Quiz section 10

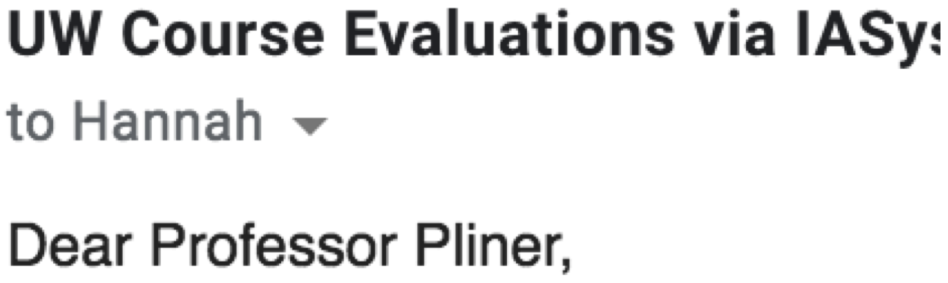
June 1, 2018

Logistics

- Bring: 1 page cheat-sheet, simple calculator
- Any last logistics questions about the final?

Logistics

- Bring: 1 page cheat-sheet, simple calculator
- Any last logistics questions about the final?
- Please do course evals for all three of the instructors (expire today!)



UW Course Evaluations via IASy

to Hannah

Dear Professor Pliner,

Course Takeaways

- Bioinformatics is not magic: there are always assumptions, uncertainties, ambiguities

- Have an understanding of what is happening inside black boxes – it might not be as complicated as it seems initially

- Start small and be clear in your own analysis and programming

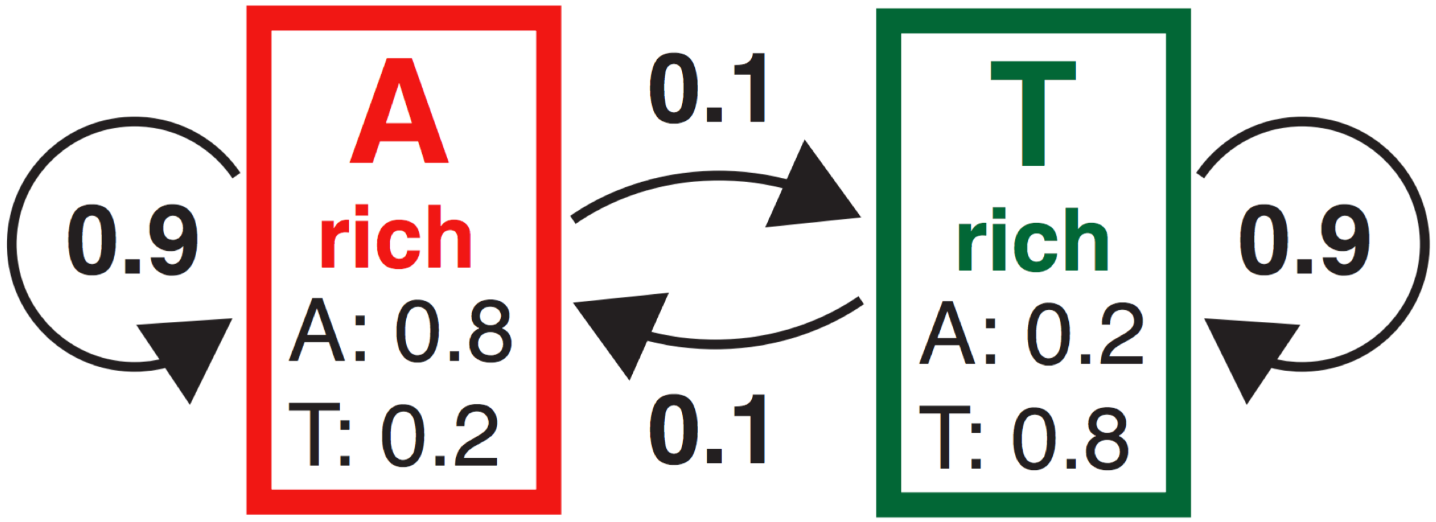
Topics from first half

- Alignments
  - Reasons to align sequences
  - Needleman-Wunsch algorithm
  - Smith-Waterman algorithm
  - Effects of parameter variation (including gap penalties)
  - Testing for statistical significance of an alignment
- Phylogenetic trees
  - Rooted and unrooted topologies
  - Defining the best tree with UPGMA and Neighbor Joining
  - Concept of parsimony
  - Fitch algorithm: quantifying how parsimonious a tree is, assigning internal states
  - Finding the most parsimonious tree: Hill climbing w/ Nearest-Neighbor interchanges
  - Bootstrapping to quantify confidence in tree partitions
- Clustering
  - Defining a clustering problem
  - Hierarchical clustering
    - Impact of using single/complete/average linkage
  - K-means: Objective and algorithm
- Networks
  - Reasons to make and analyze networks
  - Basic network definitions
  - Dijkstra's Algorithm
  - Network motifs and their uses

Topics from second half

- Gene prediction
    - Experimental methods
    - Homology based
    - Ab initio/Ad hoc
    - Markov chain/model and property
    - Hidden markov models
    - Viterbi algorithm
    - Forward-backward algorithm (general concept only)
- Machine learning
    - Definitions (objects, features, model, training data, overfitting)
    - Supervised versus unsupervised and tasks for each
    - Variant effect prediction
    - Feature trees
    - Decision trees
    - Tree generation
    - Contingency tables/confusion matrices
    - Performance stats (accuracy, TPR, TNR)
- DNA Sequencing and alignment
    - Sequencing technologies
    - Uses of HTS
    - Short read mapping (hashing, seeding, spaced seeds, difference of BWA)
    - Paired read structural variation
    - Variant calling (Phred scores)
    - Genome assembly (N50, graph-based assembly)

Markov chain/model versus hidden Markov model?

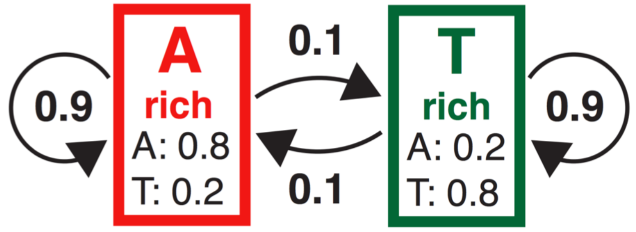


Viterbi algorithm

- What is it for?

- Big picture of how it works?

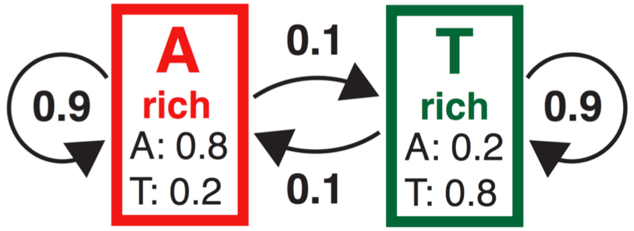
Viterbi: determine the likeliest hidden state sequence for an observed sequence



Observed sequence

	A	A	T	T	T	A
A-rich	0.5*0.8= 0.4	0.9 *0.8 = ?				
T-rich	0.5*0.2= 0.1	0.1				

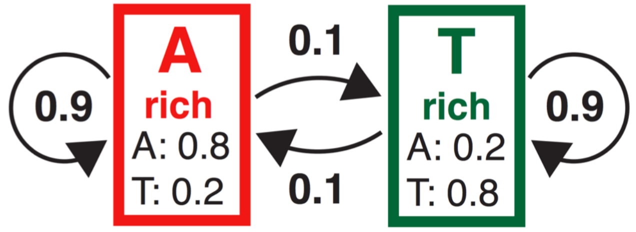
Viterbi: determine the likeliest hidden state sequence for an observed sequence



Observed sequence

	A	A	T	T	T	A
A-rich	0.4 →	0.288				
T-rich	0.1					

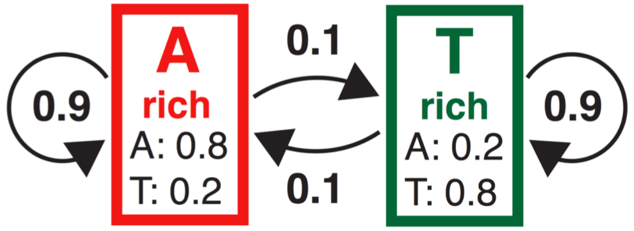
Viterbi: determine the likeliest hidden state sequence for an observed sequence



Observed sequence

	A	A	T	T	T	A
A-rich	0.4	0.288				
T-rich	0.1					

Viterbi: determine the likeliest hidden state sequence for an observed sequence



Observed sequence

	A	A	T	T	T	A
A-rich	0.4	0.288				
T-rich	0.1					

What’s a decision tree?

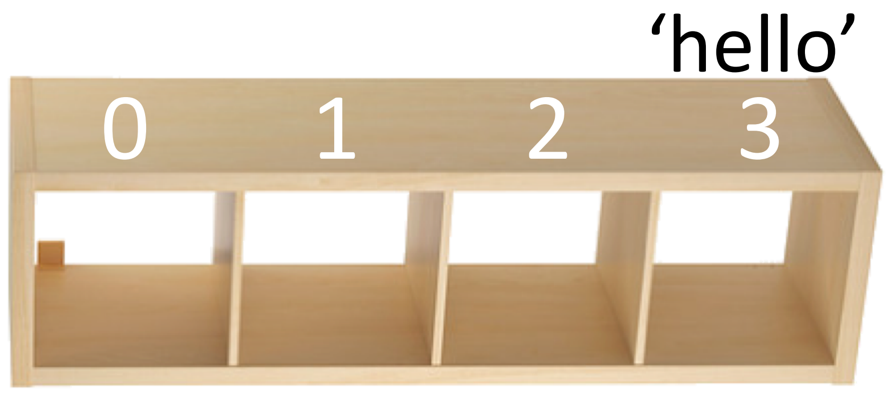
- How do you construct an optimal decision tree?

What is hashing?

- A hash function maps some object x to an integer i
- A hash function allows us to have a hash table, which is like a list that allows indexing by arbitrary objects (a python Dictionary!)
- We can compute the value of the hash function and find the index in the hash table in constant time – fast!!

hash(‘hello’) → 3

Hash table with key ‘hello’



Hashing Improves Search

- A **hash function** assigns a unique key to each unique data element (DNA sequence in our case)

```
hash(“ATGCTG”) = key1
hash(“TTTCTG”) = key2
```

…

- **Keys** encode strings in a short, easily comparable format (e.g. a number)

Hashing Improves Search

- A **hash function** assigns a unique key to each unique data element (DNA sequence in our case)

- The **hash table** is an associative array that describes the relationship between the key and the sequence and its genomic loction

Key	Hashed index	Genomic location
“GCTAGC”	Key1	Chr1 123412
…	…	…
“TTTAGC”	KeyN	Chr6 988472

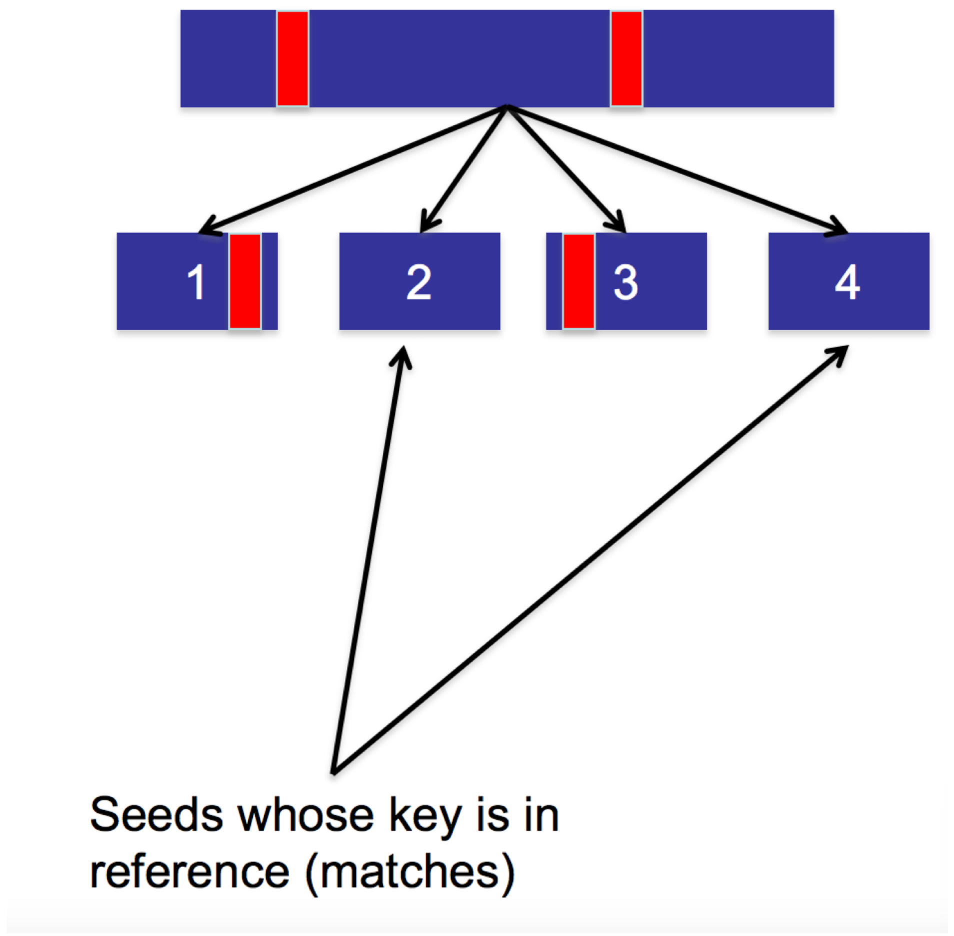
Is hashing really faster?

```
constructing dictionary: 0.0440001487732
Using the dictionary: 0.00799989700317
Using reference.index: 0.0120000839233
```

Constructing the dictionary is expensive, but you only have to do it once, and you keep reaping the benefits

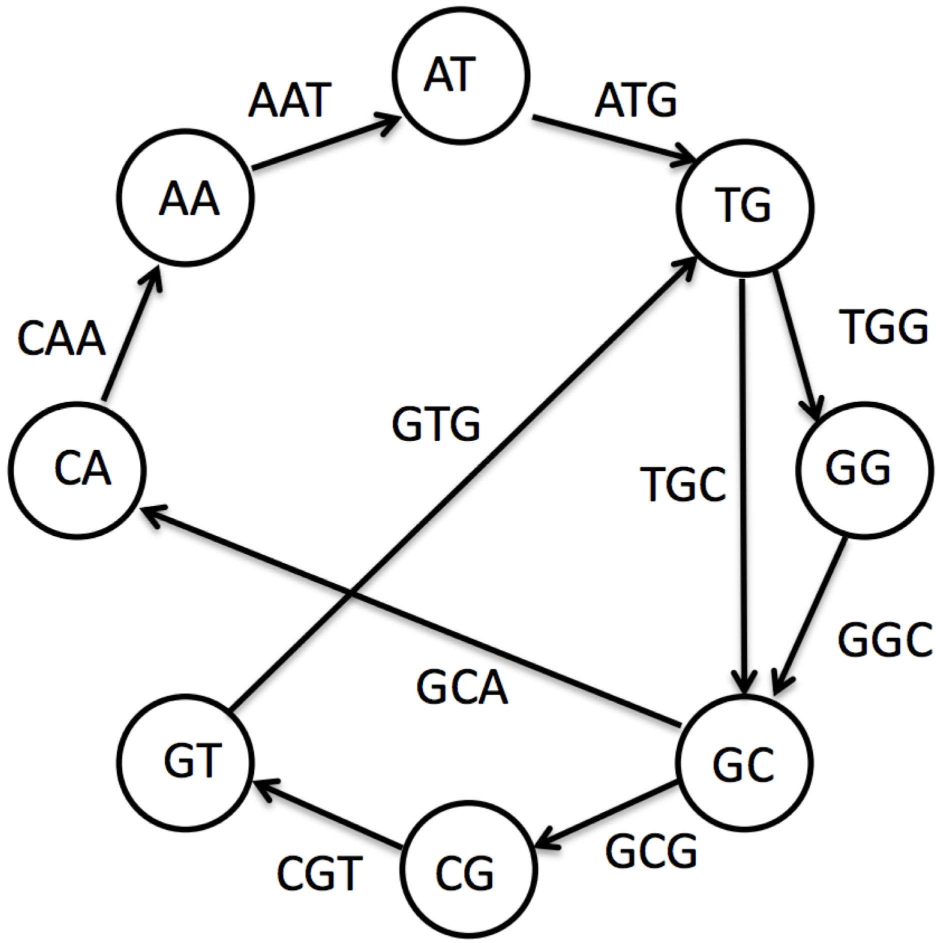
What is seeding? Spaced seeding?

- With this spaced seeding, how many mismatches will be allowed? Why?



Graph-based genome assembly

- Where is the read “CAATG” represented?



Any other questions??