Probabilistic Reasoning wrt Time

RN, Chapter 15

Decision Theoretic Agents

- Introduction to Probability [Ch13]
 - Belief networks [Ch14]
- Dynamic Belief Networks [Ch15]
 - Foundations
 - Markov Chains (Classification)
 - Hidden Markov Models (HMM)
 - Kalman Filter
 - General: Dynamic Belief Networks (DBN)
 - Applications
 - Future Work, Extensions, …
- Single Decision [Ch16]
- Sequential Decisions [Ch17]
- Game Theory [Ch 17.6 17.7]

Markovian Models

In general, X_{t+1} depends on everything ! ... X_t, X_{t-1}, ...
 Markovian means...

Future is independent of the past once you know the present. P($X_{t+1} | X_{t}, X_{t-1}, ...$) = P($X_{t+1} | X_{t}$)

- Markov Chain: "state" (everything important) is visible P(x_{t+1} | x_t, (everything)) = P(x_{t+1} | x_t)
- Eg: First-Order Markov Chain
 - **1**. Random Walk along x axis, changing x-position ± 1 at each time
 - 2. Predicting rain
- $\xrightarrow{\begin{array}{c|c}r_2 & P(r_2|r_1) \\\hline t & 0.7 \\\hline f & 0.2 \\\hline \end{array} \xrightarrow{\begin{array}{c|c}r_3 & P(r_3|r_2) \\\hline t & 0.7 \\\hline f & 0.2 \\\hline \end{array} \xrightarrow{\begin{array}{c|c}r_3 \\\hline t & 0.7 \\\hline \end{array} \xrightarrow{\begin{array}{c|c}r_3 \\\hline \end{array} \end{array}$

4

Stationarity:

 $P(x_{2} | x_{1}) = P(x_{3} | x_{2}) = ... = P(x_{t+1} | x_{t})$

Hidden Markov Model: State information not visible

Using Markov Chain, for Classification

Two classes of DNA... different di-nucleotide distribution

$\pm D($ $\downarrow \downarrow) \pm (V \downarrow V)$	+	А	С	G	Т	_	Α	С	G	Т
$a_{i,j} = P(x_i \mapsto x_j +) = p^+(X_{t+1} = x_j X_t = x_i)$	A	0.180	0.274	0.426	0.120	A	0.300	0.205	0.285	0.210
35	C	0.171	0.368	0.274	0.188	С	0.322	0.298	0.078	0.302
$a^- = D(m + m + m) = m^- (V = m + V = m)$	G	0.161	0.339	0.375	0.125	G	0.248	0.246	0.298	0.208
$a_{i,j} = P(x_i \mapsto x_j -) = p(x_{t+1} = x_j x_t = x_i)$	Т	0.079	0.355	0.384	0.182	Т	0.177	0.239	0.292	0.292

Use this to classify a nucleotide sequence
 x = (ACATTGACCA...)

A: P(x |+) = $p^{+}(x_{1} |) p^{+}(x_{2} | x_{1}) p^{+}(x_{3} | x_{2}) ... p^{+}(x_{k} | x_{k-1}) =$ $\prod_{i=1}^{k} p^{+}(x_{i} | x_{i-1}) = \prod_{i=1}^{k} a^{+}_{x_{i} | x_{i}^{-1}}$ using Markov properties

Using Markov Chain, for Classification

	+	A	C	G	Т			
	A	0.180	0.274	0.426	0.120			
	C	0.171	0.368	0.274	0.188			
\pm $D($ $+$ $) + ($ Y $+$	G	0.161	0.339	0.375	0.125			
$a_{i,j} = P(x_i \mapsto x_j +) = p^+(X_{t+1} = x_j X_t = x_i)$	Т	0.079	0.355	0.384	0.182			
	-	А	С	G	Т			
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i,j	G	0.248	0.246	0.298	0.208			
	Т	0.177	0.239	0.292	0.292			
$- \ln x - /\Lambda C \Lambda T T C \Lambda C C \Lambda T \ln \alpha^2$								
15 X = (ACATIGACCAT) POSITIVE:								

 $P(x | +) = p^{+}(x_{1} |) p^{+}(x_{2} | x_{1}) p^{+}(x_{3} | x_{2}) \dots p^{+}(x_{k} | x_{k-1})$ = p^{+}(A) p^{+}(C | A) p^{+}(A | C) \dots p^{+}(T | A)

 $= 0.25 \times 0.274 \times 0.171 \times ... \times 0.355$

 $P(x \mid -) = p^{-}(x_1 \mid) p^{-}(x_2 \mid x_1) p^{-}(x_3 \mid x_2) \dots p^{-}(x_k \mid x_{k-1})$ = p^{-}(A) p^{-}(C \mid A) p^{-}(A \mid C) \dots p^{-}(T \mid A) = 0.25 \times 0.205 \times 0.322 \times \dots \times 0.239

• Pick larger: + if p(x|+) > p(x|-)

Results (Markov Chain)

•
$$S(x) = \log \frac{P(x|+)}{P(x|-)} = \sum_{i=1}^{k} \log \frac{a_{x_{i-1},x_i}^+}{a_{x_{i-1},x_i}^-} = \sum_{i=1}^{k} \beta_{x_{i-1},x_i}$$

where $eta_{i,j} = \log rac{a_{ij}^+}{a_{ij}^-}$								
β	А	С	G	Т				
Α	-0.740	0.419	0.580	-0.803				
С	-0.913	0.302	1.812	-0.685				
G	-0.624	0.461	0.331	-0.730				
Т	-1.169	0.573	0.393	-0.679				

Results over 48 sequences:



- Here: everything is visible
- Sometimes, can't see the "states"

Phydeaux, the Dog

- Sometimes: *Grumpy* Sometimes: *Happy*
- But hides emotional state...
 Only observations:
 - { slobbers, frowns, yelps }

Known Correlations

- State { G,H } to Observations {s, f, y}
- State { G,H } on day t to state { G,H } on day t+1



Challenge: Given observation sequence: (s, s, f, y, y, f, ...) what were Phydeaux's states? ??

Umbrella+Rain Situation

- State: X_t ∈ { +rain, -rain }
- Observation: $E_t \in \{+umbrella, -umbrella\}$
- Simple Belief Net:



Note: Umbrella_t depends only on Rain_t
 Rain_t depends only on Rain_{t-1}

HMM Tasks



- 1. Filtering / Monitoring: $P(X_t | e_{1:t})$
 - What is $P(R_3 = + | U_1 = +, U_2 = +, U_3 = -)$?
 - Need distr. current state to make rational decisions
- 2. Prediction: P($X_{t+k} | e_{1:t}$)
 - What is $P(R_5 = | U_1 = +, U_2 = +, U_3 = -)$?
 - Use to evaluate possible courses of actions
- 3. Smoothing / Hindsight: P(X_{t-k} | e_{1:t})
 - What is $P(R_1 = | U_1 = +, U_2 = +, U_3 = -)$?
- 4. Likelihood: P(e_{1:t})
 - What is $P(U_1 = +, U_2 = +, U_3 = -)$?
 - For comparing different models ... classification
- 5. Most likely expl'n: argmax_{x1:t} { P(x_{1:t} | e_{1:t}) }
 - Given $\langle U_1 = +, U_2 = +, U_3 = \rangle$, what is most likely value for $\langle R_1, R_2, R_3 \rangle$?
 - Compute assignments, for DNA, sounds, . . .

1. Filtering



- At time 3: have $P(R_2 \mid u_{1:2}) = \langle P(+r_2 \mid ++), P(-r_2 \mid ++) \rangle$... then observe $u_3 = P(R_3 \mid u_{1:3}) = P(R_3 \mid u_{1:2}, u_3)$ $= 1/P(u_{1:3}) P(u_3 \mid R_3, u_{1:2}) P(R_3 \mid u_{1:2})$ $= 1/P(u_{1:3}) P(u_3 \mid R_3) P(R_3 \mid u_{1:2})$
- $P(R_3 | e_{1:2}) = \sum_{r_2} P(R_3, r_2 | e_{1:2})$ = $\sum_{r_2}^{r_2} P(R_3 | r_2, e_{1:2}) P(r_2 | e_{1:2})$ = $\sum_{r_2}^{r_2} P(R_3 | r_2) P(r_2 | e_{1:2})$

1. Filtering $R_0 \rightarrow R_1 \rightarrow R_2 \rightarrow R_3$ $U_1 = + U_2 = + U_3 = -$

• At time t:

- have P(X_t | e_{1:t})
- ... then update from e_{t+1}



Called "Forward Algorithm"

$P(x_{t}, e_{1:t}) vs P(x_{t} | e_{1:t})$

- To compute P($X_t = a | e_{1:t}$): Just compute $\langle P(X_t = 1, e_{1:t}), ..., P(X_t = k, e_{1:t}) \rangle$
- 1. Compute $P(e_{1:t}) = \sum_{i} P(X_{t}=i, e_{1:t})$ 2. Return $P(X_{t}=a \mid e_{1:t})$ $= P(X_{t}=a, e_{1:t}) / P(e_{1:t})$ $= P(X_{t}=a, e_{1:t}) / \sum_{i} P(X_{t}=i, e_{1:t})$
- Normalizing constant: $\alpha = 1/P(e_{1:t})$

Filtering – Forward Algorithm

• Let
$$f_{1:t} = P(X_t | e_{1:t})$$

= $\langle P(X_t = 1 | e_{1:t}), \dots, P(X_t = r | e_{1:t}) \rangle$
 $f_{1:t+1}(X_{t+1}) = P(X_{t+1} | e_{1:t+1})$
= $\alpha P(e_{t+1} | X_{t+1}) \sum_{x_t} P(X_{t+1} | X_t) f_{1:t}(X_t)$

• $f_{1:t+1} = \alpha$ Forward($f_{1:t+1}$, e_{t+1}) Detached!

Update (for discrete state variables):
 Constant time & Constant space!

Filtering Process



Forward() Process

- Given: $P(R_0) = \langle 0.5, 0.5 \rangle$ Evidence $\langle U_1 = +, U_2 = + \rangle$:
- Predict state distribution (before evidence)

 $P(R_1) = \sum_{r_0} P(R_1 | r_0) P(r_0)$ $= \langle 0.7, 0.3 \rangle \times 0.5 + \langle 0.2, 0.8 \rangle \times 0.5 = \langle 0.45, 0.55 \rangle$

- Predict (from t = 1 to t = 2, before new evidence) $P(R_2 | +u_1) = \sum_{r_1} P(R_2 | r_1) P(r_1 | +u_1)$ $= \langle 0.7, 0.3 \rangle 0.786 + \langle 0.2, 0.8 \rangle 0.214 \approx \langle 0.593, 0.407 \rangle$
- Incorporate "Day 2 evidence" $+u_2$: $P(R_2 |+u_1,+u_2) = P(+u_2 |R_2) P(R_2 |+u_1) =$ $\alpha \langle 0.9, 0.2 \rangle .* \langle 0.609, 0.391 \rangle = \alpha \langle 0.533, 0.081 \rangle \approx \langle 0.868, 0.132 \rangle$

HMM Tasks



- 1. Filtering / Monitoring: $P(X_t | e_{1:t})$
 - What is $P(R_3 = + | U_1 = +, U_2 = +, U_3 = -)$?
 - Need distr. current state to make rational decisions
- 2. Prediction: P($X_{t+k} | e_{1:t}$)
 - What is $P(R_5 = | U_1 = +, U_2 = +, U_3 = -)$?
 - Use to evaluate possible courses of actions
- 3. Smoothing / Hindsight: $P(X_{t-k} | e_{1:t})$
 - What is $P(R_1 = | U_1 = +, U_2 = +, U_3 = -)$?
- 4. Likelihood: P(e_{1:t})
 - What is $P(U_1 = +, U_2 = +, U_3 = -)$?
 - For comparing different models ... classification
- 5. Most likely expl'n: argmax_{x1:t} { P(x_{1:t} | e_{1:t}) }
 - Given $\langle U_1 = +, U_2 = +, U_3 = \rangle$, what is most likely value for $\langle R_1, R_2, R_3 \rangle$?
 - Compute assignments, for DNA, sounds, . . .

4. Likelihood



How to compute likelihood P(e_{1:t}) ?

• Let
$$L_{1:t} = P(X_t, e_{1:t})$$

$$\begin{split} \mathbf{L}_{1:t+1} &= \mathsf{P}(\mathsf{X}_{t+1}, \mathsf{e}_{1:t+1}) = \sum_{\mathsf{x}t} \mathsf{P}(\mathsf{x}_{t}, \mathsf{X}_{t+1}, \mathsf{e}_{1:t}, \mathsf{e}_{t+1}) \\ &= \sum_{\mathsf{x}t} \mathsf{P}(\mathsf{e}_{t+1} \mid \mathsf{X}_{t+1}, \mathsf{x}_{t}, \mathsf{e}_{1:t}) \mathsf{P}(\mathsf{X}_{t+1} \mid \mathsf{x}_{t}, \mathsf{e}_{1:t}) \mathsf{P}(\mathsf{x}_{t}, \mathsf{e}_{1:t}) \\ &= \mathsf{P}(\mathsf{e}_{t+1} \mid \mathsf{X}_{t+1}) \sum_{\mathsf{x}t} \mathsf{P}(\mathsf{X}_{t+1} \mid \mathsf{x}_{t}) \mathsf{L}_{1:t}(\mathsf{x}_{t}) \end{split}$$

- Note: Same Forward() algorithm!!
- To compute actual likelihood:

 $P(e_{1:t}) = \sum_{xt} P(X_t = X_t, e_{1:t}) = \sum_{xt} L_{1:t}(X_t)$

Best Model of Phydeaux?



Challenge: Given observation sequence: (s, s, f, y, y, f, ...) which model of Phydeaux is "correct"?? Want P₁(e) vs P₁₁(e)

Use HMMs to Classify Words in Speech Recognition

- Use one HMM for each word
 - *hmm_j* for jth word
- Convert acoustic signal to sequence of fixed duration frames (eg, 60ms)

(Assumes know start/end of each word in speech signal)

 Map each frame to nearest "codebook" frame (discrete symbol x_t)

• $e_{1:T} = \langle e_1, \dots, e_n \rangle$

- To classify sequence of frames e_{1:T}
 - 1. Compute P(e_{1:T} | *hmm_j*) likelihood e_{1:T} generated by each word *hmm_j*
 - 2. Return argmax_j { P(e_{1:T} | hmm_j) } word#j whose hmm_j gave highest likelihood

HMM Tasks



- 1. Filtering / Monitoring: $P(X_t | e_{1:t})$
 - What is $P(R_3 = + | U_1 = +, U_2 = +, U_3 = -)$?
 - Need distr. over current state to make rational decisions
- Prediction: $P(X_{t+k} | e_{1:t})$
 - What is $P(R_5 = | U_1 = +, U_2 = +, U_3 = -)$?
 - Use to evaluate possible courses of actions
- 3. Smoothing / Hindsight: P(X_{t-k} | e_{1:t})
 - What is $P(R_1 = | U_1 = +, U_2 = +, U_3 = -)$?
- 4. Likelihood: P(e_{1:t})
 - What is $P(U_1 = +, U_2 = +, U_3 = -)$?
 - For comparing different models ... classification
- 5. Most likely expl'n: argmax_{x1:t} { P(x_{1:t} | e_{1:t}) }
 - Given $\langle U_1 = +, U_2 = +, U_3 = \rangle$, what is most likely value for $\langle R_1, R_2, R_3 \rangle$?
 - Compute assignments, for DNA, sounds, . . .

2. Prediction



- Already have 1 step prediction
 Prediction (from t = 1 to t = 2, before new evidence)
 - $P(R_2 | +u_1) = \sum_{r_1} P(R_2 | r_1) P(r_1 | +u_1) = ... \approx \langle 0.627, 0.373 \rangle$
- Prediction = filtering w/o incorporating new evidence Using transition info, but not observation info

 $P(X_{t+k+1} | e_{1:t}) = \sum_{xt+k} P(X_{t+k+1} | x_{t+k}) P(x_{t+k} | e_{1:t})$

- Converge to stationary distribution P(Y | e)
 fixed-point: P(Y | e) = ∑_x P(Y | x) P(x | e)
 here < 0.5, 0.5 >
 Mixing time ≈ #steps until reach fixed point
- ⇒ Prediction meaningless unless k ≈ mixing-time More "mixing" in transitions
 ⇒ shorter mixing time, harder to predict future

3. Smoothing / Hindsight

$$R_0 \rightarrow R_1 \rightarrow R_2 \rightarrow R_3 \rightarrow R_4 \rightarrow R_5$$

 $U_1 \qquad U_2 \qquad U_3 \qquad U_4 \qquad U_5$

- Given $\langle +u_1, +u_2, -u_3, +u_4, -u_5 \rangle$, what is best estimate of r_3 ? P(R₃ | +u₁, +u₂, -u₃, +u₄, -u₅)
- Let $f_{1:k} = P(X_k | e_{1:k})$ $b_{k+1:t} = P(e_{k+1:t} | X_k)$ $P(X_k | e_{1:t}) = P(X_k | e_{1:k'} e_{k+1:t})$ $= \alpha P(X_k | e_{1:k}) P(e_{k+1:t} | X_{k'} e_{1:k})$ $= \alpha P(X_k | e_{1:k}) P(e_{k+1:t} | X_k)$ $= \alpha f_{1:k} b_{k+1:t}$
- Recursive computation for f_{1:k} ... go forward: 1, 2, 3, ...,k
- Recursive computation for b_{1:k}...go backward: T, T-1, ..., k+1

Smoothing – Backward Algorithm

$$b_{4:8}(x_3) = P(e_{4:8} | x_3)$$

 $b_{4:8}(x_3) = P(e_{4:8} | x_3)$
 $= \sum_{x4} P(e_{4:8} | x_3, x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_{4:8} | x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_{4:8} | x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_4, e_{5:8} | x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_4 | x_4) P(e_{5:8} | x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_4 | x_4) P(e_{5:8} | x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_4 | x_4) P(e_{5:8} | x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_4 | x_4) P(e_{5:8} | x_4) P(x_4 | x_3)$
 $= \sum_{x4} P(e_4 | x_4) P(e_{5:8} | x_4) P(x_4 | x_3)$

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Smoothing – Backward Algorithm

$$\mathbf{b}_{\mathbf{k+1:t}}(\mathbf{x}_{\mathbf{k}}) = P(e_{\mathbf{k+1:t}} | \mathbf{x}_{\mathbf{k}}) = \sum_{\mathbf{x}\mathbf{k+1}} P(e_{\mathbf{k+1:t}} | \mathbf{x}_{\mathbf{k}}, \mathbf{x}_{\mathbf{k+1}}) P(\mathbf{x}_{\mathbf{k+1}} | \mathbf{x}_{\mathbf{k}}) = \sum_{\mathbf{x}\mathbf{k+1}} P(e_{\mathbf{k+1:t}} | \mathbf{x}_{\mathbf{k+1}}) P(\mathbf{x}_{\mathbf{k+1}} | \mathbf{x}_{\mathbf{k}}) = \sum_{\mathbf{x}\mathbf{k+1}} P(e_{\mathbf{k+1}}, e_{\mathbf{k+2:t}} | \mathbf{x}_{\mathbf{k+1}}) P(\mathbf{x}_{\mathbf{k+1}} | \mathbf{x}_{\mathbf{k}}) = \sum_{\mathbf{x}\mathbf{k+1}} P(e_{\mathbf{k+1}} | \mathbf{x}_{\mathbf{k+1}}) P(e_{\mathbf{k+2:t}} | \mathbf{x}_{\mathbf{k+1}}) P(\mathbf{x}_{\mathbf{k+1}} | \mathbf{x}_{\mathbf{k}}) = \sum_{\mathbf{x}\mathbf{k+1}} P(e_{\mathbf{k+1}} | \mathbf{x}_{\mathbf{k+1}}) P(e_{\mathbf{k+2:t}} | \mathbf{x}_{\mathbf{k+1}}) P(\mathbf{x}_{\mathbf{k+1}} | \mathbf{x}_{\mathbf{k}})$$

- So $b_{k+1:t} = Backward(b_{k+1:t'} e_{k+2:t})$
- Initialize: $b_{t+1:t}(x_t) = P(e_{t+1:t} | x_t) = 1$
- "Forward-Backward Algorithm"
 Just polytree belief net inference!
- Fixed-lag smoothing $\langle P(X_t | e_{1:t+k}) \rangle_t$

5. Most Likely Explanation



- Given (+u₁, +u₂, -u₃, +u₄, +u₅), which is most likely rain-sequence: Perhaps
 - ? $\langle +r_1, +r_2, +r_3, +r_4, +r_5 \rangle$ but forgot on day#3?
 - ? (+r₁, +r₂, -r₃, -r₄, +r₅) but was too cautious on day#4?
 ? ... 2⁵ possibilities !
- ? Idea: Just use "3. Smoothing" ?

Use "Smoothing" for MLE ?

- ? Idea: Use "3. Smoothing" ?
 For i = 1..5
 Compute P(R₁ | u)
 Let r_i* = argmax_r { P(R_i = r | u) }
 Return 〈 r₁*, ..., r₅* 〉
- Wrong! Just local... ignores interactions!
- Eg: Suppose

P($x_{t+1} = 1 | x_t = 0$) = 0.0 [ie, *no* transitions] P($e_t = 1 | x_t = 1$) \gg P($e_t = 0 | x_t = 1$) P($e_t = 0 | x_t = 0$) \gg P($e_t = 1 | x_t = 0$) Given $e = \langle 1, 0, 1 \rangle$, tempting to say $\mathbf{x} = \langle 1, 0, 1 \rangle$... but this has **0** prob of occurring!!

Better: Path through states ... dynamic program

Need to consider ALL States





- Observe $\langle s, f, s \rangle$
- Predict $\langle H, G, H \rangle$
- But O chance of occuring!!
- Only possible sequences:
 - \blacksquare \langle H, H, H \rangle
 - \langle G, G, G \rangle

MLE: Dynamic Program



• Recursively, for each $X_k = x_k$:

compute prob of most likely path to each x_k

• $m_{1:t}(X_t) = \max_{x_{1,...,x_{t-1}}} P(x_{1,...,x_{t-1}}, X_t | e_{1:t})$

 $\mathbf{m}_{1:t+1}(\mathbf{X}_{t+1}) = \max_{x_{1},...,x_{t}} P(x_{1:t}, \mathbf{X}_{t+1} | e_{1:t+1})$ = P(e_1:t+1 | X_{t+1}) max_{xt} [P(X_{t+1} | x_{t}) max_{x_{1}:t-1} P(x_{1:t-1}, x_{t} | e_{1:t})]

= $P(e_{1:t+1} | X_{t+1}) max_{xt} [P(X_{t+1} | x_t) m_{1:t}(x_t)]$

MLE – con't

- $\mathbf{m}_{1:t+1} = \max_{x_{1,...,x_{t}}} P(x_{1:t}, X_{t+1} | e_{1:t+1})$ = P(e_{1:t+1} | X_{t+1}) max_{xt} P(X_{t+1} | x_{t}) m_{1:t}
- Just like *Filtering* except
 - Replace $f_{1:t} = P(X_t | e_{1:t})$ with $m_{1:t} = max_{x1:t-1} P(x_{1:t-1}, X_t | e_{1:t})$
 - Replace \sum_{x_t} with max_{x_t}
- To recover actual optimal-states x^{*}_k keep back-pointers!
- Viterbi Algorithm
- Linear time, linear space

Most Likely Sequence | DNA



Observe only output values

•
$$E_1 = g$$
, $E_2 = c$, $E_3 = c$, $E_4 = t$, $E_5 = a$

Want to determine:

Most likely sequence of STATES

• $X_{1:5} = \langle e e i i i i \rangle$

 $X_1 = e, X_2 = e, X_3 = i, X_4 = i, X_5 = i$ (e for exon, i for intron)

Comments on HMMs

- Results hold for
 - ANY Markov model
 - with arbitrary hidden state
- HMM is special:
 - single discrete state variable
 - *single* discrete observation variable per time $T = P(X_t | X_t)$
- \Rightarrow can use matrices

$$\Gamma = P(X_t | X_{t-1}) = \begin{pmatrix} 0.7 & 0.3 \\ 0.3 & 0.7 \end{pmatrix}$$

$$T_{ij} = P(X_t = j | X_{t-1} = i)$$

 R_2

$$O^{(1)} = \begin{pmatrix} 0.9 & 0.0 \\ 0.0 & 0.2 \end{pmatrix}$$
$$O^{(t)}_{ii} = P(e_t | X_t = i)$$
$$f_{1:t+1} = \alpha O^{t+1} T^{\top} f_{1:t}$$

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Kalman Filters

Tracking a bird in flight, based on (noisy) sensors
 Given observations

("estimates" of its position/velocity) predict its future position, . . .

- X_t = TruePosition @time t
 - \dot{X}_{t} = TrueVelocity @time t
 - Z_t = MeasuredPosition @time t
- Observation model: P($Z_t | X_t$) $Z_t \sim N(X_t, \sigma_t^2)$ Transition model: P($X_{t+1} | X_t, \dot{X}_t$) $X_{t+1} \sim N(X_t + \dot{X}_t, \sigma_t^2)$



Everything stays Gaussian!
 ... for Filtering, Smoothing, ...

Tracking Object in X-Y Plane





Smoothing

Dynamic Belief Network

- At each time slice:
 - description of state
 - description of observation
- If 1 var for state, 1 var for obs
 - \Rightarrow HMM
- But can have > 1 variable for state/observation!





STATE EVOLUTION MODEL

State.t

Percept.t

State.t+

Percept.t-

State.t-

Percept.t-

State.t-2

State.t+2

╶╈┚

Percept.t

Advantage of Dynamic BN





- Why not view DBN as HMM ? ... just "bundle"
 - the observable variables {BMeter, Z} into 1 meganode
 - the latent variables {X, X', Battery} into 1 meganode
- Answer: Spse |X| = 10; |X'| = 10; |Battery| = 10, |BMeter| = 10, |Z| = 10Now:
 - CPtables: Battery \rightarrow Bmeter: 10x10; X \rightarrow Z: 10x10 X', Battery_t \rightarrow Battery_{t+1}: 10x10 x 10; X_t, X'_t \rightarrow X'_{t+1}: 10x10 x 10
 - Total: 2,200 values

As simple HMM:

- CPtable for Transition Probability: 10x10x10 x 10x10x10 = 1M !
- CPtable for Emission Probability: $10x10x10 \times 10x10 = 100K$

Representing State as — GRAPH of Random Variables



... reduces complexity of representing P(X' | X, A) and P(E | X)

Inference in DBNs

 As DBN is Belief Net, can use std BeliefNet Inference alg
 . . . after unrolling



Sums out state variable X_{t-1} corresponds to Variable Elimination (with this temporal ordering of vars)

Actual DBN Algorithm (Filtering)

DBN alg: just keep 2 slices in memory

 $\langle X_{t-1}, e_{t-1} \rangle + \langle X_{t}, e_{t} \rangle$ $f_{1:t+1} = \alpha \text{ Forward}(f_{1:t+1}, e_{t+1})$ (a) Prediction (b) Rollap (b) Rollap

(c) Betimatic

- Constant per-update time, per-update space
- BUT. . .

• as Evidence is CHILDREN, parents become COUPLED! \Rightarrow constant = $O(d^n)$

as factor involves all state variables!

Approximate Algorithms

- Could try. . .
 - likelihood weighting, MCMC, . . .
 - ... but still problems
- Use set of TUPLES themselves as approx'n!
 - Focus on high-probability instances
 - ... tuples ≈ posterior distribution . . .
- Particle Filtering

Draw N tuples, $\{d_1^{(0)}, \ldots, d_N^{(0)}\}$, from $P(X_0)$ For j = 0..Bored For i = 1..NDraw x_i from $P(X_{t+1} | d_i^{(t)})$ Compute weight $w_i = P(e_{t+1} | d_i^{(t+1)})$ Let $\{d_i^{(t+1)}\}_i$ be N tuples drawn from $\{[x_it + 1, w_i]\}_i$

Particle Filtering

Draw N tuples,
$$\{d_1^{(0)}, \ldots, d_N^{(0)}\}$$
, from $P(X_0)$
For $j = 0..$ Bored
For $i = 1..N$
Draw x_i from $P(X_{t+1} | d_i^{(t)})$
Compute weight $w_i = P(e_{t+1} | d_i^{(t+1)})$
Let $\{d_i^{(t+1)}\}_i$ be N tuples drawn from $\{[x_it + 1, w_i]\}_i$



Hierarchical HMMs

- Can construct hierarchy of HMM's:
 - Each Sentence-HMM generates string of word-HMMs (le, each "hidden state" is a possible word)
 - Each word-HMM generates strings of phoneme-HMMs (le, each "hidden state" is a possible phoneme)
 - Each phoneme-HMM generates strings of speech frames
- "Compile" hierarchy into *frame-level HMM* that finds

whole sentence most likely to have been spoken

MLE – computed by Viterbi algorithm

Beyond First-Order

- Recall First-Order Markov Chain
 - Random Walk along x axis,
 - changing x-position 1 at each time



- (Ie, need velocity, as well as position)
- 2nd-order Markov Chain
- [Can make any process into 1st-order Markov,

by expanding state

Eg, to deal with power being consumed,

could have BatteryLevel in state

... in the limit: "state" = "all history"]

Interpolated Markov Model (GLIMMER)





Computational Biology: Find Region of Interest in DNA

Segment DNA into

- Exon vs Intron vs Intergenetic Region
- StartCodon, DonorSite, AcceptorSite, StopCodon
- Techniques: NN, DecisionTrees, HMMs

Identify "motif"

- "Significant Nucleotide Sequence"
- Intron/Exon boundary
- Sites: Promoter, Enhancer,

Transcription factor binding, Splice cite

CRP Binding site (or LexA binding site, or ...)



HMM's in Biological Sequence Data

- Given collection of similar genes

 (eg, same function, but different animals)
 find new genes in other organisms that are similar.
 [Ex: Globins (hemoglobin, myoglobin)]
 Use "4. Likelihood" alg
- Given collection of similar genes, align them to one another (identify where mutations have occurred: insertions, deletions, replacements)
 Useful for studying evolution and discovering functionally important parts
 Use "5. MLE" alg

Simple Hidden Markov Model



- Each box is "state"
- w/prob of "emitting" a letter
 Transition from state to state
 - Bottom Row: standard "emit a letter"
 - Upper Row: insert "extra" letter
 (After state3, 3/5 of sequences goto "Insert"
 Of 5 transitions from "Insert", 2 goto another insert)
- If no gaps, same as earlier model.

Profile HMM



- Special structure: "profile HMM"
- Main (level 0)
 - For "columns" of alignment
- Insert (level 1)
 - For highly-variable regions
- Delete (level 2)
 - "silent" or "null"

Example





[5] Probability of Sequence wrt HMM

• $P_{HMM}(\langle ACACATC \rangle) =$ $P(\text{emit } A \mid M_1) \times P(M_1 \rightarrow M_2) \times$ $P(\text{emit } C \mid M_2) \times P(M_2 \rightarrow M_3) \times$ $P(\text{emit } A \mid M_3) \times P(M_3 \rightarrow I_3) \times$ $P(\text{emit } C \mid I_3) \times P(I_3 \rightarrow M_4) \times$ $P(\text{emit } A \mid M_4) \times P(M_4 \rightarrow M_5) \times$ $P(\text{emit } T \mid M_5) \times P(M_5 \rightarrow M_6) \times$ $P(\text{emit } C \mid M_6)$ $= 0.8 \times 1 \times 0.8 \times 1 \times 0.8 \times 0.6 \times 0.4$ $\times 0.6 \times 1 \times 1 \times 0.8 \times 1 \times 0.8$ $\approx 4.7 \times 10^{-2}$



Here, unambiguous. . . Only consistent path through HMM is (M1, M2, M3, I3, M4, M5, M6) In general, several possible paths. . .

Recent applications of HMMs

- Proteins
 - detection of bronectin type III domains in yeast
 - a database of protein domain families
 - protein topology recognition from secondary structure
 - modeling of a protein splicing domain
- Gene finding
 - detection of short protein coding regions and analysis of translation initiation sites in Cyanobacterium
 - characterization of prokaryotic and eukaryotic promoters
 - recognition of branch points
- Also
 - prediction of protein secondary structure
 - modeling an oscillatory pattern in nucleosomes
 - modeling site dependence of evolutionary rates
 - for including evolutionary information in protein secondary structure prediction
- Free packages:
 - hmmer http://genome.wustl.edu/eddy/hmm.html
 - SAM http://www.cse.ucsc.edu/research/compbio/sam.html

Other Applications

Similar approaches work for analyzing

- Proteins (Amino-Acid sequences)
 - Similar composition, similar function, and . . .
- Protein Folding"
 - Protein sequence of a.a.'s
 - "Tertiary structure" = Complete 3D structure
 - "Secondary structure" = Simpler decomposition α -helices, β -sheets, (random) coil
- TEMPORAL sequences
 - weather prediction
 - stock-market forecasting

Future Research

Scaling up to handle larger {sequences, motifs, DBs }

Learn...

- more accurate descriptions
- in less time (fewer samples, less CPU-time)
- rep'ns that allow more efficient computation
- Exploiting other information
 - facts about a.a.'s (hierarchy?)
 - structural information

Summary

- To model temporal events
 - Use rv X_t to model X at time t
 - Stationary distribution: P(X_t) same at any time
 - Markov Property:

$$\mathsf{P}(\mathsf{X}_{t+1} \mid \mathsf{X}_{t'} \; \mathsf{X}_{t-1'} \; \dots) = \mathsf{P}(\mathsf{X}_{t+1} \mid \mathsf{X}_{t})$$

Hidden Markov Model:

- Emission P(E_t | X_t); Transition P(X_{t+1} | X_t)
- Efficient (linear time!) to predict ...
 - Current state (filtering)
 - Previous state (smoothing)
 - Future state (prediction)
 - Most likely explanation (Viterbi)
- Dynamic Belief Nets extension of HMM ... mixing ...
- Uses: Speech recognition; Tracking; BioInformatics, ...