First time using UKBiobank data:

To load R:

spack load -r /mirrusu

To make a subset of one of the HTML files in phenotypes:

zcat /athena/elementolab/scratch/nib4003/ukbiobank/phenotypes/ukb26867.csv.gz | head -100 > subset\_ukb

To open R (extremely simple and not a mistake):

R

To create dataframe once in R for subset\_ukb called uk:

uk <- read.csv("subset\_ukb", stringsAsFactors=F, header=T)

uk

To show first 10 columns for first 10 people:

uk[1:10,1:10]

To show dimension of a dataframe:

dim(uk)

To quit R:

Press Ctrl Z