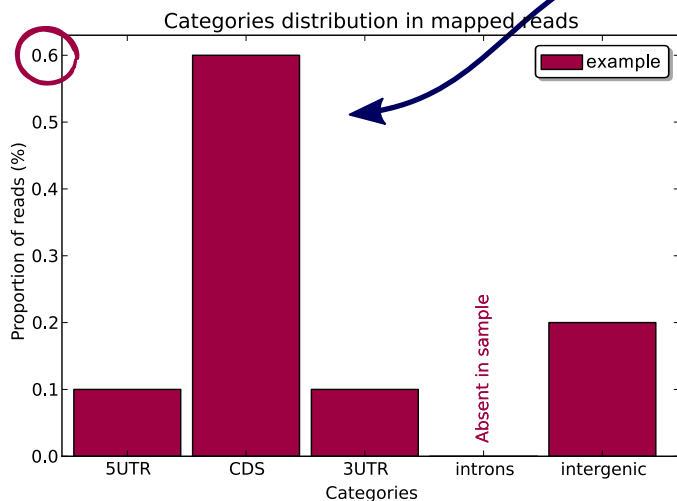


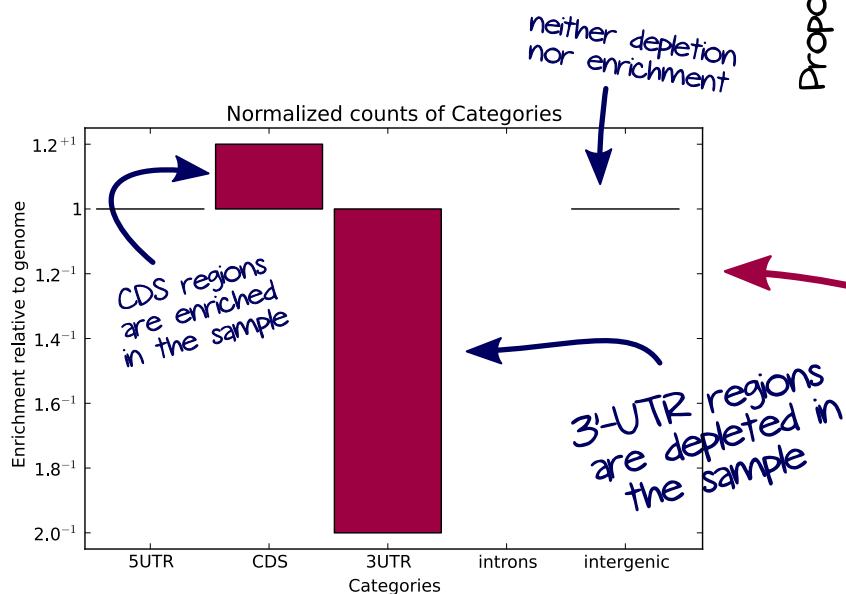
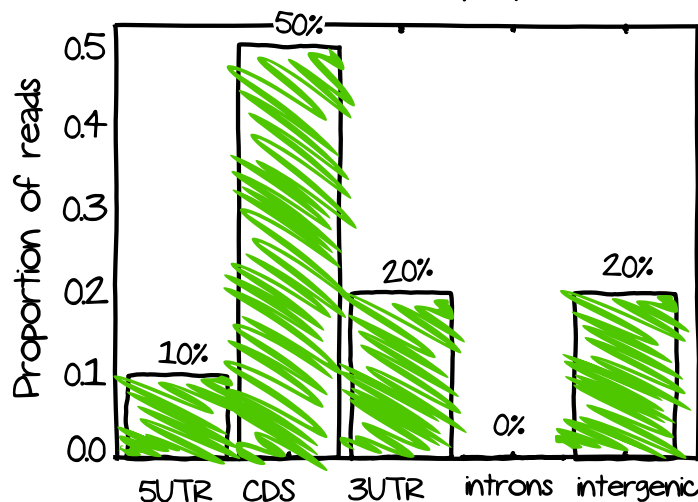
60% of the nucleotides composing the reads of the sample map to CDS regions

GTF
BAM



normalization

Genome features proportions



CDS normalization

$$\frac{60\%}{50\%} = 1.2$$