EGSEAResults

- results: list
- contrasts: character
- sampleSize: numeric
- gs.annots: list
- baseMethods: character
- combineMethod: character
- sort.by: character
- symbolsMap: data.frame
- logFC: matrix
- report.dir: character

- show, summary()
- topSets(gs.label, contrast, sort.by, number, names.only, verbose)()
- plotHeatmap(gene.set, gs.label, contrast, file.name, format, verbose)()
- plotPathway(gene.set, gs.label, contrast, file.name, verbose)()
- plotMDS(gs.label, contrast, file.name, format, verbose)()
- plotSummary(gs.label, contrast, file.name, format, x.axis, x.cutoff, verbose)()
- plotGOgraph(gs.label, contrast, sort.by, noSig, file.name, format, verbose)()
- showSetByName(gs.label, set.name)()
- showSetByID(gs.label, id)()

GSCollectionIndex

- original: list
- idx: list
- anno: data.frame
- featureIDs: character
- species: character
- name: character
- label: character

- show()
- summary()
- getSetByName(set.name)(): list
- getSetByID(id)(): list