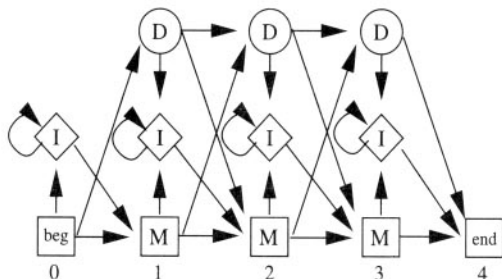


(a) Multiple alignment:

	x	x	.	.	x	
bat	A	G	-	-	C	
rat	A	-	A	G	-	C
cat	A	G	-	A	A	-
gnat	-	-	A	A	A	C
goat	A	G	-	-	-	C
	1	2	.	.	.	3

(b) Profile-HMM architecture:



(c) Observed emission/transition counts

		model position			
		0	1	2	3
match emissions	A	-	4	0	0
	C	-	0	0	4
	G	-	0	3	0
	T	-	0	0	0
insert emissions	A	0	0	6	0
	C	0	0	0	0
	G	0	0	1	0
	T	0	0	0	0
state transitions	M-M	4	3	2	4
	M-D	1	1	0	0
	M-I	0	0	1	0
	I-M	0	0	2	0
	I-D	0	0	1	0
	I-I	0	0	4	0
	D-M	-	0	0	1
	D-D	-	1	0	0
D-I	-	0	2	0	

Figure 5.7 As an example of model construction from an alignment, a small DNA multiple alignment is given (a), with three columns marked above with *x*'s. These three columns are assigned to positions 1–3 in the model architecture (b). The assignment of columns to model positions determines the symbol emission and state transition counts (c) from which probability parameters would be estimated.