

# Read Mapping: Project 3

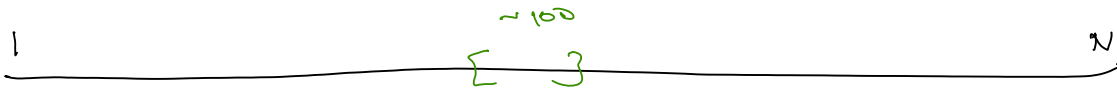
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11:45 AM

<https://eecs.wsu.edu/~ananth/CptS571/Programs/Program3/index.htm>

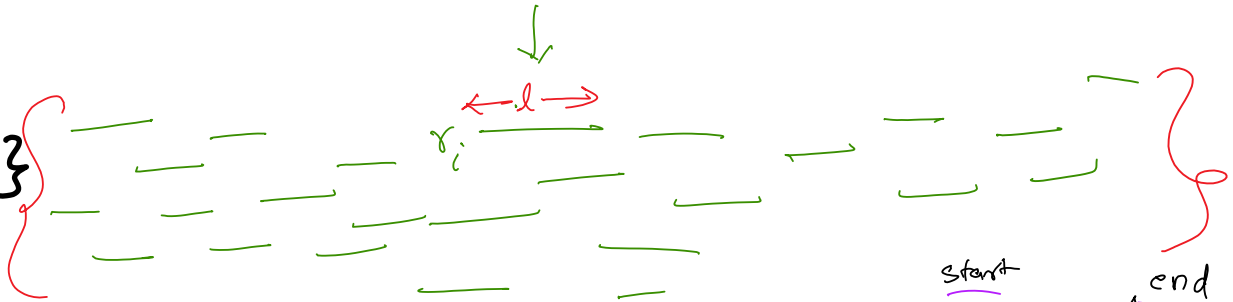
471, 571 → Proj 3  
hw  
Exam  
571 → Survey

Reference  
Genome  
 $G$ :



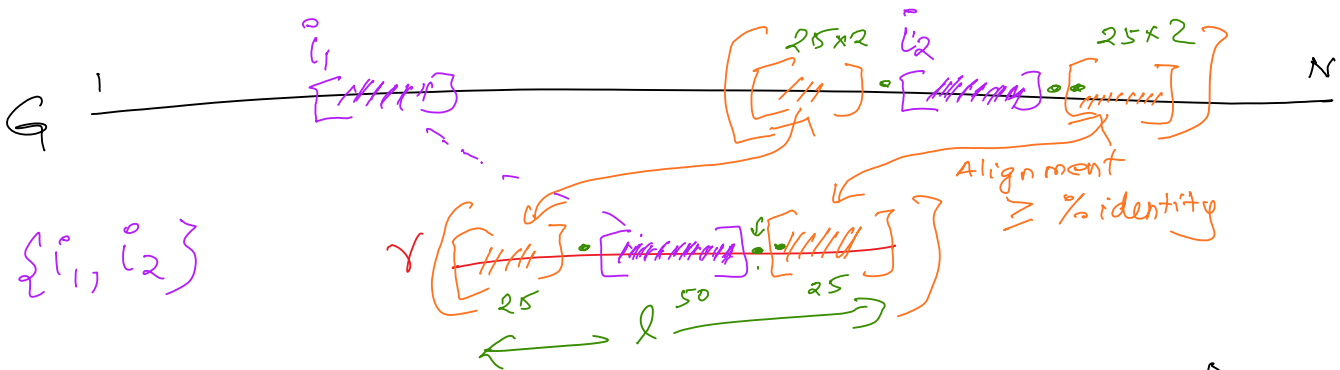
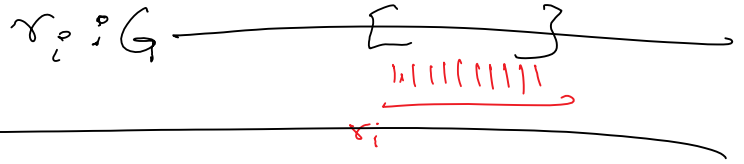
Read  
set :

$\{r_1, r_2, \dots, r_m\}$   
 $m: 10^5 - 10^6$



Output:

For every read  $r_i \in G$



Read Mapping ( $G \in \{1 \dots N\}$ ,  $R = \{r_1, r_2, \dots, r_m\}$ ) {

1. "Preprocess" ( $G$ )

2. For ( $i = 1$  to  $m$ ) // every read  $r_i$

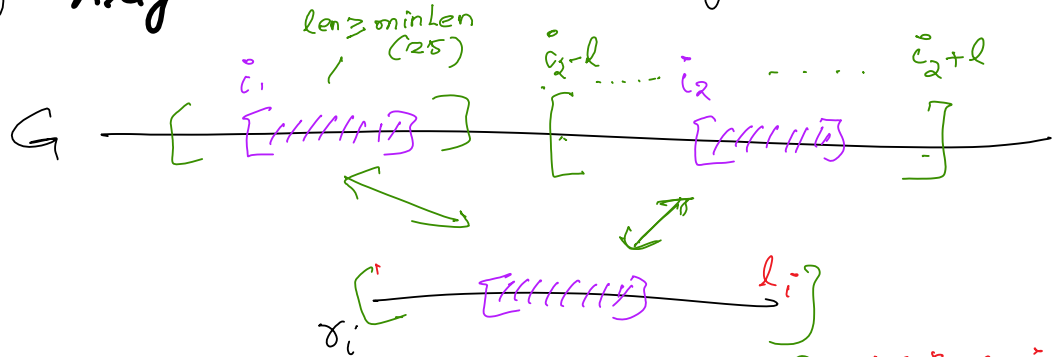
2.a)  $\{l_1, l_2, \dots, l_k\} \leftarrow \text{FindLoc}(r_i, \text{ST}(G))$  = ?  
// candidate loci which are starting indices for  
lcs ( $r_i, G$ )

# Read Mapping

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2.b) "Align" candidate loci against the read  $r_i$ .

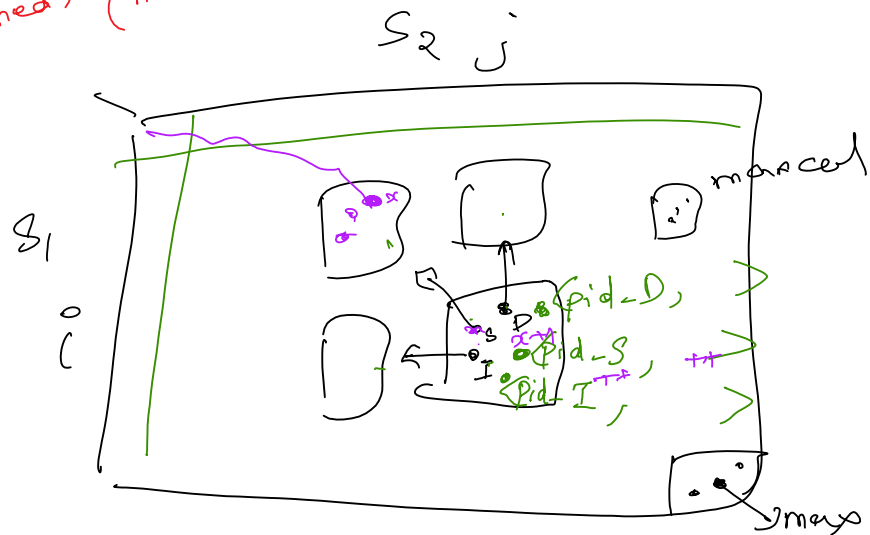


Use local Align ( $r_i[1..l_i]$  vs.  $G[i_1..i_2+l]$ )

$$\% \text{ identity} = \frac{\# \text{ matches}}{\text{Align. len}}$$

$s_1$ : a c g t - t g  
 $s_2$ : a c t t a c -  
 $\frac{3}{7}$

$\% \text{ identity} \geq \text{cutoff}$   
 Yes (aligned)  
 No (not aligned)



At the end, pick the best aligning region for each read.

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Find all locations that are starting indices on  $G$ , for  $\text{LCS}(x, G)$

$\{$   
 $\uparrow$   
 $len \leftarrow \text{FindPath}(v[i:], \text{root})$   
 $\uparrow$   
 $\text{max len} \leftarrow \text{update new len}$   
 $> \text{max len}$   
 $\}$



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↳ 1. Build  $ST(G)$

Prepare ST  $\Rightarrow$  DFS

