



**Overview and Motivation**

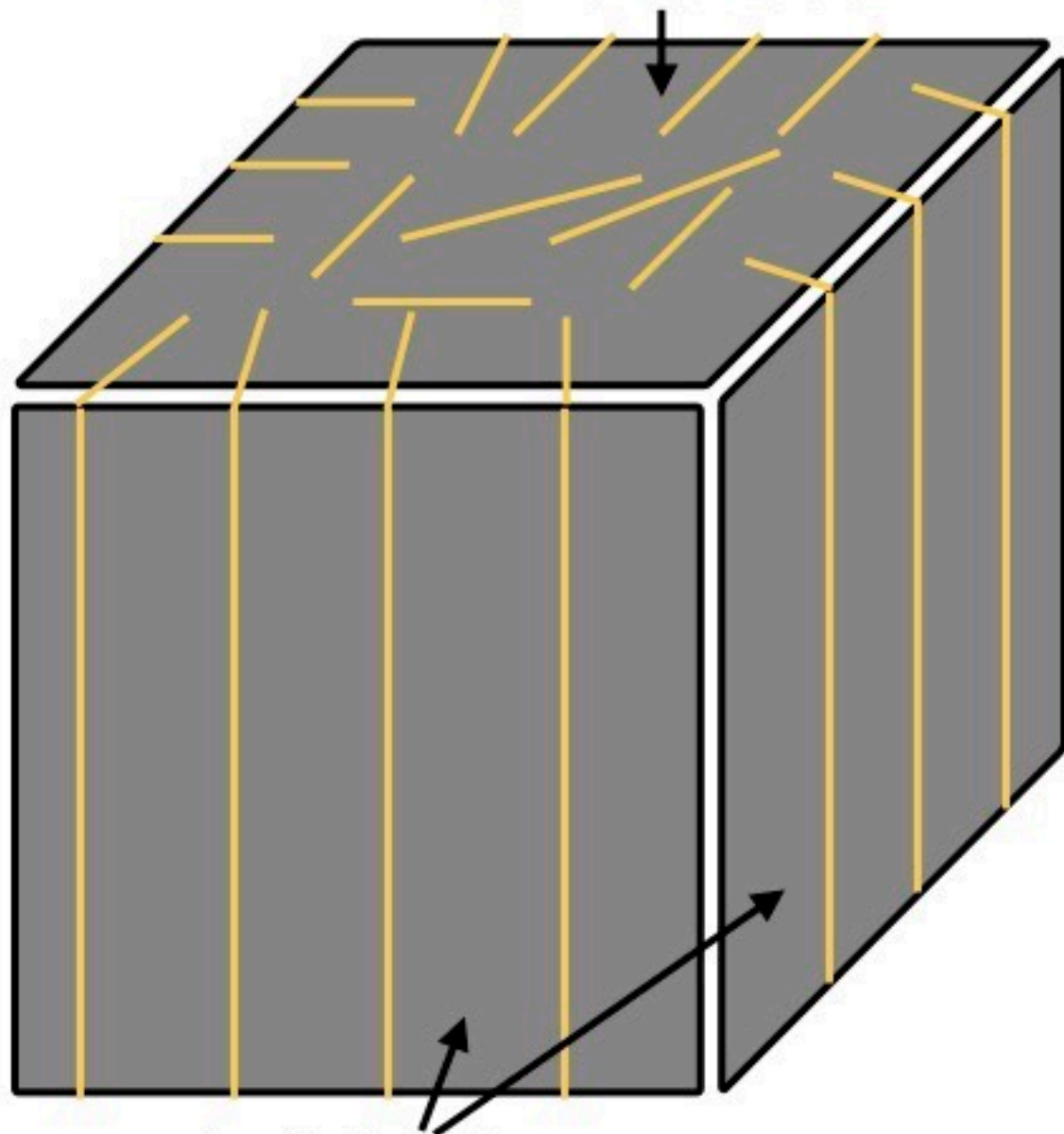
# The Plant Cell Periodical Microbial Array (PCMA) Database

- The PCMA DGG builds on the CMA DGG, and uses DGGML, which is more flexible and efficient.
- We test the effect boundary conditions and boundary shape may have on alignment.
- Key results:
  1. The array orientations of square of the square domains indicate multi-modal behavior.
  2. Arrays in rectangular domains reorient with a change of boundary conditions.

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**Periclinal Face**



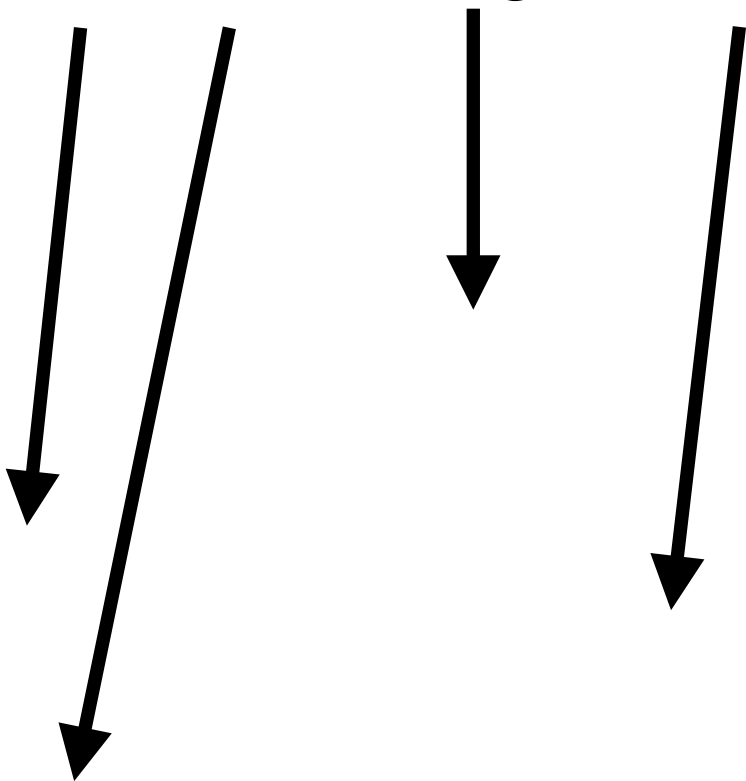
**Anticlinal Face**

Figure 39: Visualization of our approximation of the cell as a polyhedral prism, where we restrict our simulations to the periclinal face and have a “picket fence” idealization<sup>1</sup>.





CLASP uniformly localized  
on the edges.



1. (shaw, 2013)

which is more flexible and efficient.

• We test the effect boundary conditions and boundary shape may

1. The array orientations of squares are domains indicate

2. Arrays in rectangular domain oriented with angle of

• **Key results:**

have on alignment.



multi-modal behavior.

• The PGMA DGG builds on the CMADGG, and uses DGGML,

boundary conditions.

1. Square (

2. Rectangular(





• The PCMA experiments with two faces:



hours of biological time:

• Within each category 16 scenarios are run, 16 repetitions, 92 experiments for 2

(4) through (6), CLASP on the boundary with high rate of zippering.

(2) CLASP on the boundary with high rate of cross over.

(1) Collision Induced Catastrophe Boundary with high rate zippering.

(3) influx from the antichamber with high rate of zippering

$$5\mu m \times 5\mu m \equiv 25\mu m^2$$

$$8.33 \mu m \times 3 \mu m \equiv 25 \mu m^2$$



approximation of the cell as a polyhedron

finance', 'idealization'.<sup>1</sup>

Figure 39: Visualization of our

prison, wherever restrictions inculcations

to the principal factor and have a “pick

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