MAPPING & GENE EXPRESSION AND GENOME EVOLUTION 13Nov15

ANNOUNCEMENTS

MAPPING - BWT

Format specification: http://samtools.github.io/hts-specs/SAMv1.pdf

MAPPING - BWT

Alignment Fields

Col1

Col2

Col3

Col4

Col5

Col6

Col7

Col8

Col9

Col10

Col11

MAPPING - BWT

http://broadinstitute.github.io/picard/explain-flags.html

GENE EXPRESSION

GENE EXPRESSION

http://haroldpimentel.wordpress.com/2014/05/08/what-the-fpkm-a-review-rna-seq-expression-units/

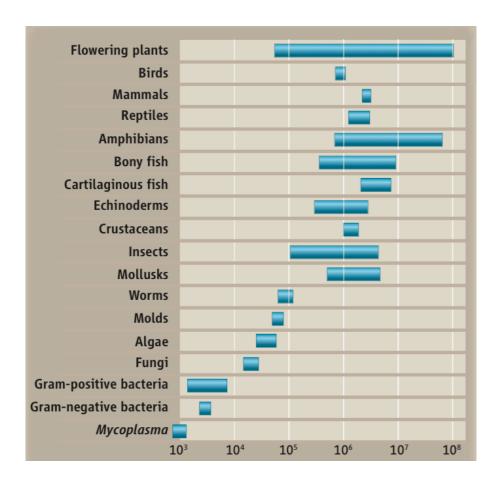
Inter- versus intra-sample comparison

GENE EXPRESSION

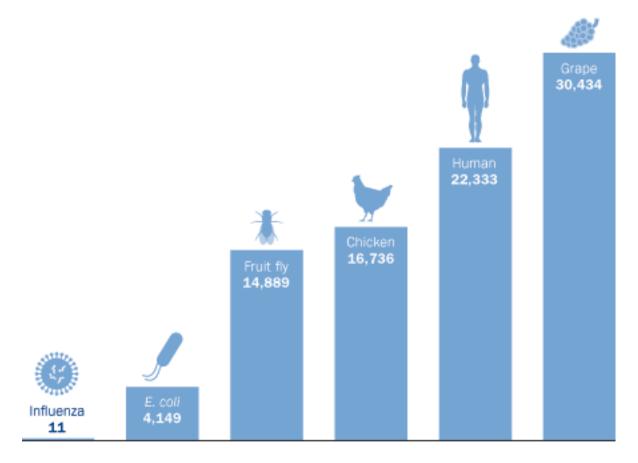
$$TPM_{i} = \frac{X_{i}}{\tilde{l}_{i}} * \left(\frac{1}{\sum_{j} \frac{X_{j}}{\tilde{l}_{j}}}\right) * 10^{6}$$

How are genomes different?

GENOME DIVERSITY: SIZE



GENOME DIVERSITY: # GENES



Species	Common name	Genome size, pg	% TEs	Gene number
Fritillaria assyriaca	lily	127.4	95-99	
Rana esculenta	frog	5.6-8.0	77	
Homo sapiens	human	3.5	45	23,000
Xenopus laevis	frog	3.5	37	
Mus musculus	mouse	3.4	40	35,000
Zea mays	maize	2.5	60	
Gallus domesticus	hen	1.25	27	20,000
Tetraodon nigroviridis	fish	0.51	0.14	22,000
Takifugu rubripes	fish	0.4	2	31,000
Anopheles gambiae	malaria mosquito	0.28	16	14,000
Drosophila melanogaster	fruit fly	0.18	15-22	14,039
Ciona intestinalis	ascidian	0.16	10	15,500
Arabidopsis thaliana	arabidopsis	0.16	14	26,000
Caenorhabditis elegans	worm	0.1	12	20,060
Saccharomyces cerevisiae	yeasts	0.012	3-5	6,680
Escherichia coli	bacterium	0.0046	0.3	4,500

