Motifs

BCH394P/364C - Systems Biology / Bioinformatics

Edward Marcotte, Univ of Texas at Austin

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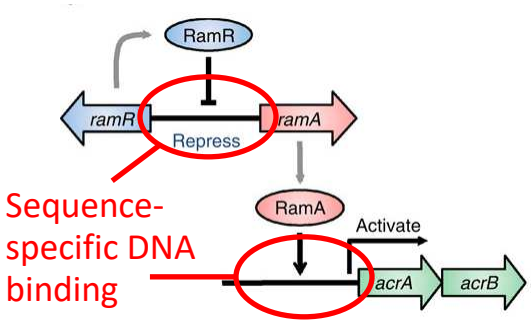
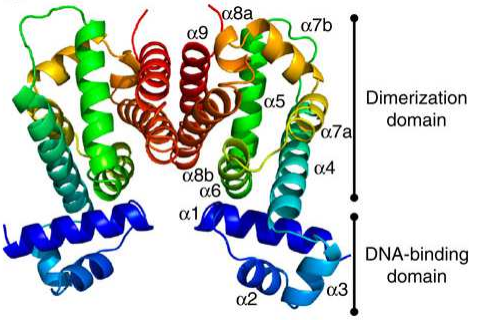
An example transcriptional regulatory cascade

Here, controlling *Salmonella* bacteria multidrug resistance



RamR represses the *ramA* gene, which encodes the activator protein for the *acrAB* drug efflux pump genes.

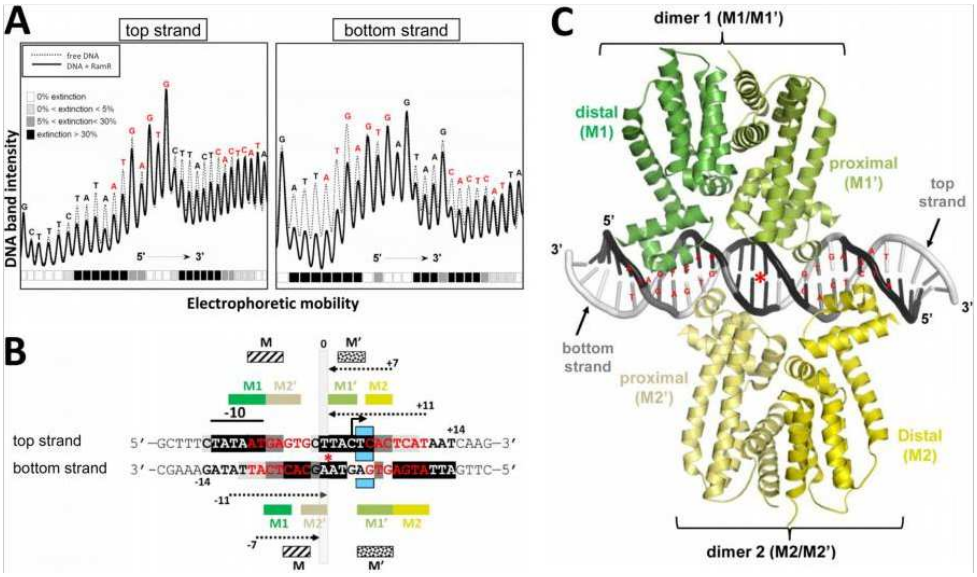


RamR dimer

Nature Communications 4, Article number: 2078 doi:10.1038/ncomms3078

2

Historically, DNA and RNA binding sites were defined biochemically (DNAse footprinting, gel shift assays, etc.)



Hydroxyl radical footprinting of *ramR-ramA* intergenic region with RamR

Antimicrob Agents Chemother. Feb 2012; 56(2): 942–948.

3

Historically, DNA and RNA binding sites were defined biochemically (DNAse footprinting, gel shift assays, etc.)

Now, many binding motifs are discovered bioinformatically

Isolate different nucleic acid segments bound by copies of the protein (e.g. all sites bound across a genome)

→ Sequence

↓

Search computationally for recurring ***motifs***

Image: Antimicrob Agents Chemother. Feb 2012; 56(2): 942–948.

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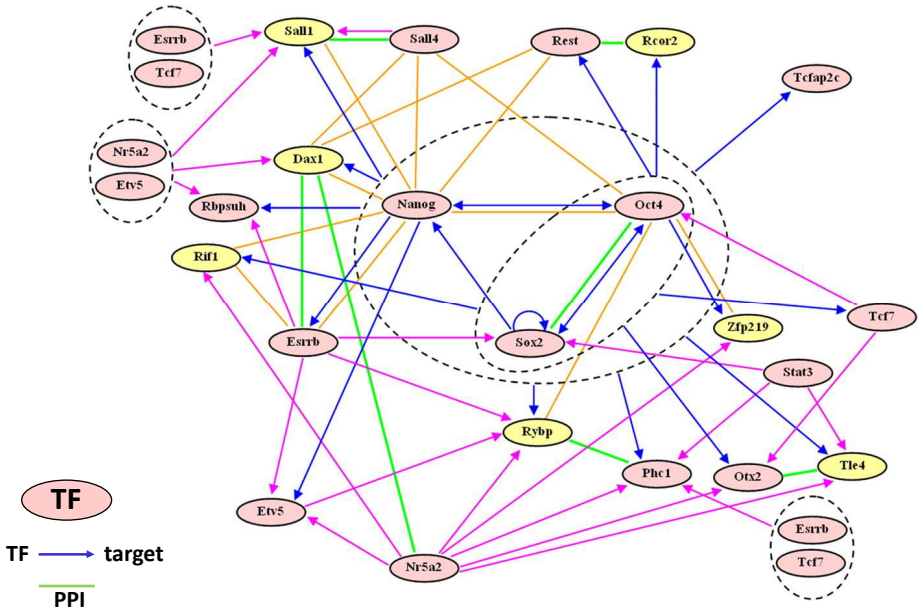
Transcription factor regulatory networks can be highly complex, e.g. as for embryonic stem cell regulators



http://www.pnas.org/content/104/42/16438

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MOTIFS

```
HEM13  CCCATTGTTCTC
HEM13  TTTCTGGTTCTC
HEM13  TCAATTGTTTAG
ANB1   CTCATTGTTGTC
ANB1   TCCATTGTTCTC
ANB1   CCTATTGTTCTC
ANB1   TCCATTGTTCGT
ROX1   CCAATTGTTTTG
```

Binding sites of the transcription factor ROX1

```
YCHATTGTTCTC
```

consensus

```
A 002700000010
C 464100000505
G 000001800112
T 422087088261
```

frequencies

frequency of nuc b at position i

$$I_{seq}(i) = -\sum_b f_{b,i} \log_2 \frac{f_{b,i}}{p_b}$$

freq of nuc b in genome

scaled by information content

NATURE BIOTECHNOLOGY VOLUME 24 NUMBER 4 APRIL 2006

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So, here's the challenge:

Given a set of DNA sequences that contain a motif (e.g., promoters of co-expressed genes), how do we discover it computationally?

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Could we just count all instances of each *k*-mer?

Why or why not?

→ promoters and DNA binding sites are not well conserved

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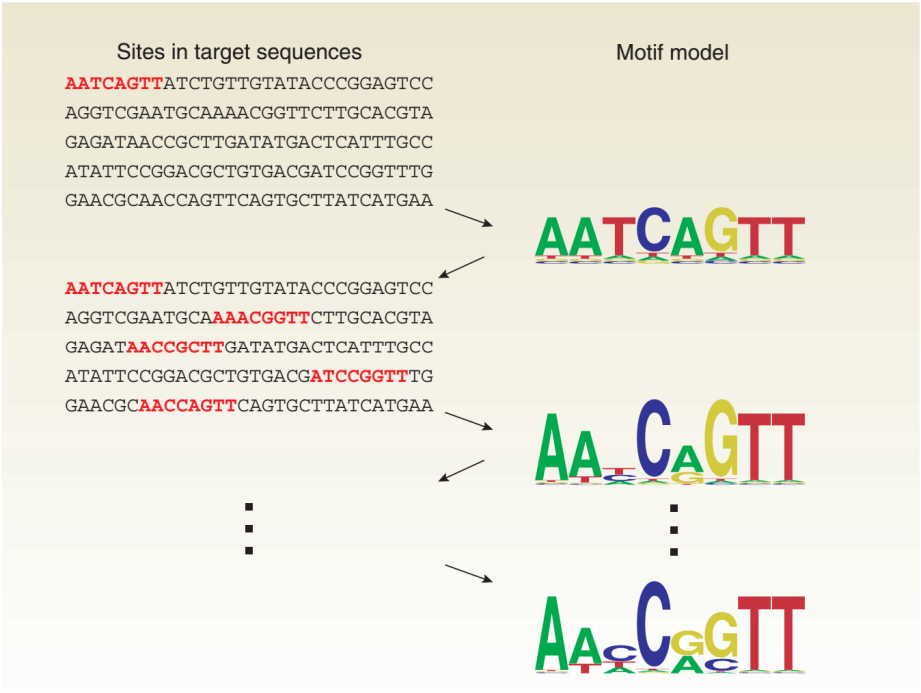
How does motif discovery work?



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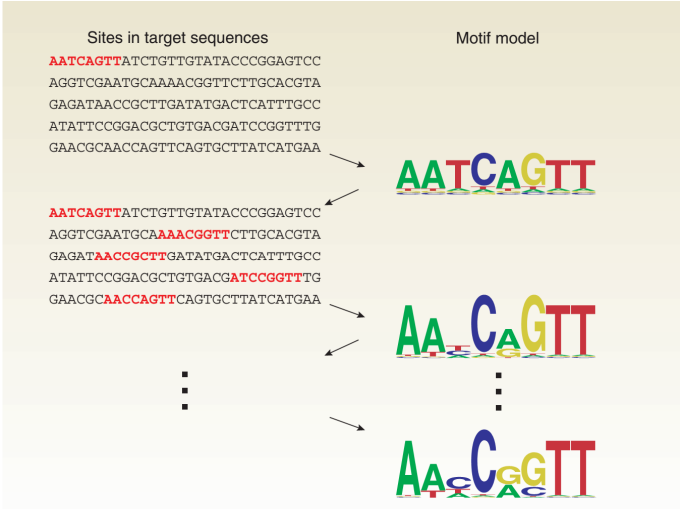
How does motif discovery work?

Assign sites to motif

Assign sites to motif

Assign sites to motif



Update the motif model

Update the motif model

Update the motif model

etc.

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How does motif discovery work?

Motif finding often uses *expectation-maximization*
***i.e.* alternating between building/updating a motif model and assigning sequences to that motif model.**

Searches the space of possible motifs for optimal solutions without testing everything.

Most common approach = *Gibbs sampling*

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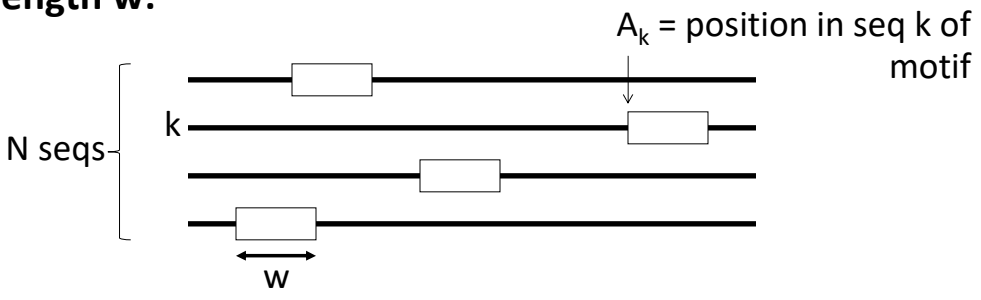
Detecting Subtle Sequence Signals: A Gibbs Sampling Strategy for Multiple Alignment

Charles E. Lawrence, Stephen F. Altschul, Mark S. Boguski, Jun S. Liu, Andrew F. Neuwald, John C. Wootton

We will consider N sequences, each with a motif of length w:



q_{ij} = probability of finding nucleotide (or aa) j at position i in motif
i ranges from 1 to w
j ranges across the nucleotides (or aa)
p_j = background probability of finding nucleotide (or aa) j

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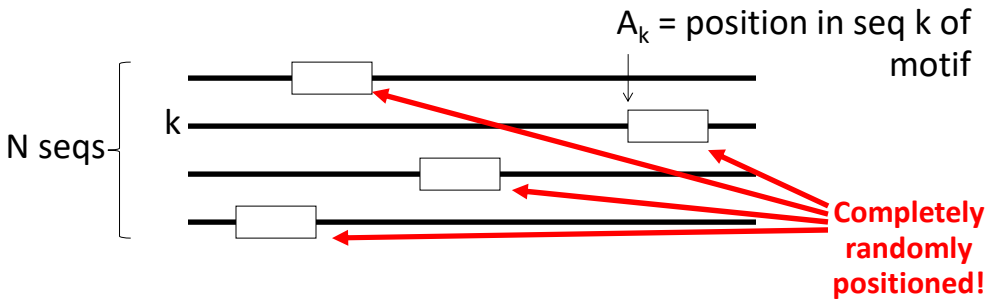
NOTE: You won't give any information at all about what or where the motif should be!

Start by choosing w and randomly positioning each motif:



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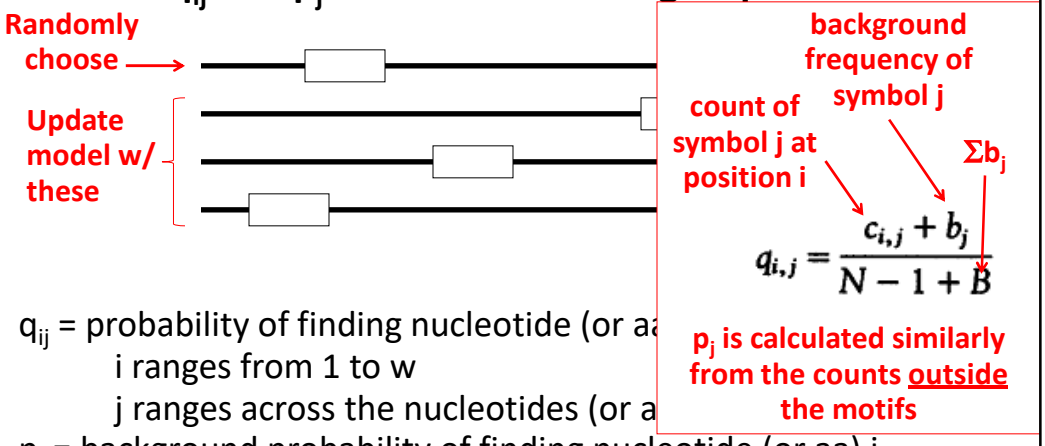
Predictive update step: Randomly choose one sequence, calculate q_{ij} and p_j from N-1 remaining sequences



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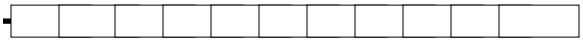
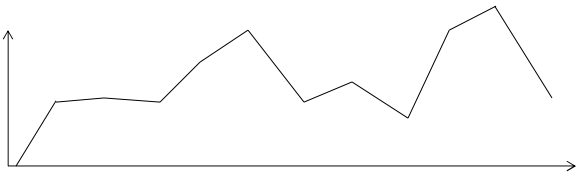
Stochastic sampling step: For withheld sequence, slide motif down sequence & calculate agreement with model

Withheld sequence →



Odds ratio of agreement with model vs. background



Position in sequence

$$\frac{\Pi(q_{ij})^{c_{xij}}}{\Pi(p_j)^{c_{xij}}}$$

(see the paper for details)

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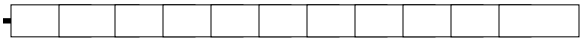
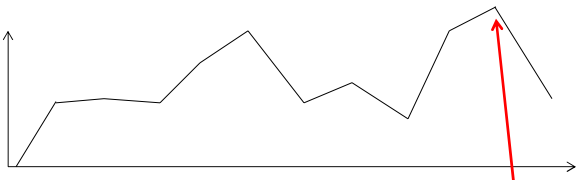
Withheld sequence →



Odds ratio of agreement with model vs. background



Position in sequence

$$\frac{\Pi(q_{ij})^{c_{xij}}}{\Pi(p_j)^{c_{xij}}}$$

(see the paper for details)

Here's the cool part: DON'T just choose the maximum.
INSTEAD, select a new A_k position proportional to this odds ratio.

Then, choose a new sequence to withhold, and repeat everything.

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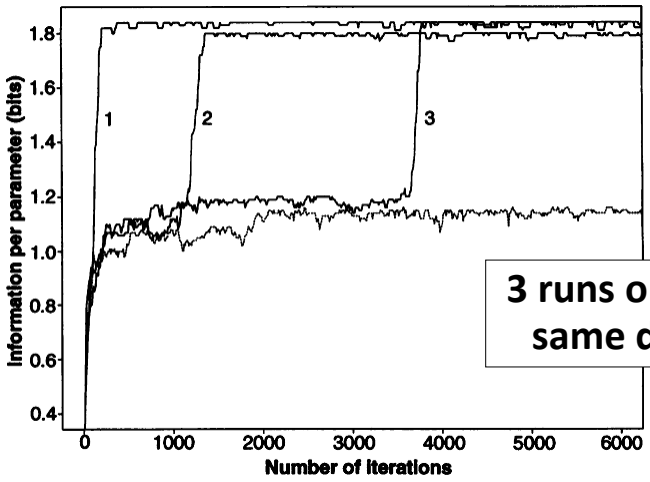
Over many iterations, this magically converges to the most enriched motifs. Note, it's stochastic:



3 runs on the same data

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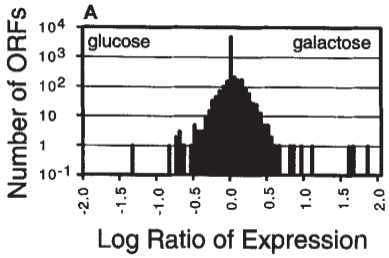
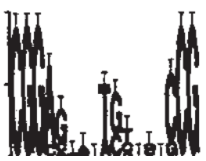
Finding DNA regulatory motifs within unaligned noncoding sequences clustered by whole-genome mRNA quantitation

Frederick P. Roth[1,2*], Jason D. Hughes[1,2*], Preston W. Estep[1], and George M. Church[1,2**]

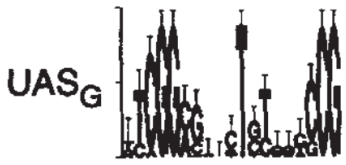


galactose vs. glucose → **Measure mRNA abundances using DNA microarrays** → **Search for motifs in promoters of glucose vs galactose controlled genes**

Discovered motifs



Known motif



Galactose upstream activation sequence

"AlignAce" NATURE BIOTECHNOLOGY VOLUME 16 OCTOBER 1998

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Finding DNA regulatory motifs within unaligned noncoding sequences clustered by whole-genome mRNA quantitation

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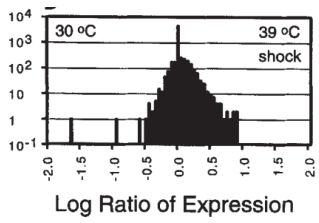
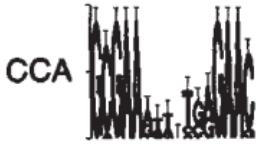


heat shock vs. 30 °C

Measure mRNA abundances using DNA microarrays → **Search for motifs in promoters of heat-induced and repressed genes**

Discovered motifs

Known motif



Cell cycle activation motif, histone activator

"AlignAce" NATURE BIOTECHNOLOGY VOLUME 16 OCTOBER 1998

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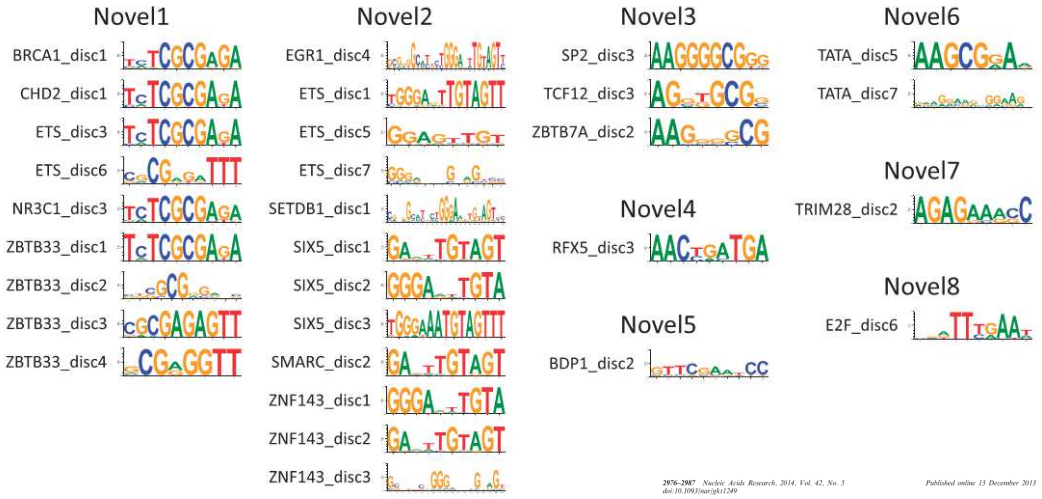
If you need them, we now know the binding motifs for 100's of transcription factors at 1000's of distinct sites in the human genome, including many new motifs.

e.g., http://compbio.mit.edu/encode-motifs/



2976–2987 Nucleic Acids Research, 2014, Vol. 42, No. 5 Published online 13 December 2013
doi:10.1093/nar/gkt1249

Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments

Pouya Kheradpour[1,2] and Manolis Kellis[1,2,*]

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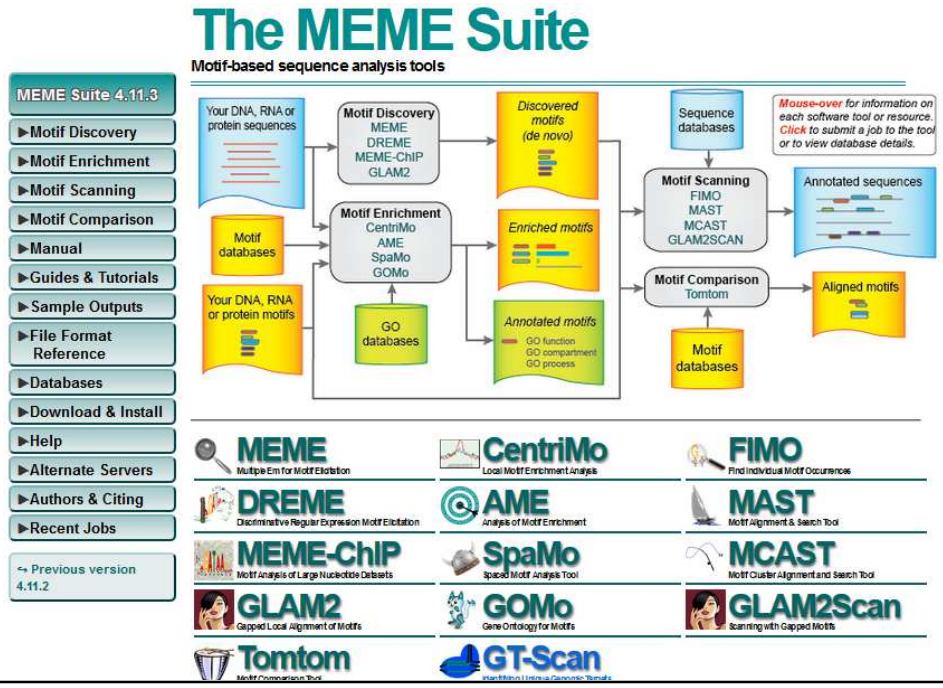
Here's a good place to start if you want to do this practically: http://meme-suite.org/



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Note: online MEME suite can sometimes be quite laggy. GibbsCluster is a good alternative for peptide motifs:
https://services.healthtech.dtu.dk/service.php?GibbsCluster-2.0

Both can also be installed on your own computer

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