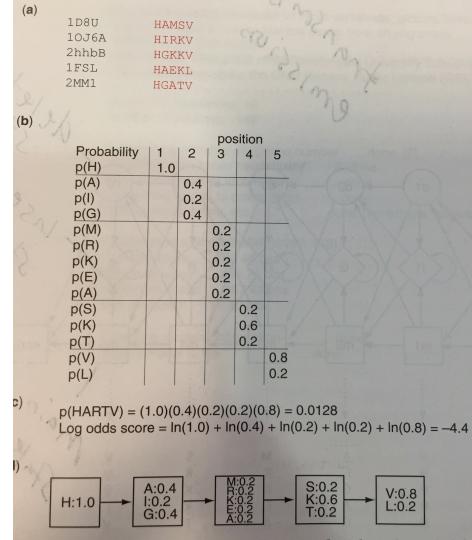
HMM

Sept 21, 2015

ANNOUNCEMENTS

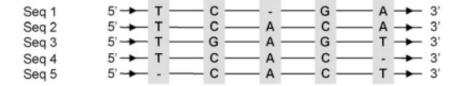
HIDDEN MARKOV MODEL

HIDDEN MARKOV MODEL

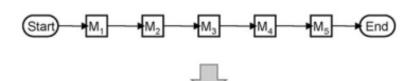


HIDDEN MARKOV MODEL

(a) Sequence Alignment

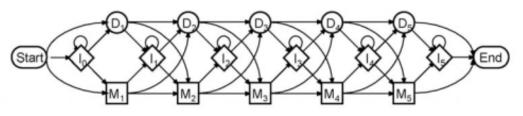


(b) Ungapped HMM



M_k Match states

(C) Profile-HMM

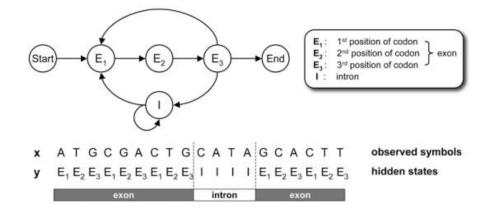


M_k Match states

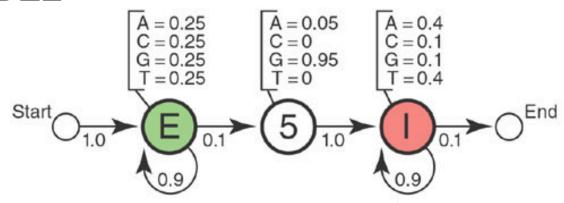
Insert states

Delete states

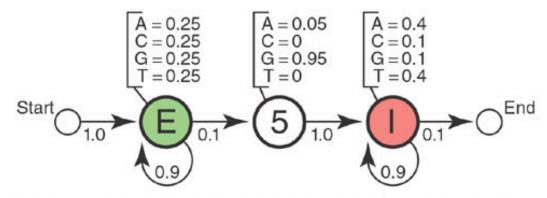
HIDDEN MARKOV MODEL



HIDDEN MARKOV MODEL

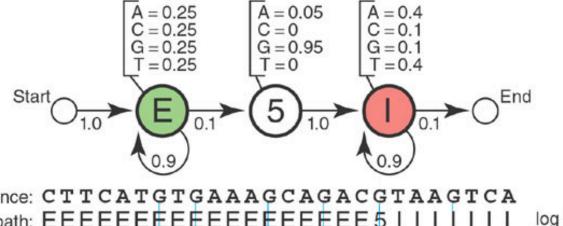


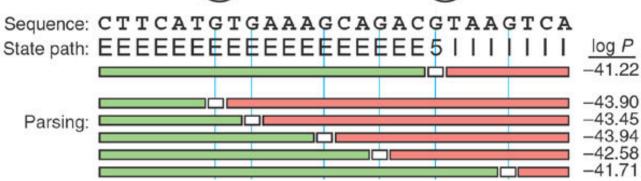
HIDDEN MARKOV MODEL



Sequence: CTTCATGTGAAAGCAGACGTAAGTCA

HIDDEN MARKOV MODEL





fastQ format and Illumina sequence data

fastQ

Description

Uses

fastQ

@HSQ-7001360:67:H88RHADXX:1:1101:1448:2158 1:N:0:CAGATC ATCTATCTGAGACTGATACGCCTTCGGCTTAATTTATACAAG +

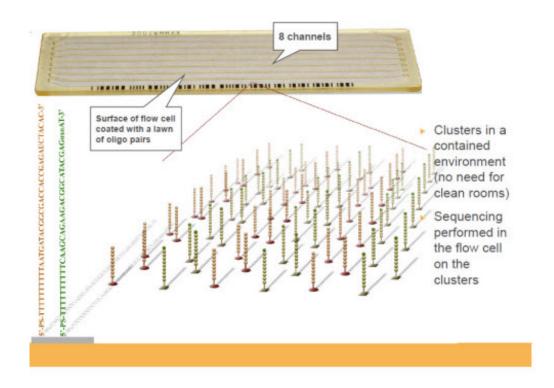
fastQ

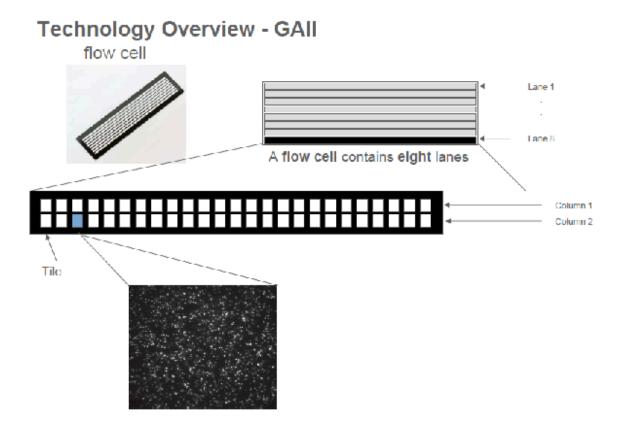
@HSQ-7001360:67:H88RHADXX:1:1101:1448:2158 1:N:0:CAGATC

- HSQ-7001360= Instrument name
- 67= run ID
- H88RHADXX=Flowcell ID
- 1=lane 1
- 1101=tile number
- 1448= x coordinate
- 2158= y coordinate
- 1=left read
- N=not filtered
- 0=control bit -> (not used anymore)
- CAGATC= adapter sequence

fastQ -> Illumina Seq

https://youtu.be/womKfikWlxM

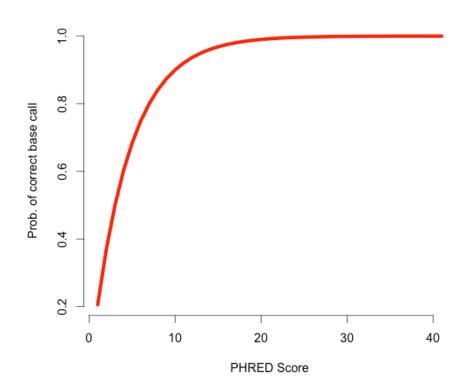


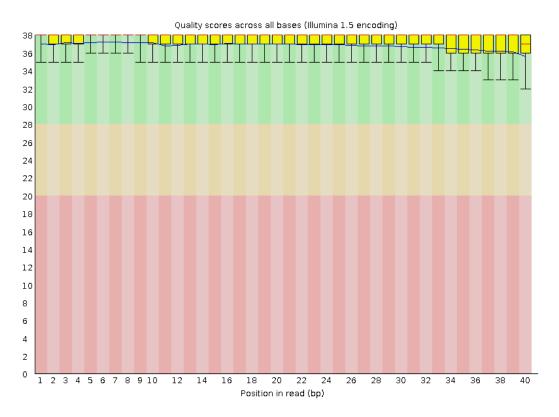


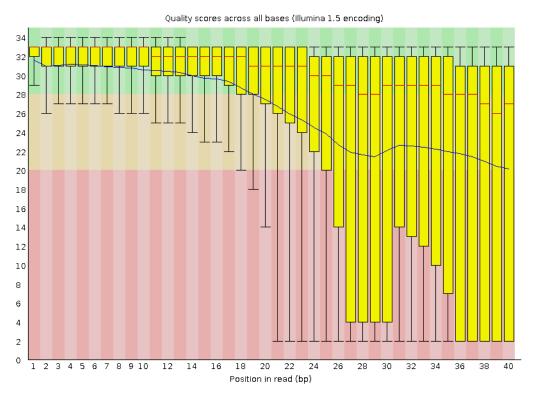
@HSQ-7001360:67:H88RHADXX:1:1101:1448:2158 1:N:0:CAGATO

- 1101=tile number
- 1448= x coordinate
- 2158= y coordinate

```
!"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKLMNOPQRSTUVWXYZ[\]^ `abcdefghijklmnopgrstuvwxyz{|}~
33
                              104
                                        126
3.....40
0.2.....41
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)
 with 0=unused, 1=unused, 2=Read Segment Quality Control Indicator (bold)
 (Note: See discussion above).
L - Illumina 1.8+ Phred+33, raw reads typically (0, 41)
```







— Figure 4. Paired-End Sequencing and Alignment ——

Paired-End Reads

