

Comp 555 - BioAlgorithms - Spring 2022



- YOU HAVE UNTIL MIDNIGHT THURSDAY TO COMPLETE P5#6
- FINAL STUDY SESSION THURSDAY APRIL 28 (2:00-3:15)?

Randomized Algorithms



Randomized Algorithms

- Randomized algorithms incorporate random, rather than deterministic, decisions
- Commonly used in situations where no exact and/or fast algorithm is known



- Works for algorithms that behave well on typical data, but poorly in special cases
- Main advantage is that no input can reliably produce worst-case results because the algorithm runs differently each time.

Select



- Select(L, k) finds the kth smallest element in L
- Select(L,1) find the smallest...

– Well known O(n) algorithm

```
minv = HUGE
for v in L:
    if (v < minv):
        minv = v</pre>
```

- Select(L, len(L)/2) find the median...
 How?
 - median = sorted(L)[len(L)/2] \Box O(n logn)
- Can we find medians, or 1st quartiles in O(n)?

Select Recursion



- **Select(L, k)** finds the kth smallest element in L
 - Select an element *m* from unsorted list L and partition L the array into two smaller lists:

 L_{lo} - elements smaller than mand L_{hi} - elements larger than m

```
 \begin{array}{l} \text{if } (\text{len}(\text{L}_{lo}) >= k) \text{ then} \\ \quad \text{Select}(\text{L}_{lo'}, k) \\ \text{elif } (k > \text{len}(\text{L}_{lo}) + 1) \text{ then} \\ \quad \text{Select}(\text{L}_{hi'}, k - (\text{len}(\text{L}_{lo}) + 1)) \\ \text{else } m \text{ is the } k^{\text{th}} \text{ smallest element} \end{array}
```



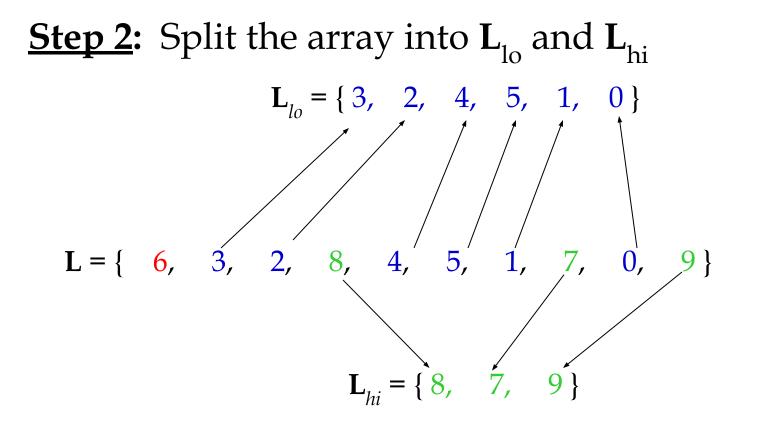
Given an array: **L** = { 6, 3, 2, 8, 4, 5, 1, 7, 0, 9 }

<u>Step 1</u>: Choose the first element as *m*

$$L = \{ 6, 3, 2, 8, 4, 5, 1, 7, 0, 9 \}$$

Our Selection







<u>Step 3</u>: Recursively call Select on either \mathbf{L}_{lo} or \mathbf{L}_{hi} until len (\mathbf{L}_{lo}) +1 = k, then return *m*.

 $len(L_{lo}) > k = 5 \square Select(\{ 3, 2, 4, 5, 1, 0 \}, 5)$

$$m = 3$$

 $L_{lo} = \{ 2, 1, 0 \}$ $L_{hi} = \{ 4, 5 \}$

 $k = 5 > len(L_{lo}) + 1 \square Select(\{4, 5\}, 5 - 3 - 1)$

 $k = 1 == len(L_{lo}) + 1 \square$ return 4

Select Code



```
In [47]: def select(L, k):
             value = L[0]
             Llo = [t for t in L if t < value]
              Lhi = [t for t in L if t > value]
             below = len(Llo) + 1
             if (len(Llo) >= k):
                  return select(Llo, k)
             elif (k > below):
                  return select(Lhi, k - below)
              else:
                  return value
         test = [6, 3, 2, 8, 4, 5, 1, 7, 0, 9]
         print(select(test, 5))
         4
```

- How fast?
- Is it really any better than sorting, and selecting?



Select with Good Splits

- Runtime depends on our selection of *m*:
 - A good selection will split L evenly such that

$$|\mathbf{L}_{lo}| = |\mathbf{L}_{hi}| = |\mathbf{L}|/2$$

- The recurrence relation is: T(n) = T(n/2)

 $n + n/2 + n/4 + n/8 + n/16 + = 2n \Box O(n)$

Same as search for minimum



However, a poor selection will split L unevenly and in the worst case, all elements will be greater or less than *m* so that one Sublist is full and the other is empty.

For a poor selection, the recurrence relation is

T(n) = T(n-1)

In this case, the runtime is $O(n^2)$.

I could have sorted First and done better

Our dilemma:

O(n) or $O(n^2)$,

depending on the list... or $O(n \log n)$ independent of it



- Select seems risky compared to Sort
- To improve Select, we need to choose *m* to give good 'splits'
- It can be proven that to achieve O(*n*) running time, we don't need a perfect splits, just reasonably good ones.
- In fact, if both subarrays are at least of size *n*/4, then running time will be O(*n*).
- This implies that half of the choices of *m* make good splitters.

A Randomized Approach



- To improve Select, *randomly* select *m*.
- Since half of the elements will be good splitters, if we choose *m* at random we will get a 50% chance that *m* will be a good choice.
- This approach will make sure that no matter what input is received, the expected running time is small.



Randomized Select

```
In [48]:
         import random
         def randomizedSelect(L, k):
             value = random.choice(L)
             Llo = [t for t in L if t < value]
             Lhi = [t for t in L if t > value]
             below = len(Llo) + 1
              if (len(Llo) >= k):
                  return randomizedSelect(Llo, k)
             elif (k > below):
                  return randomizedSelect(Lhi, k - below)
              else:
                 return value
         test = [6, 3, 2, 8, 4, 5, 1, 7, 0, 9]
         print(randomizedSelect(test, 5))
         4
```

RandomizedSelect Analysis



- Worst case runtime: $O(n^2)$
- *Expected runtime*: O(*n*).
- Expected runtime is a good measure of the performance of randomized algorithms, often more informative than worst case runtimes.
- Worst case runtimes are rarely repeated
- RandomizedSelect always returns the correct answer, which offers a way to classify Randomized Algorithms.

Types of Randomized Algorithms

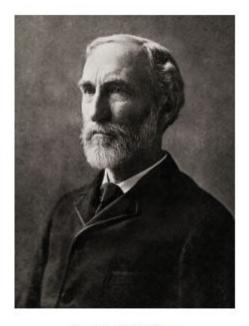
- Las Vegas Algorithms always produce the correct solution (i.e. randomizedSelect)
- Monte Carlo Algorithms do not always return the correct solution.

Of course, Las Vegas Algorithms are always preferred, but they are often hard to come by.



Gibbs Sampling

- RandomProfileMotifSearch is probably not the best way to find motifs. Depends on random guesses followed by a greedy optimization procedure.
- Gibbs Sampling estimates a distribution of each variable in turn, conditional on the current values of the other variables.
- However, we can improve the algorithm by introducing **Gibbs Sampling**, an iterative procedure that discards one *k*-mer's contribution to the profile distribution at each iteration and replaces it with a new one.
- Gibbs Sampling starts out slowly but chooses new *k*-mers with increasing the odds that it will improve the current solution.



Josiah W Gibbs



How Gibbs Sampling Works

- 1) Randomly choose starting positions $\mathbf{s} = (s_1, ..., s_t)$ and form the set of *k*-mers associated with these starting positions.
- 2) Randomly choose one of the *t* sequences.
- 3) Create a profile **P** from the remaining *t* -1 sequences.
- 4) For each position in the removed sequence, calculate the probability that the *k*-mer starting at that position was generated by **P**.
- 5) Choose a new starting position for the selected sequence at random based on the probabilities calculated in step 4.
- 6) Repeat steps 2-5 until there is no improvement



Input:

t = 5 sequences, motif length l = 8

- 1. GTAAACAATATTTATAGC
- 2. AAAATTTACCTCGCAAGG
- 3. CCGTACTGTCAAGCGTGG
- 4. TGAGTAAACGACGTCCCA
- 5. TACTTAACACCCTGTCAA



1) Randomly choose starting positions, $s=(s_{1'}s_{2'}s_{3'}s_{4'}s_5)$ in the 5 sequences:

- $s_1 = 7$ **GTAAACAATATTTATAGC**
- $s_2 = 11$ AAAATTTACCTTAGAAGG
- $s_3 = 9$ CCGTACTGTCAAGCGTGG
- s_4 =4 TGAGTAAACGACGTCCCA
- $s_5 = 1$ **TACTTAACACCCTGTCAA**



- 2) Choose one of the sequences at random: **Sequence 2:** AAAATTTACCTTAGAAGG
 - $s_1 = 7$ **GTAAACAATATTTATAGC**
 - $s_2 = 11$ AAAATTTACCTTAGAAGG
 - $s_3 = 9$ CCGTACTGTCAAGCGTGG

s₅=1

- $s_4 = 4$ TGAGTAAACGACGTCCCA
 - **TACTTAAC**ACCCTGTCAA



- 2) Choose one of the sequences at random: **Sequence 2:** AAAATTTACCTTAGAAGG
 - $s_1 = 7$ **GTAAACAATATTTATAGC**
 - $s_3=9$ CCGTACTGTCAAGCGTGG $s_4=4$ TGAGTAAACGACGTCCCA $s_5=1$ TACTTAACACCCTGTCAA



3) Create profile *P* from *l*-mers in remaining 4 sequences:

1	А	А	Т	А	Т	Т	Т	А
3	Т	С	А	А	G	С	G	Т
4	G	Т	А	А	А	С	G	А
5	Т	А	С	Т	Т	А	А	С
Α	1/4	2/4	2/4	3/4	1/4	1/4	1/4	2/4
С	0	1/4	1/4	0	0	2/4	0	1/4
Т	2/4	1/4	1/4	1/4	2/4	1/4	1/4	1/4
G	1/4	0	0	0	1/4	0	3/4	0
Consensus String	Т	А	А	А	Т	С	G	А



4) Calculate the *prob*(*a* | *P*) for every possible 8-mer in the removed sequence:

Strings Highlighted in Red

prob(**a** | **P**)

AAAATTTACCTTAGAAGG	.000732
AAAATTTACCTTAGAAGG	.000122
AAAATTTACCTTAGAAGG	0
AAAATTTACCTTAGAAGG	.000183
AAAATTTA <mark>CCTTAGAA</mark> GG	0
AAAATTTAC <mark>CTTAGAAG</mark> G	0
AAAATTTACCTTAGAAGG	0



5) Create a distribution of probabilities of k-mers prob(a | P), and randomly select a new starting position based on this distribution.

A) To create this distribution, divide each probability prob(a | P) by the total:

Starting Position 1: *prob*(AAAATTTA | P) = .706 Starting Position 2: *prob*(AAATTTAC | P) = .118 Starting Position 8: *prob*(ACCTTAGA | P) = .176



B) Select a new starting position at random according to computed distribution:

P(selecting starting position 1): .706 P(selecting starting position 2): .118 P(selecting starting position 8): .176

t = random.random()
if (t < .706):
 # use position 1
elif (t < (.706 + .118)):
 # use position 2
else:
 # use position 8</pre>

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Assume we select the substring with the highest probability – then we are left with the following new substrings and starting positions.

- $s_1 = 7$ **GTAAACAATATTTATAGC**
- $s_2=1$ AAAATTTACCTCGCAAGG
- $s_3=9$ CCGTACTGTCAAGCGTGG
- s_4 =5 TGAGTAATCGACGTCCCA
- $s_5=1$ **TACTTCACACCTGTCAA**



6) We iterate the procedure again with the above starting positions until we cannot improve the score any more.

```
In [103]: import numpy
def Score(seq, i, k, distr):
    return numpy.prod([distr[j][seq[i+j]] for j in range(k)])
def Profile(DNA, offset, k):
    profile = []
    t = len(DNA)
    for i in range(k):
        counts = {base : 0.01 for base in "acgt"}
        for j in xrange(t):
            counts[DNA[j][offset[j]+i]] += 0.96 / t
        profile.append(counts)
    return profile
```

Gibbs Sampling in Python

```
In [92]: def GibbsProfileMotifSearch(seqList, k):
              start = [random.randint(0,len(seqList[t])-k) for t in range(len(seqList))]
              bestScore = 0.0
              noImprovement = 0
              while True:
                  remove = random.randint(0,len(seqList)-1)
                  start[remove] = -1
                  distr = Profile(seqList, k, start)
                  score = 0.0
                  for t in range(len(seqList)):
                      if (start[t] < 0):</pre>
                          rScore = 0.0
                          for i in xrange(len(seqList[remove])-k+1):
                              score = Score(seqList[remove], i, k, distr)
                              if (score > rScore):
                                  rStart, rScore = i, score
                          score += rScore
                          start[t] = rStart
                      else:
                          score += Score(seqList[t], start[t], k, distr)
                  if (score > bestScore):
                      bestScore = score
                      noImprovement = 0
                  else:
                      noImprovement += 1
                      if (noImprovement > len(seqList)):
                          break
              return score, start
```





Gibbs Sampling Performance

In [116]: random.seed(2020) seqApprox = ['tagtggtcttttgagtgtagatctgaagggaaagtatttccaccagttcggggtcacccagcagggcagggtgacttaat', 'cgcgactcggcgctcacagttatcgcacgtttagaccaaaacggagttggatccgaaactggagtttaatcggagtcctt', 'gttacttgtgagcctggttagacccgaaatataattgttggctgcatagcggagctgacatacgagtaggggaaatgcgt', 'aacatcaggctttgattaaacaatttaagcacgtaaatccgaattgacctgatgacaatacggaacatgccggctccggg', 'accaccggataggctgcttattaggtccaaaaggtagtatcgtaataatggctcagccatgtcaatgtgcggcattccac', 'tagattcgaatcgatcgtgtttctccctctgtgggttaacgaggggtccgaccttgctcgcatgtgccgaacttgtaccc', 'gaaatggttcggtgcgatatcaggccgttctcttaacttggcggtgcagatccgaacgtctctggaggggtcgtgcgcta', 'atgtatactagacattctaacgctcgcttattggcggagaccatttgctccactacaagaggctactgtgtagatccgta', 'ttcttacacccttctttagatccaaacctgttggcgccatcttcttttcgagtccttgtacctccatttgctctgatgac', 'ctacctatgtaaaacaacatctactaacgtagtccggtctttcctgatctgccctaacctacaggtcgatccgaaattcg'] s, m = GibbsProfileMotifSearch(seqApprox, 10) print(s, m) for i, j in enumerate(m): print(seqApprox[i][j:j+10]) 0.0137569615302 [17, 47, 18, 33, 21, 0, 46, 70, 16, 65] tagatctgaa tggatccgaa tagacccgaa taaatccgaa taggtccaaa tagattcgaa cagatccgaa tagatccgta tagatccaaa tcgatccgaa



- Fewer profile searches, *O*(*n*), in exchange for updating the profile, *O*(*kt*), more often (tradeoff which is easier)
- Gibbs sampling can converge much faster than a fully randomized approach
- Gibbs sampling is more likely to converge to locally optimal motifs rather a fully randomized algorithm.
- Like the fully Randomized Algorithm it must be run with many randomly chosen initial seeds to achieve good results.

Next Time



WebDonuts.com We're on the West coast soif we ride into the sunset we'll drown. Mula Mar NUL

Andy, the literal Cowboy.