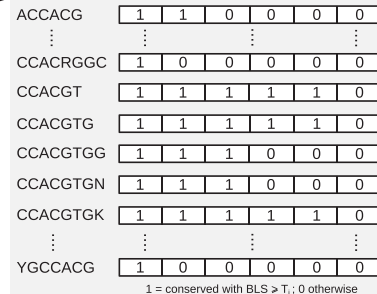


E.g. alignment-free discovery in gene family



| BLS Threshold T_i (%) | $F(T_i)$ (Conserved family count) | $F_{bg}(T_i)$ (Conserved family count) | $C(T_i)$ (Confidence score) |
|-------------------------|-----------------------------------|--|-----------------------------|
| 15 | ~1200 | ~1600 | ~0.42 |
| 50 | ~1000 | ~1200 | ~0.48 |
| 60 | ~1000 | ~1000 | ~0.45 |
| 70 | ~400 | ~200 | ~0.65 |
| 90 | ~100 | ~50 | ~0.85 |
| 95 | ~0 | ~0 | 1.00 |