HOW DOES A DICTATION MACHINE RECOGNIZE SPEECH?

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Chapter 4

How does a dictation machine recognize speech?

This Chapter is not about how to wreck a nice beach[45]

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There is magic (or is it witchcraft?) in a speech recognizer that transcribes continuous radio speech into text with a word accuracy of even not more than 50%. The extreme difficulty of this task, tough, is usually not perceived by the general public. This is because we are almost deaf to the infinite acoustic variations that accompany the production of vocal sounds, which arise from physiological constraints (co-articulation), but also from the acoustic environment (additive or convolutional noise, Lombard effect), or from the emotional state of the speaker (voice quality, speaking rate, hesitations, etc.)[46]. Our consciousness of speech is indeed not stimulated until after it has been processed by our brain to make it appear as a sequence of meaningful units: phonemes and words.

In this Chapter we will see how statistical pattern recognition and statistical sequence recognition techniques are currently used for trying to mimic this extraordinary faculty of our mind (4.1). We will follow, in Section 4.2, with a MATLAB-based proof of concept of word-based automatic speech recognition (ASR) based on Hidden Markov Models (HMM), using a bigram model for modeling (syntactic-semantic) language constraints.

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[45] It is, indeed, about *how to recognize speech*.
[46] Not to mention inter-speaker variability, nor regional dialects.

4.1 Background – Statistical Pattern Recognition

Most modern ASR systems have a pipe-line block architecture (see Fig. 4.1).

   The acoustical wave is first digitized, usually with a sampling frequency of 8 kHz for telephone applications and 16 kHz for multimedia applications. A *speech detection* module then detects segments of speech activity in the digital signal: only these segments that compose the speech signal are transmitted to the following block. The purpose of speech detection is to reduce the computational cost and the probability of ASR error when unexpected acoustic events happen. Doing this automatically, however, is by itself a difficult problem. Speech detection is sometimes implemented manually: the speaker is asked to push a button while speaking in order to activate the ASR system (*push-to-talk* mode).
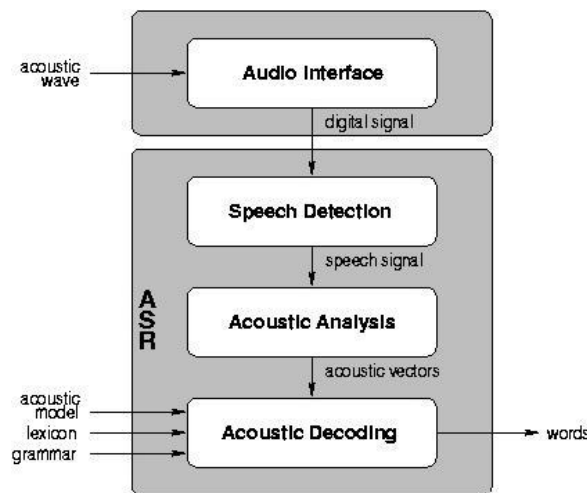
Fig. 4.1 Classical architecture of an automatic speech recognition system

   The *acoustical analysis* module processes the speech signal in order to reduce its variability while preserving its linguistic information. A time-frequency analysis is typically performed (using frame-based analysis, with 30 ms frames shifted every 10 ms), which transforms the continuous input waveform into a sequence $X = [x(1), x(2), \ldots , x(N)]$ of *acoustic*

feature vectors x(n)[47]. The performances of ASR systems (in particular, their *robustness*, i.e. their resistance to noise) are very much dependent on this formatting of the acoustic observations. Various types of feature vectors can be used, such as the LPC coefficients described in Chapter 1, although specific feature vectors, such as the Linear Prediction Cepstral Coefficients (LPCC) or the Mel Frequency Cepstral Coefficients (MFCC; Picone 1993), have been developed in practice for speech recognition, which are somehow related to LPC coefficients.

   The *acoustic decoding* module is the heart of the ASR system. During a training phase, the ASR system is presented with several examples of every possible word, as defined by the *lexicon*. A statistical model (4.1.1) is then computed for every word such that it models the distribution of the acoustic vectors. Repeating the estimation for all the words, we finally obtain a set of statistical models, the so-called *acoustic model*, which is stored in the ASR system. At run-time, the acoustic decoding module searches the sequence of words whose corresponding sequence of models is the "closest" to the observed sequence of acoustic feature vectors. This search is complex since neither the number of words, nor their segmentation, are known in advance. Efficient decoding algorithms constrain the search for the best sequence of words by a *grammar*, which defines the authorized, or at least the most likely, sequence of words. It is usually described in terms of a statistical model: the *language model.*

   In large vocabulary ASR systems, it is hard if not impossible to train separate statistical models for all words (and even to gather the speech data that would be required to properly train a word-based acoustic model). In such systems, words are described as sequences of phonemes in a *pronunciation lexicon*, and statistical modeling is applied to phonemic units. Word-based models are then obtained by concatenating the phoneme-based models. Small vocabulary systems (<50 words), on the contrary, usually consider words as basic acoustic units and therefore do not require a pronunciation lexicon.

4.1.1 The statistical formalism of ASR

The most common statistical formalism of ASR[48], which we will use throughout this Chapter, aims to produce the *most probable* word sequence

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[47] Although *x(n)* is a vector, it will not be written with a bold font in this Chapter, to avoid overloading all equations.

[48] There are numerous textbooks that explain these notions in detail. See for instance (Gold and Morgan 2000), (Bourlard and Morgan 1994) or (Bourlard

W^* given the acoustic observation sequence X. This can be expressed mathematically by the so-called *Bayesian*, or *Maximum a Posteriori* (MAP) decision rule as:

$$W^* = \arg\max_{W_i} P(W_i \mid X, \Theta) \qquad (4.1)[49]$$

where W_i represents the *i*-th possible word sequence and the conditional probability is evaluated over all possible word sequences[50], and Θ represents the set of parameters used to estimate the probability distribution.

Since each word sequence W_i may be realized as an infinite number of possible acoustic realizations, it is represented by its model $M(W_i)$, also written M_i for the sake of simplicity, which is assumed to be able to produce all such possible acoustic realizations. This yields:

$$M^* = \arg\max_{M_i} P(M_i \mid X, \Theta) \qquad (4.2)$$

where M^* is (the model of) the sequence of words representing the linguistic message in input speech X, M_i is (the model of) a possible word sequence W_i, $P(M_i \mid X, \Theta)$ is the posterior probability of (the model of) a word sequence given the acoustic input X, and the maximum is evaluated over all possible models (i.e., all possible word sequences).

Bayes' rule can be the applied to (4.2), yielding:

$$P(M_i \mid X, \Theta) = \frac{P(X \mid M_i, \Theta) P(M_i \mid \Theta)}{P(X \mid \Theta)} \qquad (4.3)$$

2007). For a more general introduction to pattern recognition, see also (Polikar 2006) or the more complete (Duda *et al.* 2000).

[49]   In equation (4.1), W_i and X are not random variables: they are values taken by their respective random variables. As a matter of fact, we will often use in this Chapter a shortcut notation for probabilities, when this does not bring confusion. The probability $P(A=a|B=b)$ that a discrete random variable A takes value a given the fact that random variable B takes value b will simply be written $P(a/b)$. What is more, we will use the same notation when A is a *continuous* random variable for referring to *probability density* $p_{A|B=b}(a)$).

[50]   It is assumed here that the number of possible word sequences is finite, which is not true for natural languages. In practice, a specific component of the ASR, the *decoder*, takes care of this problem by restricting the computation of (4.1) for a limited number of most probable sequences.

where $P(X \mid M_i, \Theta)$ represents the contribution of the so-called *acoustic model* (i.e., the likelihood that a specific model M_i has produced the acoustic observation X), $P(M_i \mid \Theta)$ represents the contribution of the so-called *language model* (i.e., the a priori probability of the corresponding word sequence), and $P(X \mid \Theta)$ stands for the a priori probability of the acoustic observation. For the sake of simplicity (and tractability of the parameter estimation process), state-of-the-art ASR systems always assume independence between the acoustic model parameters, which will now be denoted Θ_A and the parameters of the language model, which will be denoted Θ_L.

Based on the above, we thus have to address the following problems:

- *Decoding (recognition):* Given an unknown utterance X, find the most probable word sequence W^* (i.e., the most probable word sequence model M^*) such that:

$$M^* = \arg\max_{M_i} \frac{P(X \mid M_i, \Theta_A)P(M_i \mid \Theta_L)}{P(X \mid \Theta_A, \Theta_L)} \tag{4.4}$$

Since during recognition all parameters Θ_A and Θ_L are frozen, probability $P(X \mid \Theta_A, \Theta_L)$ is constant for all hypotheses of word sequences (i.e., for all choices of i) and can thus be ignored, so that (4.4) simplifies to:

$$M^* = \arg\max_{M_i} P(X \mid M_i, \Theta_A)P(M_i \mid \Theta_L) \tag{4.5}$$

- *Acoustic modeling*: Given (the model of) a word sequence, M_i, estimate the probability $P(X \mid M_i, \Theta_A)$ of the unknown utterance X.

This is typically carried out using Hidden Markov Models (HMM; see Section 4.1.3). It requires to estimate the acoustic model Θ_A. At training time, a large amount of training utterances X_j ($j = 1, \ldots, J$) with their associated models M_j are used to estimate the optimal acoustic parameter set Θ_A^*, such that:

$$\Theta_A^* = \arg\max_{\Theta_A} \prod_{j=1}^{J} P(X \mid M_i, \Theta_A)$$

$$= \arg\max_{\Theta_A} \sum_{j=1}^{J} \log(P(X \mid M_i, \Theta_A))$$

(4.6)

which is referred to as the *Maximum Likelihood* (ML), or *Maximum Log Likelihood criterion*[51].

- *Language modeling*: The goal of the language model is to estimate prior probabilities of sentence models $P(M_i \mid \Theta_L)$.

  At training time, the language model parameters Θ_L are commonly estimated from large text corpora. The language model is most often formalized as word-based Markov models (See Section 4.1.2), in which case Θ_L is the set of transition probabilities of these chains, also known as *n-grams*.

4.1.2 Markov models

A *Markov model* is the simplest form of a *Stochastic Finite State Automaton* (SFSA). It describes a sequence of observations $X = [x(1), x(2), \ldots, x(N)]$ as the output of a finite state automaton (Fig. 4.2) whose internal states $\{q_1, q_2, \ldots, q_K\}$ are univocally associated with possible observations $\{x_1, x_2, \ldots, x_K\}$ and whose state-to-state transitions are associated with probabilities: a given state q_k always outputs the same observation x_k, except initial and final states (q_I and q_F, which output nothing); the *transition probabilities* from any state sum to one. The most important constraint imposed by a (first order) Markov model is known as the
: the probability of a state (or that of the associated observation) only depends on the previous state (or that of the associated observation).

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[51] Although both criteria are equivalent, it is usually more convenient to work with the sum of *log* likelihoods. As a matter of fact, computing products of probabilities (which are often significantly lower than one) quickly exceeds the floating point arithmetic precision. Even the log of a sum of probabilities can be estimated, when needed, using log likelihoods (i.e., without having to compute likelihoods at any time), using:

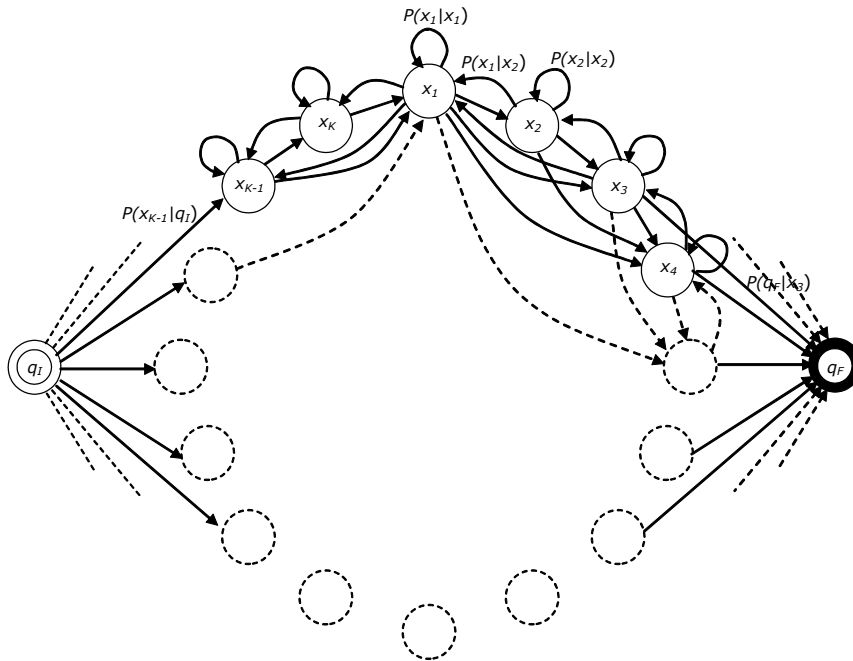$$\log(a+b) = \log(a) + \log\left(1 + e^{(\log b - \log a)}\right)$$

Fig. 4.2 A typical Markov model[52]. The leftmost and rightmost states are the initial and final states. Each internal state q_k in the center of the figure is associated to a specific observation x_k (and is labeled as such). Transition probabilities are associated to arcs (only a few transition probabilities are shown).

The probability of X given such a model reduces to the probability of the sequence of states $[q_I, q(1), q(2), ..., q(N), q_F]$ corresponding to X, i.e. to a product of transition probabilities (including transitions from state q_I and transitions to state q_F):

$$P(X) = P(q(1) \mid q_I) \left(\prod_{n=2}^{N} P(q(n) \mid q(n-1)) \right) P(q_F \mid q(N)) \qquad (4.7)$$

where $q(n)$ stands for the state associated with observation $x(n)$. Given the one-to-one relationship between states and observations, this can also be written as:

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[52] The model shown here is *ergodic*: transitions are possible from each state to all other states. In practical applications (such as in ASR, for language modeling), some transitions may be prohibited.

$$P(X) = P(x(1)|I)\left(\prod_{n=2}^{N} P\big(x(n)|x(n-1)\big)\right)P\big(F|x(N)\big) \qquad (4.8)$$

where I and F stand for the symbolic beginning and end of X.

The set of parameters, represented by the $(K \times K)$-transition probability matrix and the initial and final state probabilities:

$$\Theta = \big\{P(q_k|q_I), P(q_k|q_l), P(q_F|q_l)\big\}, \quad \text{with } k, l \text{ in } (1,...K) \qquad (4.9)$$

is directly estimated on a large amount of observation sequences (i.e., of state sequences, since states can be directly deduced from observations in a Markov model), such that:

$$\Theta^* = \arg\max_{\Theta} P(X|\Theta) \qquad (4.10)$$

This simply amounts to estimating the relative counts of observed transitions[53], i.e.:

$$P(q_k|q_l) = \frac{n_{lk}}{n_l} \qquad (4.11)$$

where n_{lk} stands for the number of times a transition from state q_l to state q_k occurred, while n_l represents the number of times state q_l was visited.

Markov models are intensively used in ASR for language modeling, in the form of *n-grams*, to estimate the probability of a word sequence $W = [w(1), w(2), ..., w(L)]$ as:

$$P(W) = P\big(w(1)|I\big)\left(\prod_{l=2}^{L} P\big(w(l)|w(l-1), w(l-2),...w(l-n+1)\big)\right).$$
$$P\big(F|w(L)\big) \qquad (4.12)[54]$$

In particular, *bigrams* further reduce this estimation to:

$$P(W) = P\big(w(1)|I\big)\left(\prod_{l=2}^{L} P\big(w(l)|w(l-1)\big)\right)P\big(F|w(L)\big) \qquad (4.13)$$

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[53] This estimate is possibly smoothed in case there is not enough training data, so as to avoid forbidding state sequences not found in the data (those which are rare but not impossible).

[54] In this case, states are not associated to words, but rather to sequences of *n-1* words. Such models are called N^{th} order Markov models.

In this case, each observation is a word from the input word sequence *W*, and each state of the model (except *I* and *F*) is characterized by a single word, which an observed word could possibly follow with a given probability.

As Jelinek (1991) pointed out: "That this simple approach is so successful is a source of considerable irritation to me and to some of my colleagues. We have evidence that better language models are obtainable, we think we know many weaknesses of the trigram model, and yet, when we devise more or less subtle methods of improvement, we come up short."

Markov models cannot be used for acoustic modeling, as the number of possible observations is infinite.

4.1.3 Hidden Markov models

Modifying a Markov model by allowing several states (if not all) to output the same observations with state-dependent *emission probabilities* (Fig. 4.3), turns it into a hidden Markov model (HMM, Rabiner 1989). In such a model, the sequence of states cannot be univocally determined from the sequence of observations (such a SFSA is called *ambiguous*). The HMM is thus called "hidden" because there is an underlying stochastic process (i.e., the sequence of states) that is not observable, but affects the sequence of observations.

While Fig. 4.3 shows a *discrete* HMM, in which the number of possible observations is finite, *continuous* HMMs are also very much used, in which the output space is a continuous variable (often even multivariate). Emission probabilities are then estimated by assuming they follow a particular functional distribution: $P(x_m/q_k)$ is computed analytically (it can no longer be obtained by counting). In order to keep the number of HMM parameters as low as possible, this distribution often takes the classical form of a (multivariate, *d*-dimensional) Gaussian[55]:

$$P(x \mid q_k) = N(x, \mu_k, \Sigma_k)$$
$$= \frac{1}{(2\pi)^{d/2} |\Sigma_k|^{1/2}} \exp\left(-\frac{1}{2}(x - \mu_k)^T \Sigma_k^{-1}(x - \mu_k) \right) \qquad (4.14)$$

where μ_k and Σ_k respectively denote the mean vector and the covariance matrix associated with state q_k. When this model is not accurate enough,

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[55] Gaussian PDFs have many practical advantages: they are entirely defined by their first two moments and are linear once derivated.

mixtures of (multivariate) Gaussians (*Gaussian mixture model*, GMM) are also used, which allow for multiple modes[56]:

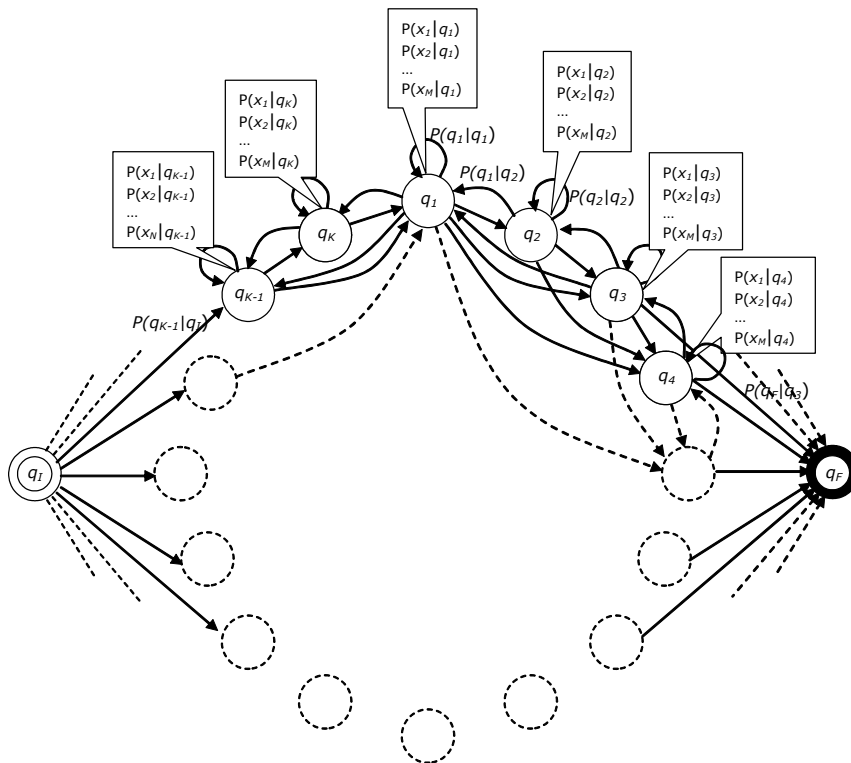$$P(x \mid q_k) = \sum_{g=1}^{G} c_{kg} N(x, \mu_{kg}, \Sigma_{kg}) \tag{4.15}$$

Fig. 4.3 A typical (discrete) hidden Markov model. The leftmost and rightmost states are the initial and final states. Each state q_k in the center of the figure is associated to several possible observations (here, to all observations $\{x_1, x_2, \dots , x_M\}$) with the corresponding emission probability. Transition probabilities are associated to arcs (only a few transition probabilities are shown). The HMM is termed as *discrete* because the number of possible observations is finite.

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[56] It is also possible (and has proved very efficient in ASR) to use artificial neural networks (ANN) to estimate emission probabilities (Bourlard and Wellekens 1990, Bourlard and Morgan 1994). We do not examine this option here.

where G is the total number of Gaussian densities and c_{kg} are the mixture gain coefficients (thus representing the prior probabilities of Gaussian mixture components). These gains must verify the constraint:

$$\sum_{g=1}^{G} c_{kg} = 1 \quad \forall k = 1,...,K \tag{4.16}$$

Assuming the total number of states K is fixed, the set of parameters Θ of the model comprises all the Gaussian means and variances, gains, and transition probabilities.

Two approaches can be used for estimating $P(X \mid M, \Theta)$.

In the *full likelihood approach*, this probability is computed as a sum on all possible paths of length N. The probability of each path is itself computed as in (4.7):

$$P(X \mid M, \Theta) = \sum_{paths\ j} P\big(q_j(1) \mid q_I\big) P\big(x(1) \mid q_j(1)\big). \tag{4.17}$$

$$\left(\prod_{n=2}^{N} P\big(q_j(n) \mid q_j(n-1)\big) P\big(x(n) \mid q_j(n)\big) \right) P\big(q_F \mid q_j(N)\big)$$

where $q_j(n)$ stands for the state in $\{q_1, q_2, ... , q_K\}$ which is associated with $x(n)$ in path j. In practice, estimating the likelihood according to (4.17) involves a very large number of computations, namely $O(NK^N)$, which can be avoided by the so-called *forward recurrence formula* with a lower complexity, namely $O(K^2N)$. This formula is based on the recursive estimation of an intermediate variable $\alpha_n(l)$:

$$\alpha_n(l) = P\big(x(1), x(2),...,x(n), q(n) = q_l\big) \tag{4.18}$$

$\alpha_n(l)$ stands for the probability that a partial sequence $[x(1), x(2), . . . , x(n)]$ is produced by the model in such a way that $x(n)$ is produced by state q_l. It can be obtained by using (Fig. 4.4):

$$\alpha_1(l) = P(x(1) \mid q_l)P\big(q_l \mid q_I\big) \quad (l = 1,...,K)$$

$$for\ n = 2,...,N\ (and\ l = 1,...,K)$$

$$\alpha_n(l) = P(x(n) \mid q_l)\sum_{k=1}^{K} \alpha_{n-1}(k)P\big(q_l \mid q_k\big) \tag{4.19}$$

$$P(X \mid M, \Theta) = \alpha_{N+1}(F) = \sum_{k=1}^{K} \alpha_N(k)P\big(q_F \mid q_k\big)$$

In the *Viterbi approximation approach,* the estimation of the data likelihood is restricted to the most probable path of length N generating the sequence X:

$$P(X \mid M, \Theta) \cong \max_{paths\ j} P\big(q_j(1) \mid I\big) P(x_1 \mid q_j(1)).$$
$$\left(\prod_{n=2}^{N} P\big(q_j(n) \mid q_j(n-1)\big) P\big(x_n \mid q_j(n)\big) \right) P\big(q_F \mid q_j(N)\big) \quad (4.20)$$

and the sums in (4.19) are replaced by the max operator. Notice it is also easy to memorize the most probable path given some input sequence by using (4.19) and additionally keeping in memory, for each $n = (1,...,N)$ and for each $l = (1,...,K)$, the value of k producing the highest term of $\alpha_{n+1}(l)$ in (4.19). Starting from the final state (i.e., the one leading to the highest term for $\alpha_{N+1}(F)$), it is then easy to trace back the best path, thereby associating one "best" state to each feature vector.
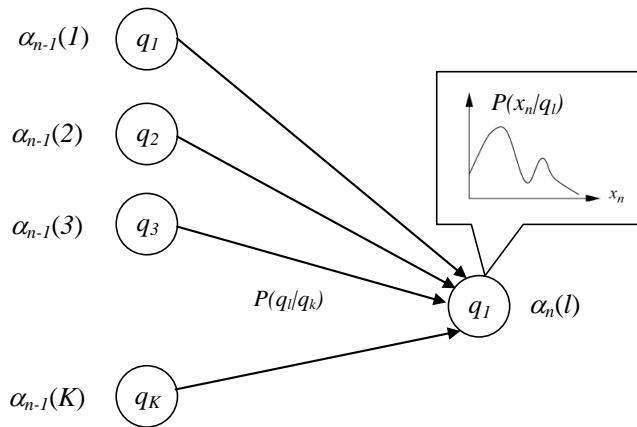

Fig. 4.4 Illustration of the sequence of operations required to compute the intermediate variable $\alpha_n(l)$

HMMs are intensively used in ASR acoustic models where every sentence model M_i is represented as a HMM. Since such a representation is not tractable due to the infinite number of possible sentences, sentence HMMs are obtained by compositing sub-sentence HMMs such as word HMMs, syllable HMMs or more generally phoneme HMMs. Words, syllables, or phonemes are then generally described using a specific HMM topology (i.e. allowed state connectivity) known as *left-to-right* HMMs

(Fig. 4.5), as opposed to the general ergodic topology shown in Fig. 4.3. Although sequential signals, such as speech, are nonstationary processes, left-to-right HMMs assume that the sequence of observation vectors is a piecewise stationary process. That is, a sequence $X = [x(1), x(2), \ldots , x(N)]$ is modeled as a sequence of discrete stationary states with instantaneous transitions between these states.

4.1.4 Training HMMs

HMM training is classically based on the Maximum Likelihood criterion: the goal is to estimate the parameters of the model which maximize the likelihood of a large number of training sequences X_j ($j = 1,\ldots , J$). For Gaussian HMMs (which we will examine here, as they are used in most ASR systems), the set of parameters to estimate comprises all the Gaussian means and variances, gains (if GMMs are used), and transition probabilities.
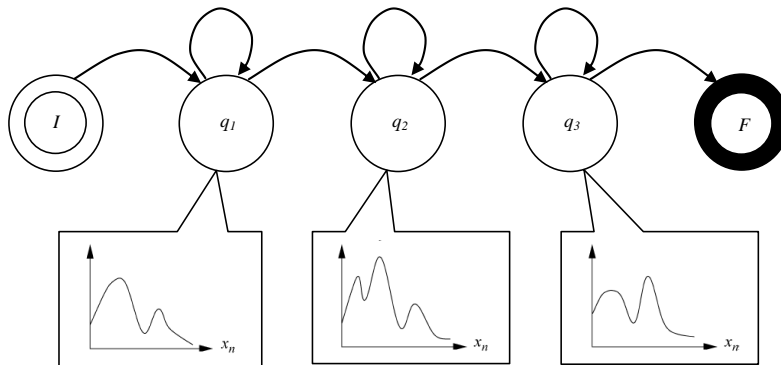

Fig. 4.5 A left-to-right continuous HMM, shown here with (univariate) continuous emission probabilities (which look like mixtures of Gaussians). In speech recognition, this could be the model of a word or of a phoneme which is assumed to be composed of three stationary parts.

Training algorithms
A solution to this problem is a particular case of the *Expectation-Maximization* (EM) algorithm (Moon 1996). Again, two approaches are possible.

In the *Viterbi approach* (Fig. 4.6), the following steps are taken:
1. Start from an initial set of parameters $\Theta^{(0)}$. With a left-to-right topology, one way of obtaining such a set is by estimating the

parameters from a linear segmentation of feature vector sequences, i.e., by assuming that each training sequence X_j ($j = 1,\dots, J$) is produced by visiting each state of its associated model M_j the same amount of times. Then apply the expectation step to this initial linear segmentation.

2. (*Expectation* step) Compute transition probabilities as in (4.11). Obtain emission probabilities for state k by estimating the Gaussian parameters in (4.14) or the GMM parameters in (4.15) and (4.16) from all feature vectors associated to state k in the training sequences (see below).

2. (*Maximization* step) For all training utterances X_j and their associated models M_j find the maximum likelihood paths ("best" paths), maximizing $P(X_j/M_j)$ using the Viterbi recursion, thus yielding a new segmentation of the training data. This step is often referred to "forced alignment", since we are forcing the matching of utterances X_j on given models M_j.

3. Given this new segmentation, collect all the vectors (over all utterances X_j) associated with states q_k and reestimate emission and transition probabilities as in the expectation step. Iterate as long as the total likelihood of the training set increases or until the relative improvement falls below a pre-defined threshold.
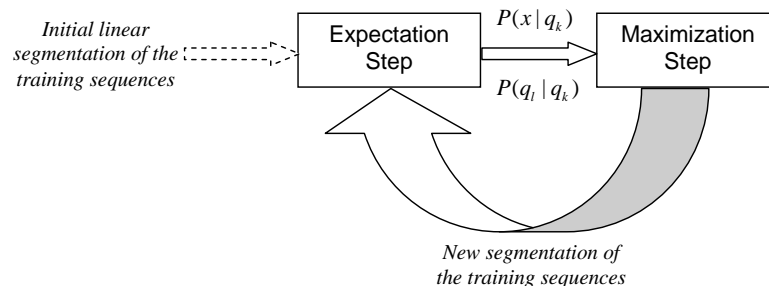

Fig. 4.6 The *Expectation-Maximization* (EM) algorithm, using the Viterbi approach.

In the *Forward-Backward*, or *Baum-Welch approach*, all paths are considered. Feature vectors are thus no longer univocally associated to states when reestimating the emission and transitions probabilities: each of them counts for some weight in the reestimation of the whole set of parameters.

The convergence of the iterative processes involved in both approaches can be proved to converge to a local optimum (whose quality will depend on the quality of the initialization).

Estimating emission probabilities

In the Viterbi approach, one needs to estimate the emission probabilities of each state q_k, given a number of feature vectors $\{x_{1k}, x_{2k}, \ldots, x_{Mk}\}$ associated to it. The same problem is encountered in the Baum-Welch approach, with feature vector partially associated to each state. We will explore the Viterbi case here, as it is easier to follow[57].

When a multivariate Gaussian distribution $N(\mu_k, \Sigma_k)$ is assumed for some state q_k, the classical estimation formulas for the mean and covariance matrix, given samples x_{ik} stored as column vectors, are:

$$\tilde{\mu}_k = \frac{1}{M} \sum_{i=1}^{M} x_{ik}$$

$$\tilde{\Sigma}_k = \frac{1}{M-1} \sum_{i=1}^{M} (x_{ik} - \tilde{\mu}_k)(x_{ik} - \tilde{\mu}_k)^T$$

(4.21)

It is easy to show that $\tilde{\mu}_k$ is the maximum likelihood estimate of μ_k. The ML estimator of Σ_k, though, is not exactly the one given by (4.21): the ML estimator normalizes by M instead of (M-1). However it is shown to be biased when the exact value of μ_k is not known, while (4.21) is unbiased.

When a multivariate GMM distribution is assumed for some state q_k, estimating its weights c_{kg}, means μ_{kg} and covariance matrices Σ_{kg} for $g=1, \ldots, G$ as defined in (4.15), cannot be done analytically. The EM algorithm is used again for obtaining the maximum likelihood estimate of the parameters, although in a more straightforward way than above (there is not such a thing as transition probabilities in this problem). As before, two approaches are possible: the *Viterbi-EM approach*, in which each feature vectors is associated to one of the underlying Gaussians, and the *EM approach*, in which each vector is associated to all Gaussians, with some weight (for a tutorial on the EM algorithm, see Moon 1996, Bilmes 1998).

The Viterbi-EM and EM algorithms are very sensitive to the initial values chosen for their parameters. In order to maximize their chances to

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[57] Details on the Baum-Welch algorithm can be found in (Bourlard, 2007).

converge to a global maximum of the likelihood of the training data, the *k-means* algorithm is sometimes used for providing a first estimate of the parameters. Starting from an initial set of *G* prototype vectors, this algorithm iterates on the following steps:

1. For each feature vector x_{ik} (i=1, …, *M*), compute the squared Euclidian distance from the kth prototype, and assign x_{ik} to its closest prototype.
2. Replace each prototype with the mean of the feature vectors assigned to it in step 1.

Iterations are stopped when no further assignment changes occur.

4.2 MATLAB proof of concept: ASP_dictation_machine.m

Although speech is by essence a non-stationary signal, and therefore calls for dynamic modeling, it is convenient to start this script by examining static modeling and classification of signals, seen as a statistical pattern recognition problem. We do this by using Gaussian multivariate models in Section 4.2.1 and extend it to Gaussian Mixture Models (GMM) in Section 4.2.2. We then examine, in Section 4.2.3, the more general dynamic modeling, using Hidden Markov Models (HMM) for isolated word classification. We follow in Section 4.2.4 by adding a simple bigram-based language model, implemented as a Markov model, to obtain a connected word classification system. We end the Chapter in Section 4.2.5 by implementing a word-based speech recognition system[58], in which the system does not know in advance how many words each utterance contains.

4.2.1 Gaussian modeling and Bayesian classification of vowels

We will examine here how Gaussian multivariate models can be used for the classification of signals.

   A good example is that of the classification of sustained vowels, i.e., of the classification of incoming acoustic feature vectors into the corresponding phonemic classes. Acoustic feature vectors are generally highly multi-dimensional (as we shall see later), but we will work in a 2D space, so as to be able to plot our results.

---

[58] Notice that we will not use the words *classification* and *recognition* indifferently. Recognition is indeed more complex than classification, as it involves the additional task of segmenting an input stream into segments for further classification.

In this Chapter, we will work on a hypothetic language, whose phoneme set is only composed of four vowels {/a/, /e/, /i/, /u/}, and whose lexicon reduces to {"why" /uai/, "you" /iu/, "we" /ui/, "are" /ae/, "hear" /ie/, "here" /ie/}. Every speech frame can then be represented as a 2-dimensional vector of speech features in the form of pairs of formant values (the first and the second spectral formants, F_1 and F_2; see Chapter 1, Section 1.1).

Our first task will be to classify vowels, by using Gaussian probability density functions (PDF) for class models and Bayesian (MAP) decision. Let us load a database of features extracted from the vowels and words of this language[59]. Vowel samples are grouped in matrices of size N x 2, where each of the N rows is a training example and each example is characterized by a formant frequency pair $[F_1, F_2]$. Supposing that the whole database covers adequately our imaginary language, it is easy to compute the prior probability $P(q_k)$ of each class q_k (q_k in {/a/,/e/,/i/,/u/}). The most common phoneme in our hypothetic language is /e/.

```
load data; % vowels={a,e,i,u};

N_samples=0;
for j=1:4
    N_samples = N_samples+size(vowels{j}.training,1);
end;
for j=1:4
    prior(j) = size(vowels{j}.training,1)/N_samples;
end;
prior
```

```
prior =  0.1500    0.4000    0.1500    0.3000
```

As can be seen in Fig. 4.7 (left), our four vowel classes have serious overlap in the 2D vector space.

```
plot(vowels{1}.training(:,1),vowels{1}.training(:,2),'k+');
hold on;
plot(vowels{2}.training(:,1),vowels{2}.training(:,2),'r*');
plot(vowels{3}.training(:,1),vowels{3}.training(:,2),'gp');
plot(vowels{4}.training(:,1),vowels{4}.training(:,2),'bs');
```

Let us now assume that we are asked to identify an unknown vowel from its (F_1, F_2) features. One way of solving this problem is by performing multivariate Gaussian modeling of each class, i.e., finding the mean and covariance matrices of the data in each class.

---

[59] These samples were actually generated from statistical models of the vowels, which we chose for tutorial purposes. See Appendix 1 in the `ASP_dictation_machine.m` script, and the `gendata.m` file.

MATLAB function involved:

- `plot_2Dgauss_pdf(mu,sigma)` plots the mean and standard deviation ellipsis of the 2D Gaussian process that has mean `mu` and covariance matrix `sigma`, in a 2D plot.

```
for j=1:4
    mu{j}=mean(vowels{j}.training)';
    sigma{j}=cov(vowels{j}.training);
    plot_gauss2D_pdf(mu{j},sigma{j})
end;
```
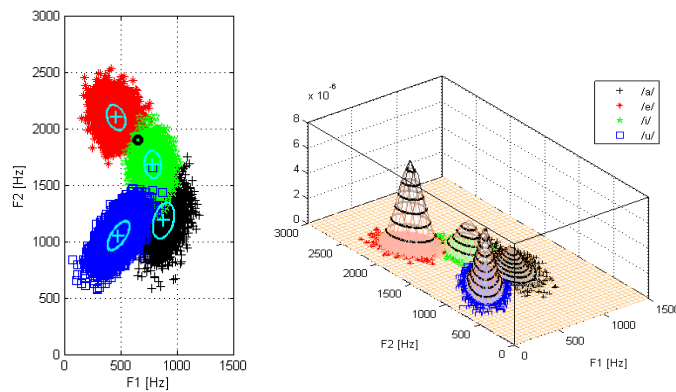

Fig. 4.7 Left: Samples of the four vowels {/a/, /e/, /i/, /u/} of our imaginary language in the (F_1,F_2) plane, superimposed with the standard deviation ellipsis of their 2D Gaussian model. Right: 2D Gaussian estimates of the PDF of these vowels in the (F_1,F_2) plane.

Fig. 4.7 shows that /i/, for instance, has its mean F_1 at 780 Hz and its mean F_2 at 1680 Hz [60]. The covariance matrix for the /i/ class is almost diagonal (the scatter plot for the class has its principal axes almost parallel to the coordinate axes, which implies that F_1 and F_2 are almost uncorrelated; see Appendix 1 of the `ASP_dictation_machine.m` file). Its diagonal elements are thus close to the square of the length of the halfmajor and halfminor axes of the standard deviation ellipsis: 76 Hz and 130 Hz, respectively.

---

[60] These values are the ones fixed in our imaginary language; they do not correspond to those of English vowels at all.

```
    mu{3}
    sqrtm(sigma{3})
```

```
ans =    1.0e+003 *
    0.7814    1.6827

ans =
   75.3491   -4.4051
   -4.4051  125.5608
```

Let us estimate the likelihood of a test feature vector given the Gaussian model of class /e/, using the classical Gaussian PDF formula. The feature vector is shown as a black dot in Fig. 4.7.

```
    sample=[650 1903];
    x = sample-mu{2};
    likelihood = exp(-0.5* x* inv(sigma{2}) *x') / sqrt((2*pi)^2 …
                 * det(sigma{2}))

    plot(sample(1),sample(2),'ko','linewidth',3)
```

```
likelihood =  7.1333e-007
```

The likelihood of this vector is higher in class /i/ than in any other class (this is also intuitively obvious from the scatter plots shown previously), as shown below.

MATLAB function involved:

- `gauss_pdf(x,mu,sigma)` returns the likelihood of sample `x` (NxD) with respect to a Gaussian process with mean `mu` (1xD) and covariance `sigma` (DxD). When a set of samples is provided as input, a set of likelihoods is returned.

```
    for j=1:4
        likelihood(j) = gauss_pdf(sample,mu{j},sigma{j});
    end;
    likelihood
```

```
likelihood =  1.0e-005 *

   0.0000    0.0713    0.1032    0.0000
```

Likelihood values are generally very small. Since we will use products of them in the next paragraphs, we will systematically prefer their log-likelihood estimates.

```
    log(likelihood)
```

```
ans =  -29.3766  -14.1533  -13.7837  -36.9803
```

Since not all phonemes have the same prior probability, Bayesian (MAP) classification of our test sample is not equivalent to finding the class with maximum likelihood. Posterior probabilities *P(class|sample)* must be estimated by multiplying the likelihood of the sample by the prior of each class, and dividing by the marginal likelihood of the sample (obtained by summing its likelihood for all classes). Again, for convenience, we compute the log of posterior probabilities. The result is that our sample gets classified as /e/ ratter than as /i/, because the prior probability of /e/ is much higher than that of /i/ in our imaginary language.

```
marginal=sum(likelihood); % is a constant
log_posterior=log(likelihood)+log(prior)-log(marginal)
```

log_posterior =   -18.0153   -1.8112   -2.4224   -24.9258

Notice that the marginal likelihood of the sample is not required for classifying it, as it is a subtractive constant for all log posterior probabilities. We will not compute it in the sequel.

Multiplying likelihoods by priors can be seen as a weighting which accounts for the intrinsic frequency of occurence of each class. Plotting the posterior probability of classes in the (F_1, F_2) plane gives a rough idea of how classes are delimited (Fig. 4.7, right).

MATLAB function involved:

- `mesh_2Dgauss_pdf(mu,sigma,prior,gridx,gridy,ratioz)` plots the PDF of a 2D-Gaussian PDF in a 3D plot. `mu` (1x2) is the mean of the density, `sigma` (2x2) is the covariance matrix of the density. `prior` is a scalar used as a multiplicative factor on the value of the PSD. `gridx` and `gridy` must be vectors of the type (x:y:z) `ratioz` is the (scalar) aspect ratio on the Z axis.

```
hold on;
for j=1:4
    mesh_gauss2D_pdf(mu{j},sigma{j},prior(j),0:50:1500, ...
        0:50:3000, 7e-9);
    hold on;
end;
```

One can easily compare the performance of max likelihood vs. max posterior classifiers on test data sets taken from our four vowels (and having the same prior distribution as from the training set). The error rate is smaller for Bayesian classification: 2.4% vs. 2.2%.

MATLAB function involved:

- `gauss_classify(x,mus,sigmas,priors)` returns the class of the point `x` (1xD) with respect to Gaussian classes, using Bayesian classification. `mus` is a cell array of the (1xD) means, `sigmas` is a cell array of the (DxD) covariance matrices. `priors` is a vector of Gaussian priors. When a set of points (NxD) is provided as input, a set of classes is returned.

```
total=0;
errors_likelihood=0;
errors_bayesian=0;
for i=1:4
    n_test=size(vowels{i}.test,1);
    class_likelihood=gauss_classify(vowels{i}.test,mu,…
        sigma,[1 1 1 1]);
    errors_likelihood=errors_likelihood…
        +sum(class_likelihood'~=i);
    class_bayesian=gauss_classify(vowels{i}.test,mu,…
        sigma,prior);
    errors_bayesian=errors_bayesian…
        +sum(class_bayesian'~=i);
    total=total+n_test;
end;
likelihood_error_rate=errors_likelihood/total
bayesian_error_rate=errors_bayesian/total
```

```
likelihood_error_rate = 0.0240
bayesian_error_rate   = 0.0220
```

4.2.2 Gaussian Mixture Models (GMM)

In the previous section, we have seen that Bayesian classification is based on the estimation of class PDFs. Up to now, we have modeled the PDF for each class /a/, /e/, /i/, /u/ as a Gaussian multivariate (one per class). This implicitly assumes that the feature vectors in each class have a (uni-modal) normal distribution, as we used the `mean` and `cov` functions, which return the estimates of the mean and covariance matrix of supposedly Gaussian multivariate data samples. It turns out that the vowel data we used had actually been sampled according to Gaussian distributions, so that this hypothesis was satisfied.

Let us now try to classify the words of our imaginary language, using the same kind of approach as above. We will use 100 samples of the six words {"why" /uai/, "you" /iu/, "we" /ui/, "are" /ae/, "hear" /ie/, "here" /ie/}[61] in our imaginary language, for which each speech frame is again

---

[61] Again, the phonetic transcriptions of these words are not those of English (while they remain easy to remember for tutorial purposes).

characterized by an [F_1, F_2] feature vector. These samples (Fig. 4.8) are stored in the **words** variable.

```
for i=1:6
    subplot(2,3,i)
    plot(words{i}.training_all(:,1),…
        words{i}.training_all(:,2),'+');
    title(words{i}.word);
hold on;
end;
```

Notice that "you" and "we" have the same statistical distribution, because of their phonemic content (in our imaginary language): /iu/ and /ui/. Notice also that "hear" and "here" also have the same distribution, because they have exactly the same phonemic transcription: /ie/. We will come back to this later.
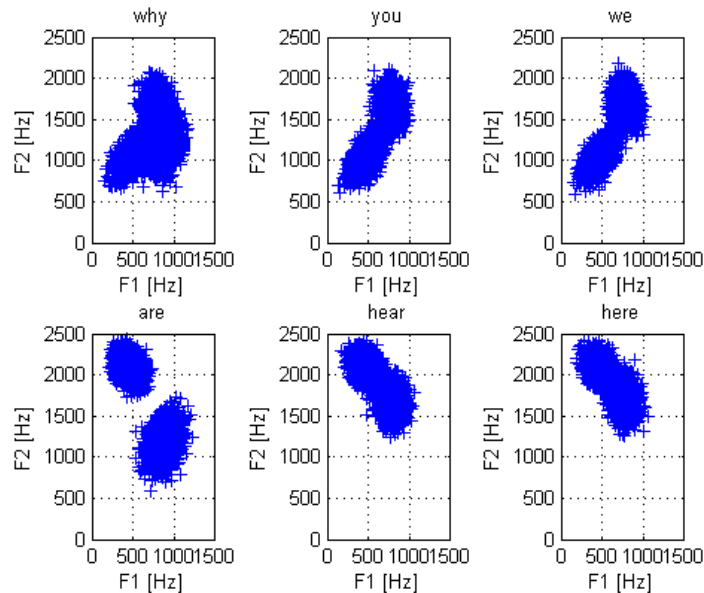

Fig. 4.8 Samples of the six words {"why" /uai/, "you" /iu/, "we" /ui/, "are" /ae/, "hear" /ie/, "here" /ie/} of our imaginary language in the (F_1,F_2) plane.

We are now facing a PDF estimation problem: the PDF of the data in each class in no longer Gaussian. This is typical of practical ASR systems: in word-based ASR, each class accounts for the realization of several phonemes and is thus better described as a multi-modal distribution, i.e. a distribution with several maxima. The same holds for phoneme-based ASR

as well. As a matter of fact, speech is very much submitted to coarticulation, which often results in several modes for the acoustic realization of each phoneme, as a function of the phonetic context in which it appears.

If we apply a uni-modal Gaussian model to word "why", for instance, we get a gross estimation of the PDF (Fig. 4.9, left). This estimation does not correctly account for the fact that several areas in the (F_1, F_2) plane are more densely crowded. The maximum value of the Gaussian PDF is very low, since it spans more of the (F_1, F_2) space than it should (and the integral is constrained to one).

```
training_set=words{1}.training_all;
test_set=words{1}.test_all;
mu_all=mean(training_set);
sigma_all=cov(training_set);

plot(training_set(:,1),training_set(:,2),'+');
hold on;
mesh_gauss2D_pdf(mu_all,sigma_all,...
        1, 0:50:1500, 0:50:2500,7e-9);
```
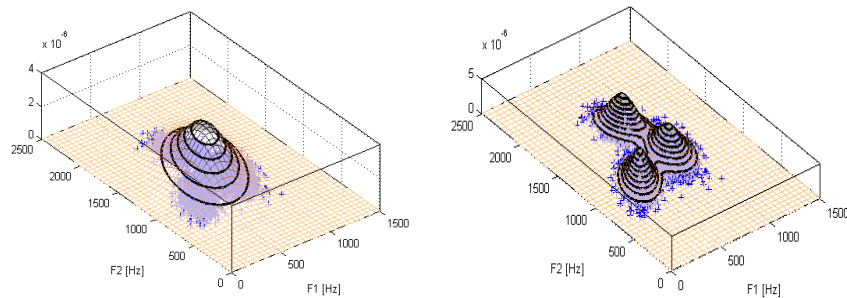

Fig. 4.9 Left: 2D Gaussian estimation of the PDF of the word "why" in the (F_1, F_2) plane. Right: The same PDF estimated from a GMM estimate (using a mixture of 3 Gaussians).

The total log likelihoods of the training and test data given this Gaussian model are obtained as sum of the log likelihoods of all feature vectors.

```
log_likelihood_training=…
    sum(log(gauss_pdf(training_set,mu_all,sigma_all)))
log_likelihood_test=…
    sum(log(gauss_pdf(test_set,mu_all,sigma_all)))
```

```
log_likelihood_training =  -7.4102e+004
log_likelihood_test = -8.3021e+004
```

One way of estimating a multi-modal PDF is by clustering data, and then estimate a uni-modal PDF in each cluster. An efficient way to do this (using a limited number of clusters) is by using *K*-means clustering. Starting with *k* prototype vectors or *centroids,* this algorithm first associates each feature vector in the training set to its closest centroid. It then replaces every centroid by the mean of all feature vectors that have been associated to it. The algorithm iterates by re-associating each feature vector to one of the newly found centroids, and so on until no further change occurs.

MATLAB function involved:

- `[new_means,new_covs,new_priors,distortion]= ...` `kmeans(data,n_iterations,n_clusters)` , where `data` is the matrix of observations (one observation per row) and `n_clusters` is the desired number of clusters, returns the mean vectors, covariance matrices, and priors of k-means clusters. `distortion` is an array of values (one per iteration) of sum of squared distances between the data and the mean of their cluster. The clusters are initialized with a heuristic that spreads them randomly around `mean(data)`. The algorithm iterates until convergence is reached or the number of iterations exceeds `n_iterations`. Using `kmeans(data,n_iterations,means)`, where `means` is a cell array containing initial mean vectors, makes it possible to initialize means.
- `plot_kmeans2D(data,means)` plots the clusters associated with `means` in `data` samples, using a Euclidian distance.

```
% Initializing prototypes "randomly" around the mean
initial_means{1} = [0,1] * sqrtm(sigma_all) + mu_all;
initial_means{2} = [0,0] * sqrtm(sigma_all) + mu_all;
initial_means{3} = [1,2] * sqrtm(sigma_all) + mu_all;

[k_means,k_covs,k_priors,totalDist]=kmeans(training_set,…
    1000,initial_means);

plot_kmeans2D(training_set, k_means);
```

The *K*-means algorithm converges monotonically, in 14 iterations, to a (local) minimum of the global distortion defined as the sum of all distances between feature vectors and their associated centroids (Fig. 4.10, left).

```
plot(totalDist,'.-');
xlabel('Iteration'); ylabel('Global LS criterion'); grid on;
```
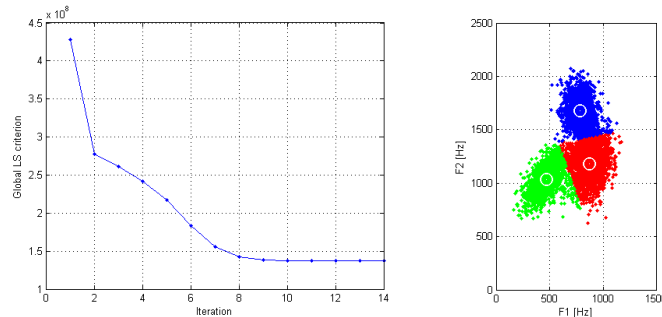
Fig. 4.10 Applying the *k*-means algorithm (with *k*=3) to the sample feature vectors for word "why". Left: Evolution of the total distortion; Right: Final clusters

The resulting sub-classes, though, do not strictly correspond to the phonemes of "why" (Fig. 4.10, right). This is because the global criterion that is minimized by the algorithm is purely geometric. It would actually be very astonishing in these conditions to find the initial vowel sub-classes. This is not a problem, as what we are trying to do is to estimate the PDF of the data, not to classify it into "meaningful" sub-classes. Once clusters have been created, it is easy to compute the corresponding (supposedly uni-modal) Gaussian means and covariance matrices for each cluster (this is actually done inside our `kmeans` function), and to plot the sum of their PDFs, weighted by their priors. This produces an estimate of the PDF of our speech unit (Fig. 4.9, right).

MATLAB function involved:

- `mesh_GMM2D_pdf(mus,sigmas,weights,gridx,gridy,ratioz)` plots the PDF of a 2D Gaussian Mixture Model PDF in a 3D plot. `mus` is a cell array of the (1x2) means, `sigmas` is a cell array of the (2x2) covariance matrices. `weights` is a vector of Gaussian weights. `gridx` and `gridy` must be vectors of the type (x:y:z) `ratioz` is the (scalar) aspect ratio on the Z axis;

```
plot(training_set(:,1),training_set(:,2),'+');
hold on;
mesh_GMM2D_pdf(k_means,k_covs,k_priors, ...
        0:50:1500, 0:50:2500,2e-8);
hold off;
```

The total log likelihoods of the training and test data are obtained as above, except we now consider that each feature vector "belongs" to each cluster with some weight equal to the prior probability of the cluster. Its

likelihood is thus computed as a weighted sum of likelihoods (one per Gaussian).

MATLAB function involved:

- `GMM_pdf(x,mus,sigmas,weights)` returns the likelihood of sample `x` (1xD) with respect to a Gaussian Mixture Model. `mus` is a cell array of the (1xD) means, `sigmas` is a cell array of the (DxD) covariance matrices. (1xD) `weight` is a vector of Gaussian weights. When a set of samples (NxD) is provided as input, a set of likelihoods is returned.

```
log_likelihood_training=…
    sum(log(GMM_pdf(training_set,k_means,k_covs,k_priors)))
log_likelihood_test=…
    sum(log(GMM_pdf(test_set,k_means, k_covs, k_priors)))
```
```
log_likelihood_training =
 -7.1310e+004

log_likelihood_test =
 -7.9917e+004
```

The *K*-means approach used above is not optimal, in the sense that it is based on a purely geometric convergence criterion. The central algorithm for training GMMs is based on the EM (Expectation-Maximization) algorithm. As opposed to *K*-means, EM truly maximizes the likelihood of the data given the GMM parameters (means, covariance matrices, and weights). Starting with *k* initial uni-modal Gaussians (one for each sub-class), it first estimates, for each feature vector, the probability of each sub-class given that vector. This is the Estimation step, which is based on soft classification: each feature vector belongs to all sub-classes, with some weights. In the Maximization step, the mean and covariance of each sub-class is updated, using all feature vectors and taking those weights into account. The algorithm iterates on the E and M steps, until the total likelihood increase for the training data falls under some threshold.

The final estimate obtained by EM, however, only corresponds to a local maximum of the total likelihood of the data, whose value may be very sensitive to the initial uni-modal Gaussian estimates provided as input. A frequently used value for these initial estimates is precisely the one provided by the K-means algorithm.

Applied to the sample feature vectors of "why", the EM algorithm converges monotonically, in 7 steps, from the *K*-means solution to a (local) maximum of the total likelihood of the sample data (Fig. 4.11).

MATLAB function involved:

- `[new_means,new_sigmas,new_priors,total_loglike]= ...`
`GMM_train(data,n_iterations,n_gaussians)`, where `data` is the matrix of observations (one observation per row) and `n_gaussians` is the desired number of clusters, returns the mean vectors, covariance matrices, and priors of GMM Gaussian components. `total_loglike` is an array of values (one per iteration) of the total likelihood of the data given the GMM model. GMMs are initialized with a heuristic that spreads them randomly around `mean(data)`. The algorithm iterates until convergence is reached or the number of iterations exceeds `n_iterations`.
`GMM_train(data,n_iterations,means,covs,priors)` makes it possible to initialize the means, covariance matrices, and priors of the GMM components.
- `plot_GMM2D(data, means, covs)` shows the standard deviation ellipsis of the Gaussian components of a GMM defined by `means` and `covs`, on a 2D plot, together with `data` samples.

```
[means,covs,priors,total_loglike]=GMM_train(training_set,…
    100,k_means,k_covs,k_priors);

plot(training_set(:,1),training_set(:,2),'+');
plot_GMM2D(training_set,means,covs);

plot(total_loglike,'.-');
xlabel('Iteration'); ylabel('Global Log Likelihood'); grid on;
```

The total log likelihoods of the training and test data given this GMM model are obtained as above. The increase compared to estimating the GMM parameters from *K*-means clustering is small, but this is due to the oversimplified PDF we are dealing with. GMMs are very much used in speech recognition for acoustic modeling.

```
log_likelihood_training=…
    sum(log(GMM_pdf(training_set,means,covs,priors)))
log_likelihood_test=…
    sum(log(GMM_pdf(test_set,means,covs,priors)))
```
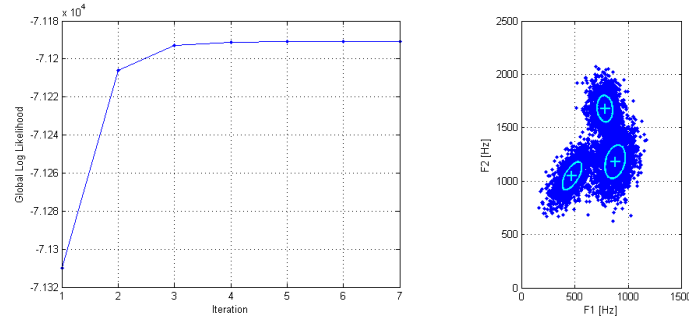
Fig. 4.11 Applying the EM algorithm (with 3 Gaussians) to the sample feature vectors for word "why". Left: Evolution of the total log likelihood of the data; Right: Standard deviation ellipses of the three Gaussian components. Notice we do not set colors to feature vectors, as EM precisely does not strictly assign Gaussians to feature vectors.

```
log_likelihood_training =
 -7.1191e+004

log_likelihood_test =
 -7.9822e+004
```

Now let us try to recognize sample words in {"why", "you", "we", "are", "hear", "here"}. We now use the sequence of feature vectors from our unknown signal (instead of a single vector as before), estimate the joint likelihood of all vectors in this sequence given each class, and obtain the posterior probabilities in the same way as above. If we assume that each sample in our sequence is independent from the others (which is in practice a rather bold claim, even for stationary signals; we will come back to this in the next section when introducing dynamic models), then the joint likelihood of the sequence is simply the product of the likelihoods of each sample.

We first estimate a GMM for each word, using 3 Gaussians per word.[62] The estimated GMMs are plotted in Fig. 4.12.

```
for i=1:6

    [GMMs{i}.means,GMMs{i}.covs,GMMs{i}.priors,total_loglike]=...
        GMM_train(words{i}.training_all,100,3);
end;

for i=1:6
    subplot(2,3,i)
```

---

[62] When 2 Gaussians are enough, one of the three ends up having very small weight.

```
    plot(words{i}.training_all(:,1),…
         words{i}.training_all(:,2),'+');
    title(words{i}.word);
    hold on;
    mesh_GMM2D_pdf(GMMs{i}.means,GMMs{i}.covs,GMMs{i}.priors, ...
         0:50:1500, 0:50:2500,8e-9);
end;
```

Let us then try to recognize the first test sequence taken from "why" (Fig. 4.13). Since we do not know the priors of words in our imaginary language, we will set them all to 1/6. As expected, the maximum log likelihood is encountered for word "why": our first test word is correctly recognized.

```
word_priors=ones(1,6)*1/6;
test_sequence=words{1}.test{1};
for i=1:6
    log_likelihood(i) = sum(log(GMM_pdf(test_sequence,...
         GMMs{i}.means,GMMs{i}.covs,GMMs{i}.priors)));
end;
log_posterior=log_likelihood+log(word_priors)
[maxlp,index]=max(log_posterior);
recognized=words{index}.word
```

```
log_posterior =
 -617.4004 -682.0656 -691.2229 -765.6281 -902.7732 -883.7884

recognized = why
```
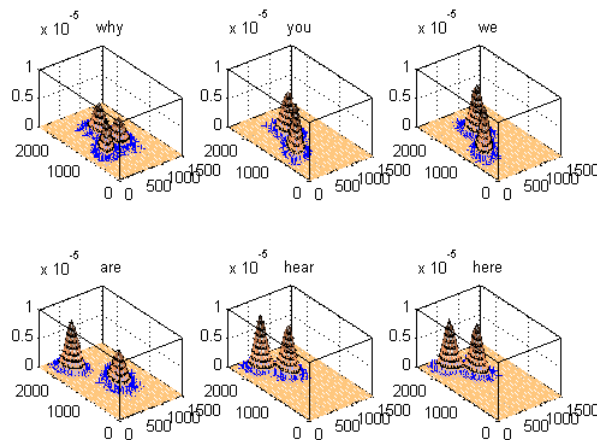

Fig. 4.12 GMMs estimated by the EM algorithm from the sample feature vectors of our six words: "why", "you", "we", "are", "hear", "here"
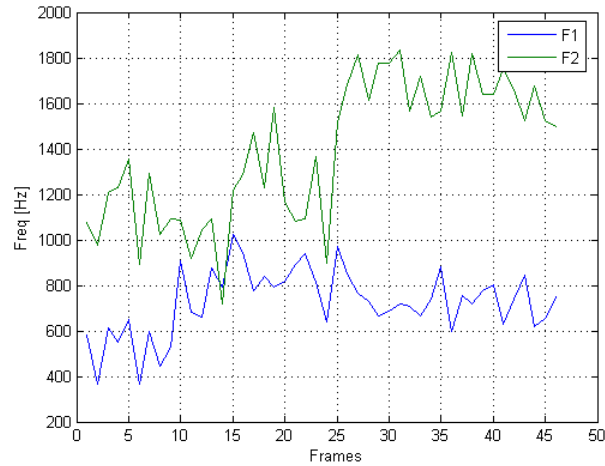
Fig. 4.13 Sequence of feature vectors of the first sample of "why". The three phonemes (each corresponding to a Gaussian in the GMM) are quite apparent.

Not all sequences are correctly classified, though. Sequence 2 is recognized as a "we".

```
test_sequence=words{1}.test{2};
for i=1:6
    log_likelihood(i) = sum(log(GMM_pdf(test_sequence,...
        GMMs{i}.means,GMMs{i}.covs,GMMs{i}.priors)));
end;
log_posterior=log_likelihood+log(word_priors)
[maxlp,index]=max(log_posterior);
recognized=words{index}.word
```

```
log_posterior =
  1.0e+003 *
   -0.6844   -0.6741   -0.6729   -0.9963   -1.1437   -1.1181

recognized = we
```

We may now compute the total word error rate on our test database.

MATLAB function involved:

• `GMM_classify(x,GMMs,priors)` returns the class of sample x with respect to GMM classes, using Bayesian classification. x {(NxD)} is a cell array of test sequences. `priors` is a vector of class priors. The function returns a vector of classes.

```
total=0;
errors=0;
```

```
for i=1:6
    n_test=length(words{i}.test);
    class=GMM_classify(words{i}.test,GMMs,word_priors);
    errors=errors+sum(class'~=i);
    class_error_rate(i)=sum(class'~=i)/n_test;
    total=total+n_test;

    subplot(2,3,i);
    hist(class,1:6);
    title(words{i}.word);
    set(gca,'xlim',[0 7]);

end;
overall_error_rate=errors/total
class_error_rate
```

```
overall_error_rate =
    0.3000

class_error_rate =
    0.0800    0.4300    0.4400    0.0100    0.3900    0.4500
```

Obviously, our static approach to word classification is not a success. Only 70% of the words are recognized. The rather high error rates we obtain are not astonishing. Except for "why" and "are", which have fairly specific distributions, "here" and "here" have identical PDFs, as well as "you" and "we". These pairs of words are thus frequently mistaken for one another (Fig. 4.14).
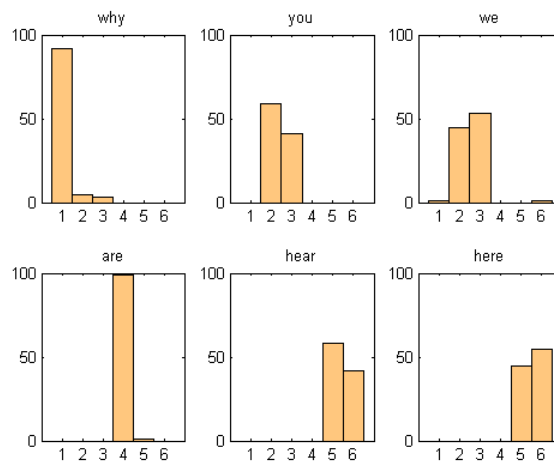

Fig. 4.14 Histograms of the outputs of the GMM-based word recognizer, for samples of each of the six possible input words. The integer values on the x axes refer to the index of the output word, in {"why", "you", "we", "are", "hear", "here"}.

4.2.3 Hidden Markov Models (HMM)

In the previous Sections, we have seen how to create a model, either Gaussian or GMM, for estimating the PDF of speech feature vectors, even with complicated distribution shapes, and have applied it to the classification of isolated words. The main drawback of such a static classification, as it stands, is that it does not take time into account. For instance, the posterior probability of a sequence of feature vectors does not change when the sequence is time-reversed, as in words "you" /iu/ and "we" /ui/. This is due to the fact that our Bayesian classifier implicitly assumed that successive feature vectors are statistically independent.

In this Section we will model each word in our imaginary language using a 2-state HMM (plus their initial and final states), except for "why", which will be modeled as a 3-state HMM. One should not conclude that word-based ASR systems set the number of internal HMM states for each word to the number of phonemes they contain. The number of states is usually higher than the number of phonemes, as phonemes are themselves produced in several articulatory steps which may each require a specific state. The reason for our choice is directly dictated by the fact that the test data we are using throughout this script was randomly generated by HMMs (see appendix 1 in the MATLAB script) in which each phoneme was produced by one HMM state modeled as a multivariate Gaussian. As a result, our test data virtually exhibits no coarticulation, and hence does not require more than one state per phoneme.

We will make one more simplification here: that of having access to a corpus of pre-segmented sentences, from which many examples of our 6 words have been extracted. This will make it possible to train our word HMMs separately. In real ASR systems, segmentation (in words or phonemes) is not known. Sentence HMMs are thus created by concatenating word HMMs, and these sentence HMMs are trained. Words (or phoneme) segmentation is then obtained as a by-product of this training stage.

We start by loading our training data and creating initial values for the left-right HMM of each word in our lexicon. Each state is modeled using a Gaussian multivariate whose mean feature vector is set to a random value close to the mean of all feature vectors in the word. The elements $trans(i,j)$ of the transition matrix give the probability of going from state q_i to q_j (state 1 being the initial state). Transitions probabilities betweeen internal (emiting) states are set to a constant value of 0.8 for staying in the same state, and 0.2 for leaving to the next state.

```
% Initializing HMM parameters
% "why" is a special case: it has 3 states
```

```
mu=mean(words{1}.training_all);
sigma=cov(words{1}.training_all);
HMMs{1}.means = {[],mu,mu,mu,[]};
HMMs{1}.covs  = {[],sigma,sigma,sigma,[]};
HMMs{1}.trans = [ 0.0 1.0  0.0  0.0  0.0
                      0.0 0.8  0.2  0.0  0.0
                      0.0 0.0  0.8  0.2  0.0
                      0.0 0.0  0.0  0.8  0.2
                      0.0 0.0  0.0  0.0  1.0 ];
for i=2:6
    mu=mean(words{i}.training_all);
    sigma=cov(words{i}.training_all);
    HMMs{i}.means = {[],mu,mu,[]};
    HMMs{i}.covs  = {[],sigma,sigma,[]};
    HMMs{i}.trans = [0.0 1.0   0.0   0.0
                      0.0 0.8   0.2   0.0
                      0.0 0.0   0.8   0.2
                      0.0 0.0   0.0   1   ];
end
```

Let us train our HMM models using the Baum-Welch (or Forward-Backward) algorithm, which is a particular implementation of the EM algorithm we already used for training our GMMs in the previous Section. This algorithm will adapt the parameters of our word HMMs so as to maximize the likelihood of each training set given each HMM model.

MATLAB function involved:

- `new_hmm = HMM_train_FB(data,old_hmm,dmin,qmax)`| returns the Maximum Likelihood re-estimation of a Gaussian Hidden Markov Model (i.e., a single, possibly multivariate, Gaussian probability density function per state) based on the forward-backward algorithm (aka. Baum-Welch re-estimation formulas). Note that most operations are performed in the log domain for accuracy[63]. `dmin` and `qmax` are respectively the minimum log-likelihood relative improvement and the maximum number of iterations until convergence.

```
for i=1:6
  HMMs{i}=HMM_gauss_train(words{i}.training,HMMs{i},0.001,50);
end;
```

The word "why" is now correctly modeled as a sequence of 3 states, each with a Gaussian multivariate PDF, which matches those of the underlying phonemes in the word: /uai/ (**Fig. 4.15**).

```
for i=2:4
    subplot(1,3,i-1)
    plot(words{1}.training_all(:,1),…
         words{1}.training_all(:,2),'+');
    title(['state ' num2str(i-1)]); % emiting states only
```

---

[63] This function uses a homemade `logsum.m` function, which computes the log of a sum of likelihoods from log-likelihoods, as mentioned in 4.1.1.

```
hold on;
mesh_gauss2D_pdf(HMMs{1}.means{i},HMMs{1}.covs{i},1, ...
    0:50:1500, 0:50:2500,1e-8);
end;
```
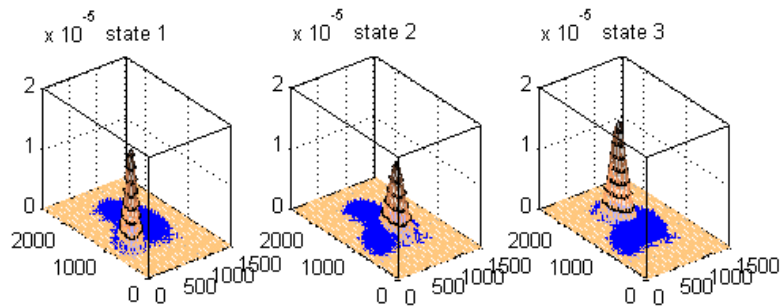

Fig. 4.15 PDF of the three Gaussian HMM states obtained from samples of "why".

The transition probabilities between the states of "why" have been updated by the Baum-Welch algorithm.

```
HMMs{1}.trans
```

```
ans =
     0    1.0000         0         0         0
     0    0.9970    0.0030         0         0
     0         0    0.9951    0.0049         0
     0         0         0    0.9387    0.0613
     0         0         0         0    1.0000
```

As a result of this better modeling, the total likelihood of the data for word "why" is higher than with our previous static GMM model. The previous model can actually be seen as a single-state HMM, whose emission probabilities are modeled by a GMM.

```
log_likelihood_training=0;
for i=1:length(words{1}.training)
    training_sequence=words{1}.training{i};
    log_likelihood_training=log_likelihood_training+...
        HMM_gauss_loglikelihood(training_sequence,HMMs{1});
end;

log_likelihood_test=0;
for i=1:length(words{1}.test)
    test_sequence=words{1}.test{i};
    log_likelihood_test=log_likelihood_test+...
        HMM_gauss_loglikelihood(test_sequence,HMMs{1});
end;
```

```
      log_likelihood_training
      log_likelihood_test
```

```
log_likelihood_training = -6.7144e+004
log_likelihood_test = -7.5204e+004
```

HMM-based isolated word classification can now be achieved by finding the maximum of the posteriori probability of a sequence of feature vectors given all 6 HMM models. The 2nd test sequence for "why" (which was not correctly recognized using GMMs and a single state) now passes our classification test.

```
      word_priors=ones(1,6)*1/6;

      test_sequence=words{1}.test{2};
      for i=1:6
          log_posterior(i) = HMM_gauss_loglikelihood(...
              test_sequence, HMMs{i})+log(word_priors(i));
      end
      log_posterior
      [tmp,index]=max(log_posterior);
      recognized=words{index}.word
```

```
log_posterior =
  1.0e+003 *
  -0.6425   -1.0390   -0.6471   -1.0427   -1.1199   -1.1057
```

```
recognized = why
```

The HMM model does not strictly assign states to feature vectors: each feature vector can be emitted by any state with a given probability. It is possible, though, to estimate the best path through the HMM given the data, by using the Viterbi algorithm (Fig. 4.16).

MATLAB function involved:

- `plot_HMM2D_timeseries(x,stateSeq)` plots a two-dimensional sequence x (one observation per row) as two separate figures, one per dimension. It superimposes the corresponding state sequence `stateSeq` as colored dots on the observations. x and `stateSeq` must have the same length.

```
      best_path=HMM_gauss_viterbi(test_sequence,HMMs{index});
      plot_HMM2D_timeseries(test_sequence,best_path);
```

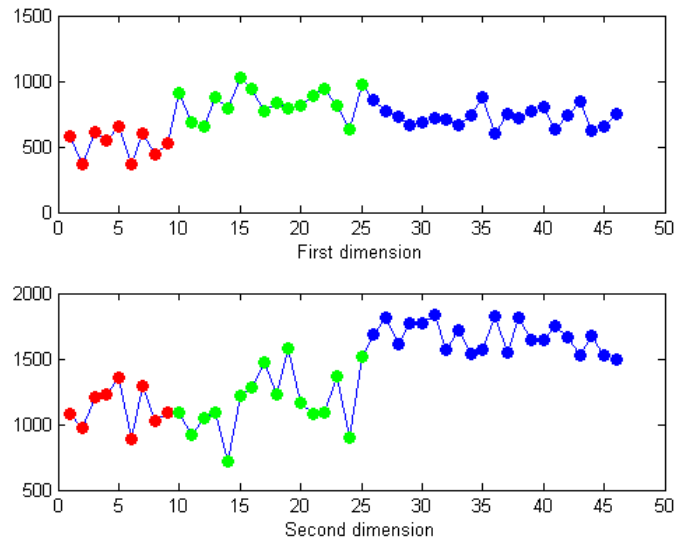We may now compute the total word error rate again.

Fig. 4.16 Best path obtained by the Viterbi algorithm, from the sequence of feature vectors of "why" in Fig. 4.13.

MATLAB function involved:

- `HMM_gauss_classify(x,HMMs,priors)` returns the class of sample x with respect to HMM classes, using Bayesian classification. HMM states are modeled by a Gaussian multivariate. x (NxD) is a cell array of test sequences. `priors` is a vector of class priors. The function returns a vector of classes.

```
total=0;
errors=0;
for i=1:6
    n_test=length(words{i}.test);
    class=HMM_gauss_classify(words{i}.test,HMMs,word_priors);
    errors=errors+sum(class'~=i);
    class_error_rate(i)=sum(class'~=i)/n_test;
    total=total+n_test;

    subplot(2,3,i);
    hist(class,1:6);
    title(words{i}.word);
    set(gca,'xlim',[0 7]);

end;
overall_error_rate=errors/total
class_error_rate
```

```
overall_error_rate = 0.1600
class_error_rate =
         0           0            0            0      0.4400      0.5200
```
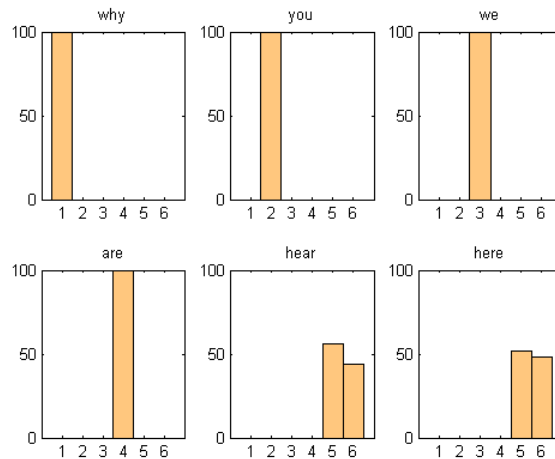

Fig. 4.17 Histograms of the outputs of the HMM-based word classifier, for samples of each of the six possible input words.

Notice the important improvement in the classification of "you" and "we" (Fig. 4.17), which are now modeled as HMMs with distinctive parameters. 84% of the (isolated) words are now recognized. The remaining errors are due to the confusion between "here" and "hear".

4.2.4 *N*-grams

In the previous Section, we have used HMM models for the words of our imaginary language, which led to a great improvement in isolated word classification. It remains that "hear" and "here", having strictly identical PDFs, cannot be adequately distinguished. This kind of ambiguity can only be resolved when words are embedded in a sentence, by using constraints imposed by the language on word sequences, i.e. by modeling the syntax of the language.

We will now examine the more general problem of connected word classification, in which words are embedded in sentences. This task requires adding a language model on top of our isolated word classification system. For convenience, we will assume that our imaginary language

imposes the same syntactic constraints as English. A sentence like "you are hear" is therefore impossible and should force the recognition of "you are here" wherever a doubt is possible. In this first step, we will also assume that word segmentation is known (this could easily be achieved, for instance, by asking the speaker to insert silences between words and detecting silences based on energy levels).

Our data file contains a list of 150 such pre-segmented sentences. Let us plot the contents of the first one ("we hear why you are here", Fig. 4.18).

```
for i=1:length(sentences{1}.test)
    subplot(2,3,i);
    test_sequence=sentences{1}.test{i}; % ith word
    plot(test_sequence(:,1),'+-');
    hold on;
    plot(test_sequence(:,2),'r*-');
    title(['Word' num2str(i)]);
end;
```

We model the syntactic constraints of our language by a bigram model, based on the probability of pairs of successive words in the language. Such an approach reduces the language model to a simple Markov model. The component bigram(i,j) of its transition matrix gives P($word_i|word_j$): the probability that the jth word in the lexicon is followed by the ith word. Clearly, "You are hear" is made impossible by bigrams(5,6)=0.
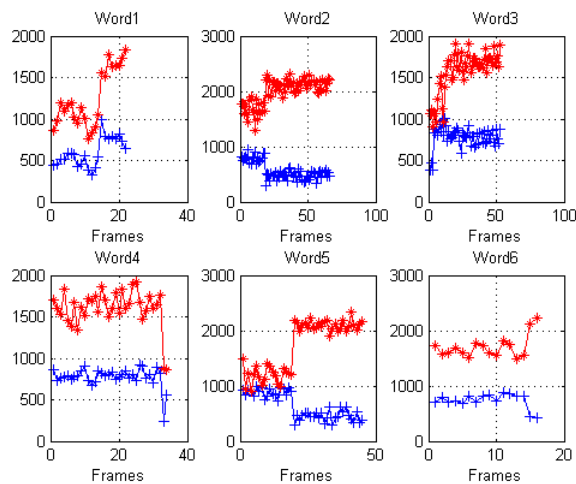

Fig. 4.18 Sequences of feature vectors for the six (pre-segmented) words in the first test sentence.

```
% states = I U {why,you,we,are,hear,here} U F
% where I and F stand for the begining and the end of a
sentence

bigrams = ...
    [0    1/6  1/6  1/6  1/6  1/6  0  ; % P(word|I)
     0    0    1/6  1/6  1/6  1/6  1/6  1/6; % P(word|"why")
     0    1/5  0    0    1/5  1/5  1/5  1/5; % P(word|"you")
     0    0    0    0    1/4  1/4  1/4  1/4; % P(word|"we")
     0    0    1/4  1/4  0    0    1/4  1/4; % P(word|"are")
     0    1/4  1/4  0    0    0    1/4  1/4; % P(word|"hear")
     0    0    1/4  1/4  1/4  0    0    1/4; % P(word|"here")
     0    0    0    0    0    0    0    1]; % P(word|F)
```

Let us now try to classify a sequence of words taken from the test set. We start by computing the log likelihood of each unknown word given the HMM model for each word in the lexicon. Each column of the log likelihood matrix stands for a word in the sequence; each line stands for a word in the lexicon {why,you,we,are,hear,here}.

```
n_words=length(sentences{1}.test);
log_likelihoods=zeros(6,n_words);

for j=1:n_words
    for k=1:6 % for each possible word HMM model
        unknown_word=sentences{1}.test{j};
        log_likelihoods(j,k) = HMM_gauss_loglikelihood(...
            unknown_word,HMMs{k});
    end;
end;

log_likelihoods
```

```
log_likelihoods =

 1.0e+003 *

  -0.2754   -0.3909   -0.2707   -0.4219   -0.6079   -0.5973
  -1.4351   -1.4067   -1.3986   -0.9186   -0.7952   -0.7977
  -0.6511   -0.8062   -0.7147   -0.9689   -0.8049   -0.8024
  -0.5203   -0.4208   -0.5043   -0.6925   -0.5306   -0.5284
  -0.9230   -1.0715   -1.0504   -0.5506   -0.6912   -0.6935
  -0.2510   -0.2772   -0.2400   -0.2851   -0.1952   -0.1953
```

With the approach we used in the previous Section, we would classify this sentence as "we hear why you are hear" (by choosing the max likelihood candidate for each word independently of its neighbors).

```
[tmp,indices]=max(log_likelihoods);
for j=1:n_words
    recognized_sequence{j}=words{indices(j)}.word;
end;
recognized_sequence
```

```
recognized_sequence =
    'we'    'hear'    'why'    'you'    'are'    'hear'
```

We implement our language model as a Markov model on top of our word HMMs. The resulting model for the sequence to recognize is a discrete HMM, in which there are as many internal states as the number of words in the lexicon (six in our case). Each state can emit any of the `n_words` input words (which we will label as '1', '2', ... 'n_words'), with emission probabilities equal to the likelihoods computed above. Bigrams are used as transition probabilities. Finding the best sequence of words from the lexicon given the sequence of observations [1, 2, ..., n_words] is obtained by looking for the best path in this model, using the Viterbi algorithm again.

As shown below, we now correctly classify our test sequence as "we hear why you are here".

MATLAB function involved:

- `[state,likelihood]  =  HMM_viterbi(transition,emission)` performs the Viterbi search (log version) of the best state sequence for a discrete Hidden Markov Model.

> `transition`: (K+2)x(K+2) matrix of transition probabilities,
>   first and last rows correspond to initial and
>   final (non-emitting) states.
> `emission`:   NxK matrix of state-conditional emission
>   probabilities corresponding to a given sequence
>   of observations of length N.
> `state`:   (Nx1) vector of state-related indexes of best sequence.
> `likelihood`: best sequence likelihood.

```
best_path=HMM_viterbi(log(bigrams),log_likelihoods);
for j=1:n_words
    recognized_sequence{j}=words{best_path(j)}.word;
end;
recognized_sequence
```

```
recognized_sequence =
    'we'     'hear'    'why'     'you'     'are'     'here'
```

We may finally compute the word error rate on our complete test data.

```
n_sentences=length(sentences);

total=0;
errors=0;
class_error_rate=zeros(1,6);
class=cell(6); % empty cells

for i=1:n_sentences

    n_words=length(sentences{i}.test);
    log_likelihoods=zeros(6,n_words);
```

```
    for j=1:n_words
        unknown_word=sentences{i}.test{j};
        for k=1:6 % for each possible word HMM model
            log_likelihoods(j,k) = HMM_gauss_loglikelihood(...
                unknown_word,HMMs{k});
        end;
    end;

    best_path=HMM_viterbi(log(bigrams),log_likelihoods);

    for j=1:n_words
        recognized_word=best_path(j);
        actual_word=sentences{i}.wordindex{j};
        class{actual_word}= [class{actual_word}, …
                            recognized_word];

        if (recognized_word~=actual_word)
            errors=errors+1;
            class_error_rate(actual_word)=…
                class_error_rate(actual_word)+1;
        end;
    end;

    total=total+n_words;

end;

overall_error_rate=errors/total
class_error_rate
```

overall_error_rate = 0.1079

class_error_rate =
*   0   0   0   0   37   31*

We now have an efficient connected word classification system for our imaginary language. The final recognition rate is now 89.2%. Errors are still mainly due to "here" being confused with "hear" (Fig. 4.19). As a matter of fact, our bigram model is not constrictive enough. It still allows non admissible sentences, such as in sentence #3: "why are you hear". Bigrams cannot solve all "hear" vs. "here" ambiguities, because of the weaknesses of this poor language model. Trigrams could do a much better job ("are you hear", for instance, will be forbidden by a trigram language model), at the expense of additional complexity.
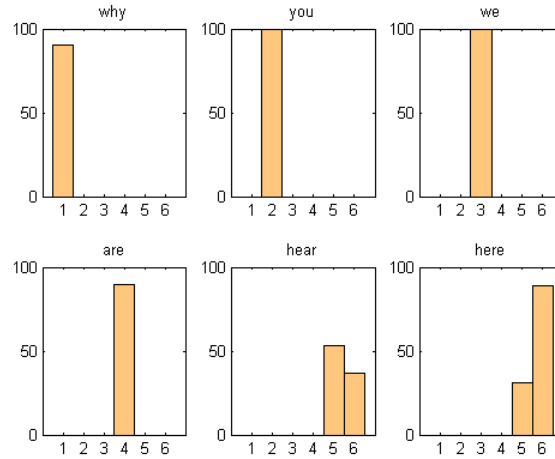
Fig. 4.19 Histograms of the outputs of the HMM-based word classifier, after adding a bigram language model.

4.2.5 Word-based continuous speech recognition

In this Section, we will relax the pre-segmentation constraint, which will turn our classification system into a true word-based speech recognition system (albeit still in our imaginary language).

The discrete sentence HMM we used previously implicitly imposed initial and final states of word HMMs to fall after some specific feature vectors[64]. When word segmentation is not known in advance, the initial and final states of all word HMMs must be erased, for the input feature vector sequence to be properly decoded into a sequence of words.

The resulting sentence HMM is a Gaussian HMM (as each word HMM state is modeled as a Gaussian) composed of all the word HMM states, connected in a left-right topology inside word HMMs, and connected in an ergodic topology between word HMMs. For the six words of our language, this makes 13 internal states, plus the sentence-initial and sentence-final states. The transition probabilities between word-internal states are taken from the previously trained word HMMs, while the transition probabilities between word-final and word-initial states are taken from our bigram model.

---

[64] The sentence HMM therefore had to be changed for each new incoming sentence.

```
sentence_HMM.trans=zeros(15,15);

% word-initial states, including  sentence-final state;
word_i=[2 5 7 9 11 13 15];
word_f=[4 6 8 10 12 14]; % word-final states;

% P(word in sentence-initial position)
sentence_HMM.trans(1,word_i)=bigrams(1,2:8);

% copying trans. prob. for the 3 internal states of "why"
sentence_HMM.trans(2:4,2:4)=HMMs{1}.trans(2:4,2:4);

% distributing P(new word|state3,"why") to the first states of
% other word models, weighted by bigram probabilities.
sentence_HMM.trans(4,word_i)=...
    HMMs{1}.trans(4,5)*bigrams(2,2:8);

% same thing for the 2-state words
for i=2:6
    sentence_HMM.trans(word_i(i):word_f(i),word_i(i):word_f(i))=...
        HMMs{i}.trans(2:3,2:3);
    sentence_HMM.trans(word_f(i),word_i)=...
        HMMs{i}.trans(3,4)*bigrams(i+1,2:8);
end;
```

The emission probabilities of our sentence HMM are taken from the word-internal HMM states.

```
k=2;
sentence_HMM.means{1}=[]; % sentence-initial state
for i=1:6
    for j=2:length(HMMs{i}.means)-1
        sentence_HMM.means{k}=HMMs{i}.means{j};
        sentence_HMM.covs{k}=HMMs{i}.covs{j};
        k=k+1;
    end;
end;
sentence_HMM.means{k}=[]; % sentence-final state
```

We search for the best path in our sentence HMM[65] given the sequence of feature vectors of our test sequence, with the Viterbi algorithm, and plot the resulting sequence of states (Fig. 4.20).

MATLAB function involved:

• [states,log_likelihood] = HMM_gauss_viterbi(x,HMM) returns the best state sequence and the associated log likelihood of the sequence of feature vectors x (one observation per row) with respect to a Markov model HMM defined by:
   HMM.means
   HMM.covs
   HMM.trans

---

[65] The new sentence model is no longer sentence-dependent: the same HMM can be used to decode any incoming sequence of feature vectors into a sequence of words.

This function implements the forward recursion to estimate the likelihood on the best path.

```
n_words=length(sentences{1}.test);
complete_sentence=[];
for i=1:n_words
    complete_sentence=[complete_sentence ; ...
        sentences{1}.test{i}];
end;

best_path=HMM_gauss_viterbi(complete_sentence,sentence_HMM);
plot_HMM2D_timeseries(complete_sentence,best_path);

state_sequence=best_path(diff([ 0 best_path])~=0)+1;
word_indices=state_sequence(ismember(state_sequence,word_i));
[tf,index]=ismember(word_indices,word_i);

recognized_sentence={};
for j=1:length(index)
    recognized_sentence{j}=words{index(j)}.word;
end;
recognized_sentence
```

```
recognized_sentence =
    'we'    'hear'    'why'    'you'    'are'    'here'
```

We may finally compute again the word error rate on our complete test data (this is done in the accompanying MATLAB script). The final error rate of our word-based continuous speech recognizer is about 86.8%. This is only 2.4% less than when using pre-segmented words, which shows the efficiency of our sentence HMM model for both segmenting and classifying words. In practice, non segmented data is used for both training and testing, which could still slightly increase the word error rate.
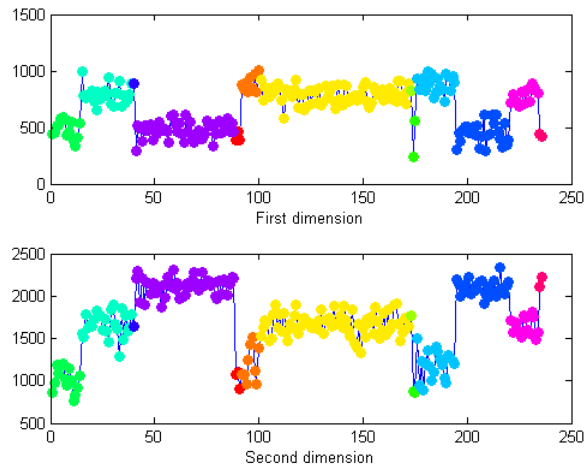

Fig. 4.20 Best path obtained by the Viterbi algorithm, from the sequence of feature vectors of the first test sentence.

4.3 Going further

Dictation machines still differ from this proof-of-concept in several ways. Mel Frequency Cepstral Coefficients (MFCCs) are used in place of our (F_1, F_2) formants for the acoustic model. Their first and second time-derivatives are added as features, as a simple way of accounting for the correlation between feature vectors *within* HMM states. Moreover, given the number of possible words in natural languages (several tens of thousands), ASR systems involve one additional layer in the statistical description of sentences: that of *phonemes*. The word HMMs we have trained above are replaced by phoneme HMMs. Word HMMs are themselves composed of phoneme HMMs (in the same way as we have built our sentence HMM from word HMMs), and additional pruning mechanisms are used in the decoder to constrain the search for the best sequence of words from the input feature vector sequence.

Several MATLAB-based HMM toolboxes are publicly available, such as Kevin Murphy's (Murphy 2005), Steinar Thorvaldsen's (Thorvaldsen 2005, applied to biology), or Olivier Cappé's (Cappé 2001). MATLAB also provides its own HMM toolbox under the Statistics Toolbox. The most famous HMM toolbox, originally developed for large vocabulary speech recognition, is the HTK toolkit developed at Cambridge University (in ANSI C; Young *et al.* 2006).

4.4 Conclusion

In this Chapter, we have seen how GMMs are used for the classification of (supposedly stationary) signals, and how HMMs provide a means of modeling non-stationary signals as sequences of stationary states. We have also implemented a simple bigram model, whose coupling with our word HMMs has resulted in a unique sentence HMM, able to perform continuous speech recognition, i.e., to find how many words are present in an incoming stream of feature vectors, and which words they are.

4.5 References

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