Introduction to Evolutionary Dynamics
Prof. Supreet Saini
Department of Chemical Engineering
Indian Institute of Technology, Bombay

Lecture - 33
Evolutionary dynamics when mutations are rapid - 3

Hi, and let us continue our discussion from the last lecture, and what we are discussing is we are interested in the time of transition of this population between these two different distributions.

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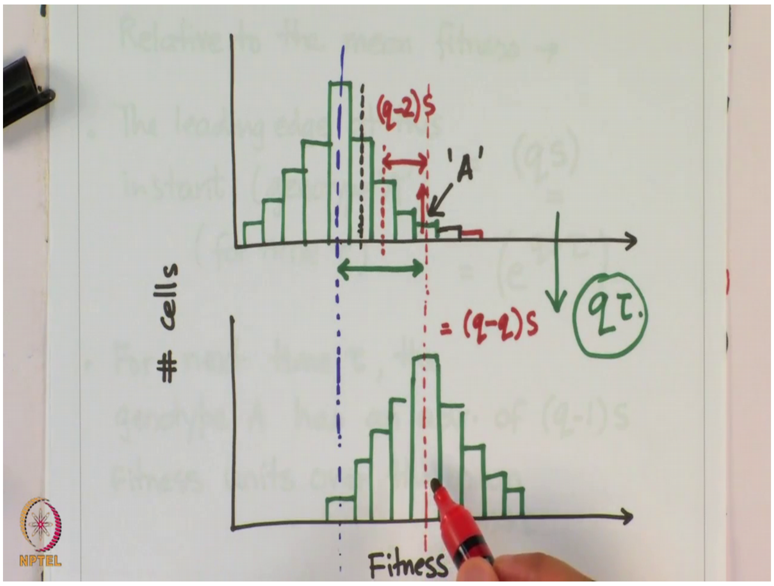

In the first distribution we are looking at this leading edge, and what we are interested in is the transition of the population from this on this fitness scale from this picture to this picture. And we know that the total amount of time that it takes to transition from this picture to this picture is equal to q times tau, because this leading edge will take tau amounts of time for each of these steps. And there are q such beneficial mutations that distinguish the leading edge from the mean of the population at any given instant, hence it will need q of these transitions hence the total time is q times tau.

Now, how do we come up with an expression for this difference of this growth of this growth of the numbers which are associated with this leading edge such that it becomes the most frequent distribution most frequent genotype in the population, and the way we are going to think about.

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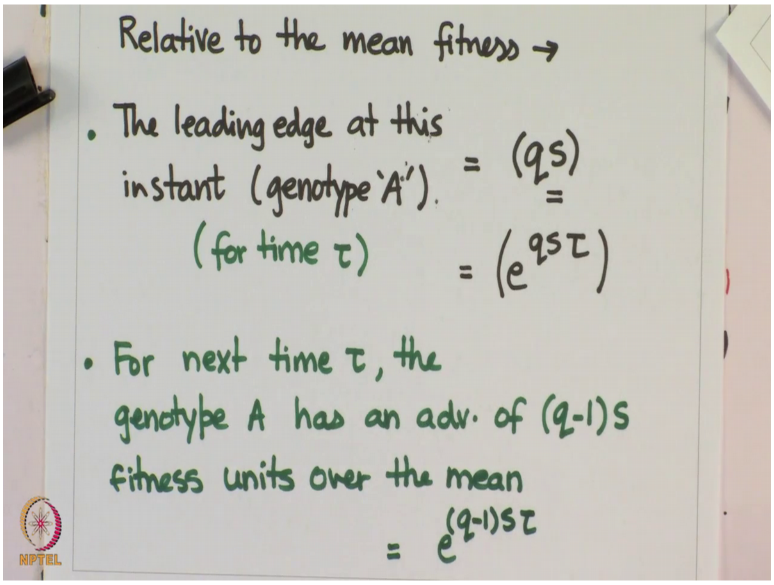

Relative to the mean fitness →

- The leading edge at this instant (genotype 'A'). $= (qs)$ $=$ $= \left(e^{qs\tau}\right)$
  (for time τ)
- For next time τ, the genotype A has an adv. of $(q-1)s$ fitness units over the mean $= e^{(q-1)s\tau}$

This is that we know that this leading edge relative to the mean fitness, the leading edge or let me call this the leading edge at this particular instant, but let me call this genotype A, because after tau units this A genotype will no longer be the leading edge and this particular genotype will be the leading edge. So, this would not be the leading edge for all time, but let us call this genotype A which happens to be the leading edge when this particular snapshot is taken.

So, the leading edge at this instant which is genotype A, is growing at a rate which relative to the means is q s is fitter than the mean by a quantity q s; that means, relative to the mean its numbers are increasing in the following manner e to the power q s and that happens for time tau while the leading edge or the genotype A is still the leading edge.

After time tau this genotype A is no longer the leading edge, but it becomes in this distribution it becomes second now this genotype A while this new beneficial mutation has become established in the population, the mean of the population the mean fitness has also moved from this particular genotype to this particular genotype. So, when this has become established because the wave is moving towards the right at a constant speed the new mean fitness of the population is being defined by this particular genotype; that means, the distance between genotype A and this new mean is no longer q s units in fitness, but q minus 1 units.

Because genotype A has remained where it was, but the mean has moved up s units; that means, that the distance the relative advantage of genotype A over the mean has now become reduced by s units and the new advantage that this genotype A holds over the mean is q minus 1 s units. So, it remains as a leading edge for time tau for then. So, this is one the second for next time tau the genotype A has an advantage of q minus 1 times s fitness units over the mean, which means that for this next tau units of time its numbers are going to grow as e to the power q minus 1 s into tau.

Similarly, what has happened in this next tau interval is that now another beneficial mutation has become established in the population and all the while these mutations are becoming established, the numbers associated with genotype A are being increased because of selection. But when this has become established now the mean has moved up another s units this red line represents the new mean and the distance between genotype A and the new mean is now q minus 2 times s and so on and so forth.

This will keep on happening till our genotype A itself becomes the mean and once genotype A itself becomes the mean as shown in this picture, what happens is that the relative advantage this will become q minus q times s and its numbers will stop growing. After this the wave would have moved to the right and this genotype A would be less fit than the mean fitness of the environment and hence its numbers will start to drop. So, this is that instant where numbers associated with this genotype A are maximum.

And what; that means, is to come from this picture to this picture we need to take q such steps at each of those each of those q steps in the first step the numbers of genotype A grow as q s e to the power q s, in the second step the numbers of genotype A grow as q minus one into e to the power q minus one s and so on and so forth. So, we can summarize this as for the first tau interval of time tau.

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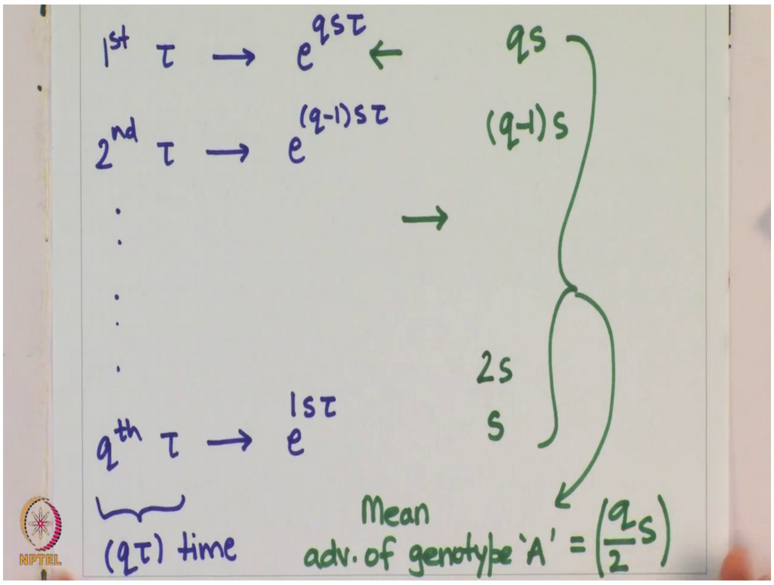

The numbers associated with genotype A grow as e to the power q s tau. For the second tau the numbers grow as e to the power q minus one s tau and so on and so forth, for the q th interval the numbers will grow as e to the power s tau one s tau and this each of this tau intervals characterizes the exact location of genotype A with respect to the mean fitness of the environment at that particular instant.

So, this is equal to a total of q tau time because these are q intervals each of time tau and in this this total time of q tau is divided between these between these q intervals where growth is happening at a different rate as described by these formula, and the simplifying assumption that we are going to make here is the following that the fastest rate in of the genotype A is occurring when itself is at the leading edge and that fastest rate is e to the power q s tau.

So, the exponent here is q s the exponent in the second interval is q minus one times s and so on and so forth coming all the way down to s and what we are going to say is that for each of these q intervals the mean advantage of genotype A is equal to q divided by 2 s. So, in the first interval the advantage that genotype A had over the mean was q s in the second interval the advantage that genotype A over the mean was q minus one s and so on and so forth coming all the way down to two s and then s. And finally, it becomes 0.

So, if we are taking all of these q intervals together the mean advantage that this genotype A has had over the mean fitness of the culture, in this entire interval of time can be approximated as simply q s by 2 which is just the mean associated with these q values. Again this is an approximation that we have made in order to come up with an article expression which describes, but this is not too bad an approximation in the sense maybe you are only interested in order of magnitude estimates of speed of evolution associated with our experiment.

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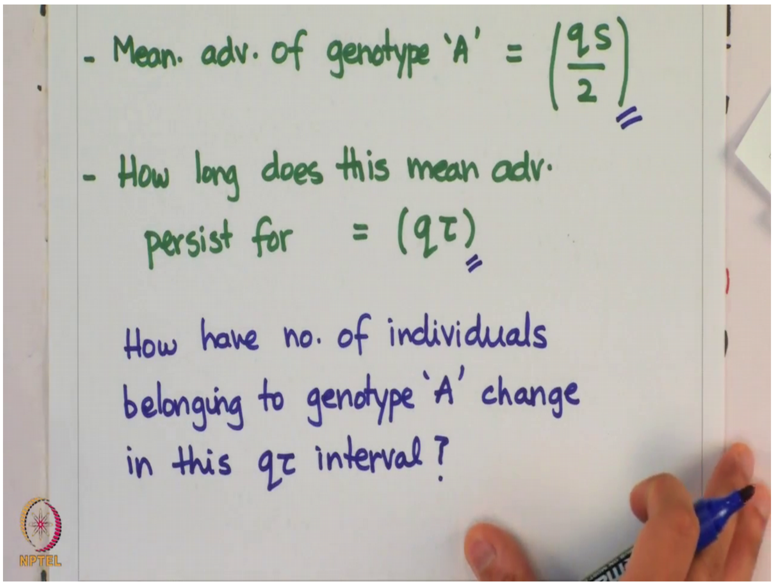

- Mean. adv. of genotype 'A' = $\left(\frac{qs}{2}\right)$
- How long does this mean adv. persist for = $(q\tau)$

How have no. of individuals belonging to genotype 'A' change in this $q\tau$ interval ?

So, we have this this mean advantage which is q s divided by 2. So, mean advantage of genotype A is equal to q s by 2, and the next question is that how long does this mean advantage of this genotype persist for. How long does this mean advantage persist for and that is just equal to q times tau.

Because if we revisit this t for first tau interval the advantage was q s, for the second tau interval the advantage was q minus 1 s and for the q-th tau interval the advantage was just s that means, these I can take the mean of these advantages as just the central value here which is q s by 2 and this mean advantage can be approximated to be had over the sum of this entire duration which is just q times tau time. So, which gives me this result that the leading edge of this culture can be approximated as this mean advantage of q s by two which has persisted for q tau amounts of time.

So, if you work with these assumptions how have number of individuals belonging to our genotype A, change in this q tau interval that is the question that we want to answer that if this is the advantage that this leading edge or genotype A had over the mean over the entire interval, and this is the time interval for which this advantage persisted what are its numbers after this interval of q tau time has passed.

And that can be approximated as number of individuals of genotype A is equal to n naught into e to the power q s by 2 into the.

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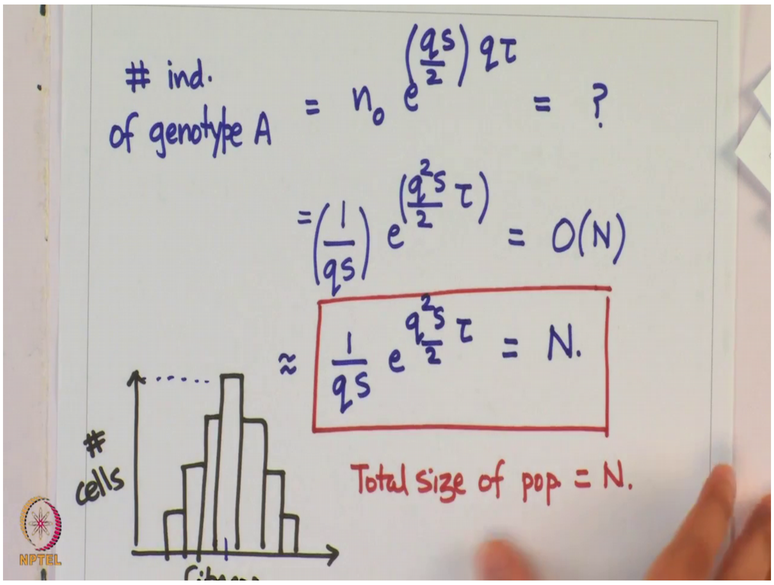

So, this is the advantage the relative growth rate with respect to the mean times the time for which this advantage persisted which is just q tau and this is equal to something and at this instant we do not know what that something is. N naught is the starting number of individuals which belong to genotype A and that we can safely assume to be one upon q s because this is the number of individuals that would we would need in that genotype A as leading edge, before we can say that genotype A became established in the population. When the numbers of genotype A were less than this then that particular genotype is still (Refer Time: 14:11) to genetic drift and it has not become established, but once the numbers reach 1 by q s that s when we say it has become established.

So, n naught is just 1 by q s, and this expression in the exponent becomes e to the power q square s by 2 into tau and this is equal to something in the right hand side which we have not yet defined, but let s revisit this again in our distribution this is fitness and this is number of cells and when genotype A has become the most frequent genotype in my distribution what that means, is that of the and I know that the total size of my population.

This experiment is being conducted in a setting where the total number of individuals in the population is always equal to n, then I can say that when genotype A has become the most frequent individual in the population, at the time we can say that the number of individuals of this genotype A is of the order of n. This is again an approximation because we do not really know exactly how many individuals belong to that particular genotype at this instant, but a good approximation is that it is of the order of n. Now that exact number could be n by 2, n by 3 or n by 4, but its, but the answer we know is most likely of the order of n and hence I am going to approximate this as one upon q s e to the power q square s by 2 times tau equals n ok.

So, this is the expression that I have right now and again I solved this whatI am interested in from this expression is the value or the expression for tau in terms of n s and q. So, I am going to rearrange these. So, I get this.

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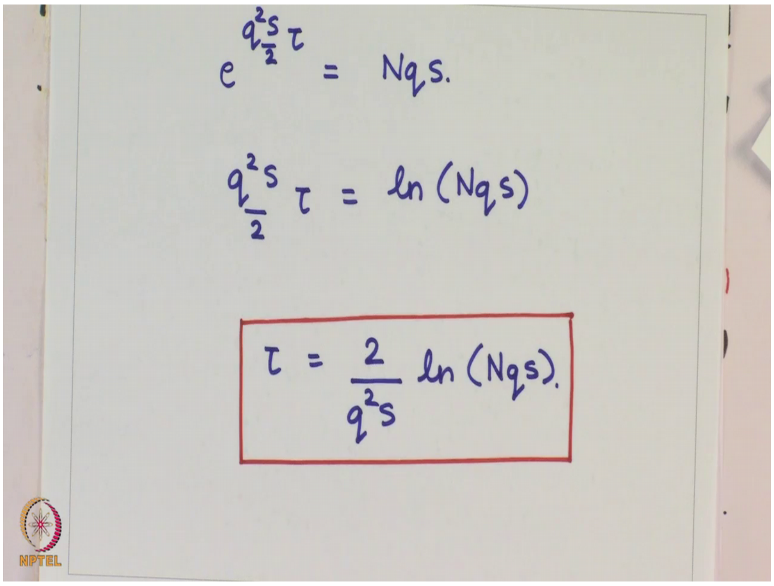

$$e^{\frac{q^2 s}{2}\tau} = Nqs.$$

$$\frac{q^2 s}{2}\tau = \ln(Nqs)$$

$$\boxed{\tau = \frac{2}{q^2 s}\ln(Nqs).}$$

So, I get an expression that tau equals this expression and if I do that what I end up getting is just e to the power q square s by two into tau is equal to NqS I take log on 2 divided by q square s into l n of NqS that s my second expression associated with the regime where mutations are happening rapidly and I come up with an expression which estimates the value of tau in terms of my variable q. Again q is somewhat arbitrarily assumed variable which defines that how far is the leading edge of this distribution that we have been talking about from the mean fitness at any given instant in time.

So, this is one instant one expression for tau which we have arrived at by looking at the distribution and calculating the time that it takes the leading edge to become the most frequent genotype in the population. In the last lecture we had done the same exercise and come up with an expression for tau where the approach there was calculating how long does it take for the leading edge to no longer be the leading edge and become next to the leading edge genotype in the distribution that we are interested in.

So, using these two approaches we have these two expressions for tau and what we want to do together want to do is now solve these two expressions together, and come up with values of q and tau.

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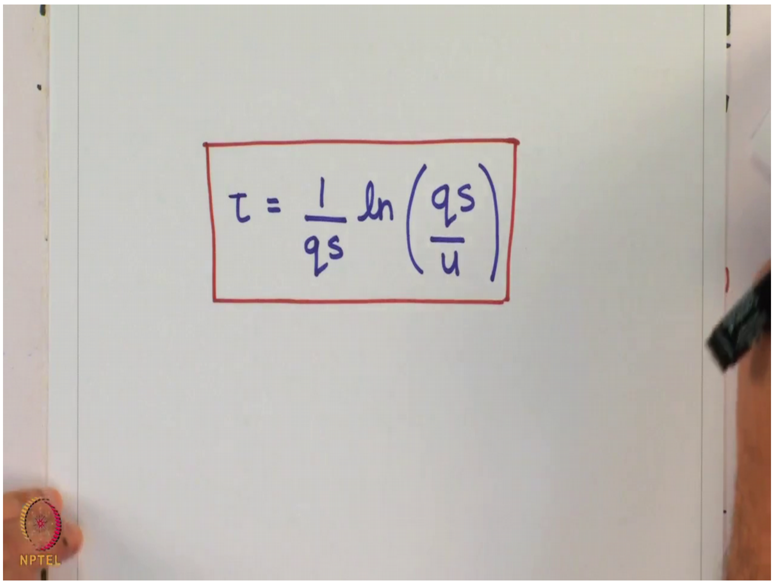

$$\boxed{\tau = \frac{1}{qs} \ln\left(\frac{qs}{u}\right)}$$

So, again this is the expression that we had obtained in the last lecture which was calculated using the logic that we were interested in the time it takes for the leading edge, to no longer be the leading edge and this is the expression for tau that we have derived in this point which is derived using the logic that how long does it take for the leading edge to become the most frequent genotype.

And now what we want to do is sort of work with both these expressions together, and solve for tau as well as q we sort of have good estimate for everything else and we have two equations in two unknowns we can solve them together. And the easiest way to do them is equate let us equate these two values we have each of these expressions is tau equals something hence the two right hand sides of these two equations are also equal to each other.

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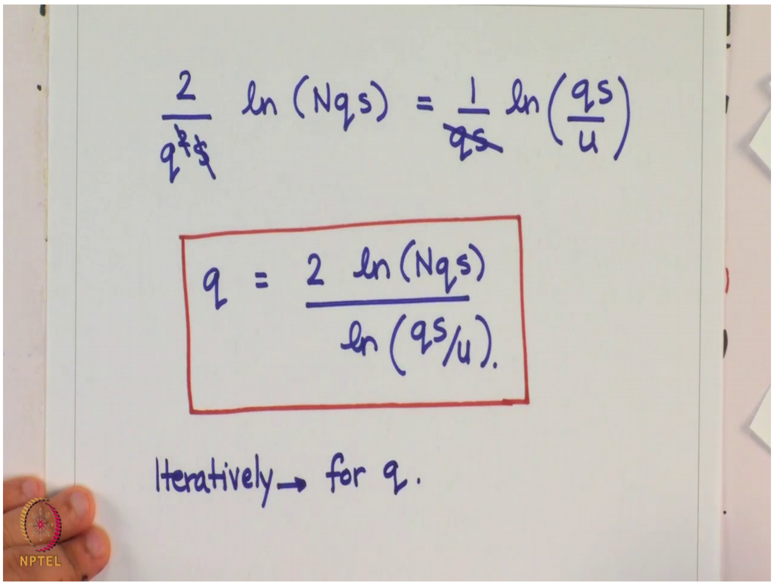

$$\frac{2}{q^{\cancel{2}}\cancel{s}} \ln(Nqs) = \frac{1}{\cancel{qs}} \ln\left(\frac{qs}{u}\right)$$

$$\boxed{q = \frac{2\ln(Nqs)}{\ln(qs/u)}.}$$

Iteratively $\rightarrow$ for q.

So, I am just going to write the right hand sides and then sort of simplify them and see how we can proceed towards solving for tau and q. If we do that we get two divided by q square s times l n of NqS equal to 1 upon q s l n of q s by u. We can simplify this we can drop this q s this s gets cancelled one of the q gets cancelled and we eventually get q equal to 2 l n of NqS divided by l N of q S by u.

So, we have this expression in q where we have gotten rid of our variable tau, we will say that we have reasonable estimates for s and n u hence q is the only unknown in this variable, but you cannot explicitly solve for q in this expression because q is occurring on the left hand side as well as right hand side. It is not trivial you cannot straightaway solve for q and an equation like this can be solved iteratively. So, we will solve this iteratively for q, and the scheme is that once we get q we can plug that q back in an expression we have already derived, and get estimates of tau and once we have tau we will we will know the speed at which that wave is moving.

So, let us try and look at how do we solve for this equation iteratively, and the approach that we are going to take is that we have q s the problem with this equation is that we have q on both left hand side and right hand side and there is no clear way to how to go about solving for q. So, the scheme that we are going to discuss is an iterative scheme where we guess values of q and consequently approach towards better values of q, which better estimate which better reflect accuracy associated with that relationship.

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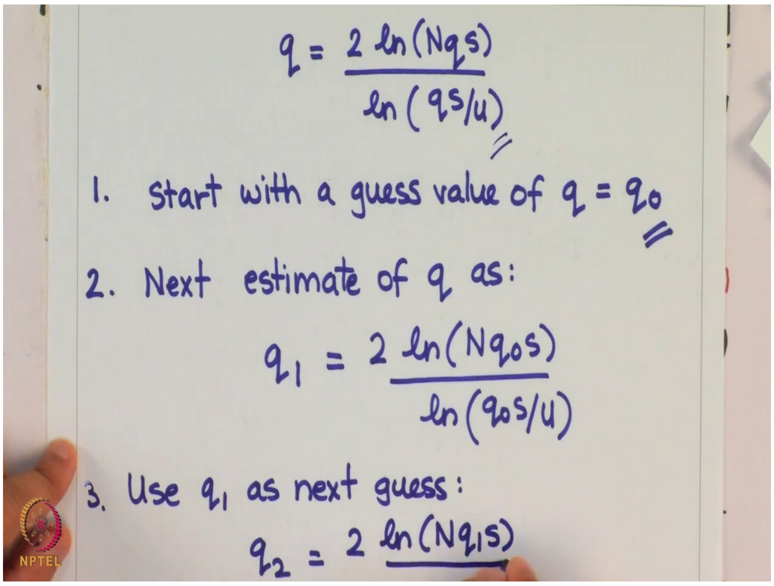

$$q = \frac{2\ln(Nqs)}{\ln(qs/u)}$$

1. Start with a guess value of $q = q_0$
2. Next estimate of q as:

$$q_1 = 2\frac{\ln(Nq_0s)}{\ln(q_0s/u)}$$

3. Use q_1 as next guess:

$$q_2 = 2\ln(Nq_1s)$$

So, let me just let me just quickly talk about this. So, our expression is q equals 2 times l n of NqS divided by l n of q s by u and to solve this iteratively, the first step that we will take is we will start with a guess value of q which is q naught. So, we just guess a value of q naught and that is our starting point from there we will get the next estimate of q as which is the next estimate I am going to call that as q 1, and that q 1 can be estimated as two times l n of n q naught s divided by l n of q naught s by u. So, what we are doing here is that we guess a value of q which is equal to q naught, and we plug this guest value of q naught only in the right hand side associated with the equation.

Now, if the guest value of q naught was 100 percent accurate then what I should get on the right hand side should also be equal to q which should be q 0, but because this was a guest value my left hand side will not be equal to q 0, but will be some other value of q which let us say is equal to q 1. So, I get q 1 here. And now I have this q 1 I am going to use q 1 as next guess and get q 2 equal to 2 times l n of n q 1 s divided by l n of q 1 s by u. So, what we have done here is that.

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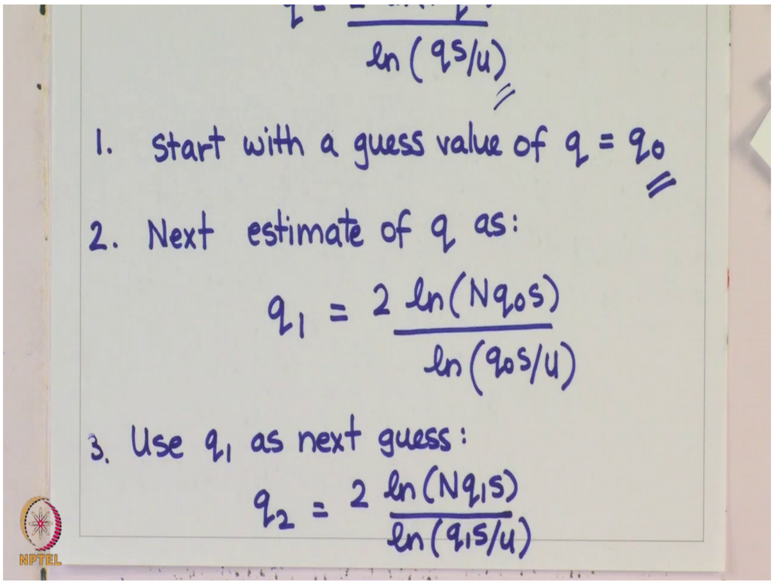

$\ln(qs/u)$

1. Start with a guess value of $q = q_0$
2. Next estimate of q as:

$$q_1 = 2\frac{\ln(Nq_0 s)}{\ln(q_0 s/u)}$$

3. Use q_1 as next guess:

$$q_2 = 2\frac{\ln(Nq_1 s)}{\ln(q_1 s/u)}$$

Now, that the value that we arrived at using my initial guess that value was q 1 and now I am going to use this next estimate of q 1 as my guest value and arrive at the next estimate of q which is q 2 and I will keep on progressing like this to higher values of q iaq I plus 1 every estimate of q q I gives me the next estimate of q which is q I plus 1.

And I will keep on doing this till I converts to a certain value of q where between two successive iterations of the scheme between q I and q I plus 1, the change that has happened in the value of q is negligible something that I am happy to ignore and that s when I that s when I will say that the scheme has converged to a particular value of q and that s the q that I am interested in. These schemes can fail sometimes and not converge. So, we just have to play around with the initial guess q naught that you are starting with and hopefully one of those starting guesses will converge to the q value that we want to solve for in this equation.

So, once we have this once we have the q value solved for using this iterative scheme, we plus this back in this expression that we had earlier derived for tau, and that gives me the time it takes that using by plugging the q value that I have solved here I can calculate the value of tau and this tau gives me the value that the leading the value of time that would take for the leading edge to no longer be the leading edge. And if I have that now I have q I have I already have n u and s those are values that I have very good estimates of depending on what kind of experiments I am doing and I have solved for q and tau.

Remember, now let us go back in our discussion and talk about what did we start with; we started with hoping to come up with an expression which tells me about speed of evolution in this experiment. So, having solved for all these quantities, I just want you to pause the video for a minute or so, and think about what would that speed of evolution be in terms of everything that we have done so far.

Now we have solved for all the variables associated can we come up with an expression which tells me about the speed of evolution associated with this experiment.

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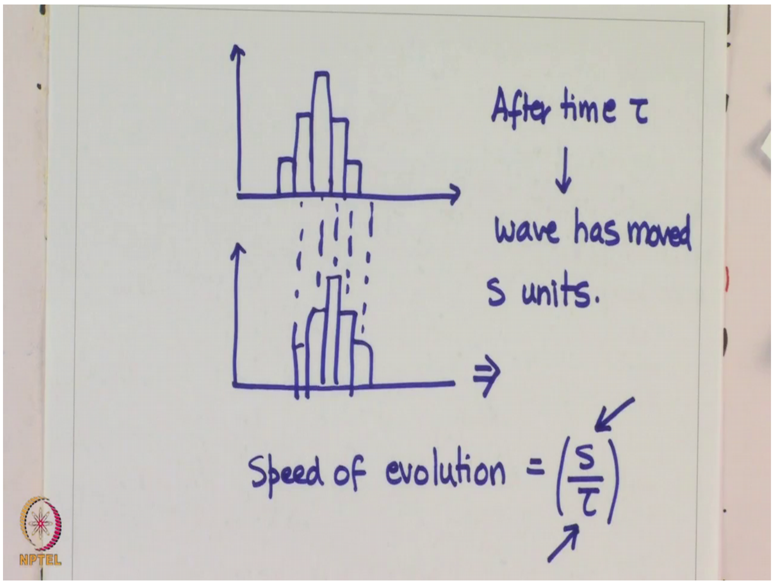

So, what you should what you should think about how you should think about this is the following that what we are saying is that there is a travelling wave distribution, and at sometime the wave maybe looks like this and what we are saying is that in exactly tau times the wave moves up s units, which means after time tau the waves the wave looks something like this.

So, this corresponds to this this corresponds to this, what we are saying that after time tau the wave has moved s units which another way to think about this is that in time tau it is almost as if every individual in the population has increased its fitness by s units imagine this travelling wave to imagine this travelling wave in a sense that everyone has jumped s units in this time tau.

Now, what that means, is if we can think of this wave in these terms that is every individual has increased its fitness by s units in time tau what that means, is that speed of evolution is just equal to s divided by tau because in this tau interval the fitness increase in every individual is s; that means, if increase in every individuals fitness is s; that means, the increase in mean fitness is also equal to s. So, in time tau the mean fitness increase is equal to s hence the speed of evolution, can be estimated as s upon tau and we have already solved for tau from the previous analysis that we just completed, and hence we have an expression for speed of evolution associated with this experiment.

So, in this way this was involved, but in this way we have been able to come up with a relatively simple expression for speed of evolution making some huge approximations, but something that hopefully gives us a good handle of order of magnitude estimates of speed of evolutions associated with these simple (Refer Time: 29:28) evolutionary experiments in lab.

We will change (Refer Time: 29:34) in the next class and we will talk about something called game theory and associated that with evolutionary dynamics.

Thank you.