Hidden Markov Models for Speech Recognition

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Recap: HMMs

- This structure is a generic representation of a statistical model for processes that generate time series.
- The “segments” in the time series are referred to as states.
  - The process passes through these states to generate time series.
- The entire structure may be viewed as one generalization of the DTW models we have discussed thus far.
Hidden Markov Models

- A Hidden Markov Model consists of two components
  - A state/transition backbone that specifies how many states there are, and how they can follow one another
  - A set of probability distributions, one for each state, which specifies the distribution of all vectors in that state

- This can be factored into two separate probabilistic entities
  - A probabilistic Markov chain with states and transitions
  - A set of data probability distributions, associated with the states
Relation to DTW: The transition structure

- The transitions in the HMM have associated probabilities
  - Derived by counting, as we saw earlier

- The transitions in the DTW template have associated penalties
  - $T_{ij} = -\log(P_{ij})$
Relation to DTW: The Node Scores

- States in the HMM have associated state output distributions
  - Typically Gaussian
  - Means and variances are obtained from all the training vectors in the segment associated with the state

- Template Nodes in DTW has an associated node cost function
  - The cost associated with any node is dependent on the observation
  - \( N_i(O) = -\log(P_i(O)) \)

- HMMs: We try to maximize probabilities
  - DTW: Minimize cost
Path Scores: Likelihoods, Log Likelihoods and Costs

- Use probabilities or likelihoods instead of cost
  - Scores combine multiplicatively along a path
  - Path Score = \( P_{11} \cdot P_{12} \cdot P_{22} \cdot P_{23} \cdot P_{33} \cdot P_{23} \)

- Alternately use log probabilities as scores: \( N_i(O) = \log(P_i(O)) \), \( T_{11} = \log(P_{11}) \)
  - Scores add as in DTW
  - Path Score = \( N_1(O_1) + T_{11} + N_1(O_2) + T_{12} + N_2(O_3) + T_{22} + N_2(O_4) + T_{23} + N_3(O_5) + T_{23} \)
    - Replace all “Min” operations in DTW by “Max”

- Alternately use negative log probabilities as cost: \( N_i(O) = \log(P_i(O)) \), \( T_{11} = -\log(P_{11}) \)
  - Cost adds as in DTW
  - Computation remains identical to DTW (with edge costs factored in)
Modelling the process of speech production

• The HMM models the process underlying the observations as going through a number of states
  – For instance, in producing the sound “W”, it first goes through a state where it produces the sound “UH”, then goes into a state where it transitions from “UH” to “AH”, and finally to a state where it produced “AH”

• The true underlying process is the vocal tract here
  – Which roughly goes from the configuration for “UH” to the configuration for “AH”
HMMs are abstractions

- The states are not directly observed
  - Here states of the process are analogous to configurations of the vocal tract that produces the signal
  - We only hear the speech; we do not see the vocal tract
  - i.e. the states are hidden

- The interpretation of states is not always obvious
  - The vocal tract actually goes through a continuum of configurations
  - The model represents all of these using only a fixed number of states

- The model abstracts the process that generates the data
  - The system goes through a finite number of states
  - When in any state it can either remain at that state, or go to another with some probability
  - When at any states it generates observations according to a distribution associated with that state
HMM as a statistical model

- An HMM is a statistical model for a time-varying process
- The process is always in one of a countable number of states at any time
- When the process visits in any state, it generates an observation by a random draw from a distribution associated with that state
- The process constantly moves from state to state. The probability that the process will move to any state is determined solely by the current state
  - i.e. the dynamics of the process are Markovian
- The entire model represents a probability distribution over the sequence of observations
  - It has a specific probability of generating any particular sequence
  - The probabilities of all possible observation sequences sums to 1
How an HMM models a process

HMM assumed to be generating data

state sequence

state distributions

observation sequence
HMM Parameters

• The *topology* of the HMM
  – No. of states and allowed transitions
  – E.g. here we have 3 states and cannot go from the blue state to the red

• The transition probabilities
  – Often represented as a matrix as here
  – $T_{ij}$ is the probability that when in state $i$, the process will move to $j$

• The probability of beginning at a particular state

• The *state output distributions*
**HMM state output distributions**

- The state output distribution represents the distribution of data produced from any state.
- In the previous lecture we assumed the state output distribution to be Gaussian:
  - Albeit largely in a DTW context.

$$P(v) = \text{Gaussian}(v; m, C) = \frac{1}{\sqrt{2\pi|C|}} e^{-0.5(v-m)^T C^{-1}(v-m)}$$

- In reality, the distribution of vectors for any state need not be Gaussian:
  - In the most general case it can be arbitrarily complex.
  - The Gaussian is only a coarse representation of this distribution.

- If we model the output distributions of states better, we can expect the model to be a better representation of the data.
A Gaussian Mixture is literally a mixture of Gaussians. It is a weighted combination of several Gaussian distributions.

\[
P(v) = \sum_{i=0}^{K-1} w_i \text{Gaussian}(v; m_i, C_i)
\]

- \(v\) is any data vector. \(P(v)\) is the probability given to that vector by the Gaussian mixture.
- \(K\) is the number of Gaussians being mixed.
- \(w_i\) is the mixture weight of the \(i^{th}\) Gaussian. \(m_i\) is its mean and \(C_i\) is its covariance.

The Gaussian mixture distribution is also a distribution:
- It is positive everywhere.
- The total volume under a Gaussian mixture is 1.0.
- Constraint: the mixture weights \(w_i\) must all be positive and sum to 1.
Node Score: The Gaussian Distribution

• What does a Gaussian distribution look like?

• For a single (scalar) variable, it is a bell-shaped curve representing the density of data around the mean

• Example:

Four different scalar Gaussian distributions, with different means and variances

The mean is represented by $\mu$, and variance by $\sigma^2$

$\mu$ and $\sigma$ are the parameters of the Gaussian distribution

(Taken from Wikipedia)
The Scalar Gaussian Function

- The Gaussian density function (the bell curve) is:

\[ p(x) = \frac{1}{\sqrt{2\pi \sigma^2}} e^{-\frac{1}{2\sigma^2} (x-\mu)^2} \]

- \( p(x) \) is the density function of the variable \( x \), with mean \( \mu \) and variance \( \sigma^2 \)

- The attraction of the Gaussian function (regardless of how appropriate it is!) comes from how easily the mean and variance can be estimated from sample data \( x_1, x_2, x_3 \ldots x_N \)
  - \( \mu = (\text{Sum } x_i)/N \)
  - \( \sigma^2 = (\text{Sum } (x_i^2 - \mu^2))/N \)
The 2-D Gaussian Distribution

• Speech data are not scalar values, but vectors!
• Needs multi-variate (multi-dimensional) Gaussians
• Figure: A Gaussian for 2-D data
  – Shown as a 3-D plot

• Distributions for higher dimensions are tough to visualize!
The Multidimensional Gaussian Distribution

• Instead of variance, the multidimensional Gaussian has a covariance matrix

• The multi-dimensional Gaussian distribution of a vector variable \( x \) with mean \( \mu \) and covariance \( \Sigma \) is given by:

\[
f(x) = (2\pi)^{-N/2} \det(\Sigma)^{-1/2} \exp\left(-\frac{1}{2}(x - \mu)^T \Sigma^{-1} (x - \mu)\right)
\]

– where \( N \) is the vector dimensionality, and \( \det \) is the determinant function

• The complexity in a full multi-dimensional Gaussian distribution comes from the covariance matrix, which accounts for dependencies between the dimensions
The Diagonal Covariance Matrix

Full covariance: all elements are non-zero

-0.5(x-\mu)^T C^{-1} (x-\mu)

Diagonal covariance: off-diagonal elements are zero

\sum_i (x_i - \mu_i)^2 / 2\sigma_i^2

- In speech recognition, we frequently assume that the feature vector dimensions are all independent of each other

- **Result:** The covariance matrix is reduced to a diagonal form
  - The exponential term becomes, simply:
    \[(\sum_i (x_i - \mu_i)^2 / \sigma_i^2) / 2, \ i\ \text{going over all vector dimensions}\]
  - The determinant of the diagonal \(\Sigma\) matrix is easy to compute

- Further, each \(\sigma_i^2\) (the \(i\)-th diagonal element in the covariance matrix) is easily estimated from \(x_i\) and \(\mu_i\) like a scalar

24 Feb 2010  HMMs
Generating an observation from a Gaussian mixture state distribution

First draw the identity of the Gaussian from the a priori probability distribution of Gaussians (mixture weights)

Then draw a vector from the selected Gaussian
Gaussian Mixtures

- A Gaussian mixture can represent data distributions far better than a simple Gaussian.
- The two panels show the histogram of an unknown random variable.
- The first panel shows how it is modeled by a simple Gaussian.
- The second panel models the histogram by a mixture of two Gaussians.
- Caveat: It is hard to know the optimal number of Gaussians in a mixture distribution for any random variable.
HMMs with Gaussian mixture state distributions

• The parameters of an HMM with Gaussian mixture state distributions are:
  – $\pi$ the set of initial state probabilities for all states
  – $T$ the matrix of transition probabilities
  – A Gaussian mixture distribution for every state in the HMM. The Gaussian mixture for the $i^{th}$ state is characterized by
    • $K_i$, the number of Gaussians in the mixture for the $i^{th}$ state
    • The set of mixture weights $w_{i,j}$  $0 < j < K_i$
    • The set of Gaussian means $m_{i,j}$  $0 < j < K_i$
    • The set of Covariance matrices $C_{i,j}$  $0 < j < K_i$
Three Basic HMM Problems

• Given an HMM:
  – What is the probability that it will generate a specific observation sequence
  – Given a observation sequence, how do we determine which observation was generated from which state
    • The state segmentation problem
  – How do we *learn* the parameters of the HMM from observation sequences
Computing the Probability of an Observation Sequence

• Two aspects to producing the observation:
  – Precessing through a sequence of states
  – Producing observations from these states
Precessing through states

HMM assumed to be generating data

state sequence

- The process begins at some state (red) here
- From that state, it makes an allowed transition
  - To arrive at the same or any other state
- From that state it makes another allowed transition
  - And so on

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HMMs
Probability that the HMM will follow a particular state sequence

\[ P(s_1, s_2, s_3, \ldots) = P(s_1) P(s_2 | s_1) P(s_3 | s_2) \ldots \]

- \( P(s_1) \) is the probability that the process will initially be in state \( s_1 \)
- \( P(s_i | s_i) \) is the transition probability of moving to state \( s_i \) at the next time instant when the system is currently in \( s_i \)
  - Also denoted by \( P_{ij} \) earlier
  - Related to edge scores in DTW as \( T_{ij} = -\log(P(s_i | s_i)) \)
Generating Observations from States

HMM assumed to be generating data

- At each time it generates an observation from the state it is in at that time
Probability that the HMM will generate a particular observation sequence given a state sequence \((\text{state sequence known})\)

\[
P(o_1,o_2,o_3,...|s_1,s_2,s_3,...) = P(o_1|s_1)P(o_2|s_2)P(o_3|s_3)...
\]

Computed from the Gaussian or Gaussian mixture for state \(s_1\)

- \(P(o_i|s_i)\) is the probability of generating observation \(o_i\) when the system is in state \(s_i\)
  - Related to node scores in DTW trellis as:
    \[N_i(O) = -\log(P(o_i|s_i))\]

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Precessing through States and Producing Observations

HMM assumed to be generating data

- At each time it produces an observation and makes a transition
Probability that the HMM will generate a particular state sequence and from it, a particular observation sequence

\[ P(o_1, o_2, o_3, \ldots, s_1, s_2, s_3, \ldots) = \]
\[ P(o_1, o_2, o_3, \ldots | s_1, s_2, s_3, \ldots) P(s_1, s_2, s_3, \ldots) = \]
\[ P(o_1 | s_1) P(o_2 | s_2) P(o_3 | s_3) \ldots P(s_1) P(s_2 | s_1) P(s_3 | s_2) \ldots \]
Probability of Generating an Observation Sequence

• If only the observation is known, the precise state sequence followed to produce it is not known
• All possible state sequences must be considered

\[
P(o_1, o_2, o_3, \ldots) = \sum_{\text{all possible state sequences}} P(o_1, o_2, o_3, \ldots, s_1, s_2, s_3, \ldots) =
\]

\[
\sum_{\text{all possible state sequences}} P(o_1 | s_1) P(o_2 | s_2) P(o_3 | s_3) \ldots P(s_1) P(s_2 | s_1) P(s_3 | s_2) \ldots
\]
Computing it Efficiently

• Explicit summing over all state sequences is not efficient
  – A very large number of possible state sequences
  – For long observation sequences it may be intractable

• Fortunately, we have an efficient algorithm for this: The forward algorithm

• At each time, for each state compute the total probability of all state sequences that generate observations until that time and end at that state
Consider a generic HMM with 5 states and a “terminating state”. We wish to find the probability of the best state sequence for an observation sequence assuming it was generated by this HMM

- \( P(s_i) = 1 \) for state 1 and 0 for others
- The arrows represent transition for which the probability is not 0. \( P(s_i \mid s_j) = a_{ij} \)
- We sometimes also represent the state output probability of \( s_i \) as \( P(o_t \mid s_i) = b_i(t) \) for brevity
The trellis is a graphical representation of all possible paths through the HMM to produce a given observation

- Analogous to the DTW search graph / trellis

- The Y-axis represents HMM states, X axis represents observations
- Every edge in the graph represents a valid transition in the HMM over a single time step
- Every node represents the event of a particular observation being generated from a particular state
The Forward Algorithm

$$\alpha_u(s,t) = P(x_{u,1}, x_{u,2}, \ldots, x_{u,t}, state(t) = s | \lambda)$$

\[\square\] \(\alpha_u(s,t)\) is the total probability of ALL state sequences that end at state \(s\) at time \(t\), and all observations until \(x_t\)
The Forward Algorithm

\[ \alpha_u(s,t) = P(x_{u,1}, x_{u,2}, \ldots, x_{u,t}, \text{state}(t) = s | \lambda) \]

Can be recursively estimated starting from the first time instant (forward recursion)

\[ \alpha_u(s,t) = \sum_{s'} \alpha_u(s', t-1)P(s'|s')P(x_{u,t} | s) \]

\( \alpha_u(s,t) \) can be recursively computed in terms of \( \alpha_u(s', t') \), the forward probabilities at time \( t-1 \)
The Forward Algorithm

\[ \text{Totalprob} = \sum_{s} \alpha_u(s, T) \]

- In the final observation the alpha at each state gives the probability of all state sequences ending at that state.
- The total probability of the observation is the sum of the alpha values at all states.

HMMs

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Problem 2: The state segmentation problem

- Given only a sequence of observations, how do we determine which sequence of states was followed in producing it?
The HMM as a generator

- The process goes through a series of states and produces observations from them.
States are Hidden

HMM assumed to be generating data

- The observations do not reveal the underlying state

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HMMs
The state segmentation problem

HMM assumed to be generating data

• State segmentation: Estimate state sequence given observations

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Estimating the State Sequence

• Any number of state sequences could have been traversed in producing the observation
  – In the worst case every state sequence may have produced it

• Solution: Identify the most probable state sequence
  – The state sequence for which the probability of progressing through that sequence and generating the observation sequence is maximum
  – i.e. \[ P(o_1, o_2, o_3, ..., s_1, s_2, s_3, ...) \] is maximum
Estimating the state sequence

• Once again, exhaustive evaluation is impossibly expensive

• But once again a simple dynamic-programming solution is available

\[
P(o_1, o_2, o_3, \ldots, s_1, s_2, s_3, \ldots) = \\
P(o_1 | s_1) P(o_2 | s_2) P(o_3 | s_3) \ldots P(s_1) P(s_2 | s_1) P(s_3 | s_2) \ldots
\]

• Needed:

\[
\arg \max_{s_1, s_2, s_3, \ldots} P(o_1 | s_1) P(s_1) P(o_2 | s_2) P(s_2 | s_1) P(o_3 | s_3) P(s_3 | s_2)
\]
Estimating the state sequence

- Once again, exhaustive evaluation is impossibly expensive
- But once again a simple dynamic-programming solution is available

\[
P(o_1, o_2, o_3, \ldots, s_1, s_2, s_3, \ldots) = \\
P(o_1|s_1)P(o_2|s_2)P(o_3|s_3)\ldots P(s_1)P(s_2|s_1)P(s_3|s_2)\ldots
\]

- Needed:

\[
\arg \max_{s_1, s_2, s_3, \ldots} P(o_1|s_1)P(s_1)P(o_2|s_2)P(s_2|s_1)P(o_3|s_3)P(s_3|s_2)
\]
The state sequence

- The probability of a state sequence ?,?,?,?,?,,sx, sy ending at time t is simply
  \[ P(?,?,?,?,?, sx, sy) = P(?,?,?,?, sx) \cdot P(o_t|s_y) \cdot P(s_y|s_x) \]

- The best state sequence that ends with sx, sy at t will have a probability equal to the probability of the best state sequence ending at t-1 at sx times
  \[ P(o_t|s_y) \cdot P(s_y|s_x) \]
  - Since the last term is independent of the state sequence leading to sx at t-1
**Trellis**

- The graph below shows the set of all possible state sequences through this HMM in five time instants.
The cost of extending a state sequence

- The cost of extending a state sequence ending at \( s_x \) is only dependent on the transition from \( s_x \) to \( s_y \), and the observation probability at \( s_y \).
The cost of extending a state sequence

- The best path to $s_y$ through $s_x$ is simply an extension of the best path to $s_x$
The Recursion

• The overall best path to $s_x$ is an extension of the best path to one of the states at the previous time.
The Recursion

- Bestpath prob(s_y,t) = Best (Bestpath prob(s?,t) * P(s_y | s?) * P(o_t|s_y))
Finding the best state sequence

• This gives us a simple recursive formulation to find the overall best state sequence:

1. The best state sequence \( X_{1,i} \) of length 1 ending at state \( s_i \) is simply \( s_i \).
   – The probability \( C(X_{1,i}) \) of \( X_{1,i} \) is \( P(o_1 \mid s_i) P(s_i) \)

2. The best state sequence of length \( t+1 \) is simply given by
   – \( \text{argmax}_{X_{t,i}} C(X_{t,i}) P(o_{t+1} \mid s_j) P(s_j \mid s_i) \) \( s_i \)

3. The best overall state sequence for an utterance of length \( T \) is given by
   \[ \text{argmax}_{X_{t,i}} C(X_{T,i}) \]
   – The state sequence of length \( T \) with the highest overall probability
Finding the best state sequence

- The simple algorithm just presented is called the VITERBI algorithm in the literature
  - After A.J. Viterbi, who invented this dynamic programming algorithm for a completely different purpose: decoding error correction codes!

- The Viterbi algorithm can also be viewed as a breadth-first graph search algorithm
  - The HMM forms the Y axis of a 2-D plane
    - Edge costs of this graph are transition probabilities $P(s|s)$. Node costs are $P(o|s)$
    - A linear graph with every node at a time step forms the X axis
    - A trellis is a graph formed as the crossproduct of these two graphs
    - The Viterbi algorithm finds the best path through this graph
Viterbi Search (contd.)

Initial state initialized with path-score $= P(s_1) b_1(1)$

All other states have score 0 since $P(s_i) = 0$ for them
Viterbi Search (contd.)

\[ P_j(t) = \max_i [P_i(t-1) a_{ij} b_j(t)] \]

- State with best path-score
- State with path-score < best
- State without a valid path-score

State transition probability, \( i \) to \( j \)

Score for state \( j \), given the input at time \( t \)

Total path-score ending up at state \( j \) at time \( t \)
Viterbi Search (contd.)

\[ P_j(t) = \max_i [P_i(t-1) a_{ij} b_j(t)] \]

State transition probability, \( i \) to \( j \)

Score for state \( j \), given the input at time \( t \)

Total path-score ending up at state \( j \) at time \( t \)
Viterbi Search (contd.)
Viterbi Search (contd.)

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Viterbi Search (contd.)

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Viterbi Search (contd.)
Viterbi Search (contd.)

THE BEST STATE SEQUENCE IS THE ESTIMATE OF THE STATE SEQUENCE FOLLOWED IN GENERATING THE OBSERVATION
Viterbi and DTW

- The Viterbi algorithm is identical to the string-matching procedure used for DTW that we saw earlier.

- It computes an estimate of the state sequence followed in producing the observation.

- *It also gives us the probability of the best state sequence*.
Problem 3: Training HMM parameters

• We can compute the probability of an observation, and the best state sequence given an observation, using the HMM’s parameters

• But where do the HMM parameters come from?

• They must be learned from a collection of observation sequences

• We have already seen one technique for training HMMs: The segmental K-means procedure
Modified segmental K-means AKA Viterbi training

- The entire segmental K-means algorithm:
  1. Initialize all parameters
     - State means and covariances
     - Transition probabilities
     - Initial state probabilities
  2. Segment all training sequences
  3. Reestimate parameters from segmented training sequences
  4. If not converged, return to 2
Segmental K-means

The procedure can be continued until convergence

Convergence is achieved when the total best-alignment error for all training sequences does not change significantly with further refinement of the model.
A Better Technique

• The Segmental K-means technique uniquely assigns each observation to one state
• However, this is only an estimate and may be wrong
• A better approach is to take a “soft” decision
  – Assign each observation to every state with a probability
Training by segmentation: Hard Assignment

\[ \mu_j = \frac{1}{\sum_{i \in \text{segment}(j)} 1} \sum_{i \in \text{segment}(j)} x_i \]

Each vector belongs uniquely to a segment
Training by segmentation: Soft Assignment

\[
\mu_j = \frac{1}{\sum f_{i,j} \sum_{i \in \text{All vectors}}} \sum_{i \in \text{All vectors}} f_{i,j} x_i
\]

\[
\sum f_{i,j} = 1
\]

Assignment is *fractioned*:
Every segment gets a piece of every vector

Means and variances are computed from fractioned vectors

Where do the fractions come from?
The “probability” of a state

• The probability assigned to any state $s$, for any observation $x_t$ is the probability that the process was at $s$ when it generated $x_t$

• We want to compute

$$P(\text{state}(t) = s \mid x_1, x_2, \ldots, x_T) \propto P(\text{state}(t) = s, x_1, x_2, \ldots, x_T)$$

• We will compute $P(\text{state}(t) = s, x_1, x_2, \ldots, x_T)$ first

  – This is the probability that the process visited $s$ at time $t$ while producing the entire observation
Probability of Assigning an Observation to a State

- The probability that the HMM was in a particular state $s$ when generating the observation sequence is the probability that it followed a state sequence that passed through $s$ at time $t$. 

![Diagram of HMM transitions](image)
Probability of Assigning an Observation to a State

- This can be decomposed into two multiplicative sections
  - The section of the lattice leading into state $s$ at time $t$ and the section leading out of it
Probability of Assigning an Observation to a State

- The probability of the red section is the total probability of all state sequences ending at state $s$ at time $t$
  - This is simply $\alpha(s,t)$
  - Can be computed using the forward algorithm

![Diagram of state transitions]
The forward algorithm

\[ \alpha_u(s, t) = P(x_{u,1}, x_{u,2}, \ldots, x_{u,t}, \text{state}(t) = s | \lambda) \]

Can be recursively estimated starting from the first time instant (forward recursion)

\[ \alpha_u(s, t) = \sum_{s'} \alpha_u(s', t - 1) P(s | s') P(x_{u,t} | s) \]

\( \lambda \) represents the complete current set of HMM parameters
The Future Paths

• The blue portion represents the probability of all state sequences that began at state $s$ at time $t$
  – Like the red portion it can be computed using a *backward recursion*
The Backward Recursion

\[ \beta_u(s, t) = P(x_{u,t+1}, x_{u,t+2}, \ldots, x_{u,T} | state(t) = s, \lambda) \]

\[ \beta_u(s, t) = \sum_{s'} \beta_u(s', t + 1)P(s' | s)P(x_{u,t+1} | s') \]

- \( \beta_u(s,t) \) is the total probability of ALL state sequences that depart from \( s \) at time \( t \), and all observations after \( x_t \)
- \( \beta(s,T) = 1 \) at the final time instant for all valid final states

Can be recursively estimated starting from the final time time instant (backward recursion)
The complete probability

\[ \alpha_u(s, t) \beta_u(s, t) = P(x_{u,1}, x_{u,2}, \ldots, x_{u,T}, \text{state}(t) = s | \lambda) \]

\[ = P(X_u, \text{state}(t) = s | \lambda) \]
Posterior probability of a state

• The probability that the process was in state $s$ at time $t$, given that we have observed the data is obtained by simple normalization

$$P(\text{state}(t) = s | \mathbf{X}_u, \lambda) = \frac{P(\mathbf{X}_u, \text{state}(t) = s | \lambda)}{\sum_{s'} P(\mathbf{X}_u, \text{state}(t) = s' | \lambda)} = \frac{\alpha_u(s,t) \beta_u(s,t)}{\sum_{s'} \alpha_u(s',t) \beta_u(s',t)}$$

• This term is often referred to as the gamma term and denoted by $\gamma_{s,t}$
Update Rules

• Once we have the state probabilities (the gammas) the update rules are obtained through a simple modification of the formulae used for segmental K-means
  – This new learning algorithm is known as the Baum-Welch learning procedure

• Case 1: State output densities are Gaussians
Update Rules

\[ \mu_s = \frac{1}{N_s} \sum_{x \in s} x \]

\[ C_s = \frac{1}{N_s} \sum_{x \in s} (x - \mu_s)^T (x - \mu_s) \]

Segmental K-means

Baum Welch

- A similar update formula reestimates transition probabilities
- The initial state probabilities \( P(s) \) also have a similar update rule

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HMMs
Case 2: State output densities are Gaussian Mixtures

- When state output densities are Gaussian mixtures, more parameters must be estimated

\[ P(x \mid s) = \sum_{i=0}^{K-1} w_{s,i} \text{Gaussian}(x; \mu_{s,i}, C_{s,i}) \]

- The mixture weights \( w_{s,i} \), mean \( \mu_{s,i} \) and covariance \( C_{s,i} \) of every Gaussian in the distribution of each state must be estimated
Splitting the Gamma

We split the gamma for any state among all the Gaussians at that state

A posteriori probability that the \( t^{th} \) vector was generated by the \( k^{th} \) Gaussian of state \( s \)

\[
\gamma_{k,s,u,t} = P(state(t) = s|X_u, \lambda)P(k^{th}. Gaussian|state(t) = s, x_{u,t}, \lambda)
\]
Splitting the Gamma among Gaussians

A posteriori probability that the $t^{th}$ vector was generated by the $k^{th}$ Gaussian of state $s$

$$\gamma_{k,s,u,t} = P(state(t) = s|X_u, \lambda) P(k^{th} Gaussian|state(t) = s, x_{u,t}, \lambda)$$

$$\gamma_{k,s,u,t} = P(state(t) = s|X_u, \lambda) \frac{w_{k,s}}{\sqrt{(2\pi)^d |C_k|}} e^{-\frac{1}{2}(x_{u,t} - \mu_{k,s})^T C_k^{-1} (x_{u,t} - \mu_{k,s})}$$

$$\sum_{k'} w_{k',s} \frac{1}{\sqrt{(2\pi)^d |C_{k',s}|}} e^{-\frac{1}{2}(x_{u,t} - \mu_{k',s})^T C_k^{-1} (x_{u,t} - \mu_{k',s})}$$
Updating HMM Parameters

\[ \tilde{\mu}_{k,s} = \frac{\sum_u \sum_t \gamma_{k,s,u,t} x_{u,t}}{\sum_u \sum_t \gamma_{k,s,u,t}} \]

\[ \tilde{C}_{k,s} = \frac{\sum_u \sum_t \gamma_{k,s,u,t} (x_{u,t} - \tilde{\mu}_{k,s}) (x_{u,t} - \tilde{\mu}_{k,s})^T}{\sum_u \sum_t \gamma_{k,s,u,t}} \]

\[ \tilde{\nu}_{k,s} = \frac{\sum_u \sum_t \sum_j \gamma_{j,s,u,t}}{\sum_u \sum_t \sum_j \gamma_{j,s,u,t}} \]

- Note: Every observation contributes to the update of parameter values of every Gaussian of every state
Overall Training Procedure: Single Gaussian PDF

• Determine a topology for the HMM
• Initialize all HMM parameters
  – Initialize all allowed transitions to have the same probability
  – Initialize all state output densities to be Gaussians
    • We’ll revisit initialization

1. Over all utterances, compute the “sufficient” statistics

\[
\sum_u \sum_t \gamma_{s,u,t} \sum_u \sum_t \gamma_{s,u,t} x_{u,t} \sum_u \sum_t \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s)
\]

2. Use update formulae to compute new HMM parameters

3. If the overall probability of the training data has not converged, return to step 1
An Implementational Detail

• Step1 computes “buffers” over all utterance

\[
\sum_{u} \sum_{t} \gamma_{s,u,t} = \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} + \ldots
\]

\[
\sum_{u} \sum_{t} \gamma_{s,u,t} x_{u,t} = \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} x_{u,t} + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} x_{u,t} + \ldots
\]

\[
\sum_{u} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s) = \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s) + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s) + \ldots
\]

• This can be split and parallelized
  – U_1, U_2 etc. can be processed on separate machines

Machine 1
\[
\sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} + \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} x_{u,t} + \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s)
\]

Machine 2
\[
\sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} x_{u,t} + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s)
\]

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An Implementational Detail

- Step 2 aggregates and adds buffers before updating the models.

\[
\sum_{u} \sum_{t} \gamma_{s,u,t} = \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} + \ldots
\]

\[
\sum_{u} \sum_{t} \gamma_{s,u,t} \mathbf{x}_{u,t} = \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} \mathbf{x}_{u,t} + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} \mathbf{x}_{u,t} + \ldots
\]

\[
\sum_{u} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s) = \sum_{u \in U_1} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s) + \sum_{u \in U_2} \sum_{t} \gamma_{s,u,t} (x - \mu_s)^T (x - \mu_s) + \ldots
\]

\[
\tilde{\mu}_{k,s} = \frac{\sum_{u} \sum_{t} \gamma_{k,s,u,t} \mathbf{x}_{u,t}}{\sum_{u} \sum_{t} \gamma_{k,s,u,t}}
\]

\[
\tilde{C}_{k,s} = \frac{\sum_{u} \sum_{t} \gamma_{k,s,u,t} (\mathbf{x}_{u,t} - \tilde{\mu}_{k,s})(\mathbf{x}_{u,t} - \tilde{\mu}_{k,s})^T}{\sum_{u} \sum_{t} \gamma_{k,s,u,t}}
\]

\[
\tilde{W}_{k,s} = \frac{\sum_{u} \sum_{t} \gamma_{k,s,u,t}}{\sum_{u} \sum_{t} \sum_{j} \gamma_{j,s,u,t}}
\]
An Implementational Detail

- **Step2 aggregates and adds** buffers before updating the models.

\[
\sum_u \sum_t \gamma_{s,u,t} = \sum_{u \in U_1} \sum_t \gamma_{s,u,t} + \sum_{u \in U_2} \sum_t \gamma_{s,u,t} + \ldots
\]

\[
\sum_u \sum_t \gamma_{s,u,t} x_{u,t} = \sum_{u \in U_1} \sum_t \gamma_{s,u,t} x_{u,t} + \sum_{u \in U_2} \sum_t \gamma_{s,u,t} x_{u,t} + \ldots
\]

\[
\sum_u \sum_t \gamma_{s,u,t} (x - \mu_s) (x - \mu_s)^T = \sum_{u \in U_1} \sum_t \gamma_{s,u,t} (x - \mu_s) (x - \mu_s)^T + \sum_{u \in U_2} \sum_t \gamma_{s,u,t} (x - \mu_s) (x - \mu_s)^T + \ldots
\]

\[
\tilde{\mu}_{k,s} = \frac{\sum_u \sum_t \gamma_{k,s,u,t} x_{u,t}}{\sum_u \sum_t \gamma_{k,s,u,t}}
\]

\[
\tilde{C}_{k,s} = \frac{\sum_u \sum_t \gamma_{k,s,u,t} (x_{u,t} - \tilde{\mu}_{k,s}) (x_{u,t} - \tilde{\mu}_{k,s})^T}{\sum_u \sum_t \gamma_{k,s,u,t}}
\]

\[
\tilde{W}_{k,s} = \frac{\sum_u \sum_t \gamma_{k,s,u,t}}{\sum_u \sum_t \sum_j \gamma_{j,s,u,t}}
\]

Computed by machine 1

Computed by machine 2

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HMMs
Training for HMMs with *Gaussian Mixture* State Output Distributions

- Gaussian *Mixtures* are obtained by splitting
  1. Train an HMM with (single) Gaussian state output distributions
  2. Split the Gaussian with the largest variance
     - Perturb the mean by adding and subtracting a small number
     - This gives us 2 Gaussians. Partition the mixture weight of the Gaussian into two halves, one for each Gaussian
     - A mixture with N Gaussians now becomes a mixture of N+1 Gaussians
  3. Iterate BW to convergence
  4. If the desired number of Gaussians not obtained, return to 2

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Splitting a Gaussian

- The mixture weight $w$ for the Gaussian gets shared as $0.5w$ by each of the two split Gaussians
Implementation of BW: underflow

- Arithmetic underflow is a problem
  \[
  \alpha_u(s,t) = \sum_{s'} \alpha_u(s',t-1)P(s|s')P(x_{u,t}|s)
  \]
  - The alpha terms are a recursive product of probability terms
    - As \( t \) increases, an increasingly greater number probability terms are factored into the alpha
  - All probability terms are less than 1
    - State output probabilities are actually probability densities
    - Probability density values \( can \) be greater than 1
    - On the other hand, for large dimensional data, probability density values are usually \( much \) less than 1
  - With increasing time, alpha values decrease
  - Within a few time instants, they underflow to 0
    - Every alpha goes to 0 at some time \( t \). All future alphas remain 0
    - As the dimensionality of the data increases, alphas goes to 0 faster

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HMMs
Underflow: Solution

• One method of avoiding underflow is to scale all alphas at each time instant
  
  – Scale with respect to the largest alpha to make sure the largest scaled alpha is 1.0
  
  – Scale with respect to the sum of the alphas to ensure that all alphas sum to 1.0
  
  – Scaling constants must be appropriately considered when computing the final probabilities of an observation sequence
Implementation of BW: underflow

• Similarly, arithmetic underflow can occur during beta computation

\[ \beta_u(s, t) = \sum_{s'} \beta_u(s', t+1) \log P(s' \mid s) P(x_{u,t+1} \mid s') \]

• The beta terms are also a recursive product of probability terms and can underflow

• Underflow can be prevented by
  – Scaling: Divide all beta terms by a constant that prevents underflow
  – By performing beta computation in the log domain
Implementation of BW: pruning

- The forward backward computation can get very expensive
- Solution: Prune
- Pruning in the forward backward algorithm raises some additional issues
  - Pruning from forward pass can be employed by backward pass
  - Convergence criteria and tests may be affected
  - More later
Building a recognizer for isolated words

• Now have all necessary components to build an HMM-based recognizer for isolated words
  – Where each word is spoken by itself in isolation
  – E.g. a simple application, where one may either say “Yes” or “No” to a recognizer and it must recognize what was said
Isolated Word Recognition with HMMs

• Assuming all words are equally likely

• Training
  – Collect a set of “training” recordings for each word
  – Compute feature vector sequences for the words
  – Train HMMs for each word

• Recognition:
  – Compute feature vector sequence for test utterance
  – Compute the forward probability of the feature vector sequence from the HMM for each word
    • Alternately compute the best state sequence probability using Viterbi
  – Select the word for which this value is highest
Issues

• What is the topology to use for the HMMs
  – How many states
  – What kind of transition structure
  – If state output densities have Gaussian Mixtures: how many Gaussians?
HMM Topology

• For speech a left-to-right topology works best
  – The “Bakis” topology
  – Note that the initial state probability \( P(s) \) is 1 for the 1\(^{st} \) state and 0 for others. This need not be learned

• States may be skipped
Determining the Number of States

• How do we know the number of states to use for any word?
  – We do not, really
  – Ideally there should be at least one state for each “basic sound” within the word
    • Otherwise widely differing sounds may be collapsed into one state
    • The average feature vector for that state would be a poor representation

• For computational efficiency, the number of states should be small
  – These two are conflicting requirements, usually solved by making some educated guesses
Determining the Number of States

• For small vocabularies, it is possible to examine each word in detail and arrive at reasonable numbers:

  ![Diagram of HMM states](image_url)

  S O M E T H I N G

• For larger vocabularies, we may be forced to rely on some *ad hoc* principles
  – *E.g.* proportional to the number of letters in the word
    • Works better for some languages than others
    • Spanish and Indian languages are good examples where this works as almost every letter in a word produces a sound
How many Gaussians

• No clear answer for this either
• The number of Gaussians is usually a function of the amount of training data available
  – Often set by trial and error
  – A minimum of 4 Gaussians is usually required for reasonable recognition
Implementation of BW: initialization of alphas and betas

• Initialization for alpha: $$\alpha_u(s,1)$$ set to 0 for all states except the first state of the model. $$\alpha_u(s,1)$$ set to 1 for the first state
  – All observations must begin at the first state

• Initialization for beta: $$\beta_u(s, T)$$ set to 0 for all states except the terminating state. $$\beta_u(s, t)$$ set to 1 for this state
  – All observations must terminate at the final state
Initializing State Output Density Parameters

1. Initially only a single Gaussian per state assumed
   • Mixtures obtained by splitting Gaussians

2. For Bakis-topology HMMs, a good initialization is the “flat” initialization
   • Compute the *global* mean and variance of all feature vectors in all training instances of the word
   • Initialize *all Gaussians* (i.e., all state output distributions) with this mean and variance
   • Their means and variances will converge to appropriate values automatically with iteration
   • Gaussian splitting to compute Gaussian mixtures takes care of the rest
Isolated word recognition: Final thoughts

• All relevant topics covered
  – How to compute features from recordings of the words
    • We will not explicitly refer to feature computation in future lectures
  – How to set HMM topologies for the words
  – How to train HMMs for the words
    • Baum-Welch algorithm
  – How to select the most probable HMM for a test instance
    • Computing probabilities using the forward algorithm
    • Computing probabilities using the Viterbi algorithm
      – Which also gives the state segmentation
Questions

• ?