

Named Entity Recognition

Using Conditional Random Field

Named Entity Recognition

⟨Google⟩₁ , headquartered in ⟨Mountain View⟩₂ ⟨Mountain View (1600 Amphitheatre Pkwy)⟩₁₂ ⟨1600⟩₁₄ ⟨Amphitheatre Pkwy⟩₇ , ⟨Mountain View⟩₂ , ⟨CA 940430⟩₈ ⟨940430⟩₁₅), unveiled the new ⟨Android⟩₃ ⟨phone⟩₅ for ⟨\$799⟩₁₃ ⟨799⟩₁₆ at the ⟨Consumer Electronic Show⟩₁₁ . ⟨Sundar Pichai⟩₄ said in his ⟨keynote⟩₉ that ⟨users⟩₆ love their new ⟨Android⟩₃ ⟨phones⟩₁₀ .

1. Google

ORGANIZATION

[Wikipedia Article](#)

Salience: 0.19

2. Mountain View

LOCATION

[Wikipedia Article](#)

Salience: 0.18

3. Android

CONSUMER GOOD

[Wikipedia Article](#)

Salience: 0.14

4. Sundar Pichai

PERSON

[Wikipedia Article](#)

Salience: 0.11

5. phone

CONSUMER GOOD

Salience: 0.10

6. users

PERSON

Salience: 0.09

Use a classifier?

- Only based on the features of the current state
- Not include sequential information
(Classes of the entities may require context information)

A Sequence Labeling Problem

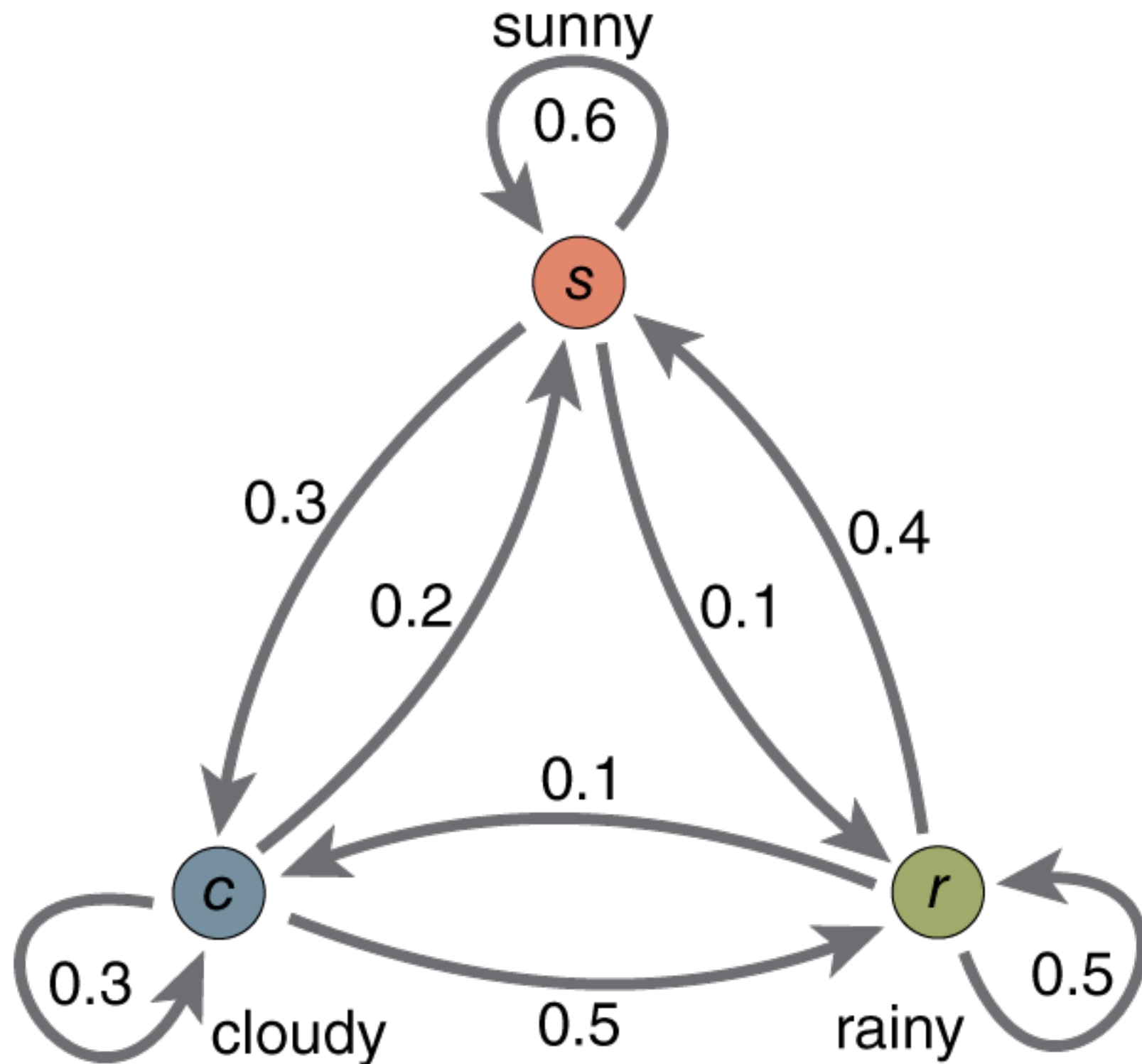
- The task of assigning label sequences to a set of observation sequences
- Given: an input sequence
 $X = x_1, x_2, \dots, x_T$
- Output: a sequence with the same length
 $Y = y_1, y_2, \dots, y_T$
- Also used for solving part-of-speech tagging problem
 $X = I, have, a, dream, .$
 $Y = pron, verb, determiner, noun, punct$

Markov Process

- For a Markov Process, the next state only depends on the current state

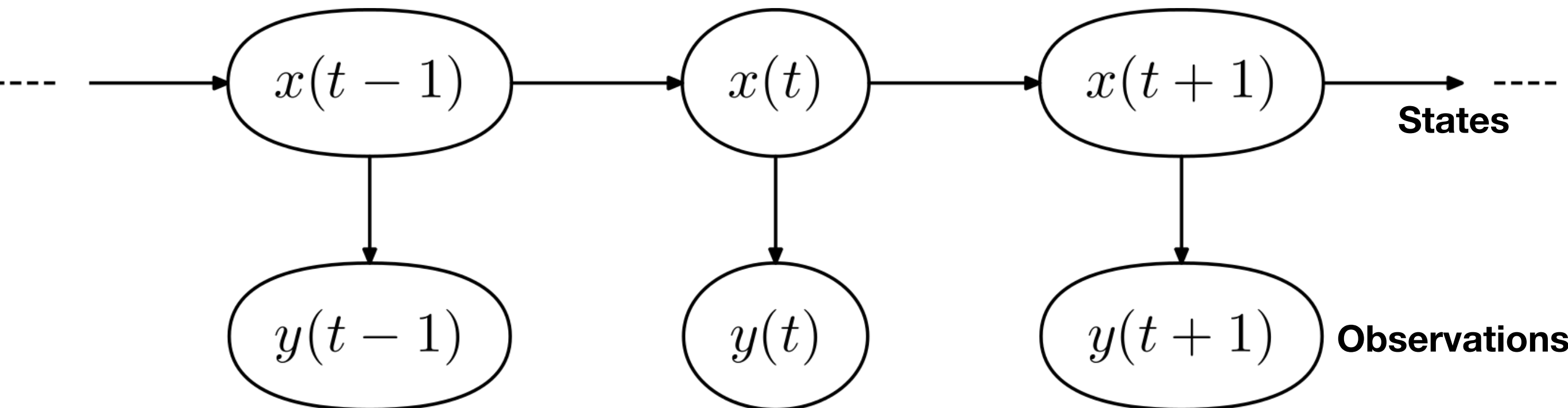
$$p(x_{t+1} \mid x_0, \dots, x_t) = p(x_{t+1} \mid x_t)$$

Markov Chain



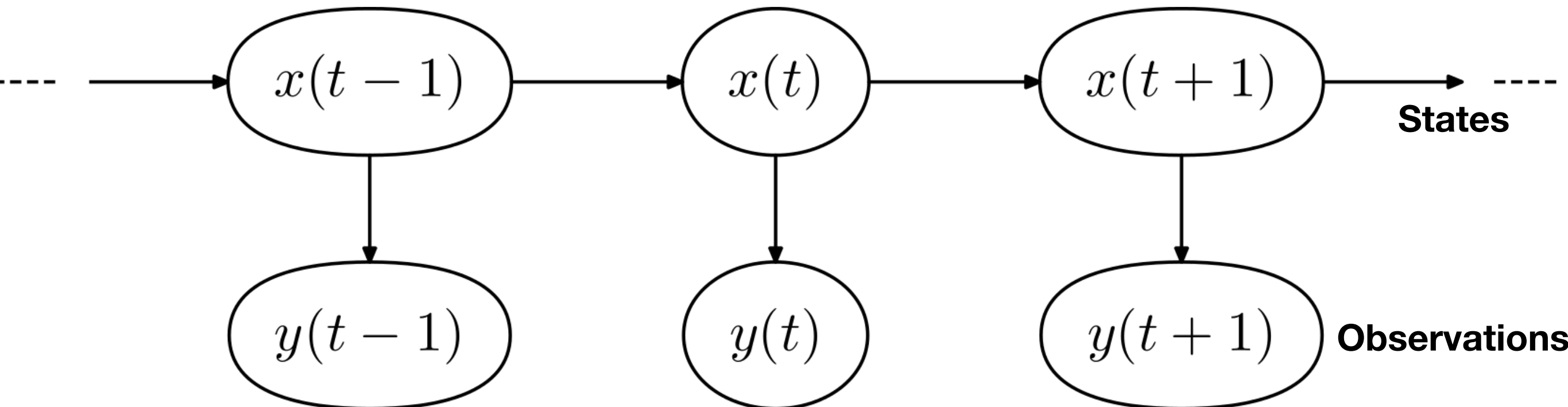
Hidden Markov Model

- Each (hidden) state is dependent on a fixed number of previous states
- Each (visible) observation only depends on the corresponding state



Hidden Markov Model

- What is the most likely states x_0, x_1, \dots, x_T producing the observations y_0, y_1, \dots, y_T ?



The Viterbi Algorithm

- Suppose we are given
 - Hidden Markov Model (HMM) with states $X = x_1, x_2, \dots, x_T$
 - Initial prob. π_i , transition prob. $a_{i,j}$, and emission prob. $b_{i,k}$
 - Observed sequence $Y = y_1, y_2, \dots, y_T$
- The Viterbi path, or the most likely state sequence x_0, x_1, \dots, x_T is:

$$V_{0,k} = P(y_0 | k) \cdot \pi_i$$

$$V_{t,k} = P(y_t | k) \cdot \max_{x \text{ in } X} (a_{x,k} \cdot V_{t-1,x})$$

$$\text{Ptr}(t, k) = P(y_t | k) \cdot \operatorname{argmax}_{x \text{ in } X} (a_{x,k} \cdot V_{t-1,x})$$

- The size of V is $T \times |X|$ and each $V_{t,k}$ take $|X|$ steps to compute
- The complexity of Viterbi algorithm is $O(T \times |X|^2)$

Define the parameters

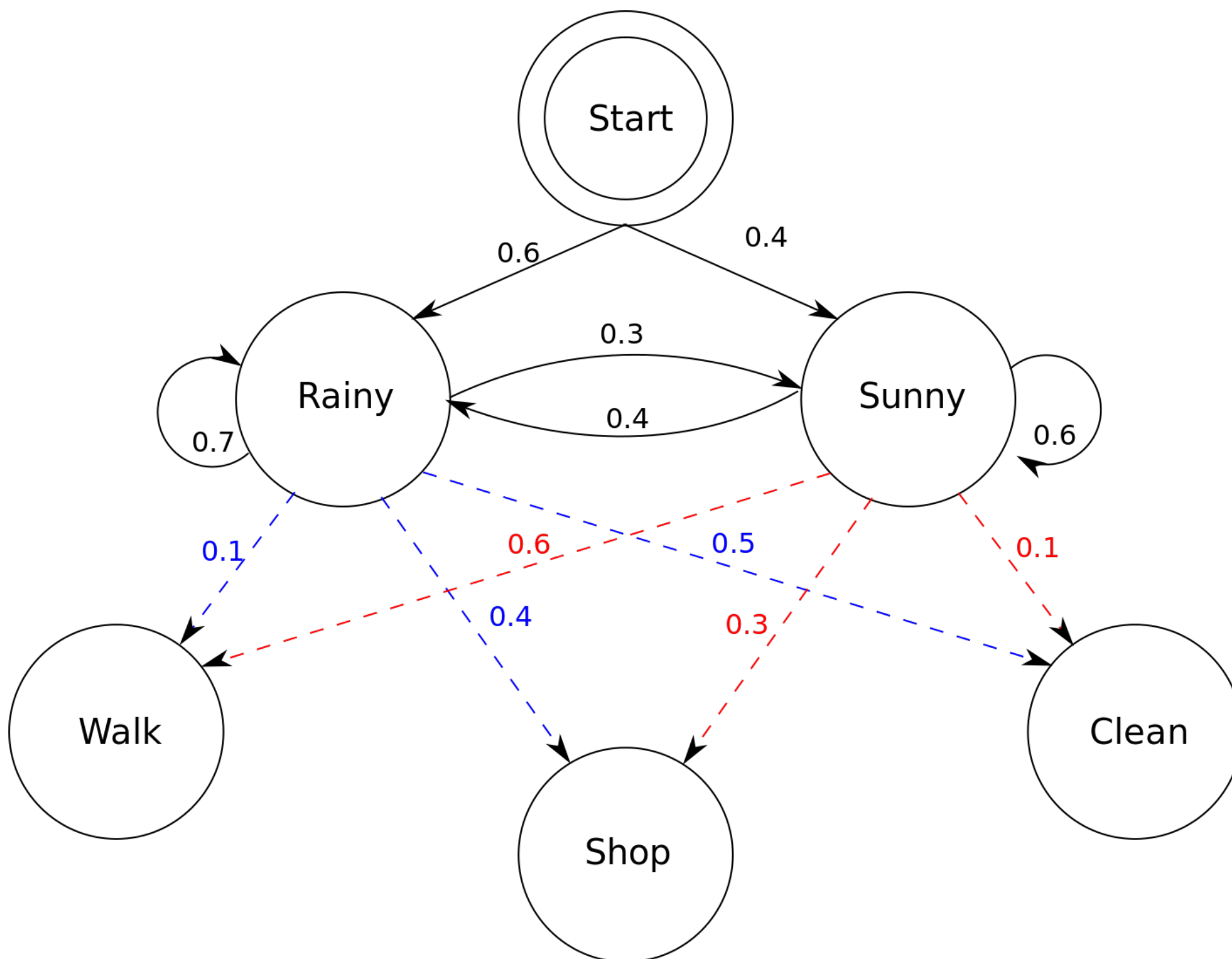
```
states = ('Rainy', 'Sunny')

observations = ('walk', 'shop', 'clean')

start_probability = {'Rainy': 0.6, 'Sunny': 0.4}

transition_probability = {
    'Rainy' : {'Rainy': 0.7, 'Sunny': 0.3},
    'Sunny' : {'Rainy': 0.4, 'Sunny': 0.6},
}

emission_probability = {
    'Rainy' : {'walk': 0.1, 'shop': 0.4, 'clean': 0.5},
    'Sunny' : {'walk': 0.6, 'shop': 0.3, 'clean': 0.1},
}
```



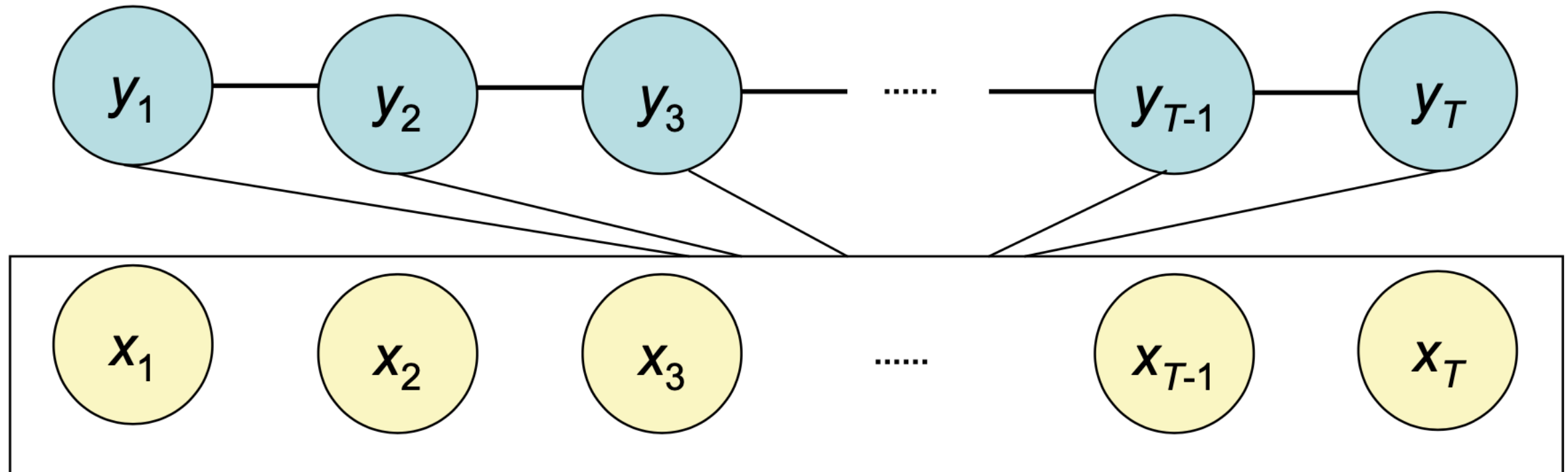
Label Bias Problem

- Lafferty, J., McCallum, A., & Pereira, F. C. (2001). Conditional random fields: Probabilistic models for segmenting and labeling sequence data.
- States with low-entropy next state distributions will take little notice of observations
(i.e., States with a single outgoing transition effectively ignores their observation)

Conditional Random Field

- A CRF defines the conditional probability for sequences

$$P(y_1, \dots, y_T \mid x_1, \dots, x_T)$$



Conditional Random Field

- Can be seen as sequential version of logistic regression
- Global normalization instead of local (e.g. HMMs)
- Relax strong independence assumptions made in HMM

$$\exp\left(\sum_l \lambda_l t_l(y_{i-1}, y_i, \mathbf{x}, i) + \sum_k \mu_k s_k(y_i, \mathbf{x}, i)\right)$$

transition feature function

state feature function

Transition Feature Function

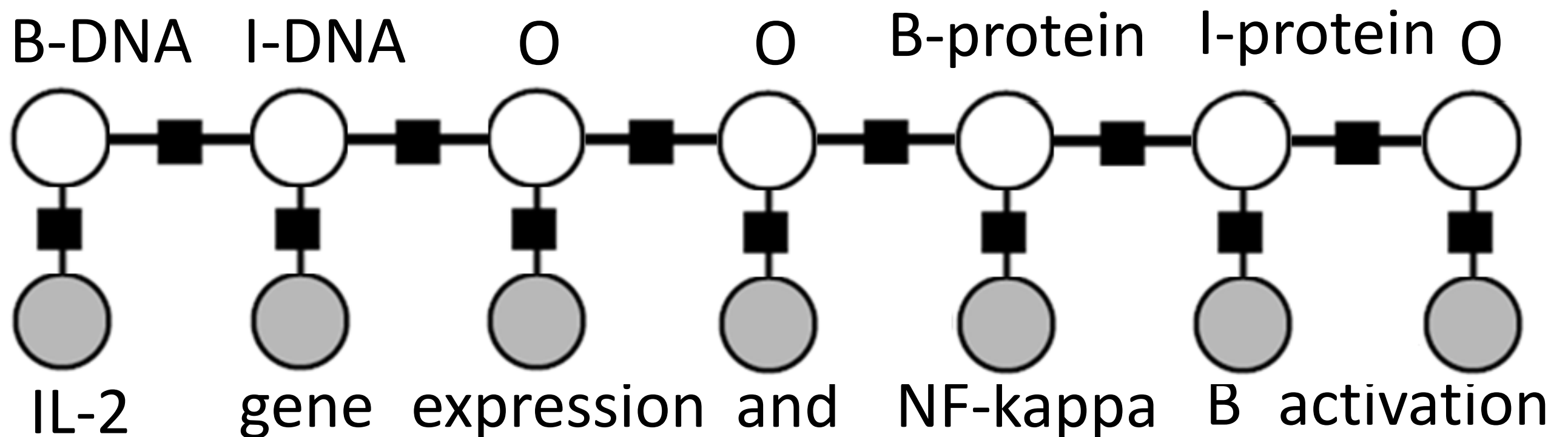
$$t_1(y_{i-1}, y_i, \mathbf{x}, i) = \begin{cases} 1 & \text{if } y_{i-1} = \text{B-DNA and } y_i = \text{I-DNA} \\ 0 & \text{otherwise} \end{cases}$$

$$i = 2: t_1 = 1;$$

$$i = 3: t_1 = 0;$$

$$i = 4: t_1 = 0;$$

...



State Feature Function

$$s_1(y_i, \mathbf{x}, i) = \begin{cases} 1 & \text{if } y_i = \text{I-DNA and } x_i = \text{gene} \\ 0 & \text{otherwise} \end{cases}$$

$$i = 1: s_1 = 0;$$

$$i = 2: s_1 = 1;$$

$$i = 3: s_1 = 0;$$

...

