TAD Viewer

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Objective and Motivations

- **Challenge:** create a data-driven visual representation of our current understanding of the human genome
- Guided by models and figures that we see on the daily
- Our Values:
  - Design for Simplicity
  - Design for Organization

	Kb		
GSE63525_GM12878_primary+replicate_HiCCUPS_looplist.txt.gz	658.8 Kb	(ftp)(http)	TXT
GSE63525_GM12878_primary+replicate_HiCCUPS_looplist_with_motifs.txt.gz	827.1 Kb	(ftp)(http)	TXT
GSE63525_GM12878_primary_HiCCUPS_looplist.txt.gz	420.0 Kb	(ftp)(http)	TXT
GSE63525_GM12878_primary_README.rtf	9.0 Kb	(ftp)(http)	RTF
GSE63525_GM12878_primary_interchromosomal_contact_matrices.tar.gz	14.6 Gb	(ftp)(http)	TAR
GSE63525_GM12878_primary_intrachromosomal_contact_matrices.tar.gz	7.1 Gb	(ftp)(http)	TAR
GSE63525_GM12878_replicate_HiCCUPS_looplist.txt.gz	372.5 Kb	(ftp)(http)	TXT
GSE63525_GM12878_replicate_README.rtf	8.9 Kb	(ftp)(http)	RTF
GSE63525_GM12878_replicate_interchromosomal_contact_matrices.tar.gz	13.5 Gb	(ftp)(http)	TAR
GSE63525_GM12878_replicate_intrachromosomal_contact_matrices.tar.gz	6.5 Gb	(ftp)(http)	TAR
GSE63525_GM12878_subcompartments.bed.gz	31.1 Kb	(ftp)(http)	BED
GSE63525_HMEC_Arrowhead_domainlist.txt.gz	104.0 Kb	(ftp)(http)	TXT
GSE63525_HMEC_HiCCUPS_looplist.txt.gz	304.9 Kb	(ftp)(http)	TXT
GSE63525_HMEC_HiCCUPS_looplist_with_motifs.txt.gz	405.0 Kb	(ftp)(http)	TXT
GSE63525_HMEC_README.rtf	8.7 Kb	(ftp)(http)	RTF

potrace-1.15.win64.zip | GSE63525_KBM7....txt.gz | GSE63525_K562_....txt.... | GSE63525_IMR9....txt.gz | GSE63525_HeLa_....txt.... | Show all

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```
        nrow = length(terms))
        mat = rbind(mat, m)
      }

    }
    if (nrow(genes) == 1) {
      terms = GOdata[GOdata[, 1] == rownames(genes), 3]
      mat = rbind(mat, c(uniques[i], rownames(genes), terms))
    }

    mat = mat[-1, ]
    write.table(
      mat,
      paste("tad", uniques[i], ".txt", sep = ""),
      quote = F,
      col.names = F,
      row.names = F,
      sep = "\t",
    )
    results = rbind(results, mat)
  }
  return(results)
```

```
if (nrow(genes) == 1) {
terms = GOdata[GOdata[, 1] == rownames(genes), 3]
mat = rbind(mat, c(uniques[i], rownames(genes), terms))
}
mat = mat[-1, ]
write.table(
mat,
paste("tad", uniques[i], ".txt", sep = ""),
quote = F,
col.names = F,
row.names = F,
sep = "\t",
ncolumns=3
)
results = rbind(results, mat)
}
return(results)
}
derp()
write.table(mat,"tad24.txt",quote=F,col.names=F,row.names=F,sep="\t")
```

```
+     mat = mat[-1, ]
+     write.table(
+       mat,
+       paste("tad", uniques[i], ".txt", sep = ""),
+       quote = F,
+       col.names = F,
+       row.names = F,
+       sep = "\t",
+       ncolumns=3
+     )
+     results = rbind(results, mat)
+   }
+   return(results)
+ }
> derp()
Error in write.table(mat, paste("tad", uniques[i], ".txt", sep = ""),  :
  unused argument (ncolumns = 3)
> write.table(mat,"tad24.txt",quote=F,col.names=F,row.names=F,sep="\t")
>
```

write.table {utils} R Documentation

Data Output

Description

`write.table` prints its required argument `x` (after converting it to a data frame if it is not one nor a matrix) to a file or connection.

Usage

```
write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ",
            eol = "\n", na = "NA", dec = ".", row.names = TRUE,
            col.names = TRUE, qmethod = c("escape", "double"),
            fileEncoding = "")
```

Future Directions

- Incorporating more data (superloops, multiple genomes, other experimental systems)
  - Add the ability to supply more raw data
- Adding an interactive panel for the user, such that the user can choose which data to display
  - Perhaps each section of the chromosome can be expanded and coded to show additional data
- External output to string-db, co-expression data, etc.
- Displaying raw Hi-C plots