

Gibbs Sampling and Random Projection

Spring 2016

Gibbs Sampling

- RandomProfileMotifSearch is probably not the best way to find motifs. Depends on random guesses followed by a greedy optimization procedure.
- Major cost is Scoring, P(**a** | **P**), and updating profiles
- 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 more slowly but chooses new k-mers with increasing the odds that it will improve the current solution.

How Gibbs Sampling Works

- 1) Randomly choose starting positions
 - $s = (s_1,...,s_t)$ 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 other *t* -1 sequences.
- 4) For each position in the removed sequence, calculate the probability that the *l*-mer starting at that position was generated by **P**.
- 5) Choose a new starting position for the removed 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	GTAAAC <mark>AATATTTA</mark> TAGC
s ₂ =11	AAAATTTACCTTAGAAGG
s ₃ =9	CCGTACTGTCAAGCGTGG
s ₄ =4	TGA <mark>GTAAACGA</mark> CGTCCCA
s ₅ =1	TACTTAAC ACCCTGTCAA



2) Choose one of the sequences at random: **Sequence 2:** AAAATTTACCTTAGAAGG

<i>s</i> ₁ =7	GTAAAC <mark>AATATTTA</mark> TAGC
s ₂ =11	AAAATTTACC <mark>TTAGAAGG</mark>
s ₃ =9	CCGTACTG <mark>TCAAGCGT</mark> GG
<i>s</i> ₄ =4	TGA <mark>GTAAACGA</mark> CGTCCCA
s ₅ =1	TACTTAAC ACCCTGTCAA



2) Choose one of the sequences at random: **Sequence 2:** AAAATTTACCTTAGAAGG

 $s_1 = 7$ GTAAACAATATTTATAGC

s ₃ =9	CCGTACTG <mark>TCAAGCGT</mark> GG
s ₄ =4	TGA <mark>GTAAACG</mark> ACGTCCCA
s ₅ =1	TACTTAAC ACCCTGTCAA



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

 $prob(\mathbf{a} \mid \mathbf{P})$

AAAATTTACCTTAGAAGG	.000732
AAAATTTACCTTAGAAGG	.000122
AAAATTTACCTTAGAAGG	0
AAA <mark>ATTTACCT</mark> TAGAAGG	0
AAAATTTACCTTAGAAGG	0
AAAATTTACCTTAGAAGG	0
AAAATT TACCTTAG AAGG	0
AAAATTT <mark>ACCTTAGA</mark> AGG	.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.

<i>s</i> ₁ =7	GTAAAC <mark>AATATTTA</mark> TAGC
s ₂ =1	AAAATTTACCTCGCAAGG
s ₃ =9	CCGTACTG <mark>TCAAGCGT</mark> GG
s ₄ =5	TGAGT <mark>AATCGACG</mark> TCCCA
s ₅ =1	TACTTCAC ACCCTGTCAA



ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎֎ՠ֎

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

Modified Profile function:

```
def Profile(seqList, k, start):
  dist = [dict([(base,0.1) for base in "acgt"]) for i in xrange(k)]
  for t in xrange(len(seqList)):
     if (start[t] < 0):
        continue
     for i, base in enumerate(seqList[t][start[t]:start[t]+k]):
        dist[i][base] += 1.0
  for i in xrange(k):
     total = sum(dist[i].values())
     for base in "acgt":
        dist[i][base] /= total
  return dist
                Comp 555
```

```
Gibbs
Sampling
in Python
```

```
def GibbsProfileMotifSearch(seqList, k):
  start = [random.randint(0,len(seqList[t])-k+1) for t in xrange(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 xrange(len(seqList)):
       if (start[t] < 0):
          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:
       nolmprovement += 1
       if (noImprovement > len(seqList)):
          break
  return score, start
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                                                                           14
```

Gibbs Sampling Performance

```
%timeit s, m = FindMotif(seqApprox, 10, 100, RandomProfileMotifSearch)
print "Random", s
for i, si in enumerate(m):
    print si, seqApprox[i][si:si+10]
print
%timeit s, m = FindMotif(seqApprox, 10, 100, GibbsProfileMotifSearch)
print "Gibbs", s
for i, si in enumerate(m):
    print si, seqApprox[i][si:si+10]
1 loops, best of 3: 473 ms per loop
Random ttgacctgat
17 tagatctgaa
47 tggatccgaa
18 tagacccgaa
33 taaatccgaa
21 taggtccaaa
0 tagattcgaa
46 cagatecgaa
70 tagatccgta
16 tagatccaaa
65 tcgatccgaa
10 loops, best of 3: 66.3 ms per loop
Gibbs ttgacctgat
17 tagatctgaa
47 tggatccgaa
18 tagacccgaa
33 taaatccgaa
21 taggtccaaa
0 tagattcgaa
46 cagatccgaa
70 tagatecgta
16 tagatccaaa
65 tcgatccgaa
```



Gibbs Sampler in Practice

- 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.



Another Randomized Approach

- **Random Projection Algorithm** is a different way to solve the Motif Finding Problem.
- **Guiding principle:** Instances of a good motif will likely agree at a subset of positions.
- However, it is unclear how to find these matching, "non-mutated" positions.
- To bypass the effect of mutations within a motif, we randomly select a subset of positions in the pattern creating a **projection** of the pattern.
- Search for that projection in a hope that the selected positions are not affected by mutations in most instances of the motif.



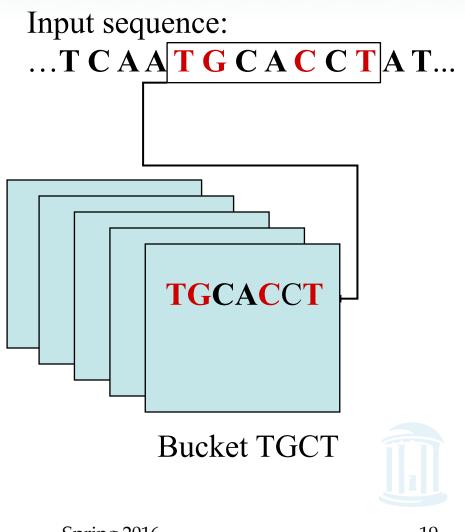
Projections

- Choose *k* positions in string of length *l*.
- Concatenate nucleotides at chosen *k* positions to form *k*-tuple.
- This can be viewed as a projection of *l*-dimensional space onto *k*-dimensional subspace.

$$l = 15$$
Projection $k = 7$
TGCTGAT
Projection = (2, 4, 5, 7, 11, 12, 13)

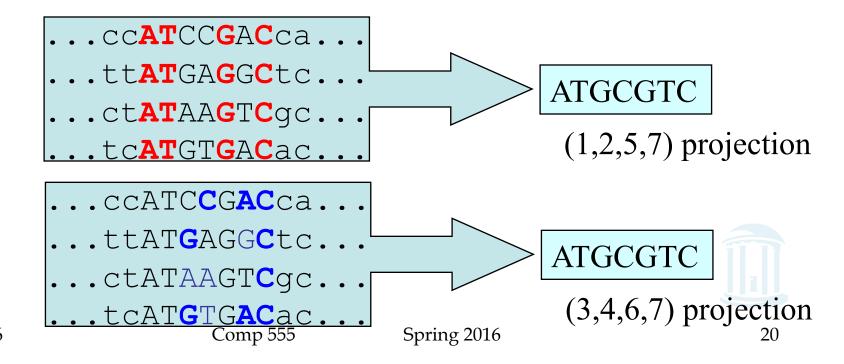
Random Projections Algorithm

- Select *k* out of *l* positions uniformly at random.
- For each *l*-tuple in input sequences, hash into buckets based on the *k* selected positions.
- Recover motif from *enriched* buckets that contain many *l*-tuples with at least one from each sequence.



Random Projections Algorithm (cont'd)

- Some projections will fail to detect motifs but if we try many of them the probability that one of the buckets fills increases.
- In the example below, the bucket **GC*AC is "bad" while the bucket AT**G*C is "good"

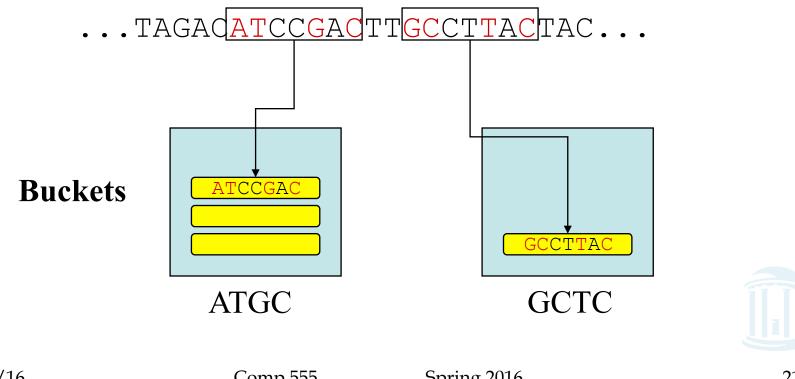


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Example

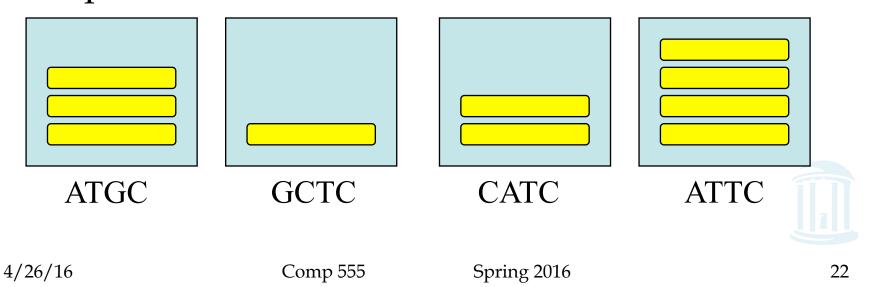
<u>֎ՠ֎֎֎֎֎֎֎֎֎֎֎֎</u>

- l = 7 (motif size), k = 4 (projection size)
- Choose projection (1,2,5,7)



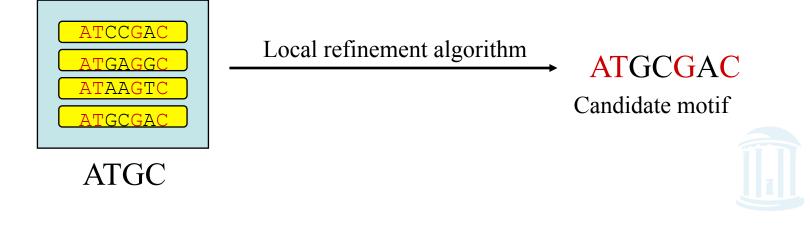
Hashing and Buckets

- Hash function *h*(*x*) obtained from *k* positions of projection.
- Buckets are labeled by values of h(x).
- *Enriched buckets*: contain more than *s l*-tuples, for some parameter *s* with representatives from all sequences



Motif Refinement

- How do we recover the motif from the sequences in enriched buckets?
- *k* nucleotides are exact matches, (hash key of bucket).
- Use information in other *l-k* positions as starting point for local refinement scheme, e.g. Gibbs sampler.



Synergy of Random Projection

- Random Projection is a procedure for finding good *starting points*: every enriched bucket is a potential starting point.
- Feeding these starting points into existing algorithms (like Gibbs sampler, or fully Randomized Search) provides good local search in vicinity of every starting point.
- These algorithms work particularly well for "good" starting points.



Random Projection

def RandomProjectionMotifStart(seqList, k): N = len(seqList)matches = random.randint(k/3,(3*k)/4) positions = sorted(random.sample(range(k), matches)) $hash = \{\}$ for t in xrange(N): for i in xrange(len(seqList[t])-k+1): pattern = ".join([seqList[t][i+j] for j in positions]) plist = hash.get(pattern,[[] for j in xrange(N)]) plist[t] += [i] hash[pattern] = plist result = [] for key in hash.iterkeys(): start = [] skipped = 0for posList in hash[key]: if (len(posList) == 0): skipped += 1 if (skipped > N/3): break start.append(-1) else: start.append(posList[0]) else: result.append(start) return result

Good Projections

seqApprox = [

'tagtggtcttttgagtgtagatctgaagggaaagtatttccaccagttcggggtcacccagcagggcagggtgacttaat', 'cgcgactcggcgctcacagttatcgcacgtttagaccaaaacggagttggatccgaaactggagttaatcggagtcctt', 'gttacttgtgagcctggttagacccgaaatataattgttggctgcatagcggagctgacatacgagtaggggaaatgcgt', 'aacatcaggctttgattaaacaatttaagcacgtaaatccgaattgacctgatgacaatacggaacatgccggctccggg', 'accaccggataggctgcttattaggtccaaaaggtagtatcgtaataatggctcagccatgtcaatgtgcggcattccac', 'tagattcgaatcgatcgtgtttctccctctgtgggttaacgaggggtccgaccttgctcgaaggtcgtgcgacttgacc', 'gaaatggttcggtgcgatatcaggccgttctcttaacttggcggtgcagatccgaacgtctcggagggggtcgtgcgcat, 'atgtatactagacattctaacgctcgcttattggcggagaccattgcccacaagagggtcctgtgcgatacgta', 'ttcttacacccttctttagatccaaacctgttggcgccatcttctttcgagtcctacaagagggtcctgtgccdat 'ttcttacacccttctttagatccaaacgtagtccggtcttccttactctgatgcccacacagagggtcctgtgccatctgatgac', 'ctacctatgtaaaacaacatctactaacgtagtccggtctttcctgatcccaacctacaggtcgatccdattccaattcc']

?at?c?aa?? [-1, 49, -1, 35, -1, 2, 48, 12, 18, 67] at?c?aa??? [-1, 50, -1, 36, -1, 3, 49, 13, 19, 68] gat???aa?? [19, 49, -1, 50, -1, 2, 48, -1, 18, 67] ?g??cc?aa? [-1, 48, 19, -1, 22, 62, 47, -1, 17, 66] ??gat???aa [17, 47, -1, 48, -1, 0, 46, -1, 16, 65] t?g?tc?g?? [17, 47, -1, -1, 48, -1, 4, 70, 67, 65] ?t?g?tc?g? [16, 46, -1, -1, 47, -1, 3, 69, 66, 64] ?g??cc?aa? [-1, 48, 19, -1, 22, 62, 47, -1, 17, 66] g??cc?aa?? [-1, 49, 20, -1, 23, 63, 48, -1, 18, 67] atc??aa??? [20, 50, -1, 36, 38, -1, 49, -1, 19, 68]

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Random Projection Performance

}} }

```
def RandomProjectionMotif(seqList,k):
    startList = []
    while len(startList) < 10:</pre>
        startList += RandomProjectionMotifStart(seqList, k)
    highScore = 0.0
    for start in startList:
        score, start = ProfileMotifSearch(seqList, k, start)
        if score > highScore:
            motif = [s for s in start]
            highScore = score
    return highScore, motif
%timeit s,m = RandomProjectionMotif(seqApprox,10)
print "RandomProjection", s
for i, si in enumerate(m):
    print si, seqApprox[i][si:si+10]
10 loops, best of 3: 65.1 ms per loop
```

RandomProjection ttgacctgat

```
17 tagatctgaa
```

- 47 tggatccgaa
- 18 tagacccgaa
- 33 taaatccgaa
- 21 taggtccaaa
- 0 tagattcgaa
- 46 cagatccgaa
- 70 tagatccgta
- 16 tagatccaaa
- 65 tcgatccgaa



Random Projection Synopsis

- Fewer starts than other randomized algorithms (10x fewer)
- Each projection is *O*(*tn*), which is the same as the full scan of in the fully Randomized Profile scan
- Generates good starts but requires either Gibbs sampling or Randomized search to refine the final solution



It's Over

- Final Monday, 5/2
 - 12:00-3:00PM
 - This room: FB007
 - Open book, open notes, open internet, online
 - Will cover material since midterm
 - Final Study session:
 - Friday 4/29, FB007 5pm-7pm

