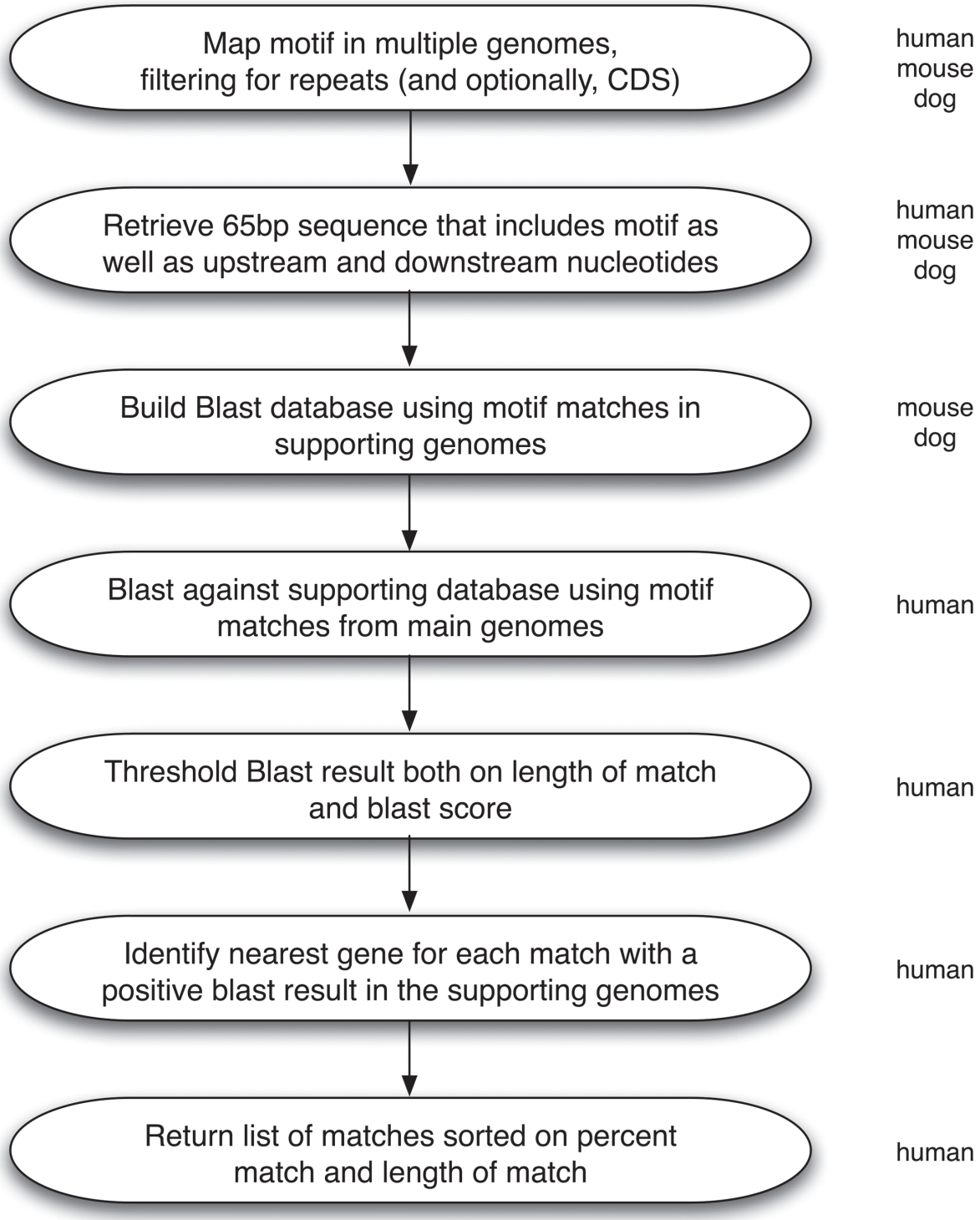
Map motif in multiple genomes, filtering for repeats (and optionally, CDS)
human mouse dog
Retrieve 65bp sequence that includes motif as well as upstream and downstream nucleotides
human mouse dog
Build Blast database using motif matches in supporting genomes
mouse dog
Blast against supporting database using motif matches from main genomes
human
Threshold Blast result both on length of match and blast score
human
Identify nearest gene for each match with a positive blast result in the supporting genomes
human
Return list of matches sorted on percent match and length of match
human