Coupled Hidden Markov Models: some computational challenges

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1. CHMMs

Coupled Hidden Markov Models (CHMMs) are a natural extension of HMMs when there are multiple observation sequences with dependencies:

Notation: *x* (*i*) $\overset{(i)}{t},y$ (*i*) *t* : hidden state/obs at time *t* in chain *i*.

 $Z_t = (X$ (1) $t^{(1)},\ldots,X$ (3) $\left(\begin{smallmatrix} 1 & 0 \ t & \end{smallmatrix} \right)$ and Y (*i*) $\left| Z_t \right| = Y$ (*i*) $\int_t^{\tau(t)}|X|$ (*i*) *t* \implies for *C* chains with *X* (*i*) $\{e^{i\theta}\}\ \in\ \{1,\dots,N\},$ $|Z_t| = N^C$.

References

Saul and Jordan (1999) Mixture Model $\mathbb{P}(X_t^{(i)}$ $\left| \frac{u}{t} \right|$ x (1:*C*) $\binom{(1:C)}{t-1} = \sum$ *C* $k=1$ ω_{ki} $\mathbb{P}(X_t^{(i)}$ $\left| \frac{u}{t} \right|$ x (*k*) $\binom{\kappa}{t-1}$

Likelihood $\mathbb{P}(Y_{1:T}^{(1:C)}% ,\mathbb{P})=\mathbb{P}(Y_{1:T}^{(1:C)}% ,\mathbb{P})=\mathbb{P}(Y_{1:T}^{(1:C)}% ,\mathbb{P})$ $\binom{I:C}{1:T} \approx \prod$ *C k*=1 $\mathbb{P}(Y^{(k)}_{1:T})$ $\binom{r(k)}{1:T} = \prod$ *C k*=1 *i*=1 \sum *N α* (*k*) $T^{(\kappa)}(i)$

with *α* (*k*) $T^{(\kappa)}_T(i)$ itself a factored approximation of the forward variable. Only $C = 2$ example.

Choi, H., Fermin, D., Nesvizhskii, A. I., Ghosh, D. and Qin, Z. S. (2013), 'Sparsely correlated hidden Markov models with application to genome-wide location studies', *Bioinformatics* **29**(5), 533–541. Holmes, C. C. and Held, L. (2006), 'Bayesian auxiliary variable models for binary and multinomial regression', *Bayesian Analysis* **1**(1), 145–168. Pakman, A. and Paninski, L. (2013), 'Auxiliary-variable exact Hamiltonian Monte Carlo samplers for binary distributions', *arXiv* (1311.2166). Saul, L. K. and Jordan, M. I. (1999), 'Mixed memory Markov models: decomposing complex stochastic processes as mixtures of simpler ones', *Machine Learning* **37**(1), 75–86. Sherlock, C., Xifara, T., Telfer, S. and Begon, M. (2013), 'A coupled hidden Markov model for disease interactions', *Journal of the Royal Statistical Society, Series C* **62**(4), 609–627. Zhong, S. and Ghosh, J. (2002), HMMs and coupled HMMs for multi-channel EEG classification, *in* 'Proceedings of the International Joint Conference on Neural Networks', Vol. 2, pp. 1154–1159.

Choi *et al.* **(2013) Logistic Regression** Similarly, a transition matrix per chain, with logistic regression transition probabilities. But, for speed, ad-hoc inferential procedure: mixture model EM to infer observation model, Viterbi to select most likely hidden sequence, IRLS on subsample to fit LR with lasso+AIC. $C = 39, N = 2, T = 15.4 \times 10^6$

3. Existing approaches

ωki can be viewed as mixing weights, or strength of effect of chain *k* on chain *i*. Now only *NC*² parameters.

Zhong and Ghosh (2002) Marginal Composite

5. Our main interest and scaling towards $C = 100$ — initial work

Sherlock *et al.* **(2013) Structured Transitions** Uses structured transition matrix for each chain, where probabilities modelled with a logistic regression with others chains (and external factors) as covariates.

 $\mathbb{P}(X^{(l)}_{T-})$ $T^{-t}_{T-t} = i \,|\, X$ (*l*) $T-t+1 = j, \mathbf{y}$ (*l*) $_{1:T}^{\left(\iota\right) },\mathbf{x}%$ $(-l)$ $\binom{-\iota}{1:T} \propto \alpha$ (*l*) (*n*−*t*+1)*ij*

4. Our hidden layer model

Funding

This work is funded under the EPSRC i-like project.

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2. The naïve approach

One might naïvely reformulate as:

Natural forward variable becomes:

Objective is inference in the minimal setting of $N = 10, C = 100, T = 10^5$. This leads to numerous challenges:

- computing forward variable \implies TN^C additions and *TC* multiplications; $\geq 10^{105}$ elementary operations
- forward variable requires $8TN^C$ bytes of memory to store; $\geq 7.45 \times 10^{96}$ GB memory • transition matrix is $N^C \times N^C$. $\geq 9.31\times 10^{190}$ GB memory

Hence, naïve approach clearly a non-starter.

$$
\alpha_t(i_1, \dots, i_C) = \mathbb{P}(Y_{1:t}^{(1:C)} = y_{1:t}^{(1:C)}, X_t^{(1:C)} = i_{1:C})
$$
\n
$$
= \left(\sum_{j_1=1}^N \dots \sum_{j_C=1}^N \alpha_{t-1}(j_1, \dots, j_C) \prod_{k=1}^C \mathbb{P}(X_t^{(k)} = i_k \mid x_{t-1}^{(1:C)} = j_{1:C}) \right) \prod_{k=1}^C f_{Y \mid X}(y_t^{(k)} \mid i_k)
$$

There is some interest in inference on model parameters, but our *primary* interest is actually in inferring dependence structure. e.g. in genomics data set this could infer ancestry. ∴ direct multinomial logistic regression transition model: a blocked spike-and-slab prior for Bayesian variable selection is then equivalent to inferring the hidden layer structure.

MCMC sampler

- Hidden states: conditional forward/ stochastic-backward **X** (*i*) $\left. \begin{matrix} 1\ 1\ 1\ \end{matrix} ; T \right| \boldsymbol{\beta}, \boldsymbol{\lambda}, \mathbf{Y}$ (*i*) $_{1:T}^{\left(\iota\right) },\mathbf{X}% _{1:T^{\left(\iota\right) },\mathbf{X}_{2}:}^{\left(\iota\right) },$ $(-i)$ $\{1:T \text{ for } i \in \{1,\ldots,C\}$ • Multinomial logistic parameters
- *β* | **X** (1:*C*) 1:*T*
- Observation model parameters *λ* | **Y** (1:*C*) $_{1:T}^{(\texttt{1:} \cup \texttt{})}, \mathbf{X}$ (1:*C*) 1:*T*

Hidden states Define conditional forward variable

$$
\alpha_{tjk}^{(l)} = \mathbb{P}(y_t^{(l)}, X_{t-1}^{(l)} = j, X_t^{(l)} = k | \mathbf{y}_{1:t-1}^{(l)}, \mathbf{x}_{1:T}^{(-l)})
$$

$$
= \left(\sum_{i=1}^N \alpha_{(t-1)ij}^{(l)}\right) \frac{\exp(\tilde{\mathbf{x}}_{t-1}^{*j} \boldsymbol{\beta}_k^{(l)})}{1 + \sum_{n=1}^{N-1} \exp(\tilde{\mathbf{x}}_{t-1}^{*j} \boldsymbol{\beta}_n^{(l)})}
$$

$$
\times f_{Y_t^{(i)} | X_t^{(i)} } \left(y_t^{(i)} | k\right)
$$

Then sample **X** (*i*) $\left. \begin{array}{l} \left(\ ^{t}\right) \ 1:T \end{array} \right|\boldsymbol{\beta},\boldsymbol{\lambda},\mathbf{Y}$ (*i*) $_{1:T}^{\left(\iota\right) },\mathbf{X}% _{1:T}^{\left(\iota\right) },\mathbf{A}^{\left(\iota\right) },$ $(-i)$ $\sum_{1:T}^{(-i)}$ backwards, since: *N*

$$
\mathbb{P}(X_T^{(l)} = j \, | \, \mathbf{y}_{1:T}^{(l)}, \mathbf{x}_{1:T}^{(-l)}) = \sum_{i=1} \alpha_{Tij}^{(l)}
$$

Logistic regression

Currently using Holmes and Held (2006).

Results

6. Current work

Probit regression

Adapting Pakman and Paninski (2013), a Hamiltonian Monte Carlo sampler for truncated multivariate Gaussian and binary distributions. Achieved substantial speedup vs author's reference C++ implementation by exploiting problem specific features.

Currently exploring GPU implementation:

boundary hit times embarassingly parallel; minimum hit time a reduction operator; entire problem can propagate on GPU. **Hidden states**

Also, exploring block sampling hidden states. Need to find an algorithm to partition chains in some sense 'optimally': mixing -vs- compute.