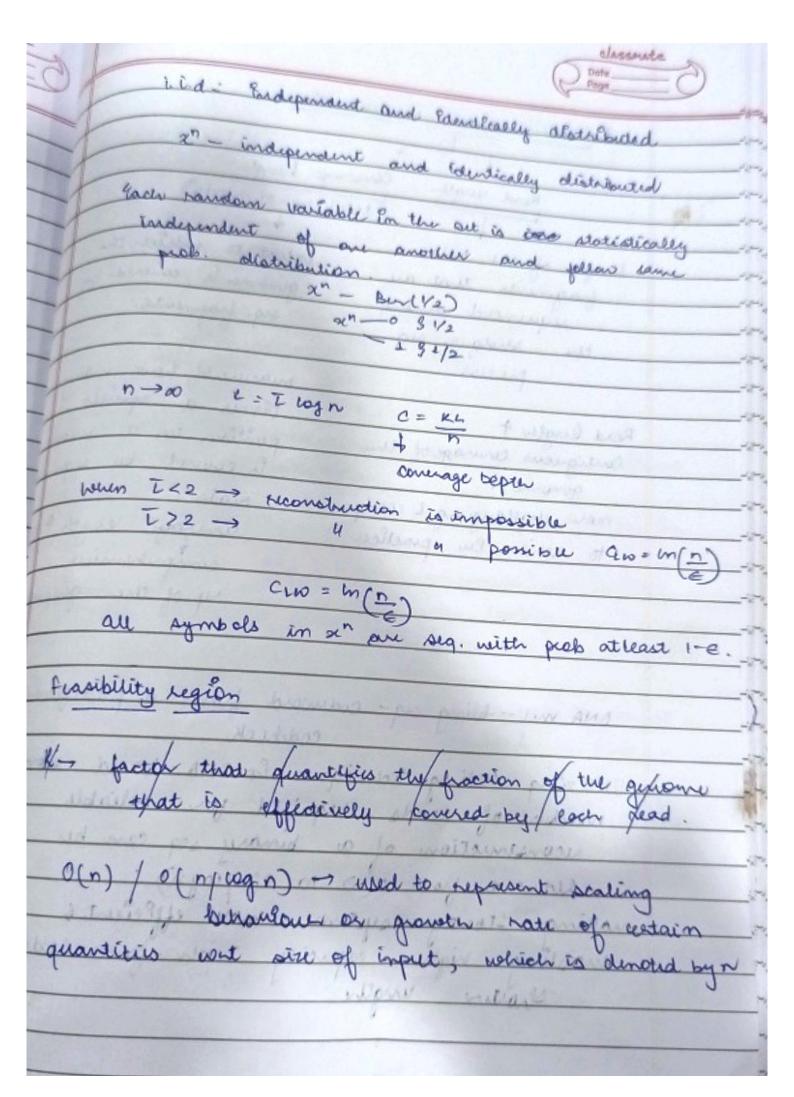


Reliable sequence monstruction coverage hengler Read length ( solar no of mode) length of the KNA fragments that are genome is conered by sequenced during seq. fragments. the shotgun seq. process marine of para worth times a specific Read length 4 Consignous compage of the position en a genome En council by sequenced genome 4 more challenging & costly Nads compage length + to achieve en practice. comprehensive sep of the genome DNA mol-being ag-coducord from a predefined codebook Utillizing coding teamiques for DNA - based sterage, number of reads bequired for reliable successmetion of a binary seq, can be (neportuge of also may promptle making Gerage system more efficients enabling higher capacity with fewer leads of Mond when



	Should line - Compline Manual
	shuffling - Sampling Channel
	she transmitted symbols are randomly harranged or permuted during the commo process.
	permeted during the comm- process.
	no of possible dealend as length sequences
	The same of the sa
	2 Trogn = nt = 0 (m/rogn) -> 0 (x)
	nt logn to as no o nt to as not on
	All the state of t
-	hoan to accompany
-	CANE
-	nt = o(n/ wan) i = n > 00
-	$n^{\overline{L}} = o(n/\log n)$ $n^{\overline{L}} \rightarrow o$ as $n \rightarrow \infty$
-	
-	when t<1
-	
-	probability that a given symbol in X" is
1	not seq by any of the x reads
	- 11- KX
	cn/L a
	= (1-4) = (1-4) /w
	$\begin{pmatrix} 1 & 1 & 1 \\ 1 & 1 & 1 \end{pmatrix} = \begin{pmatrix} 1 & 1 \\ 1 & 1 \end{pmatrix}$
	<u>·</u>
	= lim  1-L) =
	$= \lim_{n\to\infty} (1-L)^{\frac{1}{n}}$ $= \lim_{n\to\infty} (\log e^{\frac{1}{n}})^{\frac{1}{n}}$ $= \lim_{n\to\infty} \log e^{\frac{1}{n}}$
	= lim love x = th)
	n→00
	$=(e^{-c})$

