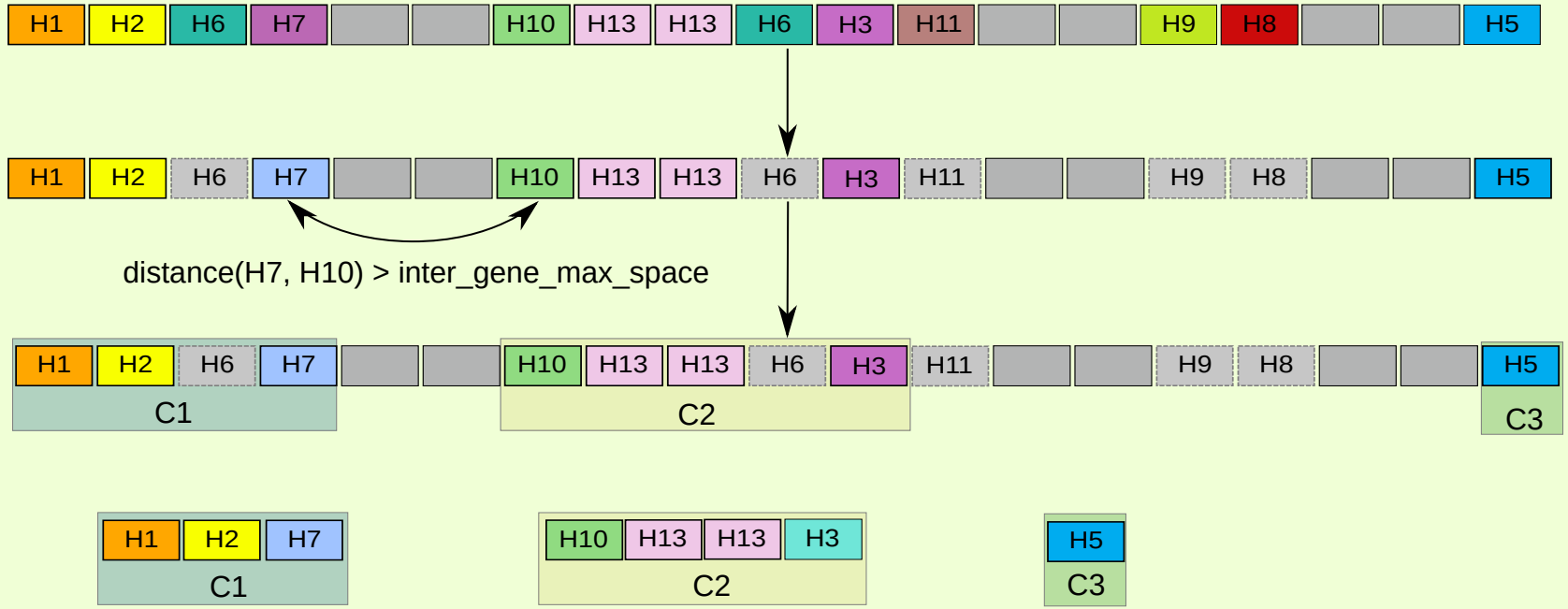
B - Scanning components

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)

- C1 => Rejected (min_genes_required)
- C2 => Rejected (min_mandatory_genes_required / min_genes_required)
- C3 => Rejected (min_mandatory_genes_required / min_genes_required)

C1; C2; C3
C2 C3
} rejected_candidates.tx/tsv

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

- **C1 C2 => System (System A #1: "SA_1")**
- **C1 C3 => System ("SA_2")**
- C2 C3 => Rejected (min_mandatory_genes_required)
- **C1 C2 C3 => System ("SA_3")**

SA_1: C1 C2
SA_2: C1 C3
SA_3: C1 C2 C3
} **all_systems.txt/tsv**