

## gene

### Make Heatmap of Gene (Q8)

```
library(ggplot2)
library(bio3d)
ls("package:bio3d")
```

##	[1]	"aa.index"	"aa.table"	"aa123"
##	[4]	"aa2index"	"aa2mass"	"aa321"
##	[7]	"aanma"	"aanma.pdb"	"aanma.pdb"
##	[10]	"aln2html"	"amsm.xyz"	"angle.xyz"
##	[13]	"as.fasta"	"as.pdb"	"as.pdb.default"
##	[16]	"as.pdb.mol2"	"as.pdb.prmtop"	"as.select"
##	[19]	"as.xyz"	"atom.index"	"atom.select"
##	[22]	"atom.select.mol2"	"atom.select.pdb"	"atom.select.pdb"
##	[25]	"atom.select.prmtop"	"atom2ele"	"atom2ele.default"
##	[28]	"atom2ele.pdb"	"atom2mass"	"atom2mass.default"
##	[31]	"atom2mass.pdb"	"atom2xyz"	"basename.pdb"
##	[34]	"bhattacharyya"	"bhattacharyya.array"	"bhattacharyya.enma"
##	[37]	"bhattacharyya.matrix"	"bhattacharyya.nma"	"bhattacharyya.pca"
##	[40]	"binding.site"	"biounit"	"blast.pdb"
##	[43]	"bounds"	"bounds.sse"	"build.hessian"
##	[46]	"bwr.colors"	"cat.pdb"	"chain.pdb"
##	[49]	"check.utility"	"clean.pdb"	"cmap"
##	[52]	"cmap.default"	"cmap.pdb"	"cmap.pdb"
##	[55]	"cmap.xyz"	"cna"	"cna.dccm"
##	[58]	"cna.ensmb"	"cnapath"	"com"
##	[61]	"com.pdb"	"com.xyz"	"combine.select"
##	[64]	"community.aln"	"community.tree"	"consensus"
##	[67]	"conserv"	"convert.pdb"	"core.cmap"
##	[70]	"core.find"	"core.find.default"	"core.find.pdb"
##	[73]	"core.find.pdb"	"cov.enma"	"cov.nma"
##	[76]	"covoverlap"	"covoverlap.enma"	"covoverlap.nma"
##	[79]	"dccm"	"dccm.egnm"	"dccm.enma"
##	[82]	"dccm.gnm"	"dccm.nma"	"dccm.pca"
##	[85]	"dccm.xyz"	"deformation.nma"	"diag.ind"
##	[88]	"difference.vector"	"dist.xyz"	"dm"
##	[91]	"dm.pdb"	"dm.pdb"	"dm.xyz"
##	[94]	"dssp"	"dssp.pdb"	"dssp.pdb"
##	[97]	"dssp.xyz"	"elements"	"entropy"
##	[100]	"ff.aaenm"	"ff.aaenm2"	"ff.anm"
##	[103]	"ff.calpha"	"ff.pfanm"	"ff.reach"
##	[106]	"ff.sdenm"	"filter.cmap"	"filter.dccm"
##	[109]	"filter.identity"	"filter.rmsd"	"fit.xyz"

## [112]	"fluct.nma"	"formula2mass"	"gap.inspect"
## [115]	"geostas"	"geostas.default"	"geostas.enma"
## [118]	"geostas.nma"	"geostas.pdb"	"geostas.pdbs"
## [121]	"geostas.xyz"	"get.blast"	"get.pdb"
## [124]	"get.seq"	"gnm"	"gnm.pdb"
## [127]	"gnm.pdbs"	"hclustplot"	"hivp"
## [130]	"hmmer"	"identify.cna"	"inner.prod"
## [133]	"inspect.connectivity"	"is.gap"	"is.mol2"
## [136]	"is.pdb"	"is.pdbs"	"is.select"
## [139]	"is.xyz"	"kinesin"	"layout.cna"
## [142]	"lbio3d"	"load.enmff"	"mask"
## [145]	"mask.dccm"	"mktrj"	"mktrj.enma"
## [148]	"mktrj.nma"	"mktrj.pca"	"mono.colors"
## [151]	"motif.find"	"mustang"	"network.amendment"
## [154]	"nma"	"nma.pdb"	"nma.pdbs"
## [157]	"normalize.vector"	"orient.pdb"	"overlap"
## [160]	"pairwise"	"pca"	"pca.array"
## [163]	"pca.pdbs"	"pca.tor"	"pca.xyz"
## [166]	"pdb.annotate"	"pdb.pfam"	"pdb2aln"
## [169]	"pdb2aln.ind"	"pdb2sse"	"pdbaln"
## [172]	"pdbfit"	"pdbfit.pdb"	"pdbfit.pdbs"
## [175]	"pdbs2pdb"	"pdbs2sse"	"pdbseq"
## [178]	"pdbsplit"	"pfam"	"plot.bio3d"
## [181]	"plot.blast"	"plot.cmap"	"plot.cna"
## [184]	"plot.cnapath"	"plot.core"	"plot.dccm"
## [187]	"plot.dmat"	"plot.ecna"	"plot.ecnapath"
## [190]	"plot.enma"	"plot.fasta"	"plot.fluct"
## [193]	"plot.geostas"	"plot.hmmer"	"plot.matrix.loadings"
## [196]	"plot.nma"	"plot.pca"	"plot.pca.loadings"
## [199]	"plot.pca.score"	"plot.pca.scree"	"plot.rmsip"
## [202]	"plotb3"	"print.cna"	"print.cnapath"
## [205]	"print.core"	"print.enma"	"print.fasta"
## [208]	"print.geostas"	"print.mol2"	"print.nma"
## [211]	"print.pca"	"print.pdb"	"print.prmtop"
## [214]	"print.rle2"	"print.select"	"print.sse"
## [217]	"print.xyz"	"project.pca"	"prune.cna"
## [220]	"pymol"	"pymol.dccm"	"pymol.modes"
## [223]	"pymol.nma"	"pymol.pca"	"pymol.pdbs"
## [226]	"read.all"	"read.cif"	"read.crd"
## [229]	"read.crd.amber"	"read.crd.charmm"	"read.dcd"
## [232]	"read.fasta"	"read.fasta.pdb"	"read.mol2"
## [235]	"read.ncdf"	"read.pdb"	"read.pdb2"
## [238]	"read.pdcBD"	"read.pqr"	"read.prmtop"
## [241]	"rgyr"	"rle2"	"rmsd"
## [244]	"rmsf"	"rmsip"	"rmsip.default"
## [247]	"rmsip.enma"	"rot.lsqr"	"rtb"
## [250]	"sdENM"	"seq2aln"	"seqaln"
## [253]	"seqaln.pair"	"seqbind"	"seqidentity"
## [256]	"setup.ncore"	"sip"	"sip.default"
## [259]	"sip.enma"	"sip.nma"	"sse.bridges"
## [262]	"store.atom"	"stride"	"struct.aln"
## [265]	"summary.cna"	"summary.cnapath"	"summary.pdb"
## [268]	"torsion.pdb"	"torsion.xyz"	"transducin"
## [271]	"trim"	"trim.mol2"	"trim.pdb"

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## [274] "trim.pdb"      "trim.xyz"      "unbound"
## [277] "uniprot"       "var.pdb"       "var.xyz"
## [280] "vec2resno"     "vmd"           "vmd.cna"
## [283] "vmd.cnapath"   "vmd.ecna"      "vmd.ecnapath"
## [286] "vmd_colors"    "wrap.tor"      "write.crd"
## [289] "write.fasta"   "write.mol2"     "write.ncdf"
## [292] "write.pdb"     "write.pir"      "write.pqr"
## [295] "xyz2atom"      "xyz2z.pca"     "z2xyz.pca"
```

```
#Import Data
multiplealn <- read.fasta("gene_multipleAlignment_Q5")
#Calculate Identity Matrix
heat <- seqidentity(multiplealn)
#Plot visualization
heatmap(heat)
```

