

HMMs – Each column of seed alignment corresponds to a column of matrix.

yeast GUGUUCGCUAC  
human -UCUUCGGCG-  
fly AGAUU-GUACU

1 5 11

1.0  
.8  
.6  
.4  
.2  
0

C  
U  
G  
U  
U  
C  
G  
C  
A  
G

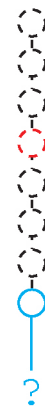


band

states



struct <<<---<--->--->>  
yeast GUGUUCGCUAC  
human -UCUUCGGCG-  
fly AGAUU-GUACU



?

CUGUUCGCAG

CMs – Each column of seed alignment corresponds to a state.

yeast	human	fly
U C	U C	U
U G	U G	U G
G•C	C•G	A•U
U•A <sup>U</sup>	U•G <sup>C</sup>	G•C <sup>A</sup>
G•C		A•U