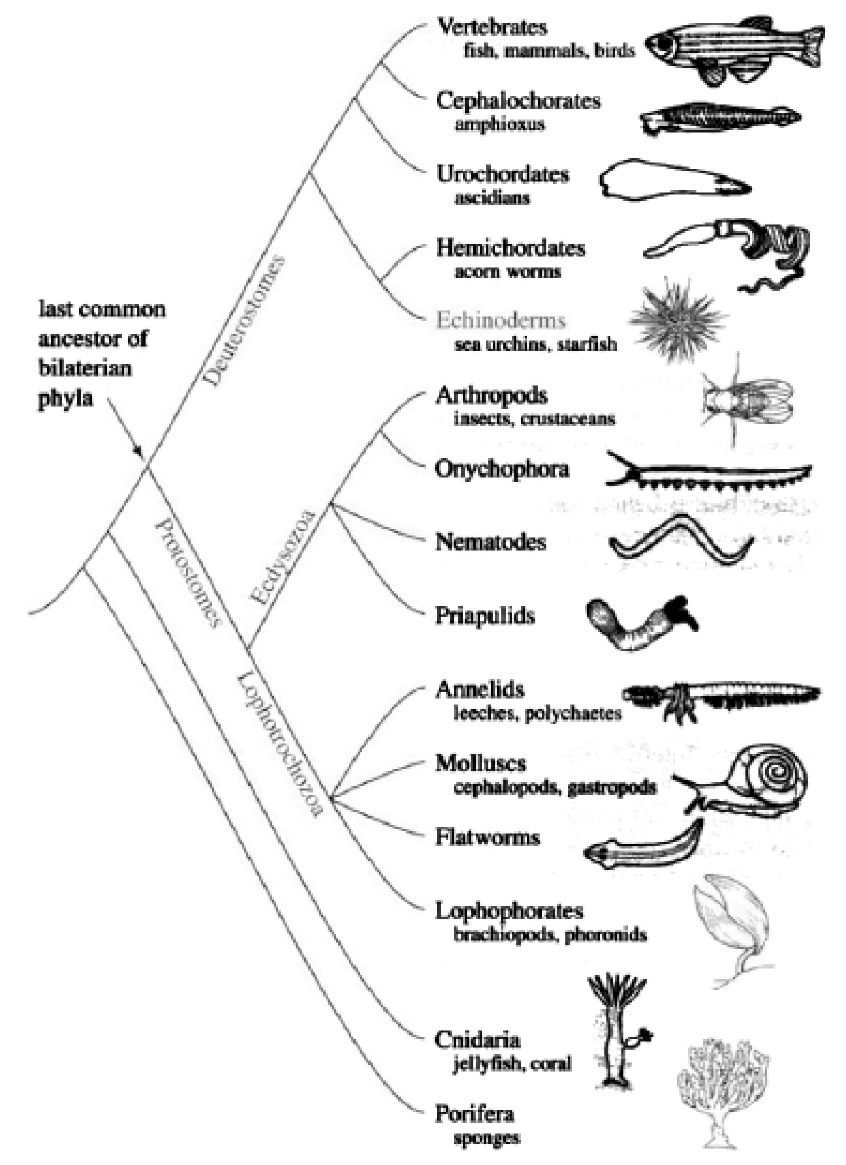
Morphogen Gradients

- Cell Migration
- Cell-layer Contraction
- Adhesion
- Growth
- Secretion of skeletal elements
- Programmed cell death

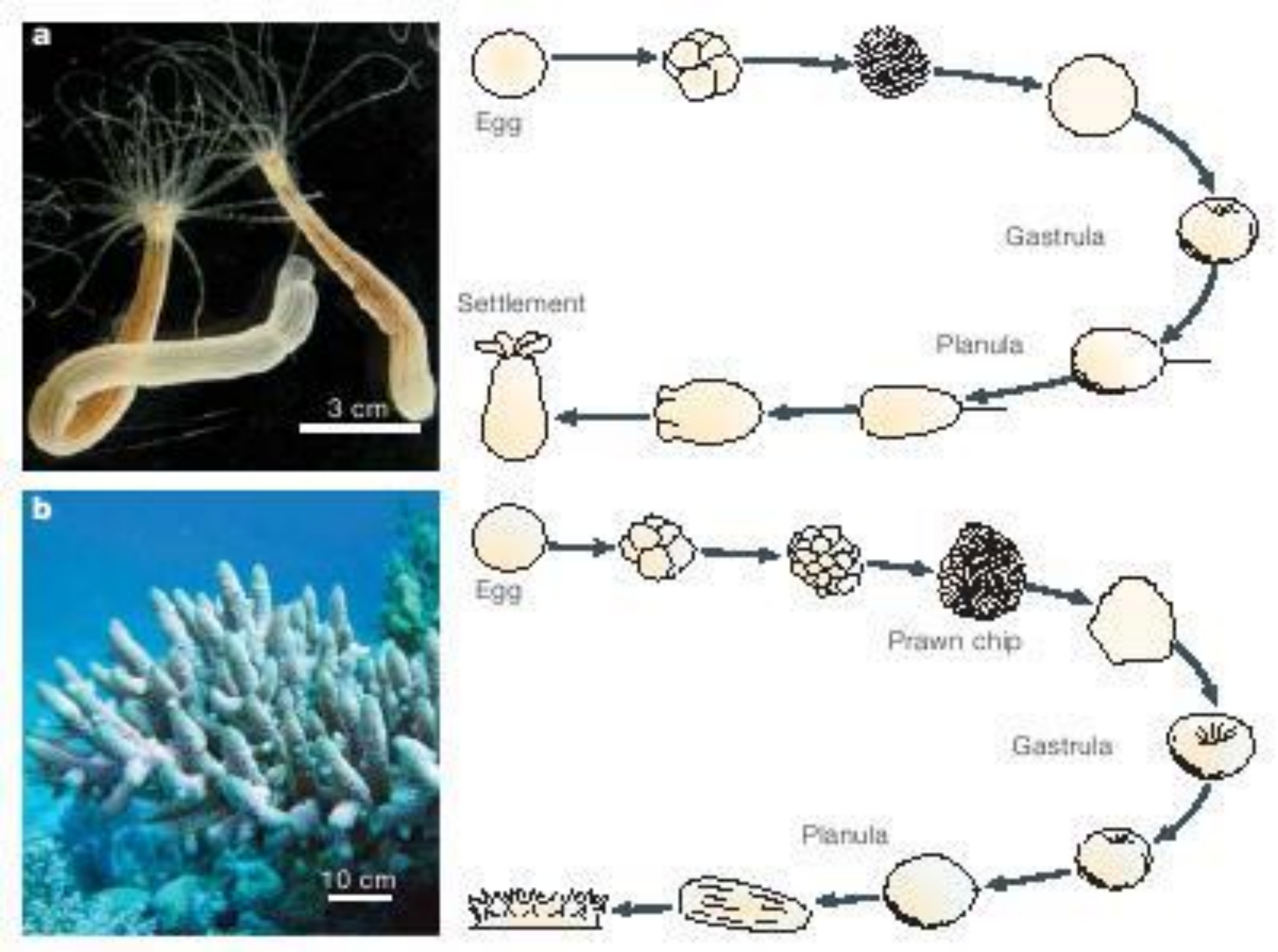
Growth form

Environmental influences

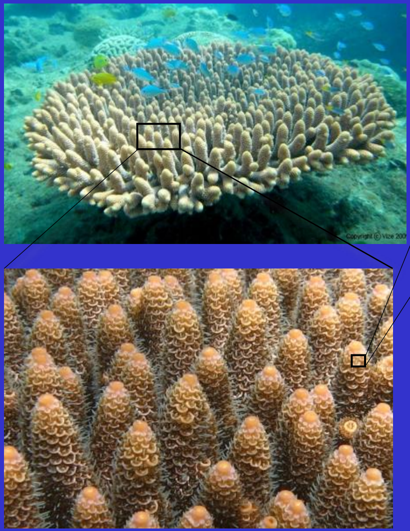
The animal kingdom



Nematostella vectensis (top) / *Acropora millepora* (bottom) (Ball et al., Nature Reviews Genetics: 567, 2004)

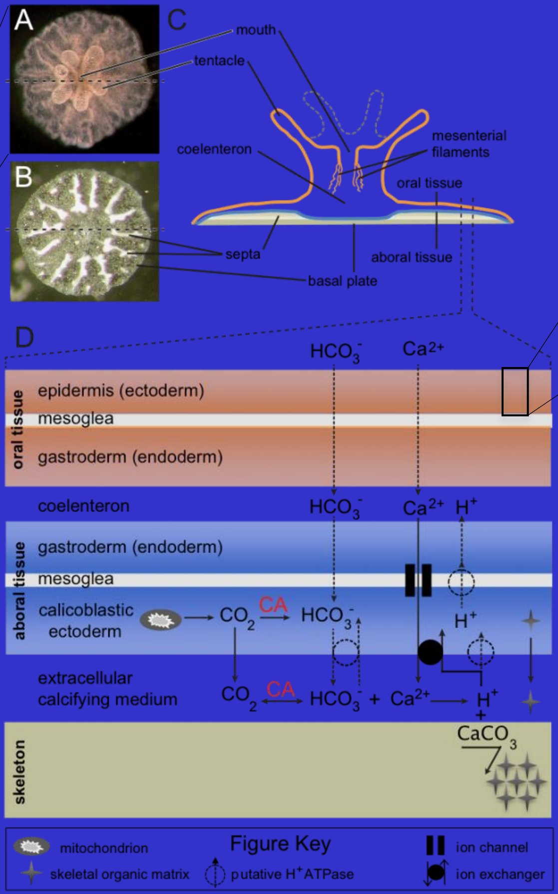


Growth of corals: a multiscale problem



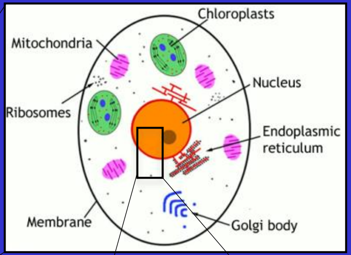
Macromorphology
cm – m
months – years

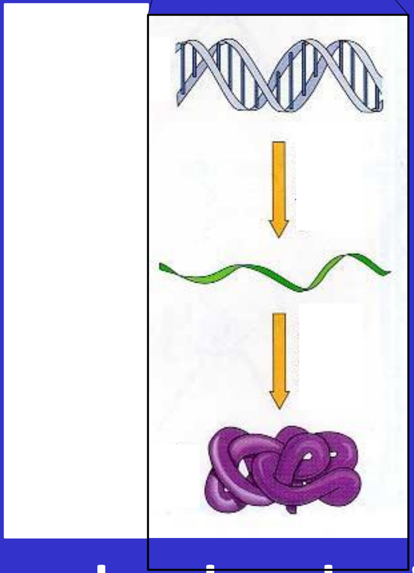
Micromorphology
µm – mm; days - weeks



tissue physiology
1 – 100 µm; ns -µs

cell physiology
1 – 10 µm; ns - hours



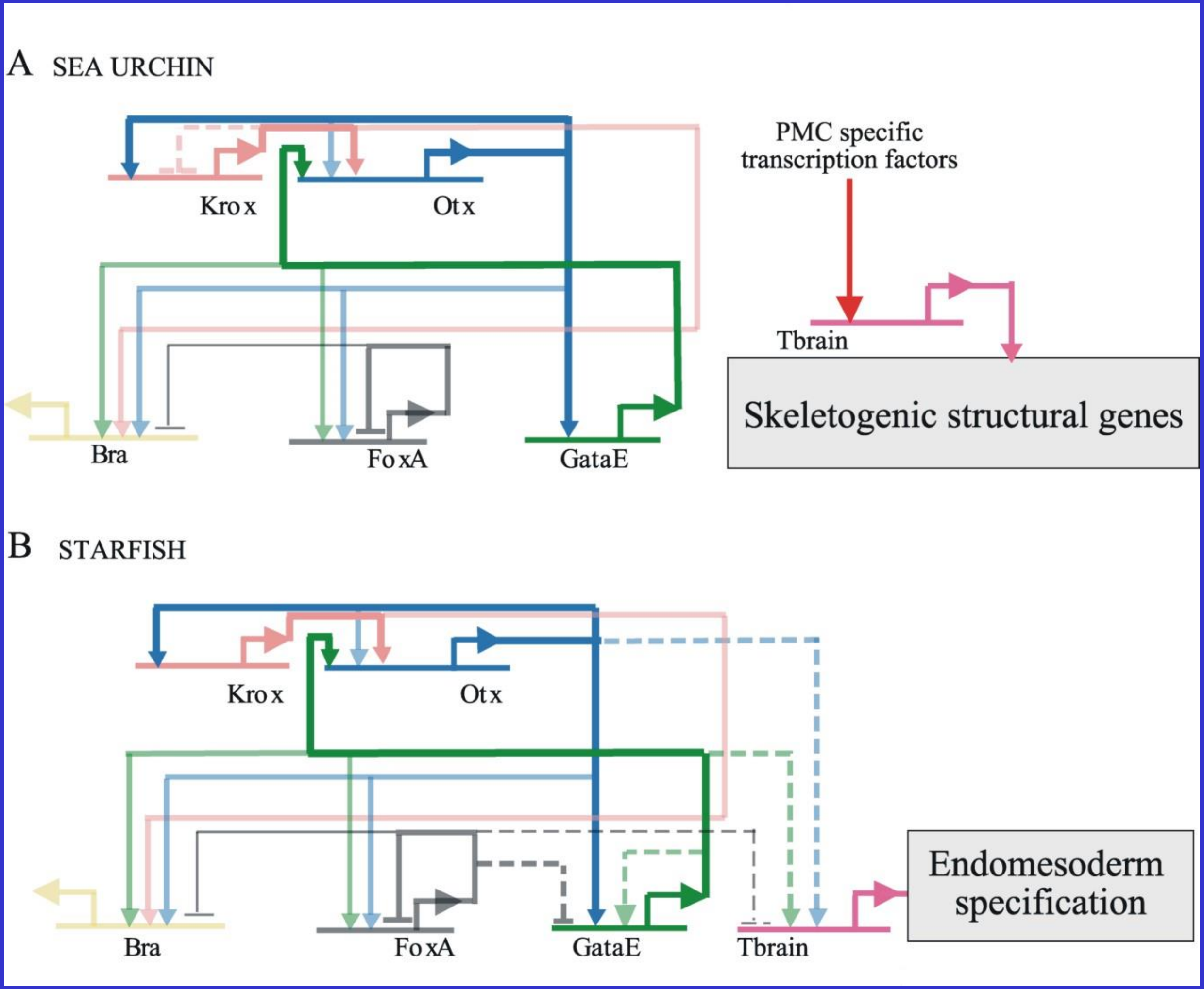


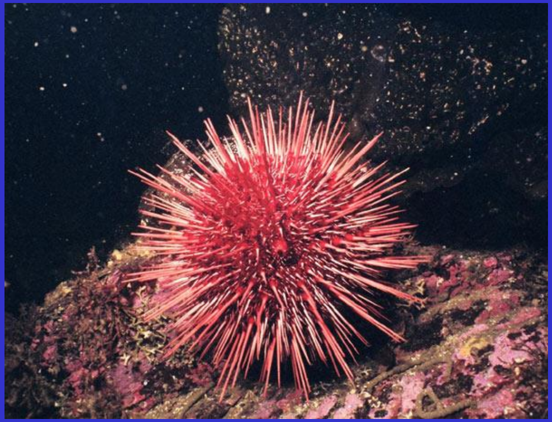
molecular physiology
Å – nm; s - mins

Overview

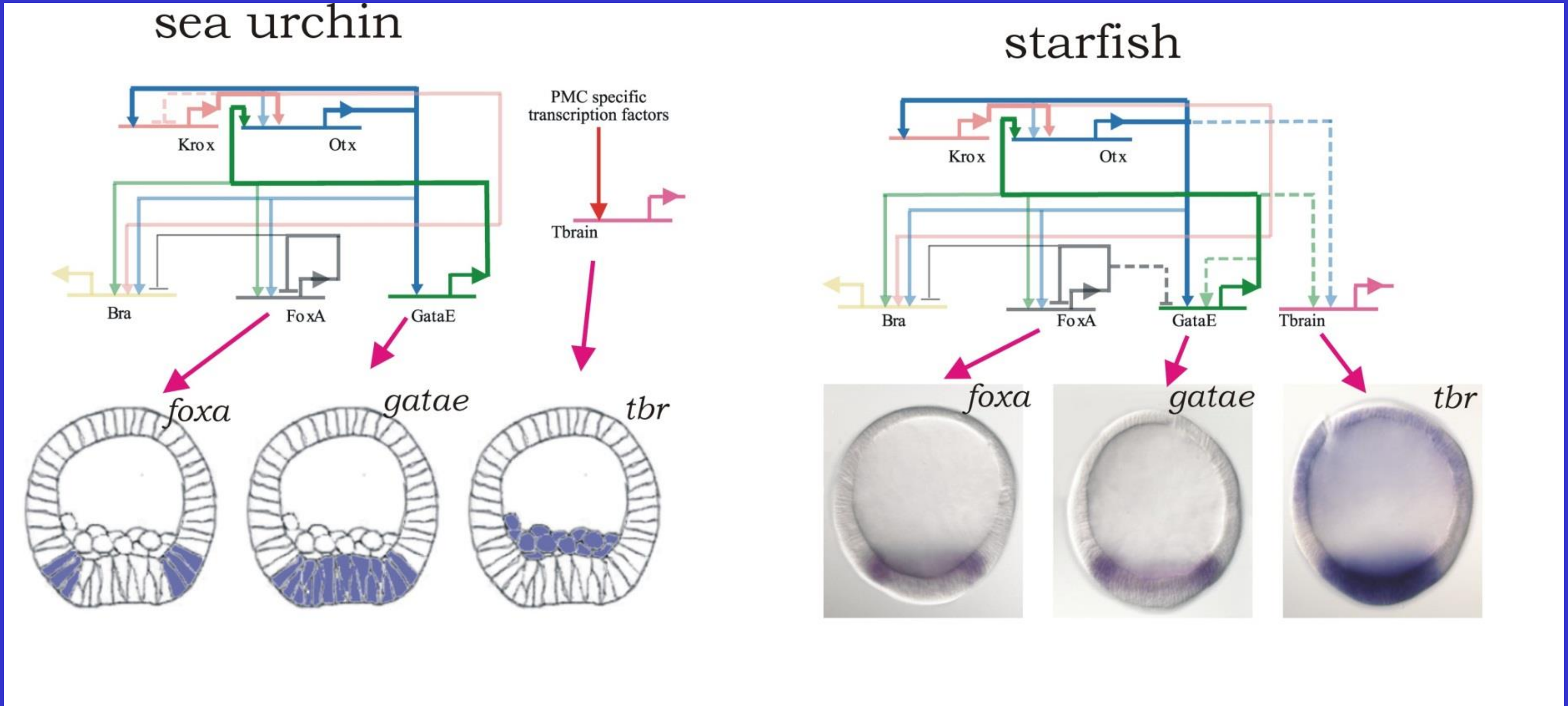
- Modelling gene regulation
- The sea anemone *Nematostella vectensis* case study modelling gene regulation
- Cell-based modelling of gastrulation in *Nematostella* and the hydrozoan *Clytia hemisphaerica*
- Biomineralisation in the scleractinian coral *Acropora millepora*
- Modelling calcification physiology in corals
- Modelling growth and form of corals (e.g *Madracis sp.*) and the impact of the physical environment

Comparison of regulatory network architectures (Hinman & Davidson, 2004)





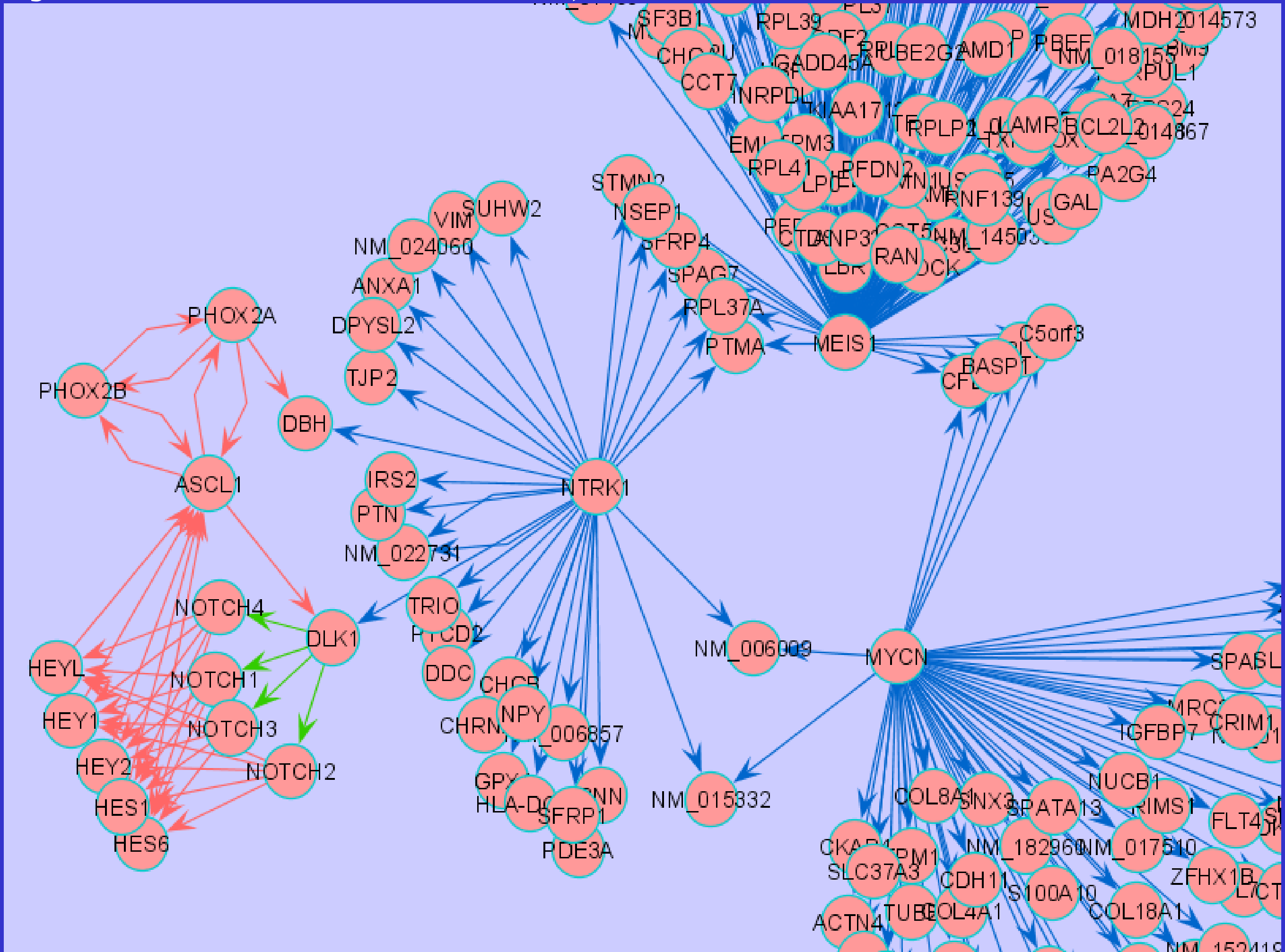
Evolutionary changes in expression patterns are predicted by alterations in upstream regulatory network architecture (Hinman & Davidson, 2004)



Example gene network

Experimentally identified
downstream pathways of three genes

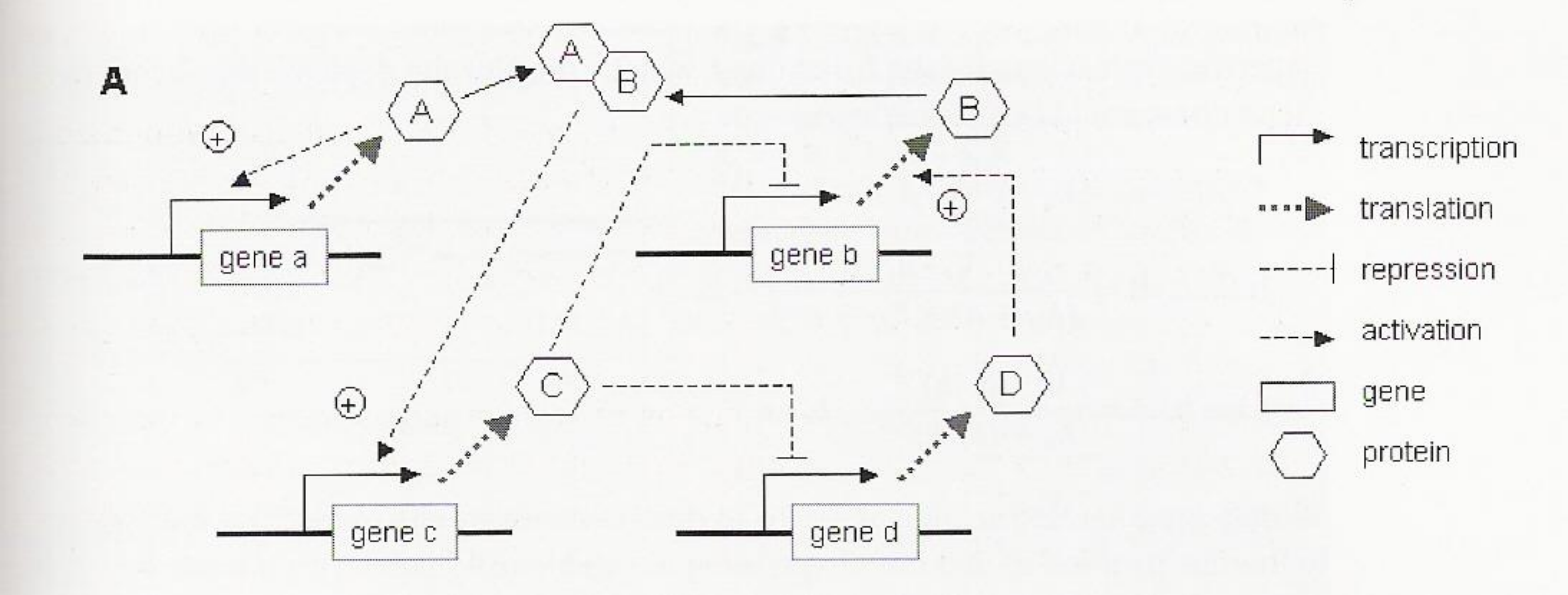
(N-myc, Meis1, NTRK1) in human neuroblastoma



Possible components in a gene network model

- Forward flow of information from gene to mRNA to protein
- Positive and negative feedback loops
- Information exchange with metabolic pathways, signalling pathways
- Biomechanics of cells
- Spatial component

Modelling genetic networks, example (Klipp et al., 2005)



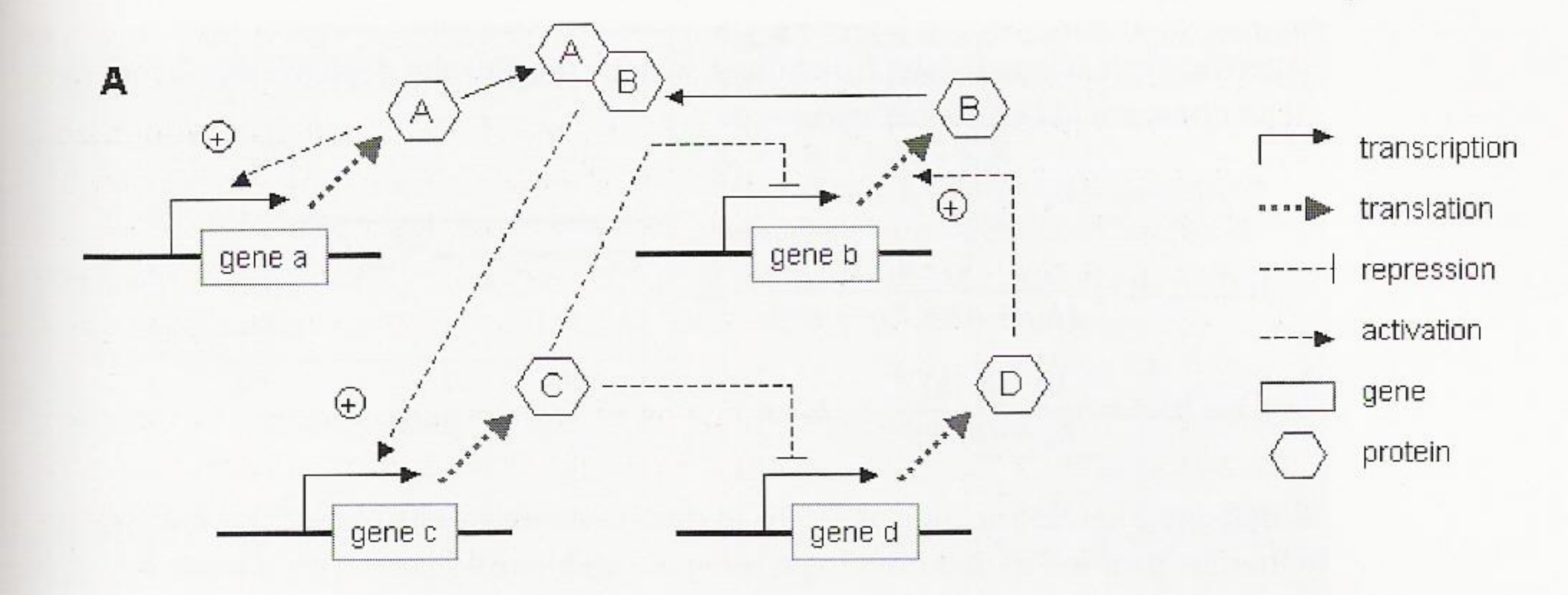
Different models for gene networks

- Boolean networks
- Ordinary differential equations
- Partial differential equations
- …

Genetic networks: the major challenges

- Understanding the dynamics and how gene networks regulate processes is a major (not solved in general) challenge! How do we model such a network? Complication: regulatory networks are very large, many details (needed in the models) are frequently missing
- major challenge: how to infer regulatory networks from gene expression data? How to infer model parameters?
- Major challenge: how do we couple models of regulatory networks and biomechanical models (for example models of growth and development)?

Modelling genetic networks, example



Modelling genetic networks with ODEs

$$\frac{dx_i}{dt} = f_i(x_1,\ldots,x_n), i = 1,\ldots,n$$

- Where x_i represent the concentrations of mRNAs, proteins, or other molecules and n number of genes

Modelling genetic networks with ODEs, example II

- Consider only mRNA quantities a,b,c and d:

$$\frac{da}{dt} = f_a(a)$$

$$\frac{db}{dt} = f_b(b,c,d)$$

$$\frac{dc}{dt} = f_a(a,b,c)$$

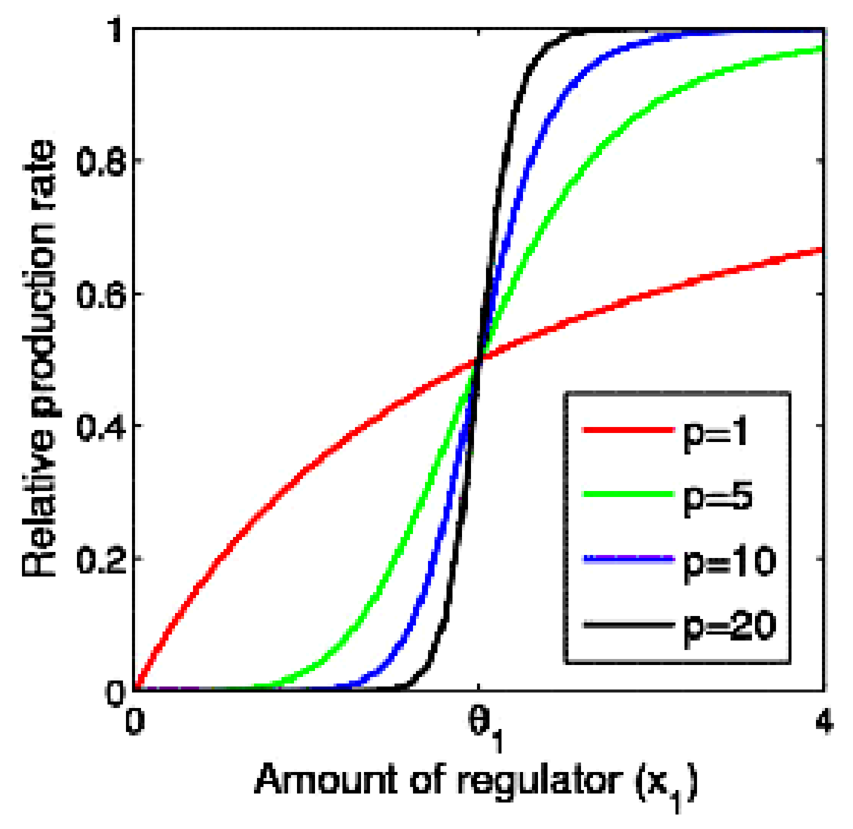
$$\frac{dd}{dt} = f_d(c,d)$$

Modelling enzyme kinetics

- Binding of ligands to proteins, case binding of n ligands (S) to a protein (E), complete cooperativity (Hill equation)

$$v = \frac{V_{\max} K_B S^n}{1 + K_B S^n}$$

Hill function



Modelling genetic networks with ODEs, example III

- A possible model of the regulatory network describing quantities of mRNA:

$$\frac{da}{dt} = v_a - k_a \cdot a$$

$$\frac{db}{dt} = \frac{V_b \cdot d^{n_d}}{(K_b + d^{n_d})(K_{Ic} + c^{n_c})} - k_b \cdot b$$

$$\frac{dc}{dt} = \frac{V_c \cdot (a \cdot b)^{n_{ab}}}{K_c + (a \cdot b)^{n_{ab}}} - k_c \cdot c$$

$$\frac{dd}{dt} = \frac{V_d}{K_{Ic} + c^{n_c}} - k_d \cdot d$$

- Here k_a,k_b,k_c,k_d are rate constants of the degradation of a,b,c and d. v_a is a constant rate of expression

Modelling genetic networks with ODEs, example III

- A possible model of the regulatory network describing quantities of mRNA:

$$\frac{da}{dt} = v_a - k_a \cdot a$$

$$\frac{db}{dt} = \frac{V_b \cdot d^{n_d}}{(K_b + d^{n_d})(K_{Ic} + c^{n_c})} - k_b \cdot b$$

$$\frac{dc}{dt} = \frac{V_c \cdot (a \cdot b)^{n_{ab}}}{K_c + (a \cdot b)^{n_{ab}}} - k_c \cdot c$$

$$\frac{dd}{dt} = \frac{V_d}{K_{Ic} + c^{n_c}} - k_d \cdot d$$

$$\frac{V_b \cdot d^{n_d}}{(K_b + d^{n_d})}$$

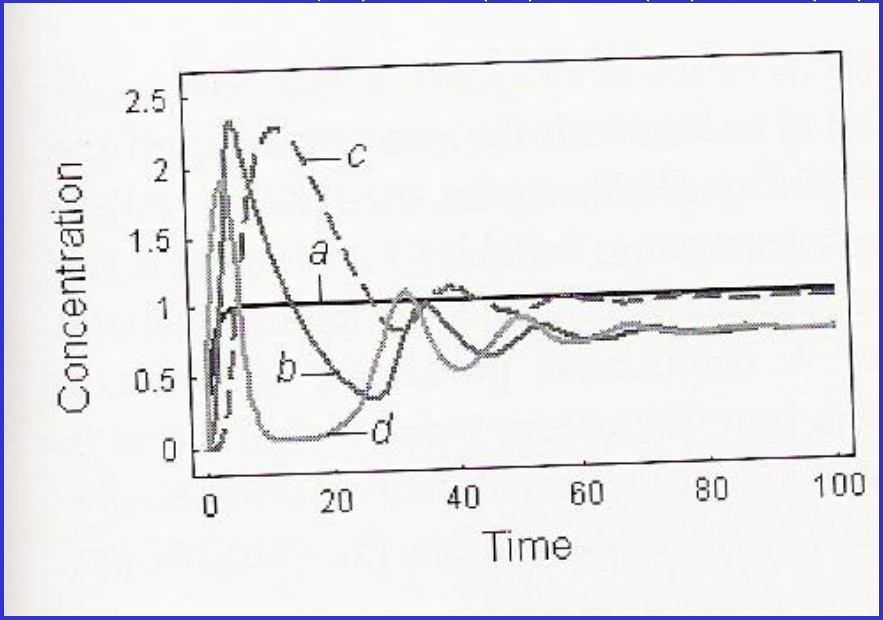
Is Hill term with Max rate V_b, Dissociation constant K_b and Hill coefficient n_d

$$(K_{Ic} + c^{n_c})$$

Is inhibition term

Modelling genetic networks with ODEs, example IV

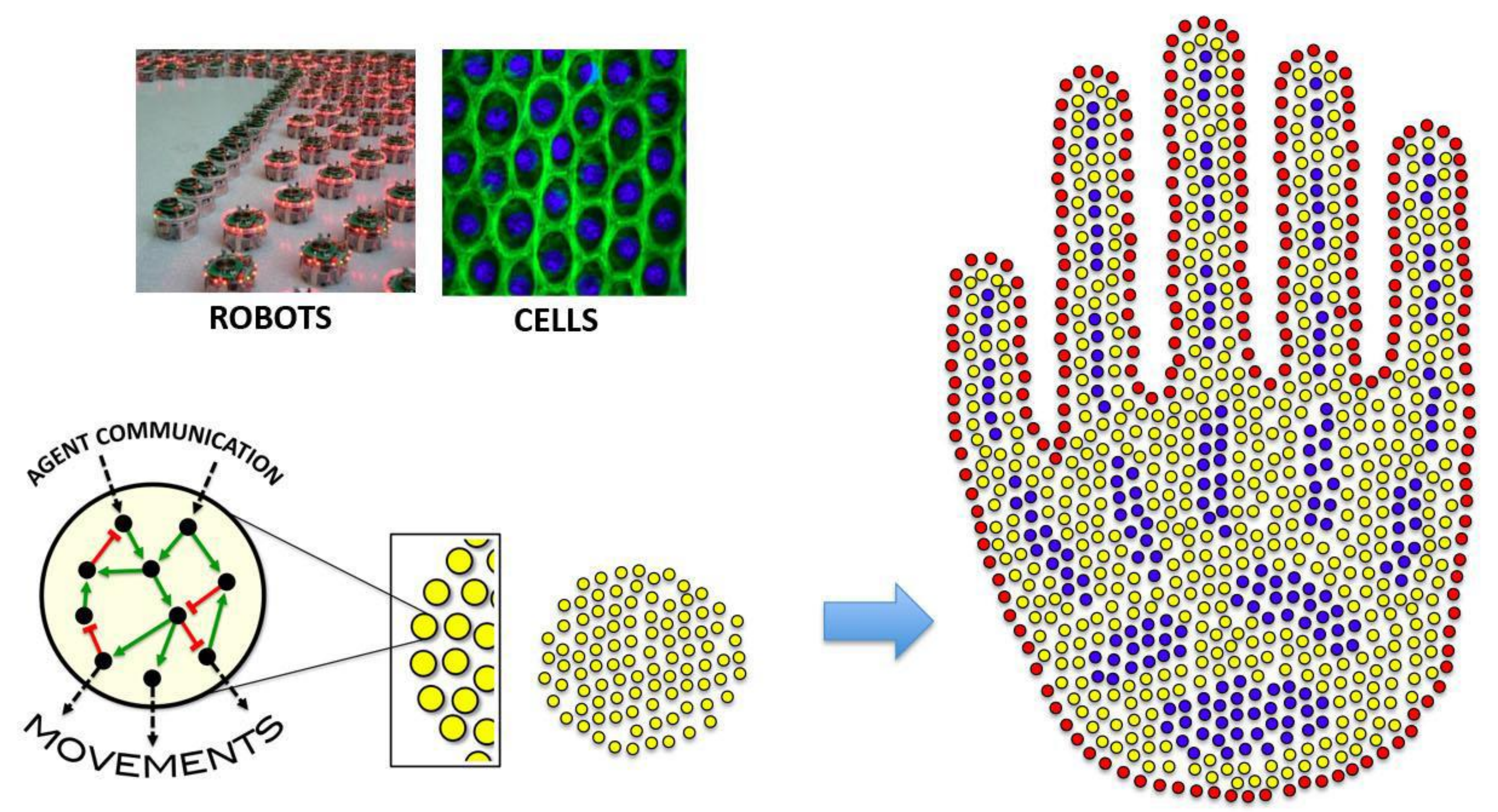
- Dynamics of the quantities of mRNA (v_a=1, k_a=1,V_b=1,K_b=5,K_{ic}=0.5, n_c=4;k_b=0.1,V_c=1,K_c=5;k_c=0.1,V_d=1, k_d=0,1; initial conditions a(0)=b(0)=c(0)=d(0)=0):



Modelling genetic networks with ODEs

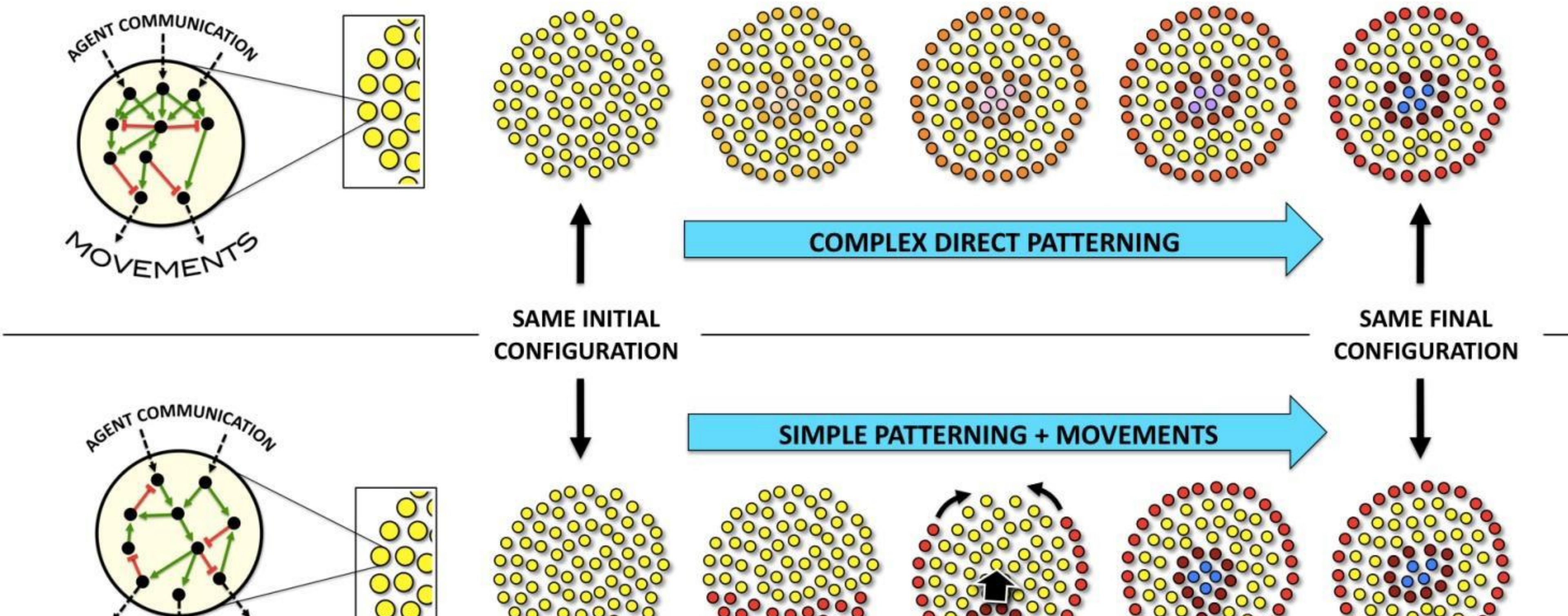
- Advantage: can take into account detailed knowledge about regulatory network (including quantitative information; temporal information for example time delays, slow and fast processes; can be extended to PDE description including spatial information)
- Disadvantage: current lack of this detailed knowledge! Many parameters are not available, you need an additional method to estimate these parameters from actual data.
- Disadvantage: the ODE description is a macroscopic one, in many steps only a few molecules are involved.
- Disadvantage: no spatial component

The central concept cells are controlled by gene regulatory networks, and display collective emergent behaviour to spatially-organise themselves into a functional multi-cellular structure.

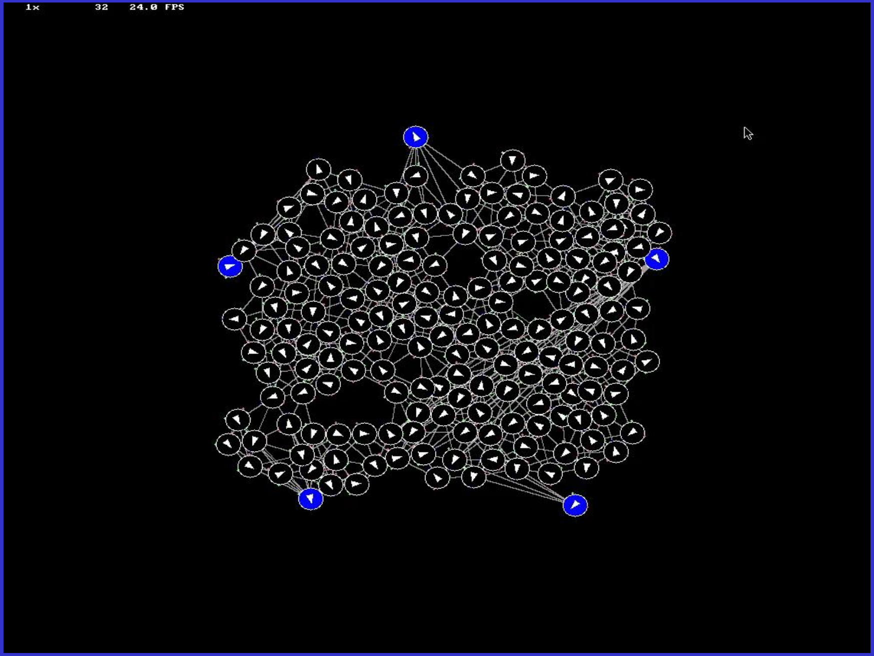


Two different ways to develop the same pattern. upper row there is hardly any cell movement. The GRN enables each cell to accurately interpret its position. (*morphostatic)* Lower row the GRN drives only a very simple patterning process occurs – dividing the initial tissue into 3 simple zones. However, cell types then display extensive rearrangements (migrations, invagination etc.) to produce the correct final configuration

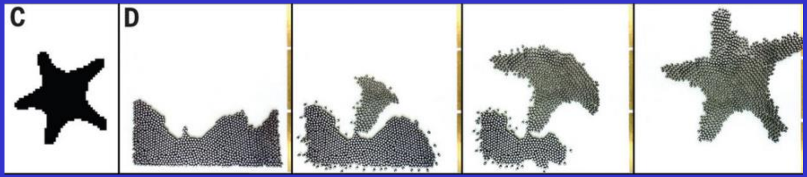
in a *morphodynamic* manner.



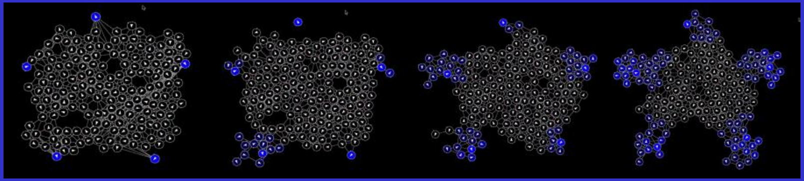
Modelling a swarm of kilo bots (Slavkov et al., Science Robotics, 2018)



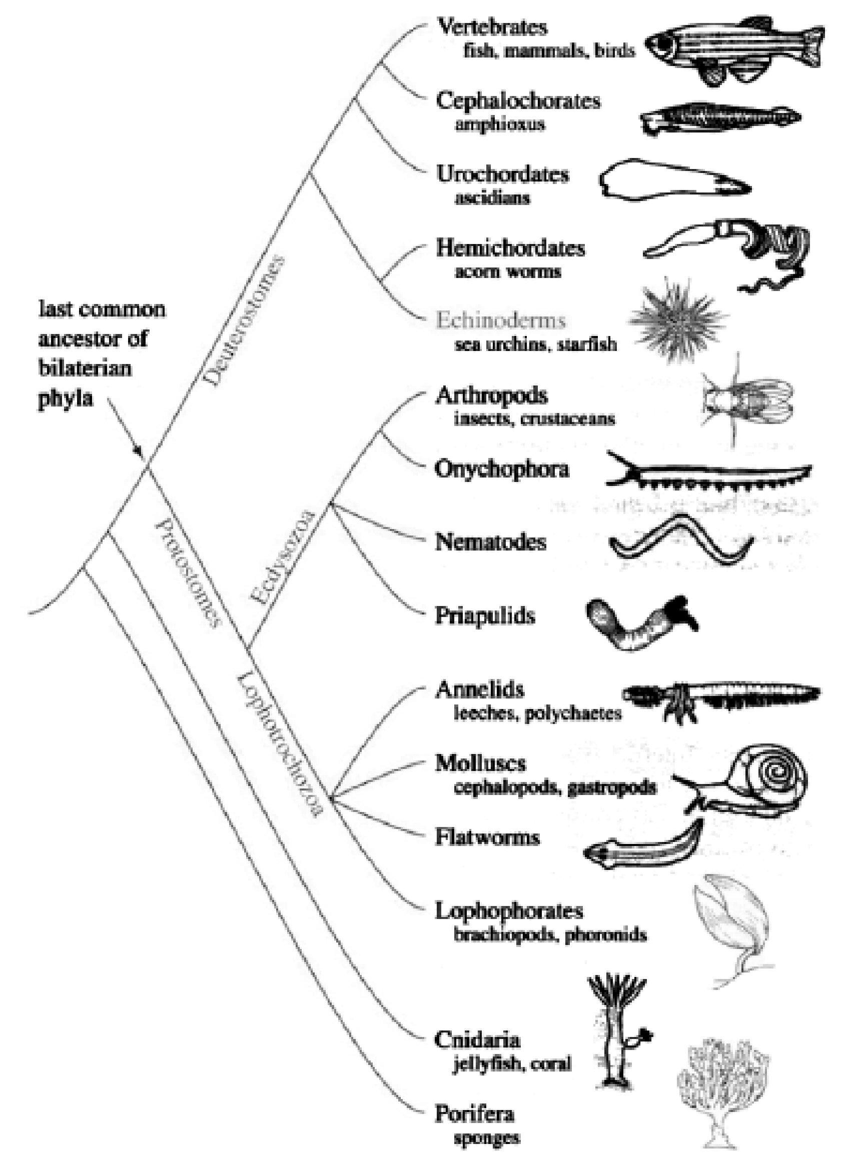
Only the edge-bots move towards the gradient



M. Rubenstein, et al. Science, Vol. 345, pp. 795-799, 2014



The animal kingdom



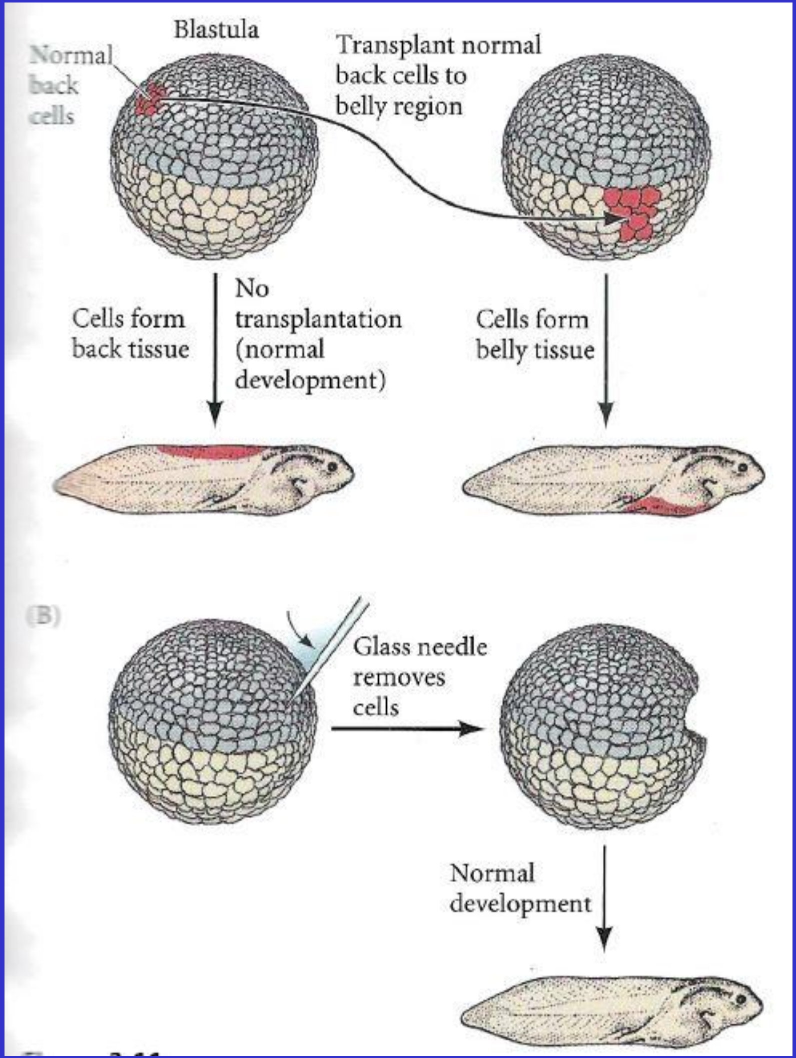
- Reconstruction of gene regulatory networks in *Nematostella vectensis*, (Botman & Kaandorp, BMC Research Notes, 2012; Abdol et al. Dev. Biol. 2017)

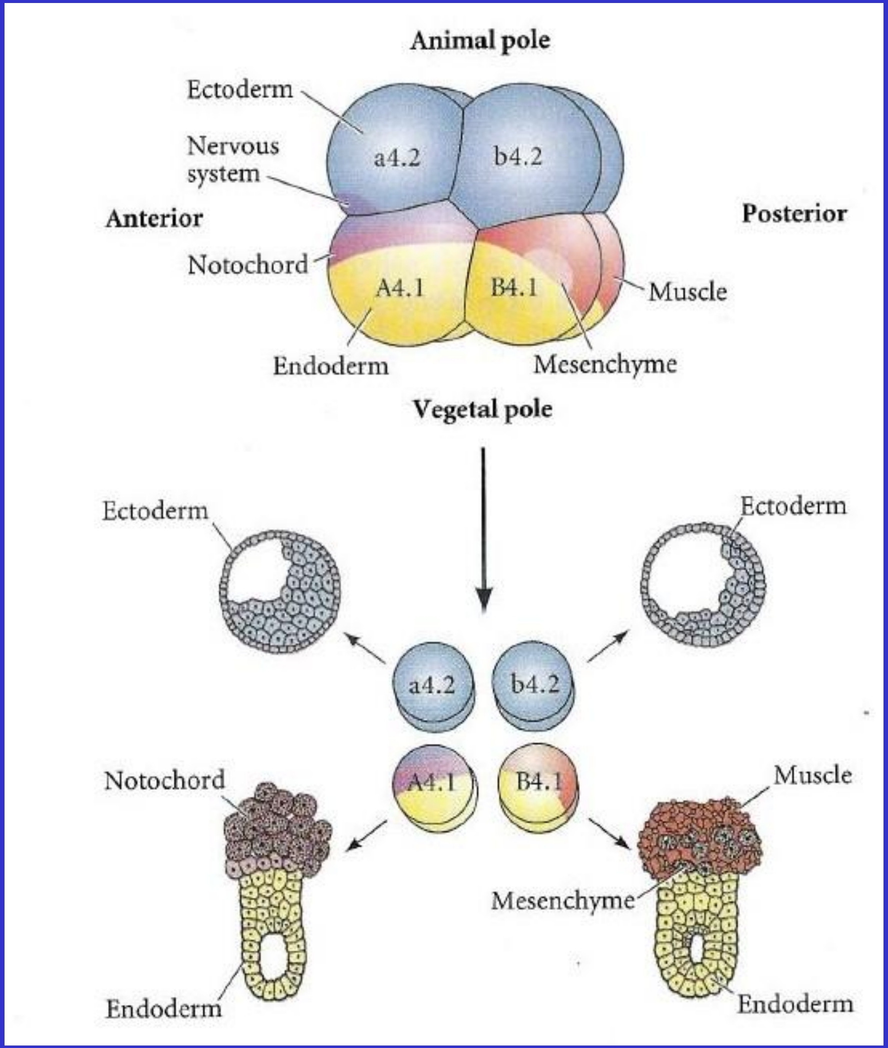
Modelling and inferring gene regulation of body plan formation in *Nematostella vectensis*: the morphodynamic case, (*Botman & Kaandorp, BMC Research Notes, 2012; Abdol et al. Dev. Biol. 2017; Vroomans et al., in prep*)

Nematostella vectensis (starlet sea anemone)

- Both *Nemostella* and *Acropora* are anthozoans (basal animals)
- Genomes have been sequenced
- Genomes close to human
- *Nematostella* is currently extensively studied
- Holoblastic cell cleavage (no complicated unequal cell cleavages)
- Development by regional specification (no pre-determined cell fate, no fate map)
- Relatively simple body plan

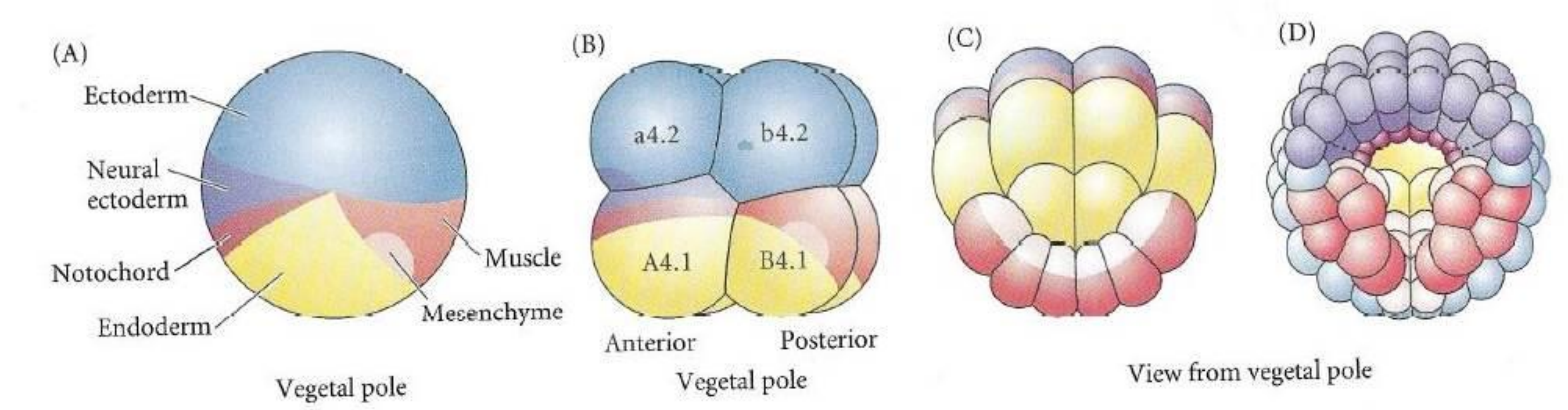
Nematostella vectensis regulative (left) vs mosaic development (right) *(Gilbert, 2000)*





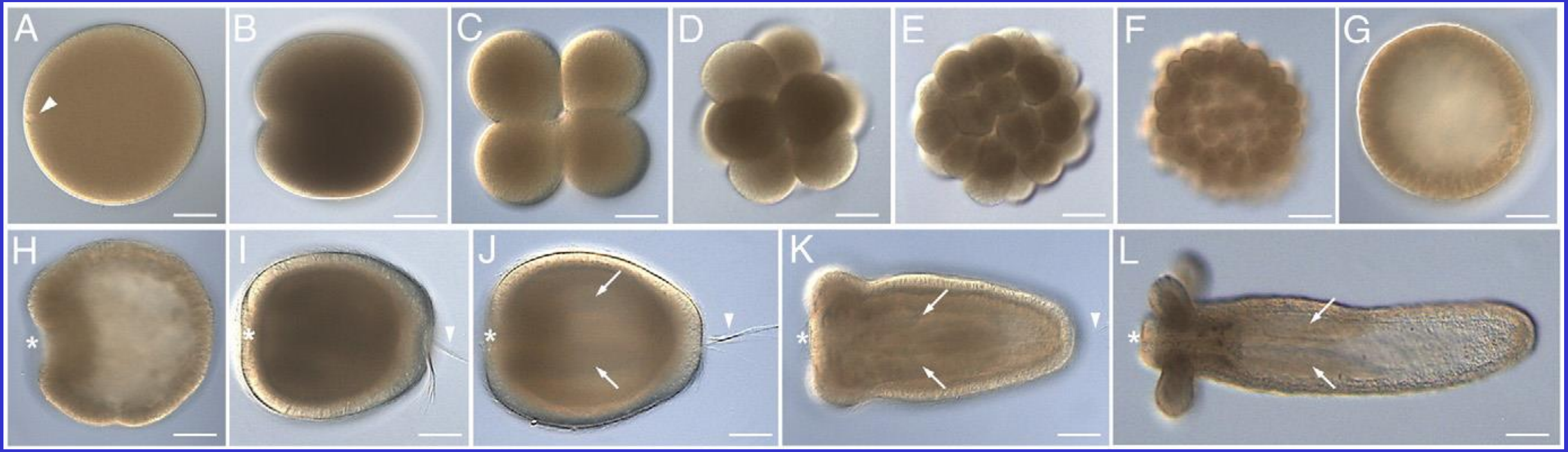
Non holoblastic cell cleavage (e.g. tunicates)

(Gilbert, 2000)



Nematostella vectensis developmental stages

Lee 2007



(**A**) egg
(**B**-**F**) cleavage to prawn chip (11 cleavage stage)
(**G**) Blastula
(**H**) Gastrula
(**I**) planula with apical tuft
(**J**) planula mesenteries grow
(**K**) Polyp early tentacle
(**L**) Polyp

Nematostella gastrulation (Magie et all 2007)

A Apical constriction

B Invagination or ingression

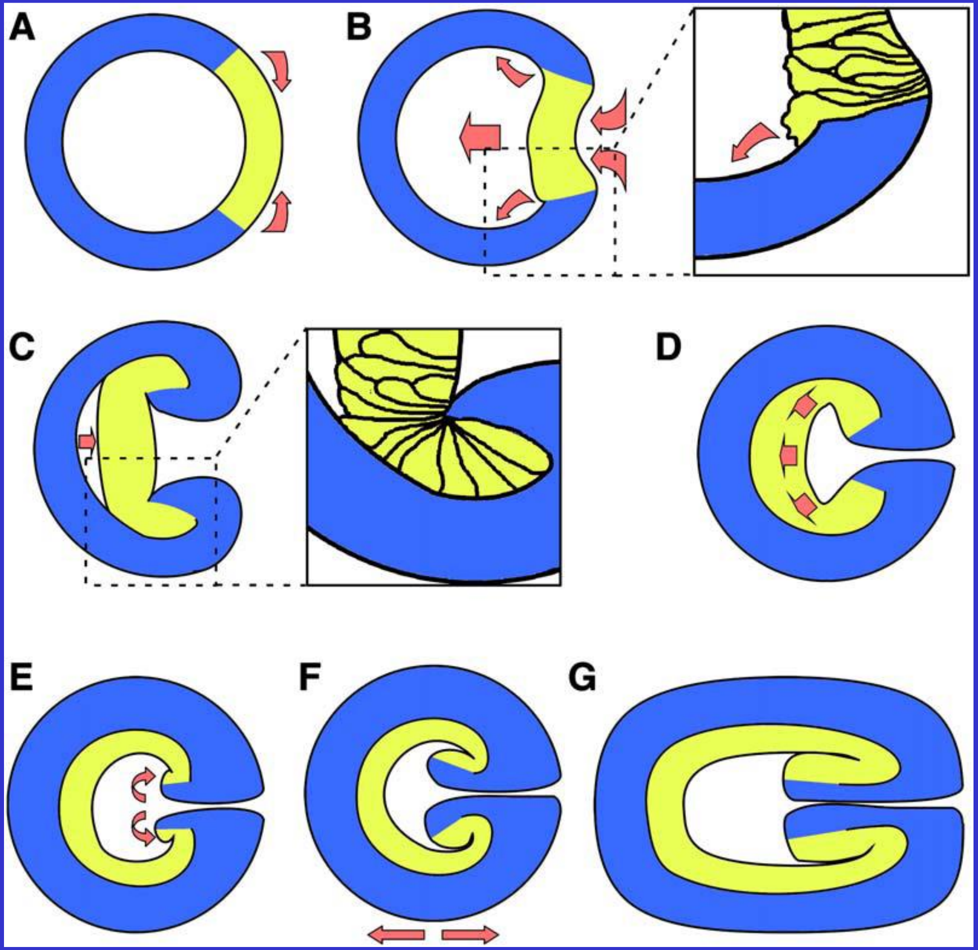
C Endoderm zipping against ectoderm, blastocoel vanishes

D Endoderm thinning

E Invagination of pharynx

F Elongation of planula

G Planlula stage

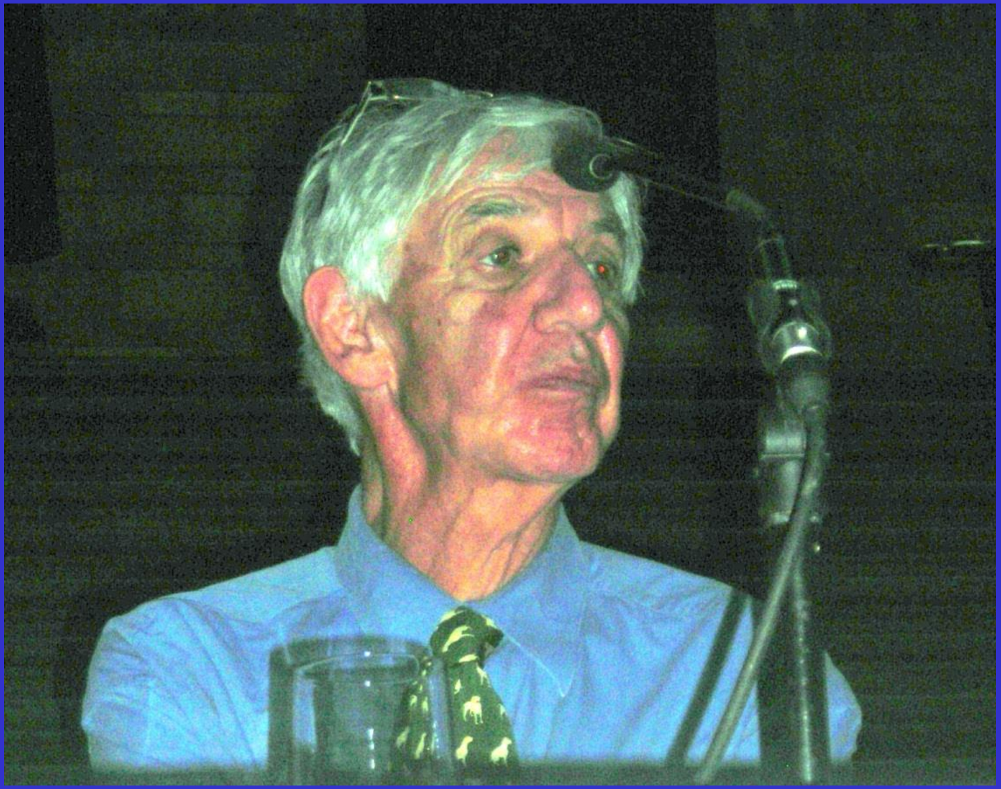


Magie 2007

Yellow is endoderm
Blue is ectoderm

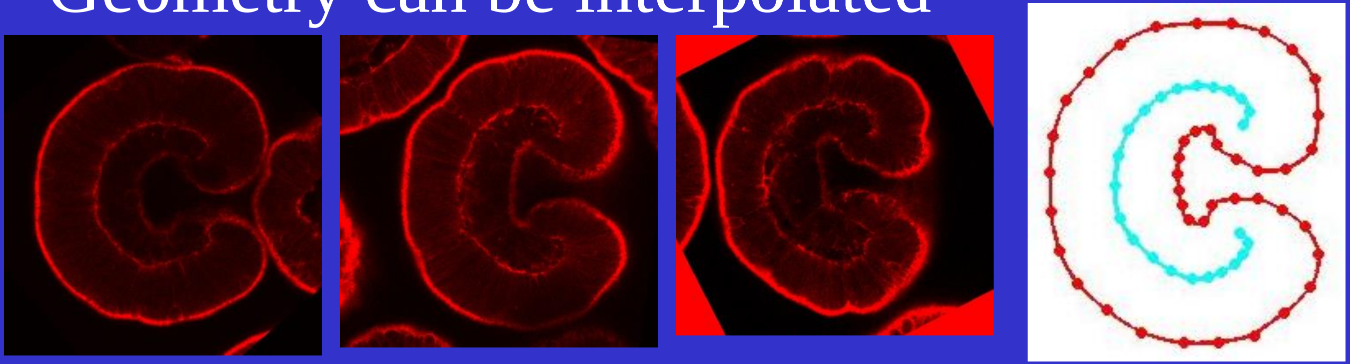
Gastrulation (Lewis Wolpert)

"It is not birth, marriage, or death, but gastrulation which is truly the most important time in your life."



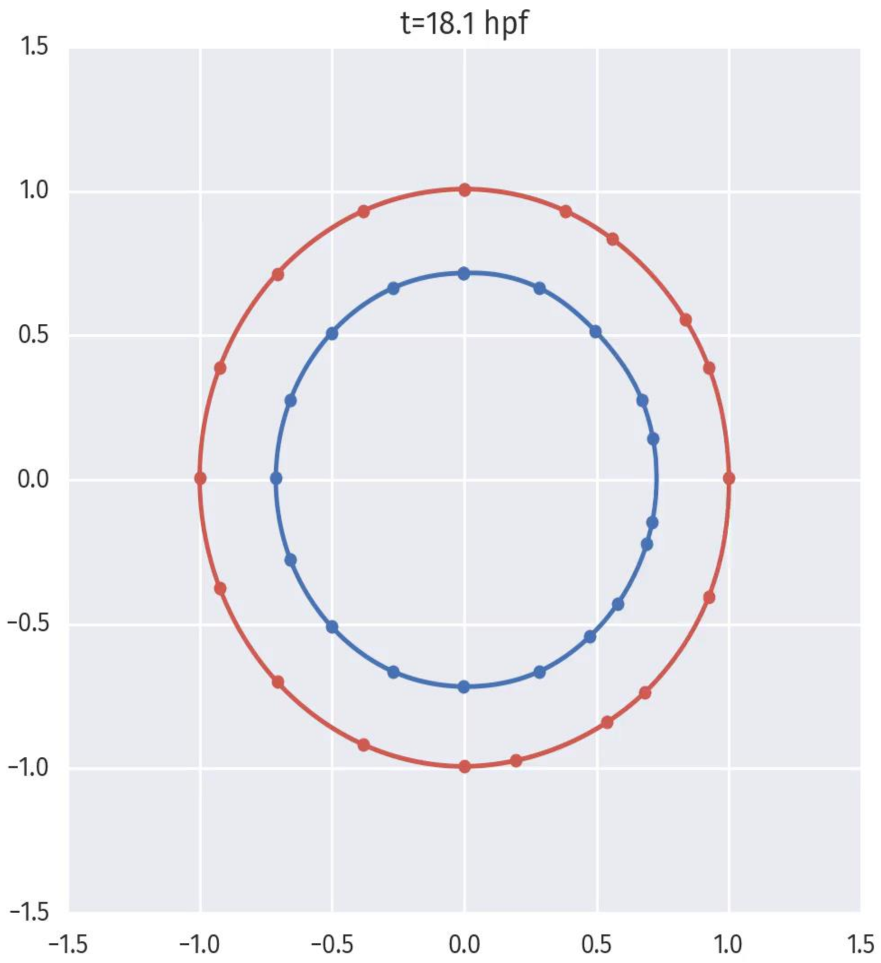
Geometry extraction in *Nematostella vectensis* using confocal data

- Cell layers are traced using splines
- Geometry can be interpolated



- resulting average geometry Three confocal images showing embryos 28 hours post fertilization

Embryo geometries

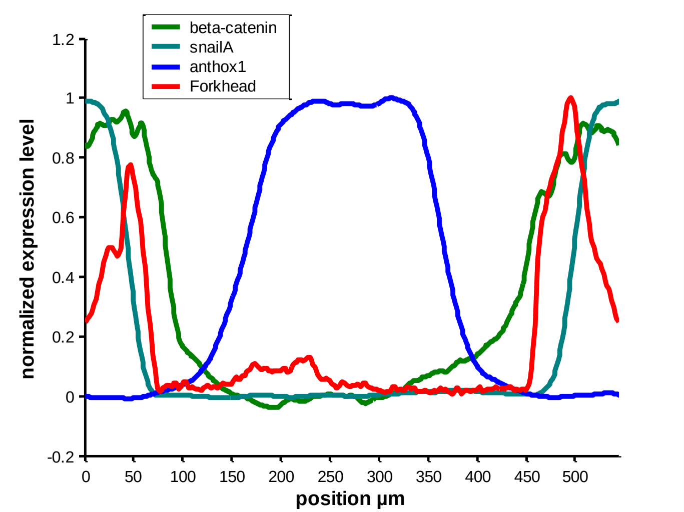


Developmental genes and signalling pathways in *Nematostella vectensis*

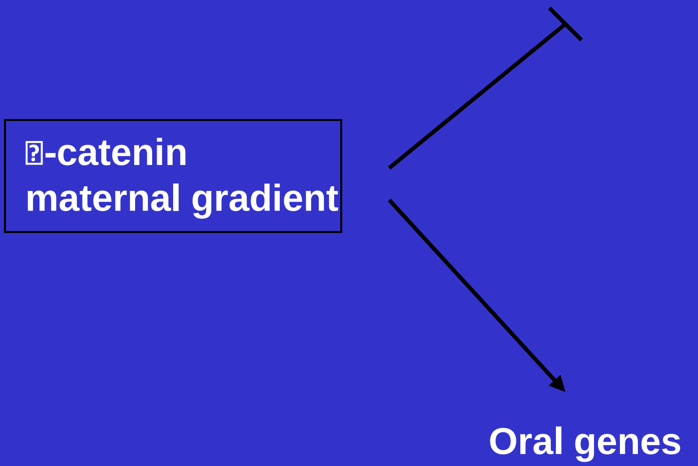
- Transpcription factors (within cell nucleus)
  - Homeobox genes
  - Sox genes
  - Fox genes
  - Other genes
- Wnt signalling pathway (diffusable ligands)
- TGF beta signalling pathway (diffusable ligands)
- FGF signalling pathway (diffusable ligands)
- …

Quantify Expression Patterns

- **Load gene expression picture**
- **Choose stage**
- **Adjust geometry to fit the real embryo shape**
- **Perform decomposition**
- **Calculate expression levels**
- **Plot the expression profile**
- **Process the data, i.e. shift, scale, reduce noise etc.**
- **Combine all patterns of the genes of interest**



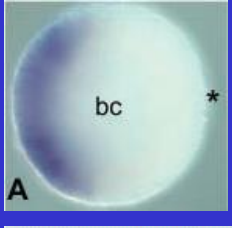
Nematostella vectensis, in situ hybridizations: genes at blastula stage (* indicates future position mouth)



β-catenin maternal gradient

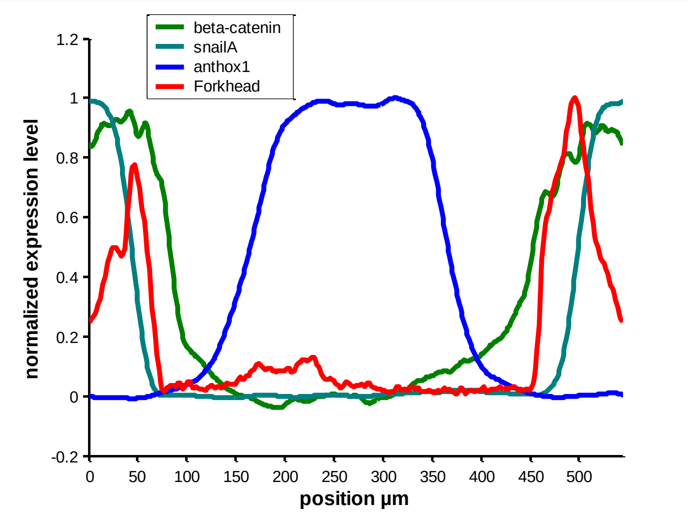
Aboral genes

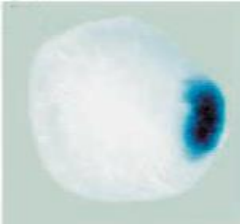
Oral genes



anthox1
Finnerty 2004

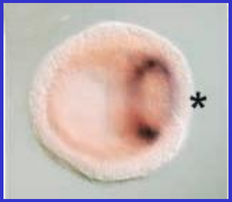
foxD1
Magie 2005





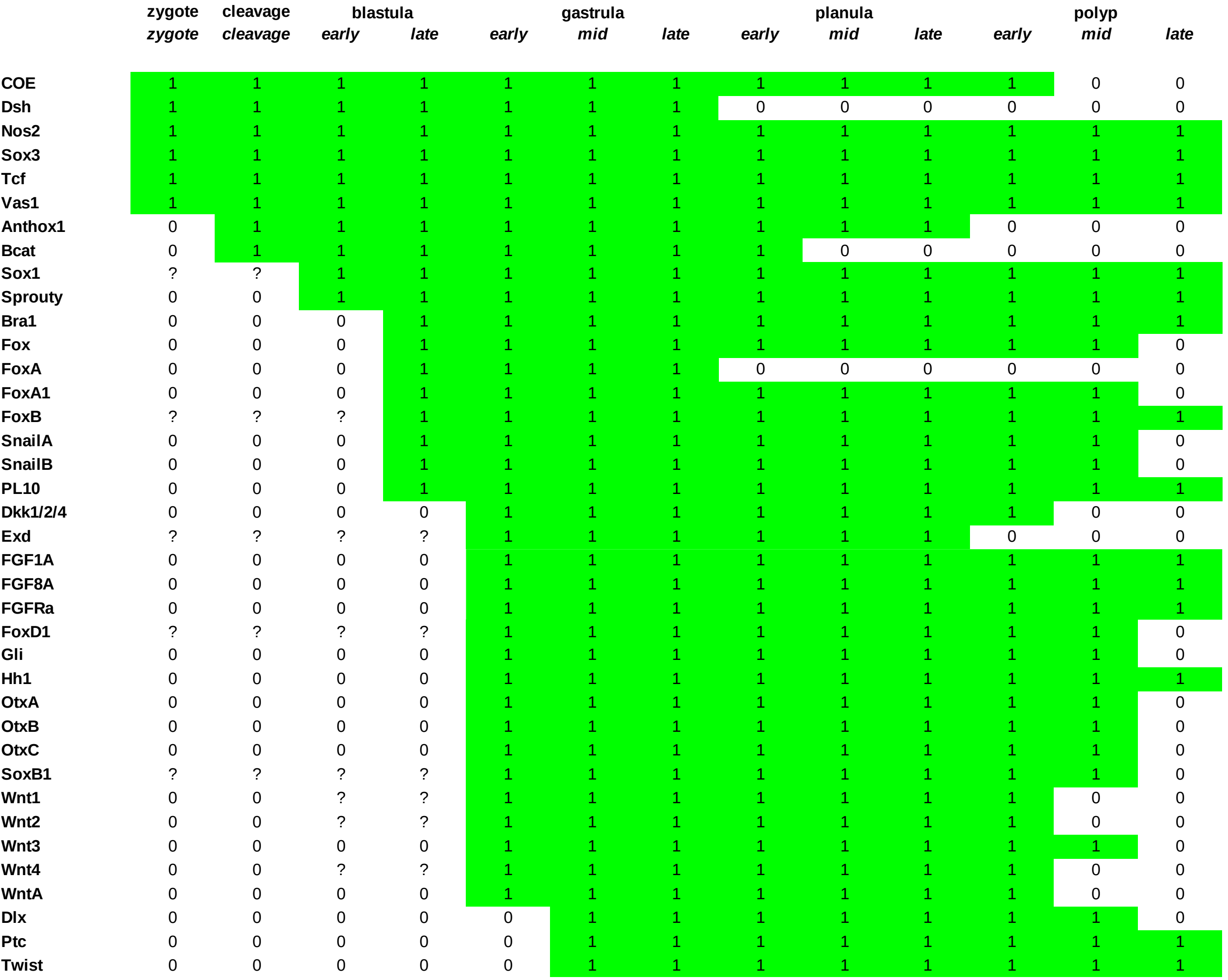
snailA/B
Martindale 2004

foxB (forkhead)
Magie 2005



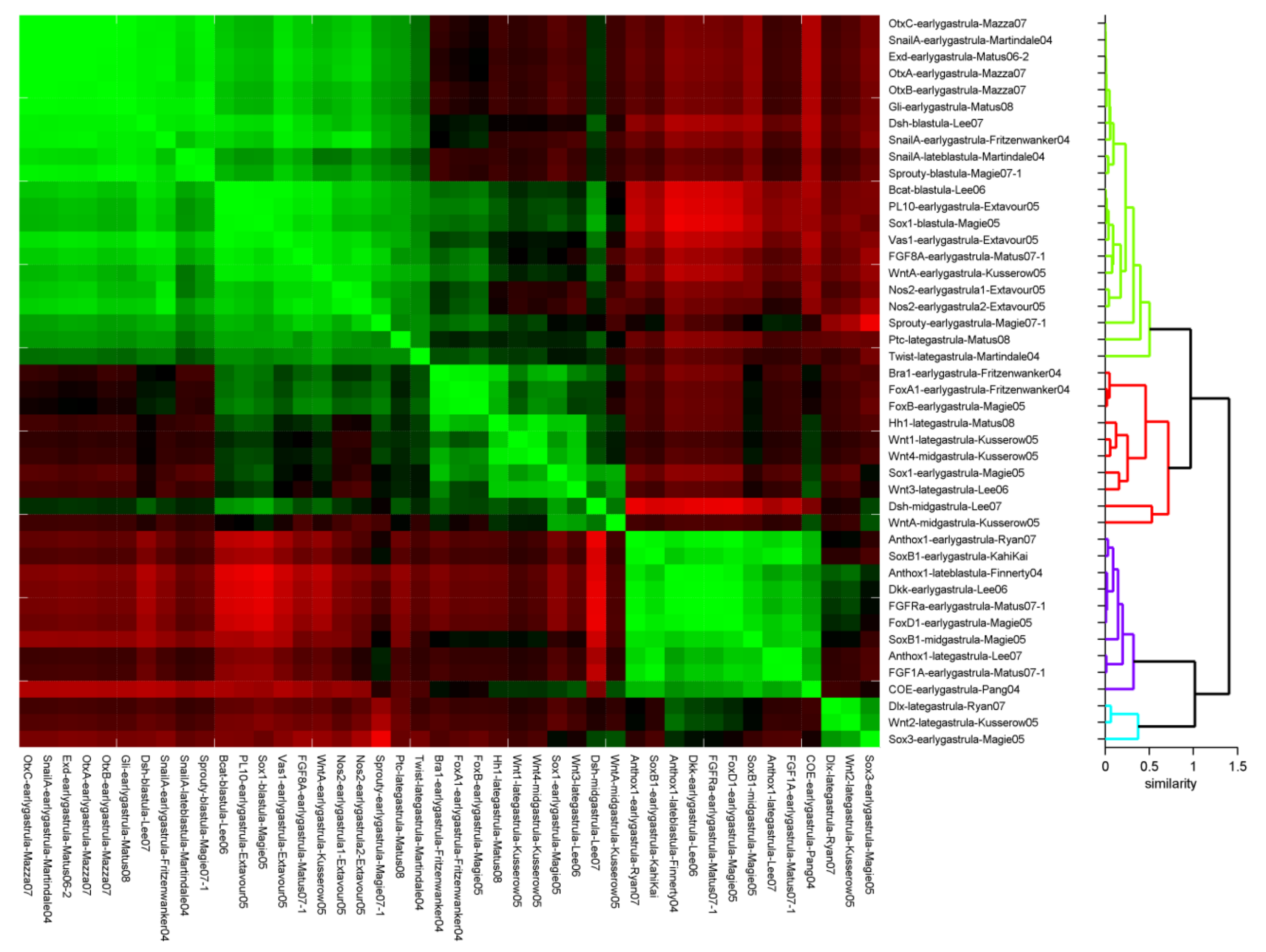
twist

Final list of genes. For this resulting set of genes quantifications were made for early developmental stages (up to mid gastrula)

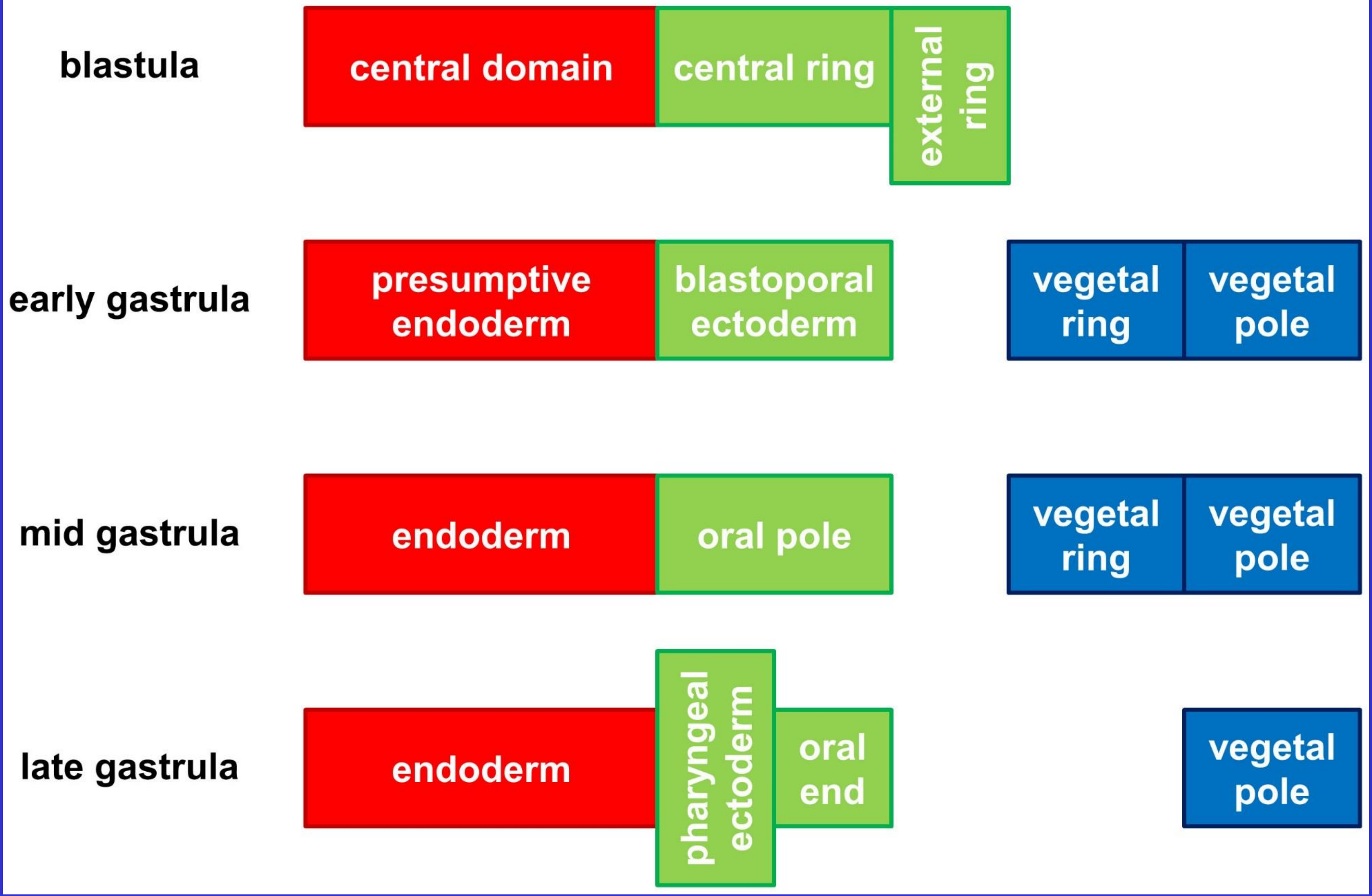


	zygote	cleavage	blastula		gastrula			planula			polyp		
	zygote	*cleavage*	*early*	*late*	*early*	*mid*	*late*	*early*	*mid*	*late*	*early*	*mid*	*late*
COE	1	1	1	1	1	1	1	1	1	1	1	0	0
Dsh	1	1	1	1	1	1	1	0	0	0	0	0	0
Nos2	1	1	1	1	1	1	1	1	1	1	1	1	1
Sox3	1	1	1	1	1	1	1	1	1	1	1	1	1
Tcf	1	1	1	1	1	1	1	1	1	1	1	1	1
Vas1	1	1	1	1	1	1	1	1	1	1	1	1	1
Anthox1	0	1	1	1	1	1	1	1	1	1	0	0	0
Bcat	0	1	1	1	1	1	1	1	0	0	0	0	0
Sox1	?	?	1	1	1	1	1	1	1	1	1	1	1
Sprouty	0	0	1	1	1	1	1	1	1	1	1	1	1
Bra1	0	0	0	1	1	1	1	1	1	1	1	1	1
Fox	0	0	0	1	1	1	1	1	1	1	1	1	0
FoxA	0	0	0	1	1	1	1	0	0	0	0	0	0
FoxA1	0	0	0	1	1	1	1	1	1	1	1	1	0
FoxB	?	?	?	1	1	1	1	1	1	1	1	1	1
SnailA	0	0	0	1	1	1	1	1	1	1	1	1	0
SnailB	0	0	0	1	1	1	1	1	1	1	1	1	0
PL10	0	0	0	1	1	1	1	1	1	1	1	1	1
Dkk1/2/4	0	0	0	0	1	1	1	1	1	1	1	0	0
Exd	?	?	?	?	1	1	1	1	1	1	0	0	0
FGF1A	0	0	0	0	1	1	1	1	1	1	1	1	1
FGF8A	0	0	0	0	1	1	1	1	1	1	1	1	1
FGFRa	0	0	0	0	1	1	1	1	1	1	1	1	1
FoxD1	?	?	?	?	1	1	1	1	1	1	1	1	0
Gli	0	0	0	0	1	1	1	1	1	1	1	1	0
Hh1	0	0	0	0	1	1	1	1	1	1	1	1	1
OtxA	0	0	0	0	1	1	1	1	1	1	1	1	0
OtxB	0	0	0	0	1	1	1	1	1	1	1	1	0
OtxC	0	0	0	0	1	1	1	1	1	1	1	1	0
SoxB1	?	?	?	?	1	1	1	1	1	1	1	1	0
Wnt1	0	0	?	?	1	1	1	1	1	1	1	0	0
Wnt2	0	0	?	?	1	1	1	1	1	1	1	0	0
Wnt3	0	0	0	0	1	1	1	1	1	1	1	1	0
Wnt4	0	0	?	?	1	1	1	1	1	1	1	0	0
WntA	0	0	0	0	1	1	1	1	1	1	1	0	0
Dlx	0	0	0	0	0	1	1	1	1	1	1	1	0
Ptc	0	0	0	0	0	1	1	1	1	1	1	1	1
Twist	0	0	0	0	0	1	1	1	1	1	1	1	1

Analysis Expression Patterns



Cluster analysis of Kahi Kai data base of in situ's diagrammitic overview of the clusters (Botman et al., BMC Syst. Biol., 2014)



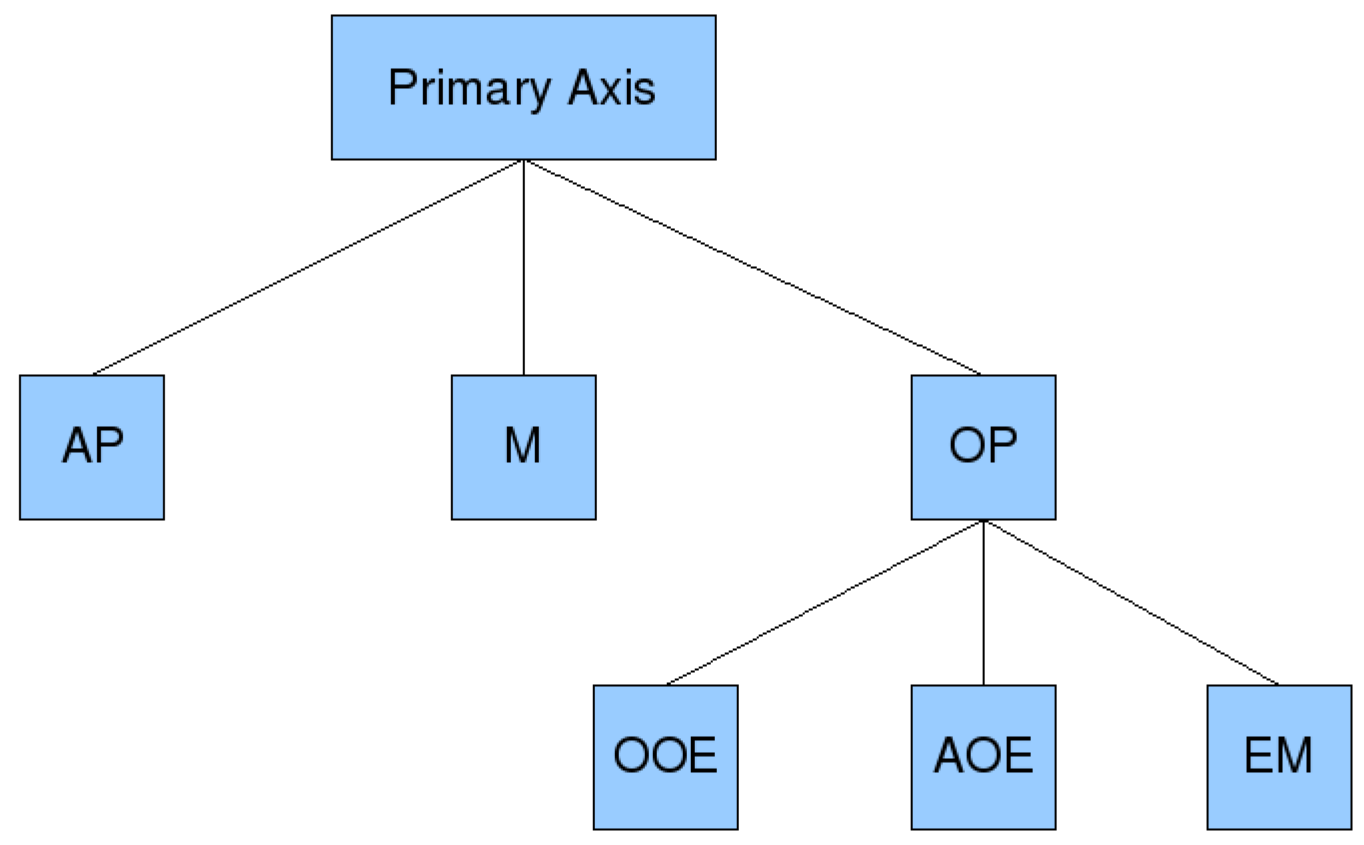
blastula
central domain
central ring
external ring

early gastrula
presumptive endoderm
blastoporal ectoderm
vegetal ring
vegetal pole

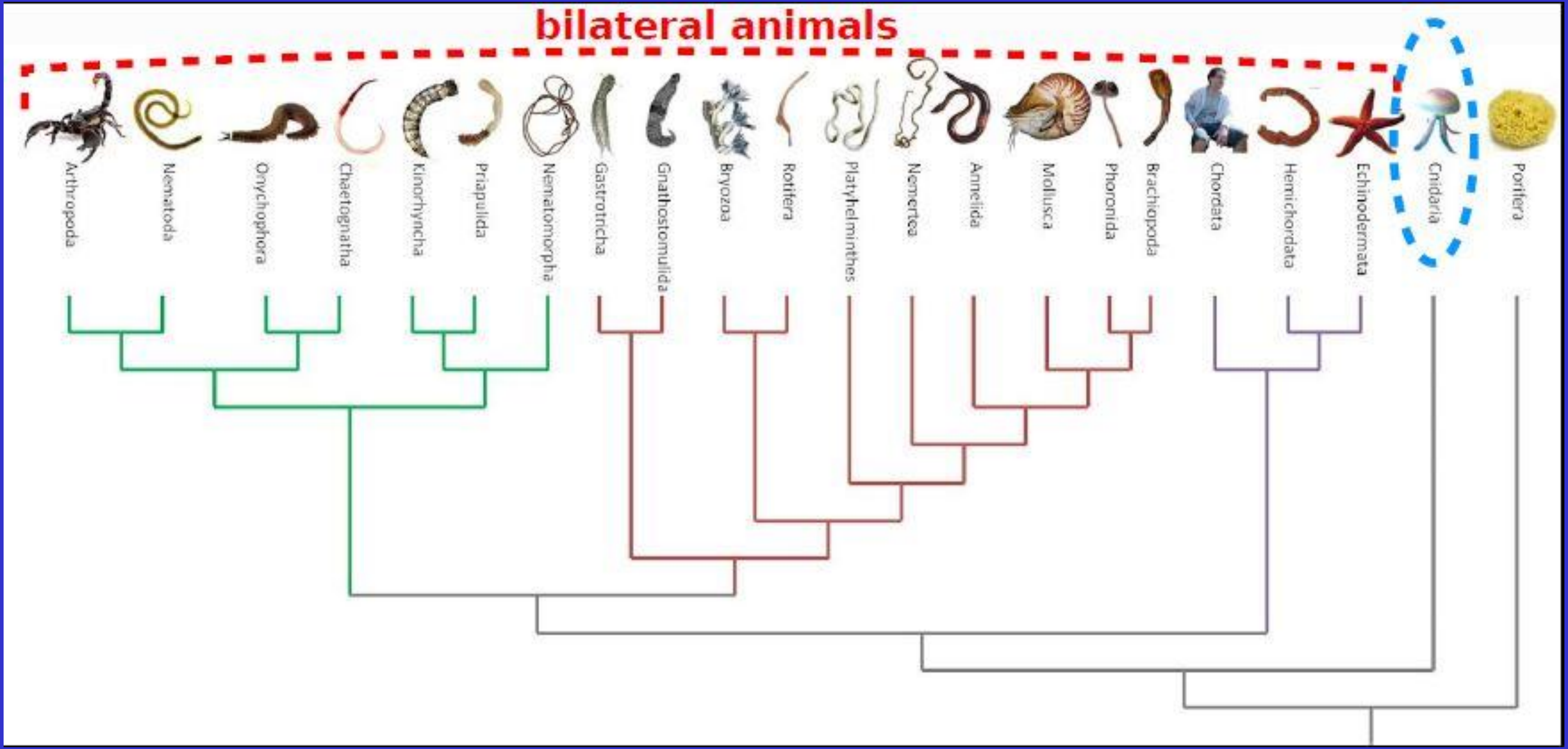
mid gastrula
endoderm
oral pole
vegetal ring
vegetal pole

late gastrula
endoderm
pharyngeal ectoderm
oral end
vegetal pole

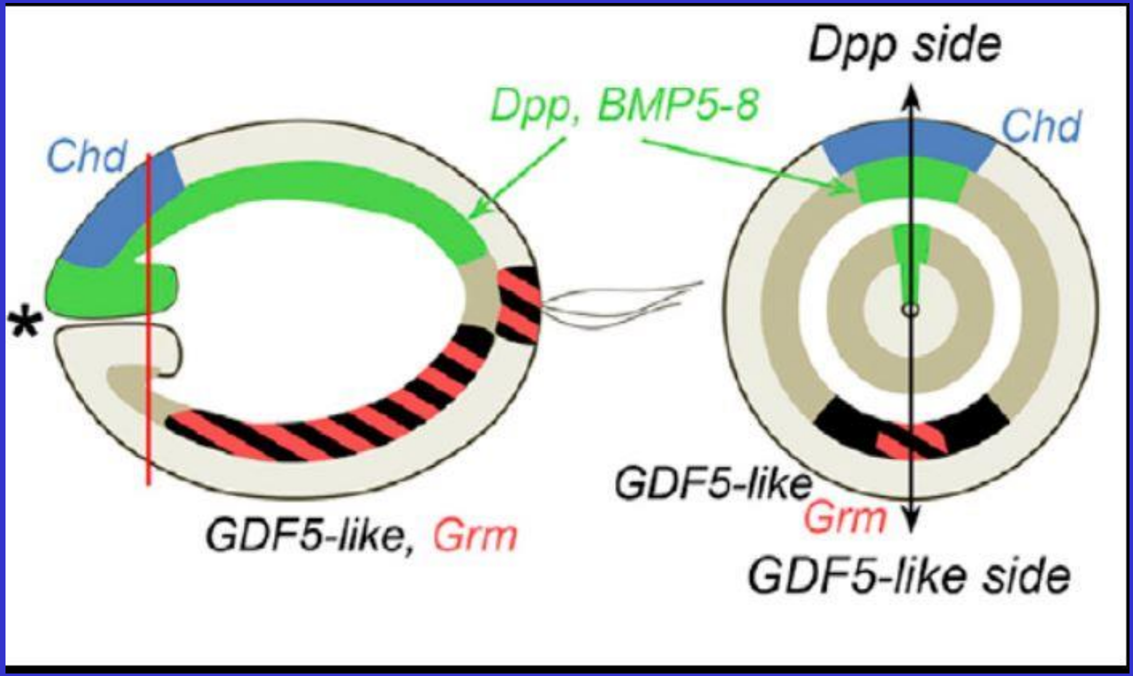
Hierarchical subdivision of the primary axis. AP = Aboral Pole; M = Middle section; OP = Oral Pole; OE = Oral Ectoderm; EM = Endoderm Markers; OOE; Oral part of Oral Ectoderm; AOE = Aboral part of Oral Ectoderm. The top level (Primary Axis) represents a yet to identify (set of) pattern(s) that initiates the setting up of the primary axis.



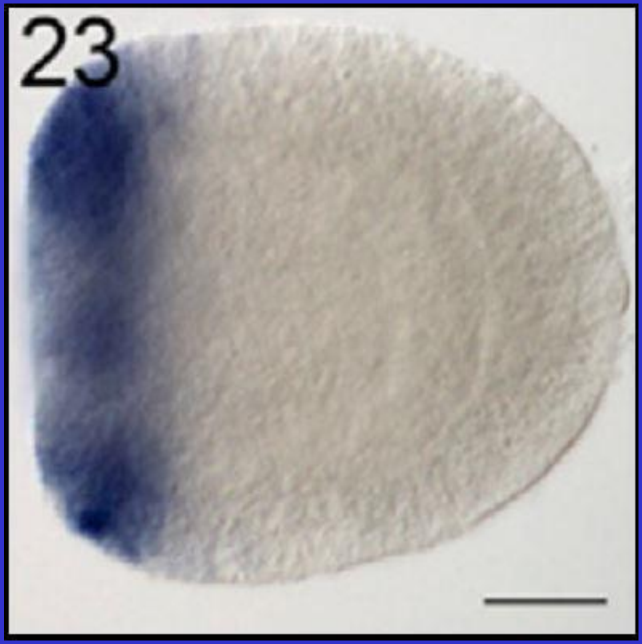
Bilateral bodyplan in animals

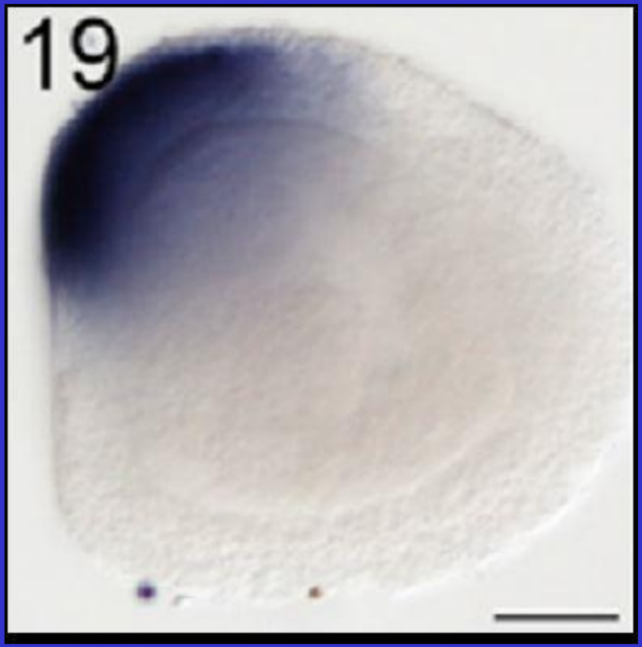


Genes involved in the specification of the second body axis (the directive axis) (Genikhovich et al., 2015), thin of fluid between ectoderm and endoderm transports molecules

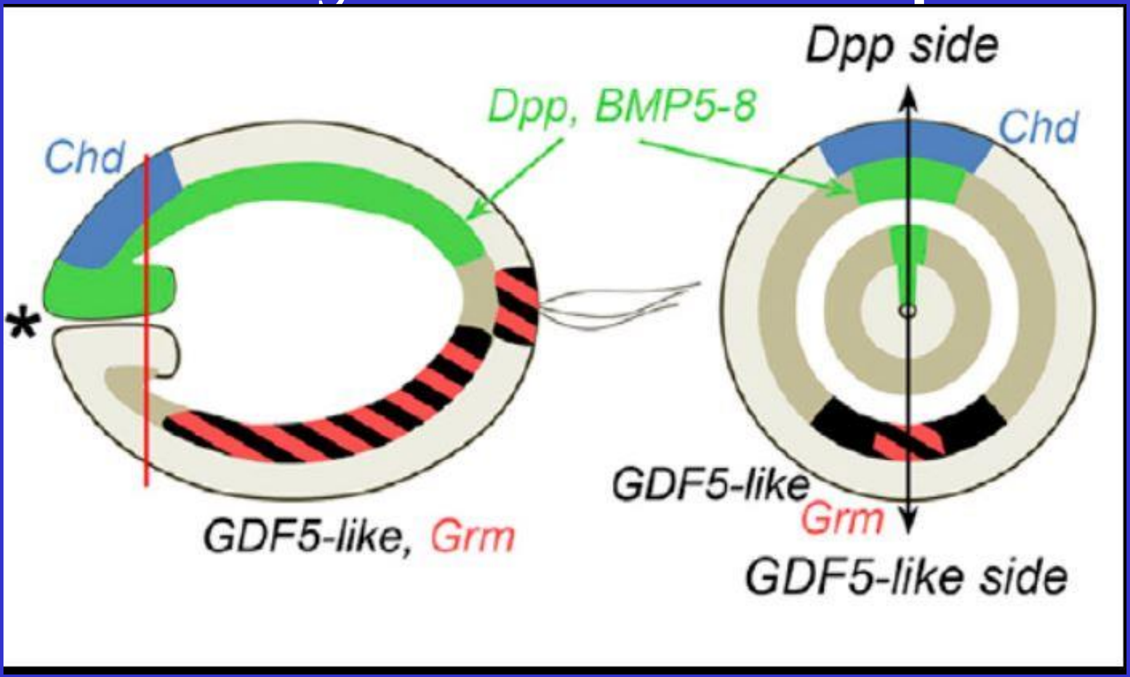


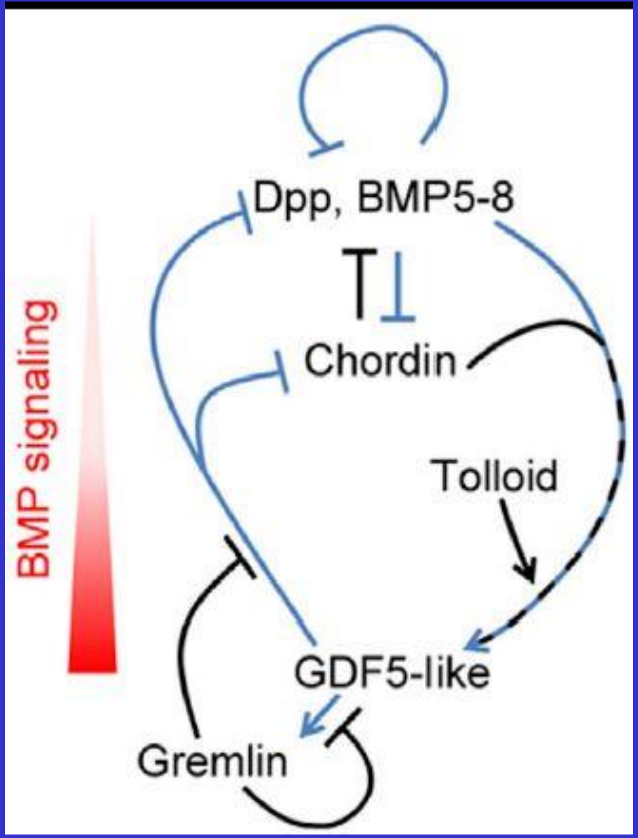
Genes involved in the second axis formation are first expressed symmetrically (chordin expression, Genikhovich et al. 2015)



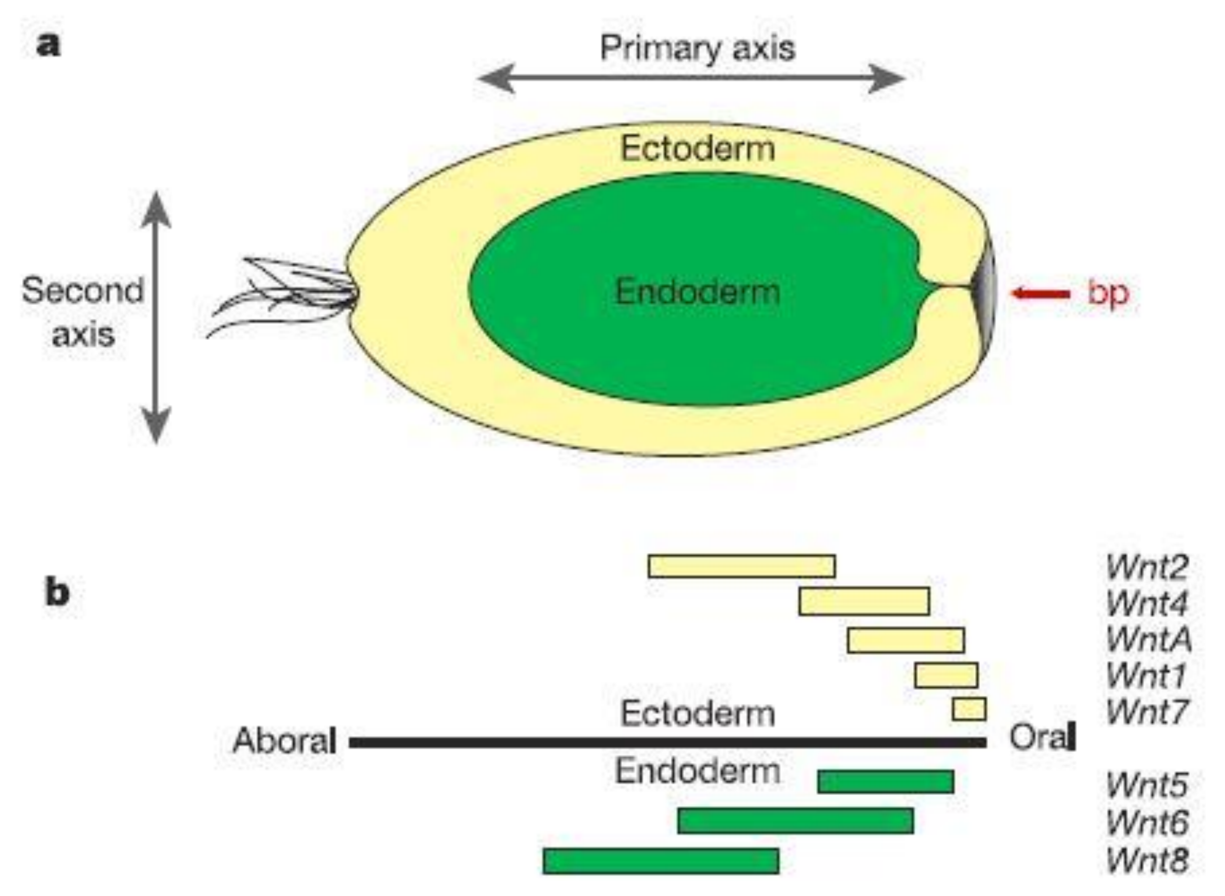


Proposed network (Genikhovich et al, 2015) assumes there is an asymmetric expression of BMP





``Segmentation" along the primary axis in *Nematostella vectensis*, diagram of 8 of the 11 expressed wnt pathways (Kusserow et al., Nature, 2005) in the planula larvae



Modelling Gene Regulatory Networks in space and time I

- Modelling and inferring gene regulatory networks in *Nematostella vectensis* , (Botman et al., Plos One, 2014; Abdol et al., Dev. Biol. 2017
- Modelling gene regulatory networks in *Nematostella vectensis* and symmetry breaking Vroomans et al., in prep)

Modelling Gene Regulatory Networks in Nematostella vectensis in space and time II: two approaches

- **Connectionist model**

Advantage we can infer the GRN from spatio-temporal data using global optimisation,

disadvantage: not suitable for modelling non-linear interactions (e.g. Hill exponent)

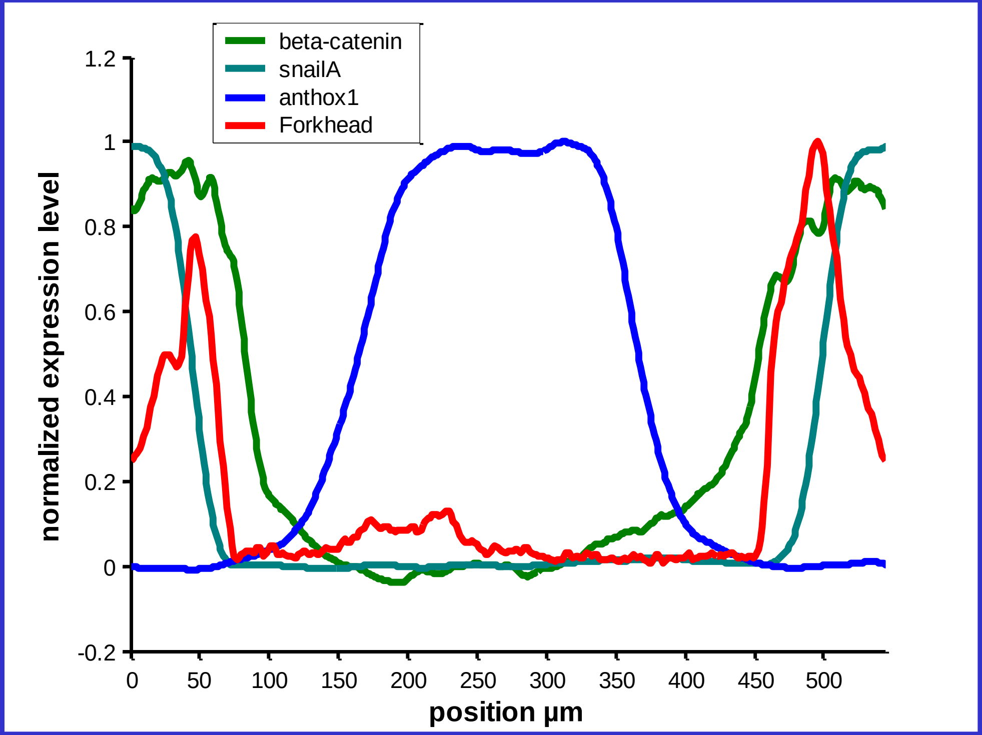
- **Modelling gene regulatory networks in using Hill equation based reaction diffusion equations**.

Advantage we can include more detailed knowledge about molecular interactions.

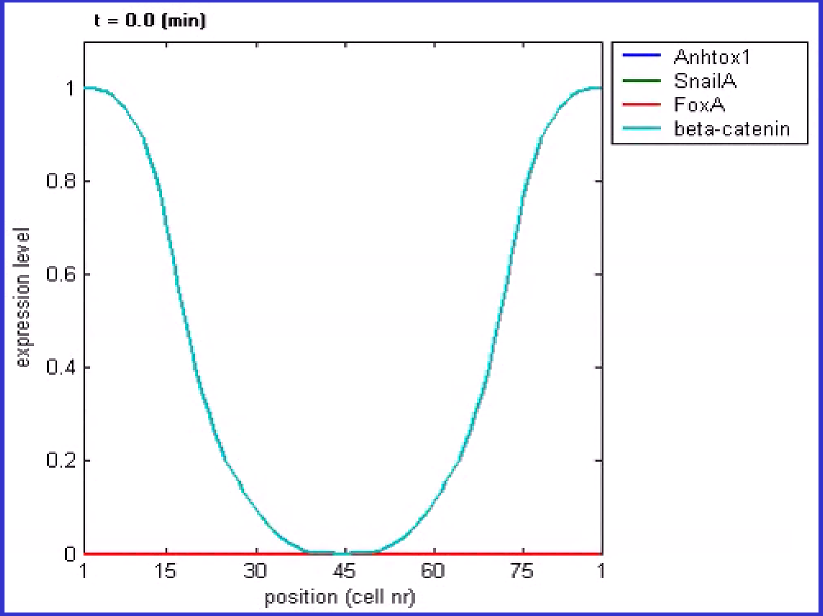
Disadvantage: inferring from expression data is challenging

Gene regulation during gastrulation in *Nematostella vectensis*

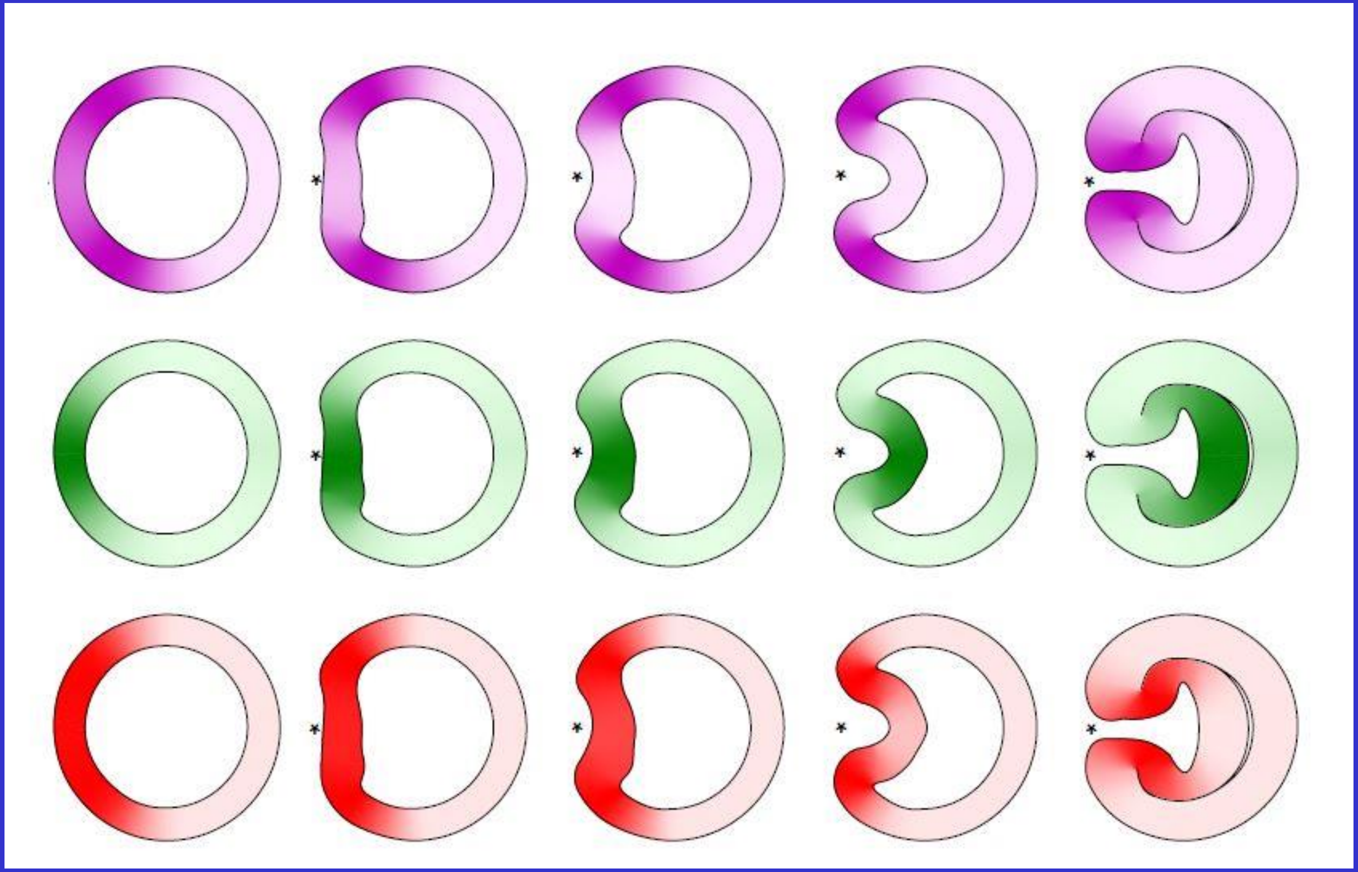
Quantified gene expression



Simulated gene expression



Spatio-temporal modelling of gene regulation in Nematostella vectensis (Botman et al., Plos One 2014; Abdol et al., Gene Expression Patterns / Developmental Biology, 2017)

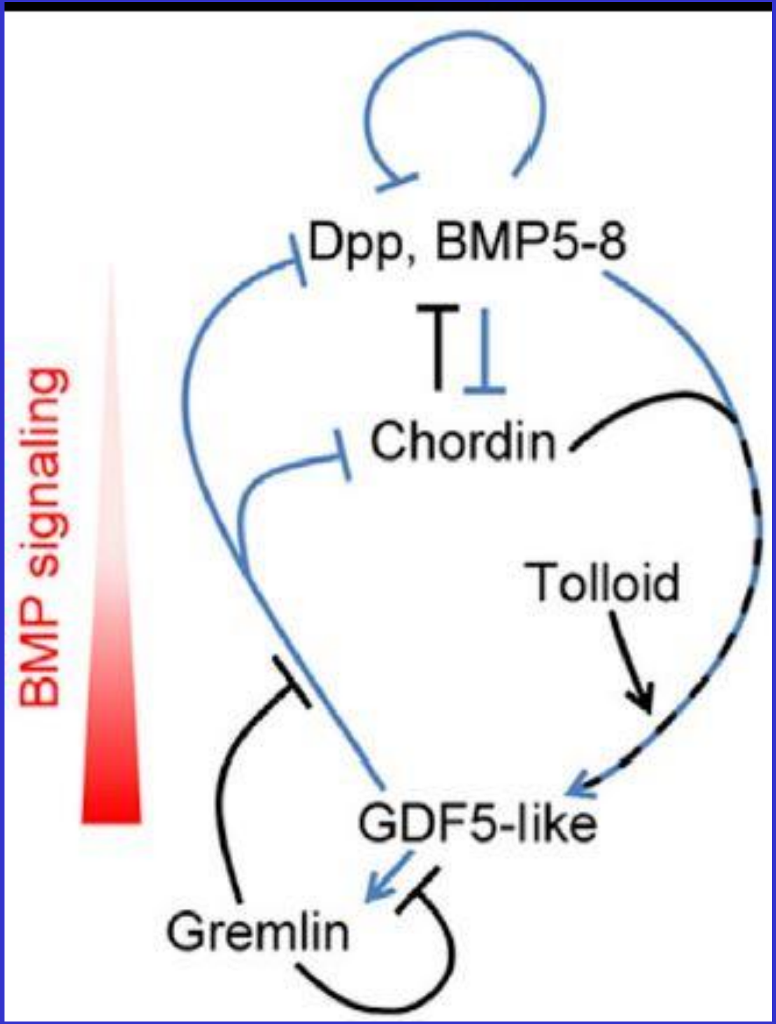


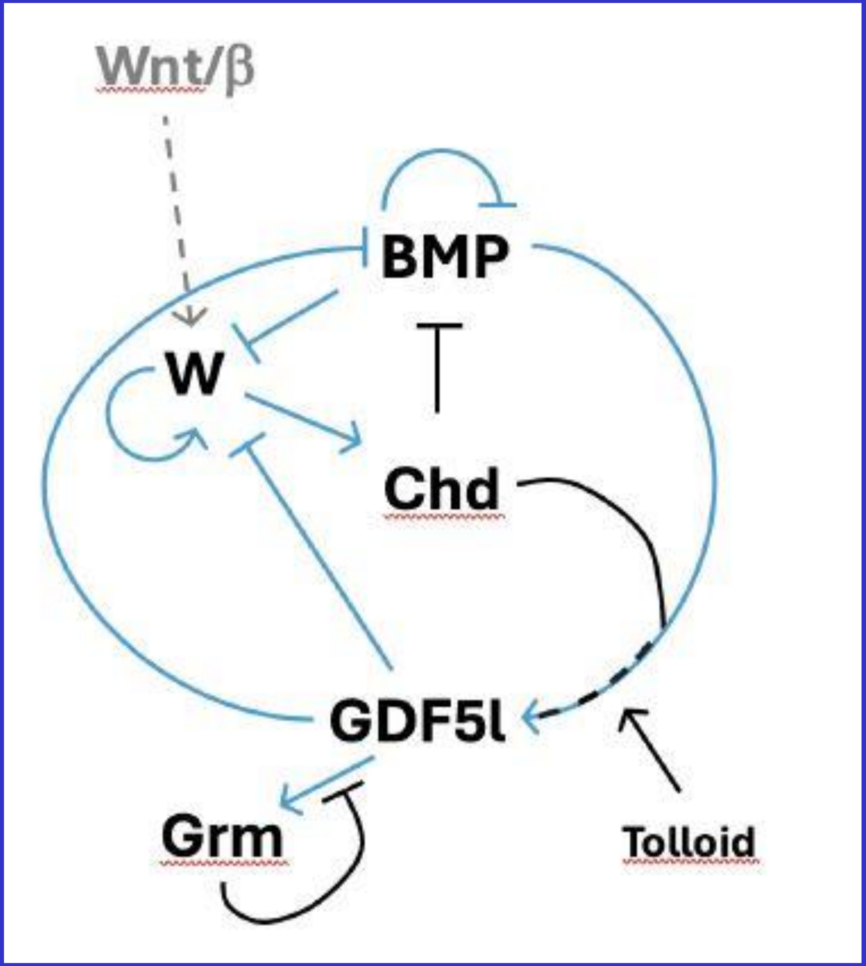
NvBra

snailA

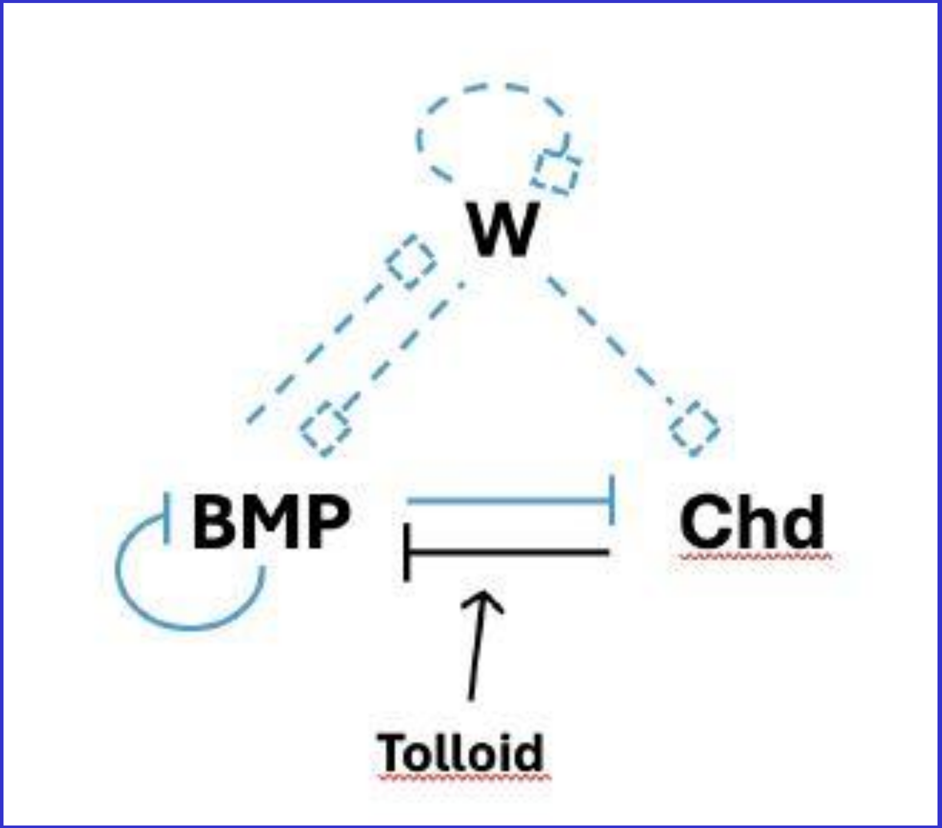
Foxa

Modelling the second axis formation: left the original proposal (Genikhovich et al. 2015), right our proposal , W is a hypothetical gene

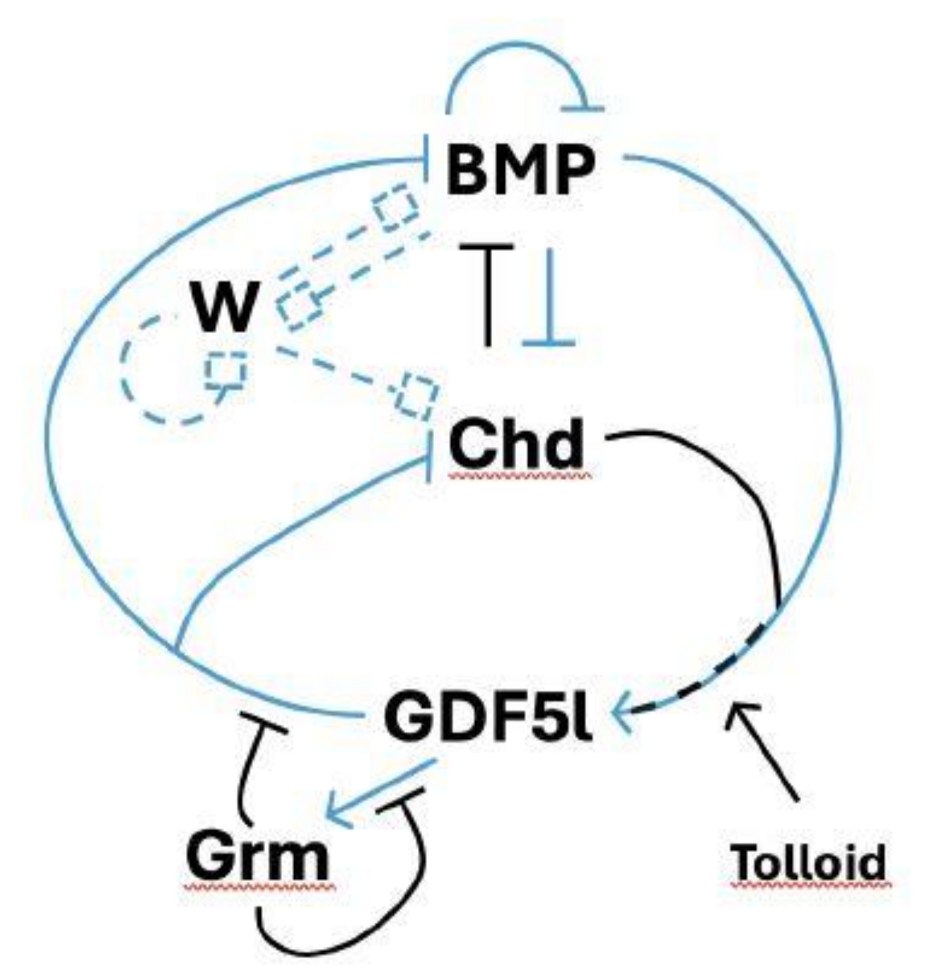




Simplified version of our proposed network (16 different possible networks)



Including template in the original network

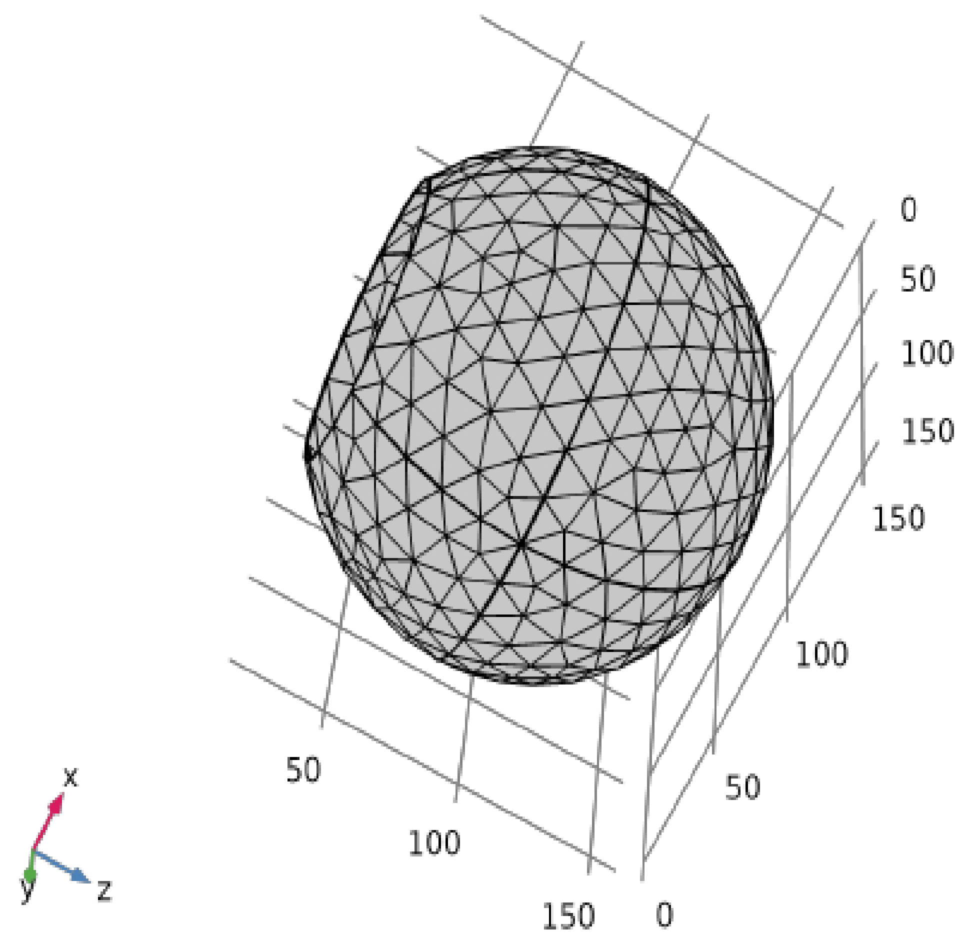


Spatial layout for Comsol simulation

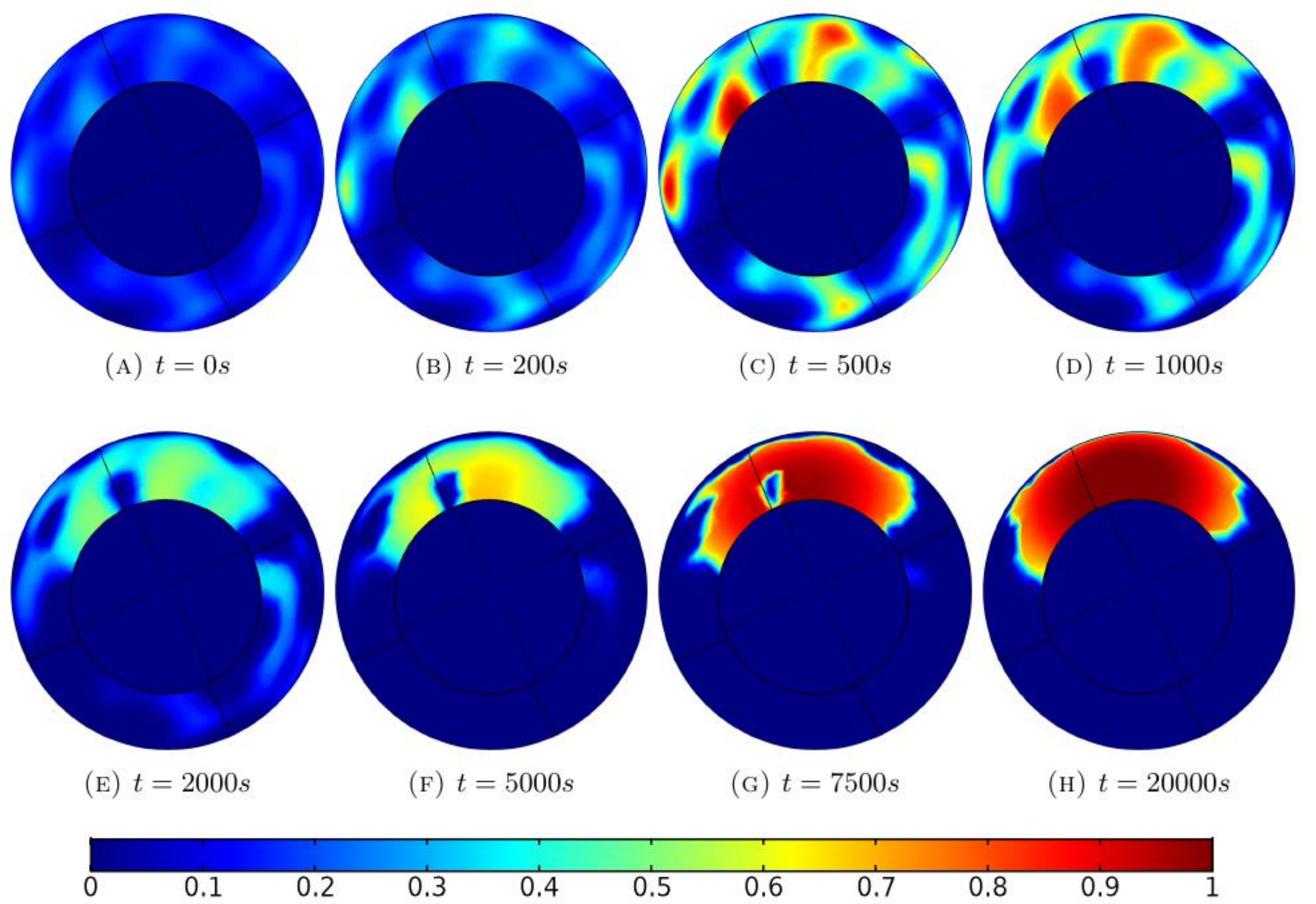
discretized through finite element method

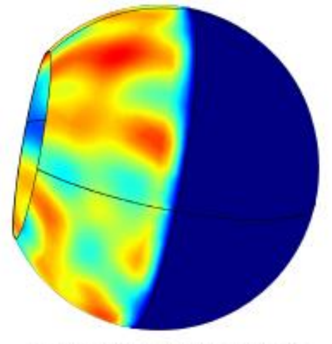
Implicit backwards differentiation

need a small timestep due to stiffness of equations



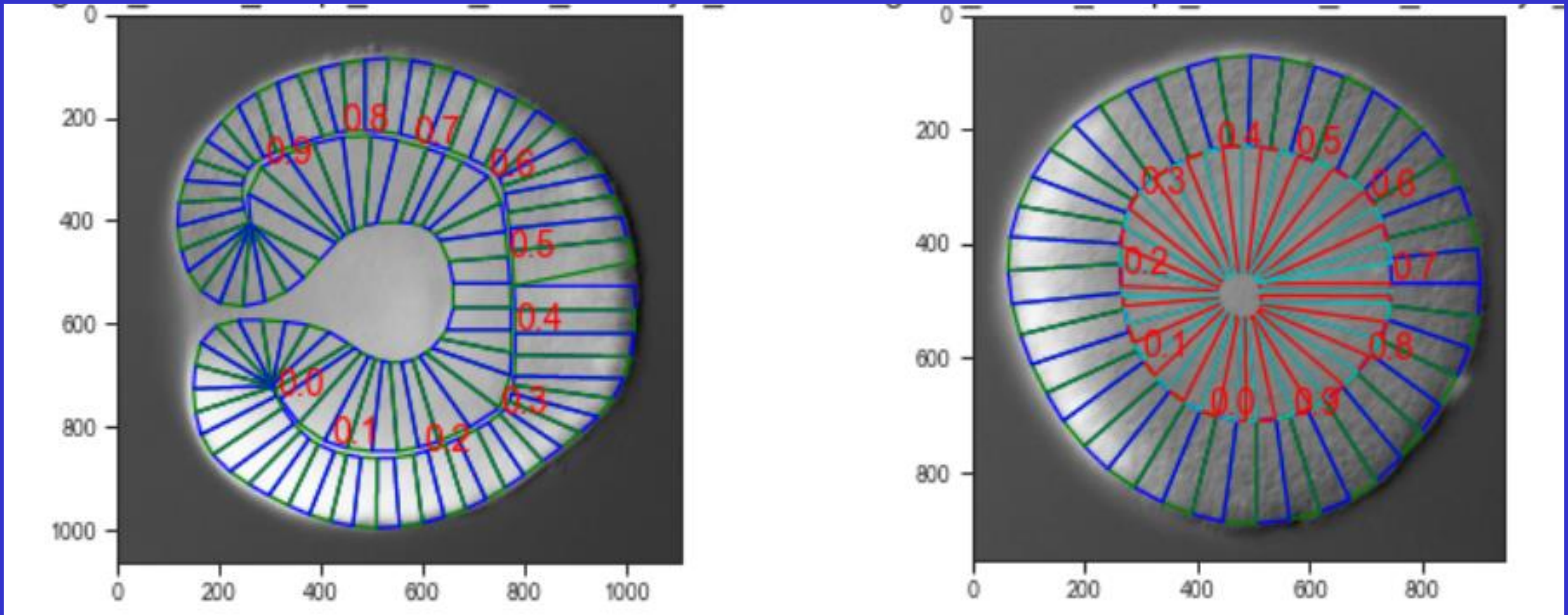
Extended model can break symmetry. Development of W expression in time. Self-activation random pertubations in W are amplified which in turn leads to stronger BMP signalling



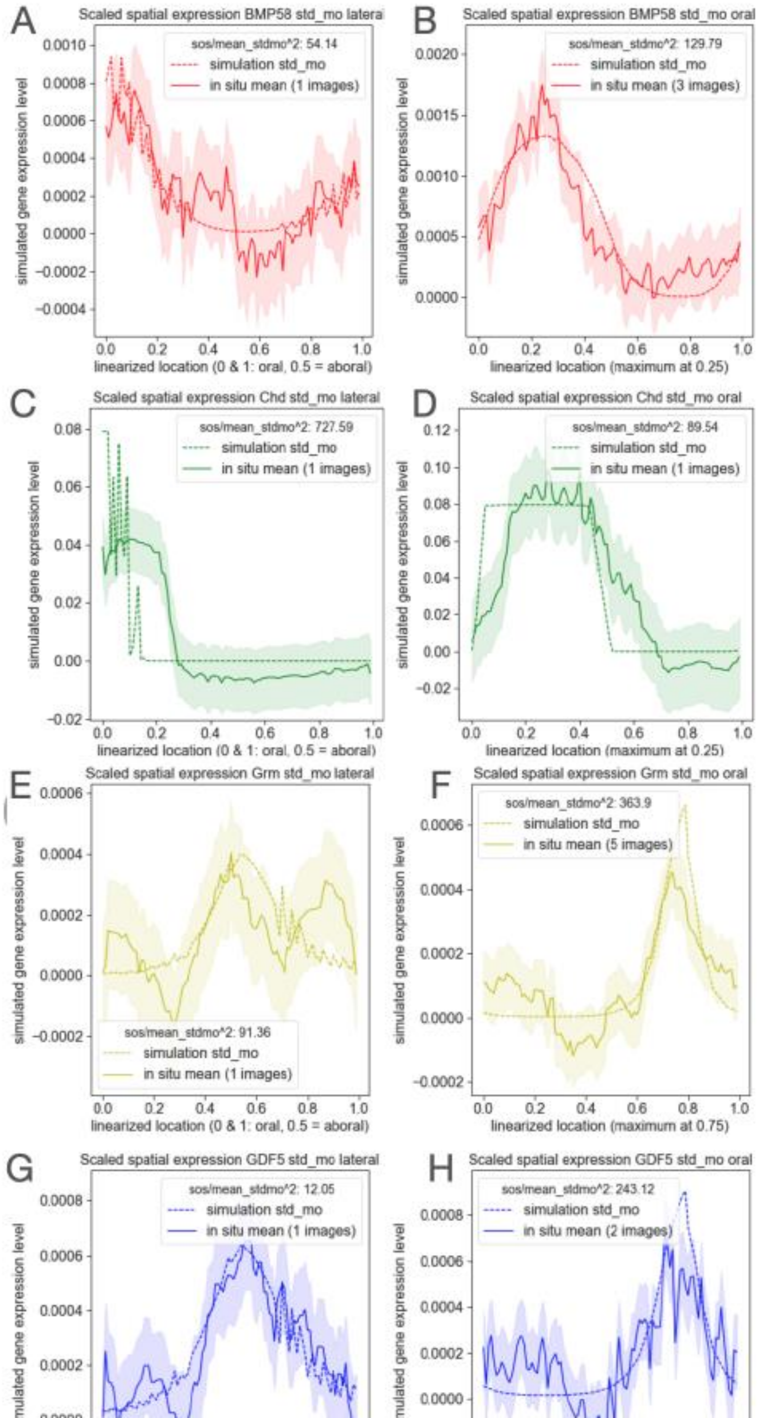


(C) Initial condition of W

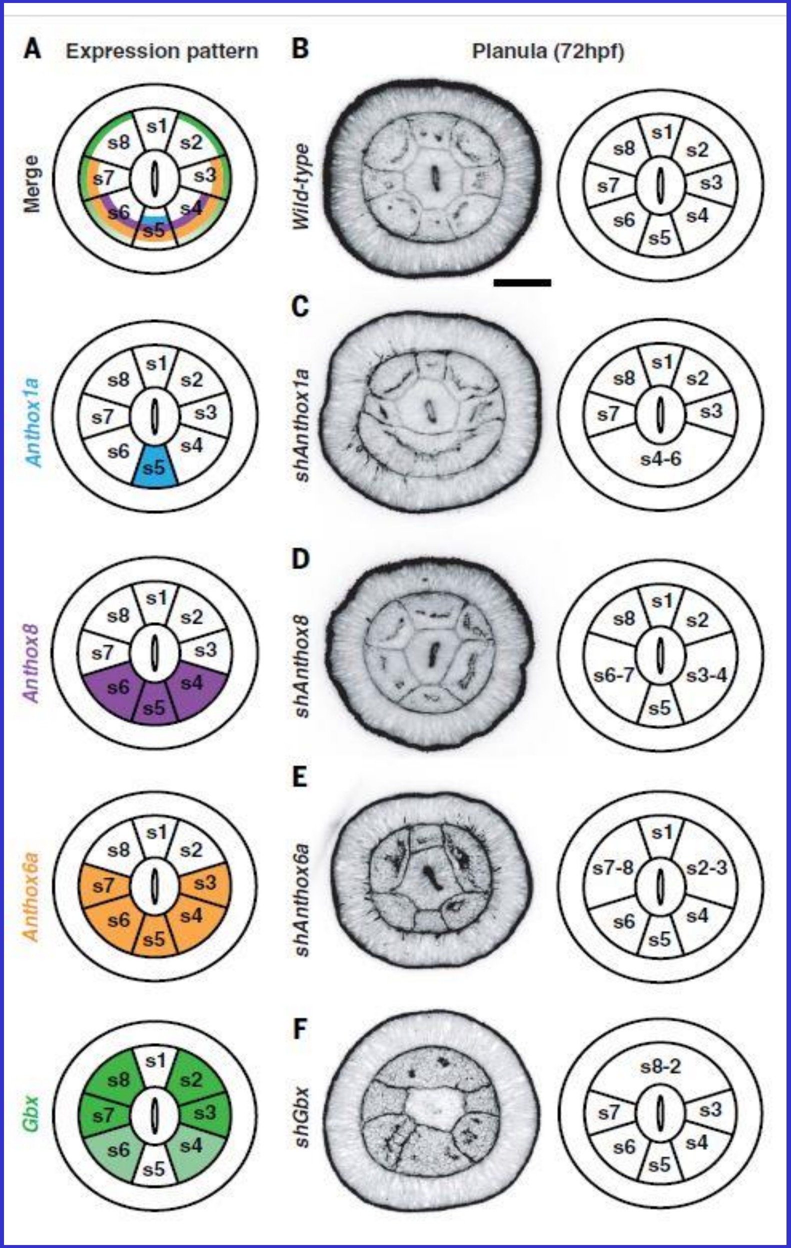
Quantify Expression Patterns
pseudocells to extract gene expression pattern
(Vroomans et al., in prep)



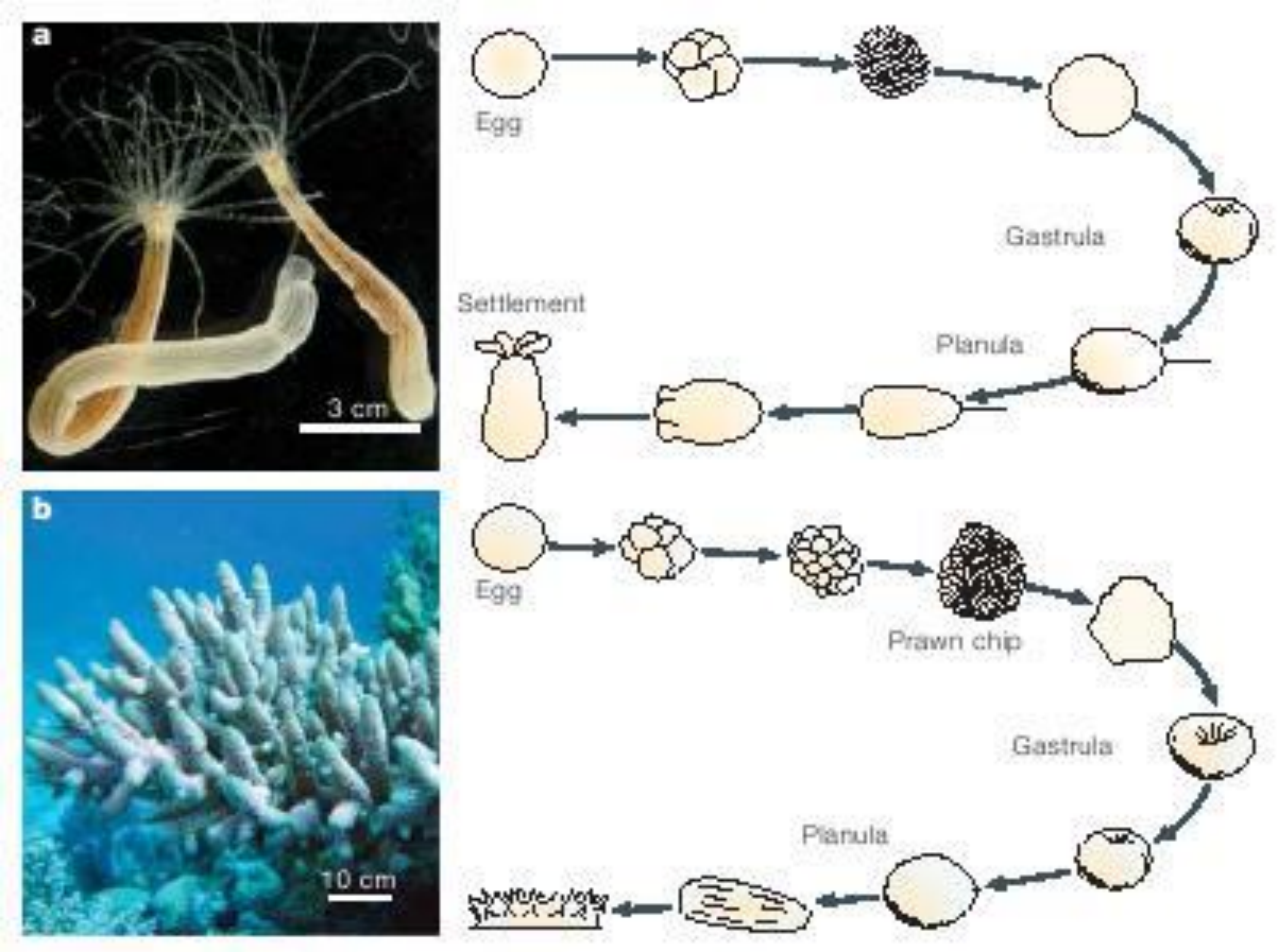
Simulated gene expression patterns match experimental data in wild type *Nematostella*



Development 8-folded symmetry in *Nematostella vectensis* (He et al., 2018)



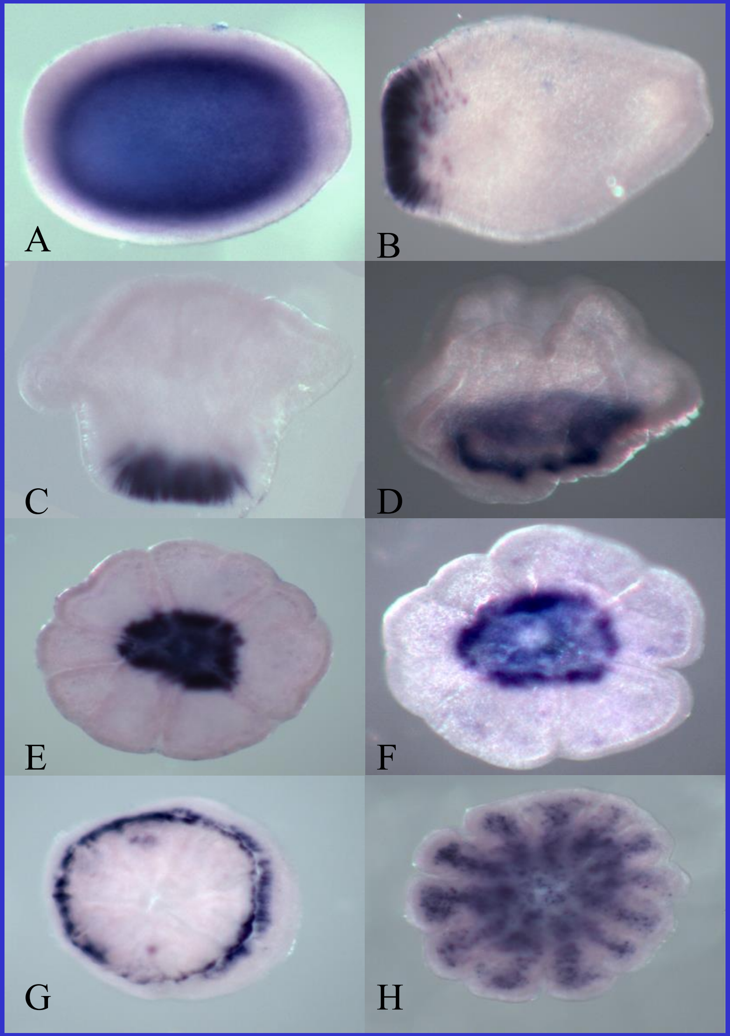
Nematostella vectensis (top) / *Acropora millepora* (bottom) (Ball et al., Nature Reviews Genetics: 567, 2004)



‘Pre-patterning of calcified structures by gene regulation in corals

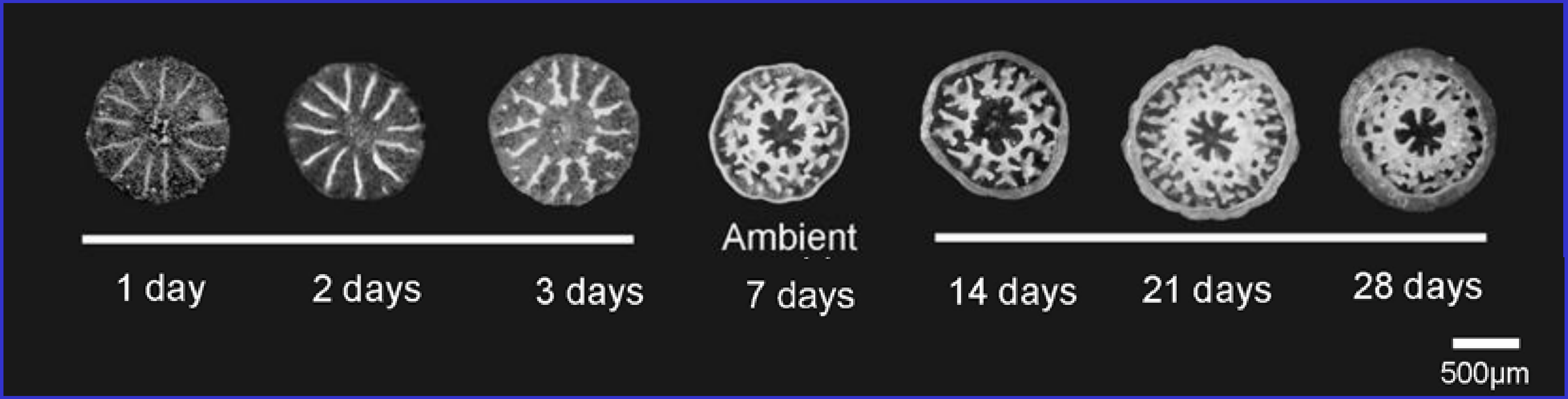
The scleractinian coral *Acropora millepora* (Great Barrier Reef Australia)

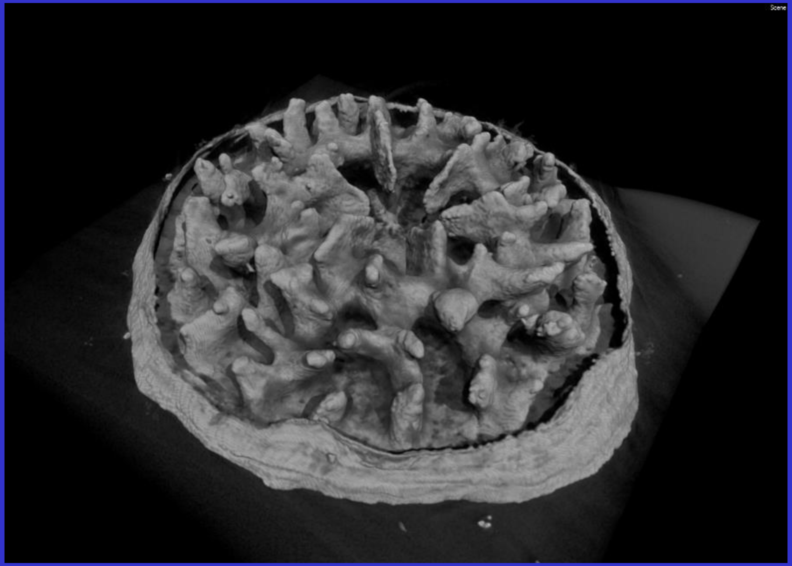
Development of a 6 (12)-folded symmetry in a coral larvae before settlement. Galaxin expression patterns in *Acropora millepora*: prepattern for calcification (after Reyes, 2009)



Am Galaxin-like

Larval Skeleton in the scleractinian coral Acropora Millepora with 6 (12-) folded symmetry (Chia-Miin, 2012)





Micro CT scan of a larval skeleton of
Acropora millepora

Conclusions and future work

- Model of the aboral axis and the second directive axis of body plan formation in *Nematostella vectensis*
- Model of spatio-temporal gene regulation of body axes formation, we can predict the outcome of perturbation experiments using morpholino’s
- In situ’s of Nematostella vectensis larvae show the formation of an 8-folded symmetrical pattern of mesenteries.
- In situ’s of Acropora millepora larvae show a six-(-12) folded pre-pattern indicating future calcification. The six (12) folded symmetry is found again in skeletons of larvae after settlement.
- Future work Modelling the emergence of an 8-folded symmetry in *Nematostella vectensis*

Modelling cells: from Sequences and consequences – (S. Brenner, Phil Trans Roy Soc B, 2010)

- ``Thus while the genome sequence is central, it is a level of abstraction which is too cryptic to be used for the organization of data and the derivation of theoretical models. Proposals to base everything on the genome sequence by annotating it with additional data will only increase its opacity. The correct level of abstraction is the cell. The cell is the fundamental unit of structure, function and organization of living systems—something we have known for 180 years.’’

Models of cells

(see also introduction PhD thesis C. Tamulonis, 2013)

- Continuum models
- Cell-based models

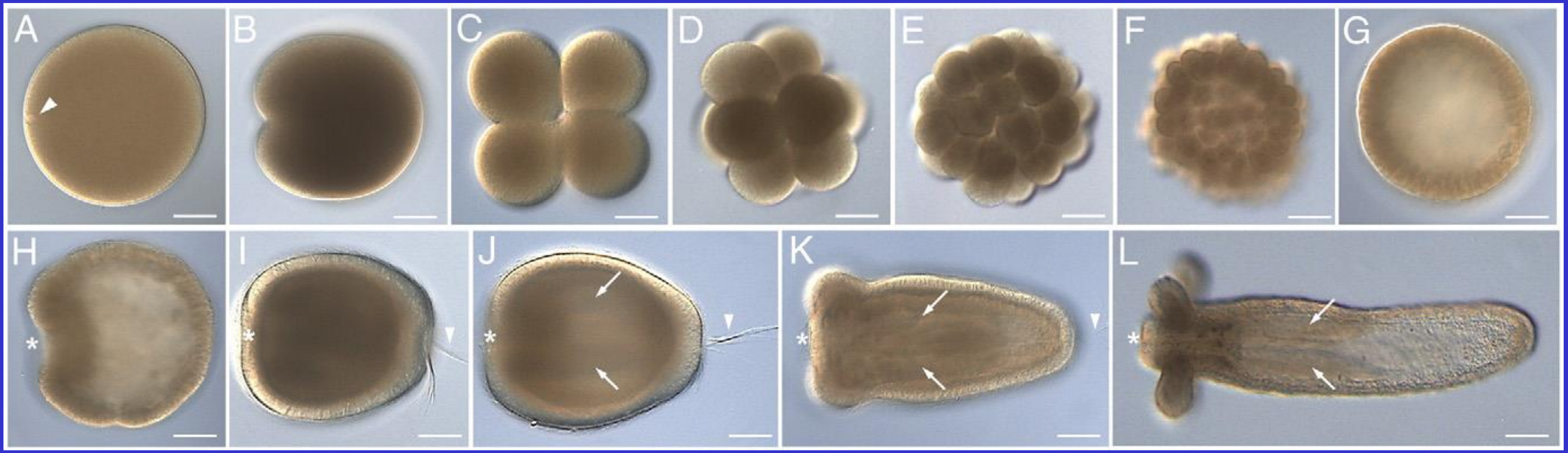
Cell-based models (a selection)

- Lattice-based models:
  a) Cellular Potts Model
- Lattice-free models:
  a) cells as spheres and ellipsoids
  b) cells as polygons
  c) cells as complex polygons (cell-boundary model)

- Cell-based modelling of gastrulation in sea anemones and jelly fish (C. Tamulonis, et al., Developmental Biology, 2011; *van der Sande et al. Dev. Biol., 2020;* R. Dries K. Renders and J.A. Kaandorp, submitted)

Nematostella vectensis developmental stages

Lee 2007



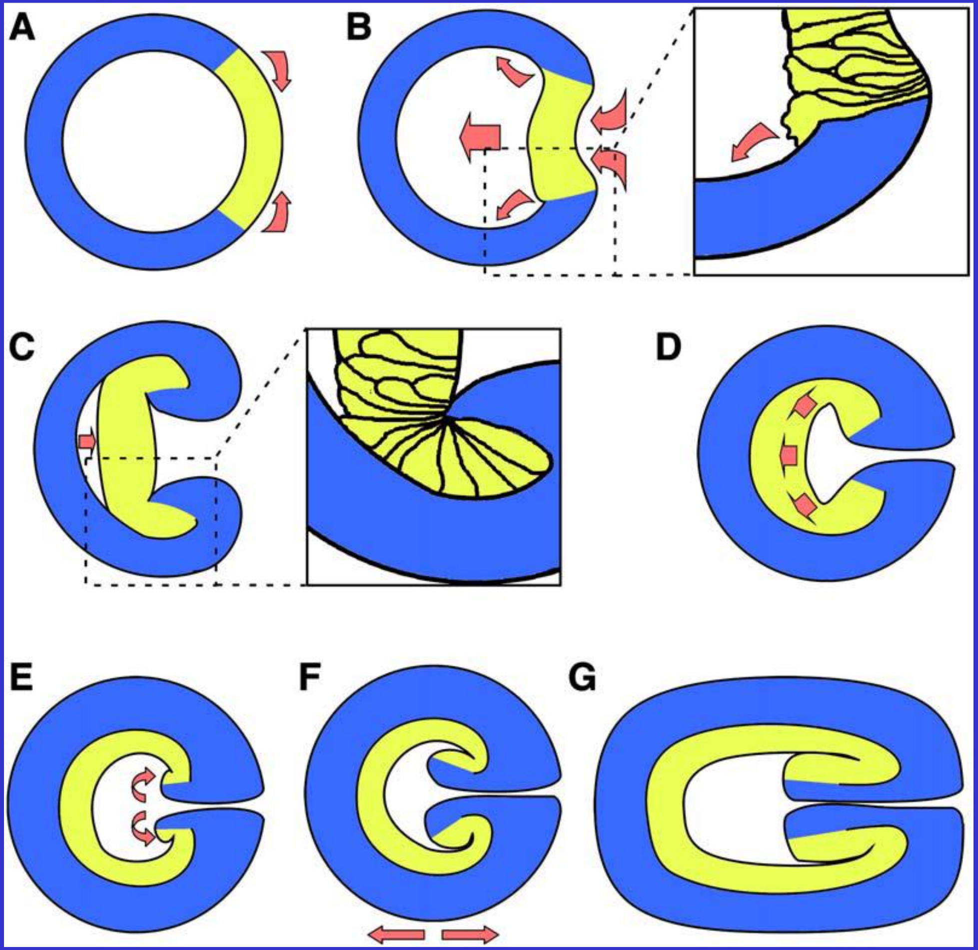
(**A**) egg
(**B**-**F**) cleavage to prawn chip (11 cleavage stage)
(**G**) Blastula
(**H**) Gastrula

(**I**) planula with apical tuft
(**J**) planula mesenteries grow
(**K**) Polyp early tentacle
(**L**) Polyp

Nematostella gastrulation

- A Apical constriction
- B Invagination or ingression
- C Endoderm zipping against ectoderm, blastocoel vanishes
- D Endoderm thinning
- E Invagination of pharynx
- F Elongation of planula
- G Planlula stage

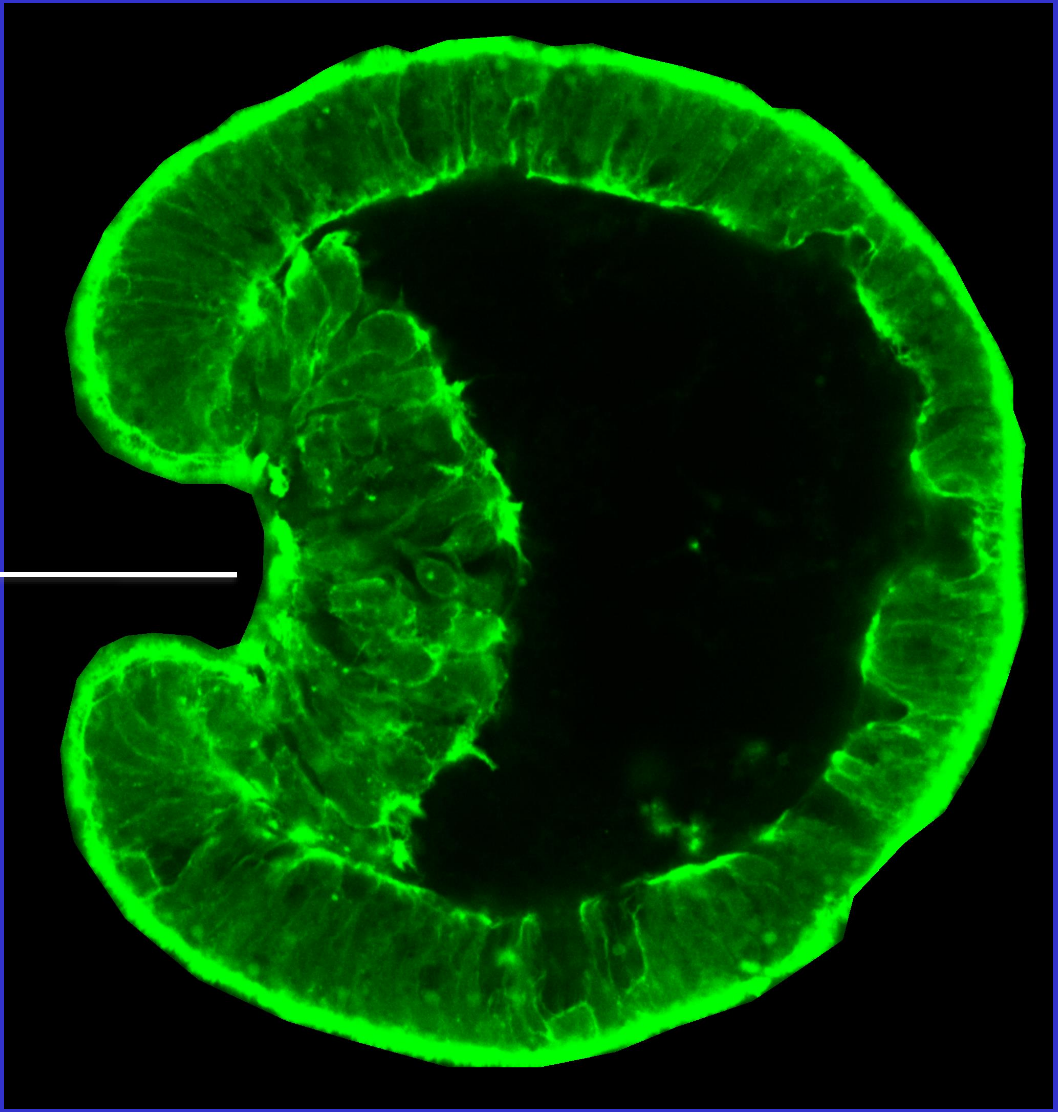
Yellow is endoderm
Blue is ectoderm



Magie 2007

Nv gastrulation V

Invagination

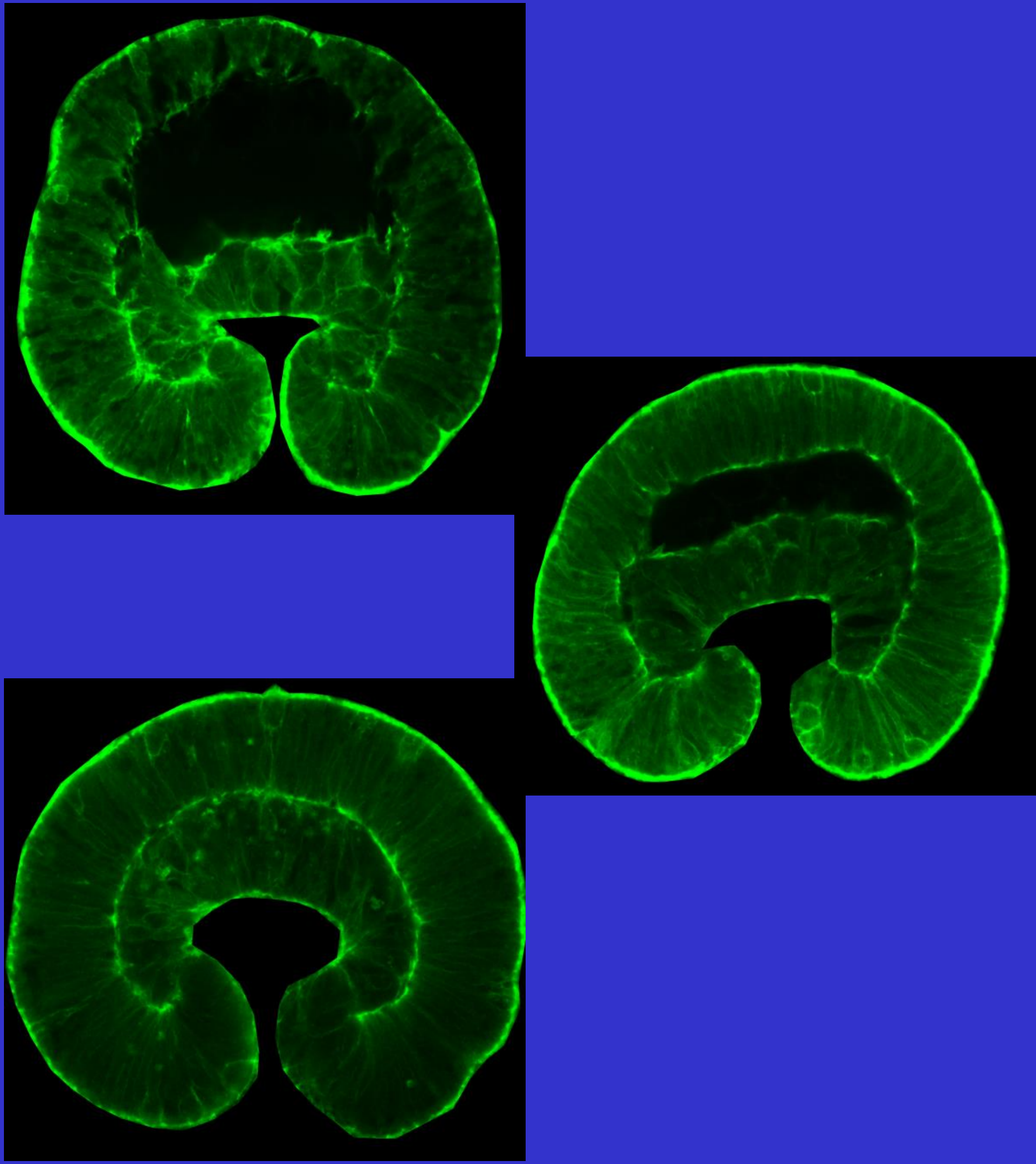


Apical constriction also induces invagination

Nv gastrulation VI

Zipping

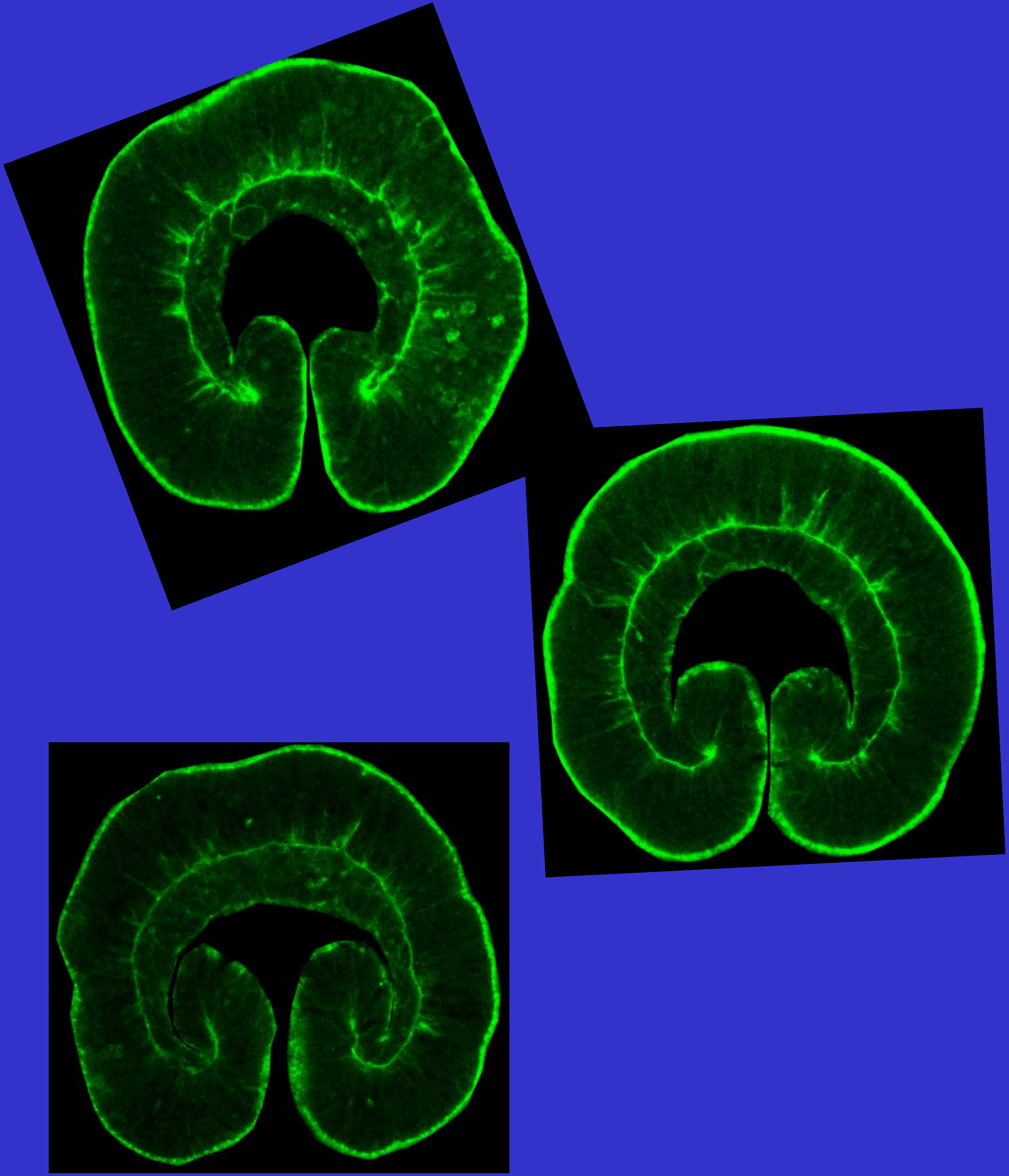
Zipping of the endoderm and ectoderm occurs via cell protrusions that pull the two layers together.



Nv gastrulation VII

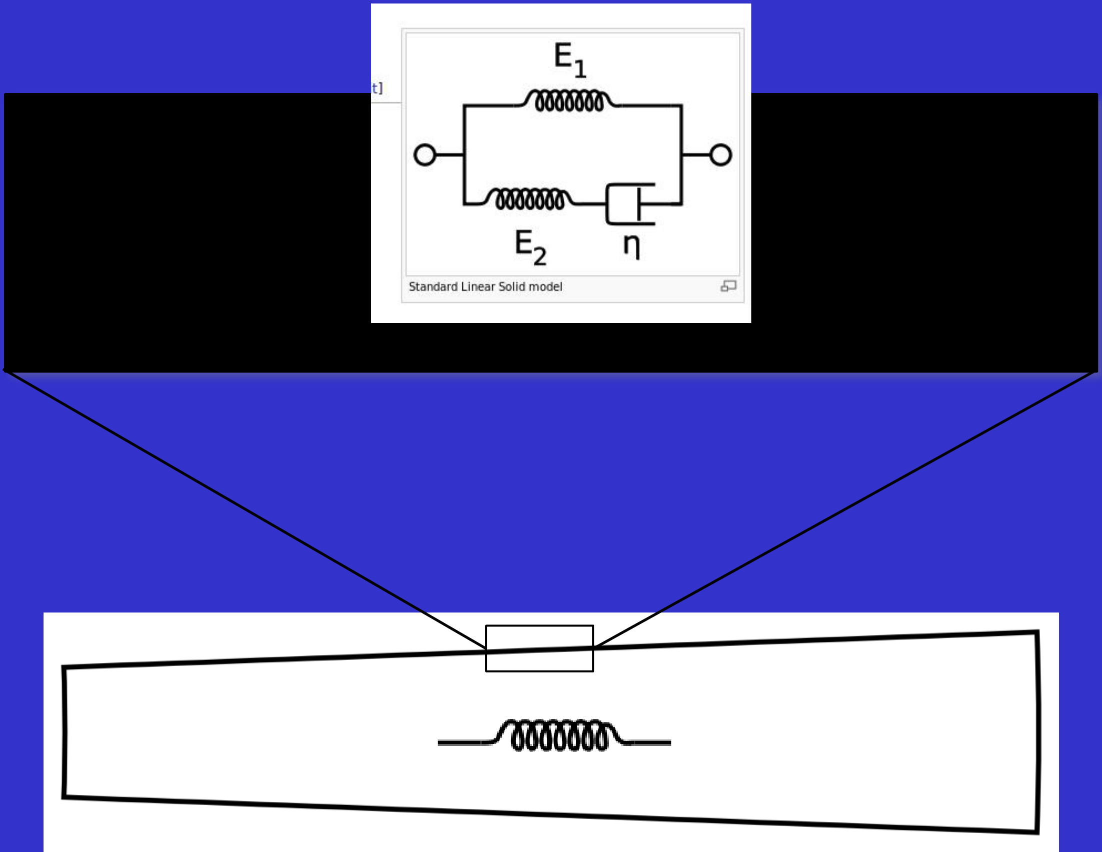
Thinning & Involution

After the endoderm has been internalized , the ectoderm involutes, forming the pharynx, as the endoderm thins.



Physical cell model

- Each edge is loaded with a viscoelastic element
- Elastic element restrains the cell area
- The dynamics of the model are driven by simple Newtonian mechanics, running a simulation step consists of determining the forces acting on each vertex and the resulting system of differential equations is solved using the Velocity Verlet numerical integration method



Intermezzo Cell-Based modelling: dynamics I

- The dynamics of the model are driven by simple Newtonian mechanics and the position of each vertex, $\mathbf{r}_{c,i}$ is governed by the equation:

$$m_{c,i}\frac{d^2 r_{c,i}}{dt^2} = F_{c,i} - \eta_{c,i}\frac{dr_{c,i}}{dt} \quad c = 1,\ldots,87 \quad v = 1,\ldots,84$$

- Where $\mathbf{F}_{c,i}$ is the total force acting on the vertex, $m_{c,i}$ and $\eta_{c,i}$ are the mass and the damping parameter of the vertex.
- All the processes in the model are described in terms of vector forces. Running a simulation step consists of determining the forces acting on each vertex and solving the resulting system of differential equations is solved using the Velocity verlet numerical integration method with timestep .

Intermezzo Intermezzo Cell-Based modelling: springs II

- Each edge of every cell is loaded with a spring that controls its length by exerting a restorative force proportional to the strain

$$F = k\frac{l - l_0}{l_0}$$

- Where k is the spring stiffness, l is the edge length and l_0 is the spring’s rest length

Intermezzo Intermezzo Cell-Based modelling: Cytosol III

- The area of a cell is given by the standard formula for the area of a polygon

$$-\frac{1}{2}\sum_{i=1}^{84} r_i \times r_{i+1} = -\frac{1}{2}\sum_{i=1}^{84} x_i y_{i+1} - x_{i+1} y_i$$

- The inner contents of a cell are assumed elastic with energy

$$E = \frac{1}{2} k_V \left(\frac{A - A_0}{A_0} \right)^2$$

- where *A* is the area of the cell, *A0* is the equilibrium area of the cell (equal to the initial area of the cell) and K_A is the stiffness of the inner area.

Intermezzo Intermezzo Cell-Based modelling: Forces IV

- Contact forces are defined between edge-vertex pairs
- Filopodia: long range adhesive mechanism

Nematostella vectensis gastrulation modelling goals

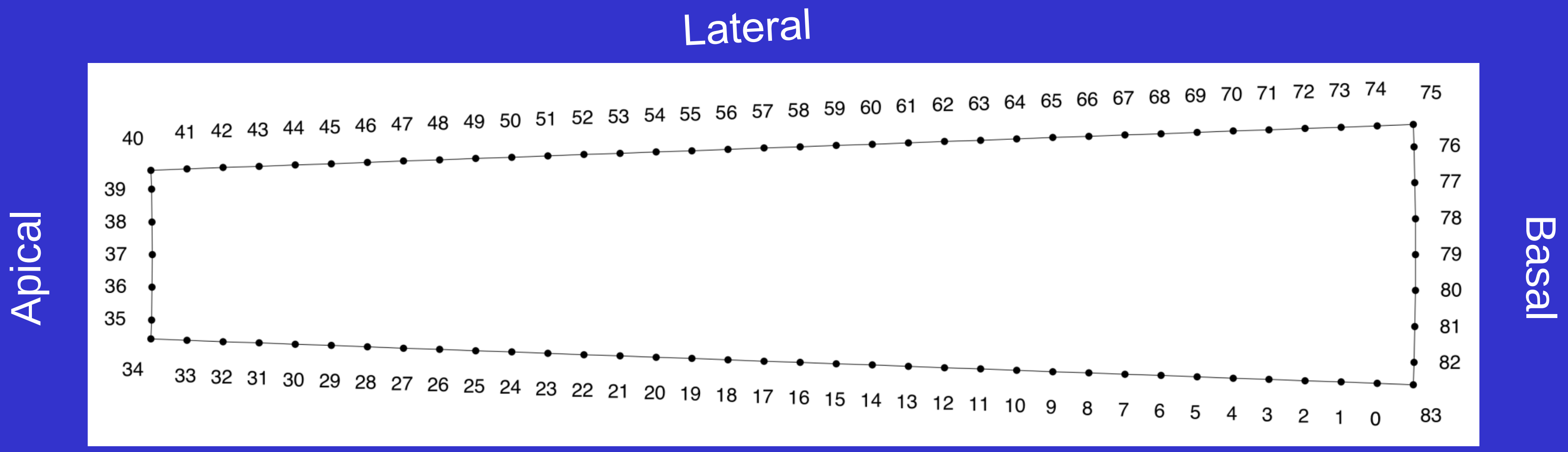
- Better understand the role of the individual processes in the collective gastrulation process

- Understand gastrulation variability through parameter variation

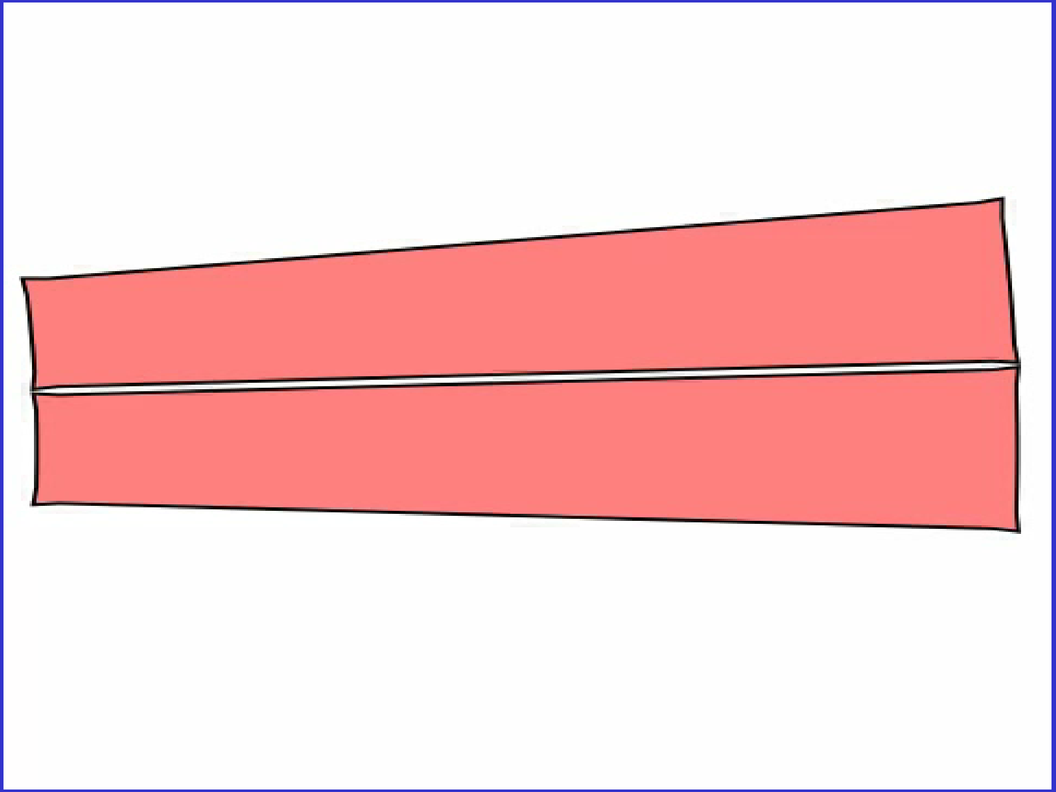
- Understand why gastrulation in *Nematostella vectensis* is so robust despite high variability

Cell representation

- Cell boundary represented as a detailed polygon
- Polygon is defined as a sequence of points
- Differential properties across the boundary, e.g. apical region may be stiffer than the baso-lateral region



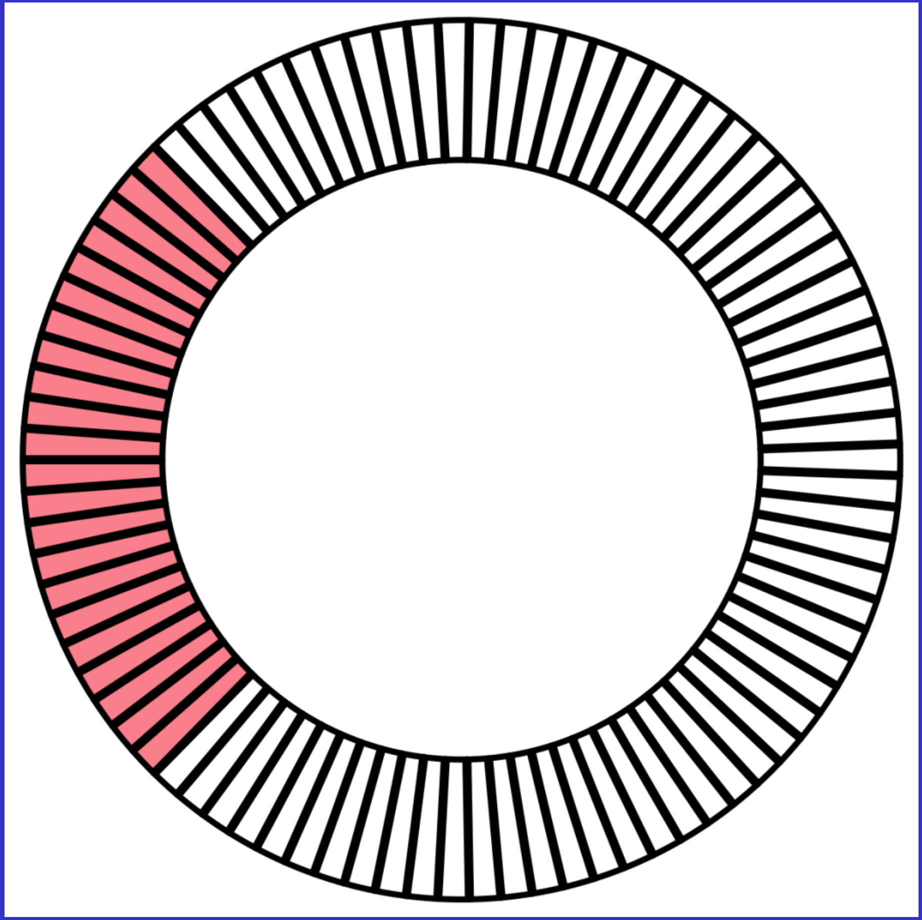
Cell adhesion



- Cell edges may express "adhesion molecules"
- When a "sticky" vertex comes within range of another sticky edge, the vertex adheres to the edge
- Adhesion junctions are dynamic and can turnover

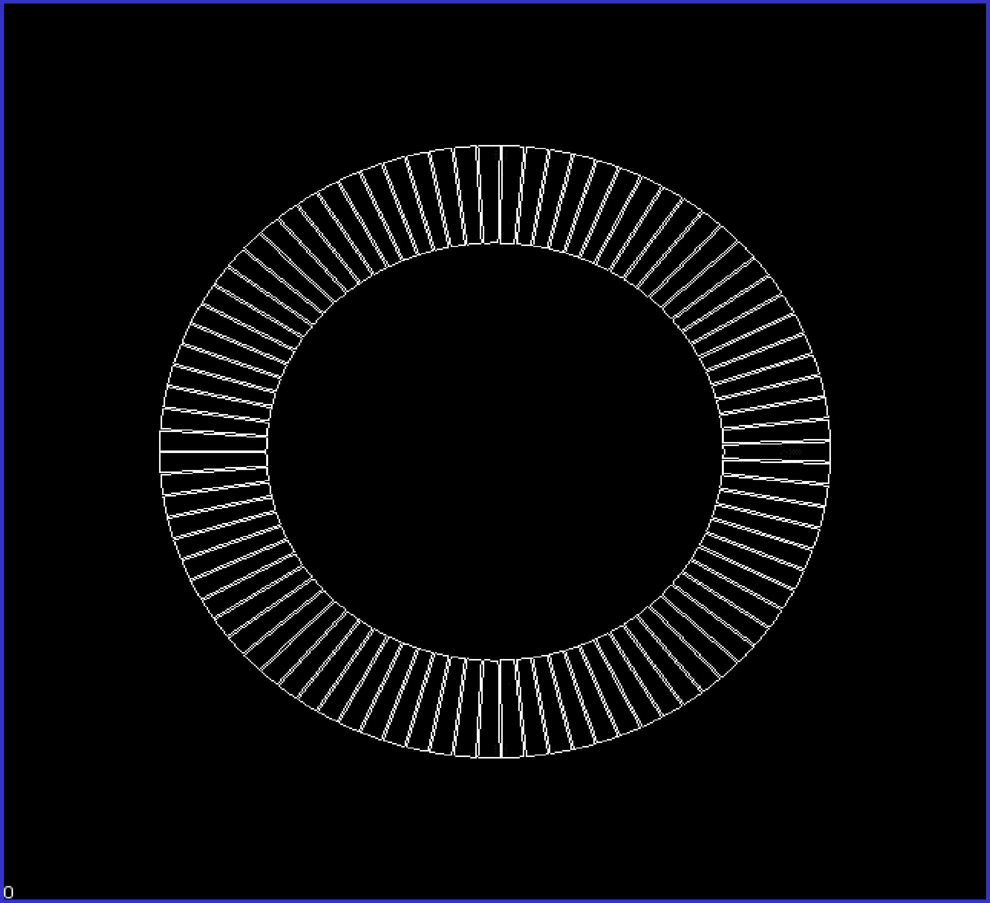
Blastula

- Blastula composed of 87 cells of equal size
- Cells are linked apically by an edge
- Differentiated into pre-ectoderm and pre-endoderm
- Pre-Ectoderm
  - ~75% of total number of cells
  - Epithelium
  - Cells express adhesion molecules all over their membranes
- Pre-Endoderm
  - Cells do not express adhesion molecules
  - Cells constrict their apices



Invagination

Emerges from apical constriction of the cells



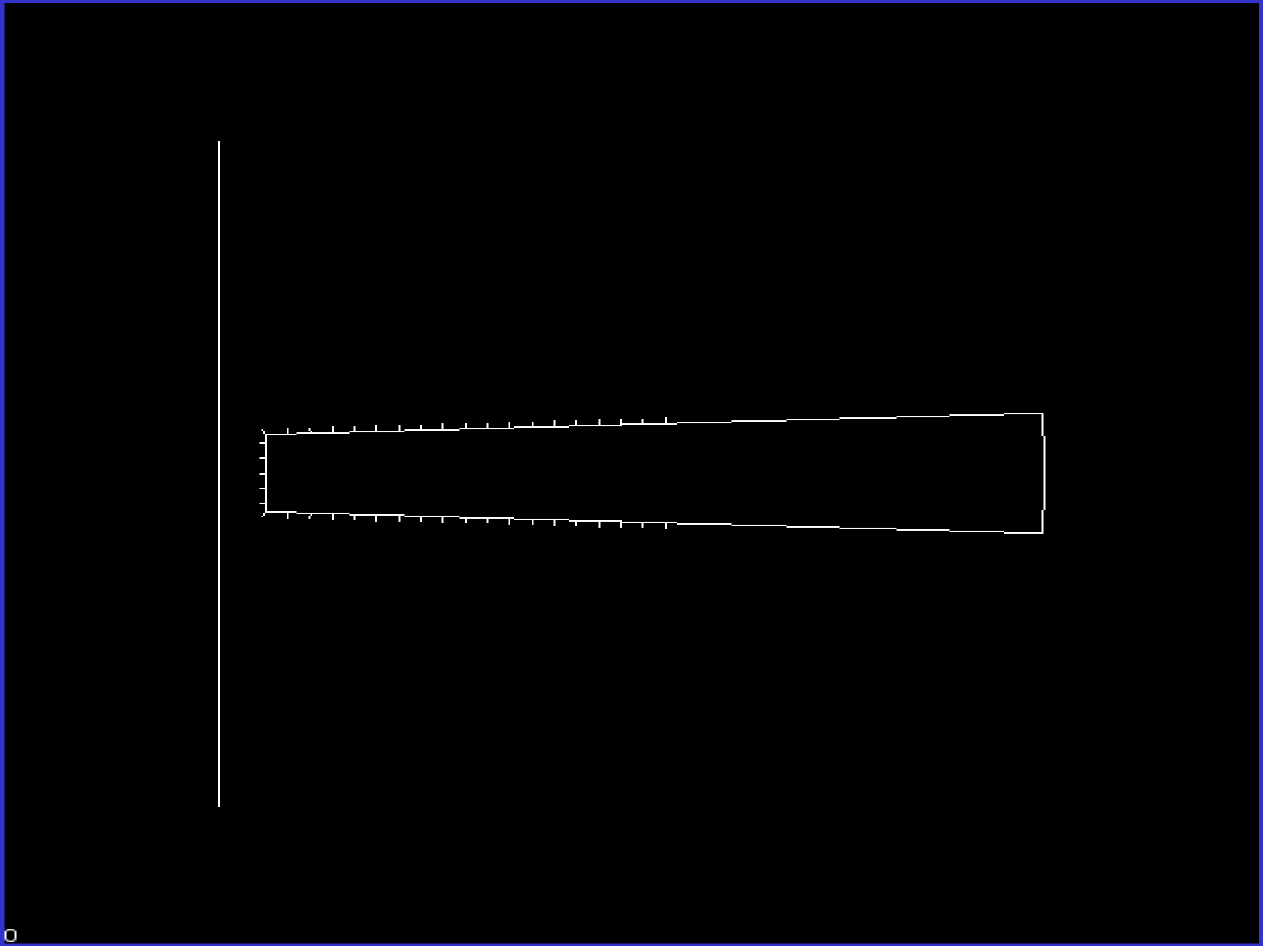
Filopodia

Placed at the basal – lateral portion of the pre-endodermal cells

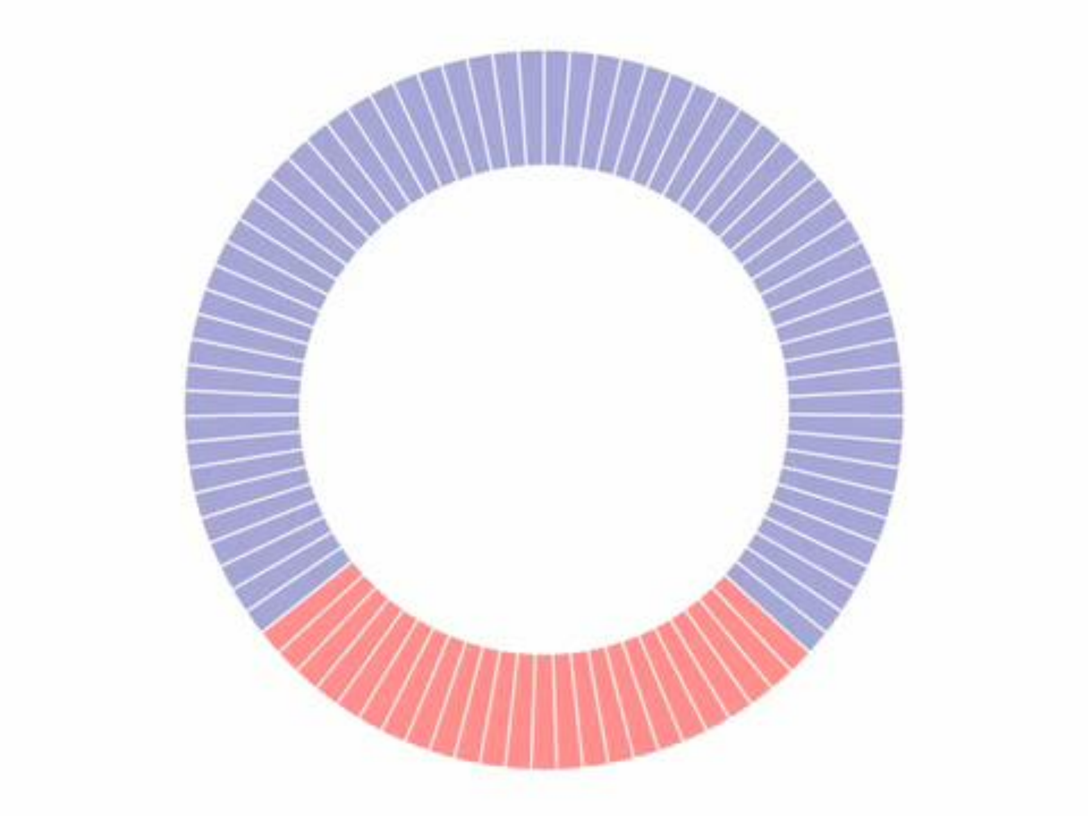
Modeled as edges which protrude from the membrane

Apex of the filopodia is "sticky"

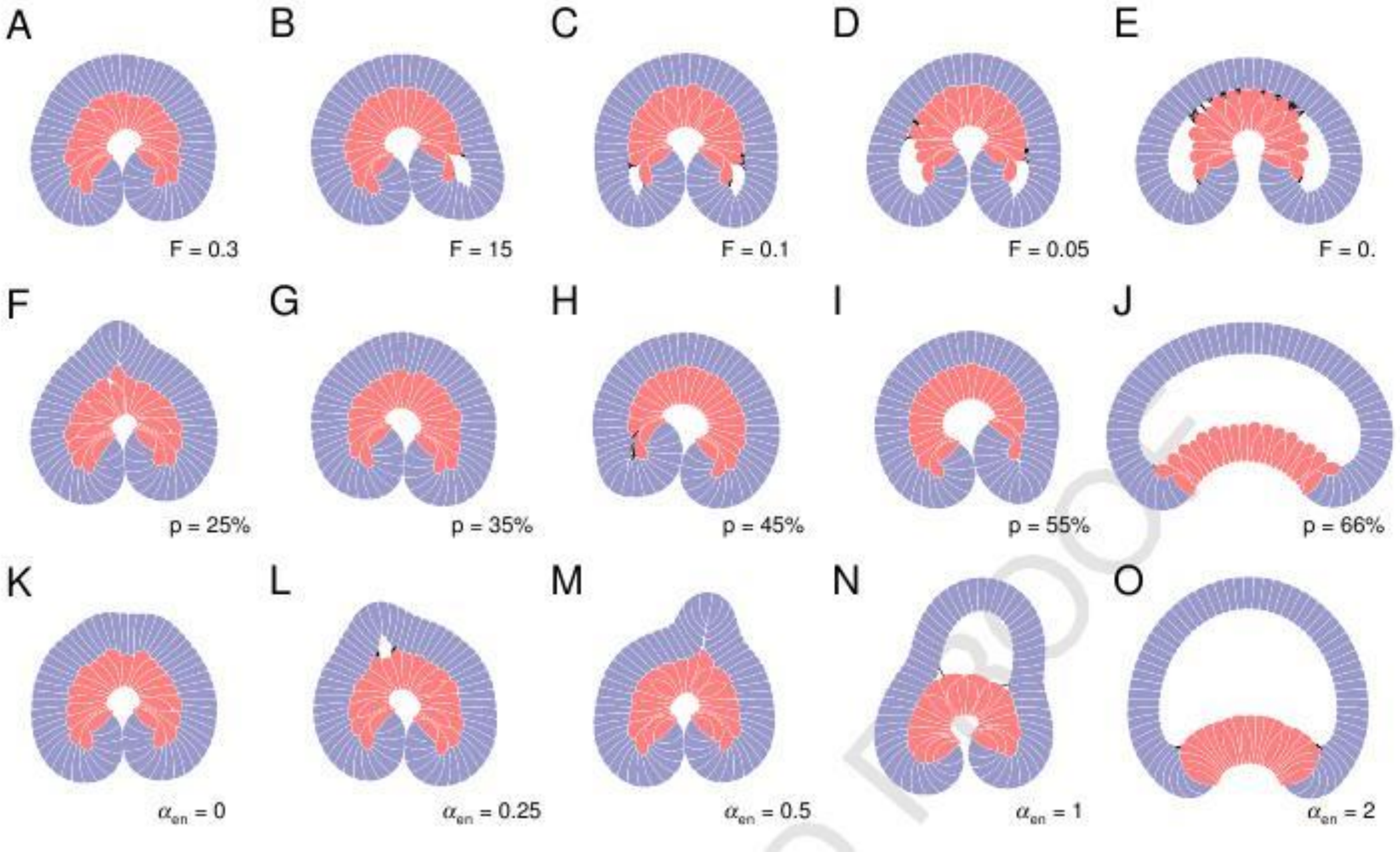
Filopodia edges are loaded with springs that "reel" the apex in as the spring shortens



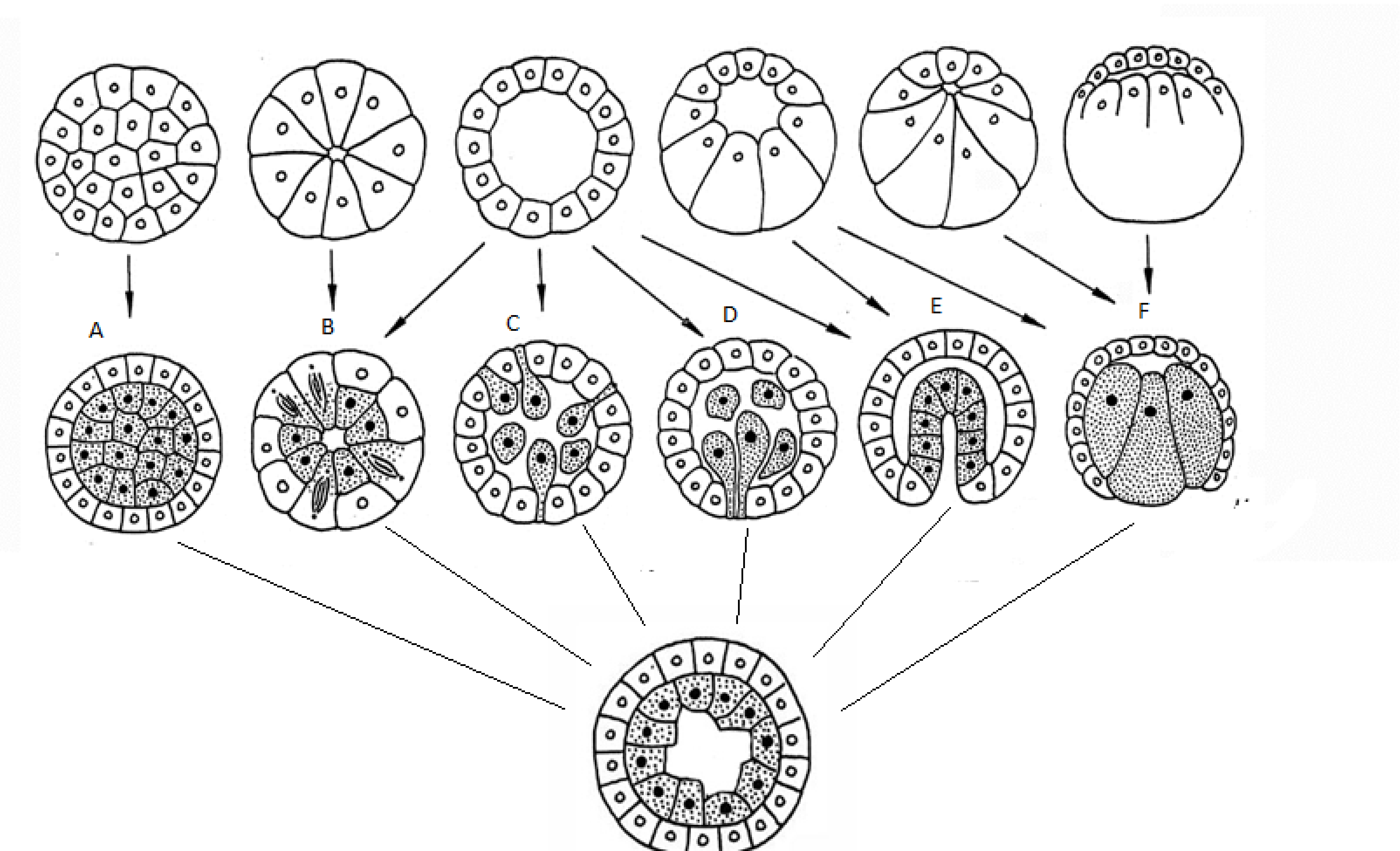
Cell-based modelling of gastrulation (C. Tamulonis, et al., Developmental Biology, 2011)



Parameter variation Generating “morphospaces” in order to better understand the contributions of each parameter to the final configuration of the blastula



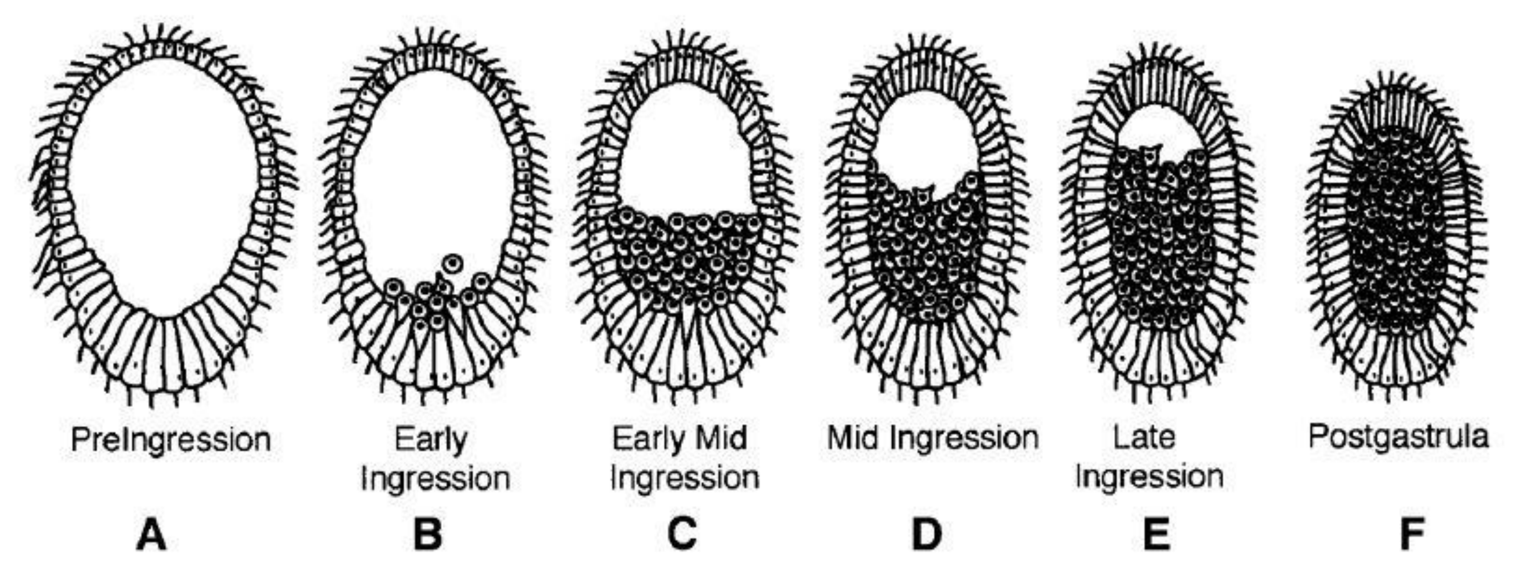
Different modes of gastrulation in metazoans. A - morular delamination, B - cellular delamination, C - multipolar ingression, D - unipolar ingression, E - invagination, F – epiboly: all different modes lead finally to the same gastrulated structure (after Ivanova-Kazas, 1995).



Gastrulation in the hydrozoan *Clytia hemisphaerica*

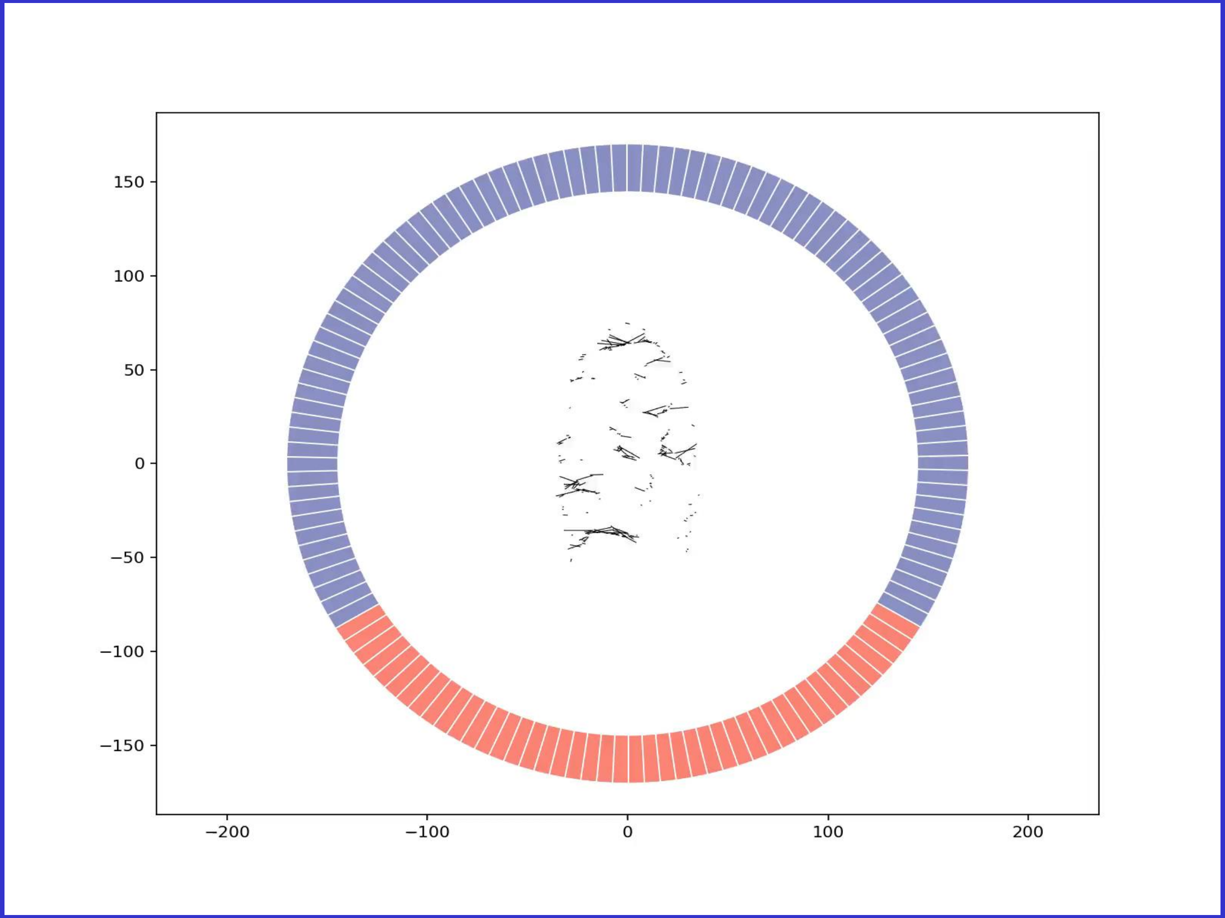
- Gastrulation by ingression

Gastrulation by ingression in the hydrozoan *Clytia sp*.

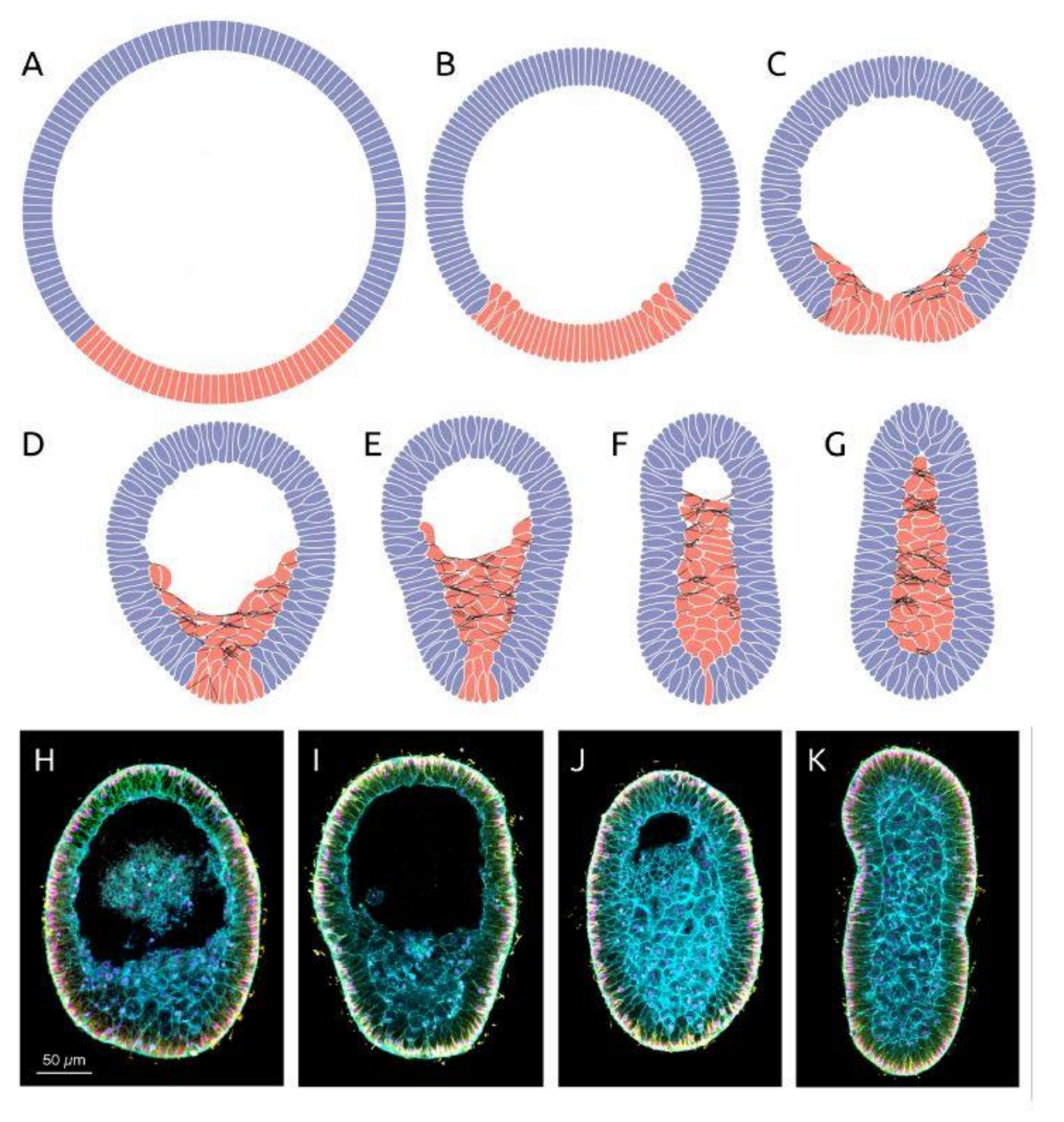


Modelling gastrulation by ingression in the hydrozoan *Clytia hemisphaerica*

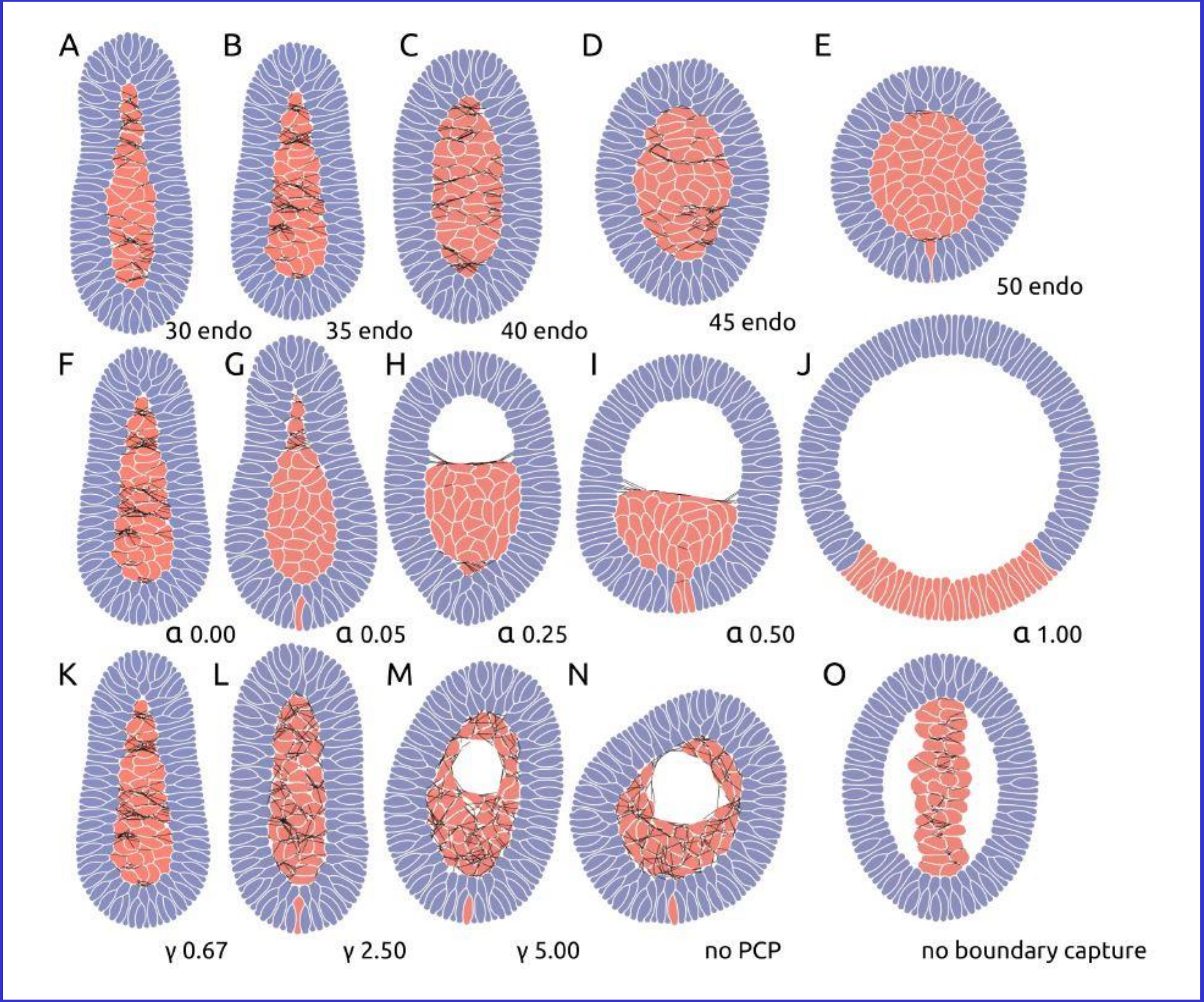
(van der Sande et al. Dev. Biol., 2020)



Comparison simulated and real *Clytia* embryo



Parameter sweep (first row size of oral domain varied; second row increasing cell-cell adhesion; third row increasing Planar Cell Polarity



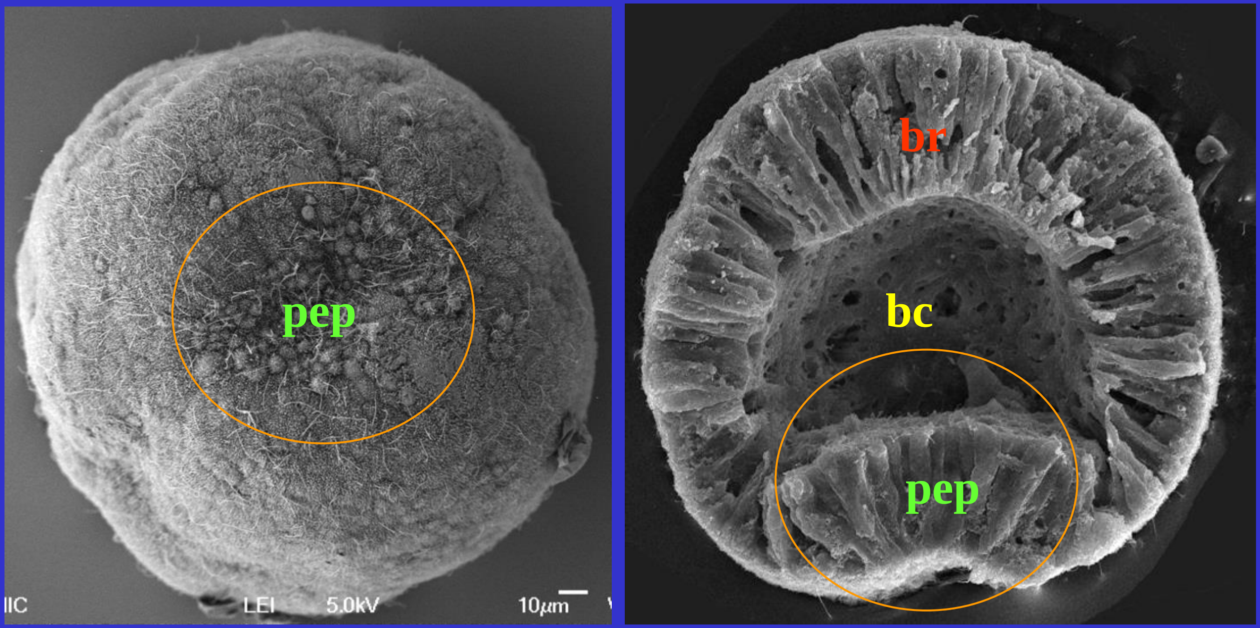
Gastrulation in the sea anemone *Nematostella vectensis* in 3D

- 3D Cell-based modelling of gastrulation in sea anemones (R. Dries K. Renders and J.A. Kaandorp, submitted)

Gastrulation in the sea anemone *Nematostella vectensis* in 3D

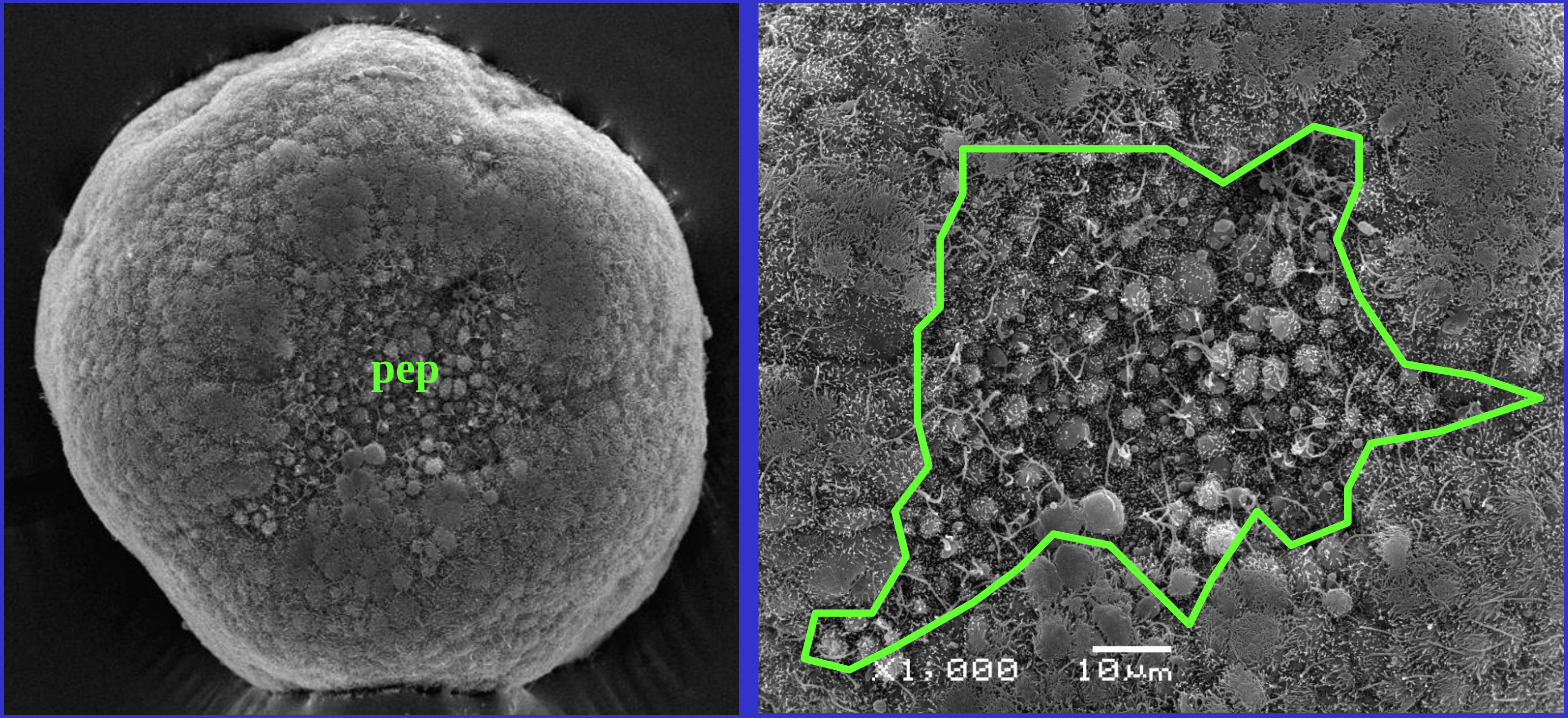
- Which aspects of gastrulation cannot be captured with a 2D model? Example the formation of a pre-endormal plate

Onset of gastrulation, formation of pre-endodermal plate (Kraus & Technau, Dev Genes Evol, 2006)



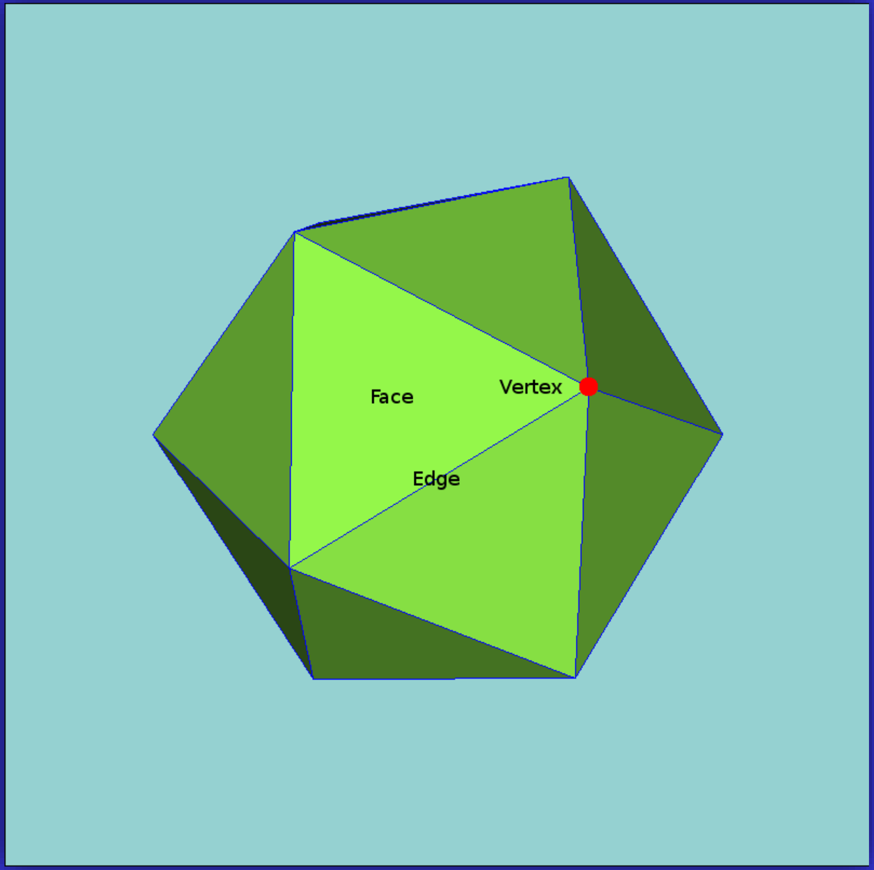
pep – pre-endodermal plate, bc – blastocoel, br – blastocoel roof

Onset of gastrulation, formation of pre-endodermal plate
(Kraus & Technau, Dev Genes Evol, 2006)

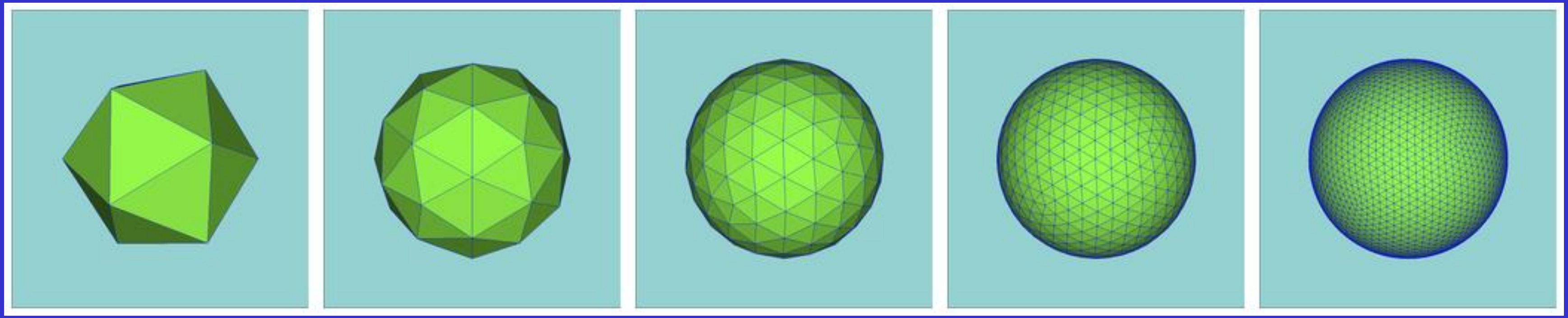


pep – pre-endodermal plate

Representation of a cell in 3D cell based model based on a Mass-Spring System

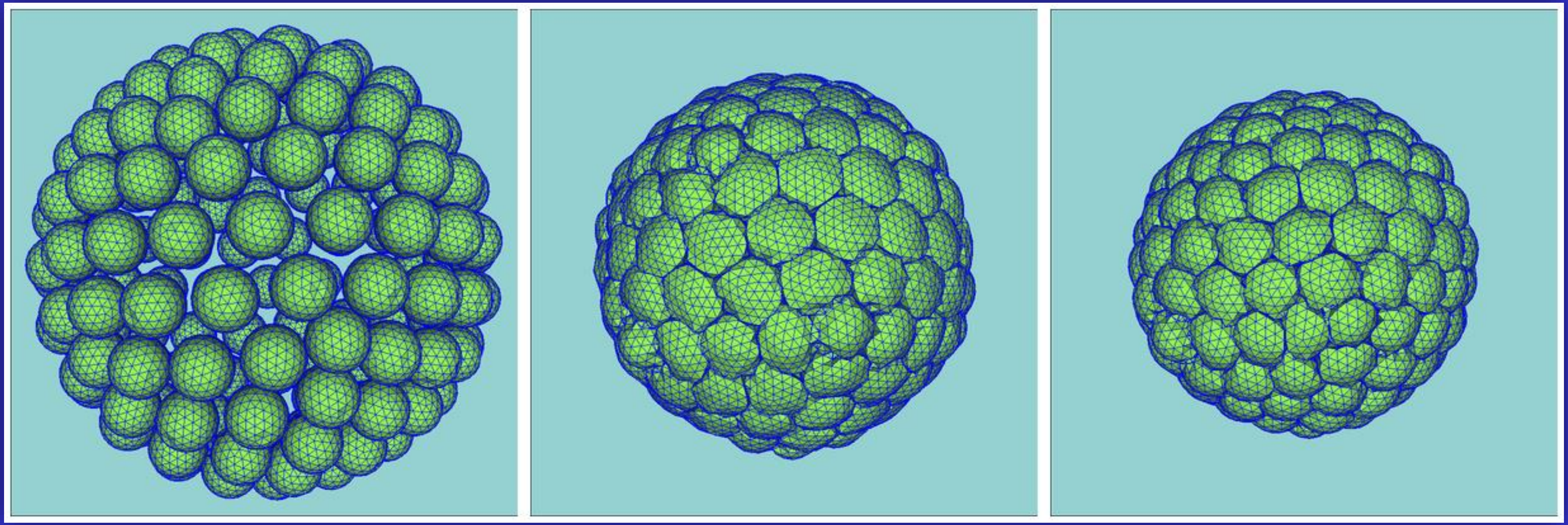


Representation of a cell in 3D cell based model using a triangulated sphere derived from an icosahedron



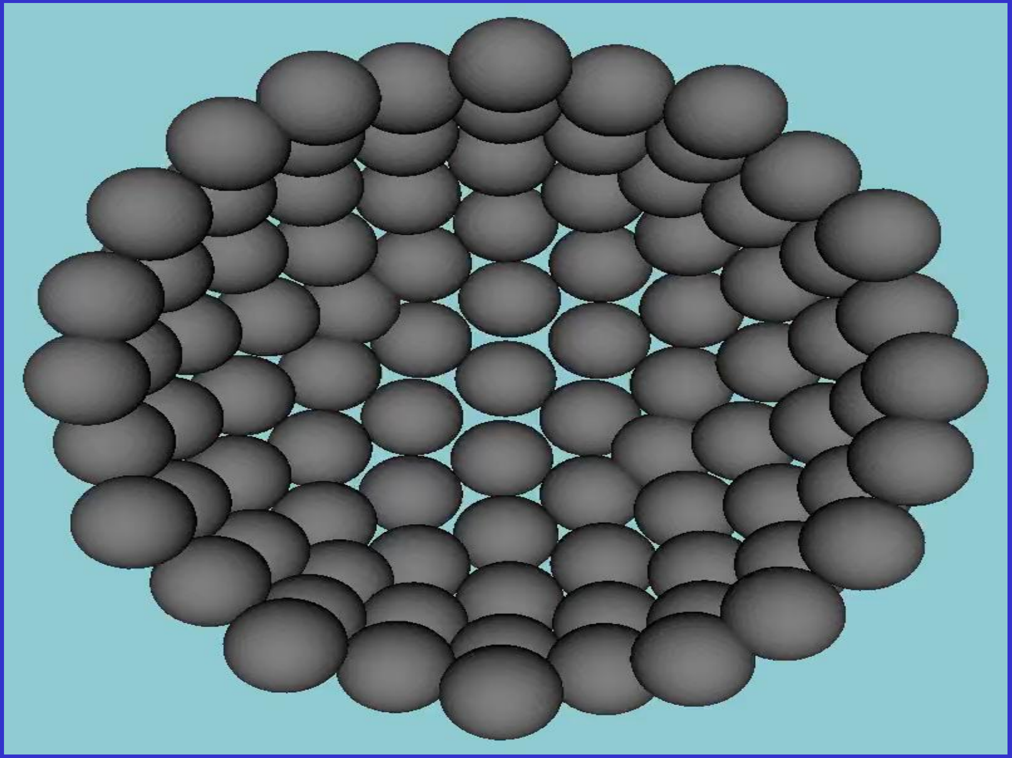
Icosahedron (N1) **N2** **N3** **N4** **N5**

Blastula Formation: packing cells using the 3D cell based model on a spherical surface

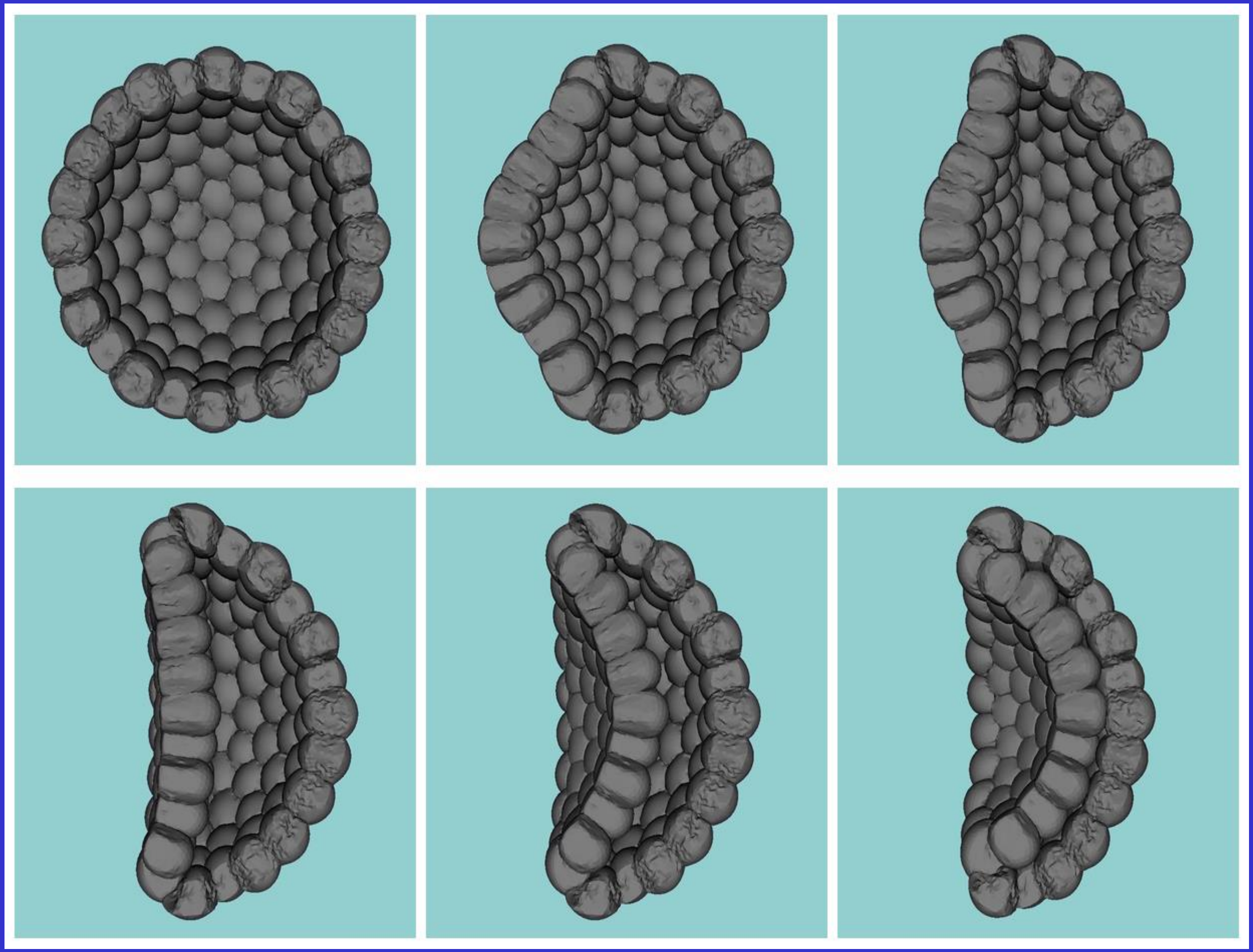


Adhesion of 162 single cells

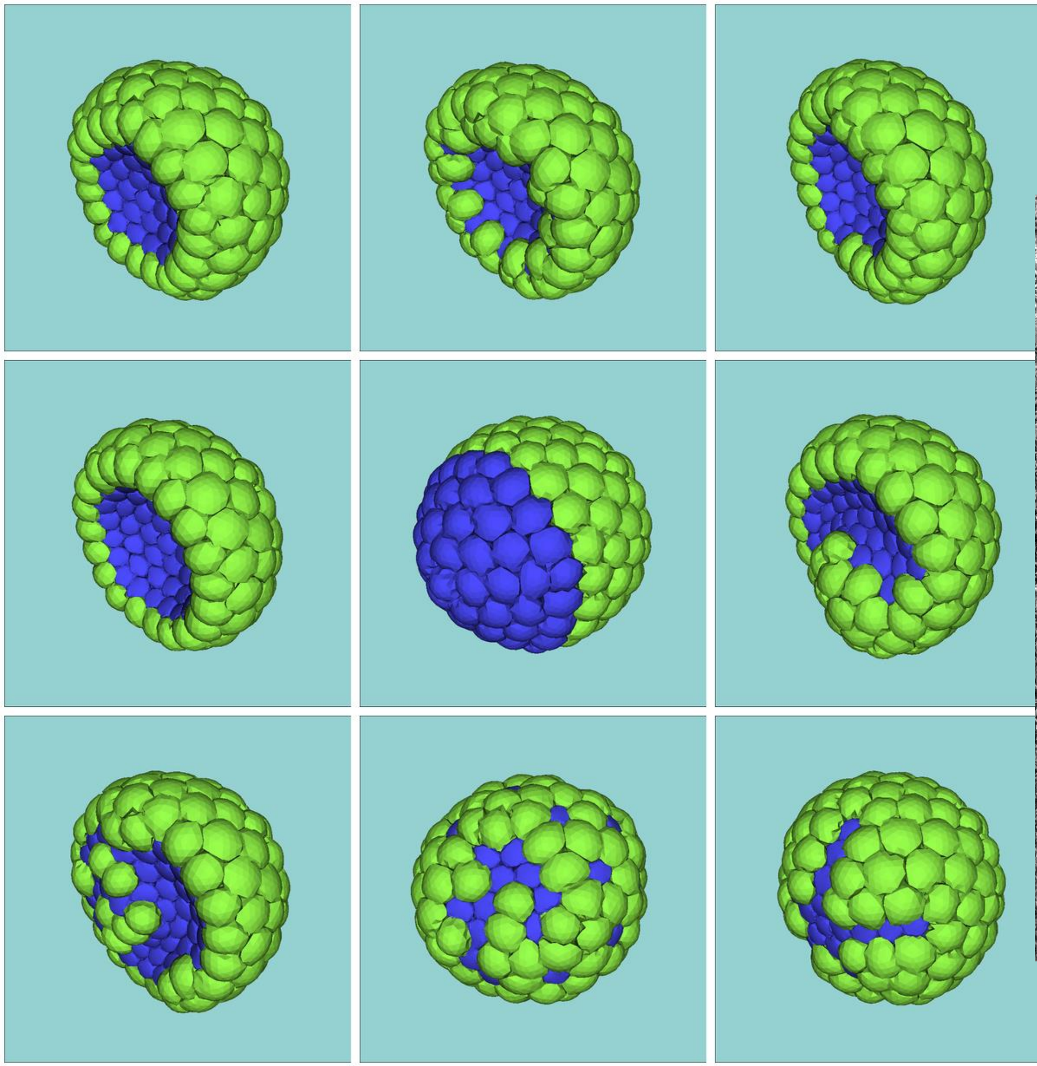
3D cell based modelling of gastrulation, (R.dries K.Renders and J.A. Kaandorp, submitted)



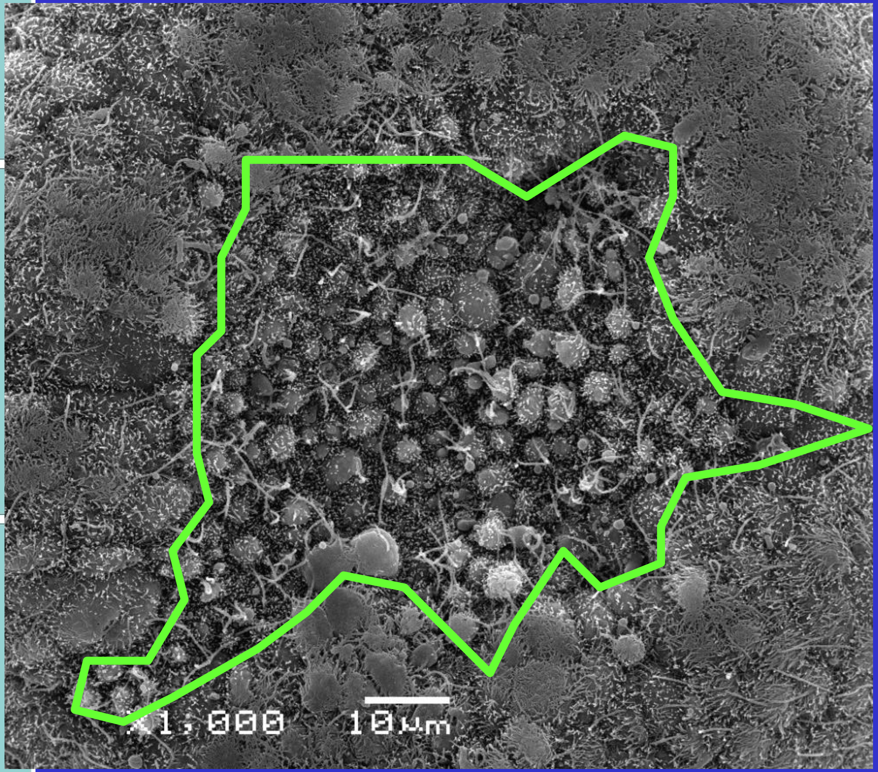
3D cell based modelling of gastrulation, (R.dries, K. Renders and J.A. Kaandorp, submitted)



3D model of gastrulation and irregular shaped pre-endodermal plates



pre-endodermal plate (Kraus & Technau, Dev Genes Evol, 2006)



Conclusions and future work

- Cell-based modelling techniques are fundamental for obtaining an understanding of morphogenesis. We need to able to model the morphology of the cell in detail and cell polarity
- Robust 2D model gastrulation (invagination and ingression), we can demonstrate bottle cell formation, apical constriction and gastrulation
- First version of a 3D cell-based model. We can demonstrate successful simulated gastrulation for different irregular shaped endodermal plates
- Future work: Couple the gastrulation model with a model of gene regulation, biomineralization etc.