### Cloud Computing and the DNA Data Race Michael Schatz

October 22, 2010 CSHL Advanced Sequencing Course





### Outline

### Part I:Theory

- I. Genome Assembly by Analogy
- 2. DNA Sequencing and Genomics
- 3. Sequence Analysis in the Clouds
  - I. Sequence Alignment
  - 2. Mapping & Genotyping
  - 3. Genome Assembly

#### Part 2: Practice

- I. AWS Mini-Tutorial
- 2. Hadoop Mini-Tutorial

### Shredded Book Reconstruction

Dickens accidentally shreds the first printing of <u>A Tale of Two Cities</u>
 – Text printed on 5 long spools



- How can he reconstruct the text?
  - 5 copies x 138, 656 words / 5 words per fragment = 138k fragments
  - The short fragments from every copy are mixed together
  - Some fragments are identical



### **Greedy Reconstruction**



The repeated sequence make the correct reconstruction ambiguous

• It was the best of times, it was the [worst/age]

Model sequence reconstruction as a graph problem.

### de Bruijn Graph Construction

- $D_k = (V, E)$ 
  - V = All length-k subfragments (k < l)</li>
  - E = Directed edges between consecutive subfragments
    - Nodes overlap by k-1 words



- Locally constructed graph reveals the global sequence structure
  - Overlaps between sequences implicitly computed

de Bruijn, 1946 Idury and Waterman, 1995 Pevzner, Tang, Waterman, 2001



### de Bruijn Graph Assembly



### Molecular Biology & DNA Sequencing



Genome of an organism encodes the genetic information in long sequence of 4 DNA nucleotides: ACGT

- Bacteria: ~3 million bp
- Humans: ~3 billion bp



Current DNA sequencing machines can sequence millions of short (25-500bp) reads from random positions of the genome

- Per-base error rate estimated at 1-2% (Simpson et al, 2009)



GCAAGGCAAACCCGAGCCCAGTTT

TCCAGTTCTAGAGTTTCACATGATC



Like Dickens, we can only sequence small fragments of the genome at once.

- Use software to analyze the sequences
- Modern Biology requires Computational Biology

## The DNA Data Race

Genome	Technology	Cost
Venter et al.	Sanger (ABI)	\$300,000,000
Levy et al.	Sanger (ABI)	\$10,000,000
Wheeler et al.	Roche (454)	\$2,000,000
Ley et al.	Illumina	\$1,000,000
Bentley et al.	Illumina	\$250,000
Pushkarev et al.	Helicos	\$48,000
Drmanac et al.	Complete Genomics	\$4,400
	Genome Venter et al. Levy et al. VVheeler et al. Ley et al. Bentley et al. Pushkarev et al. Drmanac et al.	GenomeTechnologyVenter et al.Sanger (ABI)Levy et al.Sanger (ABI)Wheeler et al.Roche (454)Ley et al.IlluminaBentley et al.IlluminaPushkarev et al.HelicosDrmanac et al.Complete Genomics

(Pushkarev et al., 2009)

Sequencing a single human genome uses ~100 GB of compressed sequence data in billions of short reads. ~20 DVDs / genome







Use massive amounts of sequencing to explore the genetic origins of life



Our best (only) hope is to use many computers:

- Parallel Computing aka Cloud Computing
- Now your programs will crash on 1000 computers instead of just 1 <sup>(2)</sup>



## **Amazon Web Services**

http://aws.amazon.com

- All you need is a credit card, and you can immediately start using one of the largest datacenters in the world
- Elastic Compute Cloud (EC2)
  - On demand computing power
    - Support for Windows, Linux, & OpenSolaris
    - Starting at  $8.5 \notin$  / core / hour
- Simple Storage Service (S3)
  - Scalable data storage
    - 10¢ / GB upload fee, 15¢ / GB monthly fee





### **Cloud Computing Spectrum**



# **Embarrassingly Parallel**

- Batch computing
  - Each item is independent
  - Split input into many chunks
  - Process each chunk separately on a different computer
- Challenges
  - Distributing work, load balancing, monitoring & restart
- Technologies
  - Condor, Sun Grid Engine
  - Amazon Simple Queue





### **Elementary School Dance**



# Loosely Coupled

- Divide and conquer
  - Independently process many items
  - Group partial results
  - Scan partial results into final answer
- Challenges
  - Batch computing challenges
  - + Shuffling of huge datasets
- Technologies
  - Hadoop, Elastic MapReduce, Dryad
  - Parallel Databases



## Junior High Dance



# Hadoop MapReduce

http://hadoop.apache.org

- MapReduce is the parallel distributed framework invented by Google for large data computations.
  - Data and computations are spread over thousands of computers, processing petabytes of data each day (Dean and Ghemawat, 2004)
  - Indexing the Internet, PageRank, Machine Learning, etc...
  - Hadoop is the leading open source implementation
- Benefits
  - Scalable, Efficient, Reliable
  - Easy to Program
  - Runs on commodity computers
- Challenges
  - Redesigning / Retooling applications
    - Not Condor, Not MPI
    - Everything in MapReduce



### K-mer Counting

- Application developers focus on 2 (+1 internal) functions
  - Map: input → key:value pairs
  - Shuffle: Group together pairs with same key

Map, Shuffle & Reduce All Run in Parallel

– Reduce: key, value-lists → output



### Hadoop Architecture



- Hadoop Distributed File System (HDFS)
  - Data files partitioned into large chunks (64MB), replicated on multiple nodes
  - Computation moves to the data, rack-aware scheduling
- Hadoop MapReduce system won the 2009 GreySort Challenge
  - Sorted 100 TB in 173 min (578 GB/min) using 3452 nodes and 4x3452 disks



• Given a reference and many subject reads, report one or more "good" end-toend alignments per alignable read

Methyl-Seq

Hi-C-Seq

- Find where the read most likely originated
- Fundamental computation for many assays
  - Genotyping
    RNA-Seq
  - Structural Variations
    Chip-Seq
- Desperate need for scalable solutions
  - Single human requires >1,000 CPU hours / genome





http://bowtie-bio.sourceforge.net/crossbow

- Align billions of reads and find SNPs
  - Reuse software components: Hadoop Streaming
- Map: Bowtie (Langmead et al., 2009)
  - Find best alignment for each read
  - Emit (chromosome region, alignment)
- Shuffle: Hadoop
  - Group and sort alignments by region
- Reduce: SOAPsnp (Li et al., 2009)
  - Scan alignments for divergent columns
  - Accounts for sequencing error, known SNPs



## Performance in Amazon EC2

http://bowtie-bio.sourceforge.net/crossbow

	Asian Individual Genome		
Data Loading	3.3 B reads	106.5 GB	\$10.65
Data Transfer	lh :15m	40 cores	\$3.40
Setup	0h : I 5m	320 cores	\$13.94
Alignment	Ih : 30m	320 cores	\$41.82
Variant Calling	I h : 00m	320 cores	\$27.88
End-to-end	4h : 00m		\$97.69

Analyze an entire human genome for ~\$100 in an afternoon. Accuracy validated at >99%

#### Searching for SNPs with Cloud Computing.

Langmead B, Schatz MC, Lin J, Pop M, Salzberg SL (2009) Genome Biology. 10:R134

# Map-Shuffle-Scan for Genomics



#### Cloud Computing and the DNA Data Race.

Schatz, MC, Langmead B, Salzberg SL (2010) Nature Biotechnology 28:691-693

# Tightly Coupled

- Computation that cannot be partitioned
  - Graph Analysis
  - Molecular Dynamics
  - Population simulations
- Challenges
  - Loosely coupled challenges
  - + Parallel algorithms design
- Technologies
  - MPI
  - MapReduce, Dryad, Pregel



## Short Read Assembly



- Genome assembly as finding an Eulerian tour of the de Bruijn graph
  - Human genome: >3B nodes, >10B edges
- The new short read assemblers require tremendous computation
  - Velvet (Zerbino & Birney, 2008) serial: > 2TB of RAM
  - ABySS (Simpson et al., 2009) MPI: 168 cores x ~96 hours
  - SOAPdenovo (Li et al., 2010) pthreads: 40 cores x 40 hours, >140 GB RAM

### K-mer Counting

- Application developers focus on 2 (+1 internal) functions
  - Map: input → key:value pairs
  - Shuffle: Group together pairs with same key

Map, Shuffle & Reduce All Run in Parallel

– Reduce: key, value-lists → output



### Graph Construction

- Application developers focus on 2 (+1 internal) functions
  - Map: input → key:value pairs
  - Shuffle: Group together pairs with same key

Map, Shuffle & Reduce All Run in Parallel

– Reduce: key, value-lists → output



### Graph Compression

- After construction, many edges are unambiguous
  - Merge together compressible nodes
  - Graph physically distributed over hundreds of computers





# High School Dance



### Warmup Exercise

- Who here was born closest to October 22?
  - You can only compare to I other person at a time



Find winner among 64 teams in just 6 rounds

#### Challenges

- Nodes stored on different computers
- Nodes can only access direct neighbors

#### Randomized List Ranking

- Randomly assign H/T to each compressible node
- Compress (Ĥ)→T links



Initial Graph: 42 nodes

#### Randomized Speed-ups in Parallel Computation.

#### Challenges

- Nodes stored on different computers
- Nodes can only access direct neighbors

#### Randomized List Ranking

- Randomly assign H/T to each compressible node
- Compress (Ĥ)→T links



Round 1: 26 nodes (38% savings)

#### Randomized Speed-ups in Parallel Computation.

#### Challenges

- Nodes stored on different computers
- Nodes can only access direct neighbors

#### Randomized List Ranking

- Randomly assign H/T to each compressible node
- Compress (Ĥ)→T links



Round 2: 15 nodes (64% savings)

#### Randomized Speed-ups in Parallel Computation.

#### Challenges

- Nodes stored on different computers
- Nodes can only access direct neighbors

#### Randomized List Ranking

- Randomly assign H/T to each compressible node
- Compress (Ĥ)→T links



Round 2: 8 nodes (81% savings)

#### Randomized Speed-ups in Parallel Computation.

#### Challenges

- Nodes stored on different computers
- Nodes can only access direct neighbors

#### Randomized List Ranking

- Randomly assign H/T to each compressible node
- Compress (Ĥ)→T links



Round 3: 6 nodes (86% savings)

#### Randomized Speed-ups in Parallel Computation.

#### Challenges

- Nodes stored on different computers
- Nodes can only access direct neighbors

#### Randomized List Ranking

- Randomly assign (H) / T to each compressible node
- Compress (Ĥ)→T links

#### Performance

- Compress all chains in log(S) rounds



Round 4: 5 nodes (88% savings)

#### Randomized Speed-ups in Parallel Computation.


#### Node Types











Isolated nodes (10%)

Tips (46%)

Bubbles/Non-branch (9%)

Dead Ends (.2%)

Half Branch (25%)

Full Branch (10%)

(Chaisson, 2009)

http://contrail-bio.sourceforge.net

#### Scalable Genome Assembly with MapReduce

- Genome: E. coli KI2 MGI655, 4.6Mbp
- Input: 20.8M 36bp reads, 200bp insert (~150x coverage)
- Preprocessor: Quality-Aware Error Correction



#### Assembly of Large Genomes with Cloud Computing.

Schatz MC, Sommer D, Kelley D, Pop M, et al. In Preparation.



Contrail

## E. coli Assembly Quality

Incorrect contigs: Align at < 95% identity or < 95% of their length

Assembler	Contigs ≥ 100bp	N50 (bp)	Incorrect contigs
Contrail PE	300	54,807	4
Contrail SE	529	20,062	0
SOAPdenovo PE	182	89,000	5
ABySS PE	233	45,362	13
Velvet PE	286	54,459	9
EULER-SR PE	216	57,497	26
SSAKE SE	931	11,450	38
Edena SE	680	16,430	6



Contrail http://contrail-bio.sourceforge.net



De novo Assembly of the Human Genome

- Genome: African male NA18507 (SRA000271, Bentley et al., 2008)
- Input: 3.5B 36bp reads, 210bp insert (~40x coverage)



#### Assembly of Large Genomes with Cloud Computing.

Schatz MC, Sommer D, Kelley D, Pop M, et al. In Preparation.

# Hadoop for NGS Analysis





#### CloudBurst

Highly Sensitive Short Read Mapping with MapReduce

100x speedup mapping on 96 cores @ Amazon

http://cloudburst-bio.sf.net

(Schatz, 2009)

#### Myrna

Cloud-scale differential gene expression for RNA-seq

Expression of 1.1 billion RNA-Seq reads in <2 hours for ~\$66



(Langmead, Hansen, Leek, 2010)

http://bowtie-bio.sf.net/myrna/

#### AMOS

Searching for SNPs in the Turkey Genome

Scan the de novo assembly to find 920k hetrozygous alleles



(Dalloul et al, 2010)

http://amos.sf.net

#### Summary

- Surviving the data deluge means computing in parallel
  - Cloud computing is an attractive platform for large scale sequence analysis and computation
- Use the right tool for the job
  - Embarassingly parallel = Condor/Hadoop
  - Loosely coupled = Hadoop/Dyrad
  - Tightly coupled = MPI/Hadoop
- Emerging technologies are a great start, but we need continued research
  - A word of caution: new technologies are new

#### Acknowledgements

#### Advisor

Steven Salzberg

#### **UMD** Faculty

Mihai Pop, Art Delcher, Amitabh Varshney, Carl Kingsford, Ben Shneiderman, James Yorke, Jimmy Lin, Dan Sommer

#### **CBCB** Students

Adam Phillippy, Cole Trapnell, Saket Navlakha, Ben Langmead, James White, David Kelley



#### Break



### Outline

Part I: Theory

- I. Genome Assembly by Analogy
- 2. DNA Sequencing and Genomics
- 3. Sequence Analysis in the Clouds
  - I. Sequence Alignment
  - 2. Mapping & Genotyping
  - 3. Genome Assembly

#### Part 2: Practice

- I. AWS Mini-Tutorial
- 2. Hadoop Mini-Tutorial

#### A Brief History of the Amazon Cloud

- Urban Legend
  - Additional capacity added every fall for the holiday shopping season, underutilized rest of the year...
- Official Story
  - Amazon is a technology company
    - Different divisions of Amazon share computation
  - Amazon Web Services is the 3<sup>rd</sup> Business Division
    - Retail & Seller Businesses



## **Amazon Web Services**

http://aws.amazon.com

- All you need is a credit card, and you can immediately start using one of the largest datacenters in the world
- Elastic Compute Cloud (EC2)
  - On demand computing power
    - Support for Windows, Linux, & OpenSolaris
    - Starting at  $8.5 \notin$  / core / hour
- Simple Storage Service (S3)
  - Scalable data storage
    - 10¢ / GB upload fee, 15¢ / GB monthly fee





#### **Other Services**



Everything you need to run a large scale service & analysis suite in the clouds.

#### **Cloud Solutions for DNA Sequence Analysis**

- Rapid & elastic deployment of vast computation
   Accessible, Reproducible, Reliable, Collaborative
- Why not?
  - Transfer: 200 GBs takes 1 hr 2 weeks
  - Privacy & security: Excellent... with care
  - Expertise: Computing on 1000 cores is complex
  - Price: The meter is always running
  - Who will be on the line for making it all work?
    - Psychological and Institutional paradigm shift

### EC2 Architecture

- Very large pool of machines
  - Effectively infinite resources
  - High-end servers with many cores and many GB RAM
- Machines run in a virtualized environment
  - Amazon can subdivide large nodes into smaller instances
  - You are 100% protected from other users on the machine
  - You get to pick the operating system, all installed software



## Instance Types

Туре	Price / hr	CPU	Resources
<b>Micro</b> Web service	2¢	I core @ I ECU	.6 GB RAM 10 GB Disk
<b>Standard</b> Light Tasks	8.5¢	I core @ I ECU	I.7 GB RAM I 60 GB Disk
<b>Extra Large</b> Mapping w/BWA	68¢	4 core @ 2 ECU	I 5 GB RAM I .7 TB Disk
HighCPU XL Mapping w/Crossbow	68¢	8 cores @ 2.5 ECU	7 GB RAM 1.7 TB Disk
HighMem Quad XL Assembly	\$2.00	8 cores @ 3.25 ECU	68.4 GB RAM 1.7 TB Disk

ECU = EC2 Compute Unit. Approximately 1.0 – 1.2 GHz Intel Xeon from 2007

Reserved Instances make it cheaper for consistent use. Pay for what you use, rounded UP to the next full hour

## Amazon Machine Images



- A few Amazon sponsored images – Suse Linux, Windows
- Many Community Images & Appliances
  - Crossbow: Hadoop, Bowtie, SOAPsnp
  - CloudBioLinux.com: Appliance for Genomics
- Build you own
  - Completely customize your environment
  - You results could be totally reproducible

## Amazon S3

- S3 provides persistent storage for large volumes of data
  - Very high speed connection from S3 to EC2 compute nodes
  - Public data sets include s3://1000genomes
- Tiered pricing by volume
  - Pricing starts at 15¢ / GB / month
  - 5.5¢ / GB / month for over 5 PB
  - Pay for transfer in and out of Amazon
- Import/Export service for large volumes
  - FedEx your drives to Amazon



## **Getting Started**

#### http://docs.amazonwebservices.com/AWSEC2/latest/GettingStartedGuide/



# Signing Up



## AWS Management Console



# Running your First Cloud Analysis

- I. Pick your AMI
  - Machine Image: Operating System & Tools
- 2. Pick your instance type & quantity
  - Micro High-Memory Quadruple Extra Large
- 3. Pick your credentials
  - SSH Keys
- 4. Configure your Firewall
  - Protect your servers
- 5. Launch!

## I. Pick your AMIs



#### CloudBioLinux

	Amazon EC2	Amazon VIII	Amozon Elettic	Amazon	Amazon BDS	Amazon CAR			
	equest Instanc	es Wizard	ManDadura	Continet	PROMOUT PROFE			Cancel x.	iii
	Choose an Amazon	Machine Image (/	catton are easi MI) from one of the ta	(connected free late) blood lists below b	y clicking its Selec	t button,			e Hol
	Quick Start My Newlog: All Image	AMIS Comm	cloudbiolinux	_		€ € 1 to	4 of 4 Isens )	м	at a
	AMI ID	Root Device	Manifest		1	Nationm			
	ami-Oaf91263	ebs	678711657553/CloudBi	oLinux 32bit 20100	716	Other Linux	Select 🔒		
m	ami-4e67a227	ebs	678711657553/CloudBi	oLinux 64bit 20100	929	Other Linux	Select 🔒	1	
	ami-6963b200	instance-store	jevicloudbiolinux/JCVI-0	Cloud-BioLinux.mar	nifest.xml	Other Linux	Select 🔒	1	
also i	ami-879c75ee	ebs	678711657553/CloudBi	oLinux 20100507		Other Linux	Select 🚺		

# 2. Pick your Instance Type

naron 53	Request Instances W	izard				Cancel (a)	
evigetio	- 0	1					
egioni =	CHOCOL IN WHICH HARAWACK	DETAAL (DEALS OF PAR (CONTRACT, PRODUCT)					a Q Ann
EC2 Dash	Provide the details for your	r Instance(s). You may also decide whether you want	to launch your	instances as "on-	demand" or "r	ipot"	ers > >
and a second							Name
Instance	Number of Enstances:	1 Availability Zone: No Preference	9				1
Spot Reg	Instance Type:	Large (m1 large, 7.5 GB)	•				pat
inter .	Note, launching at tamica	Туре	CPU Units	CPU Cores	Memory		
AMIR	Course and the second second	Large (m1.large)	4 BCUs	2 Cores	7.5 GB	-	-
Bundle T	Launch Instances	Extra Large (m1.xlarge)	8 ECUs	4 Cores	15 GB		1
	EC2 Instances let you pa	High-Memory Extra Large (m2.xlarge)	6.5 ECUs	2 Cores	17.1 68		
Volument	commonly large fixed co	High-Memory Double Extra Large (m2.2xlarge)	13 ECUs	4 Cores	34.2 68		
Snapshur	O Request Spot Inst	High-Memory Quadruple Extra Large (m2.4xlarge)	26 ECUs	8 Cores	68.4 GB		
	O Launch Instances	High-CPU Extra Large (c1.xlarge)	20 ECUs	8 Cores	7 GB	-	
Elastic IP Security Placemen Lood Ball Key Pairs							
		Contrast (1)					

# 3. Pick your Credentials

macun 53	Request Instances Wizard		Cancel A
Regioni S • EC3 Dash • EC3 Dash • Instanco • Spot Reg • AMIs • AMIs • Bundle T ELATTIC BLD • Volumes • Snapshut	Crossi Annie Instance private (Crossi Annie Instance private) Public/private key pairs allow you to secure Greate & Download your Key Pair. You generate a key pair once - not each time you Choose from your existing Key Croate a new Key Pair 1. Enter a name for your key pair:* 2. Click to create your key pair:*	An environment represent an environment by connect to your instance after it launches. To create a key pair, en will then be prompted to save the private key to your computer. Note the want to deploy an Amazon BC2 instance. Pairs (e.g., jdoekey) Create & Download your Key Pair Save the file in a place you will remember. You use the key pairs bill unch other instances in the future or visit the Key Pairs page to create or manage existing ones.	ter a name and click , you only need to Name
Elastic IB Security Placamer Lood Bala Key Pairs	O Proceed without a Key Pair	Comman []	

# 4. Configure your Firewall

terun 53	Research Textures Mr	and a		10	Canal a	
-	Request Instances W	izard			Carde (A)	
gion s	CHOCKE AN ANY INSTANCE	BETALE (BRAN)	ALT PLAT CONFIGLA	NE FREEWOLD		a Que
	Security groups determine	whether a network	port is open or blocke	d on your instances. You may use an existin	g security group, or	per 2 31
CL2 Dans	now or update your securit	new security group t ty group anytime us	to allow access to your sing the Security Group	instances using the suggested ports below. is page. All changes take effect immediately	Add addienal ports	Aleres 1
Instance	C Change and an air	an of some mulat	the French from			
Spot Reg	Choose one or mo	re of your exist	ung security Grou	ipa		par ) a
áne -	O Create a new seco	arity aroup	5			
AMIR	1. Name your Security G	noup sah+http				-
Bundle T	2. Describe your Security	Group ssh+http				n
ASTICAL	3. Define allowed Connec	tions				
Volument	Appleation	Transport	Part	Source Network (IPv4 CIDR)	Actions	
Snapshat	нттр	TCP	80	All Internet	Remove	
Electic 10	SSH	TCP	22	All internet	Ranque	
Security	Statistics a	1.22	1.372	- ballenne bare		
Placemer						
Lood Bat						
Cey Pairs	Select.			All Internet Change	All Bat	
	Sector Sector			A CONTRACTOR		

#### 5. Launch!

tou >>	Request Instances W	izard	Cancel	A
ligation Ioni (S	CROCKLAR AND INCOMES	Details could entry converse recent.		a Q Aus
C2 Date	AME	Amazon Linux AMI ID ami-Jac33653 (i386)		e Marrie I
utanco pot Reg	Description:	Amazon Linux AMI Base 1.0, EBS boot, 32-bit architecture with Amazon EC2 AMI Tools.	Edit AMI	-
Min	Number of Instances: Availability Zone:	1 No Preference		
undle T	Instance Type: Instance Class:	Micro (t1.micro) On Demand	Edit Instance Details	ſ
alumen napahah WOLCH	Monitoring: Kernel ID: RAM Disk ID: User Data:	Disabled Use Default Use Default	Edit Advanced Details	
sotic D	Key Pair Name:	mechatz	Edit Key Pair	
tacemen ood Bata ey Pairs	Security Group(s):	basic	Edit Firewall	
	- Bark	Laurch		

# Monitoring your Server

	-	20		WS Manageme	int Console				
D- C (X) %	Ce anazon com	https://console.a	aws.am	azon.com/ec2/	home#c=EC2	6s-instan	081		8
ews.amazon.com	AWS Products   De	velopers Communit	ly Sud	port   Account.				Welcome, CBC	Settings Sign
Amazon 53 Amazon E0	C2 Amazon VP	C Amazon Elas MapReduci	stic #	Amazon CloudFront	Amazo	n RDS	Amazon SNS		
Navigation	<b>Hy Instances</b>		_						
Region: 🛀 US East 💌	B Launch Instant		dell.	Reserved Instance	es =			3 ShowHide	@ Refresh   @ Help
	Viewing: All Inst	tances		Al Instance Typ	pes 📦	-		16 < 1001	of 1 Instances > >
ECT Desigoard	Name 74	Instance	AMI	Ro	ot Device	Type	Status	Security Groups	Key Pair Name
INSTANCES	D enoty	-4aab6027	ami-3a	c33653 eb		t1 micro	a subning	crossbow46474683	aso-keypair
MAGES									
MAGES AMIs Dundle Tasks									
MAGES AMIs Dundle Tasks ELASTIC BLOCK STORE Volumes Snapshots	0 EC2 Instance	a selected							
MAGES AMIS Dundle Tasks LASTIC BLOCK STORE Volumes Snapshots	0 EC2 Instance Select an in	a selected satance above							
MAGES AMIS Bundle Tasks ELASTIC BLOCK STORE Volumes Snapshots NETWORKING & SECURITY	0 BC2 Instance Select an it	a selected satarce above							
MAGES AMIS Bundle Tasks ELASTIC BLOCK STORE Volumes Snapshots Networking & SECURITY Elastic IPs Security Groups	0 BC2 Instance Select an in	s selected satance above							
IMAGES MAGES Mages Bundle Tasks ELASTIC BLOCK STORE Volumes Volumes Snapshots METWORKING & SECURITY Elastic IPs Security Groups Placement Groups	0 BC2 Instance Select an in	a selected satance above							

## Connecting (I)



## Connecting (2)



## Calling SNPs in the Cloud ©

chmod 400 mschatz.pem

scp -r -i mschatz.pem data.tgz ubuntu@ec2-174-129-123-73.compute-1.amazonaws.com: ssh -i mschatz.pem ubuntu@ec2-174-129-123-73.compute-1.amazonaws.com

<remote>

ls

```
tar xzvf data.tgz
bowtie -S data/genomes/e_coli data/reads/e_coli_10000snp.fq ec_snp.sam
samtools view -bS -o ec_snp.bam ec_snp.sam
samtools sort ec_snp.bam ec_snp.sorted
```

samtools pileup -cv -f data/genomes/NC\_008253.fna ec\_snp.sorted.bam > snps

```
samtools index ec_snp.sorted.bam
samtools tview ec_snp.sorted.bam data/genomes/NC_008253.fna
```

exit

<local>

scp -i mschatz.pem ubuntu@ec2-174-129-123-73.compute-1.amazonaws.com:snps .

#### **1000Genomes in the Cloud**

s3cmd --configure

# cp data/.s3cfg .

s3cmd ls s3://1000genomes

s3cmd ls s3://1000genomes/Pilots\_Bam/NA20828/

s3cmd get s3://1000genomes/Pilots\_Bam/NA20828/\*chr22\* .

samtools view NA20828.SLX.maq.SRP000033.2009\_09.chr22\_1\_49691432.bam

### Terminating

)-(C) (X)	Amazon.com https://console.aw	amazon.com/ec2/home#c=DC2	Mis-Instances	<u>Ω</u>
	ABS Products Developers Community	Support Account		Welcome, CBCB   Settings   Sign (
Amazon 53 Amazon B	C2 Amazon VPC Amazon Elastic MapReduce	Amazon CloudFront Amazo	n RDS Amazon SNS	
Navigation	Hy Instances			
Region: 📑 US Cast +	Launch Instance Instance Actions	Reserved instances     *		🗇 Showfride 🛛 🖓 Rafresh 🖉 Help
PC2 Participand	Viewing: Al Instances	Al Instance Types 0		€ € 1 to 1 of 1 Instances > >
Fee passionere	Name <sup>The</sup> Instance Al	ID Root Device	Type Status	Security Groups Key Pair Name
INSTANCES	🛃 empty 📑 i-4aab6027 an	A	tt.micro 🕥 running	crossbow4647468; gsg-keypair
Spot Requests  MAGES     AMIs     Bundle Tasks  ELASTIC BLOCK STORE     Volumes     Snapshots  METWORKING & SECURITY     Elastic IPs     Security Groups	1 EC2 Instance selected EC2 Instance: I-4aab6 Description Monitoring T AMI ID: ami Security Groups: crossbow464746833350-X-master Status: nor	Connect Get System Log Create Image (EBS AMI) Add/Edit Tags Launch More Like This Disassociate TP Address Instance Lifecycle Terminate Reboot Stop Start	one: ype:	us-east-1c t1.micro 46476683350
Blacement Groups	Status: num	CloudWatch Monitoring	when	464746833350
> Load Balancers	Victoriantian	Enable CloudWatch Disable CloudWatch	latement Group	
+ Key Pairs	Beservation: r-81	filceb	RAM Disk ID:	14
	Platform:		Key Pair Name	psc-keysair
	Kernel ID: aki-	407//9529	Monitoring:	disabled
	AMI Launch Index: 0		Elastic IP:	
	Root Device: /de	(sda1	Root Device Type:	abs (

Total cost: 8.5¢

### Reflections

- Launching and managing virtual clusters with the AWS Console is quick and easy
  - Entirely scriptable using ec2 tools
  - iPhone App also available
- Things get really interesting on 168 cores
  - I week CPU = I hour wall

#### Hadoop on AWS



Just 3 commands to bring up a 168 core (21 node) cluster & crunch terabytes: \$HADOOP/src/contrib/ec2/bin/hadoop-ec2 launch-cluster HADOOP 21 \$HADOOP/src/contrib/ec2/bin/hadoop-ec2 <hadoop cmd> HADOOP \$HADOOP/src/contrib/ec2/bin/hadoop-ec2 terminate-cluster HADOOP

#### Kmer Code

```
kmer-map.pl
                                             kmer-reduce.pl
#!/usr/bin/perl
                                             #!/usr/bin/perl
my $K = 15;
                                             my $mer = "";
                                             my $cnt = 0;
while (<>)
                                             while (<>)
{
 for (my \$i = 0;
                                             {
      $i < length($ )-$K;</pre>
                                               chomp;
      $i++)
                                               my ($curmer, $curcnt) = split / t/, $;
 {
  my $kmer = substr($ ,$i,$K);
  print "$kmer\t1\n";
                                               if ($curmer ne $mer)
 }
                                               {
                                                 print "$mer\t$cnt\n" if ($cnt > 0);
}
                                                 $mer = $curmer; $cnt = 0;
                                               }
                                              $cnt += $curcnt;
```

print "\$mer\t\$cnt\n" if (\$cnt > 0);
### BashReduce

#### \$ head -3 reads.txt

ATATTTTTTCTTGTTTTTTTATATCCACAAACTCTTT CCACAAAATCAATACCTTGTGGAATAAAATTGTCCA TATTTTTTCTTGTTTTTTTATATCCACAAACTCTTTT

\$ cat reads.txt	./kmer-map.pl	I	head	-3
ATATTTTTTTCTTGTT	1			
TATTTTTTTCTTGTTT	1			
ATTTTTTCTTGTTTT	1			

# Kmer Counting In Hadoop

#!/bin/sh

```
STREAMING=/usr/lib/hadoop-0.20/contrib/streaming/hadoop-
streaming-0.20.2+320.jar
```

hadoop fs -mkdir /user/mschatz/kmertest/reads hadoop fs -put reads.txt /user/mschatz/kmertest/reads

```
hadoop jar $STREAMING \
  -input /user/mschatz/kmertest/reads \
  -output /user/mschatz/kmertest/kmers \
  -mapper ./kmer-map.pl \
  -reducer ./kmer-reduce.pl \
  -file ./kmer-map.pl \
  -file ./kmer-reduce.pl \
  -jobconf mapred.map.tasks=10 \
  -jobconf mapred.reduce.tasks=1
```

```
hadoop fs -cat /user/mschatz/kmertest/kmers/part-* | head -3
hadoop fs -rmr /user/mschatz/kmertest
```

### Hadoop Output

- 10/10/21 16:03:51 INFO mapred.FileInputFormat: Total input paths to process : 1
- 10/10/21 16:03:51 INFO streaming.StreamJob: getLocalDirs(): [/scratch0/hadoop/mapred/ local]
- 10/10/21 16:03:51 INFO streaming.StreamJob: Running job: job 201009232028 2089
- 10/10/21 16:03:51 INFO streaming.StreamJob: To kill this job, run:
- 10/10/21 16:03:51 INFO streaming.StreamJob: /usr/lib/hadoop-0.20/bin/hadoop job Dmapred.job.tracker=szhdname01.umiacs.umd.edu:8021 -kill job 201009232028 2089
- 10/10/21 16:03:51 INFO streaming.StreamJob: Tracking URL: http://
- szhdname01.umiacs.umd.edu:50030/jobdetails.jsp?jobid=job\_201009232028\_2089
- 10/10/21 16:03:52 INFO streaming.StreamJob: map 0% reduce 0%
- 10/10/21 16:03:58 INFO streaming.StreamJob: map 30% reduce 0%
- 10/10/21 16:04:01 INFO streaming.StreamJob: map 100% reduce 0%
- 10/10/21 16:04:07 INFO streaming.StreamJob: map 100% reduce 20%
- 10/10/21 16:04:16 INFO streaming.StreamJob: map 100% reduce 100%
- 10/10/21 16:04:19 INFO streaming.StreamJob: Job complete: job 201009232028 2089
- 10/10/21 16:04:19 INFO streaming.StreamJob: Output: /user/mschatz/kmertest/kmers

ААААААААБТАССТА	44
АААААААGTAGCTAT	44

AAAAAAGCAAATGTG 17

## **Crossbow Webform**

http://bowtie-bio.sf.net/crossbow/ui.html

Http://ec2	2-184-73-43-172.com C Q7 Google	_
WS 10 *	<yole-ans-id></yole-ans-id>	
WS Secret Key *		
WS Keyper Neme	gag-keypar Look 8 up	
	Check Conderstate	
loti name	Crossbow-Ecol	
lati tiype	<ul> <li>Crassbow</li> <li>Just preprocess reads</li> </ul>	
input URL *	alle // «YOUR-BUCKET»/example/e_convenationantes	1
	Orack that input URL events	
betput URL *	s3n // <youb-buckets e_col="" example="" output_small<="" td=""><td></td></youb-buckets>	
	Check that output URL doesn't exet	
input type	<ul> <li>Preprocessed reads</li> <li>Manifest Ne</li> </ul>	
Fruncate length	D (Of blank or 0, truncation is deutried)	
	Skip reads shorter than truncate length	
Discard Fraction	0	
Quality encoding	(Phred+13 2)	
Senome/Annotation	(E. enk 0057967 8)	
	Specify reference (ar URL)	
	sle//	
	Check that reference ter URL exists	
lowlie options	-= 1	
SCAPeng options	-2 -u -n -q	
Additional SOAPsno sptions for haploids	-r 0.0001	
ASSESSMENT SOAPENP	L A MARKET - A ANNI	

- Enter your account info, manifest file, reference info, and pipeline settings

   List of URLs to fastq files
- Crossbow
  - Parallel ftp
  - Parallel map
  - Parallel SNPs

# More Information

- Amazon Web Services
  - <u>http://aws.amazom.com</u>
  - http://aws.amazon.com/free



- Hadoop
  - http://hadoop.apache.org
- Crossbow & Bowtie
  - <u>http://bowtie-bio.sf.net</u>





# Thank You!

http://schatzlab.cshl.edu

@mike\_schatz