

# DESeq and ExonSeq

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# Two questions

Assume you measure some quantity in different samples and/or conditions.

Example here: concentration of a transcript in samples of extracted mRNA

There are two different questions you may want to ask.

1. Given two samples, is the concentration of the transcript of interest different in the two samples?

You may say yes if the difference between the measured values is large compared to the accuracy of the measurement.

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2. Given samples from two conditions (treatment vs control), did the treatment cause a difference in transcript concentration?

You may say yes if the difference between the measured values is large compared to the typical variation of concentration between replicates.

In comparative RNA-Seq and ChIP-Seq,

- the technical noise can be predicted from theory
- the biological variation needs to be assessed by comparing replicates.

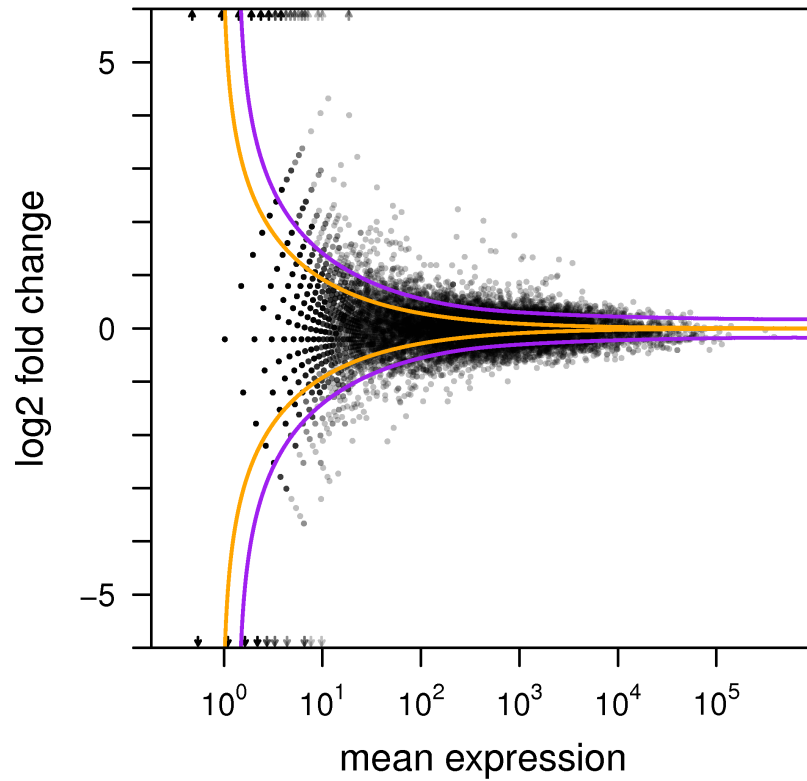
Many currently available tools ignore this issue and so produce false positives.

DESeq estimates biological variation properly and then tests for differential expression.

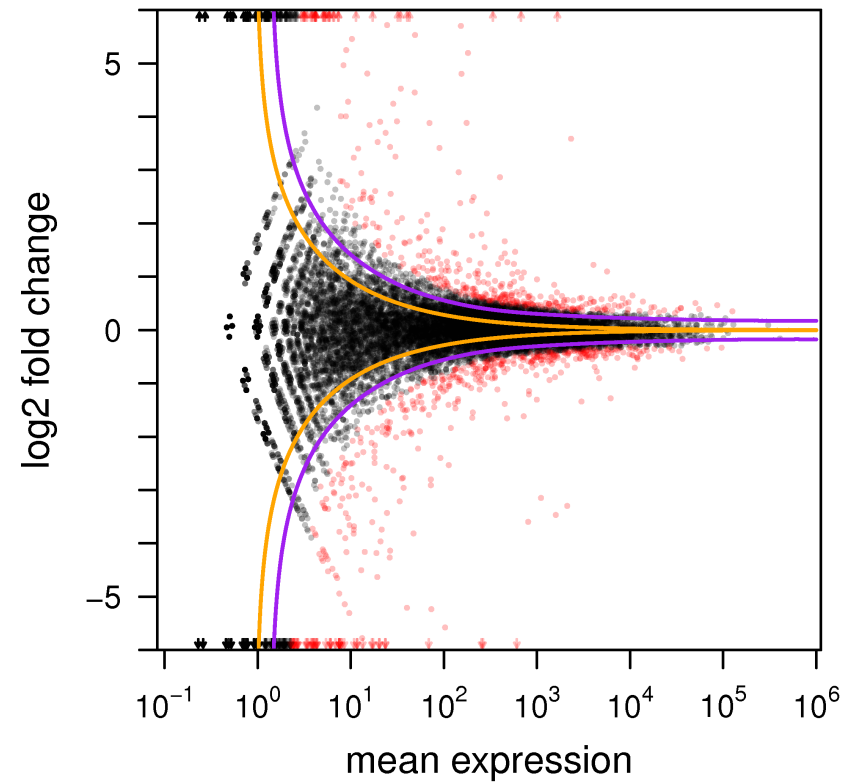
(also: edgeR, BaySeq)

# DESeq

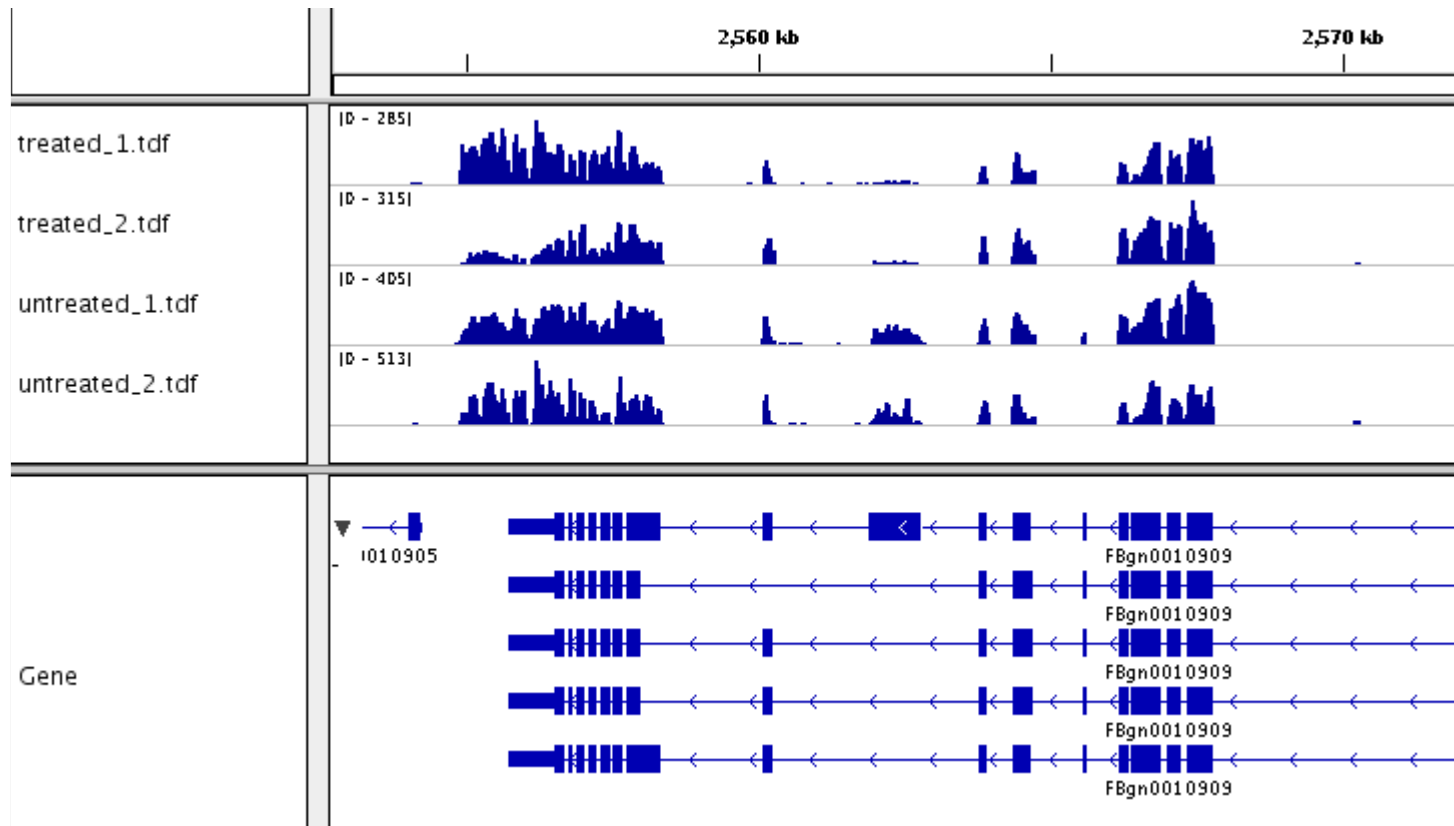
comparison of  
two replicates



comparison of  
treatment vs control



# Alternative isoform regulation



Data: Brooks et al., Genome Res., 2010

# Count table for a gene

number of reads mapped to each exon (or part of exon) in gene *msn*:

	treated_1	treated_2	control_1	control_2	
E01	398	556	561	456	
E02	112	180	153	137	
E03	238	306	298	226	
E04	162	171	183	146	
E05	192	272	234	199	
E06	314	464	419	331	
E07	373	525	481	404	
E08	323	427	475	373	
E09	194	213	273	176	
E10	90	90	530	398	<--- !
E11	172	207	283	227	
E12	290	397	606	368	<--- ?
E13	33	48	33	33	
E14	0	33	2	37	
E15	248	314	468	287	
E16	554	841	1024	680	

[...]



