MITOCW | MITRES_10_S95F20_0108_300k

PROFESSOR: So as a more technical aside, let's analyze more carefully the problem of release of viral load from a drop by process of diffusion.

So here, again, I sketch a droplet, which would typically be an aerosol droplet in the size range of, let's say, microns.

And the virion of interest has a size that is much smaller than that on the order of, let's say, 100 nanometers.

And this white path is showing how such a virion would go from its initial position R, let's say, as a radio position, to the boundary.

Now, the general problem of finding the expected first passage time from the point inside a domain to a boundary is a classical problem in the theory of stochastic processes and random walks.

And it has the following representation.

So the mean are expected first passage time from a point to an absorbing surface solves the following problem.

Is the Laplacian of that time with a minus sign is 1 over D where D is the diffusivity.

And so this is the DV that I described before, the diffusivity of the virion.

And the boundary condition for this equation is that it's an absorbing boundary, basically.

So when the virion gets to the surface it's gone.

And that's when the stochastic process finishes.

So it's tau equals 0 on radius capital R, which is the radius of the droplets.

So that's on the boundary.

So in the case of a spherical drop, then we can write this equation in spherical coordinates.

So that's minus 1 over r-squared, r derivative of r-squared D tau DR. And that's equal to 1 over capital D.

And then again, our boundary condition is the tau of capital R is equal to zero.

Another boundary condition we might mention is that D tau DR at R equals 0 is zero.

That's a symmetry boundary condition.

So when you're right in the middle, basically, there should be no-- there's no favorite direction for the diffusion process.

And so, therefore, the derivative this time with respect to R must be 0 at the center because it's a symmetry boundary condition.

OK, so we can now go ahead and solve this problem.

Let me put the r-squared on their side and use primes with no derivatives.

So let's write this as r-squared tau prime, prime equals minus r-squared over d.

And if I now integrate both sides, I get r-squared tau prime equals -- and then here we get a minus r-cubed over 3D plus a constant.

And that constant immigration according to the symmetry boundary condition has to be 0, because tau prime is 0 at r equals 0.

So we can simplify this and write tau prime is minus r over 3D.

And so then I can integrate again.

And I found that tau of r is-- well, I integrate this, I get r squared over 2 is integral of r.

So that gives that an r-squared over 6.

So there will be a 6 D and minus r-squared.

And there'll be a constant integration.

And in order to satisfy this boundary condition of vanishing a capital R, you can see that I can write the constant this way.

And I'll write it as capital R squared over 6D is a constant of integration.

So basically, the profile of the main first passage time is essentially a parabola.

So as a function of distance R from the center of the droplet, you have this shape to the mean transmission time.

And the maximum here, the maximum value is tau 0 is the maximum value.

And that is r-squared over 60.

So that's if you happen to be unlucky and right in the middle.

That's the longest you would expect to take from a particular part.

Now on the other hand, as I've sketched here, in a typical droplet, if the virions are randomly distributed, some of them, like this guy over here, happen to be very close to the surface.

So you're not going to have to wait this long for them to escape.

So now we can ask the question, what is the average escape time over all the initial positions of the virus, or virion, assuming that the virions are uniformly distributed at random in the initial condition.

So if we do that, then we're solving for the-- that's all [INAUDIBLE],, so I'll put it over here.

The average escape time or first passage time for the virus will be tau bar.

Well, what I'll do is I'll integrate over all the positions and then divide by the volume because a uniform distribution.

So I'll write the integral over the volume as 4 pi, the solid angle times integral from 0 to capital R of tau of r r-squared DR. And I'll divide by the total volume 4/3 pi capital r-cubed.

OK, so if we do this integral here, so when we plug-in this, first of all, we can see that we get, obviously, for the constant term, rsquared over 60, we just have a ratio of volume over volume, which is one.

So we get r squared over 6D is the first term, just integrating that constant.

But then it's 1 minus.

And then instead of r-squared, you have r-squared times this r-squared.

It says r to fourth. So you integrate that. You get r to the fifth over 5. And so then you get 1/5 over this 1/3 here. And that gives you 3/5. And that gives, when I subtract one minus 3/5, I get 2/5. And so that gives, when I subtract one minus 3/5, I get 2/5. And 2 over 6 is 1/3. And so this ends up being r-squared over 15D as we had previously quoted. So it's worth going through the calculation just to see. This number 15 is an order of magnitude. It's larger than 10. So while we normally estimate diffusion times to be of order length squared divided by D, so r-squared over d, this calculation shows that the actual average time is much smaller than that by a factor of 15. And that's precisely because the virus virions sometimes find themselves initially near the surface. So they get out more easily.

So you don't have to wait for diffusion across the entire drop.

That sets the overall scale.

But the average drop diffusion time is actually less than that.