Replication1

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```r
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
```

```r
library(ggpubr)
```

```
## Loading required package: ggplot2

## Loading required package: magrittr
```

```r
library(ggplot2)
library(Hmisc)
```

```
## Loading required package: lattice

## Loading required package: survival

## Loading required package: Formula

##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:dplyr':
##
##     src, summarize

## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```r
library(MASS)
```

```
##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select
```

```r
library(ppcor)
library(boot)
```

```
##
## Attaching package: 'boot'
## The following object is masked from 'package:survival':
##
##     aml
```

```
## The following object is masked from 'package:lattice':
##
##     melanoma
```

```
CorFunc <- function(d,indices){
  R <- rcorr(d$X[indices],d$Y[indices])
  return(R$r[1,2])
}

# example of difference in significance but no difference in effect.
for (i in c(1:10)){ #
  print(i)
  # set.seed(1235)  # for reproducibility
  set.seed(1234+i)
  A <- rnorm(20,0.5,1)# simulate random data
  tA <- t.test(A, mu=0)
  print(mean(A))
  print(tA$p.value)
}
```

```
## [1] 1
## [1] 0.5886905
## [1] 0.005039768
## [1] 2
## [1] 0.570992
## [1] 0.01676168
## [1] 3
## [1] 0.5471627
## [1] 0.05202813
## [1] 4
## [1] 0.4991654
## [1] 0.02134782
## [1] 5
## [1] 0.03927364
## [1] 0.8561865
## [1] 6
## [1] 0.5937153
## [1] 0.01069414
## [1] 7
## [1] 0.546981
## [1] 0.03120765
## [1] 8
## [1] 0.6472981
## [1] 0.007175651
## [1] 9
## [1] 0.3387416
## [1] 0.08353486
## [1] 10
## [1] 0.05170604
## [1] 0.8279797
```

```r
set.seed(1237)  # for reproducibility
A <- rnorm(20,0.5,0.9)# simulate random data
t.test(A, mu=0)
```

```
##
##  One Sample t-test
##
## data:  A
## t = 2.2834, df = 19, p-value = 0.03409
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.04521522 1.03967761
## sample estimates:
## mean of x
## 0.5424464
```

```r
set.seed(1238)  # for reproducibility
B <- rnorm(20,0.5,1.5)# simulate random data with larger variance
t.test(B, mu=0)
```

```
##
##  One Sample t-test
##
## data:  B
## t = 1.671, df = 19, p-value = 0.1111
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.1259521  1.1234482
## sample estimates:
## mean of x
##  0.498748
```

```r
AB=as.matrix(c(A,B))
group = factor(rep(c('A','B'),each=20));
dt = data.frame(AB,group)
t.test(A,B,var.equal = TRUE)
```

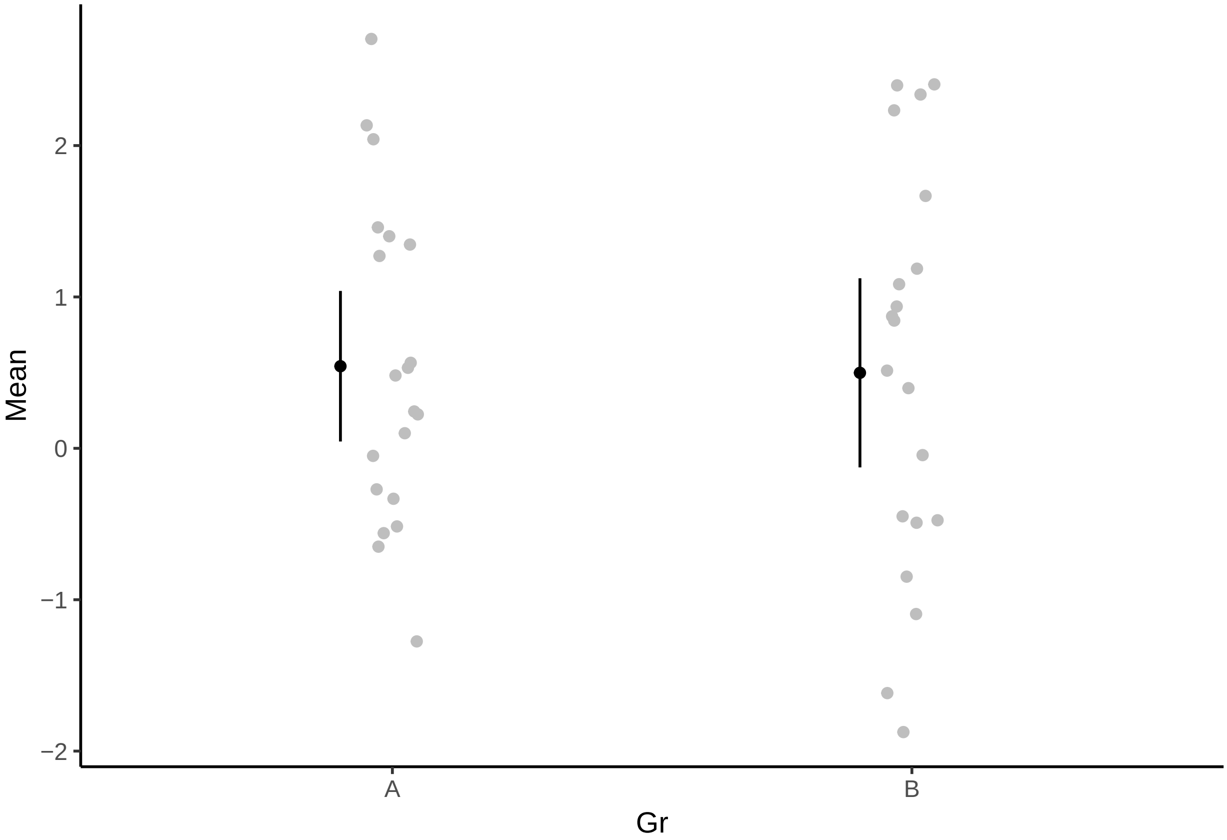
```
##
##  Two Sample t-test
##
## data:  A and B
## t = 0.11455, df = 38, p-value = 0.9094
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.7285505  0.8159472
## sample estimates:
## mean of x mean of y
## 0.5424464 0.4987480
```

```r
sumup = data.frame("Gr" = c('A','B'))

sumup<-cbind(sumup,Mean=with(dt, tapply(AB, group, mean)))
sumup<-cbind(sumup,SD=with(dt, tapply(AB, group, sd)))
sumup<-cbind(sumup,N=with(dt, tapply(AB, group, length)))
sumup<-cbind(sumup,SE =sumup$SD/sqrt(sumup$N))  # Calculate standard error of the mean
ciMult <- qt(.95/2 + .5, sumup$N-1)
```

```
sumup<-cbind(sumup,CI = sumup$SE * ciMult)

EffNieuw <- ggplot(sumup, aes(x=Gr, y=Mean)) +
  geom_errorbar(aes(ymin=Mean-CI, ymax=Mean+CI), width=NA,position = position_nudge(x = -0.1)) +
  geom_point(position = position_nudge(x = -0.1)) +
  geom_jitter(data=dt,aes(x=group,y=AB),color = "gray",width = 0.05)+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),panel.background = elemen
print(EffNieuw)
```

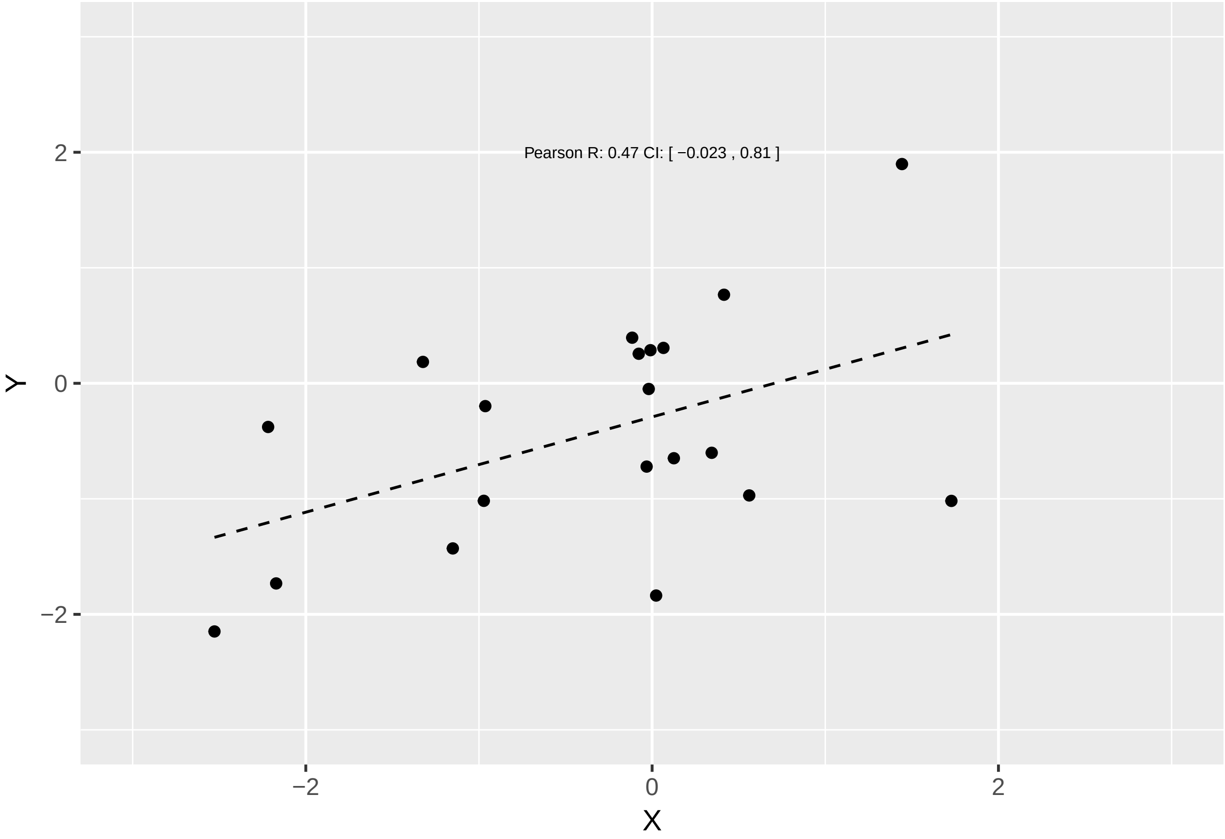


```
# figure on Nieuwenhuis with correlations
Rval <- 0.5
Sigma <- matrix(c(1,Rval,Rval,1),2,2)
for (i in c(10,26)){ #,11,8,18,22,24 --> other possible examples
  print(i)
  set.seed(1234+i)  # for reproducibility
  D <- mvrnorm(n = 20, rep(0, 2), Sigma, empirical = FALSE)
  X <- D[,1]
  Y <- D[,2]
  Add <- data.frame(X,Y)
  R<-rcorr(Add$X,Add$Y,type=c("pearson"))
  RValue = R$r[1,2]
  print(R$r[1,2])
  print(R$P[1,2])

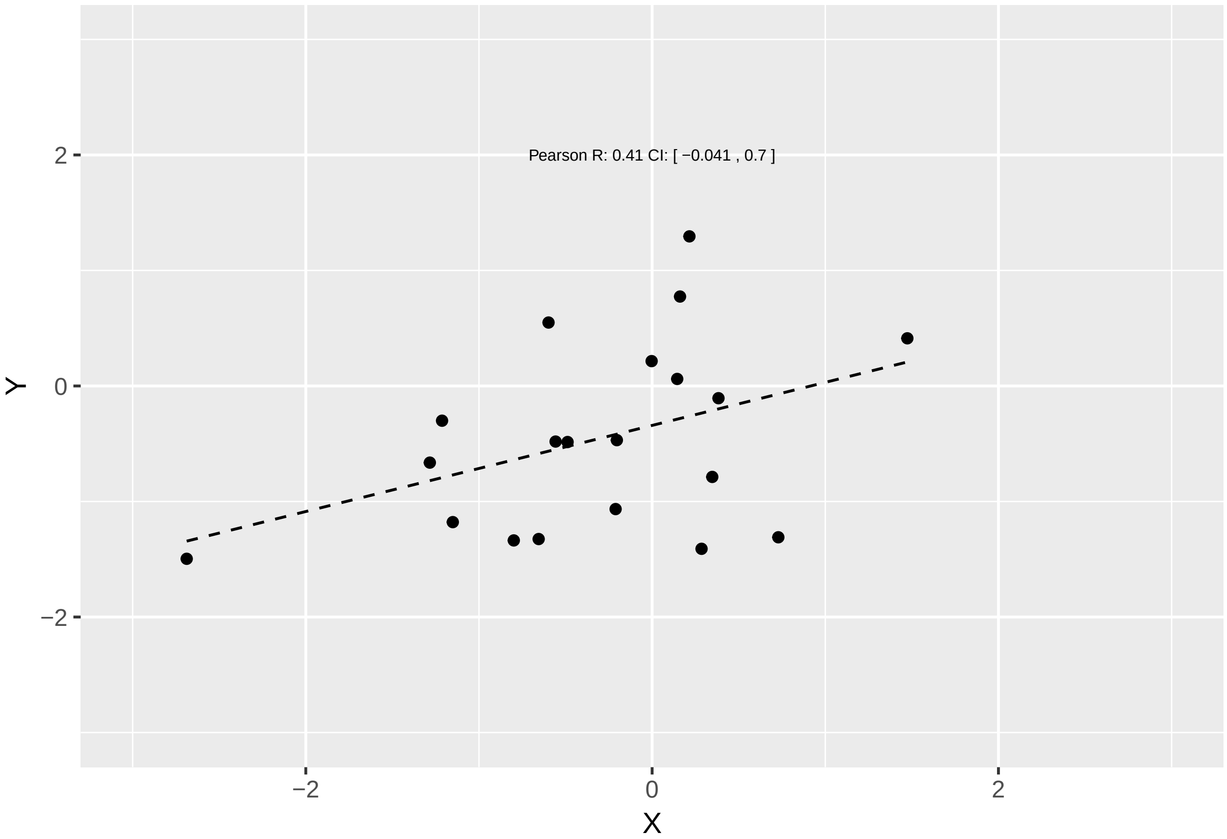
  # bootstrap CI
  cor.boot <- NULL
  N <- dim(Add)[1]
  for (i in 1:1000) {
    idx <- sample.int(N, N, replace = TRUE)
    cor.boot[i] <- cor(Add[idx, ])[1,2]
  }
  Rbci0<- quantile(cor.boot, c(.025, .975))

  txt = toString(paste("Pearson R:", format(RValue,digits=2), "CI: [",format( Rbci0[1],digits=2),",",fo
  NiewenCorr<-ggplot(Add, aes(X, Y)) +
    geom_point() +
    labs(x = "X", y = "Y") +
    geom_smooth(method="lm",color = "black",linetype = 2, size=0.5, se=FALSE) +
    coord_cartesian(xlim = c(-3,3),ylim = c(-3,3)) +
    annotate("text", x = 0, y = 2, label = txt,size=2)+
    theme(legend.position="none")
  print(NiewenCorr)
}
```

```
## [1] 10
## [1] 0.474046
## [1] 0.03472206
```



```
## [1] 26
## [1] 0.4082099
## [1] 0.07397
```



```
################################
# figure on underpower
################################
P=NA;R=NA;Cond=NA;
LowP = data.frame(P,R,Cond)
HighP= data.frame(P,R,Cond)

for (i in 1:10000){
A <- rnorm(15,0.5,1)
B <- rnorm(15,0.5,1)
R<-rcorr(A,B)
LowP <- rbind(LowP,c(R$P[1,2], R$r[1,2],R$P[1,2]<0.05))

A <- rnorm(100,0.5,1)
B <- rnorm(100,0.5,1)
R<-rcorr(A,B)
HighP <- rbind(HighP,c(R$P[1,2], R$r[1,2],R$P[1,2]<0.05))
}
LowP$Cond = factor(LowP$Cond)
HighP$Cond = factor(HighP$Cond)

L2 <-filter(LowP, Cond == "1")
R2 <-filter(HighP, Cond == "1")
  ggplot(L2, aes(x=R)) +
    geom_histogram(aes(x=R),binwidth=.025)+
    geom_histogram(data=R2,aes(x=R),binwidth=.025,fill="red")+
    xlim(-1, 1)
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).

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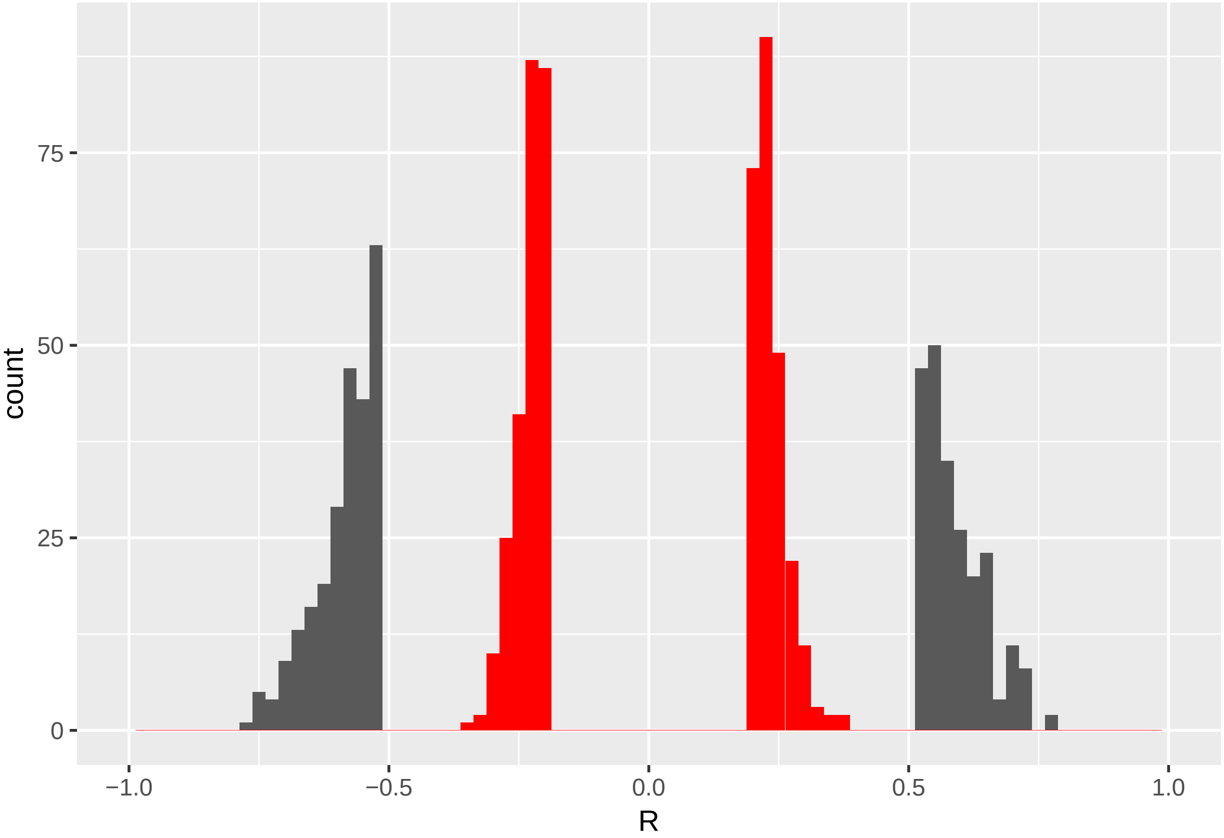
```



```
################################
# figure on correlation
################################

set.seed(1234)  # for reproducibility
PP = list()

# effect of outlier
X <- rnorm(20,0,1)
Y <- rnorm(20,0,1)
Z <- rep(1,20)
Dcor = data.frame(X,Y,Z)
for (i in c(1,3,5)){
  print(i)
  Add <- rbind(Dcor,c(i,i,2))
  R<-rcorr(Add$X,Add$Y,type=c("pearson"))
  RValue = R$r[1,2]
  print(R$P[1,2])

  # bootstrap CI
  cor.boot <- NULL
  N <- dim(Add)[1]
  for (i in 1:1000) {
    idx <- sample.int(N, N, replace = TRUE)
    cor.boot[i] <- cor(Add[idx, ])[1,2]
  }
  Rbci<- quantile(cor.boot, c(.025, .975))


  txt = toString(paste("Pearson R:", format(RValue,digits=2), "CI: [",format( Rbci[1],digits=2),",",for
  PP[[length(PP) + 1]]<-ggplot(Add, aes(X, Y),fill=factor(Z)) +
    scale_color_manual(values=c("black", "red")) +
    scale_fill_manual(values=c(NA, "red")) +
    geom_point(aes(colour = factor(Z),fill=factor(Z)),shape=21) +
    labs(x = "X", y = "Y") +
    geom_smooth(method="lm",color = "black",linetype = 2, size=0.5) +
    coord_cartesian(xlim = c(-2.5,6.5),ylim = c(-2.5,6.5)) +
    annotate("text", x = 0, y = 6, label = txt,size=2)+
    theme(legend.position="none")
}
```

```
## [1] 1
## [1] 0.5595559
```

```
## Warning in cor(Add[idx, ]): the standard deviation is zero
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## [1] 0.2610825

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## [1] 5
## [1] 0.01098973
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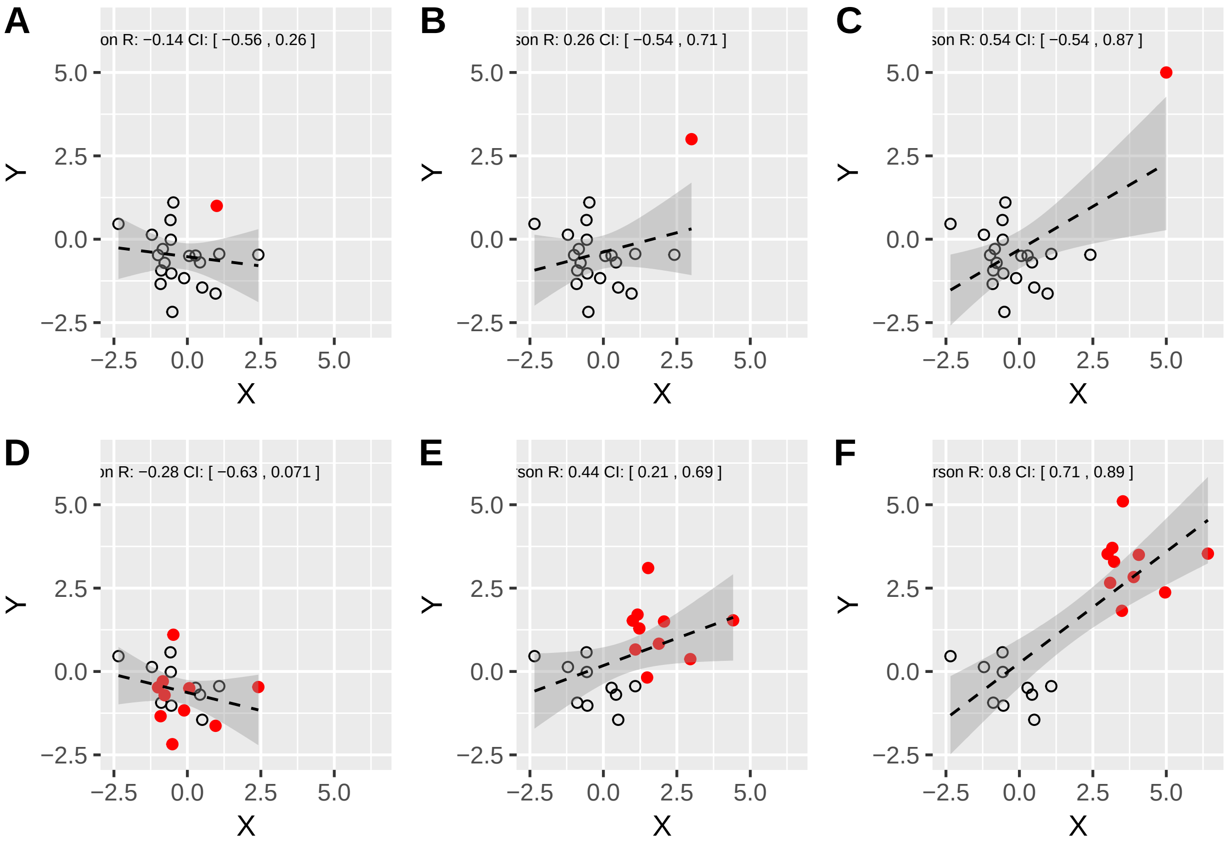
```
# effect of subgroups
set.seed(1234)  # for reproducibility
QQ = list()
Xbase <- rnorm(20,0,1)
Ybase <- rnorm(20,0,1)
Z <- c(rep(0,10),rep(1,10))

for (i in c(0,2,4)){
  print(i)
  X = Xbase+i*Z
  Y = Ybase+i*Z
  Add = data.frame(X,Y,Z)
  R<-rcorr(Add$X,Add$Y)
  RCor = R$r[1,2]
  print(R$P[1,2])
  # bootstrap CI
  cor.boot <- NULL
  N <- dim(Add)[1]
  for (i in 1:1000) {
    idx <- sample.int(N, N, replace = TRUE)
    cor.boot[i] <- cor(Add[idx, ])[1,2]
  }
  Rbci2<- quantile(cor.boot, c(.025, .975))


  txt = toString(paste("Pearson R:", format(RCor,digits=2), "CI: [",format( Rbci2[1],digits=2),",",forma
  QQ[[length(QQ) + 1]]<-ggplot(Add, aes(X, Y),fill=factor(Z)) +
    scale_color_manual(values=c("black", "red")) +
    scale_fill_manual(values=c(NA, "red")) +
    geom_point(aes(colour = factor(Z),fill=factor(Z)),shape=21) +
    labs(x = "X", y = "Y") +
    geom_smooth(method="lm",color = "black",linetype = 2, size=0.5) +
    coord_cartesian(xlim = c(-2.5,6.5),ylim = c(-2.5,6.5)) +
    annotate("text", x = 0, y = 6, label = txt,size=2)+
    theme(legend.position="none")
}
```

```
## [1] 0
## [1] 0.2378304
## [1] 2
## [1] 0.05013606
## [1] 4
## [1] 2.337339e-05
```

```
ggarrange(PP[[1]],PP[[2]],PP[[3]],QQ[[1]],QQ[[2]],QQ[[3]],ncol = 3, nrow = 2,labels = c("A","B","C","D"
```


A
on R: −0.14 CI: [−0.56 , 0.26]
B
son R: 0.26 CI: [−0.54 , 0.71]
C
son R: 0.54 CI: [−0.54 , 0.87]
D
on R: −0.28 CI: [−0.63 , 0.071]
E
son R: 0.44 CI: [0.21 , 0.69]
F
rson R: 0.8 CI: [0.71 , 0.89]
Y
X
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2.5
0.0
−2.5
−2.5
0.0
2.5
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