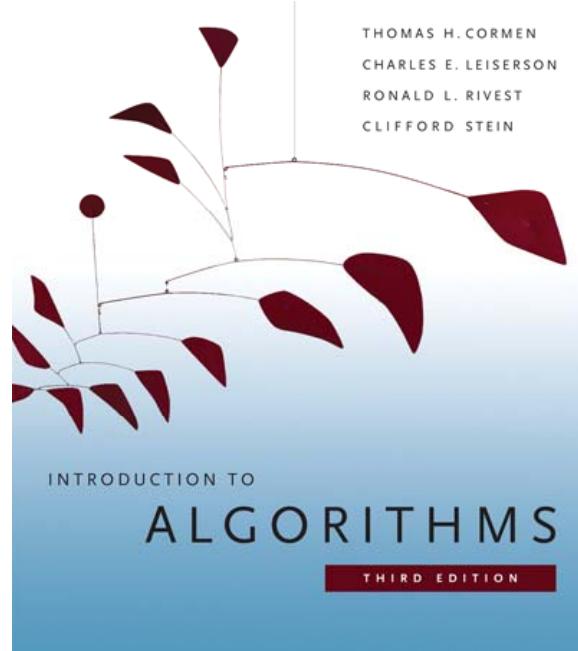


# *6.006- Introduction to Algorithms*



## *Lecture 5*

**Prof. Manolis Kellis**

# Unit #2 – Genomes, Hashing, and Dictionaries

Unit	Pset	Week	Date	Lecture (Tuesdays and Thursdays)			Recitation (Wed and Fri)	
Intro Binary Search Trees	PS1 Out: 2/1 Due: Mon 2/14 HW lab: Sun 2/13	1	Tue Feb 01	1	Introduction and Document Distance		1	Python and Asymptotic Complexity
			Thu Feb 03	2	Peak Finding Problem		2	Peak Finding correctness & analysis
		2	Tue Feb 08	3	Scheduling and Binary Search Trees		3	Binary Search Tree Operations
			Thu Feb 10	4	Balanced Binary Search Trees		4	Rotations and AVL tree deletions
Hashing	PS2 Out: 2/15 Due: Mon 2/28 HW lab:Sun 2/27	3	Tue Feb 15	5	Hashing I : Chaining, Hash Functions		5	Hash recipes, collisions, Python dicts
			Thu Feb 17	6	Hashing II : Table Doubling, Rolling Hash		6	Probability review, Pattern matching
		4	Tue Feb 22	-	President's Day - Monday Schedule - No Class		-	No recitation
			Thu Feb 24	7	Hashing III : Open Addressing		7	Universal Hashing, Perfect Hashing
Sorting	PS3. Out: 3/1 Due: Mon 3/7 HW lab: Sun 3/6	5	Tue Mar 01	8	Sorting I : Insertion & Merge Sort, Master Theorem		8	Proof of Master Theorem, Examples
			Thu Mar 03	9	Sorting II : Heaps		9	Heap Operations
		6	Tue Mar 08	10	Sorting III: Lower Bounds, Counting Sort, Radix Sort		10	Models of computation
			Wed Mar 09	Q1	Quiz 1 in class at 7:30pm. Covers L1-R10. Review Session on Tue 3/8 at 7:30pm.			
Graphs and Search	PS4. Out: 3/10 Due: Fri 3/18 HW lab:W 3/16	7	Thu Mar 10	11	Searching I: Graph Representation, Depth-1st Search		11	Strongly connected components
			Tue Mar 15	12	Searching II: Breadth-1st Search, Topological Sort		12	Rubik's Cube Solving
		8	Thu Mar 17	13	Searching III: Games, Network properties, Motifs		13	Subgraph isomorphism
			Tue Mar 29	14	Shortest Paths I: Introduction, Bellman-Ford		14	Relaxation algorithms
Shortest Paths	PS5 Out: 3/29 Due: Mon 4/11 HW lab:Sun 4/10	9	Thu Mar 31	15	Shortest Paths II: Bellman-Ford, DAGs		15	Shortest Path applications
			Tue Apr 05	16	Shortest Paths III: Dijkstra		16	Speeding up Dijkstra's algorithm
		10	Thu Apr 07	17	Graph applications, Genome Assembly		17	Euler Tours
			Tue Apr 12	18	DP I: Memoization, Fibonacci, Crazy Eights		18	Limits of dynamic programming
Dynamic Program ming	PS6 Out: Tue 4/12 Due: Fri 4/29 HW lab:W 4/27	11	Wed Apr 13	Q2	Quiz 2 in class at 7:30pm. Covers L11-R17. Review Session on Tue 4/13 at 7:30pm.			
			Thu Apr 14	19	DP II: Shortest Paths, Genome sequence alignment		19	Edit Distance, LCS, cost functions
		12	Tue Apr 19	-	Patriot's Day - Monday and Tuesday Off		-	No recitation
			Thu Apr 21	20	DP III: Text Justification, Knapsack		20	Saving Princess Peach
Numbers Pictures (NP)	PS7 out Thu4/28 Due: Fri 5/6 HW lab: Wed 5/4	13	Tue Apr 26	21	DP IV: Piano Fingering, Vertex Cover, Structured DP		21	Phylogeny
			Thu Apr 28	22	Numerics I - Computing on large numbers		22	Models of computation return!
		14	Tue May 3	23	Numerics II - Iterative algorithms, Newton's method		23	Computing the nth digit of $\pi$
			Thu May 5	24	Geometry: Line sweep, Convex Hull		24	Closest pair
Beyond		15	Tue May 10	25	Complexity classes, and reductions		25	Undecidability of Life
			Thu May 12	26	Research Directions (15 mins each) + related classes			
			Finals week	Q3	Final exam is cumulative L1-L26. Emphasis on L18-L26. Review Session on Fri 5/13 at 3pm			

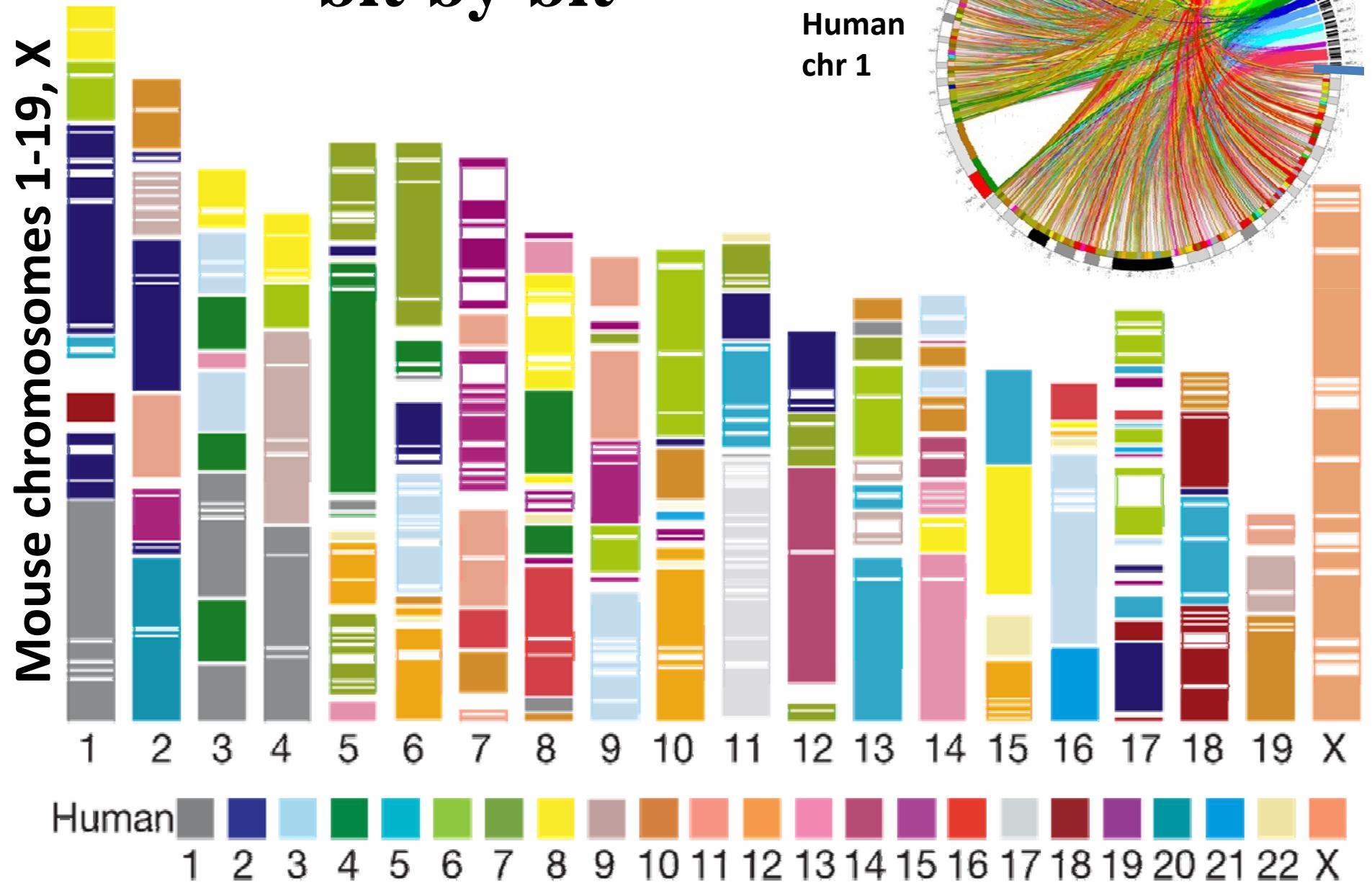
(hashing out...) **Our plan ahead**

- **Today: Genomes, Dictionaries, and Hashing**
  - Intro, basic operations, collisions and chaining
  - Simple uniform hashing assumption
  - Hash functions, python implementation
- **Thursday: Speeding up hash tables**
  - Faster comparison: Signatures
  - Faster hashing: Rolling Hash
- **Next week: Space issues**
  - Dynamic resizing and amortized analysis
  - Open addressing, deletions, and probing

# Our plan for today: Hashing I

- **Today: Genomes, Dictionaries, and Hashing**
  - Matching genome segments
  - Introduction to dictionaries
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# Comparing two genomes bit by bit



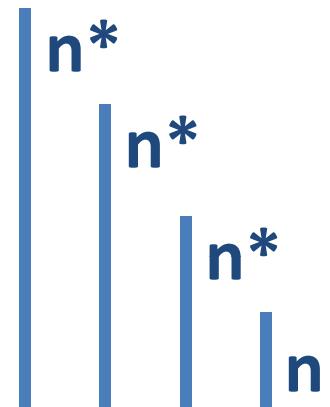
# DNA matching: All about strings

- How to find ‘corresponding’ pieces of DNA
- Given two DNA sequences
  - Strings over 4-letter alphabet
- Find longest substring that appears in both
  - Algorithm vs. Arithmetic
  - Algorithm vs. Arithmetic
  - L19: Subsequence - much harder (e.g. Algorithm)
- Other applications:
  - Plagiarism detection
  - Word autocorrect
  - Jeopardy!



# Naïve Algorithm

- Say strings S and T of length n
- For  $L = n$  downto 1
  - for all length L substrings  $X_1$  of S
    - for all length L substrings  $X_2$  of T
      - if  $X_1 = X_2$ , return L
- Runtime analysis
  - $n$  candidate lengths
  - $n$  strings of that length in  $X_1$
  - $n$  strings of that length in  $X_2$
  - $L$  time to compare the strings
  - Total runtime:  $\Omega(n^4)$



# Improvement 1: Binary Search on L

- Start with  $L=n/2$
- for all length L substrings  $X_1$  of S
- for all length L substrings  $X_2$  of T
- if  $X_1=X_2$ , success, try larger L  
           if failed, try smaller L
- Runtime analysis  
 $\Omega(n^4) \rightarrow \Omega(n^3 \log n)$

# Improvement 2: Python Dictionaries

- For every possible length  $L=n,\dots,1$ 
  - Insert all length L substrings of S into a dictionary
  - For each length L substring of T, check if it exists in dictionary
- Possible lengths for outer loop: n
- For each length:
  - at most n substrings of S inserted into dictionary, each insertion takes time  $O(1) * L$  ( $L$  is paid because we have to read string to insert it)
  - at most n substrings of T checked for existence inside dictionary, each check takes time  $O(1) * L$
  - Overall time spent to deal with a particular length  $L$  is  $O(Ln)$
- Hence overall  $O(n^3)$
- With binary search on length, total is  $O(n^2 \log n)$
- “Rolling hash” dictionaries improve to  $O(n \log n)$  (next time)

# Our plan for today: Hashing I

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# Dictionaries: Formal Definition

- It is a **set** containing **items**; each item has a **key**
- what keys and items are is quite flexible
- Supported Operations:
  - **Insert(*key*, *item*)**: add *item* to set, indexed by *key*
  - **Delete(*key*)**: delete item indexed by *key*
  - **Search(*key*)**: return the item corresponding to the given *key*, if such an item exists
  - **Random\_key()**: return a random key in dictionary
- **Assumption**: every item has its own key (or that inserting new item clobbers old)
- **Application** (and origin of name): Dictionaries
  - *Key* is word in English, *item* is word in French

# Dictionaries are everywhere

- Spelling correction
  - *Key* is misspelled word, *item* is correct spelling
- Python Interpreter
  - Executing program, see a variable name (*key*)
  - Need to look up its current assignment (*item*)
- Web server
  - Thousands of network connections open
  - When a packet arrives, must give to right process
  - *Key* is source IP address of packet, *item* is handler

# Implementation

- use BSTs!
  - can keep keys in a BST, keeping a pointer from each key to its value
  - $O(\log n)$  time per operation
- Often not fast enough for these applications!
- Can we beat BSTs?

*if only we could do all operations in  $O(1)$ ...*

# Dictionaries: Attempt #1

0	/
1	/
2	/
	/
key1	item1
	/
	/
key2	item2
	/
key3	item3
	/

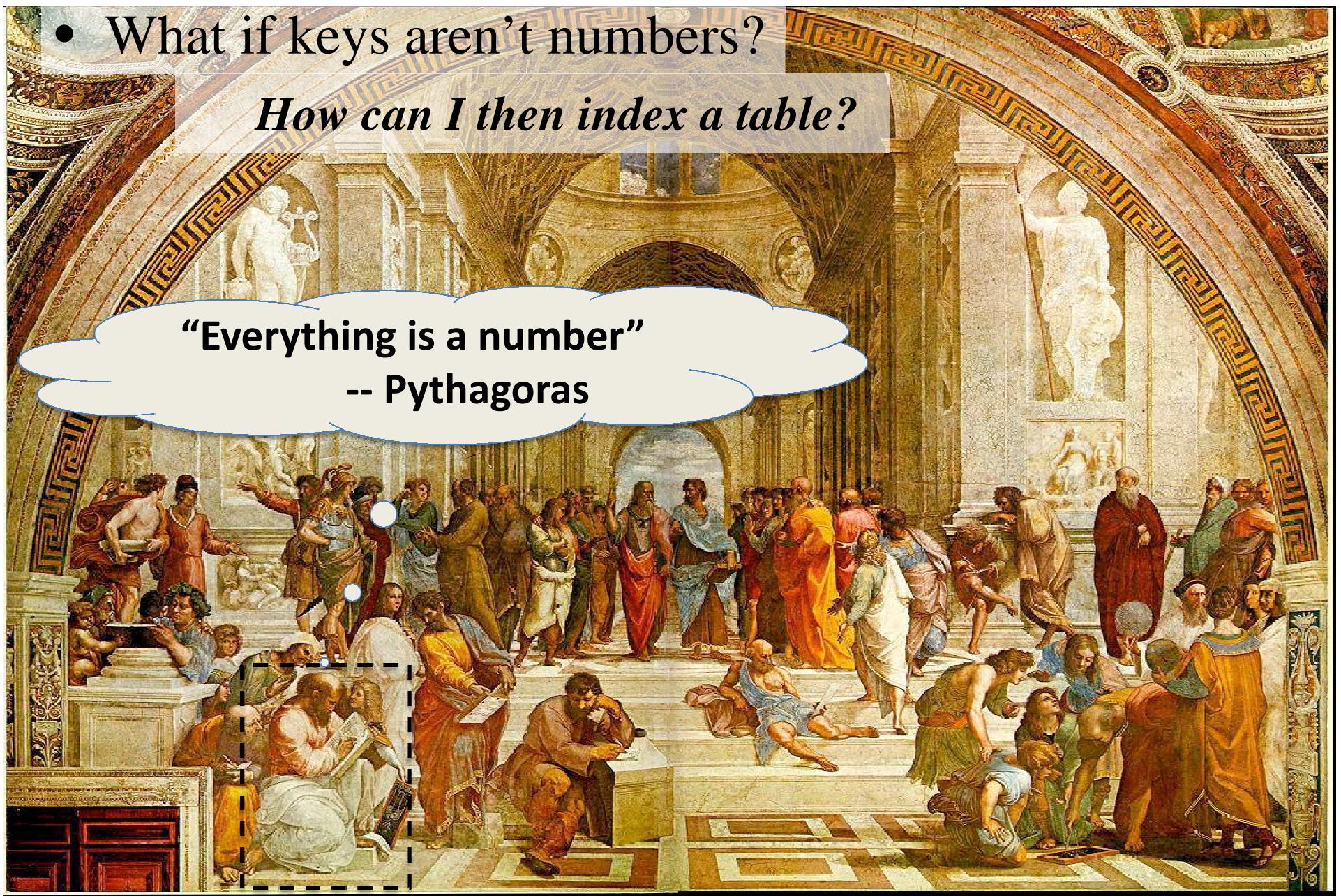
- Forget about BSTs..
- Use table, indexed by keys!

# Problems...

- What if keys aren't numbers?

*How can I then index a table?*

“Everything is a number”  
-- Pythagoras



# Interpreting words as numbers

- What if keys aren't numbers?
  - Anything in the computer is a sequence of bits
  - So we can pretend it's a number
- Example: English words
  - 26 letters in alphabet
    - ⇒ can represent each with 5 bits
  - Antidisestablishmentarianism has 28 letters
  - $28 \times 5 = 140$  bits
  - So, store in array of size  $2^{140}$  ....oops
- Isn't this too much space for 100,000 words?

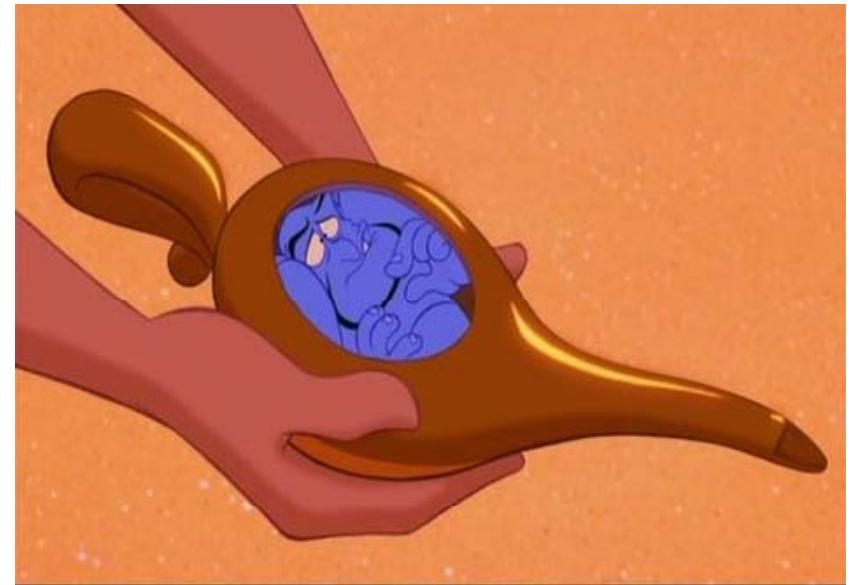
# Our plan for today: Hashing I

- **Today: Genomes, Dictionaries, and Hashing**
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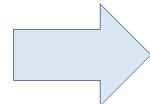
# Hash Functions

- Exploit sparsity
  - Huge universe  $U$  of possible keys
  - But only  $n$  keys actually present
  - Want to store in table (array) of size  $m \sim n$
- Define **hash function**  $h: U \rightarrow \{1..m\}$ 
  - Filter key  $k$  through  $h(\cdot)$  to find table position
  - Table entries are called **buckets**
- Time to insert/find key is
  - Time to compute  $h$  (generally length of key)
  - Plus one time step to look in array

# The ‘magic’ of hash functions



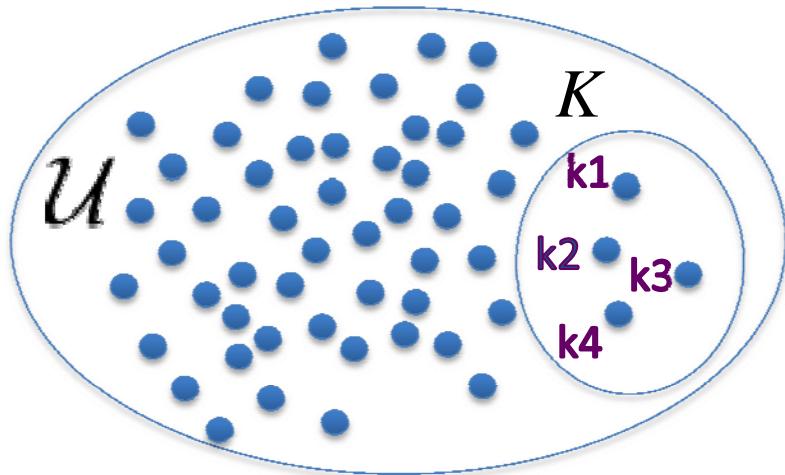
**PHENOMENAL  
COSMIC  
POWERS!!**



itty bitty living space

With apologies to Disney

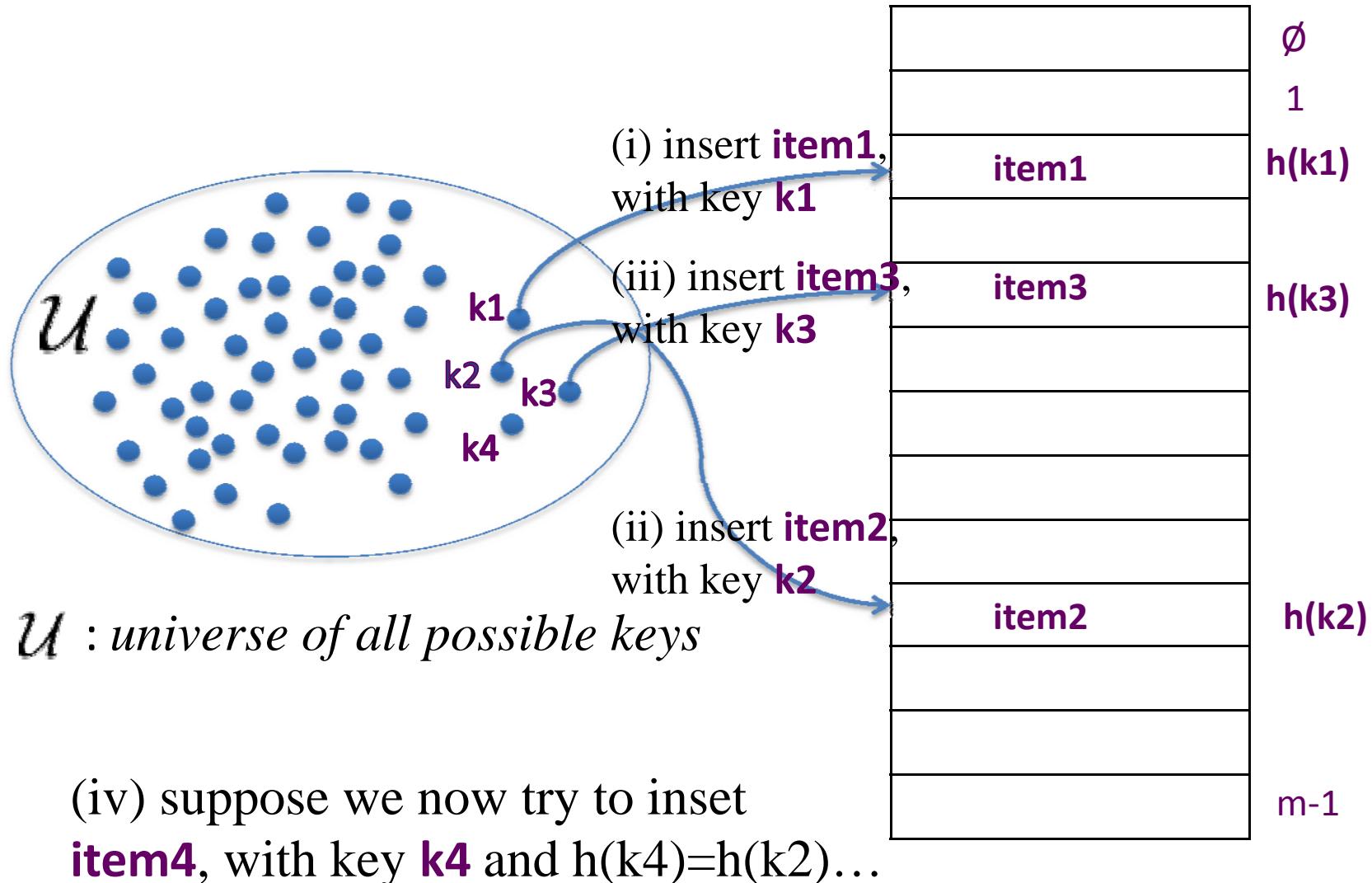
# Hashing exploits sparsity of space



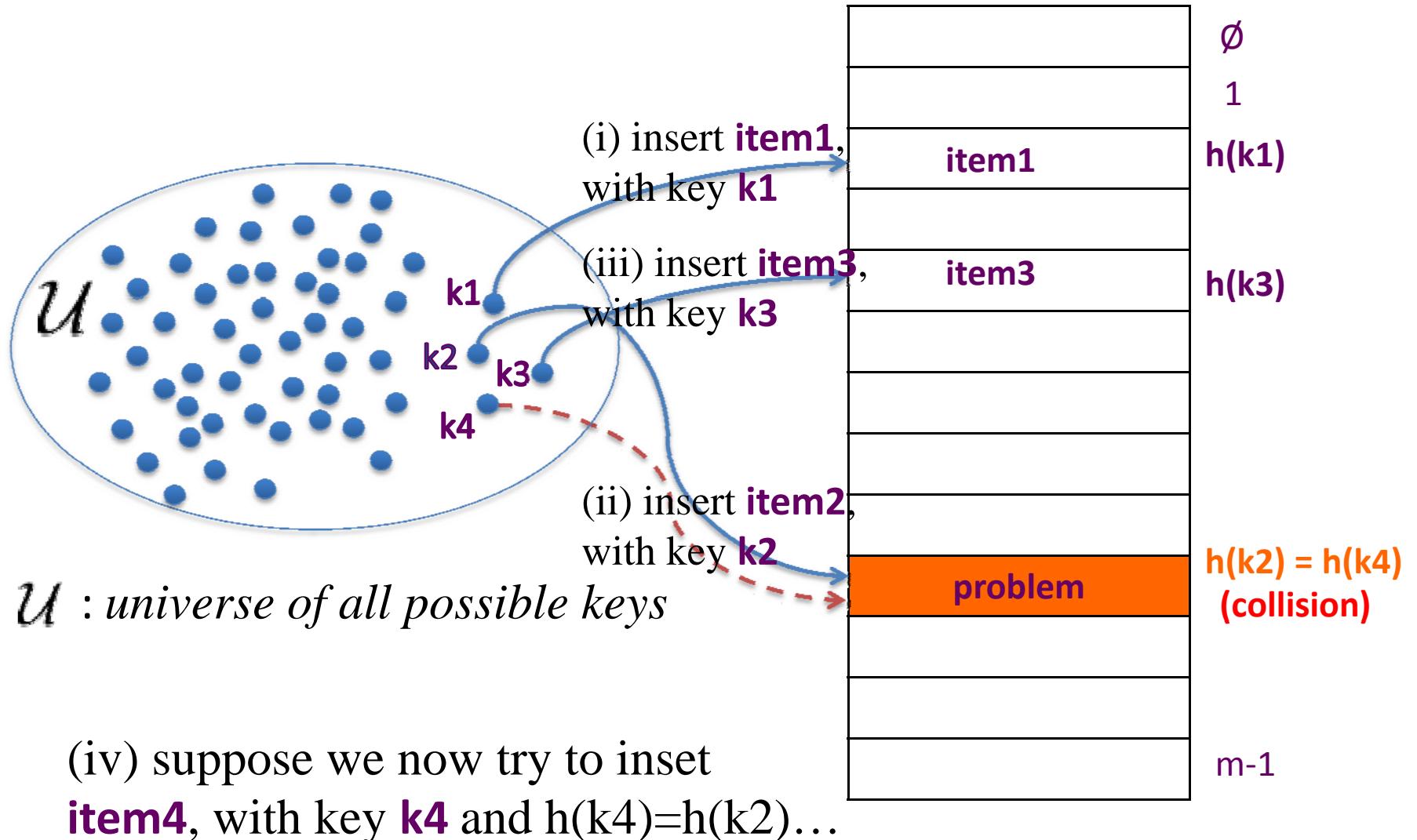
$\mathcal{U}$  : *universe of all possible keys;  
huge set*

$K$  : *actual keys; small set but not  
known in advance*

# All keys map to small space...



# ... leading to collisions



# Our plan for today: Hashing I

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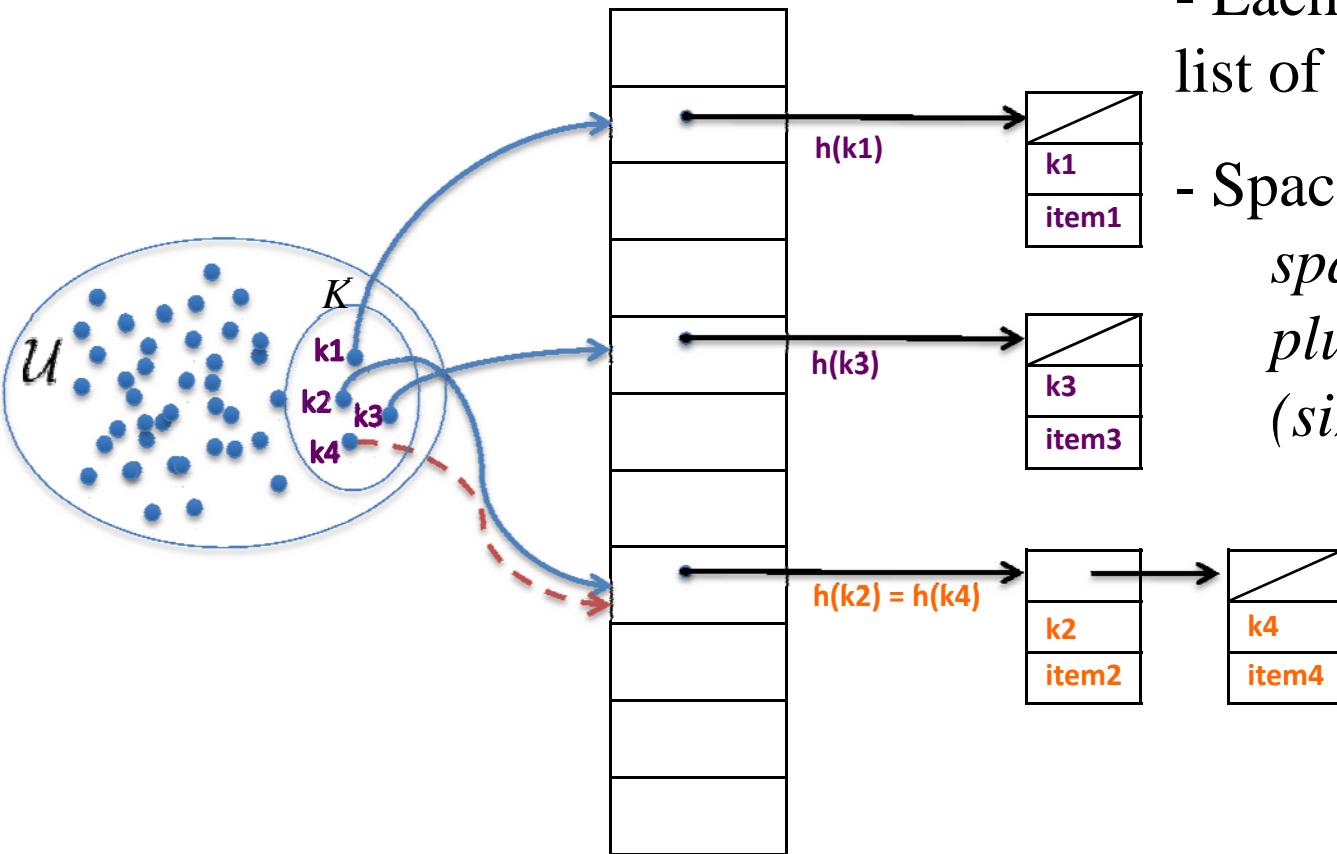
# Collisions

- What went/can go wrong?
  - Distinct keys  $x$  and  $y$
  - But  $h(x) = h(y)$
  - Called a **collision**
- This is unavoidable: if table smaller than range, **some** keys **must** collide...
  - Pigeonhole principle
- What do you put in the bucket?

# Coping with collisions

- **Idea1:** Change to a new “uncolliding” hash function and re-hash all elements in the table
  - Hard to find, and can take a long time if  $m=O(n)$
- **Idea2:** Chaining
  - Linked list of hashed items for each bucket (today)
- **Idea3:** Open addressing
  - Find a different, empty bucket for  $y$  (next lecture)
- **Idea4:** Perfect hashing (not covered in 6.006)
  - Create a 2<sup>nd</sup>-level hash table of size  $k^2$  for each  $k$ -element bin, and try several 2<sup>nd</sup>-level hash functions until no collisions are found (see 6.046)

# Chaining



$\mathcal{U}$  : universe of all possible keys

$K$  : actual keys, not known in advance

- Each bucket, linked list of contained items
- Space used is *space of table plus one unit per item (size of key and item)*

# Problem Solved?

- To find key, must scan whole list in key's bucket
- Length  $L$  list costs  $L$  key comparisons
- If all keys hash to same bucket, lookup cost  $\Theta(n)$

**Solution: optimism**

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# Simple uniform hashing assumption

- Definition:
  - Each key  $k \in K$  of keys is equally likely to be hashed to any slot of table  $T$ , independent of where other keys are hashed.

Let  $n$  be the number of keys in the table, and let  $m$  be the number of slots.

Define the ***load factor*** of  $T$  to be

$$\alpha = n/m$$

= average number of keys per slot.

# Chaining Analysis under SUHA

## Average case analysis:

- n items in table of m buckets
- Average number of items/bucket is  $\alpha=n/m$
- So expected time to find some key x is  $(1+\alpha)$
- $O(1)$  if  $\alpha=O(1)$ , i.e.  $m=\Omega(n)$

*apply hash  
function  
and access  
slot*

*search  
the  
list*

# Summary (rehash)

- Matching big genomes is a hard problem
  - And you will tackle it in your problem set!
- Dictionaries are pervasive
- Hash tables implement them efficiently
  - Under an optimistic assumption of random keys
  - Can be “made true” by heuristic hash functions
- Key idea for beating BSTs: Indexing
  - Sacrificed operations: previous, successor
- Chaining strategy for collision resolution
- Next two lectures: speed & space improvements

# Unit #2: Genomes, Hashing, Dictionaries

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