

# Self-Assembly of a Lamellae-Forming Block Copolymer on Sparse Nanopatterns



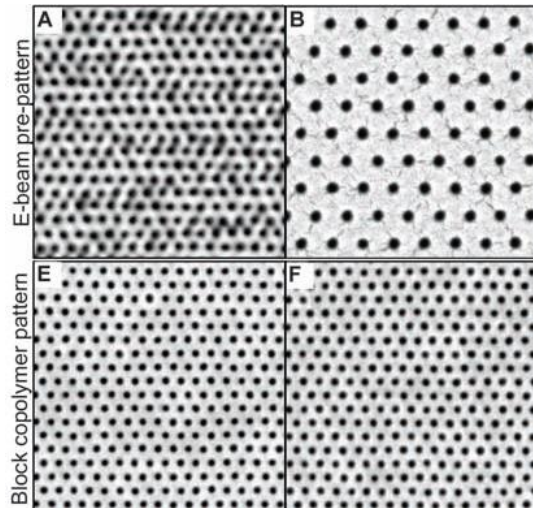
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Liu, P.F. Nealey and J. J. de Pablo

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# Interpolation on sparse nanopatterns

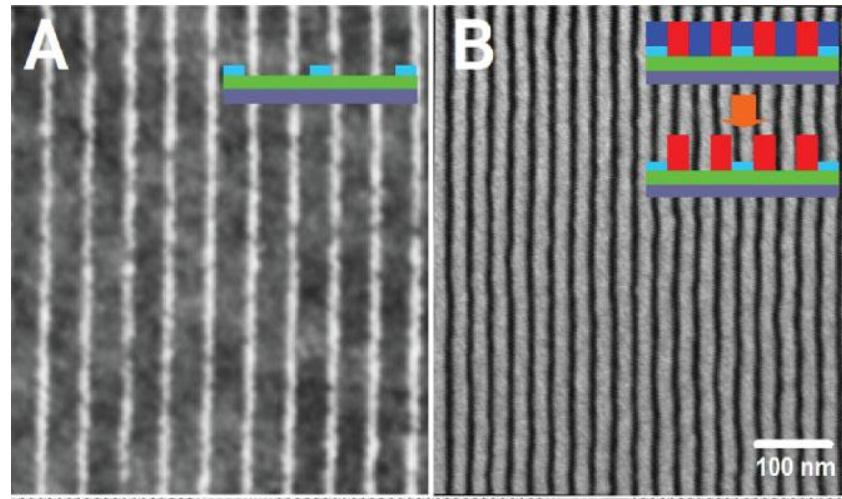
Block-copolymers can form defect-free structures on sparse patterns.

cylinder-forming copolymer



Ruiz, R. *et al. Science*, **2008**.  
One spot for 4 cylinders

lamellae-forming copolymer



Cheng, J. Y. *et al. Adv. Mat.*, **2008**  
One stripe for 2 lamellae

What morphologies arise in density multiplication with symmetric copolymers?  
How robust is the multiplication process ?

# Interpolation on sparse nanopatterns

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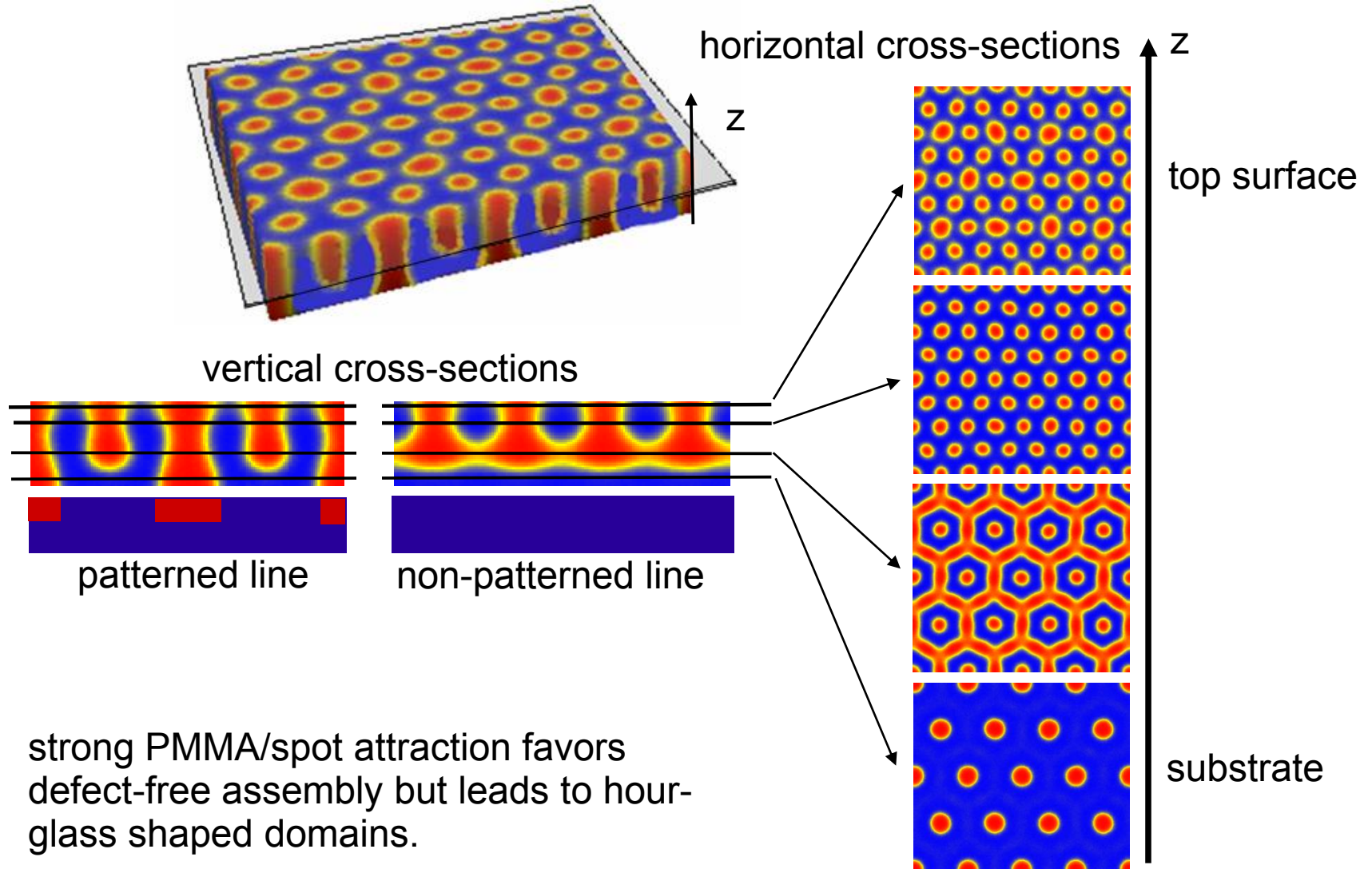
What are the conditions for a successful interpolation?

*Two ways to envision the problem:*

1. The block copolymer mostly adopts its bulk morphology. The nanopattern serves only to pin the domains and enforce long-range alignment.

2. The nanopattern induces non-bulk morphologies and interpolation is only possible with a careful choice of the pattern properties

# Non-bulk morphology in interpolation of cylinders

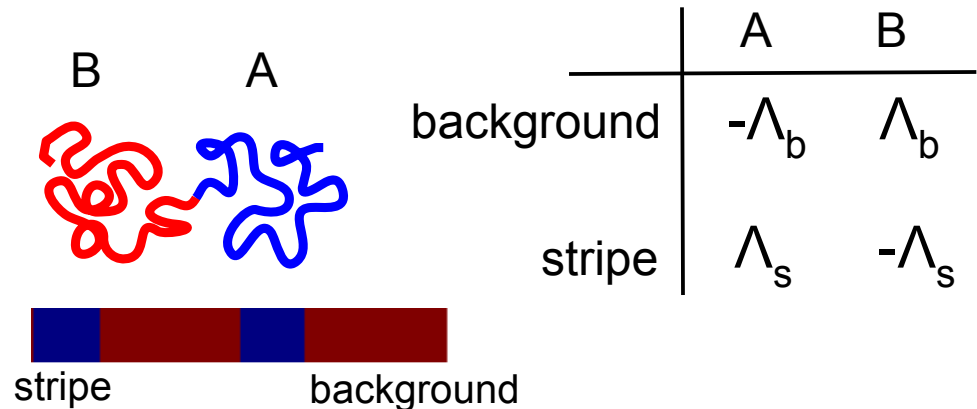
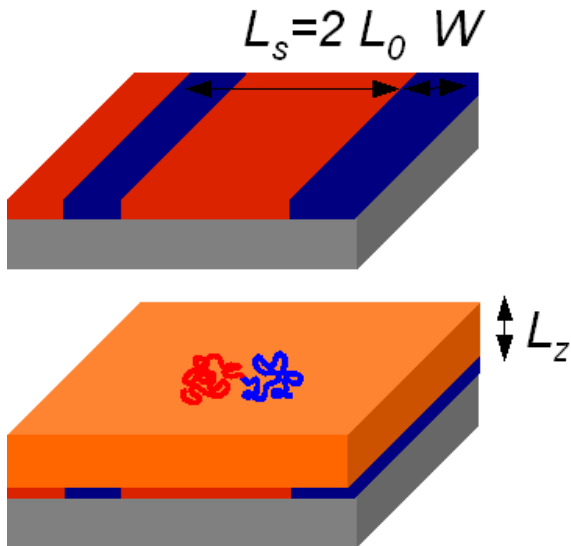


# Experimental system

A symmetric diblock on a stripe-patterned substrate

A large parameter space

- film thickness  $L_z$
- pattern periodicity  $L_s$
- stripe width  $W$
- block/pattern strength of interaction

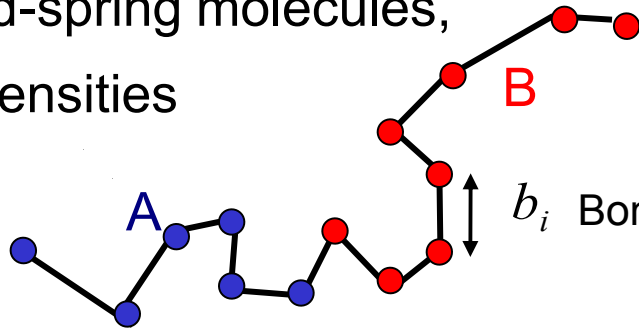


A combinatorial exploration of the parameter space is needed

# A coarse-grained model

## A mesoscopic description

Gaussian chains, discretized into bead-spring molecules, interact via a functional of the local densities

$$H / kT = 3/2 \sum_i b_i^2 + E_{int}[\phi_A, \phi_B]$$


$b_i$  Bond length

Interaction energy:

$$E_{int}[\phi_A, \phi_B] / \sqrt{N} \sim \underbrace{\chi N \int dr \phi_A \phi_B}_{\text{incompatibility}} + \underbrace{\kappa N \int dr (\phi_A - \phi_B)^2}_{\text{finite compressibility}}$$

Helfand, J. Chem. Phys. (1975)

## Coarse-grained parameters

$R_e$  end-to-end distance

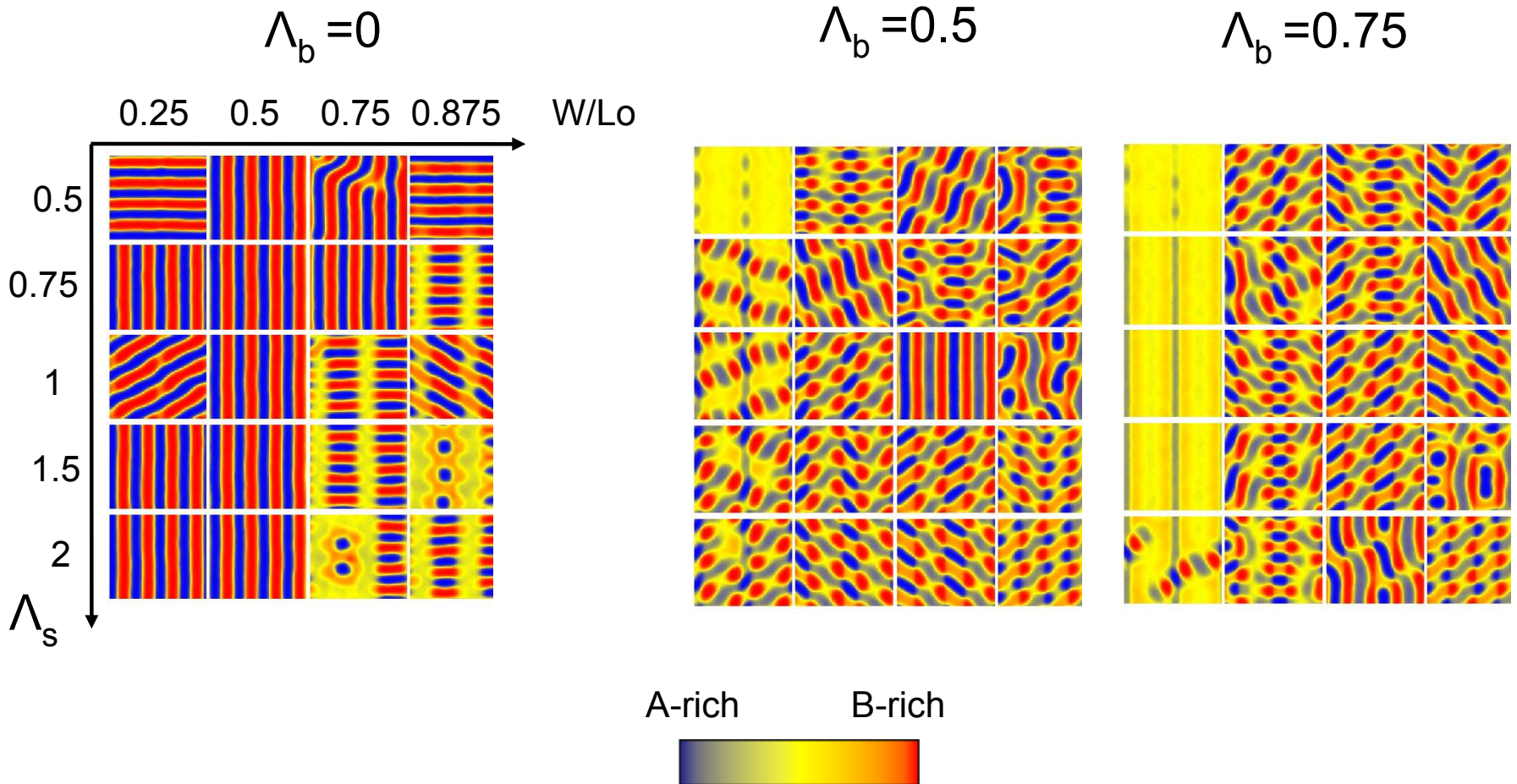
$\sqrt{N}$  number of chains in the volume occupied by a chain

$\chi N, \kappa N$   $N$ , number of beads per chain  $\sqrt{N} = \rho_{chain} R_e^3$

# A combinatorial approach

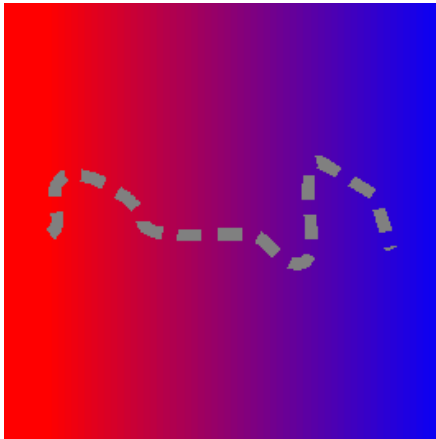
A simulated system typically includes 10000 chains.

The method is efficient enough to consider hundreds of parameter combinations.



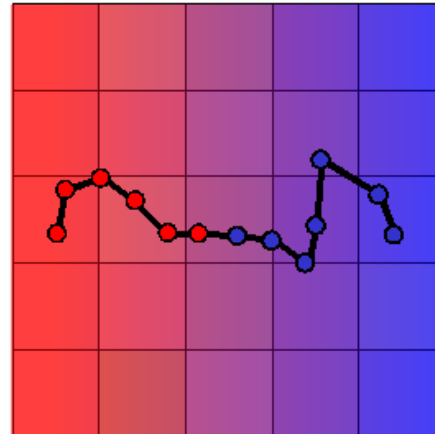
# Methods

## Self-consistent field theory



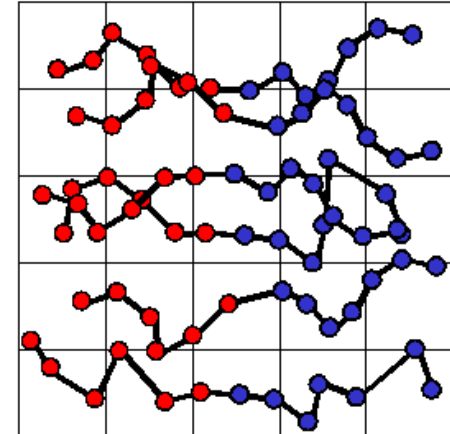
- field-based
- neglect fluctuations
- modified diffusion equation

## Single-chain in mean-field simulations



- particle-based but fields
- includes fluctuations
- two-step cycle

## Monte Carlo simulations



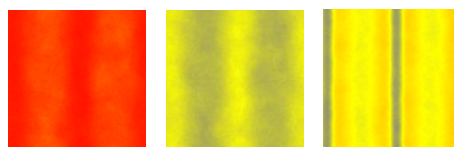
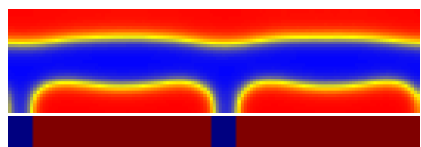
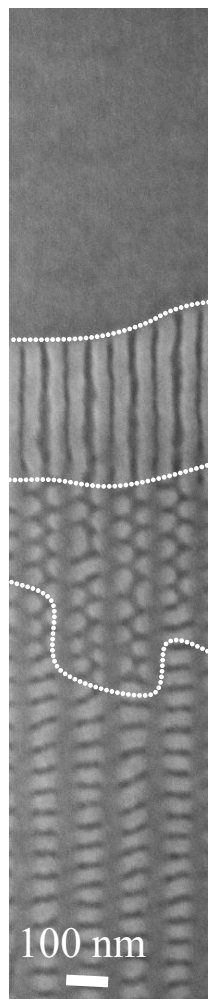
- particle-based, no fields
- includes fluctuations
- genuine MC simulation



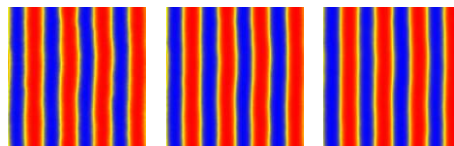
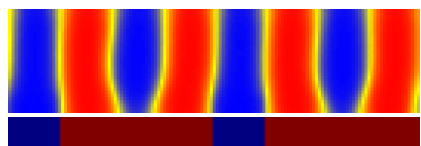
# A variety of morphologies

Side views:

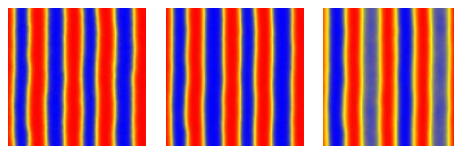
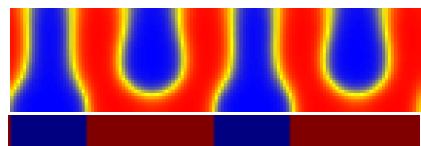
Top views:



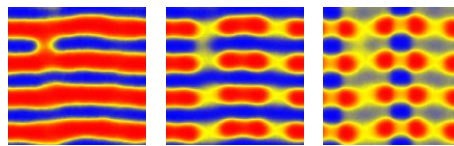
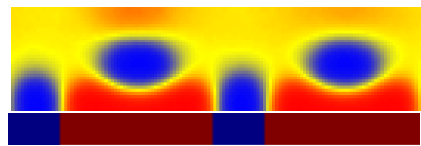
Horizontal lamellae



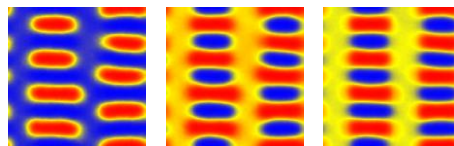
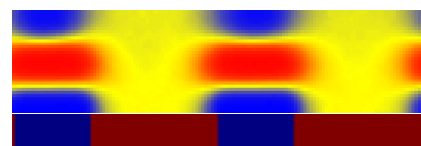
Vertical lamellae



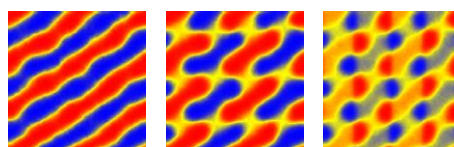
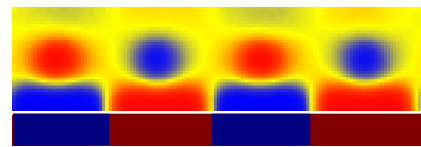
Vertical lamellae  
(asymmetric)



Dots



Mixed lamellae



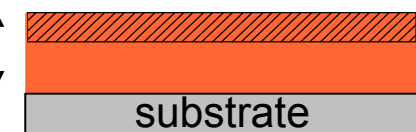
Checkerboard

$d/H=1/4$

$1/2$

$1$

$H$



$d$

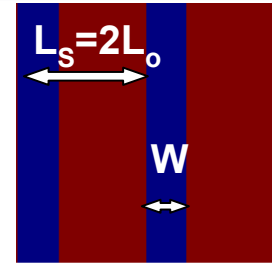
$H$

substrate

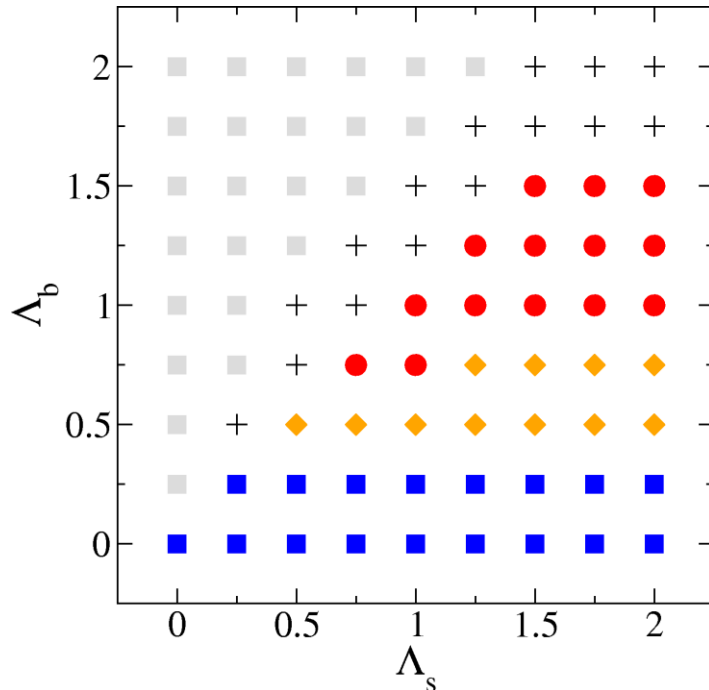
# Exploring the parameter space

Effect of changing the pattern selectivity

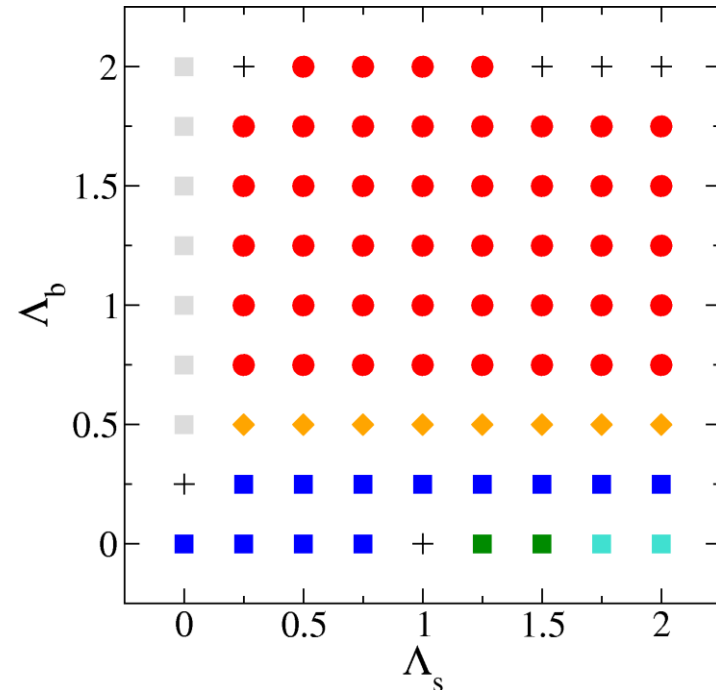
Fixed interpolation ratio  $L_s/L_o=2$   
 Fixed thickness  $H=L_o$



$W/L_o=0.5$



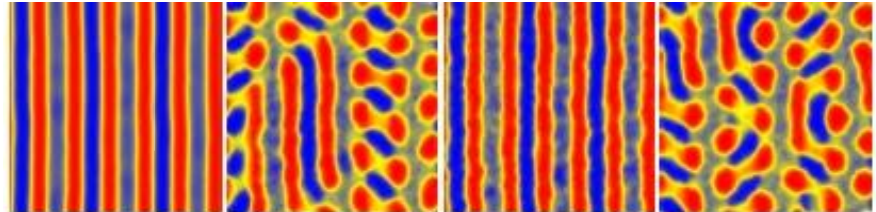
$W/L_o=0.75$



- Horizontal Lamellae
- Vertical Lamellae
- Mixed lamellae
- Dots
- ▲ Checkerboard
- ◆ Dots and lamellae
- Horizontal and mixed lamellae
- + Hybrid

# Thermodynamic integration

- Two competing morphologies  
Which one is equilibrium?



4 distinct  
simulations

- Free energy difference  
going from state 1 to state 2  
:

$$\Delta F_{1 \rightarrow 2} = \int du \left\langle \frac{\partial H}{\partial u} \right\rangle$$

The integration path must be fully reversible and continuous.

- Impose an external field that constrains the system to stay  
in the desired state:

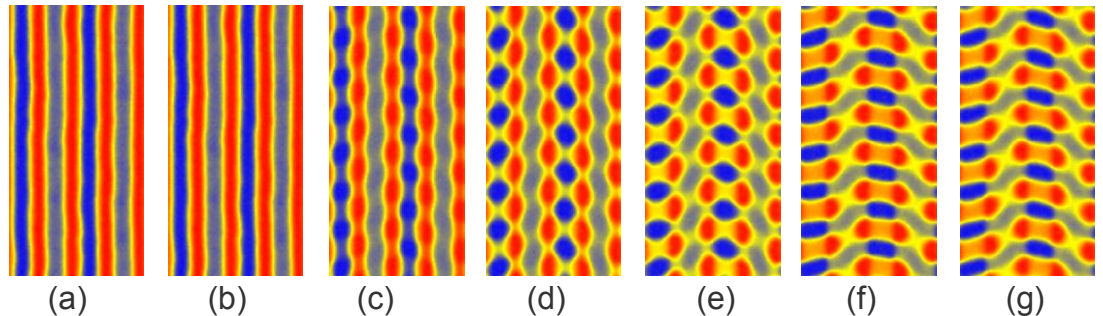
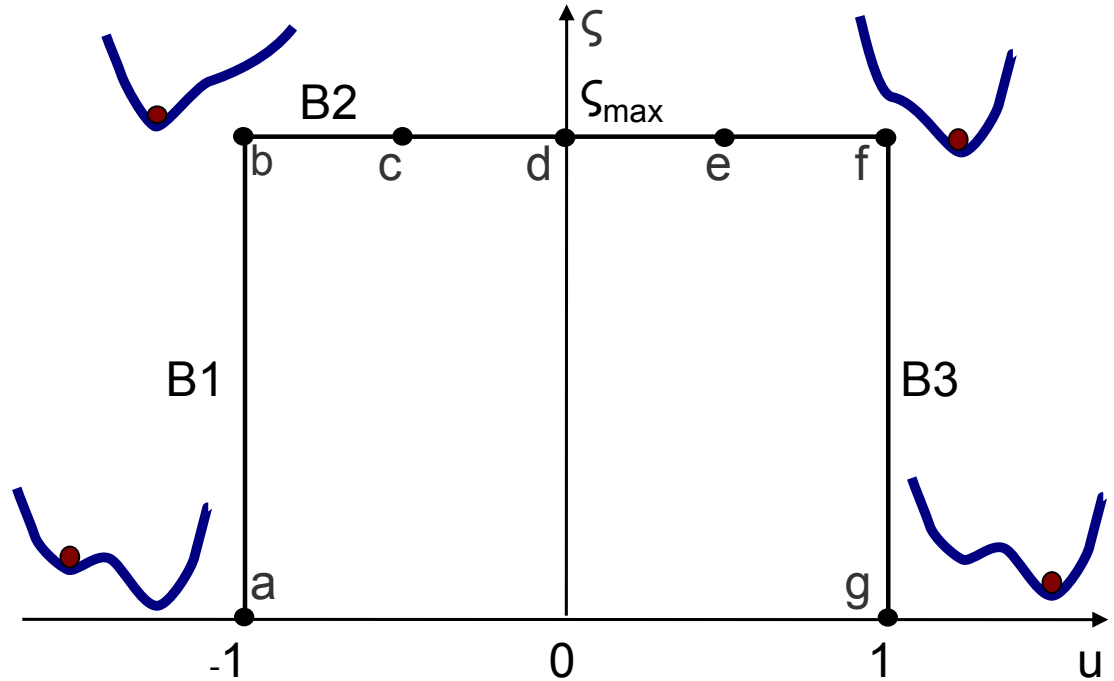
$$H_{ext} = \sum U_{ext}(\epsilon_i, K_i) \quad U_{ext}(\epsilon, K) = -\zeta f_{ext}(\epsilon) \mathcal{E}_K$$

# A Reversible path: from lamellae to dots

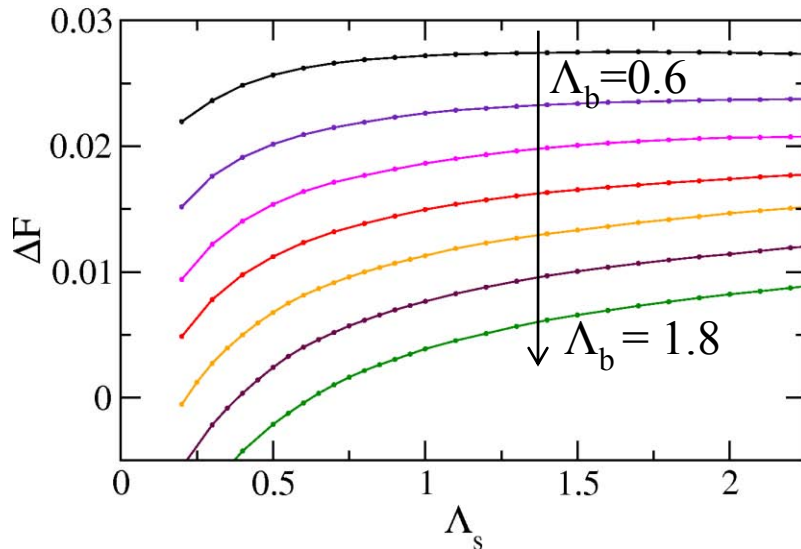
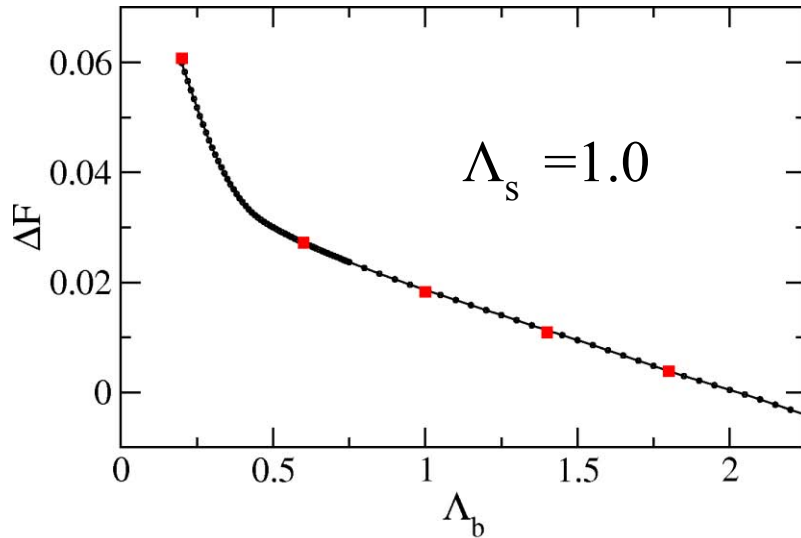
$$\Delta F = F_{dot} - F_{lam}$$

Three branches:

- Field branch B1: Start from lamellae and impose a lamellae-like external field to further stabilize morphology of the lamellae
- Mixing branch B2 : gradually convert lamellae into dots using an interpolated field
- Field branch B3 : decrease the dot-like field to zero.



# Free energy calculations



$$\Delta F = F_{dot} - F_{lam} \quad \Delta F \text{ in } k_b T / \text{chain}$$

- Absolute value of  $\Delta F$  computed along the external field path
- $\Delta F$  computed from the reference point by simple thermodynamic integration:

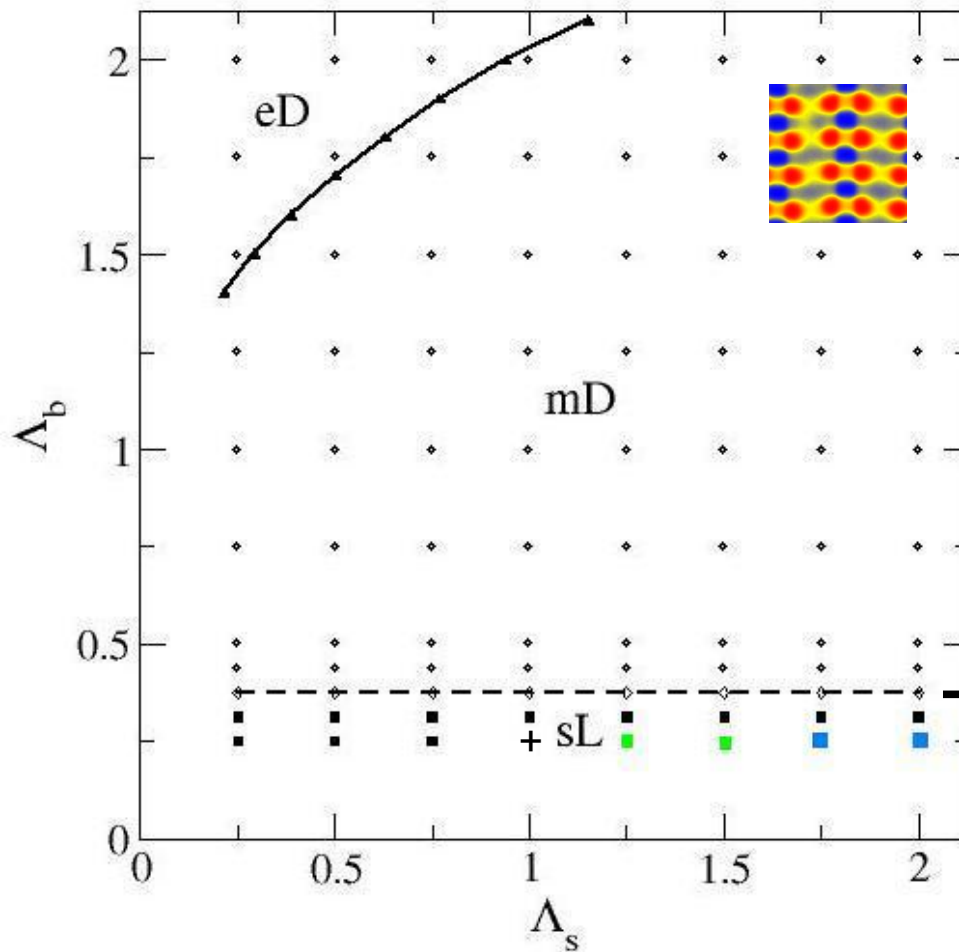
$$\Delta F = \int d\lambda_b \left\langle \frac{\partial H}{\partial \lambda_b} \right\rangle$$

→ good agreement between the two procedures

$\Delta F$  can then be computed for the entire plane  $\Lambda_s - \Lambda_b$ .

# Metastability vs equilibrium

$$W/L_0=0.75$$



Morphology obtained in simulations:

: lamellae

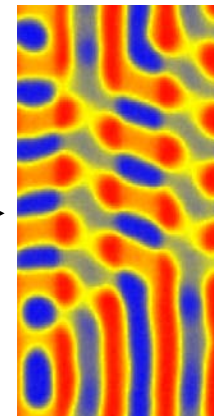
: dots

Three regions:

- eD : equilibrium dots

- mD: metastable dots

- sL : stable lamellae



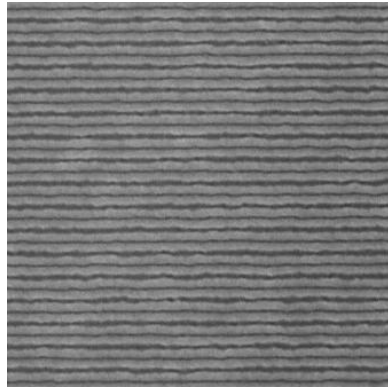
Formation of dots and lamellae in the same simulation box

This region of the parameter space is dominated by metastable dots.

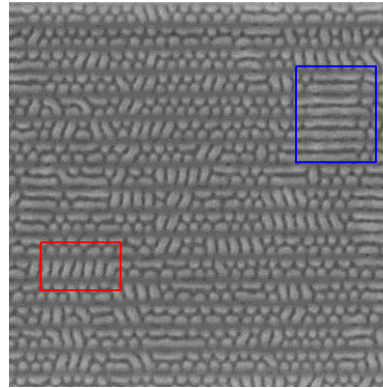
# Interpretation of experiments

Experiments

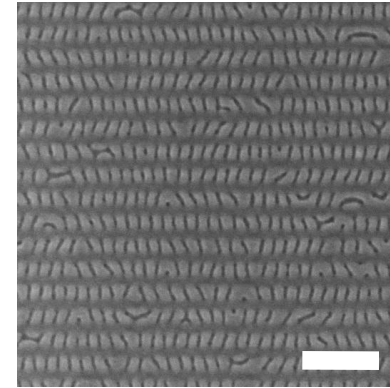
$W/L_0=0.57$



0.79



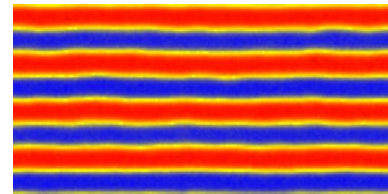
1.08



PMMA

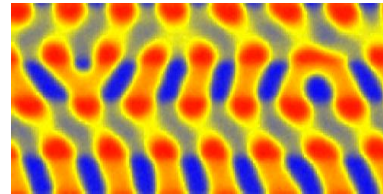
PS

Simulations



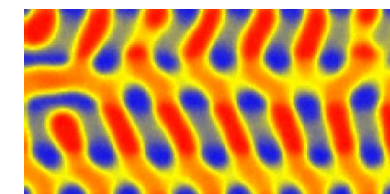
$W/L_0=0.5$   
 $\Lambda_b=0.3$

lamellae



0.75  
 $\Lambda_b=0.4$

metastable "red" dots



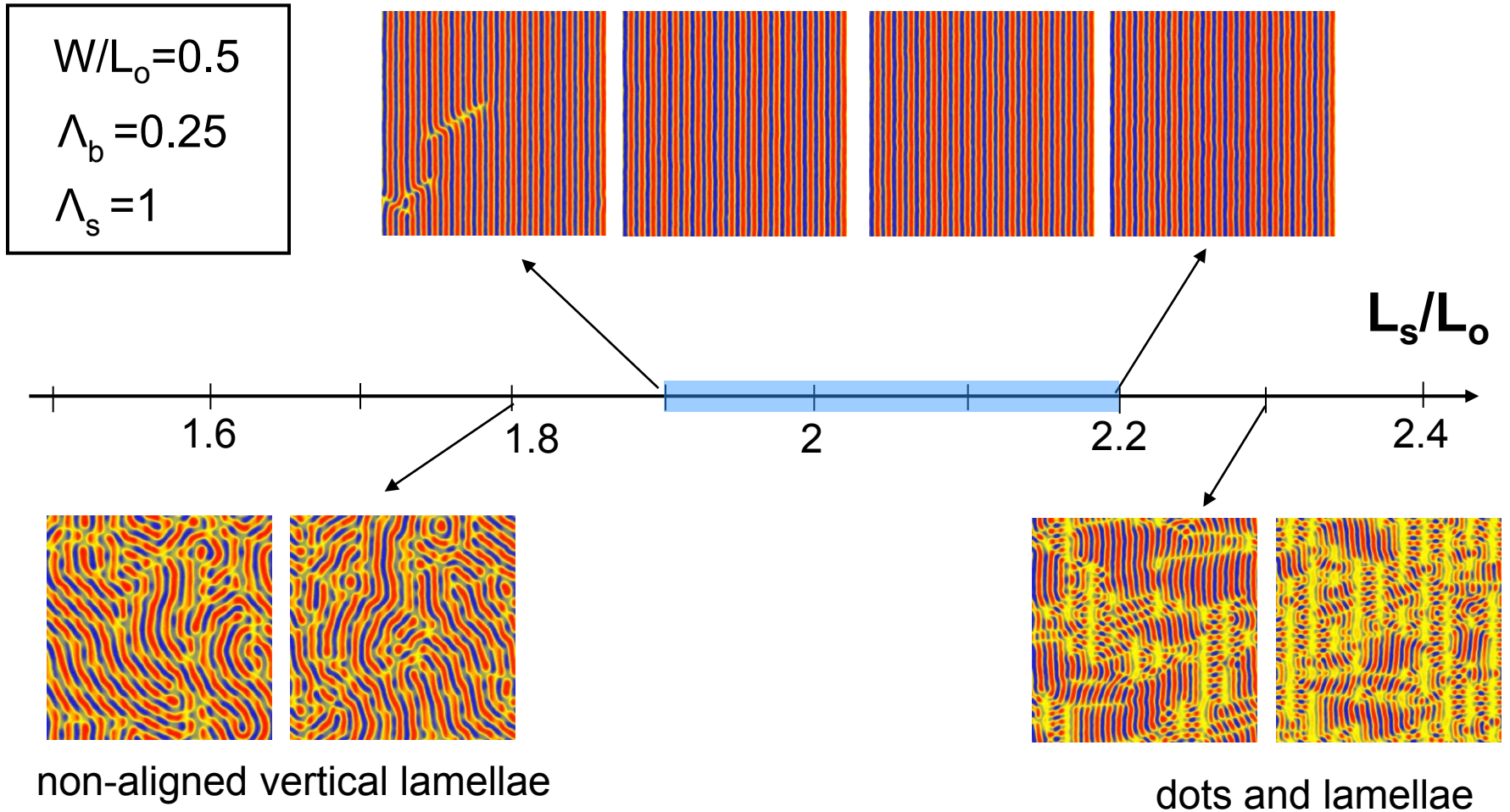
1  
 $\Lambda_b=0.4$

"blue dots"

PMMA

PS

# Effect of pattern commensurability





# Conclusions

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- Using MC simulations of a coarse-grained model, we can efficiently simulate three-dimensional systems and explore wide regions of parameter space.
- Thermodynamic integration can be used to determine the free energy difference between two ordered morphologies.
- The process of pattern interpolation with lamellae produces distinct morphologies: horizontal, vertical, vertical asymmetric, mixed lamellae, dots and checkerboard.
- In the vicinity of  $W/L_0=0.5$ , metastable dot structures are predominant. Only low strength of the background are lamellae preferred both thermodynamically and dynamically.



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# **Control of characteristic period, range of interpolation, and defects through homopolymer addition**

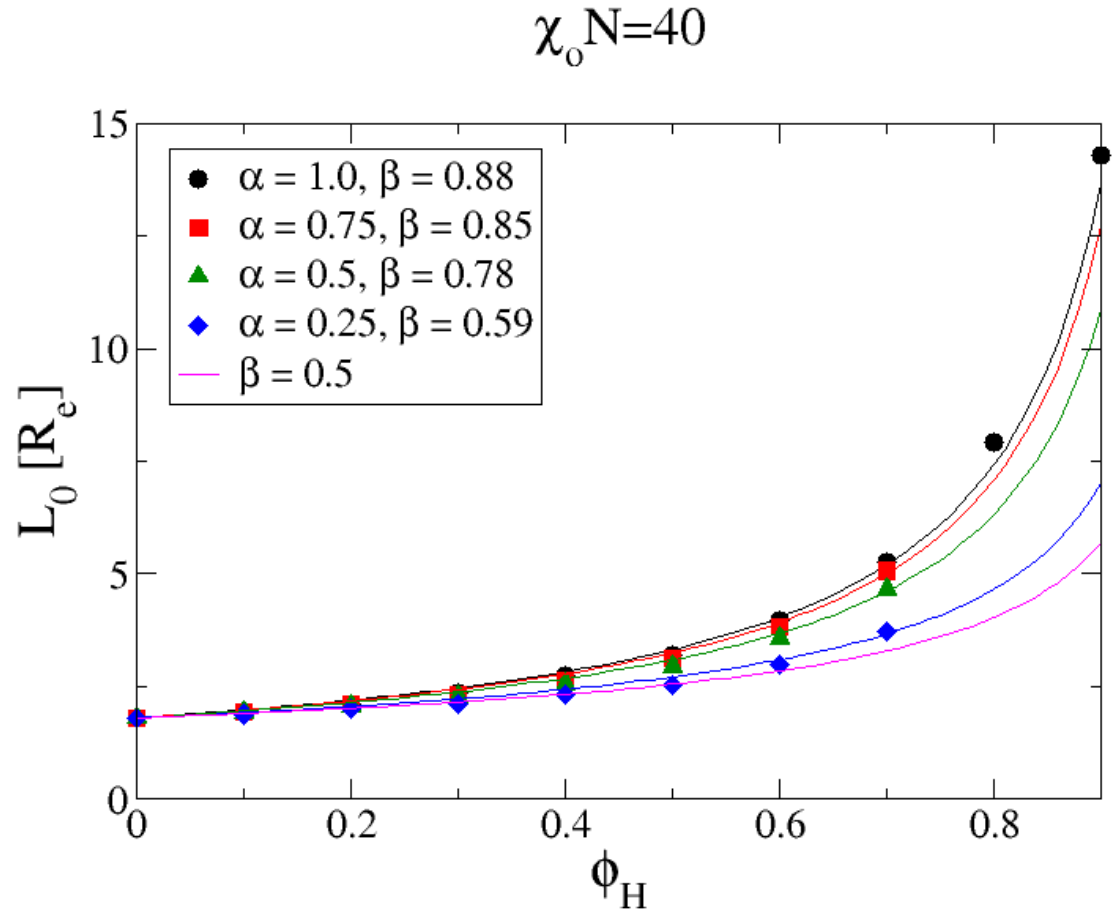
Darin Pike, Guoliang Liu, Paul Nealey, Juan de Pablo

# Ternary Mixtures, Optimal Period

The diblock copolymer can be swollen by each homopolymer, increasing the period.

The swelling can be fitted to the equation

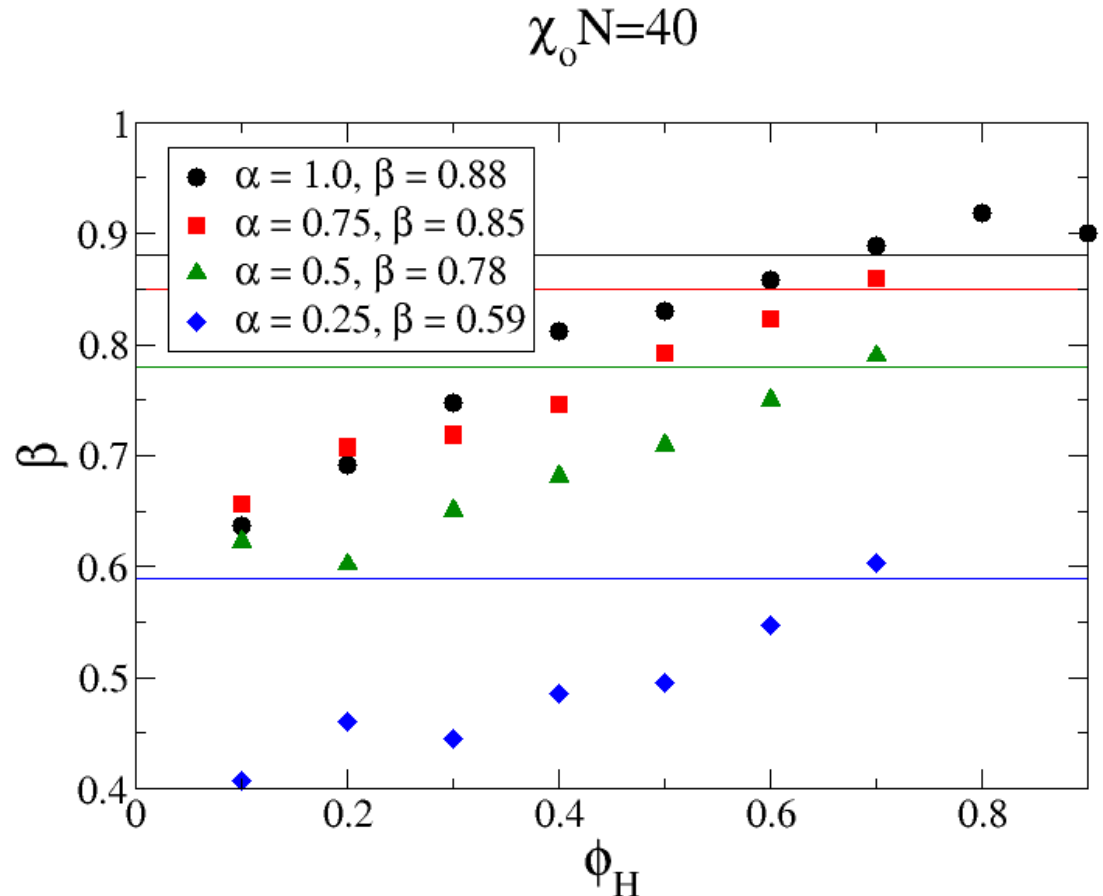
$$L_0(\phi_H) = \frac{L_0(\phi_H = 0)}{(1 - \phi_H)^\beta}$$



# Values of $\beta$

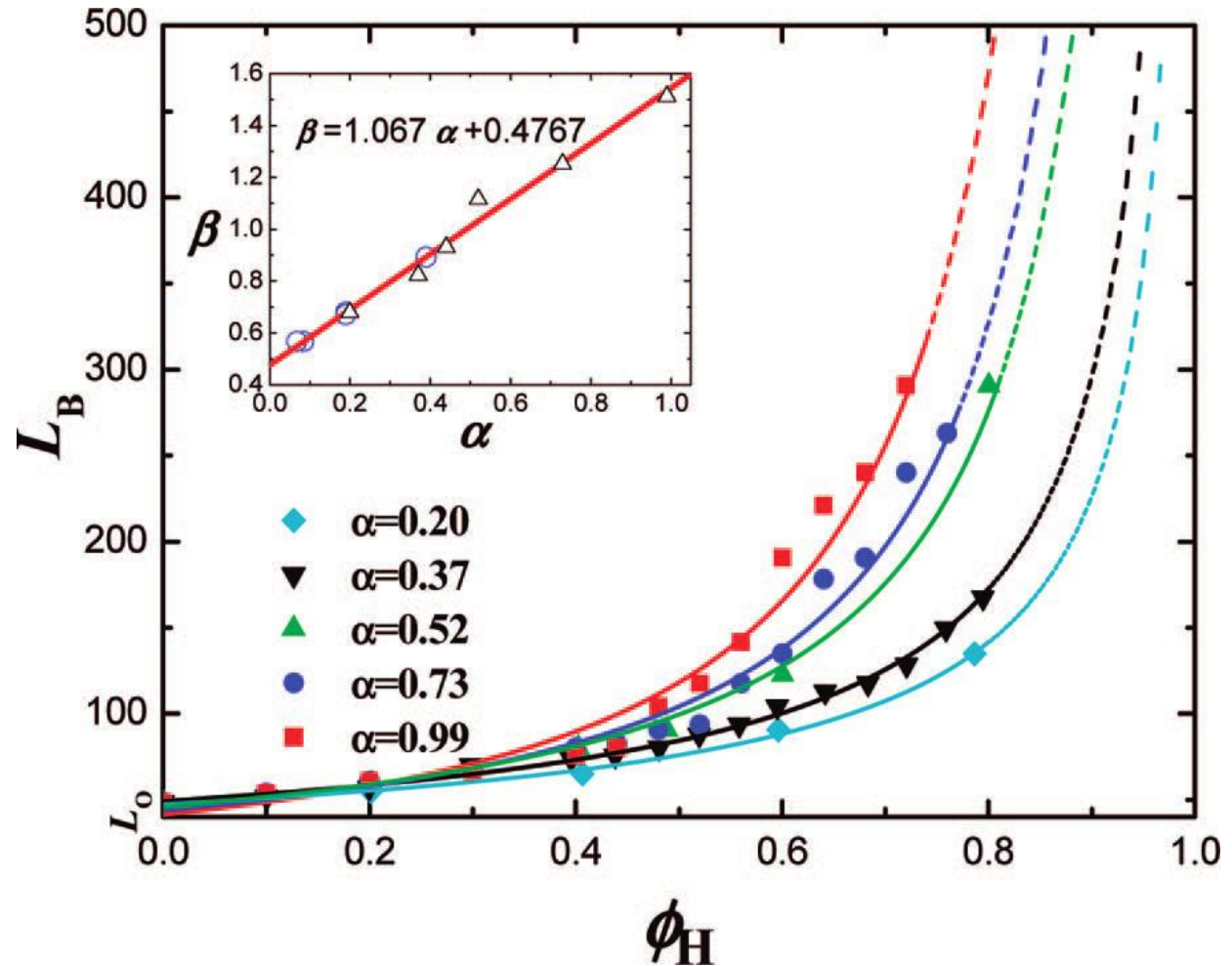
The value of  $\beta$  drifts as the lamellae become more swollen with homopolymers.

The curves on the preceding slide use the  $\beta$  values at around  $\phi_H = 0.7$ .



# Experimental Results

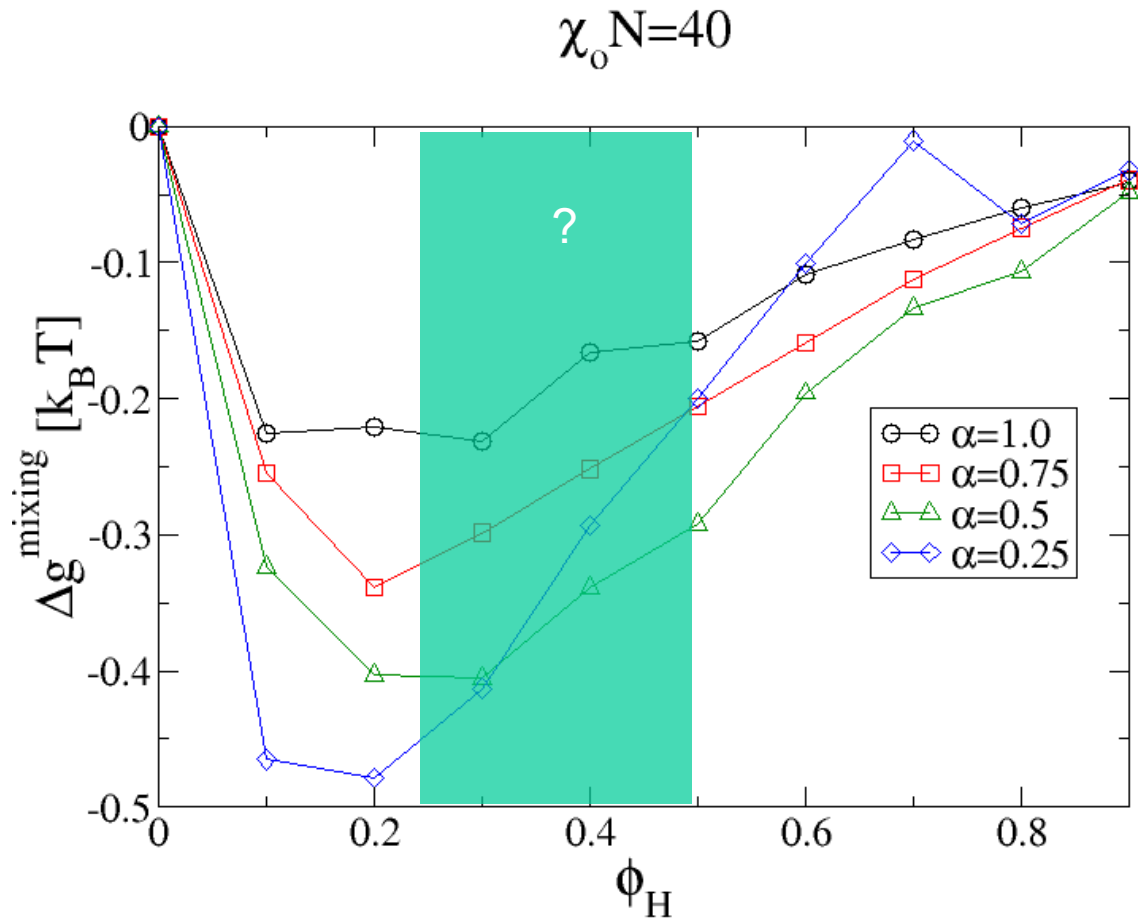
Experimentally, Guoliang produced larger values of  $\beta$  with a linear dependence in  $\alpha$ .



# Energy of Mixing

Free energy of mixing can be determined from Monte Carlo simulations.

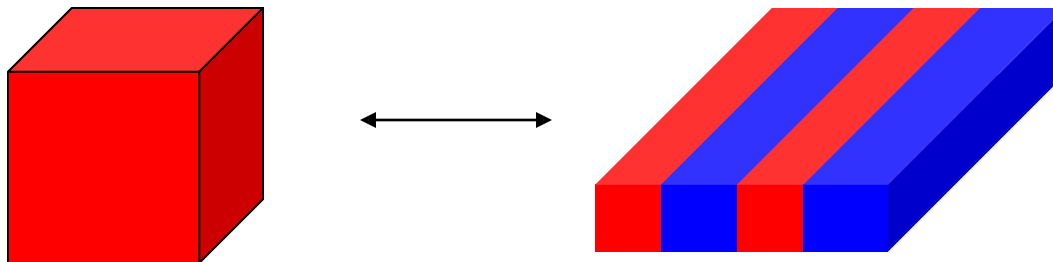
This value, along with interfacial energy and surface energy, can be used to determine where defect free structures are possible.



# Optimal Swelling with Gibbs ensemble

To determine the ideal swelling of the lamellae with homopolymers, a Gibbs ensemble simulation is run.

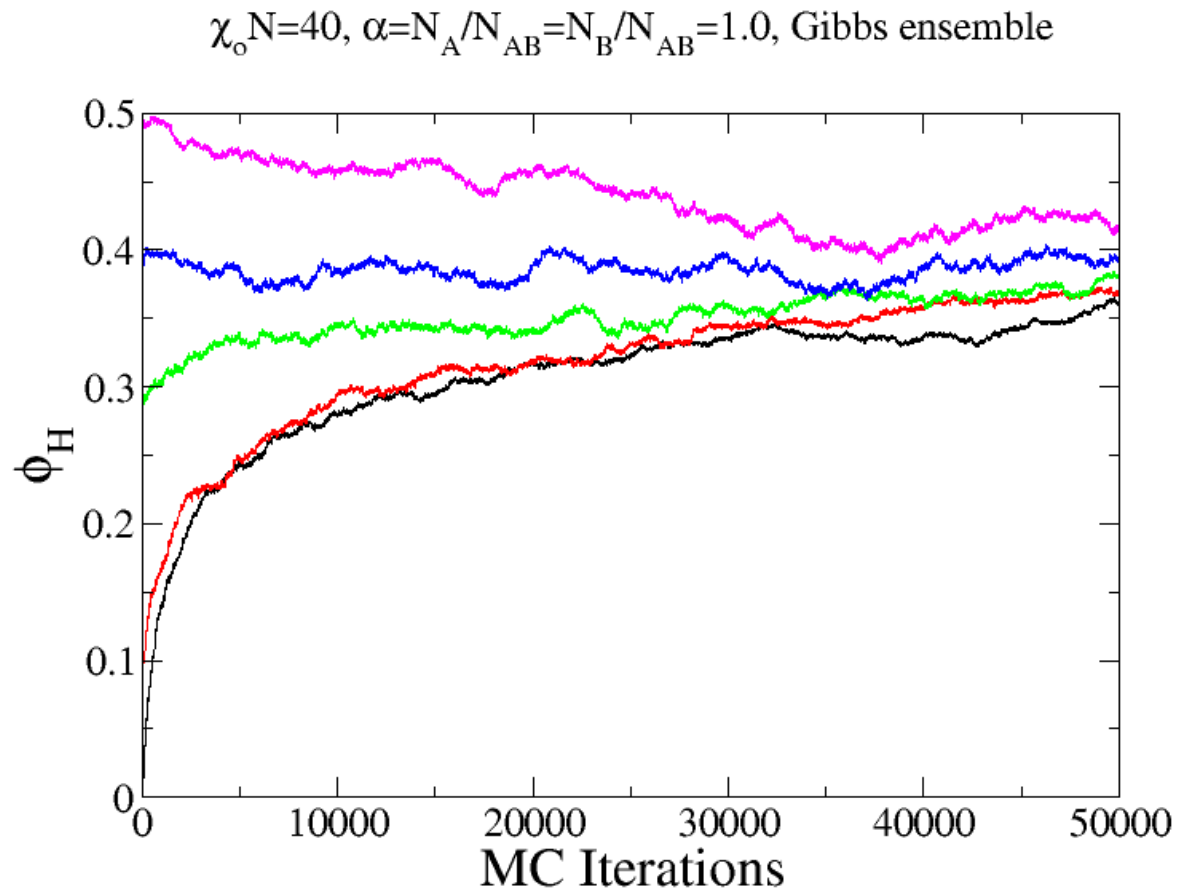
One simulation box is lamellae, the other is A-rich. The A-rich simulation box doubles as a B-rich simulation box.





# Optimal Swelling with Gibbs ensemble

Optimally, the lamellae is swollen with a volume fraction of 0.39 homopolymers when all chains are the same length.



# Comparing chemical potential

$\mu^{\text{ex}}$  includes the ideal mixing term.

	Lamellar phase	A-rich phase
$\mu^{\text{ex}}$ of copolymer	47.6	47.8
$\mu^{\text{ex}}$ of A polymer	43.3	43.3
The average volume fraction of copolymers in the A-rich phase is $2.1 \cdot 10^{-5}$ . The error in this value may be up to 20%, so it is close enough to $1.8 \cdot 10^{-5}$ , the value that gives $\mu^{\text{ex}}=47.6$ .	43.3	-

For  $\mu^{\text{ex}}$  of the B homopolymer to match in the 2 phases listed above, the volume fraction in the A-rich phase must be  $8.3 \cdot 10^{-14}$ . In the Monte Carlo simulation, there is never a B homopolymer in the A-rich phase. The simulation would need to be run over 100 years before a B homopolymer ends up in the A-rich phase.

# Comparing to SCFT

The ideal MC volume fractions in the A-rich phase (from chemical potential calculations) match closely with the SCFT:

A-rich phase	MC, $\chi_0 N=40$ , $\chi N=32.8$	SCFT, $\chi N=30$	SCFT, $\chi N=35$
$\phi_{\text{copolymer}}$	$1.8 \cdot 10^{-5}$	$2.7 \cdot 10^{-5}$	$3.0 \cdot 10^{-6}$
$\phi_{\text{B homopolymer}}$	$0.33$	$0.31$	$0.30$

The SCFT predicts slightly less homopolymers in the lamellar phase:

Lamellar phase	MC, $\chi_0 N=40$ , $\chi N=32.8$	SCFT, $\chi N=30$	SCFT, $\chi N=35$
$\phi_{\text{homopolymers}}$	0.39	0.36	0.34

# Optimal Period

The A-rich phase is almost pure A.

Thus, the maximally swollen lamellae can be approximated by equating the chemical potential of the homopolymers in the pure phase with that in the lamellae.

I will verify this trend with Gibbs ensemble, as it is opposite to what is expected.

