Alignment of Time Course Microarray Data with Hidden Markov Models

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Gene expression

Gene expression

DNA is transcribed into mRNA mRNA is translated into protein



Tinsley, R. (2011) 'MOTHER NATURE', On Dit 79(6), 12-13.



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Hidden Markov model

A hidden Markov model (HMM) is a collection of RVs that form:

- **1** A Markov chain, S_1, S_2, \ldots 'state sequence'
- 2 An additional sequence, X_1, X_2, \ldots 'emission sequence'



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Hidden Markov model



$$p(\mathbf{x}_{1:T}, \mathbf{s}_{1:T} | \lambda) = \mathbf{a}_{\mathbf{s}_1} \prod_{t=2}^T \mathbf{a}_{\mathbf{s}_{t-1}\mathbf{s}_t} \left(\prod_{t=1}^T f(\mathbf{x}_t | \mu_{\mathbf{s}_t}, \sigma_{\mathbf{s}_t}^2) \right)$$

where

$$\lambda = \{\mathbf{a}, \mathbf{A}, \mu_1, \sigma_1^2, \mu_2, \sigma_2^2, \dots, \mu_N, \sigma_N^2\}.$$

HMM framework

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| Model | Data |
|-------------------|------------------------------|
| emission sequence | expression profile |
| state sequence | underlying behaviour of gene |

L(t)-fold HMM

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$$p(\mathbf{x}_{1:T}, s_{1:T} | \lambda) = a_{s_1} \prod_{t=2}^{T} a_{s_{t-1}s_t} \Big(\prod_{t=1}^{T} \prod_{l=1}^{L(t)} f(x_t^{(l)} | \mu_{s_t}, \sigma_{s_t}^2) \Big).$$

Alignment model

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$$L(t) = \begin{cases} 1 & \text{if } t = G_1 \text{ or } G_2 \\ 2 & \text{otherwise.} \end{cases}$$

 $1 < G_1 < G_2 \leq 19$



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Parameter estimates



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Diagnostics





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HMMs in general

Bilmes, J. (2002) What HMMs Can Do, Technical Report UWEETR-2002-0003, UWEE.

HMMs in MATLAB

Murphy, K. (2005) The HMM Toolbox, http://www.cs.ubc.ca/~murphyk/Software/HMM/hmm.html