modeling development (1)
classical models of pattern formation
segmentation patterns
One more level between genotype and phenotype:
Modeling development (and its evolution)

pattern formation (dependent on shape)

Pattern formation $\rightarrow$ shape

pattern formation $\leftarrow$ shape

TODAY: Classical models of pattern formation / segmentation

Supervised modeling
Top down modeling:
- Given observed pattern/behaviour $X$ and assumptions $A$
  CAN $A \rightarrow X$ (AND does it generate $X++$)
- Data driven models, quantitative fitting

Theme: specific and/or general mechanisms
and/or specific instantiations (?)
development: cell differentiation, pattern formation and morphogenesis

Classically most studied: pattern formation

Prepattern → cell differentiation → morphogenesis

3 most discussed general mechanisms for stationary pattern formation for development

Turing patterns (Turing 1952) introduced term 'morphogen'

Positional information (Wolpert 1969) morphogen gradient - coordinate system

"Clock and wavefront" Cook and Zeeman 1976 temporal oscillation → spatial pattern

compare: "pattern is 'default"

however here specific positioning/orientation

in continuous medium
Segmented bodyplans

from Ten Tusscher EPJE

reinventions (?)
generic mechanism?
homologous at molecular, pathway level?
A generic regular pattern formation mechanisms

Turing Patterns

Can DIFFUSION create patterns from homogeneous state?

- 2 interacting substances
- stable homogeneous equilibrium in absence of diffusion
- unstable for spatial heterogeneous perturbations
- with diffusion: stable (+ regular) stable patterns
Turing patterns: formal requirements

\[
\begin{align*}
\frac{\partial A}{\partial t} & = D_a \Delta A + f_1(A,I) \\
\frac{\partial I}{\partial t} & = D_i \Delta I + f_2(A,I)
\end{align*}
\]

without diffusion stable:
\[\text{tr} J = a_{11} + a_{22} < 0\]
\[\text{det} J = a_{11} * a_{22} - a_{21} * a_{12} > 0\]

with diffusion unstable
\[
\begin{align*}
a_{11} + a_{22} & < 0 \\
a_{11} * a_{22} - a_{21} * a_{12} & > 0 \\
D_a a_{22} + D_i a_{11} & > 2 \sqrt{D_a D_i \times (a_{11} * a_{22} - a_{21} * a_{12})} > 0
\end{align*}
\]
simplified requirements

\[
\begin{align*}
& \begin{aligned}
& a_{11} + a_{22} < 0 \\
& a_{11} \cdot a_{22} - a_{21} \cdot a_{12} > 0 \\
& D_a a_{22} + D_i a_{11} > 0
\end{aligned}\\
& a_{11} > 0 \text{ and } a_{22} < 0 \quad \frac{D_i}{|a_{22}|} > \frac{D_a}{|a_{11}|}
\end{align*}
\]

Diffusion I >> Diffusion A: short range activation, long range inhibition

Positive feedback system: \((+ \quad +)\)

Variables vary over space in phase:

Activator – inhibitor system: \((+ \quad -)\)
Turing patterns

In 2D:

NB wavelength
regular patterns seen in e.g. coat patterns

Not only regular patterns, but also domain dependence shifting with irregular domains

Zebra: ’face recognition’

However sometimes “wrong” small domain: spots; large domain only 2 phases

“the stripes are easy, but what about the horse part?”, Turing
applicable in Biology? If so HOW?

Strictly speaking:
Needs homogeneous initial state;
Needs diffusion
Needs large difference in diffusion;

_HAS been sought but NOT BEEN FOUND_

Less strictly speaking

Needs SOME mechanism of
local activation / longer range inhibition
Classical Modeling Fallacy
Drosophila stripes as Turing patterns

Observe stripes

Turing instability $\rightarrow$ stripes

Hence $\Rightarrow$ Turing pattern

SHAME om “US” Math Biologists
Activation/inhibition scheme: fish stripes, Kondo-group

“looks like Turing patterns” (stripes)
“looks like turing patterns after ablation”
“short range activation, long range inhibition demonstrated by ablation experiments in pigment cells (no molecular interactions known)”
Conclusions Turing Patterns

Elegant, very general

beyond Original diffusion – > pattern

However Stripes: too degenerate pattern to infer anything (needs ++)

Domain / disturbance variations more informative

However random positioning - but may be tweaked

Often invoked, eg. limb– >digitis

Also for vegetation patterns
"French flag": different morphogen concentrations → activate different genes

Alternative attractors: maintain expression domains when morphogen gradient disappears

mutual negative feedback
Positional information/ french flag problem
Wolpert 1969

Source/sink/diffusion for gradient formation
‘read-out’ of concentration – > cell differentiation
(stabilization by mutual inhibition)

french flag problem: how to be scale invariant?

source/sink diffusion is scale invariant!
(but not a likely solution...)

problems: spatial/temporal scaling of diffusion
in tissue: cell boundaries may not allow gradients
how to have precise quantitative readout?
“simple mechanism may not be simple”
noise

“pathways which produce and use positional information”
receptors disturb gradient cf Kerzberg and Wolpert 1998

several potential solutions proposed
early patterning in Drosophila

Model 1: gap gene expression in Drosophila (pre-gastrulation / pre cellularization)

paradigm system for positional information

Maternal gradient (Bicoid) (measured)
In syncytium stage (no cell walls to pass)

paradigm system for data driven quantitative modeling

Very precise description of pattern in space/time available
Much experimental knowledge about genes involved and their interactin

many papers main authors J. Reinitz anf J. Jaeger; here used:
Manu, .... Reinitz 2009 Canalization of Gene Expression in the Drosophila Blastoderm by Gap Gene Cross Regulation, Pos Biology
J.Jaeger .. Reinitz 2004.Dynamic control of positional information in the early Drosophila embryo Nature
modelled space-time frame

gap gene expression in late stage: black line: modeled area
modeling gene regulation: ODE for each nucleus

\[
\frac{dv_i^a}{dt} = R^a g\left(\sum_{b=1}^{N} T^{ab}v_i^b + m^a v_i^{Bcd} + \sum_{\beta=1}^{N_e} E^{a\beta}v_i^{\beta}(t) + h^a\right) + D^a(n)\left[(v_{i-1}^a - v_i^a) + (v_{i+1}^a - v_i^a)\right] - \lambda^a v_i^a.
\]

T interaction between gap genes; m interaction with bicid;
E interaction of gap genes with time varying external factors; \( \lambda \) decay; \( D \) diffusion

interphase: production, diffusion and decay;
mitosis: only diffusion and decay
division: nuclei divide, inherit state,
distance between them halved

g(u^a) = \frac{1}{2} \left[ \left(\frac{u^a}{\sqrt{(u^a)^2 + 1}}\right) + 1 \right]

transcription:
“data driven modeling”: massive fitting using simulated annealing

use: ’known genes’, initial conditions, spatial/temporal variation of nonregulated regulators.

Fit model output in all M nuclei, for all genes, at all N timepoints for which data are available.

\[ E = \sum_{\text{all } a, t, t, \text{ and genotypes for which data exists}} (v_i^a(t)_{\text{model}} - v_i^a(t)_{\text{data}})^2 + \text{(penalty terms)} \]

Do this Z=65 times gives Z different outcomes; and select good fits, no major patterning defects, no known regulatory mistakes (23/65) similar networks
used example of 'good' network

<table>
<thead>
<tr>
<th>Target gene a</th>
<th>bcd</th>
<th>cad</th>
<th>tll</th>
<th>hb</th>
<th>Kr</th>
<th>gt</th>
<th>kni</th>
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</thead>
<tbody>
<tr>
<td>hb</td>
<td>0.025</td>
<td>0.004</td>
<td>0.003</td>
<td>0.021</td>
<td>-0.001</td>
<td>0.022</td>
<td>-0.112</td>
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<tr>
<td>Kr</td>
<td>0.118</td>
<td>0.021</td>
<td>-0.203</td>
<td>-0.026</td>
<td>0.035</td>
<td>-0.042</td>
<td>-0.062</td>
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<tr>
<td>gt</td>
<td>0.256</td>
<td>0.023</td>
<td>-0.011</td>
<td>-0.028</td>
<td>-0.202</td>
<td>0.007</td>
<td>0.003</td>
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<tr>
<td>kni</td>
<td>0.012</td>
<td>0.020</td>
<td>-0.187</td>
<td>-0.082</td>
<td>0.000</td>
<td>-0.017</td>
<td>0.013</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameter</th>
<th>hb</th>
<th>Kr</th>
<th>gt</th>
<th>kni</th>
</tr>
</thead>
<tbody>
<tr>
<td>$R^a$</td>
<td>15.000</td>
<td>10.354</td>
<td>15.000</td>
<td>15.000</td>
</tr>
<tr>
<td>$D^a$</td>
<td>0.166</td>
<td>0.200</td>
<td>0.103</td>
<td>0.200</td>
</tr>
<tr>
<td>$t_{1/2}$</td>
<td>9.529</td>
<td>15.908</td>
<td>9.438</td>
<td>13.062</td>
</tr>
</tbody>
</table>

above: model: early - late; below av. exp. early-late
classical question
developmental patterning very precise, despite differences in
e.g. size of embryo or gradient noise

Manu et al 2009: is due to regulatory circuit.
robustness to variation in bicoid gradient
robustnes to size variation (20%)

without cross regulation gap-genes
model also reproduces shifts in expression patterns over time
Jaeger et al 2004 op.cit
“Quantitative system drift compensates for altered maternal inputs to the gap gene network of the scuttle fly Megaselia abdita” Wotton et al, eLife 2015
Some, but only tiny differences in expression patterns
Fitting not very robust: alternative “as good” fits with even opposite signs of interaction (filtered to agree with experimental knowledge)

because of shifting “better” fitting because less degenerate supervised modeles: Fits

++ = scaling property and noise reduction

++ insight in evolutionary drift / compensation in conserved patterning
Positional information (?):

yes - gradient given and provides “coordinate system”

no - not simple concentration readout
readout itself ‘makes the pattern’

scale invariant (tolerant) because of regulation / not invariant
bicoid gradient
However there appears to be a common mechanism in segmentation development in many organisms. Clock and wavefront mechanisms from temporal to spatial pattern. Cooke and Zeeman 1976

clock: internal cellular oscillations, phase synchronized between cells
wavefront: competence wave moving from anterior to posterior at constant speed
gradients which appear to play a role

“arrest” can be autonomous (Hopf or other bifurcation or extern because of bistability Goldbeter 20..

\[ \text{similar result} \]

resistant to noise

distance governed by posterior rate of growth.
proposed “implementation” as 3 tier mechanism in somitogenesis

A Bottom tier: single cell oscillators
B Middle tier: local synchronization
C Upper tier: global control of slowing and arrest

single cell oscillator: delayed auto-feedback systems
delay determines number of segments
Indeed: intron deletion speeds up the clock
Harima et al Cell 2012
neighbour synchronization: with delay: longer period
reinvented or conserved, which genes oscillate?

GO terms: signalling and transcription

Krol et al Development 2011

orthologs
Only 2 overlapping orthologs involved in segmentation clock

first estimate:

after filtering:
Only 2 orthologs: but members of 3 pathways in all

(this analysis first to find member WNT pathway)
conclusion: very high plasticity!

Only small subset of the 3 pathways oscillate: enough for functional oscillations? “just in time assembly”

Similar (non) conservation pattern in cell cycle mechanisms yeast and pombe

Conservered HER/HES delayed oscillator also in medaka, Xenopus, and invertebrates (e.g. cockroach)!!

Segmentation lost? reinvented?
Is segmentation “the same” in the different organisms??

RA knockout leads to asymmetric somatogenesis which is different for different vertebrate species

HOW/WHY??

Model in more detail to find out which difference in regulatory network may explain difference in phenotype of RA knockouts
<table>
<thead>
<tr>
<th>organism</th>
<th>pErk dynamics</th>
<th>oscillating pathways</th>
<th>left-right phenotype</th>
<th>Slower osc</th>
<th>FGF8</th>
<th>delay (somite nr)</th>
<th>somite size diff</th>
<th>return to symmetry</th>
</tr>
</thead>
<tbody>
<tr>
<td>chick</td>
<td>smoothly retracting</td>
<td>FGF, Wnt, Notch</td>
<td>right side</td>
<td>symmetric, more anterior</td>
<td>no; left somites smaller</td>
<td>yes</td>
<td>unclear</td>
<td></td>
</tr>
<tr>
<td>zebrafish</td>
<td>retracts in jumps</td>
<td>Notch</td>
<td>right side</td>
<td>right side more anterior</td>
<td>right side 2-3 somites delayed</td>
<td>no</td>
<td>yes</td>
<td></td>
</tr>
<tr>
<td>mouse</td>
<td>oscillates</td>
<td>FGF, Wnt, Notch</td>
<td>right side</td>
<td>right side more anterior</td>
<td>right side 2-3 somites delayed</td>
<td>sometimes</td>
<td>yes</td>
<td></td>
</tr>
</tbody>
</table>

Vroomans & ten Tusscher 2017, Modelling asymmetric somitogenesis: Deciphering the mechanisms behind. species differences
Vroomans & ten Tusscher 2017: 
Indeed, our results suggest that rather than focussing on a catch-all mechanism in all vertebrate species and assuming that species differences merely reflect neutral developmental systems drift, we should keep an open mind for the possibility of functionally significant species differences.

OR

Side-effects of neutral drift
But what about Drosophila?

2 (3) mechanisms in insects short vs long germband (+intermediate)

clock-wavefront (sequential) mechanism might be ancestral - reinvention of simultaneous mechanism long germband??