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PROFESSOR: So until now, we based the safety guideline on the indoor reproductive number, which is essentially the effective number of new infections from a single infected person or per infected person in the room.

And in many cases, that is the right variable to think about.

In fact, it's essentially the most conservative definition that allows us to limit the spread of the disease at the level of the population.

If every room were doing that, we would control the spread of the epidemic.

But we also should think about the role of the prevalence of infection in a given region.

In particular, as the number of infected people in the population goes up, we should be increasing restrictions to a certain point.

And also, as the pandemic recedes, we should then be decreasing those restrictions.

So there has to be a role also to be played in using the guideline for the prevalence of infection.

So to describe this, let's think of a random number of transmissions that's going to occur.

So this T here is going to be the random-- it's a random variable, which will be the random number of transmissions in the room with all the usual features so in time tau and all the other assumptions about this indoor space that we've been talking about.

But the important thing is that this is random because we don't know-- what we're going to focus on here is we don't know how many people are in the room.

So there are I infected people.

And I here is the random number of infected people.

There are S susceptible people, which also is a random number.

And then there is a transmission rate, which is the expected number of-- which is the number of-- random number of transmissions per pair.

So if you take an infected person and a central person in this time, there's a certain probability of transmission, which is described by this random variable TMN.

And so what we're going to assume here is-- I'll just mention some technical assumptions, first of all, that this tau or TMN is a Poisson process with a certain mean rate calculated by the previous model that we've been dealing with with a mean rate beta times tau.

So up to a certain point in time, there's an average transmission rate beta average.

And that's a Poisson process.

So what that actually means is that the occurrence of transmission between a pair of individuals can happen randomly in the time sequence.

At any infinitesimal time step, it has no memory of the past.

And it's an independent random event with fairly low probability in a given small time interval but which achieves this certain random rate here.

So in probability statistics, we refer to that as a Poisson process.

We also assume that each TMN is independent and identically distributed Poisson processes.

So in other words, if I take two different pairs of individuals, and I consider the transmission, they're not correlated.

That is an assumption.

Because, of course, if the infected person is sitting in one place, you might expect the people nearby even, say, within six feet might be more likely to be infected.

We are leaving that out because we are considering airborne transmission in a well-mixed room where this should not be any such correlations as a first approximation.

Furthermore, we assume that not only each transmission is independent but also that the number of infected people I and all these transmissions are also independent, are uncorrelated.

So basically, the arrival of infected people is uncorrelated to how they're transmitting.

So for example, if we have a pack of infected people that arrive, we're not somehow changing the transmission rate to change that.

And that's partly we can make the assumption because we are interested in the limit of a small number infected people.

In fact, it's almost always going to be 0 or 1 because the prevalence is not going to be that high in the population generally.

And so we can make that assumption.

And so if we do that, then what we're really interested in is what is the expected number of transmissions so the expected value of this T here.

So if you have a random sum of random variables, then the expectation is easy to calculate.

If also the random number is independent from the variables you're adding up so there's no correlation between them, this would just be the expected number of the total number of those variables, which is IS, just the total number of pairs infected and susceptible, times the expected value of this tau MN, which is beta bar tau.

And just for completeness, let me also remind you actually what this beta bar is just so that when I keep writing it, we're clear on it.

It's 1 over tau integral from 0 to tau of beta dt.

So it's the time average beta.

And we have further approximated this by writing the beta inverse average is approximately the steady state value inverse times 1 plus lambda C tau inverse.

So that was a convenient approximation.

So in our subsequent calculations, whenever you see this expression average of beta times tau, you could imagine substituting this expression where beta bar is given by all the physical parameters that we've been discussing.

So this is a very simple model of the random transmission that can occur when you take into account the randomness in the number of infected people.

So now let's start to write down a model for the number of iffected people.

So the simplest thing there is that-- I'll write here the random number of infected persons is that this should be a binomial random variable.

And that means that the probability that the infected number is equal to some value N is the number of ways you can choose little n infected people out of N total people in the room times the probability that any one of them is infected, which we'll call pI, and then qI is the probability that the others are not infected.

So the important new variable that we have here is pI is the probability a person randomly selected from the population and placed in this room is infected.

And this is also sometimes called the prevalence of the infection in the population.

And then this qI, of course, is just 1 minus pI.

So it's standard notation for binomial distribution is to use q is 1 minus p.

And so let's make some further assumptions about this random number of infected people.

So first of all, by assuming this binomial distribution, we are assuming that at any moment in time, the number of iffected people is somehow refreshed continuously to reflect the same kind of distribution that you find in the population.

So the variable I is refreshed continuously in time to reflect the population prevalence.

So people are coming and going from the room.

But there's always a certain number of inffected people that reflects the chance of running into an infected person in the population.

So that's a reasonable assumption.

A more sophisticated model for a given space might take into account the actual probability or rate of arrival and the rate of removal of people and, similar to models from queuing theory, might derive a distribution which is more complicated and depends on those other parameters for the fluctuations in the number of infected people in a room.

But this is the simplest way to start is that the room essentially reflects the population statistically.

Another assumption, though, which we're going to make, which gives us some more simplicity and also allows us to be more conservative, is that we neglect exposure and essentially allow infection to happen at the same rate more than once even and allow transmission to proceed at the same rate where we essentially are assuming that S is N minus I.

So in other words, the susceptibles never get converted into an exposed group that can no longer be infected again.

We'll just say that the rate is still always going to be I times S where S is just N minus I.

So we're letting the number of infected people fluctuate.

But everyone else in the room is considered susceptible.

That's a conservative approximation.

Because in reality, the number of susceptible people would go down as they converted to the exposed Group.

Over very long times, eventually there be new infected people generated.

But that's really relevant for situations like the Diamond Princess quarantine where same people are confined to the same space for a period, a longer period.

Here, we're really thinking of just this indoor space that is reflecting the statistics of prevalence in the population.

Let me now do a couple quick calculations based on this model of some quantities that we're going to need.

So the first is that given a binomial distribution, the expected value of this random variable I is just the number in the room times pI the prevalence.

And furthermore, the variance of I, which is the expected value of I squared minus the expected value of I quantity squared, is NpIqI-- basic result for a binomial random variable.

From there, if you then take these two relationships, you can solve for the expected value of I squared and find that that is equal to this Npq plus the Np quantity squared-- I'll just write that-- Npq plus Np quantity squared.

That's wrong.

And so that's can be written as I expected value times-- well, let's see here.

We have a qI plus expected value of I.

And now using this relationship, if we look at the number of susceptibles, S, the expected value, is just N minus the expected value of I, which is Np.

And finally, to calculate transmissions, what we're really interested in, the expected value of I times s-- so that would be, if we substitute, that would be N times the expected value of I minus the expected value of I squared, which we have right here.

And if we substitute this expression here, you see we have a factor of I-- expected value that we can factor out, and then we get N minus the expected value I minus q, qI.

And then, finally, substituting the expected value of Is and pI, and 1 minus pI is qI, you can find that this is pIqI N N minus 1, which can also be written sigma I squared N minus 1.

So now we basically have an expression for the transmission rate in terms of the number of people in the room.

So essentially, it's N minus 1, which, in fact, you may recall, was the transmission rate when there's one infected person and N minus 1 susceptibles.

But time is factor sigma I squared, which is actually the fluctuation in the infected number.