

Quick introduction to genomic file types
Preliminary quality control (lab)

File types overview

- Fasta/fastq qual
- Fastq
- SAM

Text files

- BAM
- sff

Binary files

- ...
- ...

<http://www.molecularrevolution.org/resources/fileformats>

Fasta

- Most basic file format for nucleotide or amino-acid sequences
- Each sequence requires:
 - A single description line (shouldn't exceed 80 characters):
 - Starts with ">"
 - Followed by **sequence ID** and a space
 - More information (**description**)
 - The sequence, over one or several lines
(the number of characters per line is generally 70 or 80, but it doesn't matter)

↓ ↓ ↓
>Protein1 Description of protein 1
MTEITAAMVKELRESTGAGMMDCKNALSETNGDFDKAVQLLREKGLGKAAKKADRLAAEG
LVSVKVSDDFTIAAMRPSYLSYEDLDMTFVENEYKALVAELEKENEERRRLKDPNKPEHK
>DNA1 Description of dna segment 1
AACTCTCGCGTAGCTCAGAGAAGAGCTTGATCGATCGTGCTGCTGCTAGATGCTGTAGCG
CCGCTAGTAGCTGTAGATCGTGCTAGTCAGCATCGATGCTAGCTAGCTAGCTAATTACGC

Fasta qual

- Fasta-like quality format
- Always paired with a fasta file (sequences with same IDs, same order)
- Description line as in fasta format
- Qualities: a number for each base in the corresponding fasta, separated by spaces
- Can be gzip-ped and used as such by some programs



>DNA1 quality of dna segment 1

23 23 22 24 23 12 3 34 23 23 22 21 23 34 32 9 14 25 21 21 21
22 24 23 12 3 34 23 23 22 21 23 34 32 9 14 25 21 21 21 3 21

Quality - Phred scores

- Most common representation of qualities
- Related to the probability of errors (P) in a particular base

$$Q = -10\log_{10} P$$

$$P = 10^{\frac{-Q}{10}}$$

Phred Quality Score	Probability of incorrect base call	Base call accuracy
10	1 in 10	90 %
20	1 in 100	99 %
30	1 in 1000	99.9 %
40	1 in 10000	99.99 %
50	1 in 100000	99.999 %

- Solexa runs < 1.3 use a different calculation:
 - Equivalent for high quality
 - Different for low quality (negative values of Q allowed)

FastQ

- A more compact format to store sequence and qualities
- Normally on 4 lines:
 - “@” followed by the sequence ID
 - Sequence
 - “+”
 - The quality score

→ @SEQ_ID
→ GATTGCGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAA
→ +
→ !' '* (((* * * +)) % % % + +) (% % % %) . 1 * * * - + * ' ') * * 55CCF>>>>>

Example taken from Wikipedia

FastQ (contd.)

- **Quality score:**
 - ASCII encoding of phred scores
 - Sanger has one scale
 - Illumina has 3 different
- Can be gzip-ped and used as such by some programs

ASCII decimal codes

Dec	Symbol	Dec	Symbol	Dec	Symbol
32	Space	64	@	96	`
33	!	65	A	97	a
34	"	66	B	98	b
35	#	67	C	99	c
36	\$	68	D	100	d
37	%	69	E	101	e
38	&	70	F	102	f
39	'	71	G	103	g
40	(	72	H	104	h
41	)	73	I	105	i
42	*	74	J	106	j
43	+	75	K	107	k
44	,	76	L	108	l
45	-	77	M	109	m
46		78	N	110	n
47	/	79	O	111	o
48	0	80	P	112	p
49	1	81	Q	113	q
50	2	82	R	114	r

- Solexa picked different quality definition and ranges over time, all different from Sanger values
- Ask your sequence provider!
- Guessing by getting the range of all values in all/many reads (not foolproof)

```

SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS.....
.....XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX.....
.....IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII.....
.....JJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJ.....
!"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNPOQRSTUVWXYZ[\]^_`abcdefghijklmnopqrstuvwxyz{|}~
|               |       |               |
33             59      64            73                     104                               126
                -----
S - Sanger          Phred+33,   raw reads typically (0, 40)
X - Solexa          Solexa+64,  raw reads typically (-5, 40)
I - Illumina 1.3+   Phred+64,   raw reads typically (0, 40)
J - Illumina 1.5+   Phred+64,   raw reads typically (3, 40)

```


SAM/BAM

- SAM (Sequence Alignment/Map) format is the alignment of sequences (e.g. reads) to a reference sequence (e.g. genome)
 - Simple to read and parse (text, tab-delimited)
 - Flexible (possibility to add custom fields)
 - Compact in file size
 - Can store paired-end information
- Reference document:
<http://samtools.sourceforge.net/SAM1.pdf>
- **BAM** is a binary (more compact) representation of SAM

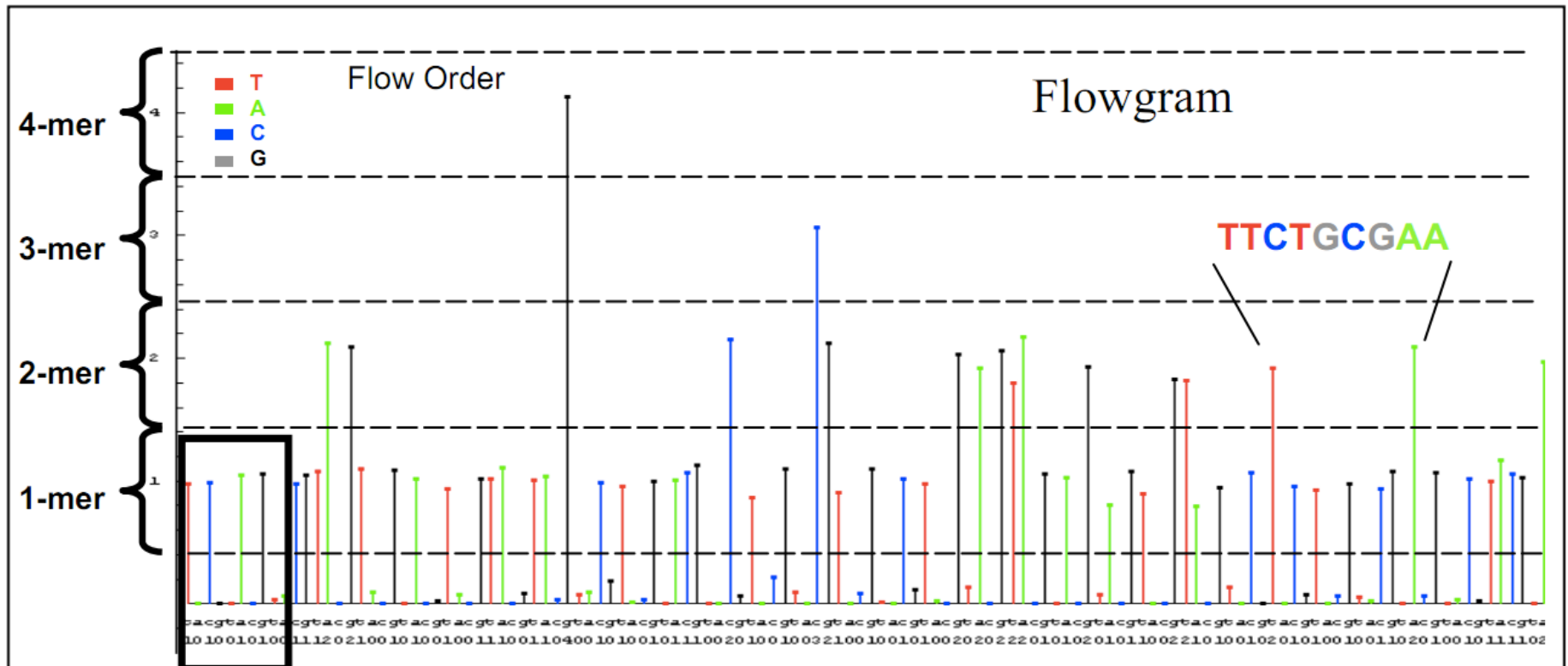
- Query (pair) name
- Reference name
- Position
- Mapping quality
- CIGAR string
- Seq and quality
- Tag:type:value fields

```
@HD      VN:1.0
@SQ      SN:chr20 LN:62435964
@RG      ID:L1 PU:SC_1_10 LB:SC_1 SM:NA12891
@RG      ID:L2 PU:SC_2_12 LB:SC_2 SM:NA12891
read_28833_29006_6945 99 chr20 28833 20 10M1D25M = 28993 1
AGCTTAGCTAGCTACCTATATCTTGGTCTTGCCG <<<<<<<<<<<<<<<
NM:i:1 RG:Z:L1
read_28701_28881_323b 147 chr20 28834 30 35M = 28701 -
ACCTATATCTTGGCCTTGGCCGATGCGGCCCTTGCA <<<<;<<<<7;:<<<
MF:i:18 RG:Z:L2
```

sff

- Binary format provided by 454 sequencing
- Contains
 - A header with information on the run (name, key sequence, number of reads, etc.)
 - For each read:
 - Name, length of the read
 - Clipping information (quality and adaptor)
 - Numeric representation of the flowgrams (454 equivalent to chromatograms)
 - Base sequence called from flowgrams
 - Qualities

454 flowgram



Key sequence = TCAG for signal calibration

Exercise: preliminary quality control of raw sequences

- number of sequences, length, average, distribution
- fasta/fastq conversion
- fastq statistics
- fasta quality chart/boxplot
- nucleotide distribution
- clipping/trimming reads