

Manual vs Seurat CLR Normalization

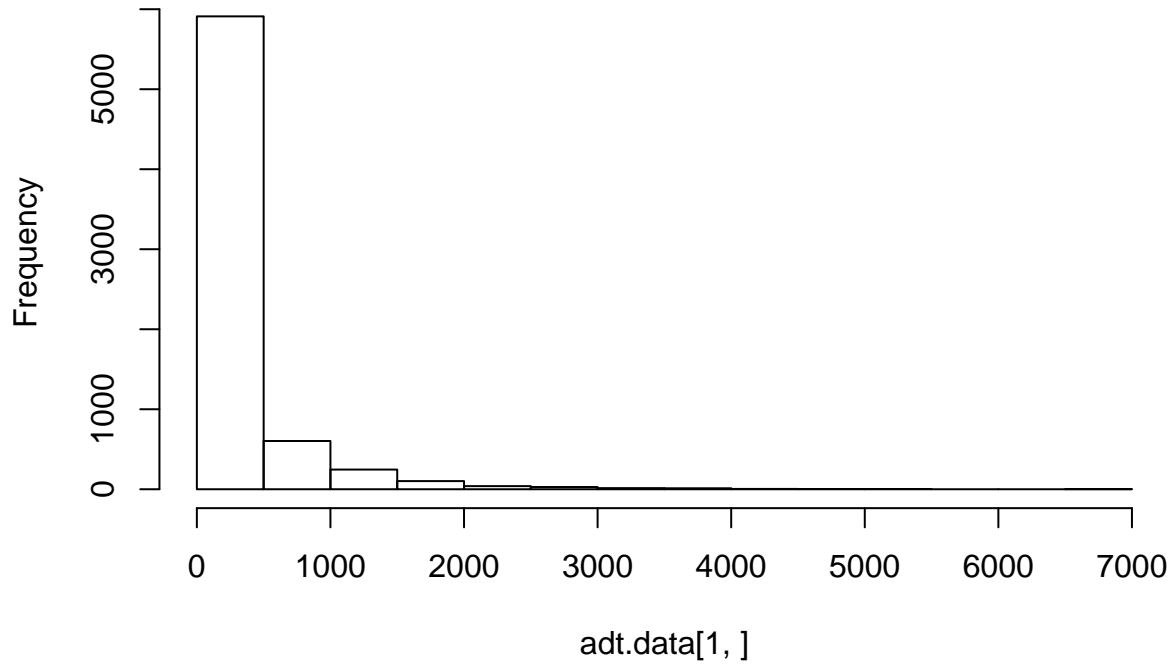
```
# load lab ADT dataset
# Load in the ADT UMI matrix
adt.data <- as.sparse(read.csv(file = "~/HarderLab/singlecellgenomicspractice/multimodal_tutorial/ADT_r
header = TRUE, row.names = 1))
```

```
##          AACCTGAGAAGGCCT.1 AACCTGAGCGGCTTC.1 AACCTGAGTGGGTTG.1
## CD115          669          25          13
## CD11b          226          14          41
## CD11c          119           9           0
## CD274          214           0         100
## FcgRIV        1285           3          12
##          AACCTGCAATGGTCT.1 AACCTGCAATTGCTG.1
## CD115           0           0
## CD11b          22          68
## CD11c           0          14
## CD274          25          19
## FcgRIV           9           0
```

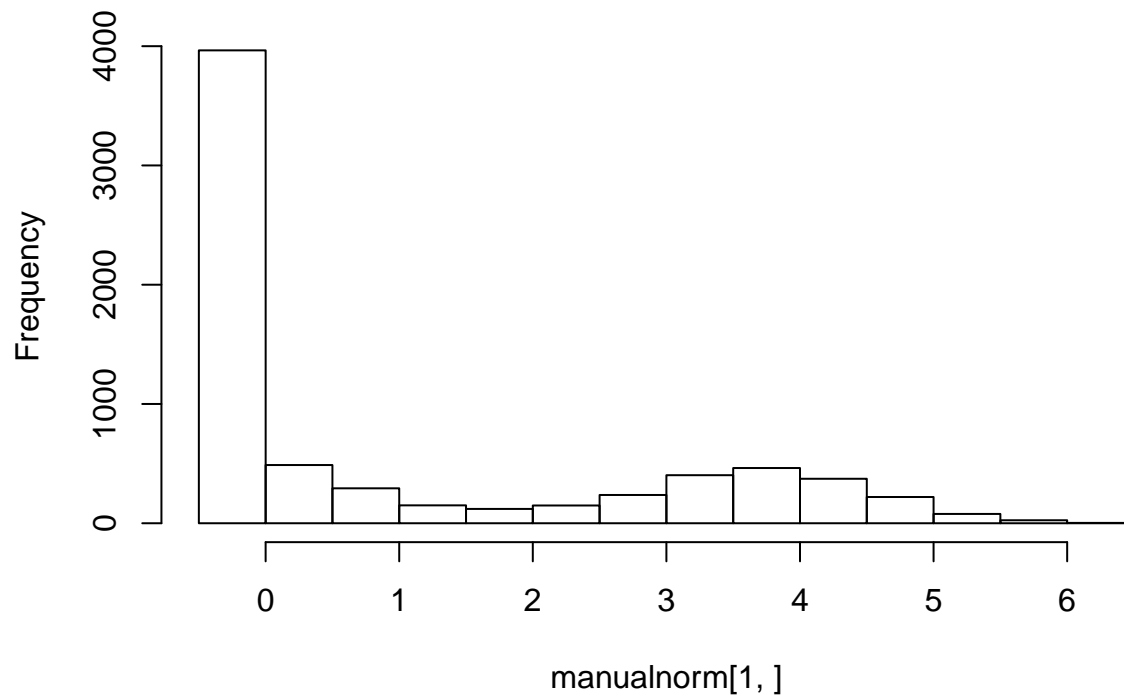
```
## Normalizing across features
```

```
##          AACCTGAGAAGGCCT.1 AACCTGAGCGGCTTC.1 AACCTGAGTGGGTTG.1
## CD115    3.88127697308693 1.0204768944278721 0.653756012054162
## CD11b    1.82140766251579 0.2783278420047390 0.662602783139913
## CD11c    3.18780271903729 1.0142438874549093 0.000000000000000
## CD274    3.48086672689090 0.0000000000000000 2.754549298500183
## FcgRIV   3.25810539159340 0.0567264891812861 0.209827431773392
##          AACCTGCAATGGTCT.1 AACCTGCAATTGCTG.1
## CD115    0.0000000000000000 0.0000000000000000
## CD11b    0.408328715424756 0.939518974498525
## CD11c    0.0000000000000000 1.317357712854883
## CD274    1.542975248123633 1.333856156438056
## FcgRIV   0.161352304495265 0.0000000000000000
```

Histogram of adt.data[1,]



Histogram of manualnorm[1,]



Histogram of seuratnorm[1,]

