



## countData

gene	ctrl_1	ctrl_2	exp_1	exp_1
geneA	10	11	56	45
geneB	0	0	128	54
geneC	42	41	59	41
geneD	103	122	1	23
geneE	10	23	14	56
geneF	0	1	2	0
...	...	...	...	...
...	...	...	...	...
...	...	...	...	...

## colData

id	treatment	sex
ctrl_1	control	male
ctrl_2	control	female
exp_1	treatment	male
exp_2	treatment	female

Sample names:  
**ctrl\_1**, **ctrl\_2**, **exp\_1**, **exp\_2**

**countData** is the count matrix  
(number of reads mapping to each gene for each sample)

**colData** describes metadata about the *columns* of countData

**First column of colData must match column names of countData (-1st)**