SPIRAL: Efficient and Exact Model Identification for Hidden Markov Models

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Motivation

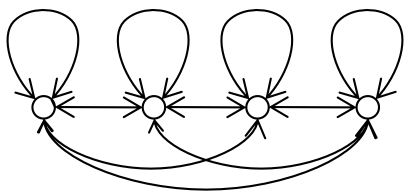
- HMM(Hidden Markov Model)
  - Mental task classification
    - Understand human brain functions with EEG signals
  - Biological analysis
    - Predict organisms functions with DNA sequences
  - Many other applications
    - Speech recognition, image processing, etc
- Goal
  - Fast and exact identification of the highest-likelihood model for large datasets

Mini-introduction to HMM

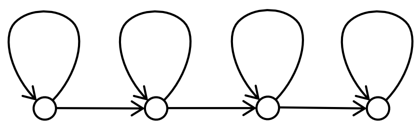
- Observation sequence $X = (x_1, x_2, \cdots, x_n)$ is a probabilistic function of states
- Consists of the three sets of parameters:
  - Initial state probability : $\pi = \{\pi_i\} \quad (1 \le i \le m)$
    - State u_i at time $t = 1$
  - State transition probability: $a = \{a_{ij}\} \quad (1 \le i, j \le m)$
    - Transition from state u_i to u_j
  - Symbol probability: $b(v) = \{b_i(v)\} \quad (1 \le i \le m)$
    - Output symbol v in state u_i

Mini-introduction to HMM

- HMM types
  - Ergodic HMM
    - Every state can be reached from every other state
  - Left-right HMM
    - Transitions to lower number states are prohibited
    - Always begin with the first state
    - Transition are limited to a small number of states



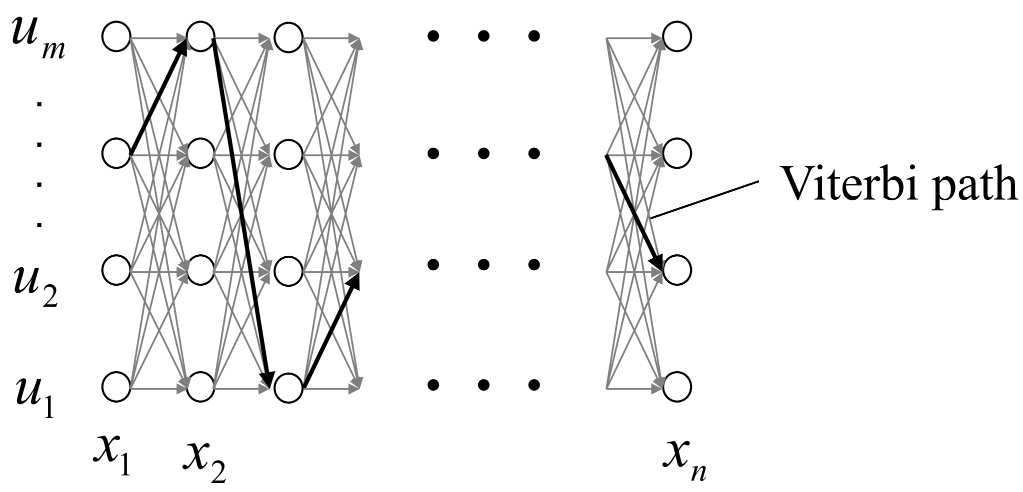
Ergodic HMM



Left-right HMM

Mini-introduction to HMM

- Viterbi path in the trellis structure
  - Trellis structure: states lie on the vertical axis, the sequence is aligned along the horizontal axis
  - Viterbi path: state sequence which gives the likelihood



Trellis structure

Mini-introduction to HMM

- Viterbi algorithm
  - Dynamic programming approach
  - Maximize the probabilities from the previous states

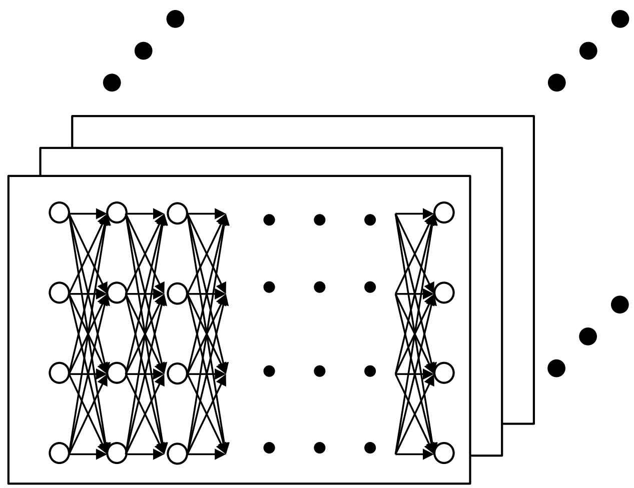
$$P = \max_{1 \le i \le m} (p_{in})$$

$$p_{it} = \begin{cases} \max\limits_{1 \le j \le m} \left(p_{j(t-1)} \cdot a_{ji}\right) \cdot b_i(x_t) & (2 \le t \le n) \\ \pi_i \cdot b_i(x_1) & (t = 1) \end{cases}$$

p_{it} : the maximum probability of state u_i at time t

Problem Definition

- Given
  - HMM dataset
  - Sequence $X = (x_1, x_2, \cdots, x_n)$ of arbitrary length
- Find
  - Highest-likelihood model, estimated with respect to *X*, from the dataset



Why not 'Naive'

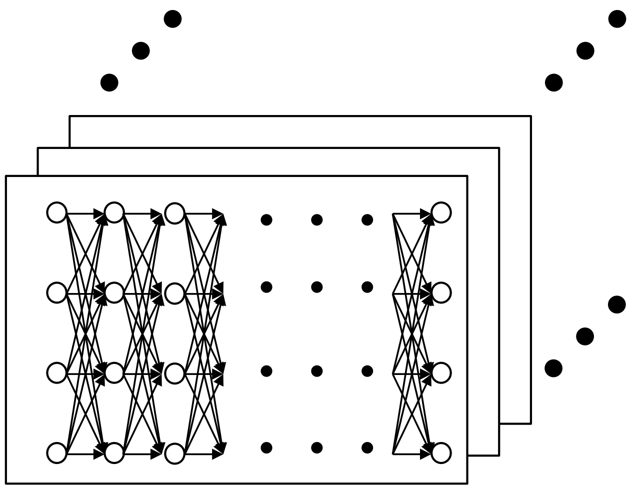
- Naïve solution
  1. Compute the likelihood for every model using the Viterbi algorithm
  2. Then choose the highest-likelihood model

But..

- High search cost: $O(nm^2)$ time for every model
  - Prohibitive for large HMM datasets

m: # of states

n: sequence length of X

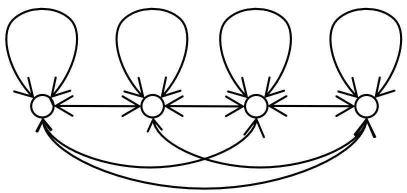


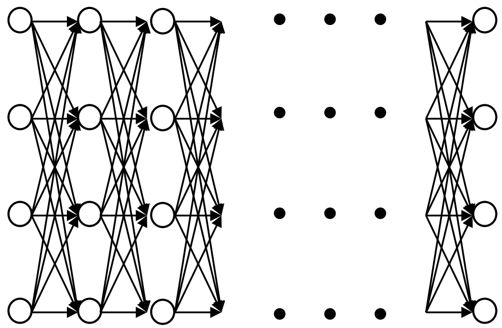
Our Solution, SPIRAL

- Requirements:
  - High-speed search
    - Identify the model efficiently
  - Exactness
    - Accuracy is not sacrificed
  - No restriction on model type
    - Achieve high search performance for any type of models

Likelihood Approximation

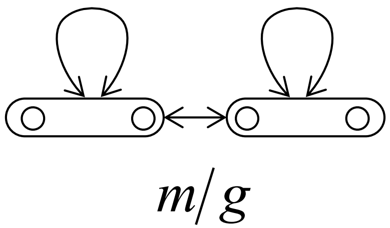
Reminder: Naive

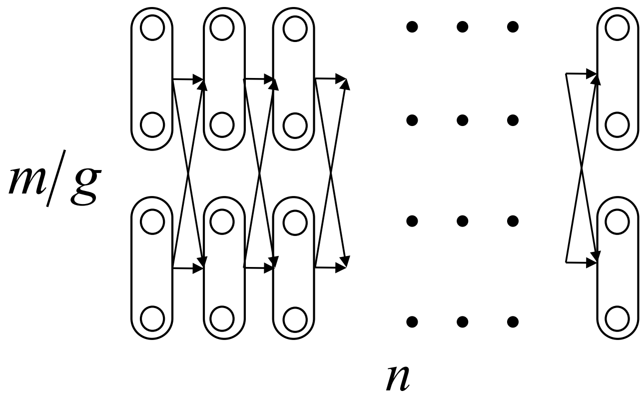




Likelihood Approximation

- Create compact models (reduce the model size)
  - For given m states and granularity g,
  - Create m/g states by merging 'similar' states





Likelihood Approximation

- Use the vector F_i of state u_i for clustering

$$F_i = \left(\pi_i; a_{i1}, \cdots, a_{im}, a_{1i}, \cdots, a_{mi}; b_i(v_1), \cdots, b_i(v_s)\right)$$

s: number of symbols

- Merge all the states u_i in a cluster C and create a new state u_C
- Choose the highest probability among the probabilities of u_i

$$\pi'_C = \max_{u_i \in C}(\pi_i) \quad a'_{Cj} = \max_{u_i \in C, u_j \notin C}(a_{ij})$$

$$a'_{CC} = \max_{u_i, u_k \in C}(a_{ik}) \quad a'_{jC} = \max_{u_i \in C, u_j \notin C}(a_{ji}) \quad b'_C(v) = \max_{u_i \in C}(b_i(v))$$

Obtain the upper bounding likelihood

Likelihood Approximation

- Compute approximate likelihood P' from the compact model

$$P' = \max_{1 \le i \le m'} \left(p'_{in} \right)$$

$$p'_{it} = \begin{cases} \max\limits_{1 \le j \le m'} \left(p'_{j(t-1)} \cdot a'_{ji} \right) \cdot b'_i(x_t) & (2 \le t \le n) \\ \pi'_i \cdot b'_i(x_1) & (t = 1) \end{cases}$$

p'_{it}: maximum probability of states

- Upper bounding likelihood
  - For approximate likelihood P', $P' \ge P$ holds
  - Exploit this property to guarantee exactness in search processing

Likelihood Approximation

Advantages

- The best model can not be pruned
  - The approximation gives the upper bounding likelihood of the original model
- Support any model type
  - Any probabilistic constraint is not applied to the approximation

Multi-granularities

- The likelihood approximation has the trade-off between accuracy and computation time
  - As the model size increases, accuracy improves
  - But the likelihood computation cost increases
- Q: How to choose granularity g ?

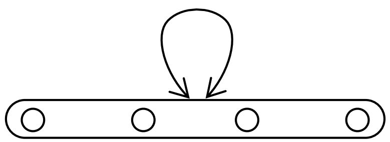
Multi-granularities

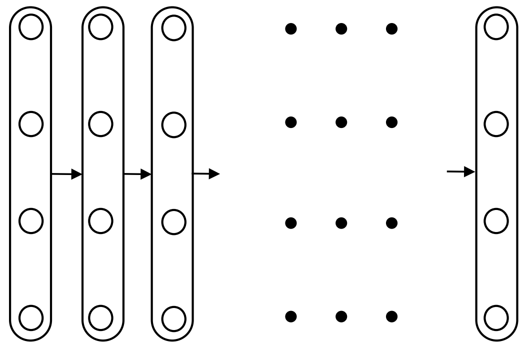
- The likelihood approximation has the trade-off between accuracy and computation time
  - As the model size increases, accuracy improves
  - But the likelihood computation cost increases
- Q: How to choose granularity g ?
- A: Use multiple granularities
  - $h+1\left(h=\lfloor \log_2 m \rfloor\right)$ distinct granularities that form a geometric progression $g_i=2^i$ (i=0,1,2,…,h)
  - Geometrically increase the model size

Multi-granularities

- Compute the approximate likelihood P' from the coarsest model as the first step
  - Coarsest model has $\lfloor m/2^h \rfloor (=1)$ states
- Prune the model if $P' < \theta$, otherwise

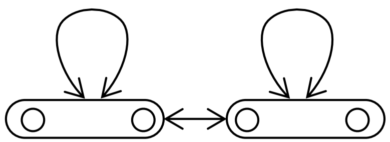
θ : threshold

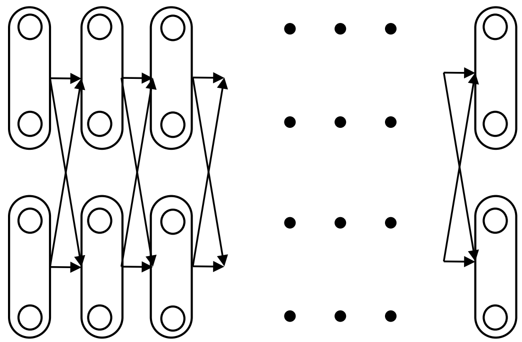




Multi-granularities

- Compute the approximate likelihood P' from the second coarsest model
  - Second coarsest model has $\lfloor m/2^{h-1} \rfloor$ states
- Prune the model if $P' < \theta$



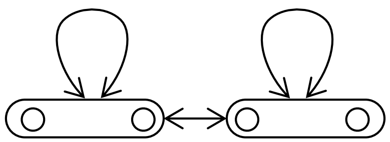


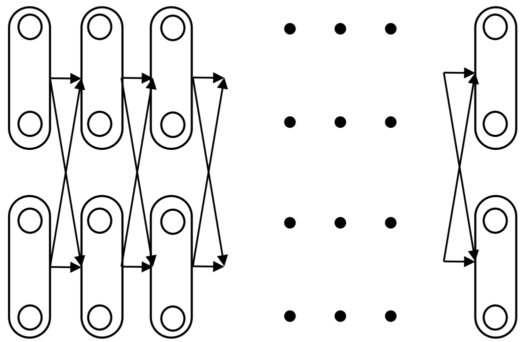
Multi-granularities

- Threshold θ
  - Exploit the fact that we have found a good model of high likelihood
    - θ : exact likelihood of the best-so-far candidate during search processing
  - θ is updated and increases when promising model is found
  - Use θ for model pruning

Multi-granularities

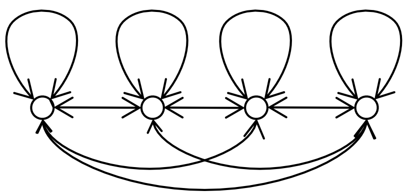
- Compute the approximate likelihood P' from the second coarsest model
  - Second coarsest model has $\lfloor m/2^{h-1} \rfloor$ states
- Prune the model if $P' < \theta$, otherwise
  - θ : exact likelihood of the best-so-far candidate

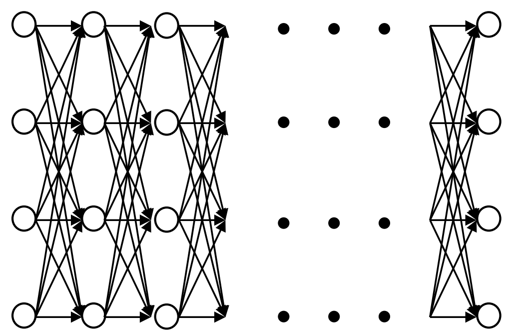




Multi-granularities

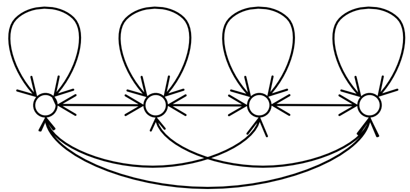
- Compute the likelihood P' from more accurate model
- Prune the model if $P' < \theta$

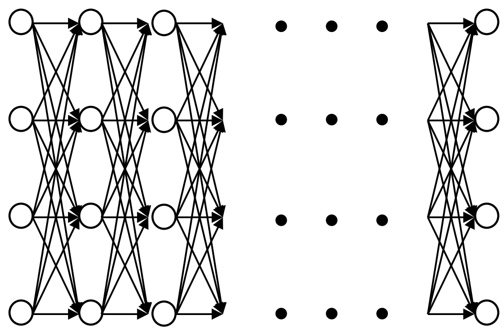




Multi-granularities

- Repeat until the finest granularity (the original model)
- Update the answer candidate and best-so-far likelihood if $P \geq \theta$



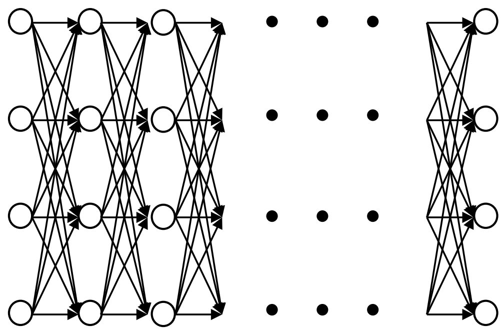


Multi-granularities

- Optimize the trade-off between accuracy and computation time
  - Low-likelihood models are pruned by coarse-grained models
  - Fine-grained approximation is applied only to high-likelihood models
- Efficiently find the best model for a large dataset
  - The exact likelihood computations are limited to the minimum number of necessary

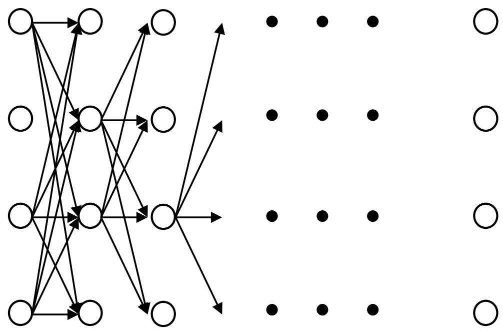
Transition Pruning

- Trellis structure has too many transitions
- Q: How to exclude unlikely paths



Transition Pruning

- Trellis structure has too many transitions
- Q: How to exclude unlikely paths
- A: Use the two properties
  - Likelihood is monotone non-increasing (likelihood computation)
  - Threshold is monotone non-decreasing (search processing)



Transition Pruning

- In likelihood computation, compute the estimate e_{it}

$$e_{it} = \begin{cases} p_{it} \cdot (a_{\max})^{n-t} \cdot \prod_{j=t+1}^{n} b_{\max}(x_j) & (1 \le t \le n-1) \\ p_{in} & (t = n) \end{cases}$$

where $a_{\max} = \max_{1 \le i, j \le m} (a_{ij}), \quad b_{\max}(v) = \max_{1 \le i \le m} b_i(v)$

  - e_{it} : conservative estimate of the likelihood p_{it} of state u_i at time t

- If $e_{it} < \theta$, prune all paths that pass through u_i at t
  - θ : exact likelihood of the best-so-far candidate

Transition Pruning

- Terminate the likelihood computation
  if all the paths are excluded
- Efficient especially for long sequences
- Applicable to approximate likelihood computation

Accuracy and Complexity

- SPIRAL needs the same order of memory space, while can be up to m^2 times faster

	Accuracy	Complexity	
		Memory Space	Computation time
Viterbi	Guarantee exactness	$O(m^2 + ms)$	$O(nm^2)$
SPIRAL			At least $O(n)$ At most $O(nm^2)$

Experimental Evaluation

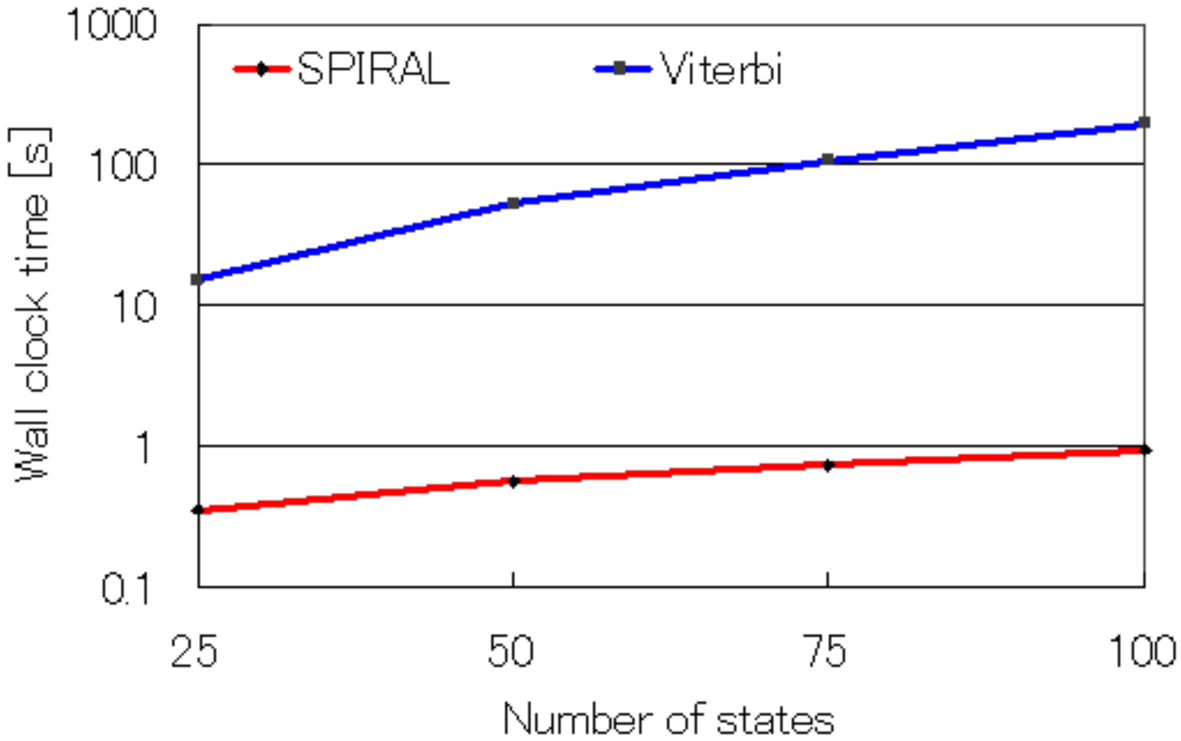
- Setup
  - Intel Core 2 1.66GHz, 2GB memory
- Datasets
  - *EEG, Chromosome, Traffic*
- Evaluation
  - Mainly computation time
  - Ergodic HMM
  - Compared the Viterbi algorithm and Beam search
    - Beam search: popular technique, but does not guarantee exactness

Experimental Evaluation

- Evaluation
  - Wall clock time versus number of states
  - Wall clock time versus number of models
  - Effect of likelihood approximation
  - Effect of transition pruning
  - SPIRAL vs Beam search

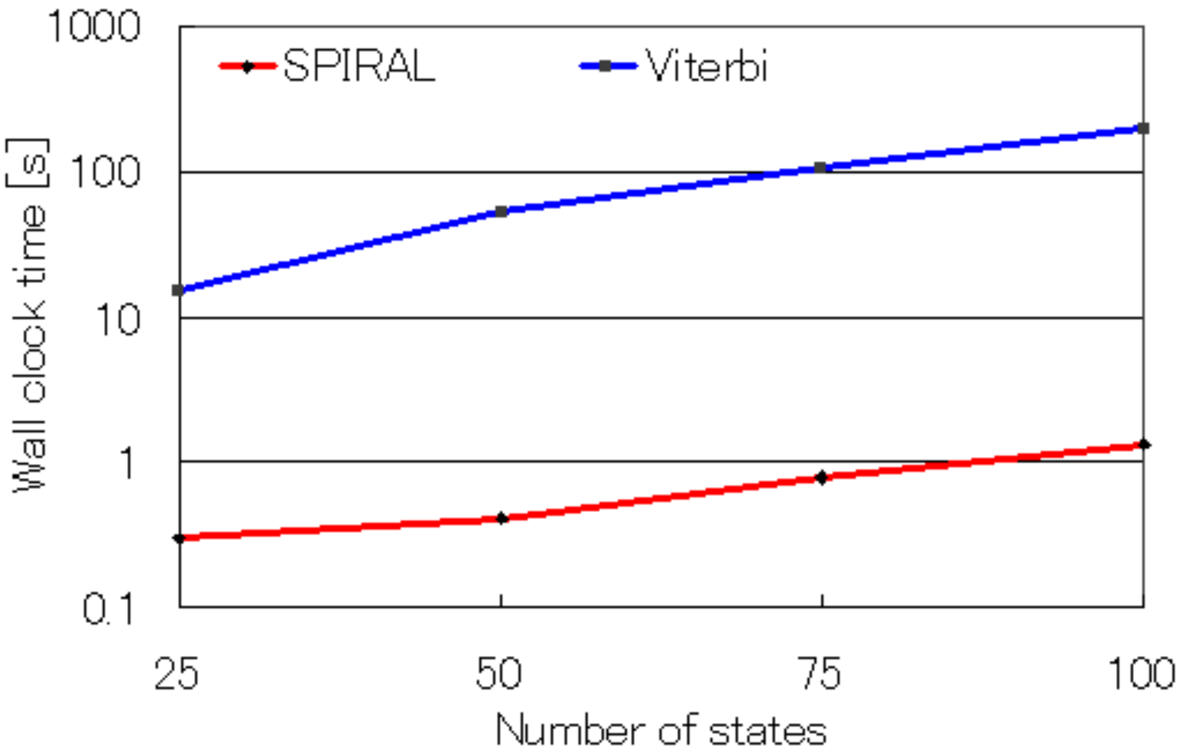
Experimental Evaluation

- Wall clock time versus number of states
  - *EEG*: up to 200 times faster



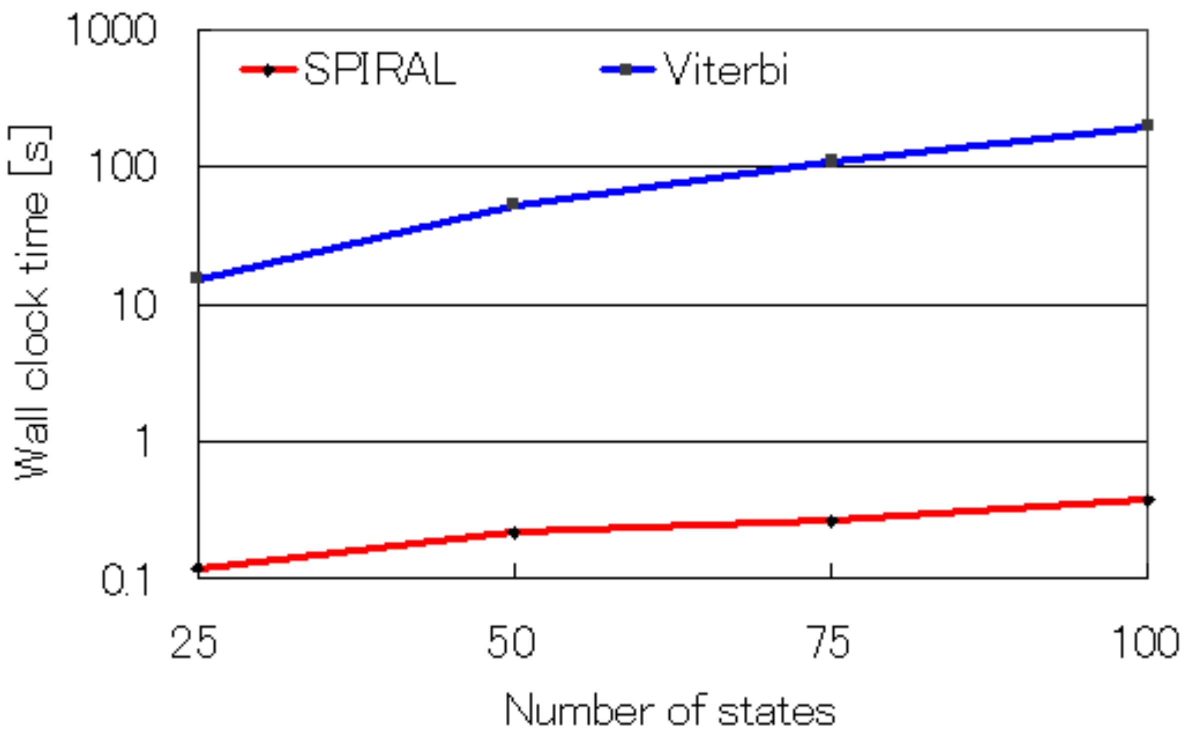
Experimental Evaluation

- Wall clock time versus number of states
  - *Chromosome*: up to 150 times faster



Experimental Evaluation

- Wall clock time versus number of states
  - *Traffic*: up to 500 times faster



Experimental Evaluation

- Evaluation
  - Wall clock time versus number of states
  - Wall clock time versus number of models
  - Effect of likelihood approximation
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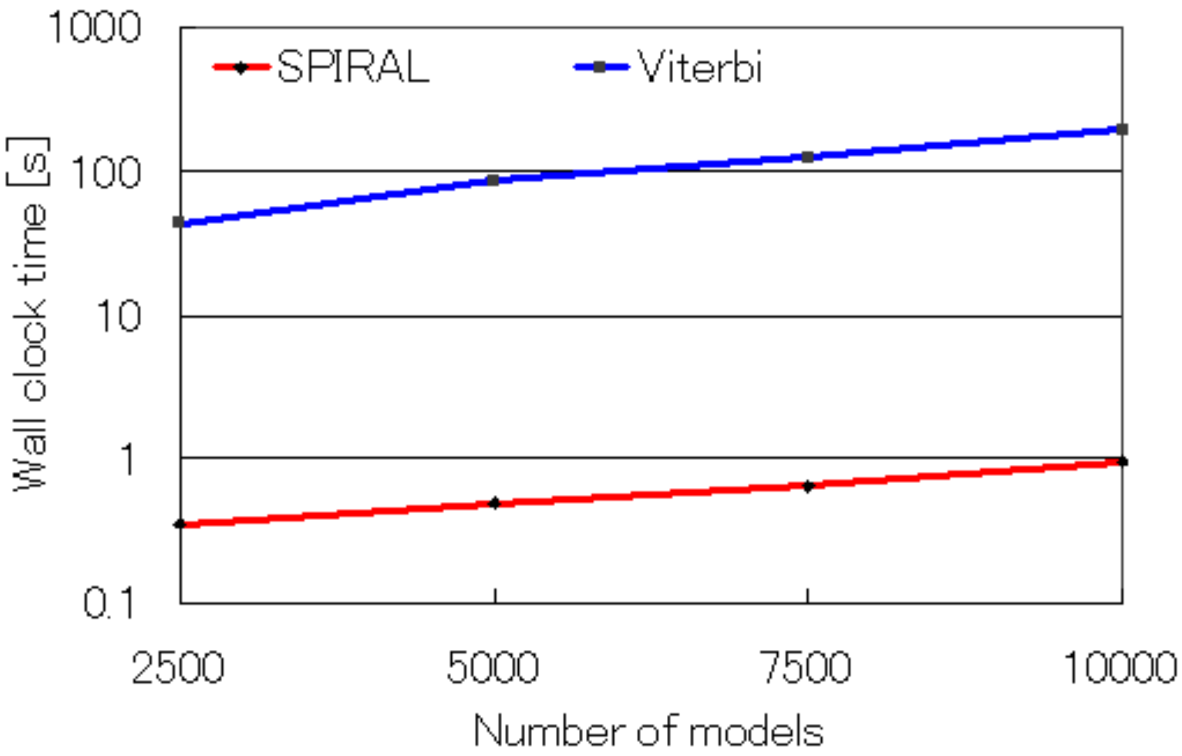
  - SPIRAL vs Beam search

Experimental Evaluation

- Wall clock time versus number of models
  - *EEG*: up to 200 times faster



Experimental Evaluation

- Evaluation
  - Wall clock time versus number of states
  - Wall clock time versus number of models
  - Effect of likelihood approximation
  - Effect of transition pruning
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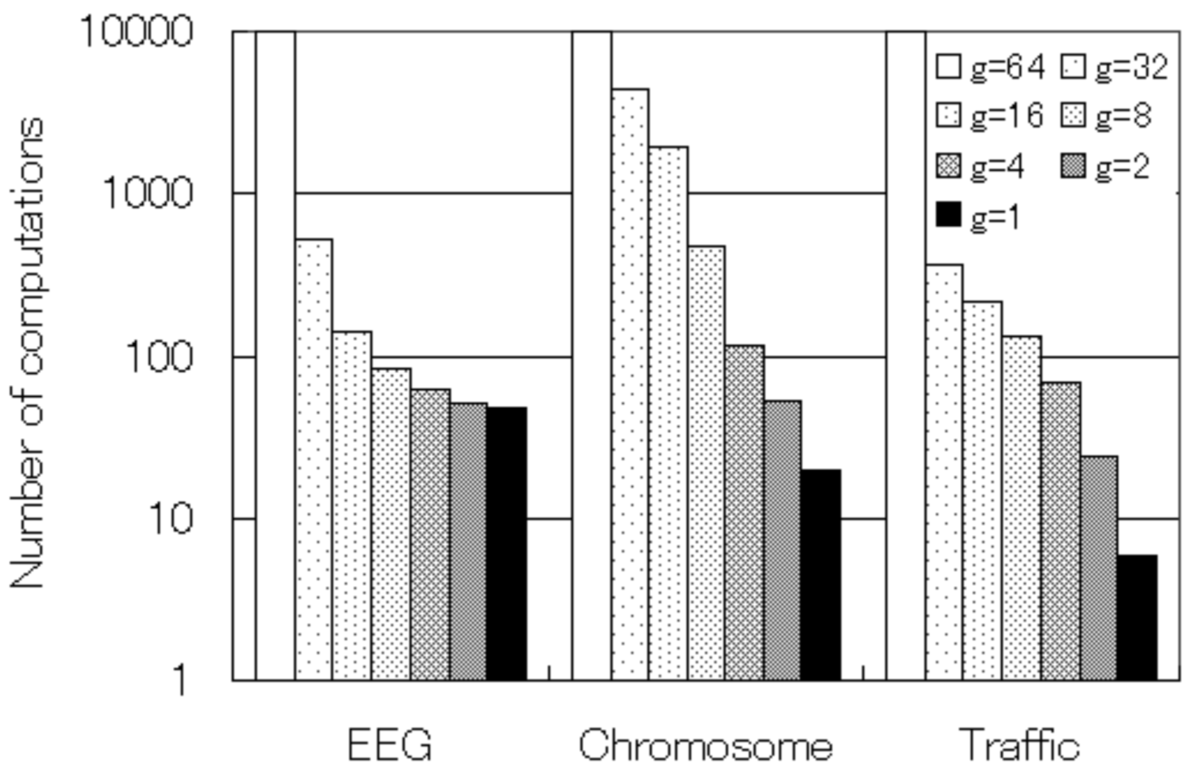
Experimental Evaluation

- Effect of likelihood approximation
  - Most of models are pruned by coarser approximations

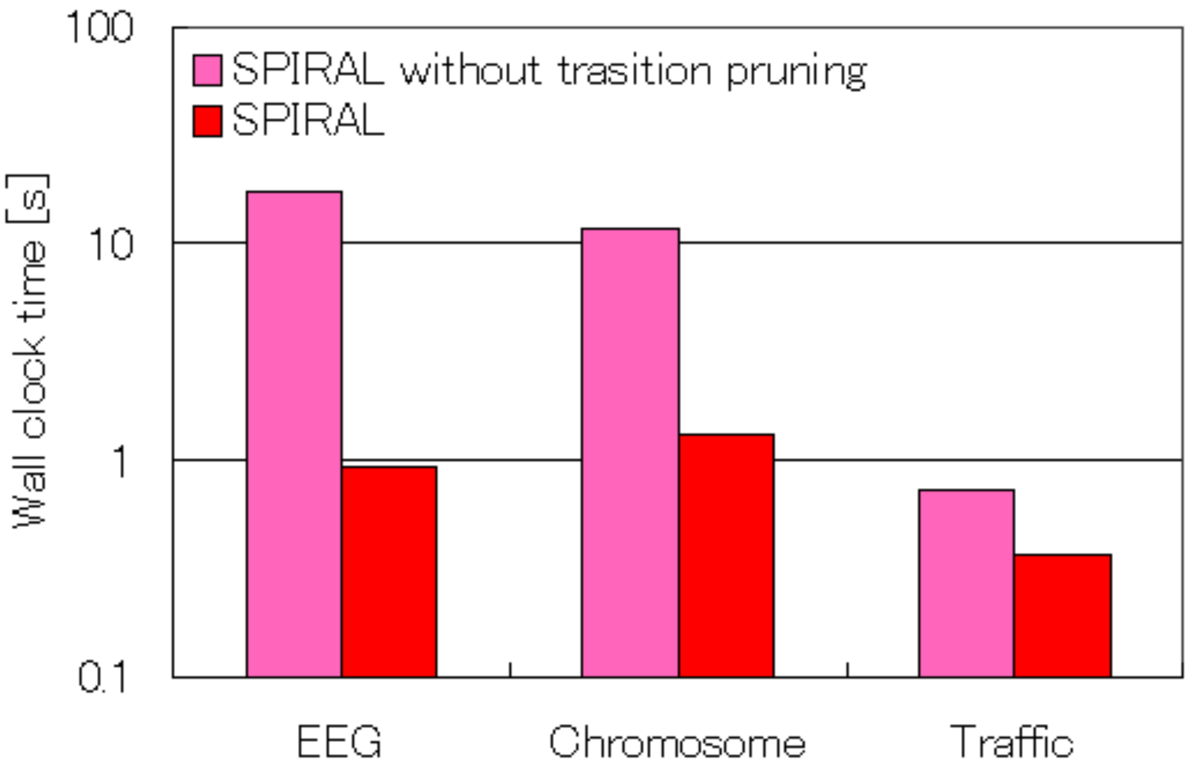


Experimental Evaluation

- Evaluation
  - Wall clock time versus number of states
  - Wall clock time versus number of models
  - Effect of likelihood approximation
  - Effect of transition pruning
  - SPIRAL vs Beam search

Experimental Evaluation

- Effect of transition pruning
  - SPIRAL find the highest-likelihood model more efficiently by transition pruning

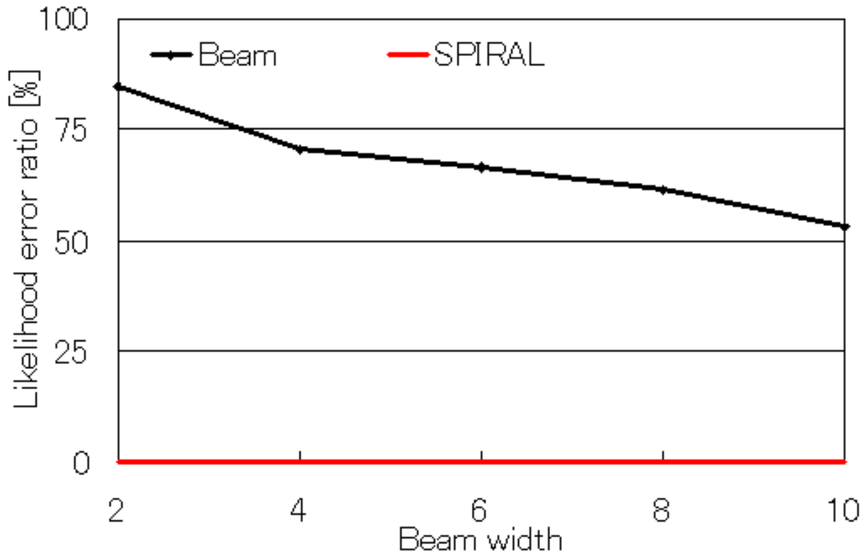


Experimental Evaluation

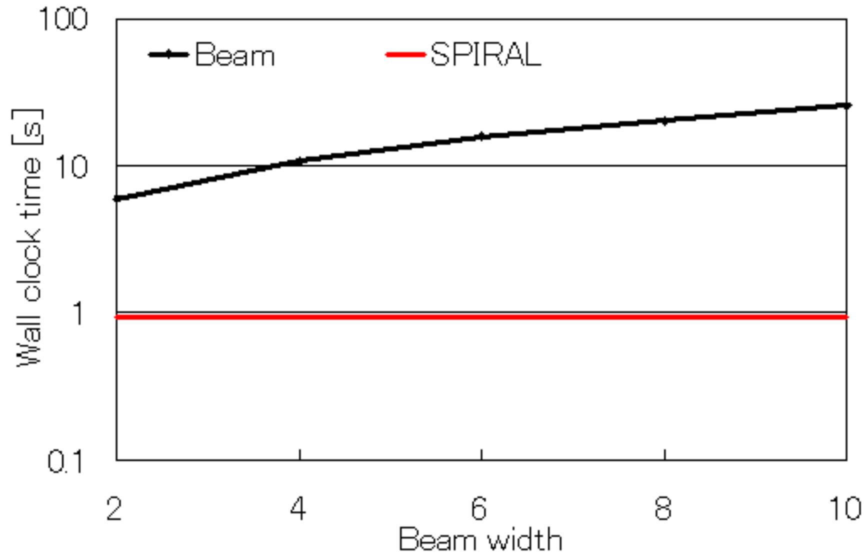
- Evaluation
  - Wall clock time versus number of states
  - Wall clock time versus number of models
  - Effect of likelihood approximation
  - Effect of transition pruning
  - SPIRAL vs Beam search

Experimental Evaluation

- SPIRAL vs Beam search
  - SPIRAL is significantly faster while it guarantees exactness



Likelihood error ratio
Note: SPIRAL gives no error



Wall clock time
SPIRAL is up to 27 times faster

Conclusion

- Design goals:
  - High-speed search
    - SPIRAL is significantly (up to 500 times) faster
  - Exactness
    - We prove that it guarantees exactness
  - No restriction on model type
    - It can handle any HMM model type
- SPIRAL achieves all the goals