SNP detection and Genome Wide Association Study using Hadoop-BAM, CrossBow and Apache HIVE in Hadoop Cluster

Jyotsna Singh – PGDBD201901006

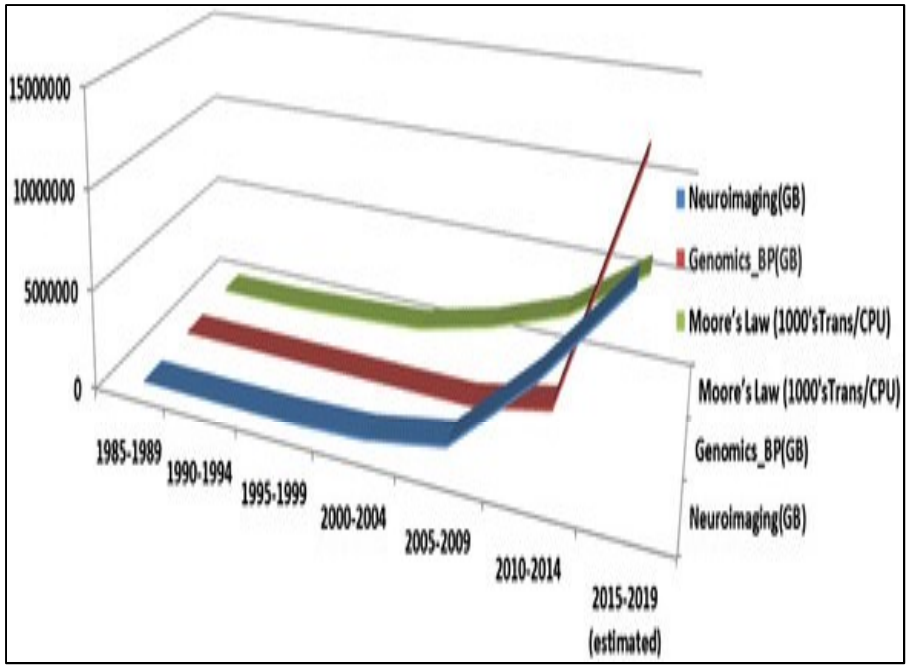
Paulami Das – PGDBD201901009

Poushali Gupta – PGDBD201901010

Institute of Bioinformatics & Applied Biotechnology, Bangalore

Next Generation Sequencing & Big Data

- The amount of NGS Data worldwide is predicted to double every 5 months which is must faster than Moore's law
- 1000 Genomes projects has Petabytes of human genome data sets
- In many GWAS and WGS studies multiple large files has to be processed sequentially



Kryder's law: Exponential growth of neuroimaging and genomics data, relative to increase of number of transistors per chip. By 2025 more than 100 PB of sequenced genome and 1 TB of neuroimaging data will be generated daily.

Different File Formats of Genomic Data

```
@HD     VN:1.0  SO:coordinate
@SQ     SN:chr20        LN:64444167
@PG     ID:TopHat       VN:2.0.14       CL:/srv/dna_tools/tophat/tophat -N 3 --read-edit-dist 5 --read-rea
lign-edit-dist 2 -i 50 -I 5000 --max-coverage-intron 5000 -M -o out /data/user446/mapping_tophat/index/chr
20 /data/user446/mapping_tophat/L6_18_GTGAAA_L007_R1_001.fastq
HWI-ST1145:74:C101DACXX:7:1102:4284:73714       16      chr20   190930  3       100M    *       0       0
       CCGTGTTTAAAGGTGGATGCGGTCACCTTCCCAGCTAGGCTTAGGGATTCTTAGTTGGCCTAGGAAATCCAGCTAGTCCTGTCTCTCAGTCCCCCCTCT
C    BBDCCDDCCDDDDCDDDDDDCDCCCDBC?DDDDDDDDDDDDDDCCDCDDDDDDDDDDCCCCEDDDC?DDDDDDDDDDDDDDDDDDDDDBDHFFFFDC@@
    AS:i:-15        XM:i:3  XO:i:0  XG:i:0  MD:Z:55C20C13A9 NM:i:3  NH:i:2  CC:Z:=  CP:i:55352714   HI:i:0
HWI-ST1145:74:C101DACXX:7:1114:2759:41961       16      chr20   193953  50      100M    *       0       0
       TGCTGGATCATCTGGTTAGTGGCTTCTGACTCAGAGGACCTTCGTCCCCTGGGGCAGTGGACCTTCCAGTGATTCCCCTGACATAAGGGGCATGGACGA
G    DCDDDDEDDDDDDDCDDDDDDDCCCDDDCDDDDDEEC>DFFFEJJJJJIGJJJJIHGBHHGJIJJJJJJGJJJIJJJJJIHJJJJJJHHHHHFFFFFCCC
    AS:i:-16        XM:i:3  XO:i:0  XG:i:0  MD:Z:60G16T18T3 NM:i:3  NH:i:1
HWI-ST1145:74:C101DACXX:7:1204:14760:4030       16      chr20   270877  50      100M    *       0       0
       GGCTTTATTGGTAAAAAAGGAATAGCAGATTTAATCAGAAATTCCCACCTGGCCCAGCAGCACCAACCAGAAAGAAGGGAAGAAGACAGGAAAAAACCA
C    DDDDDDDDDCCDDDDDDDDDDEEEEEEEFFFEFFEGHHHHFGDJJIHJJIJIJJJIIIIGGFJJIHIIIIJJJJJJIGHHFAHGFHJHFGGHFFFDD@BB
    AS:i:-11        XM:i:2  XO:i:0  XG:i:0  MD:Z:0A85G13    NM:i:2  NH:i:1
HWI-ST1145:74:C101DACXX:7:1210:11167:8699       0       chr20   271218  50      50M4700N50M     *       0
       0       GTGGCTCTTCCACAGGAATGTTGAGGATGACATCCATGTCTGGGGTGCACTTGGGTCTCCGAAGCAGAACATCCTCAAATATGACCTCTCG
accepted_hits.sam
```

SAM/BAM Files

```
>@HWI-ST216_0180:4:1101:1096:2196#GGCTAC/1
TTTTCAGNGAATACTGCAAATCAATAAACTCTTTAG
>@HWI-ST216_0180:4:1101:1158:2236#GGCTAC/1
AAAAGCTCATTTCCTATAGTTAACAGGACATGCCTT
>@HWI-ST216_0180:4:1101:1448:2211#GGCTAC/1
ATTATATAAGATAGCGGCTTTTTCCGTTAGTTTCCT
>@HWI-ST216_0180:4:1101:1331:2227#GGCTAC/1
CACGTTCTCTGTCCCCAATGGTATTTGCATCCCTGT
>@HWI-ST216_0180:4:1101:1376:2237#GGCTAC/1
GCGTCCCTTAGCTGAACTACCCAAACGTACGAATGC
```

Fasta Files

```
@HWI-ST216_0180:4:1101:1096:2196#GGCTAC/1
TTTTCAGNGAATACTGCAAATCAATAAACTCTTTAG
+HWI-ST216_0180:4:1101:1096:2196#GGCTAC/1
ceedb]]B[[]]]][fffff\ddddedeeedf_fbd
@HWI-ST216_0180:4:1101:1158:2236#GGCTAC/1
AAAAGCTCATTTCCTATAGTTAACAGGACATGCCTT
+HWI-ST216_0180:4:1101:1158:2236#GGCTAC/1
gggggggggggggggggeggfffgggggggggfg
@HWI-ST216_0180:4:1101:1448:2211#GGCTAC/1
ATTATATAAGATAGCGGCTTTTTCCGTTAGTTTCCT
```

Fastq Files

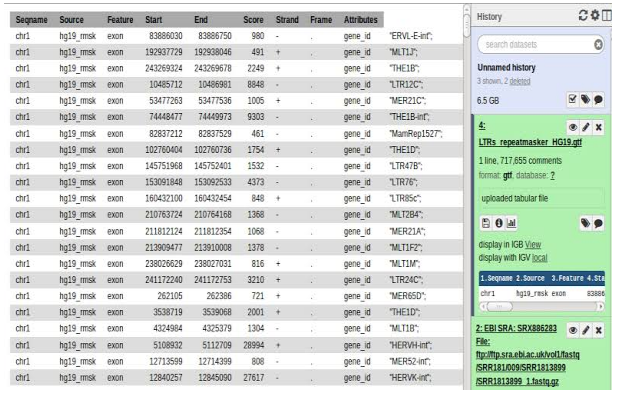
ReferenceGenome	Homo_sapiens\UCSC\hg19\Sequence\WholeGenomeFASTA				
[Regions]					
Name	Chromosome	Start	End	Upstream Probe Length	Downstream Probe Len
WASH5P-chr1-14363-14829	chr1	14363	14829	0	
WASH5P-chr1-14970-15038	chr1	14970	15038	0	
WASH5P-chr1-15796-15947	chr1	15796	15947	0	
WASH5P-chr1-16607-16765	chr1	16607	16765	0	
WASH5P-chr1-16858-17055	chr1	16858	17055	0	
WASH5P-chr1-17233-17368	chr1	17233	17368	0	
WASH5P-chr1-17606-17742	chr1	17606	17742	0	

BED Files

```
##fileformat=VCF4.2
##INFO=<ID=SVTYPE,Number=1,Type=String,
Description="Type of structure variant">
##INFO=<ID=END,Number=1,Type=Integer,
Description="End position of the variant described in this record">
#CHROM POS ID REF ALT QUAL FILTER INFO
```

```
1 160929435 rs7520618 G A . . SVTYPE=SNP;END=160929436
1 160932043 rs113387749   A . . SVTYPE=INS;END=160932043
1 160932206 rs5778188 C   . . SVTYPE=DEL;END=160932207
1 160932771 rs2256505 A G . . SVTYPE=SNP;END=160932772
1 160934077 rs2481074 T A . . SVTYPE=SNP;END=160934078
1 160934818 rs1023115 A G . . SVTYPE=SNP;END=160934819
1 160935328 . AAA TGC . . SVTYPE=SUB;END=160935331
1 160935334 rs75452934 AA TC . . SVTYPE=SUB;END=160935336
```

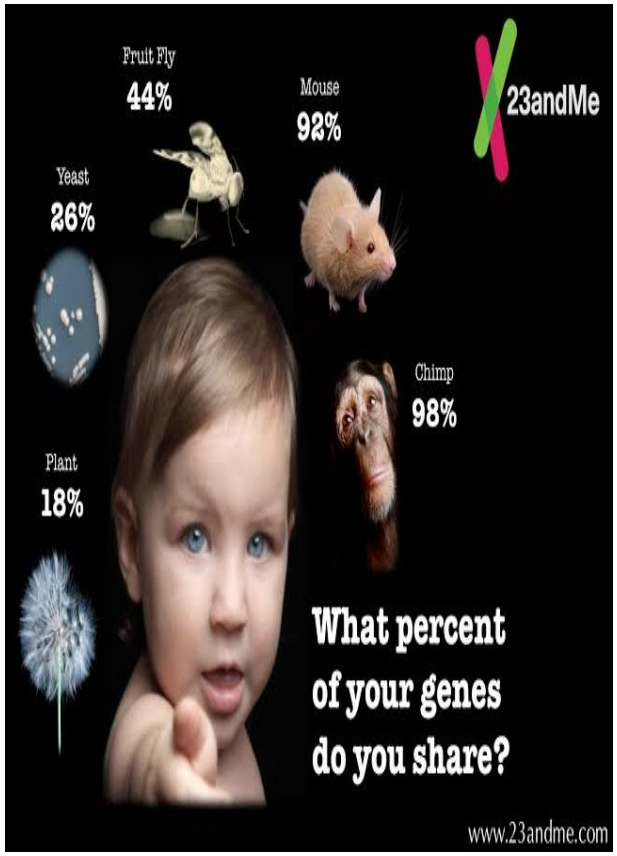
VCF Files



GTF Files

Properties of Our Data Set

- Semi-Structured
- Reference Genome – Fasta Format
  3.2 GB
  62743362 bp
- Raw Data – Fastq Format
  4.1 GB
  27999799 bp
  Sequence length - 36 bp
  GC Content – 44%
- Output File – BAM Format, VCF Format
  42 GB, 30 KB



Relationship of Human Genome with Other Species

Advantages of Hadoop

- **Hadoop is Open Source distributed data processing system**
- Based on Google's **MapReduce** architecture design
- Cheap commodity hardware for storage
- Fault tolerant distributed filesystems: **HDFS**
- Batch processing systems: **Hadoop MapReduce, Apache Hive, Apache Pig (HDD), Apache Spark (RAM)**
- Parallel SQL implementations for analytics: **Apache Hive, Cloudera Impala, Apache Spark**
- Fault tolerant distributed database: **Hbase**
- **Distributed machine learning libraries, text indexing & search**

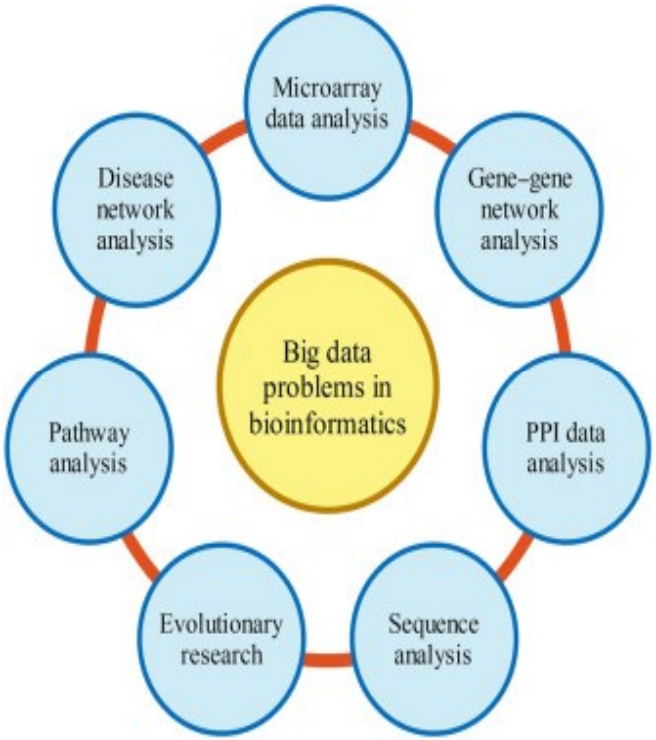
Hadoop in Different Biological Aspects

- In Cancer treatments
- In monitoring Patient Vitals
- In the Hospital Network
- In Healthcare Intelligence
- In Structural Bioinformatics –

  1) Molecular Docking

  2) Clustering of Protein-Ligand complex

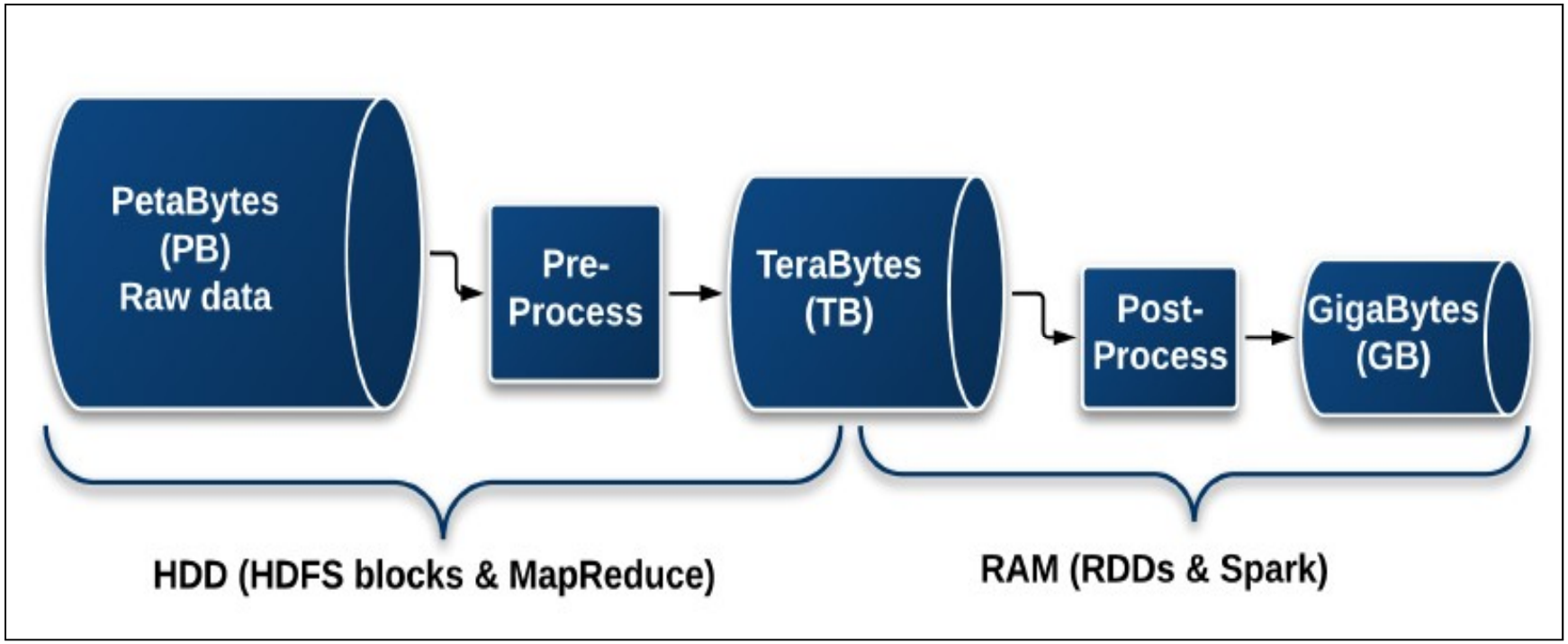
  3) Structural Alignment
- In Genomic Data Analysis



Tools used in Hadoop For Biological Data Analysis

- **Cloud Burst** – Uses Hadoop as a platform for alignment of short reads.
- **Crossbow** – Uses Hadoop for SNP genotyping from short reads.
- **Contrail** – Uses Hadoop for denovo assembly from short sequencing reads
- **Myrna** – Uses Bowtie and R/Bioconductor for calculating differential gene expression from large RNASeq data sets
- **Cloud Blast** – Uses Gene Set Enrichment Analysis in Hadoop
- **BlueSNP** - Implements GWAS statistical tests in R & executes the calculations with Apache Hadoop using MapReduce formalism.
- **HadoopBAM** – A library for processing NGS data format in parallel with both Hadoop and Spark.
- **Amazon Elastic Compute Cloud & MapReduce.**

Typical Genomics Data Analysis Using HDFS



Processing Data in main memory instead of files in hard disks = minimal I/O operations. Map/Reduce data from Petabytes to Gigabytes (million times less in the end

Project Proposal

- Genome Alignment using HADOOP-BAM
- SNP Detection using Crossbow (Bowtie+SOAPsnp) and HadoopBAM and comparing both
- Genome Wide Association Study (GWAS) using Apache HIVE across Human Genome of Different Population

SNP Detection using MapReduce Algorithm in Crossbow

- Copying the Fastq raw data and Fasta reference genome from Local File System to HDFS

↓

- Running the Crossbow pipeline in Hadoop Cluster

↓

- Crossbow's Map phase align reads with Bowtie 2 which employs a compact index of reference sequence requiring about 3 GB of memory using HG19

↓

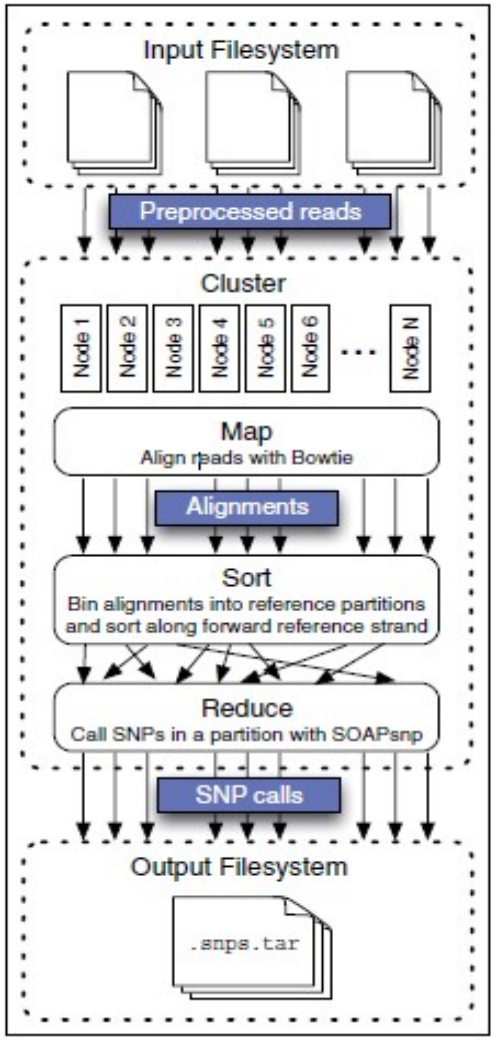
- The index is distributed to all computers in cluster via hadoop file or by instructing each node to independently obtain the index from a shared file

↓

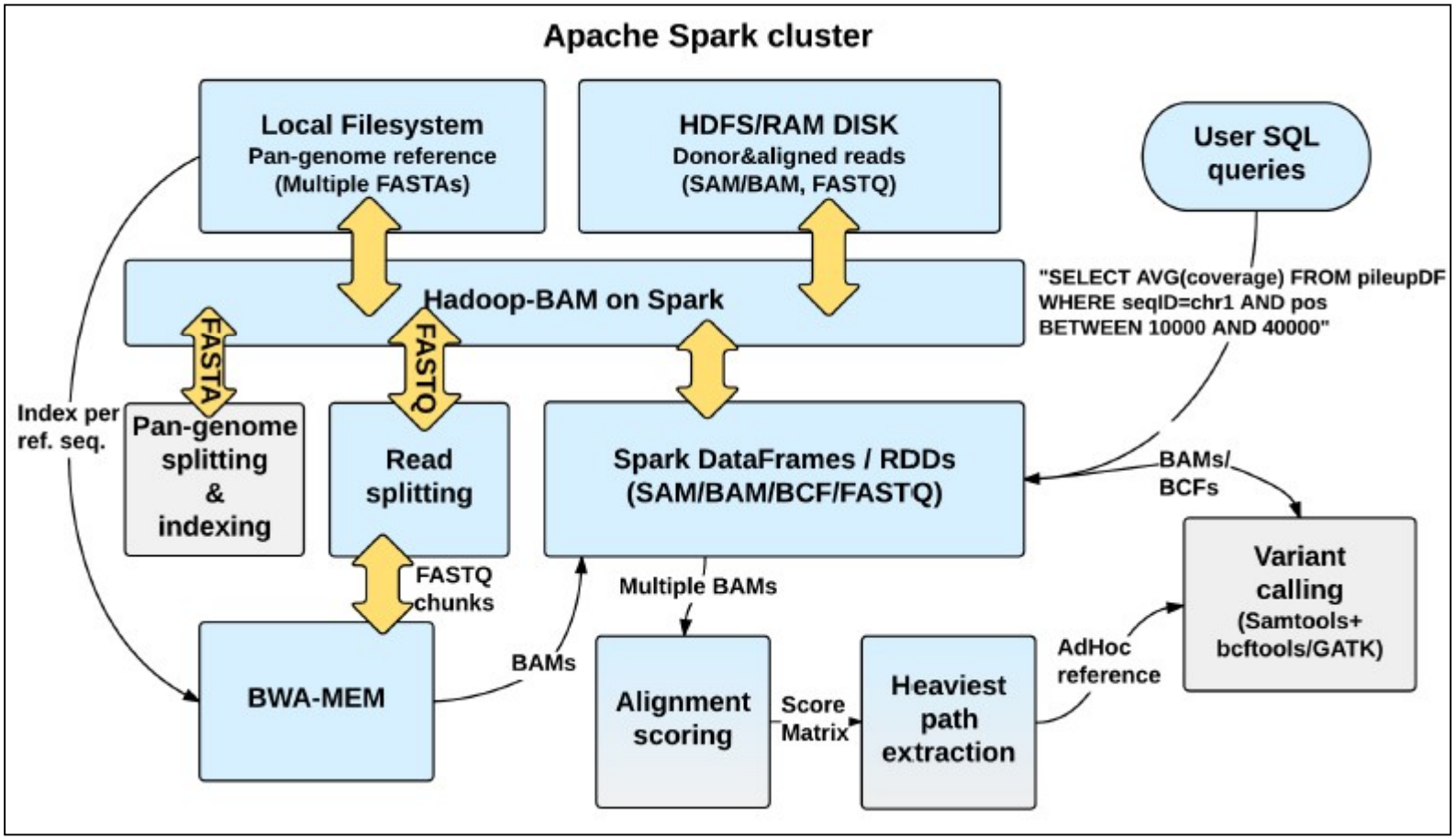
- The reduce phase performs SOAPsnp

↓

- The output of Reduce phase is SNP tuple which stored on the Clustered distributed File System which can be transferred to Local File System.

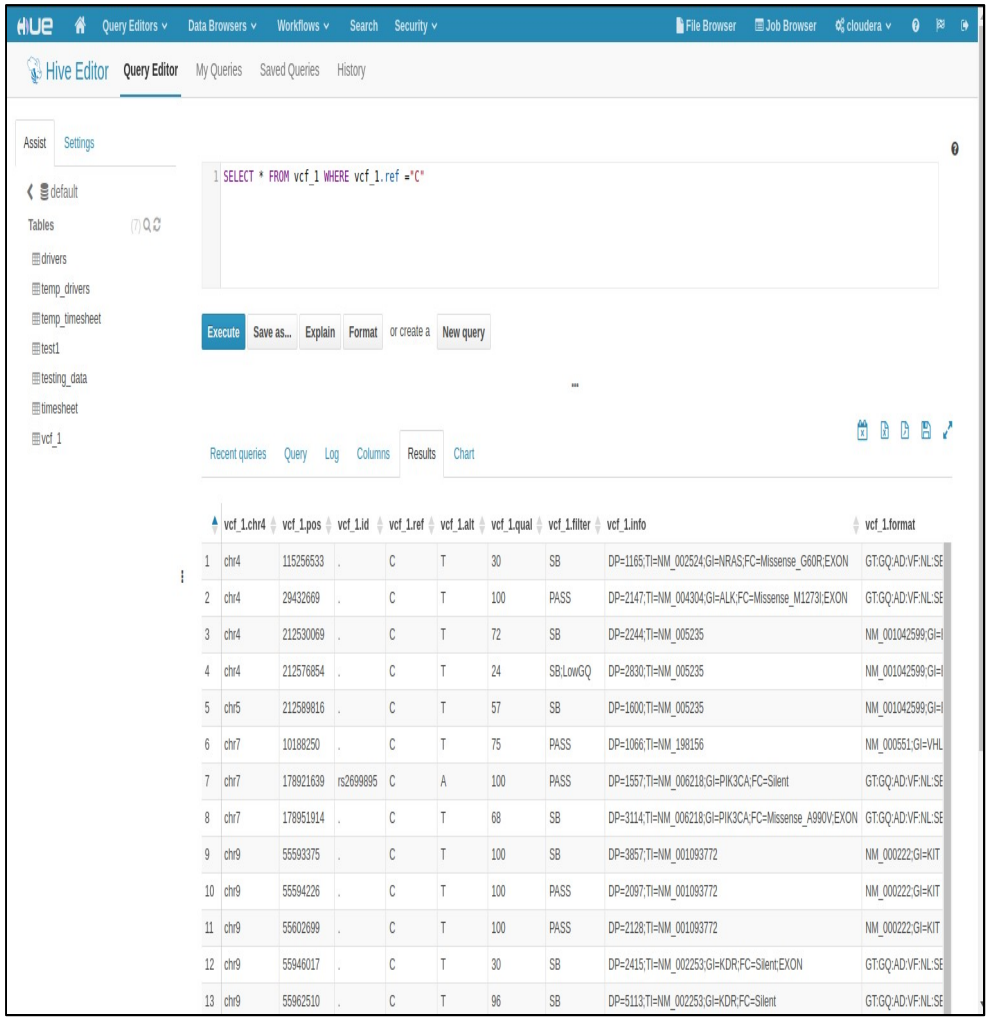


SNP Detection using HadoopBAM



Genome Wide Association Study using Apache HIVE

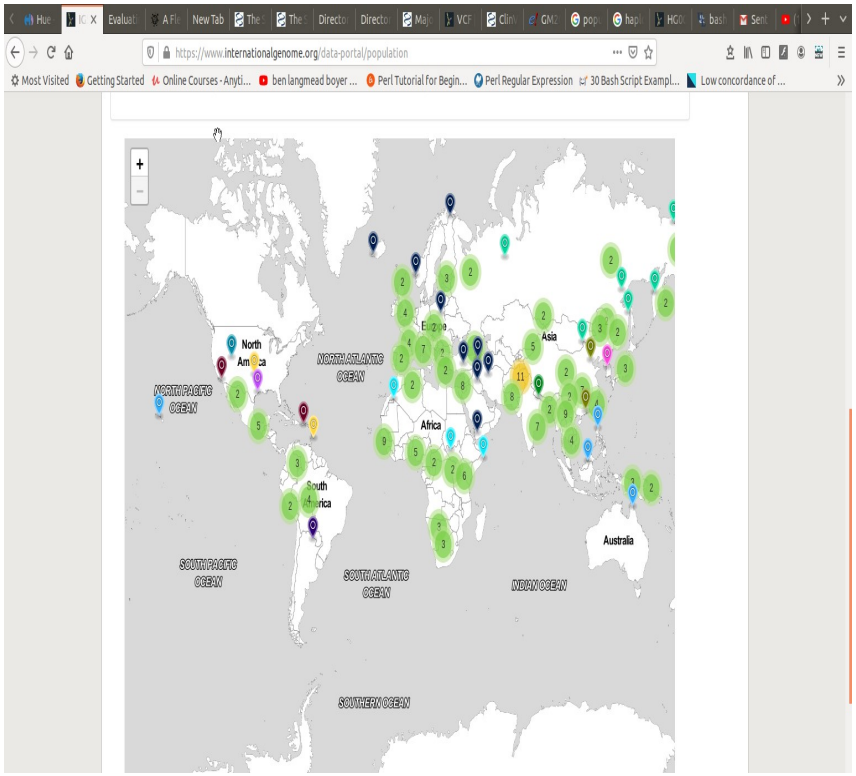
- Processing of VCF Files in Data Browser and query using Apache HIVE
- Counting the Allele Frequency
- Taking Input Data from different population and finding Genome wide association using Log odds ratio/Likelihood ratio/Chi-square test across different population

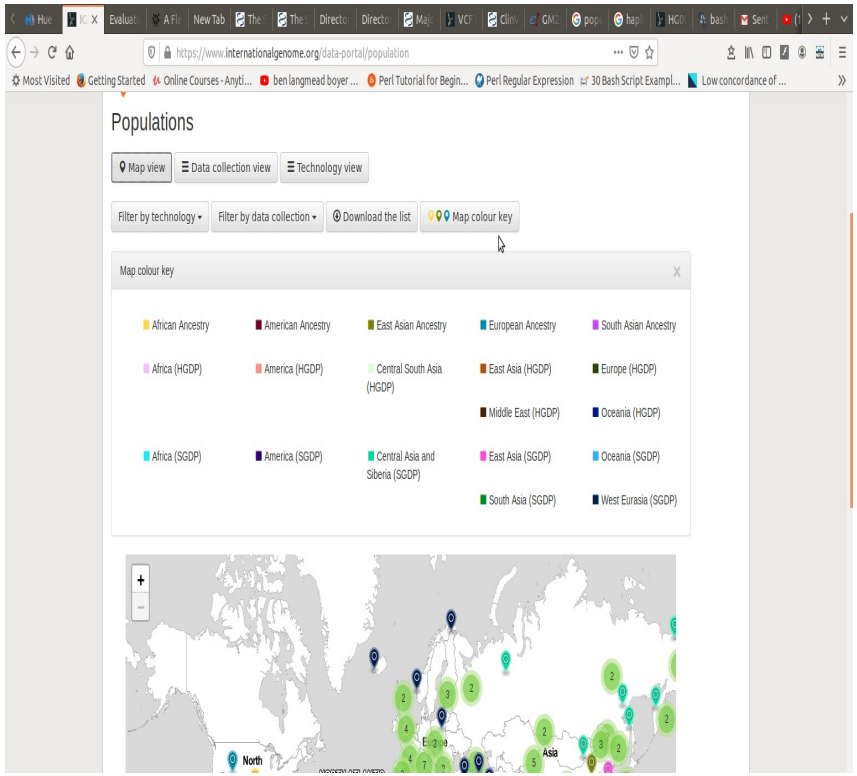


	vcf_1.chr4	vcf_1.pos	vcf_1.id	vcf_1.ref	vcf_1.alt	vcf_1.qual	vcf_1.filter	vcf_1.info	vcf_1.format
1	chr4	115256533	.	C	T	30	SB	DP=1165;TI=NM_002524;GI=NRAS;FC=Missense_G60R;EXON	GT:GQ:AD:VF:NL:SE
2	chr4	29432669	.	C	T	100	PASS	DP=2147;TI=NM_004304;GI=ALK;FC=Missense_M1273I;EXON	GT:GQ:AD:VF:NL:SE
3	chr4	212530069	.	C	T	72	SB	DP=2244;TI=NM_005235	NM_001042599;GI=I
4	chr4	212576854	.	C	T	24	SB;LowGQ	DP=2830;TI=NM_005235	NM_001042599;GI=I
5	chr5	212589816	.	C	T	57	SB	DP=1600;TI=NM_005235	NM_001042599;GI=I
6	chr7	10188250	.	C	T	75	PASS	DP=1066;TI=NM_198156	NM_000551;GI=VHL
7	chr7	178921639	rs2699895	C	A	100	PASS	DP=1557;TI=NM_006218;GI=PIK3CA;FC=Silent	GT:GQ:AD:VF:NL:SE
8	chr7	178951914	.	C	T	68	SB	DP=3114;TI=NM_006218;GI=PIK3CA;FC=Missense_A990V;EXON	GT:GQ:AD:VF:NL:SE
9	chr9	55593375	.	C	T	100	SB	DP=3857;TI=NM_001093772	NM_000222;GI=KIT
10	chr9	55594226	.	C	T	100	PASS	DP=2097;TI=NM_001093772	NM_000222;GI=KIT
11	chr9	55602699	.	C	T	100	PASS	DP=2128;TI=NM_001093772	NM_000222;GI=KIT
12	chr9	55946017	.	C	T	30	SB	DP=2415;TI=NM_002253;GI=KDR;FC=Silent;EXON	GT:GQ:AD:VF:NL:SE
13	chr9	55962510	.	C	T	96	SB	DP=5113;TI=NM_002253;GI=KDR;FC=Silent	GT:GQ:AD:VF:NL:SE

SNP Detection using Crossbow

- Downloaded fastq files from 1000 Genomes Project of different populations





Work Flow

Installed Crossbow, Bowtie, soapSNP, HadoopBAM

⇩

Indexed using Bowtie and Detected SNPs using soapSNP

```
                -T <FILE> Only call consensus on regions specified in FILE. Format: ChrName\tStart\tEnd
ibab@IBAB-PGDBD-Comp07:~/Applications/AM_Assignment/GENOMICS/20feb/AlignmentFiles$ soapsnp -B cancer_sorted.bam -o out
Authorized!
Illumina Fastq System Set
                ****************************************************************
                *                  Software name :SOAPsnp                      *
                *                        Version : v 1.05                      *
                *                    Last Update : 2011.9.25                   *
                *                         Author:Core Development Group        *
                *                                Fan Zhang & Bill Tang         *
                *                        E_mail : zhangfan@genomics.org.cn     *
                *                                 zhouguyue@genomics.org.cn    *
                *                      Copyright : BGI. All Rights Reserved.    *
                ****************************************************************
Parameters:
                -i <String> Input SORTED Soap Result or list
                -S <String> Input SORTED SAM Result or list
                -B <String> Input SORTED BAM Result or list
                -l  Specify this option will enable the alignments' filelist input
                -P <Int> Set the thread number[1]
                -d <String> Reference Sequence in fasta format
                -o <String> (<DIR> if input is file list) Output consensus file Optional Parameters:(Default in [])
                -z <Char> ASCII chracter standing for quality==0 [@]
                -g <Double> Global Error Dependency Coefficient, 0.0(complete dependent)~1.0(complete independent)[0.9]
                -p <Double> PCR Error Dependency Coefficient, 0.0(complete  dependent)~1.0(complete independent)[0.5]
                -r <Double> novel altHOM prior probability [0.0005]
                -e <Double> novel HET prior probability [0.0010]
                -t set transition/transversion ratio to 2:1 in prior probability
                -s <String> Pre-formated dbSNP information
                -2 specify this option will REFINE SNPs using dbSNPs information [Off]
                -a <Double> Validated HET prior, if no allele frequency known [0.1]
                -b <Double> Validated altHOM prior, if no allele frequency known [0.05]
                -j <Double> Unvalidated HET prior, if no allele frequency known [0.02]
                -k <Double> Unvalidated altHOM rate, if no allele frequency known [0.01]
                -u Enable rank sum test to give HET further penalty for better accuracy [Off]
                -m Enable monoploid calling mode, this will ensure all consensus as HOM  and you probably should SPECIFY
                   higher altHOM rate [Off]
                -q Only output potential SNPs. Useful in Text output mode [Off]
                -M <FILE>(<DIR> if set -l parameter) Output the quality calibration matrix;the matrix can be reused with -I
                   if you rerun the program
                -I <FILE>(<FILELIST> if set -l parameter) Input previous quality calibration matrix. It cannot be used
                   simutaneously with -M
                -L <Short> maximum length of read [45]
                -Q <Char> maximum FASTQ quality score, using ASCII chracter standing for quality[h]
                -F <Int> Output format. 0: Text; 1: GLFv2; 2: GPFv2.[0]
```

GWAS using Apache Hive – Flow Chart

- From the generated VCF files we chose only two populations – 1) Bengalis in Bangladesh
  2) British in Scotland

- Next we preprocessed the VCF files
- Randomly we chose chromosome 20 for further analysis

Preprocessing of VCF files

- Selection of lines which contain the information about SNP

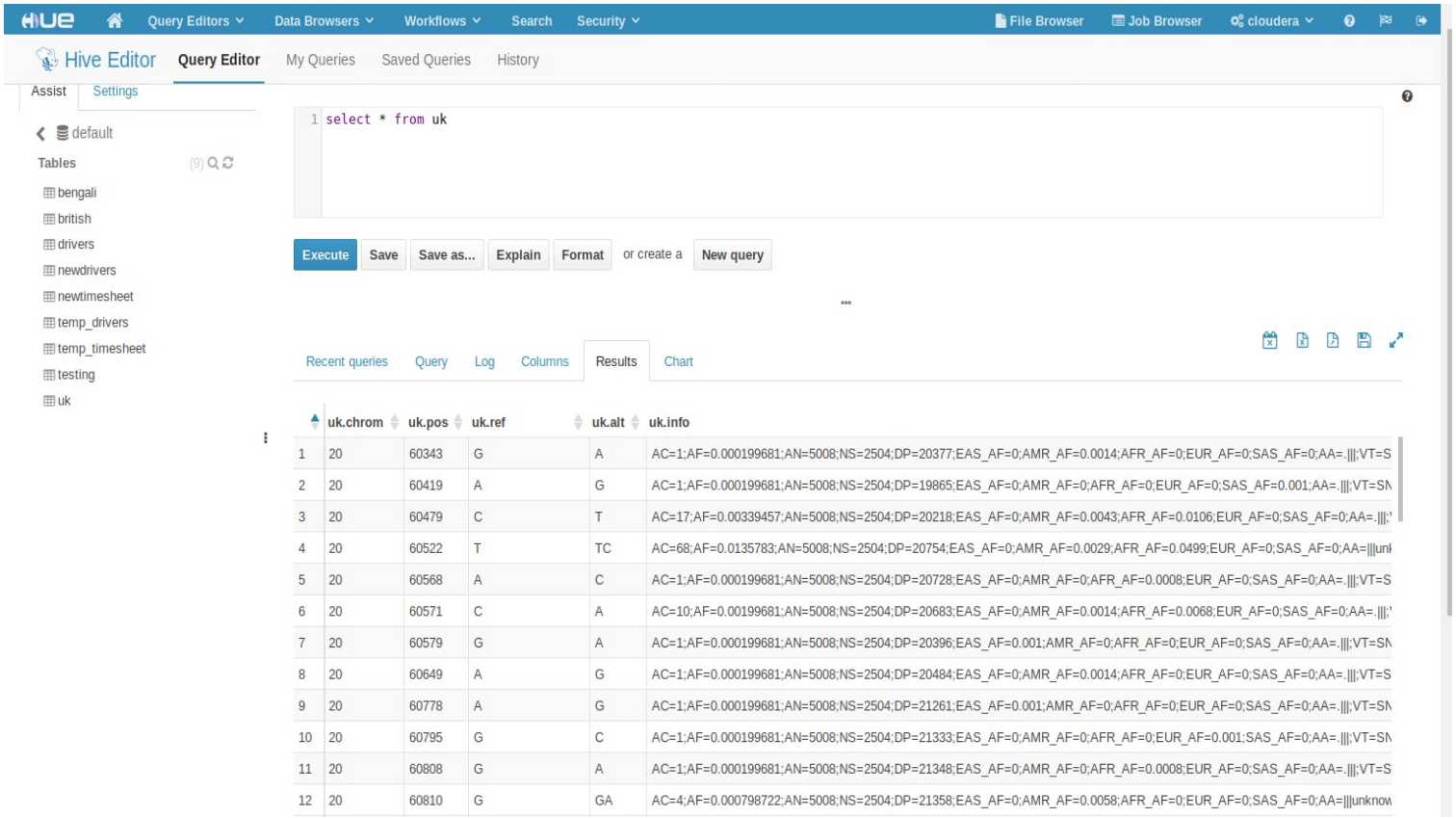
```
ibab@IBAB-PGDBD-Comp07:~/SecondSemester/VCFS$ cat ALL.chr20.phase3_shapeit2_mvnc
all_integrated_v5a.20130502.genotypes.vcf | grep "^20" > british_in_scotland.csv
```

- Extracted relevant columns : chrom, pos, ref, alt, info, format

```
ibab@IBAB-PGDBD-Comp07:~/SecondSemester/VCFS$ awk '{print $1,$2,$4,$5,$8,$9}' br
itish_in_scotland.csv > british_in_scotland_1.csv
```

Continued…

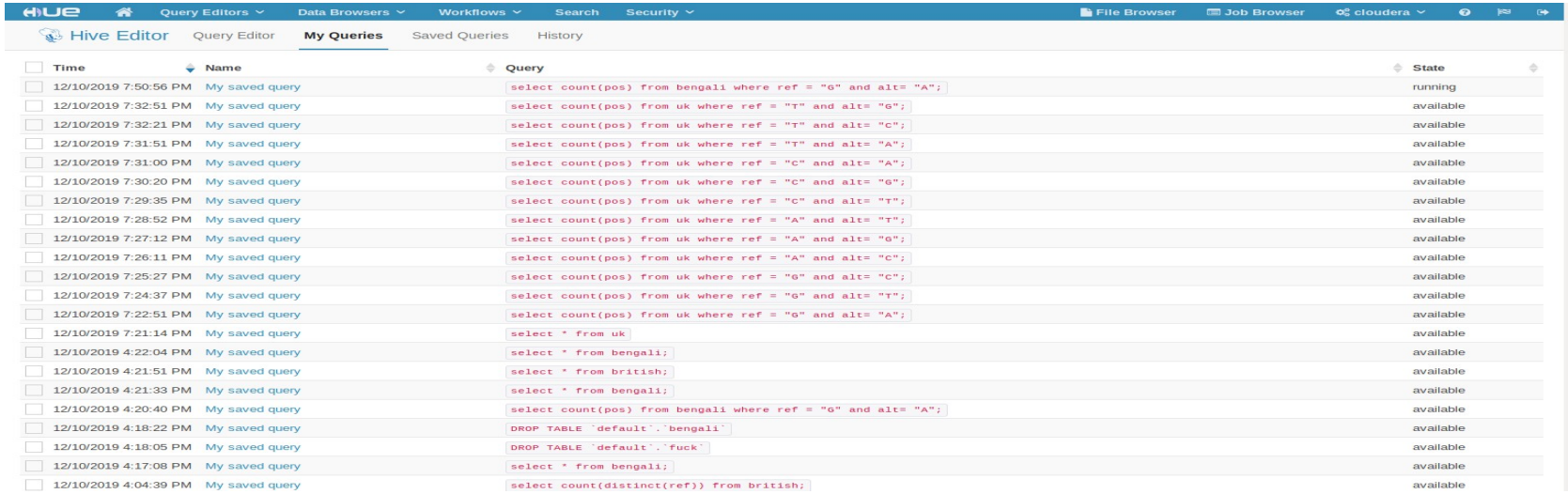
- Uploaded processed VCF files in Apache Hive



	uk.chrom	uk.pos	uk.ref	uk.alt	uk.info
1	20	60343	G	A	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=20377;EAS_AF=0;AMR_AF=0.0014;AFR_AF=0;EUR_AF=0;SAS_AF=0;AA=.|||;VT=S
2	20	60419	A	G	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=19865;EAS_AF=0;AMR_AF=0;AFR_AF=0;EUR_AF=0;SAS_AF=0.001;AA=.|||;VT=SN
3	20	60479	C	T	AC=17;AF=0.00339457;AN=5008;NS=2504;DP=20218;EAS_AF=0;AMR_AF=0.0043;AFR_AF=0.0106;EUR_AF=0;SAS_AF=0;AA=.|||
4	20	60522	T	TC	AC=68;AF=0.0135783;AN=5008;NS=2504;DP=20754;EAS_AF=0;AMR_AF=0.0029;AFR_AF=0.0499;EUR_AF=0;SAS_AF=0;AA=|||unk
5	20	60568	A	C	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=20728;EAS_AF=0;AMR_AF=0;AFR_AF=0.0008;EUR_AF=0;SAS_AF=0;AA=.|||;VT=S
6	20	60571	C	A	AC=10;AF=0.00199681;AN=5008;NS=2504;DP=20683;EAS_AF=0;AMR_AF=0.0014;AFR_AF=0.0068;EUR_AF=0;SAS_AF=0;AA=.|||
7	20	60579	G	A	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=20396;EAS_AF=0.001;AMR_AF=0;AFR_AF=0;EUR_AF=0;SAS_AF=0;AA=.|||;VT=SN
8	20	60649	A	G	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=20484;EAS_AF=0;AMR_AF=0.0014;AFR_AF=0;EUR_AF=0;SAS_AF=0;AA=.|||;VT=S
9	20	60778	A	G	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=21261;EAS_AF=0.001;AMR_AF=0;AFR_AF=0;EUR_AF=0;SAS_AF=0;AA=.|||;VT=SN
10	20	60795	G	C	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=21333;EAS_AF=0;AMR_AF=0;AFR_AF=0;EUR_AF=0.001;SAS_AF=0;AA=.|||;VT=SN
11	20	60808	G	A	AC=1;AF=0.000199681;AN=5008;NS=2504;DP=21348;EAS_AF=0;AMR_AF=0;AFR_AF=0.0008;EUR_AF=0;SAS_AF=0;AA=.|||;VT=S
12	20	60810	G	GA	AC=4;AF=0.000798722;AN=5008;NS=2504;DP=21358;EAS_AF=0;AMR_AF=0.0058;AFR_AF=0;EUR_AF=0;SAS_AF=0;AA=|||unknow

Queries in Hive

- Queried for all possible base changes : purine to purine (A -> G) , pyriminidine to pyrimidine (T ->C) , purine to pyrimidine(A ->T, A->C, G->T,G->C and vice versa)



Time	Name	Query	State
12/10/2019 7:50:56 PM	My saved query	select count(pos) from bengali where ref = "G" and alt= "A";	running
12/10/2019 7:32:51 PM	My saved query	select count(pos) from uk where ref = "T" and alt= "G";	available
12/10/2019 7:32:21 PM	My saved query	select count(pos) from uk where ref = "T" and alt= "C";	available
12/10/2019 7:31:51 PM	My saved query	select count(pos) from uk where ref = "T" and alt= "A";	available
12/10/2019 7:31:00 PM	My saved query	select count(pos) from uk where ref = "C" and alt= "A";	available
12/10/2019 7:30:20 PM	My saved query	select count(pos) from uk where ref = "C" and alt= "G";	available
12/10/2019 7:29:35 PM	My saved query	select count(pos) from uk where ref = "C" and alt= "T";	available
12/10/2019 7:28:52 PM	My saved query	select count(pos) from uk where ref = "A" and alt= "T";	available
12/10/2019 7:27:12 PM	My saved query	select count(pos) from uk where ref = "A" and alt= "G";	available
12/10/2019 7:26:11 PM	My saved query	select count(pos) from uk where ref = "A" and alt= "C";	available
12/10/2019 7:25:27 PM	My saved query	select count(pos) from uk where ref = "G" and alt= "C";	available
12/10/2019 7:24:37 PM	My saved query	select count(pos) from uk where ref = "G" and alt= "T";	available
12/10/2019 7:22:51 PM	My saved query	select count(pos) from uk where ref = "G" and alt= "A";	available
12/10/2019 7:21:14 PM	My saved query	select * from uk	available
12/10/2019 4:22:04 PM	My saved query	select * from bengali;	available
12/10/2019 4:21:51 PM	My saved query	select * from british;	available
12/10/2019 4:21:33 PM	My saved query	select * from bengali;	available
12/10/2019 4:20:40 PM	My saved query	select count(pos) from bengali where ref = "G" and alt= "A";	available
12/10/2019 4:18:22 PM	My saved query	DROP TABLE `default`.`bengali`	available
12/10/2019 4:18:05 PM	My saved query	DROP TABLE `default`.`fuck`	available
12/10/2019 4:17:08 PM	My saved query	select * from bengali;	available
12/10/2019 4:04:39 PM	My saved query	select count(distinct(ref)) from british;	available

Frequency Table

Reference Allele	Alternative Allele	Count
T	A	53024
A	T	53692
C	G	72349
G	C	71959
C	T	373871
T	C	210950
T	G	56328
A	G	219805
A	C	56018
C	A	79395
G	T	81070
G	A	377981

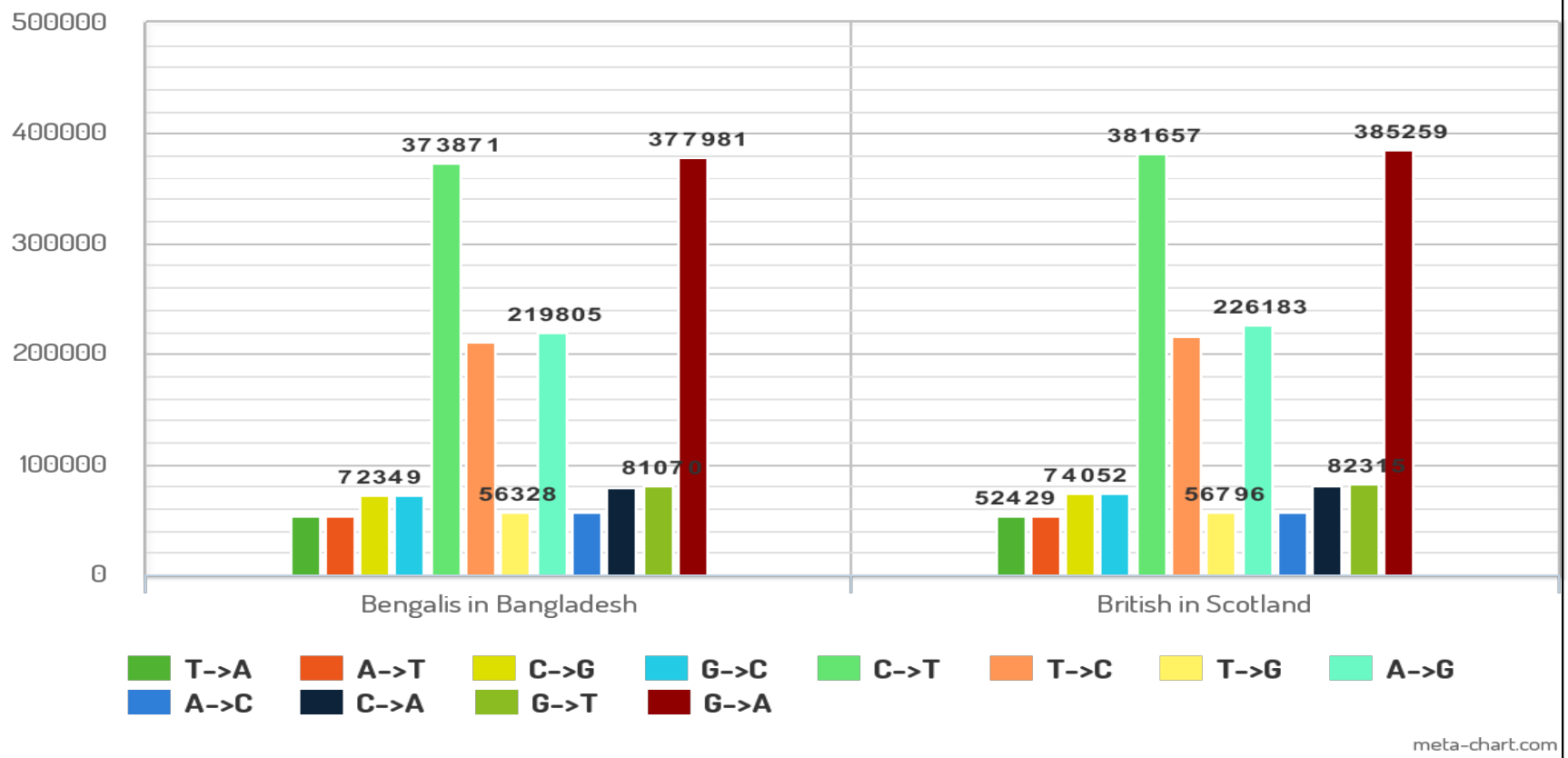
Benagali in Bangladesh

Reference Allele	Alternative Allele	Count
T	A	52429
A	T	53218
C	G	74052
G	C	73639
C	T	381657
T	C	216606
T	G	56796
A	G	226183
A	C	56717
C	A	80439
G	T	82315
G	A	385264

British in Scotland

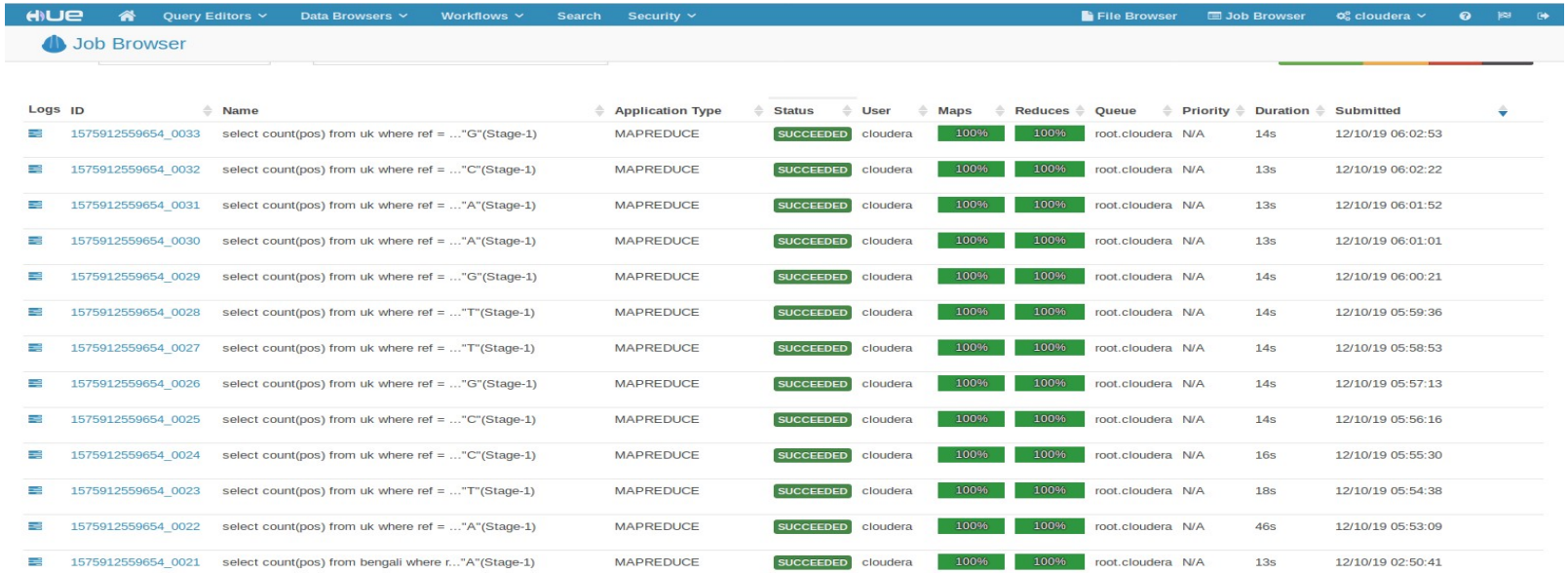
Visualization of the result

- Histogram of the VCF's of the two populations



Hive is Fast!

- Processing of files in hive was very fast as compared to running in local environment



Logs	ID	Name	Application Type	Status	User	Maps	Reduces	Queue	Priority	Duration	Submitted
	1575912559654_0033	select count(pos) from uk where ref = ..."G"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	14s	12/10/19 06:02:53
	1575912559654_0032	select count(pos) from uk where ref = ..."C"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	13s	12/10/19 06:02:22
	1575912559654_0031	select count(pos) from uk where ref = ..."A"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	13s	12/10/19 06:01:52
	1575912559654_0030	select count(pos) from uk where ref = ..."A"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	13s	12/10/19 06:01:01
	1575912559654_0029	select count(pos) from uk where ref = ..."G"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	14s	12/10/19 06:00:21
	1575912559654_0028	select count(pos) from uk where ref = ..."T"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	14s	12/10/19 05:59:36
	1575912559654_0027	select count(pos) from uk where ref = ..."T"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	14s	12/10/19 05:58:53
	1575912559654_0026	select count(pos) from uk where ref = ..."G"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	14s	12/10/19 05:57:13
	1575912559654_0025	select count(pos) from uk where ref = ..."C"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	14s	12/10/19 05:56:16
	1575912559654_0024	select count(pos) from uk where ref = ..."C"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	16s	12/10/19 05:55:30
	1575912559654_0023	select count(pos) from uk where ref = ..."T"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	18s	12/10/19 05:54:38
	1575912559654_0022	select count(pos) from uk where ref = ..."A"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	46s	12/10/19 05:53:09
	1575912559654_0021	select count(pos) from bengali where r..."A"(Stage-1)	MAPREDUCE	SUCCEEDED	cloudera	100%	100%	root.cloudera	N/A	13s	12/10/19 02:50:41

References

- **Searching for SNPs with cloud computing**

  Ben Langmead, Michael C Schatz, Jimmy Lin, Mihai Pop and Steven L Salzberg
- **The application of Hadoop in Structural Bioinformatics**

  Jamie Alnasir, Hugh P. Shanahan
- **Big Data Processing for Genomics**

  Altti Ilari Maarala, Keijo Heljanko, Andre Schumacher, Ridvan Dongelci, Luca Pireddu, Matti Niemenmaa, Aleksi Kallio, Eija Korpelainen and Gianluigi Zanetti

Thank You