

# GWAS-based Mendelian Randomization Path Analysis

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## Abstract

*GMRP* can perform analyses of Mendelian randomization (*MR*), correlation, path of causal variables onto disease of interest and *SNP* annotation analysis. *MR* includes *SNP* selection with given criteria and regression analysis of causal variables on the disease to generate beta values of causal variables on the disease. Using the beta vectors, *GMRP* performs correlation and path analyses to construct path diagrams of causal variables to the disease. *GMRP* consists of 8 *R* functions: `chrp`, `fmerge`, `mktable`, `pathdiagram`, `pathdiagram2`, `path`, `snpPositAnnot`, `ucscannot` and 5 datasets: `beta.data`, `cad.data`, `lpd.data`, `SNP358.data`, `SNP368annot.data`. `chrp` is used to separate string vector `hg19` into two numeric vectors: chromosome number and *SNP* chromosome position. Function `fmerge` is used to merge two GWAS result datasets into one dataset. Function `mktable` performs *SNP* selection and creates a standard beta table for function `path` to do *MR* and path analyses. Function `pathdiagram` is used to create a path diagram of causal variables onto a given disease or onto outcome. Function `pathdiagram2` can merge two-level *pathdiagrams* into one nested *pathdiagram* where inner *pathdiagram* is a *pathdiagram* of causal variables contributing to outcome and the outside *pathdiagram* is a path diagram of causal variables including outcome onto the disease. The five datasets provide examples for running these functions. `lpd.data` and `cad.data` provide an example to create a standard beta dataset for path function to do path analysis and *SNP* data for *SNP* annotation analysis by performing `mktable` and `fmerge`. `beta.data` are a standard beta dataset for path analysis. `SNP358.data` provide an example for `snpPositAnnot` to do *SNP* position annotation analysis and `SNP368annot.data` are for `ucscannot` to perform *SNP* function annotation analysis.

## Contents

1	Introduction . . . . .	2
2	Loading Data . . . . .	3
3	Preparation of Standard Beta Table . . . . .	5
4	Two-way Scatter Plots for Beta Values of Disease and Undefined Causal Variables . . . . .	8
5	MR and Path Analysis . . . . .	9

6	Create Path Diagram. . . . .	10
7	Create Two-level Nested Path Diagram . . . . .	11
8	SNP Annotation Analysis . . . . .	13
9	Session Info . . . . .	18

## 1 Introduction

---

As an example of human disease, coronary artery disease (*CAD*) is one of the causes leading to death and infirmity worldwide [1]. Low-density lipoprotein cholesterol (*LDL*) and triglycerides (*TG*) are viewed as risk factors causing *CAD*. In epidemiological studies, plasma concentrations of increasing *TG* and *LDL* and decreasing high-density lipoprotein cholesterol (*HDL*) have been observed to be associated with risk for *CAD* [2, 3]. However, from observational studies, one could not directly infer that these cholesterol concentrations in plasma are risk factors causing *CAD* [4, 3, 5, 6]. A big limitation of observational studies is to difficultly distinguish between causal and spurious associations due to confounding [7]. An efficient approach to overcome this limitation is *Mendelian Randomization (MR)* analysis [5, 8] where genetic variants are used as instrumental variables. For this reason, many investigators tried to use genetic variants to assess causality and estimate the causal effects on the diseases.

*MR* analysis can perfectly exclude confounding factors associated with disease. However, when we expand one causal variable to many, *MR* analysis becomes challenged and complicated because the genetic variant would have additional effects on the other risk factors, which violate assumption of no pleiotropy. An unknown genetic variant in *MR* analysis possibly provides a false instrument for causal effect assessment of risk factors on the disease. The reason is that if this genetic variant is in *LD* with another gene that is not used but has effect on the disease of study [5, 9]. It then violates the third assumption. These two problems can be addressed by using multiple instrumental variables. For this reason, Do *et al* (2013) developed statistic approach to address this issue [4]. However, method of Do *et al* [4] cannot disentangle correlation effects among the multiple undefined risk factors on the disease of study. The beta values obtained from regression analyses are not direct causal effects because their effects are entangled with correlations among these undefined risk factors.

The best way to address the entanglement of multiple causal effects is path analysis that was developed by Wright [12, 11]. This is because path analysis can dissect beta values into direct and indirect effects of causal variables on the disease. However, path analysis has not broadly been applied to diseases because diseases are usually binary variable. The method of Do [4] makes it possible to apply path analysis to disentangle causal effects of undefined risk factors on diseases. For doing so, we here provide **R package GMRP** (*GWAS-based MR and path analysis*) to solve the above issues.

This vignette is intended to give a rapid introduction to the commands used in implementing *MR* analysis, regression analysis, and path analysis, including *SNP* annotation and chromosomal position analysis by means of the *GMRP* package.

We assume that user has the *GWAS* result data from *GWAS* analysis or *GWAS* meta analysis of *SNPs* associated with risk or confounding factors and a disease of study. If all studied causal variables of *GWAS* data are separately saved in different sheet files, then files are assumed to have the same sheet format and they are required to be merged by using function `fmerge` into one sheet file without disease *GWAS* data. After a standard beta table is created

with `mktable`, user can use function `path` to perform *RM* and path analyses. Using the result of path analysis, user can draw path `plot(pathdiagram)` with functions `pathdiagram` and `pathdiagram2`. These will be introduced in detail in the following examples.

We begin by loading the *GMRP* package.

```
> library(GMRP)
```

## 2 Loading Data

*GMRP* provides five data files: `beta.data`, `cad.data`, `lpd.data`, `SNP358.data` and `SNP368annot.data` where

`lpd.data` was a subset (1069 SNPs) of four GWAS result datasets for *LDL*, *HDL*, *TG* and *TC*. These GWAS result data sheets were downloaded from the website<sup>1</sup> where there are 120165 SNPs on 23 chromosomes and 40 variables. Four GWAS result datasets for *LDL*, *HDL*, *TG* and *TC* were merged into one data sheet by using `fmerge(fl1,fl2,ID1,ID2,A,B,method)` where `fl1` and `fl2` are two GWAS result data sheets. `ID1` and `ID2` are key *id* in files `fl1` and `fl2`, respectively, and required. `A` and `B` are respectively postfix for `fl1` and `fl2`. Default values are `A=""` and `B=""`. `method` is method for merging. In the current version, there are four methods: `method="No"` or `"no"` or `"NO"` or `"N"` or `"n"` means that the data with unmatched SNPs in `file1` and `file 2` are not saved in the merged file; `method="ALL"` or `"All"` or `"all"` or `"A"` or `"a"` indicates that the data with all unmatched SNPs in `file 1` and `file 2` are saved in the unpaired way in the merged data file; If `method="file1"`, then those with unmatched SNPs only from `file1` are saved or if `method="file2"`, `fmerge` will save the data with unmatched SNPs only from `file2`". Here is a simple example:

```
> data1 <- matrix(NA, 20, 4)
> data2 <- matrix(NA, 30, 7)
> SNPID1 <- paste("rs", seq(1:20), sep="")
> SNPID2 <- paste("rs", seq(1:30), sep="")
> data1[,1:4] <- c(round(runif(20), 4), round(runif(20), 4), round(runif(20), 4), round(runif(20), 4))
> data2[,1:4] <- c(round(runif(30), 4), round(runif(30), 4), round(runif(30), 4), round(runif(30), 4))
> data2[,5:7] <- c(round(seq(30)*runif(30), 4), round(seq(30)*runif(30), 4), seq(30))
> data1 <- cbind(SNPID1, as.data.frame(data1))
> data2 <- cbind(SNPID2, as.data.frame(data2))
> dim(data1)
> dim(data2)
> colnames(data1) <- c("SNP", "var1", "var2", "var3", "var4")
> colnames(data2) <- c("SNP", "var1", "var2", "var3", "var4", "V1", "V2", "V3")
> data1<-DataFrame(data1)
> data2<-DataFrame(data2)
> data12 <- fmerge(fl1=data1, fl2=data2, ID1="SNP", ID2="SNP", A=".dat1", B=".dat2", method="No")
```

User can take the following approach to merge all four lipid files into a data sheet: `LDLHDL<-fmerge(fl1=LDLfile,fl2=HDLfile, ID1="SNP", ID2="SNP", A=".LDL", B=".HDL", method="No")`

`TGTC<-fmerge(fl1=TGfile,fl2=TCfile, ID1="SNP", ID2="SNP", A=".TG", B=".TC", method="No")`

`lpd<-fmerge(fl1=LDLHDL,fl2=TGTC,ID1="SNP",ID2="SNP",A="",B="",method="No")`

<sup>1</sup><http://csg.sph.umich.edu/abecasis/public/lipids2013/>

## GWAS-based Mendelian Randomization Path Analysis

`cad.data` was also a subset (1069 SNPs) of original GWAS meta-analyzed dataset that was downloaded from the website<sup>2</sup> and contains 2420360 SNPs and 12 variables.

`beta.data` that was created by using function `mktable` and `fmerge` from `lpd.data` and `cad.data` is a standard beta table for MR and path analyses.

`SNP358.data` contains 358 SNPs selected by `mktable` for SNP position annotation analysis.

`SNP368annot.data` is the data obtained from function analysis with <http://snp-nexus.org/index.html> SNP Annotation Tool and provides example of performing function `ucscanno` to draw a 3D pie and output the results of proportions of SNPs coming from gene function various elements.

```
> data(cad.data)
> #cad <- DataFrame(cad.data)
> cad<-cad.data
> head(cad)
```

	SNP	chr_pos_b36	reference_allele	other_allele	ref_allele_frequency	pvalue
1	rs3091242	chr1:25547372	C	T	0.4630502	0.9036396
2	rs926438	chr1:25626225	C	T	0.4661719	0.4769371
3	rs11802413	chr1:25633507	C	T	0.4651288	0.4698333
4	rs7541095	chr1:25633878	C	T	0.5329650	0.8293105
5	rs10903129	chr1:25641524	G	A	0.5345702	0.3804964
6	rs12746810	chr1:26885720	G	A	0.8749898	0.0945896

```
het_pvalue log_odds log_odds_se N_case N_control model
1 0.90432143 -0.0018321 0.0151330 17085 58384 FE
2 0.97388037 -0.0098335 0.0138259 21913 62220 FE
3 0.95992310 -0.0100090 0.0138485 21885 62197 FE
4 0.83943112 0.0030565 0.0141775 20039 60965 FE
5 0.95534970 0.0122634 0.0139836 21600 59352 FE
6 0.04893363 -0.0409198 0.0244784 19722 60854 FE
```

```
> data(lpd.data)
> #lpd <- DataFrame(lpd.data)
> lpd<-lpd.data
> head(lpd)
```

	SNP_hg18.HDL	SNP_hg19.HDL	rsid.HDL	A1.HDL	A2.HDL	beta.HDL	se.HDL	N.HDL
1	chr19:19379316	chr19:19518316	rs1000237	a	t	0.0083	0.0051	92630.00
2	chr4:88283455	chr4:88064431	rs10023050	g	a	0.0174	0.0049	92768.00
3	chr5:156366229	chr5:156433651	rs10036890	t	a	0.0044	0.0062	92644.98
4	chr19:11085181	chr19:11224181	rs1003723	t	c	0.0051	0.0050	86071.10
5	chr5:74753409	chr5:74717653	rs10038723	t	c	0.0043	0.0059	92790.02
6	chr11:116227036	chr11:116721826	rs10047459	t	c	0.0203	0.0070	76329.02

```
P.value.HDL Freq.A1.1000G.EUR.HDL SNP_hg18.LDL SNP_hg19.LDL rsid.LDL A1.LDL
1 0.127300 0.3272 chr19:19379316 chr19:19518316 rs1000237 t
2 0.001186 0.4222 chr4:88283455 chr4:88064431 rs10023050 a
3 0.551000 0.8417 chr5:156366229 chr5:156433651 rs10036890 t
4 0.337800 0.4578 chr19:11085181 chr19:11224181 rs1003723 t
5 0.488600 0.2375 chr5:74753409 chr5:74717653 rs10038723 t
6 0.013370 0.8074 chr11:116227036 chr11:116721826 rs10047459 c
A2.LDL beta.LDL se.LDL N.LDL P.value.LDL Freq.A1.1000G.EUR.LDL SNP_hg18.TG
```

<sup>2</sup><http://www.cardiogramplusc4d.org/downloads/>

## GWAS-based Mendelian Randomization Path Analysis

1	a	0.0373	0.0054	82988.90	2.755e-11	0.6728	chr19:19379316
2	g	0.0141	0.0052	83123.00	1.457e-02	0.5778	chr4:88283455
3	a	0.0245	0.0066	83022.99	3.848e-04	0.8417	chr5:156366229
4	c	0.0335	0.0053	77777.00	1.508e-09	0.4578	chr19:11085181
5	c	0.0605	0.0063	83135.02	1.381e-19	0.2375	chr5:74753409
6	t	0.0056	0.0073	71581.06	5.302e-01	0.1926	chr11:116227036
SNP_hg19.TG rsid.TG A1.TG A2.TG beta.TG se.TG N.TG P.value.TG							
1	chr19:19518316	rs1000237	t	a	0.0368	0.0049	86629.00 2.116e-12
2	chr4:88064431	rs10023050	a	g	0.0293	0.0048	86765.00 2.449e-09
3	chr5:156433651	rs10036890	t	a	0.0160	0.0060	86658.99 6.558e-03
4	chr19:11224181	rs1003723	t	c	0.0004	0.0048	81143.90 8.068e-01
5	chr5:74717653	rs10038723	t	c	0.0013	0.0058	86781.02 9.066e-01
6	chr11:116721826	rs10047459	c	t	0.0560	0.0066	74837.95 1.523e-14
Freq.A1.1000G.EUR.TG SNP_hg18.TC SNP_hg19.TC rsid.TC A1.TC A2.TC beta.TC							
1	0.6728	chr19:19379316	chr19:19518316	rs1000237	t	a	0.0374
2	0.5778	chr4:88283455	chr4:88064431	rs10023050	a	g	0.0162
3	0.8417	chr5:156366229	chr5:156433651	rs10036890	t	a	0.0351
4	0.4578	chr19:11085181	chr19:11224181	rs1003723	t	c	0.0288
5	0.2375	chr5:74753409	chr5:74717653	rs10038723	t	c	0.0515
6	0.1926	chr11:116227036	chr11:116721826	rs10047459	c	t	0.0079
se.TC N.TC P.value.TC Freq.A1.1000G.EUR.TC							
1	0.0051	92528.90	1.557e-12	0.6728			
2	0.0049	92675.00	1.499e-03	0.5778			
3	0.0063	92553.21	3.974e-08	0.8417			
4	0.0051	85814.00	1.681e-08	0.4578			
5	0.0060	92698.92	4.354e-17	0.2375			
6	0.0069	80331.01	2.155e-01	0.1926			

## 3 Preparation of Standard Beta Table

The standard beta table for *MR* and path analyses must have the standard format. It has columns: *chrn*, *posit*, *rsid*,  $a1.x_1$ ,  $a1.x_2$ ,  $\dots$ ,  $a1.x_n$ ,  $freq.x_1$ ,  $freq.x_2$ ,  $\dots$ ,  $freq.x_n$ ,  $beta.x_1$ ,  $beta.x_2$ ,  $\dots$ ,  $beta.x_n$ ,  $sd.x_1$ ,  $sd.x_2$ ,  $\dots$ ,  $sd.x_n$ ,  $pv_j$ ,  $N.x_1$ ,  $N.x_2$ ,  $\dots$ ,  $N.x_n$ ,  $pc_j$ ,  $hg.d$ ,  $SNP.d$ ,  $freq.d$ ,  $beta.d$ ,  $N.d$ ,  $freq.case$ ,  $pd_j$  where  $x_1, x_2, \dots, x_n$  are variables.

*beta* is vector of beta values of *SNPs* on variable vector  $X=(x_1, x_2, \dots, x_n)$ .

*freq* is vector of frequency of allele 1 with respect to variable vector  $X=(x_1, x_2, \dots, x_n)$ .

*sd* is vector of standard deviations of variable  $(x_1, x_2, \dots, x_n)$  specific to *SNP*. If *sd* does not specifically correspond to *SNP*, then  $sd.x_i$  has the same value for all *SNPs*.

*d* denotes disease.

*N* is sample size.

*freq.case* is frequency of disease.

*chrn* is vector of chromosome number.

*posit* is position vector of *SNPs* on chromosomes. Some time, *chrn* and *posit* are combined into string *hg19* or *hg18*.

## GWAS-based Mendelian Randomization Path Analysis

$pv_j$  is defined as  $p$ -value,  $pc_j$  and  $pd_j$  as proportions of sample size for  $SNP\ j$  to the maximum sample size in causal variables and in disease, respectively.

We use function `mktable` to choose  $SNPs$  and make a standard beta table for  $MR$  and path analyses. For convenience, we first assign `lpd.data` to `lpd` and `cad.data` to `cad`:

The standard beta table will be created via 15 steps:

Step1: calculate  $pv_j$

```
> pvalue.LDL <- lpd$P.value.LDL
> pvalue.HDL <- lpd$P.value.HDL
> pvalue.TG <- lpd$P.value.TG
> pvalue.TC <- lpd$P.value.TC
> pv <- cbind(pvalue.LDL, pvalue.HDL, pvalue.TG, pvalue.TC)
> pvj <- apply(pv, 1, min)
```

Step2: retrieve causal variables from data `lpd` and construct a matrix for beta:

```
> beta.LDL <- lpd$beta.LDL
> beta.HDL <- lpd$beta.HDL
> beta.TG <- lpd$beta.TG
> beta.TC <- lpd$beta.TC
> beta <- cbind(beta.LDL, beta.HDL, beta.TG, beta.TC)
```

Step3: construct a matrix for `allele1`:

```
> a1.LDL <- lpd$A1.LDL
> a1.HDL <- lpd$A1.HDL
> a1.TG <- lpd$A1.TG
> a1.TC <- lpd$A1.TC
> allele1 <- cbind(a1.LDL, a1.HDL, a1.TG, a1.TC)
```

Step4: give sample sizes of causal variables and calculate  $pc_j$

```
> N.LDL <- lpd$N.LDL
> N.HDL <- lpd$N.HDL
> N.TG <- lpd$N.TG
> N.TC <- lpd$N.TC
> ss <- cbind(N.LDL, N.HDL, N.TG, N.TC)
> sm <- apply(ss, 1, sum)
> pcj <- round(sm/max(sm), 6)
```

Step5: Construct matrix for frequency of `allele1` in each causal variable in `1000G.EUR`

```
> freq.LDL <- lpd$Freq.A1.1000G.EUR.LDL
> freq.HDL <- lpd$Freq.A1.1000G.EUR.HDL
> freq.TG <- lpd$Freq.A1.1000G.EUR.TG
> freq.TC <- lpd$Freq.A1.1000G.EUR.TC
> freq <- cbind(freq.LDL, freq.HDL, freq.TG, freq.TC)
```

Step6: construct matrix for  $sd$  of each causal variable (here  $sd$  is not specific to  $SNP\ j$ ). The following  $sd$  values for `LDL`, `HDL`, `TG` and `TC` were means of standard deviations of these lipoprotein concentrations in plasma over 63 studies from Willer *et al* [10].

## GWAS-based Mendelian Randomization Path Analysis

```
> sd.LDL <- rep(37.42, length(pvj))
> sd.HDL <- rep(14.87, length(pvj))
> sd.TG <- rep(92.73, length(pvj))
> sd.TC <- rep(42.74, length(pvj))
> sd <- cbind(sd.LDL, sd.HDL, sd.TG, sd.TC)
```

Step7: *SNPID* and position are retrieved from *lpd* data:

```
> hg19 <- lpd$SNP_hg19.HDL
> rsid <- lpd$rsid.HDL
```

Step8: separate chromosome number and *SNP* position using *chrp*:

```
> chr<-chrp(hg=hg19)
```

Step9: get new data:

```
> newdata<-cbind(freq,beta,sd,pvj,ss,pcj)
> newdata<-cbind(chr,rsid,allele,as.data.frame(newdata))
> dim(newdata)
```

Step10: retrieve data from *cad* and calculate *pdj* and frequency of coronary artery disease *cad*, *freq.case* in case population:

```
> hg18.d <- cad$chr_pos_b36
> SNP.d <- cad$SNP #SNPID
> a1.d<- tolower(cad$reference_allele)
> freq.d <- cad$ref_allele_frequency
> pvalue.d <- cad$pvalue
> beta.d <- cad$log_odds
> N.case <- cad$N_case
> N.ctr <- cad$N_control
> N.d <- N.case+N.ctr
> freq.case <- N.case/N.d
```

Step11: combine these *cad* variables into new data sheet using *cbind*

```
> newcad <- cbind(freq.d, beta.d, N.case, N.ctr, freq.case)
> newcad <- cbind(hg18.d, SNP.d, a1.d, as.data.frame(newcad))
> dim(newcad)
```

Step12: give name vector of causal variables:

```
> varname <-c("CAD", "LDL", "HDL", "TG", "TC")
```

Step13: choose *SNPs* using parameters *LG*, *Pv*, *Pc* and *Pd* and create **standard beta table** using *mktable*(*cdata*, *ddata*, *rt*,*varname*,*LG*, *Pv*, *Pc*,*Pd*)where

*cdata* is beta data of *SNPs* regressed on causal variables. Here *cdata*=*newdata*.

*ddata* is beta data of *SNPs* regressed on the disease (here *CAD*). Here *ddata*=*newcad*.

*LG*: a numeric parameter. *LG* is used to choose *SNPs* with given interval threshold for linkage disequilibrium (*LD*). Default *LG* = 10.

## GWAS-based Mendelian Randomization Path Analysis

*Pv*: a numeric parameter. *Pv* is used to choose *SNPs* with a given *p*-value cutoff. Default  $Pv = 5 \times 10^{-8}$ .

*Pc*: a numeric parameter. *Pc* is used to choose *SNPs* with a given cutoff for the proportion of sample size to maximum sample size in causal variable data. Default  $Pc=0.979$ .

*Pd*: a numeric parameter. *Pd* is used to choose *SNP* with a given cutoff for the proportion of sample size to the maximum sample size in disease data. Default  $Pd = 0.979$ .

*rt* has two options: "beta" and "path". If *rt*="beta" or "Beta" or "B", then `mktable` return a beta coefficient matrix of *SNPs* regressed on causal variables and disease, if *rt*="path" or "Path" or "P" it returns a path coefficient matrix of *SNPs* directly contributing to causal variables and disease.

```
> mybeta <- mktable(cdata=newdata, ddata=newcad, rt="beta", varname=varname, LG=1, Pv=0.00000005, Pc=0.979, Pd=0.979)
> dim(mybeta)
> beta <- mybeta[,4:8] # standard beta table for path analysis
> snp <- mybeta[,1:3] # snp data for annotation analysis
> beta<-DataFrame(beta)
> head(beta)
```

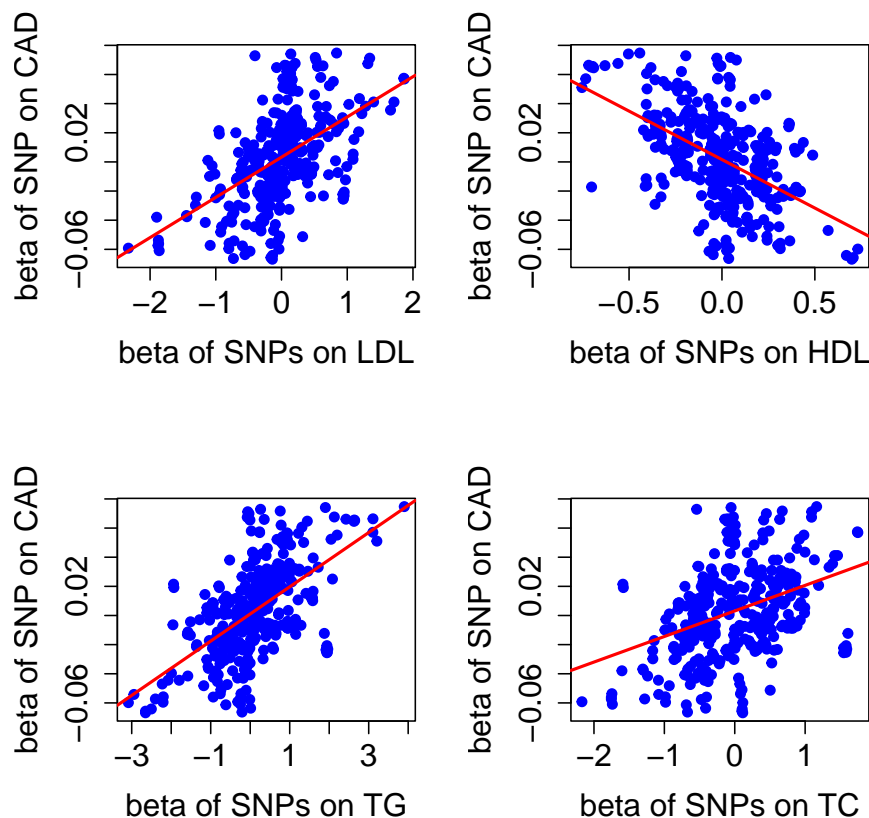
## 4 Two-way Scatter Plots for Beta Values of Disease and Undefined Causal Variables

To roughly display relationship of the undefined causal variables to disease of study, we use simple **R** `plot` function to create two-way plots of beta of multiple *SNP* regressed on the undefined causal variable versus the disease.

```
> data(beta.data)
> beta.data<-DataFrame(beta.data)
> CAD <- beta.data$cad
> LDL <- beta.data$ldl
> HDL <- beta.data$hdl
> TG <- beta.data$tg
> TC <- beta.data$tc
```

```
> par(mfrow=c(2, 2), mar=c(5.1, 4.1, 4.1, 2.1), oma=c(0, 0, 0, 0))
> plot(LDL,CAD, pch=19, col="blue", xlab="beta of SNPs on LDL", ylab="beta of SNP on CAD", cex.lab=1.5, cex.axis=1.5)
> abline(lm(CAD~LDL), col="red", lwd=2)
> plot(HDL, CAD, pch=19,col="blue", xlab="beta of SNPs on HDL", ylab="beta of SNP on CAD", cex.lab=1.5, cex.axis=1.5)
> abline(lm(CAD~HDL), col="red", lwd=2)
> plot(TG, CAD, pch=19, col="blue", xlab="beta of SNPs on TG", ylab="beta of SNP on CAD",cex.lab=1.5, cex.axis=1.5)
> abline(lm(CAD~TG), col="red", lwd=2)
> plot(TC,CAD, pch=19, col="blue", xlab="beta of SNPs on TC", ylab="beta of SNP on CAD", cex.lab=1.5, cex.axis=1.5)
> abline(lm(CAD~TC), col="red", lwd=2)
```





**Figure 1:** Scatter plots of lipid versus coronary artery disease (CAD) based on beta values of 368 SNPs regression analyses

## 5 MR and Path Analysis

After **standard beta table** was successfully created by `mktable`, user can use function `path` to perform RM analysis (regression analysis of causal variable beta values on the disease or outcome beta values), correlation among the undefined causal variables and disease and path analyses with model of

$$y \sim x_1 + x_2 + \dots + x_m$$

where  $y$  is disease or outcome variable,  $x_i$  is undefined causal variable  $i$ . Path analysis is based on *RM* analysis (regression coefficients of the causal beta on the disease beta). `path` will produce three tables: beta coefficients, *sd* values and *t*-test results of causal variables on disease or outcome, correlation matrix and path matrix (direct and indirect path coefficients)

```
> data(beta.data)
> mybeta <- DataFrame(beta.data)
> mod <- CAD~LDL+HDL+TG+TC
> pathvalue <- path(betav=mybeta, model=mod, outcome="CAD")
```

## 6 Create Path Diagram

Once user finished performance of path, user will have correlation matrix and direct path coefficients of undefined causal variable onto the disease. User is required to open a *csv* file saving results of path analysis and make table in **R Console** or copy correlation matrix without disease correlation coefficients to *excel* and copy direct path coefficients to the last column. Here is an example of making correlation and path table:

```
> mypath <- matrix(NA,3,4)
> mypath[1,] <- c(1.000000, -0.066678, 0.420036, 0.764638)
> mypath[2,] <- c(-0.066678, 1.000000, -0.559718, 0.496831)
> mypath[3,] <- c(0.420036, -0.559718, 1.000000, 0.414346)
> colnames(mypath) <- c("LDL", "HDL", "TG", "path")
> mypath<-as.data.frame(mypath)
> mypath
```

	LDL	HDL	TG	path
1	1.000000	-0.066678	0.420036	0.764638
2	-0.066678	1.000000	-0.559718	0.496831
3	0.420036	-0.559718	1.000000	0.414346

The last column is direct path coefficients, we use "path" to name this column. With this table (for example, `mypath`), user can use function `pathdiagram(pathdata,disease,R2,range)` to create path diagram. Here

*pathdata* is path result data consisting of causal correlation matrix and direct path coefficient vectors.

*disease* is a string that specifies disease name. If the disease name is long or has multiple words, then we suggest an abbreviated name, for example, coronary artery disease are shorted as "CAD".

*R2*, a numeric parameter, is *R*-square obtained from path analysis.

*range* is range of specified columns for correlation matrix. For example, `range = c(2:4)` means the correlation coefficient begins with column 2 and end at column 4. For our current example, `range=c(1:3)`.

```
> library(diagram)
```

```
> pathdiagram(pathdata=mypath, disease="CAD", R2=0.988243, range=c(1:3))
```



**Figure 2:** Path diagram demo. This path diagram shows the direct risk effects of causal variables *LDL*, *HDL* and *TG* on the disease *CAD* and their correlations.

## 7 Create Two-level Nested Path Diagram

Consider one of the causal variables is outcome of the other causal variables, but we also concern if all variables are risk factors for the disease of study. In this case we want to construct two-level nested path diagram using function `pathdiagram2(pathD,pathO,rangeD,rangeO,disease,R2D,R2O)` where

*pathD* is a *R* object that is disease path result data consisting of correlation matrix of undefined causal variables to be identified in Mendelian randomization analysis and path coefficient vector of these variables directly causing the disease of study.

*pathO* is a *R* object that is outcome path result data consisting of correlation matrix of undefined causal variables and path coefficient vector of these variables directly contributing to outcome. This outcome variable may be one of risk factors or causal variables in disease path data. These variables in *pathO* are the same with those in *pathD*.

*rangeD* is numeric vector, specifies column range for correlation coefficient matrix in *pathD*, for example, *rangeD=c(2:4)* means the correlation coefficient begins with column 2 and end at column 4.

## GWAS-based Mendelian Randomization Path Analysis

*rangeO* is numeric vector, specifies column range for correlation coefficient matrix in *pathO*, see example in *rangeD*.

*disease* is a string that specifies disease name. If the disease name is long or has multiple words, then we suggest an abbreviated name, for example, "coronary artery disease" can be shortened as "CAD".

Here is an example of *pathD* data:

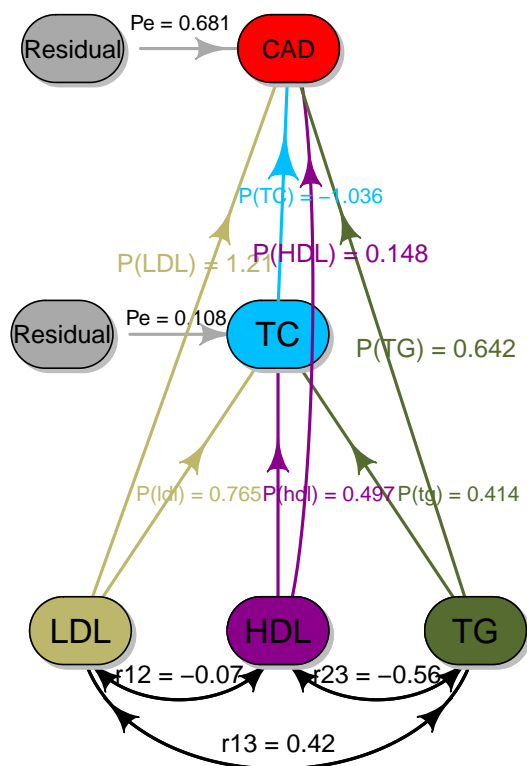
```
> pathD<-matrix(NA,4,5)
> pathD[1,] <- c(1,          -0.070161, 0.399038, 0.907127, 1.210474)
> pathD[2,] <- c(-0.070161,      1, -0.552106, 0.212201, 0.147933)
> pathD[3,] <- c(0.399038, -0.552106, 1, 0.44100, 0.64229)
> pathD[4,] <- c(0.907127, 0.212201, 0.441007, 1, -1.035677)
> colnames(pathD) <- c("LDL", "HDL", "TG", "TC", "path")
> pathD<-as.data.frame(pathD)
> pathD
```

	LDL	HDL	TG	TC	path
1	1.000000	-0.070161	0.399038	0.907127	1.210474
2	-0.070161	1.000000	-0.552106	0.212201	0.147933
3	0.399038	-0.552106	1.000000	0.441000	0.642290
4	0.907127	0.212201	0.441007	1.000000	-1.035677

Using *pathD* and *mypath*, we can perform function `pathdiagram2` to create a two-level nested path diagram:

```
> pathdiagram2(pathD=pathD,path0=myspath,rangeD=c(1:4),range0=c(1:3),disease="CAD", R2D=0.536535,R20=0.988243,
```

Note that in the current version, *GMRP* can just create two-level nested path diagram, maybe in the later version, *GMRP* will create more complex path diagrams such as more than one inner path diagram and/or multiple-disease path diagram using structure equations.



**Figure 3:** Demo of two-level nested *pathdiagram*. The outside *pathdiagram* shows the direct risk effects of undefined causal variables *LDL*, *HDL*, *TG* and *TC* on the disease *CAD*, the inner *pathdiagram* indicates the direct contributions of *LDL*, *HDL* and *TG* to *TC* and the correlation relationships among these variables.

## 8 SNP Annotation Analysis

*SNPs* chosen will be annotated in function and chromosome position. Position annotation analysis will give position information of these selected *SNPs* on chromosomes including chromosome distribution and averaged intervals between *SNPs*. We use `snpposit` to perform *SNP* position annotation. This package provides 358 *SNPs* selected by `mktable`.

```
> data(SNP358.data)
> SNP358 <- as.data.frame(SNP358.data)
> head(SNP358)
```

	rsid	chr	posit
1	rs10056022	5	74969415
2	rs10059560	5	156405784
3	rs10061689	5	74771387
4	rs10075465	5	74970975
5	rs10115928	9	107650843
6	rs10161126	12	110042348

## GWAS-based Mendelian Randomization Path Analysis

`head` displays data format required by `snpposit`. User can create similar table for *SNP* position annotation analysis. To create chromosome position histogram, we need *graphics*:

```
> library(graphics)
```

With *SNP* data `SNP358`, we can perform *SNP* position annotation using function `snppositAnnot` (`SNPdata,SNPhg19,main`) where

*SNPdata* is R object that may be *hg19* that is a string vector(`chr##.#####`) or two numeric vectors (chromosome number and *SNP* position).

*SNPhg19* is a string parameter. It may be "*hg19*" or "*chr*". If *SNPhg19*="*hg19*", then *SNPdata* contains a string vector of *hg19* or if *SNPhg19*="*chr*", then *SNPdata* consists of at least two numeric columns: *chr* and *posit*. *chr* is chromosome number and *posit* is *SNP* physical position on chromosomes. Note that "*chr*" and "*posit*" are required column names in *SNPdata* if *SNPhg19* = "*chr*".

*main* is a string which is title of graph. If no title is given, then *main*="". Its default is "A".

```
> snppositAnnot(SNPdata=SNP358,SNP_hg19="chr",main="A")
```

*SNP* function annotation analysis has two steps:

Step 1: copy *SNP IDs* selected to **Batch Query** box in [SNP Annotation Tool](#). After setting parameters and running by clicking *run button*, *SNP* annotation result will be obtained after running for a while. Choose consequence sheet of *UCSC* and copy the results to excel sheet, "*Predicted function*" column name is changed to "*functionunit*" name and save it as csv format.

Step2: input the csv file into *R Console* using **R** function `read.csv`. In *GMRP* package, we have provided data for *SNP* function annotation analysis.

```
> data(SNP368annot.data)
```

```
> SNP368<-as.data.frame(SNP368annot.data)
```

```
> SNP368[1:10, ]
```

	SNP	Allele	Strand	Symbol	Gene	function_unit
1	rs10056022	G A	1	P0C5	uc003keg.4	3downstream
2	rs10056022	G A	1	P0C5	uc003keh.4	3downstream
3	rs10056022	G A	1	ANKDD1B	uc010izt.4	3downstream
4	rs10056022	G A	1	P0C5	uc010izu.3	3downstream
5	rs10061689	G A	1	COL4A3BP	uc003kds.3	intronic
6	rs10061689	G A	1	COL4A3BP	uc003kdt.3	intronic
7	rs10061689	G A	1	COL4A3BP	uc003kdu.2	intronic
8	rs10061689	G A	1	COL4A3BP	uc011csu.2	intronic
9	rs10075465	C G	1	P0C5	uc003keg.4	intronic
10	rs10075465	C G	1	P0C5	uc003keh.4	intronic

We perform function `ucscannot` to summarize proportions of *SNPs* coming from gene various elements such as code region, introns, etc, and then create 3D pie using `pie3D` of *plotrix*.

```
> library(plotrix)
```

`ucscannot` has four parameters to be inputted: *SNPn*, *A*, *B* and *C*, a method and *UCSC* annotated data:

*UCSCannot* is annotation data obtained by performing *SNP* tools.



**Figure 4:** Chromosomal histogram of 358 selected *SNPs*. Averaged lengths of *SNP* intervals on chromosome mean that the *SNPs* on a chromosome have their averaged lengths of intervals between them. All averaged lengths over 2000kb on chromosomes were truncated, the *SNPs* on these chromosomes have at least 2000*kbp* length of interval. Numbers above *chr* columns are numbers of *SNP* distributed on the chromosomes

*SNPn* is numeric parameter for number of SNPs contained in *UCSCannot*

*A* is numeric parameter for title size, default=2.5.

*B* is numeric parameter for label size, default=1.5.

*C* is numeric parameter for *labelrad* distance,default=1.3.

*method* is numeric parameter for choosing figure output methods. It has two options: *method*=1 has no legend but color and pie components are labeled with gene elements, *method*=2 has legend over pie. The default = 1.

```

> ucscannot(UCSCannot=SNP368,SNPn=368)

      genes      exons      introns      TUR3      UTR5      intergenes      upstream      downstream
[1,]  166 0.01234568 0.8138651 0.01424501 0.001899335 0.004748338 0.05508072 0.09781576

> ucscannot(UCSCannot=SNP368,SNPn=368,A=3,B=2,C=1.3,method=2)

      genes      exons      introns      TUR3      UTR5      intergenes      upstream      downstream

```

	genes	exons	introns	TUR3	UTR5	intergenes	upstream	downstream
[1,]	166	0.01234568	0.8138651	0.01424501	0.001899335	0.004748338	0.05508072	0.09781576

Distribution of 368 SNPs within 16

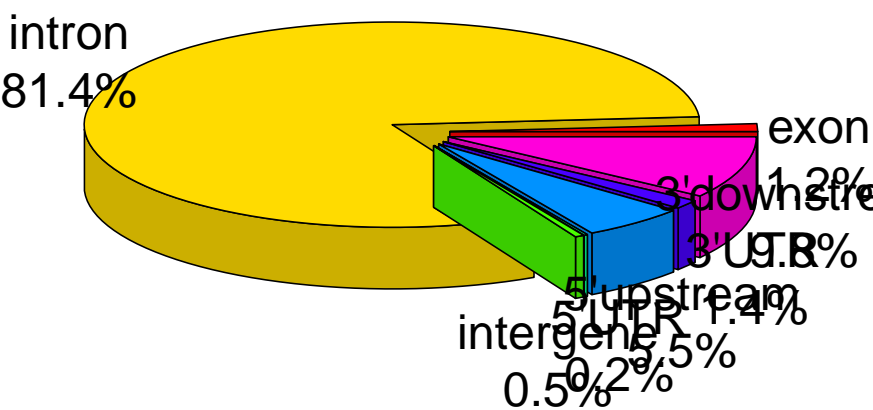


Figure 5: Distribution of the selected SNPs in gene function elements.

[1,]	166	0.01234568	0.8138651	0.01424501	0.001899335	0.004748338	0.05508072	0.09781576
------	-----	------------	-----------	------------	-------------	-------------	------------	------------



	genes	exons	introns	TUR3	UTR5	intergenes	upstream	downstream
[1,]	166	0.01234568	0.8138651	0.01424501	0.001899335	0.004748338	0.05508072	0.09781576

Distribution of 368 SNPs within 16

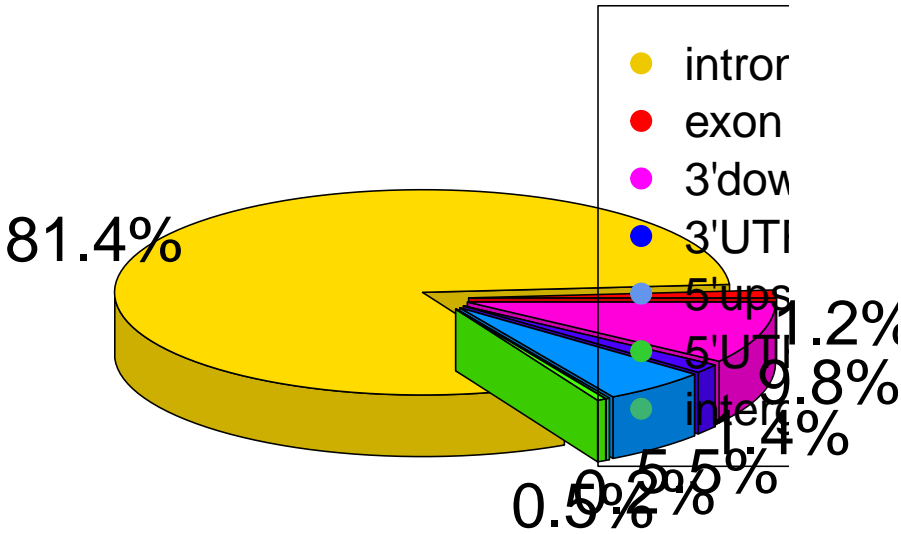


Figure 6: Distribution of the selected SNPs in gene function elements.

## 9 Session Info

```
> sessionInfo()

R version 4.6.0 Patched (2026-05-01 r89994)
Platform: aarch64-apple-darwin23
Running under: macOS Tahoe 26.3.1

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.6/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.6/Resources/lib/libRlapack.dylib; LAPACK version 3.12.1

locale:
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats4      stats      graphics  grDevices  utils      datasets  methods    base

other attached packages:
[1] GMRP_1.41.0      GenomicRanges_1.65.0 Seqinfo_1.3.0      IRanges_2.47.1
[5] S4Vectors_0.51.2 BiocGenerics_0.59.2 generics_0.1.4     plotrix_3.8-14
[9] diagram_1.6.5    shape_1.4.6.1

loaded via a namespace (and not attached):
[1] digest_0.6.39      fastmap_1.2.0      xfun_0.57          knitr_1.51
[5] htmltools_0.5.9    rmarkdown_2.31     cli_3.6.6          compiler_4.6.0
[9] tools_4.6.0        evaluate_1.0.5     yaml_2.3.12        otel_0.2.0
[13] BiocManager_1.30.27 rlang_1.2.0        BiocStyle_2.41.0
```

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## GWAS-based Mendelian Randomization Path Analysis

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