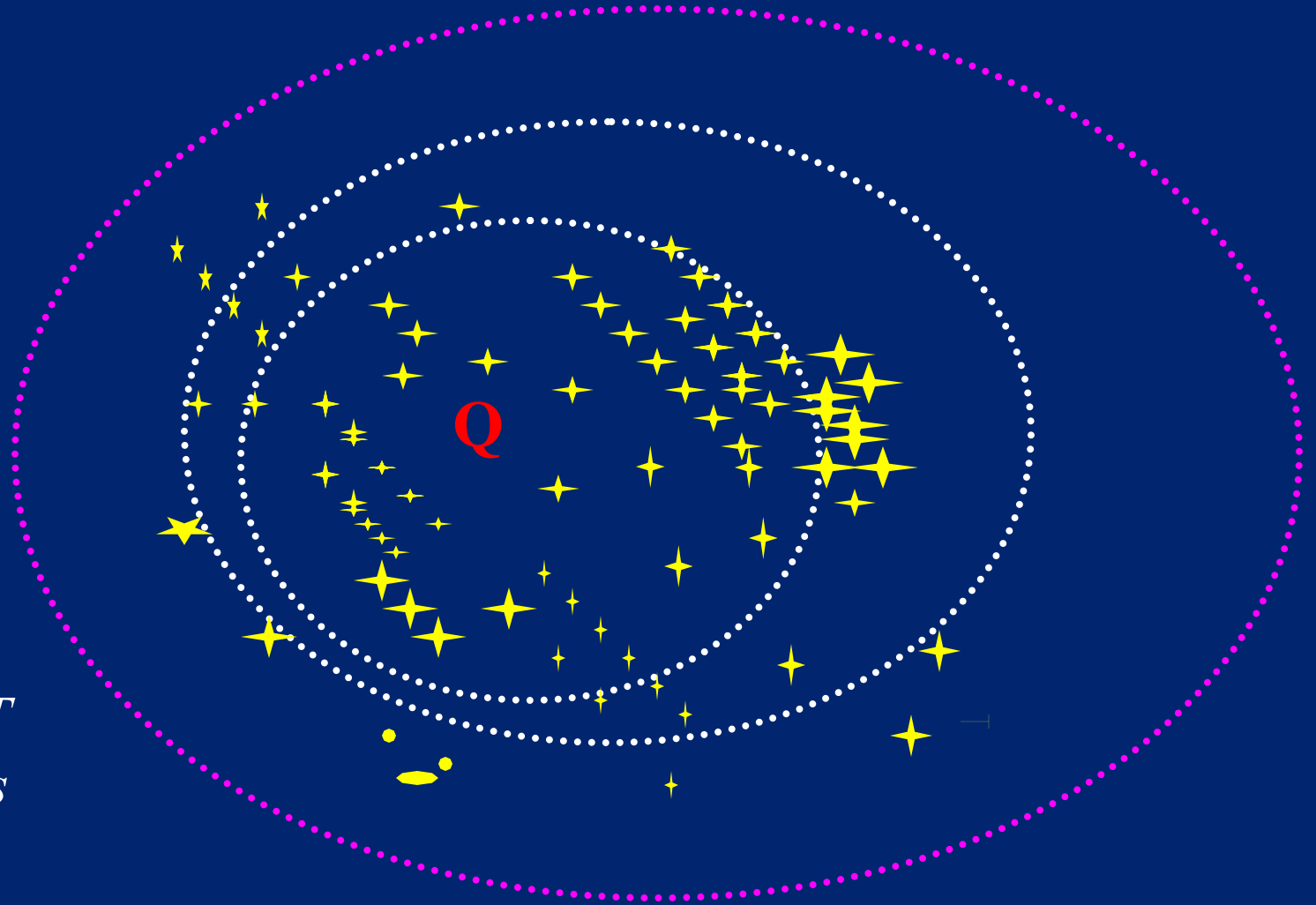
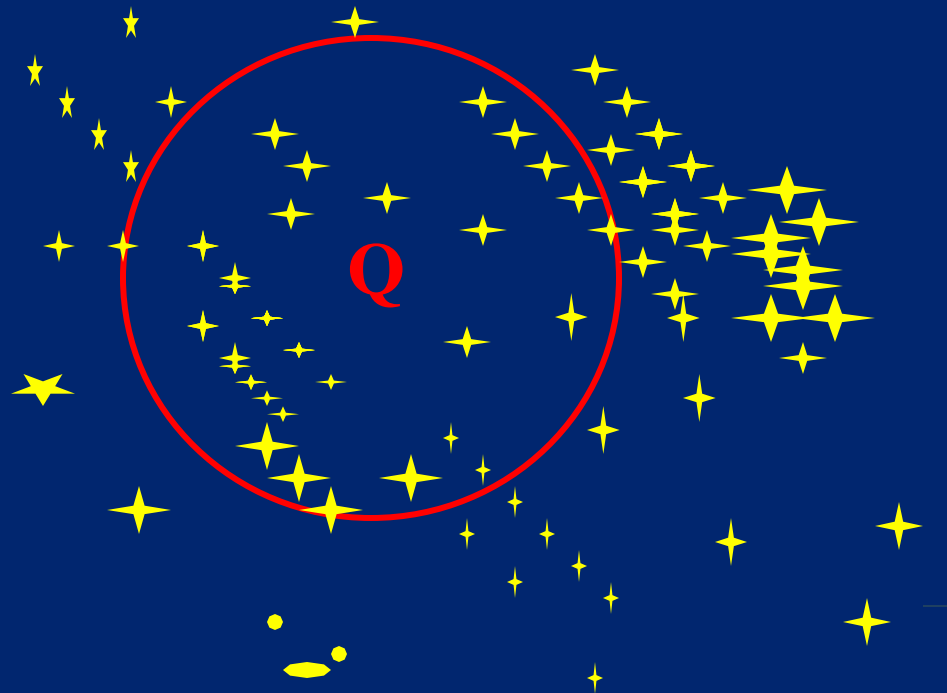


Step 1: Identify putative homologs to query sequence (Q)

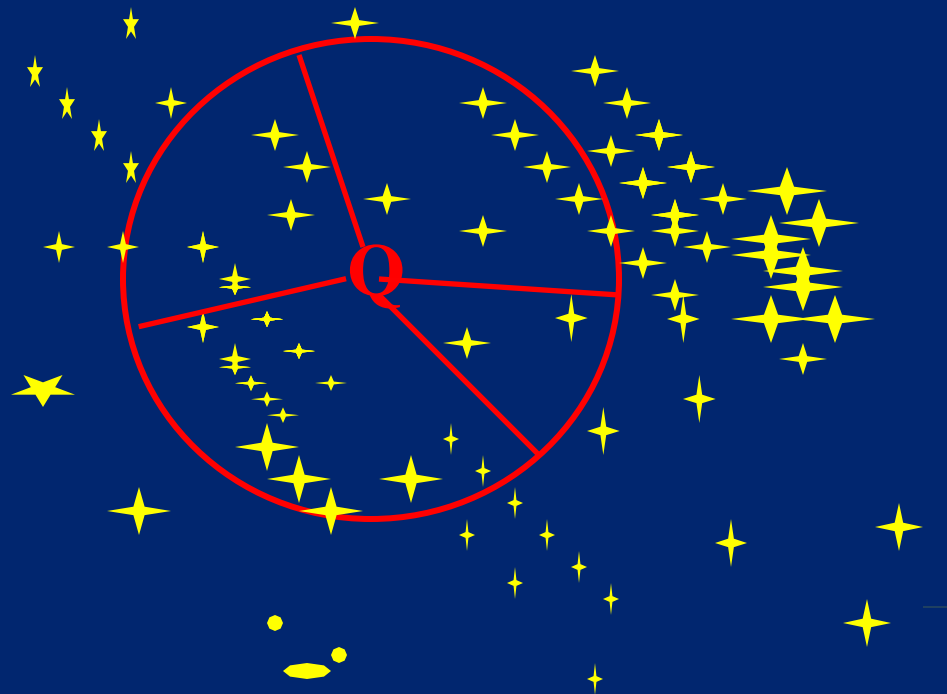


PSI-BLAST
3 iterations
E-3 cutoff

Step 2: Select initial training set

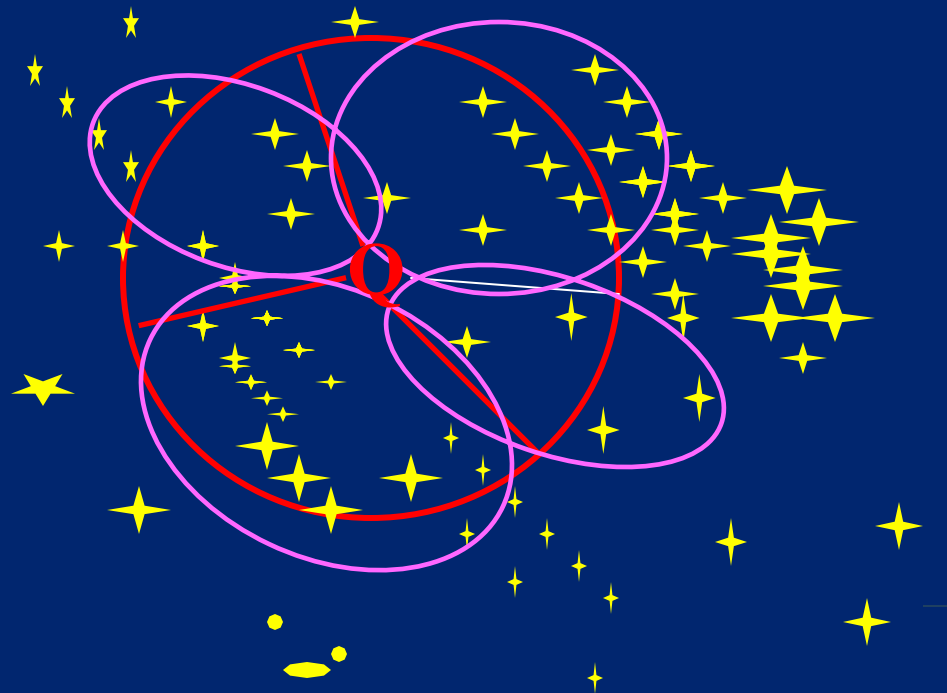


Step 3: Align initial set, identify subfamilies, and build subfamily HMMs.

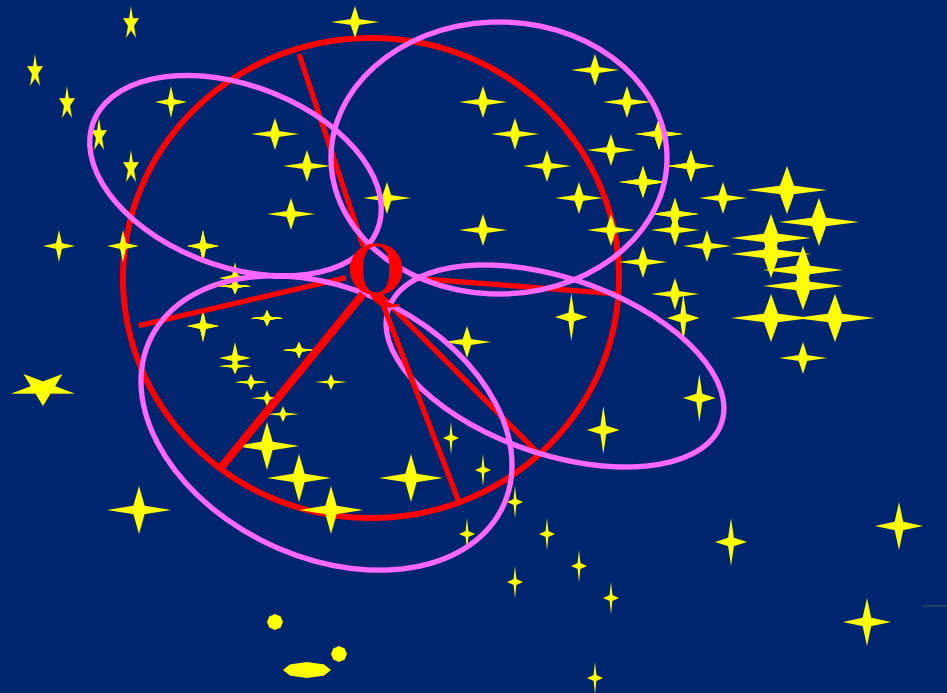


Step 4: Identify and align new homologs.

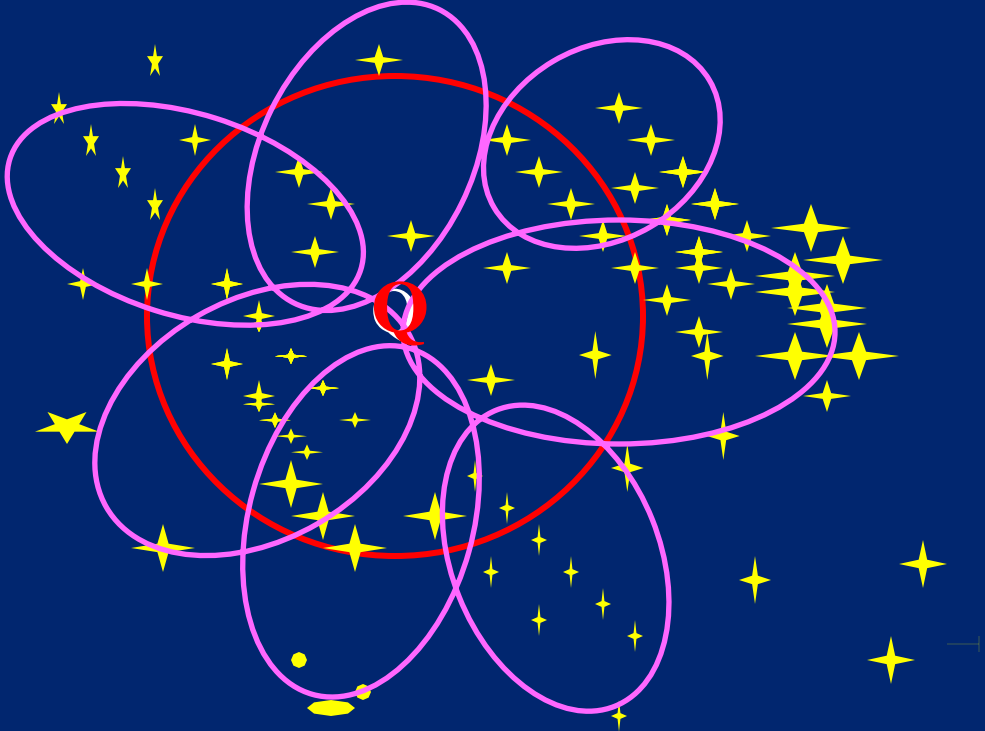
1. Search with subfamily and general HMMs.
2. Accept hits above threshold.
3. Align accepted hits to closest HMM.



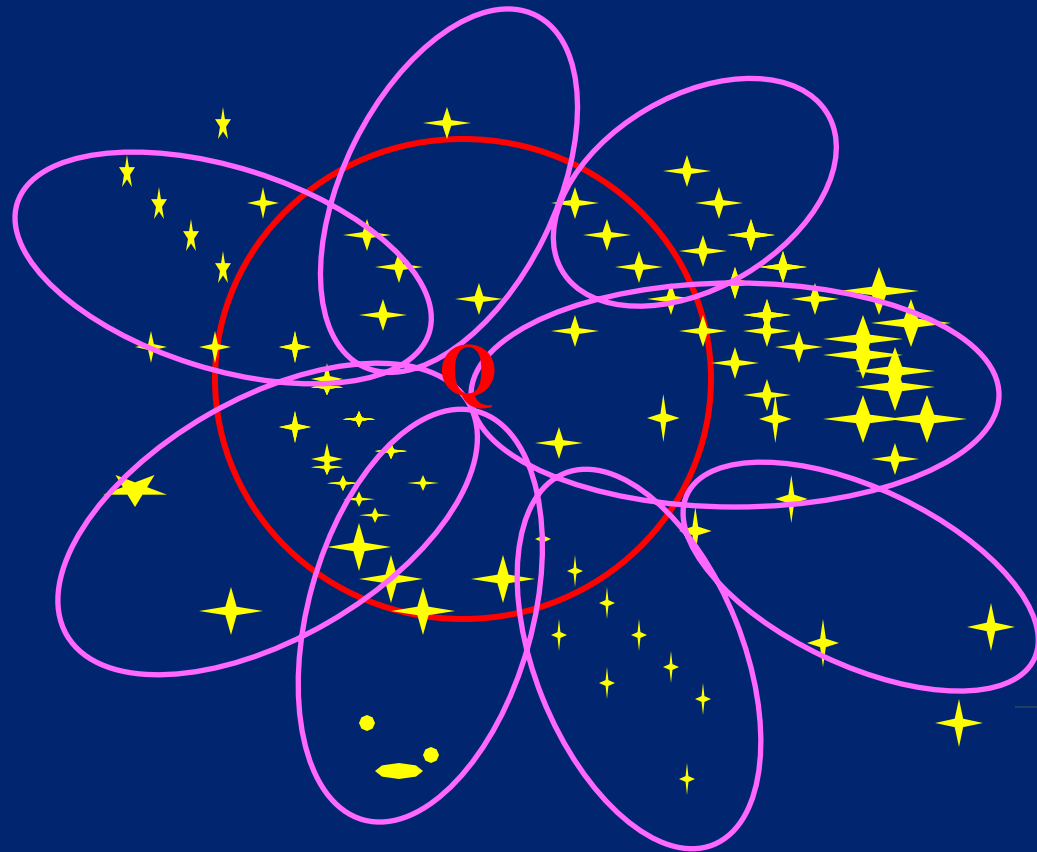
Step 5: Run BETE to identify subfamilies, and build new subfamily HMMs.



Step 6: Iterate



until ...



convergence.

