

01.3_ProcessCredDfs.Rmd

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March 15, 2017

This script simply reformats the credible set dataframes from the DIAGRAM and MetaboChip studies

Setup libraries and directories

```
"%&%&" <- function(a,b) paste0(a,b)
library("dplyr")

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
library("data.table")

## -----
## data.table + dplyr code now lives in dtplyr.
## Please library(dtplyr)!
## -----

##
## Attaching package: 'data.table'
## The following objects are masked from 'package:dplyr':
##
##   between, first, last
library("ggplot2")

## Warning: package 'ggplot2' was built under R version 3.3.2

serv.dir <- "/Users/jtorres/FUSE/"
rds.dir <- serv.dir %&%& "projects/wtsa/enhancer_driven/probe_design/rds/"
txt.dir <- serv.dir %&%& "projects/wtsa/enhancer_driven/probe_design/txt/"

df1 <- readRDS(file=rds.dir%&%&"fgwas.cred.diag.df.RDS")
df2 <- readRDS(file=rds.dir%&%&"fgwas.cred.metab.df.RDS")
```

Process data frames

```
df1$STUDY <- rep("DIAGRAM",dim(df1)[1])
df2$STUDY <- rep("MetaboChip",dim(df2)[1])
df2 <- df2[,c(1,2,3,4,5,7,8,6,9)]
df1$CHROM <- as.integer(gsub("chr", "", df1$CHR))
df2$CHROM <- as.integer(gsub("chr", "", df2$CHR))
df1 <- arrange(df1,CHROM,POS)
df2 <- arrange(df2,CHROM,POS)
```

```
df1 <- df1[,1:9]
df2 <- df2[,1:9]

gz1 <- gzfile(txt.dir%%"fgwas-cred-diag.txt.gz", "w")
write.table(x=df1,gz1,sep="\t",quote=FALSE,row.names=F)
close(gz1)

gz2 <- gzfile(txt.dir%%"fgwas-cred-metab.txt.gz", "w")
write.table(x=df2,gz1,sep="\t",quote=FALSE,row.names=F)
close(gz2)
```