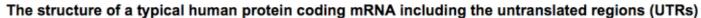
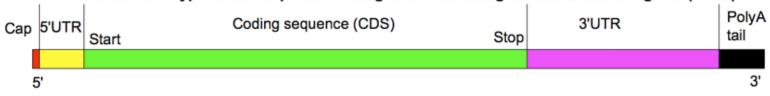
RNASeq Introduction

Malay (malay@uab.edu)

Structure of mRNA

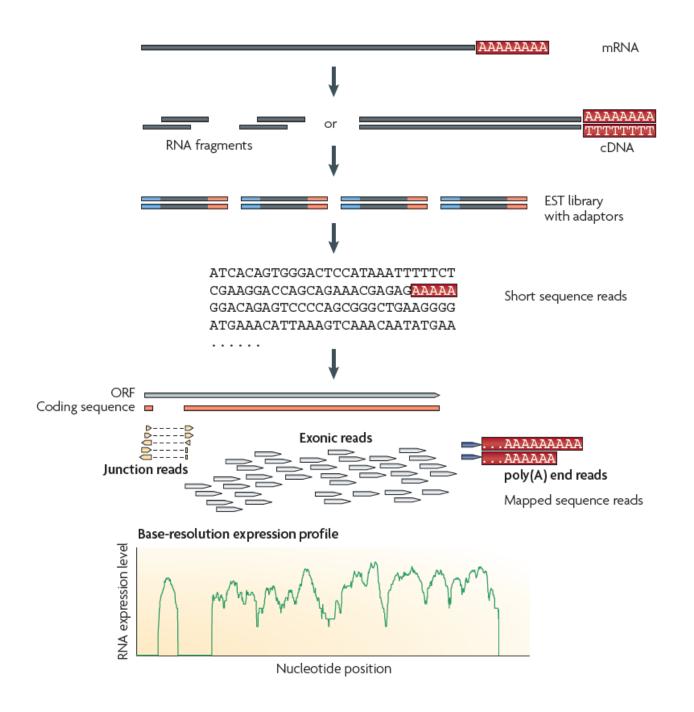




Other RNAs:

	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

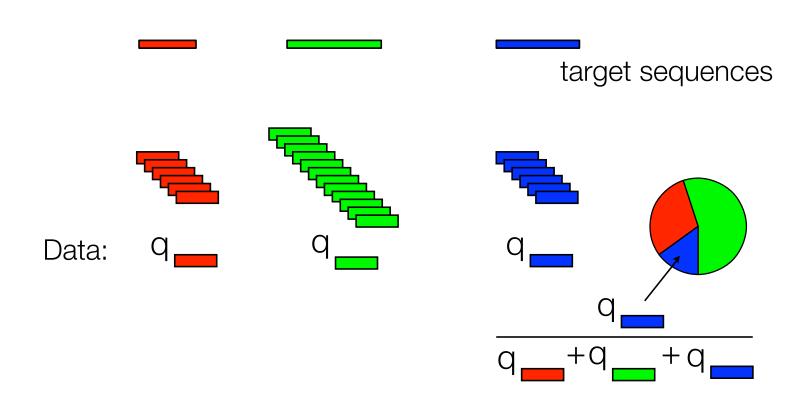
RNASeq overview



Various applications of RNASeq

Differential expression
Novel transcript detection
Fusion transcript detection
Mutation detection (not common)

The fragment assignment problem



Example count tables:

http://bowtie-bio.sourceforge.net/recount/

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.

TPM: comes from RSEM

$$RPKM = \frac{Count}{\frac{N}{10^6} \times \frac{length}{10^3}}$$

$$TPM_i = \frac{X_i}{\tilde{l}_i} \cdot \left(\frac{1}{\sum_j \frac{X_j}{\tilde{l}_j}}\right) \cdot 10^6$$

$$TPM_i = \left(\frac{FPKM_i}{\sum_j FPKM_j}\right) \cdot 10^6$$

Upper quartile normalization

Sample_ID gene raw_1Kb_read_count

1 Act7 1000

1 GapDH 2000

1 Sec4 500

. . .

1 Bglob1 10000000

TOTAL WITH Bglob1: 12,000,000

TOTAL WITHOUT: 2,000,000

2 Act7 500

2 GapDH 1000

2 Sec4 250

. .

2 Bglob1 10

TOTAL WITH Bglob1: 1,000,010

TOTAL WITHOUT: 1,000,000

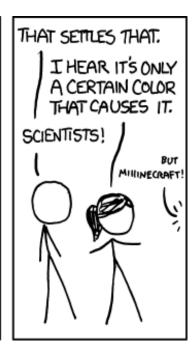
$$FPKMAct7 = \frac{1000}{\frac{1000}{10^3} \times \frac{12^6}{10^6}} = 83.3 \qquad FPKMAct7 = \frac{500}{\frac{1000}{10^3} \times \frac{1,000,010}{10^6}} = 499.995$$

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

False Discovery Rate and q-value







WE FOUND NO LINK BETWEEN BLUE JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN TEAL JELLY BEANS AND ACNE (P > 0.05),



WE FOUND NO LINK BETWEEN PURPLE JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN BROWN JELLY BEANS AND ACNE (P > 0.05)



WE FOUND NO LINK BETWEEN PINK JELLY BEANS AND ACNE (P > 0.05).



WE FOUND A LINK BETWEEN GREEN JELLY BEANS AND ACNE (P<0.05).



WE FOUND NO LINK BETWEEN MAUVE JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN MAGENTA JELLY BEANS AND ACNE (P > 0.05)



WE FOUND NO LINK BETWEEN YELLOW JELLY BEANS AND ACNE (P > 0.05).



WE FOUND NO LINK BETWEEN SALMON JELLY BEANS AND ACNE (P > 0.05).



WE FOUND NO LINK BETWEEN RED JELLY BEANS AND ACNE (P > 0.05).



WE FOUND NO LINK BETWEEN TURQUOISE JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN PEACH JELLY BEANS AND ACNE (P > 0.05).



WE FOUND NO LINK BETWEEN ORANGE JELLY BEANS AND ACNE (P > 0.05),



WE FOUND NO LINK BETWEEN BLUE JELLY BEANS AND ACNE (P > 0.05)



WE FOUND NO LINK BETWEEN TEAL JELLY BEANS AND ACNE (P > 0.05)



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WE FOUND NO LINK BETWEEN TURQUOISE JELLY BEANS AND ACNE (P>0.05)

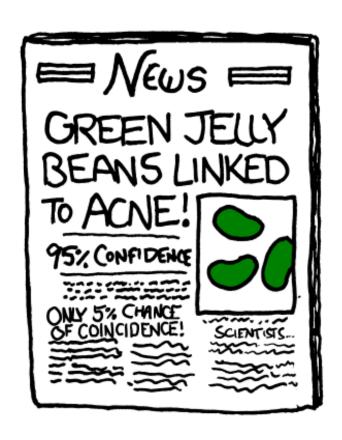


WE FOUND NO LINK BETWEEN PEACH JELLY BEANS AND ACNE (P > 0.05),



WE FOUND NO LINK BETWEEN ORANGE JELLY BEANS AND ACNE (P > 0.05),





n samples

We're doing p simultaneous tests!

þ genes

 $H_1, H_2, H_3, ..., H_p$

Bonferonni Correction

Storey's q-value

