Exercise

Get data from ivhgenes.txt. The right-most column has Entrez Gene IDs. Input can be a vector of gene IDs or a vector of fold-change values or t-scores with Entrez Gene IDs as names.

```r
library("clusterProfiler"); library("org.Hs.eg.db");
library("enrichplot")
```

Run different types of functional enrichment and visualize. Discuss how to create queries and how to interpret them. What can you say about this list of genes, involved in intraventricular hemorrhage in infants born preterm?


```r
goenrichment <- enrichGO(gene = topgenes,
  OrgDb = org.Hs.eg.db, ont = "BP",
  pAdjustMethod = "BH", pvalueCutoff = 0.05,
  qvalueCutoff = 0.05, readable = TRUE)
```

Example from previous slide; your job is to choose how to run enrichment analyses (perhaps not just enrichGO) for this problem.