# CS6220: DATA MINING TECHNIQUES

## Sequence Data

**Instructor: Yizhou Sun**

yzsun@ccs.neu.edu

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## Reminder

- Homework 1
  - 3 students need to talk to Moon during the break
  - Rakesh Viswanathan, Xin Huang, and Laxmi Rambhatla

- Midterm
  - Next Tuesday (Nov. 5), 2-hour (6-8pm) in class
  - Closed-book exam, and one A4 size cheating sheet is allowed
  - Bring a calculator (NO cell phone)
  - Cover to today's lecture

## Sequence Data

- What is sequence data?
- Sequential pattern mining
- Hidden Markov Model
- Summary

# Sequence Database

- A sequence database consists of sequences of ordered elements or events, recorded with or without a concrete notion of time.

| SID | sequence |
|---|---|
| 10 | <a(<u>ab</u>c)(a<u>c</u>)d(cf)> |
| 20 | <(ad)c(bc)(ae)> |
| 30 | <(ef)(<u>ab</u>)(df)<u>c</u>b> |
| 40 | <eg(af)cbc> |

## Sequence Data

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## Sequence Databases & Sequential Patterns

- Transaction databases vs. sequence databases
- Frequent patterns vs. (frequent) sequential patterns
- Applications of sequential pattern mining
  - Customer shopping sequences:
    - First buy computer, then CD-ROM, and then digital camera, within 3 months.
  - Medical treatments, natural disasters (e.g., earthquakes), science & eng. processes, stocks and markets, etc.
  - Telephone calling patterns, Weblog click streams
  - Program execution sequence data sets
  - DNA sequences and gene structures

# What Is Sequential Pattern Mining?

- Given a set of sequences, find the complete set of *frequent* subsequences

A *sequence* : $<\boxed{(ef)}\boxed{(ab)}\ \boxed{(df)}\boxed{c}\boxed{b}>$

An element may contain a set of items. Items within an element are unordered and we list them alphabetically.

A *sequence database*

| SID | sequence |
|---|---|
| 10 | <a(abc)(ac)d(cf)> |
| 20 | <(ad)c(bc)(ae)> |
| 30 | <(ef)(ab)(df)cb> |
| 40 | <eg(af)cbc> |

<a(bc)dc> is a *subsequence* of <a(abc)(ac)d(cf)>

Given *support threshold* *min_sup* =2, <(ab)c> is a *sequential pattern*

## Sequence

- Event / element
  - An non-empty set of items, e.g., e=(ab)
- Sequence
  - An ordered list of events, e.g., $s =< e_1 e_2 \ldots e_l >$
- Length of a sequence
  - The number of instances of items in a sequence
  - The length of < (ef) (ab) (df) c b > is 8 (Not 5!)

# Subsequence

- Subsequence
  - For two sequences $\alpha =< a_1 a_2 \dots a_n >$ and $\beta =< b_1 b_2 \dots b_m >$, $\alpha$ is called a subsequence of $\beta$ if there exists integers $1 \le j_1 < j_2 < \cdots < j_n \le m$, such that $a_1 \subseteq b_{j_1}, \dots, a_n \subseteq b_{j_n}$
- Supersequence
  - If $\alpha$ is a subsequence of $\beta$, $\beta$ is a supersequence of $\alpha$

<a(bc)dc> is a *subsequence* of
<a(abc)(ac)d(cf)>

## Sequential Pattern

- Support of a sequence $\alpha$
  - Number of sequences in the database that are supersequence of $\alpha$
  - $Support_S(\alpha)$
- $\alpha$ is frequent if $Support_S(\alpha) \geq \min\_support$
- A frequent sequence is called sequential pattern
  - l-pattern if the length of the sequence is l

# Example

A *sequence database*

| SID | sequence |
|---|---|
| 10 | <a(abc)(ac)d(cf)> |
| 20 | <(ad)c(bc)(ae)> |
| 30 | <(ef)(ab)(df)cb> |
| 40 | <eg(af)cbc> |

Given *support threshold* *min_sup* =2, <(ab)c> is a *sequential pattern*

## Challenges on Sequential Pattern Mining

- A huge number of possible sequential patterns are hidden in databases
- A mining algorithm should
  - find the complete set of patterns, when possible, satisfying the minimum support (frequency) threshold
  - be highly efficient, scalable, involving only a small number of database scans
  - be able to incorporate various kinds of user-specific constraints

## Sequential Pattern Mining Algorithms

- Concept introduction and an initial Apriori-like algorithm
  - Agrawal & Srikant. Mining sequential patterns, ICDE'95
- Apriori-based method: GSP (Generalized Sequential Patterns: Srikant & Agrawal @ EDBT'96)
- Pattern-growth methods: FreeSpan & PrefixSpan (Han et al.@KDD'00; Pei, et al.@ICDE'01)
- Vertical format-based mining: SPADE (Zaki@Machine Leanining'00)
- Constraint-based sequential pattern mining (SPIRIT: Garofalakis, Rastogi, Shim@VLDB'99; Pei, Han, Wang @ CIKM'02)
- Mining closed sequential patterns: CloSpan (Yan, Han & Afshar @SDM'03)

## The Apriori Property of Sequential Patterns

- A basic property: Apriori (Agrawal & Sirkant'94)
  - If a sequence S is not frequent
  - Then none of the super-sequences of S is frequent
  - E.g, <hb> is infrequent → so do <hab> and <(ah)b>

| Seq. ID | Sequence |
|---|---|
| 10 | <(bd)cb(ac)> |
| 20 | <(bf)(ce)b(fg)> |
| 30 | <(ah)(bf)abf> |
| 40 | <(be)(ce)d> |
| 50 | <a(bd)bcb(ade)> |

Given *support threshold*
*min_sup* =2

## GSP—Generalized Sequential Pattern Mining

- GSP (Generalized Sequential Pattern) mining algorithm
  - proposed by Agrawal and Srikant, EDBT'96
- Outline of the method
  - Initially, every item in DB is a candidate of length-1
  - for each level (i.e., sequences of length-k) do
    - scan database to collect support count for each candidate sequence
    - generate candidate length-(k+1) sequences from length-k frequent sequences using Apriori
  - repeat until no frequent sequence or no candidate can be found
- Major strength: Candidate pruning by Apriori

## Finding Length-1 Sequential Patterns

- Examine GSP using an example
- Initial candidates: all singleton sequences
  - <a>, <b>, <c>, <d>, <e>, <f>, <g>, <h>
- Scan database once, count support for candidates

| Cand | Sup |
|---|---|
| **<a>** | **3** |
| **<b>** | **5** |
| **<c>** | **4** |
| **<d>** | **3** |
| **<e>** | **3** |
| **<f>** | **2** |
| ~~<g>~~ | 1 |
| ~~<h>~~ | 1 |

*min_sup* =2

| Seq. ID | Sequence |
|---|---|
| 10 | <(bd)cb(ac)> |
| 20 | <(bf)(ce)b(fg)> |
| 30 | <(ah)(bf)abf> |
| 40 | <(be)(ce)d> |
| 50 | <a(bd)bcb(ade)> |

# GSP: Generating Length-2 Candidates

51 length-2 Candidates

| | <a> | <b> | <c> | <d> | <e> | <f> |
|---|---|---|---|---|---|---|
| <a> | <aa> | <ab> | <ac> | <ad> | <ae> | <af> |
| <b> | <ba> | <bb> | <bc> | <bd> | <be> | <bf> |
| <c> | <ca> | <cb> | <cc> | <cd> | <ce> | <cf> |
| <d> | <da> | <db> | <dc> | <dd> | <de> | <df> |
| <e> | <ea> | <eb> | <ec> | <ed> | <ee> | <ef> |
| <f> | <fa> | <fb> | <fc> | <fd> | <fe> | <ff> |

| | <a> | <b> | <c> | <d> | <e> | <f> |
|---|---|---|---|---|---|---|
| <a> | | <(ab)> | <(ac)> | <(ad)> | <(ae)> | <(af)> |
| <b> | | | <(bc)> | <(bd)> | <(be)> | <(bf)> |
| <c> | | | | <(cd)> | <(ce)> | <(cf)> |
| <d> | | | | | <(de)> | <(df)> |
| <e> | | | | | | <(ef)> |
| <f> | | | | | | |

Without Apriori property, 8*8+8*7/2=92 candidates

Apriori prunes 44.57% candidates

# How to Generate Candidates in General?

- From $L_{k-1}$ to $C_k$
- Step 1: join
  - $s_1$ $and$ $s_2$ can join, if dropping first item in $s_1$ is the same as dropping the last item in $s_2$
  - Examples:
    - <(12)3> join <(2)34> = <(12)34>
    - <(12)3> join <(2)(34)> = <(12)(34)>
- Step 2: pruning
  - Check whether all length k-1 subsequences of a candidate is contained in $L_{k-1}$

# The GSP Mining Process

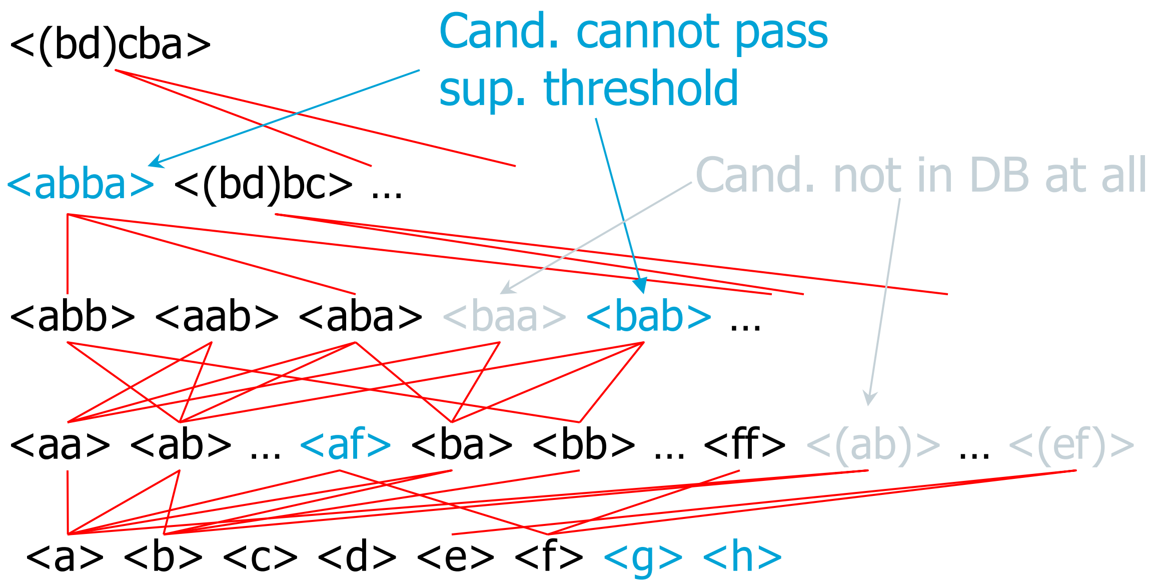
5th scan: 1 cand. 1 length-5 seq. pat.

4th scan: 8 cand. 7 length-4 seq. pat.

3rd scan: 46 cand. 20 length-3 seq. pat. 20 cand. not in DB at all

2nd scan: 51 cand. 19 length-2 seq. pat. 10 cand. not in DB at all

1st scan: 8 cand. 6 length-1 seq. pat.



<(bd)cba>
Cand. cannot pass sup. threshold
<abba> <(bd)bc> …
Cand. not in DB at all
<abb> <aab> <aba> <baa> <bab> …
<aa> <ab> … <af> <ba> <bb> … <ff> <(ab)> … <(ef)>
<a> <b> <c> <d> <e> <f> <g> <h>

*min_sup* =2

| Seq. ID | Sequence |
|---|---|
| 10 | <(bd)cb(ac)> |
| 20 | <(bf)(ce)b(fg)> |
| 30 | <(ah)(bf)abf> |
| 40 | <(be)(ce)d> |
| 50 | <a(bd)bcb(ade)> |

## Candidate Generate-and-test: Drawbacks

- A huge set of candidate sequences generated.
    - Especially 2-item candidate sequence.
- Multiple Scans of database needed.
    - The length of each candidate grows by one at each database scan.
- Inefficient for mining long sequential patterns.
    - A long pattern grow up from short patterns
    - The number of short patterns is exponential to the length of mined patterns.

# The SPADE Algorithm

- SPADE (Sequential PAttern Discovery using Equivalent Class) developed by Zaki 2001
- A vertical format sequential pattern mining method
- A sequence database is mapped to a large set of
  - Item: <SID, EID>
- Sequential pattern mining is performed by
  - growing the subsequences (patterns) one item at a time by Apriori candidate generation

# The SPADE Algorithm

| SID | EID | Items |
|---|---|---|
| 1 | 1 | a |
| 1 | 2 | abc |
| 1 | 3 | ac |
| 1 | 4 | d |
| 1 | 5 | cf |
| 2 | 1 | ad |
| 2 | 2 | c |
| 2 | 3 | bc |
| 2 | 4 | ae |
| 3 | 1 | ef |
| 3 | 2 | ab |
| 3 | 3 | df |
| 3 | 4 | c |
| 3 | 5 | b |
| 4 | 1 | e |
| 4 | 2 | g |
| 4 | 3 | af |
| 4 | 4 | c |
| 4 | 5 | b |
| 4 | 6 | c |

| a | | b | | . . . |
|---|---|---|---|---|
| SID | EID | SID | EID | . . . |
| 1 | 1 | 1 | 2 | |
| 1 | 2 | 2 | 3 | |
| 1 | 3 | 3 | 2 | |
| 2 | 1 | 3 | 5 | |
| 2 | 4 | 4 | 5 | |
| 3 | 2 | | | |
| 4 | 3 | | | |

**Join two tables**

| ab | | | ba | | | . . . |
|---|---|---|---|---|---|---|
| SID | EID (a) | EID(b) | SID | EID (b) | EID(a) | . . . |
| 1 | 1 | 2 | 1 | 2 | 3 | |
| 2 | 1 | 3 | 2 | 3 | 4 | |
| 3 | 2 | 5 | | | | |
| 4 | 3 | 5 | | | | |

| aba | | | | . . . |
|---|---|---|---|---|
| SID | EID (a) | EID(b) | EID(a) | . . . |
| 1 | 1 | 2 | 3 | |
| 2 | 1 | 3 | 4 | |

## Bottlenecks of GSP and SPADE

- A huge set of candidates could be generated
  - 1,000 frequent length-1 sequences generate s huge number of length-2 candidates!

$$1000 \times 1000 + \frac{1000 \times 999}{2} = 1{,}499{,}500$$

- Multiple scans of database in mining
- Breadth-first search
- Mining long sequential patterns
  - Needs an exponential number of short candidates
  - A length-100 sequential pattern needs $10^{30}$ candidate sequences!

$$\sum_{i=1}^{100} \binom{100}{i} = 2^{100} - 1 \approx 10^{30}$$

## Prefix and Suffix (Projection)

**Assume a pre-specified order on items, e.g., alphabetical order**

- <a>, <aa>, <a(ab)> and <a(abc)> are *prefixes* of sequence <a(abc)(ac)d(cf)>
  - Note <a(ac)> is not a prefix of <a(abc)(ac)d(cf)>
- Given sequence <a(abc)(ac)d(cf)>

| Prefix | *Suffix* (Prefix-Based *Projection)* |
|---|---|
| <a> | <(abc)(ac)d(cf)> |
| <aa> | <(_bc)(ac)d(cf)> |
| <a(ab)> | <(_c)(ac)d(cf)> |

# Mining Sequential Patterns by Prefix Projections

- Step 1: find length-1 sequential patterns
  - <a>, <b>, <c>, <d>, <e>, <f>
- Step 2: divide search space. The complete set of seq. pat. can be partitioned into 6 subsets:
  - The ones having prefix <a>;
  - The ones having prefix <b>;
  - …
  - The ones having prefix <f>

| SID | sequence |
|---|---|
| 10 | <a(abc)(ac)d(cf)> |
| 20 | <(ad)c(bc)(ae)> |
| 30 | <(ef)(ab)(df)cb> |
| 40 | <eg(af)cbc> |

## Finding Seq. Patterns with Prefix <a>

- Only need to consider projections w.r.t. <a>
  - <a>-projected database:
    - <(abc)(ac)d(cf)>
    - <(_d)c(bc)(ae)>
    - <(_b)(df)cb>
    - <(_f)cbc>

| SID | sequence |
|---|---|
| 10 | <a(abc)(ac)d(cf)> |
| 20 | <(ad)c(bc)(ae)> |
| 30 | <(ef)(ab)(df)cb> |
| 40 | <eg(af)cbc> |

- Find all the length-2 seq. pat. Having prefix <a>: <aa>, <ab>, <(ab)>, <ac>, <ad>, <af>
  - Further partition into 6 subsets
    - Having prefix <aa>;
    - …
    - Having prefix <af>

## Why are those 6 subsets?

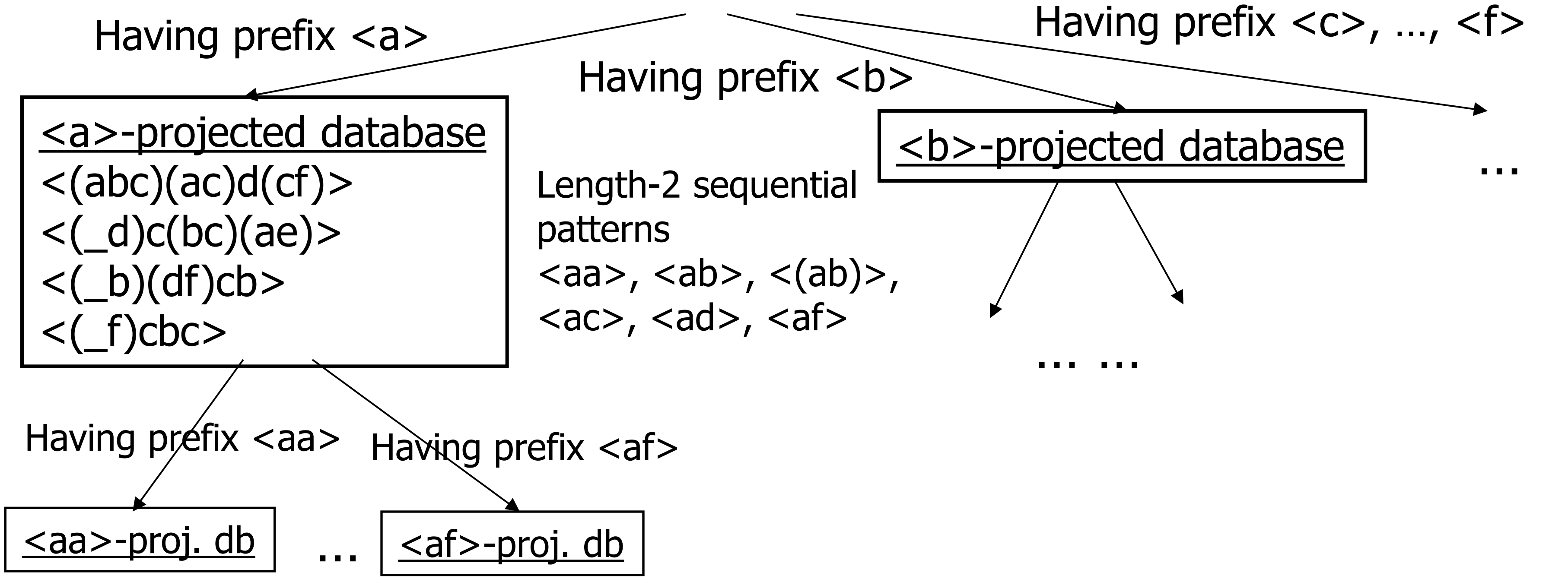
- By scanning the <*a*>-projected database once, its locally frequent items are identified as
  - $a : 2$, $b : 4$, $\_b : 2$, $c : 4$, $d : 2$, and $f : 2$.
- Thus all the length-2 sequential patterns prefixed with <*a*> are found, and they are:
  - $<aa> : 2$, $<ab> : 4$, $<(ab)> : 2$, $<ac> : 4$, $<ad> : 2$, and $<a\,f> : 2$.

# Completeness of PrefixSpan

SDB

| SID | sequence |
|---|---|
| 10 | <a(abc)(ac)d(cf)> |
| 20 | <(ad)c(bc)(ae)> |
| 30 | <(ef)(ab)(df)cb> |
| 40 | <eg(af)cbc> |

Length-1 sequential patterns
<a>, <b>, <c>, <d>, <e>, <f>

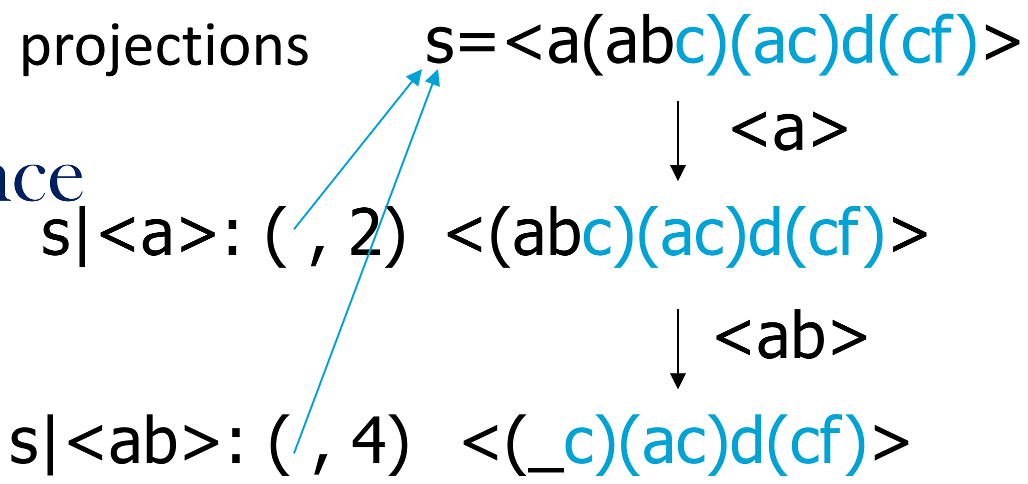


## Efficiency of PrefixSpan

- No candidate sequence needs to be generated
- Projected databases keep shrinking
- Major cost of PrefixSpan: Constructing projected databases
  - Can be improved by pseudo-projections

# Speed-up by Pseudo-projection

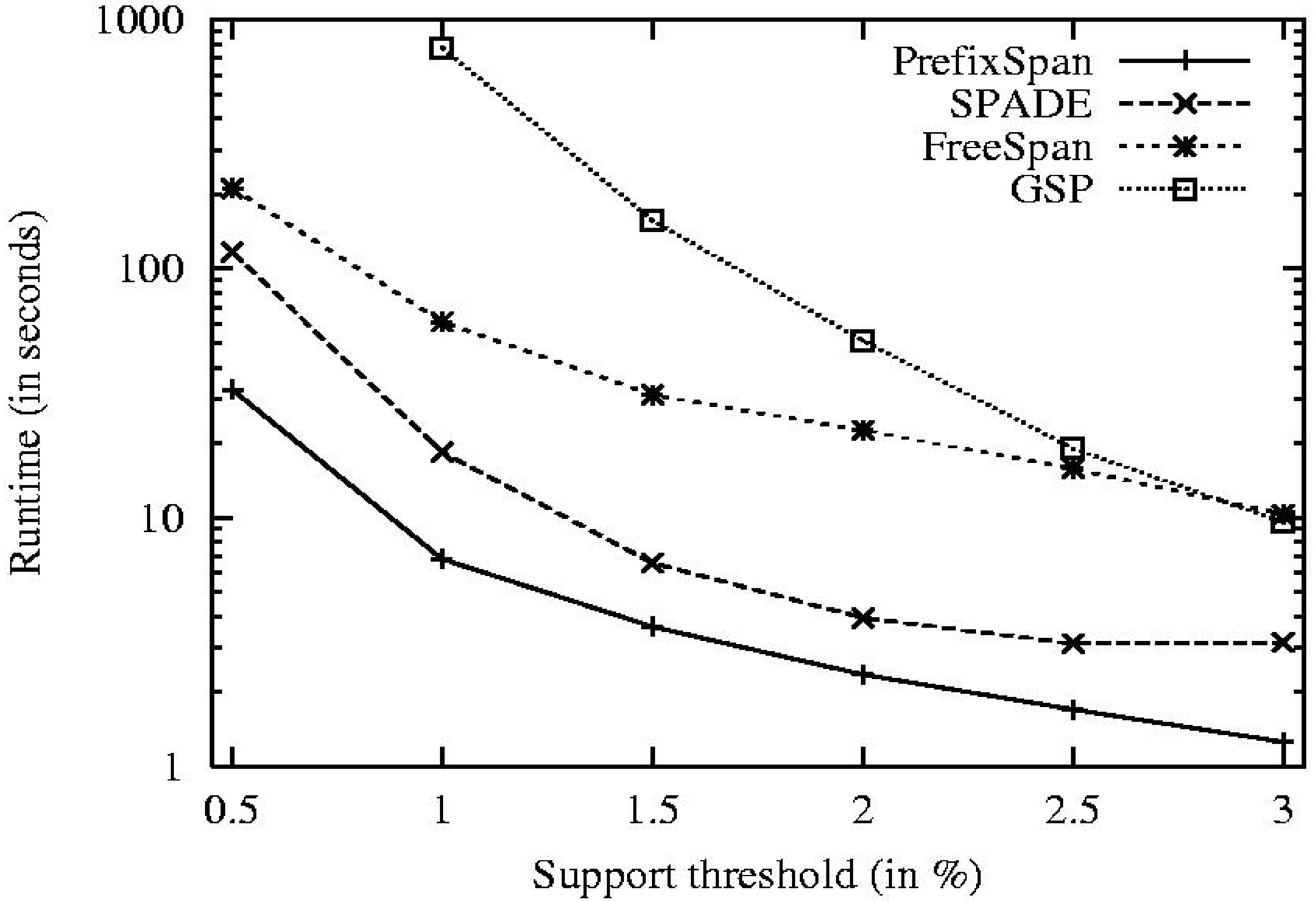
- Major cost of PrefixSpan: projection
  - Postfixes of sequences often appear repeatedly in recursive projected databases
- When (projected) database can be held in main memory, use pointers to form projections
  - Pointer to the sequence
  - Offset of the postfix


s=<a(abc)(ac)d(cf)>
<a>
s|<a>: ( , 2) <(abc)(ac)d(cf)>
<ab>
s|<ab>: ( , 4) <(_c)(ac)d(cf)>

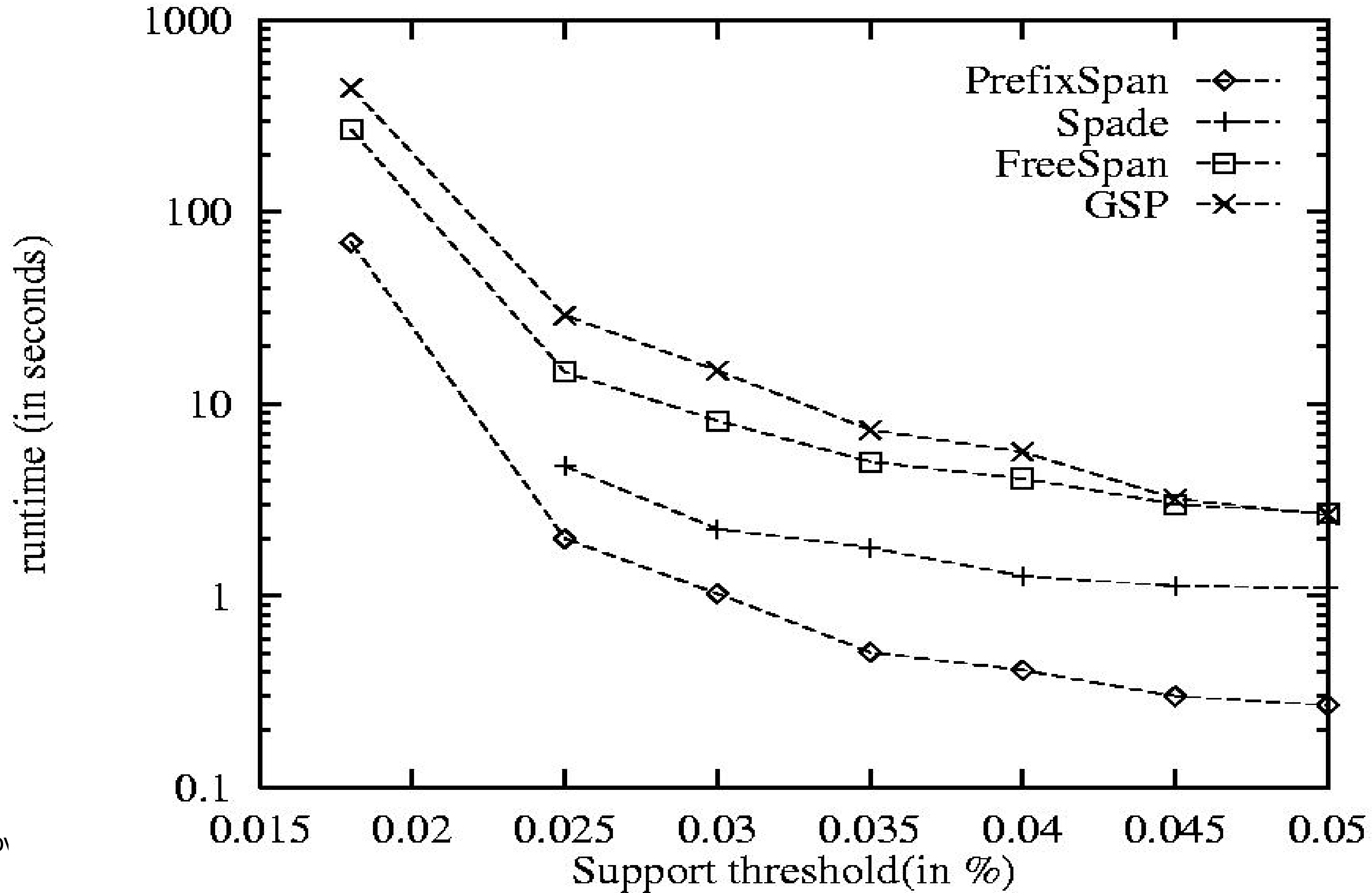
## Pseudo-Projection vs. Physical Projection

- Pseudo-projection avoids physically copying postfixes
    - Efficient in running time and space when database can be held in main memory
- However, it is not efficient when database cannot fit in main memory
    - Disk-based random accessing is very costly
- Suggested Approach:
    - Integration of physical and pseudo-projection
    - Swapping to pseudo-projection when the data set fits in memory

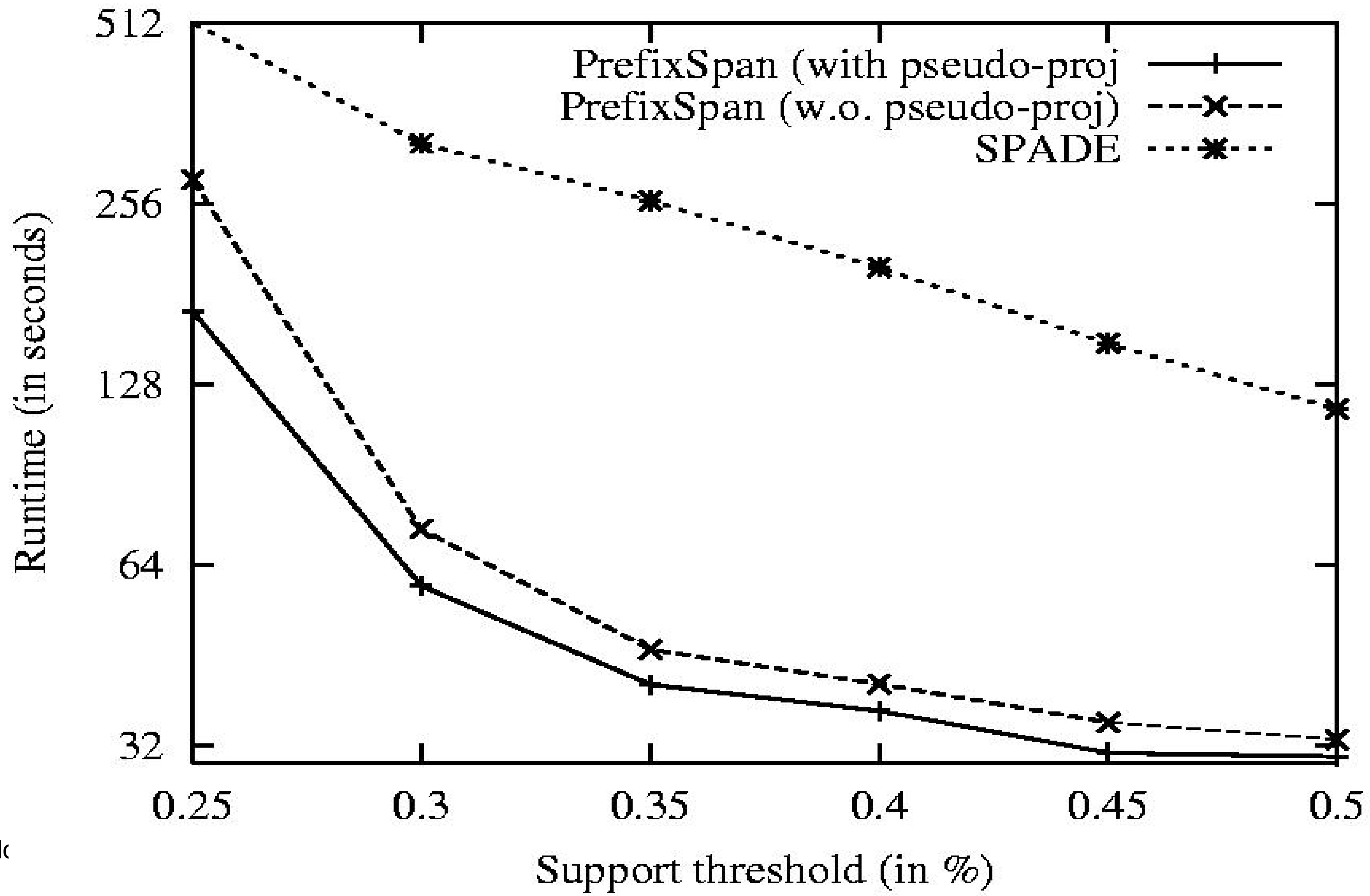
## Performance on Data Set C10T8S8I8



## Performance on Data Set Gazelle



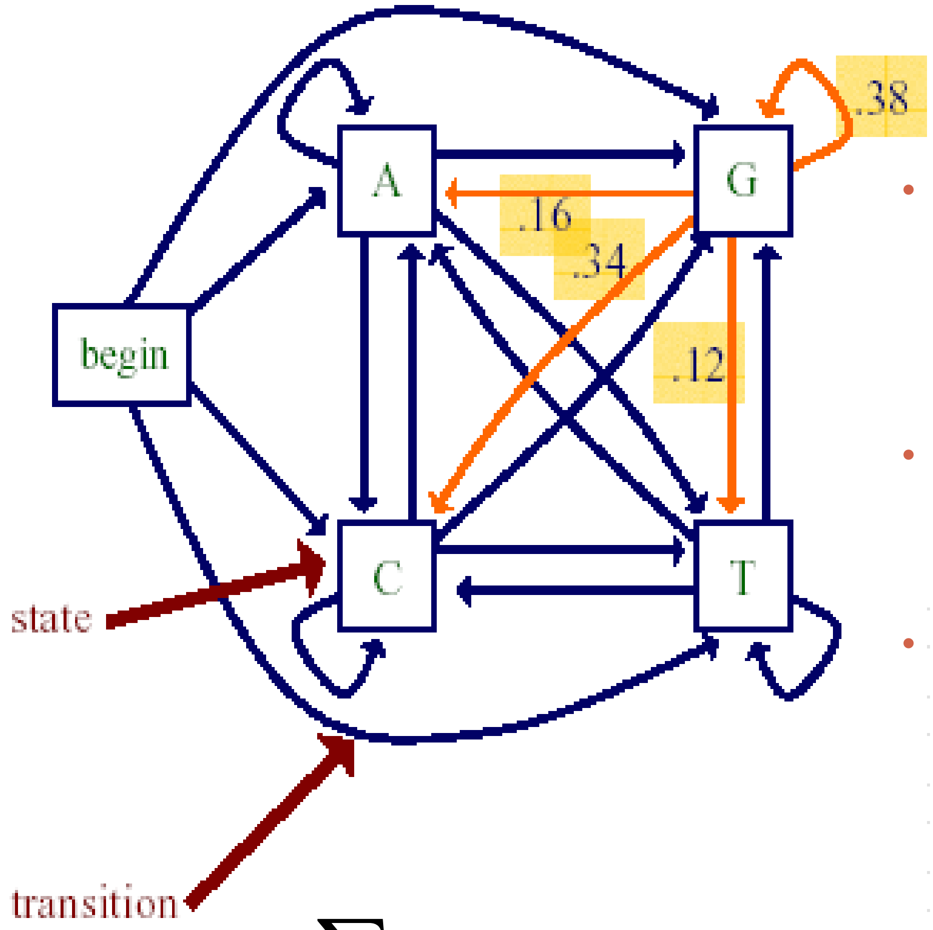
## Effect of Pseudo-Projection



## Sequence Data

- What is sequence data?
- Sequential pattern mining
- Hidden Markov Model
- Summary

# A Markov Chain Model



$$\sum \Pr(x_i \mid x_{i-1} = g) = 1$$

- **Markov property: *Given the present state, future states are independent of the past states***
- At each step the system may change its state from the current state to another state, or remain in the same state, according to a certain probability distribution
- The changes of state are called ***transitions***, and the probabilities associated with various state-changes are called ***transition probabilities***
- Transition probabilities
  - $\Pr(x_i=a|x_{i-1}=g)=0.16$
  - $\Pr(x_i=c|x_{i-1}=g)=0.34$
  - $\Pr(x_i=g|x_{i-1}=g)=0.38$
  - $\Pr(x_i=t|x_{i-1}=g)=0.12$

# Definition of Markov Chain Model

- A Markov chain model is defined by

Each event of a sequence here is Considered containing only one state

  - A set of states
    - Some states emit symbols
    - Other states (e.g., the begin state) are silent
  - A set of transitions with associated probabilities
    - The transitions emanating from a given state define a distribution over the possible next states

## Markov Chain Models: Properties

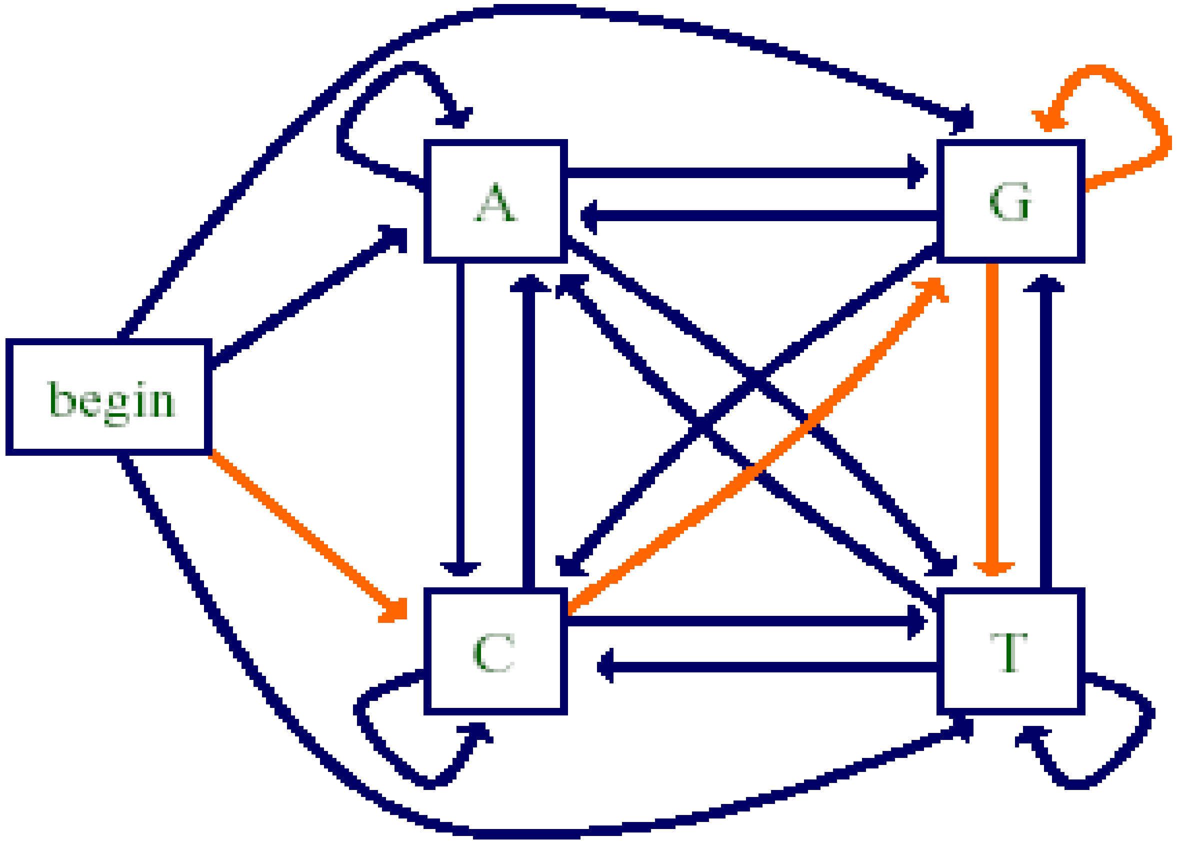
- Given some sequence x of length L, we can ask how probable the sequence is given our model
- For any probabilistic model of sequences, we can write this probability as

$$\Pr(x) = \Pr(x_L, x_{L-1}, \ldots, x_1)$$
$$= \Pr(x_L \mid x_{L-1}, \ldots, x_1) \Pr(x_{L-1} \mid x_{L-2}, \ldots, x_1) \ldots \Pr(x_1)$$

- key property of a (1st order) Markov chain: the probability of each $x_i$ depends only on the value of $x_{i-1}$

$$\Pr(x) = \Pr(x_L \mid x_{L-1}) \Pr(x_{L-1} \mid x_{L-2}) \ldots \Pr(x_2 \mid x_1) \Pr(x_1)$$
$$= \Pr(x_1) \prod_{i=2}^{L} \Pr(x_i \mid x_{i-1})$$

## The Probability of a Sequence for a Markov Chain Model



$$\Pr(cggt)=\Pr(c)\Pr(g|c)\Pr(g|g)\Pr(t|g)$$

# Example Application

- CpG islands
  - CG dinucleotides are rarer in eukaryotic genomes than expected given the marginal probabilities of C and G
  - but the regions upstream of genes are richer in CG dinucleotides than elsewhere – CpG islands
  - useful evidence for finding genes
- Application: Predict CpG islands with Markov chains
  - one to represent CpG islands
  - one to represent the rest of the genome

# Markov Chains for Discrimination

- Suppose we want to distinguish CpG islands from other sequence regions
- Given sequences from CpG islands, and sequences from other regions, we can construct
  - a model to represent CpG islands
  - a null model to represent the other regions
- can then score a test sequence by:

$$score(x) = \log \frac{\Pr(x \mid CpGModel)}{\Pr(x \mid nullModel)}$$

# Markov Chains for Discrimination

- Why use

$$score(x) = \log \frac{\Pr(x \mid CpGModel)}{\Pr(x \mid nullModel)}$$

- According to Bayes' rule

$$\Pr(CpG \mid x) = \frac{\Pr(x \mid CpG)\Pr(CpG)}{\Pr(x)}$$

$$\Pr(null \mid x) = \frac{\Pr(x \mid null)\Pr(null)}{\Pr(x)}$$

- If we are not taking into account of prior probabilities of two classes, we just need to compare Pr(x|CpG) and Pr(x|null)

## Higher Order Markov Chains

- The Markov property specifies that the probability of a state depends only on the probability of the previous state
- But we can build more “memory” into our states by using a higher order Markov model
- In an n-th order Markov model

$$\Pr(x_i \mid x_{i-1}, x_{i-2}, \ldots, x_1) = \Pr(x_i \mid x_{i-1}, \ldots, x_{i-n})$$

# Higher Order Markov Chains

- An n-th order Markov chain over some alphabet A is equivalent to a first order Markov chain over the alphabet of n-tuples: $A^n$
- Example: A 2nd order Markov model for DNA can be treated as a 1st order Markov model over alphabet

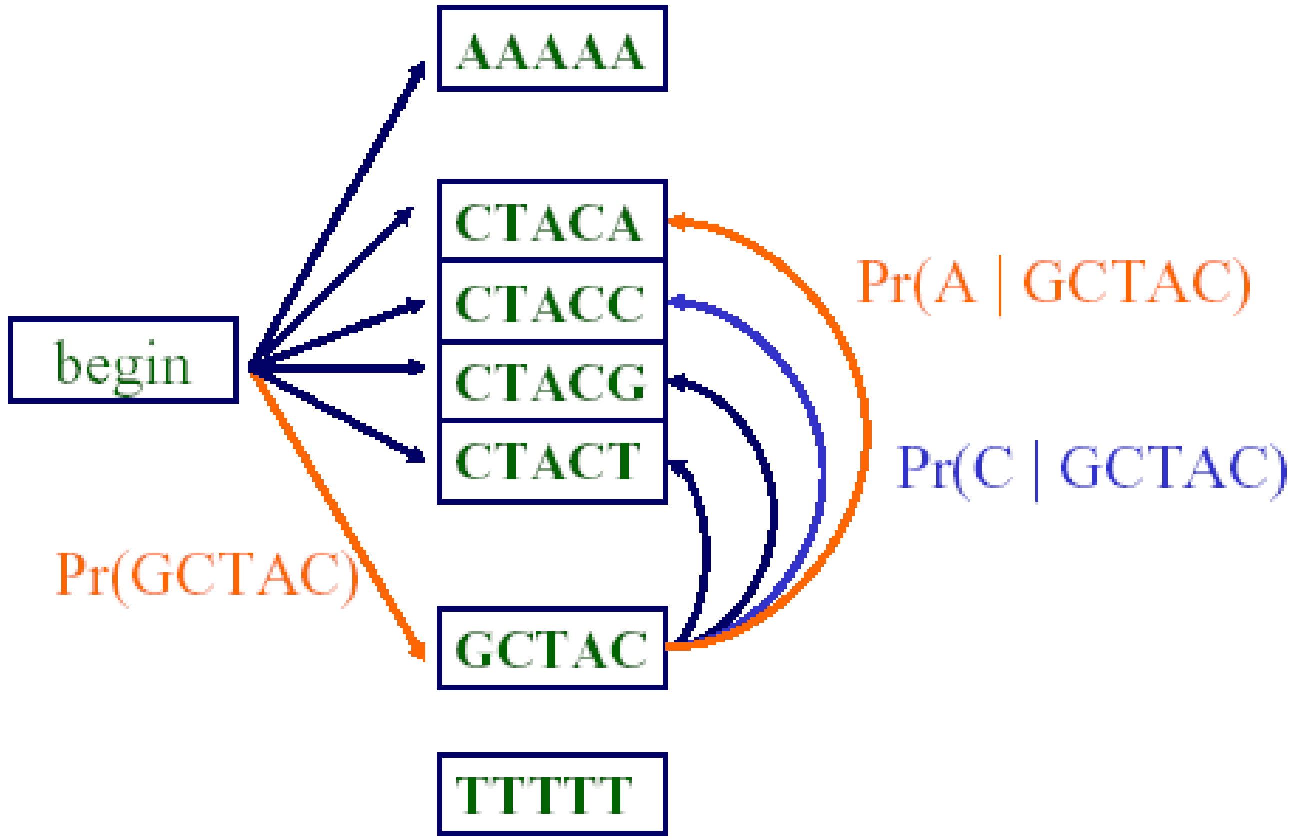
AA, AC, AG, AT

CA, CC, CG, CT

GA, GC, GG, GT

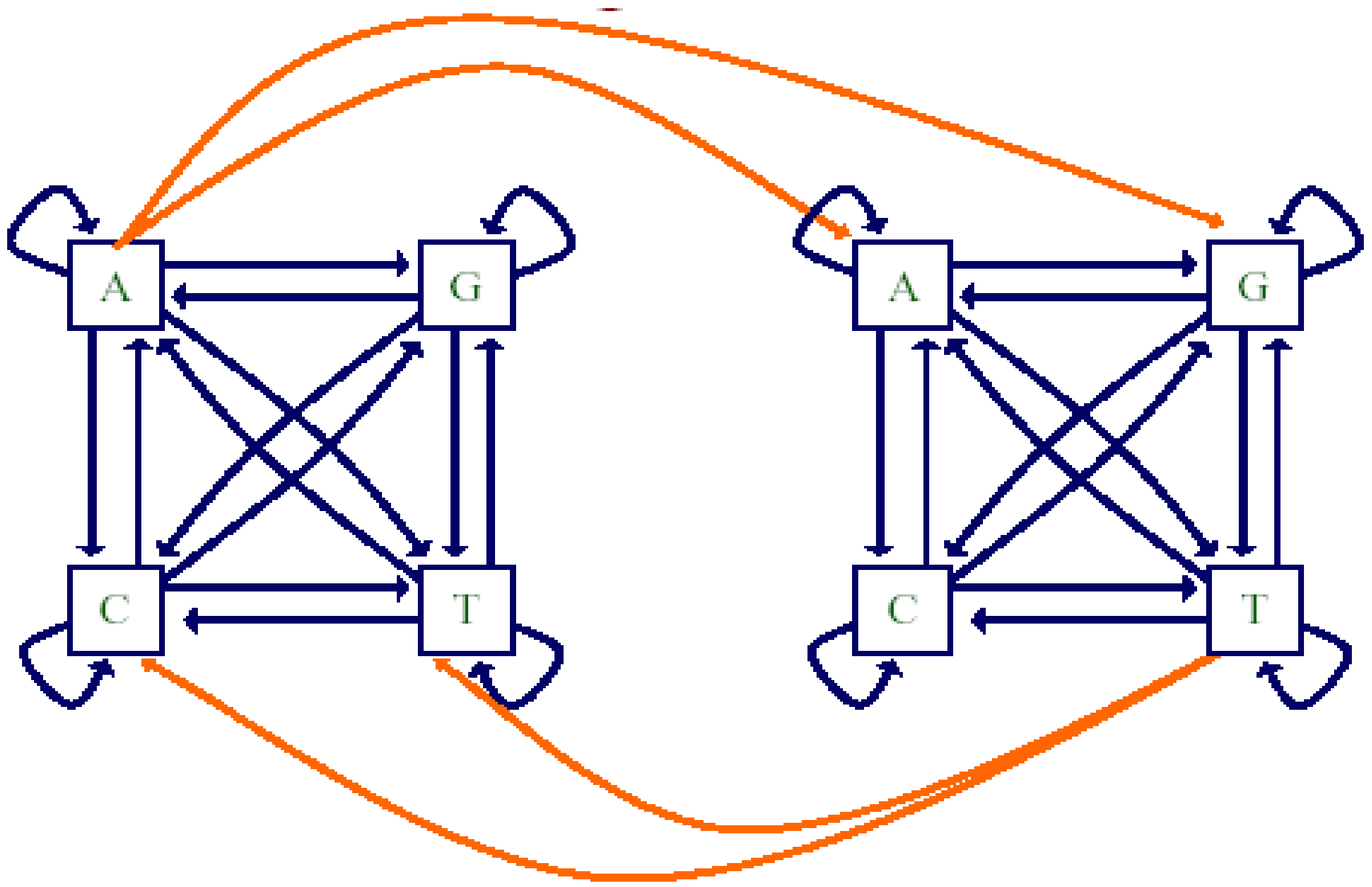
TA, TC, TG, TT

# A Fifth Order Markov Chain



Pr(gctaca)=Pr(gctac)Pr(a|gctac)

## Hidden Markov Model



Given observed sequence AGGCT, which state emits every item?

## Hidden Markov Model

- A **hidden Markov model** (**HMM**): A statistical model in which the system being modeled is assumed to be a Markov process with *unknown parameters*
  - The state is not directly visible, but variables influenced by the state are visible
  - Each state has a probability distribution over the possible output tokens. Therefore the sequence of tokens generated by an HMM gives some information about the sequence of states.
- The challenge is to determine the hidden parameters from the observable data. The extracted model parameters can then be used to perform further analysis
- An HMM can be considered as the simplest dynamic Bayesian network

## Learning and Prediction Tasks

- Learning
  - Given a model, a set of training sequences
  - Find model parameters that explain the training sequences with relatively high probability (goal is to find a model that *generalizes* well to sequences we haven't seen before)
- Classification
  - Given a set of models representing different sequence classes, a test sequence
  - Determine which model/class best explains the sequence
- Segmentation
  - Given a model representing different sequence classes, a test sequence
  - Segment the sequence into subsequences, predicting the class of each subsequence

## The Parameters of an HMM

- Transition Probabilities

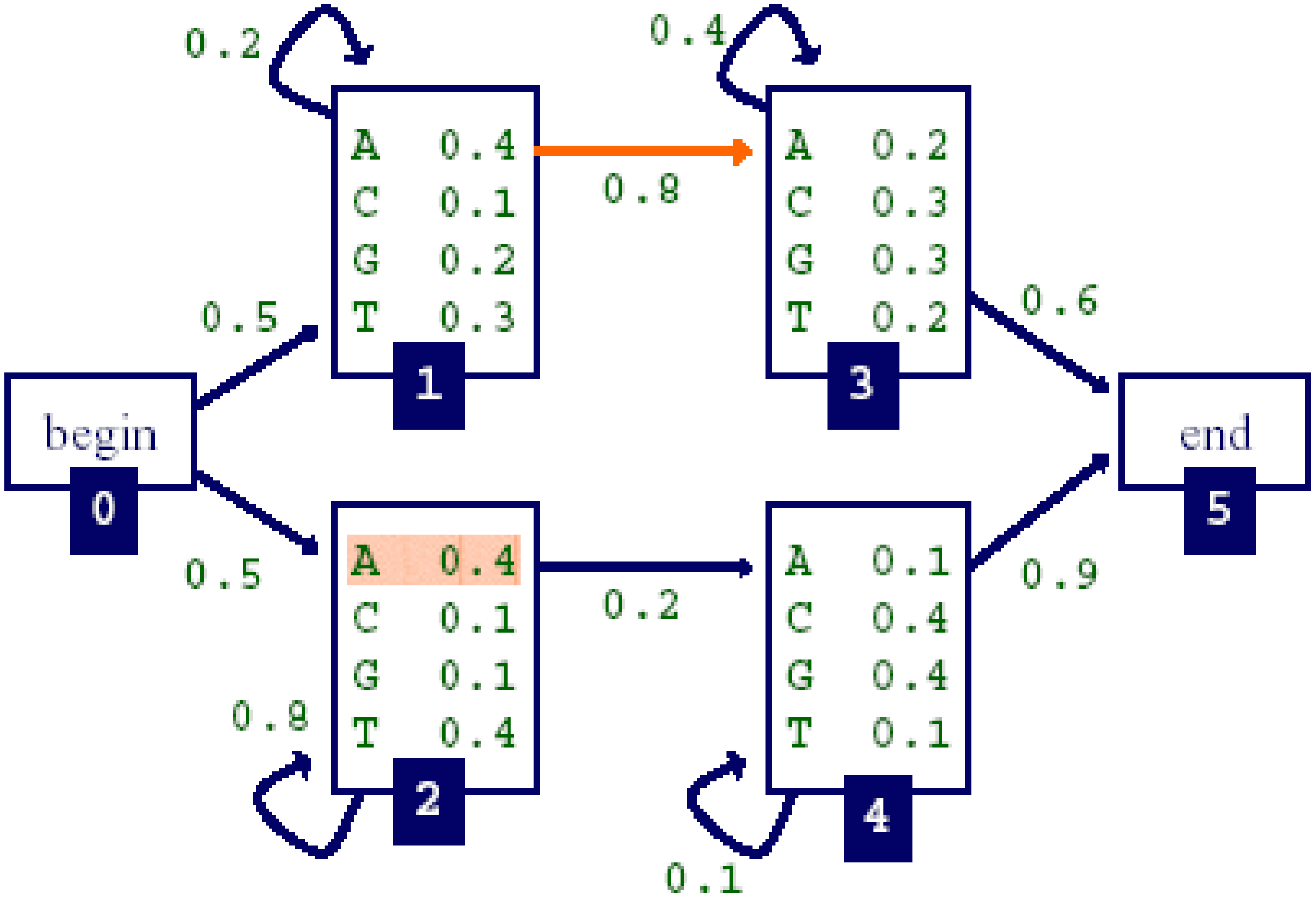
$$a_{kl} = \Pr(\pi_i = l \mid \pi_{i-1} = k)$$

  - Probability of transition from state k to state l
- Emission Probabilities

$$e_k(b) = \Pr(x_i = b \mid \pi_i = k)$$

  - Probability of emitting character b in state k

# An HMM Example



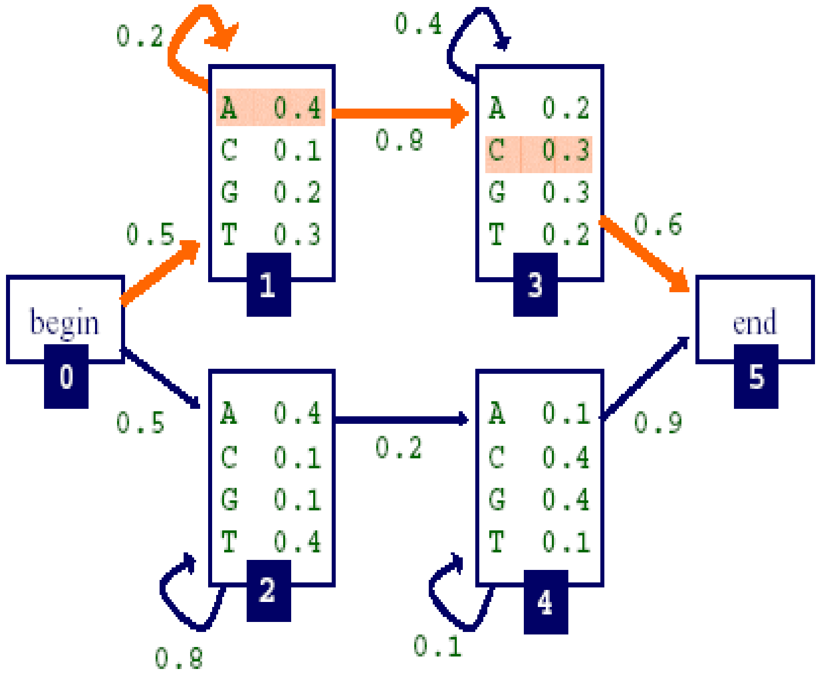
## Three Important Questions

- How likely is a given sequence?
  - The Forward algorithm
- What is the most probable "path" for generating a given sequence?
  - The Viterbi algorithm
- How can we learn the HMM parameters given a set of sequences?
  - The Forward-Backward (Baum-Welch) algorithm

# How Likely is a Given Sequence?

- The probability that the path is taken and the sequence is generated:

$$\Pr(x_1 \ldots x_L, \pi_0 \ldots \pi_N) = a_{0\pi_1} \prod_{i=1}^{L} e_{\pi_i}(x_i) a_{\pi_i \pi_{i+1}}$$



$$\Pr(AAC, \pi)$$
$$= a_{01} \times e_1(A) \times a_{11} \times e_1(A)$$
$$\times a_{13} \times e_3(C) \times a_{35}$$
$$= .5 \times .4 \times .2 \times .4 \times .8 \times .3 \times .6$$

## How Likely is a Given Sequence?

- The probability over all paths is

$$\Pr(x_1 \ldots x_L) = \sum_{\pi} \Pr(x_1 \ldots x_L, \underbrace{\pi_0 \ldots \pi_N}_{\pi})$$

- But the number of paths can be exponential in the length of the sequence...
- The Forward algorithm enables us to compute this efficiently
  - Define *$f_k(i)$* to be the probability of being in state *k* having observed the first *i* characters of sequence x
  - To compute *Pr(x)*, the probability of being in the end state having observed all of sequence x
  - Can define this recursively
  - use dynamic programming

# The Forward Algorithm

- Initialization
  - $f_0(0) = 1$ for start state; $f_i(0) = 0$ for other state
- Recursion
  - For emitting state (i = 1, … L)

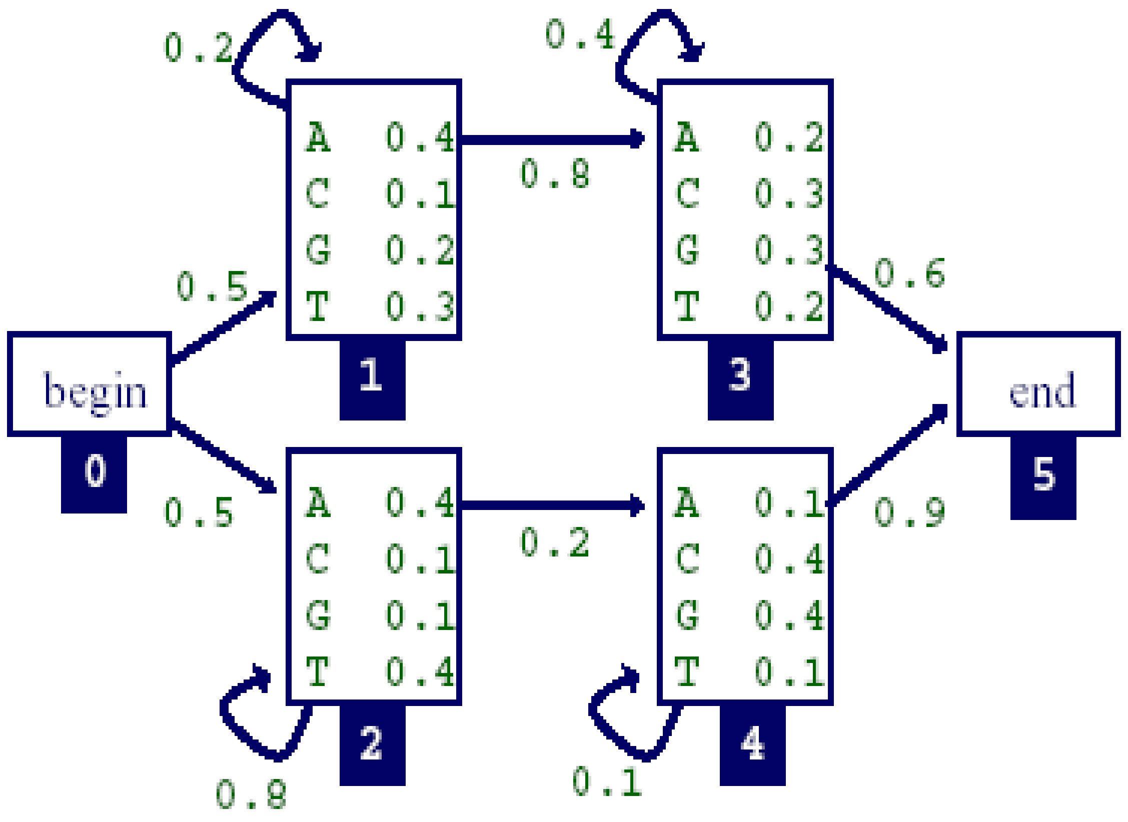
$$f_l(i) = e_l(xi) \sum_k f_k(i-1) a_{kl}$$

- Termination

$$\Pr(x) = \Pr(x_1 \ldots x_L) = \sum_k f_k(L) a_{kN}$$

N: ending state;
denoted as 0 in textbook

# Forward Algorithm Example



Given the sequence x=TAGA

# Forward Algorithm Example

- Initialization
  - $f_0(0)=1$, $f_1(0)=0...f_5(0)=0$
- Computing other values
  - $f_1(1)=e_1(T)*(f_0(0)a_{01}+f_1(0)a_{11})$
    $=0.3*(1*0.5+0*0.2)=0.15$
  - $f_2(1)=0.4*(1*0.5+0*0.8)$
  - $f_1(2)=e_1(A)*(f_0(1)a_{01}+f_1(1)a_{11})$
    $=0.4*(0*0.5+0.15*0.2)$

  ...
  - $Pr(TAGA)= f_5(4)=f_3(4)a_{35}+f_4(4)a_{45}$

## Three Important Questions

- How likely is a given sequence?
- What is the most probable “path” for generating a given sequence?
- How can we learn the HMM parameters given a set of sequences?

## Find the most probable "path" for generating a given sequence

- Decoding
  - $\pi^* = \mathrm{argmax}_{\pi} \mathrm{P}(\pi|x)$
- Given a length L sequence, how many possible underlying paths?
  - |Q|^L
  - Where |Q| is the number of possible state

## Finding the Most Probable Path: The Viterbi Algorithm

- Define $v_k(i)$ to be the probability of the most probable path accounting for the first i characters of x and ending in state k
- We want to compute $v_N(L)$, the probability of the most probable path accounting for all of the sequence and ending in the end state
- Can define recursively
- Can use DP to find $v_N(L)$ efficiently

## Algorithm

**Method:**

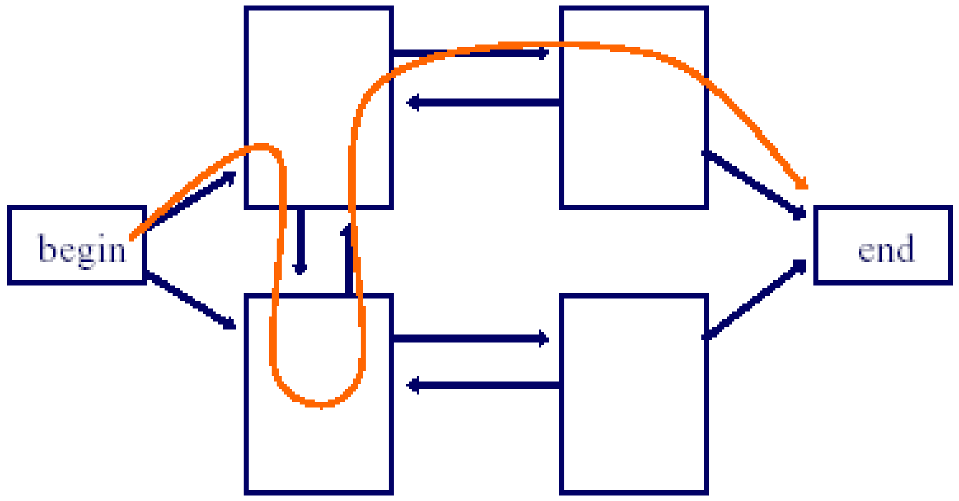
| | | |
|---|---|---|
| (1) | Initialization ($i = 0$): | $v_0(0) = 1, v_k(0) = 0$ for $k > 0$ |
| (2) | Recursion ($i = 1 \ldots L$): | $v_l(i) = e_l(x_i) max_k(v_k(i-1)a_{kl})$ |
| | | $ptr_i(l) = argmax_k(v_k(i-1)a_{kl})$ |
| (3) | Termination: | $P(x, \pi^*) = max_k(v_k(L)a_{k0})$ |
| | | $\pi^*_L = argmax_k(v_k(L)a_{k0})$ |

## Three Important Questions

- How likely is a given sequence?
- What is the most probable “path” for generating a given sequence?
- How can we learn the HMM parameters given a set of sequences?

# Learning Without Hidden State

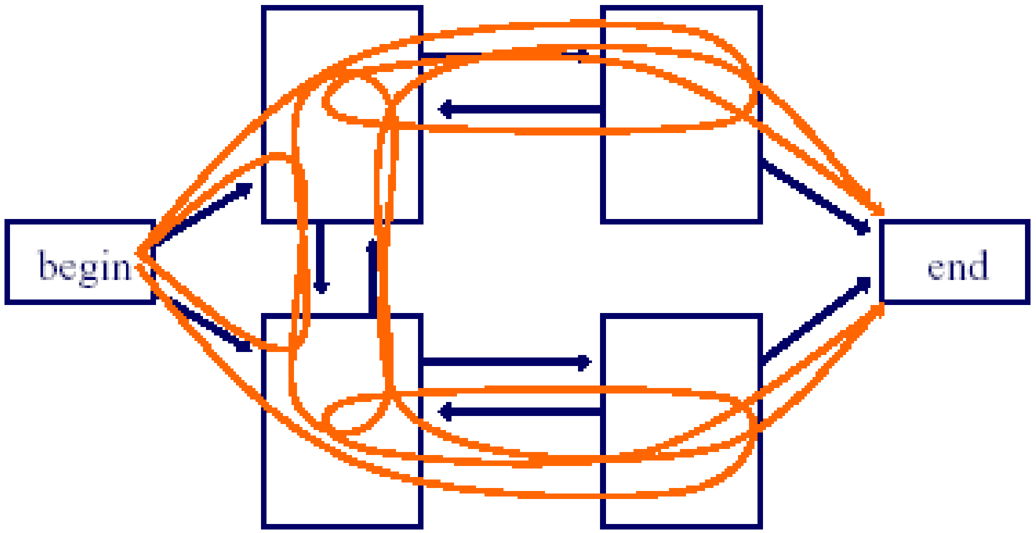
- Learning is simple if we know the correct path for each sequence in our training set



- estimate parameters by counting the number of times each parameter is used across the training set

## Learning With Hidden State

- If we don't know the correct path for each sequence in our training set, consider all possible paths for the sequence



- Estimate parameters through a procedure that counts the expected number of times each parameter is used across the training set

## *Learning Parameters: The Baum-Welch Algorithm

- Also known as the Forward-Backward algorithm
- An Expectation Maximization (EM) algorithm
  - EM is a family of algorithms for learning probabilistic models in problems that involve hidden state
- In this context, the hidden state is the path that best explains each training sequence

## *Learning Parameters: The Baum-Welch Algorithm

- Algorithm sketch:
  - initialize parameters of model
  - iterate until convergence
    - calculate the *expected* number of times each transition or emission is used
    - adjust the parameters to *maximize* the likelihood of these expected values

## Computational Complexity of HMM Algorithms

- Given an HMM with S states and a sequence of length L, the complexity of the Forward, Backward and Viterbi algorithms is $O(S^2L)$
  - This assumes that the states are densely interconnected
- Given M sequences of length L, the complexity of Baum Welch on each iteration is $O(MS^2L)$

## Sequence Data

- What is sequence data?
- Sequential pattern mining
- Hidden Markov Model
- Summary

## Summary

- Sequential Pattern Mining
  - GSP, SPADE, PrefixSpan
- Hidden Markov Model
  - Markov chain, HMM