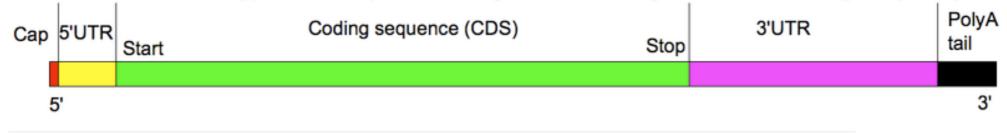
RNASeq Introduction Malay (malay@uab.edu)

Structure of mRNA

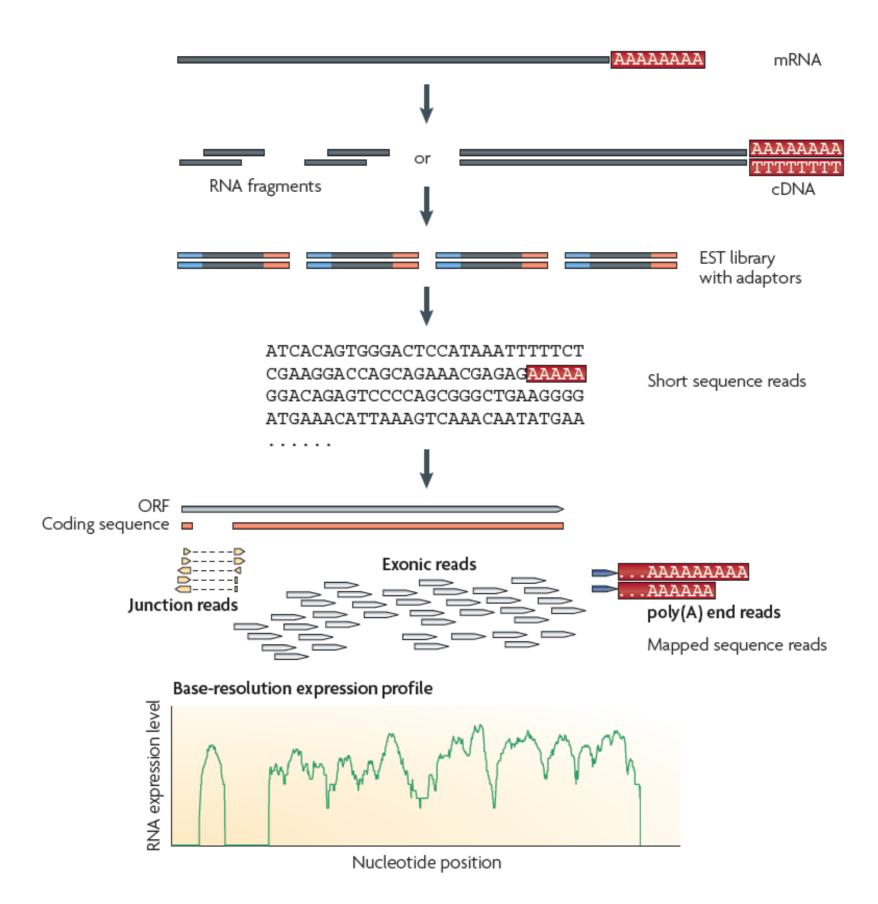
The structure of a typical human protein coding mRNA including the untranslated regions (UTRs)



Other RNAs:

	Туре	Size	Function
•	microRNA (miRNA)	21-23 nt	regulation of gene expression
•	small interfering RNA (siRNA)	19-23 nt	antiviral mechanisms
•	piwi-interacting RNA (piRNA)	26-31 nt	interaction with piwi proteins/spermatogenesis
•	small nuclear RNA (snRNA)	100-300 nt	RNA splicing
•	small nucleolar RNA (snoRNA)	-	modification of other RNAs

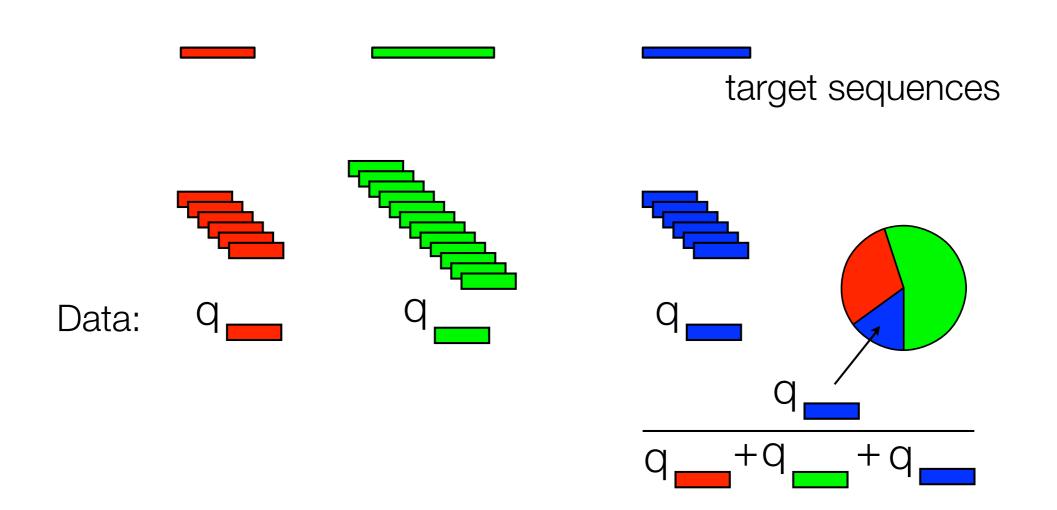
RNASeq overview



Various applications of RNASeq

Differential expression Novel transcript detection Fusion transcript detection Mutation detection (not common) Example count tables: <u>http://bowtie-bio.sourceforge.net/recount/</u>

The fragment assignment problem



Normalization methods in RNASeq

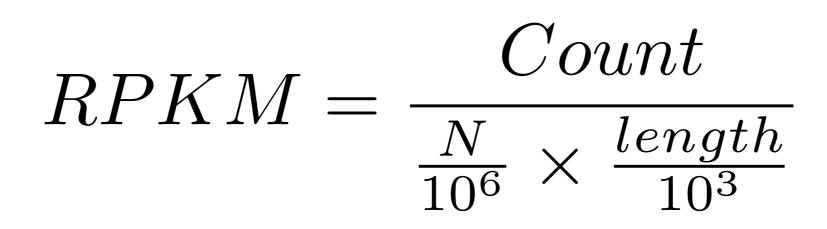
Upper Quartile (UQ): Very similar in principle to TC, the total counts are replaced by the upper quartile of counts different from 0 in the computation of the normalization factors.

DESeq: This normalization method is included in the DESeq

Trimmed Mean of M-values (TMM): This normalization method is implemented in the edgeR

Reads Per Kilobase per Million mapped reads (RPKM): This approach was initially introduced to facilitate comparisons between genes within a sample and combines between- and within-sample normalization.

FPKM: Same as RPKM, but for fragments.



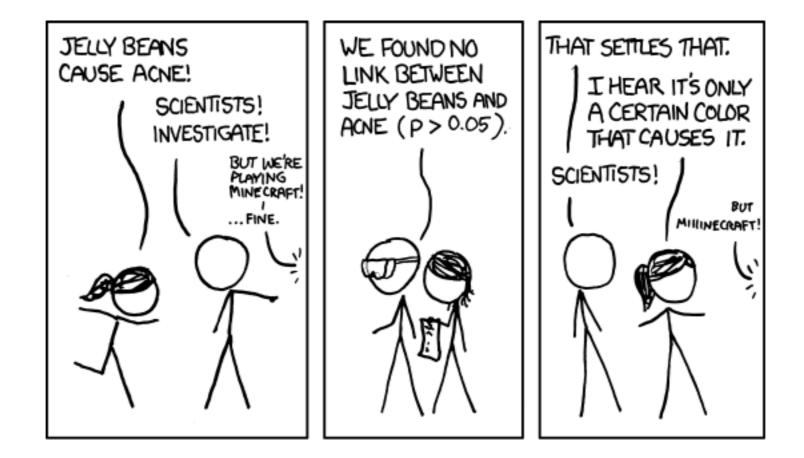
Upper quartile normalization

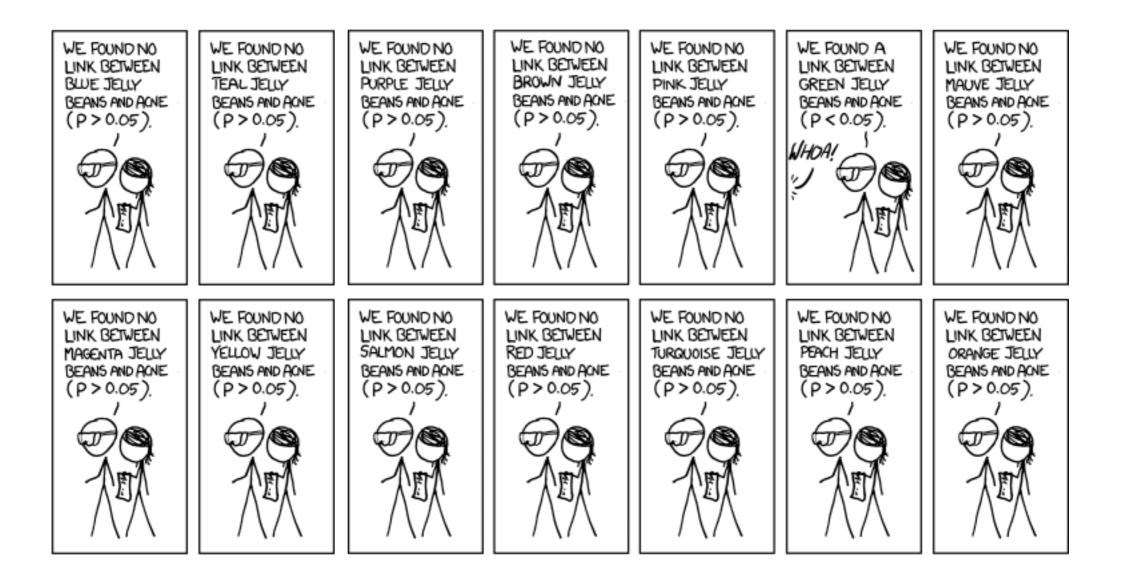
2 Act7 500
2 GapDH 1000
2 Sec4 250
2 Bglob1 10
TOTAL WITH Bglob1: 1,000,010
TOTAL WITHOUT: 1,000,000

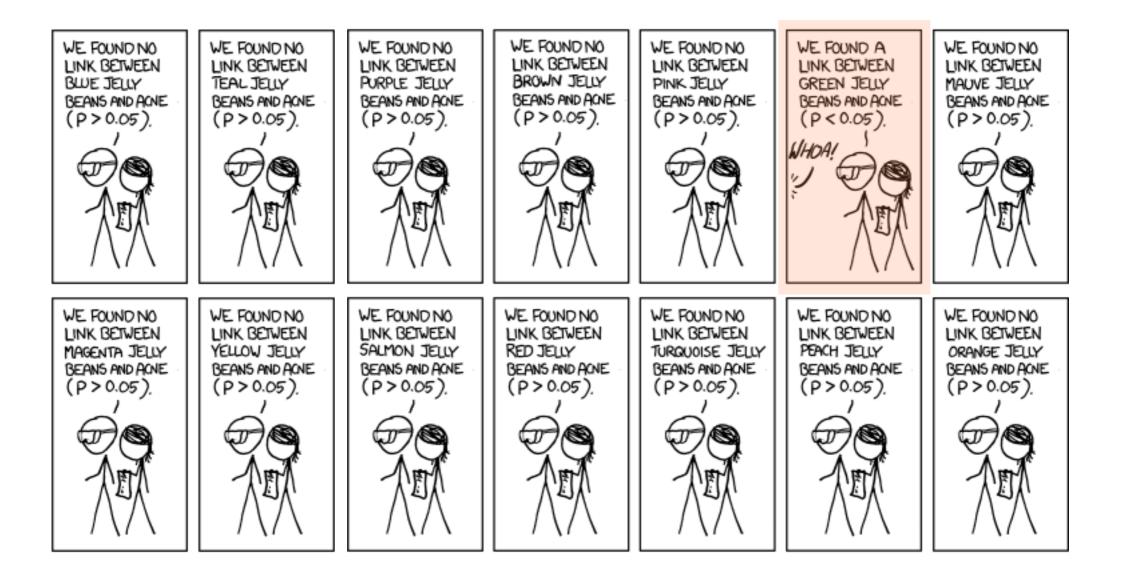
$$FPKMAct7 = \frac{1000}{\frac{1000}{10^3} \times \frac{12^6}{10^6}} = 83.3 \qquad FPKMAct7 = \frac{500}{\frac{1000}{10^3} \times \frac{1,000,010}{10^6}} = 499.995$$

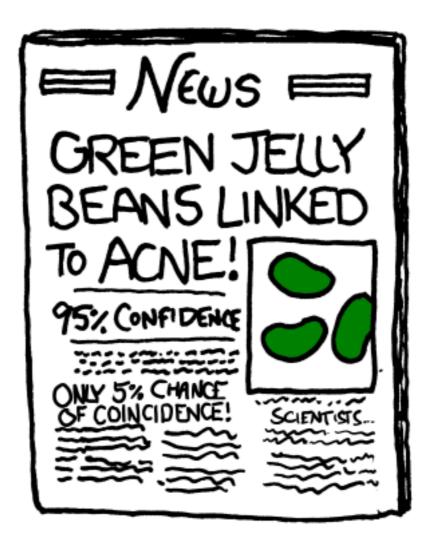
$$FPKMAct7 = \frac{1000}{\frac{1000}{10^3} \times \frac{2^6}{10^6}} = 500 \qquad FPKMAct7 = \frac{1000}{\frac{1000}{10^3} \times \frac{1^6}{10^6}} = 500$$

False Discovery Rate and q-value

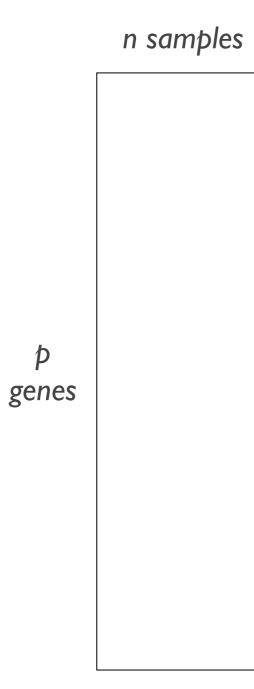








Multiple Testing



We're doing p simultaneous tests!

H₁, H₂, H₃, ..., H_P

Bonferonni Correction

Storey's q-value