

# 近似ベイズ計算法を用いた 生物数理モデルの構築と展望

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謝辞

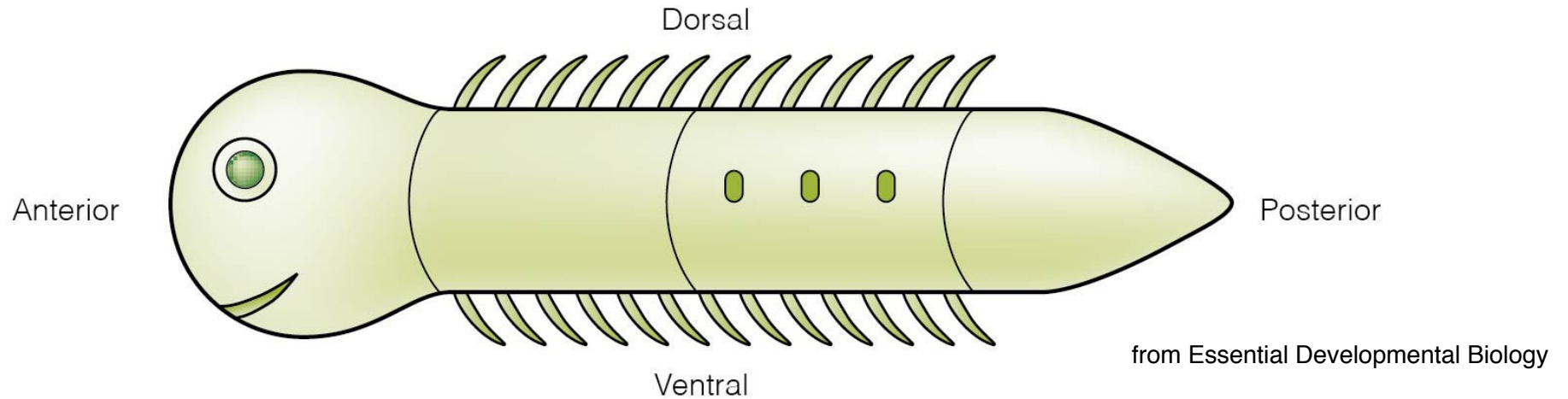
猪股秀彦, 笹井芳樹

RIKEN Center for Developmental Biology (CDB)

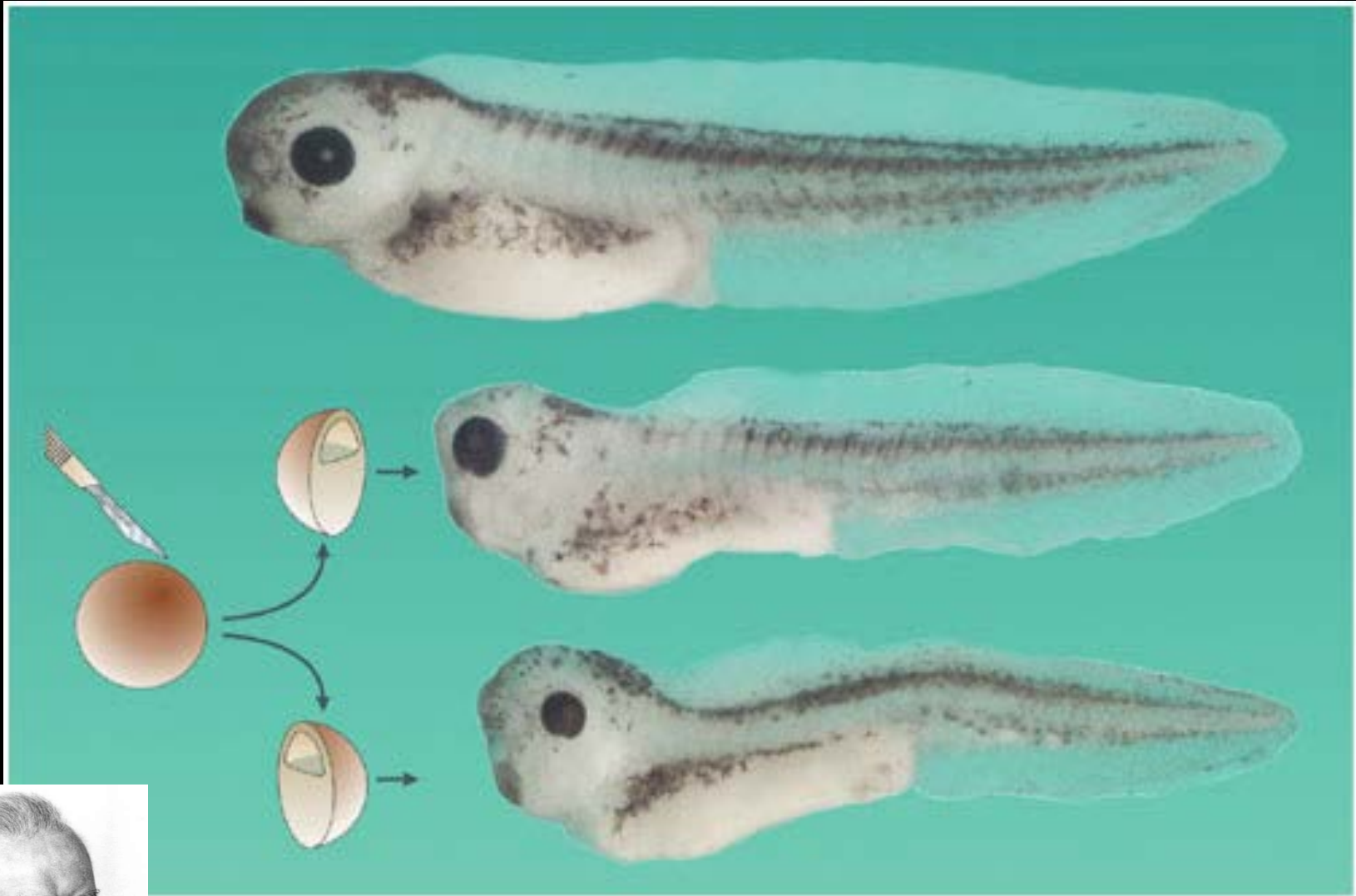
# ライフサイエンスのチャレンジ

- 分子や相互作用の知識の蓄積
- 働きを理解するには不十分
- シミュレーションによる再構成 => 理解
- しかし、基礎方程式は不確実
- 数理モデル = 仮説の構築
- パラメータ値の不可知性

# からだの基本的な3つの軸



- Anterior-Posterior (AP axis、前後軸)
- Dorsal-Ventral (DV axis、背腹軸)
- Left-Right (左右軸)

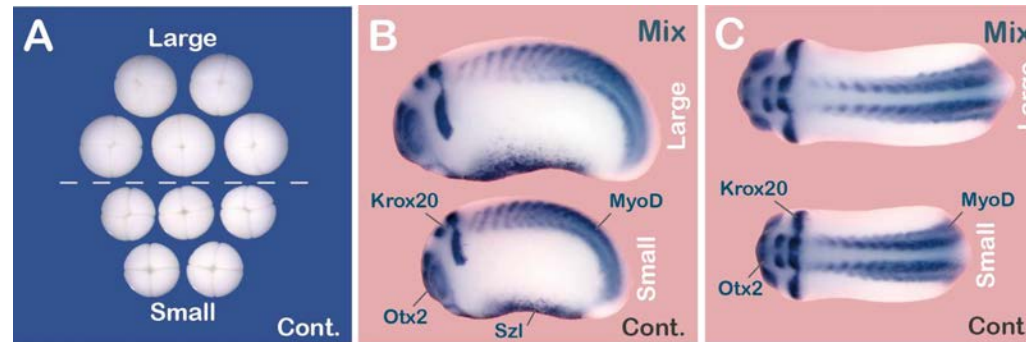


Hans Spemann

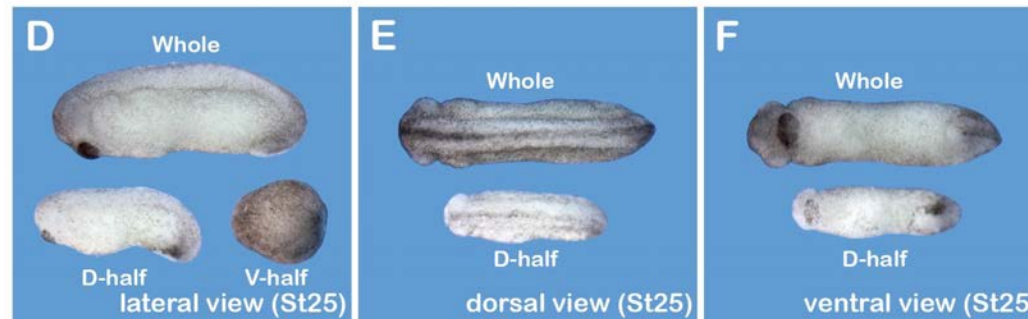
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# 背腹軸パターン形成のスケールリング性

*Xenopus laevis*



whole  
Bisection

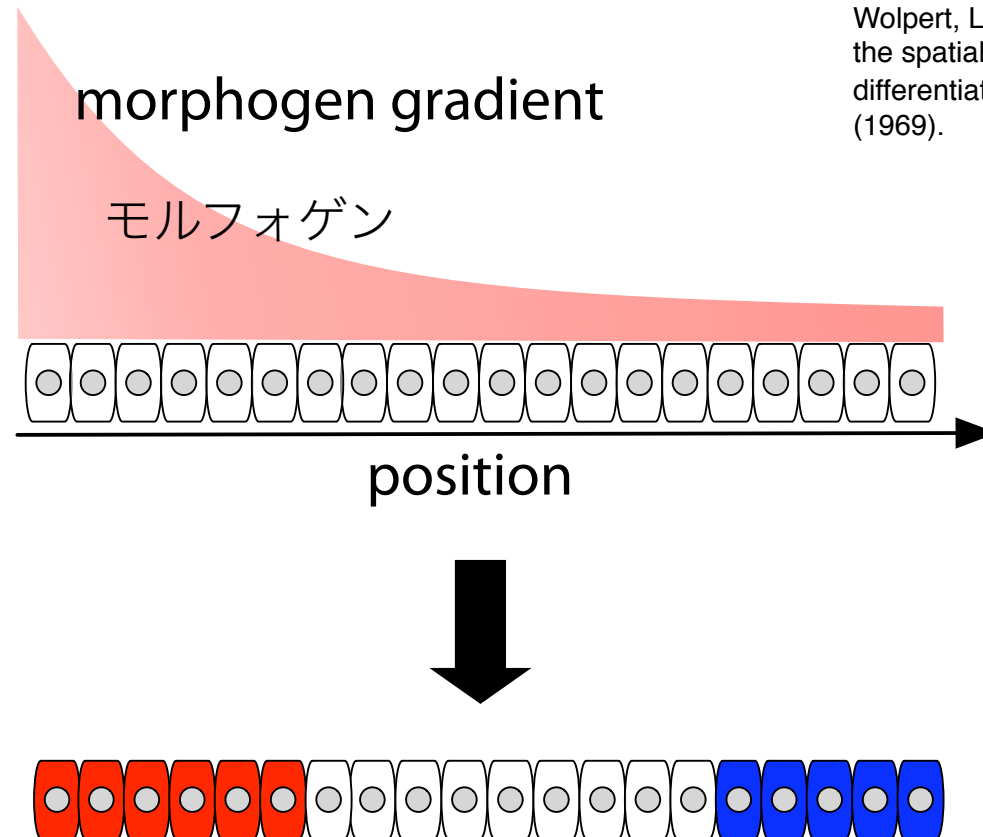


- 胚のサイズの違いにもかかわらず、背腹軸のパターン形成はプロポーシオンが維持されている。
- 背腹軸のパターンを体のサイズに適応させる仕組みは何か？
- 「スケールリング性のあるパターン形成」

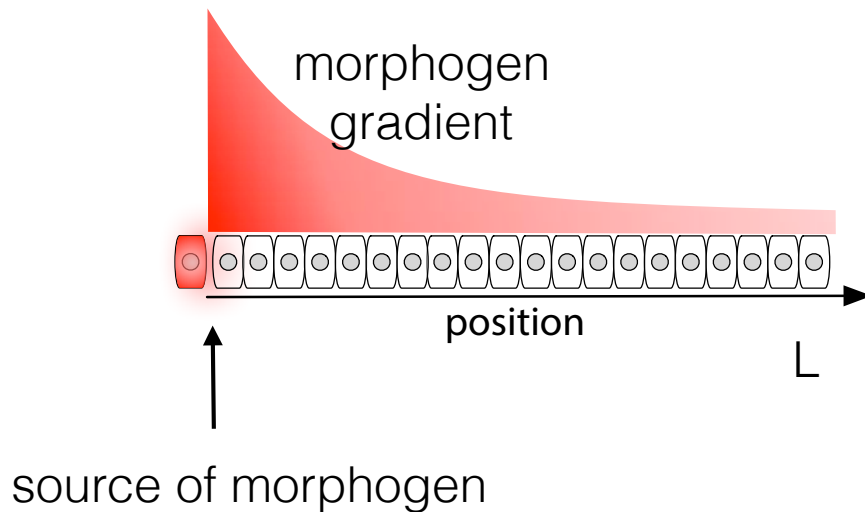
# 濃度勾配が位置情報を与える

Wolpert's "French flag" model

Wolpert, L. Positional information and the spatial pattern of cellular differentiation. *J Theor Biol* 25, 1–47 (1969).



# 拡散係数と分解レートが濃度勾配を決める



$$\frac{\partial c}{\partial t} = -\lambda c + D \frac{\partial^2 c}{\partial x^2}$$

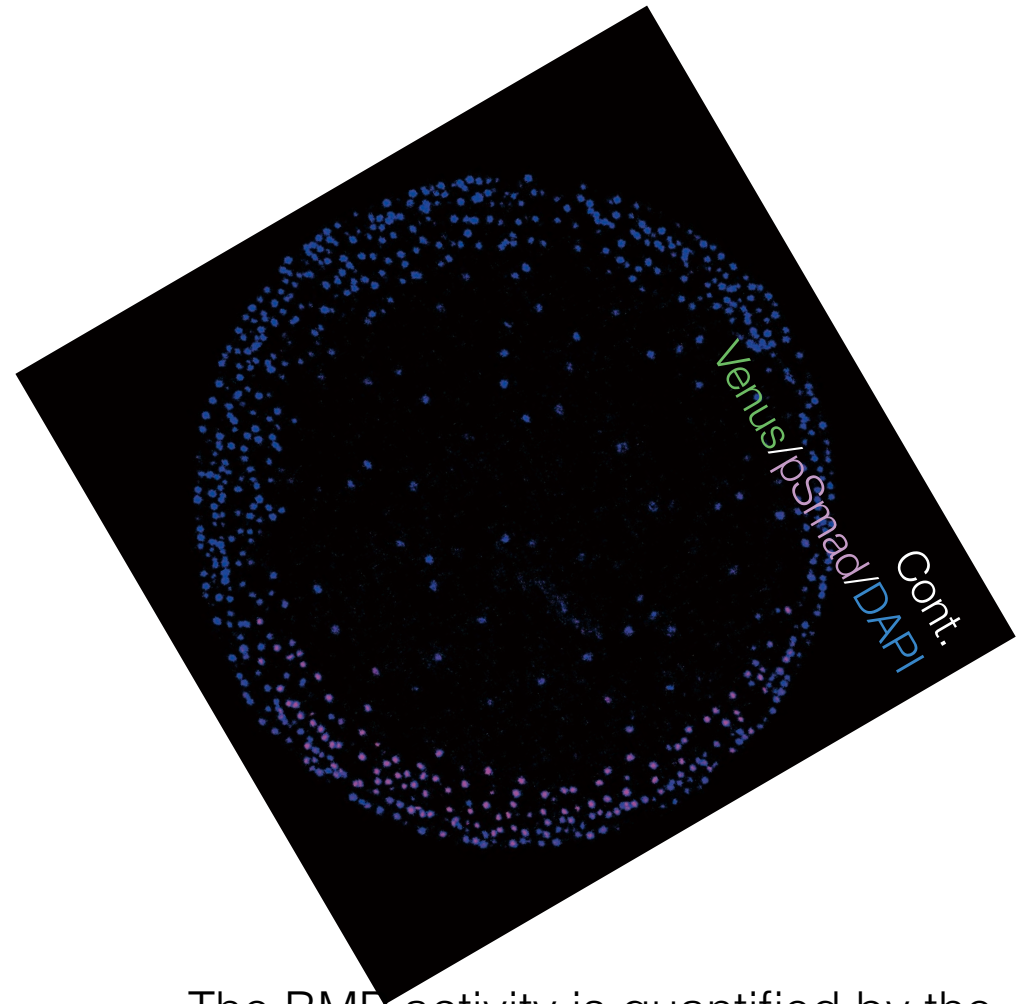
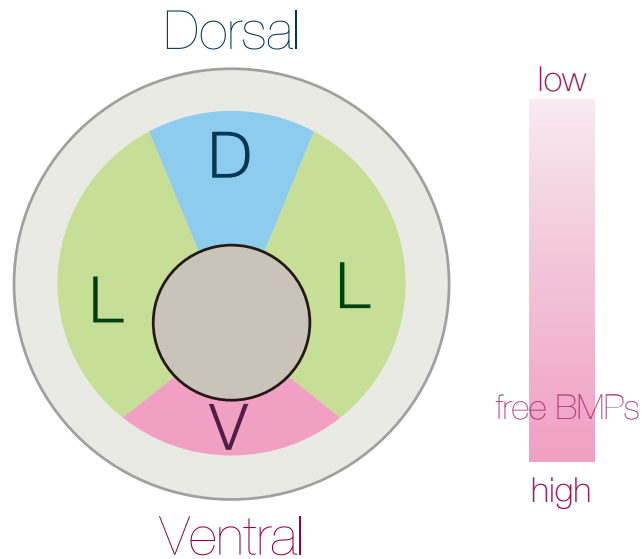
$$D \frac{\partial c}{\partial x} \Big|_{x=0} = -J$$

The morphogen gradient:  $C(x) = \frac{J}{\sqrt{D\lambda}} e^{-\frac{x}{\sqrt{D/\lambda}}}$

The diffusion distance  $\ell = \sqrt{D/\lambda} (\mu m)$

- 体のサイズは濃度勾配に影響しない！

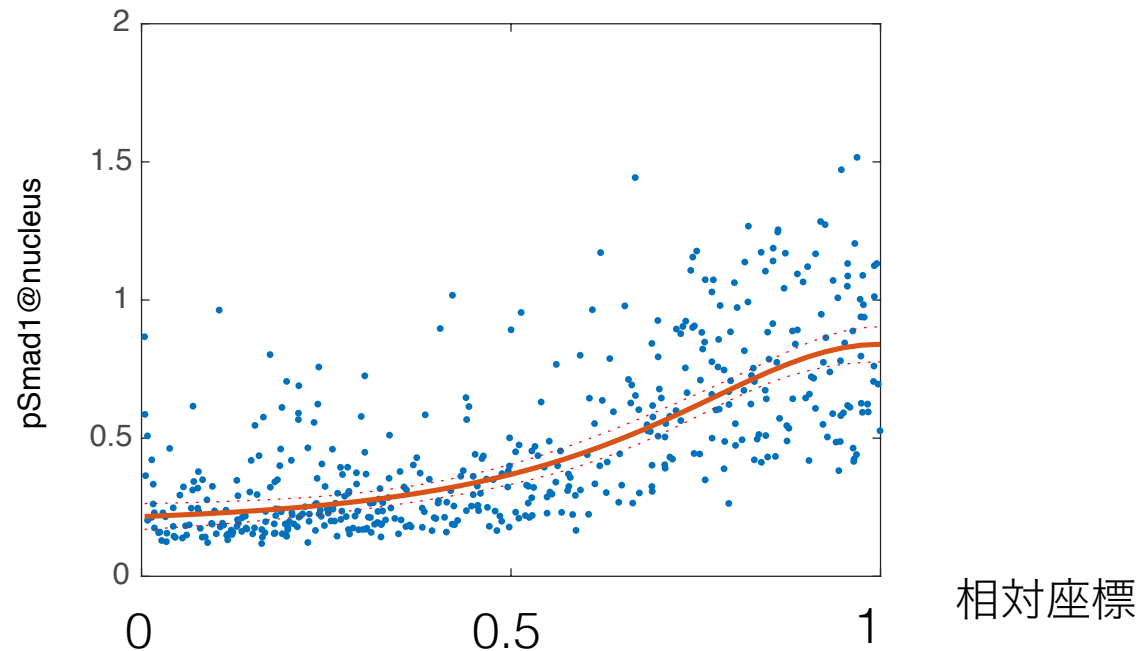
# BMP の濃度勾配が背腹軸を決めている



The BMP activity is quantified by the nuclear phospho-Smad1 (pSmad1) signal.



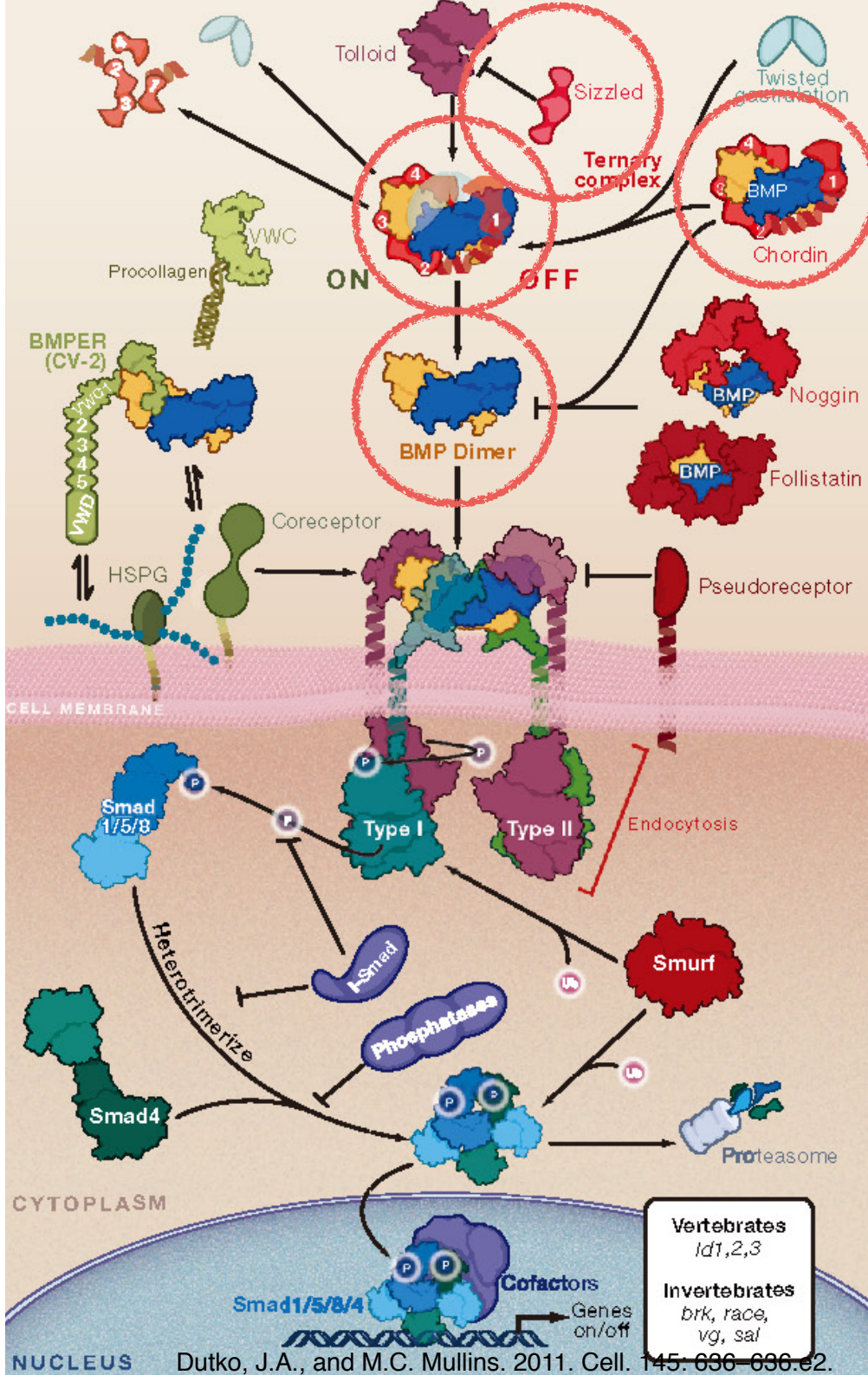
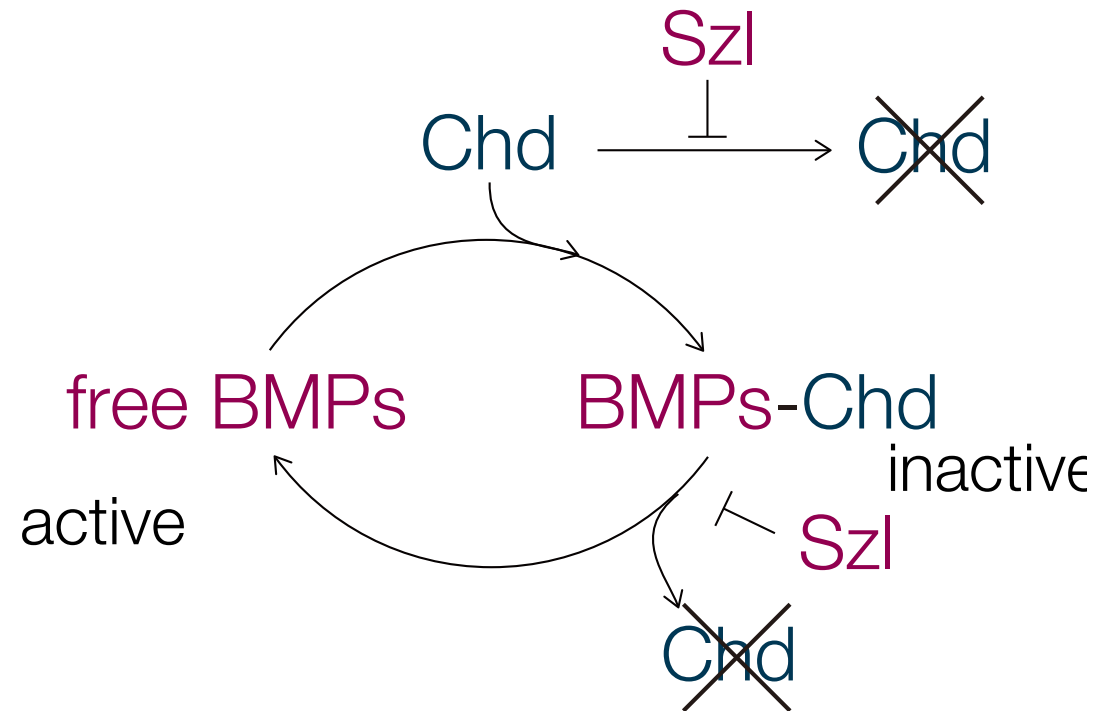
# 背腹軸に沿ったモルフォゲン濃度勾配



- 疑問：体のサイズに対して、いつも同じ割合で変化する濃度勾配は、どのように作られるか？

# BMP濃度勾配を調節する分子ネットワーク

Sizzled, a inhibitor for Chordin protease, stabilizing Chordin and BMPs-Chd complexes



# 背腹軸パターン形成の数理モデル

- (**A**) ADMP
- (**C**) Chordin
- (**AC**) ADMP-Chd
- (**BC**) BMP4-Chd
- (**B**) BMP4
- (**S**) Sizzled

$$\frac{\partial C}{\partial t} = V_C \frac{K_C^{h_C}}{K_C^{h_C} + (A+B)^{h_C}} - \lambda_C \frac{C}{1+S/K_i + (C+BC+AC)/K_m} - k_{chdbmp} C \cdot B - k_C \cdot A + D_{chd} \Delta C$$

$$\frac{\partial B}{\partial t} = V_B \frac{(A+B)^{h_B}}{K_B^{h_B} + (A+B)^{h_B}} - \lambda_B B + \lambda_C \frac{BC}{1+S/K_i + (C+BC+AC)/K_m} - k_{chdbmp} C \cdot B + D_{bmp} \Delta B$$

$$\frac{\partial A}{\partial t} = V_A \frac{K_A^{h_A}}{K_A^{h_A} + (A+B)^{h_A}} - \lambda_B A + \lambda_C \frac{AC}{1+S/K_i + (C+BC+AC)/K_m} - k_{chdadmp} C \cdot A + D_{admp} \Delta A$$

(1) BMP-dependent production

$$\frac{\partial S}{\partial t} = V_S \frac{(A+B)^{h_S}}{K_S^{h_S} + (A+B)^{h_S}} - \lambda_S S + D_{szl} \Delta S$$

(2) Degradation

(3) Association between BMPs & Chordin

$$\frac{\partial BC}{\partial t} = -\lambda_C \frac{BC}{1+S/K_i + (C+BC+AC)/K_m} + k_{chdbmp} C \cdot B + D_{chdbmp} \Delta BC$$

(4) Sizzled-regulated Chordins degradation

$$\frac{\partial AC}{\partial t} = -\lambda_C \frac{AC}{1+S/K_i + (C+BC+AC)/K_m} + k_{chdadmp} C \cdot A + D_{chdadmp} \Delta AC$$

(5) Diffusion

$$D \nabla C|_{x=0} = -J_C$$

$$D \nabla B|_{x=0} = D \nabla A|_{x=0} = D \nabla S|_{x=0} = D \nabla BC|_{x=0} = D \nabla S|_{x=0} = 0$$

(6) Chd production at dorsal end

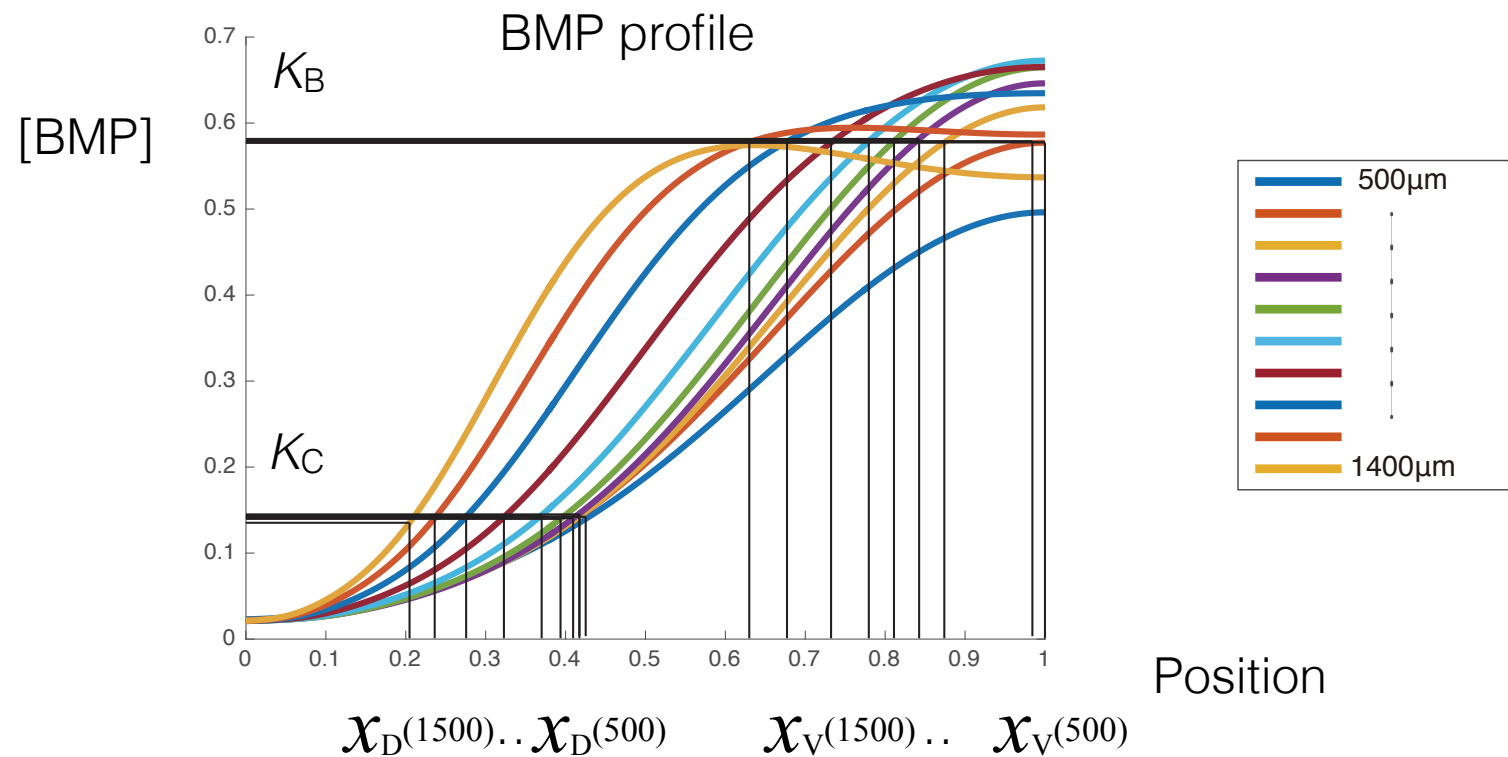
$$D \nabla C|_{x=L} = D \nabla B|_{x=L} = D \nabla A|_{x=L} = D \nabla S|_{x=L} = D \nabla BC|_{x=L} = D \nabla S|_{x=L} = 0$$

# パラメータ

$V_c, K_c, h_c$	}	..... (1) BMP-dependent production rate, Hill coefficient, threshold
$V_B, K_B, h_B$		
$V_A, K_A, h_A$		
$V_s, K_s, h_s$		
$\lambda_B, \lambda_s$	..... (2) Degradation	
$k_{BC}$	..... (3) Association between BMPs & Chordin	
$\lambda_c, K_m, K_i$	..... (4) Sizzled-regulated Chordins degradation	
$D_C, D_B, D_A, D_S, D_{CB}, D_{CA}$	..... (5) Diffusion	
$J_c$	..... (6) Chordin production at dorsal end	
$L$	..... (7) embryo size	

- パラメータの数 >> 変数の数

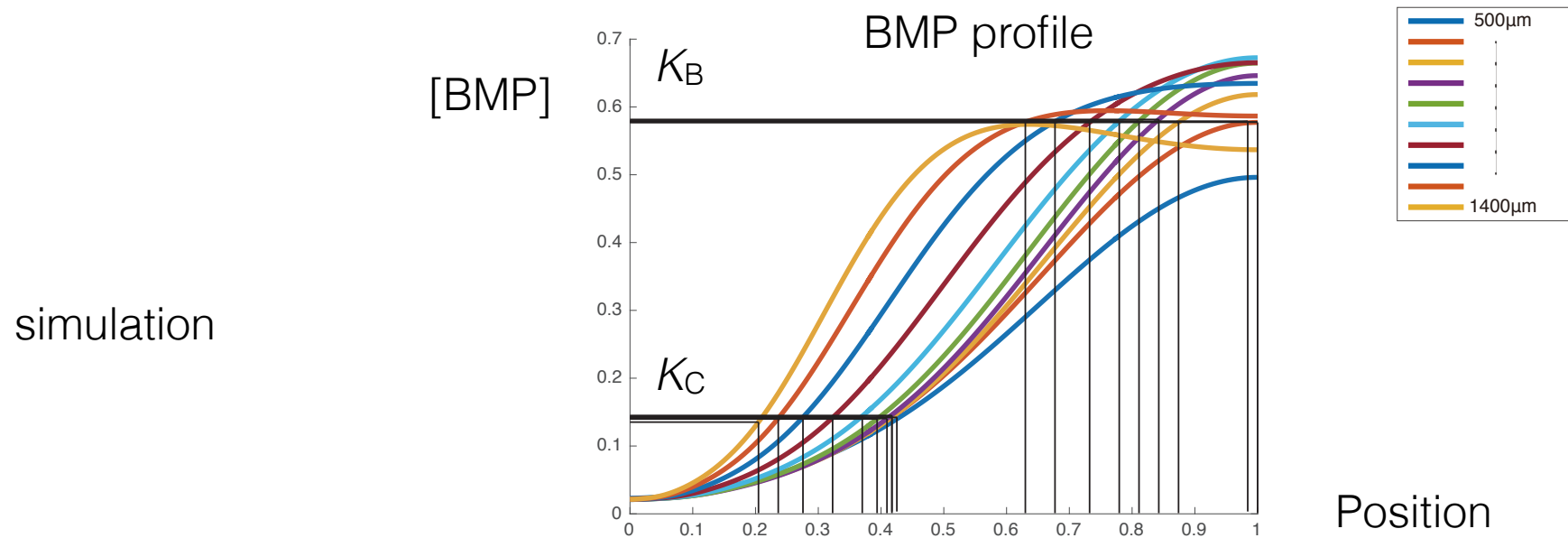
# 異なるサイズに対する モルフォゲン濃度勾配の数値計算



- [BMP] =  $K_C$ , 背領域の境界,  $x_D$
- [BMP] =  $K_B$ , 腹領域の境界,  $x_V$

$$b = \{x_D^{(1500)}, \dots, x_D^{(500)}, x_V^{(1500)}, \dots, x_V^{(500)}\}$$

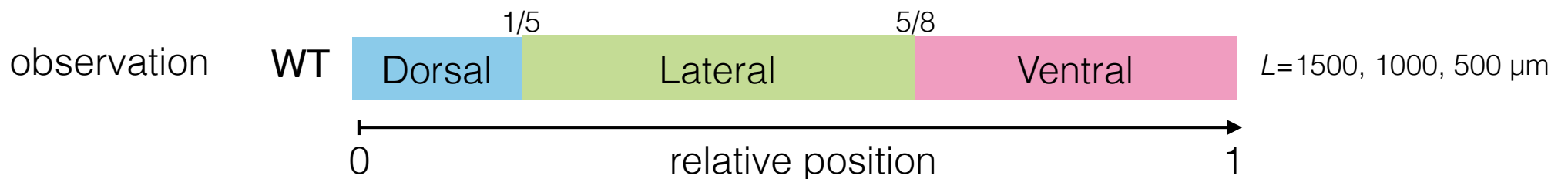
# 実験結果を説明するパラメータの推定



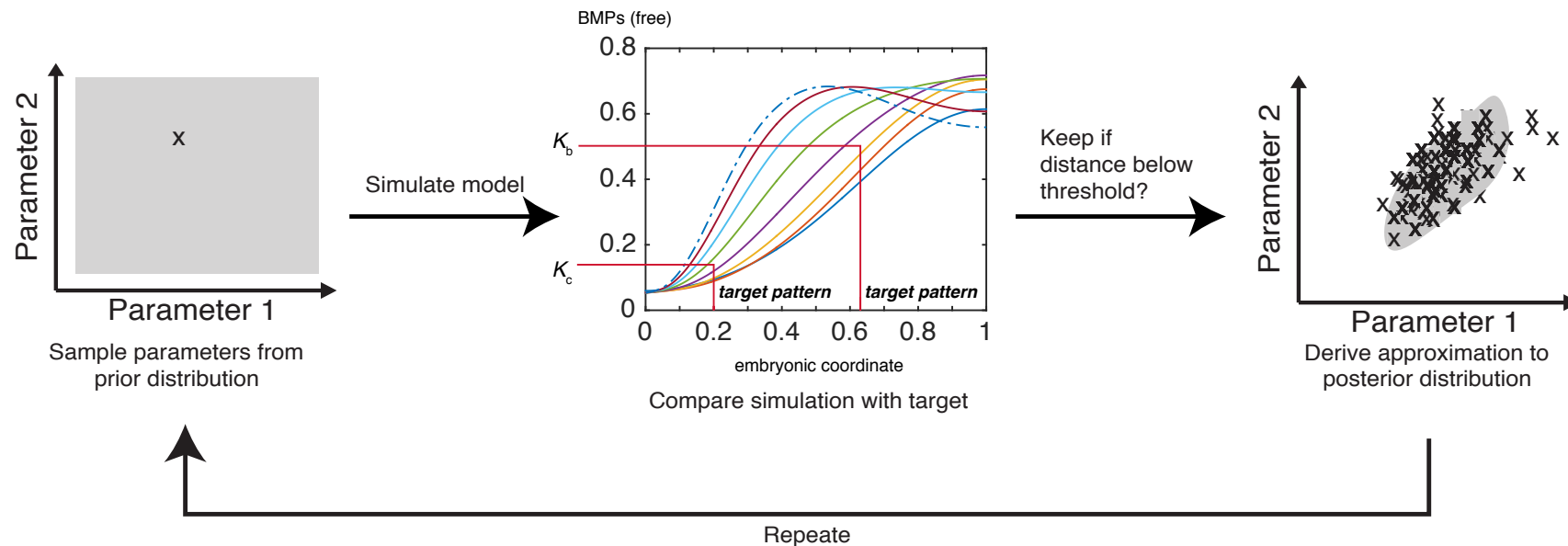
$$b = \{x_D^{(1500)}, \dots, x_D^{(500)}, x_V^{(1500)}, \dots, x_V^{(500)}\}$$



$$b^* = \{x_D^{(1500)}=1/5, \dots, x_D^{(500)}=1/5, x_V^{(1500)}=5/8, \dots, x_V^{(500)}=5/8\}$$

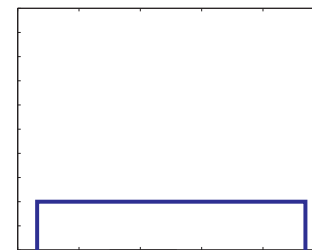


# 近似ベイズ法を用いたパラメータ推定



Liepe, Juliane, Liepe, Juliane, Paul Kirk, Paul Kirk, Sarah Filippi, Sarah Filippi, Tina Toni, Chris P Barnes & Michael P H Stumpf "A framework for parameter estimation and model selection from experimental data in systems biology using approximate Bayesian computation". Nat Protoc 9, 439–456 (2014).

# Approximate Bayesian computation (ABC) with sequential Monte Carlo (SMC) method



$$P_0(\theta)$$

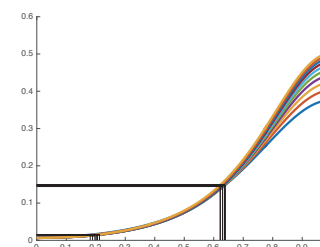
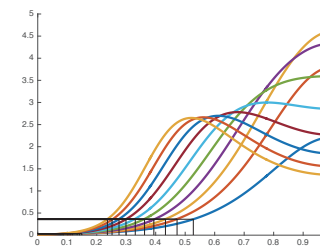
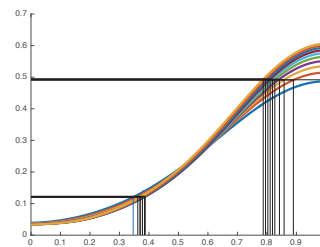
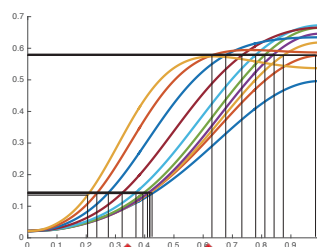
prior distribution of model parameters  $\theta$

1. pick a parameter value from the prior distribution  $P_{n-1}(\theta)$

2. perform simulation

3. compute D, V positions

$$b = \{x_D^{(1500)}, \dots, x_D^{(500)}, x_V^{(1500)}, \dots, x_V^{(500)}\}$$

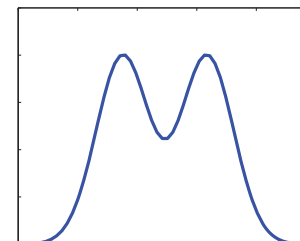


4. compute *error* from target,  $\rho(b, b^*)$

5. accept parameter  $\theta$  that errors  $\rho(b, b^*) < \epsilon$

6. Approximate the posterior distribution  $P_n(\theta)$ .

Use  $P_n(\theta)$  as the prior distribution for the next iteration. Repeat this procedure until the error  $\rho$  are sufficiently small

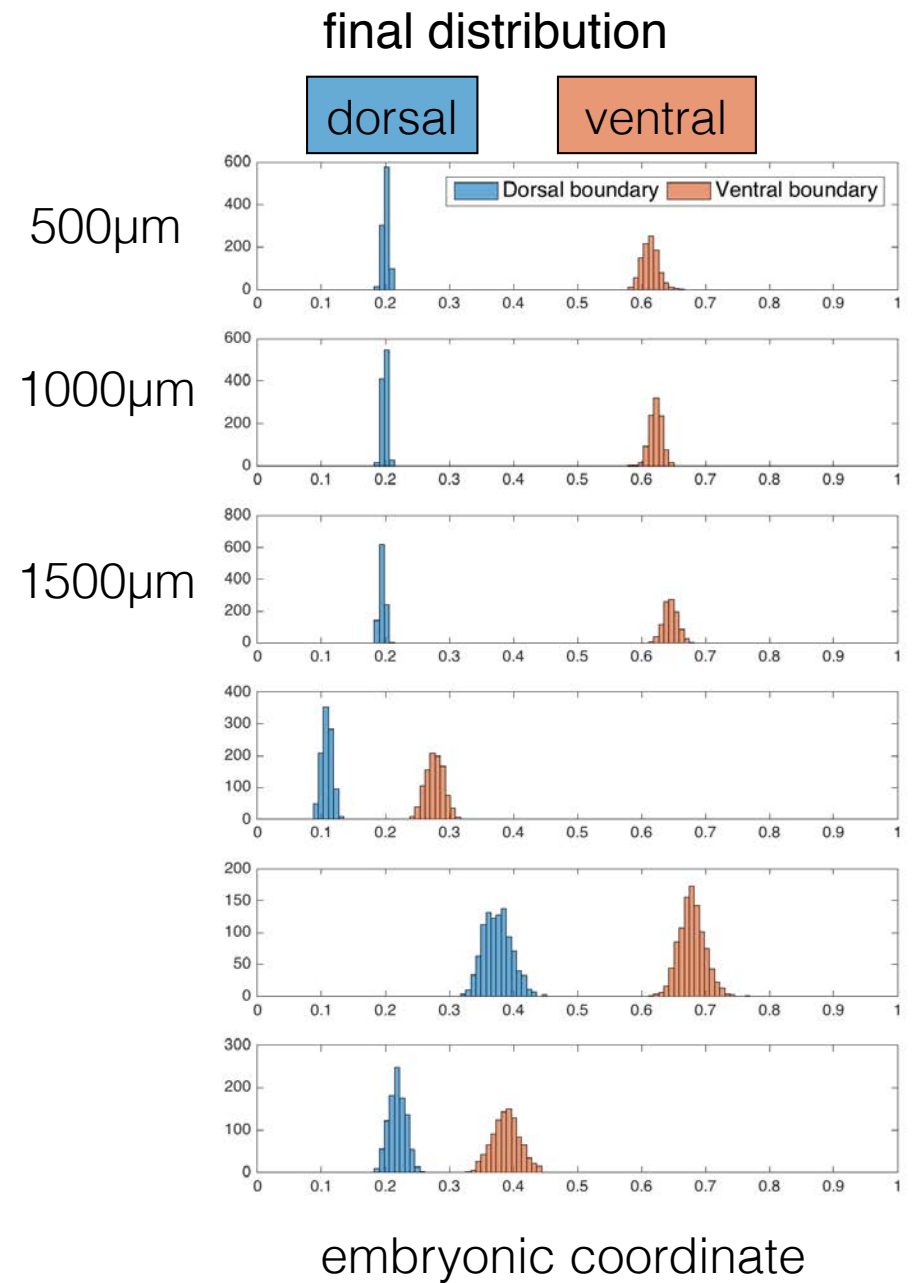
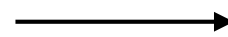
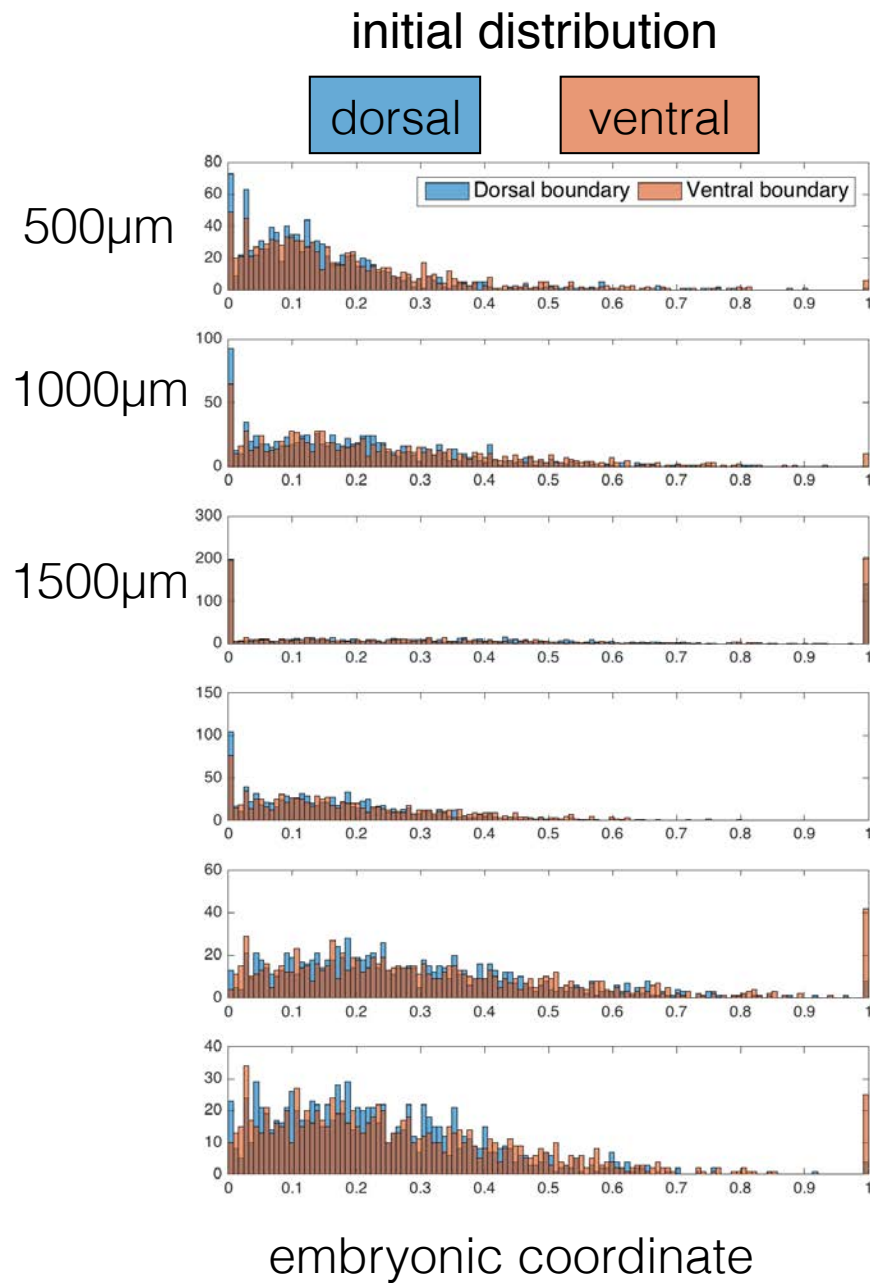


$$P_n(\theta)$$

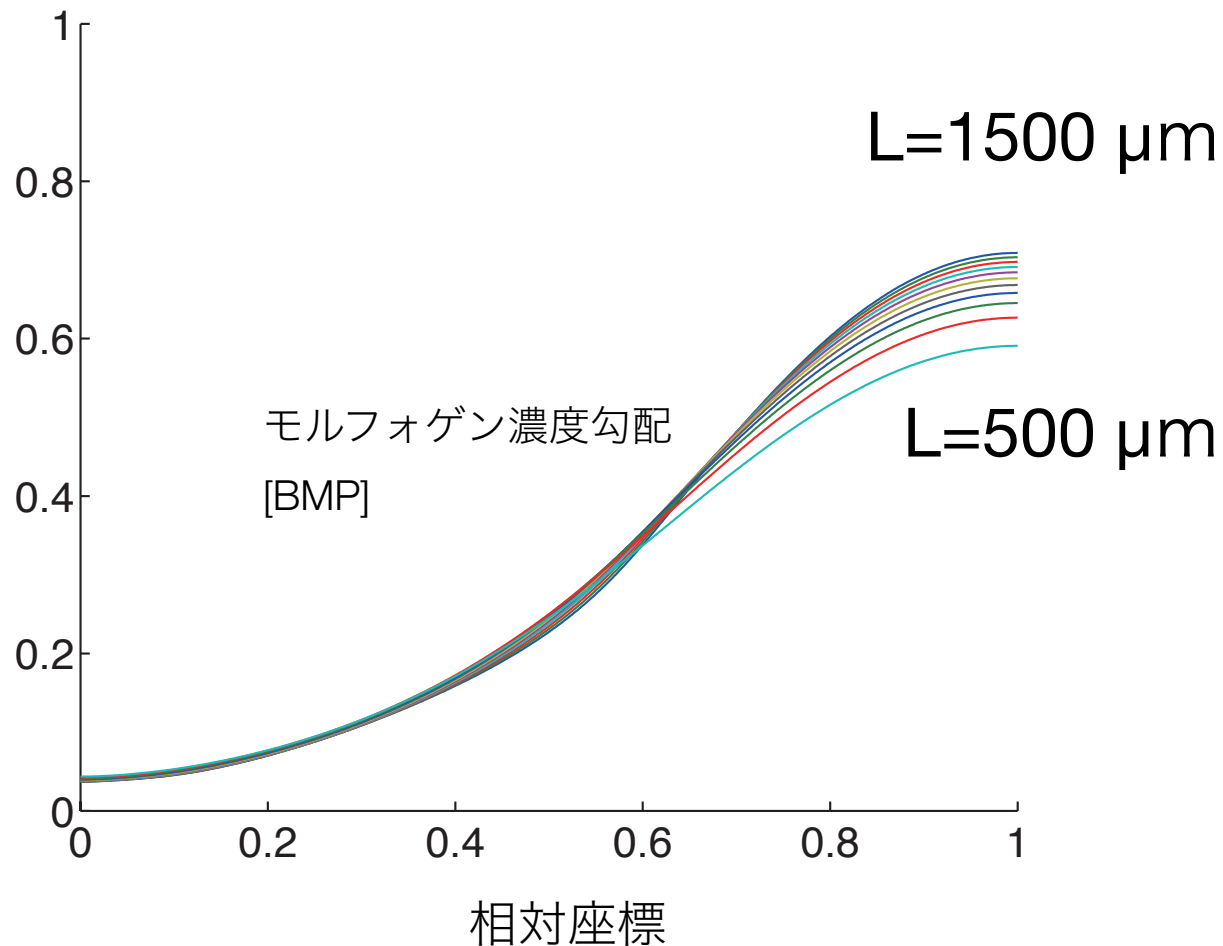
Posterior distribution of model parameters  $\theta$



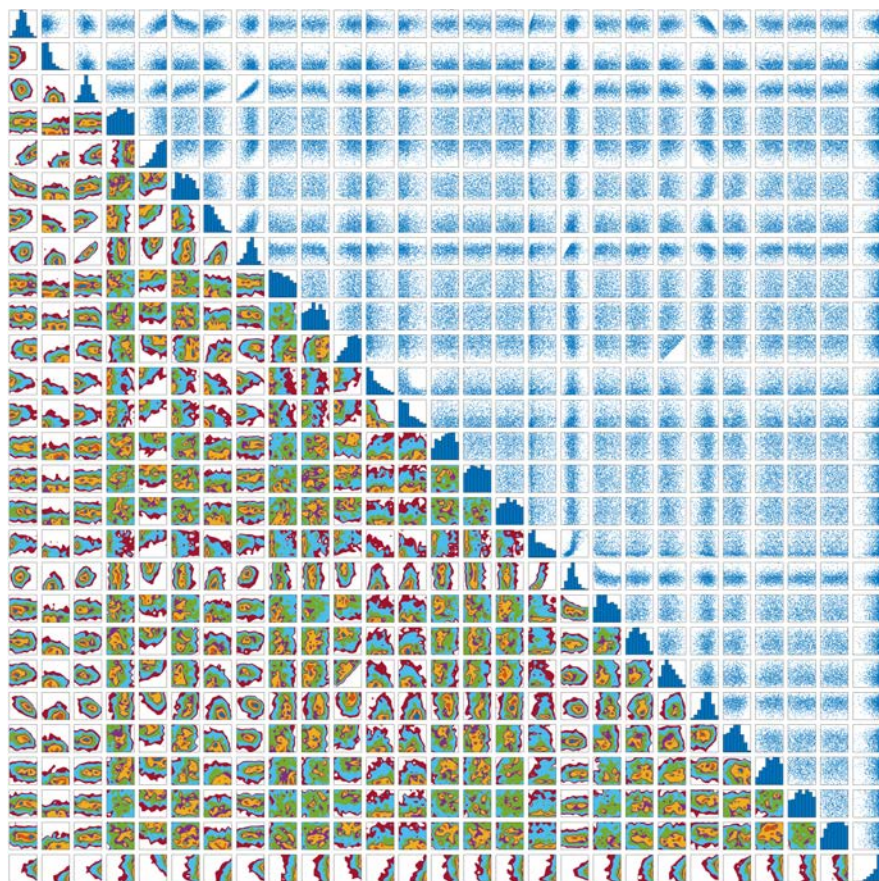
# 背腹境界の分布の推移



# モルフォゲン濃度勾配は 同じ割合で変化する



# データ駆動で本質を見抜く



$$\frac{\partial C}{\partial t} = V_C \frac{K_C^{h_C}}{K_C^{h_C} + (A+B)^{h_C}} - \lambda_C \frac{C}{1+S/K_i + (C+BC+AC)/K_m} - kC \cdot B - kC \cdot A + D\Delta C$$

$$\frac{\partial B}{\partial t} = V_B \frac{(A+B)^{h_B}}{K_B^{h_B} + (A+B)^{h_B}} - \lambda_B B + \lambda_C \frac{BC}{1+S/K_i + (C+BC+AC)/K_m} - kC \cdot B + D\Delta B$$

$$\frac{\partial A}{\partial t} = V_A \frac{K_A^{h_A}}{K_A^{h_A} + (A+B)^{h_A}} - \lambda_B A + \lambda_C \frac{AC}{1+S/K_i + (C+BC+AC)/K_m} - kC \cdot A + D\Delta A$$

$$\frac{\partial S}{\partial t} = V_S \frac{(A+B)^{h_S}}{K_S^{h_S} + (A+B)^{h_S}} - \lambda_S S + D\Delta S$$

$$\frac{\partial BC}{\partial t} = -\lambda_C \frac{BC}{1+S/K_i + (C+BC+AC)/K_m} + kC \cdot B + D\Delta BC$$

$$\frac{\partial AC}{\partial t} = -\lambda_C \frac{AC}{1+S/K_i + (C+BC+AC)/K_m} + kC \cdot A + D\Delta AC$$

データ駆動型の縮約

- スケーリング性の数理構造を、データ解析から抽出する