

	1	2	3	4	5	6	7	8	9	10	11	
yeast	G	U	C	A	U	U	C	G	G	C	...	AC
fly	G	C	C	.	U	U	-	G	G	A	...	GC
cow	G	C	A	.	U	U	C	G	U	C	...	-C
mouse	G	C	A	.	U	U	-	G	A	U	...	GC
human	G	C	G	A	U	U	C	G	C	U	...	GC
chicken	G	U	A	.	U	U	C	G	U	A	...	AC
snake	G	U	G	A	U	U	C	G	C	G	...	AC
croc	G	U	U	.	U	U	-	G	A	G	...	AC
worm	G	-	G	.	U	U	C	G	C	G	c	aAC
starfish	G	-	U	.	U	U	C	G	A	U	...	-C
urchin	G	U	U	.	U	U	C	-	A	A	...	AC

One HMM node per alignment column

3 states per node:

(M) Match: emits residues

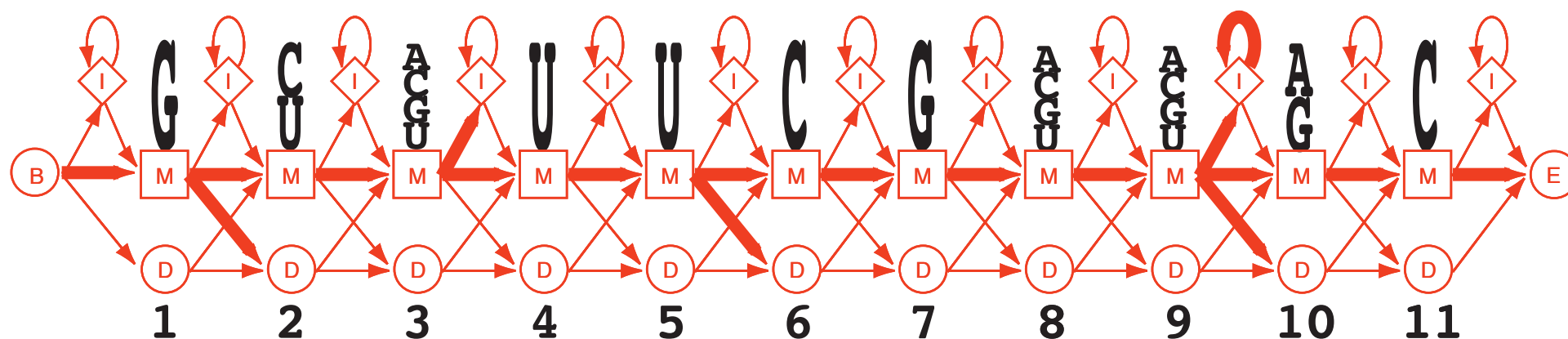
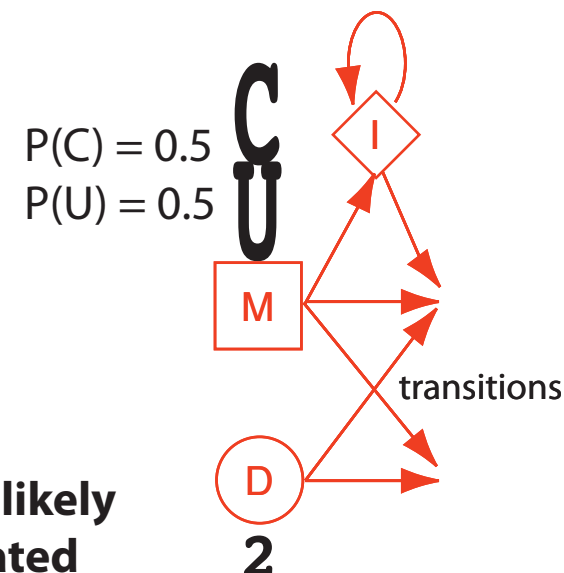
(I) Insert: inserts extra residues

(D) Delete: deletes residues

HMMs generate homologous sequences.

Given a sequence, the most likely path that could have generated that sequence can be computed.
This path implies an alignment.

Node for column 2:



urchin

