

# Variational Inference for Large-Scale and Streaming Sequential Data

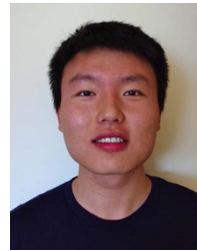
Emily Fox



Nick Foti



Alex Tank

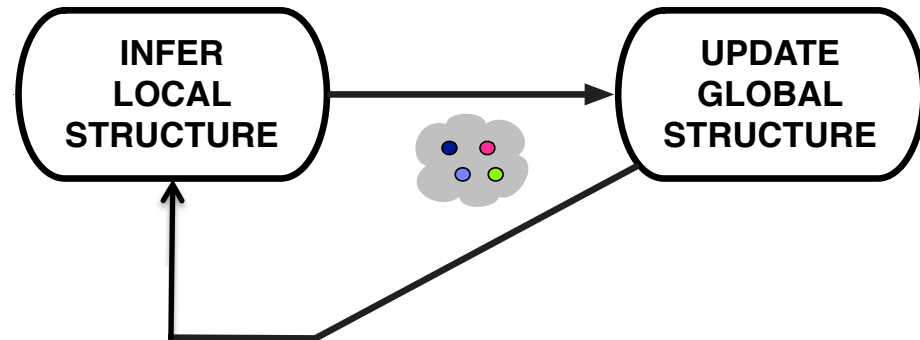


Jason Xu



Dillon Laird

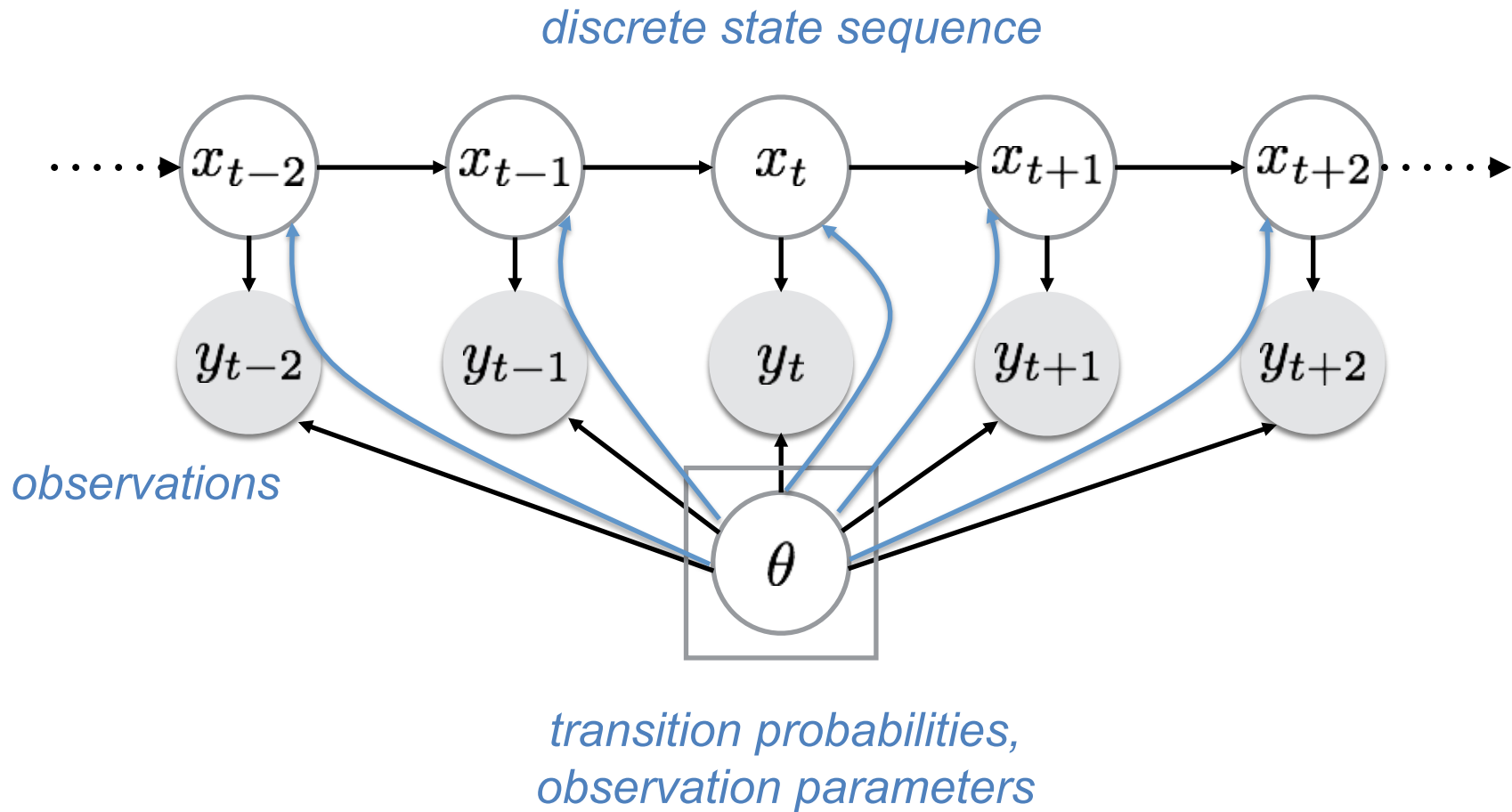
# Minibatch-Based Algorithms



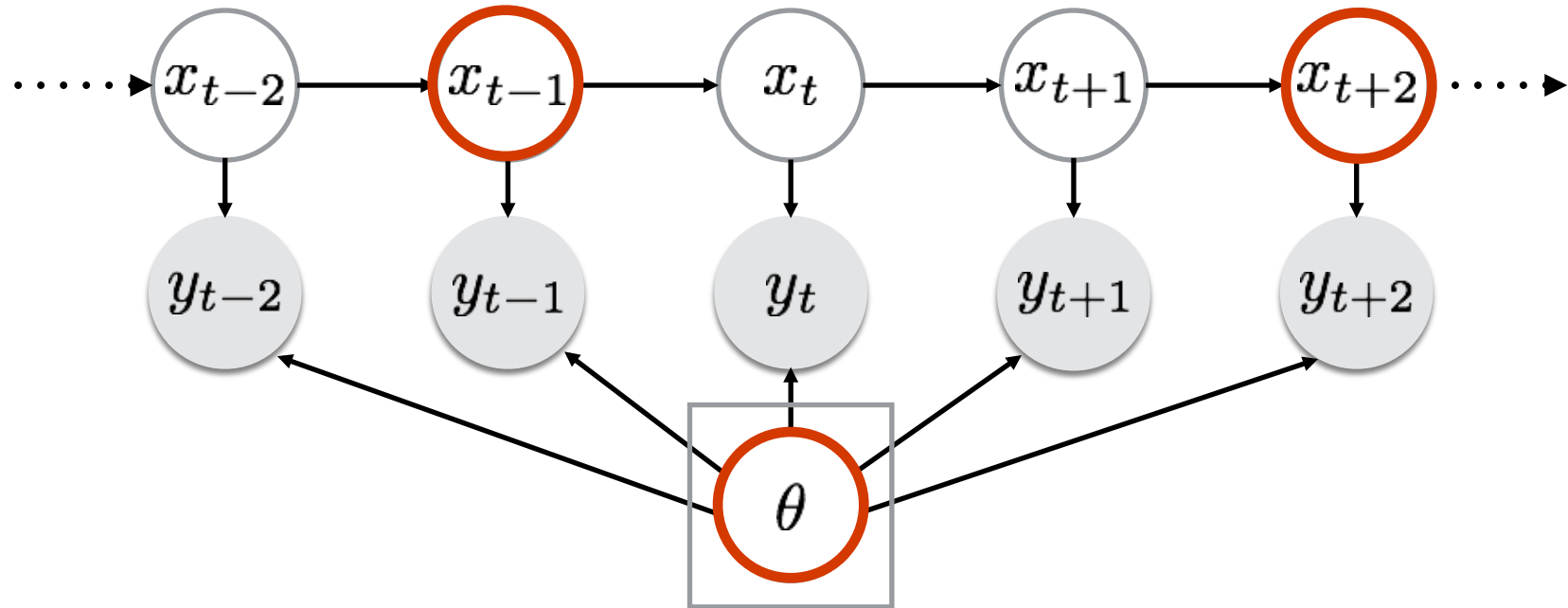
- Many ML/stat algorithms (e.g., gradient descent, Gibbs sampling,...) iterate between
  - operations involving **all data**
  - **updating parameters**
- Costly for large data / infeasible for streaming data
- Common approach for scalability:
  - **subsample data** → noisy operation
  - **noisy update** of parameters

**Not appropriate for  
dependent data**

# Hidden Markov Models (HMMs)



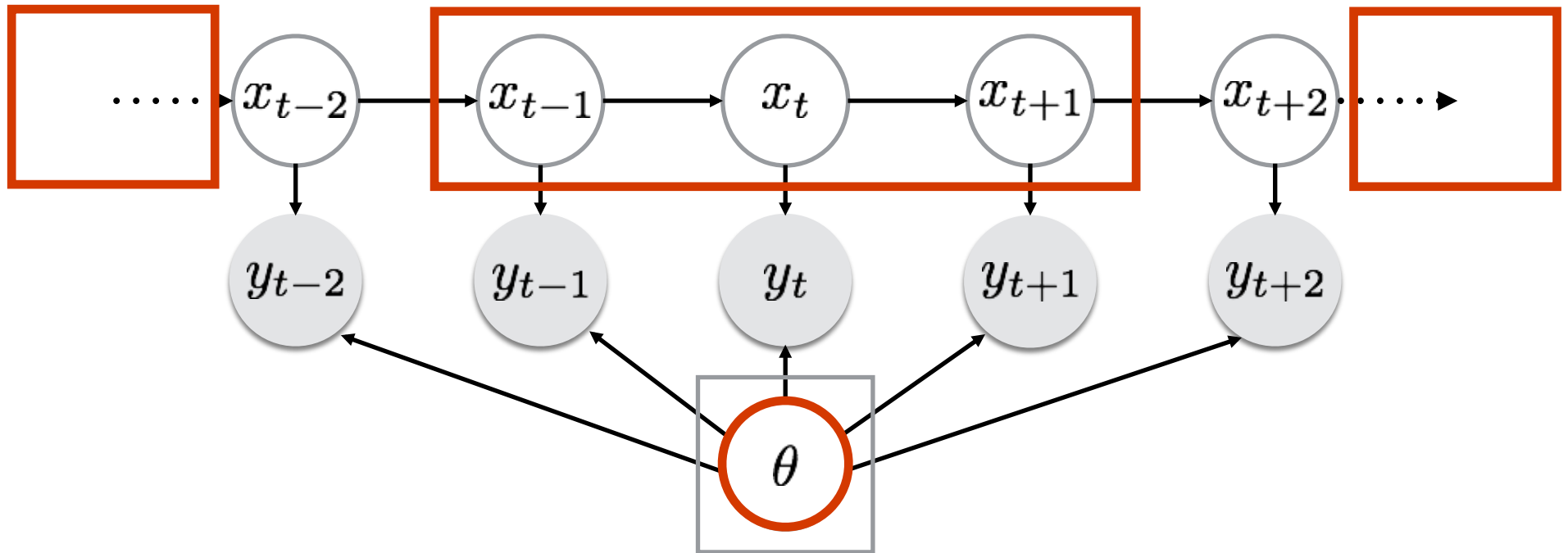
# Minibatches for HMMs



- Why not just subsample observations independently?
- Cannot learn transition structure

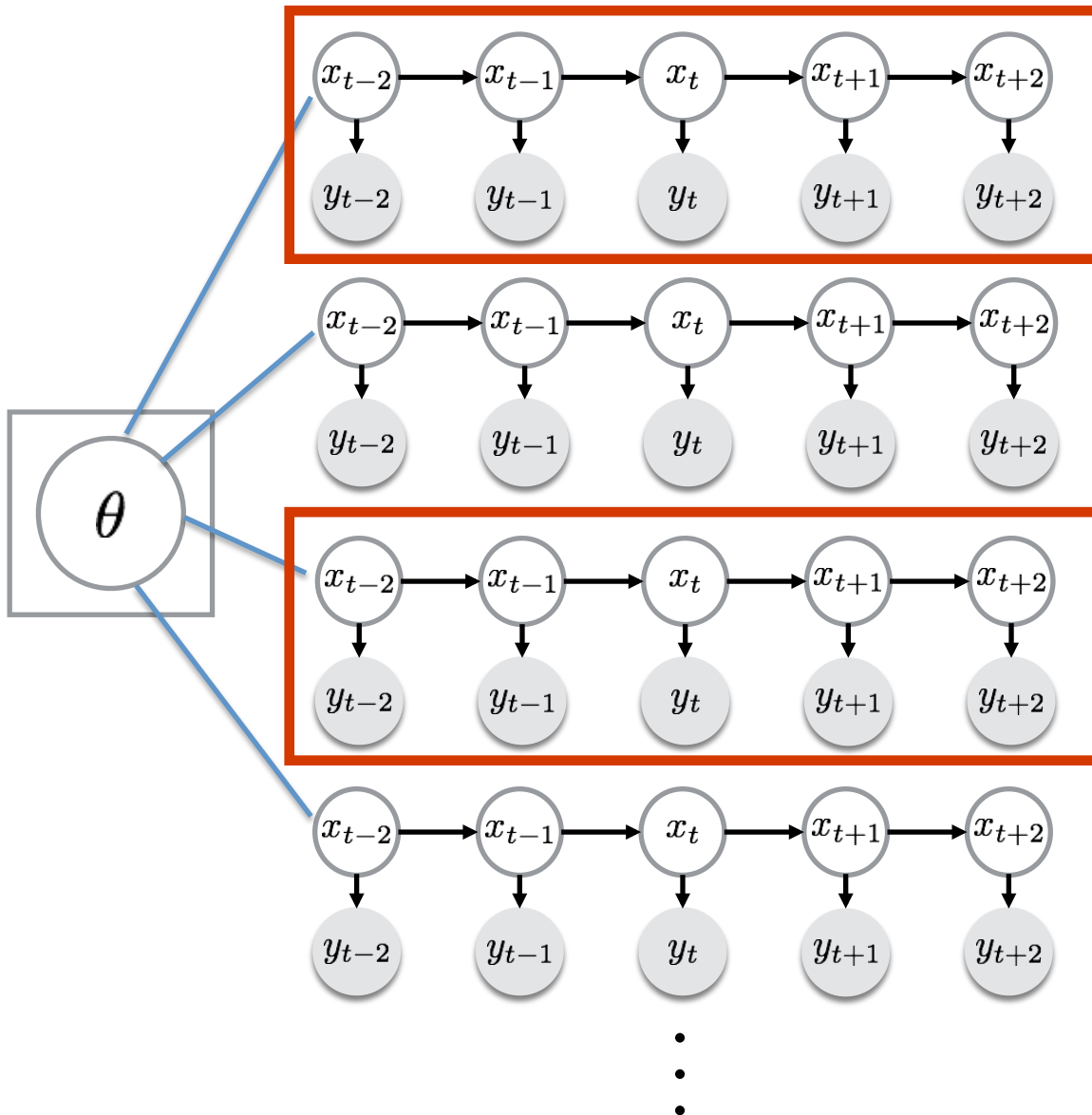
$$p(\mathbf{y}, \mathbf{x}, \theta) = p(\theta)\pi(x_1) \prod_{t=2}^T p(x_t | x_{t-1}, \theta_A) p(y_t | x_t, \theta_\phi)$$

# Minibatches for HMMs



- How about sampling *subchain*?  $x^S = (x_{t-L}, \dots, x_t, \dots, x_{t+L})$
- Do we just *sever dependencies* between subchains and analyze *separately*?

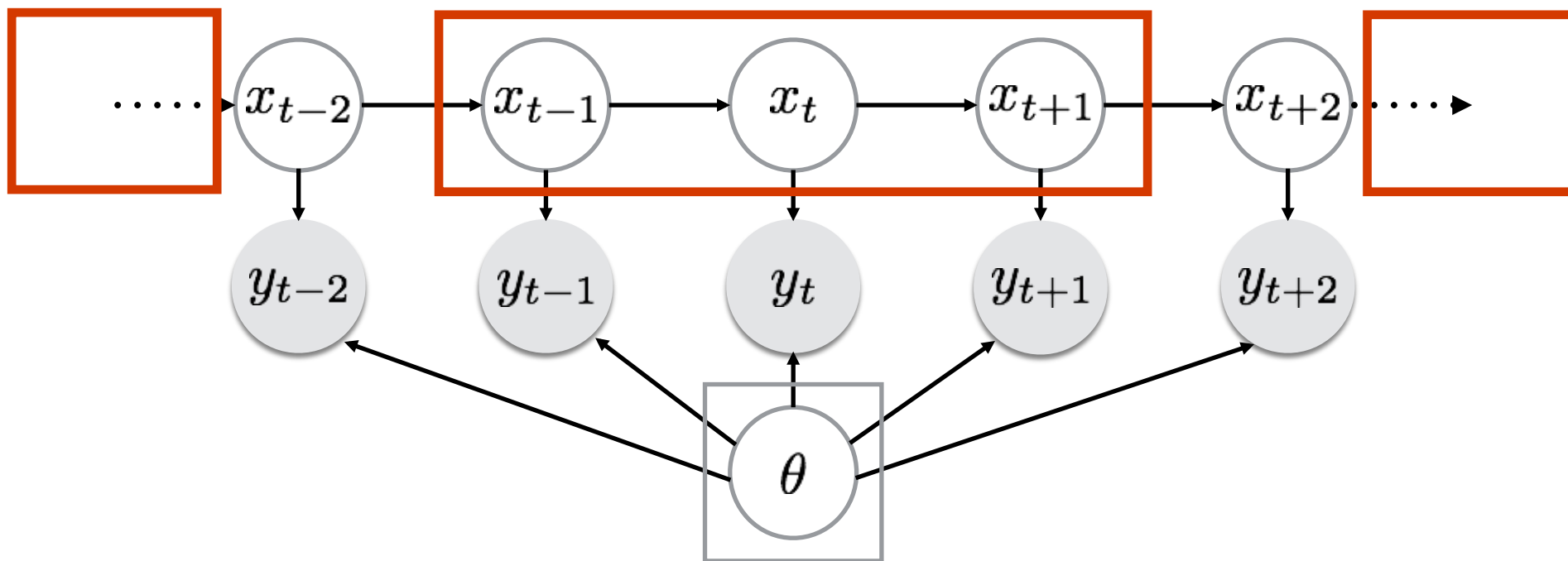
# Large Collections of Short Chains



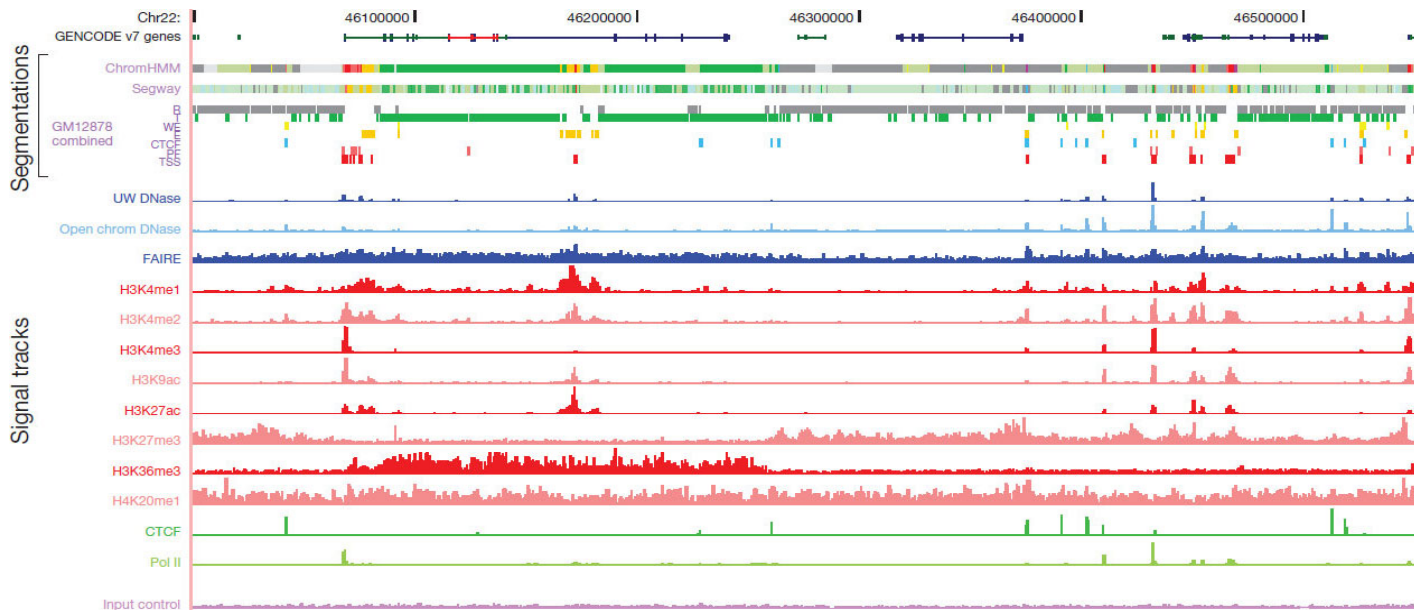
Johnson and Willsky,  
ICML 2014

Hughes et al.,  
NIPS 2015

# One Long Chain



# Human Chromatin Segmentation



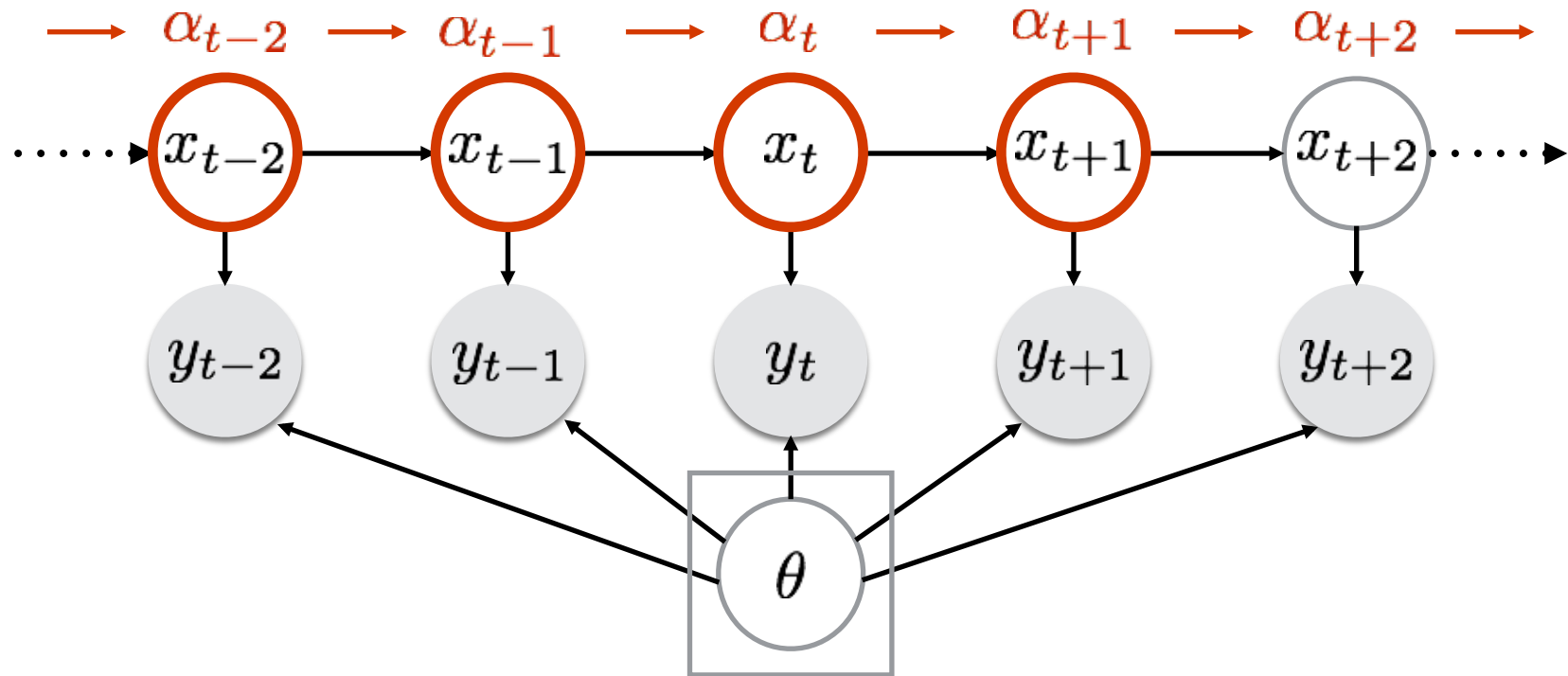
- Chromosome data set from the ENCODE project
  - ENcyclopedia Of DNA Elements
- 12 dimensional observations **T = 250 million**
- **Goal:** segment sequences



# **BATCH LEARNING FOR HMMs**

A quick review

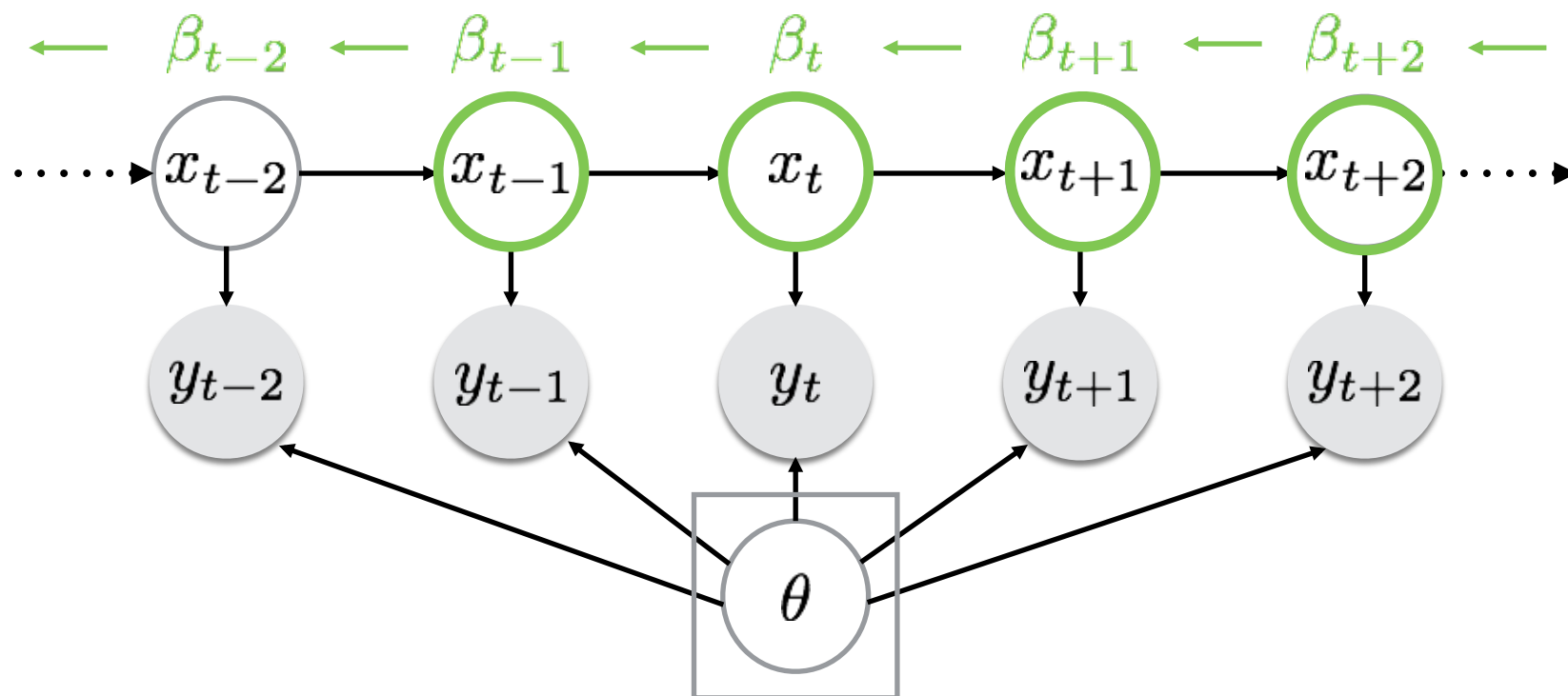
# Batch Learning for HMMs



- Use current  $\theta$  to form local state beliefs:
  - Propagate info forwards to form  $\alpha_t = p(y_1, \dots, y_t, x_t)$

$$\alpha_{t+1,k} = p(y_{t+1} \mid x_{t+1} = k) \sum_{j=1}^K \alpha_{t,j} p(x_{t+1} = k \mid x_t = j)$$

# Batch Learning for HMMs

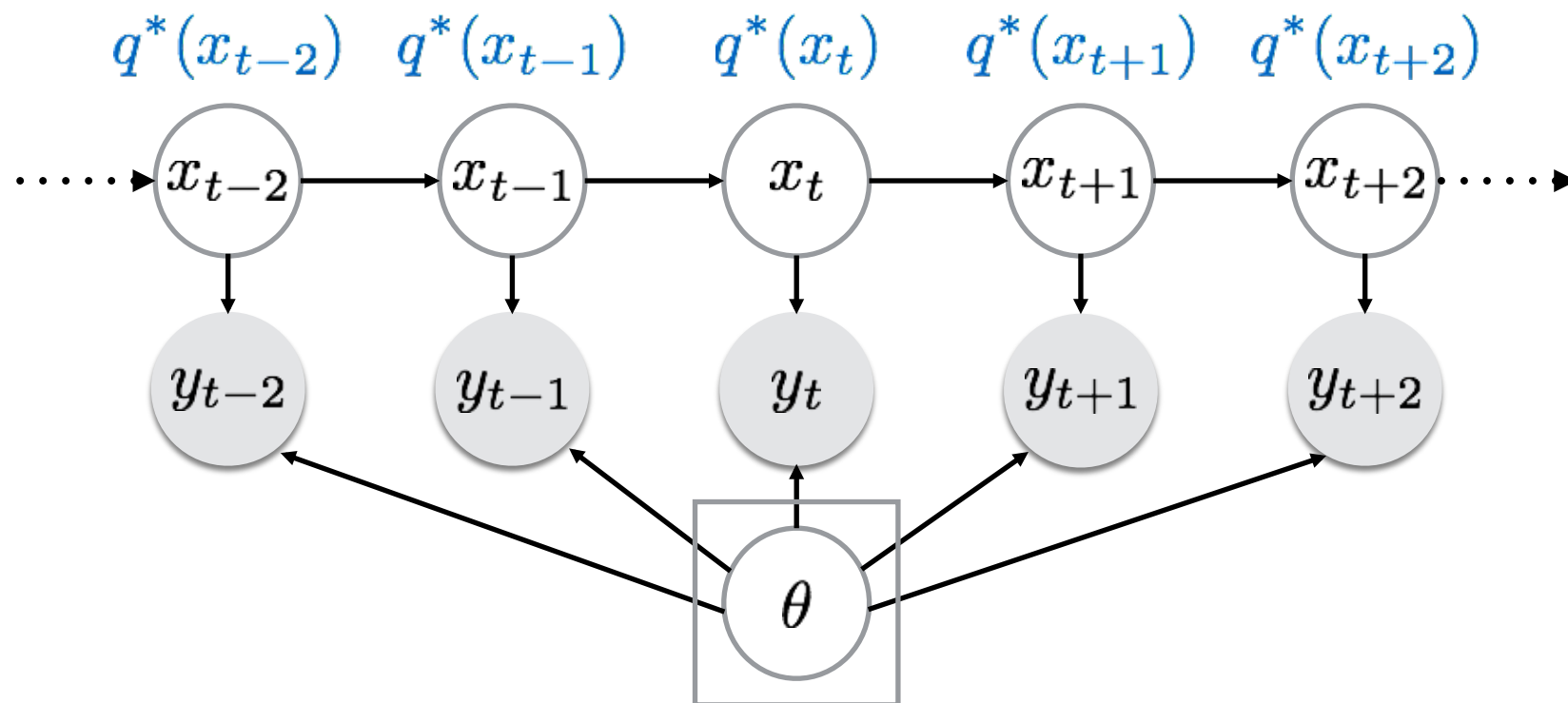


- Use current  $\theta$  to form local state beliefs:

– Propagate info backwards  $\beta_t = p(y_{t+1}, \dots, y_T | x_t)$

$$\beta_{t,k} = \sum_{j=1}^K p(y_{t+1} | x_{t+1} = j) p(x_{t+1} = j | x_t = k) \beta_{t+1,k}$$

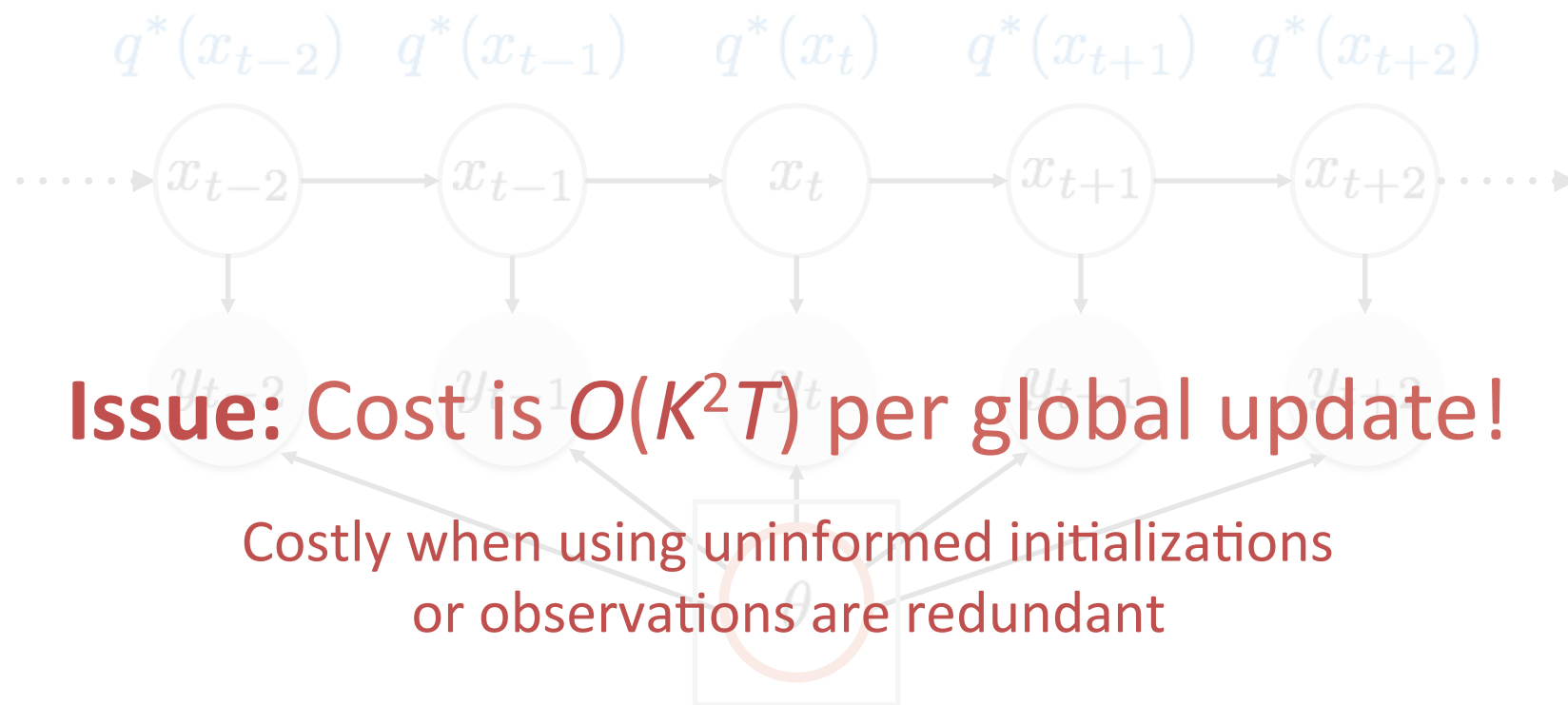
# Batch Learning for HMMs



- Combine to form *smoothed* local state belief:

$$p(x_t \mid y_1, \dots, y_T, \theta) \propto q^*(x_t) \propto \alpha_t \beta_t$$

# Batch Learning for HMMs

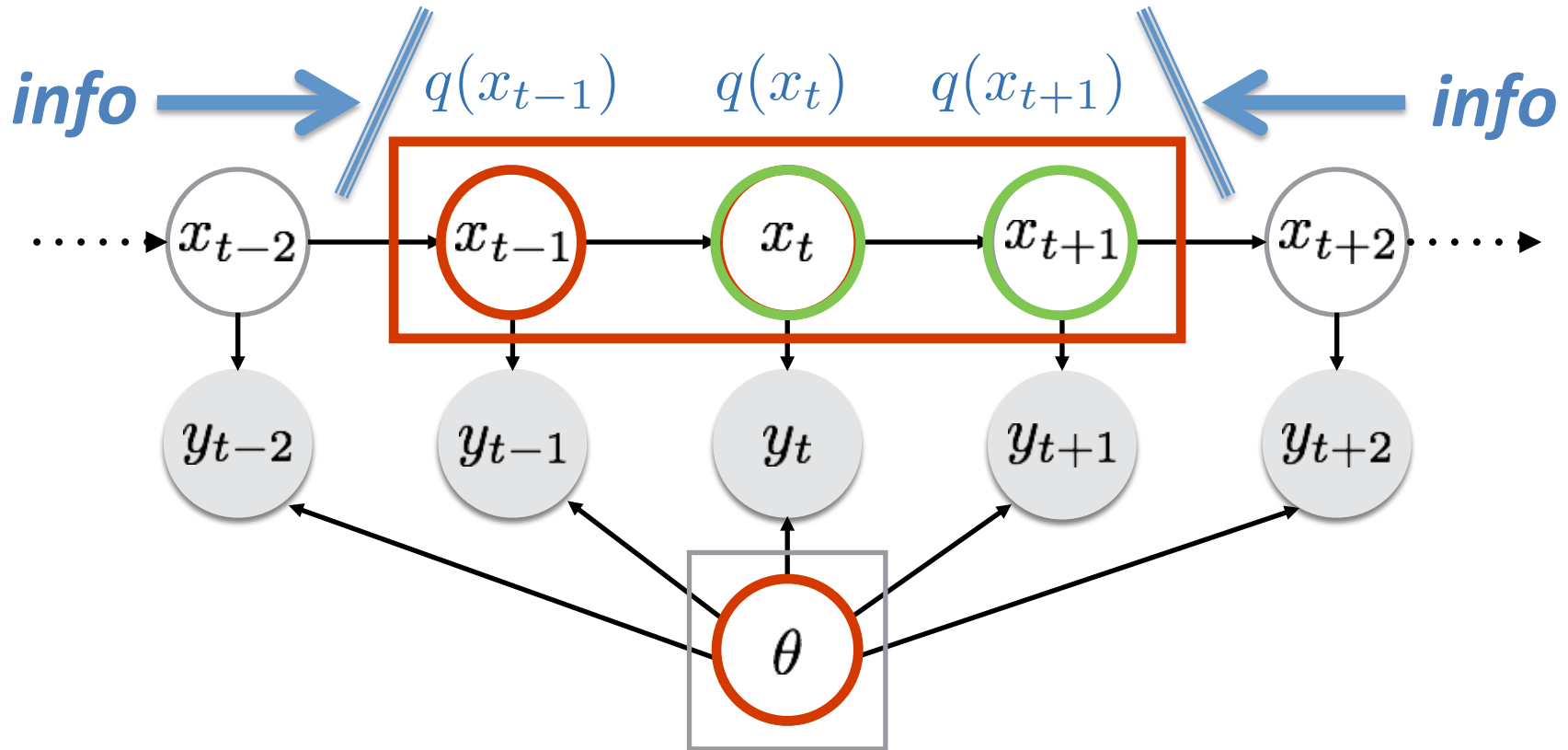


- Given local beliefs, update global parameter  
 $T = 250$  million

# **MINIBATCH LEARNING FOR HMMs?**

Issues and solutions

# Minibatch Inference for HMMs

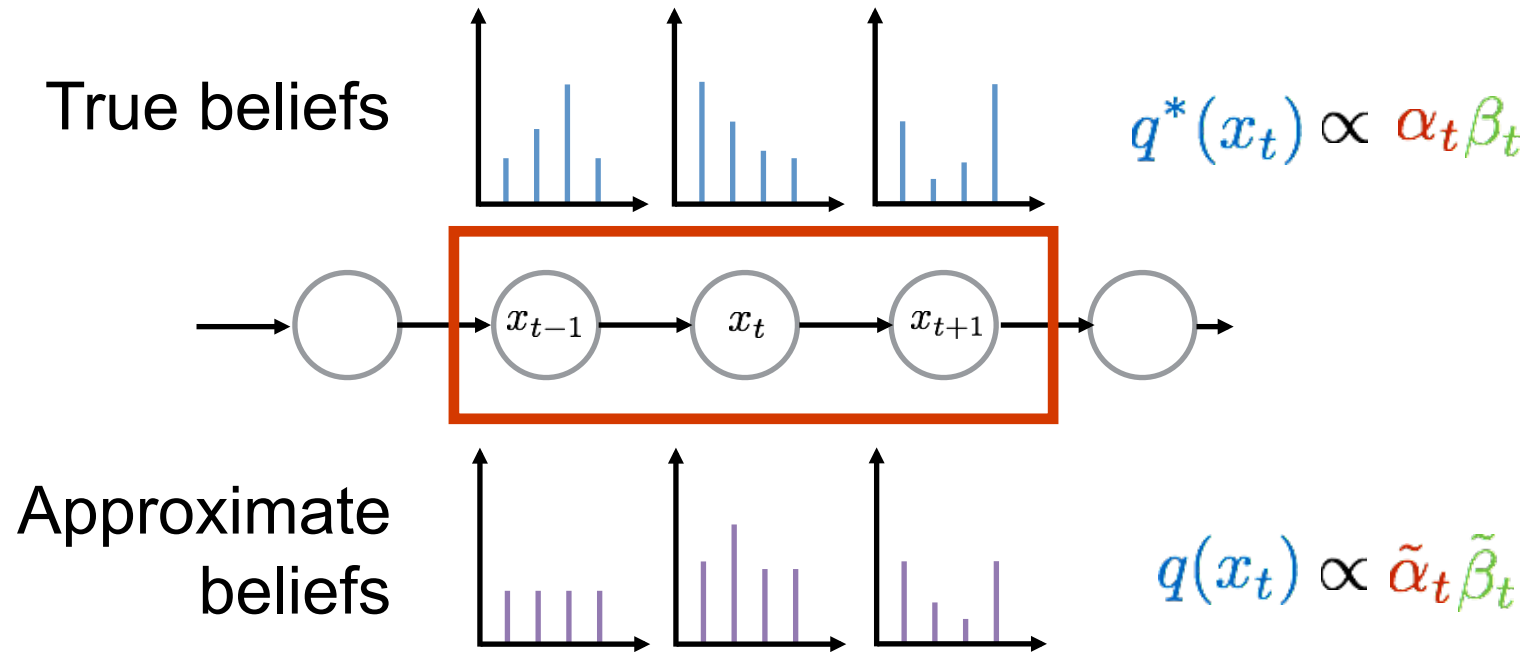


- Form **local** beliefs  $q(x_t) \propto \tilde{\alpha}_t \tilde{\beta}_t \rightarrow$  perform **global** update

Local forward message

Local backward message

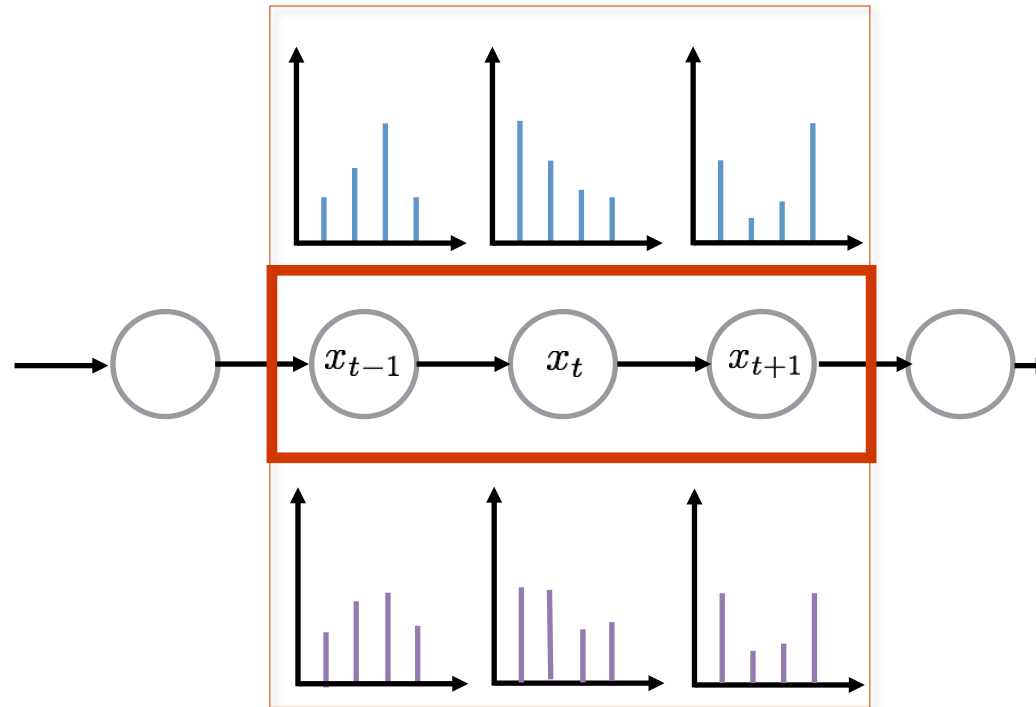
# Harnessing Memory Decay



Do we expect  $x_t$  to influence  $x_{t+1,000,000}$ ?



# Buffering Subchains



$$q^*(x_t) \propto \alpha_t \beta_t$$

$$q(x_t) \propto \tilde{\alpha}_t \tilde{\beta}_t$$

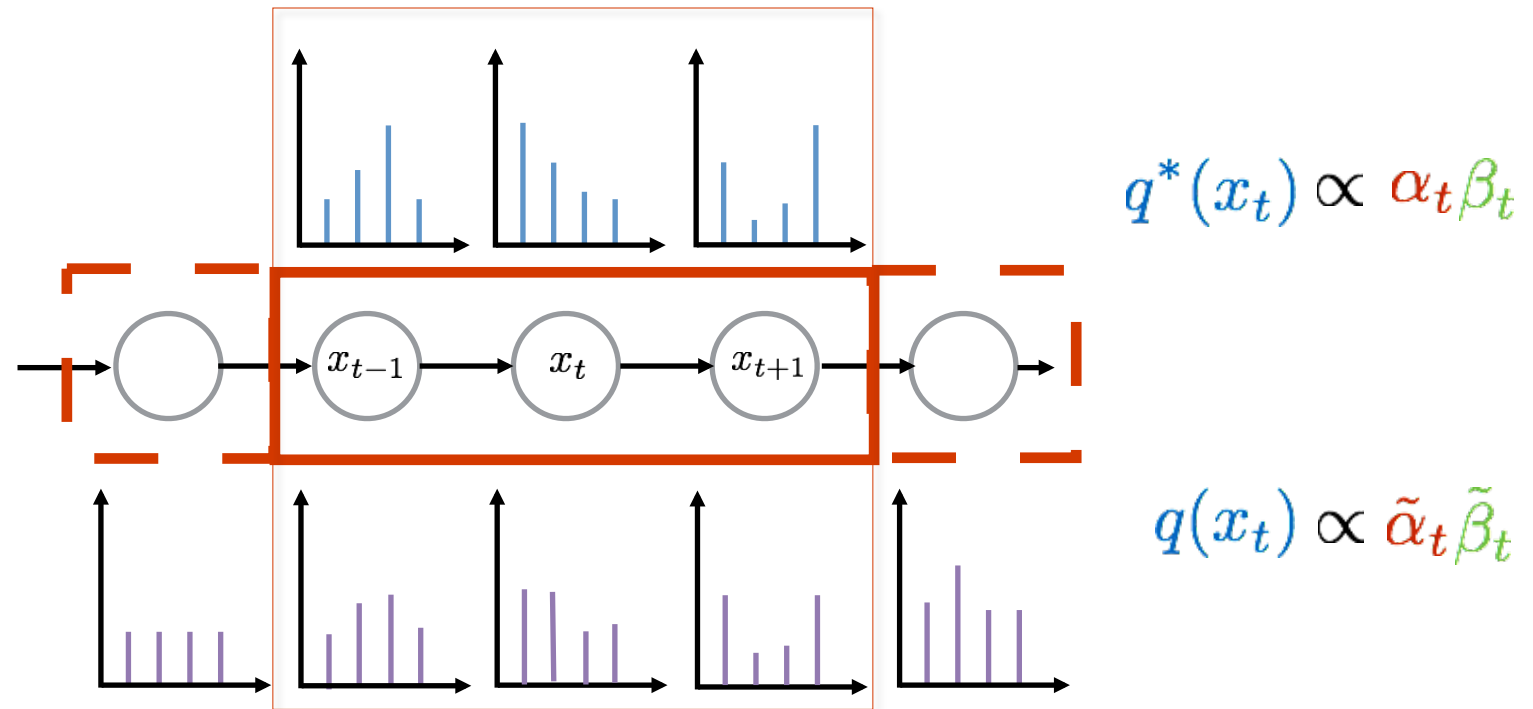
Check that subchain marginals are approximated well:

$$\max_{i \in S} \|q(x_i) - q^*(x_i)\| < \epsilon \quad ?$$

Local subchain  
marginal

Full data marginal

# Buffering Subchains



Check that subchain marginals are approximated well:

$$\max_{i \in S} \|q(x_i) - q^*(x_i)\| < \epsilon \quad ?$$

Local subchain  
marginal

Full data marginal

# Buffering Subchains

– Only need limited buffer

$$q^*(x_t) \propto \alpha_t \beta_t$$

– Complexity is now  $O(K^2 L_{buffer})$  per iteration

Large savings for  $L + \text{buffer} \ll T$

$$q(x_t) \propto \tilde{\alpha}_t \tilde{\beta}_t$$

– Similar idea as Splash BP (parallelizing BP)

[Gonzalez, et. al. 2009]

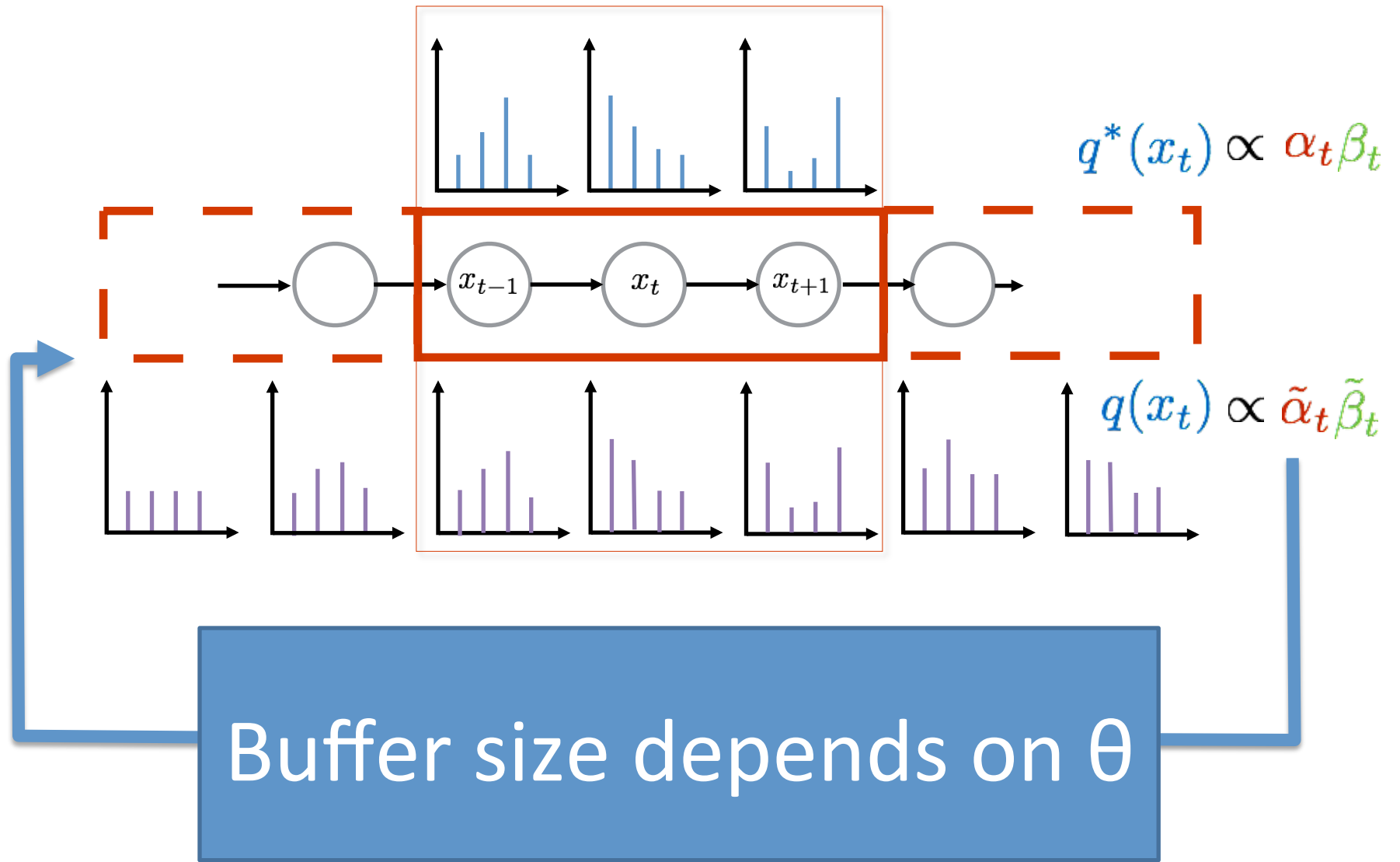
Check that subchain marginals are approximated well:

*But, uncertain parameter setting here*

Local subchain  
marginal

Full data marginal

# Buffering for Learning

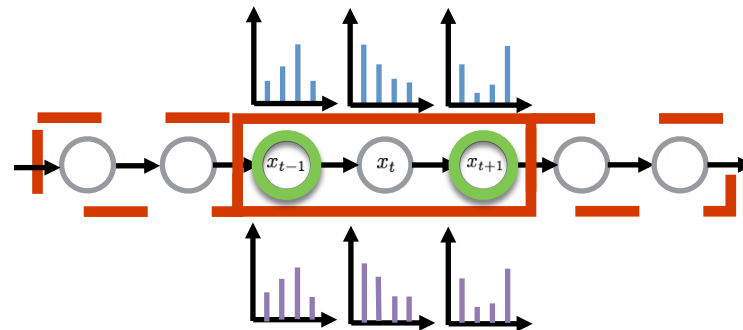


# Buffering in Practice

- We do not actually know the true marginals
- Monitor changes in approximate subchain beliefs:

$$\max_{i \in S} \left| \left| q(x_i)^{\text{new}} - q(x_i)^{\text{old}} \right| \right| < \epsilon$$

- Chain structuring implies that only endpoints must be checked



- During buffer expansions, forward-backward passes can reuse computations of previous buffer

# **A CASE STUDY: SVI-HMM**

Minibatch-based variational Bayes for HMMs

# Variational Bayes (VB)

- Approximate posterior with variational distribution

$$p(x, \theta | y) = \frac{p(y|x, \theta)p(x, \theta)}{p(y)} \approx q(x, \theta)$$

parameters  
↓  
latent variables    observations

- Minimize  $\text{KL}(q||p) \leftrightarrow$  maximize “ELBO”:

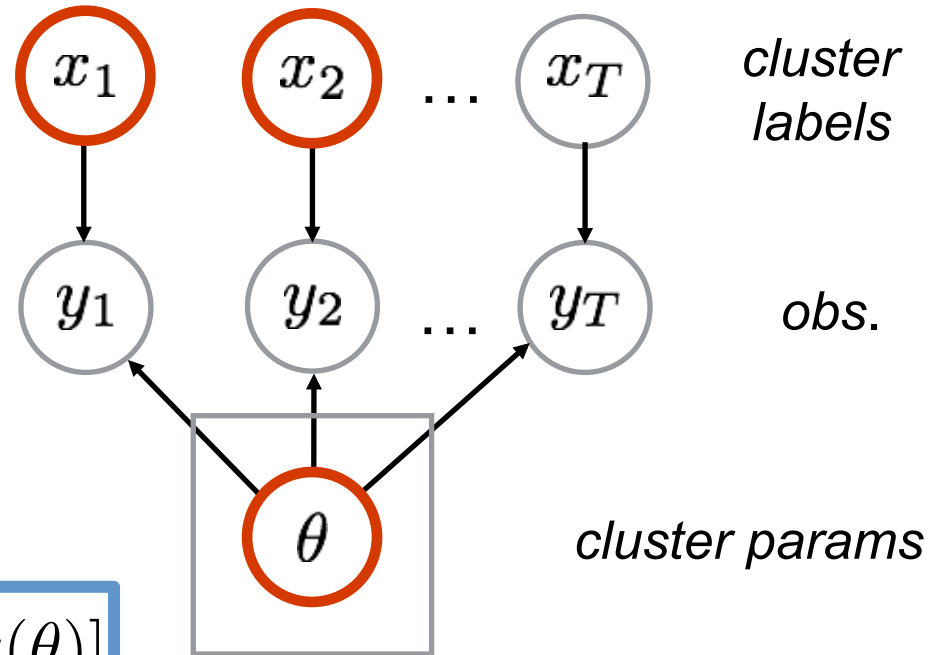
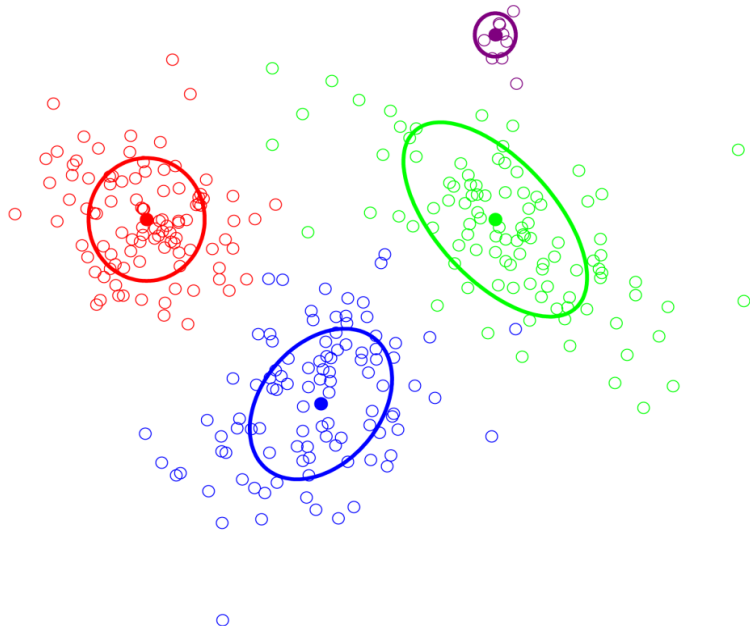
$$\mathcal{L}(q) = \mathbb{E}_q[\log p(y, x, \theta)] - \mathbb{E}_q[\log q(x, \theta)] \leq \log p(y)$$

- Common to make mean-field assumption:

$$q(x, \theta) = q(x)q(\theta)$$

# VB Example: Mixture Model

Maximize ELBO with *coordinate-ascent*  $\frac{\partial \mathcal{L}}{\partial q(\mathbf{x})} = 0 \longleftrightarrow \frac{\partial \mathcal{L}}{\partial q(\theta)} = 0$



$$\mathcal{L} = E_{q(\theta)} [\ln p(\theta)] - E_{q(\theta)} [\ln q(\theta)] + \sum_{i=1}^T E_{q(x_i)} [\ln p(y_i, x_i | \theta)] - E_{q(x_i)} [\ln q(x_i)]$$



# SVI Example: Mixture Model

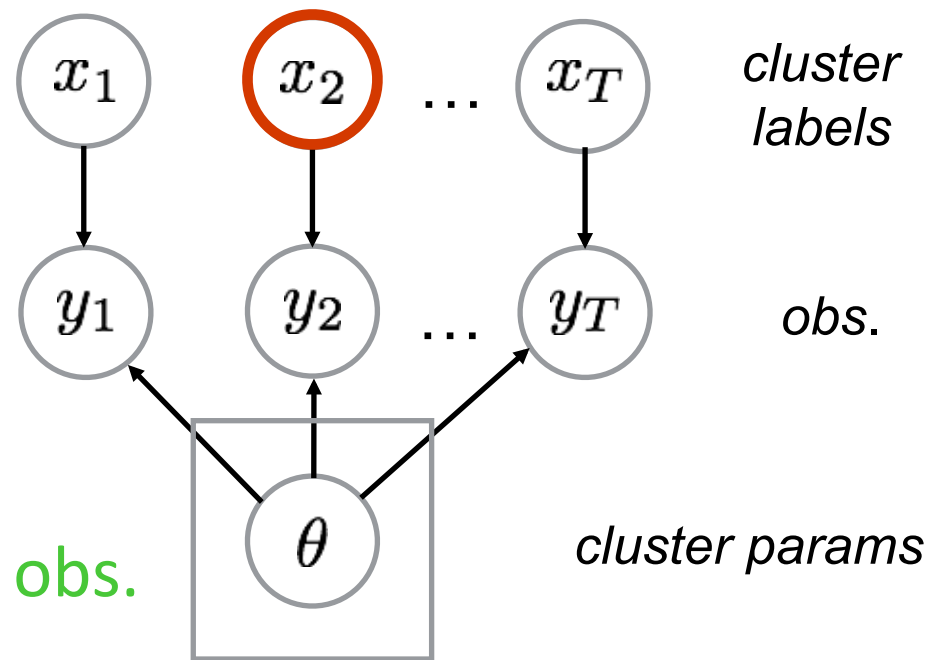
For scalability, stochastic variational inference (SVI) replaces **global** coordinate step with *stochastic gradient* step  
[Hoffman, et. al. 2013]

1. Sample observation uniformly at random

$$x^S \sim \text{Unif}(x_1, \dots, x_T)$$

2. Form noisy, unbiased ELBO:

$$\mathcal{L}^S = E_{q(\theta)} [\ln p(\theta)] - E_{q(\theta)} [\ln q(\theta)] \\ + T \cdot (E_{q(x_s)} [\ln p(y_s, x_s | \theta)] - E_{q(x_s)} [\ln q(x_s)])$$



# SVI Example: Mixture Model

3. Take standard coordinate step for  $x^s$

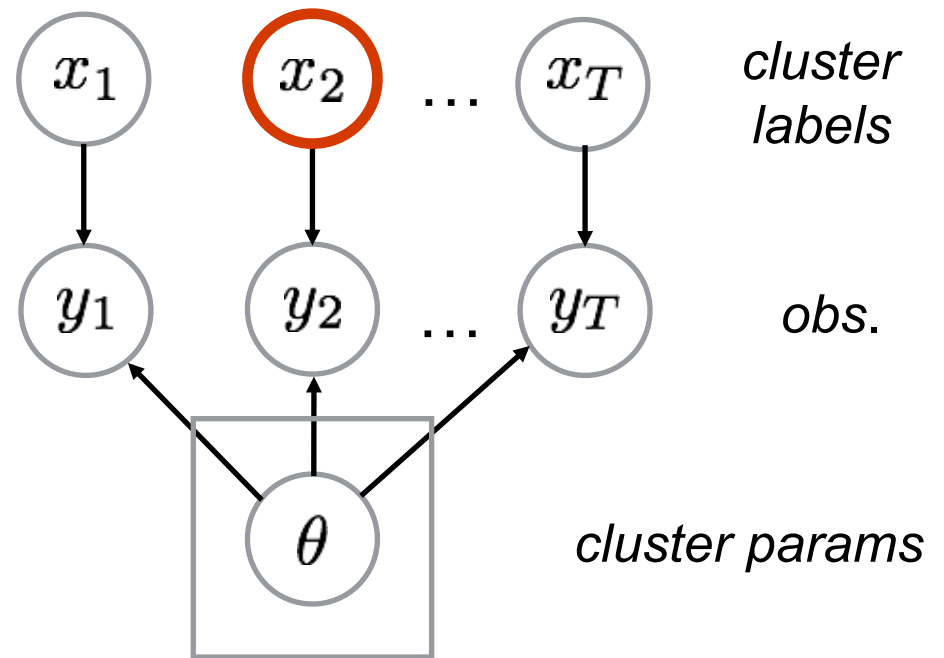
$$\frac{\partial \mathcal{L}^s}{\partial q(x_s)} = 0$$

4. Take **stochastic natural gradient** step for  $\theta$

$$\mathbf{w}^{(t)} = \mathbf{w}^{(t-1)} + \rho_t \tilde{\nabla}_{\mathbf{w}} \mathcal{L}^S$$

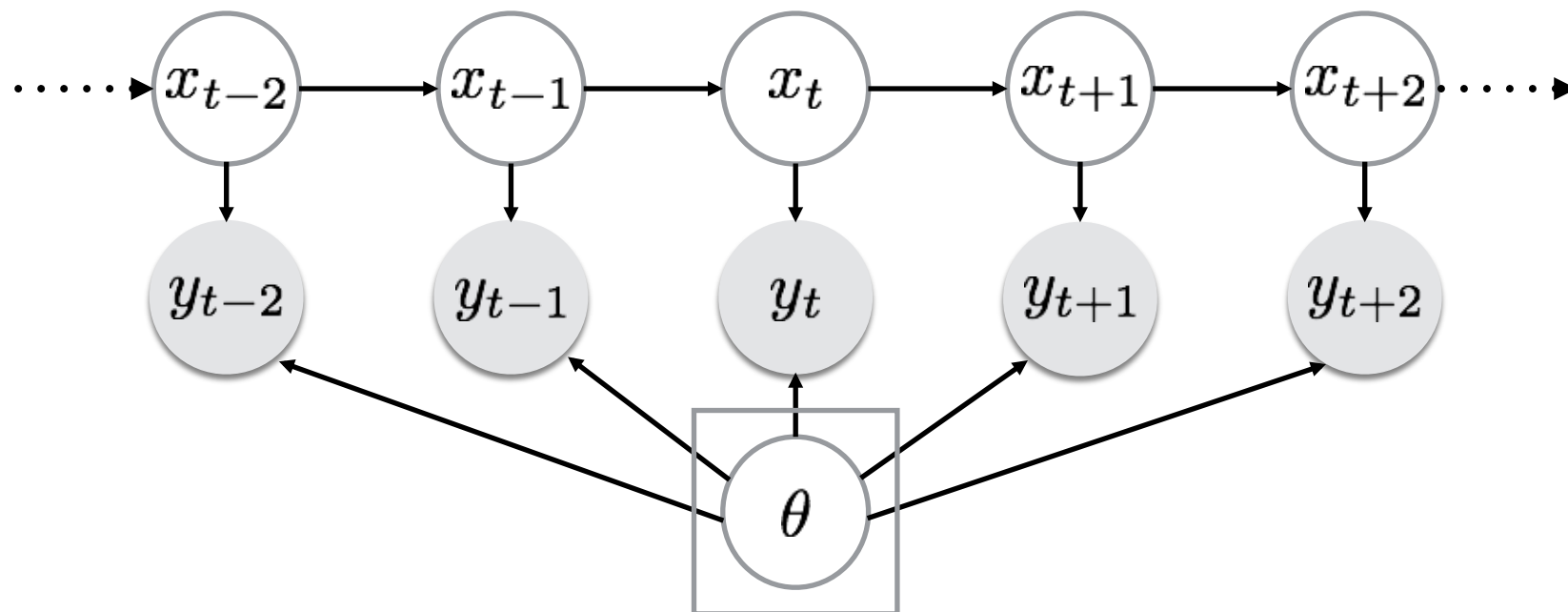
Hyperparams for  $q(\theta)$

5. Iterate



$$\mathcal{L}^s = E_{q(\theta)} [\ln p(\theta)] - E_{q(\theta)} [\ln q(\theta)] + T \cdot (E_{q(x_s)} [\ln p(y_s, x_s | \theta)] - E_{q(x_s)} [\ln q(x_s)])$$

# Variational Inference for HMMs

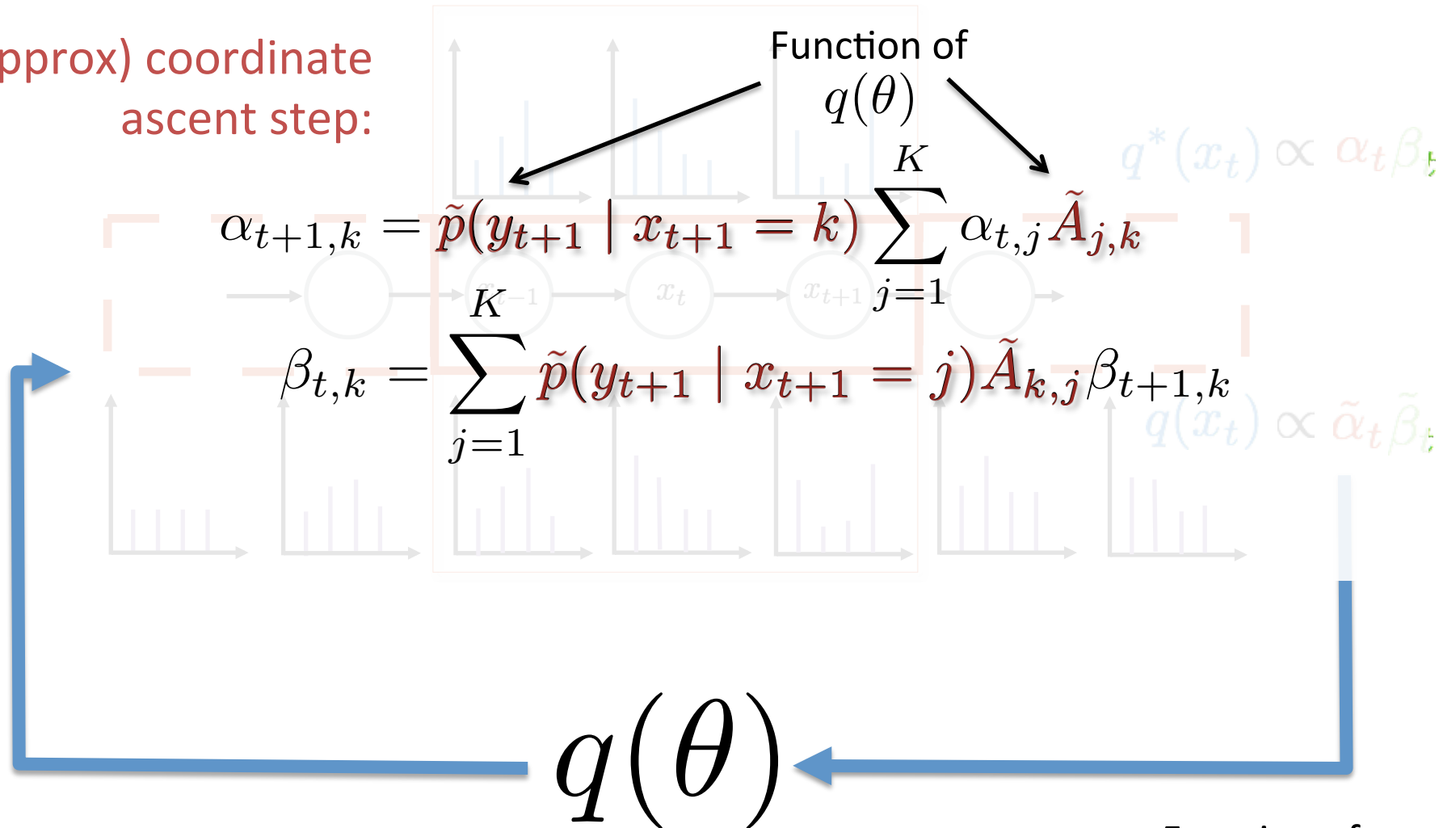


Use structured mean-field approximation:

$$p(x_1, x_2, \dots, x_T, \theta \mid y_1, y_2, \dots, y_T) \approx q(x_1, x_2, \dots, x_T)q(\theta)$$

# SVI for HMMs

(Approx) coordinate ascent step:



Stochastic natural gradient step:

$$\mathbf{w}^{(t)} = \mathbf{w}^{(t-1)} + \rho_t \tilde{\nabla}_{\mathbf{w}} \mathcal{L}^S$$

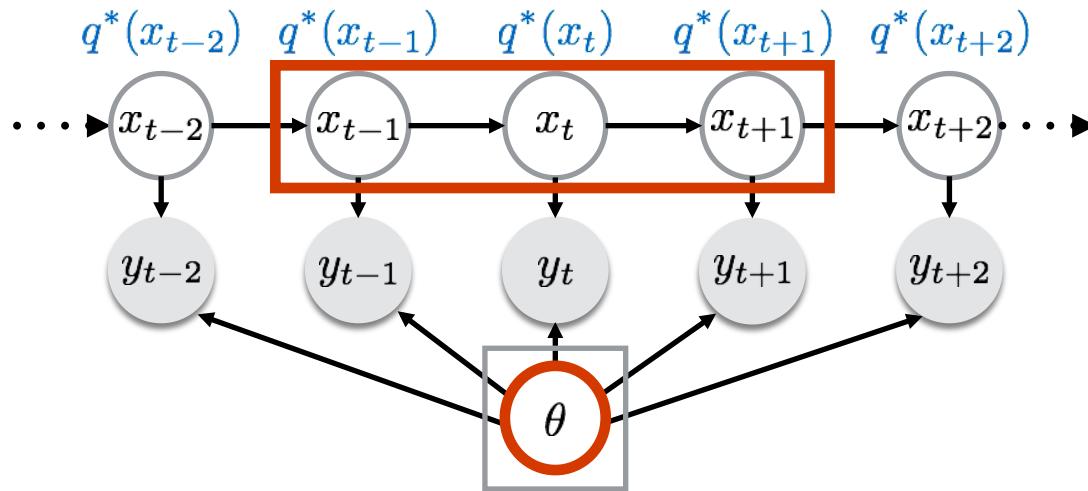
Function of  $q(\mathbf{x})$

# Differences from i.i.d. Case

- Minibatches are *correlated*
  - Data in one is not independent of data in another
- Minibatch marginals  $\neq$  batch marginals
  - Impact of latent chain
  - Mitigated by buffering

# Correlated Minibatches

- Pretend we have exact local distribution  $q^*(x^S)$



As if we had run batch forward-backward

- Typical arguments for convergence to local mode rely on *unbiased* + *independent* noisy gradients [c.f., Bottou 1998, Hoffman 2013]
  - Our SGs are *dependent* since subchains are correlated
- Using [Polyak and Tsytkin 1973], unbiasedness suffices for convergence of  $\mathbf{w}^{(t)} = \mathbf{w}^{(t-1)} + \rho_t \tilde{\nabla}_{\mathbf{w}} \mathcal{L}^S$

# Effect of Approximated Marginals

## SVI-HMM iterates:

buffer minibatches to **approx  $q(x)$**   $\leftrightarrow$  **update  $q(\theta)$**   
*coordinate ascent step* *stochastic*  
*(natural) gradient step*

For  $\epsilon$  sufficiently small (sufficiently long buffer)

- Approximate marginals “close enough” to true marginals
- Noisy gradient in same half-plane as true gradient



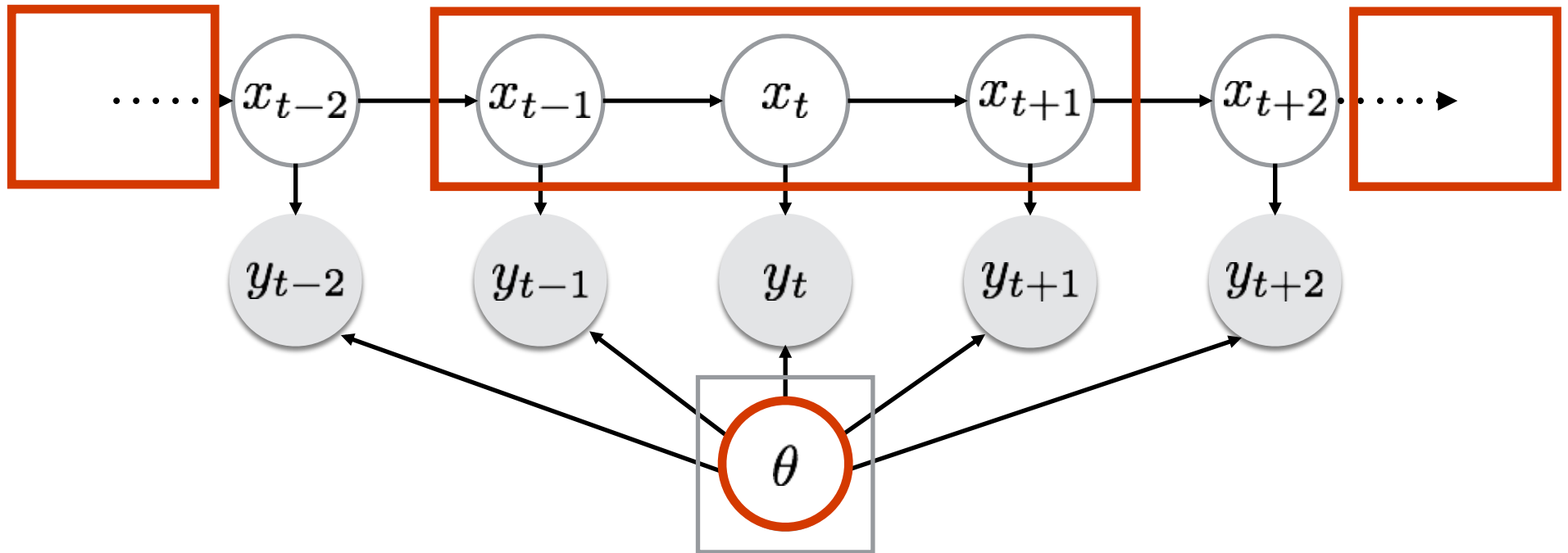
iterative algorithm converges to local mode of ELBO

# Experiments

- Synthetic data:
  - **Diagonally Dominant:** Long memory chain with large self-transitions
  - **Reversed Cycles:** Two overlapping cycles with opposite directions
- **Human chromatin application**



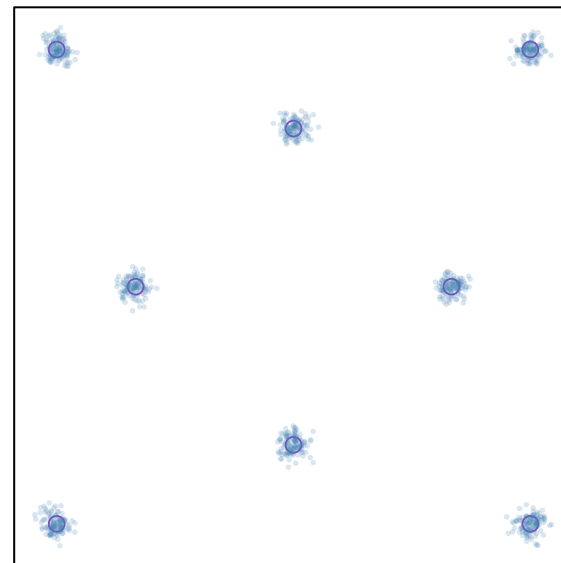
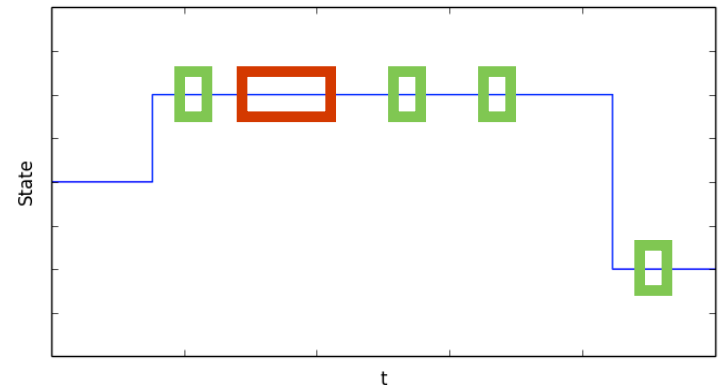
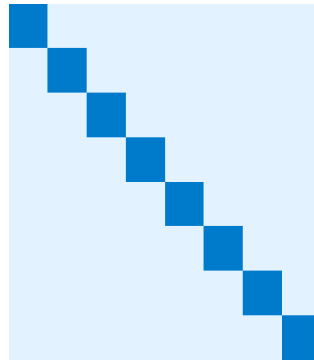
# Minibatch of Subchains



Minibatch consists of  $M$  subchains each of length  $L$

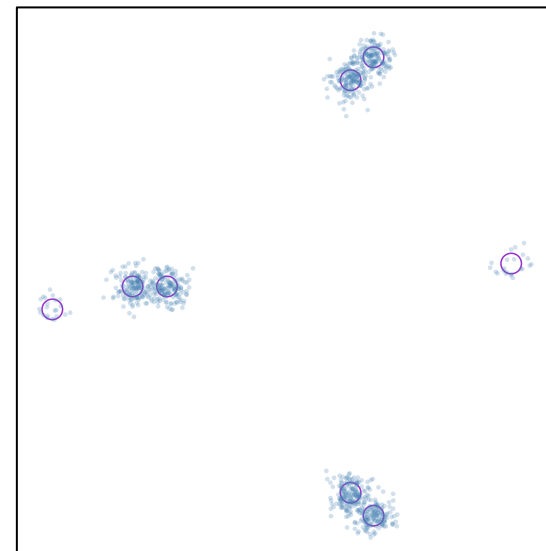
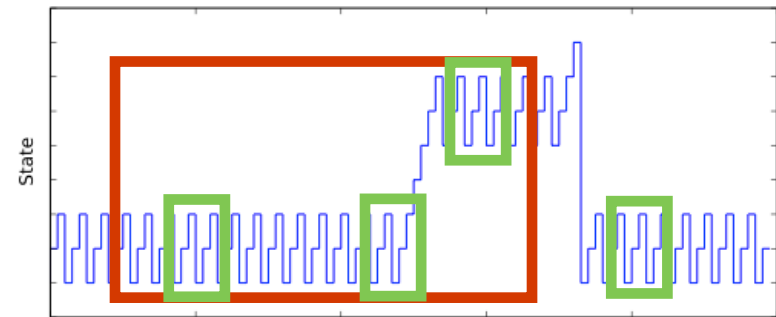
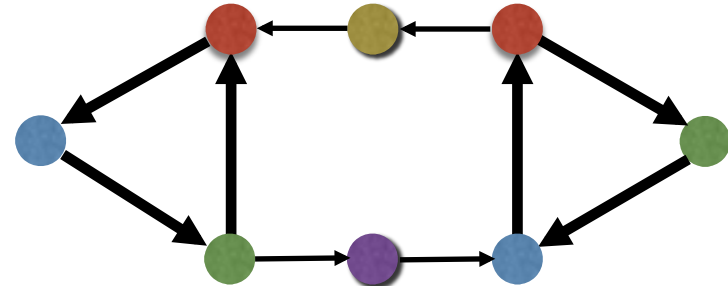
# Diagonally Dominant

- 8 latent states
- 2d Gaussian emissions
- *High auto-correlation*  
→ few long subchains converge slowly  
(small  $M$ , large  $L$ )
- *Emissions identifiable*  
→ many small subchains perform better  
(large  $M$ , small  $L$ )

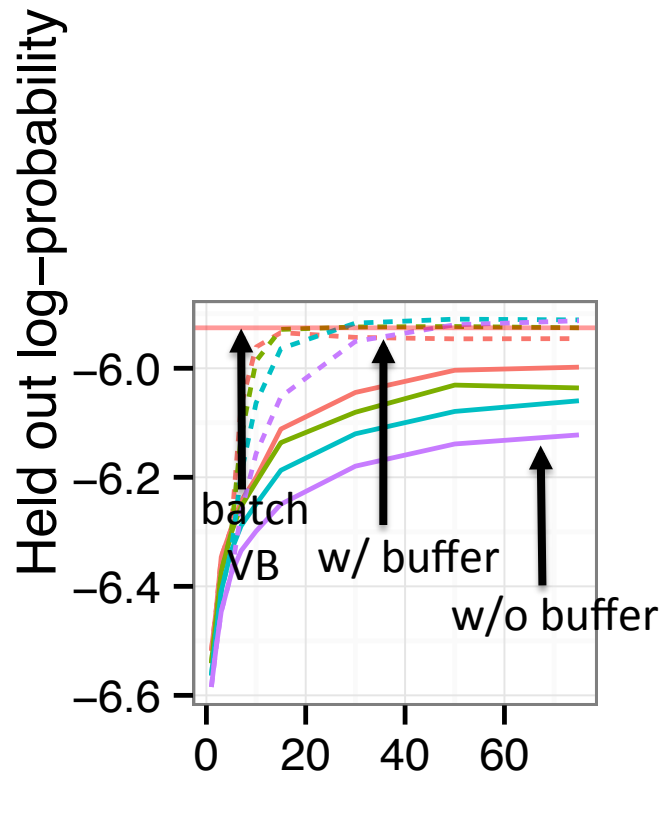
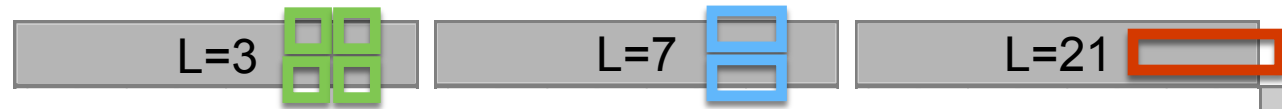


# Reversed Cycles

- 8 latent states
- 2d Gaussian emissions
- *Emission distributions overlap*
- *Direction* of cycles important to identify states
  - Singleton observations insufficient
  - Without buffering, need  $L > 3$  to learn effectively
- Longer subchains more likely to capture structure



# Subchain Buffering

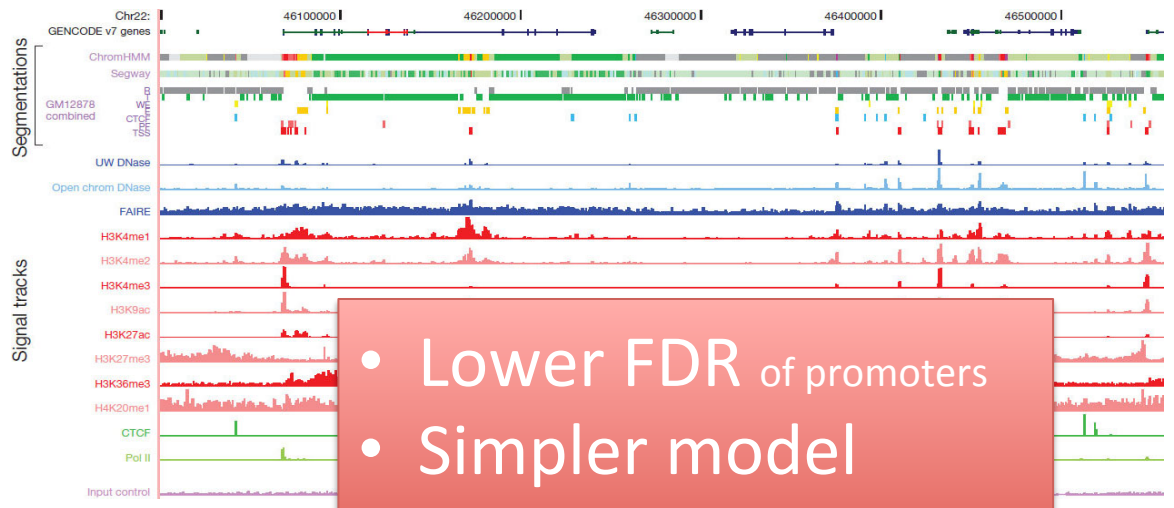


Diag. Dom.

Rev. Cycles

# Human Chromatin Segmentation

- Chromosome data from ENCODE project
- 12 dimensional observations
- **Goal:** segment sequences
- **T = 250 million**



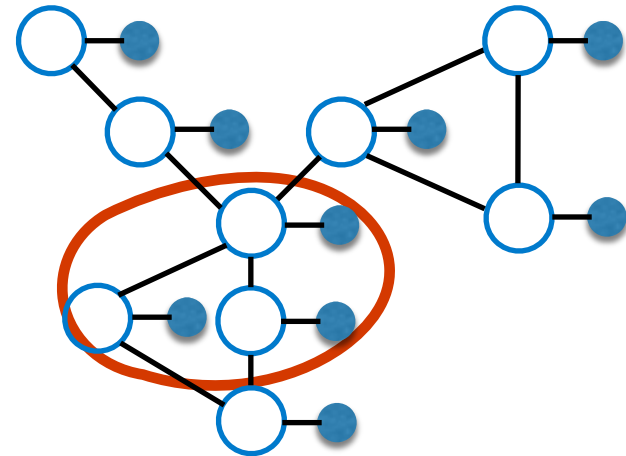
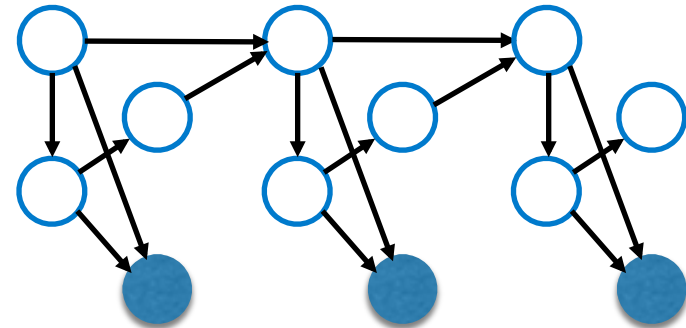
• Lower FDR of promoters  
• Simpler model  
• Uses all of the data

- [Hoffman et. al. 2012] used **dynamic Bayesian network**
    - Broke sequence into pieces to perform inference via EM
    - Severs long-range dependencies
- ← Runtime = days

- Adaptive subsampling on **HMM** (*simpler model*)
- Runtime = under 1 hr →

# BNP and Other Extensions

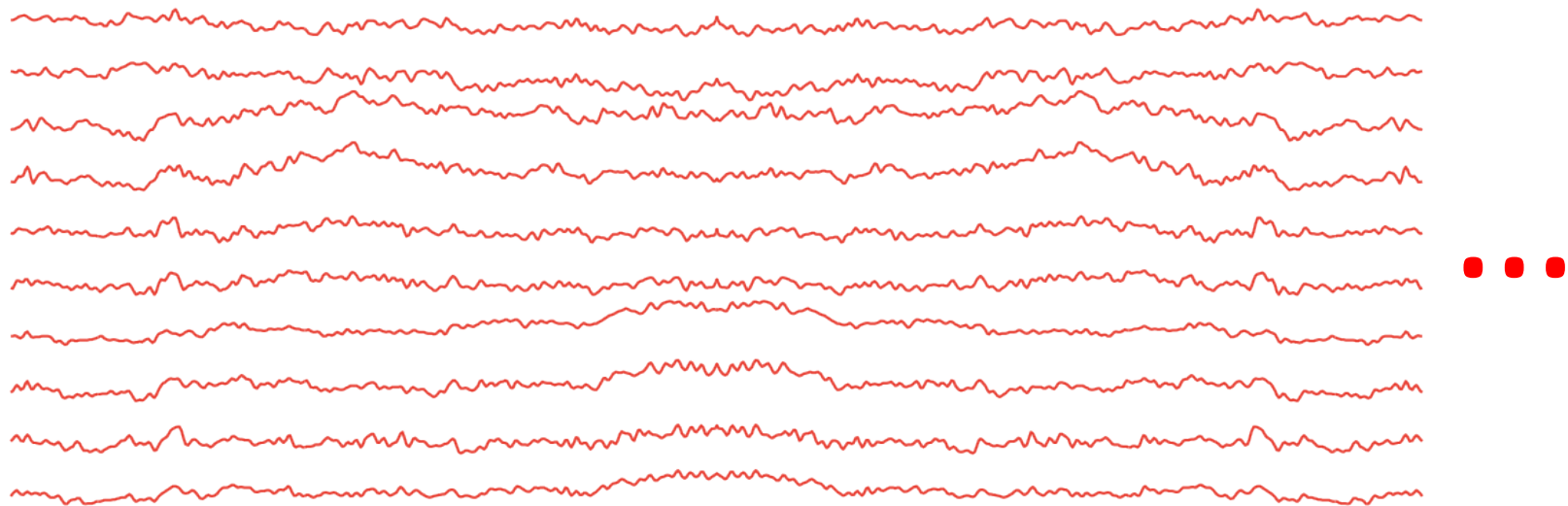
- Presented finite HMM case, but ideas could generalize to:
  - Nonparametric HMMs
  - DBN and MRF models
- Applications to:
  - Large spatial fields
  - Spatio-temporal data, etc.



# **WHAT ABOUT STREAMING DATA?**

Issues, solutions, and more issues...

# What if data arrive without bound?



Often, not just large dataset, but **streaming**



# Assumed Density Filtering

Interested in  $p(\theta|x_{1:n})$

- Assume we have  $q_{n-1}(\theta) \approx p(\theta|x_{1:n-1})$
- Incorporate new data  $\hat{p}(\theta|x_{1:n}) = p(x_n|\theta)q_{n-1}(\theta)$
- Project onto tractable family  $\arg \min_{q_n} \text{KL}(\hat{p}||q_n)$

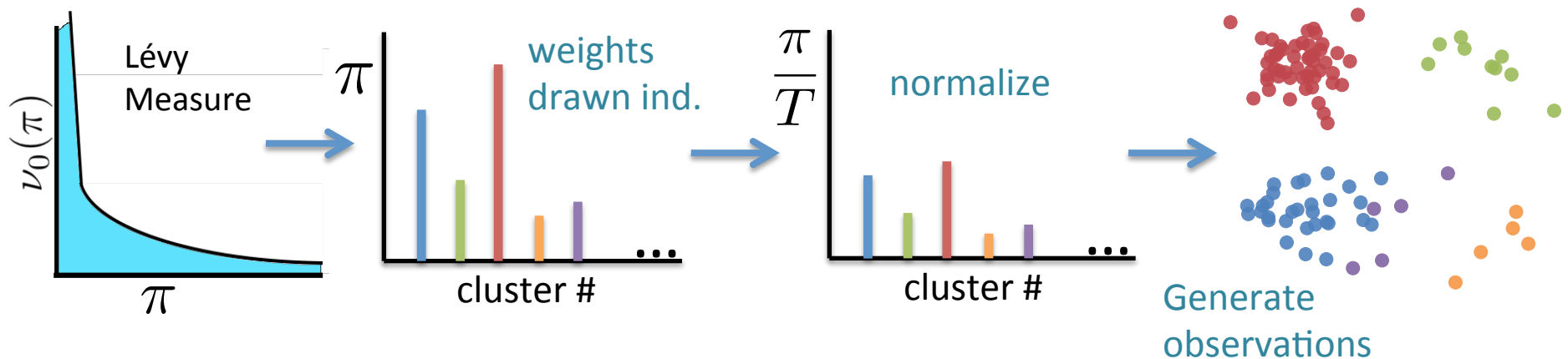


Cycling through data multiple times results in the **expectation propagation** algorithm.

# Explored ADF for BNP Mixture Models

Bayesian nonparametrics well suited to streaming case since **model complexity can adapt**

- Existing approaches only for the Dirichlet process (DP)
- We cast DP approach as ADF, and extend to more flexible class of **normalized random measures (NRMs)**



# ADF for NRM Mixture Models

Posterior of n data points can be written as a product of **factors**:

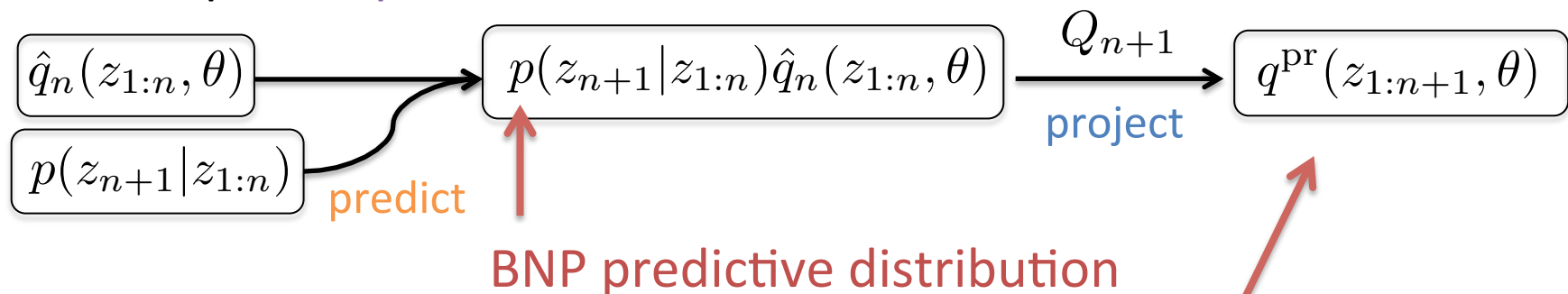
$$p(z_{1:n}, \theta | x_{1:n}) \propto p(\theta) \prod_{i=1}^n p(x_i | z_i, \theta) p(z_i | z_{1:i-1})$$

**likelihood** factor:  $p(x_i | z_i, \theta)$

**predictive** factor:  $p(z_i | z_{1:i-1})$

Iteratively project onto factorized family  $Q_n = \{q; q = \prod_{i=1}^n q(z_i) \prod_{k=1}^{\infty} q(\theta_k)\}$

1. Incorporate **predictive** factor via ADF:



*Only relies on summaries of soft-assignments, rather than full history*

$$\sum_{i=1}^t q_t(z_i = k)$$

# ADF for NRM Mixture Models

Posterior of  $n$  data points can be written as a product of **factors**:

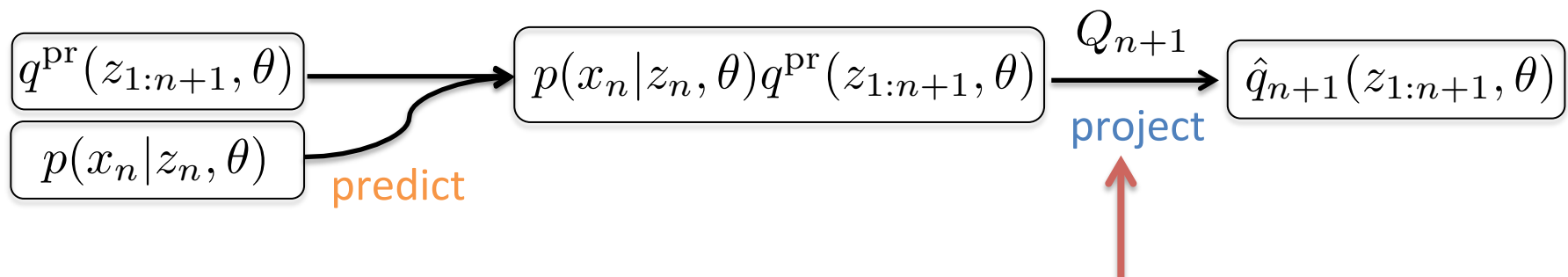
$$p(z_{1:n}, \theta | x_{1:n}) \propto p(\theta) \prod_{i=1}^n p(x_i | z_i, \theta) p(z_i | z_{1:i-1})$$

**likelihood** factor:  $p(x_i | z_i, \theta)$

**predictive** factor:  $p(z_i | z_{1:i-1})$

**Iteratively project** onto factorized family  $Q_n = \{q; q = \prod_{i=1}^n q(z_i) \prod_{k=1}^{\infty} q(\theta_k)\}$

2. Incorporate **likelihood** via second ADF step:

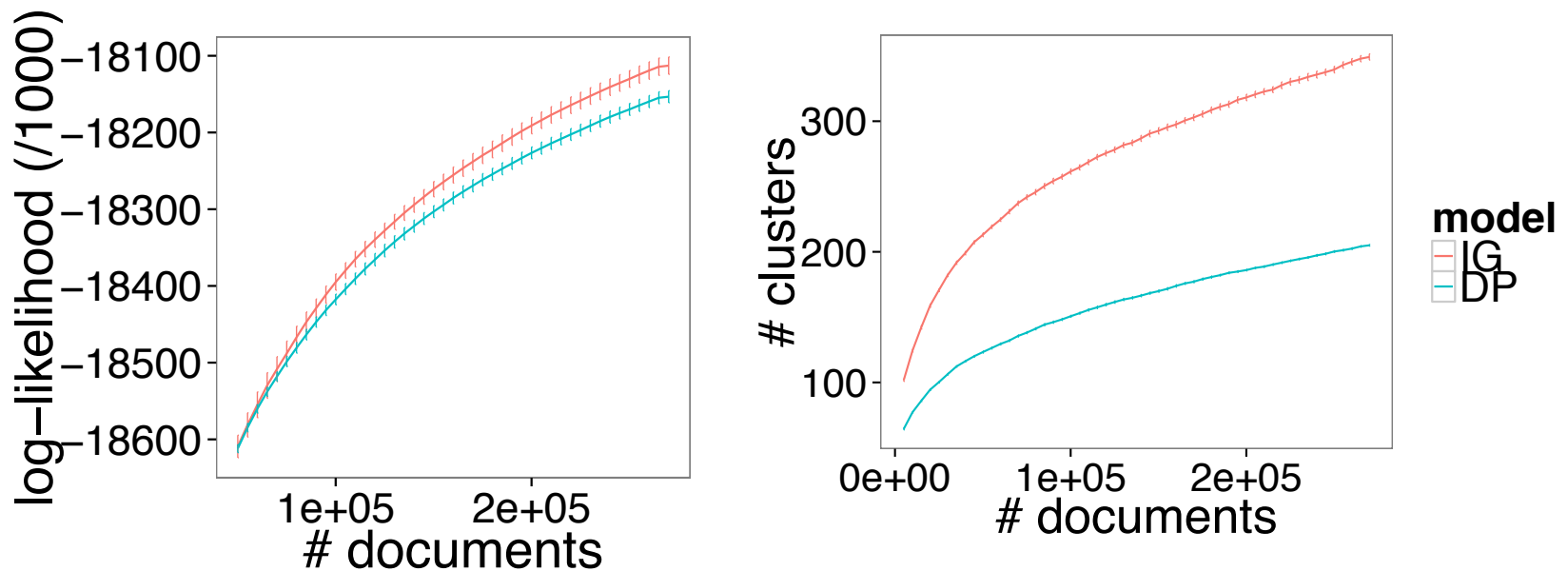


Typically intractable, so replace with VB update (*reverse KL*)

Similar to what's suggested in Broderick et al. 2013 (SVB)

# Online Document Clustering

**NYT corpus (N = 266k documents):**



## Top IG clusters after 1 epoch

Topic 1	Topic 2	Topic 3	Topic 4
athletes (.83)	merger (.36)	reform (.31)	quarterback (.45)
weight (.75)	revenue (3.3)	conservative (.26)	yankees (.45)
exercise (.68)	shares (.31)	senator (.24)	scored (.43)
steroid (.55)	cable (.31)	parties (.22)	pitcher (.38)
supplement (.49)	businesses (.29)	supporter (.22)	offense (.37)

# Some challenges...

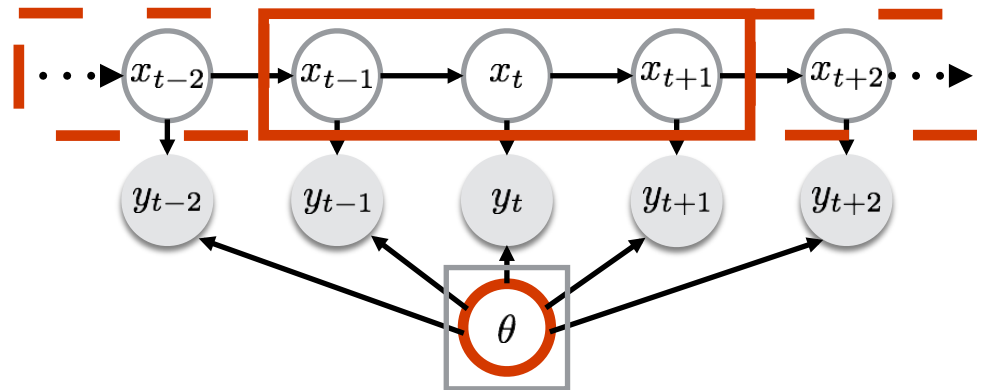
Iterating VB steps leads to more and more concentrated beliefs

- BNP adapts model capacity (i.e., new clusters), which allows one to continue learning
- Don't need to observe all clusters/modes in initial batches
- Harder in HMM case because you have “clusters” and transitions between them...often dwell in one for a while

Theis & Hoffman (2015) trust region approach can help

# Summary

- Stochastic variational inference for handling *dependent observations*
  - Harness *memory decay* to form local beliefs on *buffered subchains*
  - Bounding error in approx., can prove *convergence* of iterative algorithm
- Demonstrated on large genomics dataset where batch methods are infeasible



- Discussed promising approaches to streaming case, and challenges for time series data