

Applied Multivariate Analysis

Prof. Amit Mitra

Prof. Sharmishtha Mitra

Department of Mathematics and Statistics

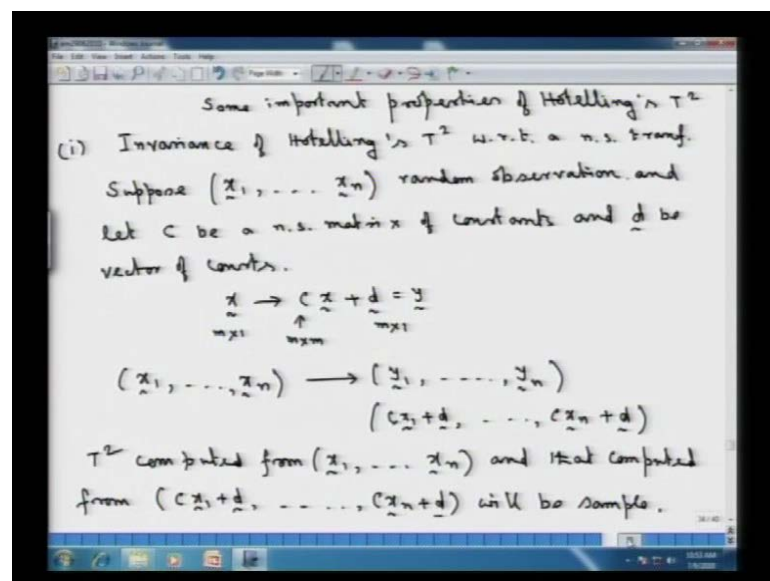
Indian Institute of Technology, Kanpur

Lecture No. # 15

Hotelling's T² Distribution and Profile Analysis

In the last lecture, we had looked at some applications of Hotelling's T square statistic, and also we had looked at how to use Hotelling's T square statistic when we have two sample normal problem, and related inference regarding that. Now, what we will do today is we will look at some important properties of the Hotelling's T square statistic.

(Refer Slide Time: 00:37)



Some important properties of the Hotelling's T square. Now, the first property that we are going to discuss is the invariance of the Hotelling's T square statistic with respect to a non-singular transformation. So, invariance of Hotelling's T square statistic with respect to a non-singular transformation. Now, what we mean by saying is that is the following that suppose we have this data x_1, x_2, x_n the random observations from a multivariate normal distribution with appropriate dimensions, and mean vector and then non-singular positive definite covariance matrix. Let c be a non-singular matrix of constants, and d be

a vector of constants. Now using this c non-singular matrix and d the vector of constants, we can actually make a transformation from this x to $c x$ plus d .

Suppose all these x s are m dimensional; we will take this c to be an m by m non-singular matrix and this to be an m by 1 vector. So, this is a new vector that is derived from this x random vector. Suppose we have this x_1, x_2, x_n , the original data through the transformation will be getting a new set of observations that is y_1, y_2, y_n which are nothing but $c x_1$ plus $d, c x_2$ plus d and so on, and the last one is $c x_n$ plus d . Now, the T square statistic computed from this x_1, x_2, x_n is going to be the same, that is going to be computed from $c x_1$ plus $d, c x_2$ plus d and $c x_n$ plus d . In that sense actually, T square will be invariant or rather I will just write that T square computed from x_1, x_2, x_n and that computed from $c x_1$ plus $d, c x_2$ plus $d, c x_n$ plus d will be same.

(Refer Slide Time: 04:29)

The image shows a whiteboard with handwritten mathematical derivations. At the top right, it states $\underline{x} \sim N_m(\underline{\mu}, \Sigma), \Sigma > 0$. Below this, several transformations are listed: $\underline{x} \rightarrow c\underline{x} + \underline{d}$, $\underline{\mu} \rightarrow c\underline{\mu} + \underline{d}$, and $\Sigma \rightarrow c\Sigma c'$. The null hypothesis $H_0: \underline{\mu} = \underline{\mu}_0$ and the alternate hypothesis $H_A: \underline{\mu} \neq \underline{\mu}_0$ are also written. Further down, the transformed mean $\underline{\mu}_0 \rightarrow c\underline{\mu}_0 + \underline{d}$ and the transformed sample mean $\bar{\underline{x}} \rightarrow c\bar{\underline{x}} + \underline{d}$ are shown. The final part of the derivation shows the transformation of the scatter matrix: $(n-1)S = \sum_{j=1}^n (\underline{x}_j - \bar{\underline{x}})(\underline{x}_j - \bar{\underline{x}})'$ is transformed into $\sum_{j=1}^n (c\underline{x}_j + \underline{d} - c\bar{\underline{x}} - \underline{d})(c\underline{x}_j + \underline{d} - c\bar{\underline{x}} - \underline{d})'$.

How do we claim this? We claim this particular invariance in the following way that since we are made this non-singular transformation, the x random vector the underlying random vector will get changed to $c x$ plus d . the corresponding x to follow a multivariate normal m with a mean vector μ and a covariance matrix as σ . Then with this transformation, this μ will be changed to $c \mu$ plus d and then this σ matrix the associated variance covariance matrix to be positive definite. So, this σ is going to be changed to $c \sigma c$ prime. Now, T square statistics comes into existence actually for testing null hypothesis of the form that μ is equal to μ naught to be tested against an alternate hypothesis H_A that μ is not equal to μ naught.

So, where does this mu naught go to? mu naught is a known vector. So, this known vector mu naught will be shifted to c mu naught plus d. Now, when we have such transformations and place what happens to this x bar quantity? Now, x bar is the sample mean vector that is obtained from x 1, x 2, x n. So, this x bar is computed from x 1, x 2, x n, the data. So, this will be changed to c x bar plus d and n minus 1 s say with a divisor n minus 1; that is given by x j minus x bar x j vector minus x bar vector transpose j equal to 1 to up to n. Now, where does this gets changed to when we are looking at the transformed observations, this x to be replaced by c x j plus d.

Now, what happens to x bar? x bar is c x bar minus d in to the transpose of that. So, it is c x j plus d minus c x bar minus d transpose. So, this d vector cancels out from both the quantities and what happens is, the following we will have here c is a non-singular matrix. So, this c can be taken out from the left, c transpose can be taken out from the right and what will be having is the following that, the quantity that I had written is going to be, c times summation j equal to 1 to n x j minus x bar then x j minus x bar transpose c transpose and this term is equal to n minus 1 times s with the divisor n minus 1.

(Refer Slide Time: 07:13)

$$\begin{aligned}
 &= c \sum_{j=1}^n (x_j - \bar{x})(x_j - \bar{x})' c' \\
 &= c (n-1) S c' \\
 \Rightarrow S &\rightarrow c S c' \\
 T^2 \text{ computed from } (x_1, \dots, x_n) &\text{ is} \\
 T^2 &= n (\bar{x} - \mu_0)' S^{-1} (\bar{x} - \mu_0) \\
 &\rightarrow n (c \bar{x} + d - c \mu_0 - d)' (c S c')^{-1} (c \bar{x} - c \mu_0) \\
 &= n (\bar{x} - \mu_0)' d' (c S)^{-1} d' (\bar{x} - \mu_0) \\
 &= n (\bar{x} - \mu_0)' S^{-1} (\bar{x} - \mu_0) \rightarrow T^2 \text{ computed from } (x_1, \dots, x_n)
 \end{aligned}$$

So, what we have seen is the following that this quantity out here that n minus 1 s. Now, with this non-singular transformation is going to c times n minus 1 s c prime. This would imply that this s the sample variance covariance matrix is going to c s c transpose. Now, once we have these things in place the T square computed form x 1, x 2, x n the original set of observations is given by T square is equal to n times x bar minus mu naught

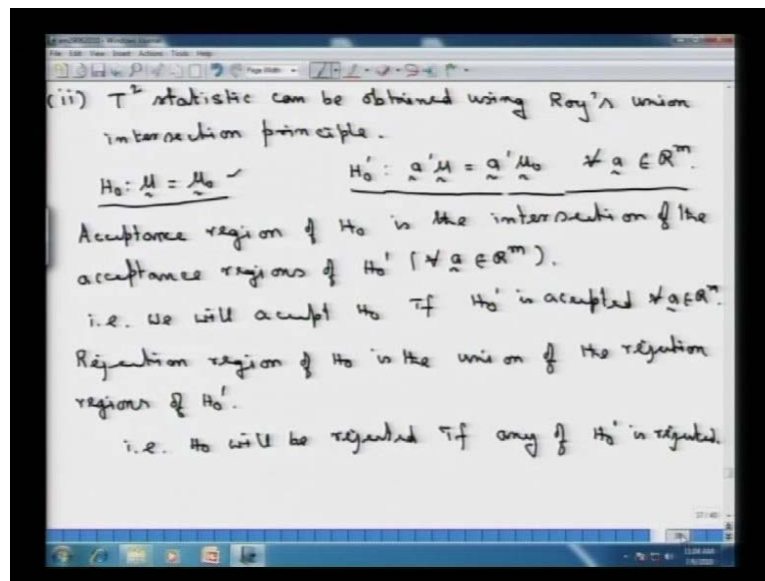
transpose $S^{-1}(\bar{x} - \mu_0)$. So, we had seen this and again this is basically that Hotelling's T^2 when we are looking at x_1, x_2, \dots, x_n ; n observations from a multivariate normal distribution for testing the null hypothesis $\mu = \mu_0$ against $\mu \neq \mu_0$.

Now, where does this go to? We will have this under the non-singular transformation that we are discussing; this \bar{x} is now $C\bar{x} + d$. Where is μ_0 ? μ_0 is $C\mu_0 - d^T$. Now S is going to CS^T . So, here what we have is this is just CS^T whole inverse and then that is multiplied by the transpose of this particular quantity what would remain? This d is cancelling out and we will have $C\bar{x} - C\mu_0$ on this side. Now, this is equal to n times; now this C can come out side with a transpose; this goes here and what will be having here is this $\bar{x} - \mu_0$.

So, this C with a transpose comes here and then we will have this term here. So, which is $C^T S^{-1} C^{-1}$ and then we will take C from this side as well; this is $C\bar{x} - C\mu_0$. So, this C into C^{-1} will give us an identity matrix; this C^T into $C^T S^{-1}$ will also give us an identity matrix. So, what will be having is n times $\bar{x} - \mu_0$ into S^{-1} times $\bar{x} - \mu_0$. Now, what is this quantity? This is the T^2 statistics which is computed from the y observations; because this is nothing but \bar{y} ; this is nothing but the mean corresponding to the y random variables.

This is the sample variance covariance matrix that is computed from the y observations that is what we had seen out here; that we have these under the transformation here; that we are making that x_1, x_2, \dots, x_n is transformed to y_1, y_2, \dots, y_n . Then what happens to the corresponding means? This is the mean vector corresponding to the y observations. This is the variance covariance matrix corresponding to the y observations and what we have proved is that the T^2 computed from the x_1, x_2, \dots, x_n which is equal to what is this quantity. This is the T^2 computed from the y observations computed from y_1, y_2, \dots, y_n . So, what we have proved is that the T^2 statistics remains invariant with respect to this non-singular transformation.

(Refer Slide Time: 11:38)



So, that was the first important property that, we can say about this Hotelling's T square. Now, the second thing is that the T square statistic can be obtained using Roy's union intersection principle. Now, what is that? We have this null hypothesis H_0 that μ equal to μ_0 . Suppose we take this alternate type of hypothesis H_0' , which is $a' \mu = a' \mu_0$. This is for every a belonging to the appropriate dimension R to the power m ; because we have got a multivariate normal which is m dimensional. So, what is the correspondence between the two hypothesis H_0 and H_0' ? Now, the acceptance region note that this is a single hypothesis here and there are a number of hypothesis for possible choices of the a vector belonging to R to the power m on the right hand side.

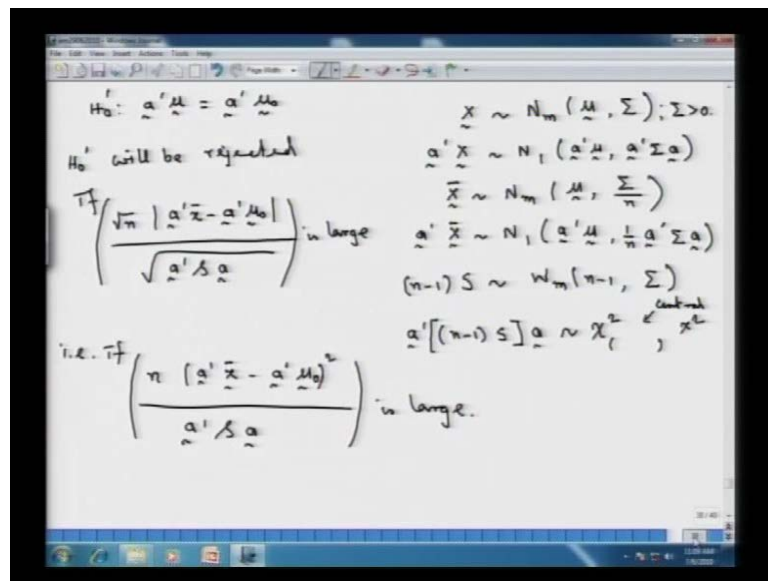
Now, the acceptance region the relationship that is what we are talking about; the acceptance region of H_0 is the intersection of the acceptance regions of H_0' for every a belonging to R to the power m . Now, what does that mean? That means, this H_0 null hypothesis is going to be accepted. If we have this H_0' hypotheses to be accepted for every value of this a vector; that is, we will accept H_0 . If H_0' is accepted for every a belonging to R to the power m and that is quite obvious; because if for some a this null hypothesis H_0' hypothesis is rejected, we cannot take this hypothesis to be accepted.

Now, this is about the acceptance region. So, the acceptance region of this would be the intersection of the acceptance region of H_0' . What about the rejection region? The rejection region has the following relationship between the H_0 and H_0'

naught prime hypothesis. The rejection region of H_0 is the union of the rejection regions of these H_0 prime set of hypothesis; that is H_0 will be rejected if any of H_0 prime hypothesis is rejected. So, rejection of any one of these H_0 prime hypothesis would leading to the rejection of the main hypothesis; that is H_0 .

Accordingly, the rejection region of H_0 would be the union of the rejection region of H_0 prime hypothesis for a varying in R to the power m . So, this basically is what we talk about the union intersection. It is called the union intersection principle; because the rejection region of this H_0 hypothesis is the union of the rejection region of these set of hypothesis. The acceptance region of this H_0 is going to be the intersection of the acceptance region of this H_0 prime set of hypothesis. Now, what we will do is that we will basically look at when is this H_0 prime hypotheses going to be rejected? On what sort of theory, we are going to actually base our rejection region. So, H_0 prime is a prime μ equal to a prime μ_0 .

(Refer Slide Time: 16:12)



Suppose, I have take this one hypothesis here; H_0 prime is a prime μ equal to a prime μ_0 for particular a vector. Now, in order to test this particular hypothesis, what we are going to make use of is the following. Now, we have x to follow a multivariate normal m dimension with a mean vector μ and a covariance matrix σ positive definite. So, we will have σ to be positive definite out here. So, x has got this particular normal distribution. So, what happens to the distribution of a prime x ? a prime x will have a multivariate normal distribution which is a prime μ and a prime σ as its variance.

Now, from here what we can also say is that this \bar{x} has got a multivariate normal distribution with a mean vector μ and a covariance matrix as σ^2 . So, this would imply that for this a prime vector, this a prime \bar{x} is going to have this N is going to be one. This is $N(1)$; because this is that particular 1 by n dimensional vector. Now, this also is a univariate normal random variable with mean as a prime μ and a covariance matrix 1 upon n a prime σ^2 . Now, the variance covariance matrix n minus 1 times s the sample variance covariance matrix; this has got a **wishart** m n minus 1 times σ^2 .

From the previous results, what we can say is that this a prime n minus 1 s times a . This is going to follow a central chi square that is what we had seen earlier that this has got central chi square on what degrees of freedom n minus 1 minus m plus 1 degrees of freedom and it is going to be a central chi square. So, this is a central chi square on the degrees of freedom which is going to given by n minus 1 minus m plus 1 . So, using these facts actually we are in a position to test this particular null hypothesis. How we are going to frame that? H_0 is will be rejected, if the following quantity is large; if \sqrt{n} absolute value of a prime \bar{x} minus a prime μ divided by under root of a prime s is large.

Why is that so? It is simple to see that; because we have a prime \bar{x} to have a normal distribution. This a prime \bar{x} minus a prime μ that divided by this variance out here; that is going to have a normal 0 1 distribution; but this σ^2 matrix is unknown to us. And hence, we also need to use this distribution chi square here. Eventually, what we are going to have? This distribution is going to be a tedious distribution; because that would be ratio of standard normal distribution to that of a central chi square random variable. So, we are going to reject H_0 , if this quantity is large; that is if this square of it is large. So, there is a reason why we are looking at this square of that particular quantity; this a prime μ whole square that divided by a prime s is large.

Now, this is as far as rejection of this one single hypothesis, H_0 for a given a prime belonging to R to the power m . So, the large quantity of this particular observed thing based on x_1, x_2, \dots, x_n is what is going to lean us to the rejection of H_0 . Now, what is the relationship between this rejection of this hypothesis for a particular a belonging to R to the power m and the rejection of H_0 hypothesis; that is, μ equal to μ_0 and what we will be having is the following. This H_0 the null

hypothesis $\mu = \mu_0$ will be rejected, if we have the supremum over a of these quantities, which is n times $(\bar{x} - \mu_0)^2$ divided by a .

(Refer Slide Time: 20:54)

And $H_0: \mu = \mu_0$ will be rejected if

$$\sup_{a \in \mathbb{R}^m} n \frac{(a' \bar{x} - a' \mu_0)^2}{a' \delta a} \text{ is large}$$

i.e. if $n \sup_{a \in \mathbb{R}^m} \left[\frac{(a' (\bar{x} - \mu_0))^2}{a' \delta a} \right]$ is large.

Recall that $\sup_{u \neq 0} \frac{(u' v)^2}{u' A u} = v' A^{-1} v$ (follows from C-S inequality)

Take $u = a$; $v = (\bar{x} - \mu_0)$; $A = \delta$

So, this is basically the supremum over every a belonging to \mathbb{R}^m ; that is, for all possible hypothesis H_0 , when a varies in \mathbb{R}^m to the power m . If we have supremum of these quantities for varying a is large, now we need to look at what is this; that is we are going to reject H_0 , if now n is constant; n just sits outside. So, it is the supremum over a belonging to \mathbb{R}^m of this particular quantity. Now, how do we write this particular quantity out here? I will take a prime outside here. This is $(\bar{x} - \mu_0)^2$ divided by a is large. Now, in order to find out the supremum of this particular quantity, supremum over this term out here; we recall that we have something called a **cauchy-schwarz** inequality.

So, we may recall the following result; recall that supremum over u not equal to zero. Ofcourse, we also will take u not equal to zero; because u equal to zero does not mean anything; because we are going to test null hypothesis that $0 = 0$; that does not make any sense. So, it is over all vectors which are non-null of this $u' v$ whole square divided by $u' A u$, where A is non-singular. This is going to be given by $v' A^{-1} v$. Now, this follows from the **cauchy-schwarz** inequality straight forward. So, we have this general result that for a non-singular matrix A , we will have the supremum of this particular quantity to be given by this. Now, here we will use this result, in order to find out what is the supremum of this.

So, we can take here, this a vector to be equal to this u vector; the v vector to be equal to this x bar minus mu naught vectors; this A to be equal to this s matrix. Now, if sigma is positive definite then with probability 1, this sample variance covariance matrix s is non-singular and hence, this s that we are talking about ofcourse, is going to be non-singular with probability 1; because, we have chosen sigma to be positive definite matrix and thus, this would imply that this H naught will be rejected, if we have this quantity n times; now I will plug in the supremum value of that is going to be given by, this x bar which is v transpose; then a inverse is s inverse x bar minus mu naught is large.

(Refer Slide Time: 24:26)

Handwritten text on a whiteboard:

$$\Rightarrow H_0 \text{ will be rejected if}$$

$$n (\bar{x} - \mu_0)' S^{-1} (\bar{x} - \mu_0) \text{ is large}$$

i.e. if T^2 is large

$$\text{i.e. if } \frac{T^2}{n-1} \cdot \frac{(n-1)-m+1}{m} \text{ is large}$$

$$\text{i.e. if } \left(\frac{T^2}{n-1} \cdot \frac{n-m}{m} \right) \text{ is large.}$$

So, this follows from this equation that this is going to be rejected. This is coming through the H naught prime set of hypothesis and then that is going to be rejected, if this is large. Or in other words, if this is large; that is this term is equal to the T square statistics only; that is if T square is large. Or in other words, we can plug in the constant; that is if T square by n minus 1 into n minus 1 minus m plus 1 divided by m is large; that is, if this T square by n minus 1; now this one cancels out and you will have this here as n minus m by m is large. Now, we know what the null distribution of this particular quantity is.

The null distribution under the null hypothesis H naught mu equal to mu naught. This is going to have an F distribution; a central F distribution on what degrees of freedom; n minus m degrees of freedom and hence, statistic is equivalent to what we have already seen. So, that is why one says that we have actually shown that the T square statistics for testing H naught mu equal to mu naught can alternatively be obtained through this union

intersection principle; wherein you consider this set of null hypothesis H_0 which is a prime $\mu = \mu_0$. And then, the rejection region of that actually leads us to seeing that this basically based on the T square statistic itself. Now, next what we are going to talk about is something about confidence intervals.

(Refer Slide Time: 26:51)

(iii) Confidence region for μ (X_1, \dots, X_n r.s. from $N_m(\mu, \Sigma)$)

Note that

$$\frac{n(\bar{X} - \mu)' S^{-1} (\bar{X} - \mu)}{n-1} \cdot \frac{n-m}{m} \sim F_{m, n-m}$$

$$\Rightarrow P\left(\frac{n(\bar{X} - \mu)' S^{-1} (\bar{X} - \mu)}{m(n-1)} \leq F_{m, n-m}(\alpha)\right) = 1 - \alpha$$

$$\Rightarrow 100(1-\alpha)\% \text{ Confidence region for } \mu \text{ is } \left\{ \mu : (\bar{X} - \mu)' S^{-1} (\bar{X} - \mu) \leq \frac{m(n-1)}{n(n-m)} F_{m, n-m}(\alpha) \right\}$$

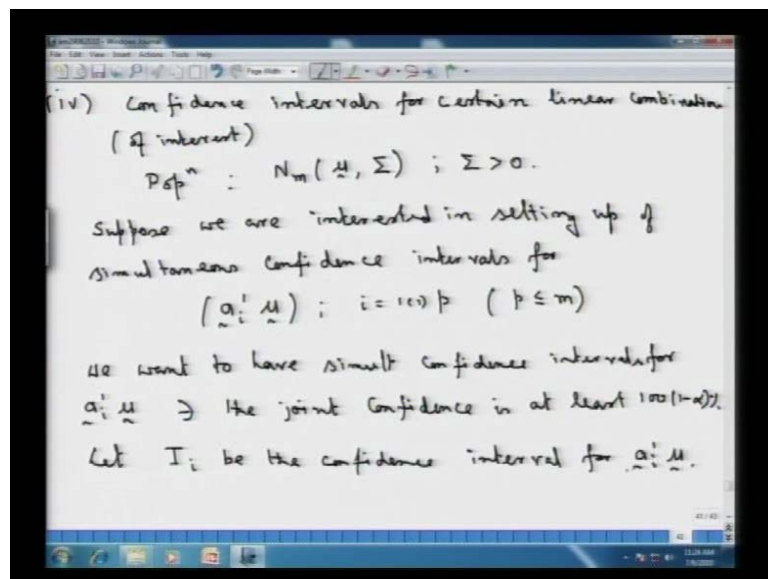
So, we will have these terms here that let me first talk about confidence region for the mean vector μ . Now this is what we have that we have x_1, x_2, \dots, x_n random sample from a multivariate normal $N_m(\mu, \Sigma)$ where Σ is a positive definite matrix. So, we are interested actually in giving confidence regions for the unknown mean vector; that is μ . Now, how are we going to do that? We know that this T square by degrees of freedom $n - 1$ $n - m$ by m ; this follows an F distribution. I will just write the full form of it. So, that it becomes easy to frame the confidence region. Note that, we will have this n times \bar{x} minus μ transpose; then we have S^{-1} \bar{x} minus μ this term here.

This is the T square statistic divided by degrees of freedom which is $n - 1$, that multiplied by $n - 1$ minus $n - 1$. So, that is $n - m$ divided by m , this will follow an F distribution; now this F distribution has degrees of freedom m $n - m$. Now, if we have this particular term to hold true; this would imply that the probability of this \bar{x} minus μ transpose S^{-1} \bar{x} minus μ ; this multiplied by all these constants out here; n times $n - m$ divided by m times $n - 1$; this less than or equal to $F_{m, n-m}(\alpha)$.

What is this probability going to be equal to 1 minus alpha, wherein this particular term is upper alpha percent point of a central F distribution on m n minus m degrees of freedom? So, the area to the right of this particular point is alpha and hence, the area to the left of it is 1 minus alpha. So, I will just write it that probability of an F statistic on m n minus m degrees of freedom greater than this $F_{m, n-m, \alpha}$; this is a given point. So, this right tail probability is equal to alpha and hence, since this has got an F distribution on m n minus m degrees of freedom. The probability that this less than or equal to 1 minus alpha.

So, this would imply that a 100 into 1 minus alpha percent confidence region for this unknown vector mu is going to be given by the set of all mu values such that we will have this $\bar{x} - \mu^T S^{-1} \bar{x} - \mu$. This is less than or equal to m times n minus 1 divided by n times n minus m times $F_{m, n-m, \alpha}$. So, what we have is ellipsoid; ellipsoidal region actually is giving us a 100 into 1 minus alpha percent confidence region for every mu; that is satisfying this particular condition that it is within this particular boundary region here. We will have that ellipsoid to lead us to 100 into 1 minus alpha percent confidence region for this mean vector mu.

(Refer Slide Time: 31:25)

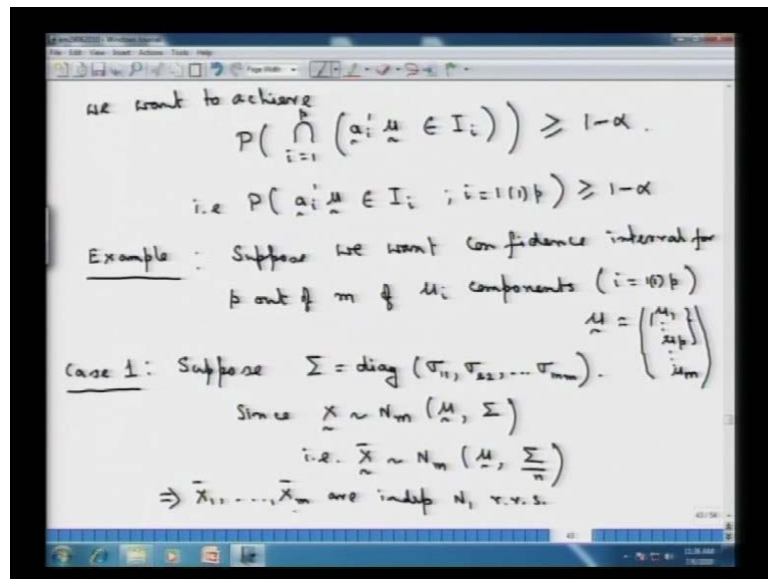


Now, let us move on to simultaneous confidence intervals for certain linear combinations of interest. Now, the underlying population still is a multivariate normal. So, the population is a multivariate normal n dimensional with a mean vector mu and a covariance matrix sigma, which is assumed to be positive definite. So, we have this sigma matrix to be positive definite. Suppose we are interested in setting up of

simultaneous confidence intervals for quantities of the form that it is a $a_i \mu$; this i is for 1 to up to p ; where this p is less than or equal to m . So, we have p such linear combinations $a_i \mu$ and these are linear combinations of the parameter. Say for example, we are interested in setting up of simultaneous confidence interval for μ_1 minus μ_2 and μ_p minus μ_{p-2} something.

So, we are interested in such p linear combinations of the unknown mean vector μ and we are trying to setup confidence intervals in such a way that we want to have simultaneous confidence intervals for these $a_i \mu$; such that the joint confidence or the joint coverage actually is at least $100(1 - \alpha)$ percent. So, that is what is our objective; we have p such linear combinations. We are trying to put up simultaneous confidence intervals for this; such that the joint confidence is at least $100(1 - \alpha)$ percent. Now, what we are going to do is that let I_i be the confidence interval for this $a_i \mu$ component. So, if we have this I_i to be the confidence interval for $a_i \mu$ what we are trying to achieve is the following.

(Refer Slide Time: 34:46)



We want to achieve the following probability statement. This is intersection of each of these i equal to 1 to p that $a_i \mu$; this belonging to I_i . So, this is an event that $a_i \mu$ belongs to I_i . So, that I_i is what we are defined to be the confidence interval for particular term out there and then the intersection of all such events this probability we required that to be equal to $1 - \alpha$. So, we will show I we can achieve under different setups such a probability statement that the joint probability of all these $a_i \mu$ quantities belonging to the respective intervals that we are going to create. The

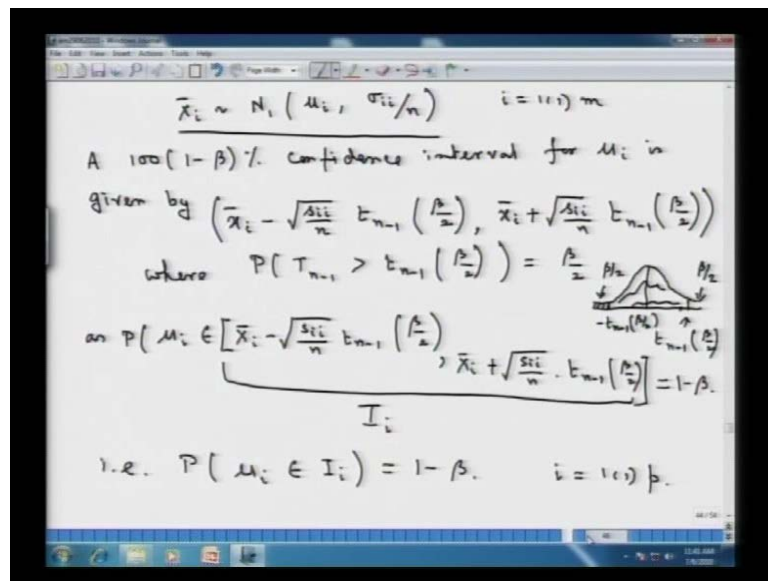
joint probability intersection of all such events is going to be greater than or equal to $1 - \alpha$.

So, this is the statement that we are going to make that this basically is the joint probability statements. So, this alternatively can be written in the following form that it is probability that this $a_i' \mu$ is belonging to this I_i interval; this is for i equal to 1 to up to p for all these linear parametric functions $a_i' \mu$; that is greater than or equal to $1 - \alpha$. Basically, this is going to give us the confidence region for each of these p linear combination of these mean vector μ and we will ensure that, this probabilities at least $1 - \alpha$. Let us take an example and then, try to illustrate how this type of problems, simultaneous confidence intervals is achieved? Now, suppose we want confidence interval for some p out of m of μ_i components without loss of generality, we take that we are interested in the first p of those components.

So, we will have this as i equal to 1 to up to p . So, these are μ_i components; we had this mean vector μ was $\mu_1, \mu_2, \dots, \mu_m$. So, we are looking at the first p components; suppose these p are important once and we are looking at setting up simultaneous confident interval for $\mu_1, \mu_2, \dots, \mu_p$; such that the joint probability of μ_i being contained in that particular random interval; that joint probability is greater than or equal to $1 - \alpha$. So, this is just an illustration; this can be anything other than these μ components also. Now we can encounter two different cases. The first case is a very simple case. Case one is suppose Σ is equal to diagonal $\Sigma_{11}, \Sigma_{22}, \dots, \Sigma_{mm}$. Now, this Σ matrix is diagonal matrix.

Now, Σ matrix being diagonal matrix implies that since we have got x to be multivariate normal with mean vector μ and a covariance matrix Σ ; in other words, this \bar{x} has got a multivariate normal m with a mean vector μ and a covariance matrix Σ by n . This would imply that $\bar{x}_1, \bar{x}_2, \dots, \bar{x}_m$ which are the constituent elements of this x vector, which is the sample mean random vector. So, this $\bar{x}_1, \bar{x}_2, \dots, \bar{x}_m$ are independent $N(1)$ random variables; because we have Σ to be diagonal matrix. Since Σ is diagonal matrix, the half diagonal entries which are going to give us a covariance terms for the components of this x vector. They are going to be zero and since the joint distribution is multivariate normal, we will have these components to be independently distributed.

(Refer Slide Time: 39:32)



Since we have this $\bar{x}_1, \bar{x}_2, \dots, \bar{x}_m$ to be independent $N(1)$ random variables; in particular, what we can write is that this \bar{x}_i would follow a univariate normal distribution with mean as μ_i , which is the corresponding component in the mean vector and this variance has σ_{ii} divided by n . This is true for every i equal to 1 to up to m and in particular, this would be the case if we are looking at any p of the components which are there in μ and the corresponding components in \bar{x} random vector. Now, from this statement what we can write is the following; a $100(1-\beta)$ percent confidence interval for this μ_i is given by \bar{x}_i .

This is the interval; \bar{x}_i minus root over σ_{ii} by n , where σ_{ii} is the corresponding diagonal element of the sample variance covariance matrix. So, this σ_{ii} by n multiplied by t_{n-1} and then we will require this to be $\beta/2$. I will say what is this equal to this is \bar{x}_i plus root over σ_{ii} by n t_{n-1} $\beta/2$ where probability that T distribution on $n-1$ degrees of freedom greater than $t_{n-1}(\beta/2)$; this would be equal to $\beta/2$. So, if we have the probability of a T random variable exceeding this t_{n-1} . This is basically the right tail cut off point. So, we will have t distribution is symmetric.

Suppose this is a point here; this point is my $t_{n-1}(\beta/2)$. So, the area to the right of that particular point is $\beta/2$; this is symmetric distribution. So, we will have $-t_{n-1}(\beta/2)$ point. Similarly, the area to the left of that would also be equal to $\beta/2$ and hence the area in between these two points, which is this area is going to be $1-\beta$. So, we will have this particular as

confidence interval; this as probability that this μ_i belonging to the random interval. Now, in terms of the random interval, this is \bar{x}_i minus square root of s_i by n times $t_{n-1, \beta/2}$; this \bar{x}_i random interval plus root over s_i divided by n times $t_{n-1, 1-\beta/2}$.

So, this is that interval. This is the lower confidence point. This is the upper confidence limit. This probability is equal to $1 - \beta$. So, this is as far as the μ_i component is concerned. Now, note that these \bar{x}_i quantities are independent due to the structure of sigma matrix that we have assumed. So, let us denote this particular interval what we have here to be this I_i interval that is probability that this μ_i belonging to this I_i . This is exactly equal to $1 - \beta$. Now, similar to one μ_i component here, one can take this for every I_i equal to $1 - \beta$ up to p .

(Refer Slide Time: 43:46)

$$\begin{aligned} &\Rightarrow P(\mu_i \in I_i; i=1 \text{ to } p) \\ &= P\left(\bigcap_{i=1}^p (\mu_i \in I_i)\right) \\ &= \prod_{i=1}^p P(\mu_i \in I_i) \\ &= (1-\beta)^p \rightarrow \text{set this to be equal to } 1-\alpha \\ \text{i.e. } &(1-\beta)^p = 1-\alpha \\ \text{i.e. } &1-\beta = (1-\alpha)^{1/p} \quad \text{given } \alpha (0 < \alpha < 1) \\ \text{i.e. } &\underline{\beta = 1 - (1-\alpha)^{1/p}} \quad \text{obtain } \beta \end{aligned}$$

Now, because we have the sigma matrix to be diagonal, the independence would imply that probability that μ_i belongs to I_i ; this simultaneously for i equal to 1 to up to p . This is going to be given by probability. This is actually intersection of i equal to 1 to up to p ; these events are μ_i belonging to this I_i . Now, these events are going to be independent; because we have chosen the sigma matrix to be a diagonal matrix. Hence, this is going to be the product i equal to 1 to up to p of the respective probabilities; because, the underlying p events with which we are looking at the intersection.

They are independent events and hence we will be having this as μ_i belonging to this I_i . Now, we have obtained these probabilities. I_i is given by this particular random

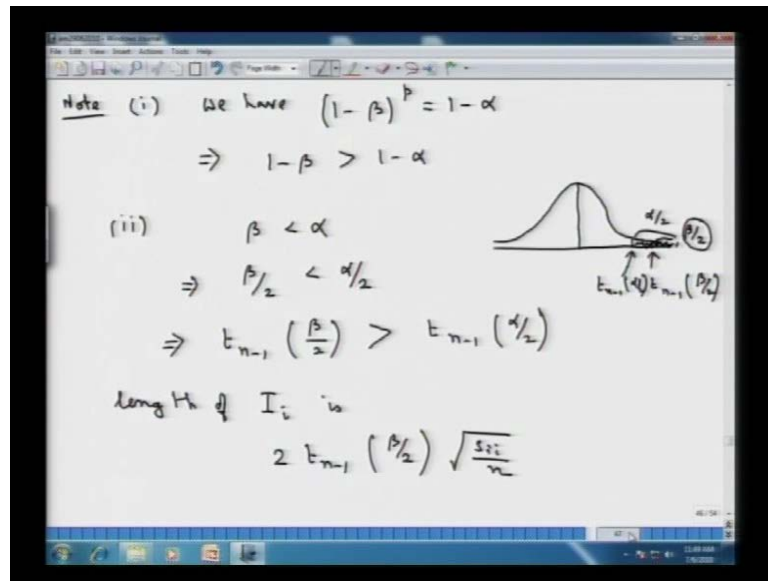
interval and what we will be having is the coverage that the probability that μ_i belonging to a particular I_i ; that probability is $1 - \beta$. So, we will have this as $1 - \beta$ whole raise to the power p . Now, what do we require? We require in order to setup a simultaneous confidence interval; see here, what we had stated out here that in order to give us the simultaneous confidence interval.

We would require this statement of this type that probability that μ_i belonging to I_i , for i equal to 1 to p ; this is greater than or equal to $1 - \alpha$. So, for a given problem if we set this $1 - \beta$ to the power p to be equal to $1 - \alpha$, then we will be able to achieve. So, we set this to be equal to $1 - \alpha$ and then we can solve for β . And then that solution β would lead us to the simultaneous confidence interval; that is, we set here $1 - \beta$ to the power p to be equal to $1 - \alpha$; that is $1 - \beta$ to be equal to $1 - \alpha$ to the power $1/p$; that is what we have is this β to be equal to $1 - (1 - \alpha)^{1/p}$.

So, from this statement out here, what we will be able to do is given α lies between 0 and 1; that is associated with $100 - \alpha$ percent confidence region. So, given α obtain β using this particular equation; because you know what is p . We know how many of these components we are actually trying to include in the joint confidence interval. So, we can obtain β from here and then using that particular β what we will do? We will go back to this particular equation here, where we can easily obtain what is an $100 - \beta$ percent confidence interval for μ_i .

So, we can use that β in this statement out here and we will be able to find out the confidence interval corresponding to that particular μ_i components. Once we have the confidence interval corresponding to one μ_i component, we can use that in the statement out here and get a $100 - \alpha$ percent simultaneous confidence interval for p of these quantities here. Now, this p can also be all the m quantities, all the m components. Now, make a note of the following observations.

(Refer Slide Time: 47:25)



Now, since we have 1 minus beta to the power p is equal to 1 minus alpha, this would imply that 1 minus beta is going to be greater than 1 minus alpha; because both alpha and beta lie between 0 and 1. So, we have 1 minus beta a quantity raise to the power p that is equal to 1 minus alpha and hence, we would require 1 minus beta to be greater than 1 minus alpha; that is straight forward. Number two is an important thing is to look at the comparison between this simultaneous confidence interval that we are setting up for each of this p component here.

And then, we would like to compare this confidence interval that we are obtaining through this simultaneous approach to that of the confidence interval 100 into 1 minus alpha percent confidence interval for a particular mu component only. So, the difference here is that in one confidence interval we are setting up a 100 into 1 minus alpha percent confidence interval for mu i only and in the second, we are obtaining a 100 into 1 minus alpha percent simultaneous confidence interval for p mu i components in which, mu i is 1 of them. So, what does the intuition? Basically, the intuition will say that the confidence interval, where we are concentrating only on one mu i component.

And then, setting up 100 into 1 minus alpha percent confidence interval for that is going to be shorter than the simultaneous confidence intervals for p such components and we are going to have 100 into 1 minus alpha percent simultaneous coverage for all those p components. So, the intuition would suggest that the expected length of the confidence interval, when we are looking at the simultaneous 100 into 1 minus alpha percent

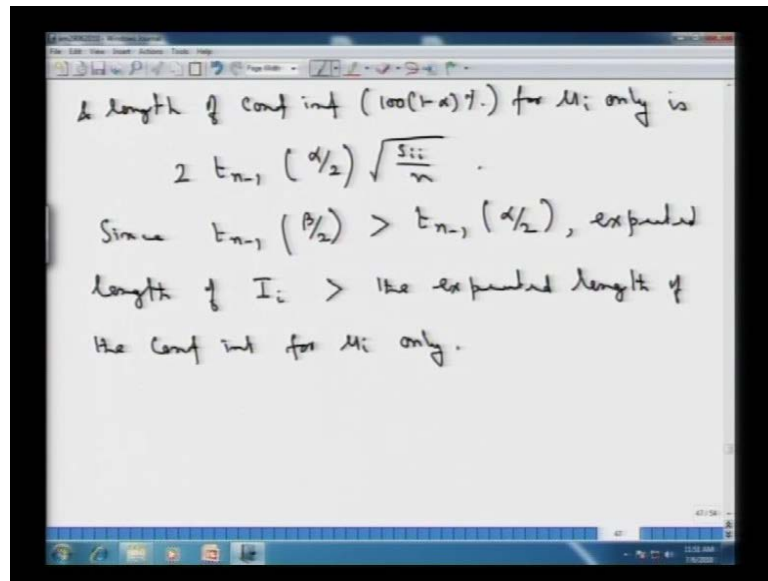
confidence interval; that is going to be larger than the one, when we are concentrating on one such μ_i component. Let us see how we prove that intuition of ours.

So, in order to prove that we start with this particular equation here; that $1 - \beta$ is greater than $1 - \alpha$; this would imply that β is less than α . Now, if β is less than α this would imply that $\beta/2$ is less than $\alpha/2$. Now, this would further imply that t_{n-1} . Now let us try to find out the logic behind this particular relationship between these two cut off points. How does this relationship between these two cut off points come across? Suppose, this is the t distribution **pdf** which is symmetric around 0.0 we have.

Here a point, now what do we have $\beta/2$ is less than $\alpha/2$. So, we have two points here; $\beta/2$ is less than $\alpha/2$ and these are going to be two cut off points. So, suppose I take this particular region here, $\beta/2$ is less than $\alpha/2$. So, I take this region here to have an area which is $\beta/2$ and then the area which is actually coming from the right of this particular point. So, this entire point here is $\alpha/2$. So, we will have $\beta/2$ which is to the right of this particular point here; having an area to the right $\beta/2$ and the area to the right of this point here, first point which is $\alpha/2$.

So, since $\beta/2$ is less than $\alpha/2$, we will have this point as $t_{n-1, \beta/2}$ and this point is $t_{n-1, \alpha/2}$. So, we will have this $t_{n-1, \beta/2}$ cut off point to be greater than $t_{n-1, \alpha/2}$. So, we will have this particular relationship. Since we have this particular relationship, it is now easy to see what is the expected length of the two types of confidence intervals that I was talking about. So, this is going to be the following that length of I_i that we have already constructed is given by $2 \times t_{n-1, \beta/2}$. This is s_i / n and length of confidence interval 100 into $1 - \alpha$ percent for μ_i only is going to be given by similarly $2 \times t_{n-1, \alpha/2}$.

(Refer Slide Time: 52:06)



Since we are looking at μ_i only, this is going to be given by $t_{n-1} \alpha/2$ and multiplier is exactly the same as this. Since, we have $t_{n-1} \beta/2$ as we have seen $t_{n-1} \beta/2$ to be greater than $t_{n-1} \alpha/2$ expected length of the confidence interval. Expected length of this I_i is going to be greater than the expected length of the confidence interval for μ_i only. So, this basically justifies our intuition that we said that our intuition suggest that; if we are trying make a 100 into 1 minus α percent confidence interval for μ_i only, then that is basically taking care of one μ_i component.

If we are going to have a simultaneous confidence interval for p such μ_i 's and trying to ensure that all those p components, the coverage that μ_i belongs to respective I_i interval that the simultaneous coverage probability is 100 into 1 minus α percent. Now, that is going to look at p such components and this is going to look at only one μ_i component and hence, we would require in the simultaneous confidence interval set, a larger interval; larger in the sense of having the expected length of that I_i to be higher.

So, this basically tells us that if we are looking at such simultaneous confidence intervals, the expected length of that confidence interval is expected to be higher. So, we will stop here today. We will look at in the next lecture what happen if σ is not necessarily a diagonal matrix. So, we will consider a general positive definite matrix and then look at how to construct such simultaneous confidence interval for μ_i components or in general for linear combinations p such linear combinations. Thank you.