

Biostatistics 615/815 Lecture 23: The Baum-Welch Algorithm Advanced Hidden Markov Models

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April 12th, 2011

Key components in 815 Presentations

- Duration : 15 minutes
- Describe / illustrate what the problem is
- Key idea
- Results
- Challenges and lessons from implementations
- Comparisons with other alternatives (if possible)

Annoucement

Homework

- Final homework is announced.
- Implementing two among E-M algorithm, Simulated Annealing, and Gibbs Sampler

815 Project

- Presentation : Tuesday April 19th.
- Final report : Friday April 29th.

Final Exam

- Thursday April 21st, 10:30AM-12:30PM.

Recap - Gibbs Sampler Algorithm

- ① Consider a particular choice of parameter values $\lambda^{(t)}$.
- ② Define the next set of parameter values by
 - Selecting a component to update, say i .
 - Sample value for $\lambda_i^{(t+1)}$, from $p(\lambda_i|x, \lambda_1, \dots, \lambda_{i-1}, \lambda_{i+1}, \dots, \lambda_k)$.
- ③ Increment t and repeat the previous steps.

Recap - Gibbs Sampling for Gaussian Mixture

- Observed data : $\mathbf{x} = (x_1, \dots, x_n)$
- Parameters : $\mathbf{z} = (z_1, \dots, z_n)$ where $z_i \in \{1, \dots, k\}$.
- Sample each z_i conditioned by all the other \mathbf{z} .

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Today

Baum-Welch Algorithm

- An E-M algorithm for HMM parameter estimation
- Three main HMM algorithms
 - The forward-backward algorithm
 - The Viterbi algorithm
 - The Baum-Welch Algorithm

Advanced HMM

- Expedited inference with uniform HMM
- Continuous-time Markov Process

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Recap - Simulated Annealing and Gibbs Sampler

Both Methods are Markov Chains

- The distribution of $\lambda^{(t)}$ only depends on $\lambda^{(t-1)}$
- Update rule defines the transition probabilities between two states, requiring aperiodicity and irreducibility.

Both Methods are Metropolis-Hastings Algorithms

- Acceptance of proposed update is probabilistically determined by relative probabilities between the original and proposed states

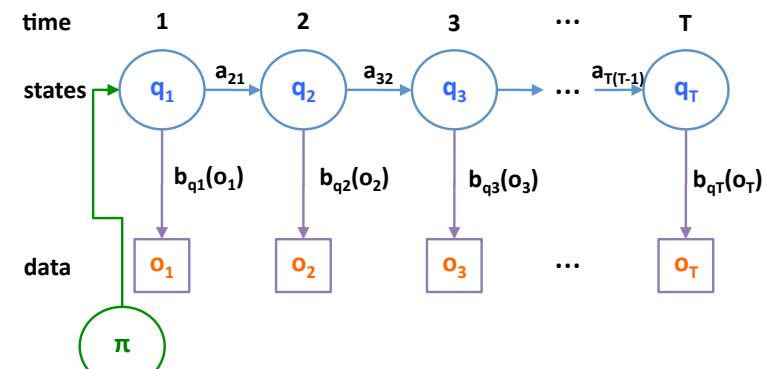
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Revisiting Hidden Markov Model



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Statistical analysis with HMM

HMM for a deterministic problem

- Given
 - Given parameters $\lambda = \{\pi, A, B\}$
 - and data $\mathbf{o} = (o_1, \dots, o_T)$
- Forward-backward algorithm
 - Compute $\Pr(q_t | \mathbf{o}, \lambda)$
- Viterbi algorithm
 - Compute $\arg \max_{\mathbf{q}} \Pr(\mathbf{q} | \mathbf{o}, \lambda)$

HMM for a stochastic process / algorithm

- Generate random samples of \mathbf{o} given λ

Using Stochastic Process for HMM Inference

Using random process for the inference

- Randomly sampling \mathbf{o} from $\Pr(\mathbf{o} | \lambda)$.
- Estimating $\arg \max_{\lambda} \Pr(\mathbf{o} | \lambda)$.
 - No deterministic algorithm available
 - Simplex, E-M algorithm, or Simulated Annealing is possible apply
- Estimating the distribution $\Pr(\lambda | \mathbf{o})$.
 - Gibbs Sampling

Deterministic Inference using HMM

- If we know the exact set of parameters, the inference is deterministic given data
 - No stochastic process involved in the inference procedure
 - Inference is deterministic just as estimation of sample mean is deterministic
- The computational complexity of the inference procedure is exponential using naive algorithms
- Using dynamic programming, the complexity can be reduced to $O(n^2 T)$.

Recap : The E-M Algorithm

Expectation step (E-step)

- Given the current estimates of parameters $\theta^{(t)}$, calculate the conditional distribution of latent variable \mathbf{z} .
- Then the expected log-likelihood of data given the conditional distribution of \mathbf{z} can be obtained

$$Q(\theta | \theta^{(t)}) = \mathbf{E}_{\mathbf{z}|\mathbf{x}, \theta^{(t)}} [\log p(\mathbf{x}, \mathbf{z} | \theta)]$$

Maximization step (M-step)

- Find the parameter that maximize the expected log-likelihood

$$\theta^{(t+1)} = \arg \max_{\theta} Q(\theta | \theta^t)$$

Baum-Welch for estimating $\arg \max_{\lambda} \Pr(\mathbf{o}|\lambda)$

Assumptions

- Transition matrix is identical between states
 - $a_{ij} = \Pr(q_{t+1} = i|q_t = j) = \Pr(q_t = i|q_{t-1} = j)$
- Emission matrix is identical between states
 - $b_i(j) = \Pr(o_t = j|q_t = i) = \Pr(o_{t-1} = j|q_{t-1} = i)$
- This is NOT the only possible assumption.
 - For example, a_{ij} can be parameterized as a function of t .
 - Multiple sets of \mathbf{o} independently drawn from the same distribution can be provided.
 - Other assumptions will result in different formulation of E-M algorithm

M-step of the Baum-Welch Algorithm

Let $\lambda^{(\tau+1)} = (\pi^{(\tau+1)}, A^{(\tau+1)}, B^{(\tau+1)})$

$$\begin{aligned}\pi^{(\tau+1)}(i) &= \frac{\sum_{t=1}^T \Pr(q_t = i|\mathbf{o}, \lambda^{(\tau)})}{T} = \frac{\sum_{t=1}^T \gamma_t(i)}{T} \\ a_{ij}^{(\tau+1)} &= \frac{\sum_{t=1}^{T-1} \Pr(q_t = j, q_{t+1} = i|\mathbf{o}, \lambda^{(\tau)})}{\sum_{t=1}^{T-1} \Pr(q_t = j|\mathbf{o}, \lambda^{(\tau)})} = \frac{\sum_{t=1}^{T-1} \xi_t(j, i)}{\sum_{t=1}^{T-1} \gamma_t(j)} \\ b_i(k)^{(\tau+1)} &= \frac{\sum_{t=1}^T \Pr(q_t = i, o_t = k|\mathbf{o}, \lambda^{(\tau)})}{\sum_{t=1}^T \Pr(q_t = i|\mathbf{o}, \lambda^{(\tau)})} = \frac{\sum_{t=1}^T \gamma_t(i) I(o_t = k)}{\sum_{t=1}^T \gamma_t(i)}\end{aligned}$$

A detailed derivation can be found at

- Welch, "Hidden Markov Models and The Baum Welch Algorithm", IEEE Information Theory Society News Letter, Dec 2003

E-step of the Baum-Welch Algorithm

- Run the forward-backward algorithm given $\lambda^{(\tau)}$

$$\begin{aligned}\alpha_t(i) &= \Pr(o_1, \dots, o_t, q_t = i|\lambda^{(\tau)}) \\ \beta_t(i) &= \Pr(o_{t+1}, \dots, o_T|q_t = i, \lambda^{(\tau)}) \\ \gamma_t(i) &= \Pr(q_t = i|\mathbf{o}, \lambda^{(\tau)}) = \frac{\alpha_t(i)\beta_t(i)}{\sum_k \alpha_t(k)\beta_t(k)}\end{aligned}$$

- Compute $\xi_t(i, j)$ using $\alpha_t(i)$ and $\beta_t(i)$

$$\begin{aligned}\xi_t(i, j) &= \Pr(q_t = i, q_{t+1} = j|\mathbf{o}, \lambda^{(\tau)}) \\ &= \frac{\alpha_t(i)a_{ij}b_j(o_{t+1})\beta_{t+1}(j)}{\Pr(\mathbf{o}|\lambda^{(\tau)})} \\ &= \frac{\alpha_t(i)a_{ij}b_j(o_{t+1})\beta_{t+1}(j)}{\sum_{(k,l)} \alpha_t(k)a_{kl}b_l(o_{t+1})\beta_{t+1}(l)}\end{aligned}$$

Implementing HMM Algorithms

```
class HMM615 {
public:
    int T;                                // number of instances
    int N;                                // number of states
    int O;                                // number of possible values
    std::vector<double> pis;               // pis[i]      : Pr(q_0=i)
    std::vector<double> trans;              // trans[i*N+j] : Pr(q_t=j|q_{t-1}=i)
    double symmTrans;
    std::vector<double> emis;              // emis[i*N+j] : Pr(o_t=j|q_t=i)
    std::vector<int> obs;                  // obs[t] : observed data from 0..O

    std::vector<double> alphas;            // alphas[t*n+i] : Pr(o_{1..t},q_t=i|lambda)
    std::vector<double> betas;              // betas[t*n+i]  : Pr(o_{t+1..T}|q_t=i,lambda)
    std::vector<double> gammas;             // gammas[t*n+i] : Pr(q_t=i|lambda,o_{1..T})

    double computeForwardBackward();
    double computeBaumWelch(double tol);
};
```

Implementing Forward algorithm : $\alpha_t(i)$

```
void HMM615::computeForwardBackward() {
    double sum = 0;
    // initialize alpha values
    for(int i=0; i < N; ++i)
        sum += (alphas[0*N + i] = pis[i] * emis[i*0+obs[0]]);
    for(int i=0; i < N; ++i) alphas[0*N + i] /= sum; // normalize sum(alphas)
    // iterate over alphas for each t
    for(int t=1; t < T; ++t) {
        for(int i=0; i < N; ++i) {
            alphas[t*N + i] = sum = 0;
            for(int j=0; j < N; ++j)
                alphas[t*N + i] += (alphas[(t-1)*N + j] * trans[j*N + i]);
            sum += (alphas[t*N + i] *= emis[i*0+obs[t]]);
        }
        for(int i=0; i < N; ++i) alphas[t*N + i] /= sum; // normalize sum(alphas)
    }
    // (continued to next slides)
}
```

Combining forward-backward algorithm : $\gamma_t(i)$

```
// compute gammas = Pr(q_t|o,lambda)
for(int t=0; t < T; ++t) {
    sum = 0;
    for(int i=0; i < N; ++i)
        sum += (gammas[t*N + i] = alphas[t*N + i] * betas[t*N + i]);
    for(int i=0; i < N; ++i)
        gammas[t*N + i] /= sum; // normalize sum(gammas)
}
}
```

Implementing Backward algorithm : $\beta_t(i)$

```
// initialize the last element of betas
sum = 0;
for(int i=0; i < N; ++i) sum += emis[i*0+obs[T-1]];
for(int i=0; i < N; ++i) betas[(T-1)*N + i] = 1./sum;
// main body of backward algorithm
for(int t=T-2; t >= 0; --t) {
    for(int i=0; i < N; ++i) {
        betas[t*N + i] = sum = 0;
        for(int j=0; j < N; ++j)
            betas[t*N + i] += (betas[(t+1)*N + j] * trans[i*N + j]
                                 * emis[j*0+obs[t+1]]);
        sum += (betas[t*N+i] * emis[i*0+obs[t]]);
    }
    sum = 0;
    // normalize sum (betas * emis )
    for(int i=0; i < N; ++i) betas[t*N + i] /= sum;
}
// (continued to next slide)
```

Implementation Notes : Forward-backward algorithm

- Forward-backward algorithm for arbitrary numbers of states and observations.
- Normalization of $\sum_t \alpha_t(i)$ and $\sum_i \beta_t(i) b_i(o_t)$ at each step
 - Only relative values of $\alpha_t(i)$ and $\beta_t(i)$ are important
 - Avoids potential overflow / underflow due to numerical precision
 - Why normalize $\sum_i \beta_t(i) b_i(o_t)$ instead of $\sum_i \beta_t(i)$?

A small utility function : update

```
// assign newVal to dst, after computing the relative differences between them
// note that dst is call-by-reference, and newVal is call-by-value
double HMM615::update(double& dst, double newVal) {
    // calculate the relative differences
    double relDiff = fabs((dst-newVal)/(newVal+ZEPS));
    // update the destination value
    dst = newVal;
    // update the destination value
    return relDiff;
}
```

The Baum-Welch Algorithm : E-step

```
// calculate \sum_t gamma_t(i)
for(int t=0; t < T; ++t) {
    for(int i=0; i < N; ++i) {
        sumGammas[i] += gammas[t*N + i];
        sumObsGammas[i*0 + obs[t]] += gammas[t*N + i];
    }
}
// calcupate \sum_t xi_t(i,j)
for(int t=0; t < T-1; ++t) {
    sum = 0;
    for(int i=0; i < N; ++i) {
        for(int j=0; j < N; ++j)
            sum += ( xis[i*N+j] = ( alphas[t*N + i] * trans[i*N + j] *
                           betas[(t+1)*N + j] *emis[j*0 + obs[t+1]] ) );
    }
    for(int i=0; i < N*N; ++i)    sumXis[i] += (xis[i] /= sum);
}
```

The Baum-Welch Algorithm : Initialization

```
void HMM615::computeBaumWelch(double tol) {
    double tmp, sum, relDiff = 1e9;

    std::vector<double> sumGammas(N,0), sumObsGammas(N*0,0);
    std::vector<double> xis(N*N,0), sumXis(N*N,0);

    // iterate until the difference is small enough
    for(int iter = 0; (iter < MAX_ITERATION) && ( relDiff > tol ); ++iter) {
        relDiff = 0;
        computeForwardBackward(); // run forward-backward algorithm
        for(int i=0; i < N; ++i)    sumGammas[i] = 0;
        for(int i=0; i < N*0; ++i) sumObsGammas[i] = 0;
        for(int i=0; i < N*N; ++i) xis[i] = sumXis[i] = 0;
```

The Baum-Welch Algorithm : M-step

```
// update transition matrix
for(int i=0; i < N; ++i) {
    for(int j=0; j < N; ++j) {
        tmp = sumXis[i*N+j] / (sumGammas[i]-gammas[(T-1)*N+i]+ZEPS);
        relDiff += update( trans[i*N+j], tmp );
    }
}

// update pis and emission matrix
for(int i=0; i < N; ++i) {
    relDiff += update( pis[i], sumGammas[i]/T );
    for(int j=0; j < O; ++j)
        relDiff += update (emis[i*O+j], sumObsGammas[i*O+j]/(sumGammas[i]+ZEPS));
}
} // repeat until relative difference is small enough
```

A working example : Biased coin example

Model

- Observations : $O = \{1(Head), 2(Tail)\}$
- Hidden states : $S = \{1(Fair), 2(Biased)\}$
- Initial states : $\pi = \{0.8, 0.2\} = A^\infty \pi_0$
- Transition probability : $A(i, j) = a_{ij} = \begin{pmatrix} 0.95 & 0.2 \\ 0.05 & 0.8 \end{pmatrix}$
- Emission probability : $B(i, j) = b_j(i) = \begin{pmatrix} 0.5 & 0.9 \\ 0.5 & 0.1 \end{pmatrix}$

Biased coin example : Results

```
user@host:~/baumWelchCoin biasedCoinInput.10000.txt
Iteration 216,
normDiff = 0.000982141,
pis = (0.80249, 0.19751),
trans = (0.942284, 0.0577156, 0.234439, 0.765561),
emis = (0.493703, 0.506297, 0.905311, 0.0946887)

user@host:~/baumWelchCoin biasedCoinInput.1000.txt
Iteration 621,
normDiff = 0.00099904,
pis = (0.544055, 0.455945),
trans = (0.723604, 0.276396, 0.330778, 0.669222),
emis = (0.291926, 0.708074, 0.904004, 0.0959957)
```

Biased coin example : main() function

```
int main(int argc, char** argv) {
    // input/output routines ... omitted
    // assign an initial starting point
    double theta0 = 0.1;
    std::vector<double> trans(4, theta0);
    std::vector<double> emis(4, 0.5);
    std::vector<double> pis(2, 0.5); // initial pi = (0.5, 0.5)
    trans[0] = trans[3] = 1-theta0; // initial A = (0.9, 0.1; 0.1, 0.9)
    emis[2] = 0.7; emis[3] = 0.3; // initial B = (0.5, 0.7; 0.5; 0.3)

    HMM615 hmm(pis, trans, emis, observations); // constructor omitted in the slides
    hmm.computeBaumWelch(1e-3); // run Baum-Welch algorithm

    return 0;
}
```

Summary : Baum-Welch Algorithm

- E-M algorithm for estimating HMM parameters
- Assumes identical transition and emission probabilities across t
- The framework can be accommodated for differently constrained HMM
- Requires many observations to reach a reliable estimates

Rapid Inference with Uniform HMM

Uniform HMM

- Definition
 - $\pi_i = 1/n$
 - $a_{ij} = \begin{cases} \theta & i \neq j \\ 1 - (n-1)\theta & i = j \end{cases}$
 - $b_i(k)$ has no restriction.
- Independent transition between n states
- Useful model in genetics and speech recognition.

Forward Algorithm with Uniform HMM

Original Forward Algorithm

$$\alpha_t(i) = \Pr(o_1, \dots, o_t, q_t = i | \lambda) = \left[\sum_{j=1}^n \alpha_{t-1}(j) a_{ij} \right] b_i(o_t)$$

Rapid Forward Algorithm for Uniform HMM

$$\begin{aligned} \alpha_t(i) &= \left[\sum_{j=1}^n \alpha_{t-1}(j) a_{ij} \right] b_i(o_t) \\ &= \left[(1 - (n-1)\theta) \alpha_{t-1}(i) + \sum_{j \neq i} \alpha_{t-1}(j) \theta \right] b_i(o_t) \\ &= [(1 - n\theta) \alpha_{t-1}(i) + \theta] b_i(o_t) \end{aligned}$$

- Assuming normalized $\sum_i \alpha_t(i) = 1$ for every t .
- The total time complexity is $O(nT)$.

Rapid Inference with Uniform HMM

Uniform HMM

- Definition
 - $\pi_i = 1/n$
 - $a_{ij} = \begin{cases} \theta & i \neq j \\ 1 - (n-1)\theta & i = j \end{cases}$
 - $b_i(k)$ has no restriction.
- Independent transition between n states
- Useful model in genetics and speech recognition.

The Problem

- The time complexity of HMM inference is $O(n^2 T)$.
- For large n , this still can be a substantial computational burden.
- Can we reduce the time complexity by leveraging the simplicity?

Backward Algorithm with Uniform HMM

Original Forward Algorithm

$$\beta_t(i) = \Pr(o_{t+1}, \dots, o_T | q_t = i, \lambda) = \sum_{j=1}^n \beta_{t+1}(j) a_{ji} b_j(o_{t+1})$$

Rapid Forward Algorithm for Uniform HMM

$$\begin{aligned} \beta_t(i) &= \sum_{j=1}^n \beta_{t+1}(j) a_{ji} b_j(o_{t+1}) \\ &= (1 - (n-1)\theta) \beta_{t+1}(i) b_i(o_{t+1}) + \theta \sum_{j \neq i} \beta_{t+1}(j) b_j(o_{t+1}) \\ &= (1 - n\theta) \beta_{t+1}(i) b_i(o_{t+1}) + \theta \end{aligned}$$

Assuming $\sum_i \beta_t(i) b_i(o_t) = 1$ for every t . (Now we know why!)

Summary : Uniform HMM

- Rapid computation of forward-backward algorithm leveraging symmetric structure
- Rapid Baum-Welch algorithm is also possible in a similar manner
- It is important to understand the computational details of existing methods to further tweak the method when necessary.

Key Idea of CTMP

Transition Rate instead of Transition Probability

- In discrete MP, a_{ij} defines the transition probability between states
- In CTMP, transition rate ρ defines the transition probability within some time intervals.

$$\Pr(q_s = i, \forall s \in (t, t+r) | q_t = i) = \exp(-\rho_{ii}r)$$

Difference from discrete HMM

- The transition probability between time points are no longer identical
- However, the transition probability can be parameterized using ρ and the interval size
- Developing E-M algorithm for estimating ρ is more sophisticated than the Baum-Welch algorithm

Continuous-time Markov Process (CTMP)

Example : Single dimensional Brownian motion

- A particle is moving along a line at a constant velocity v .
- At a rate λ times per second, the particle changes the direction.
- The position of particle is observed at arbitrary time points t_1, t_2, \dots, t_n .
- How can we model the trajectory of the particles given observations?

Other Applications

- Queueing theory
- Modeling recombination in diploid organisms
- Many other infinitesimal Models

Summary

Today

- The Baum-Welch Algorithm
- Rapid inference with Uniform HMM
- Continuous-time Markov Process (CTMP)

Next Lecture

- Overview for the Final Exam