

```

run.hyper <- function(b, cond, levs=levels(cond), th=2){
  results <- NULL
  for(k in levs){
    if(sum(cond[b]==k) > th){
      row <- c(k,
        sum( cond[b]==k ), # hits, number of tumour type k
                           # samples in selected samples
        sum( cond==k ), # foreground, total number of
                           # tumour type k samples in data set
        sum( cond!=k ), # total number of non tumour type k
                           # samples in dataset
        sum( b ),      # sample size
        1-phyper(sum( cond[b]==k ), # p-value for enrichment
                 sum( cond==k ),
                 sum( cond!=k ),
                 sum( b )))
      if(is.null(results)){
        results <- rbind(row)
        colnames(results) <- c("tumour.type",
                              "hits",
                              "foreground",
                              "background",
                              "sample.size",
                              "p.value")
      }else{
        results <- rbind(results, row)
      }
    }
  }
  results
}

```

```

phyper.expo <- function(decide, pdat, th=2){

  results <- list()

  for(ci in colnames(pdat)){
    results[[ci]] <- list()
    results[[ci]]$up <- run.hyper(decide==1,
                                   pdat[,ci],
                                   th=th)
    results[[ci]]$down <- run.hyper(decide==-1,
                                     pdat[,ci],
                                     th=th)
    results[[ci]]$mixed <- run.hyper(decide!=0,
                                       pdat[,ci],
                                       th=th)
  }
  results
}

```