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> options(width = 75, continue = " ")
> library("Gviz")
> library("trioClasses")
> library("TxDb.Hsapiens.UCSC.hg18.knownGene")
> data("pedigrees", package = "CleftCNVAssoc")
> data("penncnvjoint", package = "CleftCNVAssoc")

> data("cnv", package = "trioClasses")
> cnv.beaty.obj <- cnv.obj
> se.beaty <- SummarizedExperiment(assays = SimpleList(cnv = t(cnv.beaty.obj$cnv.mat)),
  colData = DataFrame(id = rownames(cnv.beaty.obj$cnv.mat),
    row.names = rownames(cnv.beaty.obj$cnv.mat)), rowData = cnv.beaty.obj$cmp.gr)
> beaty.trios <- MinimumDistance:::trios(beaty.pedigree)
> beaty.ped <- DataFrame(famid = do.call("rbind", strsplit(beaty.trios$O,
  "_"))[, 1], id = beaty.trios$O, fid = beaty.trios$F,
  mid = beaty.trios$M, sex = NA, dx = NA)
> ped <- PedClass(beaty.ped)
> fe.beaty <- FamilyExperiment(se.beaty, pedigree = ped)

> data("cnv.pitt", package = "trioClasses")
> cnv.pitt.obj <- cnv.obj
> se.pitt <- SummarizedExperiment(assays = SimpleList(cnv = t(cnv.pitt.obj$cnv.mat)),
  colData = DataFrame(id = rownames(cnv.pitt.obj$cnv.mat),
    row.names = rownames(cnv.pitt.obj$cnv.mat)), rowData = cnv.pitt.obj$cmp.gr)
> pitt.trios <- MinimumDistance:::trios(pitt.pedigree)
> pitt.ped <- DataFrame(famid = pitt.trios$O, id = pitt.trios$O,
  fid = pitt.trios$F, mid = pitt.trios$M, sex = NA, dx = NA)
> ped.pitt <- PedClass(pitt.ped)
> fe.pitt <- FamilyExperiment(se.pitt, pedigree = ped.pitt)

> save(fe.beaty, fe.pitt, file = "../data/fe.RData")

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