



countData

| | ctrl_1 | ctrl_2 | exp_1 | exp_2 |
|-------|--------|--------|-------|-------|
| 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

| | 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

colnames(countData) == rownames(colData)