
Variant Calling (using High-throughput Sequencing Data)

Autumn 2016

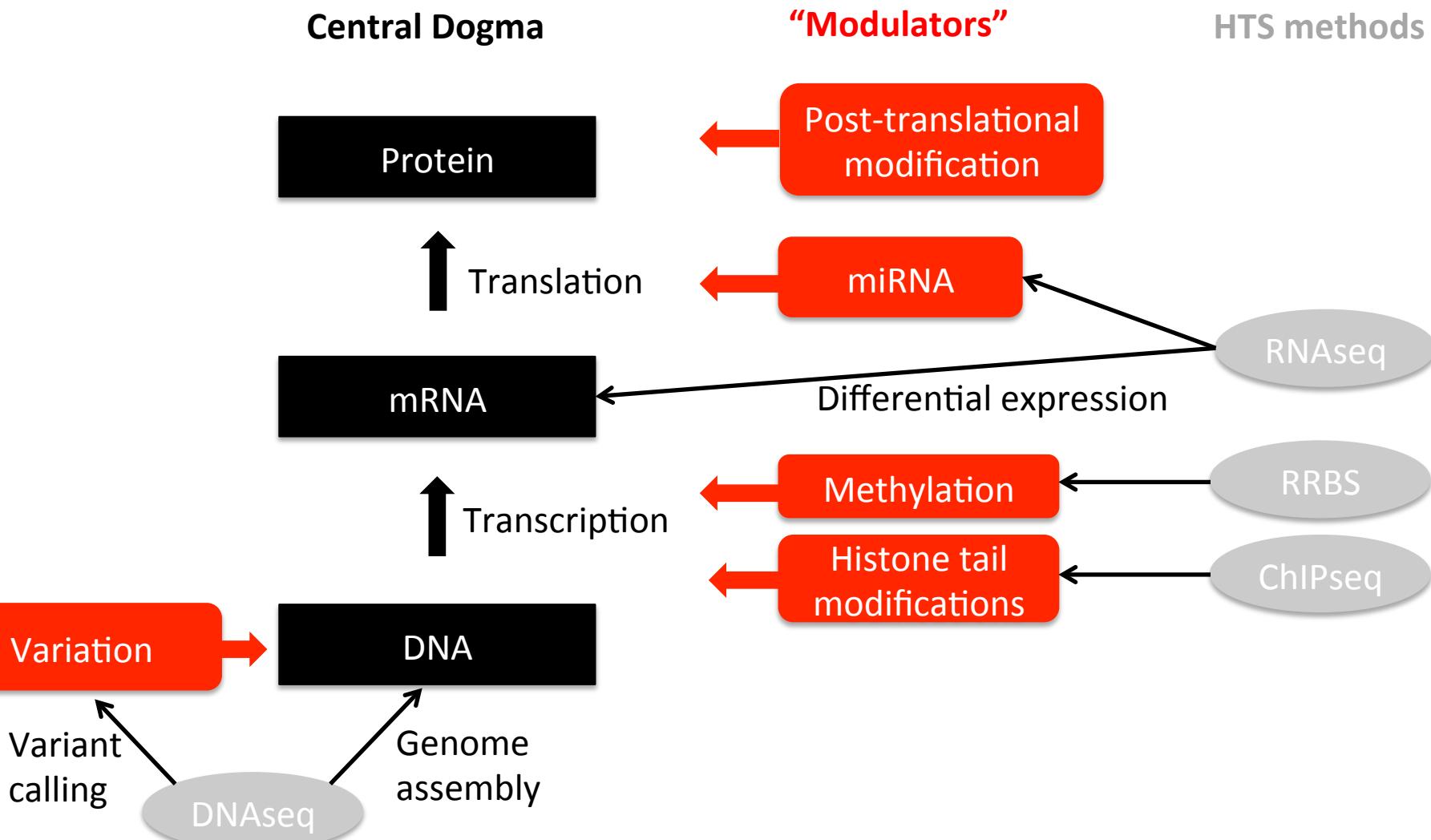
Gigsaw from University of Dundee

- Four people in each group
- Set up the reference sequence: both forward and reverse (reverse complement)
- Each person takes 10 reads. **Notice that reads are reverse complemented on the back. So use the side that is most convenient.**
- Map individually in parallel: two persons can map to forward and two to reverse.
- Then combine the reads to variant call together.
- In 10 mins, I want to know what you have found out

Gigsaw thoughts....

- Did you find some other interesting positions?
- Did all reads map perfectly
- Could this be a diploid organism?
- What if you had only had:
 - one of the references?
 - one side of the read?

Central dogma and HTS



Common concepts and themes across modules

- Technical / bioinformatic
 - Study design (RNA-seq, Statistical genomics)
 - Mapping principles (Genome assembly, Gene expression, Variant calling)
 - Alignment principles (Genome assembly and particularly variant calling)
 - Alternative splicing (Gene expression, variant calling)
 - Model system vs non-model system organisms
- The practice of bioinformatics / computational biology (!!! relevant for all modules !!!)
 - Reproducibility
 - Best practices
 - Testing (in the sense of trying code on a toy dataset where output is known)
 - Documenting
 - Statistics and hypothesis testing
 - Summary statistics and visualisation
 - Sanity checking / validation of results

ABOUT THE COURSE

INF-BIOX121

INF-BIOX121



- The tough challenges:
 - High Throughput Sequencing
 - Biological Applications
 - Informatics
- What is the secret for 18 hours with me
 - to be fun for you?
 - to be fun for me?
 - you to learn as much as possible?
- An attitude that works well in all walks of life
 - take initiative for problem solving
 - then ask for help

Who is teaching?

- People
 - Tim – bioinformatics – HTS since 2009
 - Even and Srinidhi – both took the course last year
- What we know about HTS
- I have run this course many times
 - its going not going to be easy
 - its probably going to be messy
 - but you will go away having learnt a lot, we hope ☺

Our goal for the participants

- Finish the course with an understanding of all major concepts
- Know how to run a variant calling pipeline
- Ready to make informed choice about whether you may need a simpler or more complex pipeline
- Focus is on Variant Calling and functional annotation
 - Previous courses have expressed need for more downstream analysis
 - So we have included more of this
- You might experience some overlap with other modules of the course, but repetition can be beneficial



Biologist advice to a biologist



- 1st advice: DON'T PANIC
2nd advice: DON'T PANIC
3rd advice: DON'T
- Do the unix part of tutorial of Unix and perl primer for biologists:
http://korflab.ucdavis.edu/Unix_and_Perl/, alternatively:
 - http://linuxcommand.org/learning_the_shell.php#contents
 - <http://www.tuxfiles.org/linuxhelp/cli.html>

You are not the first to have problems

- search for it on the net
- or, if you can't find the answer, ask in a forum

- Learn to write a very simple script
- Make a list of your favourite commands as you learn them.

Often when something is difficult to understand it is often either because:

- It is not clear what is being done
- Or because it is not clear why it should be done

So stop me and ask if the WHAT or the WHY is unclear!!!

Some thoughts about scientific problems vs. techniques

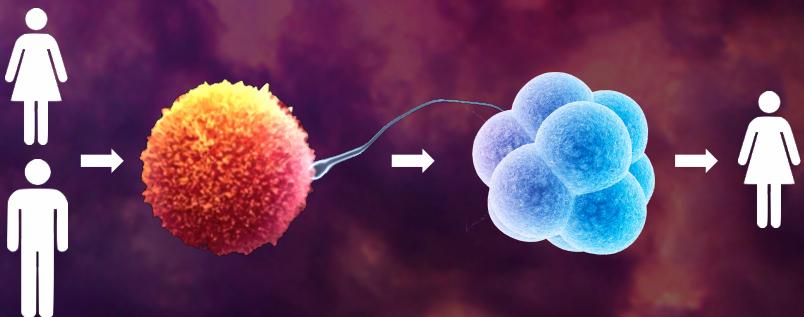
- Always keep in mind what the basic goal is and what the basic issues are with attaining that goal.
- Learn to switch from the broad picture to the details and back again.
- In my opinion it is mistake to focus too much on specific techniques. Become good at different techniques, but learn them because they help you solve problems.
- Don't go looking for things you can apply a technique to or at least be careful to not do only this.
 - Antony van Leeuwenhoek is a good counter-example

An exception to not focussing on techniques
Antony van Leeuwenhoek (1632-1723)





Humans and other multicellular organisms



A reproducing system which is:

- * Self-assembling
- * Self-repairing
- * Self-operating
- * Self-upgrading
- * Self-aware
- * Social and spiritual

The full information underlying this system is stored in the DNA of EVERY cell

Even more amazing than what we are, is
the unlikely story of our evolution?

An interesting digression on the greater
scheme of things

The Fermi paradox

“Where are all the extra-terrestrials”

The Drake equation

$$N = R \times f_p \times n_e \times f_l \times f_i \times f_c \times L$$

N = The number of civilizations in our galaxy with which communication might be possible

R = The number of stars in our galaxy

20 bn

f_p = The fraction of those stars that have planets

1

n_e = The average number of planets that can potentially support life per star that has planets

0.25

f_l = The fraction of planets that could support life that actually develop life at some point

1

f_i = The fraction of planets with life that actually go on to evolve intelligent life (civilizations)

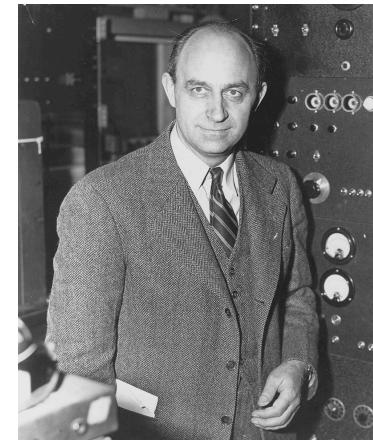
?

f_c = The fraction of civilizations that develop a technology that releases detectable signs of their existence into space

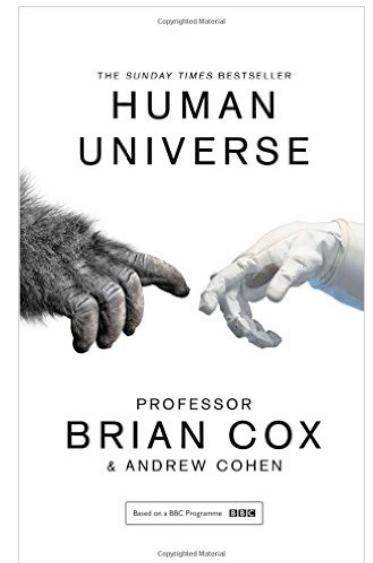
1

L = The length of time for which such civilisations release detectable signals into space

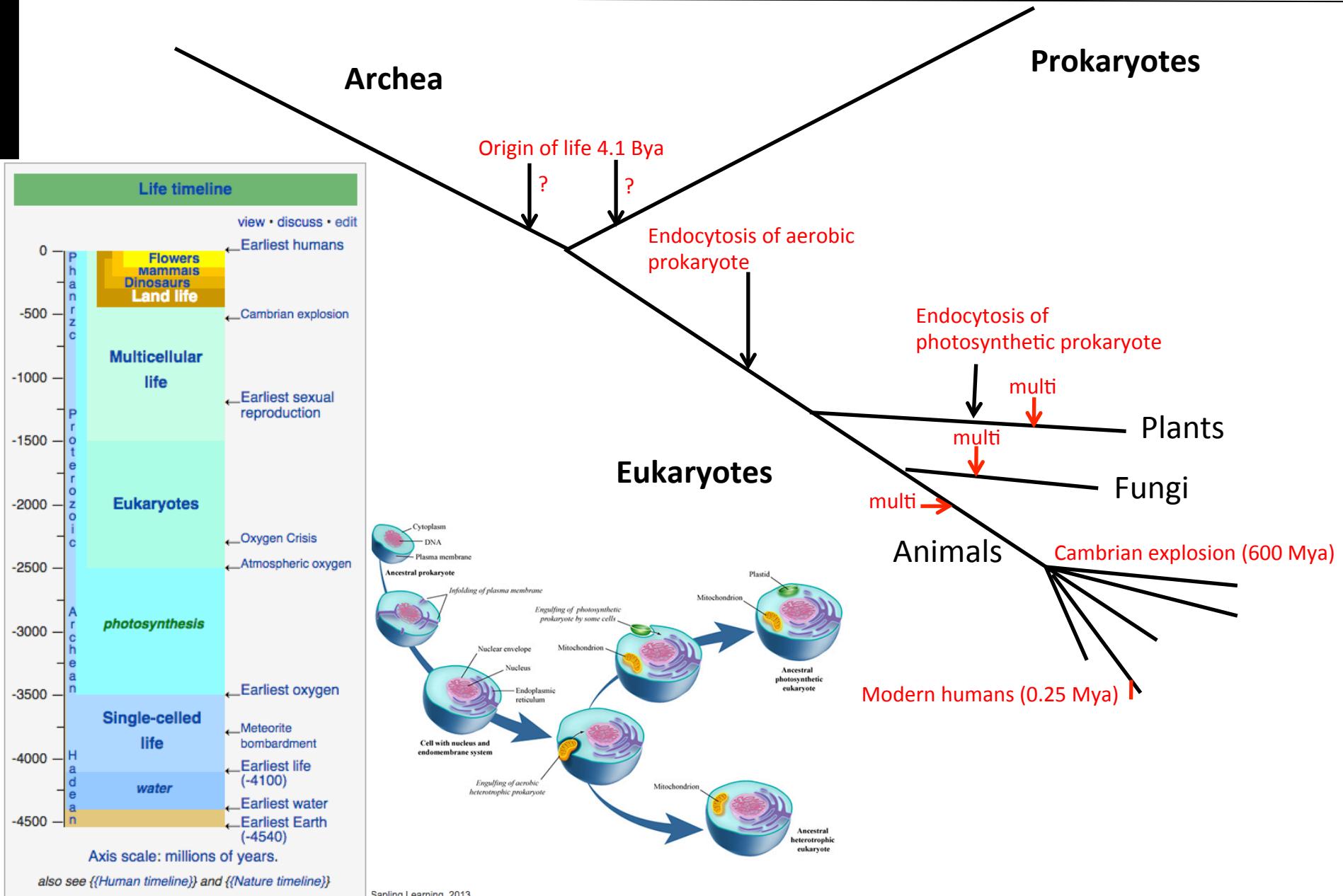
?



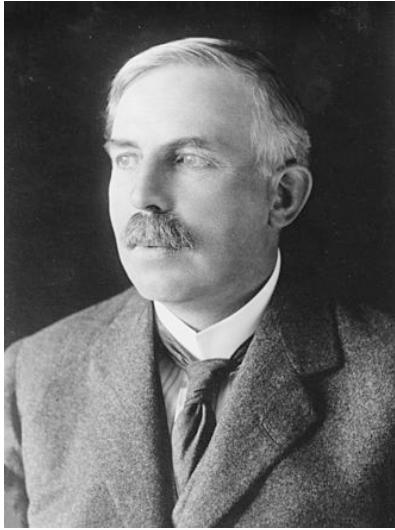
Enrico Fermi



3 kingdoms and major events



Or could it be L that is very small?



1911 Rutherford discovers the atomic nucleus



1903 Wright brothers complete powered flight

The Drake equation

$$N = R \times f_p \times n_e \times f_l \times f_i \times f_c \times L$$

only 34 years
→
Universe **12 bn** years
Life **3.5 bn** years

Active destruction



1945 Hiroshima

Or **passive** destruction: global warming
Takes only slightly longer (few hundred years)

More concretely, why study variation?

- To know the DNA sequence
- Why is the DNA sequence of interest?
- Biology
 - Understanding populations e.g. out of africa hypothesis AND population bottleneck
 - Genetic basis of behaviour
- Medicine
 - Monogenic diseases (e.g. Medical Genetics)
 - Polygenic disease (see next slides)

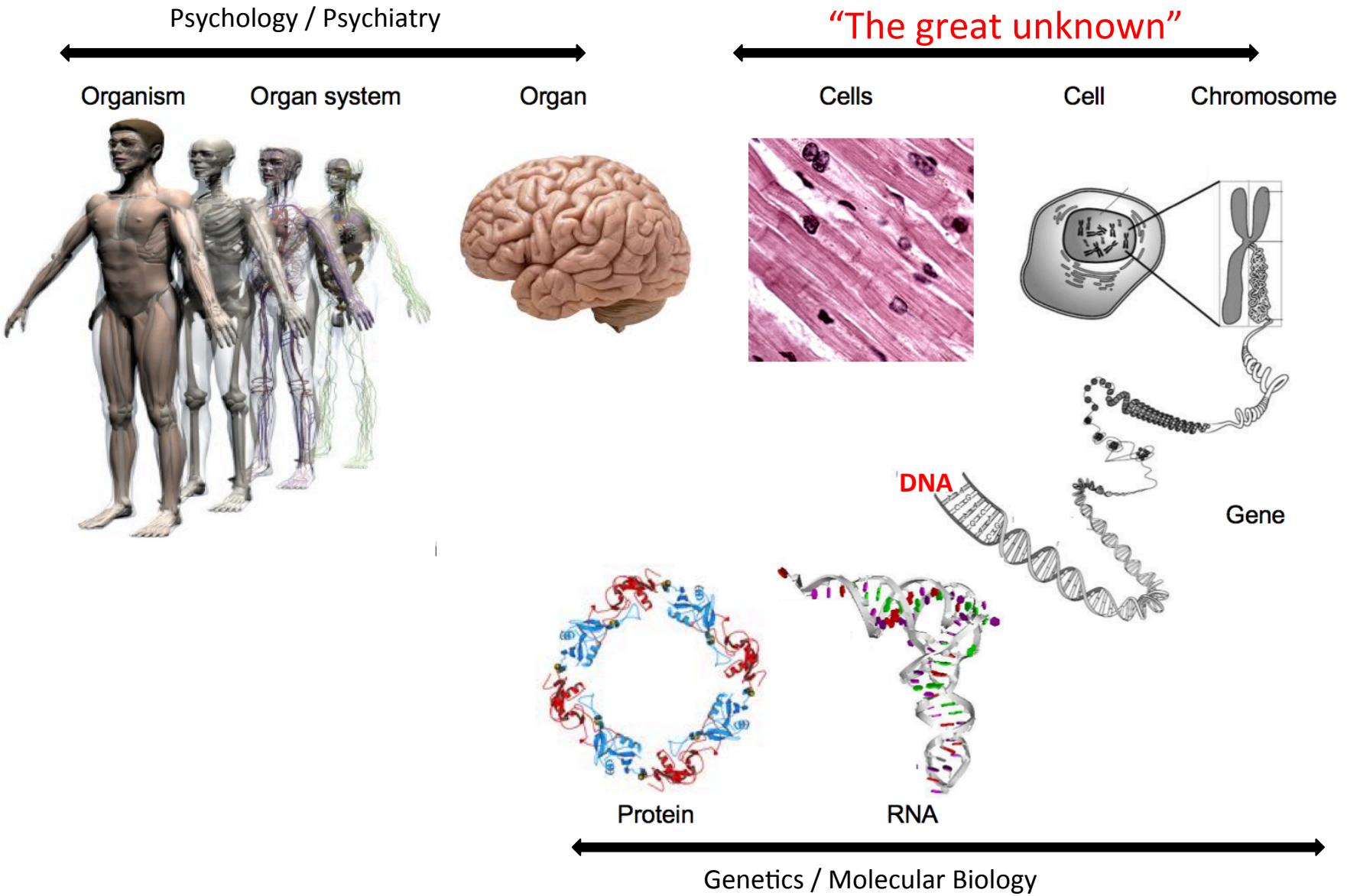
Natural courtship song variation caused by an intronic retroelement in an ion channel gene

Yun Ding¹, Augusto Berrocal^{1†}, Tomoko Morita¹, Kit D. Longden¹ & David L. Stern¹

Tracing the Route of Modern Humans out of Africa by Using 225 Human Genome Sequences from Ethiopians and Egyptians

Luca Paganin, Stephan Schiffels, Deepa Gurdasani, Petr Danecek, Aylwyn Scally, Yuan Chen, Yali Xue, Marc Haber, Rosemary Ekong, Tamiru Oljira, Ephrem Mekonnen, Donata Luiselli, Neil Bradman, Endashaw Bekele, Pierre Zalloua, Richard Durbin, Toomas Kivisild, Chris Tyler-Smith

The biological “stack”



Genome Wide Association Study

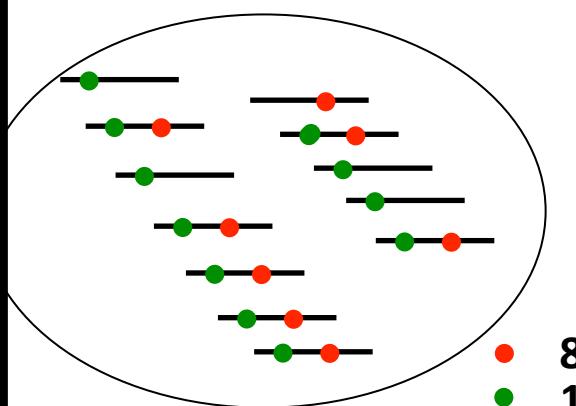
	SNP site	SNP site
Individual 1 T A T A G G G T C C A T G A T G A C T G T C A T	
Individual 2 T A T A G G G T C C A T G A T G A C T G T C A T	
Individual 3 T A T A G G G C C C A T G A T G A C T G T C A T	
Individual 4 T A T A G G G C C C A T G A T G A C T A T C A T	
Individual 5 T A T A G G G C C C A T G A T G A C T A T C A T	

↔

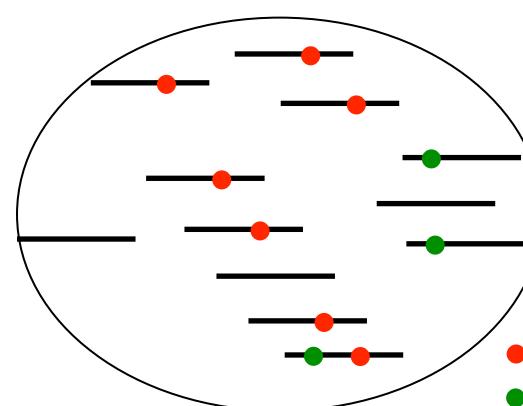
Genotyped SNPs typically 10k apart
(Genome is 3 billion base and array is 300k)

If a region of DNA has no effect on the phenotype of interest,
we expect same frequency (or odds) of SNP in case and controls

Controls



Cases



**OR= Odds of the SNP in the cases /
Odds of the SNP in the controls**

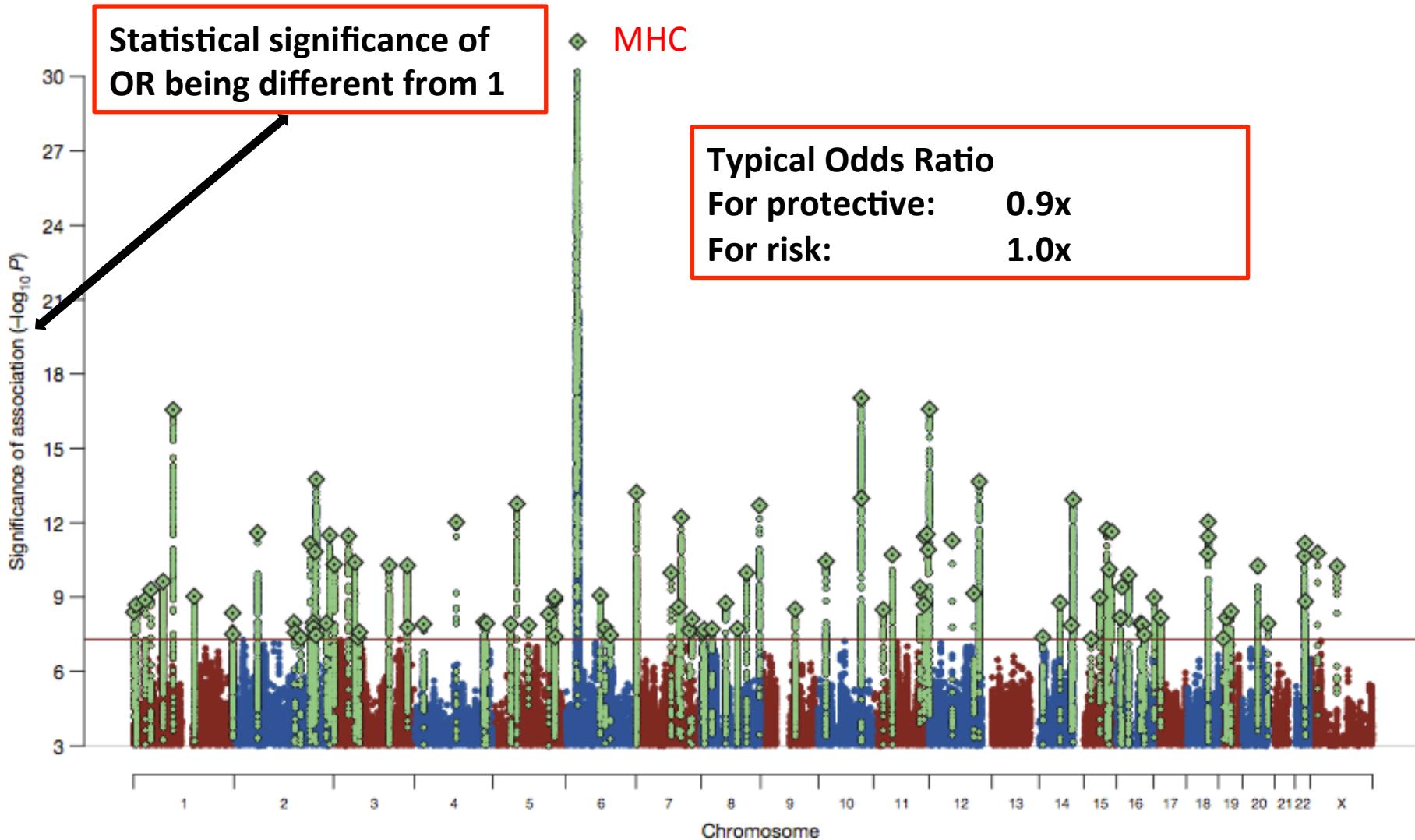
OR > 1: risk SNP

OR < 1: protective SNP

7
3

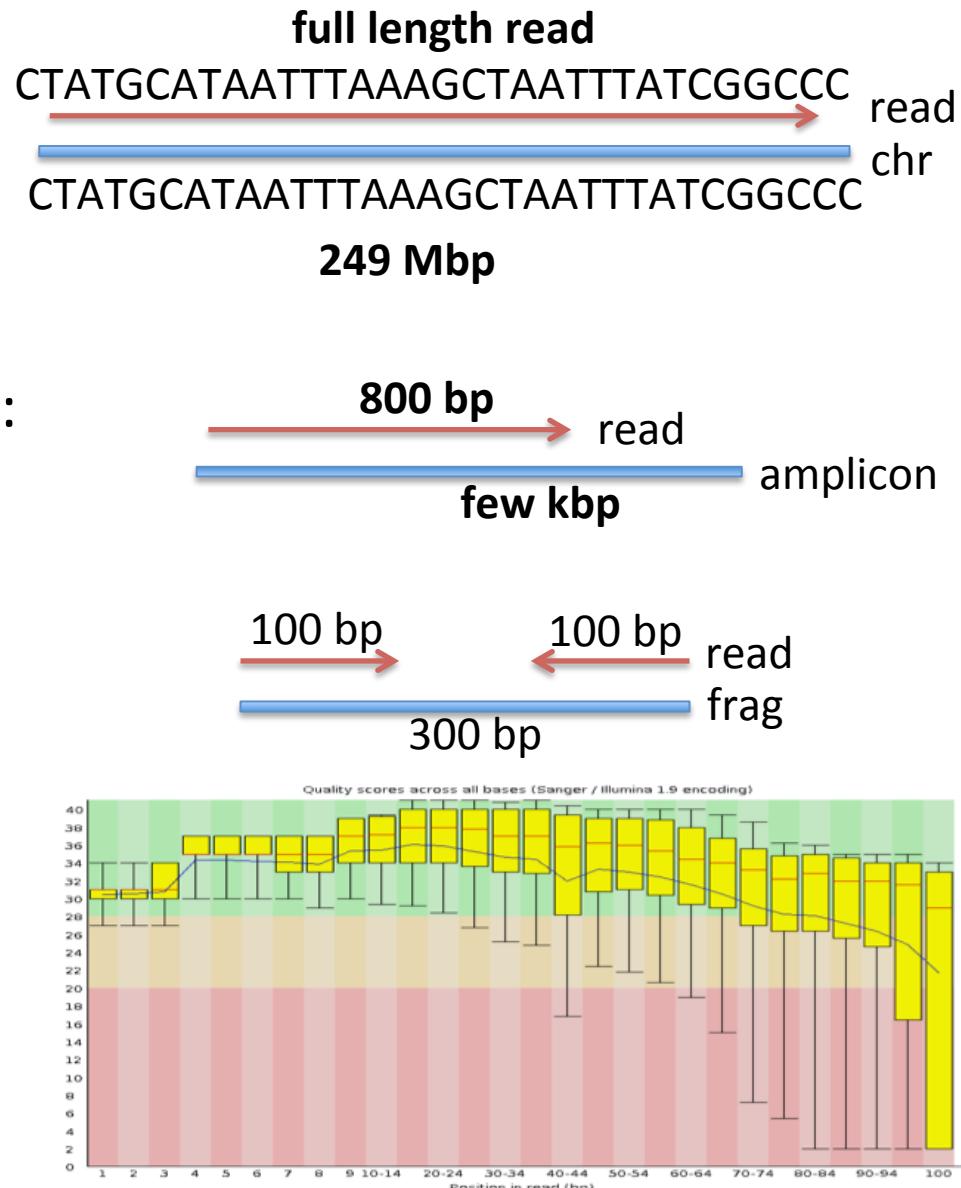
GWAS results

Biological insights from 108 schizophrenia-associated genetic loci (2014)



In a perfect world – Perfect sequencing

- Perfect sequencing:
 - single molecule (no PCR)
 - **full length**
 - no deterioration of quality
- The real world has improved but is not perfect:
 - Sanger
 - PCR
 - length: some kb
 - limited number of reads
 - high quality
 - HTS (Illumina)
 - PCR
 - 100-300 bp
 - Paired-end option (PE)
 - **billions** of reads
 - high quality, but deteriorating along read

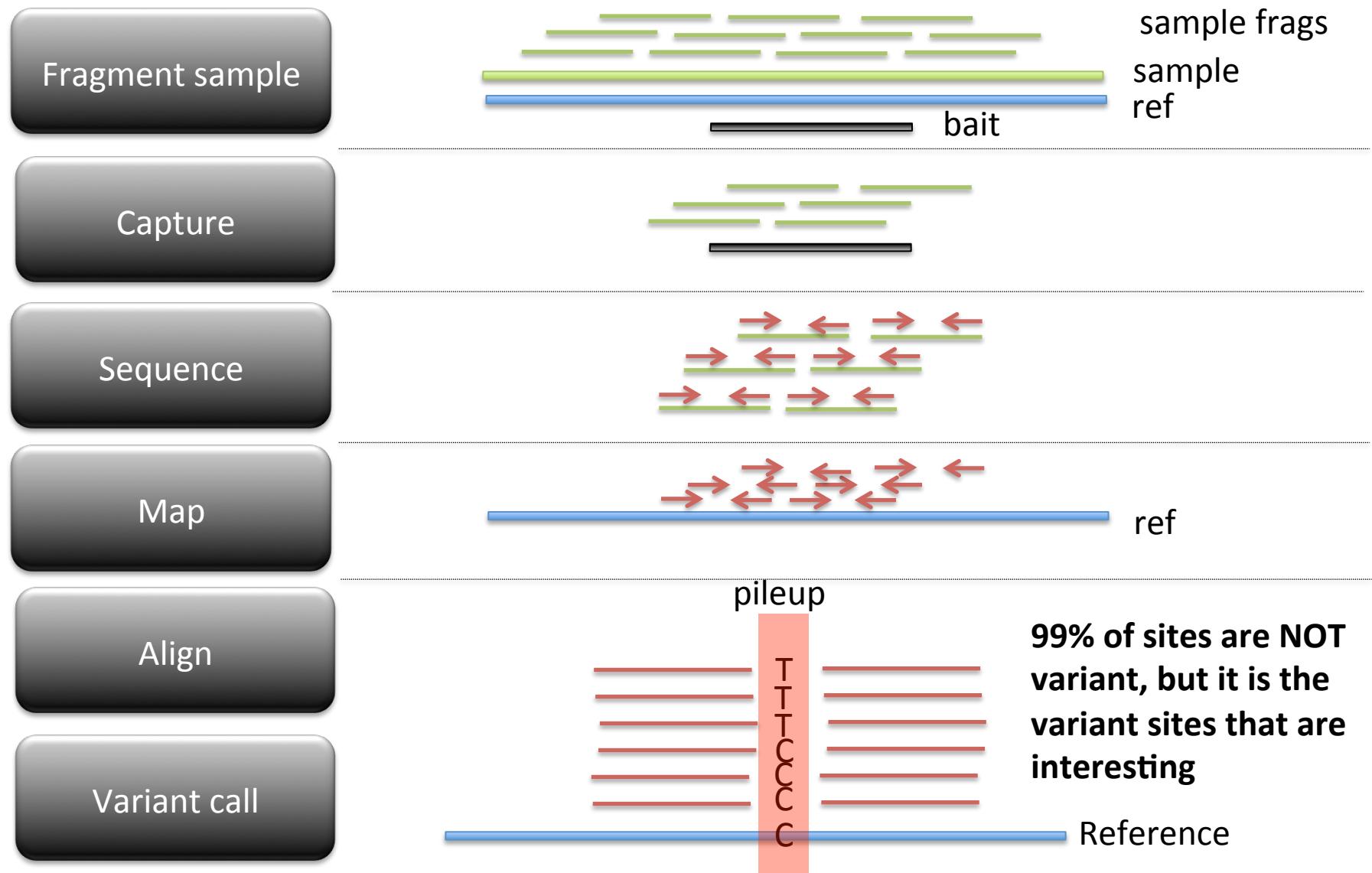


Looking for a ping pong ball in a stadium

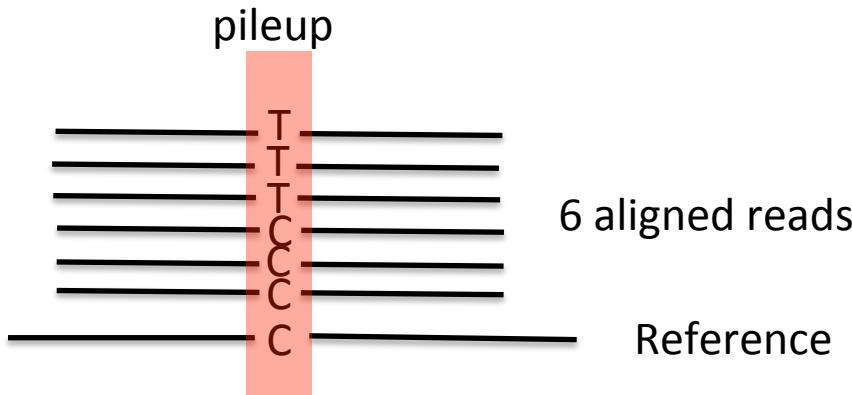
- With a hand torch!!

Or with the lights on?

A quick overview of the HTS workflow

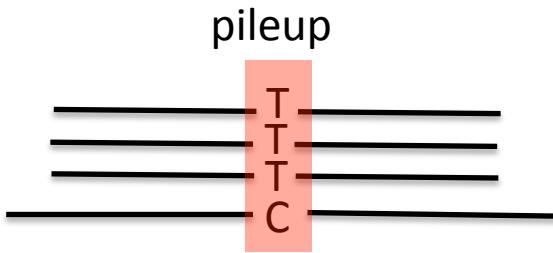


Variant sites



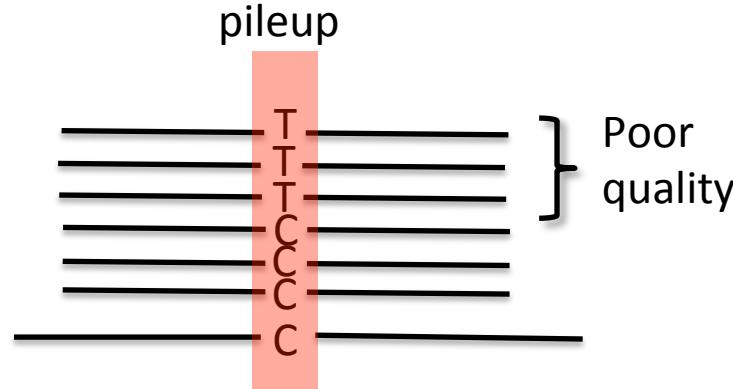
The common and easy case

- Good mapping of reads
- Good base qualities
- Good depth



Poor depth

- May not have sampled both alleles
- Could be C/T or T/T



Poor quality

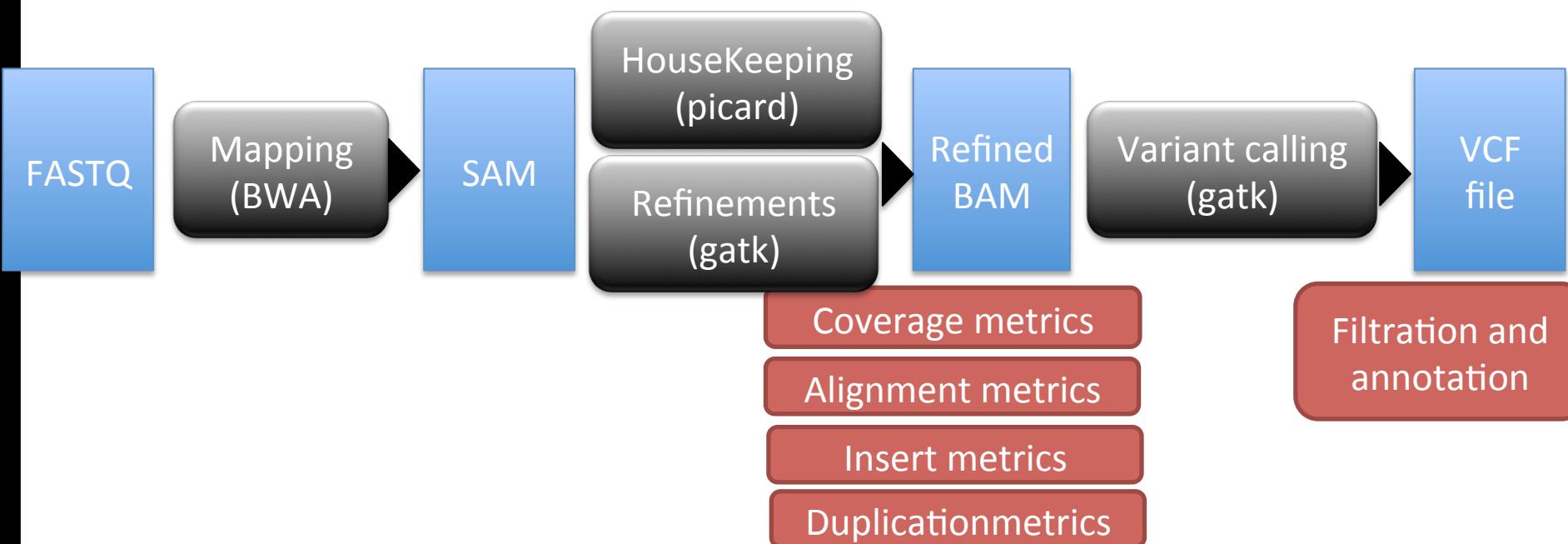
- of base calls
- of read mapping

Can lead to false variant calls: site could be ref
C/C and Ts are just base call errors

Our pedagogical approach



Multiple iterations with increasing complexity

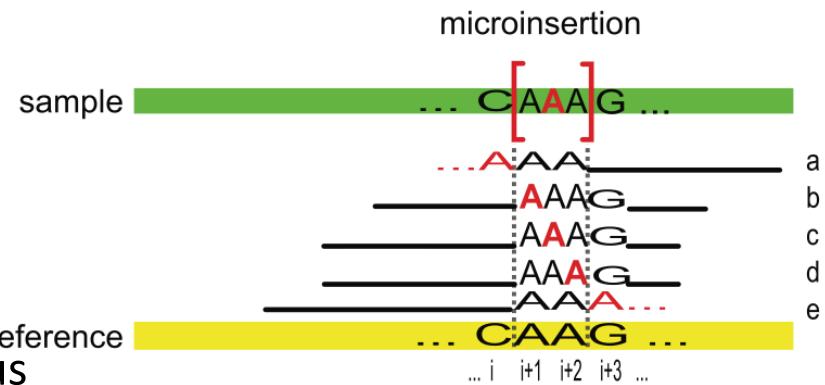


What do we aim to achieve with this approach

- Hoped for advantages of approach:
 - simple to understand most basic pipeline and easy to run
 - practice in each iteration
- Don't worry if you do not understand everything at the first iteration
- With bioinformatic pipelines it is generally a good idea to quickly create a simple version before make it more complex
 - prototyping
 - Check out Tom Wujec's TED talk "**The marshmellow challenge**"
- We will focus on single sample analysis, and will discuss more complicated setups later
 - multi-sample
 - pooled

Why do we need a “complex” pipeline?

- The biggest problem with variant calling is large numbers of FPs and FNs:
 - Mainly driven by bad alignments
 - FNs often create FPs
 - Can be systematic across samples, thus creating consistent SNPs across samples that are just machine artifacts.
- FPs and FNs, may result in:
 - the signal in our data drowning in noise → no result
 - false results → erroneous result
- You may find that reviewers will object to a pipeline which is not state-of-the-art, which creates trouble for you in the review process even though you may actually have a result.



Choice of example dataset

- Human data – arbitrary
- What if you work on other species?
 - if you have a reference genome and reads from a sample you can run the most basic pipelines
 - For more advanced pipeline you may have to spend some effort finding or generating auxiliary files in correct format
 - dbSNP
 - Genome annotation
 - You may find that they are already available for many species
 - Check out the GSA/GATK website
 - Check out <http://getsatisfaction.com/gsa>

GSA team at the Broad Institute

- A large fraction of the materials and software in this course are produced by the **Genome Sequencing and Analysis Group** team at the Broad Institute
- Information sources
 - <http://www.broadinstitute.org/gsa/wiki>
 - <http://www.getsatisfaction.com/gsa>
- People
 - [Mark A. DePristo](#), Manager of Medical and Population Genetics Analysis
 - [Eric Banks](#), Team Lead
 - [Guillermo del Angel](#)
 - [Ryan Poplin](#)
 - [Kiran Garimella](#), Team Lead
 - [Mauricio Carneiro](#)
 - Chris Hartl
 - Khalid Shakir, Team Lead
 - Matthew Hanna
 - David Roazen
- Others at the Broad
 - Heng Li: samtools and bwa
 - Tim Fennell: picard
 - Alec Wysoker: picard
 - Brac Chapman: bcbio.variation
- And others outside the Broad
 - sources at bottom of slides

For each practical

- Most key concepts explained up front
 - sometimes concepts will be first introduced in the practical (this will be the exception)
- Run through of the practical in plenum
- Read carefully through the practicals. All the information you need for doing the practical should be in the file
- Practical session
 - Try to get it running
 - If fail or computation takes time ➔ go to exercisesResults directory
- You will be doing “copy and paste”
 - that is OK
 - but you must understand what you are copying and pasting
 - if you don’t ask for explanations
- Use of labels to indicate status: “finished” and “needing help”
- It is hard!
 - new concepts
 - new environment (Unix)
 - try to understand both **and take notes!**

- I would rather you focus on working on the course
- If you cannot, do not disrupt me or fellow students:
 - silent phones
 - no youtubing or videos
 - no chatting
 - no knitting
- Alternatively, you can leave



Other dos and donts

- Do
 - Sign the attendance sheet
 - Remember that there are wide differences in competence
 - Consolidate your knowledge if you get ahead
 - Talk and get help from your neighbours
- **Do not:**
 - ask questions in plenum if you get ahead, instead consolidate what you have learnt (tool websites)
 - think that the slides are a substitute for taking notes

Unix attitude

- **Get used to having to know where you are and to tell the computer where things are**

```
java -Xmx2G -jar ${swDir}/picard-tools-1.67/MarkDuplicates.jar \
INPUT=aln.posiSrt.clean.bam \
OUTPUT=aln.posiSrt.clean.dedup.bam \
METRICS_FILE=aln.posiSrt.clean.dedup.bam_metrics.duplication.txt
```



- **Be as precise as you are in your field**

```
..../vc/exerSandbox/03_advancedPipeline
```



- **Pay attention to detail and changes**

```
-rw-rw-r-- 1 timothyh timothyh 26M Oct 2 14:30 aln.posiSrt.clean.dedup.bam
-rw-rw-r-- 1 timothyh timothyh 145K Oct 2 14:30 aln.posiSrt.clean.dedup.bai
```

- **String commands together if you can**

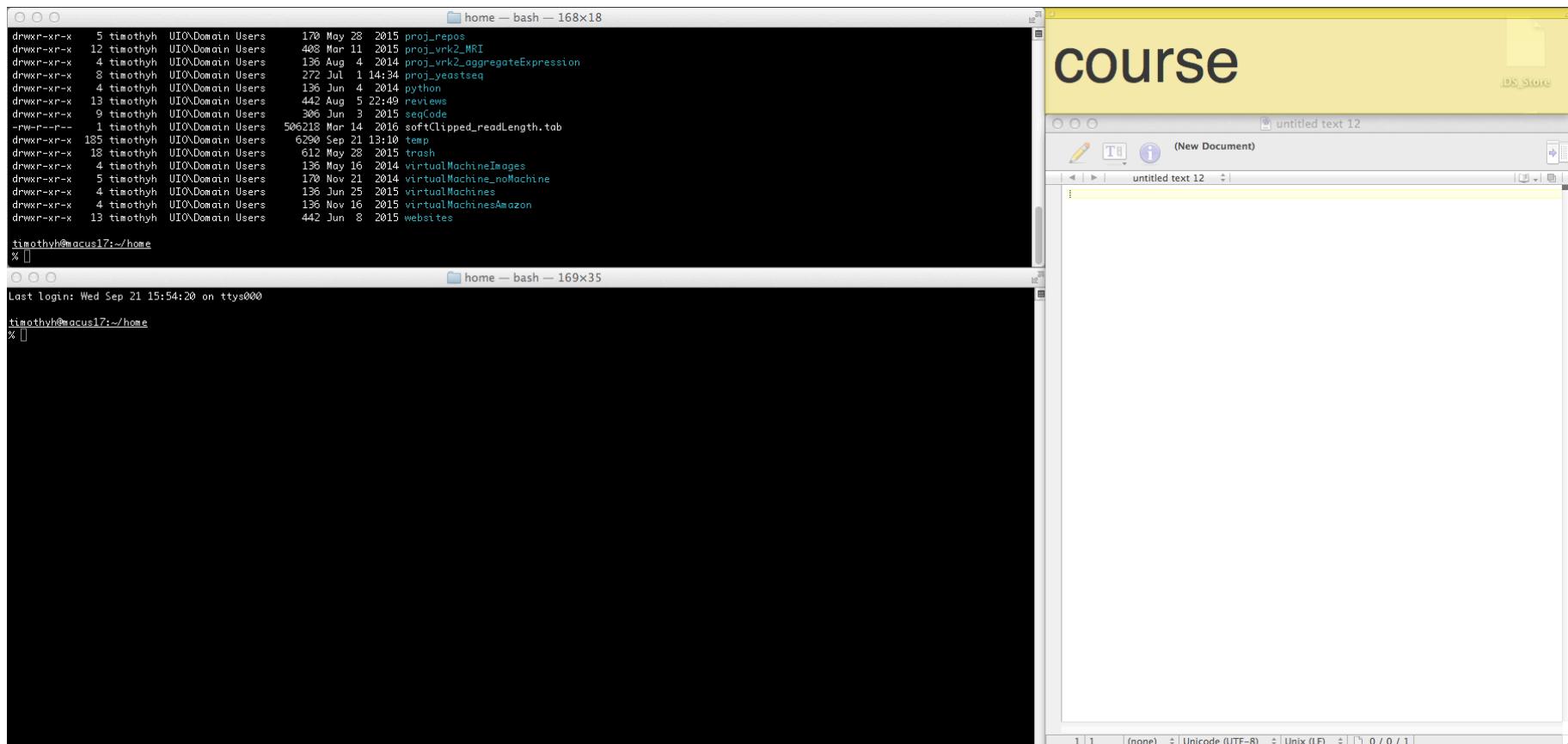
```
cat ${dataDir}/reads_agilentV1_chr5/simul_indels/deletions.vcf | grep -v "^#" | wc -l
```

Some useful unix shortcuts

- Ctrl + a: go to beginning of line
- Ctrl + e: go to end of line
- Ctrl + k: remove text after pointer
- Ctrl + u: remove text before pointer
- Arrow up and down to scroll through history
- Ctrl + r: reverse search history

Organising your desktop

- Keep an electronic notepad of file paths
- Useful to have multiple terminals
- Sometimes issues with code over several lines >> use wide terminals



Kahoot!

On your phone or in a browser go to the webpage: kahoot.it

*And punch in the code for the **Unix skills and bash variables** quiz*

I will explain answers as we go along

Why use variables for file paths?

- There are many different files in the exercises
 - with long paths (bcse there is a directory structure)
- A lot of errors in exercises are due students getting file paths wrong
AND the primary goal of this course is not to teach file paths
- If one wishes to change a file path that is used in multiple locations / exercises one needs to make multiple changes in multiple locations
- You should learn to use variables in your own scripts
- If you ever get confused, just execute the following command to see what a variable contains
 - `echo $variableName`

SOFTWARE AND DATASET – SETUP AND INTRODUCTION

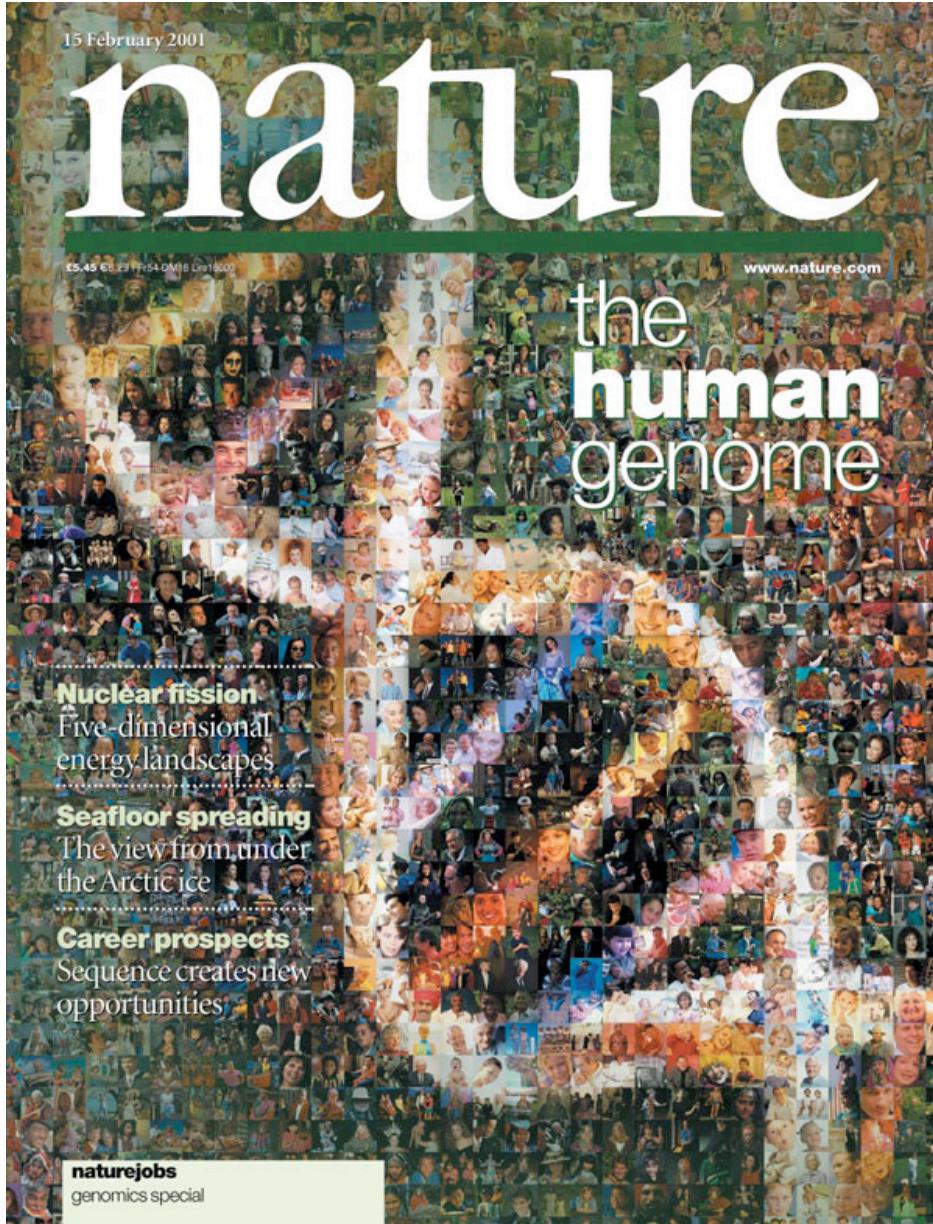
Software and data installation – mini practical

- Use the terminal or a file explorer to take a look at the central repository
 - **exerDefinitions** contains all the practicals
 - **exerResults** contains pre-computed results of practicals
 - **inputData** contains all the datasets we will be working on
- Software
 - for documentation of how the tools work for a lot of commands you get a quick help by typing the following at the command line: **command** or **command -h**
 - **If this does not work, the best is to google the tool and read the online documentation.**
- Lets take a quick look at the data >> mini practical (see next slide)

Introduction of datasets in `inputData`

- `reads_exomeCapt_chr5` in fastq format
(`reads_agilentV1_chr5`)
 - real reads from exome capture (`real_patient`)
 - simulated: known mutations (mainly indels) and simulated reads (`simul_indels`) – same regions as real dataset
 - simulated: known mutations (mainly indels) and simulated reads (`simul_NA12878`) – same regions as real dataset
- reference data (**`human_g1k_v37_chr5`**)
 - **agilentV1** >> definition of capture tiles in different formats
 - **gatkBundle** >> reference data in fasta format and vcf files of known variants (dbSNP, 1000 genomes, hapmap)
- Formats >> we will return to these later

The reference genome



Or the species of your choice.

Some kind of reference is necessary for variant calling.

It is possible to use closely related species as a reference.

Naming and ordering of chromosome/contigs

	Hg18 (UCSC)	B36 (NCBI)
Contig prefix	chr	none
Mitochondrial contig	chrM	MT
Contig order	chrM, chr1, chr2,, chrX, chrY	1, 2,, X, Y, MT

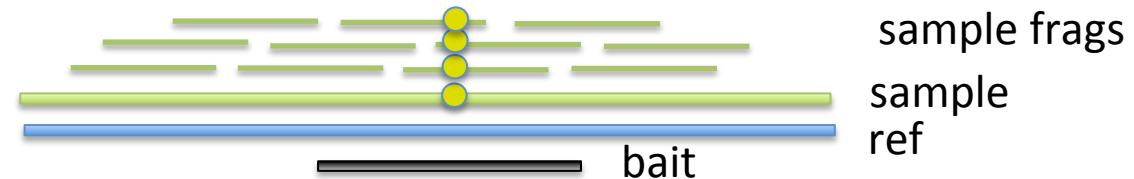
- Genome references
 - Fasta file: must have .fasta extension + respect naming and order
 - Fai file (created by samtools faidx): contig, size, location, basesPerLine → for efficient random access
 - Dict file (created by Picard CreateSequenceDictionary): SAM style header describing the contents of the fasta file → for names and length of original file
- ROD (reference ordered data)
 - GATK supports several common file formats for reading ROD data: VCF, UCSC formatted dbSNP, BED
- dbSNP files
 - Must also be ROD
 - Generated by GSA from the dbSNP db using a bit of bash, awk and a perl script: sortByRef.pl. Full details: http://www.broadinstitute.org/gsa/wiki/index.php/The_DBNSNP_rod
- All of the above delivered for human as part of the **GATK resource bundle**
 - Other species may also be available
 - Help on generating for another species see GATK wiki or getsatisfaction.com/gsa

The FASTQ reads: Motivating the simulation

- Why simulate in variant calling?
 - with real data we do not know the “truth”
 - in a simulation, we can define the “truth” and then “hide” it and test how well our methods can recover this “truth”
 - in a real dataset, most variants are single nucleotide polymorphisms and these are usually very easy to correctly call
- Drawbacks of simulation: usually will not accurately model all aspects of real data

The simulation

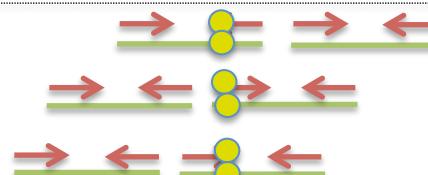
Fragment sample



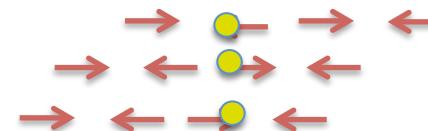
Capture



Sequence



Map



Align



Variant call

Are we able to correctly call this site as variant?

Potential challenges are:

- depth of coverage
- position in read
- size of indel

The simulated dataset

Placed in true agilent tiles on chr 5

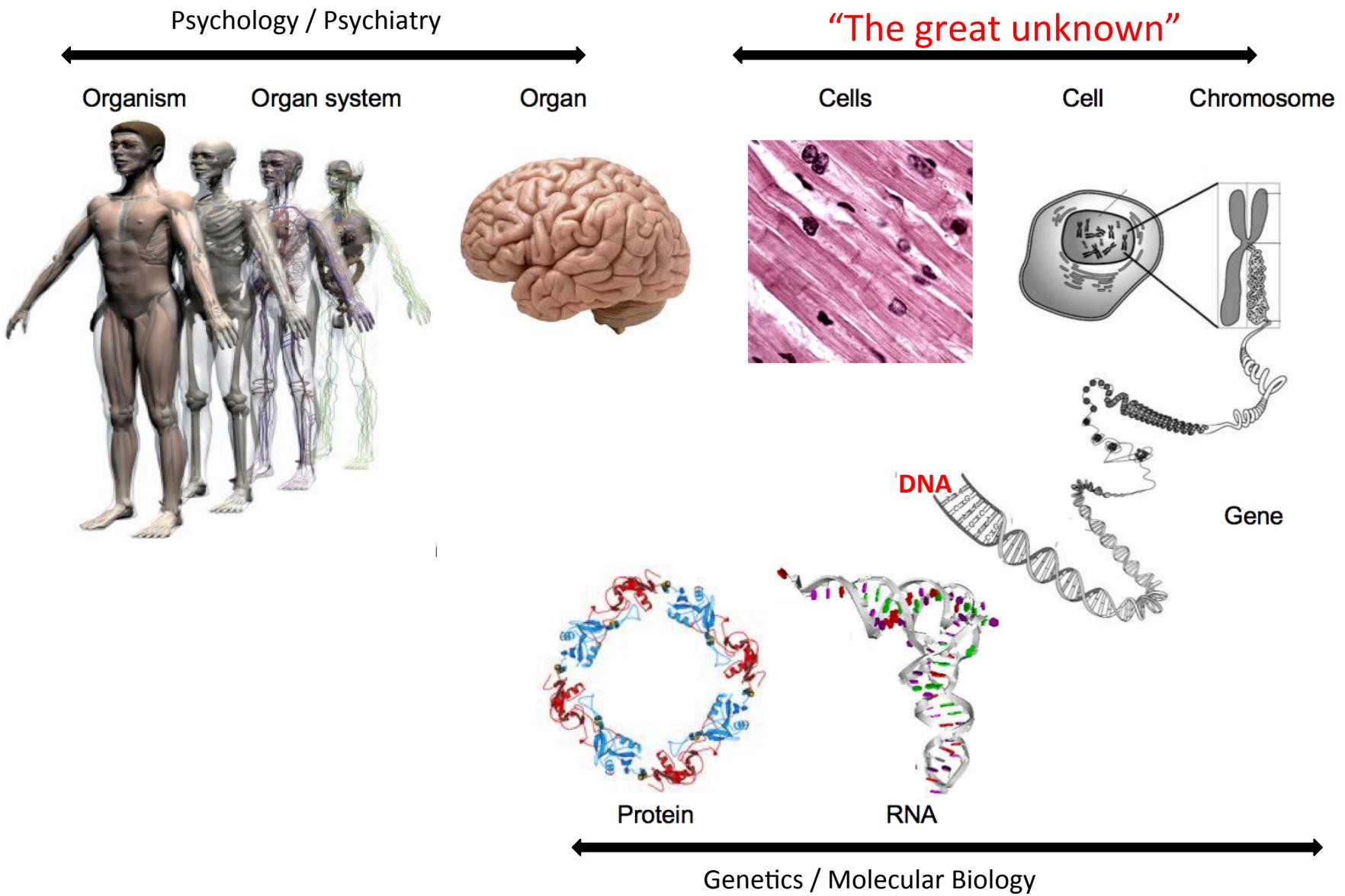
- SNPs – 100 of each type >> 600 in total
 - 3 strands (1 hetero, 2 hetero, 3 homo)
 - 2 positions in tile
- Deletions – 5 of each type >> 1800 in total
 - 3 strands (1 hetero, 2 hetero, 3 homo)
 - 2 positions in tile (at edge or well inside)
 - size: 1 to 60
- Insertions – 5 of each type >> 1800 in total
 - 3 strands (1 hetero, 2 hetero, 3 homo)
 - 2 positions in tile (at edge or well inside)
 - size: 1 to 60
- **A highly unrealistic set of variation but useful for studying the intricacies of variant calling**

Practical 01 – setting up your home directory

- We do this real SLOOOOOOOOW.....
- We need to create a place where you can do the exercises in your home directory
- Start two terminal windows
- First setup the environment, you need:
 - in a terminal: `source /data/vc/exerDefinitions/setupEnv.bash`
 - **Nota Bene: you should always run this when you start a new terminal**
 - test it: `echo $localVcDir`
 - you should output something like `/share/inf-biox121/home/timothyh/vc`
- Get your copy of the files you need from the central location:
 - in a terminal: `/data/vc/exerDefinitions/copyFiles.bash`
 - The files were copied to this location: `echo $localVcDir`
 - Check out the contents of this directory: `ls $localVcDir`
 - You should see a list of files which are your copies of the inputData, slides and exercises (exerDefinitions) and a location where you should do all exercises (exerSandbox)

GENETICS 101

The biological “stack”



Basic concepts – Take notes

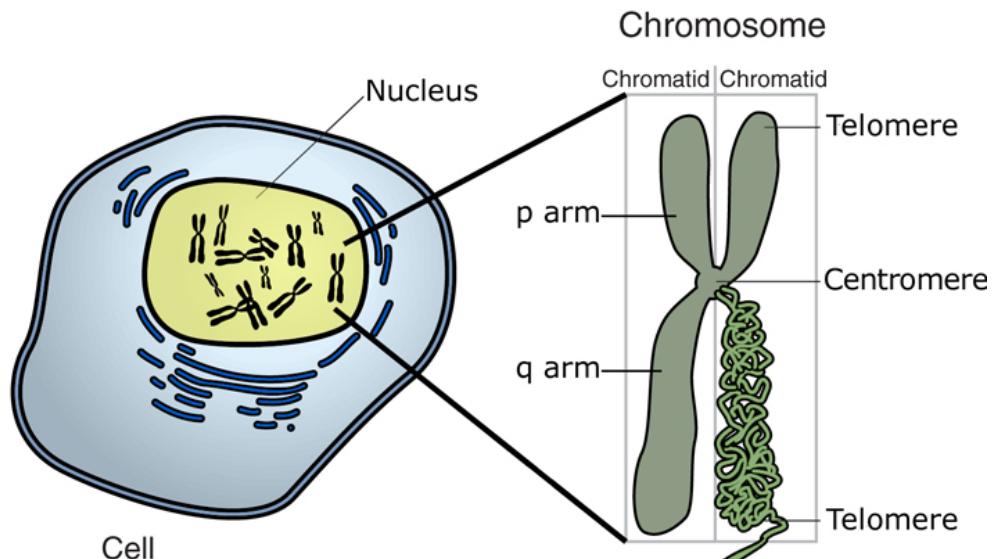
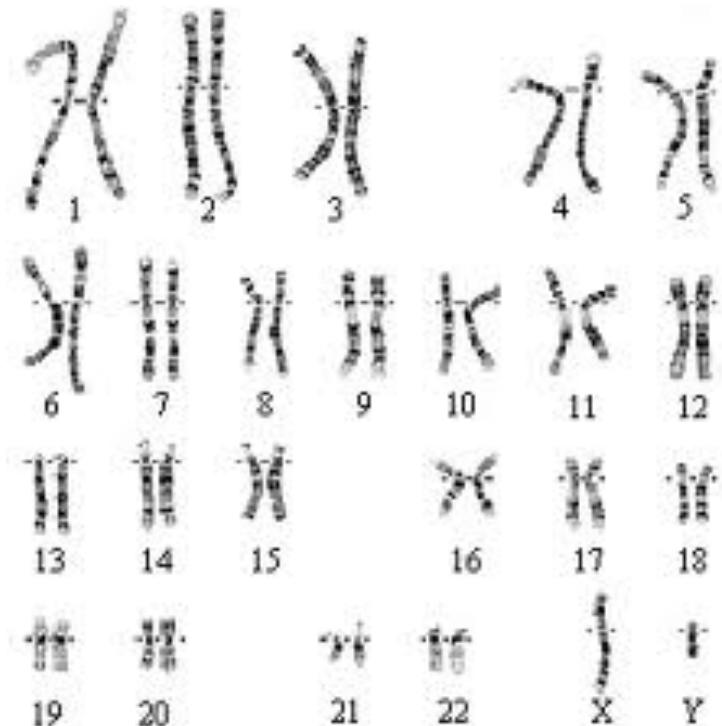


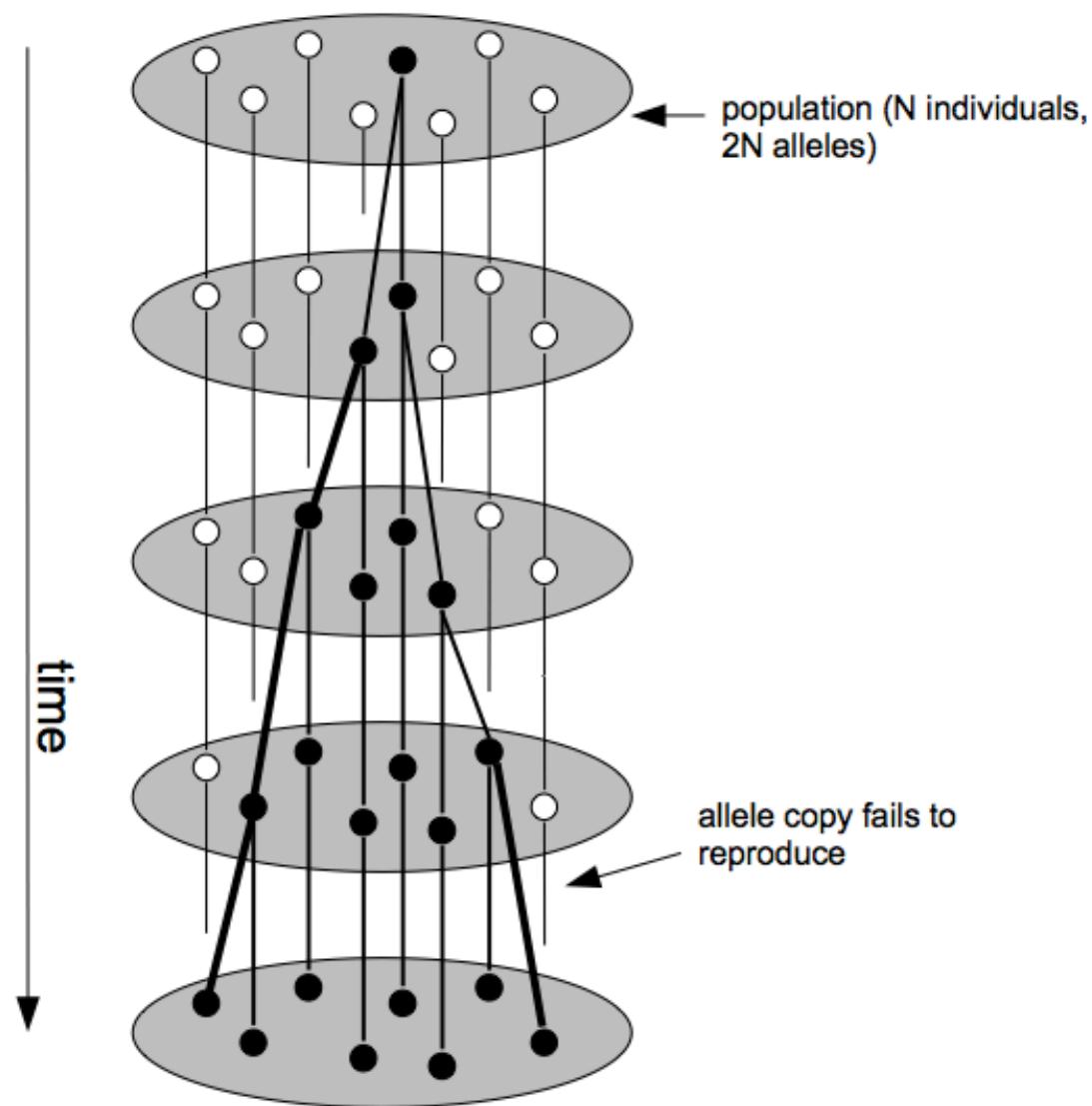
Image adapted from: National Human Genome Research Institute.



- Cells
- Chromosomes (ploidy)
- DNA complementarity and strands
- Variant site (SNPs are the most simple)
- Genotype: homozygote / heterozygote
- Haplotype

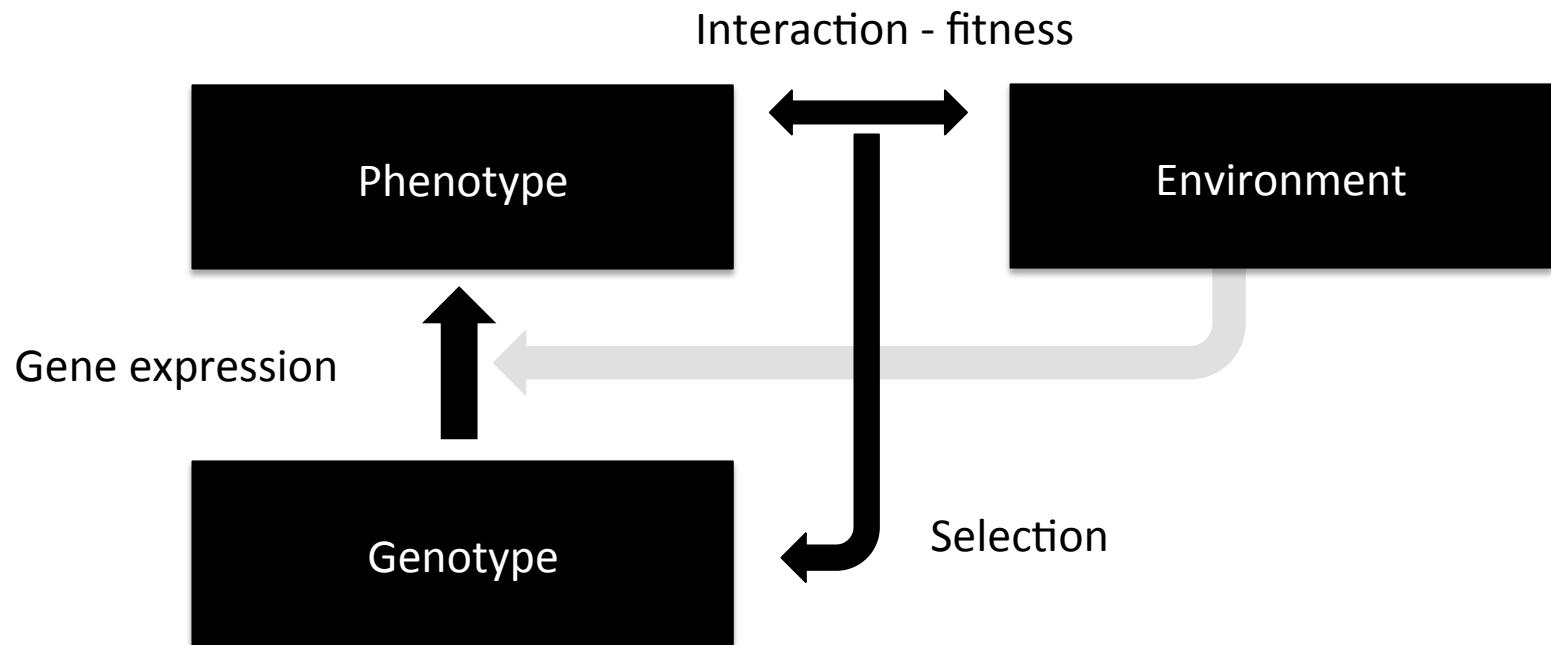
Neutral drift and selection of genomic events

New black allele arises through mutation of a white allele



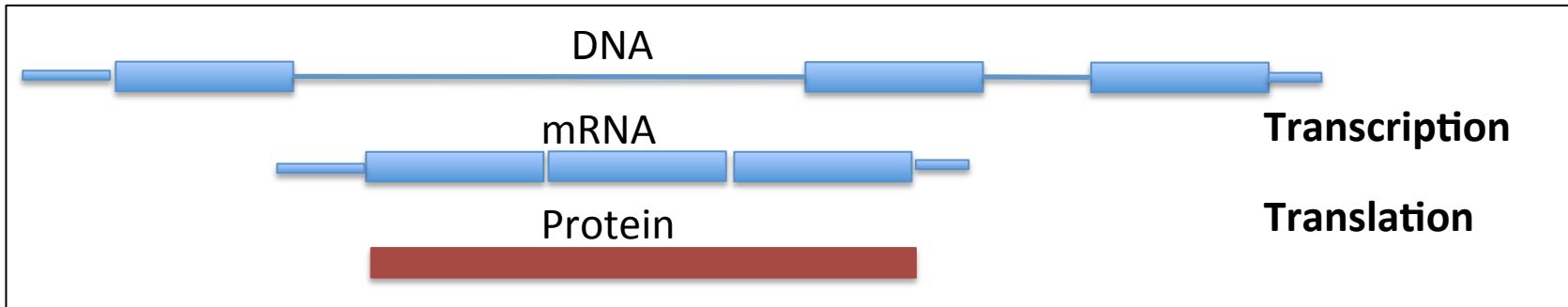
Black allele reaches fixation
(but this outcome only occurs with a small probability as it is very likely that the black allele fails to reproduce)

An abstract view of forces shaping evolution

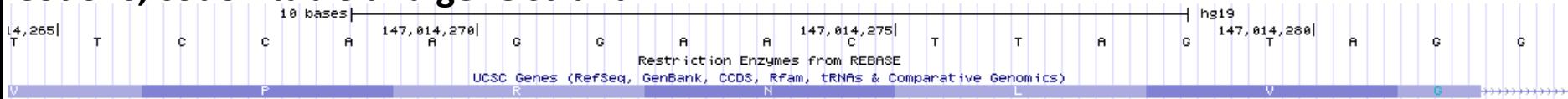


What is a gene?

Central Dogma

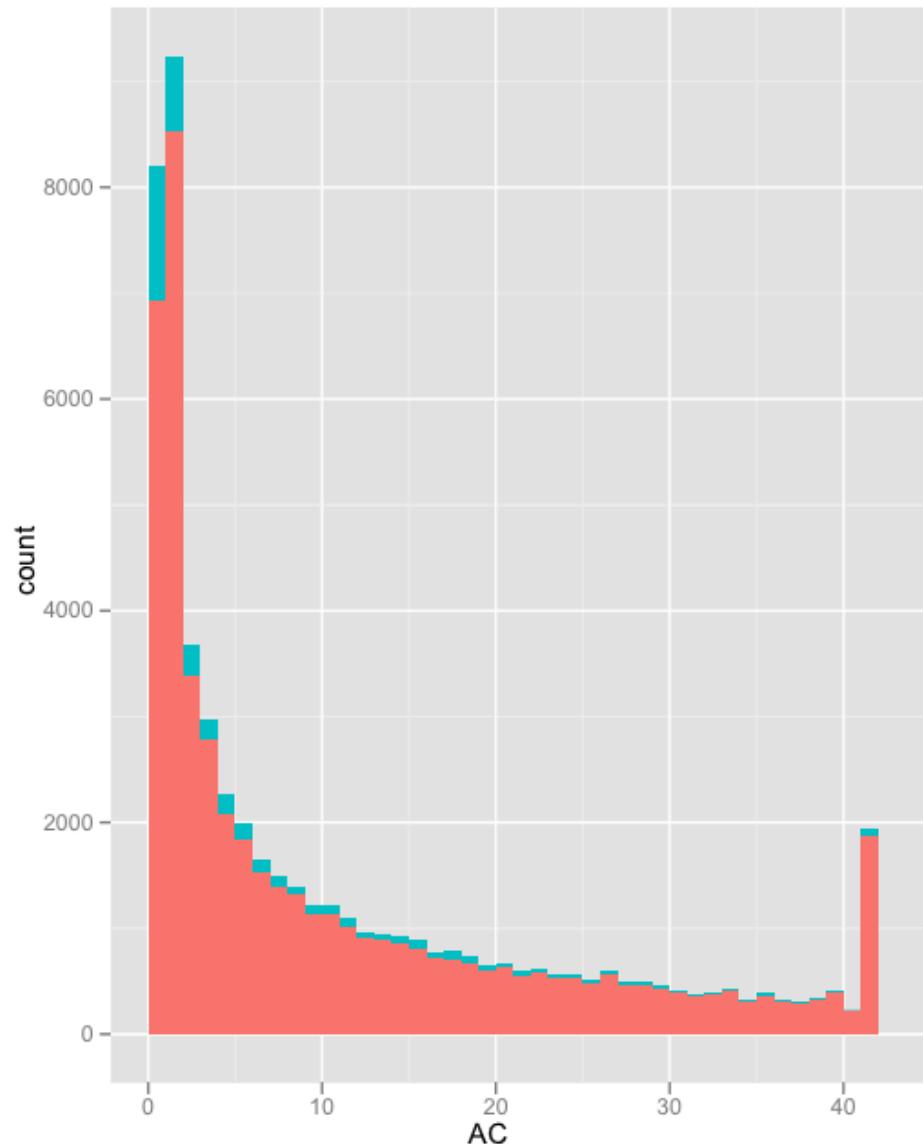


Codons, codon table and gene strand



- There are large numbers of genes in multicellular organisms
- Not all organisms have multiple exons per gene and thus do not need splicing
- Outside genes are regulatory elements that control when and where genes are expressed

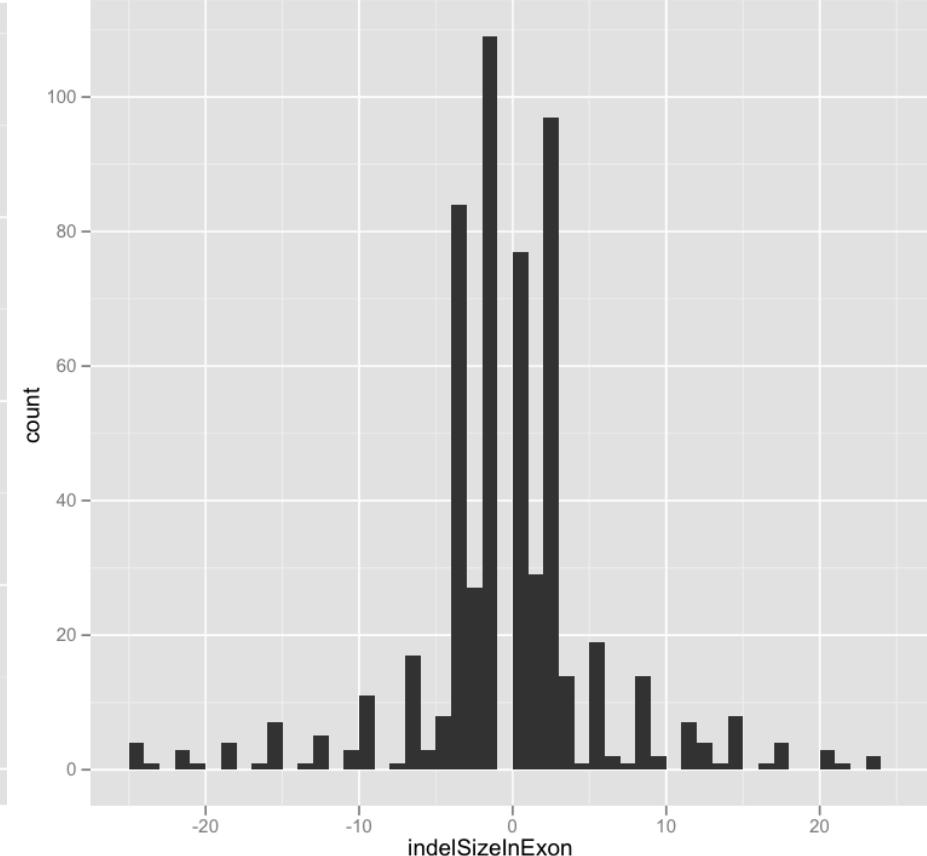
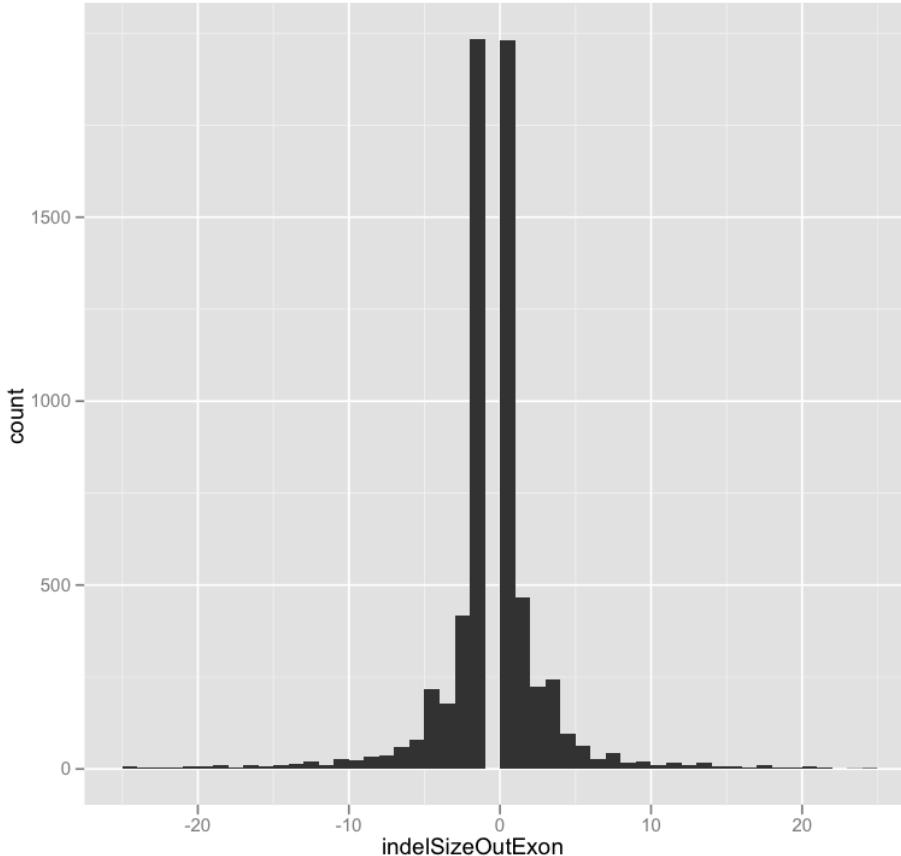
Distribution of Allele Count across 21 exomes



21 individual exomes (of diploid humans) i.e. 42 alleles

SNP numbers and indel size distribution

- Sequencing of human exome
 - 23,602 SNPs in coding exons (approx. 25M bp size)
 - 40,621 SNPs outside coding exons (approx. 25M bp size)



Notice both numbers and pattern in indel figures

Kahoot!

On your phone or in a browser go to the webpage: kahoot.it

And punch in the code for the Genetics and genomics quiz

This time I will NOT explain as we go along, instead you will get answers in a later lecture

MAPPING AND ALIGNMENT 101

Mapping

- Read mapping is the process of locating where in the reference genome a read originates from
- We typically have millions of 100-150 bp sequence reads which we need to map to a reference genome (often billions of bases)
- In addition, there will often not be an exact match between the read and the reference due to:
 - base call errors in individual reads
 - variation in the sample relative to the reference.
- One way of locating the origin of a read is to scan the whole genome looking for a match but this method is obviously very time consuming
 - later in the course we will study an algorithm which speeds this up

After mapping - Alignment

Ref A A A C A A T T A A G T

Sample AAAT

Sample A A A C A A A T A A T T A A G T

Ref A A A C - - - A A T T A A G T

Sample A A A C A A A T A A T T A A G T

Correct alignment

Sample read A A A C A A A T A A T T

Ref A A A C - - - A A T T A A G T

Sample read A A A C A A A T A A T T

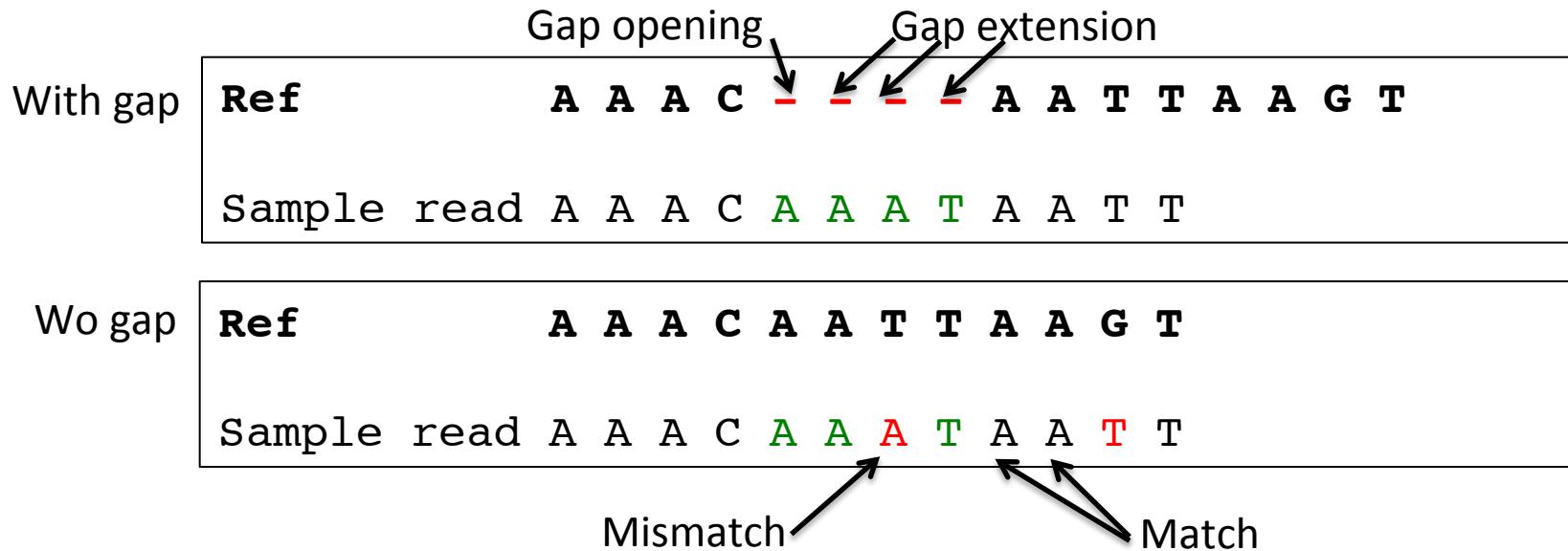
Correct alignment

Ref A A A C A A T T A A G T

Sample read A A A C A A A T A A T T

Possible alignment

Alignment



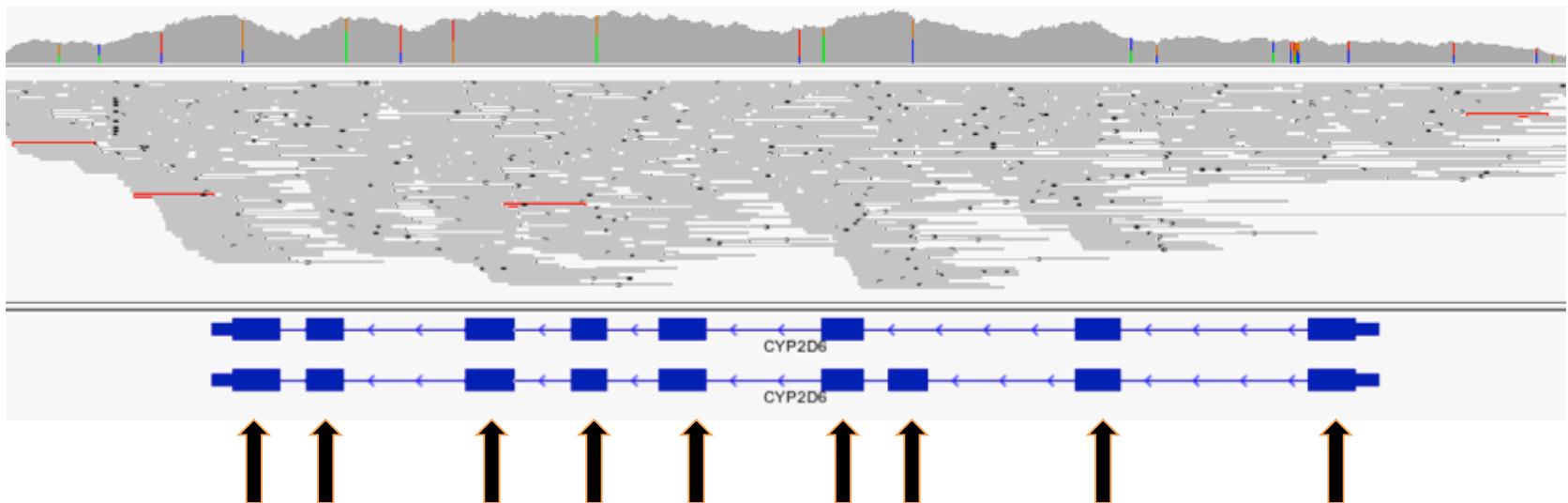
- Key component of alignment algorithm is the scoring
 - negative contribution to score
 - opening a gap
 - extending a gap
 - mismatches
 - positive contribution to score
 - matches
- The exact score contributions determine which alignment is chosen
- **Smith-Waterman** is an algorithm for finding optimal alignment given a scoring scheme without exhaustively enumerating and scoring all possible alignments



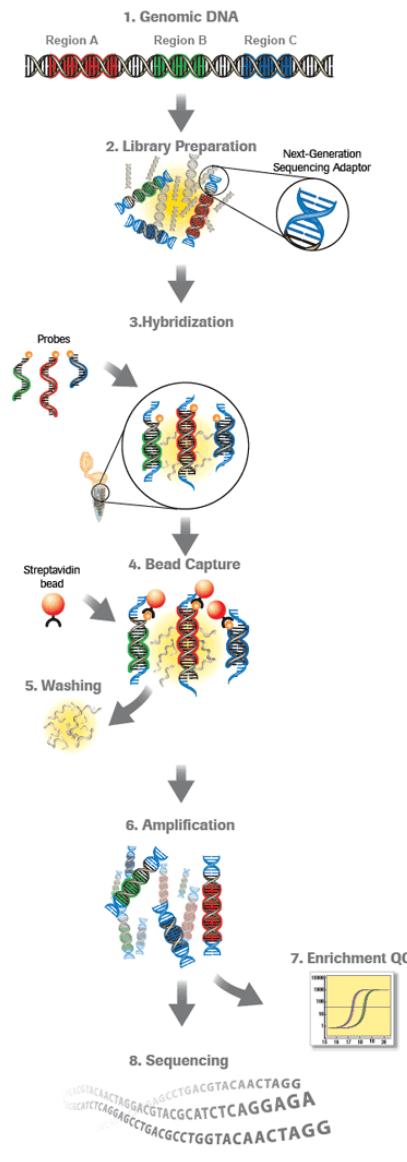
EXOME CAPTURE – ESSENTIALS

Sequencing a whole genome

- We could sequence a whole genome BUT only a small fraction is actually genes
 - in human less than 2% of the genome codes for proteins
- It saves a lot of sequencing to “capture” the regions we are interested in and sequence them



An overview of exome capture



Sonication

Library prep
(sequencing
adaptors on)

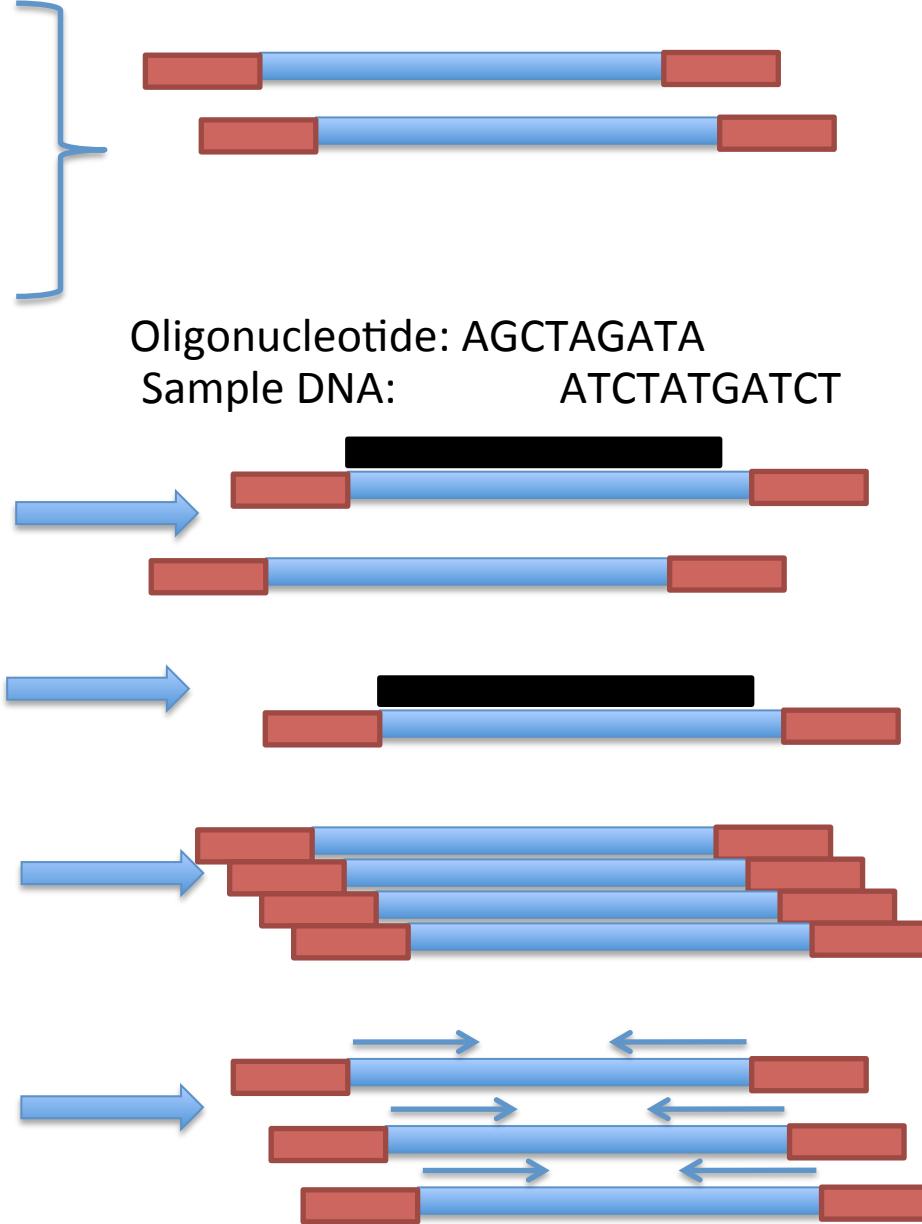
Hybridisation
to probes

Bead capture

Amplification

Sequencing

Oligonucleotide: AGCTAGATA
Sample DNA: ATCTATGATCT



Practical 02 – calling variants in the blind

- We look at the read datasets in local copy
 - Done together with instructor
- Open script 020_basicPipeline.bash (this should be your own copy under \${HOME}/vc/exerDefinitions)
- Explanation and execution of commands together with instructor

IGV mini practical

- Open a new terminal and start IGV
- Let us load up some data and explore some of the features of IGV
- We will load two datasets:
 - The dataset that you generated in the previous exercise
 - \${HOME}/vc/exerSandbox/02_basicPipeline
 - Another more realistic simulated dataset
 - \${HOME}/vc/inputData/reads_agilentV1_chr5/simul_NA12878
- Some the things we will do
 - loading files (locally or from server)
 - navigating (zoom in and out, back and forward)
 - getting access to details (on hover or click)
 - changing the way you view things (squish/expand, colours, pairs)
 - moving tracks and panels around and resizing
 - sessions
 - marking regions of interest
 - changing preferences like soft-clipped bases



SEQUENCE – ESSENTIALS

Sequencing

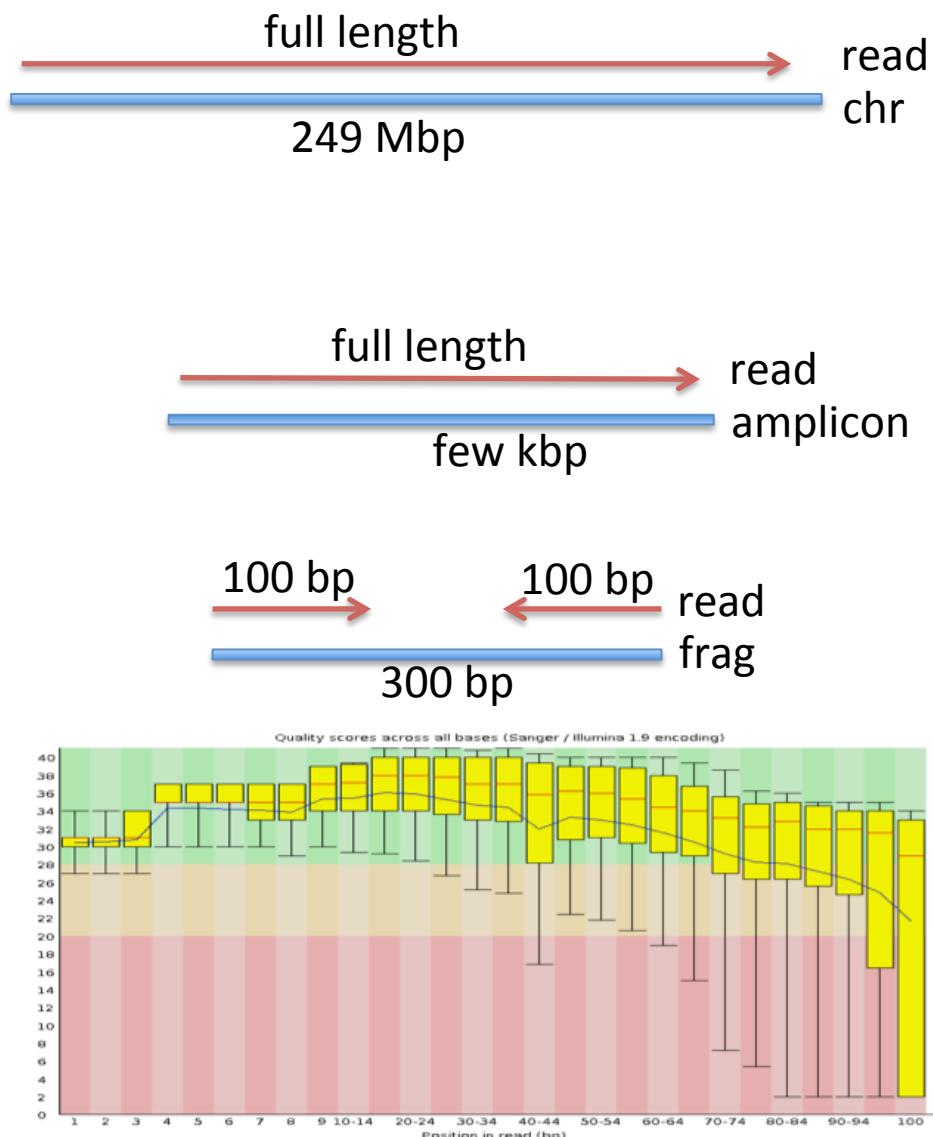
- Here we will be assuming that sequencing was covered in a previous module of the course



FASTQ FORMAT – ESSENTIALS

In a perfect world – Perfect sequencing

- Perfect sequencing:
 - single molecule (no PCR)
 - **full length**
 - no deterioration of quality
- While we are waiting:
 - Sanger
 - PCR
 - length: some kb
 - limited number of reads
 - high quality
 - HTS (Illumina)
 - PCR
 - 100 bp PE
 - billions of reads
 - high quality, but deteriorating along read



Fastq format – fasta with qualities

```
@SEQ_ID
GATTTGGGGTCAAAGCAGTATCGATCAAATAGTAAATCCATTGTTCAACTCACAGTTT
+
! ' * ( ( ( ****+ ) % % + + ) ( % % % ) . 1 *** - + * ' ) ) ** 55CCF >>>> CCCCCCCC65
```

- $p = \text{the probability that the corresponding base call is wrong}$
- Qualities $Q_{\text{sanger}} = -10 \log_{10} p$
 - $p = 0.1 \rightarrow Q = 10$
 - $p = 0.01 \rightarrow Q = 20$
 - $P = 0.001 \rightarrow Q = 30$
- Encoding: Sanger/Phred format can encode a quality score from 0 to 93 using ASCII 33 to 126: $Q + 33 \rightarrow \text{ASCII code}$

Dec	Hx	Oct	Html	Chr	Dec	Hx	Oct	Html	Chr
32	20	040	 	Space	64	40	100	@	Ø
33	21	041	!	!	65	41	101	A	A
34	22	042	"	"	66	42	102	B	B
35	23	043	#	#	67	43	103	C	C
36	24	044	$	\$	68	44	104	D	D
37	25	045	%	%	69	45	105	E	E
38	26	046	&	&	70	46	106	F	F
39	27	047	'	'	71	47	107	G	G
40	28	050	((72	48	110	H	H
41	29	051))	73	49	111	I	I
42	2A	052	*	*	74	4A	112	J	J
43	2B	053	+	+	75	4B	113	K	K
44	2C	054	,	,	76	4C	114	L	L
45	2D	055	-	-	77	4D	115	M	M
46	2E	056	.	.	78	4E	116	N	N
47	2F	057	/	/	79	4F	117	O	O
48	30	060	0	0	80	50	120	P	P
49	31	061	1	1	81	51	121	Q	Q
50	32	062	2	2	82	52	122	R	R
51	33	063	3	3	83	53	123	S	S
52	34	064	4	4	84	54	124	T	T
53	35	065	5	5	85	55	125	U	U
54	36	066	6	6	86	56	126	V	V
55	37	067	7	7	87	57	127	W	W
56	38	070	8	8	88	58	130	X	X
57	39	071	9	9	89	59	131	Y	Y
58	3A	072	:	:	90	5A	132	Z	Z
59	3B	073	;	;	91	5B	133	[[
60	3C	074	<	<	92	5C	134	\	\
61	3D	075	=	=	93	5D	135]]
62	3E	076	>	>	94	5E	136	^	^
63	3F	077	?	?	95	5F	137	_	_

Different quality formulas and encodings

- Beware of different versions

- With sequence data recently produced, you do not need to worry
 - For older data, be careful
 - Tools such as BWA have an option for older formats

Illumina sequence identifiers

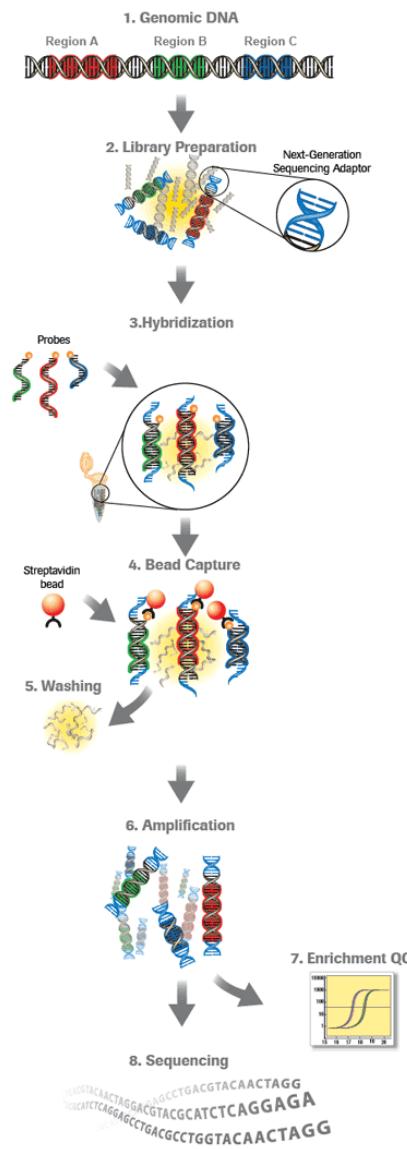
```
@SEQ_ID  
GATTTGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTGTTCAACTCACAGTTT  
+  
! ' * ( ( ( **** ) ) % % + + ) ( % % % ) . 1 * * * - + * ' ' ) ) * * 55CCF>>>>CCCCCCCC65
```

```
@EAS139:136:FC706VJ:2:2104:15343:197393 1:Y:18:ATCACG
```

EAS139	the unique instrument name
136	the run id
FC706VJ	the flowcell id
2	flowcell lane
2104	tile number within the flowcell lane
15343	'x'-coordinate of the cluster within the tile
197393	'y'-coordinate of the cluster within the tile
1	the member of a pair, 1 or 2 (<i>paired-end or mate-pair reads only</i>)
Y	Y if the read is filtered, N otherwise
18	0 when none of the control bits are on, otherwise it is an even number
ATCACG	index sequence

CLEANING UP FASTQ FILES (NOT CURRICULUM)

An overview of exome capture



Sonication

Library prep
(sequencing adaptors on)

Hybridisation
to probes

Bead capture

Amplification

Sequencing



Problem: adaptor seq (red) in reads

Possible biases in sequences that hybridise

Possible biases in sequences that elute

Possible biases in sequences that amplify

Possible biases in sequences that bridge PCR

The importance of clean up



Problem: adaptor seq in reads

- There will be non-genomic sequences in reads
 - this will often prevent mapping
- Consequences
 - if short fragments are randomly distributed >> less reads mapping >> reduced coverage >> not a big problem as long as the fraction of reads affected is not too large
 - if short fragments are not randomly distributed (e.g. Halo capture) >> specific areas will suffer from reduced/no coverage >> **big problem**
 - **It all depends on the sample whether something really matters or not**

Chip-seq example

Pre-sequencing sample prep



Partially successful removal of adaptors



Sequencing sample prep



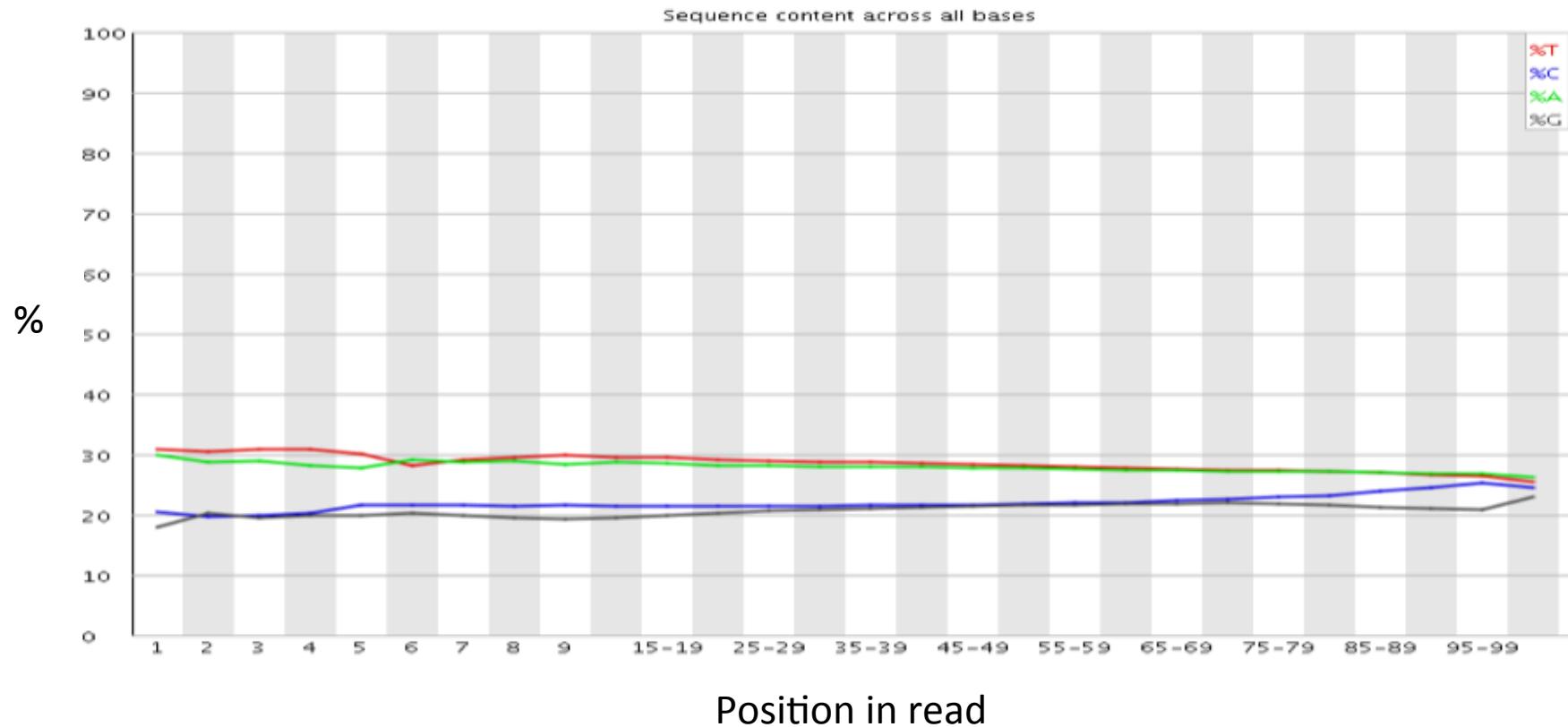
Sequencing



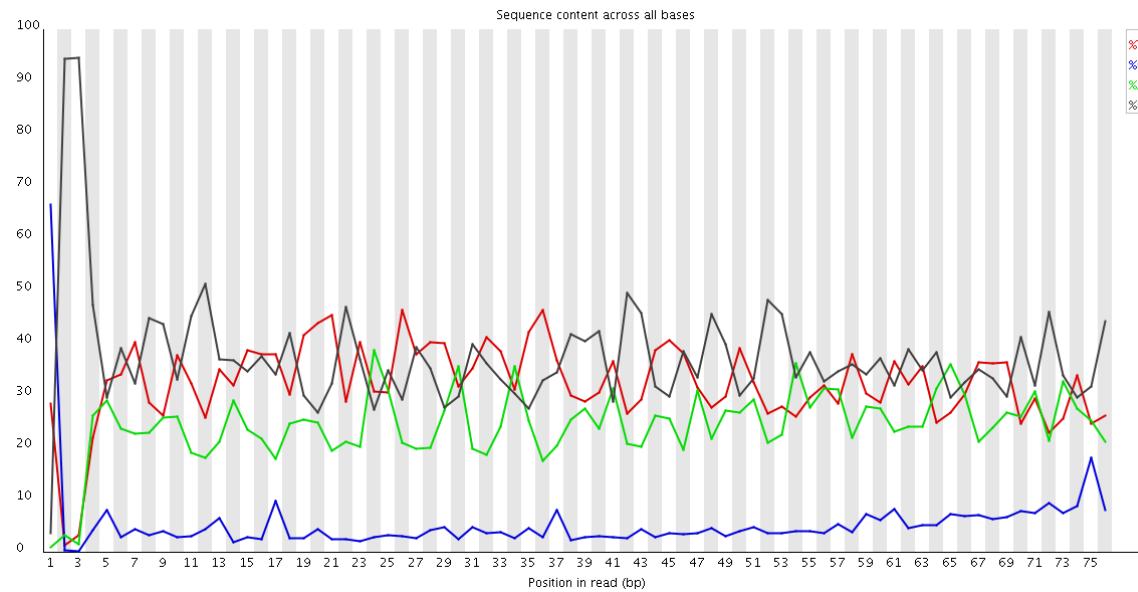
- If there are adaptors still attached to the genomic fragments in the material entering sequencing sample prep, the situation can be even more complicated.

- Fastqc report is essential to get a feel for whether clean-up is required

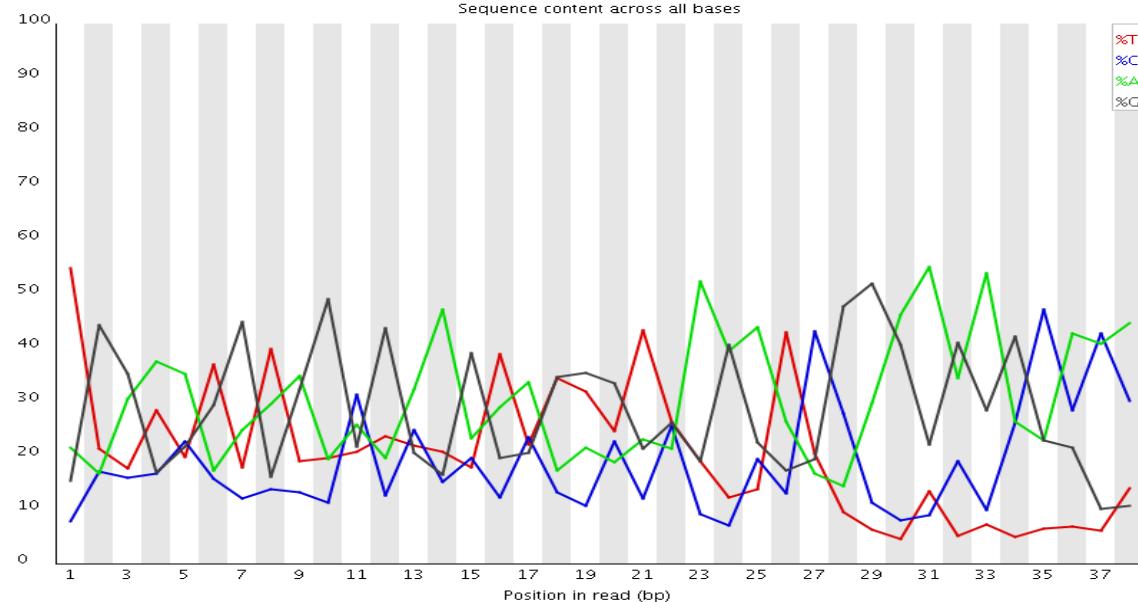
Per cycle sequence content



Per cycle sequence content



?



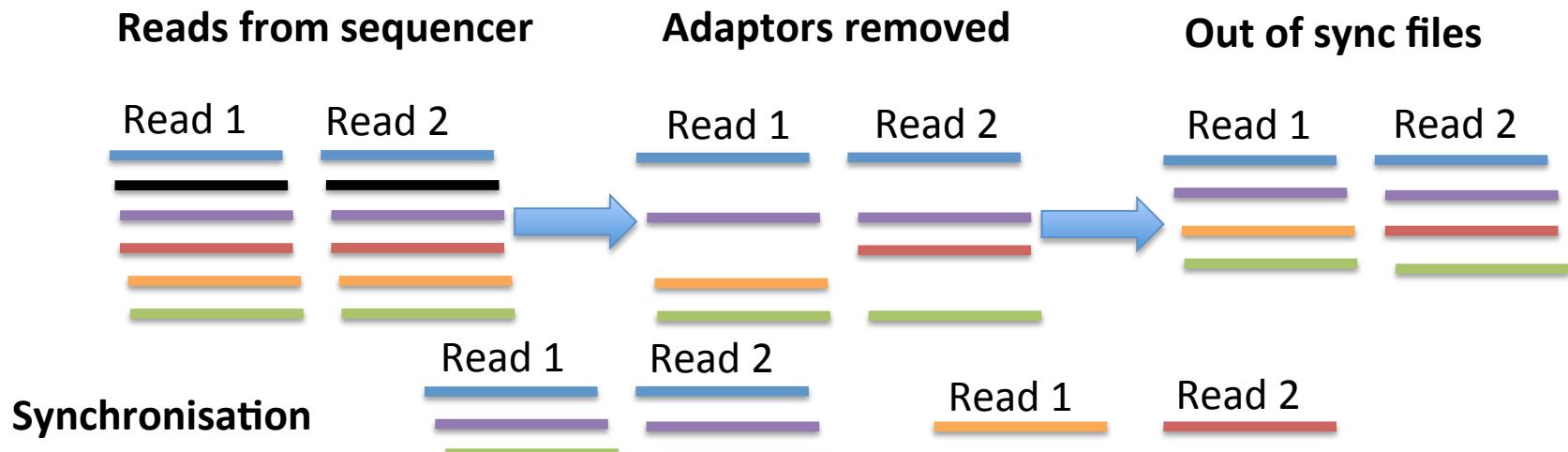
?

Manipulating fasta and fastq files

- Fastx toolkit: http://hannonlab.cshl.edu/fastx_toolkit/
- FASTQ trimmer
- FASTQ quality filter
- FASTQ quality trimmer
- Can do most of the obvious manipulations of fastq/a you may need

How to perform clean up

- Get an overview of the sample preparation both:
 - pre-sequencing
 - sequencing sample prep
- Run fastqc on the data
 - pay particular attention to the base distribution results
- Clean up using
 - fastx-toolkit
 - cutadapt
 - other tools
- Remember that you need to synchronise the R1 and R2 files (with PE)



**NB: Synchronisation is very important even when not clipping off adaptors
(files can be unsynchronised for other reasons)**



MAPPING WITH BWA

Why mapping?

- The biggest difference with Sanger
 - we did not design and use primers for sequence amplification
 - we sonicated
 - >> we do not know where the reads “originate” from
- For each read
 - we need to determine its likely origin
 - how likely it is that we have correctly identified its origin

- The Burrows-Wheeler Transform (BWT) is a way of permuting the characters of a string T into another string $BWT(T)$
- For example for $T = abaaba\$$
- $\$$ defined to be a character that does **not** appear elsewhere in T and which is **lexicographically prior** to all other characters
- The rotations of T

Burrows-Wheeler Matrix $BW M(T)$

\$	a	b	a	a	b	a
a	\$	a	b	a	a	b
b	a	\$	a	b	a	a
a	b	a	\$	a	b	a
a	a	b	a	\$	a	b
b	a	a	b	a	\$	a
a	b	a	a	b	a	\$

Lexicographic
sorting of rows

\$	a	b	a	a	b	a
a	\$	a	b	a	a	b
a	a	b	a	\$	a	b
a	b	a	\$	a	b	a
a	b	a	a	b	a	\$
b	a	\$	a	b	a	a
b	a	a	b	a	\$	a

$BWT(T)$

$BWT(T) = abba\$aa$

Relationship to suffix array

- Suffix array = sorted array of all suffixes of a string
- $T = abaaba\$$

All suffixes of T	Sorted suffixes	Matching order	
0 a b a a b a \$	6 \$	BWM:	SA: Suffixes given by SA:
1 b a a b a \$	5 a \$	\$abaaba	6 \$
2 a a b a \$	2 a a b a \$	a\$abaab	5 a\$
3 a b a \$	3 a b a \$	aaba\$ab	2 aaba\$
4 b a \$	0 a b a a b a \$	aba\$aba	3 aba\$
5 a \$	4 b a \$	abaaba\$	0 abaaba\$
6 \$	1 b a a b a \$	ba\$abaa	4 ba\$
		<u>baaba\$a</u>	1 baaba\$

The LF mapping property of the BWT

- $\text{BWT}(\text{abaaba\$}) = \text{abba\$aa}$
- Seem like we have lost which **a** in $\text{BWT}(T)$ corresponds to which **a** in T
- BUT we have not thanks to an important property of the BWT called **LF mapping**

\$	a	b	a	a	b	a
a	\$	a	b	a	a	b
a	a	b	a	\$	a	b
a	b	a	\$	a	b	a
a	b	a	a	b	a	\$
b	a	\$	a	b	a	a
b	a	a	b	a	\$	a

$$T = a_0 b_0 a_1 a_2 b_1 a_3 \$$$

The subscript corresponds to
the number of times the
character has previously been
seen in T

\$	a_0	b_0	a_1	a_2	b_1	a_3
a_3	\$	a_0	b_0	a_1	a_2	b_1
a_1	a_2	b_1	a_3	\$	a_0	b_0
a_2	b_1	a_3	\$	a_0	b_0	a_1
a_0	b_0	a_1	a_2	b_1	a_3	\$
b_1	a_3	\$	a_0	b_0	a_1	a_2
b_0	a_1	a_2	b_1	a_3	\$	a_0

We call the subscript the rank
\$ does not require rank as
occurs only once

The LF mapping states: the i^{th} occurrence of a character c in the last column has the same rank as the i^{th} occurrence of c in the first column

We will not
prove why!!

How do we reverse BWT? Useful for compression

We re-rank them:

Skipped

- * Before we ranked according how many times occurred previously in T ie T ranking
- * Now we re-rank according to how many times previously seen in BWT(T) ie B ranking

F	L	rank
\$	a	0
a	b	0
a	b	1
a	a	1
a	\$	0
b	a	2
b	a	3

Start with \$

F	L	rank
\$	a	0
a	b	0
a	b	1
a	a	1
a	\$	0
b	a	2
b	a	3

Rows are rotations of T so last col of the first row contains the character to left of \$ in T: a



Rank array tells us this is a with rank 0



How do we get the character to the left of a_0 ?



We can do this if we know the row that begins with a_0



The LF mapping states: the i^{th} occurrence of a character c in the last column has the same rank as the i^{th} occurrence of c in the first column



The LF tells us which row begins with a_0 : the first row containing an "a"

Assuming first row is 0, we visit rows: 0, 1, 5, 3, 2, 6, 4

$\xrightarrow{\quad\quad\quad} a_3 b_1 a_1 a_2 b_0 a_0 \$$

Reversible means useful for compression

FM index – key to searching a string

- Ferragina and Manzini: BWT can be used as a space-efficient index of T
- Searching for occurrences of P = aba
- The BWM is sorted, so any rows having P as a **prefix** will be **consecutive**

First find the rows beginning with the shortest **suffix** of P i.e. “a”

>> rows 1,2,3 and 4

1

F	a	b	a	a	b
\$	a	\$	a	b	a
a	\$	a	b	a	a
a	a	b	a	\$	a
a	b	a	\$	a	b
a	b	a	a	b	a
b	a	\$	a	b	a
b	a	a	b	a	\$

2

Second find all rows begin with the **next** longest **suffix** of P i.e. “ba”

>> these are rows 1 and 2 (**rows are rotations of T**)

3

The **LF mapping** and rank array tell us which rows have “ba” as a prefix: rows beginning with b0 and b1

The LF mapping states: the i^{th} occurrence of a character c in the last column has the same rank as the i^{th} occurrence of c in the first column

Searching T

F	L	$rank$
\$	a	0
a	\$	0
a	a	1
a	b	1
a	a	1
b	a	2
b	a	3

4

The LF mapping and rank array tell us which rows have “ba” as a prefix: row beginning with b0 and b1

3

F	L	$rank$
\$	a	0
a	\$	0
a	a	1
a	b	1
a	a	1
b	a	2
b	a	3

6

Occurrences of “ba” are preceded by a2 and a3

5

Backward matching: apply LF mapping repeatedly to find range of rows **prefixed** by successively longer proper **suffixes of P until range is empty or run out of suffixes**

With only 3 backward matching (LF mapping and rotations) operations we have found the rows prefixed with occurrences of “aba”

Looking up offsets

So far we have discussed how to use the FM Index to determine whether and how many times a substring P occurs within T , but we have not discussed how to find *where* P occurs, i.e. the substring's offset into T .

If our index included the suffix array $SA(T)$, we could simply look this up in $SA(T)$. For example, here was the range we ended up with after searching for $P = aba$ within $BWT(abaaba\$)$:

SA and BWM have a corresponding order

F	L	$SA(T)$	BWM:	SA:	Suffixes given by SA:
\$	a b a a b	a	6	\$abaaba	6 \$
a	\$ a b a a	b	5	a\$abaab	5 a\$
a	a b a \$ a	b	2	aaba\$ab	2 aaba\$
a	b a \$ a b	a	3	aba\$aba	3 aba\$
a	b a a b a	\$	0	abaaba\$	0 abaaba\$
b	a \$ a b a	a	4	ba\$abaa	4 ba\$
b	a a b a \$	a	1	baaba\$a	1 baaba\$

$SA(T)$ tells us these matches occurred at T offsets 0 and 3.

$T=abaaba$

012345

Maybe that did not seem impressive.....

<i>F</i>	<i>L</i>	<i>rank</i>
\$	a	0
a	\$	0
a	a	1
a	b	1
a	a	0
b	a	2
b	a	3

I could have found the offsets of “aba” in T. Yes,

BUT:

- either you then scan T with “aba” >> exhaustive search
- or you have to store the whole BWM matrix

When the string you are searching is 3 billion bases long that means:

- either you check for a match at every 3 bn positions
- or you need to store a matrix that is 3bn x 3bn

If you use the BWT and suffix array:

- You only need to store the first and last columns of the BWM (not the blue section)
- You need to do **X** backward matching operations to locate a string of **length X**

There are many optimisation to:

- Decrease space requirements
- Decrease time requirements
- Allow for mismatches

Application to read mapping

- You need to build an index of the genome you wish to search
- Reads are 100 bp long
- But, the longer the string searched for the longer the search time (**longer backtracking**), thus an advantage to search with a shorter string.
- There are 4 different nucleotides and 3.0E09 bases of genome
 - $4^{16} = 4.0\text{E}09$
 - $4^{17} = 17.0\text{E}09$
- Assuming complex sequence, 16 to 17 bp should be enough for a unique match
- BUT
 - variation in sample relative to reference
 - base call errors
 - **THUS** 17 bp search string is not enough
- BWA searches with a “seed” of 32 and allows 2 differences in the seed
- **Reads with seed matches are aligned using Smith-Waterman**

The Fasta, BWA index and other indexes in inputData

- Log into the machines and run
cd vc/inputData/human_g1k_v37_chr5/gatkBundle
ls -l *fasta*
- The biggest file is **human_g1k_v37_chr5.fasta**
- Take a look at this file with **less**
- Next biggest is **human_g1k_v37_chr5.fasta.bwt** What do you think this is?
- Another big one is **human_g1k_v37_chr5.fasta.sa** What do you think this is?
- Files with extension: amb, ann, pac, bwt and sa are generated by indexing of .fasta file
- .dict and .fai are very simple files needed by Picard and other programs

```
bwa index -a bwtsw genome.fa
samtools faidx genome.fa
java -jar CreateSequenceDictionary.jar R=genome.fa O=genome.dict
samtools dict genome.fa
```

What are desirable characteristics of a read mapper?

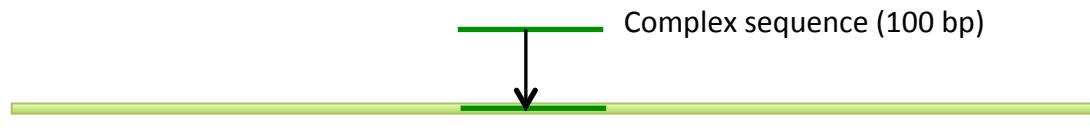
- Accurately predict the source of a read
 - in the normal range of base error rates
 - in the normal range of indel frequency and size
- But, not necessary to get the alignment exactly right as this can be done later using multiple sequence alignment (MSA)

Reference Sample	NNNNNCAAGNNNN	Reference Correct read align	NNNNNCA A AGGNNN
	NNNNNCA A AGNNNN		NNNNNCA A AGNNNN
		Reference Alt. align	NNNNNCAAGGNNN
			NNNNNCA A AGNNNN

- Produce an accurate estimate of the reliability of prediction

Factors complicating mapping

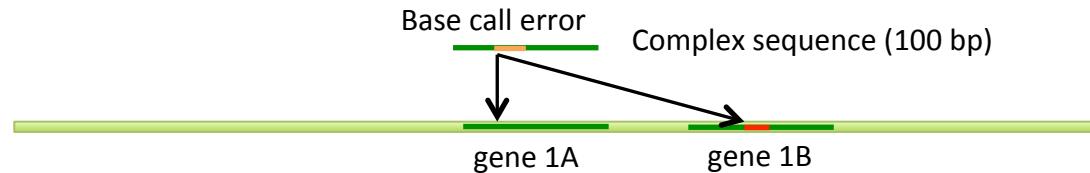
The simple case



Millions of reads

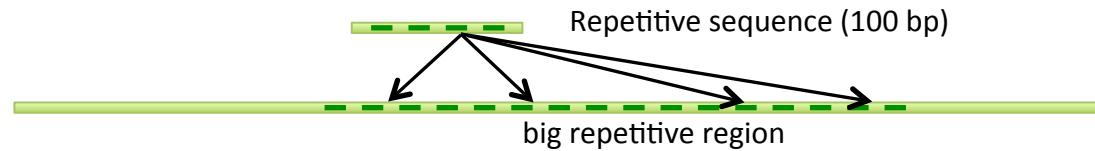
Billions of positions
in human genome

Homologous regions



Risk of mismatching

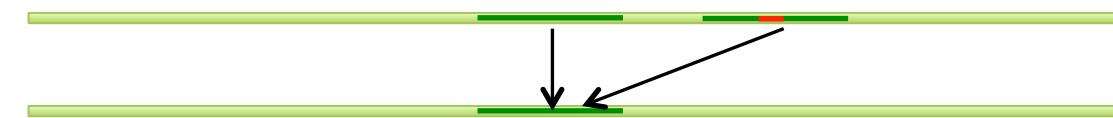
Repetitive region



Impossible to be
map correctly

Structural variation (not in reference)

Duplication in sample which is not present in the reference



Definite
"mismapping"

Different programs

- BWA
- Novoalign
- BOWTIE
- SOAP
-
- Most based on BWT: Burrows-Wheeler Transform
 - a very neat computer algorithm for finding the location of substrings within a string
 - can I find atgc in attgcatcgatcga.....
 - requires indexing of string / reference, but enables
 - rapid search, necessary when mapping billions of reads
 - manageable RAM footprint: 2.3 GB for single reads and 3GB for paired-end (for BWA), so runs on an ordinary computer

Mapping quality scores

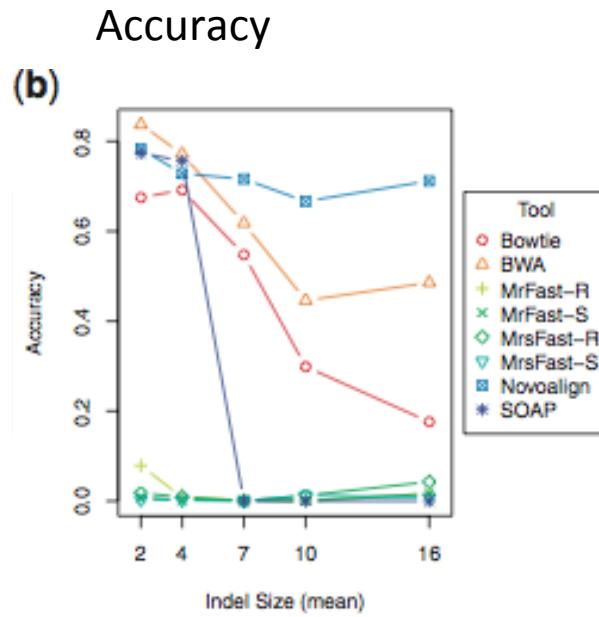
- The mapping quality score is the Phred-scaled probability of the mapping being **incorrect**.
- Probability is computed from the qualities of the mismatched bases between read and reference and quality features of the second best hit (see Li, Ruan, and Durbin 2008)
- All programs do not necessarily produce good estimates of mapping quality
- BWA provides good mapping qualities with slight overestimation of quality score:
 - empirical error rate 7×10^{-6} for Q60 mappings

$$Q_{\text{sanger}} = -10 \log_{10} p$$

BWA

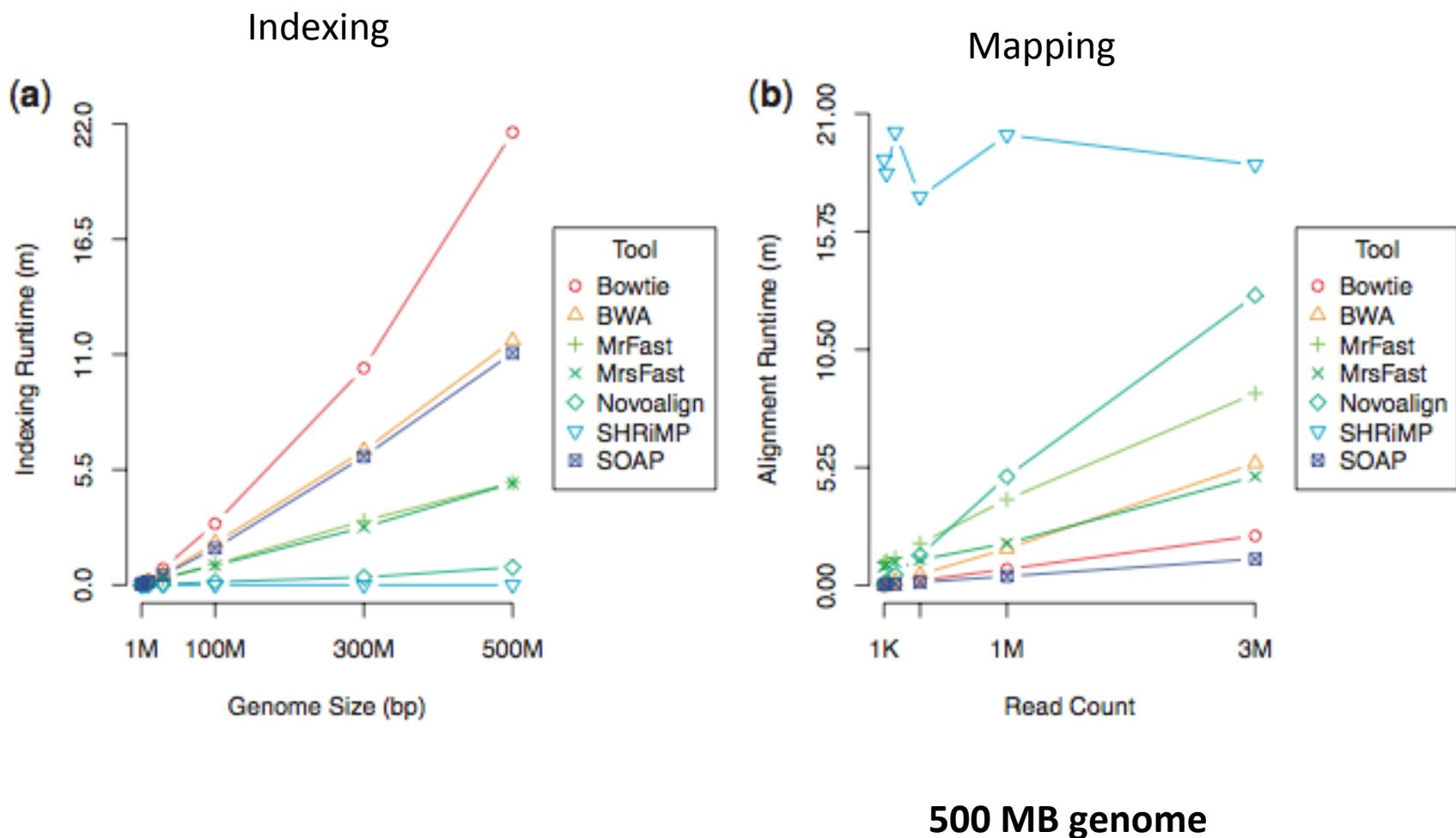
- Fast and accurate short read alignment with Burrows-Wheeler Transform
- But, in practice, makes changes to algorithm to adapt to biological reality and increase speed
- Paired-end mapping
- Like similar programs, randomly places a repetitive read across the multiple equally best positions and mapping quality 0
- Supports multi-threading (as do all BWT aligners)

Accuracy with varying indel sizes



- BWA and Novoalign are best performing

Runtime



Words of caution about the comparison

- Note this results are for SR 50 bp reads
 - reads are often longer with Illumina
 - can be much longer with other technologies and will require different mapper (see Fast and accurate long-read alignment with Burrows-Wheeler transform)
- **But, in summary:**
 - **mappers are not all of the same quality**
 - **bwa and novoalign are amongst the best for Illumina reads**

Alignment errors after mapping

Base stacks

coor	sample	coor	12345678901234	5678901234567890123456	
ref	pileup	ref	aggttttataaaaac	----aattaagtctacagagcaacta	
9	t ttt	sample	aggttttataaaaac	AAATaattaagtctacagagcaacta	
10	a aaaC	read1	aggttttataaaaac	<u>aaAt</u> aa	
11	a aaaaa	read2	ggttttataaaaac	<u>aaAt</u> aaTt	Incorrect
12	a aaaaaa	read3	ttataaaaac	AAATaattaagtctaca	
13	a aaaaaaa	read4	CaaaT	aattaagtctacagagcaac	
14	c cccTTT	read5	<u>aaT</u>	aattaagtctacagagcaact	
15	a aaaaaaa	read6	T	aattaagtctacagagcaacta	
16	a aaaaaaa	read1	aggttttataaaaac	<u>aaat</u> aa	
17	t AAffff	read2	ggttttataaaaac	<u>aaat</u> aatt	Correct
18	t ffffff	read3	ttataaaaac	<u>aaat</u> aattaagtctaca	
19	a aaaaaaa	read4	caaataattaagtctacagagcaac		
20	a aaaaaaa	read5	<u>aaat</u> aattaagtctacagagcaact		
21	g Tgggg	read6	taattaagtctacagagcaacta		

>> Can be solved by alignment: considering all mapping reads and reference together (as we shall see later)



SAM FORMAT

What does the SAM file look like?

BSQ	SN:1	LN:249250621
BSQ	SN:2	LN:243199373
BSQ	SN:3	LN:198022430
BSQ	SN:4	LN:191154276
BSQ	SN:5	LN:180915260
BSQ	SN:6	LN:171115067
BSQ	SN:7	LN:159138663
BSQ	SN:8	LN:146364022
BSQ	SN:9	LN:141213431
BSQ	SN:10	LN:135534747
BSQ	SN:11	LN:135006516

Header

Data lines (one per read)

Col	Field	Type	Regexp/Range	Brief description
1	QNAME	String	[!-?A-~]{1,255}	Query template NAME
2	FLAG	Int	[0,2 ¹⁶ -1]	bitwise FLAG
3	RNAME	String	* [!-()+-<>-~] [!-~]*	Reference sequence NAME
4	POS	Int	[0,2 ²⁹ -1]	1-based leftmost mapping POSition
5	MAPQ	Int	[0,2 ⁸ -1]	MAPping Quality
6	CIGAR	String	* ([0-9]+[MIDNSHPX=])+	CIGAR string
7	RNEXT	String	* = [!-()+-<>-~] [!-~]*	Ref. name of the mate/next segment
8	PNEXT	Int	[0,2 ²⁹ -1]	Position of the mate/next segment
9	TLEN	Int	[-2 ²⁹ +1,2 ²⁹ -1]	observed Template LENgth
10	SEQ	String	* [A-Za-z.=.]+	segment SEQuence
11	QUAL	String	[!-~]+	ASCII of Phred-scaled base QUALity+33

Inspecting one record

PCUS-319-EAS487_0001:7:1:1002:1094#0

pPr2

5

484690

29

76M

=

484585

-181

ATGCTTGGTGAAGCGCGTCACCAGCGACAGAAGGAAGGCGAA

; ; ; ; ; ; ; 3 / < 5 ; ; : 58 ? 65 < ' = ? ? ? < ; @ ? BBA ? BB = @ @ ? @ A

Col	Field	Type	Regexp/Range	Brief description
1	QNAME	String	[!-?A-~]{1,255}	Query template NAME
2	FLAG	Int	[0,2 ¹⁶ -1]	bitwise FLAG
3	RNAME	String	* [!-()+-<>-~] [!-~]*	Reference sequence NAME
4	POS	Int	[0,2 ²⁹ -1]	1-based leftmost mapping POSition
5	MAPQ	Int	[0,2 ⁸ -1]	MAPping Quality
6	CIGAR	String	* ([0-9]+[MIDNSHPX=])+	CIGAR string
7	RNEXT	String	* = [!-()+-<>-~] [!-~]*	Ref. name of the mate/next segment
8	PNEXT	Int	[0,2 ²⁹ -1]	Position of the mate/next segment
9	TLEN	Int	[-2 ²⁹ +1,2 ²⁹ -1]	observed Template LENgth
10	SEQ	String	* [A-Za-z.=.]+	segment SEQuence
11	QUAL	String	[!-~]+	ASCII of Phred-scaled base QUALity+33

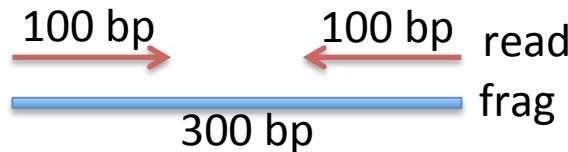
Difference between 1-based and 0-based coordinates

NNCTGGTNNNN

123456789 ==> specified as closed interval ==> coords 3-7 ==> length = 7 - 3 + 1
012345678 ==> specified as half-closed half-open ==> coords 2-7 ==> length = 7 - 2

- SAM (+ VCF and GFF) are 1-based
- BED are 0-based
- Can be very important when manipulating SNP coordinates >> be careful

The FLAG column – a bit wise flag



p=0x1 (paired sequencing)

P=0x2 (properly paired after mapping)

u=0x4 (unmapped)

U=0x8 (mate unmapped)

r=0x10 (reverse)

R=0x20 (mate reverse)

1=0x40 (first read in pair)

2=0x80 (second read in pair)

s=0x100 (not primary) ==> if read has multiple mappings one must be primary

f=0x200 (failure) ==> does not pass filter

d=0x400 (duplicate) ==> PCR or optical duplicate

- Translate from bit wise flag to readable codes by using **samtools view -X**
- OR take a look at <https://broadinstitute.github.io/picard/explain-flags.html>

Introducing flags - What is a duplicate?



About the SAM file produced by BWA

- It contains **all** the reads >> the Picard/GATK paradigm: information is annotated (and not filtered)
 - unique
 - ambiguous
 - unmapped
- It has a number of short comings
 - it takes a lot of space → convert to BAM
 - the mates are not fully updated on each others existence → fixmate
 - it is not sorted → sort
 - it contains PCR duplicates → mark or remove duplicates
 - it does not contain meta-data on the reads (sample, sequencer, etc)

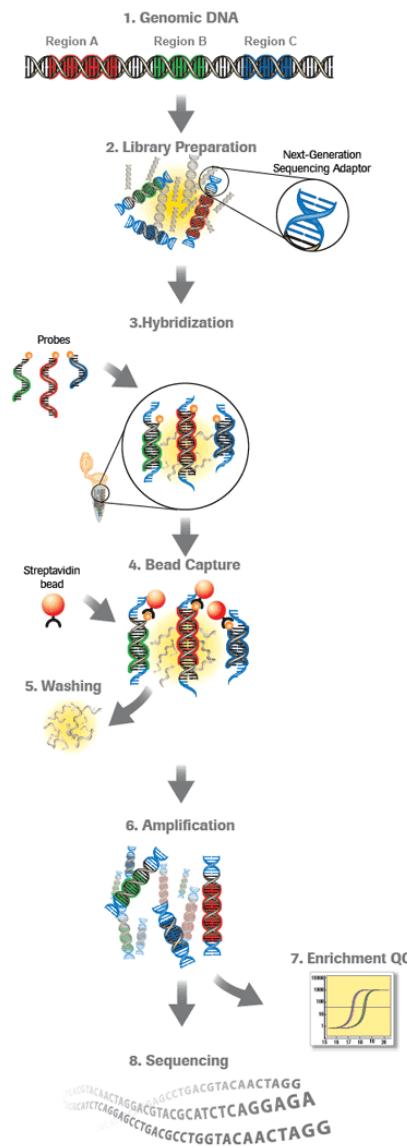
What tools can I use to manipulate the data?

- Two alternative software packages for doing this
 - samtools
 - basic
 - easy to use
 - picard
 - advanced functionality
 - used by GATK team
- For simple tasks like viewing, indexing, sorting → samtools
- For more advanced tasks and preparing for downstream analysis → Picard due to GATKs pickyness
- These tools will be introduced in more detail in the practicals
- **Brief practical: Take a look at your SAM file**



COMPUTING ADVANCED METRICS – PICARD

An overview of exome capture – weak points



Sonication

Library prep
(sequencing adaptors on)

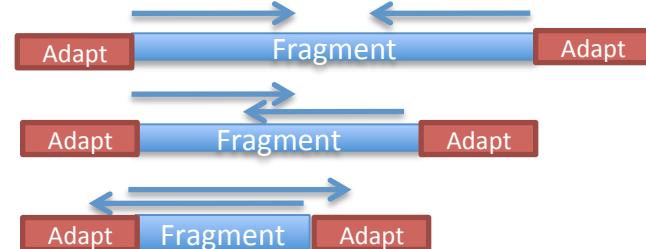
Hybridisation
to probes

Bead capture

Amplification

Sequencing

Problem: error in sonication >> adaptor seq in reads >> unmapped reads



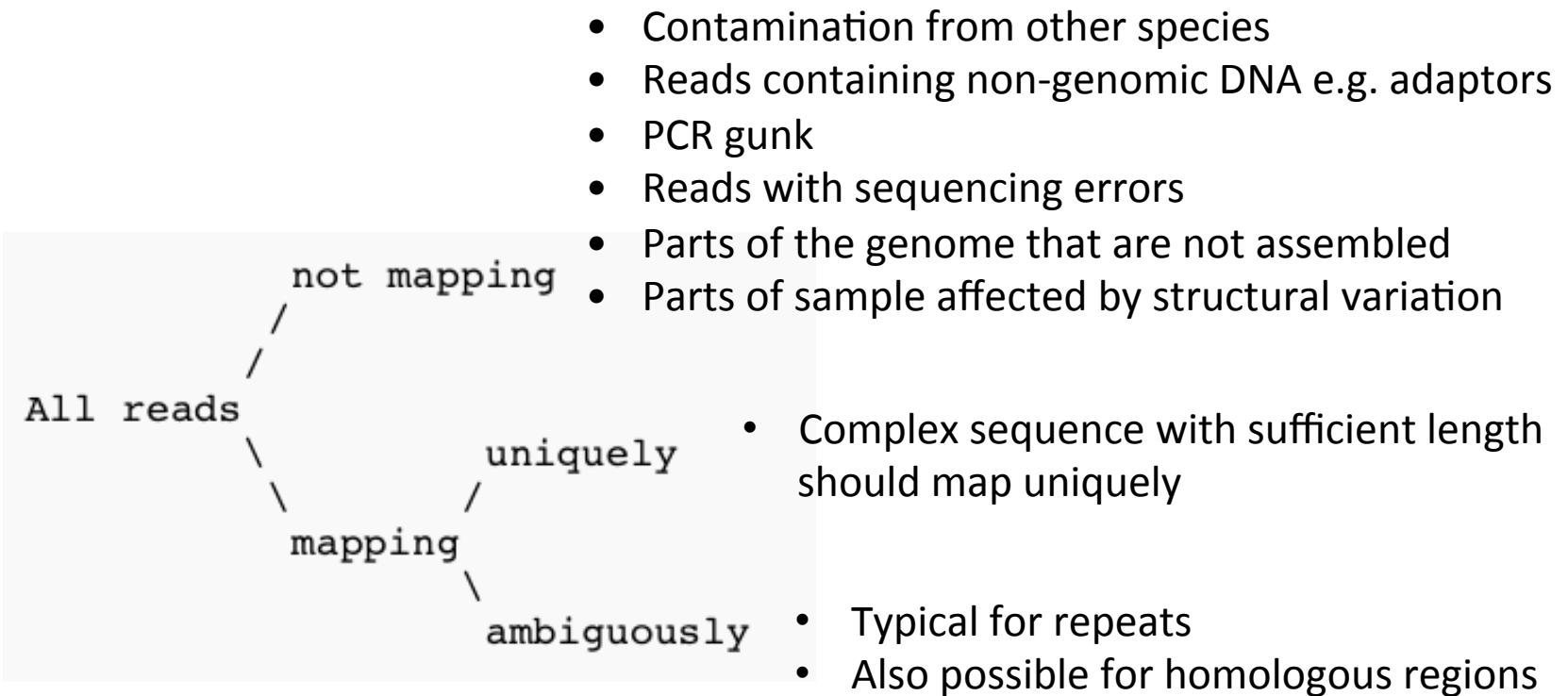
Possible biases in sequences that hybridise >> **coverage bias**

Possible biases in sequences that elute >> **coverage bias**

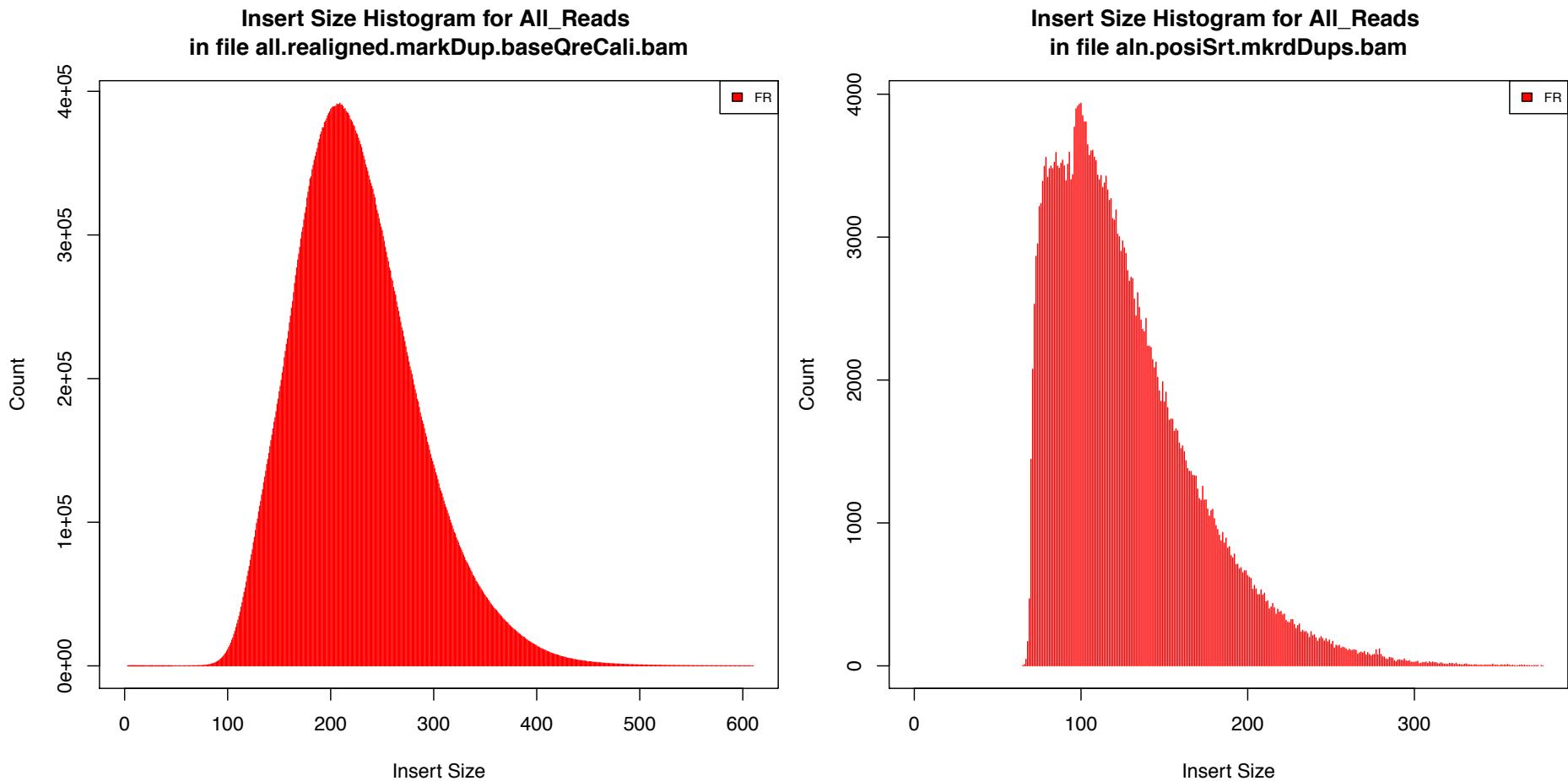
Possible biases in sequences that amplify >> **sequence PCR duplicates**

Possible biases in sequences that bridge PCR >> **coverage bias**

Metrics - Basic read classification

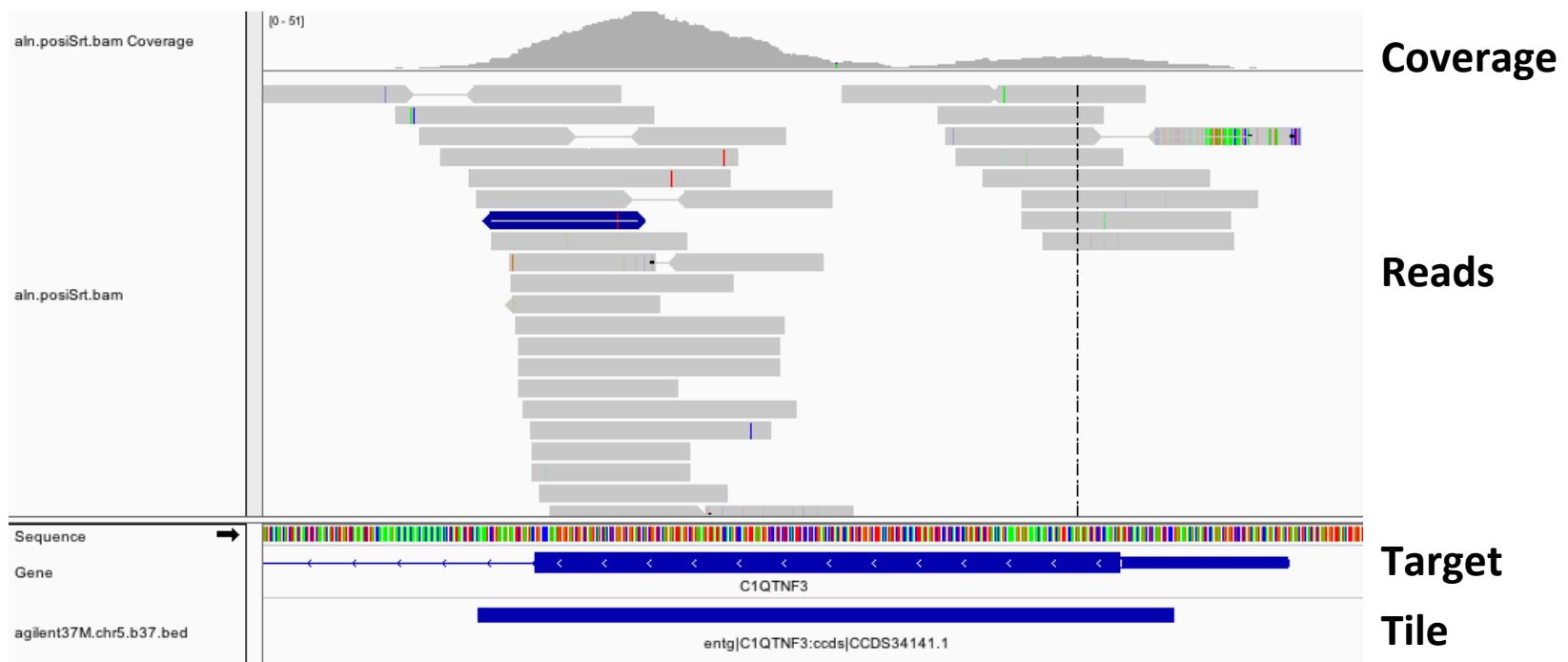


Metrics – Insert sizes

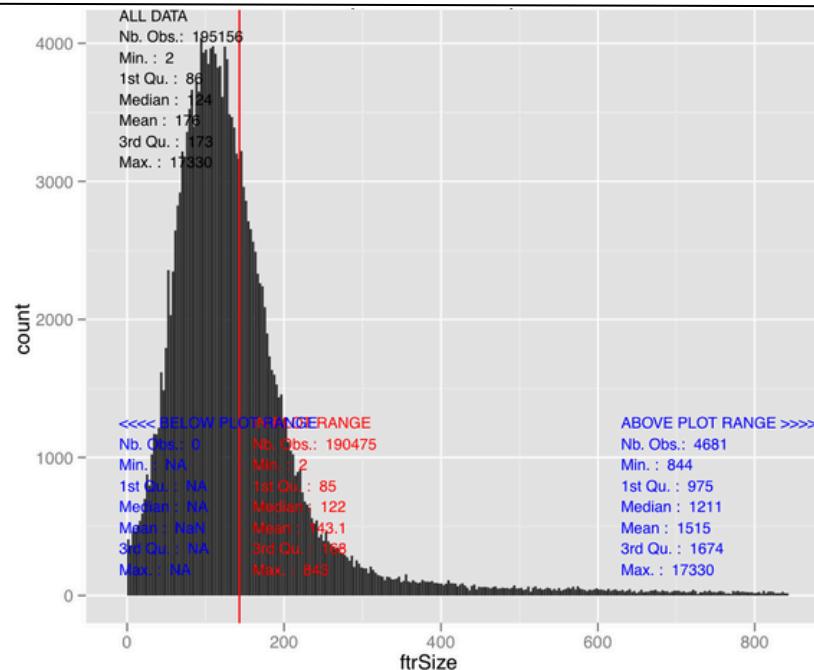


Metrics - Coverage

- Even if doing Whole Genome Sequencing (WGS) >> coverage issues
 - due to repetitive regions
 - due to properties of the DNA e.g. GC content
- Exome sequencing >> Capture by hybridisation



Exome capture – The nature of the target



CCDS exon length distribution

Exon(x) - the target:
(R=repeat, I=intro)

IIIIIXXXXXXXXXXXXXXRRRRXXXXXXIIII

Nimblegen (avoid repeats and tiles no longer than need to be)
The tiled (T) region (or bait): TTTTTTTTTTTTTTT
The oligos(O) (or probes): 00000 0000000
00000 0000
00000 0000
00000 0000
00000 0000

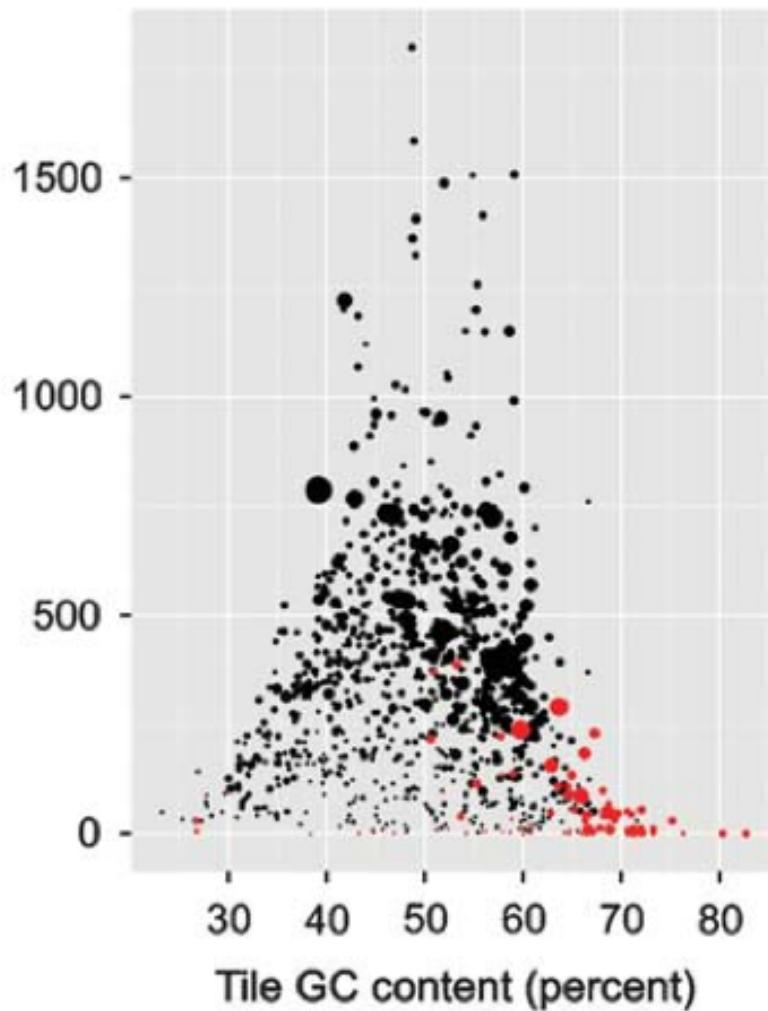
Agilent (no attempt to avoid repeats and no oligo overlap so tiles are always multiple of 120 so often sequence well into introns)
The tiled (T) region (or bait): TTTTTTTTTTTTTTTTTTTTTTTTTTT
The oligos(O) (or probes): 0000000000000000|0000000000000000

There may be more than one tiled region per target
.e.g. if the target contains repeats.
Oligo spacing: distance between start positions of oligos
Oligo overlap: number of overlapping bases between oligos

Coverage metrics – Effect of GC content

a

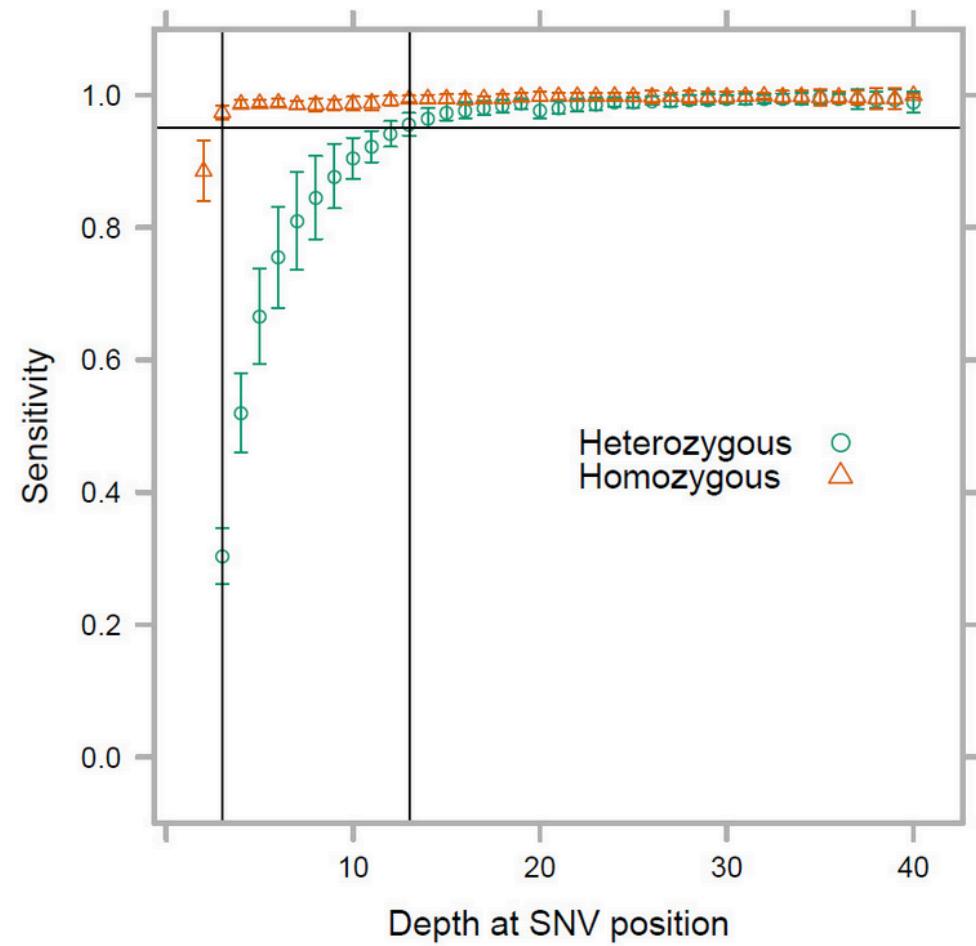
Average coverage depth of tile



ZERO_CVG_TARGETS_PCT	0.031204
FOLD_80_BASE_PENALTY	2.955833
PCT_TARGET_BASES_2X	0.930749
PCT_TARGET_BASES_10X	0.634677
PCT_TARGET_BASES_20X	0.334935
PCT_TARGET_BASES_30X	0.16685

The effect of depth on errors

- Heterozygotes vs homozygote variant sites
- Equal sampling of alleles



From "Quantifying single nucleotide variant detection sensitivity in exome sequencing"
BMC Bioinformatics 2013

Duplicate metrics



Duplicates potentially introduce variant calling errors

021_generatingReports.bash

- Time to see how we can do some of this in practice
- Walk through the fastq and SAM/BAM part of the practical
- Stop when we get to VCF part!
- **Walk through this together with instructor**

VCF FILE - BASICS

VCF format

```
##fileformat=VCFv4.0
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=1000GenomesPilot-NCBI36
##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=.,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
20 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2
20 17330 . T A 3 q10 NS=3;DP=11;AF=0.017
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
20 1230237 . T . 47 PASS NS=3;DP=13;AA=T
20 1234567 microsat1 GTCT G,GTACT 50 PASS NS=3;DP=9;AA=G
```

Meta data:
definitions of
tags used
elsewhere in
data lines

Header line

FORMAT	NA00001	NA001
GT:GQ:DP:HQ	0 0:48:1:51,51	
GT:GQ:DP:HQ	0 0:49:3:58,50	
GT:GQ:DP:HQ	1 2:21:6:23,27	
GT:GQ:DP:HQ	0 0:54:7:56,60	
GT:GQ:DP	0/1:35:4	

Data lines

Variant columns

Genotype columns

Columns of data lines

- **CHROMO:** chromosome / contig
- **POS:** the reference position with the 1st base having position 1
- **ID:** an id; rs number if dbSNP variant
- **REF:** reference base.
 - The value in POS refers to the position of the first base in the string
 - for indels, the reference string must include the base before the event (and this must be reflected in POS)
- **ALT:** comma separated list of alternate non-ref alleles called on at least one of the samples
 - if no alternate alleles then the missing value should be used “.”
- **QUAL:** phred-scaled quality score of the assertion made in ALT (whether variant or non-variant)
- **FILTER:** PASS if the position has passed all filters (defined in meta-data).
- **INFO:** additional information

REF and ALT

Reference a t C g a >> C is reference base

		REF	ALT
Variant	a t G g a >> C is a G	20 3 .	C G
Variant	a t - g a >> C is deleted	20 2 .	TC T
Variant	a t Cag a >> A is inserted	20 3 .	C CA

REF and ALT

Reference a t C g a >> C is reference base

		REF	ALT
Variant	a t G g a >> C is a G	20 3 .	C G
Variant	a t - g a >> C is deleted	20 2 .	TC T
To represent both in the same record		20 2 .	TC T,TG

Comparing VCF files: normalisation

- The VCF format is quite precise but still leaves room for representing one variant in multiple ways
 - VCF files need normalisation before comparison
- **Parsimony**
 - Pos: 5, Ref: ATC, Alt: AT
 - Or Pos: 6, Ref: TC, Alt: T >> most parsimonious
- **Left alignment**, suppose context: pos 8, ref: ATTTT, T deletion
 - Pos: 10, Ref: TT, Alt: T
 - Or Pos: 8, Ref: AT, Alt: A >> left aligned
- **MNP on separate lines**
 - 150 TCT CCC
 - Can be decomposed into two records: 150 T C AND 152 T C
- **One should also ensure that the same reference naming is used in both comparison files and that both files have the same sort order**
- More details at:
<https://github.com/chapmanb/bcbio.variation/wiki/Normalized-variant-representation> and http://genome.sph.umich.edu/wiki/Variant_Normalization

021_generatingReports.bash (part II: VCF file)

- Time to take a look at the VCF part of the practical
- **Do this together**

Practical 022_workingWithFormats

- introduction to manipulation of:
 - SAM/BAM
 - VCF
- **Walk through this together**

APPENDIX

Overview of topics (not in chrono order)

- Software and datasets setup and intro
- Fastq format
- Read mapping (SAM/BAM format)
- IGV
- Variant calling (VCF format)
- Metrics reports (esp coverage – BED format)
- Alignment refinement
- Base quality score recalibration
- Variant annotation and functional filtration

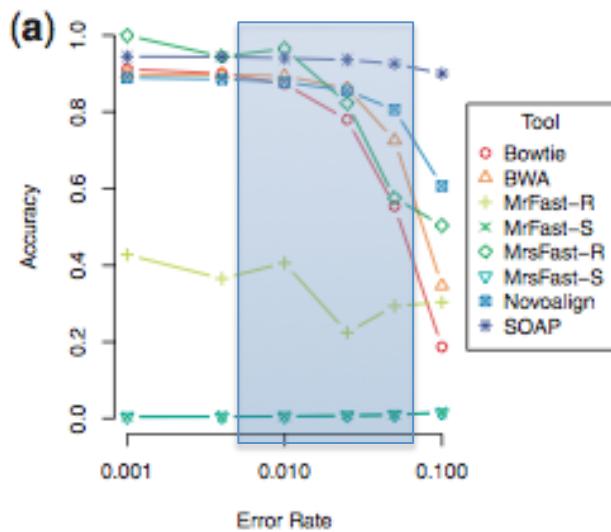
Comparison of different programs (optional)

- Comparison analysis of algorithms for next-generation sequencing read alignment, Ruffalo et al. 2011
 - generate genome in silico with certain indel properties (size and frequency)
 - simulate reads from this genome with certain error rate
 - measure mapper accuracy: the true location of a read is considered the truth and a mapping is considered a prediction
- What to look out for on the next slide
 - Ignore the Fast tools as they are poor mappers (green in legend)
 - Only focus on the parts of the plots that cover realistic range of parameters
- In summary, BWA and Novoalign are both good mapping tools

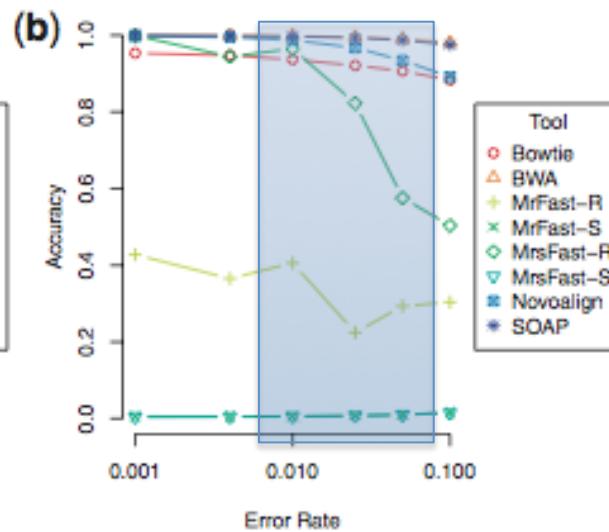
Accuracy with varying error rate

With mapping quality threshold 10

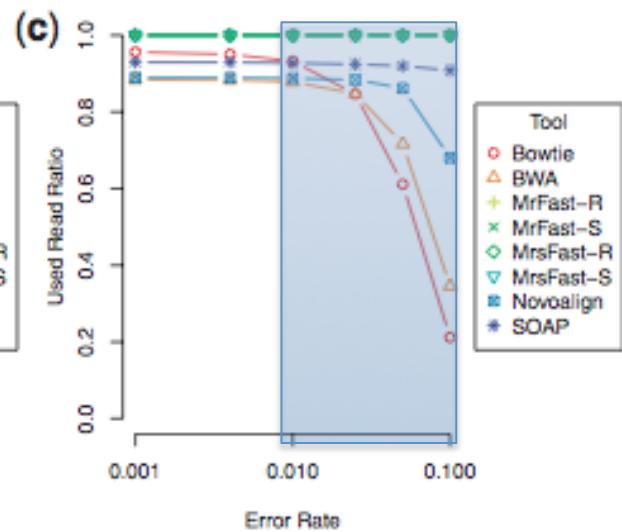
Accuracy



Accuracy



Used read ratio

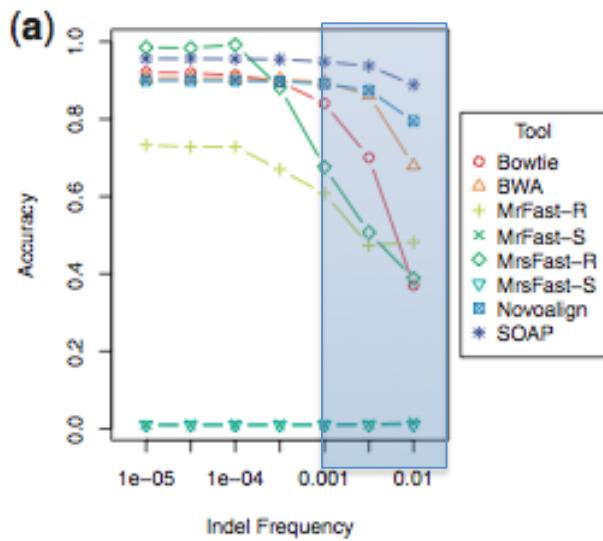


- No indels
- Higher range of error rate is unrealistic
- Minor differences between good algorithms in range

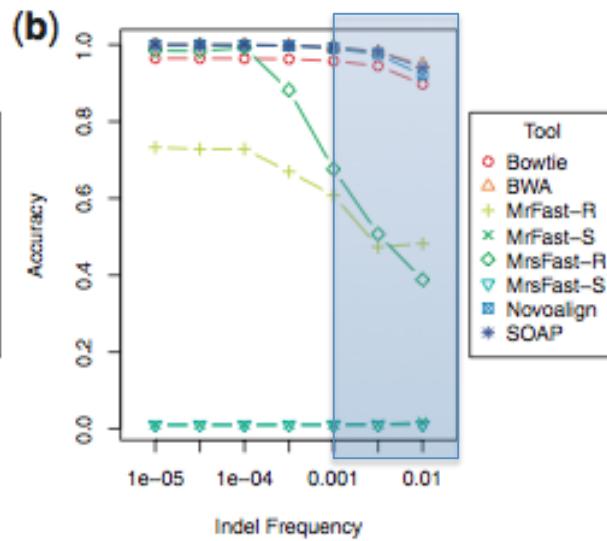
Accuracy with varying indel frequency

With mapping quality threshold 10

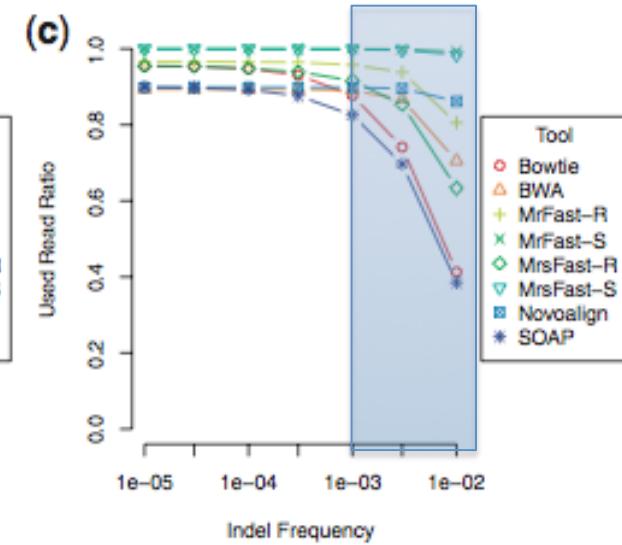
Accuracy



Accuracy



Used read ratio



- indel size fixed at 2 → small
- error rate fixed at 0.01 → somewhat high
- only lower indel frequencies are realistic → small differences between programs in relevant range
- soap would have looked a lot worse if indel size had been bigger