

Lecture 13: Quantifying Cell Behavior

1. Cell Cultures

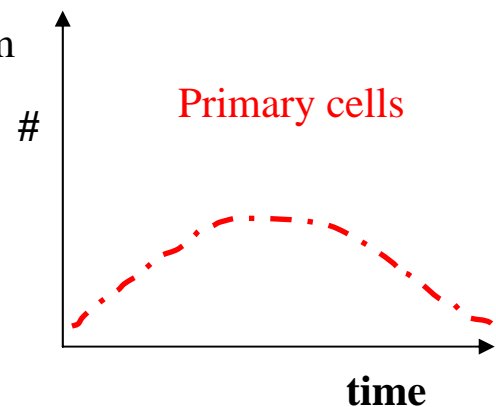
a. Why use cell cultures?

	<i>in vivo</i> (living organisms)	<i>in vitro</i> (glass, i.e., culture)
Pros	1. native 3D environment 2. all relevant signals present	1. simplified model systems 2. study parameters independently 3. observe as function of time
Cons	1. many variables – noisy data 2. animal rights concerns	1. unnatural 2D environment 2. may lack important signals

b. Types of cell cultures

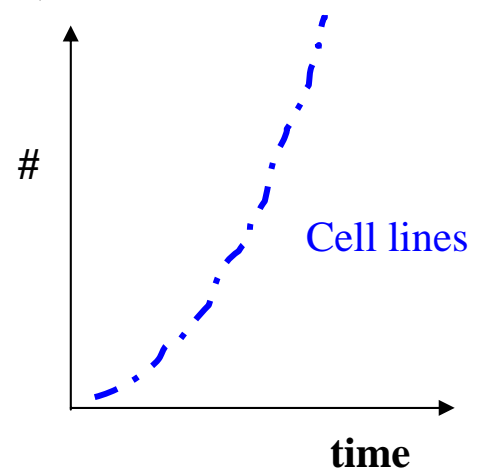
Primary cultures: directly from living organism

- ☺ reflect function of real organism
- ☹ eventually die off;
- ☹ some cell types poor dividers (nerve)



Cell lines: derived from primary cells (not clones)

- ☺ altered genes \Rightarrow immortality
 - isolated spontaneous mutation
 - tumor cells
 - viral oncogene transfection



2. Assays of Cell Function

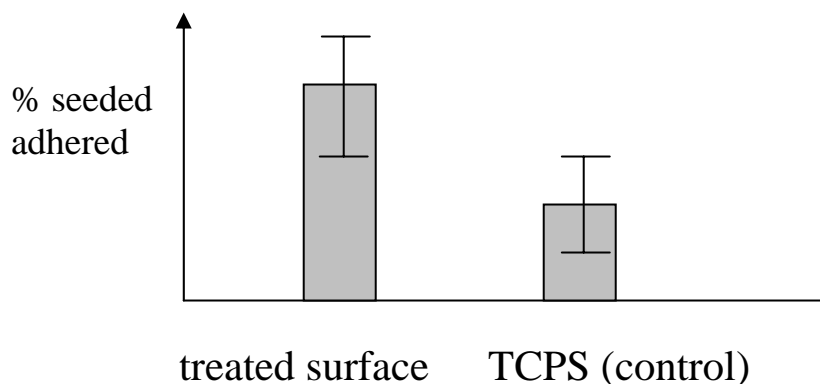
- Adhesion
- Migration
- Proliferation
- Differentiation (change in phenotype, ex. blood stem cells ⇒ leukocytes)
- Secretion (protein production)

a. Cell Adhesion Assays

Importance: cell adhesion is necessary for many other cell functions—provides biophysical and biochemical stimulation

➤ *Sedimentation assay:*

1. Cell type seeded onto surface of interest at given density (#/area) for a specified time *in vitro*
2. Surface is gently washed, and remaining cells counted, e.g., by optical microscopy or Coulter counter (cells detached, suspended & “count” by electrical resistance change thru narrow channel)



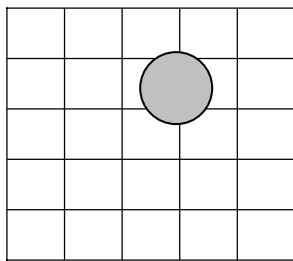
3. For testing cell resistance, serum-containing medium is a stricter test than cells seeded in protein-free solution.

Note: plasma vs. serum
 plasma—liquid portion of blood (cells removed)
 serum—plasma with coagulants (e.g., FGN) removed

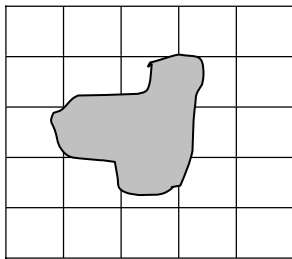
⇒ Sedimentation assays give **no info. on strength** of adhesion.

➤ *Cell Spreading Assay*

1. Cell type seeded onto surface of interest at given density (#/area) for a specified time
2. Measure projected surface area (optical microscopy)



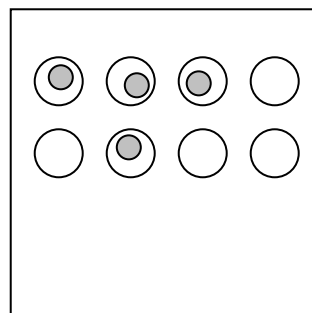
Closer in spirit, but still not a direct adhesion measurement

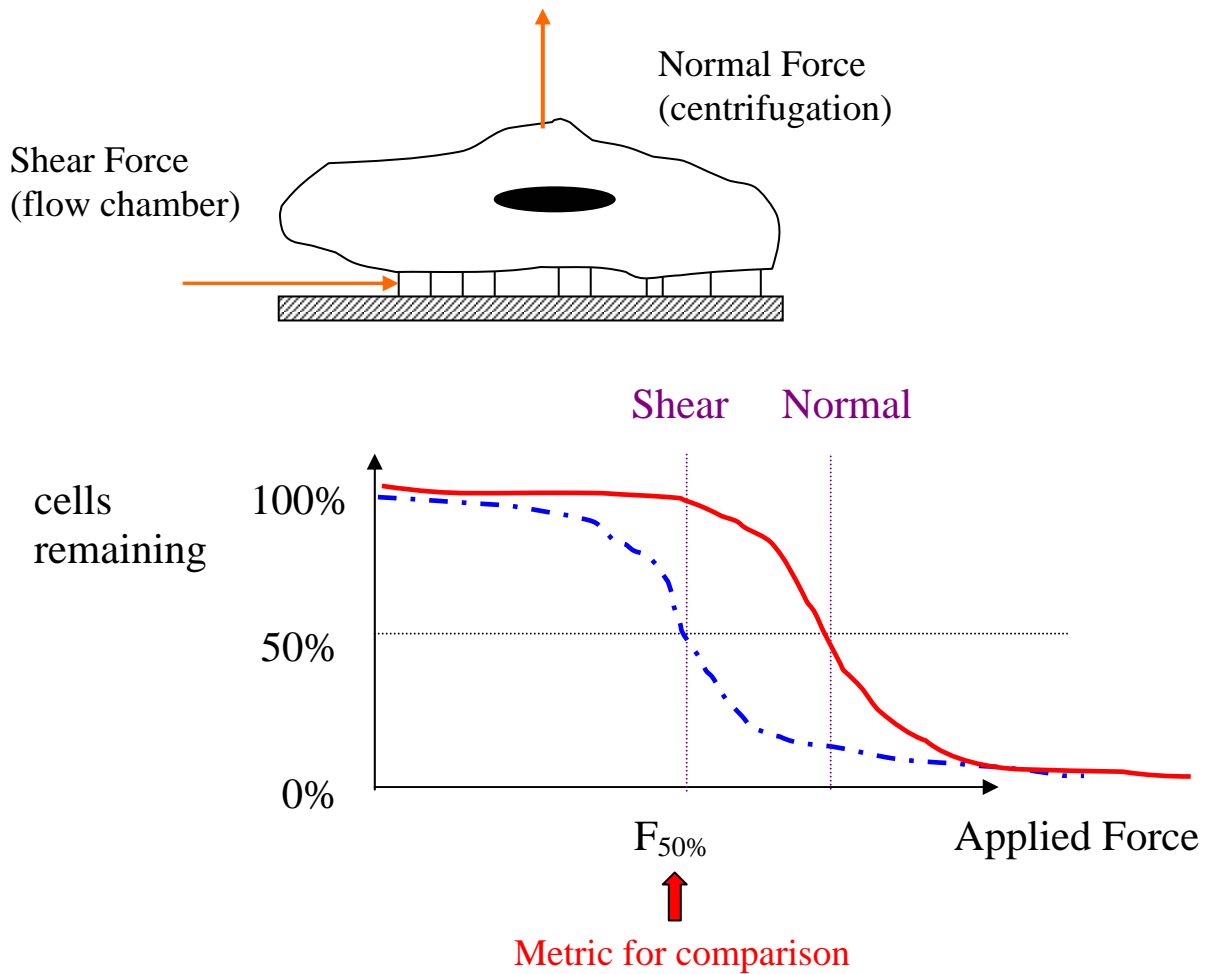


Spreading indicates focal contact formation—metabolic activity

➤ *Centrifugation assay: (normal force)*

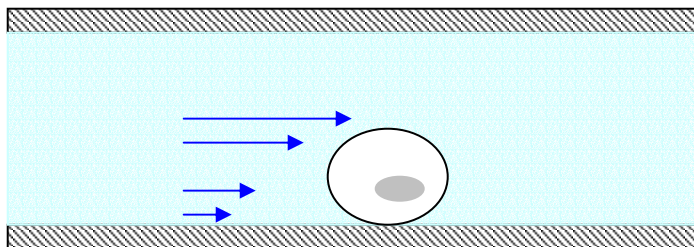
1. Cell type seeded into 24-well plate with surface coating for a specified time
2. Plate is inverted in centrifuge and cells attached vs. applied force is measured





➤ *Flow Chamber assay: (shear force)*

1. Cells seeded into parallel plate chamber
2. Fluid flow velocity gradient results in shear force on cell-surface bonds – pop like a “seam”



b. Cell Migration Assays

Importance:

- tissue organization (embryonic)
- immune and inflammatory response (chemotaxis of white blood cells)
- angiogenesis—endothelial cell migration to form vasculature
- wound healing—fibroblast migration to form connective tissue
- tumor metastasis

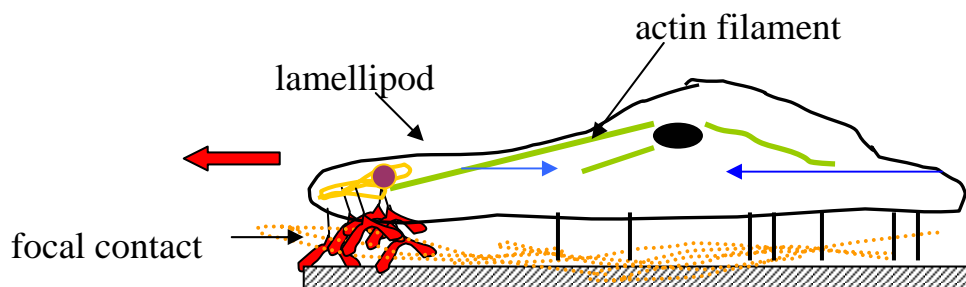
How do cells migrate?

Actin polymerization in cytoskeleton \Rightarrow “lamellipod” extension

Contractile force generated on actin filaments

Force translated to substrate through *focal contacts*

\Rightarrow net translation



Over short times: cell motion appears **directional**

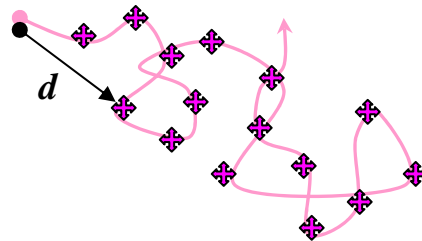
Over long times: cell motion is analogous to a **diffusive** process
(in absence of chemical gradients or physical barriers)

Quantification approaches:

1. individual cell measurements
2. migration of cell populations

➤ *Individual Cell Measurements:*

Time-lapse videomicroscopy tracks cell motion (beneath fluid or gel) on a surface as a function of time elapsed.



1. Measure distance traveled from starting pt. (d) as a function of time (t)
2. Fit data to model to obtain *rms speed* (S) and *persistence time* (P) (cell dependent)

P : time before memory of initial direction is lost (typically min-hrs)

S : measure of centroid displacement per time (typically 1-50 $\mu\text{m/h}$)

Persistent Random Walk Model: $\langle d(t)^2 \rangle = nS^2 [Pt - P^2(1 - e^{-t/P})]$

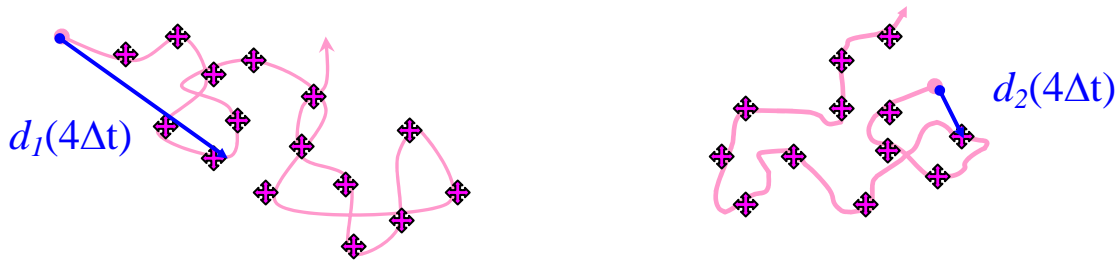
of dimensions (2)

where $\langle d(t)^2 \rangle = \frac{1}{M} \sum_{i=1}^M d_i(t)^2$

M = # of measurements

Note: $\langle \mathbf{d}(t) \rangle \equiv 0, t \gg P$
Why?

M = # of cells if each time step used as a single data point



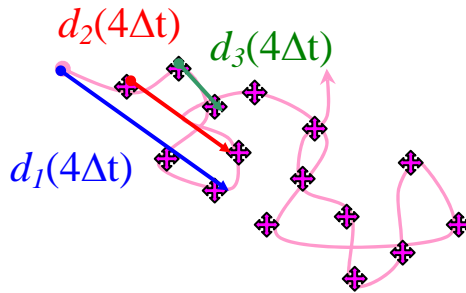
Cell 1 path

Cell 2 path

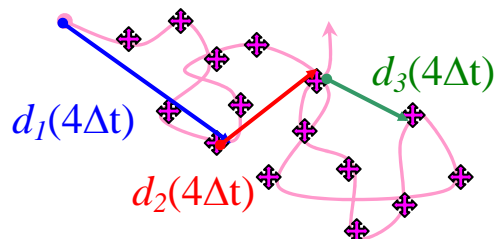
Requires measuring many cell paths for good statistics (TEDIOUS!!)

Alternately, we can use *data from a single cell*:

Strategy (i): count each pt. on its trajectory as a “starting pt.” (all sampling points are equivalent)



Strategy (ii): break migration path into $M = N/j$ segments of $j\Delta t$ steps (N =total # of sampling intervals Δt)



Fitting to the Persistent Random Walk Model

$$\langle d(t)^2 \rangle = nS^2 \left[Pt - P^2 (1 - e^{-t/P}) \right]$$

For short times $t < P$:

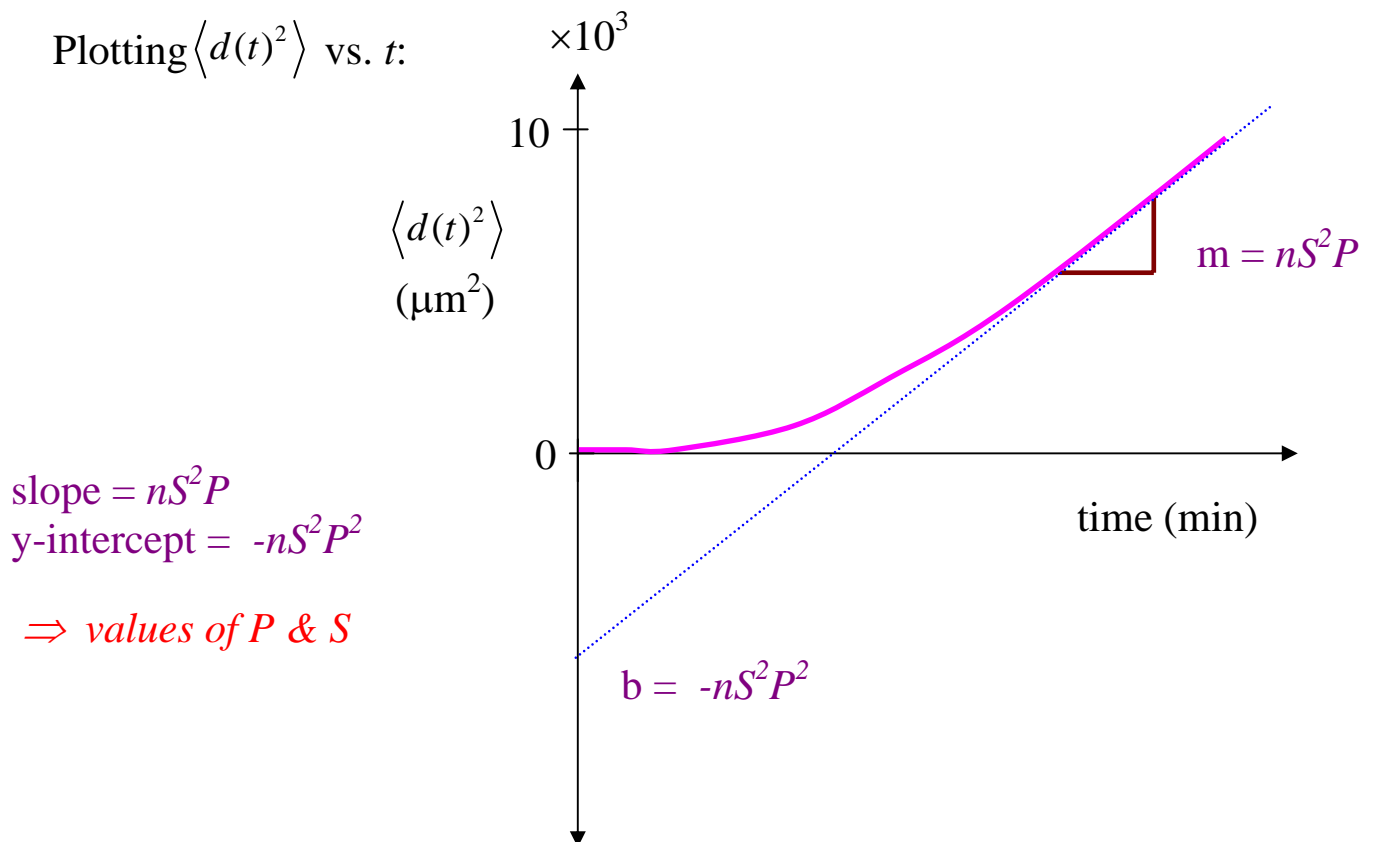
$$\exp(-ax) \approx 1 - ax + \frac{(ax)^2}{2} - \dots$$

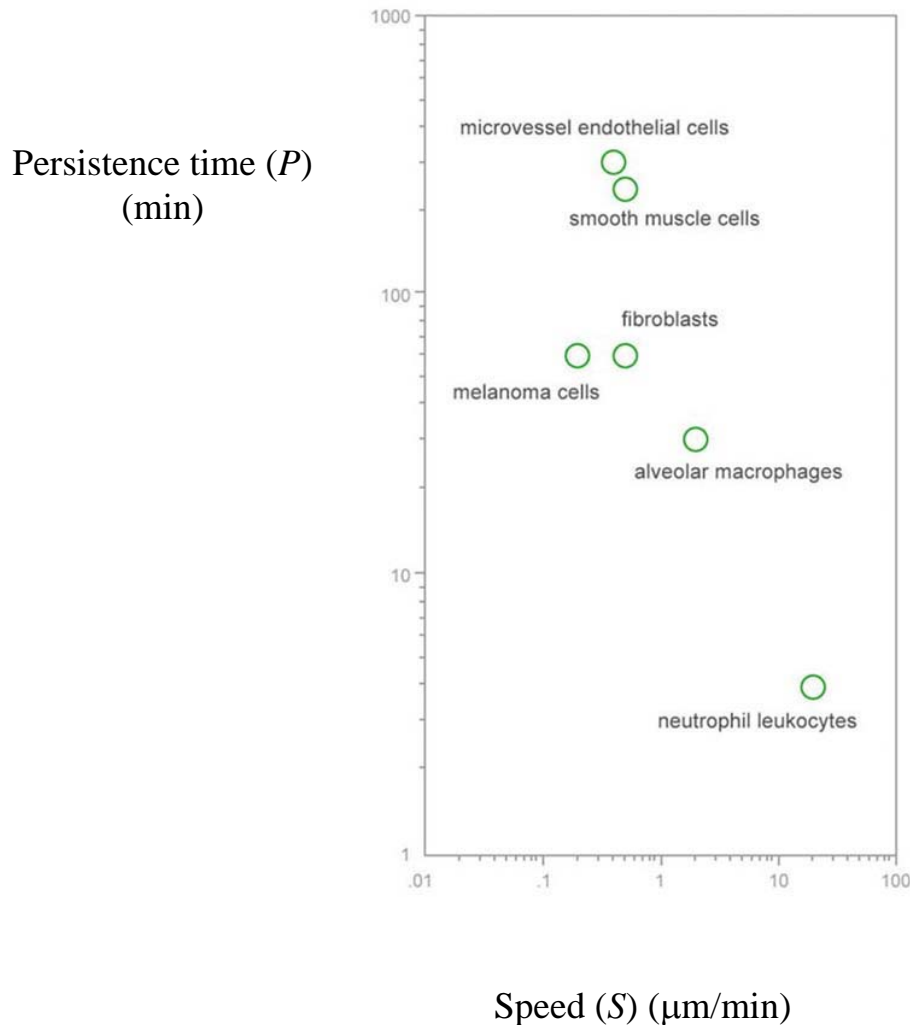
$$\langle d(t)^2 \rangle = S^2 t^2$$

or $\langle d(t)^2 \rangle^{1/2} = St$ **distance traveled = speed \times time**
(directional motion)

For long times $t > P$: $\langle d(t)^2 \rangle = nS^2 Pt - nS^2 P^2$

Plotting $\langle d(t)^2 \rangle$ vs. t :





Comparison of P & S for different cell types migrating on same substrate...

How do speeds relate to event sequence in the inflammatory response?

Figure by MIT OCW.

From D.A. Lauffenburger & J.J. Linderman, *Receptors: Models for Binding, Trafficking and Signaling*, Oxford U. Press, 1993.

$$\text{For } t \gg P: \langle d(t)^2 \rangle = nS^2Pt$$

$$\text{or } \langle d(t)^2 \rangle^{1/2} = S\sqrt{nPt} \quad \text{distance traveled} \sim \text{time}^{1/2} \text{ (diffusive motion)}$$

Analogous to the diffusion coefficient (D) for atoms and molecules, we can define a motility coefficient, μ , for cells:

$$\mu = S^2P/n \quad \Rightarrow \quad \langle d(t)^2 \rangle = n^2\mu t \quad \text{or } \langle d^2 \rangle^{1/2} = \sqrt{4\mu t} \quad \text{for 2d}$$

Typical values:
 $\mu \sim 10^{-9} - 10^{-8} \text{ cm}^2/\text{sec}$

Chemotaxis

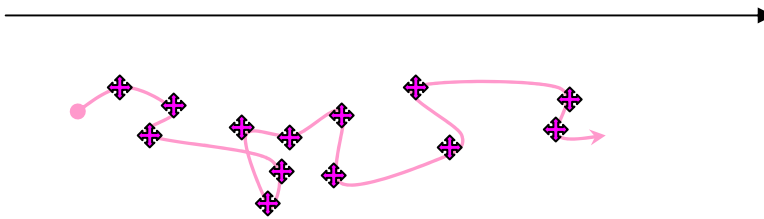
If chemotactic or haptotactic (surface-bound signaling) agent is present, mean displacement $\langle \mathbf{d}(t) \rangle$ is nonzero.

We can quantify the degree of chemotacticity of a migration with the *Chemotactic Index, CI*:

$$CI = \frac{|\langle \mathbf{d}(t) \rangle|}{L_{path}} \left\{ 1 - \left(\frac{t}{P} \right)^{-1} \left[1 - e^{-t/P} \right] \right\}^{-1}$$

where $\langle \mathbf{d}(t) \rangle$ is the mean displacement up a concentration gradient, and L_{path} is the *total cell path (contour) length*.

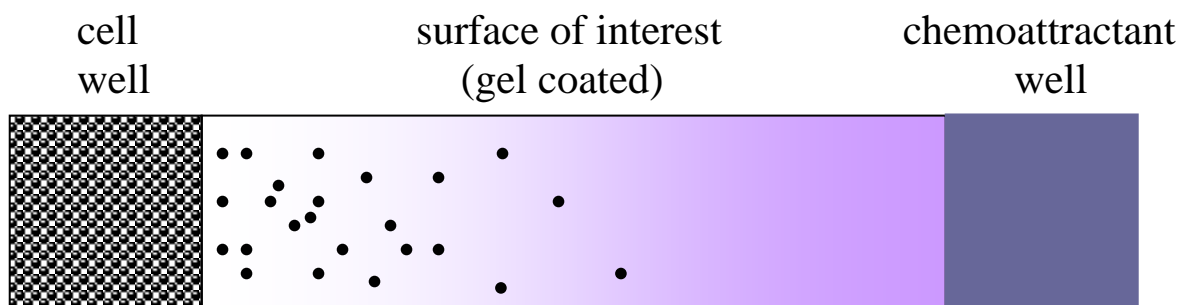
Concentration gradient of chemotactic agent in x-direction



For long times ($t \gg P$): $CI = \frac{|\langle \mathbf{d}(t) \rangle|}{\langle L_{path}(t) \rangle} \quad (0 < CI < 1)$

➤ Migration of Cell Populations

- Cells are seeded in a well (typically under a gel) from which they migrate
- cell density (c , cells/area or cells/volume) is measured at various distances from well at different times



Governing expression for cell density, c (cells/area):

$$\frac{\partial c}{\partial t} = -\frac{\partial \mathbf{J}_c}{\partial x}$$

where \mathbf{J}_c is cell flux (cells/distance-time)

$$\frac{\partial c}{\partial t} = -\frac{\partial}{\partial x} \left[\underbrace{-\mu \frac{\partial c}{\partial x} + c \left\{ -\frac{1}{2} \frac{\partial \mu}{\partial L} + \chi \right\} \frac{\partial L}{\partial x}}_{\text{where } \mathbf{J}_c \text{ is cell flux (cells/distance-time)}} \right]$$

$L =$ chemotactic agent conc. (mol/liter)
 $\chi =$ chemotaxis coefficient (area/time-M)

random-walk motion
 μ -dependence on chemotactic agent concentration
 directional bias from chemotactic agent

$$\chi \text{ related to single cell properties thru: } \chi = \frac{S \cdot CI}{\nabla L} - \frac{1}{n} \left(\frac{d \ln P}{dL} - \frac{d \ln S}{dL} \right)$$

Cells can exhibit chemotaxis in any situation where μ exhibits concentration dependence.

Macrophage motility coefficient μ dependence on C5a concentration

From D.A. Lauffenburger & J.J. Linderman, *Receptors: Models for Binding, Trafficking and Signaling*, Oxford U. Press, 1993.

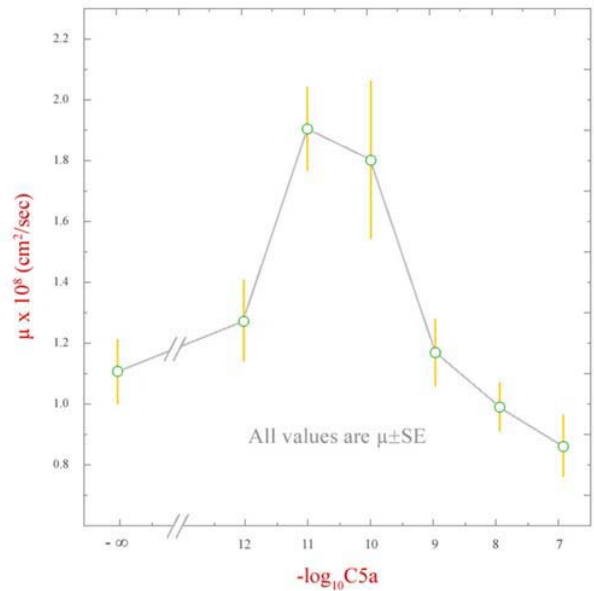


Figure by MIT OCW.

$$\frac{\partial c}{\partial t} = -\frac{\partial}{\partial x} \left[-\mu \frac{\partial c}{\partial x} + c \left\{ -\frac{1}{2} \frac{\partial \mu}{\partial L} + \chi \right\} \frac{\partial L}{\partial x} \right]$$

A fit of cell data to the model requires solving the above equation for the appropriate boundary conditions.

Example: For random cell motion with continually replenished cells:

$$c(0,t) = c_o \quad t > 0$$

$$c(\infty,t) = 0$$

$$\frac{c(x,t)}{c_o} = \operatorname{erfc} \left(\frac{x}{\sqrt{4\mu t}} \right)$$

obtain $\mu(L)$ for different L values

can determine μ from fitting $c(x,t)$ data