

More specifically, we can ask the following

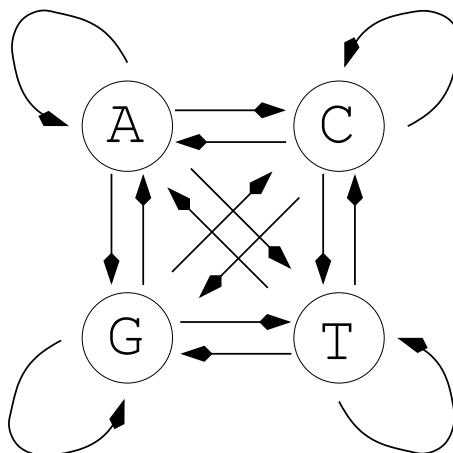
Questions.

1. Given a (short) segment of genomic sequence.
How to *decide* whether this segment is from a CpG-island or not?
2. Given a (long) segment of genomic sequence.
How to *find* all CpG-islands contained in it?

8.2 Markov chains

Our goal is to come up with a probabilistic model for CpG-islands. Because pairs of consecutive nucleotides are important in this context, we need a model in which the probability of one symbol depends on the probability of its predecessor. This dependency is captured by the concept of a *Markov chain*.

Example.



- Circles = *states*, e.g. with names A, C, G and T.
- Arrows = possible *transitions*, each labeled with a *transition probability* a_{st} . Let x_i denote the state at time i . Then $a_{st} := P(x_{i+1} = t \mid x_i = s)$ is the conditional probability to go to state t in the next step, given that the current state is s .

Definition.

A (time-homogeneous) *Markov chain* (of order 1) is a system (Q, A) consisting of a finite set of *states* $Q = \{s_1, s_2, \dots, s_n\}$ and a *transition matrix* $A = \{a_{st}\}$ with $\sum_{t \in Q} a_{st} = 1$ for all $s \in Q$ that determines the probability of the transition $s \rightarrow t$ by

$$P(x_{i+1} = t \mid x_i = s) = a_{st}.$$

At any time i the Markov chain is in a specific state x_i , and at the tick of a clock the chain changes to state x_{i+1} according to the given transition probabilities.

Remarks on terminology.

- *Order 1* means that the transition probabilities of the Markov chain can only “remember” 1 state of its history. Beyond this, it is *memoryless*. The “memorylessness” condition is a very important. It is called the *Markov property*.
- The Markov chain is *time-homogenous* because the transition probability

$$P(x_{i+1} = t \mid x_i = s) = a_{st}.$$

does not depend on the time parameter i .

Example.

Weather in Tübingen, daily at midday: Possible states are “rain”, “sun”, or “clouds”.

Transition probabilities:

	R	S	C
R	.5	.1	.4
S	.2	.6	.2
C	.3	.3	.4

Note that all rows add up to 1.

Weather: . . . rrrrrrrccsssssscscscsccrrrcrccssss . . .

Given a sequence of states $s_1, s_2, s_3, \dots, s_L$. What is the probability that a Markov chain $x = x_1, x_2, x_3, \dots, x_L$ will step through precisely this sequence of states? We have

$$\begin{aligned} &P(x_L = s_L, x_{L-1} = s_{L-1}, \dots, x_1 = s_1) \\ &= P(x_L = s_L \mid x_{L-1} = s_{L-1}, \dots, x_1 = s_1) \\ &\quad \cdot P(x_{L-1} = s_{L-1} \mid x_{L-2} = s_{L-2}, \dots, x_1 = s_1) \\ &\quad \cdots P(x_2 = s_2 \mid x_1 = s_1) \cdot P(x_1 = s_1) \end{aligned}$$

using the “expansion”

$$P(A \mid B) = \frac{P(A \cap B)}{P(B)} \iff P(A \cap B) = P(A \mid B) \cdot P(B).$$

Now

$$P(x_i = s_i \mid x_{i-1} = s_{i-1}, \dots, x_1 = s_1) = P(x_i = s_i \mid x_{i-1} = s_{i-1})$$

by the Markov property. Thus

$$\begin{aligned} &P(x_L = s_L, x_{L-1} = s_{L-1}, \dots, x_1 = s_1) \\ &= P(x_L = s_L \mid x_{L-1} = s_{L-1}) \\ &\quad \cdot P(x_{L-1} = s_{L-1} \mid x_{L-2} = s_{L-2}) \\ &\quad \cdots P(x_2 = s_2 \mid x_1 = s_1) \cdot P(x_1 = s_1) \\ &= P(x_1 = s_1) \prod_{i=2}^L a_{s_{i-1}s_i}. \end{aligned}$$

Hence the probability of a path is the product of the probability of the initial state and the transition probabilities of its edges.

8.3 Modeling the begin and end states

A Markov chain *starts* in state x_1 with an initial probability of $P(x_1 = s)$. For simplicity we would like to model this as a transition, too.

Therefore we add a *begin state* to the model that is labeled 'b'. We also impose the constraint that $x_0 = b$ holds. Then:

$$P(x_1 = s) = a_{bs}.$$

This way, we can store all probabilities in one matrix and the "first" state x_1 is no longer special:

$$P(x_L = s_L, x_{L-1} = s_{L-1}, \dots, x_1 = s_1) = \prod_{i=1}^L a_{s_{i-1}s_i}.$$

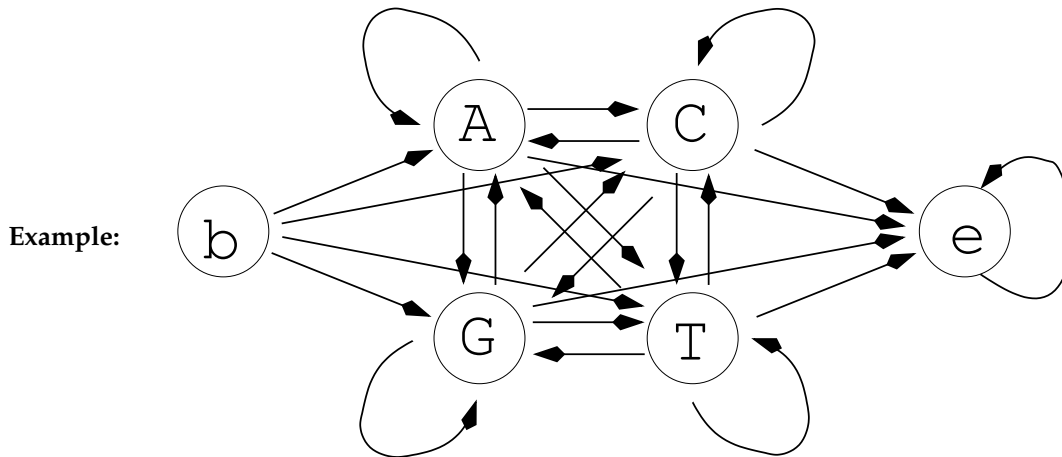
Similarly, we explicitly model the *end* of the sequence of states using an *end state* 'e'. Thus, the probability that the Markov chain stops is

$$P(x_L = t) = a_{t,e}.$$

if the current state is t .

We think of b and e as *silent states*, because they do not correspond to letters in the sequence. (More applications of silent states will follow.)

Later we will use 0 for the begin *and* end state. (Then, formally, we have the same index set for rows and columns.)



```
# Markov chain that generates CpG islands
# (Source: DEMK98, p 50)
# Number of states:
6
# State labels:
A, C, G, T, *=b, +=e
# Transition matrix:
0.1795 0.2735 0.4255 0.1195 0 0.002
0.1705 0.3665 0.2735 0.1875 0 0.002
0.1605 0.3385 0.3745 0.1245 0 0.002
0.0785 0.3545 0.3835 0.1815 0 0.002
0.2495 0.2495 0.2495 0.2495 0 0.002
0.0000 0.0000 0.0000 0.0000 0 1.000
```

A word on stochastic regular grammars. One can view Markov chains as nondeterministic finite automata, where each transition is assigned a probability.

This also translates to grammars: A *stochastic regular grammar* is a regular grammar where each production is assigned a probability.

8.4 Determining the transition matrix

How do we find transition probabilities that explain a given set of sequences best? It can be proven that the following is optimal.

The transition matrix A^+ for DNA that comes from a CpG-island, is determined as follows:

$$a_{st}^+ = \frac{c_{st}^+}{\sum_{t'} c_{st'}^+},$$

where c_{st} is the number of positions in a training set of CpG-islands at which state s is followed by state t . We can calculate these counts in a single pass over the sequences and store them in a $\Sigma \times \Sigma$ matrix.

We obtain the matrix A^- for non-CpG-islands from empirical data in a similar way.

In general, the matrix of transition probabilities is not symmetric.

Two examples of Markov chains.

<pre># Markov chain for CpG islands # (Source: DEMK98, p 50) # Number of states: 6 # State labels: A C G T * + # Transition matrix: .1795 .2735 .4255 .1195 0 0.002 .1705 .3665 .2735 .1875 0 0.002 .1605 .3385 .3745 .1245 0 0.002 .0785 .3545 .3835 .1815 0 0.002 .2495 .2495 .2495 .2495 0 0.002 .0000 .0000 .0000 .0000 0 1.000</pre>	<pre># Markov chain for non-CpG islands # (Source: DEMK98, p 50) # Number of states: 6 # State labels: A C G T * + # Transition matrix: .2995 .2045 .2845 .2095 0 .002 .3215 .2975 .0775 .3015 0 .002 .2475 .2455 .2975 .2075 0 .002 .1765 .2385 .2915 .2915 0 .002 .2495 .2495 .2495 .2495 0 .002 .0000 .0000 .0000 .0000 0 1.000</pre>
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Note the different values for CpG: $a_{CG}^+ = 0.2735$ versus $a_{CG}^- = 0.0775$.

8.5 Testing hypotheses

When we have two models, we can ask which one explains the observation better.

Given a (short) sequence $x = (x_1, x_2, \dots, x_L)$. Does it come from a CpG-island (model⁺)?

We have

$$P(x | \text{model}^+) = \prod_{i=0}^L a_{x_i x_{i+1}}^+,$$

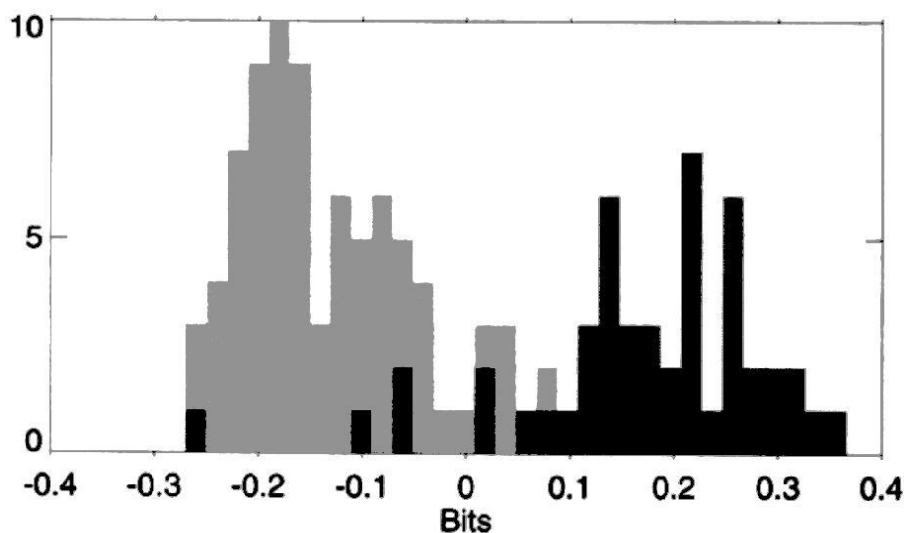
with $x_0 = \text{b}$ and $x_{L+1} = \text{e}$. Similar for (model⁻).

To compare the models, we calculate the *log-odds ratio*:

$$S(x) = \log \frac{P(x | \text{model}^+)}{P(x | \text{model}^-)} = \sum_{i=0}^L \log \frac{a_{x_{i-1} x_i}^+}{a_{x_{i-1} x_i}^-}.$$

Then this ratio is normalized by the length of x . This resulting *length-normalized log-odds score* $S(x)/|x|$ can be used to classify x . The higher this score is, the higher the probability is that x comes from a CpG-island.

The histogram of the length-normalized scores for the sequences from the training sets for A^+ and A^- shows that $S(x)/|x|$ is indeed a good classifier for this data set. (Since the base two logarithm was used, the unit of measurement is called “bits”.)



Example.

Weather in Tübingen, daily at midday: Possible states are rain, sun or clouds.

Types of questions that the Markov chain model can answer:

If it is sunny today, what is the probability that the sun will shine for the next seven days?

And what is more unlikely: 7 days sun or 8 days rain?

8.6 Hidden Markov Models (HMMs)

Motivation: Question 2, how to *find* CpG-islands in a long sequence?

We could approach this using Markov Chains and a “window technique”: a window of width w is moved along the sequence and the score (as defined above) is plotted. However the results are somewhat unsatisfactory: It is hard to determine the boundaries of CpG-islands, and which window size w should one choose? ...

Another approach is to merge the two Markov chains model^+ and model^- to obtain a so-called *Hidden Markov Model*. (But HMMs are much more general than this.)

8.7 Hidden Markov Models

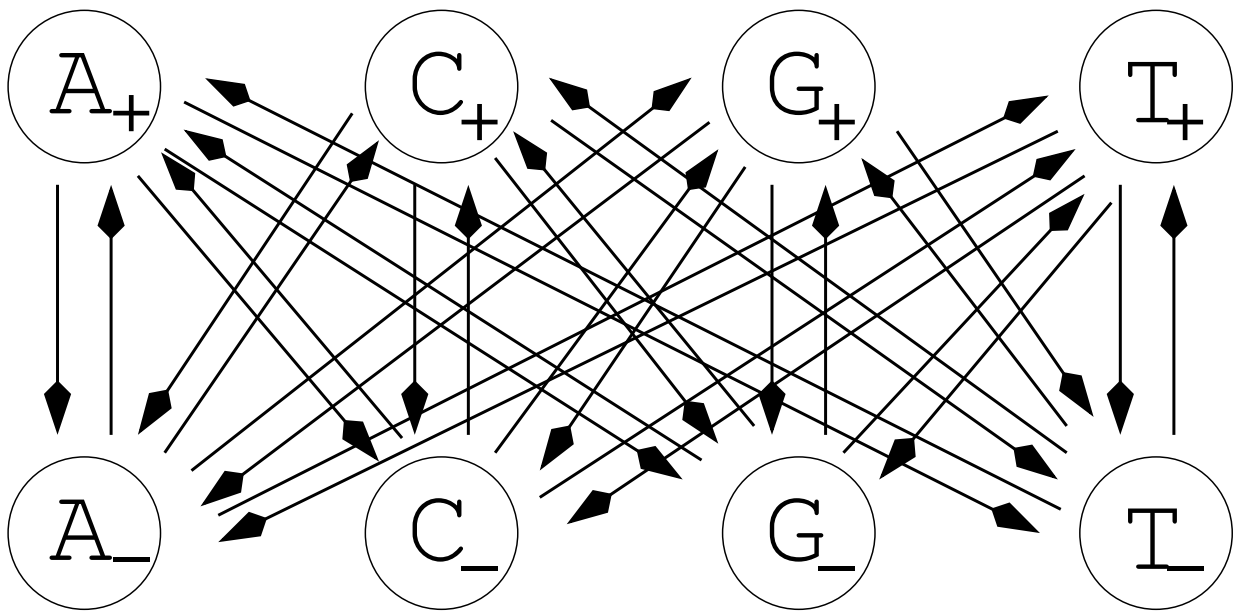
Definition.

An HMM is a system $M = (\Sigma, Q, A, e)$ consisting of

- an alphabet Σ ,
- a set of states Q ,
- a matrix $A = \{a_{kl}\}$ of transition probabilities a_{kl} for $k, l \in Q$, and
- an emission probability $e_k(b)$ for every $k \in Q$ and $b \in \Sigma$.

8.8 Example

An HMM for CpG-islands:



Now we also have all transitions between states in either of the two sets that carry over from the two Markov chains model⁺ and model⁻. The old edges within the two models are still there, but not shown here.

8.9 HMM for CpG-islands

```

# Number of states:
9
# Names of states (begin/end, A+, C+, G+, T+, A-, C-, G- and T-):
0 A+ C+ G+ T+ A- C- G- T-
# Number of symbols:
4
# Names of symbols:
a c g t
# Transition matrix, probability to change from +island to -island (and vice versa) is 10E-4
#      0      A+      C+      G+      T+      A-      C-      G-      T-
0      0.0000000 0.0725193 0.1637630 0.1788242 0.0754545 0.1322050 0.1267006 0.1226380 0.1278950
A+     0.0010000 0.1762237 0.2682517 0.4170629 0.1174825 0.0035964 0.0054745 0.0085104 0.0023976
C+     0.0010000 0.1672435 0.3599201 0.2679840 0.1838722 0.0034131 0.0073453 0.0054690 0.0037524
G+     0.0010000 0.1576223 0.3318881 0.3671328 0.1223776 0.0032167 0.0067732 0.0074915 0.0024975
T+     0.0010000 0.0773426 0.3475514 0.3759440 0.1781818 0.0015784 0.0070929 0.0076723 0.0036363
A-     0.0010000 0.0002997 0.0002047 0.0002837 0.0002097 0.2994005 0.2045904 0.2844305 0.2095804
C-     0.0010000 0.0003216 0.0002977 0.0000769 0.0003016 0.3213566 0.2974045 0.0778441 0.3013966
G-     0.0010000 0.0001768 0.0002387 0.0002917 0.0002917 0.1766463 0.2385224 0.2914165 0.2914155
T-     0.0010000 0.0002477 0.0002457 0.0002977 0.0002077 0.2475044 0.2455084 0.2974035 0.2075844
# Emission probabilities:
#   a c g t
0   0 0 0 0
A+  1 0 0 0
C+  0 1 0 0
G+  0 0 1 0
T+  0 0 0 1
A-  1 0 0 0
C-  0 1 0 0
G-  0 0 1 0
T-  0 0 0 1

```

Note the emission probabilities: The model emits the letters A, C, G, T, but for each letter there are two states where the letter can come from. Thus we cannot reconstruct the path the HMM has taken from the sequence alone.

In general, the emission probabilities need not be zero-one. But in the HMM for CpG-islands every state emits a unique letter. Thus the emitted symbol is not really “random” for a given state.

Next we look at an example where the states and the emitted symbols are associated in a looser way.

8.10 Example: fair/loaded die

An *occasionally dishonest casino* uses two dice, a *fair* and a *loaded* one:

- Given an HMM and a sequence of states and symbols. What is the *probability* to get this sequence?
- Given an HMM and a sequence of symbols. Can we *reconstruct* the corresponding sequence of states, assuming that the sequence was generated using the HMM?

8.12 Probability for given states and symbols

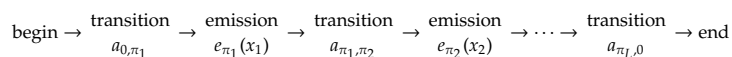
Definitions.

- A *path* $\pi = (\pi_1, \pi_2, \dots, \pi_L)$ in an HMM $M = (\Sigma, Q, A, e)$ is a sequence of states $\pi_i \in Q$.
- Given a sequence of *symbols* $x = (x_1, \dots, x_L)$ and a *path* $\pi = (\pi_1, \dots, \pi_L)$ through M . Then the *joint probability* is:

$$P(x, \pi) = a_{0\pi_1} \prod_{i=1}^L e_{\pi_i}(x_i) a_{\pi_i\pi_{i+1}},$$

with $\pi_{L+1} = 0$.

Schematically,



All we need to do is multiply these probabilities up.

This answers the first question. However, we usually do not *know* the path π through the model! That information is *hidden*.

8.13 The decoding problem

The *decoding problem* is the following: We have observed a sequence x of symbols that was generated by an HMM and we would like to “decode” the sequence of states from it.

Example: The sequence of symbols CGCG has a number of possible “explanations” within the CpG-model, e.g.:

(C_+, G_+, C_+, G_+) , (C_-, G_-, C_-, G_-) and (C_-, G_+, C_-, G_+) .

Among these, the first one is more likely than the second. The third one is very unlikely because the “signs” alternate, and those transitions have small probabilities.

A path through the HMM determines which parts of the sequence x are classified as CpG-islands (+/-). Such a classification of the observed symbols is also called a decoding. But here we will only consider the case where we want to reconstruct the passed states themselves, and not a “projection” of them.

Historical remark.

In *speech recognition*, HMMs have been applied since the 1970s. One application is the following. A speech signal is sliced into pieces of 10-20 milliseconds, each of which is assigned to one of e.g. 256 categories. We want to find out what sequence of phonemes was spoken. Since the precise pronunciation of words in natural language varies a lot, we are faced with a decoding problem.

The most probable path. To solve the decoding problem, we want to determine the path π^* that maximizes the probability of having generated the sequence x of symbols, that is:

$$\pi^* = \arg \max_{\pi} \Pr(\pi | x) = \arg \max_{\pi} \Pr(\pi, x).$$

For a sequence of n symbols there are $|Q|^n$ possible paths, therefore we cannot solve the problem by full enumeration.

Luckily, the “most probable path” π^* can be computed by *dynamic programming*. The recursion involves the following entities:

Definition. Given a prefix (x_1, x_2, \dots, x_i) of the sequence x which is to be decoded. Then let $(\pi_1^*, \pi_2^*, \dots, \pi_i^*)$ be a *path of states* with $\pi_i^* = s$ which maximizes the probability that the HMM followed these states and emitted the symbols (x_1, x_2, \dots, x_i) along its way. That is,

$$(\pi_1^*, \dots, \pi_i^*) = \arg \max \left\{ \prod_{k=1}^i a_{\pi_{k-1}, \pi_k} e_{\pi_k}(x_k) \mid (\pi_1, \dots, \pi_i) \in Q^i, \pi_i = s, \pi_0 = 0 \right\}.$$

Also, let $V(s, i)$ denote the *value* of this maximal probability.

Clearly we can store the values $V(s, i)$ in a $Q \times [1 \dots L]$ dynamic programming matrix.

Initialization.

Every path starts at state 0 with probability 1. Hence, the *initialization* for $i = 0$ is $V(0, 0) = 1$, and $V(s, 0) = 0$ for $s \in Q \setminus \{0\}$.

Recursion.

Now for the *recurrence formula*, which applies for $i = 1, \dots, L$. Assume that we know the most likely path for x_1, \dots, x_{i-1} under the additional constraint that the last state is s , for all $s \in Q$. Then we obtain the most likely path to the i -th state t by maximizing the probability $V(s, i-1)a_{st}$ over all predecessors $s \in Q$ of t . To obtain $V(t, i)$ we also have to multiply by $e_t(x_i)$ since we have to emit the given symbol x_i .

That is, we have

$$V(t, i) = \max\{ V(s, i-1)a_{st} \mid s \in Q \} \cdot e_t(x_i)$$

for all $t \in Q$. (Again, note the use of the Markov property!)

Termination.

In the last step, we enter state 0 but do not emit a symbol. Hence $P(x, \pi^*) = \max\{ V(s, L)a_{s,0} \mid s \in Q \}$.

8.14 Viterbi algorithm

Input: HMM $M = (\Sigma, Q, A, e)$
and symbol sequence x

Output: Most probable path π^* .

Initialization ($i = 0$): $V(0, 0) = 1, V(s, 0) = 0$ for $s \in Q \setminus \{0\}$.

Recurrence:

For all $i = 1, \dots, L, t \in Q$: $V(t, i) = e_t(x_i) \max\{ V(s, i - 1)a_{st} \mid s \in Q \}$
 $T(t, i) = \arg \max\{ V(s, i - 1)a_{st} \mid s \in Q \}$

Termination ($i = L + 1$): $P(x, \pi^*) = \max\{ V(s, L)a_{s,0} \mid s \in Q \}$
 $\pi_L^* = \arg \max\{ V(s, L)a_{s,0} \mid s \in Q \}$

Traceback:

For all $i = L, \dots, 1$: $\pi_{i-1}^* = T(\pi_i^*, i)$

x_0	x_1	x_2	x_3	...	x_{i-2}	x_{i-1}	x_i	...	x_L	x_{L+1}
0					0
	A_+	A_+	A_+	...	A_+	A_+	A_+	...	A_+	
	C_+	C_+	C_+	...	C_+	C_+	C_+	...	C_+	
	G_+	G_+	G_+	...	G_+	G_+	G_+	...	G_+	
	T_+	T_+	T_+	...	T_+	T_+	T_+	...	T_+	
	A_-	A_-	A_-	...	A_-	A_-	A_-	...	A_-	
	C_-	C_-	C_-	...	C_-	C_-	C_-	...	C_-	
	G_-	G_-	G_-	...	G_-	G_-	G_-	...	G_-	
	T_-	T_-	T_-	...	T_-	T_-	T_-	...	T_-	

We need not consider the values in the 0 row except for the initialization and the termination of the DP.

The *running time* is $|Q|^2|L|$, as each entry of the $Q \times L$ matrix requires $|Q|$ calculations.

The repeated multiplication of probabilities will quickly produce very small numbers. In order to avoid *underflow arithmetic errors*, the calculations in the Viterbi algorithm should therefore be done in “log scale”, i.e., we store $\log V(s, i)$ instead of $V(s, i)$. This makes multiplications become additions (which are calculated faster), and the numbers stay in a reasonable range. Moreover, $\log a_{s,t}$ and $\log e_t(y)$ might be rounded to discrete steps so that we can use (unsigned) integer arithmetic.

E.g. a probability $p = 10^{-12345}$ might be stored as $-[1000 \cdot \log_{10} p] = 12345000$.

8.15 Examples for Viterbi

Given the sequence CGCG and the HMM for CpG-islands. Here is the DP table V . (Some traceback pointers are indicated in $[\]$):

8.17 Forward algorithm

We have already seen a closed formula for the probability $P(x, \pi)$ that M generated x using the path π . Summing over all possible paths, we obtain the probability that M generated x :

$$P(x) = \sum_{\pi} P(x, \pi).$$

Calculating this sum is done by “replacing the max with a sum” in the Viterbi algorithm.

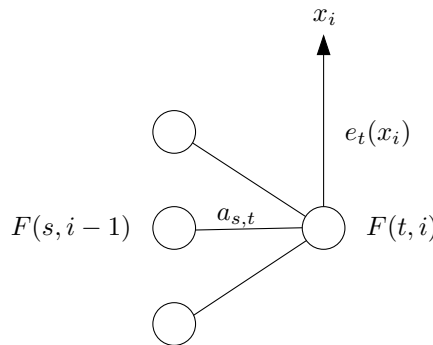
Formally, we define the *forward-variable*:

$$F(s, i) = \Pr(x_1 \dots x_i, \pi_i = s),$$

This is the probability that the sequence generated by the HMM has the sequence (x_1, \dots, x_i) as a prefix, and the i -th state is $\pi_i = s$.

Using the distributive law (and a similar reasoning as for $\Pr(x, \pi)$), we obtain the recursion

$$F(t, i) = e_t(x_i) \cdot \sum_{s \in Q} F(s, i-1) a_{s,t}.$$



The resulting algorithm is actually simpler, since we do not have to maintain backtrace pointers:

Input: HMM $M = (\Sigma, Q, A, e)$
and symbol sequence x

Output: Probability $\Pr(x)$.

Initialization ($i = 0$): $F(0, 0) = 1, F(s, 0) = 0$ for $s \in Q \setminus \{0\}$.

Recurrence:

For all $i = 1 \dots L, t \in Q$: $F(t, i) = e_t(x_i) \sum_{s \in Q} F(s, i-1) a_{st}$

Termination ($i = L + 1$): $\Pr(x) = \sum_{s \in Q} F(s, L) a_{L,0}$

The “log-scale” transform is a bit more complicated in this case, since we have to *add* probabilities. But there are efficient ways to calculate $\log(p + q)$ from $\log p$ and $\log q$: Let $r := p + q$, w.l.o.g. $p > q$. Then

$$\begin{aligned} \log r &= \log(e^{\log p} + e^{\log q}) \\ &= \log(e^{\log p}) + \log(1 + e^{\log q} / e^{\log p}) \\ &= \log p + \log(1 + e^{\log q - \log p}) \end{aligned}$$

and in this way it can be calculated using an numerical approximation for the function $x \mapsto \log(1 + e^{-x}), x \geq 0$.

Alternatively, one can apply *scaling methods*. The idea is to multiply all entries of a column of the DP matrix with the same factor, if they become too small.

8.18 Backward algorithm

Recall the definition of the *forward-variables*:

$$F(s, i) = \Pr(x_1 \dots x_i, \pi_i = s).$$

This is the probability that the sequence generated by the HMM has the sequence (x_1, \dots, x_i) as a *prefix*, and the i -th state is $\pi_i = s$.

For the posterior decoding we need to compute the conditional probability that M emitted x_i from state π_i , when it happened to generate x :

$$\Pr(\pi_i = s \mid x) = \frac{\Pr(\pi_i = s, x)}{\Pr(x)}.$$

Since $\Pr(x)$ is known by the forward algorithm, it suffices to calculate $\Pr(\pi_i = s, x)$. Now, by the Markov property,

$$\begin{aligned} \Pr(x, \pi_i = s) &= \Pr(x_1, \dots, x_i, \pi_i = s) \Pr(x_{i+1}, \dots, x_L \mid x_1, \dots, x_i, \pi_i = s) \\ &= \Pr(x_1, \dots, x_i, \pi_i = s) \Pr(x_{i+1}, \dots, x_L \mid \pi_i = s). \end{aligned}$$

Hence, if we define the *backward-variables*:

$$B(s, i) = \Pr(x_{i+1} \dots x_L \mid \pi_i = s),$$

then

$$\begin{aligned} \Pr(x, \pi_i = s) &= \Pr(x_1, \dots, x_i, \pi_i = s) \Pr(x_{i+1}, \dots, x_L \mid \pi_i = s) \\ &= F(s, i) B(s, i). \end{aligned}$$

$B(s, i)$ is the probability that the HMM will generate the sequence (x_{i+1}, \dots, x_L) “when it is started in state π_i ”, until it reaches state 0. It is computed by the *backward algorithm*.

Input: HMM $M = (\Sigma, Q, A, e)$
and symbol sequence x

Output: Probability $\Pr(x)$.

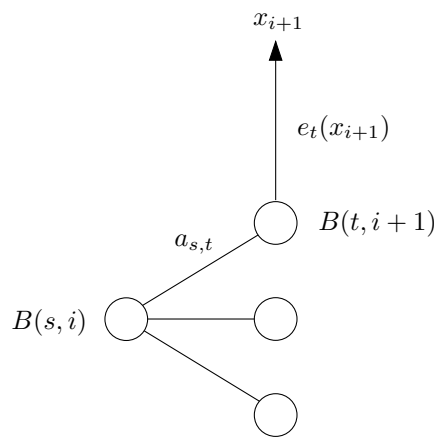
Initialization ($i = L$): $B(s, L) = a_{s,0}$ for all $s \in Q$.

Recurrence:

For all $i = l - 1 \dots 1, s \in Q$: $B(s, i) = \sum_{t \in Q} a_{st} e_t(x_{i+1}) B(t, i + 1)$

Termination ($i = 0$): $\Pr(x) = \sum_{t \in Q} a_{0,t} e_t(x_1) B(t, 1)$

The reasoning behind the recurrences is similar to the forward algorithm.



Usually one is mainly interested in the backward *variables*, since $\Pr(x)$ can be computed by the forward algorithm as well.

8.19 Posterior decoding

The probabilities $\Pr(\pi_i | x)$, $i = 1, \dots, L$ are called *posterior probabilities*, because they are determined *after* observing the (random) sequence x . They are conditional probabilities when we have a partial knowledge of the actual outcome of a random experiment.

The sequence of states $\hat{\pi}$ obtained by posterior decoding is defined thus:

$$\hat{\pi}_i = \arg \max_{s \in Q} P(\pi_i = s | x).$$

In other words, at every position we choose the most probable state for that position.

Pros and cons of posterior decoding:

- Posterior probabilities provide an alternative means to decode the observed sequence. It is often superior to the Viterbi algorithm, especially if there are *many paths* which have *almost the same probability* as the most probable one.
- Posterior decoding is useful if we are interested in *the state at a specific position i* and not in the whole sequence of states.
- Also the *posterior probabilities* can serve as a *quantitative measurement* of the *confidence* in the predicted states.
- Although the posterior decoding is defined by maximizing the probabilities at each state, *the path as a whole might not be taken very likely* by the HMM. If the transition matrix forbids some transitions (i.e., $a_{st} = 0$), then this decoding may even produce a sequence that is *not a valid path*, because its probability is 0!

8.20 The design of Hidden Markov Models

How does one come up with an HMM?

First step: Determine its “*topology*”, i.e. the number of states and how they are connected via transitions of non-zero probability. – This is kind of an art. We will later see profile HMMs as an example of a commonly used topology.

Second step: Set the *parameters*, i.e. the transition probabilities a_{st} and the emission probabilities $e_s(x)$.

We consider the second step. Given a set of example sequences. Our goal is to “train” the parameters of the HMM using the example sequences, that is, to set the parameters in such a way that the probability, with which the HMM generates the given example sequences, is maximized.

8.21 Training when the states are known

Let $M = (\Sigma, Q, A, e)$ be an HMM.

Given a list of sequences of symbols $x^{(1)}, x^{(2)}, \dots, x^{(n)}$ and a list of corresponding paths $\pi^{(1)}, \pi^{(2)}, \dots, \pi^{(n)}$. (E.g., DNA sequences with annotated CpG-islands.) We consider the probability that the HMM generates them “one after another”.

We want to choose the parameters (A, e) of the HMM M *optimally*, such that:

$$(A, e) = \arg \max \left\{ \Pr_{M'} \left((x^{(1)}, \pi^{(1)}), \dots, (x^{(n)}, \pi^{(n)}) \right) \mid M' = (\Sigma, Q, A', e') \right\}$$

In other words, we want to determine the *maximum likelihood estimator* (ML-estimator) for the parameters (A, e) .

(Recall: If we consider $P(D \mid M)$ as a function of D , then we call this a *probability*; as a function of M , then we use the word *likelihood*.)

Not surprisingly, it turns out (analytically) that the likelihood is maximized by the estimators

$$\tilde{A}_{st} := \frac{\tilde{A}_{st}}{\sum_{t'} \tilde{A}_{s,t'}} \quad \text{and} \quad \tilde{e}_{st} := \frac{\tilde{e}_{st}}{\sum_{t'} \tilde{e}_{s,t'}},$$

where

$$\begin{aligned} \tilde{A}_{st} &:= \text{Observed number of transitions from state } s \text{ to state } t, \\ \tilde{e}_{sb} &:= \text{Observed number of emissions of symbol } b \text{ in state } s. \end{aligned}$$

(However this presumes that we have sufficient training data.)

8.22 Training the *fair/loaded* HMM

Given example data x and π :

Symbols x : 1 2 5 3 4 6 1 2 6 6 3 2 1 5
States π : F F F F F F U U U U F F F

State transitions:

$$\begin{array}{c|ccc} \tilde{A}_{kl} & 0 & F & U \\ \hline 0 & & & \\ F & & & \\ U & & & \end{array} \quad \rightarrow \quad \begin{array}{c|ccc} \tilde{A}_{kl} & 0 & F & U \\ \hline 0 & & & \\ F & & & \\ U & & & \end{array}$$

Emissions:

$\bar{e}_k(b)$	1	2	3	4	5	6	→	$\tilde{e}_k(b)$	1	2	3	4	5	6
0								0						
F								F						
U								U						

Given example data x and π :

Symbols x : 1 2 5 3 4 6 1 2 6 6 3 2 1 5
 States π : F F F F F F U U U U F F F

State transitions:

\bar{A}_{kl}	0	F	U	→	\tilde{A}_{kl}	0	F	U
0	0	1	0		0	0	1	0
F	1	8	1		F	$\frac{1}{10}$	$\frac{8}{10}$	$\frac{1}{10}$
U	0	1	3		U	0	$\frac{1}{4}$	$\frac{3}{4}$

Emissions:

$\bar{e}_k(b)$	1	2	3	4	5	6	→	$\tilde{e}_k(b)$	1	2	3	4	5	6
F	3	2	1	1	2	1		F	.3	.2	.1	.1	.2	.1
U	0	1	1	0	0	2		U	0	$\frac{1}{4}$	$\frac{1}{4}$.0	.0	$\frac{1}{2}$

8.23 Pseudocounts

One common problem in training is *overfitting*. For example, if some possible transition (s, t) is never seen in the example data, then we will set $\tilde{a}_{st} = 0$ and the transition is then forbidden in the resulting HMM. Moreover, if a given state s is never seen in the example data, then $\tilde{e}_s(b)$ resp. $\tilde{e}_s(b)$ is undefined for all t, b .

To solve this problem, we introduce *pseudocounts* r_{st} and $r_s(b)$ and *add* them to the observed transition resp. emission frequencies.

Small pseudocounts reflect “little pre-knowledge”, large ones reflect “more pre-knowledge”. The effect of pseudocounts can also be thought of as “smoothing” the model parameters using a background model (i. e., a *prior distribution*).

8.24 Training when the states are unknown

Now we assume we are given a list of sequences of symbols $x^{(1)}, x^{(2)}, \dots, x^{(n)}$ and we do *not* know the list of corresponding paths $\pi^{(1)}, \pi^{(2)}, \dots, \pi^{(n)}$, as is usually the case in practice.

Then the problem to choose the parameters (A, e) of the HMM M *optimally*, such that:

$$(A, e) = \arg \max \left\{ \Pr_{M'}(x^{(1)}, \dots, x^{(n)}) \mid M' = (\Sigma, Q, A', e') \right\}$$

is NP-hard and hence we cannot solve it exactly in polynomial time.

The quantity

$$\log \Pr_{M'}(x^{(1)}, \dots, x^{(n)}) = \sum_{j=1}^n \log \Pr_{M'}(x^{(j)})$$

is called the *log-likelihood* of the model M .

It serves as a measure of the quality of the model parameters.

The Baum-Welch algorithm finds a locally optimal solution to the HMM training problem. It starts from an arbitrary initial estimate for (A, e) and the observed frequencies \bar{A}, \bar{e} . Then it applies a reestimation step until convergence or timeout.

- In each reestimation step, the forward and backward algorithm is applied (with the current model parameters) to each example sequence.
- Using the posterior state probabilities, one can calculate the expected emission frequencies. (In a loop we add for each training sequence a term to the current \bar{e}).
- Using the forward and backward variables, one can also calculate the expected transition frequencies. (In a loop we add for each training sequence a term to \bar{A}).
- The new model parameters are calculated as maximum likelihood estimates based on \bar{A}, \bar{e} .

8.25 Baum-Welch algorithm

- Input:* HMM $M = (\Sigma, Q, A, e)$,
training data $x^{(1)}, \dots, x^{(n)}$,
pseudocounts r_{st} and $r_s(b)$ (if desired).
- Output:* HMM $M' = (\Sigma, Q, A', e')$ with an improved score.
- Initialization:* Pick some arbitrary model parameters (A, e) .
Set some initial "observation frequencies" (\bar{A}, \bar{e}) .
- Reestimation:* For each sequence $x^{(j)}, j = 1, \dots, n$:
Calculate $F^{(j)}$ using the forward algorithm.
Calculate $B^{(j)}$ using the backward algorithm.
Update \bar{A} and \bar{e} using the posterior probabilities.
Calculate new model parameters (A, e) from (\bar{A}, \bar{e}) .
Calculate the new log-likelihood of the model.
Repeat.
- Termination:* Stop if the change of log-likelihood becomes too small,
or the maximal number of iterations is exceeded.

Updating \bar{e} : The probability that the model with parameters (A, e) was in state $\pi_i = s$ when it generated the symbol $x_i^{(j)}$ of $x^{(j)}$ is just the posterior state probability

$$\Pr(\pi_i^{(j)} = s \mid x^{(j)}) = \frac{F^{(j)}(s, i)B^{(j)}(s, i)}{\Pr(x^{(j)})}.$$

Thus we increase $\bar{e}_s(b)$ by

$$\sum_{j=1}^n \sum_{i: x_i^{(j)}=b} \frac{F^{(j)}(s, i)B^{(j)}(s, i)}{\Pr(x^{(j)})}.$$

Updating \bar{A} : The probability that the model with parameters (A, e) stepped from state $\pi_i = s$ to state $\pi_{i+1} = t$ when it generated the symbols $x_i^{(j)}, x_{i+1}^{(j)}$ of $x^{(j)}$ is

$$\begin{aligned} \Pr(\pi_i = s, \pi_{i+1} = t \mid x) &= \Pr(x_1, \dots, x_i, \pi_i = s) \cdot \Pr(x_{i+1}, \pi_i = s, \pi_{i+1} = t) \cdot \Pr(x_{i+2}, \dots, x_L \mid \pi_{i+1} = t) \\ &= \frac{F(s, i)a_{st}e_t(x_{i+1})B(t, i + 1)}{\Pr(x^{(j)})}. \end{aligned}$$

Thus we increase \bar{a}_{st} by

$$\sum_{j=1}^n \sum_{i=0}^{|x^{(j)}|} \frac{F(s, i)a_{st}e_t(x_{i+1})B(t, i + 1)}{\Pr(x^{(j)})}.$$

(Here we let $e_t(x_{|x^{(j)}|+1}) := 1$.)

Remark: One can prove that the log-likelihood-score converges to a local maximum using the Baum-Welch-algorithm.

However, this doesn't imply that the parameters converge!

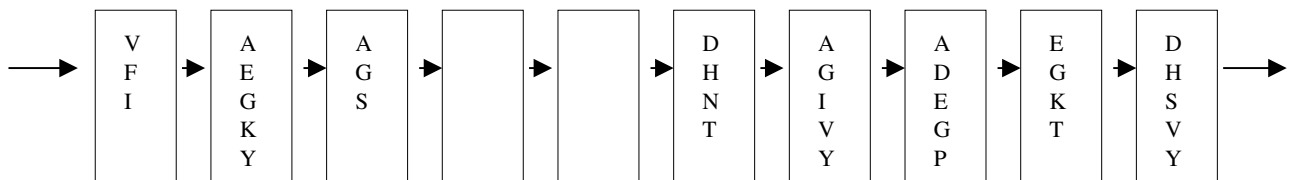
Local maxima can be avoided by considering many different starting points.

Additionally, any standard optimization approaches can also be applied to solve the optimization problem.

8.26 Profile HMMs

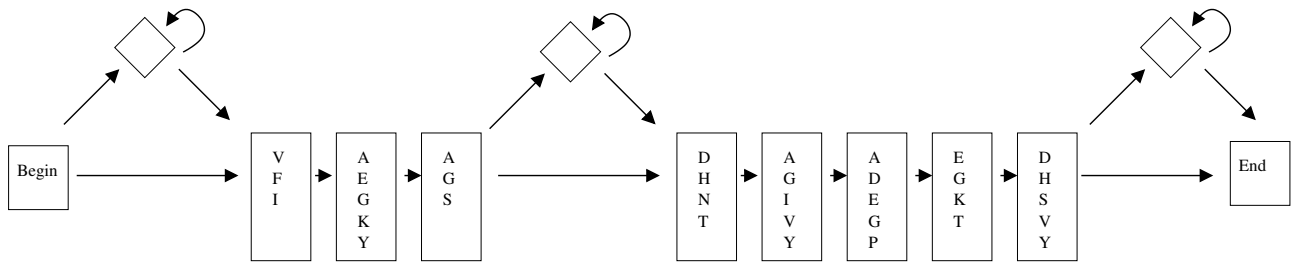
```
HBA_HUMAN    ...VGA--HAGEY...
HBB_HUMAN    ...V---NVDEV...
MYG_PHYCA    ...VEA--DVAGH...
GLB3_CHITP   ...VKG-----D...
GLB5_PETMA   ...VYS--TYETS...
LGB2_LUPLU   ...FNA--NIPKH...
GLB1_GLYDI   ...IAGADNGAGV...
"Matches":   ***  *****
```

We first consider a simple HMM that is equivalent to a PSSM (*Position Specific Score Matrix*):



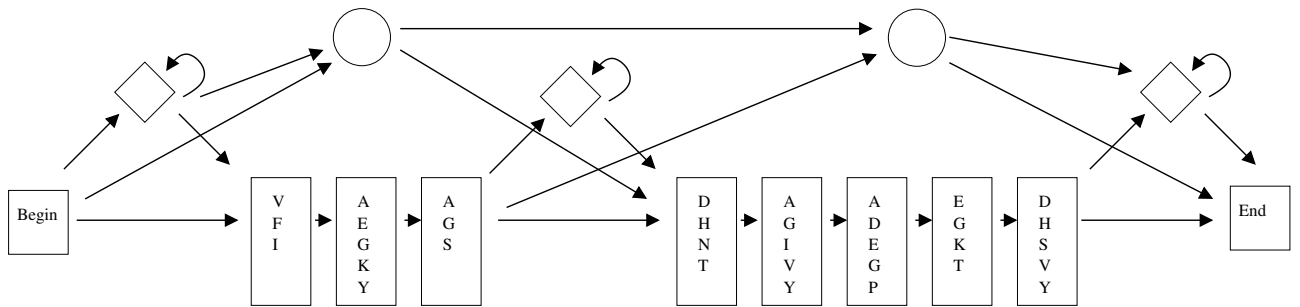
(The listed amino-acids have a higher emission-probability.)

We introduce so-called *insert*-states that emit symbols based on their background probabilities.



This allows us to model segments of sequence that lie outside of conserved domains.

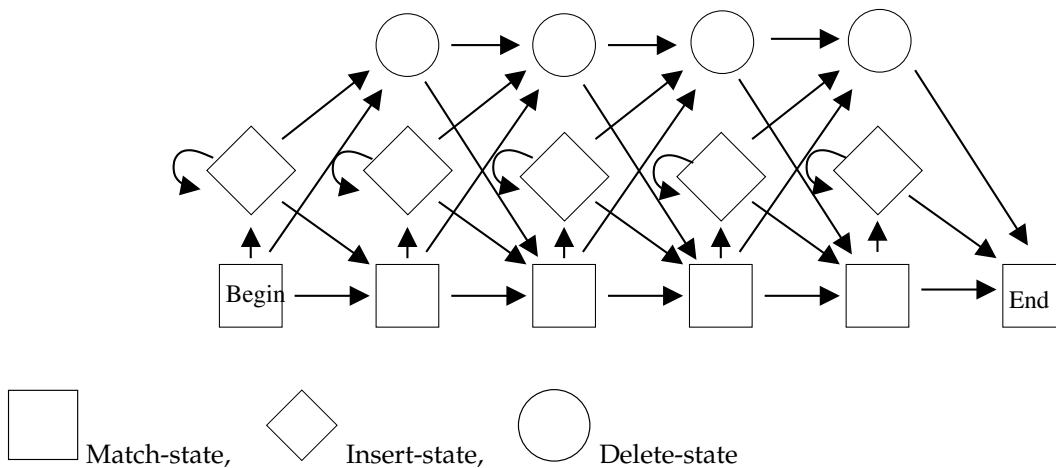
We introduce so-called *delete-states* that are *silent* and do not emit any symbols.



This allows us to model the absence of individual domains.

Silent states can be included into HMMs if we provide some changes to the algorithms. We consider the case where the HMM does not contain cycles involving silent states. Of course, silent states have no factor for the emission probability in the recurrences. In the DP recurrence, for each column the silent states are processed after the emitting states. They receive incoming paths from the same column. We do not describe the details here.

The general topology of a profile HMM is as follows.



Given a multiple alignment of a family of sequences. How to design a profile HMM from it? We could apply the Baum-Welch algorithm, but there are more direct ways to assign the model parameters.

First we must decide which positions of the alignment are to be modeled as match- and which positions are to be modeled as insert-states. Rule-of-thumb: columns with more than 50% gaps should be modeled as insert-states.

We determine the transition and emission probabilities simply by counting the observed transitions \bar{a}_{st} and emissions $\bar{e}_s(b)$.

The insert states emit with a background distribution as obtained from unaligned sequence.

Obviously, it may happen that certain transitions or emissions do not appear in the training data and thus we use the *Laplace-rule* and add 1 to each count.

8.27 Excursion: Higher-order Markov chains

Remark.

One can also define Markov chains of order k , where the transition probabilities have the form $P(x_{i+1} = t \mid x_i = s_1, \dots, x_{i-k+1} = s_k)$, but these are not easily visualized as graphs and can (at least in principle) be reduced to the order 1 case.

Idea:

Assume that we are given a 2-nd order Markov chain over an alphabet (state set) Σ with transition probabilities

$$a_{s,t,u} = \Pr(x_{i+1} = u \mid x_i = t, x_{i-1} = s).$$

Here the “output” of a state is simply its label.

Then this is equivalent to a 1-st order Markov chain over the alphabet Σ^2 with transition probabilities

$$\tilde{a}_{(s,t),(t',u)} := \begin{cases} a_{s,t,u} & t = t' \\ 0 & \text{otherwise} \end{cases}$$

The “output” of a state (t, u) is its last entry, u .

Begin and end of a sequence can be modeled using a special state 0, as before. The reduction of k -th order Markov chains uses Σ^k in a similar way. (Proof: exercise.) – However, usually it is better to modify the algorithms rather than blow up the state space.