

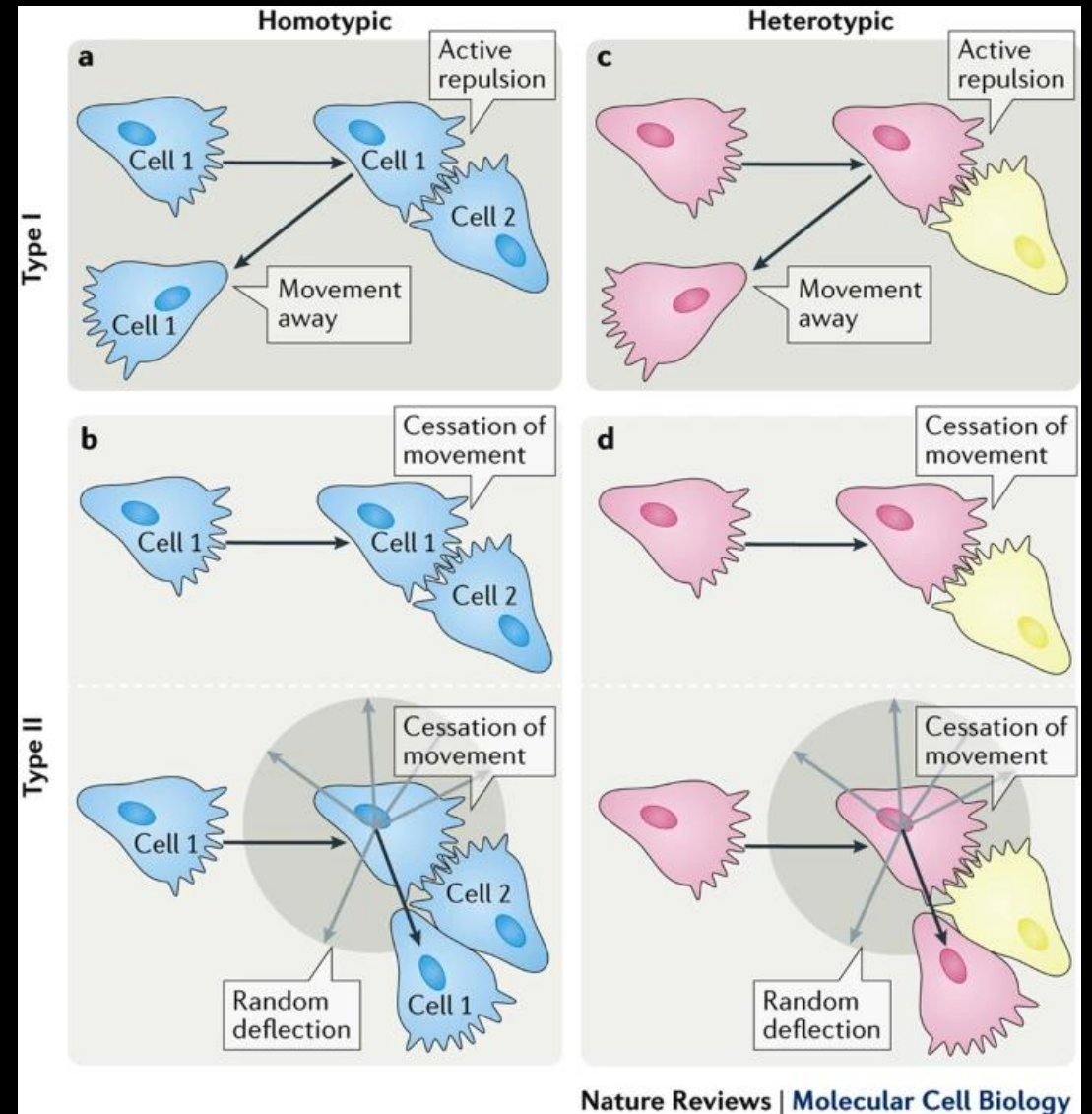
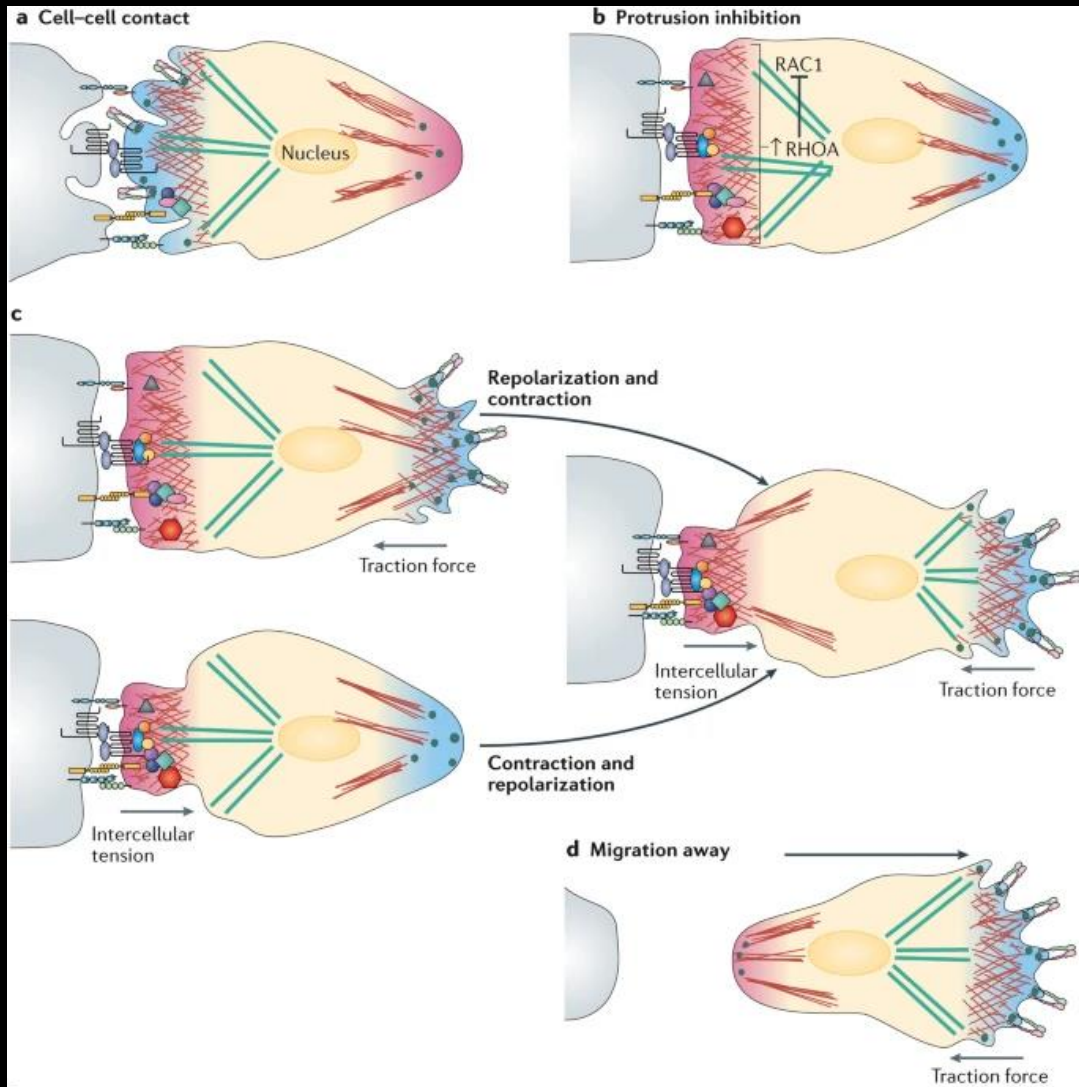
# Modeling Contact Inhibition of Locomotion

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&

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# What is Contact Inhibition of Locomotion, (CIL)?



# Why model CIL?

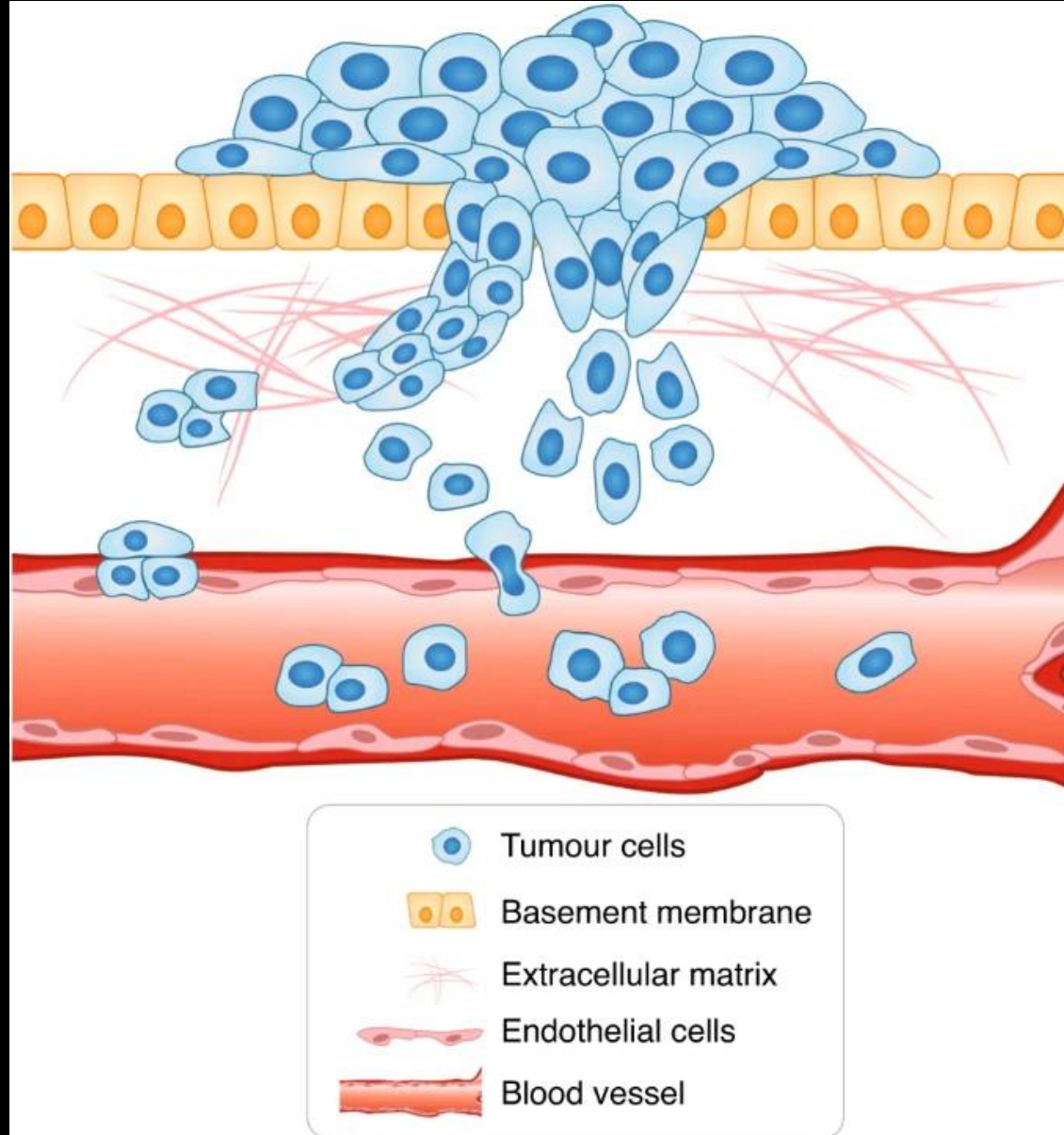
CIL has now been observed in vivo:

- Cancer
- Neural crest cells
- Neurons
- Hemocytes
- Early endoderm

Models add to the understanding of CIL's role within migration, such as:

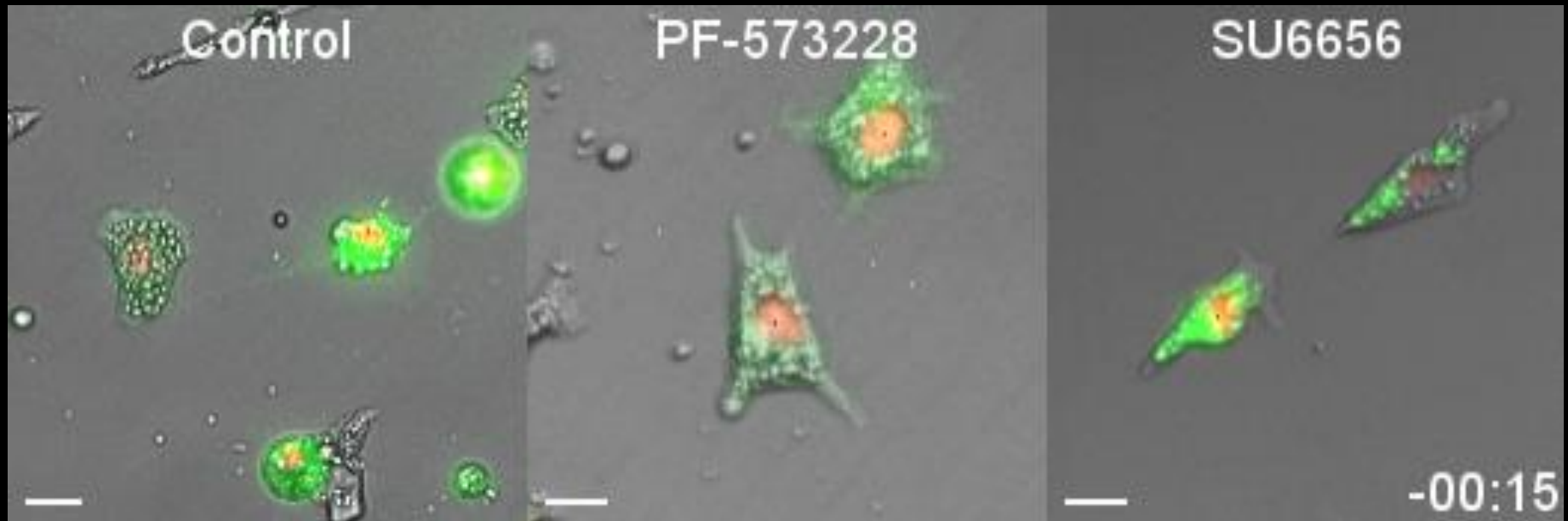
- Driving cellular dispersion
- Inducing cellular tiling
- Coordinating collective cell migration

# Cancer



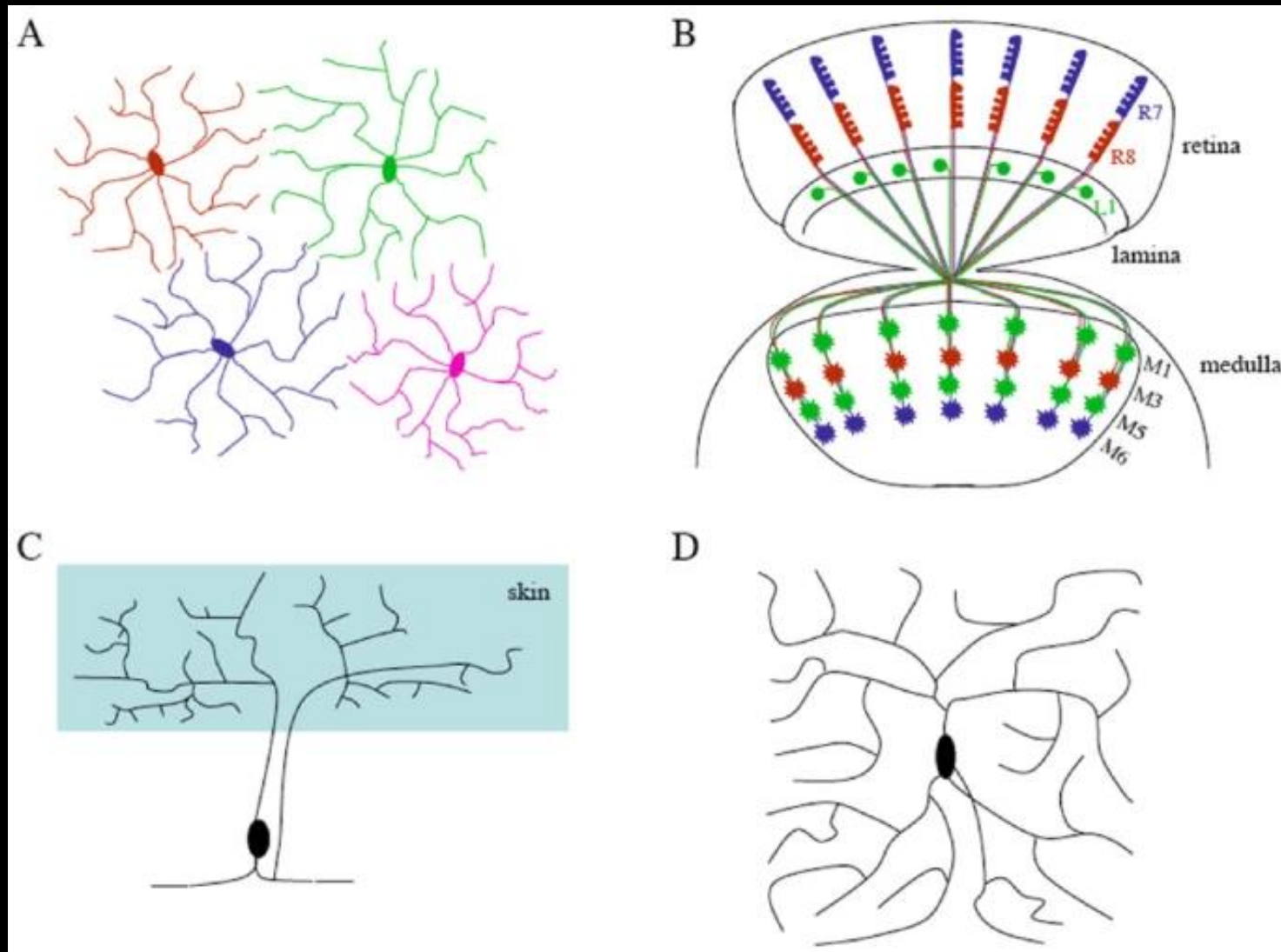
<https://doi.org/10.1038/s41416-020-01149-0>

# Neural crest cells



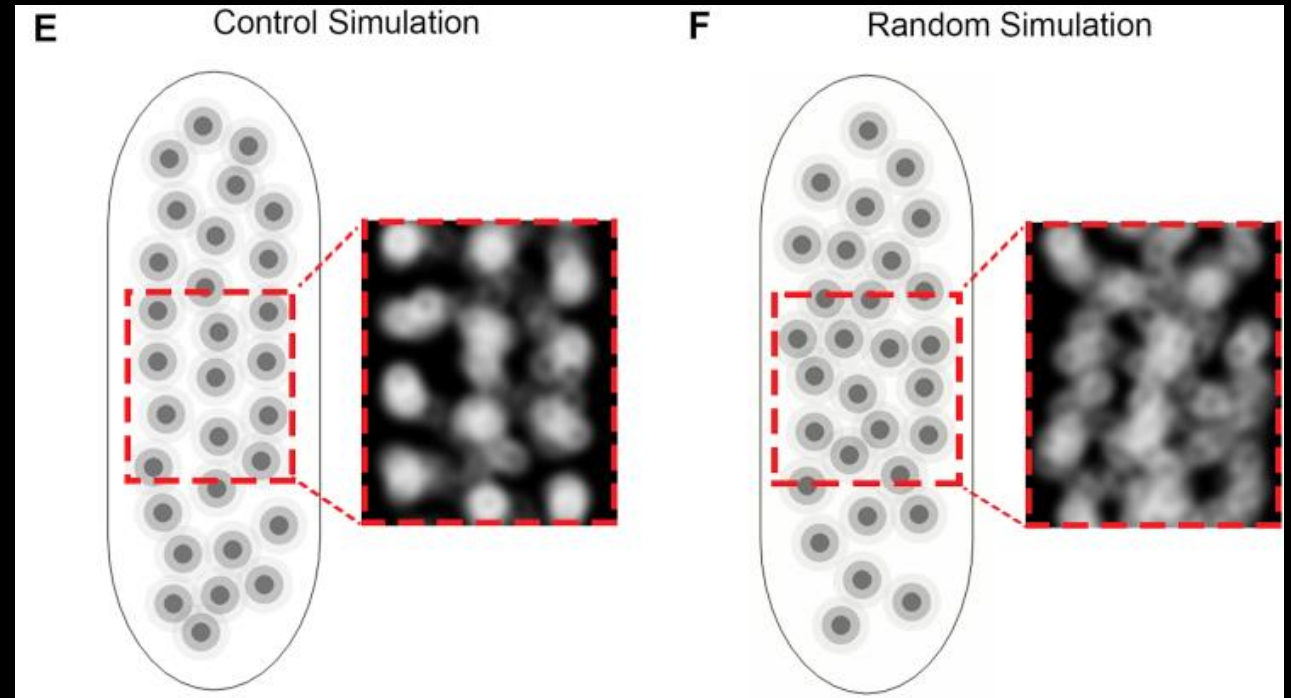
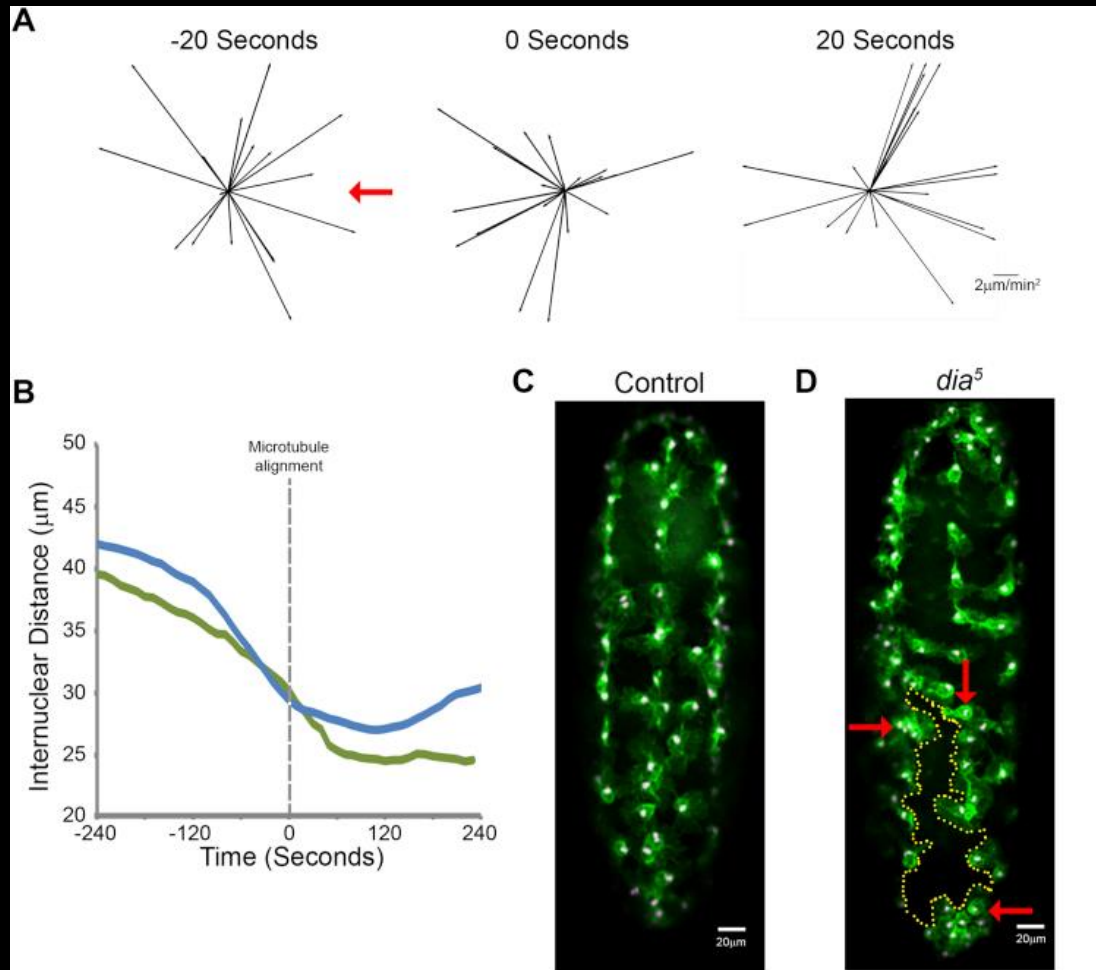
<https://doi.org/10.1016/j.devcel.2018.05.003>

# Neuronal tiling

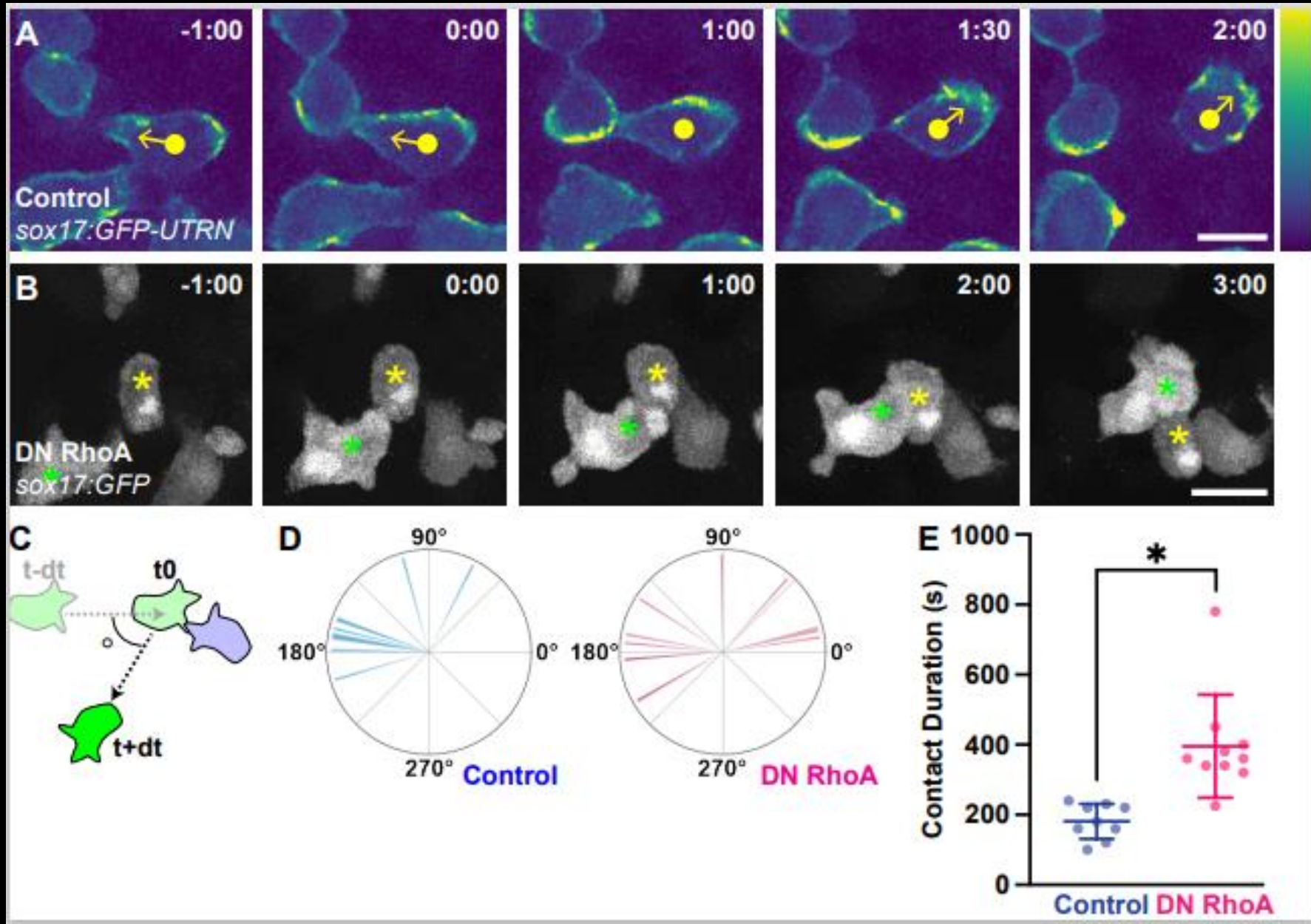




# Hemocytes



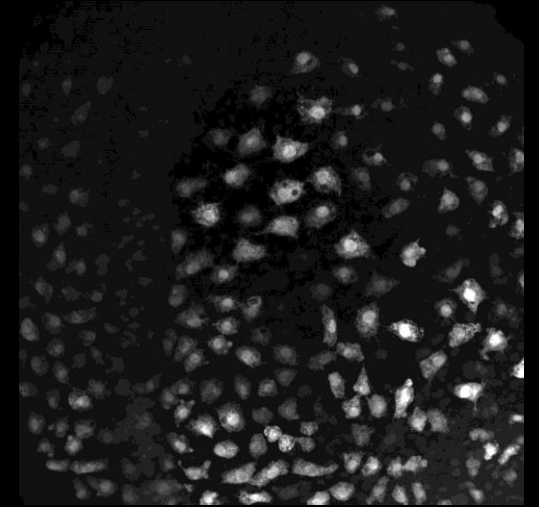
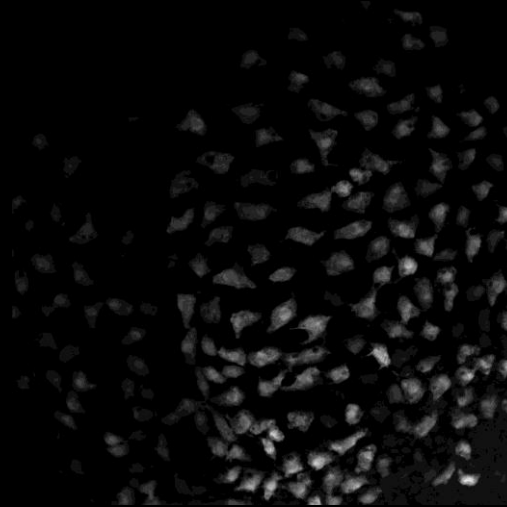
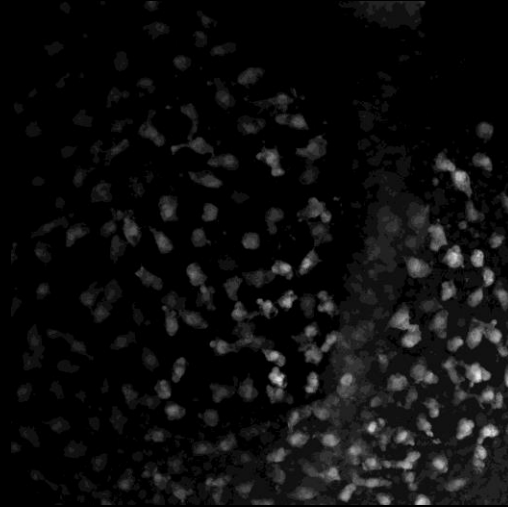
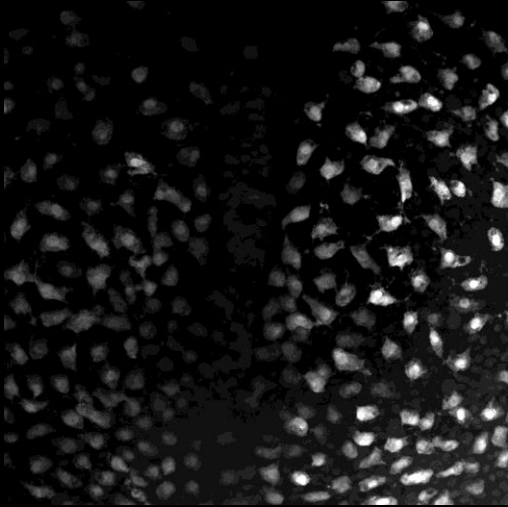
# Disruption of CL in endoderm



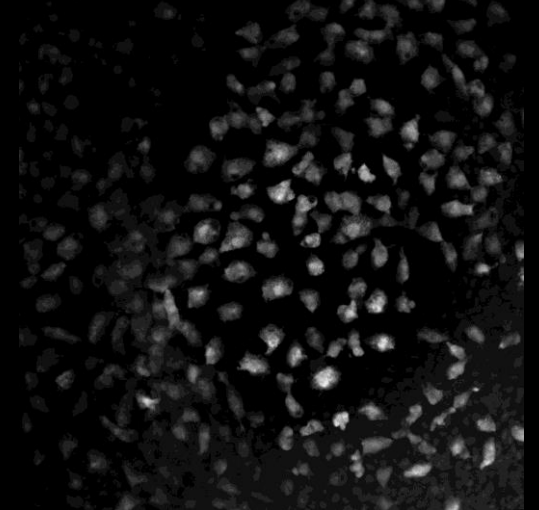
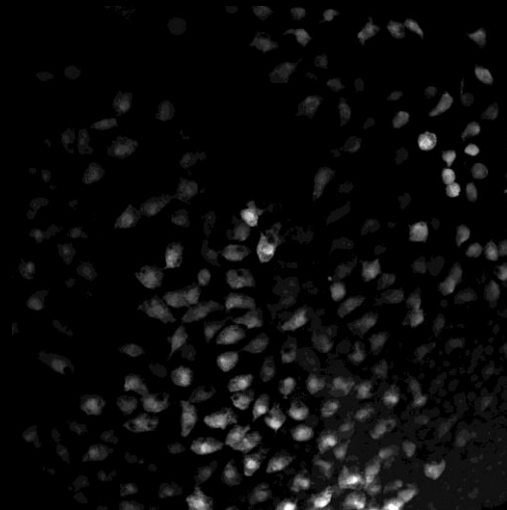
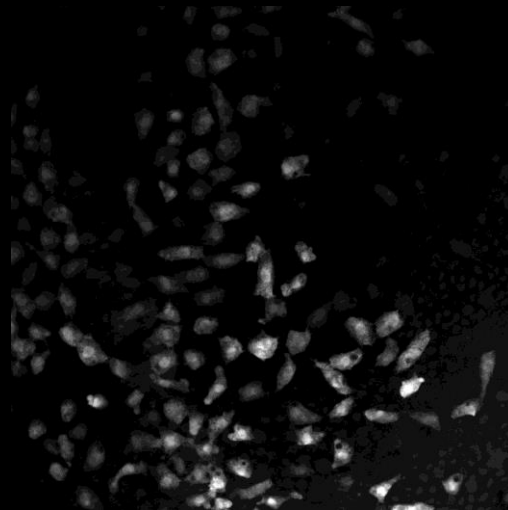
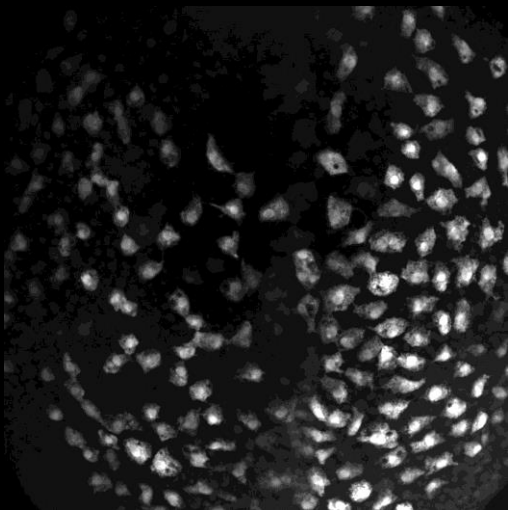


# Disruption of spacing regularity

Tg(sox17:GFP)



Tg(sox17:GFP) DN RhoA  
mRNA



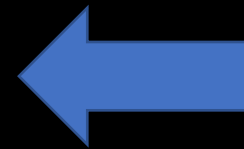
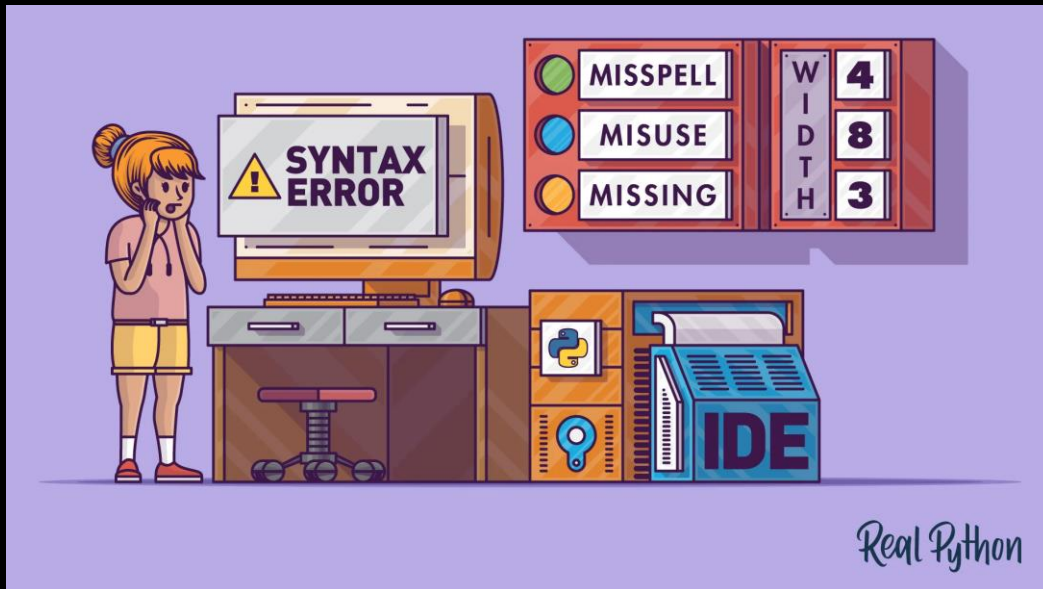
Is a simple model for CL enough to account for regular spacing of early endoderm cells?

# Project Aims

- **Aim 1** - Utilize the Matlab code from a lab mate which modeled the movement of early endoderm cells within a rectangular region. The code will be run with no more than 10 cells to start.
- **Aim 2** - The model from aim 1 will be used however, cells will be aligned at the lower half of the rectangle and repulsion will be taken away to mimic experimental data.
- **Aim 3** - The model from aim 2 will be run on the surface of a hemisphere instead of a rectangular region.

# Aim 1

- We received a MATLAB code
- I tried to convert the MATLAB code to PYTHON using an online converter.



- Parentheses instead of brackets
- Periods instead of commas
- This happened in almost every line

# Aim 1

```
R = np.array([[np.transpose(X(:,tt - 1))],[np.transpose(Y(:,tt - 1))]])
```

SyntaxError: invalid syntax

```
script_R[ri,:,rj] = R(:,ri) - R(:,rj)
```

SyntaxError: invalid syntax

```
mag_script_R[ri,rj] = np.sqrt(np.dot(script_R(ri,:,rj),script_R(ri,:,rj)))
```

SyntaxError: invalid syntax

```
theta_avg[row_idx_flock[ii]] = mean(Theta(temp_mat(:,2),tt - 1))
```

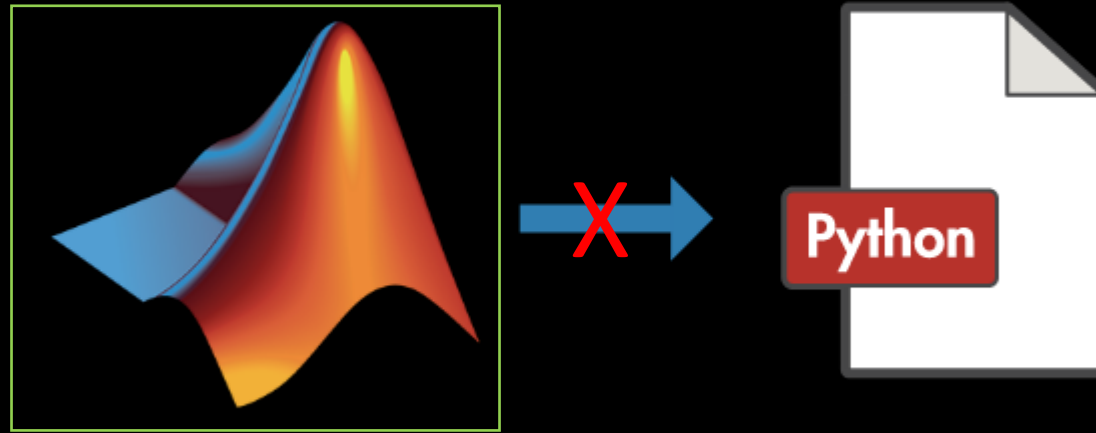
SyntaxError: invalid syntax

```
F_attractive[row_idx_attract,:,col_idx_attract] = F_attractive(row_idx_attract,:,col_idx_attract) - np.multiply(alpha / inv  
Sq_script_R(row_idx_attract,:,col_idx_attract),script_R_hat(row_idx_attract,:,col_idx_attract))
```

SyntaxError: invalid syntax

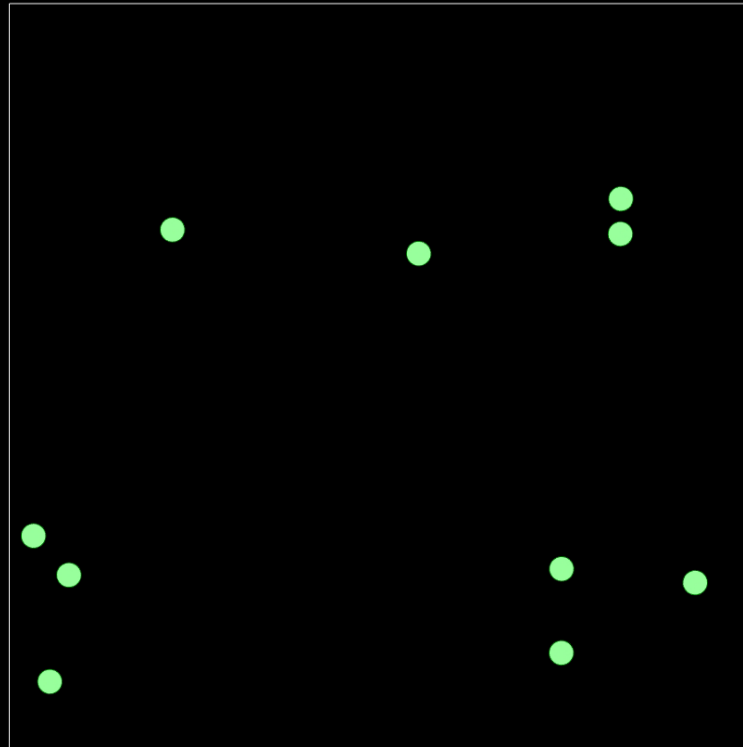


# Aim 1



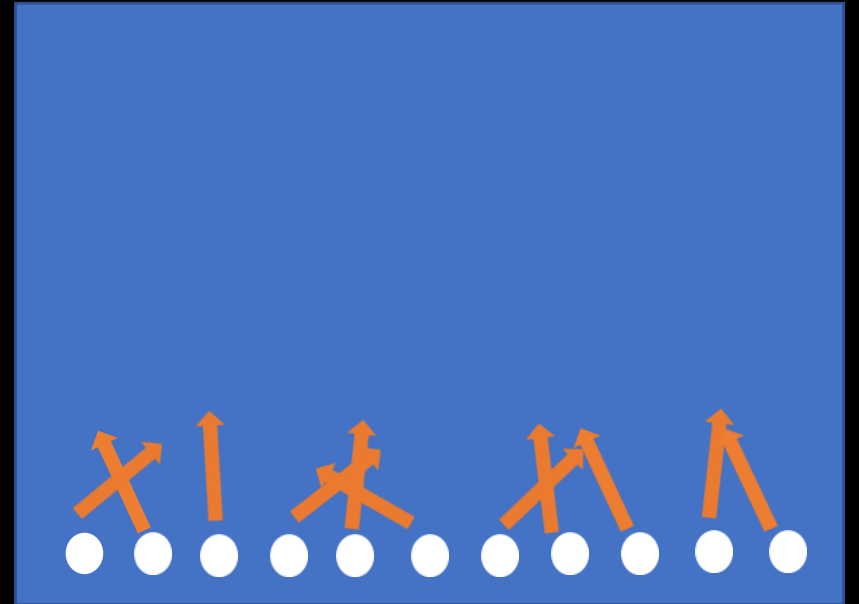
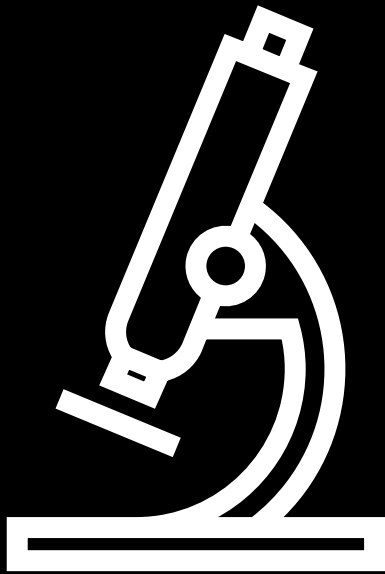
- Then I downloaded a package so that I could get the program to run and reduced the number of cells to 10.

# Aim 1 - Video



## Aim 2

- **Aim 2** - The model from aim 1 will be used however, cells will be aligned at the lower half of the rectangle and allow overlapping of the cells to mimic experimental data.

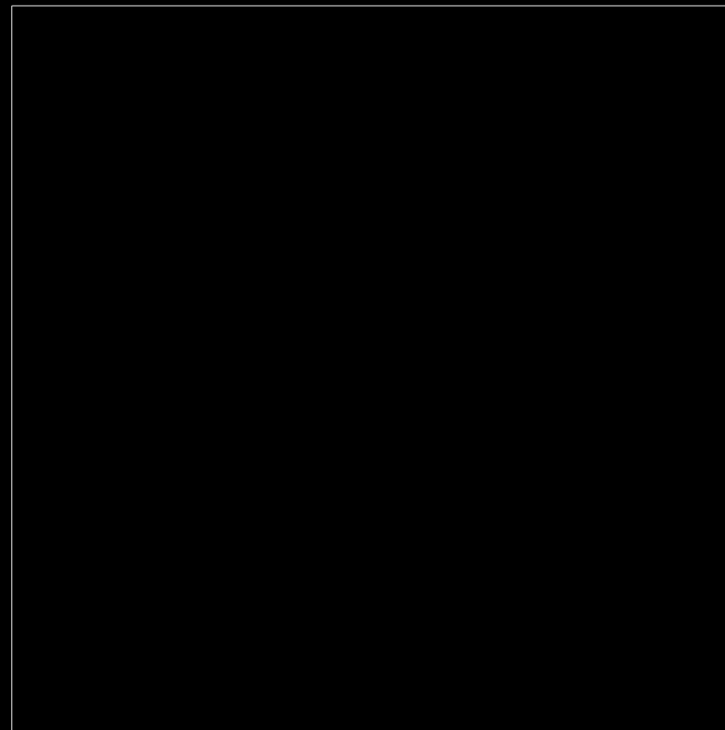
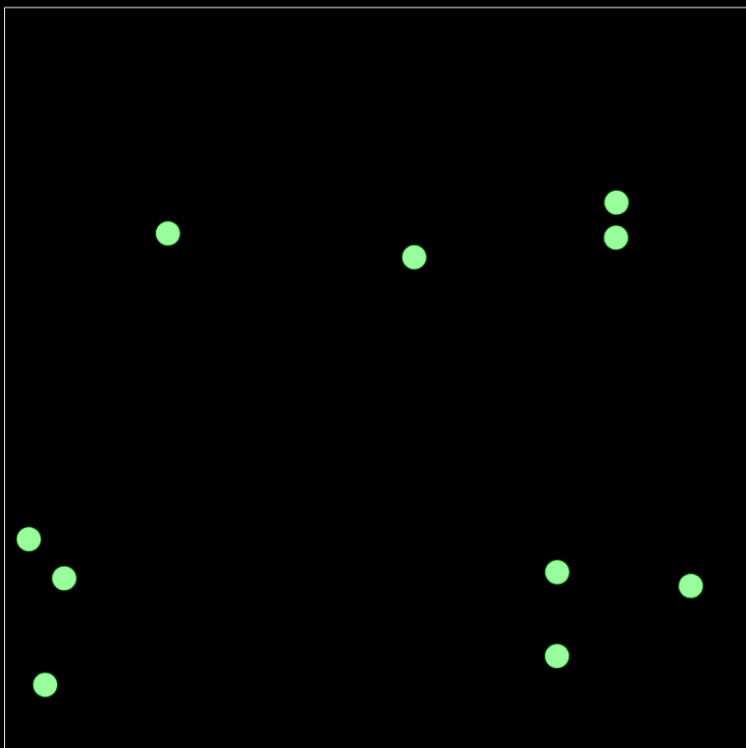


# Aim 2 - Video

- Changes I made to the original code:
  - Increase attractive force – simulate a reduction in repulsion
  - Allowing overlap – disabling initial check for overlapping cells
  - Removed the y-axis noise to create a straight line



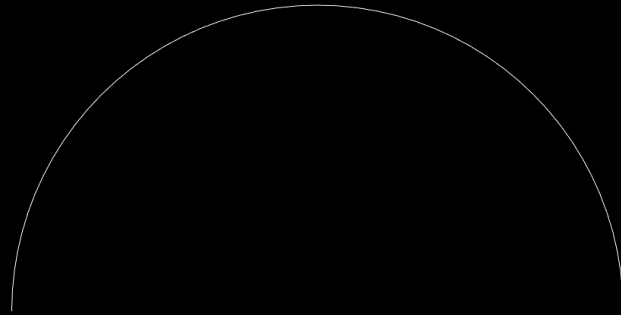
# Aim 1 vs Aim 2





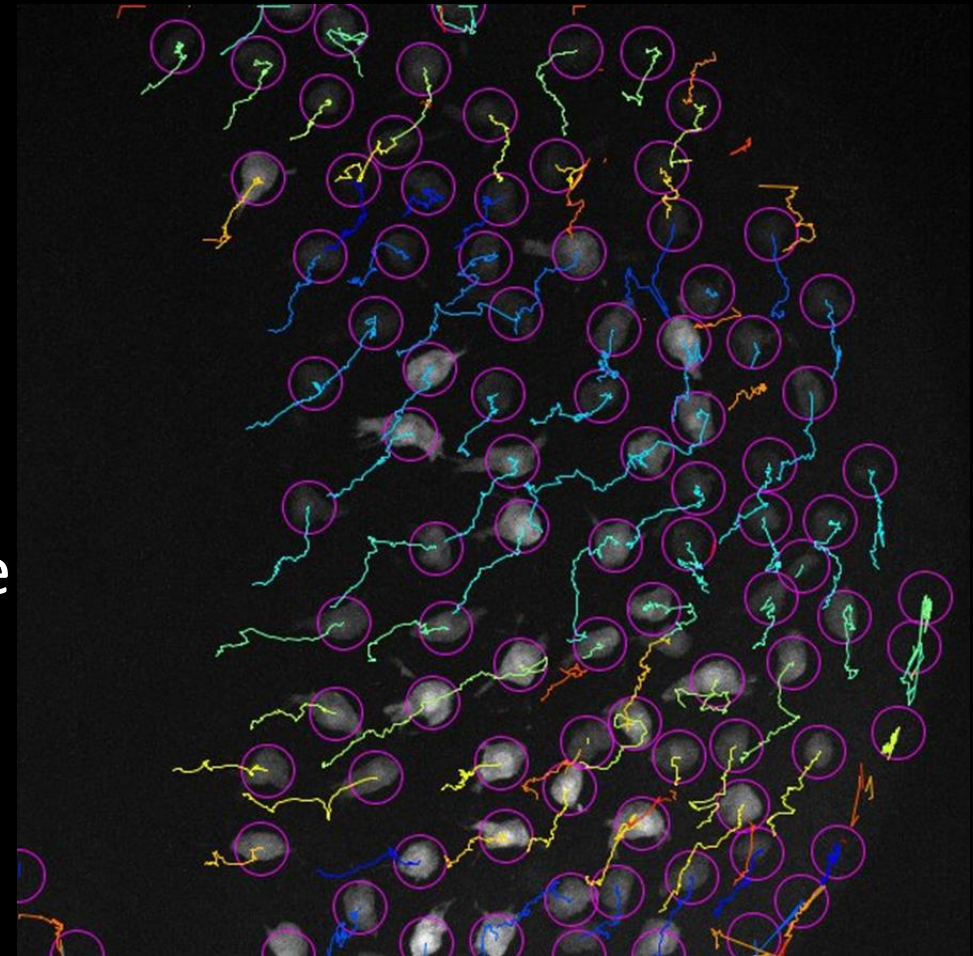
# Aim 3

- Where I am currently.
- I am trying to get some of the cells inside of a hemisphere.
- I still need to..
  - align the cells at the bottom
  - adjust the boundaries



# Future plans

- Apply data obtained from in vivo cell tracking of early endoderm
  - Average velocity
  - Average duration of contact
  - Average angle of repulsion
  - Cell to embryo size ratio
  - Average number of cells
- Run simulation with and without CIL
- Observe spacing between cells in each case



# Final Result

- Changes made to final code:
  - Simulated collisions between the hemisphere/bottom of hemisphere and cells
  - Used Pythagorean Theorem to determine collisions
  - The hemisphere was translated to make calculations easier
  - Cells sometime go outside of the hemisphere, but typically return

