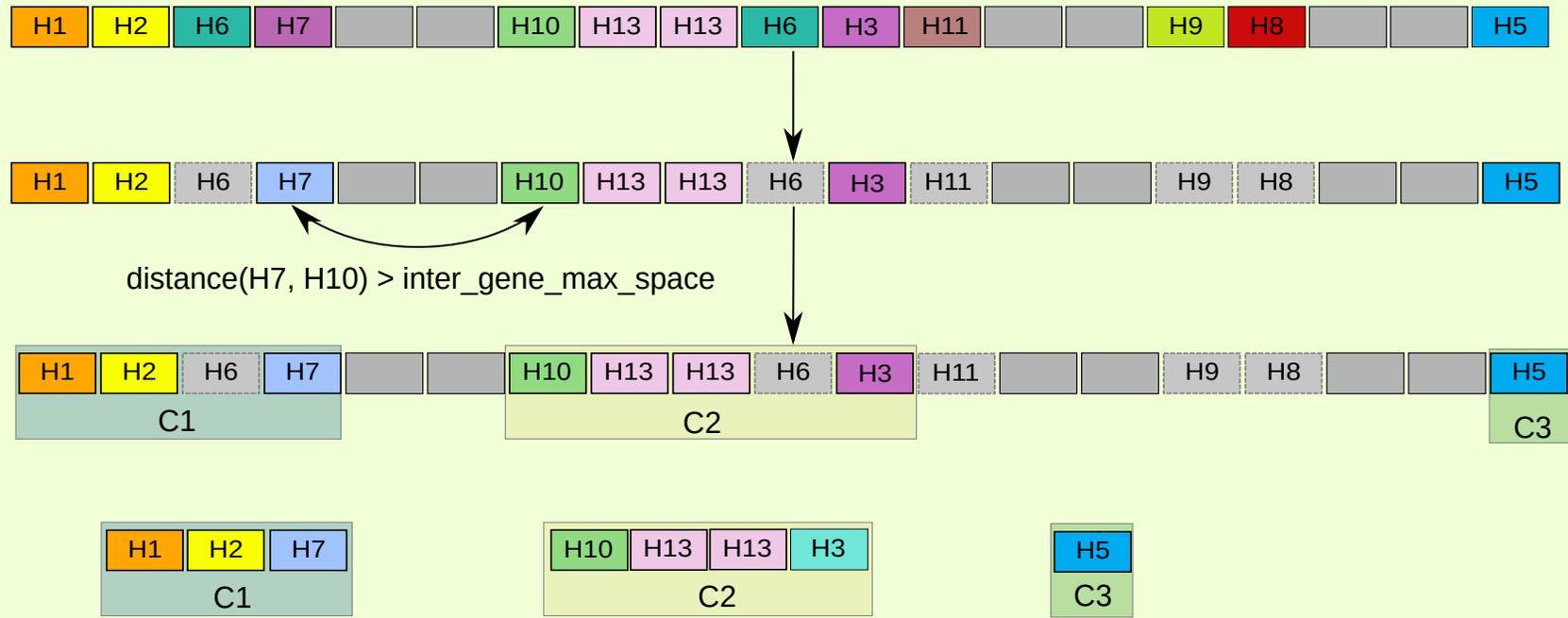


B

Step 1

Consider the first Model (A) to filter hits
 (Genes of model (A): G1, G2, G3, G4, G5, G7, G10, G13)

Build clusters "C" with
 co-localizing sets of Hits



Step 2

Check quorum:
 - from clusters only
 ("single_locus" search mode)

+ from combinations
 of clusters
 ("multi_loci" search mode)

C1	=> Rejected (min_genes_required)	C1; C2; C3 } rejected_clusters.txt
C2	=> Rejected (min_mandatory_genes_required / min_genes_required)	
C3	=> Rejected (min_mandatory_genes_required / min_genes_required)	
C1 C2	=> System (System A #1: "SA_1")	SA_1: C1 C2 } all_systems.txt/tsv
C1 C3	=> System ("SA_2")	
C2 C3	=> Rejected (min_mandatory_genes_required)	
C1 C2 C3	=> System ("SA_3")	SA_3: C1 C2 C3 }