

Calculating Correlation Between Mutation Operators

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Installing and loading packages

```
install.packages("ggpubr")
```

```
## Installing package into '/home/beatriz/R/x86_64-pc-linux-gnu-library/3.4'  
## (as 'lib' is unspecified)
```

```
install.packages("ggplot2")
```

```
## Installing package into '/home/beatriz/R/x86_64-pc-linux-gnu-library/3.4'  
## (as 'lib' is unspecified)
```

```
install.packages("reshape2")
```

```
## Installing package into '/home/beatriz/R/x86_64-pc-linux-gnu-library/3.4'  
## (as 'lib' is unspecified)
```

```
library("ggplot2")  
library("reshape2")  
library("ggpubr")
```

```
## Loading required package: magrittr
```

Reading data

```

evoResults1 <- read.csv('/home/beatriz/Desktop/pibicDataSet/evoResults.csv', sep =
",", header = TRUE)
evoResults2 <- read.csv('/home/beatriz/Desktop/pibicDataSet/evoResults2.csv', sep =
",", header = TRUE)
evoResults3 <- read.csv('/home/beatriz/Desktop/pibicDataSet/evoResults3.csv', sep =
",", header = TRUE)

randoopResults1 <- read.csv('/home/beatriz/Desktop/pibicDataSet/randoopResults.csv',
sep = ",", header = TRUE)
randoopResults2 <- read.csv('/home/beatriz/Desktop/pibicDataSet/randoopResults2.csv',
sep = ",", header = TRUE)
randoopResults3 <- read.csv('/home/beatriz/Desktop/pibicDataSet/randoopResults3.csv',
sep = ",", header = TRUE)

manualResults1 <- read.csv('/home/beatriz/Desktop/pibicDataSet/manualSuitesResults.c
v', sep = ",", header = TRUE)
manualResults2 <- read.csv('/home/beatriz/Desktop/pibicDataSet/manualSuitesResults2.c
sv', sep = ",", header = TRUE)
manualResults3 <- read.csv('/home/beatriz/Desktop/pibicDataSet/manualSuitesResults3.c
sv', sep = ",", header = TRUE)

```

Merging data

```

evoResults12 <- merge(evoResults1, evoResults2, all = TRUE)
#evo12
evoResults123 <- merge(evoResults12, evoResults3, all = TRUE)
#evoResults123

randoopResults12 <- merge(randoopResults1, randoopResults2, all = TRUE)
#randoopResults12
randoopResults123 <- merge(randoopResults12, randoopResults3, all = TRUE)
#randoopResults123

manualResults12 <- merge(manualResults1, manualResults2, all = TRUE)
#manualResults12
manualResults123 <- merge(manualResults12, manualResults3, all = TRUE)
#manualResults123

evoAndRandoopDataSet <- merge(evoResults123, randoopResults123, all = TRUE)
completeDataSet <- merge(evoAndRandoopDataSet, manualResults123, all = TRUE)
#completeDataSet

```

ReturnValsMutator

ReturnValsMutator vs ConditionalsBoundaryMutator

```
par(mfrow = c(2,2))
plot(evoResults123$ConditionalsBoundaryMutator ~ evoResults123$ReturnValsMutator, dat
a = evoResults123)
plot(randoopResults123$ConditionalsBoundaryMutator ~ randoopResults123$ReturnValsMuta
tor, data = randoopResults123)
plot(manualResults123$ConditionalsBoundaryMutator ~ manualResults123$ReturnValsMutato
r, data = manualResults123)

cor.test(evoResults123$ConditionalsBoundaryMutator, evoResults123$ReturnValsMutator,
method='spearman')
```

```
## Warning in cor.test.default(evoResults123$ConditionalsBoundaryMutator,
## evoResults123$ReturnValsMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$ConditionalsBoundaryMutator and evoResults123$ReturnValsMutat
or
## S = 24839000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8509665
```

```
cor.test(randoopResults123$ConditionalsBoundaryMutator, randoopResults123$ReturnValsM
utator, method='spearman')
```

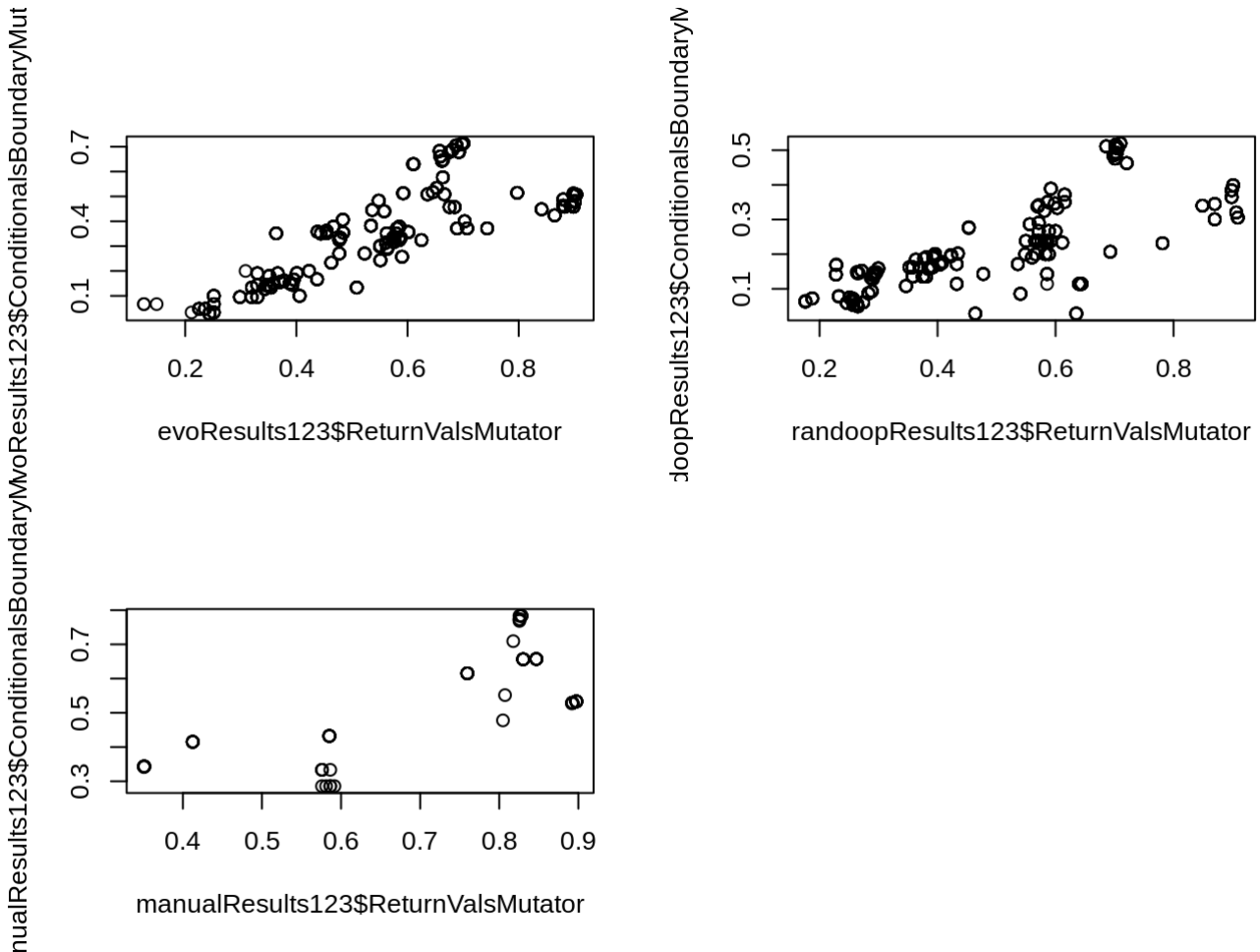
```
## Warning in
## cor.test.default(randoopResults123$ConditionalsBoundaryMutator, : Cannot
## compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$ConditionalsBoundaryMutator and randoopResults123$ReturnV
alsMutator
## S = 33167000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8009974
```

```
cor.test(manualResults123$ConditionalsBoundaryMutator, manualResults123$ReturnValsMut
ator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$ConditionalsBoundaryMutator, :
## Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data: manualResults123$ConditionalsBoundaryMutator and manualResults123$ReturnValsMutator
## S = 60426, p-value = 9.996e-13
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6374082
```



ReturnValsMutator vs VoidMethodCallMutator

```
par(mfrow = c(2,2))
plot(evoResults123$VoidMethodCallMutator ~ evoResults123$ReturnValsMutator, data = evoResults123)
plot(randomResults123$VoidMethodCallMutator ~ randomResults123$ReturnValsMutator, data = randomResults123)
plot(manualResults123$VoidMethodCallMutator ~ manualResults123$ReturnValsMutator, data = manualResults123)

cor.test(evoResults123$VoidMethodCallMutator, evoResults123$ReturnValsMutator, method = 'spearman')
```

```
## Warning in cor.test.default(evoResults123$VoidMethodCallMutator,  
## evoResults123$ReturnValsMutator, : Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: evoResults123$VoidMethodCallMutator and evoResults123$ReturnValsMutator  
## S = 44012000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.6377623
```

```
cor.test(randoopResults123$VoidMethodCallMutator, randoopResults123$ReturnValsMutator,  
method='spearman')
```

```
## Warning in cor.test.default(randoopResults123$VoidMethodCallMutator,  
## randoopResults123$ReturnValsMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: randoopResults123$VoidMethodCallMutator and randoopResults123$ReturnValsMutator  
## S = 24164000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.801122
```

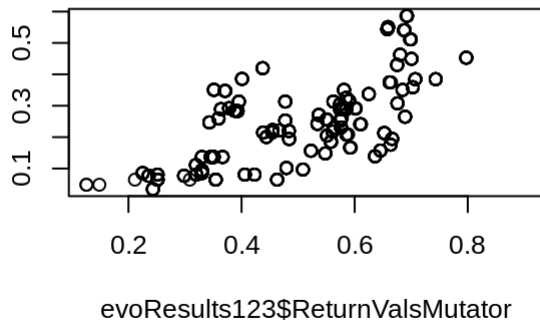
```
cor.test(manualResults123$VoidMethodCallMutator, manualResults123$ReturnValsMutator,  
method='spearman')
```

```
## Warning in cor.test.default(manualResults123$VoidMethodCallMutator,  
## manualResults123$ReturnValsMutator, : Cannot compute exact p-value with  
## ties
```

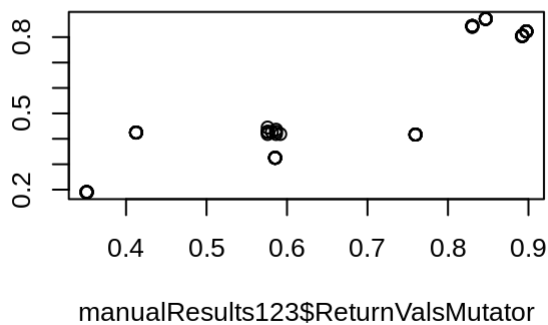
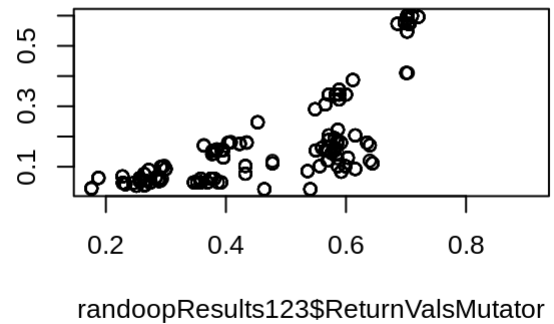
```
##  
## Spearman's rank correlation rho  
##  
## data: manualResults123$VoidMethodCallMutator and manualResults123$ReturnValsMutator  
## S = 31439, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.7412076
```

evoResults123\$VoidMethodCallMutator

manualResults123\$VoidMethodCallMutator



randoopResults123\$VoidMethodCallMutator



ReturnValsMutator vs IncrementsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$IncrementsMutator ~ evoResults123$ReturnValsMutator, data = evoResults123)
plot(randoopResults123$IncrementsMutator ~ randoopResults123$ReturnValsMutator, data = randoopResults123)
plot(manualResults123$IncrementsMutator ~ manualResults123$ReturnValsMutator, data = manualResults123)
```

```
cor.test(evoResults123$IncrementsMutator, evoResults123$ReturnValsMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$IncrementsMutator,
## evoResults123$ReturnValsMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data: evoResults123$IncrementsMutator and evoResults123$ReturnValsMutator
## S = 46886000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7186818
```

```
cor.test(randoopResults123$IncrementsMutator, randoopResults123$ReturnValsMutator, method='spearman')
```

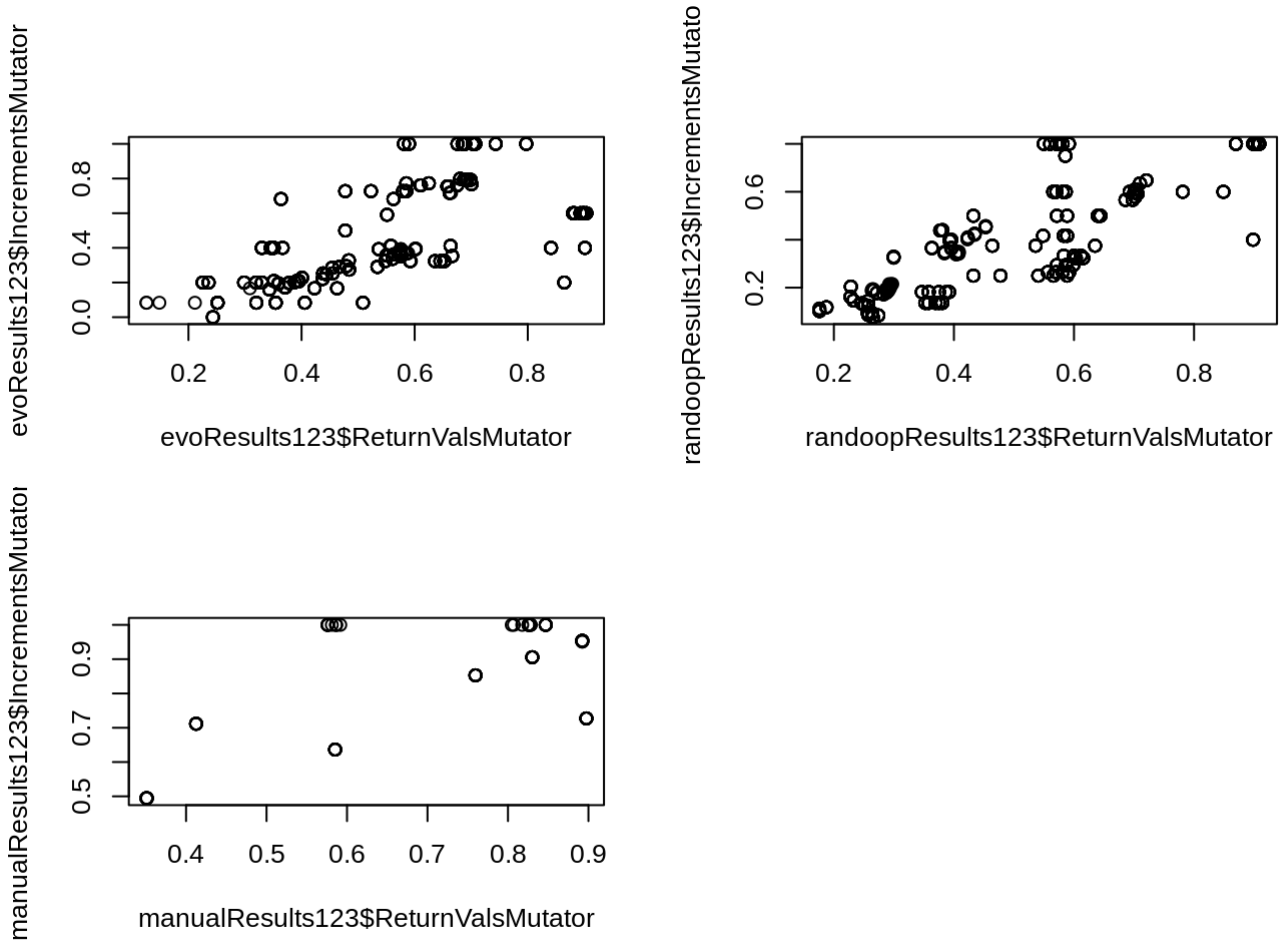
```
## Warning in cor.test.default(randoopResults123$IncrementsMutator,  
## randoopResults123$ReturnValsMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: randoopResults123$IncrementsMutator and randoopResults123$ReturnValsMutator  
## S = 34897000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.7906195
```

```
cor.test(manualResults123$IncrementsMutator, manualResults123$ReturnValsMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$IncrementsMutator,  
## manualResults123$ReturnValsMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: manualResults123$IncrementsMutator and manualResults123$ReturnValsMutator  
## S = 88465, p-value = 8.499e-07  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.4691569
```



ReturnValsMutator vs NegateConditionalsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$NegateConditionalsMutator ~ evoResults123$ReturnValsMutator, data
     = evoResults123)
plot(randoopResults123$NegateConditionalsMutator ~ randoopResults123$ReturnValsMutato
     r, data = randoopResults123)
plot(manualResults123$NegateConditionalsMutator ~ manualResults123$ReturnValsMutator,
     data = manualResults123)
```

```
cor.test(evoResults123$NegateConditionalsMutator, evoResults123$ReturnValsMutator, me
thod='spearman')
```

```
## Warning in cor.test.default(evoResults123$NegateConditionalsMutator,
## evoResults123$ReturnValsMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$NegateConditionalsMutator and evoResults123$ReturnValsMutator
## S = 14059000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9156459
```



```
cor.test(randoopResults123$NegateConditionalsMutator, randoopResults123$ReturnValsMutator, method='spearman')
```

```
## Warning in cor.test.default(randoopResults123$NegateConditionalsMutator, :  
## Cannot compute exact p-value with ties
```

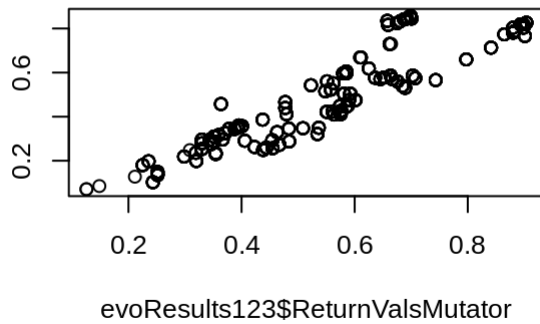
```
##  
## Spearman's rank correlation rho  
##  
## data: randoopResults123$NegateConditionalsMutator and randoopResults123$ReturnValsMutator  
## S = 15379000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.907728
```

```
cor.test(manualResults123$NegateConditionalsMutator, manualResults123$ReturnValsMutator, method='spearman')
```

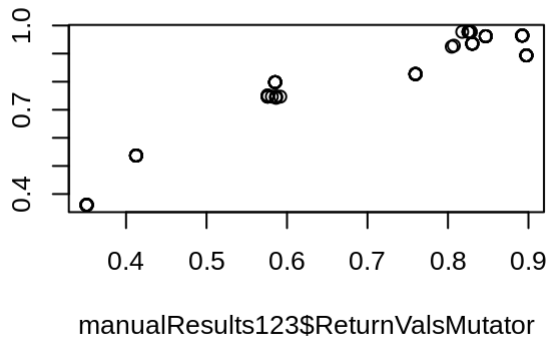
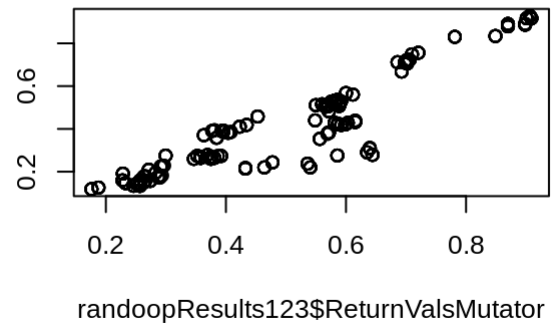
```
## Warning in cor.test.default(manualResults123$NegateConditionalsMutator, :  
## Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: manualResults123$NegateConditionalsMutator and manualResults123$ReturnValsMutator  
## S = 30624, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.8162364
```

anualResults123\$NegateConditionalsNuevoResults123\$NegateConditionalsMuta



ndoopResults123\$NegateConditionalsMl



ReturnValsMutator vs MathMutator

```
par(mfrow = c(2,2))
plot(evoResults123$MathMutator ~ evoResults123$ReturnValsMutator, data = evoResults123)
plot(randoopResults123$MathMutator ~ randoopResults123$ReturnValsMutator, data = randoopResults123)
plot(manualResults123$MathMutator ~ manualResults123$ReturnValsMutator, data = manualResults123)
```

```
cor.test(evoResults123$MathMutator, evoResults123$ReturnValsMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$MathMutator,
## evoResults123$ReturnValsMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data: evoResults123$MathMutator and evoResults123$ReturnValsMutator
## S = 23672000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8579672
```

```
cor.test(randoopResults123$MathMutator, randoopResults123$ReturnValsMutator, method='spearman')
```

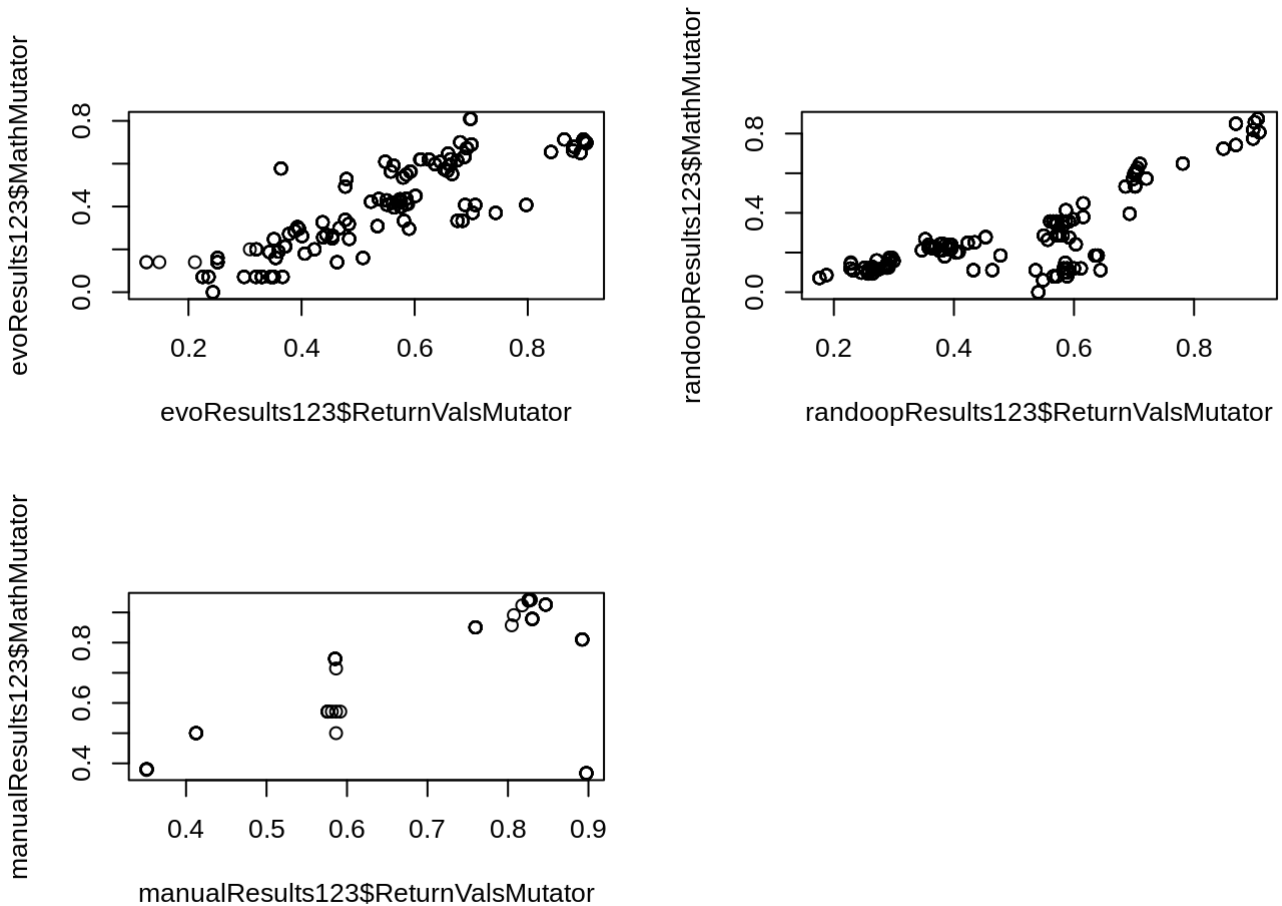
```
## Warning in cor.test.default(randoopResults123$MathMutator,  
## randoopResults123$ReturnValsMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: randoopResults123$MathMutator and randoopResults123$ReturnValsMutator  
## S = 52585000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.6844883
```

```
cor.test(manualResults123$MathMutator, manualResults123$ReturnValsMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$MathMutator,  
## manualResults123$ReturnValsMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: manualResults123$MathMutator and manualResults123$ReturnValsMutator  
## S = 116710, p-value = 0.002455  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.2996617
```



ReturnValsMutator vs InvertNegsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$InvertNegsMutator ~ evoResults123$ReturnValsMutator, data = evoResults123)
plot(randoopResults123$InvertNegsMutator ~ randoopResults123$ReturnValsMutator, data = randoopResults123)
plot(manualResults123$InvertNegsMutator ~ manualResults123$ReturnValsMutator, data = manualResults123)
```

```
cor.test(evoResults123$InvertNegsMutator, evoResults123$ReturnValsMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$InvertNegsMutator,
## evoResults123$ReturnValsMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data: evoResults123$InvertNegsMutator and evoResults123$ReturnValsMutator
## S = 4260100, p-value = 0.3576
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.0532983
```

```
cor.test(randoopResults123$InvertNegsMutator, randoopResults123$ReturnValsMutator, method='spearman')
```

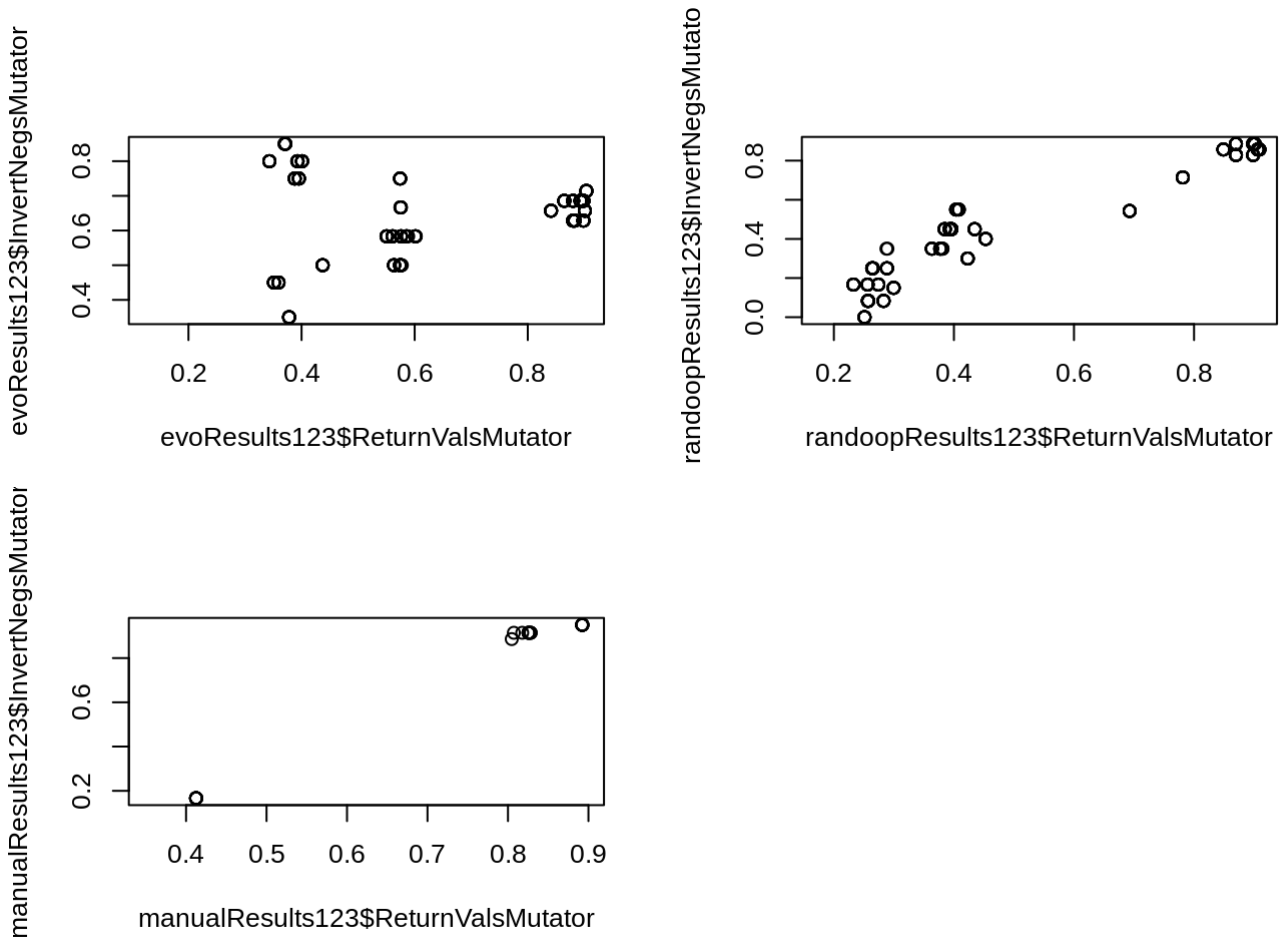
```
## Warning in cor.test.default(randoopResults123$InvertNegsMutator,
## randoopResults123$ReturnValsMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$InvertNegsMutator and randoopResults123$ReturnValsMutator
## S = 337060, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.925096
```

```
cor.test(manualResults123$InvertNegsMutator, manualResults123$ReturnValsMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$InvertNegsMutator,
## manualResults123$ReturnValsMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$InvertNegsMutator and manualResults123$ReturnValsMutator
## S = 100.43, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9776568
```



ConditionalsBoundaryMutator

ConditionalsBoundaryMutator vs VoidMethodCallMutator

```
par(mfrow = c(2,2))
plot(evoResults123$VoidMethodCallMutator ~ evoResults123$ConditionalsBoundaryMutator,
data = evoResults123)
plot(randoopResults123$VoidMethodCallMutator ~ randoopResults123$ConditionalsBoundary
Mutator, data = randoopResults123)
plot(manualResults123$VoidMethodCallMutator ~ manualResults123$ConditionalsBoundaryMu
tator, data = manualResults123)

cor.test(evoResults123$VoidMethodCallMutator, evoResults123$ConditionalsBoundaryMutat
or, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$VoidMethodCallMutator,
## evoResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-value
## with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$VoidMethodCallMutator and evoResults123$ConditionalsBoundaryM
utator
## S = 52736000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.5659579
```

```
cor.test(randoopResults123$VoidMethodCallMutator, randoopResults123$ConditionalsBound
aryMutator, method='spearman')
```

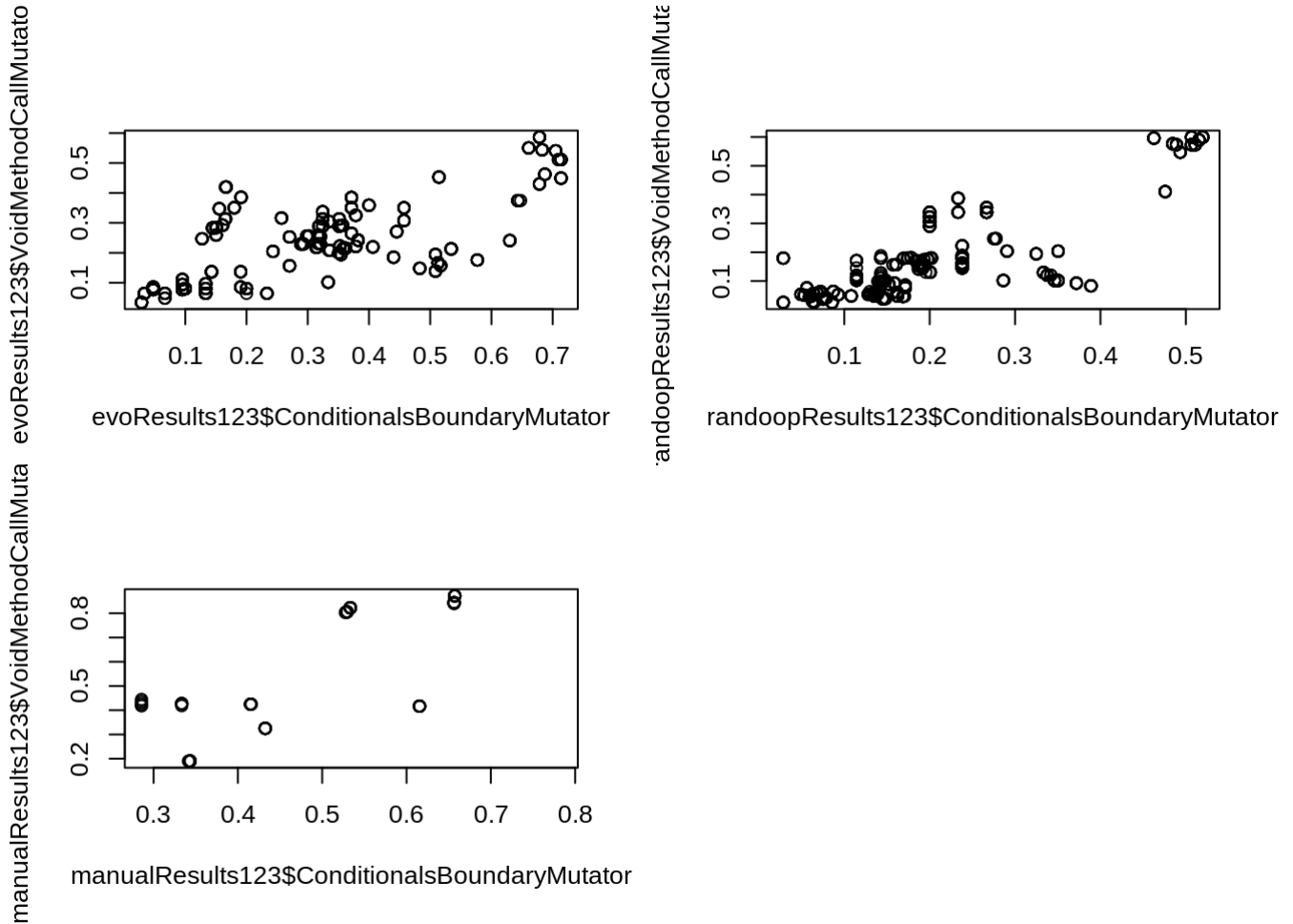
```
## Warning in cor.test.default(randoopResults123$VoidMethodCallMutator,
## randoopResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-
## value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$VoidMethodCallMutator and randoopResults123$ConditionalsB
oundaryMutator
## S = 28908000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7620775
```

```
cor.test(manualResults123$VoidMethodCallMutator, manualResults123$ConditionalsBoundar
yMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$VoidMethodCallMutator,
## manualResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-
## value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$VoidMethodCallMutator and manualResults123$ConditionalsBou
ndaryMutator
## S = 39394, p-value = 2.742e-13
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6757302
```



ConditionalsBoundaryMutator vs IncrementsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$IncrementsMutator ~ evoResults123$ConditionalsBoundaryMutator, data = evoResults123)
plot(randoopResults123$IncrementsMutator ~ randoopResults123$ConditionalsBoundaryMutator, data = randoopResults123)
plot(manualResults123$IncrementsMutator ~ manualResults123$ConditionalsBoundaryMutator, data = manualResults123)

cor.test(evoResults123$IncrementsMutator, evoResults123$ConditionalsBoundaryMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$IncrementsMutator,
## evoResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-value
## with ties
```



```
##  
## Spearman's rank correlation rho  
##  
## data:  evoResults123$IncrementsMutator and evoResults123$ConditionalsBoundaryMutator  
## S = 58370000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.6497802
```

```
cor.test(randoopResults123$IncrementsMutator, randoopResults123$ConditionalsBoundaryMutator, method='spearman')
```

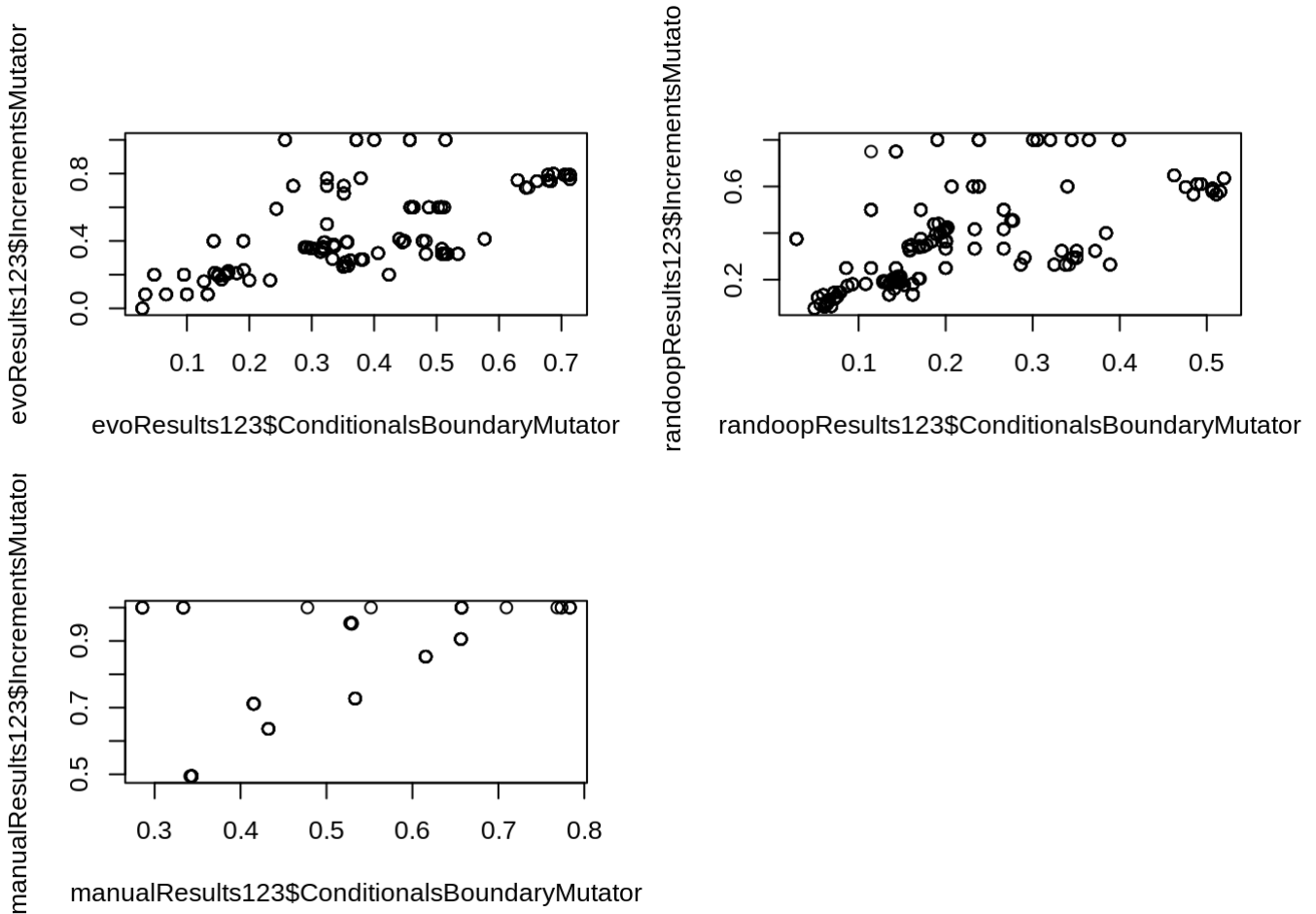
```
## Warning in cor.test.default(randoopResults123$IncrementsMutator,  
## randoopResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-  
## value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  randoopResults123$IncrementsMutator and randoopResults123$ConditionalsBoundaryMutator  
## S = 52853000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.6828823
```

```
cor.test(manualResults123$IncrementsMutator, manualResults123$ConditionalsBoundaryMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$IncrementsMutator,  
## manualResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-  
## value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  manualResults123$IncrementsMutator and manualResults123$ConditionalsBoundaryMutator  
## S = 92376, p-value = 3.371e-06  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.44569
```



ConditionalsBoundaryMutator vs NegateConditionalsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$NegateConditionalsMutator ~ evoResults123$ConditionalsBoundaryMutator, data = evoResults123)
plot(randoopResults123$NegateConditionalsMutator ~ randoopResults123$ConditionalsBoundaryMutator, data = randoopResults123)
plot(manualResults123$NegateConditionalsMutator ~ manualResults123$ConditionalsBoundaryMutator, data = manualResults123)
```

```
cor.test(evoResults123$NegateConditionalsMutator, evoResults123$ConditionalsBoundaryMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$NegateConditionalsMutator,
## evoResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-value
## with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$NegateConditionalsMutator and evoResults123$ConditionalsBoundaryMutator
## S = 27770000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8333786
```

```
cor.test(randoopResults123$NegateConditionalsMutator, randoopResults123$ConditionalsBoundaryMutator, method='spearman')
```

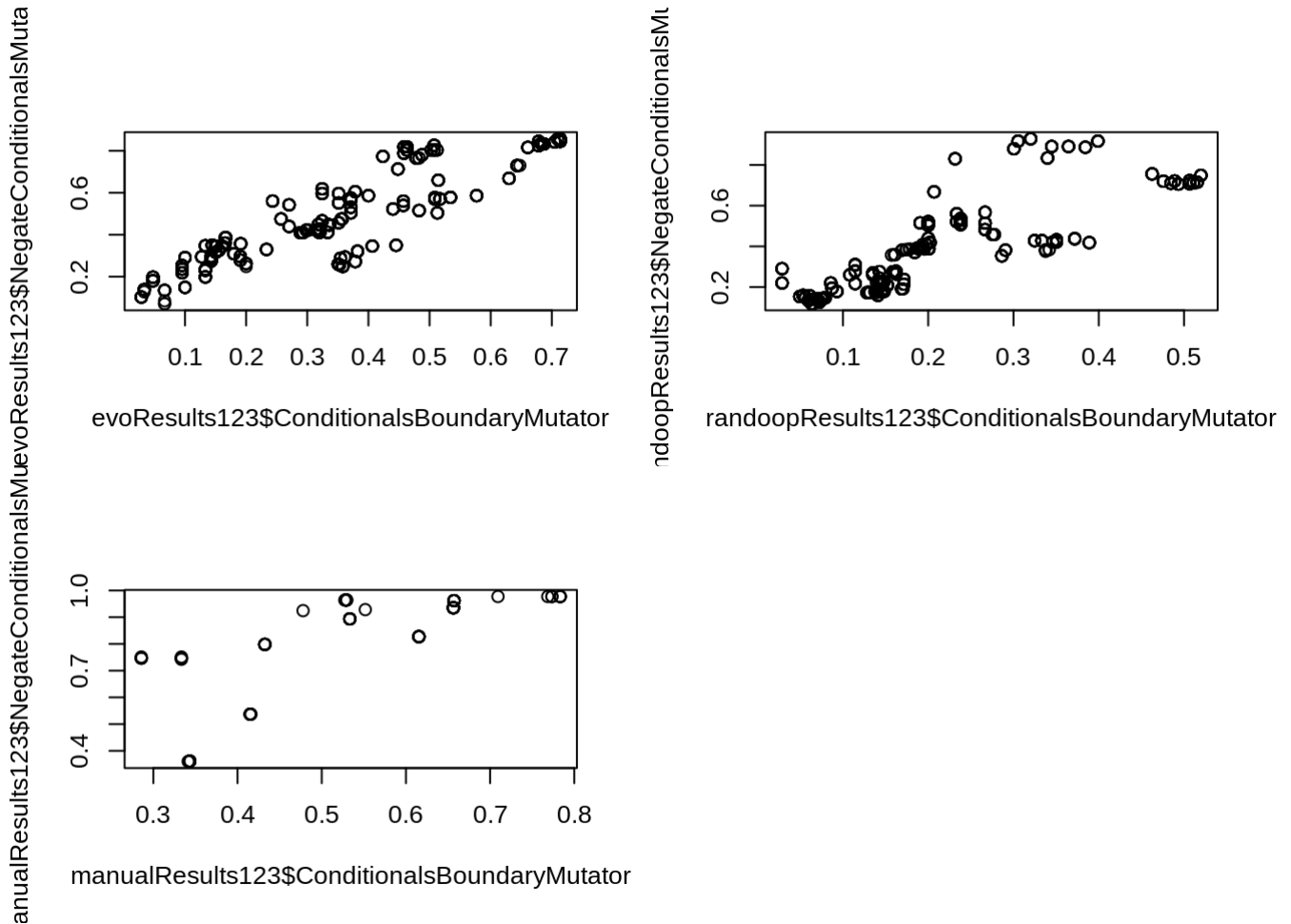
```
## Warning in cor.test.default(randoopResults123$NegateConditionalsMutator, :
## Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$NegateConditionalsMutator and randoopResults123$ConditionalsBoundaryMutator
## S = 22926000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8624461
```

```
cor.test(manualResults123$NegateConditionalsMutator, manualResults123$ConditionalsBoundaryMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$NegateConditionalsMutator, :
## Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$NegateConditionalsMutator and manualResults123$ConditionalsBoundaryMutator
## S = 30608, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8163363
```



ConditionalsBoundaryMutator vs MathMutator

```
par(mfrow = c(2,2))
plot(evoResults123$MathMutator ~ evoResults123$ConditionalsBoundaryMutator, data = evoResults123)
plot(randoopResults123$MathMutator ~ randoopResults123$ConditionalsBoundaryMutator, data = randoopResults123)
plot(manualResults123$MathMutator ~ manualResults123$ConditionalsBoundaryMutator, data = manualResults123)

cor.test(evoResults123$MathMutator, evoResults123$ConditionalsBoundaryMutator, method = 'spearman')
```

```
## Warning in cor.test.default(evoResults123$MathMutator,
## evoResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-value
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  evoResults123$MathMutator and evoResults123$ConditionalsBoundaryMutator  
## S = 26058000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.8436492
```

```
cor.test(randoopResults123$MathMutator, randoopResults123$ConditionalsBoundaryMutator,  
method='spearman')
```

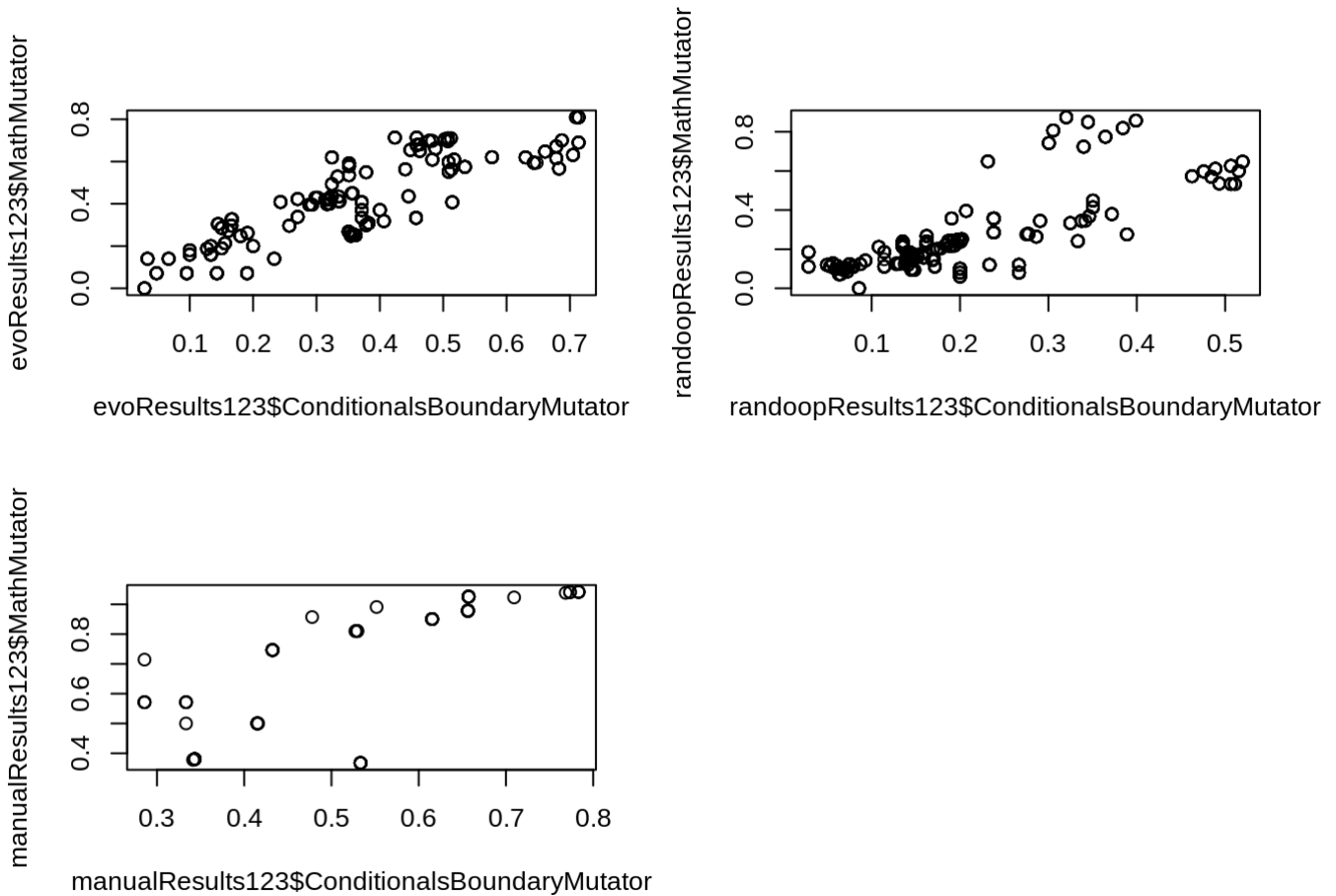
```
## Warning in cor.test.default(randoopResults123$MathMutator,  
## randoopResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-  
## value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  randoopResults123$MathMutator and randoopResults123$ConditionalsBoundaryMutator  
## S = 41864000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.7488137
```

```
cor.test(manualResults123$MathMutator, manualResults123$ConditionalsBoundaryMutator,  
method='spearman')
```

```
## Warning in cor.test.default(manualResults123$MathMutator,  
## manualResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-  
## value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  manualResults123$MathMutator and manualResults123$ConditionalsBoundaryMutator  
## S = 38558, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.7686271
```



ConditionalsBoundaryMutator vs InvertNegsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$InvertNegsMutator ~ evoResults123$ConditionalsBoundaryMutator, data = evoResults123)
plot(randoopResults123$InvertNegsMutator ~ randoopResults123$ConditionalsBoundaryMutator, data = randoopResults123)
plot(manualResults123$InvertNegsMutator ~ manualResults123$ConditionalsBoundaryMutator, data = manualResults123)

cor.test(evoResults123$InvertNegsMutator, evoResults123$ConditionalsBoundaryMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$InvertNegsMutator,
## evoResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-value
## with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$InvertNegsMutator and evoResults123$ConditionalsBoundaryMutator
## S = 4460300, p-value = 0.8791
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.008822251
```

```
cor.test(randoopResults123$InvertNegsMutator, randoopResults123$ConditionalsBoundaryMutator, method='spearman')
```

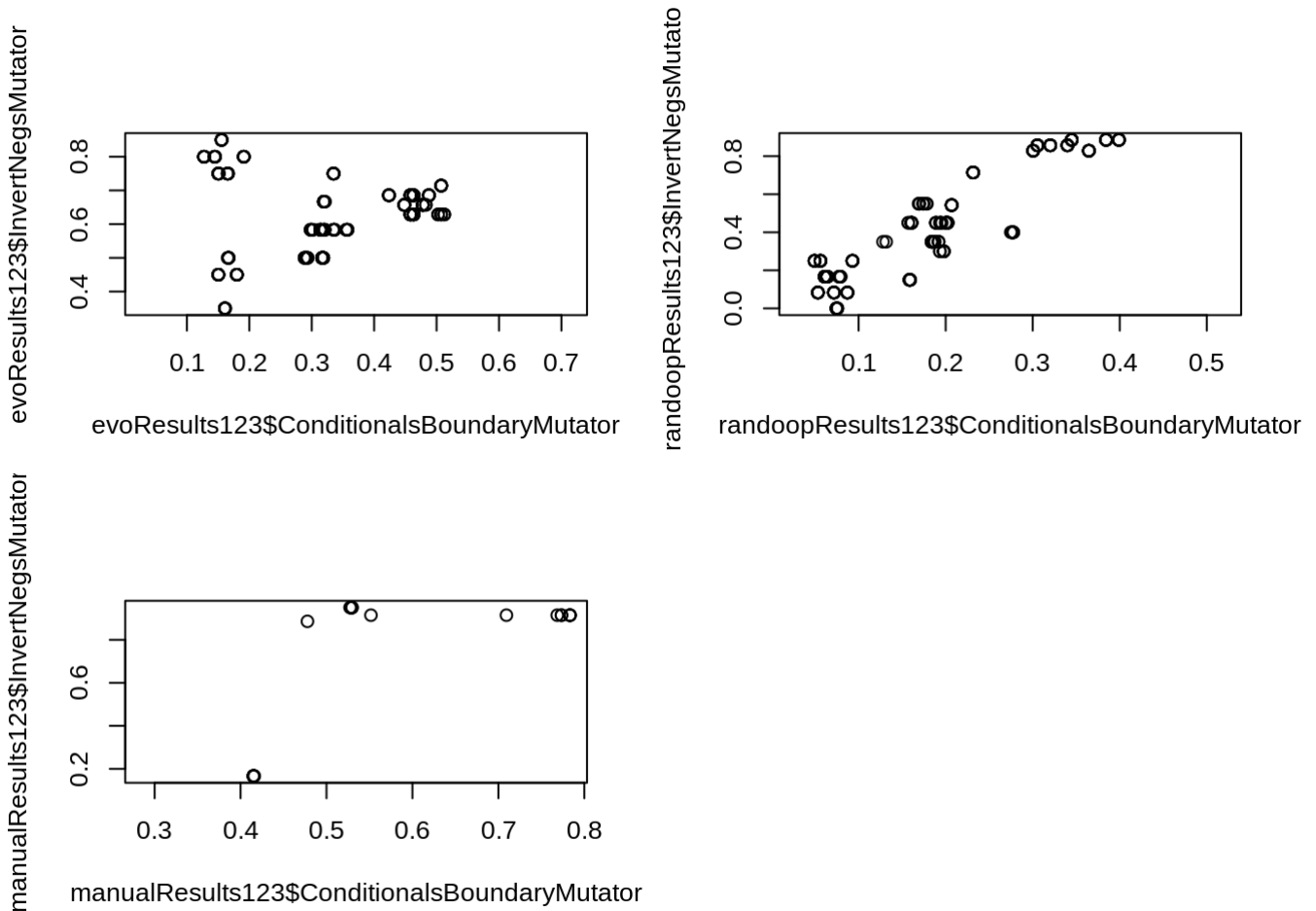
```
## Warning in cor.test.default(randoopResults123$InvertNegsMutator,
## randoopResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-
## value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$InvertNegsMutator and randoopResults123$ConditionalsBoundaryMutator
## S = 476730, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8940598
```

```
cor.test(manualResults123$InvertNegsMutator, manualResults123$ConditionalsBoundaryMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$InvertNegsMutator,
## manualResults123$ConditionalsBoundaryMutator, : Cannot compute exact p-
## value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$InvertNegsMutator and manualResults123$ConditionalsBoundaryMutator
## S = 1980.4, p-value = 0.001309
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.5594228
```



VoidMethodCallMutator

VoidMethodCallMutator vs IncrementsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$IncrementsMutator ~ evoResults123$VoidMethodCallMutator, data = evoResults123)
plot(randoopResults123$IncrementsMutator ~ randoopResults123$VoidMethodCallMutator, data = randoopResults123)
plot(manualResults123$IncrementsMutator ~ manualResults123$VoidMethodCallMutator, data = manualResults123)

cor.test(evoResults123$IncrementsMutator, evoResults123$VoidMethodCallMutator, method = 'spearman')
```

```
## Warning in cor.test.default(evoResults123$IncrementsMutator,
## evoResults123$VoidMethodCallMutator, : Cannot compute exact p-value with
## ties
```



```
##  
## Spearman's rank correlation rho  
##  
## data:  evoResults123$IncrementsMutator and evoResults123$VoidMethodCallMutator  
## S = 41914000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.6550297
```

```
cor.test(randoopResults123$IncrementsMutator, randoopResults123$VoidMethodCallMutator,  
method='spearman')
```

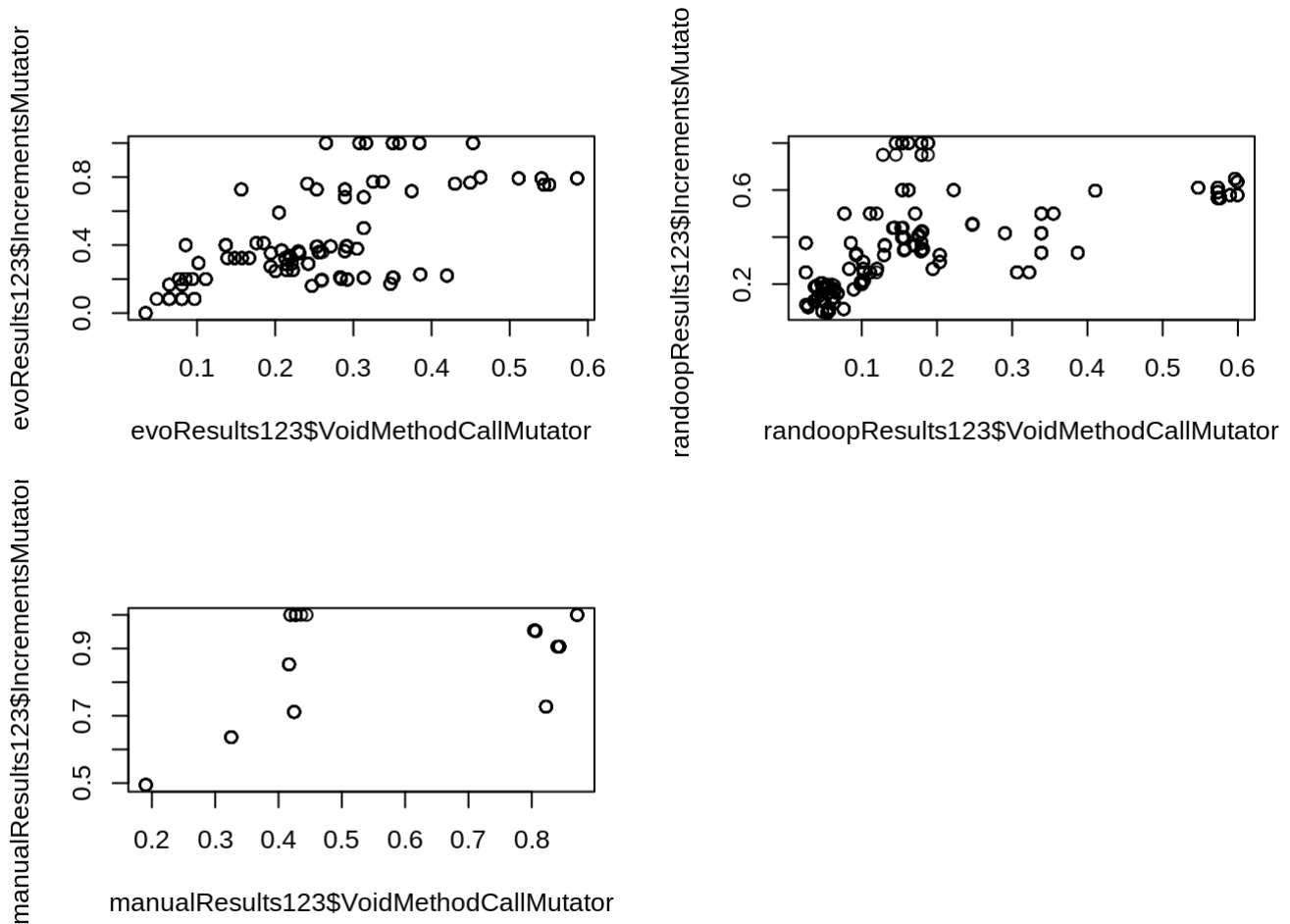
```
## Warning in cor.test.default(randoopResults123$IncrementsMutator,  
## randoopResults123$VoidMethodCallMutator, : Cannot compute exact p-value  
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  randoopResults123$IncrementsMutator and randoopResults123$VoidMethodCallMutator  
## S = 30760000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.746832
```

```
cor.test(manualResults123$IncrementsMutator, manualResults123$VoidMethodCallMutator,  
method='spearman')
```

```
## Warning in cor.test.default(manualResults123$IncrementsMutator,  
## manualResults123$VoidMethodCallMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  manualResults123$IncrementsMutator and manualResults123$VoidMethodCallMutator  
## S = 35642, p-value = 7.176e-15  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.7066131
```



VoidMethodCallMutator vs NegateConditionalsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$NegateConditionalsMutator ~ evoResults123$VoidMethodCallMutator, data = evoResults123)
plot(randoopResults123$NegateConditionalsMutator ~ randoopResults123$VoidMethodCallMutator, data = randoopResults123)
plot(manualResults123$NegateConditionalsMutator ~ manualResults123$VoidMethodCallMutator, data = manualResults123)
```

```
cor.test(evoResults123$NegateConditionalsMutator, evoResults123$VoidMethodCallMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$NegateConditionalsMutator,
## evoResults123$VoidMethodCallMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$NegateConditionalsMutator and evoResults123$VoidMethodCallMutator
## S = 36576000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6989666
```

```
cor.test(randoopResults123$NegateConditionalsMutator, randoopResults123$VoidMethodCallMutator, method='spearman')
```

```
## Warning in cor.test.default(randoopResults123$NegateConditionalsMutator, :
## Cannot compute exact p-value with ties
```

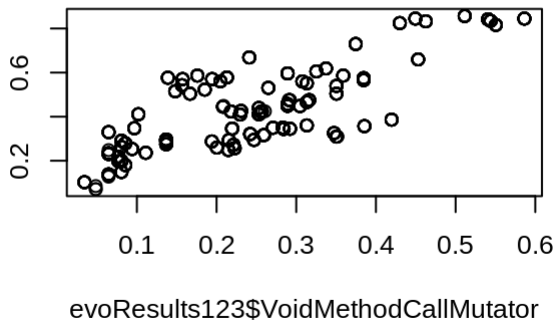
```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$NegateConditionalsMutator and randoopResults123$VoidMethodCallMutator
## S = 15558000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8719493
```

```
cor.test(manualResults123$NegateConditionalsMutator, manualResults123$VoidMethodCallMutator, method='spearman')
```

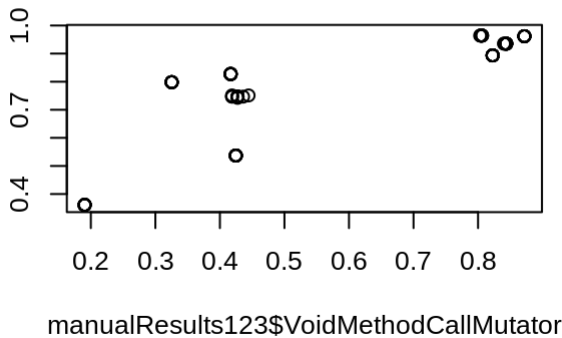
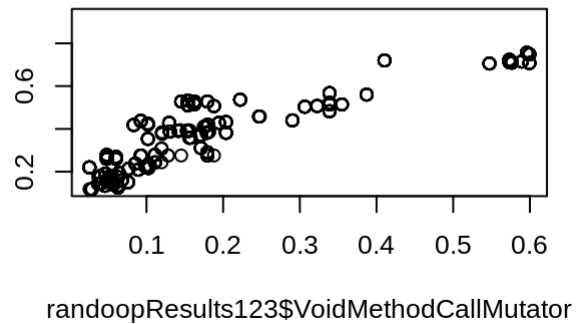
```
## Warning in cor.test.default(manualResults123$NegateConditionalsMutator, :
## Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$NegateConditionalsMutator and manualResults123$VoidMethodCallMutator
## S = 29251, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7592183
```

anualResults123\$NegateConditionalsNuevoResults123\$NegateConditionalsMuta



ndoopResults123\$NegateConditionalsMl



VoidMethodCallMutator vs MathMutator

```
par(mfrow = c(2,2))
plot(evoResults123$MathMutator ~ evoResults123$VoidMethodCallMutator, data = evoResults123)
plot(randoopResults123$MathMutator ~ randoopResults123$VoidMethodCallMutator, data = randoopResults123)
plot(manualResults123$MathMutator ~ manualResults123$VoidMethodCallMutator, data = manualResults123)
```

```
cor.test(evoResults123$MathMutator, evoResults123$VoidMethodCallMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$MathMutator,
## evoResults123$VoidMethodCallMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data: evoResults123$MathMutator and evoResults123$VoidMethodCallMutator
## S = 50821000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.5817195
```

```
cor.test(randoopResults123$MathMutator, randoopResults123$VoidMethodCallMutator, method='spearman')
```

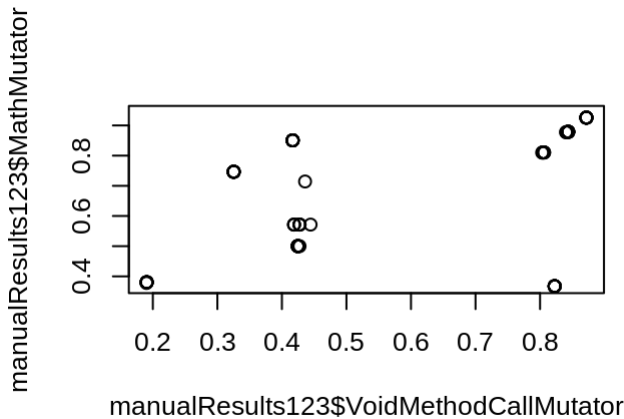
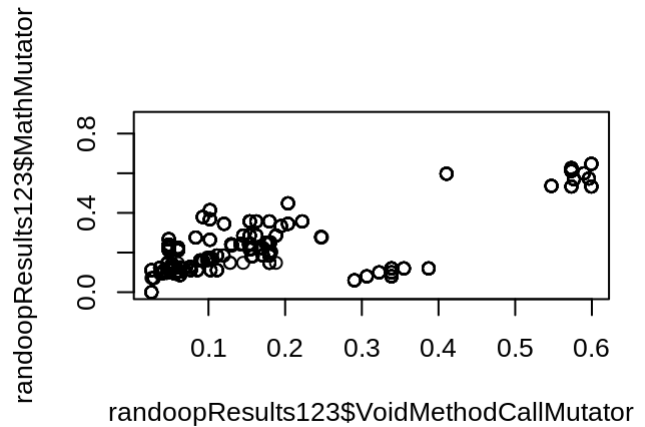
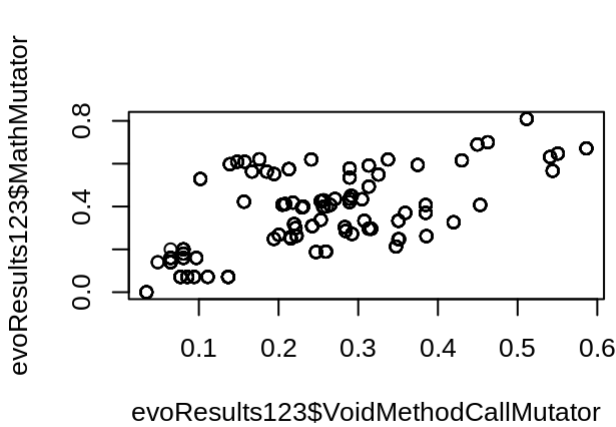
```
## Warning in cor.test.default(randoopResults123$MathMutator,  
## randoopResults123$VoidMethodCallMutator, : Cannot compute exact p-value  
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: randoopResults123$MathMutator and randoopResults123$VoidMethodCallMutator  
## S = 66640000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.451523
```

```
cor.test(manualResults123$MathMutator, manualResults123$VoidMethodCallMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$MathMutator,  
## manualResults123$VoidMethodCallMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: manualResults123$MathMutator and manualResults123$VoidMethodCallMutator  
## S = 65563, p-value = 4.997e-06  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.4603198
```



VoidMethodCallMutator vs InvertNegsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$InvertNegsMutator ~ evoResults123$VoidMethodCallMutator, data = evoResults123)
plot(randoopResults123$InvertNegsMutator ~ randoopResults123$VoidMethodCallMutator, data = randoopResults123)
plot(manualResults123$InvertNegsMutator ~ manualResults123$VoidMethodCallMutator, data = manualResults123)
```

```
cor.test(evoResults123$InvertNegsMutator, evoResults123$VoidMethodCallMutator, method = 'spearman')
```

```
## Warning in cor.test.default(evoResults123$InvertNegsMutator,
## evoResults123$VoidMethodCallMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data: evoResults123$InvertNegsMutator and evoResults123$VoidMethodCallMutator
## S = 1242100, p-value = 0.3361
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.06837242
```

```
cor.test(randoopResults123$InvertNegsMutator, randoopResults123$VoidMethodCallMutator, method='spearman')
```

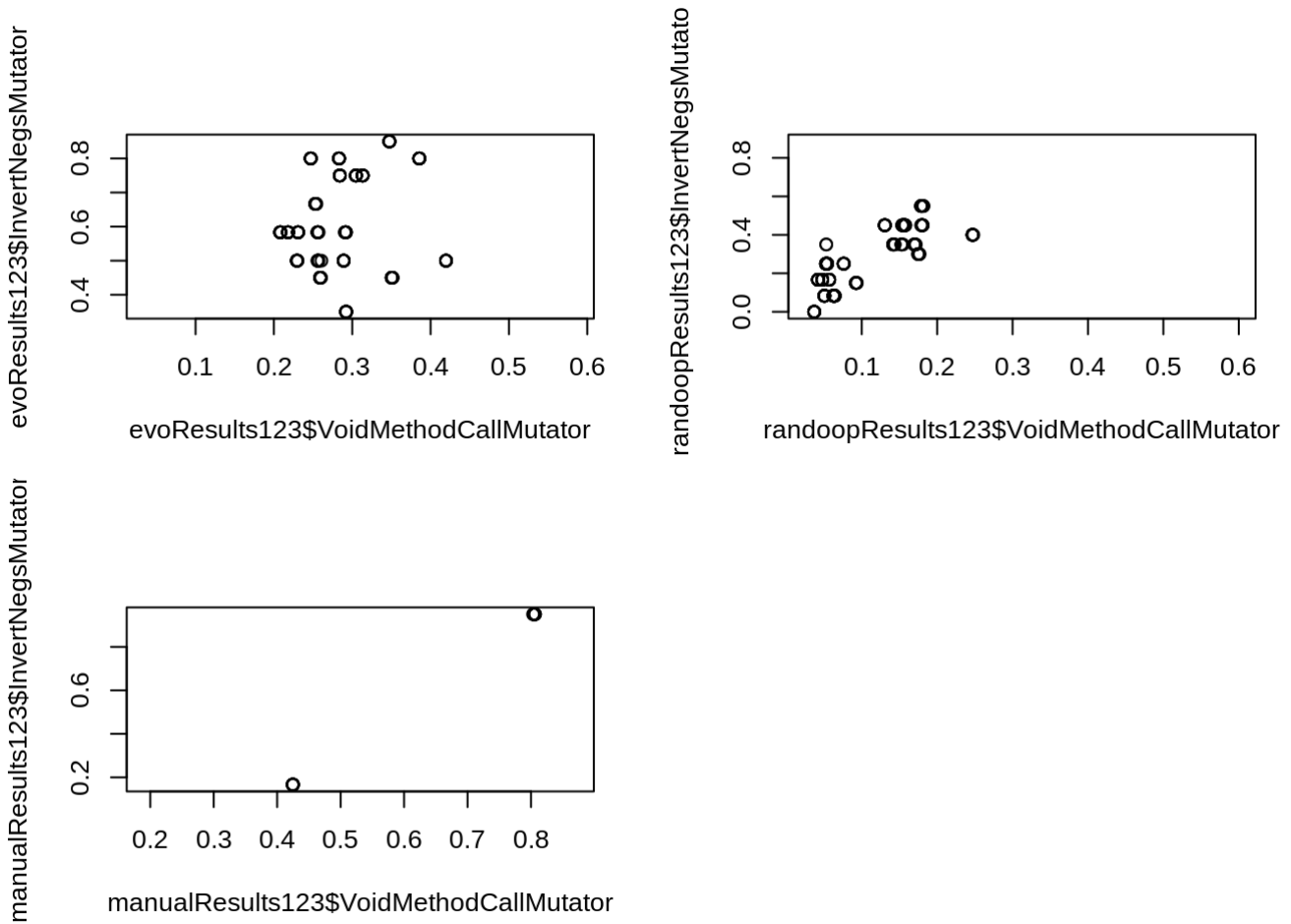
```
## Warning in cor.test.default(randoopResults123$InvertNegsMutator,
## randoopResults123$VoidMethodCallMutator, : Cannot compute exact p-value
## with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$InvertNegsMutator and randoopResults123$VoidMethodCallMutator
## S = 306080, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7704334
```

```
cor.test(manualResults123$InvertNegsMutator, manualResults123$VoidMethodCallMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$InvertNegsMutator,
## manualResults123$VoidMethodCallMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$InvertNegsMutator and manualResults123$VoidMethodCallMutator
## S = 113.34, p-value = 1.647e-08
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9147787
```



IncrementsMutator

IncrementsMutator vs NegateConditionalsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$NegateConditionalsMutator ~ evoResults123$IncrementsMutator, data
     = evoResults123)
plot(randoopResults123$NegateConditionalsMutator ~ randoopResults123$IncrementsMutator, data
     = randoopResults123)
plot(manualResults123$NegateConditionalsMutator ~ manualResults123$IncrementsMutator, data
     = manualResults123)

cor.test(evoResults123$NegateConditionalsMutator, evoResults123$IncrementsMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$NegateConditionalsMutator,
## evoResults123$IncrementsMutator, : Cannot compute exact p-value with ties
```



```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$NegateConditionalsMutator and evoResults123$IncrementsMutator
## S = 38314000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7701139
```

```
cor.test(randoopResults123$NegateConditionalsMutator, randoopResults123$IncrementsMutator, method='spearman')
```

```
## Warning in cor.test.default(randoopResults123$NegateConditionalsMutator, :
## Cannot compute exact p-value with ties
```

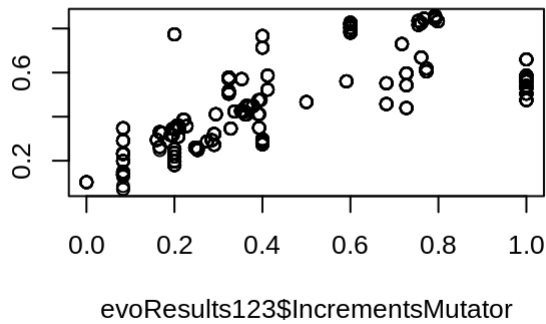
```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$NegateConditionalsMutator and randoopResults123$Increment
sMutator
## S = 25692000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8458451
```

```
cor.test(manualResults123$NegateConditionalsMutator, manualResults123$IncrementsMutator, method='spearman')
```

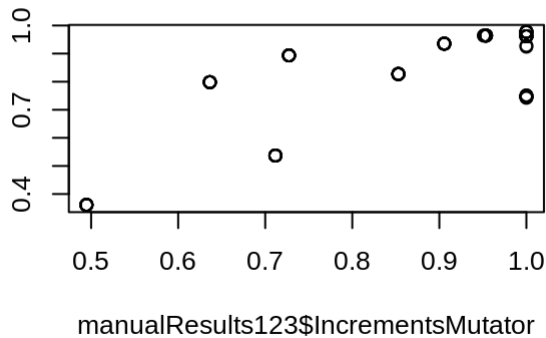
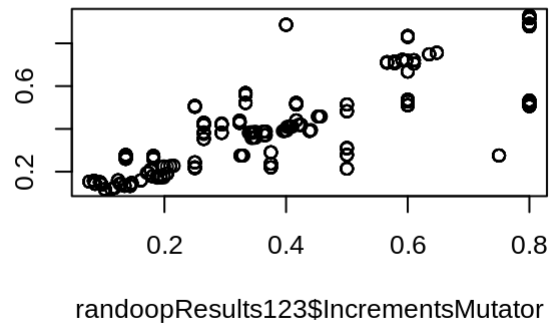
```
## Warning in cor.test.default(manualResults123$NegateConditionalsMutator, :
## Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$NegateConditionalsMutator and manualResults123$IncrementsM
utator
## S = 55331, p-value = 3.158e-14
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6679829
```

anualResults123\$NegateConditionalsNuevoResults123\$NegateConditionalsMuta



ndoopResults123\$NegateConditionalsMl



IncrementsMutator vs MathMutator

```
par(mfrow = c(2,2))
plot(evoResults123$MathMutator ~ evoResults123$IncrementsMutator, data = evoResults123)
plot(randoopResults123$MathMutator ~ randomoopResults123$IncrementsMutator, data = randomoopResults123)
plot(manualResults123$MathMutator ~ manualResults123$IncrementsMutator, data = manualResults123)
```

```
cor.test(evoResults123$MathMutator, evoResults123$IncrementsMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$MathMutator,
## evoResults123$IncrementsMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data: evoResults123$MathMutator and evoResults123$IncrementsMutator
## S = 65554000, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.6066734
```

```
cor.test(randoopResults123$MathMutator, randoopResults123$IncrementsMutator, method='spearman')
```

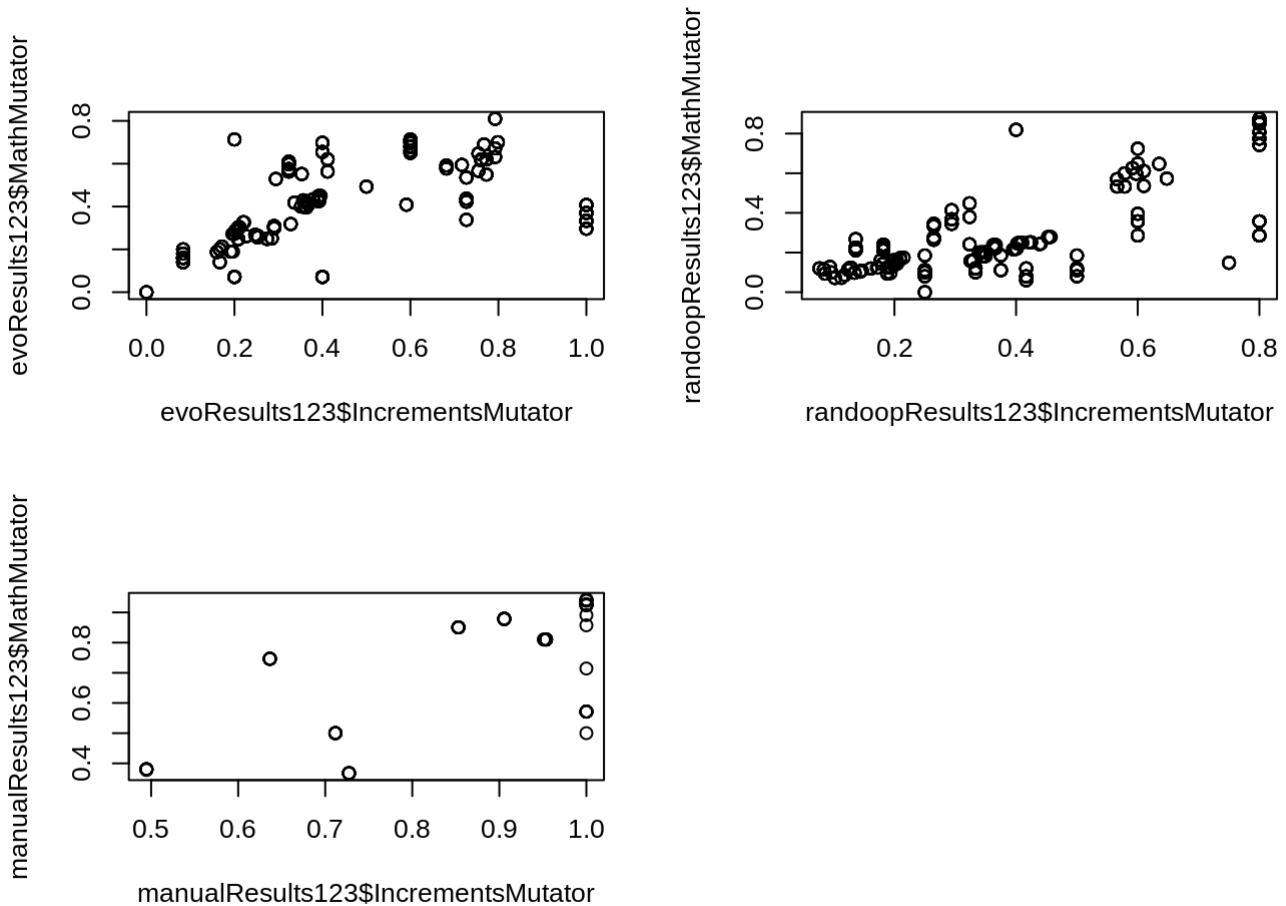
```
## Warning in cor.test.default(randoopResults123$MathMutator,  
## randoopResults123$IncrementsMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: randoopResults123$MathMutator and randoopResults123$IncrementsMutator  
## S = 61222000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.6326653
```

```
cor.test(manualResults123$MathMutator, manualResults123$IncrementsMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$MathMutator,  
## manualResults123$IncrementsMutator, : Cannot compute exact p-value with  
## ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: manualResults123$MathMutator and manualResults123$IncrementsMutator  
## S = 57229, p-value = 1.199e-13  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.6565901
```



IncrementsMutator vs InvertNegsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$InvertNegsMutator ~ evoResults123$IncrementsMutator, data = evoResults123)
plot(randoopResults123$InvertNegsMutator ~ randoopResults123$IncrementsMutator, data = randoopResults123)
plot(manualResults123$InvertNegsMutator ~ manualResults123$IncrementsMutator, data = manualResults123)
```

```
cor.test(evoResults123$InvertNegsMutator, evoResults123$IncrementsMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$InvertNegsMutator,
## evoResults123$IncrementsMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data: evoResults123$InvertNegsMutator and evoResults123$IncrementsMutator
## S = 4507100, p-value = 0.9782
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## -0.001586923
```

```
cor.test(randoopResults123$InvertNegsMutator, randoopResults123$IncrementsMutator, method='spearman')
```

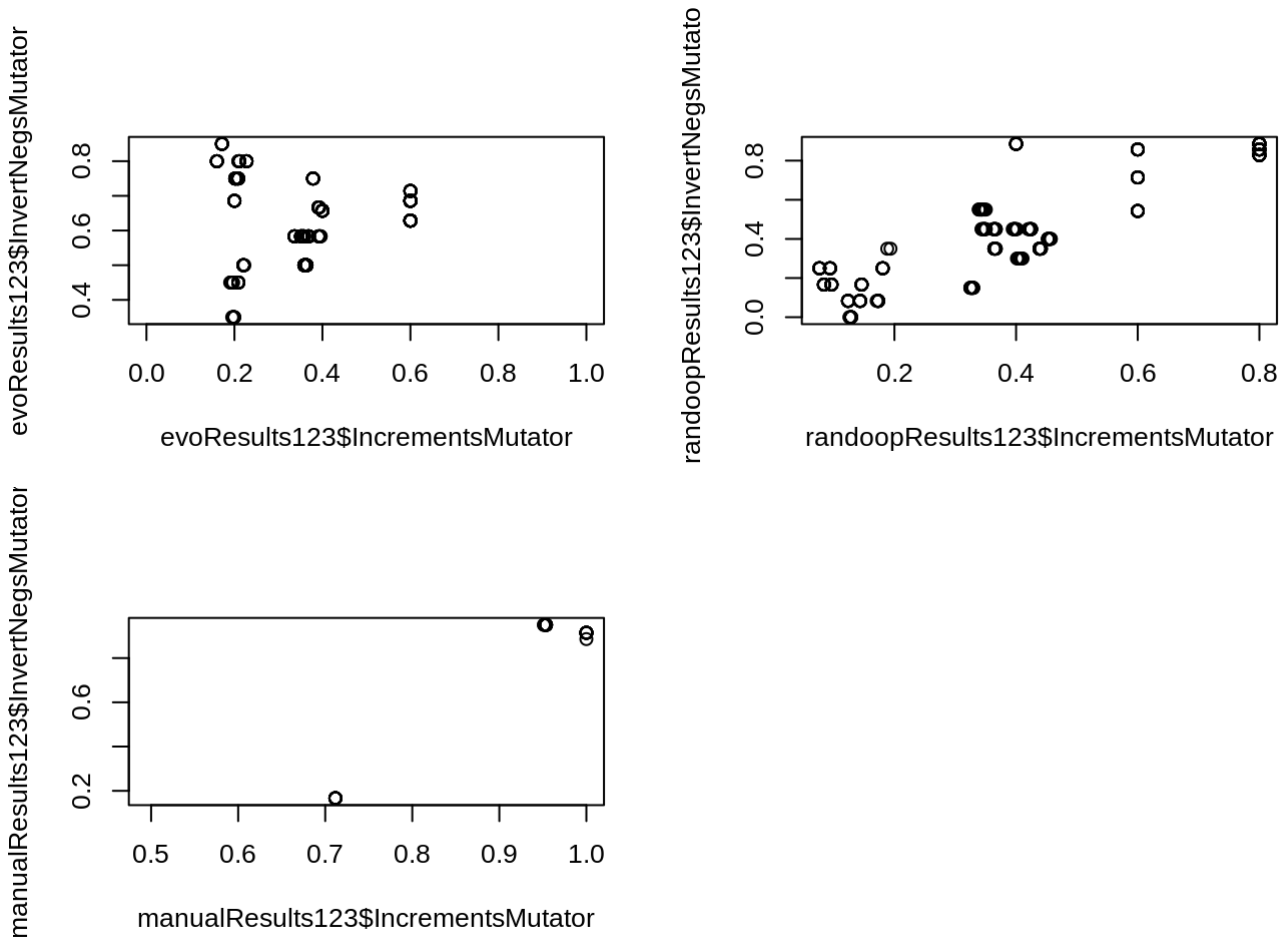
```
## Warning in cor.test.default(randoopResults123$InvertNegsMutator,
## randoopResults123$IncrementsMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data: randoopResults123$InvertNegsMutator and randoopResults123$IncrementsMutator
## S = 722680, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8394029
```

```
cor.test(manualResults123$InvertNegsMutator, manualResults123$IncrementsMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$InvertNegsMutator,
## manualResults123$IncrementsMutator, : Cannot compute exact p-value with
## ties
```

```
##
## Spearman's rank correlation rho
##
## data: manualResults123$InvertNegsMutator and manualResults123$IncrementsMutator
## S = 2282.1, p-value = 0.005717
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.4923123
```



NegateConditionalsMutator

NegateConditionalsMutator vs MathMutator

```
par(mfrow = c(2,2))
plot(evoResults123$MathMutator ~ evoResults123$NegateConditionalsMutator, data = evoResults123)
plot(randoopResults123$MathMutator ~ randoopResults123$NegateConditionalsMutator, data = randoopResults123)
plot(manualResults123$MathMutator ~ manualResults123$NegateConditionalsMutator, data = manualResults123)

cor.test(evoResults123$MathMutator, evoResults123$NegateConditionalsMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$MathMutator,
## evoResults123$NegateConditionalsMutator, : Cannot compute exact p-value
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  evoResults123$MathMutator and evoResults123$NegateConditionalsMutator  
## S = 14107000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.9153585
```

```
cor.test(randoopResults123$MathMutator, randoopResults123$NegateConditionalsMutator,  
method='spearman')
```

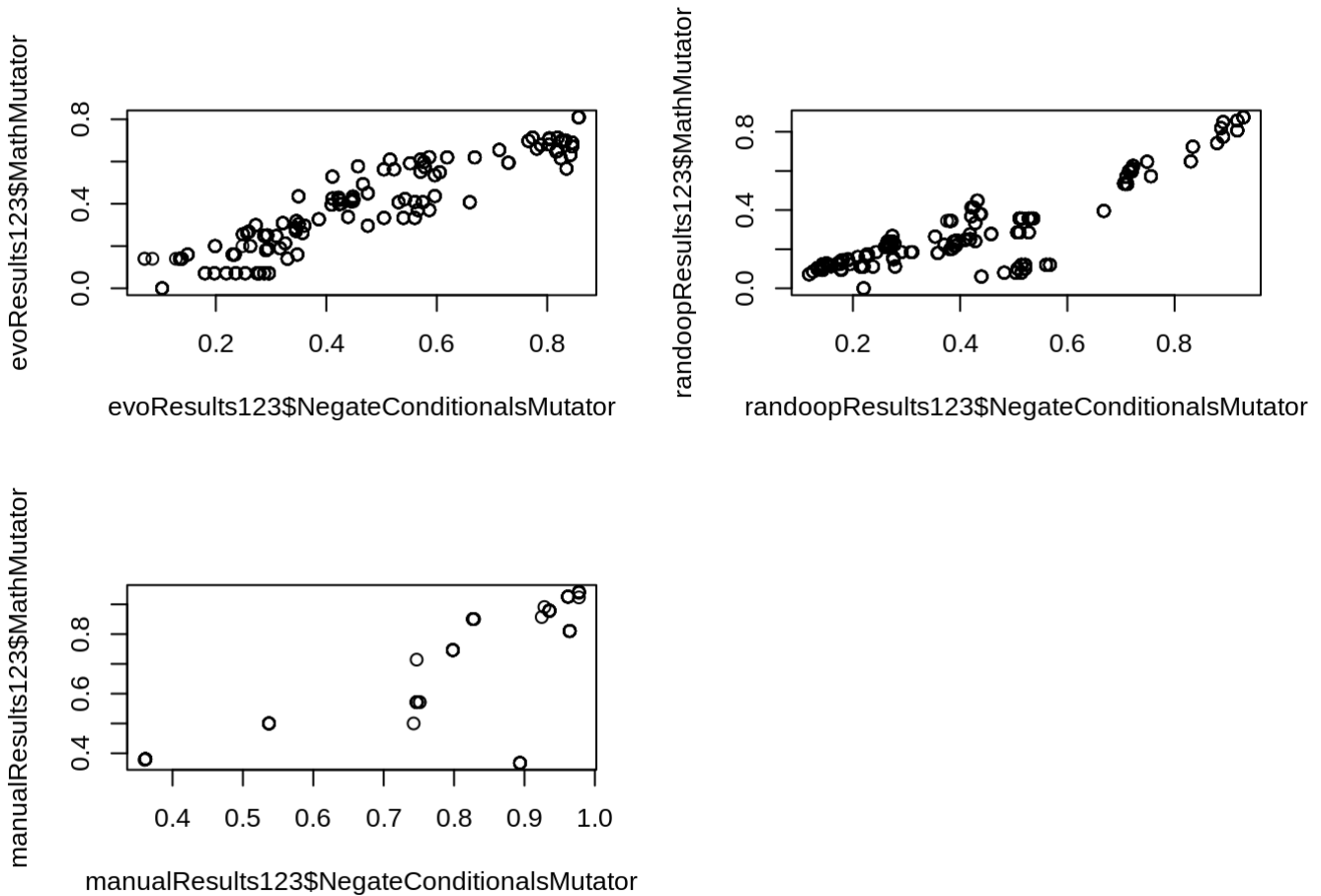
```
## Warning in cor.test.default(randoopResults123$MathMutator,  
## randoopResults123$NegateConditionalsMutator, : Cannot compute exact p-value  
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  randoopResults123$MathMutator and randoopResults123$NegateConditionalsMutat  
or  
## S = 43154000, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.7410753
```

```
cor.test(manualResults123$MathMutator, manualResults123$NegateConditionalsMutator, me  
thod='spearman')
```

```
## Warning in cor.test.default(manualResults123$MathMutator,  
## manualResults123$NegateConditionalsMutator, : Cannot compute exact p-value  
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  manualResults123$MathMutator and manualResults123$NegateConditionalsMutator  
## S = 46608, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.7203218
```



NegateConditionalsMutator vs InvertNegsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$InvertNegsMutator ~ evoResults123$NegateConditionalsMutator, data
     = evoResults123)
plot(randoopResults123$InvertNegsMutator ~ randoopResults123$NegateConditionalsMutator,
     data = randoopResults123)
plot(manualResults123$InvertNegsMutator ~ manualResults123$NegateConditionalsMutator,
     data = manualResults123)

cor.test(evoResults123$InvertNegsMutator, evoResults123$NegateConditionalsMutator, me
thod='spearman')
```

```
## Warning in cor.test.default(evoResults123$InvertNegsMutator,
## evoResults123$NegateConditionalsMutator, : Cannot compute exact p-value
## with ties
```



```
##  
## Spearman's rank correlation rho  
##  
## data:  evoResults123$InvertNegsMutator and evoResults123$NegateConditionalsMutator  
## S = 4254800, p-value = 0.3469  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.05448819
```

```
cor.test(randoopResults123$InvertNegsMutator, randoopResults123$NegateConditionalsMutator, method='spearman')
```

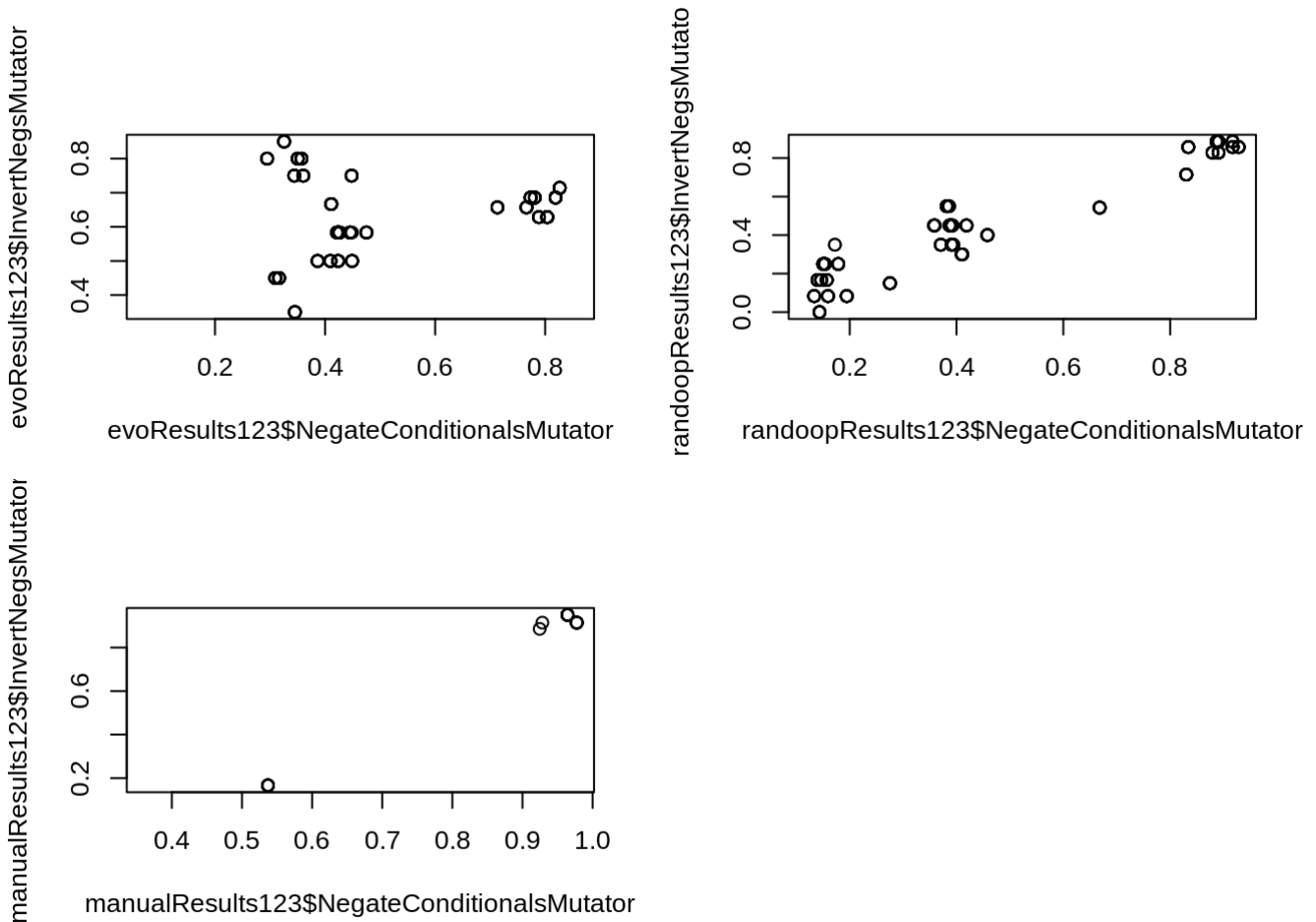
```
## Warning in cor.test.default(randoopResults123$InvertNegsMutator,  
## randoopResults123$NegateConditionalsMutator, : Cannot compute exact p-value  
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  randoopResults123$InvertNegsMutator and randoopResults123$NegateConditionalsMutator  
## S = 428800, p-value < 2.2e-16  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.9047108
```

```
cor.test(manualResults123$InvertNegsMutator, manualResults123$NegateConditionalsMutator, method='spearman')
```

```
## Warning in cor.test.default(manualResults123$InvertNegsMutator,  
## manualResults123$NegateConditionalsMutator, : Cannot compute exact p-value  
## with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data:  manualResults123$InvertNegsMutator and manualResults123$NegateConditionalsMutator  
## S = 1728.5, p-value = 0.0002946  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.6154649
```



MathMutator

MathMutator vs InvertNegsMutator

```
par(mfrow = c(2,2))
plot(evoResults123$InvertNegsMutator ~ evoResults123$MathMutator, data = evoResults123)
plot(randoopResults123$InvertNegsMutator ~ randoopResults123$MathMutator, data = randoopResults123)
plot(manualResults123$InvertNegsMutator ~ manualResults123$MathMutator, data = manualResults123)

cor.test(evoResults123$InvertNegsMutator, evoResults123$MathMutator, method='spearman')
```

```
## Warning in cor.test.default(evoResults123$InvertNegsMutator,
## evoResults123$MathMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  evoResults123$InvertNegsMutator and evoResults123$MathMutator
## S = 4200300, p-value = 0.2502
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.06659821
```

```
cor.test(randoopResults123$InvertNegsMutator, randoopResults123$MathMutator, method=
'spearman')
```

```
## Warning in cor.test.default(randoopResults123$InvertNegsMutator,
## randoopResults123$MathMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  randoopResults123$InvertNegsMutator and randoopResults123$MathMutator
## S = 393740, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.912502
```

```
cor.test(manualResults123$InvertNegsMutator, manualResults123$MathMutator, method='sp
earman')
```

```
## Warning in cor.test.default(manualResults123$InvertNegsMutator,
## manualResults123$MathMutator, : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data:  manualResults123$InvertNegsMutator and manualResults123$MathMutator
## S = 2289.6, p-value = 0.005911
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.4906282
```

