PMLS2/e: External Media

This document corresponds to the second edition of *Physical models of living systems*. If you want materials related to the first edition, please instead visit www.physics.upenn.edu/biophys/PMLS/index.html .

Here is a list of movies and other media mentioned in *PMLS*. Some of these are available directly via links below; in other cases, the link below takes you to the original journal article's media section (you may need an institutional subscription to view those ones).

- If your browser balks when you click a URL, you may succeed by instead copying it, then pasting it into the browser's address space.
- If a file name appears below without a URL, and clicking its name doesn't deliver it, try looking the Media section of *PMLS*'s web site.
- Many videos available at journal web sites will no longer play in Apple software such as Quicktime or Safari. You may nevertheless be successful with a different browser, or with free software such as VLC (which can also convert to modern formats). If you have this problem with a video on *PMLS*'s web site, look for a version in `.mp4` or `.m4v` format (not `.mov`).

#1: See
https://cdn.rcsb.org/pdb101/learn/resources/structural-biology-of-hiv/index.html .

#2: Molecular visualization data and tools are available at the RCSB Protein Database. [The PDB is operated by the Research Collaboratory for Structural Bioinformatics (RCSB).]
Overview: https://www.rcsb.org .
Once you enter a molecule's accession code, you'll have the option of various Web-based viewers to visualize it. The JSmol viewer can report the distance between any two atoms in the structure: Double-click one atom. Then as you hover your pointer over any other atom (or double-click it), you'll see a distance report. Some viewers offer high-quality image output suitable for publication (or homework assignment).
Alternatively, you can download the PDB coordinate file for the molecule that interests you, then use a standalone visualization application on your computer. One good option is JMol, which may require that you first install Java on your computer. It's freely available at sourceforge.net/projects/jmol/ . Other viewers are listed here: www.rcsb.org/docs/third-party-resources/molecular-graphics-software = perma.cc/JAM9-5HTK .

#3: https://www.youtube.com/watch?v=cDcprgWiQEY: Free Brownian motion of micrometer-scale particles.
BrownianBerner.mp4: (Courtesy William Berner.) TPM.avi, TPM.mov, TPM.m4v, TPM.wmv: Brownian motion of particles tethered to a microscope slide by single strands of DNA (not visible) (courtesy Laura Finzi, Emory University). One particle breaks loose from its tether and escapes.
BeadJump.avi, BeadJump.mov, BeadJump.m4v: Brownian motion of a single particle in a double potential energy well, showing thermally activated hopping between two local equilibria. [Courtesy Adam J Simon; see Adam Simon and Albert Libchaber. Escape and synchronization of a Brownian particle. Phys. Rev. Lett. **68**, 3375 (1992).]
Flipper.mov: Simulation.

#4: Files shotNoise.aiff and shotNoise.mp3 contain clicks representing the actual arrival times of photon detection events. [Data courtesy John F Beausang and Yale E Goldman.] File pprocess.aiff and pprocess.m4a contain simulated clicks drawn from a Poisson process with the same mean rate for comparison.

#5: Files 60Hz.aiff and 60Hz.mp3 contain equally spaced clicks at rate 60/s.

#6: DRIFTescapeTraj.mp4: A random walker is shown moving under constant force. The force is indicated as minus the slope of a potential energy function (*blue line*). The walker gradually drifts rightward. Each video frame summarizes 23 time steps in the simulated trajectory, a total of 6900 steps.
TRAPescapeTraj.mp4: A random walker is shown moving in a harmonic restoring potential. The force is indicated as minus the slope of a potential energy function (*blue line*). Each video frame summarizes 5 time steps in the simulated trajectory, for a total of 6000 steps.
escapeHisto01-side.mp4: Many identical walkers in a symmetric harmonic restoring potential were released near

to the potential minimum. The animation shows a histogram of positions occupied by the walkers at subsequent times. Whenever a walker crosses position $x = 100$, it is deemed to have "escaped" and the trapped population goes down. The cumulative number of escaped particles at each time is indicated by a red dot on the right side. (A hard wall prevents escape on the left side.) After a very fast equilibration, the histogram settles down to a nearly Gaussian form (quasi-equilibrium), with total area under the curve gradually decreasing as more walkers escape. The dimensionless "force field" as a function of position was taken to be slightly tilted: The probability to step right was $\mathcal{P}_+ = \frac{1}{2}\big(1 - 0.0025(x - 50) + 0.01\big)$.

#7: See Supplementary Movie S1 at
https://www.science.org/doi/10.1126/science.1084398 = FIONA-Yildiz.mp4: "Movement of a single fluorescent dye attached to myosin V for the lower right trace shown in Fig. 3. Each pixel is 86 nm. Discrete 74-nm steps are clearly visible." [Supplement to A Yildiz et al. Myosin V walks hand-over-hand: Single fluorophore imaging with 1.5-nm localization. Science (2003) **300** (5628) pp. 2061–2065.]

#8: Files myoV.mov and myoV.avi show motion of the molecular motor myosin-V. Myosin-V was labeled by the fluorescent dye rhodamine (green) and is seen walking along actin filaments labeled with Alexa 647 (blue). The actin filaments in turn are attached to a quartz microscope slide, in the presence of 5 μM ATP. The motion consists of about four steps per second, giving an overall speed of about 140 nm/s. [Courtesy John F Beausang and Yale E Goldman.]

#9: https://www.science.org/doi/10.1126/science.1127344 movie S1 = Betzig1127344s1.mov: "Partial summed molecule TIRF image (center) and PALM image (right) constructed during the acquisition of 300 single molecule frames (left) out of the 20 000 frames used to construct the images in Fig. 2. Scale bar is 0.5 μm." [Supplement to E Betzig et al. Imaging intracellular fluorescent proteins at nanometer resolution. Science (2006) vol. **313** (5793) pp. 1642–1645.]
Similar processing applied to lights on the Eiffel Tower: https://www.youtube.com/watch?v=RE70GuMCzww
= Eiffel.m4v .

#10: See
https://www.nature.com/articles/nature09450 Supplementary Movie S2 = Ando2010nature.mov: "High-speed AFM movies showing hand-over-hand movement of M5-HMM. The dynamic process was filmed at 6.8 frames/s and the obtained movies are played at 7 frames/s." [Supplement to N Kodera et al. Video imaging of walking myosin V by high-speed atomic force microscopy. Nature (2010) **468** (7320) pp. 72–76.]

#11: DavidRogersNeutrophil.mp4 shows a neutrophil chasing *Staphylococcus aureus* (David Rogers, Vanderbilt University). This video shows this process at about twice actual speed. "A human polymorphonuclear leukocyte (neutrophil) on a blood film, crawling among red blood cells, notable for their dark color and principally spherical shape. The neutrophil is 'chasing' *Staphylococcus aureus* microorganisms, added to the film.
The chemoattractant derived from the microbe is unclear but may be complement fragment C5a, generated by the interaction of antibodies in the blood serum with the complement cascade, and/or bacterial N-formyl peptides. Blood platelets adherent to the underlying glass are also visible. Notable is the characteristic asymmetric shape of the crawling neutrophil with an organelle-excluding leading lamella and a narrowing at the opposite end culminating in a 'tail' that the cell appears to drag along. Contraction waves are visible along the surface of the moving cell as it moves forward in a gliding fashion. As the neutrophil relentlessly pursues the microbe it ignores the red cells and platelets. However, its leading edge is sufficiently stiff (elastic) to deform and displace the red cells it bumps into.
The internal contents of the neutrophil also move, and granule motion is particularly dynamic near the leading edge. These granules only approach the cell surface membrane when the cell changes direction and redistributes its peripheral 'gel.' After the neutrophil has engulfed the bacterium, note that the cell's movements become somewhat more jerky, and that it begins to extend more spherical surface projections. These bleb-like protuberances resemble the blebs that form constitutively in the M2 melanoma cells missing the actin filament crosslinking protein filamin-1 (ABP-280) and may be telling us something about the mechanism of membrane protrusion."
Text: Thomas P. Stossel (Brigham and Women's Hospital and Harvard Medical School), June 22, 1999.

#12: https://jlb.onlinelibrary.wiley.com/doi/full/10.1189/jlb.0506346 supplemental movie 1 =
jlb1281-sup-0001.mov : "Wild-type leukocyte response to fin wound. A wild-type zebrafish embryo was wounded in the ventral fin and observed by time-lapse DIC microscopy; the region imaged is the ventral fin in the midsection of the

embryo, just below the vasculature and ICM. Note the migration of apparent leukocytes from the vasculature/ICM to the wound site." [Supplement to J R Mathias et al. Resolution of inflammation by retrograde chemotaxis of neutrophils in transgenic zebrafish. J. Leukoc. Biol. (2006) vol. **80** (6) pp. 1281–8.]

http://dictybase.org/Multimedia/development/ax320x.mov = ax320x.mov: Aggregation of *Dictyostelium discoideum* amebæ toward a pipette emitting the chemoattractant cAMP. [R Firtel, University of California, San Diego.] (More at http://dictybase.org/Multimedia/.)

www.rsc.org/suppdata/ib/c0/c0ib00033g/c0ib00033g_1.mov = Skogec0ib00033g1.mov: A *Dictyostelium* cell expressing the F-actin reporter ΔlimE - GFP chemotaxing in a gradient chamber. Confocal fluorescence images were taken at both the cell-glass (red) and cell-PDMS (green) contact planes and superimposed at each frame. [Supplement to M Skoge et al. Gradient sensing in defined chemotactic fields. Integr. Biol. (Camb.) (2010) vol. **2** (11–12) pp. 659–68.]

#13: See https://www.cell.com/cell/fulltext/S0092-8674(10)00352-1 supplementary movie S1 = http://doi.org/10.1016/j.cell.2010.03.034 = ZengCELL2010-mmc2.mp4. [Zeng, L, Skinner, SO, Zong, C, Sippy, J, Feiss, M, and Golding, I. (2010). Decision making at a subcellular level determines the outcome of bacteriophage infection. Cell, **141**(4), 682–691.]

#14: See Movie S1 and its caption at https://www.science.org/doi/full/10.1126/science.1161427 = ChoiSCIENCEmovieS1.m4v [Supplement to P Choi et al. A stochastic single-molecule event triggers phenotype switching of a bacterial cell. Science (2008) vol. **322** (5900) pp. 442–446.]

#15: https://www.nature.com/articles/nature07389#Sec8 supplementary movie 11 = 41586-2008-BFnature07389-MOESM217-ESM.mp4: "Timelapse microscopy of JS013 cells (negative feedback only), continuously induced with 0.6 mM IPTG at 37°C. The phase-contrast image is shown in gray, and fluorescence is shown in green. Total time of movie is 210 min with a sampling rate of one image every 3 min." [Stricker, J, Cookson, S, Bennett, MR, Mather, WH, Tsimring, LS, and Hasty, J. (2008). A fast, robust and tunable synthetic gene oscillator. Nature, **456**(7221), 516–519.]

#16: https://static-content.springer.com/esm/art%3A10.1038%2Fnature19841/MediaObjects/41586_2016_BFnature19841_MOESM73_ESM.mov: Oscillations are reported by a YFP (green) while a constitutive CFP is expressed as segmentation marker (blue). The video is played at 10 frames/s and the images were acquired every 5 min. [3rd video in supplement to Potvin-Trottier, L, Lord, N, Vinnicombe, G et al., Synchronous long-term oscillations in a synthetic gene circuit. Nature **538**, 514–517 (2016). doi.org/10.1038/nature19841 .]

#17: relaxationOsc.mov and relaxationOsc.mp4: Operation of a mechanical relaxation oscillator similar to the one in Figure 13.4. There are differences between this realization and the idealized one in the text: (*i*) Switching between the two buckets is done manually: The feedback loop consists of a human continuously observing the bucket positions and supplying beads always to the higher bucket. The human does not, however, impose any particular periodicity. (*ii*) The system has friction, but is not in a high-friction regime where inertia may be neglected. Indeed, the system displays bounces, also visible in the traces shown in the figures below. (*iii*) There are "hard stops" at the extreme values of θ. (*iv*) The toggle element is implemented by magnets in each bucket, similar to Figure 12.13a, so it only comes into effect at the extreme values of θ. Despite these differences, the system displays the basic behavior expected for a relaxation oscillator.

relaxationOscResults.pdf: Time series recorded from this apparatus, showing the operation of the oscillator with (a) no toggle, and with (b) weak and (c) strong toggle elements. [Realization courtesy William Berner.]

#18: https://www.nature.com/articles/nature07389#Sec8 supplementary movie 1 = 41586-2008-BFnature07389-MOESM207-ESM.mp4: "A timelapse microscopy of JS011 cells continuously induced with 0.7% arabinose and 2 mM IPTG at 37 C. The brightfield image is shown in gray, and fluorescence is shown in green. Total time of movie is 228 min with a sampling rate of one image every 3 min." [Stricker et al. op. cit.]

#19: T-TsaiXenopus.mov and T-TsaiXenopus.gif: Timelapse microscopy of cell division in a *Xenopus* embryo. The overall size of the embryo is about 1 mm diameter throughout the video; the real-time duration of each division

cycle is about 25 min. Video micrograph courtesy Tony Yu-Chen Tsai [see also T Tsai et al. Changes in oscillatory dynamics in the cell cycle of early *Xenopus laevis* embryos. PLoS Biol. (2014) vol. **12** (2) e1001788].

#20: Suel2006video2.mp4: "Movie of a *B. subtilis* microcolony under nutrient limitation conditions, showing PcomG and PcomS activities in red and green colors, respectively. comS is expressed in all cells, but only one [cell] becomes competent. The two promoter activities are negatively correlated during competence." [Süel, GM, Garcia-Ojalvo, J, Liberman, LM, and Elowitz, MB (2006). An excitable gene regulatory circuit induces transient cellular differentiation. Nature, **440**(7083), 545–550. doi.org/10.1038/nature04588].