

# Managing Big Data Reaching Back to the 11<sup>th</sup> Century

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#### **Ancestry.com** mission



Our mission is to help everyone

discover, preserve and share

their family history.



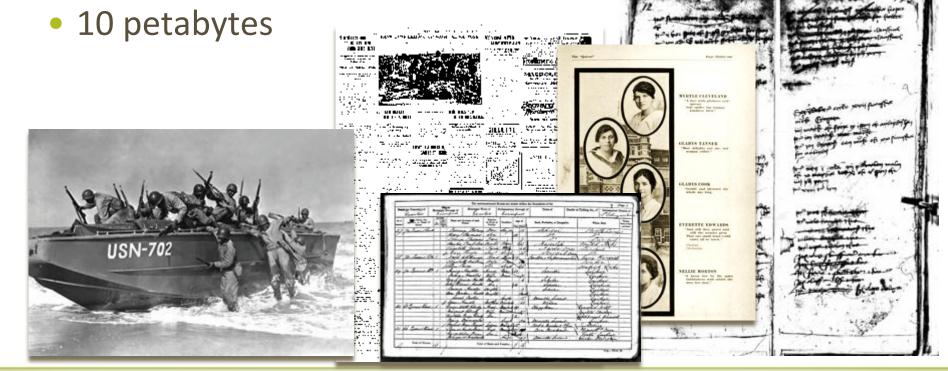
#### Data is our product

It's the "aha" moment of a discovery that drives our



#### World's largest online family history resource

- Over 30,000 historical content collections
- Records dating back to 11<sup>th</sup> century
- 12 billion records and images

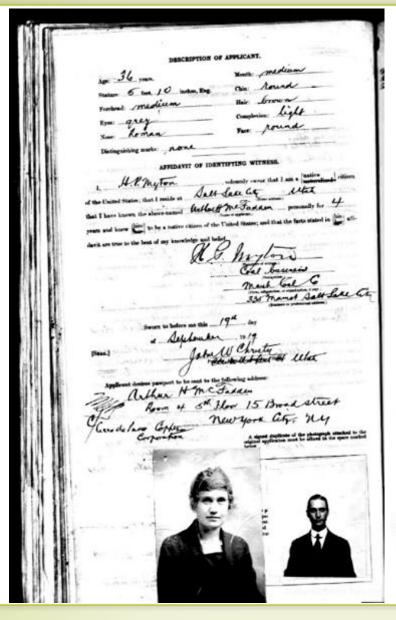


#### User contributed content and structure

- 50 million family trees
- More than 5 billion profiles
- 200 million stories and photos



#### **Behavioral data**



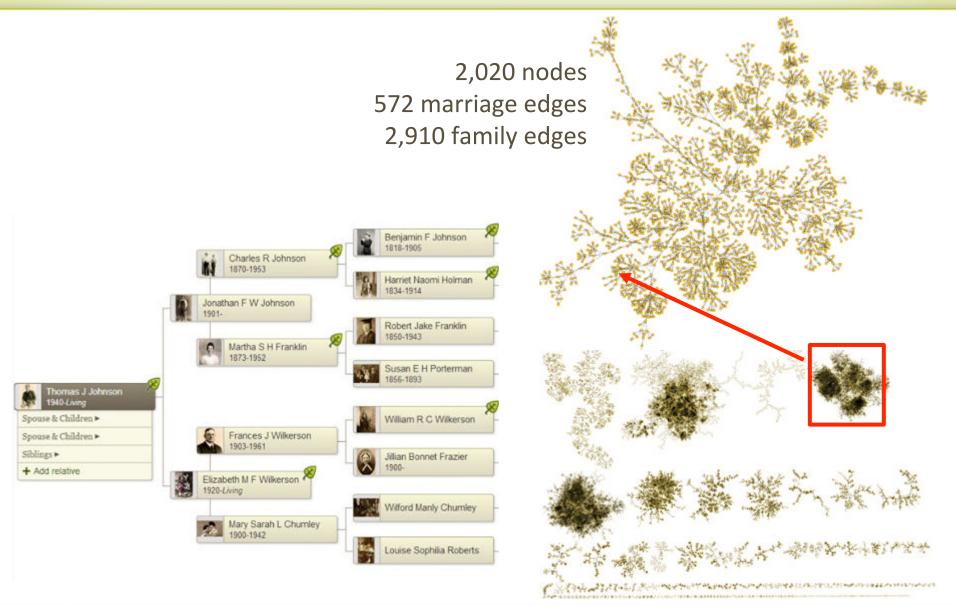
#### **Next Best Discovery Algorithm**

40 million searches/day

 10 million people added to trees/day



#### The math behind our big data equation



#### We've barely scratched the surface

 Making the site more social through sharing





 Mobile extends the core users experience and attracts a new demographic



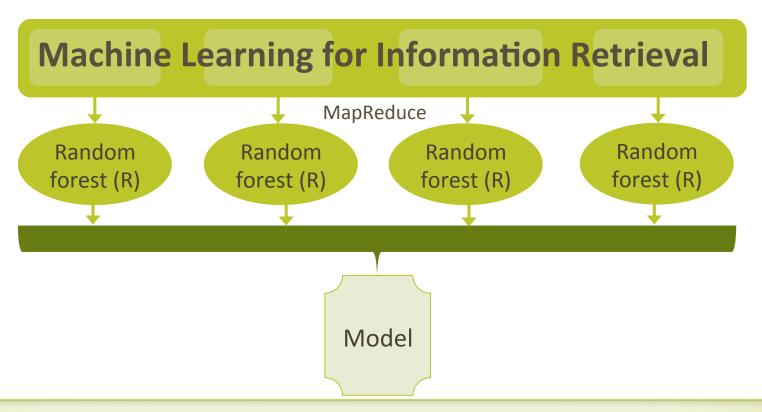


 New experiences like AncestryDNA



#### **Our transition to Hadoop**





#### How we're using Hadoop



- 1. Machine Learning
- 2. Predictive analytics
- 3. Natural Language Processing and Entity Extraction
- 4. DNA Processing

#### **Ancestry DNA**

#### Spit in a tube, pay \$99, learn your past

Autosomal DNA tests
Samples from over 200,000 people
700,000 SNPs for each sample
10,000,000 4<sup>th</sup> cousin matches



#### **Discover Your Ethnicity**

Find out if you're part Irish, Native American, or maybe Cameroonian.

**NEWLY UPDATED** 



#### Connect with new relatives

Imagine meeting a 3rd cousin for the 1st time.

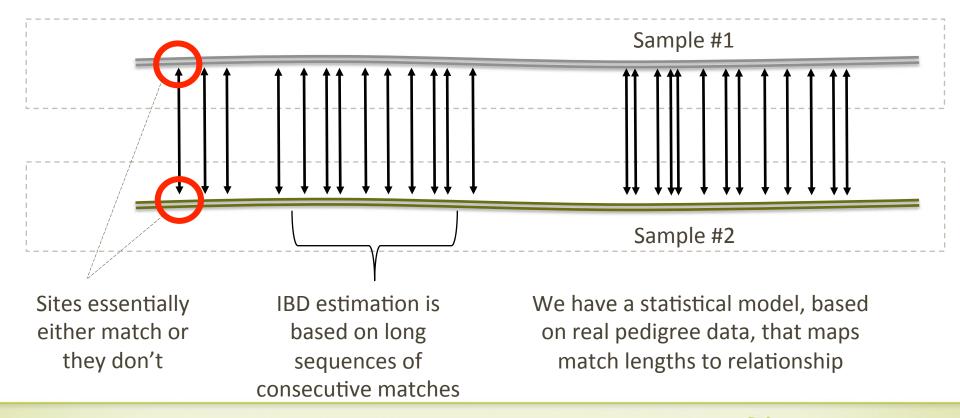


#### Family history is in our DNA

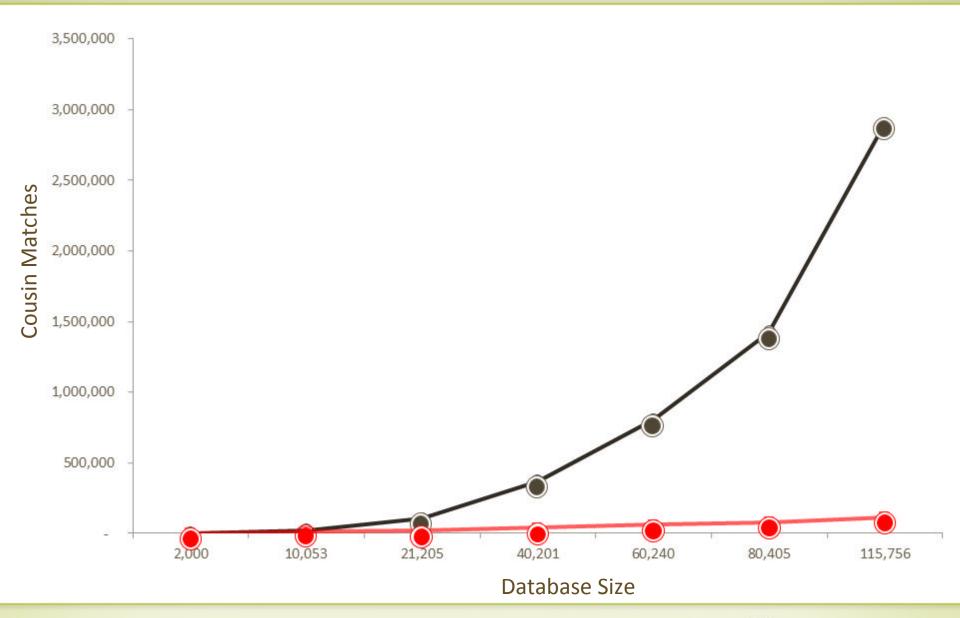
Even more powerful when combined with Ancestry.com.

#### **Estimating IBD (matching)**

- We identify "long" DNA segments shared by two individuals.
- These segments are said to be Identical-by-Descent (IBD) and identify recent shared genetic ancestry.



#### **Network effect & cousin matches**

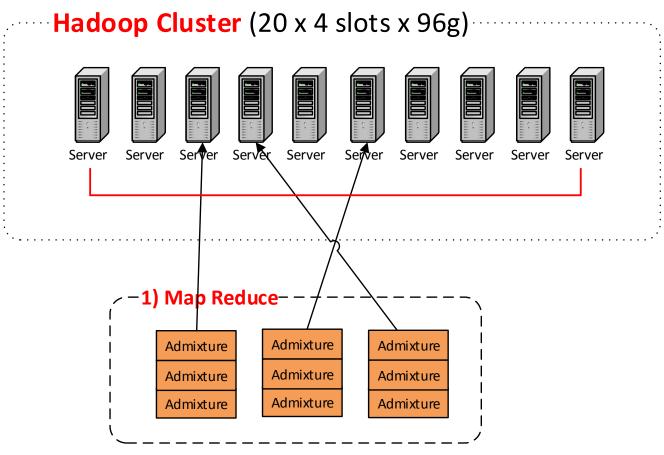


#### Algorithms in the pipeline

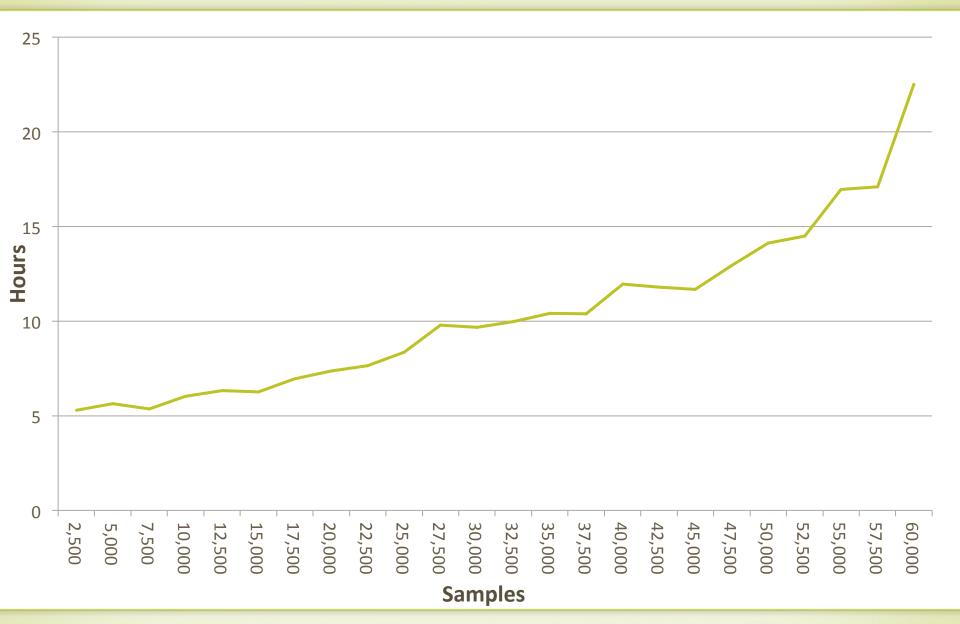




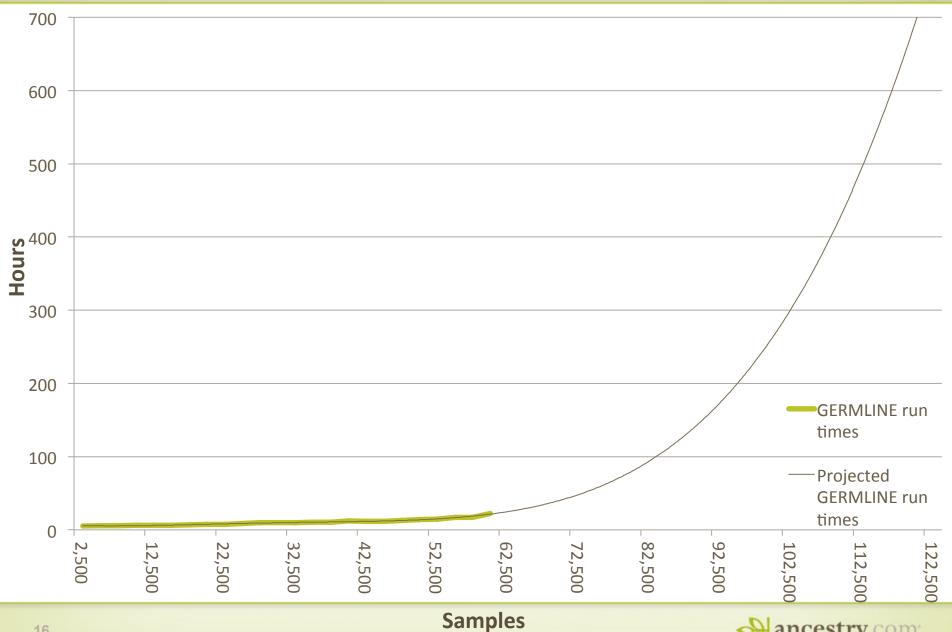




#### **GERMLINE** run times (in hours)



#### **Projected GERMLINE run times (in hours)**





Kara Thrace, aka Starbuck

- Ace viper pilot
- Has a special destiny
- Not to be trifled with

### The Input

Starbuck : ACTGACCTAGTTGAC Adama : TTAAGCCTAGTTGAC



**Admiral Adama** 

- Admiral of the Colonial Fleet
- Routinely saves humanity from destruction

### Separate into words



0 1 2

Starbuck : ACTGA CCTAG

TTGAC

Adama: TTAAG CCTAG

TTGAC



#### **Build the hash table**



0 1 2
Starbuck : ACTGA CCTAG TTGAC
Adama : TTAAG CCTAG TTGAC

ACTGA\_0 : Starbuck

TTAAG\_0 : Adama

CCTAG\_1 : Starbuck, Adama

TTGAC\_2: Starbuck, Adama



### Iterate through genome and find matches



0 1 2

Starbuck: ACTGA CCTAG TTGAC

Adama: TTAAG CCTAG TTGAC

ACTGA\_0 : Starbuck

TTAAG 0: Adama

CCTAG\_1: Starbuck, Adama

TTGAC\_2: Starbuck, Adama



Starbuck and Adama match from position 1 to position 2

### Does that mean they're related?







...maybe

#### **But wait... what about Baltar?**

Baltar: TTAAGCCTAGGGGCG



**Gaius Baltar** 

- Handsome
- Genius
- Kinda evil

## The jermline way

#### Step one: Update the hash table.

	Starbuck	Adama
2_ACTGA_0	1	
2_TTAAG_0		1
2_CCTAG_1	1	1
2_TTGAC_2	1	1



Baltar: TTAAG CCTAG GGGCG



New sample to add

Key : [CHROMOSOME]\_[WORD]\_[POSITION]

Cell value: A byte set to 1, denoting that the user has that word at that position on

that chromosome

### The jermline way

## Step two: Find matches, update the results table

	2_Starbuck	2_Adama
2_Starbuck		{ (1, 2),}
2_Adama	{ (1, 2),}	



Baltar and Adama match from position 0 to position 1
Baltar and Starbuck match at position 1



Key : [CHROMOSOME]\_[USER ID]

Cell value: A list of ranges where the two users match on a chromosome

## The jermline way

Hash Table					
	Starbuck	Adama	Baltar		
2_ACTGA_0	1				
2_TTAAG_0		1	1		
2_CCTAG_1	1	1	1		
2_TTGAC_2	1	1			
2_GGGCG_2			1		

Results Table					
	2_Starbuck	2_Adama	2_Baltar		
2_Starbuck		{ (1, 2),}	{ (1),}		
2_Adama	{ (1, 2),}		{ (0,1),}		
2_Baltar	{ (1),}	{ (0,1),}			

## But wait ... what about Zarek, Roslin, Hera, and Helo?









### Run them in parallel with Hadoop!



Photo by Benh Lieu Song

#### **Parallelism with Hadoop**

Batches are usually about a thousand people.

 Each mapper takes a single chromosome for a single person.

MapReduce Jobs :

Job #1 : Match Words

Updates the hash table

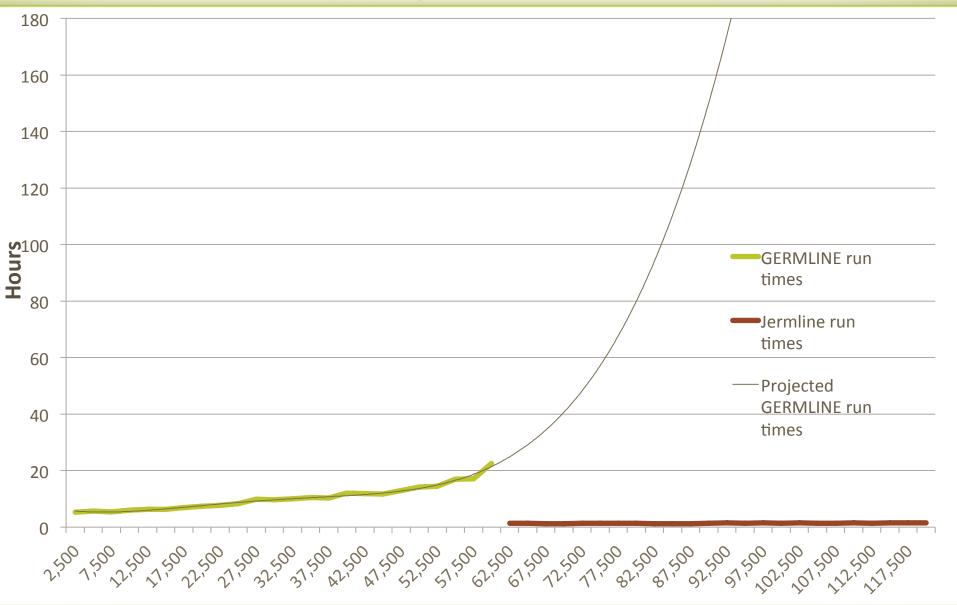
Job #2 : Match Segments

Identifies areas where the samples match

#### Run times for matching (in hours)



#### Run times for matching (in hours)



#### **AncestryDNA – Cast of characters**



#### **Scientists**

Think they can code:

- Linux
- MySQL
- PERL and/or Python



#### **Software Engineers**

Think they are Scientists:

- Math
- Statistics
- Read science papers

#### Pressures of a startup business

Release a product, learn, and then scale

#### Other lessons learned

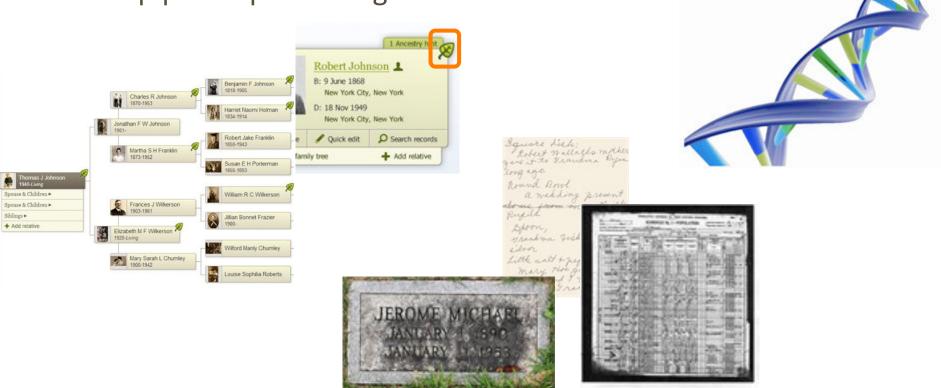
- Prototyping is key to overcoming resistance to change
- Technical architecture is heavily influenced by people organization
- Developing a team of experienced Hadoop users can often be done using internal employees
- A culture of experimentation and innovation yields the best results



#### Using Hadoop to drive scalable results

- Machine learning and predictive analytics
- Entity extraction and product development

DNA pipeline processing





# Questions?

Tech Roots blog - <a href="http://blogs.ancestry.com/techroots/">http://blogs.ancestry.com/techroots/</a>