# Probabilistic Models: Spring 2014 <br> Gene Finding Example 

We are given the following hidden Markov model describing the (simplified) behavior of DNA.


| $S_{0}$ | $\Theta_{S_{0}}$ |
| :---: | :--- |
| Genic | .5 |
| Intergenic | .5 |


| $S_{t-1}$ | $S_{t}$ | $\Theta_{S_{t} \mid S_{t-1}}$ |
| :---: | :---: | :--- |
| Genic | Genic | .7 |
| Genic | Intergenic | .3 |
| Intergenic | Genic | .3 |
| Intergenic | Intergenic | .7 |


| $S_{i}$ | $O_{i}$ | $\Theta_{O_{i} \mid S_{i}}$ |
| :---: | :---: | :--- |
| Genic | AT | .9 |
| Genic | CG | .1 |
| Intergenic | AT | .2 |
| Intergenic | CG | .8 |

1. Use the forward algorithm to calculate the predictive posterior distribution over $S_{1} \ldots S_{4}$ given the following observations: $A T, A T$, $C G, A T$.

Table 1: The forward messages.

| Time $t$ | $P\left(S_{t}=\right.$ genic $\left.\mid O_{1} \ldots O_{t}\right)$ | $P\left(S_{t}=\right.$ intergenic $\left.\mid O_{1} \ldots O_{t}\right)$ |
| :---: | :--- | :--- |
| 1 | 0.8182 | 0.1818 |
| 2 | 0.8834 | 0.1166 |
| 3 | 0.1907 | 0.8093 |
| 4 | 0.7308 | 0.2692 |

2. Use the backward algorithm to calculate the smoothed posterior distribution over $S_{1}$ given the observations: $A T, A T$.

Note that we can reuse the forward message from the previous question. So we just need to compute the backward message.

$$
\begin{aligned}
P\left(O_{2}=\mathrm{AT} \mid S_{1}=\text { genic }\right) & =\sum_{S_{2}} P\left(O_{2}=\mathrm{AT} \mid S_{2}\right) P\left(S_{2} \mid S_{1}=\text { genic }\right) P\left(O_{3} \ldots O_{t} \mid S_{2}\right) \\
& \text { We do not have any more observations, so we can drop the third term. } \\
& =P\left(O_{2}=\mathrm{AT} \mid S_{2}=\text { genic }\right) P\left(S_{2}=\text { genic } \mid S_{1}=\text { genic }\right)+ \\
& P\left(O_{2}=\mathrm{AT} \mid S_{2}=\text { intergenic }\right) P\left(S_{2}=\text { intergenic } \mid S_{1}=\text { genic }\right) \\
& =.9(.7)+.2(.3) \\
& =.69
\end{aligned}
$$

Similarly, $P\left(O_{2}=\mathrm{AT} \mid S_{1}=\right.$ intergenic $)=.41$. Combining this with the forward message, we get that

$$
P\left(S_{1}=\operatorname{genic} \mid O_{1}=\operatorname{AT}, O_{2}=\mathrm{AT}\right) \propto 0.8182(0.69), \text { and }
$$

$$
P\left(S_{1}=\operatorname{intergenic} \mid O_{1}=\mathrm{AT}, O_{2}=\mathrm{AT}\right) \propto 0.1818(0.41)
$$

Multiplying and then normalizing gives that

$$
\begin{aligned}
P\left(S_{1}=\operatorname{genic} \mid O_{1}\right. & \left.=\mathrm{AT}, O_{2}=\mathrm{AT}\right) \approx 0.883, \text { and } \\
P\left(S_{1}=\text { intergenic } \mid O_{1}\right. & \left.=\mathrm{AT}, O_{2}=\mathrm{AT}\right) \approx 0.117 .
\end{aligned}
$$

3. Use the Viterbi algorithm to find the most likely instantiation of $S_{1} \ldots S_{4}$ given the observations: $A T, A T, C G, C G$.

To find the most likely instantiation of $S_{1}$, we need to find the value of $S_{0}$ which maximizes $P\left(S_{1}=s_{1}, S_{0} \mid O_{1}=\right.$ AT $)$ for each value of $S_{1}$.
First, we consider when $S_{1}=$ genic.

$$
\begin{aligned}
P\left(S_{1}=s_{1} \mid O_{1}=\mathrm{AT}\right) & \propto P\left(O_{1}=\mathrm{AT} \mid S_{0}, S_{1}=\text { genic }\right) P\left(S_{1}=\text { genic } \mid S_{0}\right) \\
& =P\left(O_{1}=\mathrm{AT} \mid S_{1}=\text { genic } \max _{S_{0}} P\left(S_{1}=\operatorname{genic} \mid S_{0}\right) P\left(S_{0}\right)\right. \\
& \text { We now consider } S_{0}=\text { genic } \\
& =P\left(O_{1}=\mathrm{AT} \mid S_{1}=\text { genic }\right) P\left(S_{1}=\text { genic } \mid S_{0}=\text { genic }\right) P\left(S_{0}=\text { genic }\right) \\
& =.9(.7)(.5) \\
& =0.315
\end{aligned}
$$

We now consider $S_{0}=$ intergenic
$=P\left(O_{1}=\mathrm{AT} \mid S_{1}=\right.$ genic $) P\left(S_{1}=\right.$ genic $\mid S_{0}=$ intergenic $) P\left(S_{0}=\right.$ intergenic $)$
$=.9(.3)(.5)$
$=0.135$
We take the max over $S_{0}$ and find that $P\left(S_{1}=s_{1} \mid O_{1}=\mathrm{AT}\right) \propto 0.315$.
A similar set of calculations shows that $P\left(S_{1}=s_{1} \mid O_{1}=\mathrm{AT}\right) \propto 0.070$. Since this is the first state on the path, we normalize these values to find that $\left.P\left(S_{1} \mid O_{1}=\mathrm{AT}\right) \approx<0.8182,0.1818\right\rangle$.
To find the most likely instantiation of $S_{2}$, we need to find the value of $S_{1}$ which maximizes $P\left(S_{2}=s_{2}, S_{1} \mid O_{1}=\right.$ AT, $O_{2}=$ AT for each value of $S_{2}$.

First, we consider when $S_{2}=$ genic.

$$
\begin{aligned}
P\left(S_{2}=s_{2}, S_{1} \mid O_{1}=\mathrm{AT}, O_{2}=\mathrm{AT}\right) & \propto P\left(O_{2}=\mathrm{AT} \mid S_{2}=\text { genic }\right) P\left(S_{2}=\operatorname{genic} \mid S_{1}\right) \\
& =P\left(O_{2}=\mathrm{AT} \mid S_{2}=\text { genic }\right) \max _{S_{1}} P\left(S_{2}=\text { genic } \mid S_{1}\right) \max _{s_{0}} P\left(s_{0}, s_{1} \mid O_{1}=\mathrm{AT}\right)
\end{aligned}
$$

The second "max" is simply the numbers we calculated in the previous step.
We now consider $S_{1}=$ genic
$=P\left(O_{2}=\mathrm{AT} \mid S_{2}=\right.$ genic $) P\left(S_{2}=\right.$ genic $\mid S_{1}=$ genic $) \max _{s_{0}} P\left(s_{0}, s_{1} \mid O_{1}=\mathrm{AT}\right)$
$=.9(.7)(.8182)$
$=0.5155$
We now consider $S_{1}=$ intergenic

$$
\begin{aligned}
& =P\left(O_{2}=\mathrm{AT} \mid S_{2}=\text { genic }\right) P\left(S_{2}=\text { genic } \mid S_{0}=\text { intergenic }\right) \max _{s_{0}} P\left(s_{0}, s_{1} \mid O_{1}=\mathrm{AT}\right) \\
& =.9(.3)(.1818) \\
& =0.0491
\end{aligned}
$$

We take the max over $S_{1}$ and find that $P\left(S_{2}=\right.$ genic, $\left.S_{1}=s_{1} \mid O_{1}=\mathrm{AT}, O_{2}=\mathrm{AT}\right) \propto 0.5155$
A similar set of calculations shows that $P\left(S_{2}=\right.$ intergenic, $\left.S_{1}=s_{1} \mid O_{1}=\mathrm{AT}, O_{2}=\mathrm{AT}\right) \propto 0.0491$. Since this is not the first state on the path, these values give us the probabilities of the paths and do not need to be normalized.
Similar calculations show that the values for all of the states are as follows.

| Table 2: The path probabilities. |  |  |
| :---: | :--- | :--- |
| Time $t$ | $P\left(S_{1} \ldots S_{t}=\right.$ genic $\left.\mid O_{1} \ldots O_{t-1}\right)$ | $P\left(S_{1} \ldots S_{t}=\right.$ intergenic $\left.\mid O_{1} \ldots O_{t-1}\right)$ |
| 1 | 0.8182 | 0.1818 |
| 2 | 0.5155 | 0.0491 |
| 3 | 0.0361 | 0.1237 |
| 4 | 0.0037 | 0.0693 |

## Some useful equations

The forward algorithm
$P$ (next state|observations so far, next observation) $\propto P$ (next observation|next state) $\sum_{\text {current state }} P$ (next state| current state) $P$ (current state|observations so far) $P\left(S_{t+1} \mid O_{1}, O_{2}, \ldots, O_{t+1}\right) \propto P\left(O_{t+1} \mid S_{t+1}\right) \sum_{S_{t}=s_{t}} P\left(S_{t+1} \mid S_{t}\right) P\left(S_{t}=s_{t} \mid O_{1}, \ldots, O_{t}\right)$
The backward algorithm
$P\left(S_{k} \mid O_{1}, \ldots, O_{t}\right) \propto$ forward $(k) P\left(O_{k+1}, \ldots, O_{t} \mid S_{k}\right)$
$P($ remaining observations $\mid$ current state $)=\sum_{\text {next state }} P($ next state $\mid$ current state $) P$ (next observation $\mid$ next state $) P($ further observations|next state)
$P\left(O_{k+1}, \ldots, O_{t} \mid S_{k}\right)=\sum_{S_{k+1}=s_{k+1}} P\left(S_{k+1}=s_{k+1} \mid S_{k}\right) P\left(O_{k+1} \mid S_{k+1}\right) P\left(O_{k+2}, \ldots, O_{t} \mid S_{k+1}=s_{k+1}\right)$

## The Viterbi algorithm

$\max _{\text {path so far }} P$ (path so far, next state in path| observations so far, next observation)
$\quad \propto P($ next observation $\mid$ next state $)\left\{\max _{\text {current state }} P(\right.$ next state $\mid$ current state $)\left\{\max _{\text {previous states }} P(\right.$ previous states, current statelobservations so far $\left.\}\right\}$
$\max _{\ldots s_{t}} P\left(s_{1} \ldots s_{t}, S_{t+1} \mid O_{1} \ldots O_{t+1}\right) \propto P\left(O_{t+1} \mid S_{t+1}\right)\left\{\max _{s_{t}} P\left(S_{t+1} \mid s_{t}\right)\left\{\max _{s_{1} \ldots s_{t-1}} P\left(s_{1} \ldots s_{t-1}, s_{t} \mid O_{1} \ldots O_{t}\right)\right\}\right\}$

