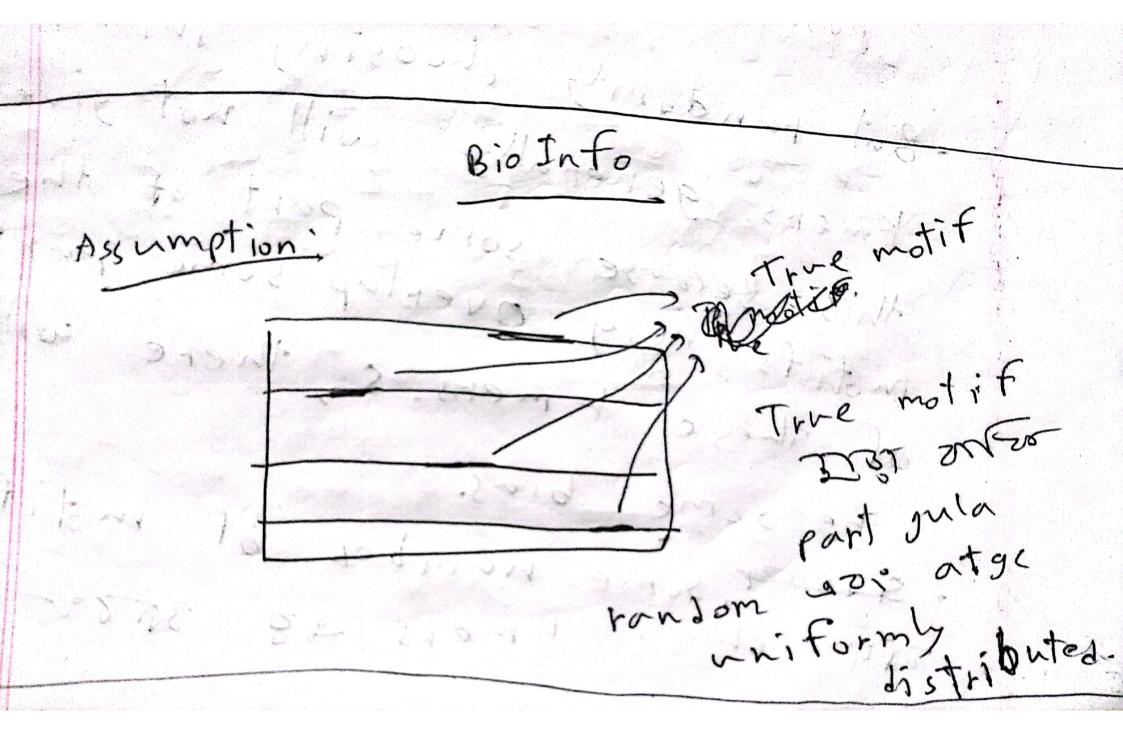
BioInfo 31/1/24 15 length pattern Biological problem 9 357

gene high-rate & express JONES cell to cell Functionality vary zogg, zvf3 whole genome cell

BioInfo Companison companison.

motif logo = 2- entropy we have \$ 4 characters. So 2 bits score string problem median

5/2/24 BioInfo Greedy Notif Search (n-k+1) x + x (n-k+1) = t(n-k+(b)2))im = (3)% To fondo mis ted motifisearch t(n-k+1) on each iteration



According to assumption, for pools parts not motif, profile will be a almost: K . 12 . 52 . 58 . 58 It will not be good, scores will alway remain some for all position! lo interes ex · But randomly choosing initial Kmers, generally, will not give this Because some part of the overlap some part motifs may overlap some part of these kmers. So, there will be some bias. some number of motifs Mistra ichose knew as 3500

स्तिक राष्ट्र, ठारेटल torge drastic change 280 moo, 400 search space 2220, 23 work 2251 converge at 2000 chitical point M60,

Solution - aibbs To Sampling KL-divergence - 100tT background distribution us som ansordit distribution compare 2000. For to motifi search - background distribution 200 350 2500 input 0 string so (upstream of all genes) E CONTRACT character young distribution. प्रकार कार्य letter उठाका अगत् all, 57 system @18 m zooso Services of the services of th