

Comparison of liger with mhg

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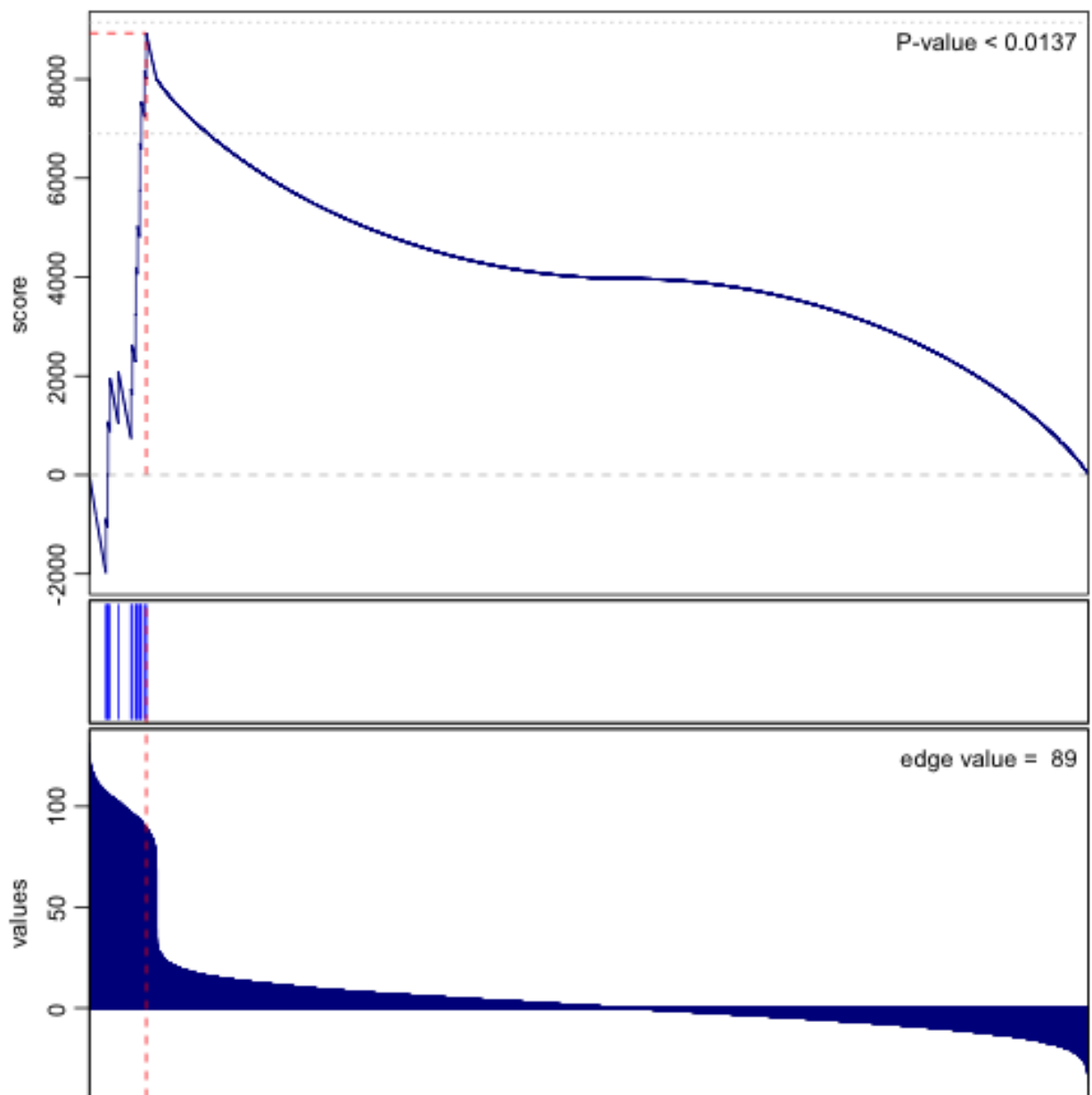
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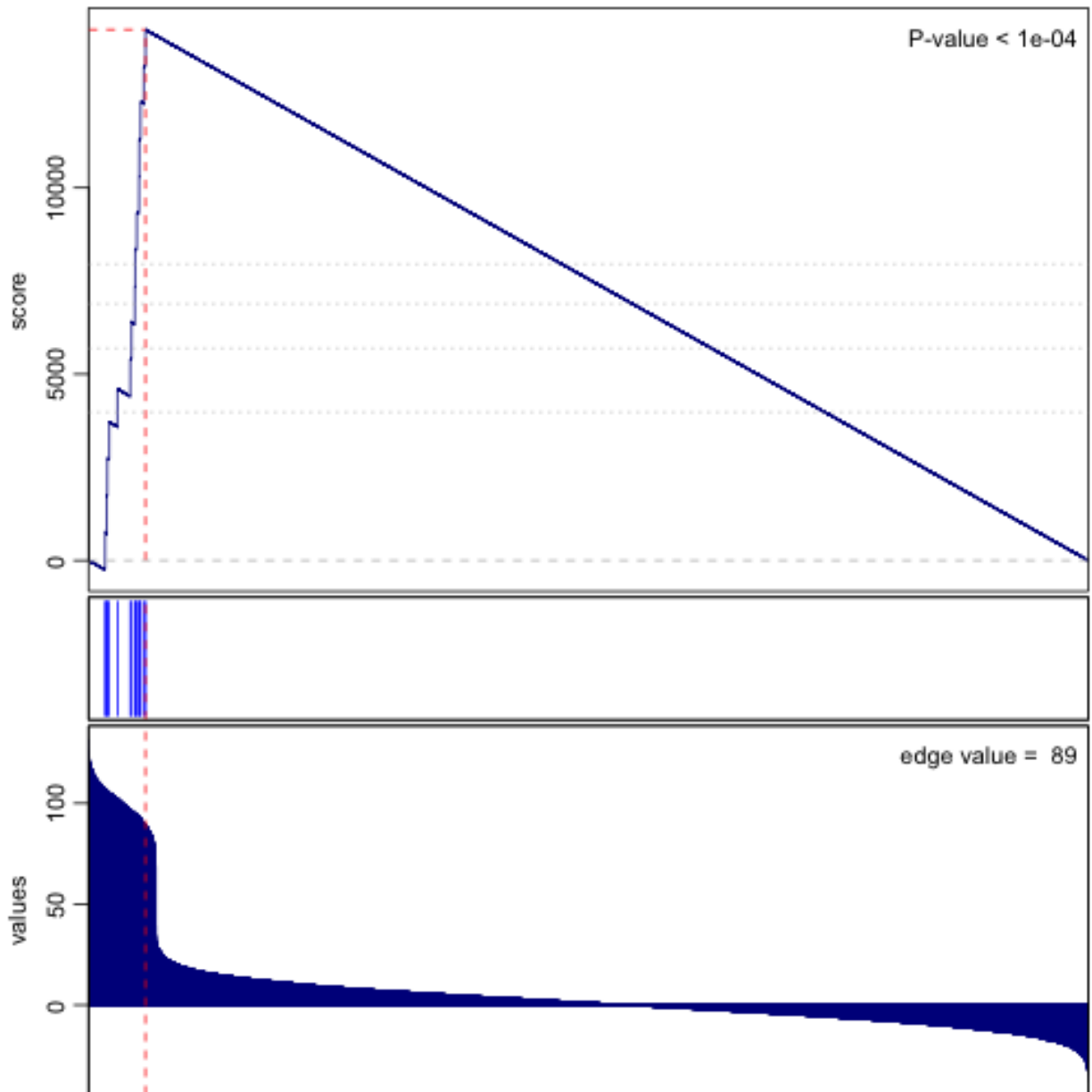
```
library(liger)
library(mhg)

# Simulate

library(liger)
# load gene set
data("org.Hs.G02Symbol.list")
# get universe
universe <- unique(unlist(org.Hs.G02Symbol.list))
# get a gene set
gs <- org.Hs.G02Symbol.list[[1]]
# fake dummy example where everything in gene set is perfectly enriched
vals <- rnorm(length(universe), 0, 10)
names(vals) <- universe
vals[gs] <- rnorm(length(gs), 100, 10)
# add some noise
vals[sample(1:length(universe), 1000)] <- rnorm(1000, 100, 10)
# test previously perfectly enriched gene set again
gs <- org.Hs.G02Symbol.list[[1]]

# Run liger
liger1 <- gsea(values=vals, geneset=gs)
liger2 <- gsea(values=vals, geneset=gs, rank=TRUE)
```





```
# Wrapper for mhg
mhgsea <- function(values, geneset) {
  # Fold change
  fc <- sort(values, decreasing=TRUE)
  # Size of the population.
  N <- length(values)
  # Successes in the population.
  K <- sum(geneset %in% names(values))
  # Only consider enrichments in the first L observations.
  L <- N
  # Require at least X successes in the first L observations.
  X <- 1
  # Define items in the population as successes.
  x <- as.numeric(names(fc) %in% geneset)
```

```

# Test for enrichment.
res <- mhg_test(x, N, K, L, X)
# This is how you can plot the results.
plot_mhg(
  values = fc,
  x = x,
  res = res,
  n = L,
  value = bquote("values")
)
return(res)
}

# Run mhg
res <- mhgsea(values=vals, geneset=gs)

```

