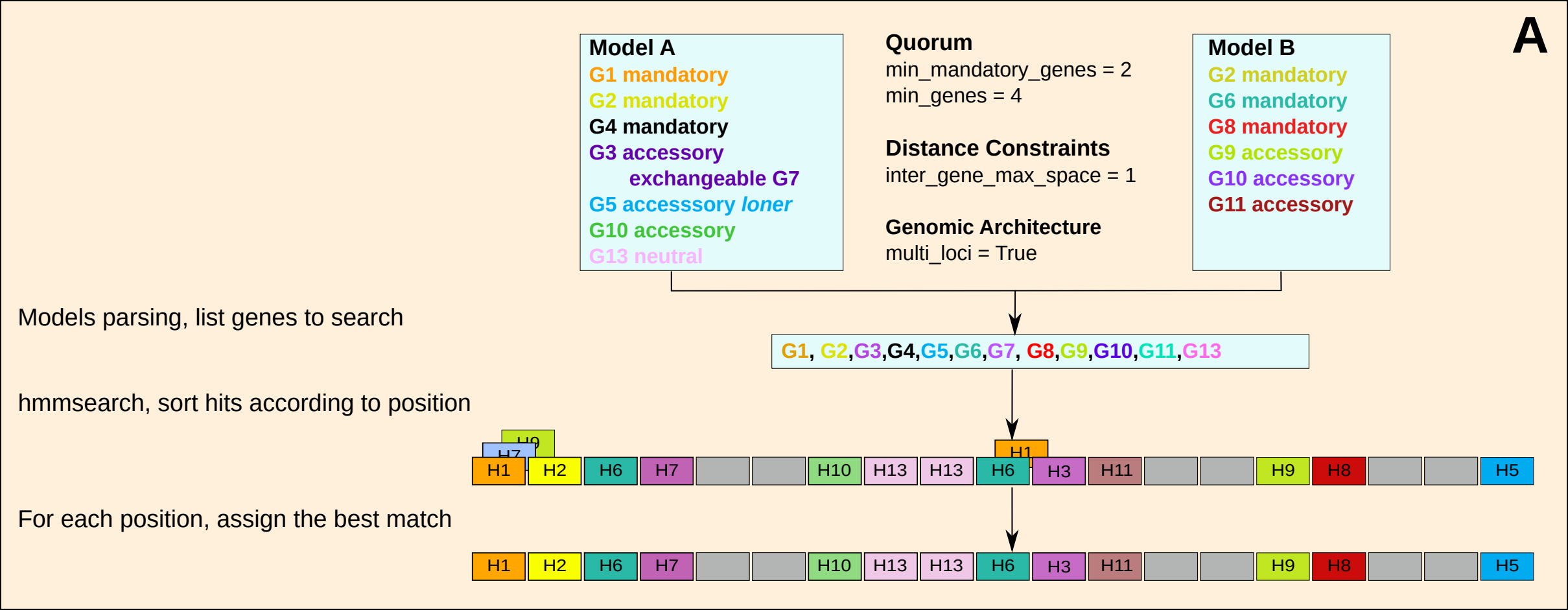
A
Model A
G1 mandatory
G2 mandatory
G4 mandatory
G3 accessory
exchangeable G7
G5 accesssory loner
G10 accessory
G13 neutral
Quorum
min_mandatory_genes = 2
min_genes = 4
Distance Constraints
inter_gene_max_space = 1
Genomic Architecture
multi_loci = True
Model B
G2 mandatory
G6 mandatory
G8 mandatory
G9 accessory
G10 accessory
G11 accessory
Models parsing, list genes to search
G1, G2,G3,G4,G5,G6,G7, G8,G9,G10,G11,G13
hmmsearch, sort hits according to position
H1 H2 H6 H7 H10 H13 H13 H6 H3 H11 H9 H8 H5
For each position, assign the best match
H1 H2 H6 H7 H10 H13 H13 H6 H3 H11 H9 H8 H5