

Variant calling

Detecting variants in NGS data

The Genome Analysis ToolKit (GATK)

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4th March 2014

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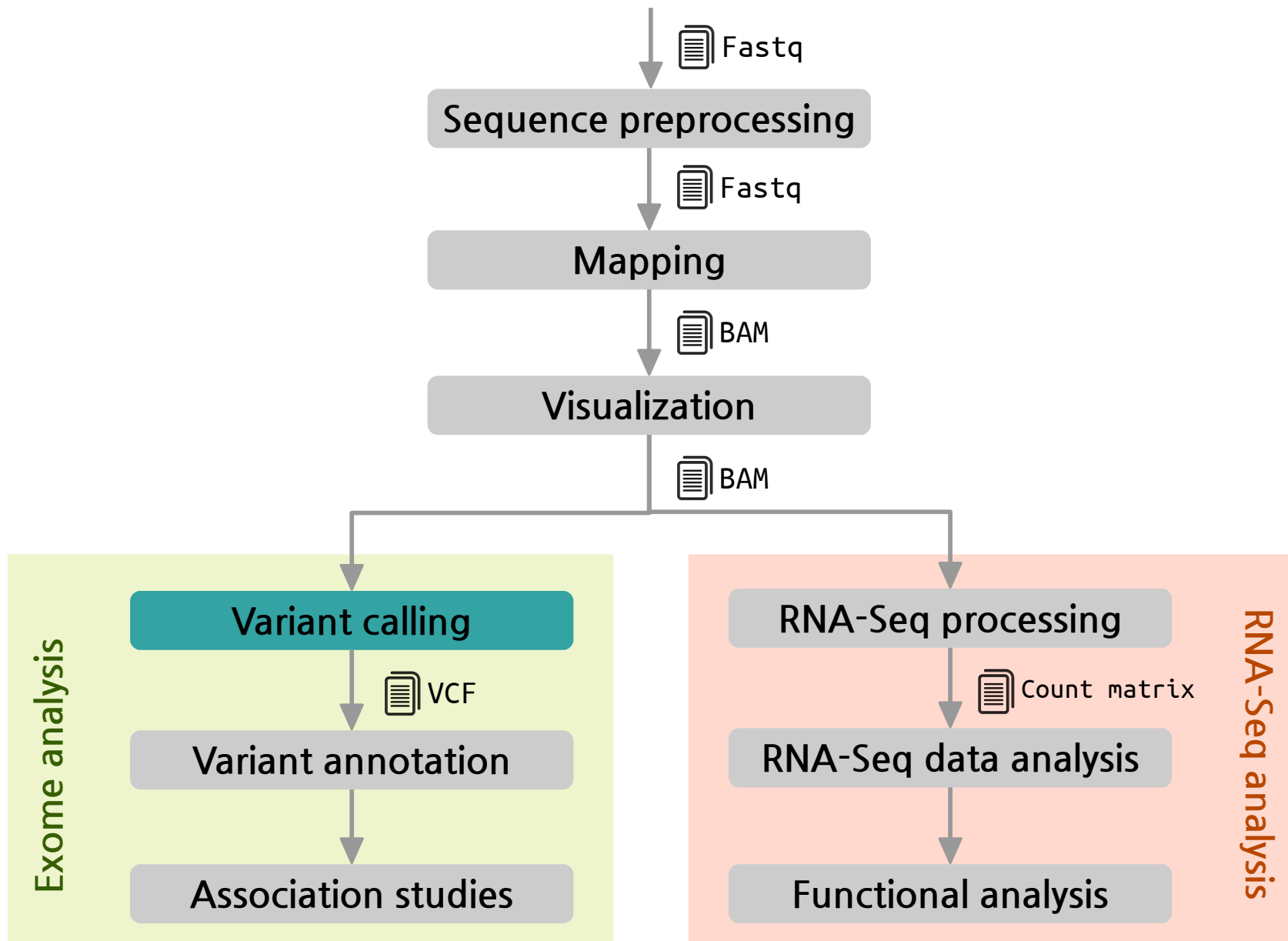
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The pipeline



Genomic variation

Terminology

- **Variant:** sequence data difference that exists between individuals in a population
- **Mutation:** molecular event that created a variant
- **Allele:** alternative state of a sequence variant
- **Genotype:** allelic state in a specific individual
 - AA homozygous or AT heterozygous at specific base
- **Polymorphism:** sequence variation that is common within a population
 - "SNP on chromosome 16 associated with obesity"

Types of Genome Sequence Variants

1. Single Nucleotide Variants (SNVs)

Single base changes, e.g., A→T.

2. Insertions-Deletions (Indels)

Consisting of one or a few bases, e.g., +ATGA, ΔT.

3. Structural Variants (SVs)

Everything else: large deletions, insertions, duplications, inversions, translocations, mobile element insertions, horizontal gene transfer

Objective

- Some variation observed in BAM files is caused by mapping and sequencing artifacts
- **Separate true variation from machine artifacts**
- Balance between:
 - **Sensitivity:** minimize false negatives (i.e.: failing to identify real variants)
 - **Specificity:** minimize false positives (i.e.: failing to reject artifacts)

Processing pipeline

1. Mark duplicates

Duplicates shouldn't be counted as additional evidence

2. Local realignment around INDELS

Reads mapping on the edges of INDELS often get mapped with mismatching bases introducing false positives

3. Base quality score recalibration (BQSR)

Calling algorithms rely on the base quality score

Quality scores provided by sequencing machines are generally inaccurate and biased

4. Variant calling

Discover variants and their genotypes

1. Mark duplicates

- All NGS **sequencing platforms are NOT single molecule sequencing** → the same DNA molecule can be sequenced several times
- **PCR** → duplicate DNA fragments in the final library
- If there is a base variation it will have **high depth support**
- Can result in **false variant calls**

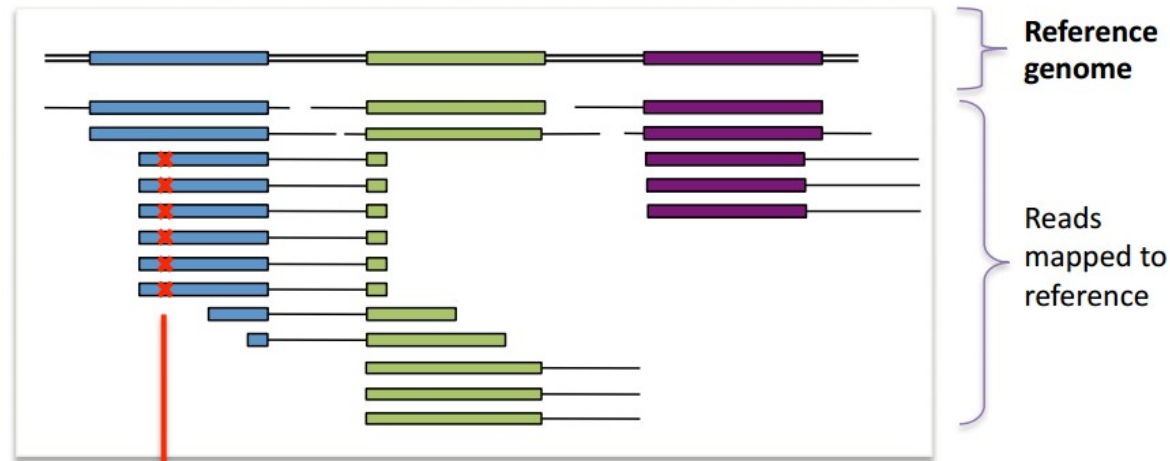
Tools

- **Samtools**: `samtools rmdup` or `samtools rmdupse`
- **Picard/GATK**: `MarkDuplicates`

1. Mark duplicates

The reason why duplicates are bad

✗ = sequencing error propagated in duplicates



After marking duplicates, the GATK will only see :

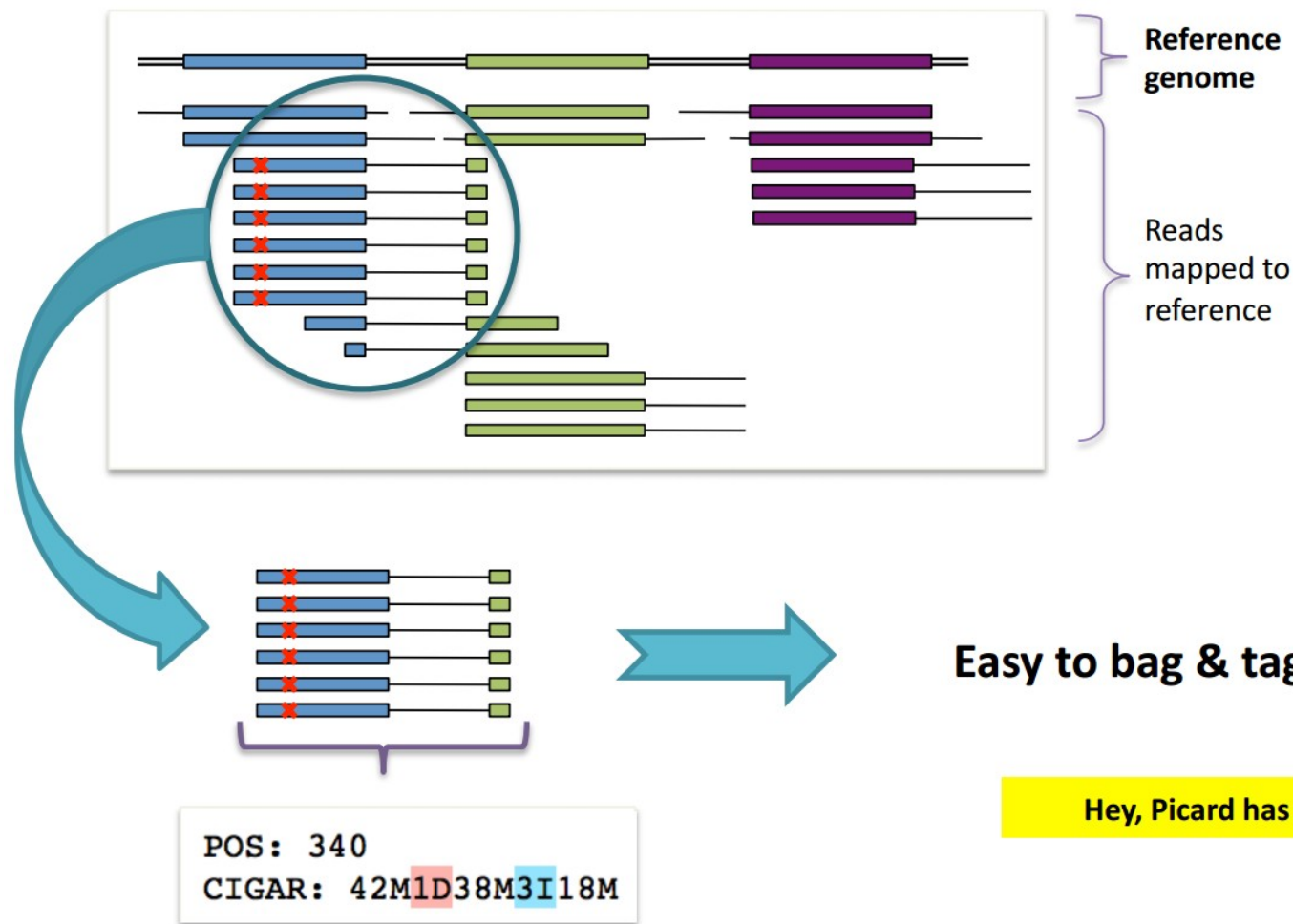


... and thus be more likely to make the right call

1. Mark duplicates

Duplicate identification

Duplicates have the same starting position and the same CIGAR string



1. Mark duplicates

Duplicated induce biased SNP calls

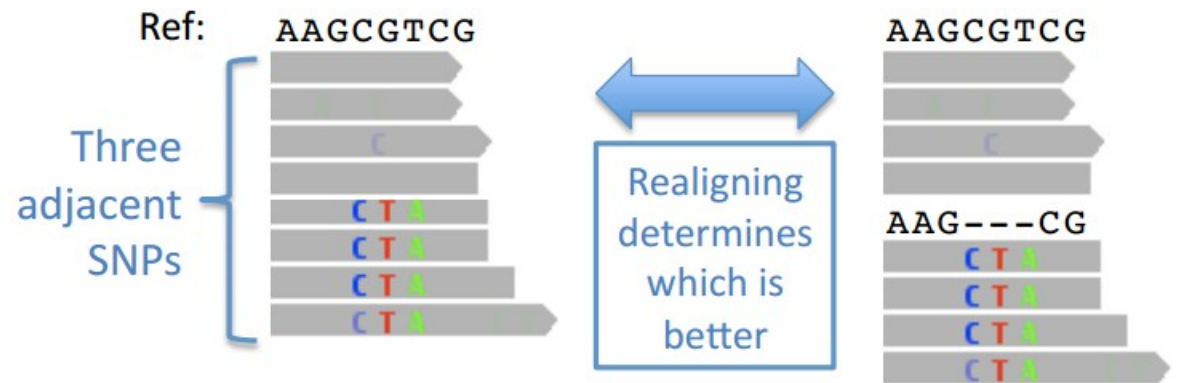


But it is not perfect...

- Does not account for **sequencing errors**
- Does not account for **natural duplicates**
- Does not account for duplicate reads with **different mapping locations**

2. Local realignment around INDELS

- Alignment algorithms tend to produce some **artifacts**
- Reads **near INDELS** are mapped with mismatches
- **Realignment** can identify the most consistent placement for these reads
 1. **Identify** problematic regions
 2. **Determine the optimal** consensus sequence
- **Minimizes mismatches** with the reference sequence
- **Refines** location of **INDELS**



3. Base quality score recalibration

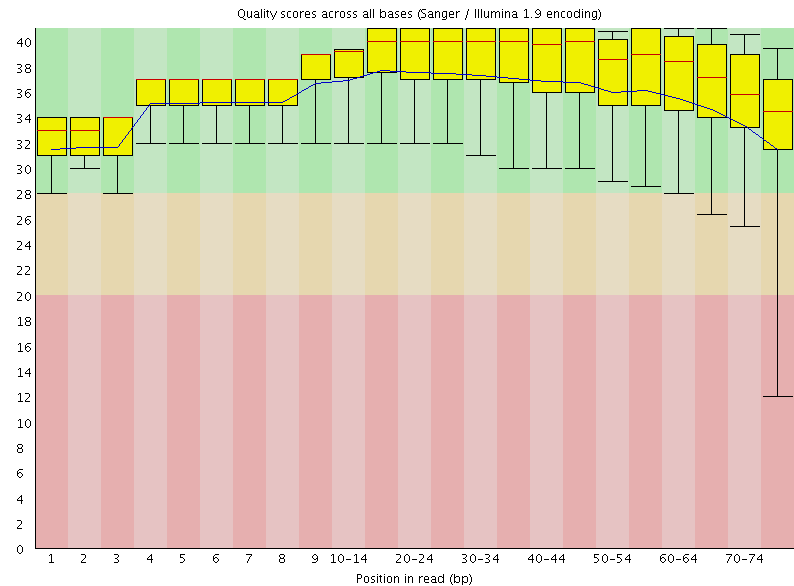
- **Calling algorithms** rely heavily on the **quality scores** assigned to the individual base calls in each sequence read
- Unfortunately, the scores produced by the machines are subject to various sources of **systematic error**, leading to over- or under-estimated base quality scores in the data

How?

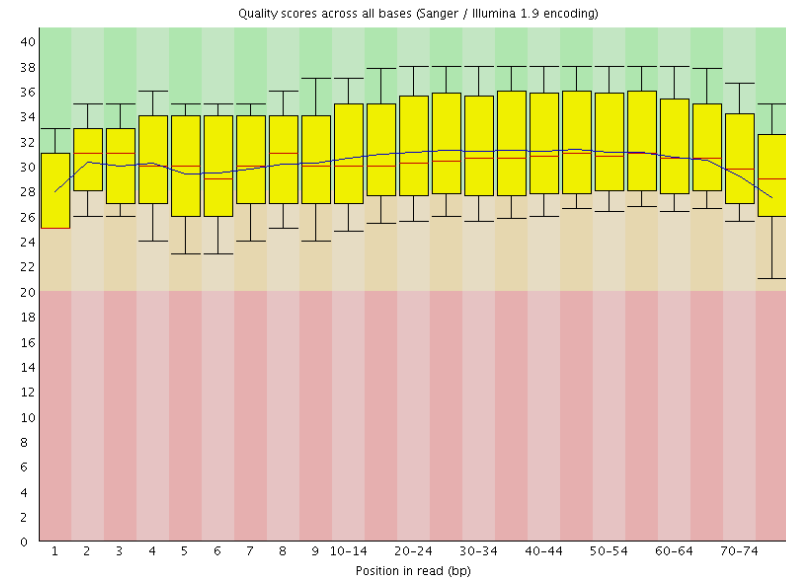
1. **Analyse covariation** among several features of a base:
 - Reported quality score
 - Position within the read
 - Preceding and current nucleotide
 2. Use a set of **known variants** (i.e.: dbSNP) to model error properties of real polymorphism and determine the **probability that novel sites are real**
 3. **Adjust** the quality scores of all reads in a BAM file
- Requires a reference genome and a catalog of known variable sites.

3. Base quality score recalibration

Before



After



Phred Quality score:

$$Q_{\text{Phred}} = -10 \log_{10} P(\text{error}).$$

A score of 20 corresponds to 1 % error rate in base calling

4. Variant calling

Variant discovery process

Steps

1. **Variant calling:** Identify the positions that differ from the reference
2. **Genotype calling:** calculate the genotypes for each sample at these sites

Initial approach

Independent base assumption

Counting the number of times each allele is observed

Evolved approach

Bayesian inference → Compute genotype likelihood

Advantages:

Provide statistical measure of **uncertainty**

Lead to **higher accuracy** of genotype calling

4. Variant calling

Two different methods

UnifiedGenotyper

Call **SNPs and indels separately** by considering each variant locus independently

Accepts any ploidy

Pooled calling

High sample numbers

HaplotypeCaller

Call SNPs, indels, and some SVs **simultaneously** by performing a local de-novo assembly

More accurate, especially for indels

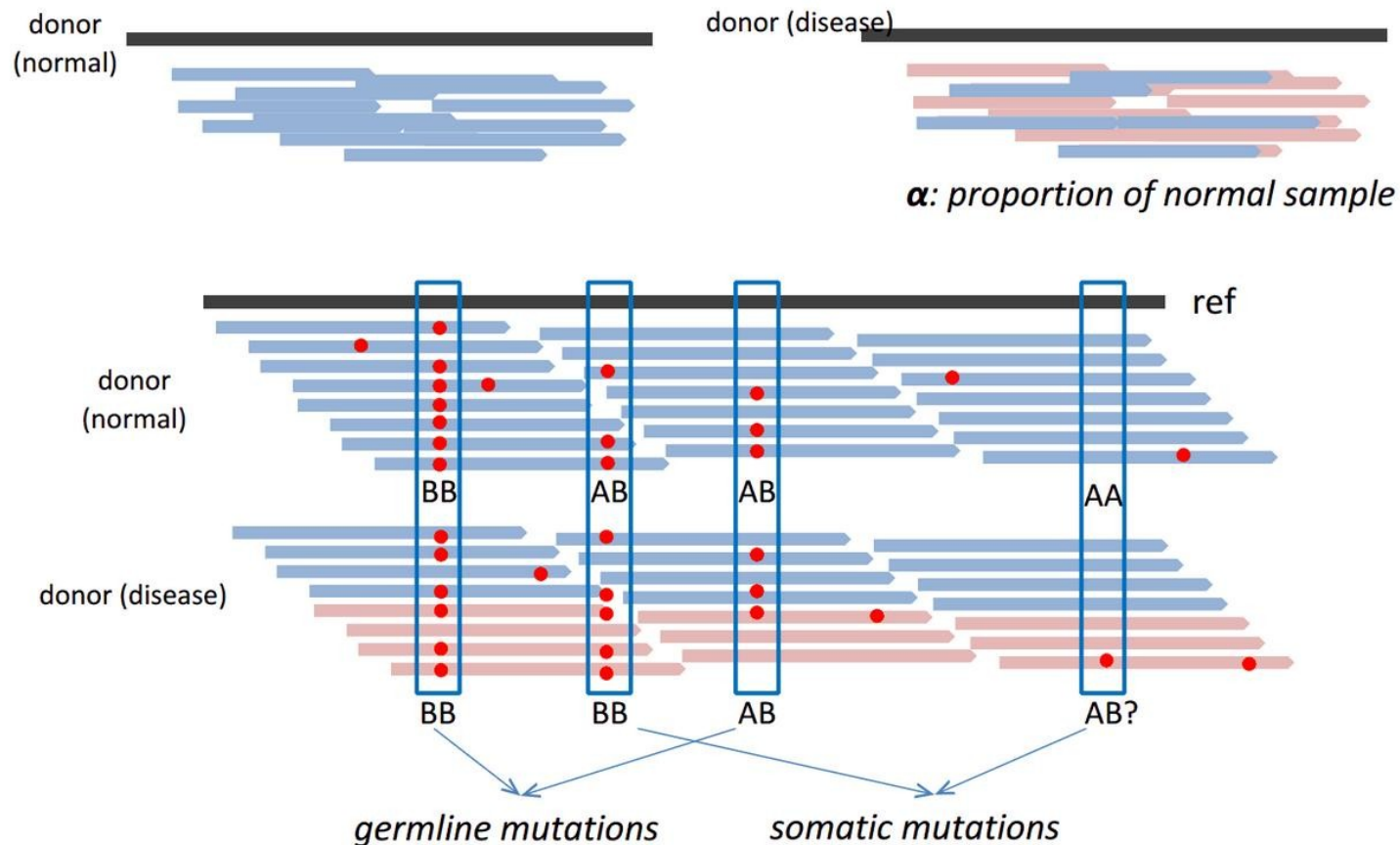
Will eventually replace UG

Somatic calling

Detenting somatic SNVs in cancer

Challenges:

- Somatic variants occur at low frequency in genome
- Most tumors are impure and heterogeneous



VCF file format

- Specification defined by the 1000 genomes (current version 4.2):
<http://www.1000genomes.org/wiki/Analysis/Variant%20Call%20Format/vcf-variant-call-format-version-41>
- Commonly **compressed and indexed** with bgzip/tabix
- Single-sample or multi-sample VCF

```
##fileformat=VCFv4.1
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a6e0c7f379d618ff66beb2da,species="Homo sapiens",taxonomy=x>
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT NA000001 NA000002 NA000003
20 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2 GT:GQ:DP:HQ 0|0:48:1:51,51 1|0:48:8:51,51 1/1:43:5:.,.
20 17330 . T A 3 q10 NS=3;DP=11;AF=0.017 GT:GQ:DP:HQ 0|0:49:3:58,50 0|1:3:5:65,3 0/0:41:3
20 1110696 rs6040355 A G,T 67 PASS NS=2;DP=10;AF=0.333,0.667;AA=T;DB GT:GQ:DP:HQ 1|2:21:6:23,27 2|1:2:0:18,2 2/2:35:4
20 1230237 . T . 47 PASS NS=3;DP=13;AA=T GT:GQ:DP:HQ 0|0:54:7:56,60 0|0:48:4:51,51 0/0:61:2
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9;AA=G GT:GQ:DP 0/1:35:4 0/2:17:2 1/1:40:3
```

VCF file format

```
##fileformat=VCFv4.1
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a6e0c7f379d618ff66beb2da,species="Homo sapiens",taxonomy=x>
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
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20 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2 GT:GQ:DP:HQ 0|0:48:1:51,51 1|0:48:8:51,51 1/1:43:5:.,.
20 17330 . T A 3 q10 NS=3;DP=11;AF=0.017 GT:GQ:DP:HQ 0|0:49:3:58,50 0|1:3:5:65,3 0/0:41:3
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20 1230237 . T . 47 PASS NS=3;DP=13;AA=T GT:GQ:DP:HQ 0|0:54:7:56,60 0|0:48:4:51,51 0/0:61:2
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9;AA=G GT:GQ:DP 0/1:35:4 0/2:17:2 1/1:40:3
```

- CHROM: chromosome
- POS: position
- ID: identifier
- REF: reference base(s)
- ALT: non-reference allele(s)
- QUAL: quality score of the calls (phred scale)
- FILTER: "PASS" or a filtering tag
- INFO: additional information
- FORMAT: describes the information given by sample

INFO column

INFO column: semicolon-separated fields. `<key>=<data>[,data]`

Some reserved (but optional) keys:

- AA ancestral allele
- AC allele count in genotypes, for each ALT allele, in the same order as listed
- AF allele frequency
- CIGAR cigar string describing how to align an alternate allele to the reference allele
- DB dbSNP membership
- MQ RMS mapping quality, e.g. MQ=52
- MQ0 Number of MAPQ == 0 reads covering this record
- NS Number of samples with data
- SB strand bias at this position
- SOMATIC indicates that the record is a somatic mutation, for cancer genomics
- VALIDATED validated by follow-up experiment

Software

Software	Available from	Calling method	Prerequisites	Comments	Refs
SOAP2	http://soap.genomics.org.cn/index.html	Single-sample	High-quality variant database (for example, dbSNP)	Package for NGS data analysis, which includes a single individual genotype caller (SOAPsnp)	15
realSFS	http://128.32.118.212/thorfinn/realSFS/	Single-sample	Aligned reads	Software for SNP and genotype calling using single individuals and allele frequencies. Site frequency spectrum (SFS) estimation	-
Samtools	http://samtools.sourceforge.net/	Multi-sample	Aligned reads	Package for manipulation of NGS alignments, which includes a computation of genotype likelihoods (samtools) and SNP and genotype calling (bcftools)	53
GATK	http://www.broadinstitute.org/gsa/wiki/index.php/The_Genome_Analysis_Toolkit	Multi-sample	Aligned reads	Package for aligned NGS data analysis, which includes a SNP and genotype caller (Unified Genotyper), SNP filtering (Variant Filtration) and SNP quality recalibration (Variant Recalibrator)	32,33
Beagle	http://faculty.washington.edu/browning/beagle/beagle.html	Multi-sample LD	Candidate SNPs, genotype likelihoods	Software for imputation, phasing and association that includes a mode for genotype calling	42
IMPUTE2	http://mathgen.stats.ox.ac.uk/impute/impute_v2.html	Multi-sample LD	Candidate SNPs, genotype likelihoods	Software for imputation and phasing, including a mode for genotype calling. Requires fine-scale linkage map	44
QCall	ftp://ftp.sanger.ac.uk/pub/rd/QCALL	Multi-sample LD	'Feasible' genealogies at a dense set of loci, genotype likelihoods	Software for SNP and genotype calling, including a method for generating candidate SNPs without LD information (NLDA) and a method for incorporating LD information (LDA). The 'feasible' genealogies can be generated using Margarita (http://www.sanger.ac.uk/resources/software/margarita)	54
MaCH	http://genome.sph.umich.edu/wiki/Thunder	Multi-sample LD	Genotype likelihoods	Software for SNP and genotype calling, including a method (GPT_Freq) for generating candidate SNPs without LD information and a method (thunder_glf_freq) for incorporating LD information	-

A more complete list is available from <http://seqanswers.com/wiki/Software/list>. LD, linkage disequilibrium; NGS, next-generation sequencing.

GATK (Genome Analysis ToolKit)

<http://www.broadinstitute.org/gatk/>

- Probabilistic method: **Bayesian estimation** of the most likely genotype
- Calculates many **parameters** for each position of the genome
- SNP and INDEL calling
- Used in **many NGS projects**, including the 1000 Genomes Project, The Cancer Genome Atlas, etc.
- Base quality recalibration
- INDEL realignment
- Uses standard input and output files
- **Multi-sample** calling

GATK prerequisites

- Requires Java (<http://www.oracle.com/technetwork/java/javase/downloads/index.html>)

- Check your java version

```
java -version
```

GATK \geq 2.6 → Requires Java version 1.7

- Picard

- Website: <http://picard.sourceforge.net/>
- Go to Download page and select
[Download picard-tools-1.108.zip \(47.0 MB\)](#)

- Testing:

```
java -jar AddOrReplaceReadGroups.jar -h
```

- Usage

```
java -jar <ToolName> [options]
```

General Information

[FAQ](#)

[Download Page](#)

[Getting help](#)

[Picard SourceForge Project Page](#)

[SAMTools Home Page](#)

[SAM Format Specification](#)

[SAMTools mailing Lists](#)

[SVN Browse](#)


[Explain SAM Flags](#)

[Description of output of metrics programs](#)

GATK installation

- GATK 2.8 download

<http://www.broadinstitute.org/gatk/>

- We need to register before download
- Go to Downloads and click 
- Accept the license agreement
- Extract the file in the applications folder

You must be logged into the forums to proceed

You do not seem to be logged into the forums

Register

Login Here »

- Check if GATK is working

Show GATK help

```
java -jar GenomeAnalysisTK.jar -h
```

- Usage

```
java -jar GenomeAnalysisTK.jar -T <ToolName> [arguments]
```

MuTect installation

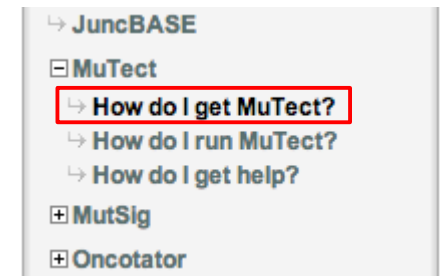
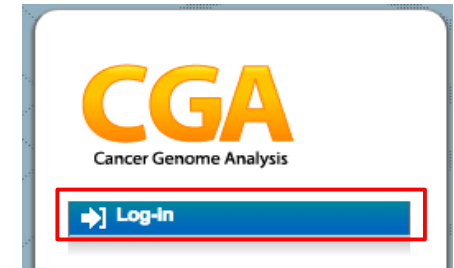
- MuTect download

<http://www.broadinstitute.org/cancer/cga/mutect>

- Click *Log-in* and go to the *Create new account* tab
- Fill the form
- Go to *How do I get mutect* and accept the license agreement
- Download the latest version

[muTect-1.1.4-bin.zip](#)

- Extract the file in the applications folder



- Check if MuTect is working

```
java -jar muTect-1.1.4.jar -h
```

- Usage

```
java -jar muTect-1.1.4.jar --analysis_type MuTect [arguments]
```


THANK YOU.