Exploring Nondeterminism in Tools That Automatically Generate or Analyse Test Suites

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Installing and loading packages

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

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

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

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

```
install.packages("reshape")
```

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

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

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

```
install.packages("dplyr")
```

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

```
library("ggplot2")
library("reshape")
library("reshape2")
```

```
##
## Attaching package: 'reshape2'
## The following objects are masked from 'package:reshape':
##
##     colsplit, melt, recast
```

```
library("ggpubr")
```

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

```
library("dplyr")
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:reshape':
##
##     rename
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

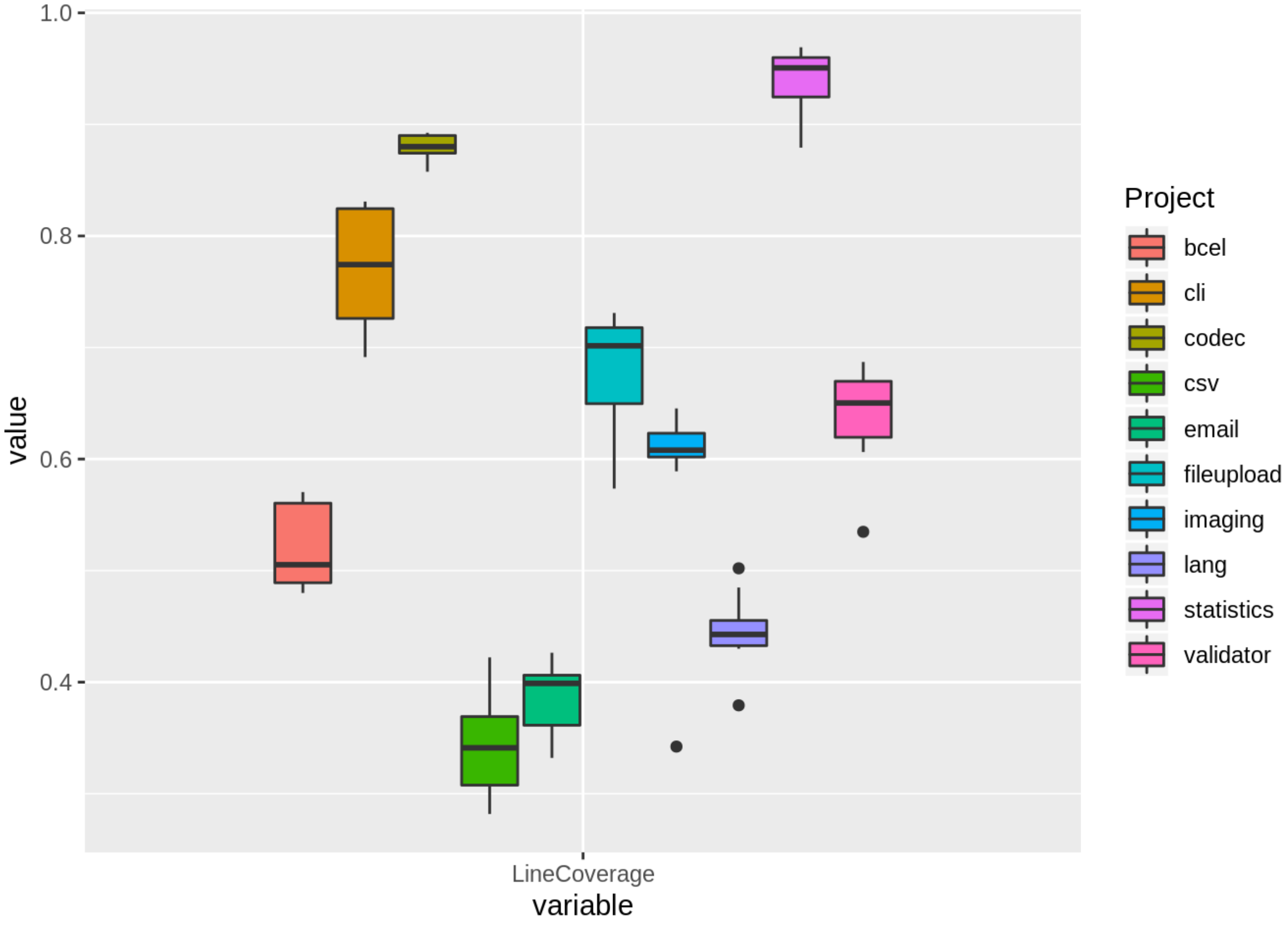
Reading data

```
evo <- read.csv('/home/raul/Desktop/evo1Execution.csv', sep = ",", header = TRUE)
evo.lineCoverage <- melt(evo, id.var = "Project", measure.var = "LineCoverage")
evo.mutationCoverage <- melt(evo, id.var = "Project", measure.var = "MutationCoverage")

randoop <- read.csv('/home/raul/Desktop/randoop1Execution.csv', sep = ",", header = TRUE)
randoop.lineCoverage <- melt(randoop, id.var = "Project", measure.var = "LineCoverage")
randoop.mutationCoverage <- melt(randoop, id.var = "Project", measure.var = "MutationCoverage")

pitEvo <- read.csv('/home/raul/Desktop/pitSameProjectSameTestSuiteEvo.csv', sep = ",", header = TRUE)
pitEvo.lineCoverage <- melt(pitEvo, id.var = "Project", measure.var = "LineCoverage")
pitEvo.mutationCoverage <- melt(pitEvo, id.var = "Project", measure.var = "MutationCoverage")

pitRandoop <- read.csv('/home/raul/Desktop/pitSameProjectSameTestSuiteRandoop.csv', sep = ",", header = TRUE)
pitRandoop.lineCoverage <- melt(pitRandoop, id.var = "Project", measure.var = "LineCoverage")
pitRandoop.mutationCoverage <- melt(pitRandoop, id.var = "Project", measure.var = "MutationCoverage")

pitManual <- read.csv('/home/raul/Desktop/pitSameProjectSameTestSuiteManual.csv', sep = ",", header = TRUE)
pitManual.lineCoverage <- melt(pitManual, id.var = "Project", measure.var = "LineCoverage")
pitManual.mutationCoverage <- melt(pitManual, id.var = "Project", measure.var = "MutationCoverage")
```

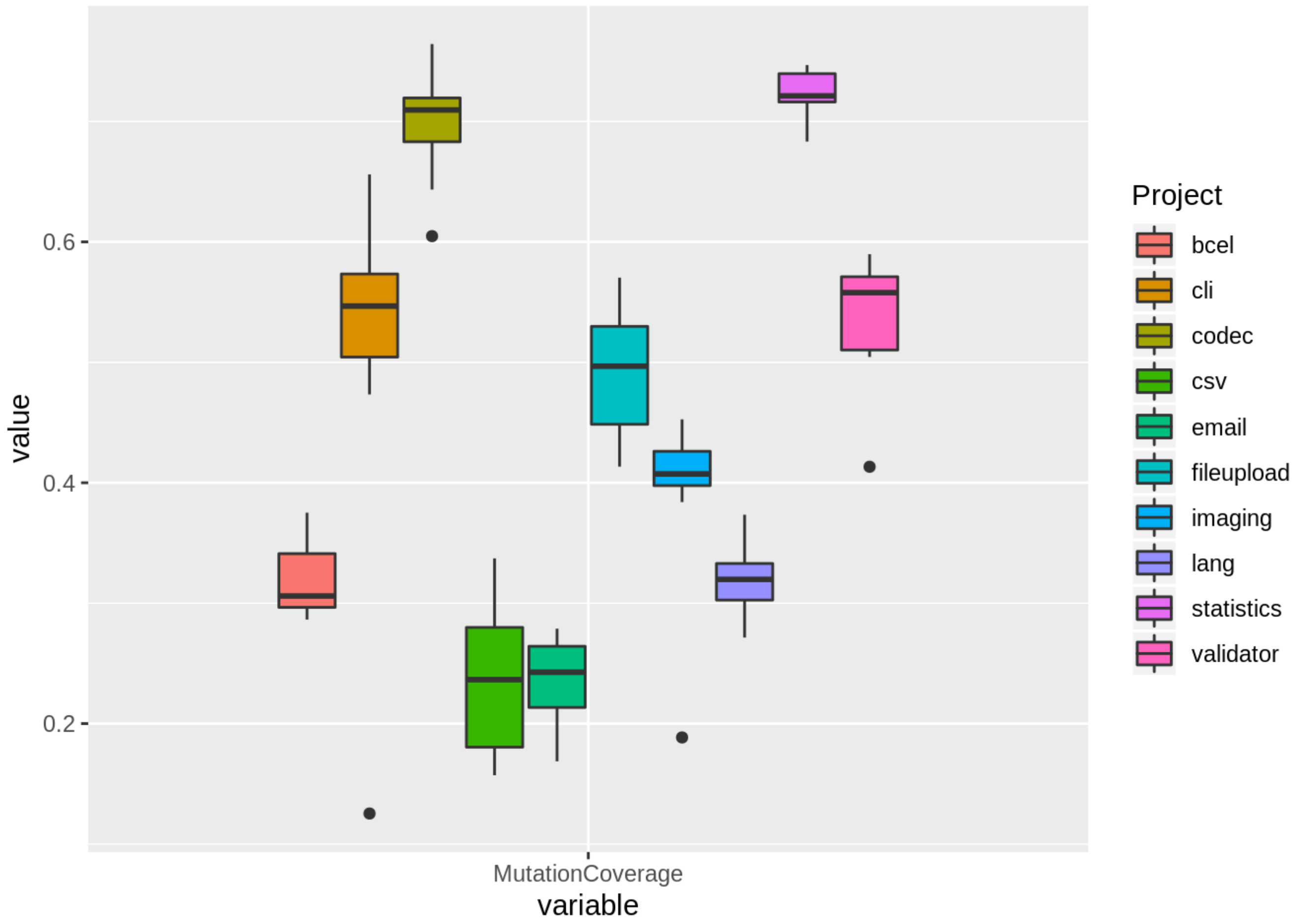
Ploting Box-plots

#EvoSuite

```
par(mfrow = c(1,2))

ggplot(data = evo.lineCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("LineCoverage"))
```



```
ggplot(data = evo.mutationCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("MutationCoverage"))
```

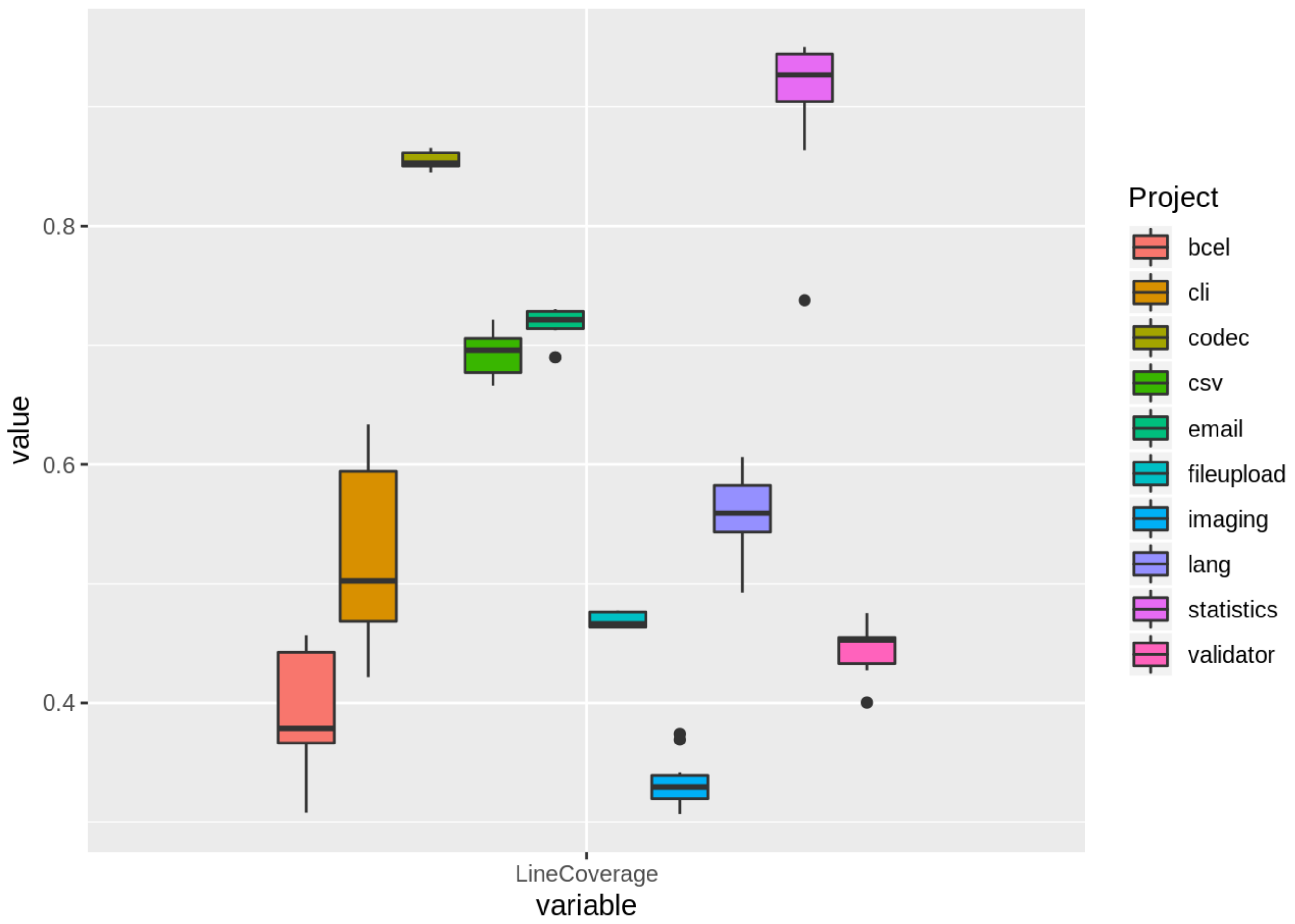


```
evo %>% group_by(Project) %>% summarise(MutationCoverageAverage = mean(MutationCovera
ge), MutationCoverageVariation = var(MutationCoverage), MutationCoverageStandardDevia
tion = sd(MutationCoverage))
```

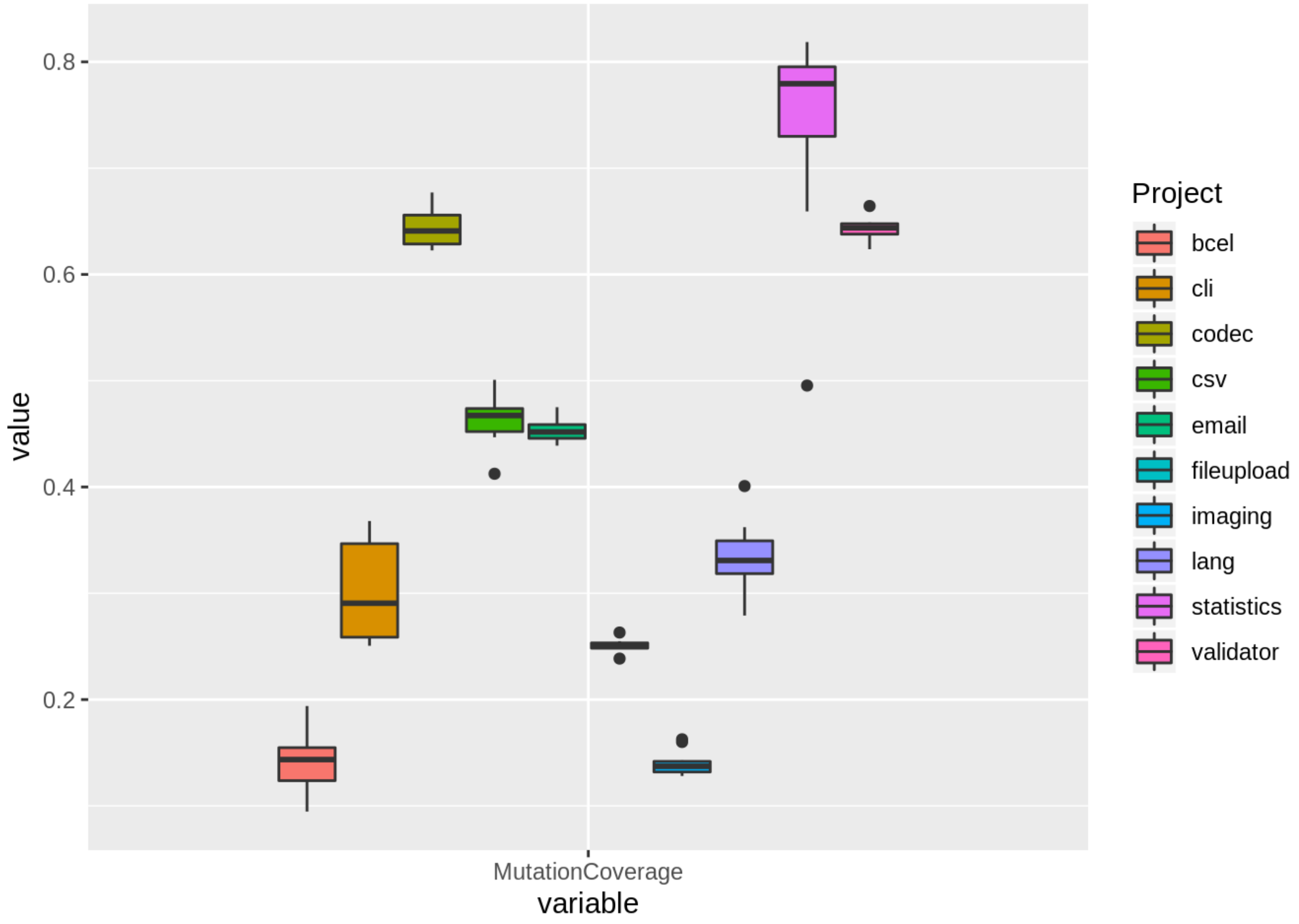
```
## # A tibble: 10 x 4
##    Project   MutationCoverageAv… MutationCoverageVa… MutationCoverageStand…
##    <fct>                   <dbl>               <dbl>                  <dbl>
##  1 bcel                    0.319            0.000983                 0.0314
##  2 cli                     0.510            0.0207                   0.144
##  3 codec                   0.696            0.00205                  0.0453
##  4 csv                     0.239            0.00423                  0.0650
##  5 email                   0.234            0.00148                  0.0385
##  6 fileuplo…               0.491            0.00299                  0.0547
##  7 imaging                 0.391            0.00547                  0.0740
##  8 lang                    0.318            0.000806                 0.0284
##  9 statisti…               0.724            0.000356                 0.0189
## 10 validator               0.536            0.00276                  0.0525
```

Randoop

```
ggplot(data = randoop.lineCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("LineCoverage"))
```



```
ggplot(data = randoop.mutationCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("MutationCoverage"))
```



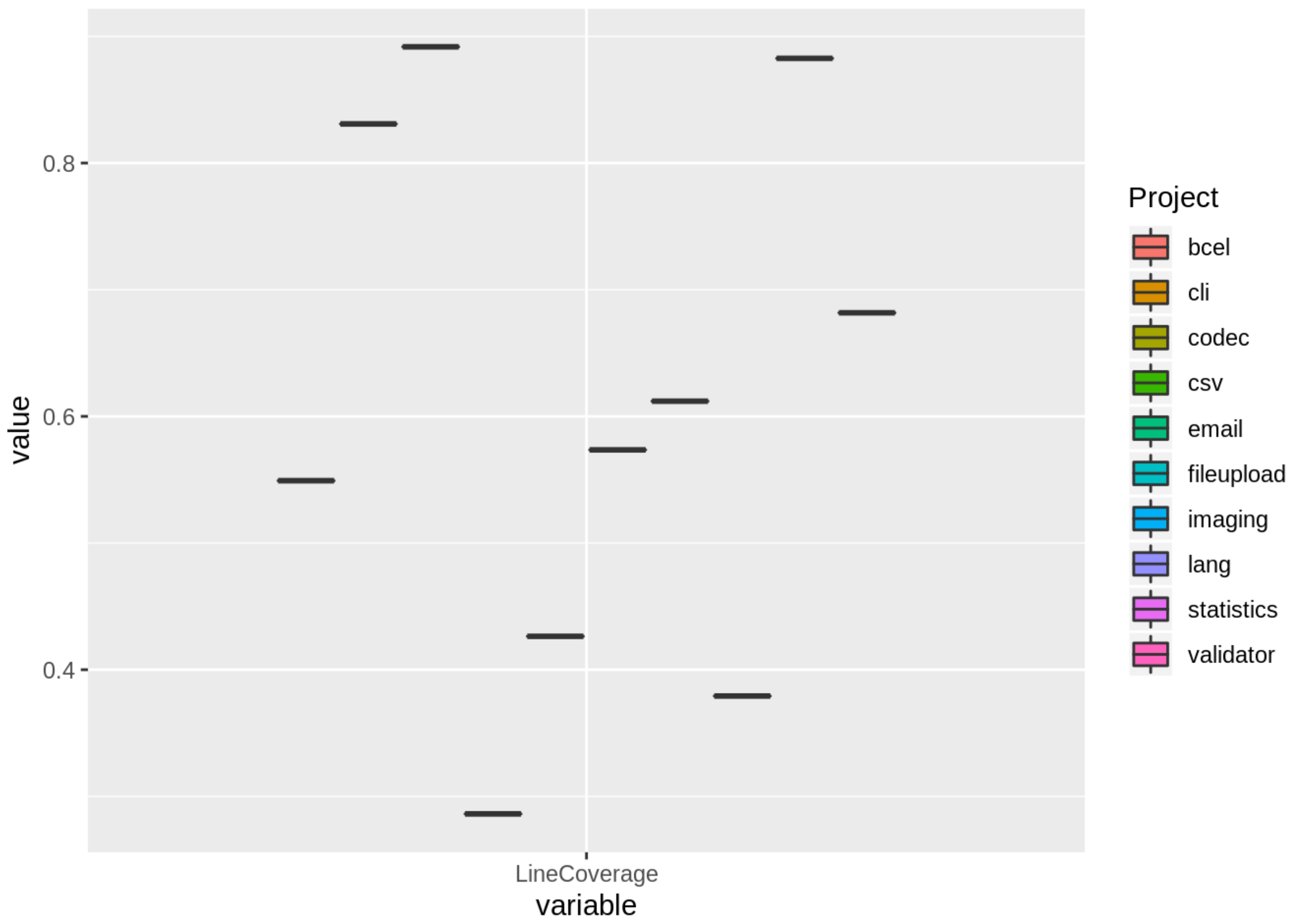
```
randoop %>% group_by(Project) %>% summarise(LineCoverageAverage = mean(LineCoverage),
LineCoverageVariation = var(LineCoverage), LineCoverageStandardDeviation = sd(LineCov
erage))
```

```
## # A tibble: 10 x 4
##    Project   LineCoverageAvera… LineCoverageVariat… LineCoverageStandardDe…
##    <fct>                  <dbl>               <dbl>                   <dbl>
##  1 bcel                   0.389          0.00294                    0.0543
##  2 cli                    0.524          0.00537                    0.0733
##  3 codec                  0.855          0.0000472                  0.00687
##  4 csv                    0.692          0.000353                   0.0188
##  5 email                  0.717          0.000233                   0.0153
##  6 fileuplo…              0.469          0.0000431                  0.00657
##  7 imaging                0.334          0.000488                   0.0221
##  8 lang                   0.559          0.00109                    0.0330
##  9 statisti…              0.905          0.00417                    0.0646
## 10 validator              0.447          0.000507                   0.0225
```

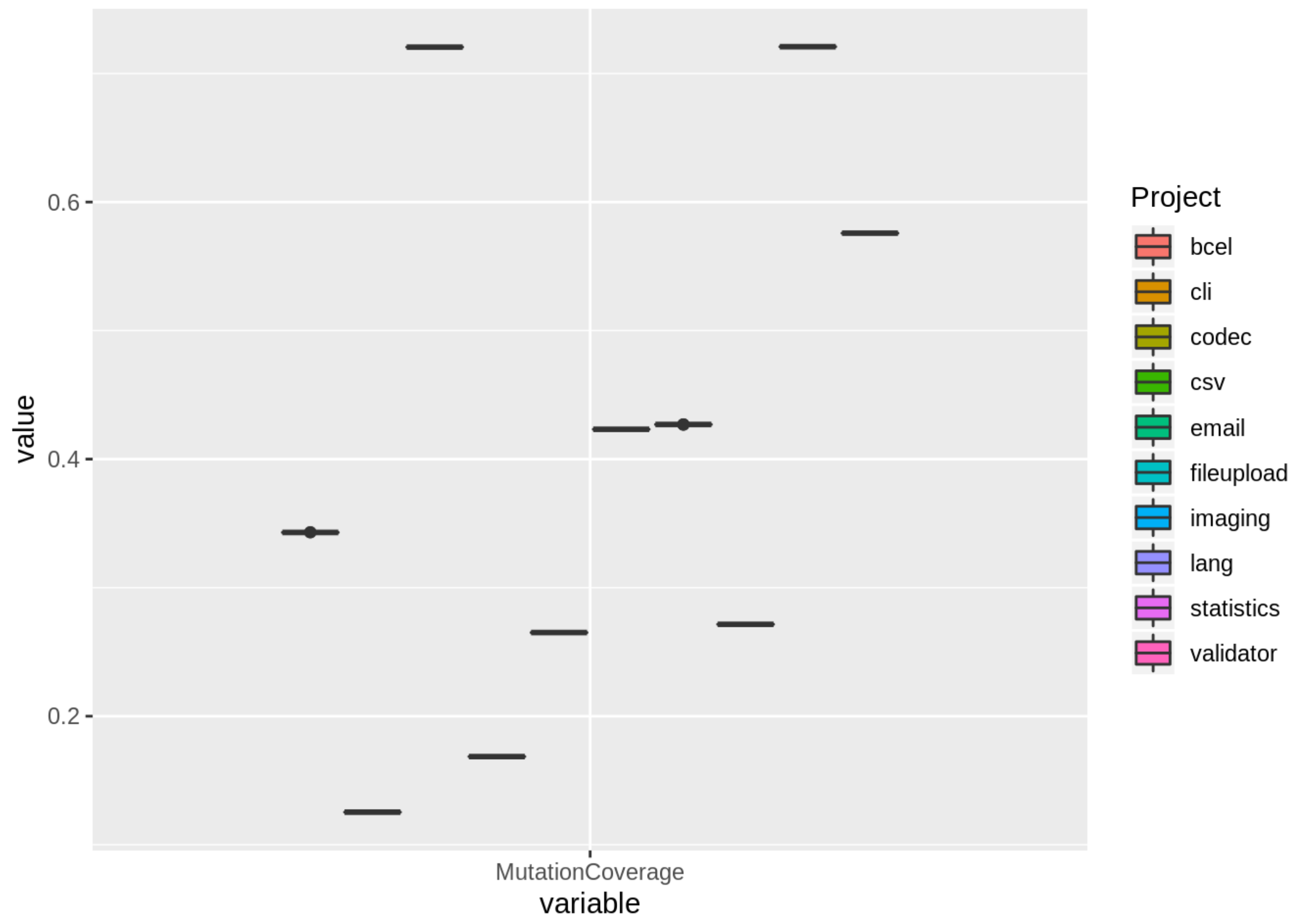
PIT

EvoSuite

```
ggplot(data = pitEvo.lineCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("LineCoverage"))
```

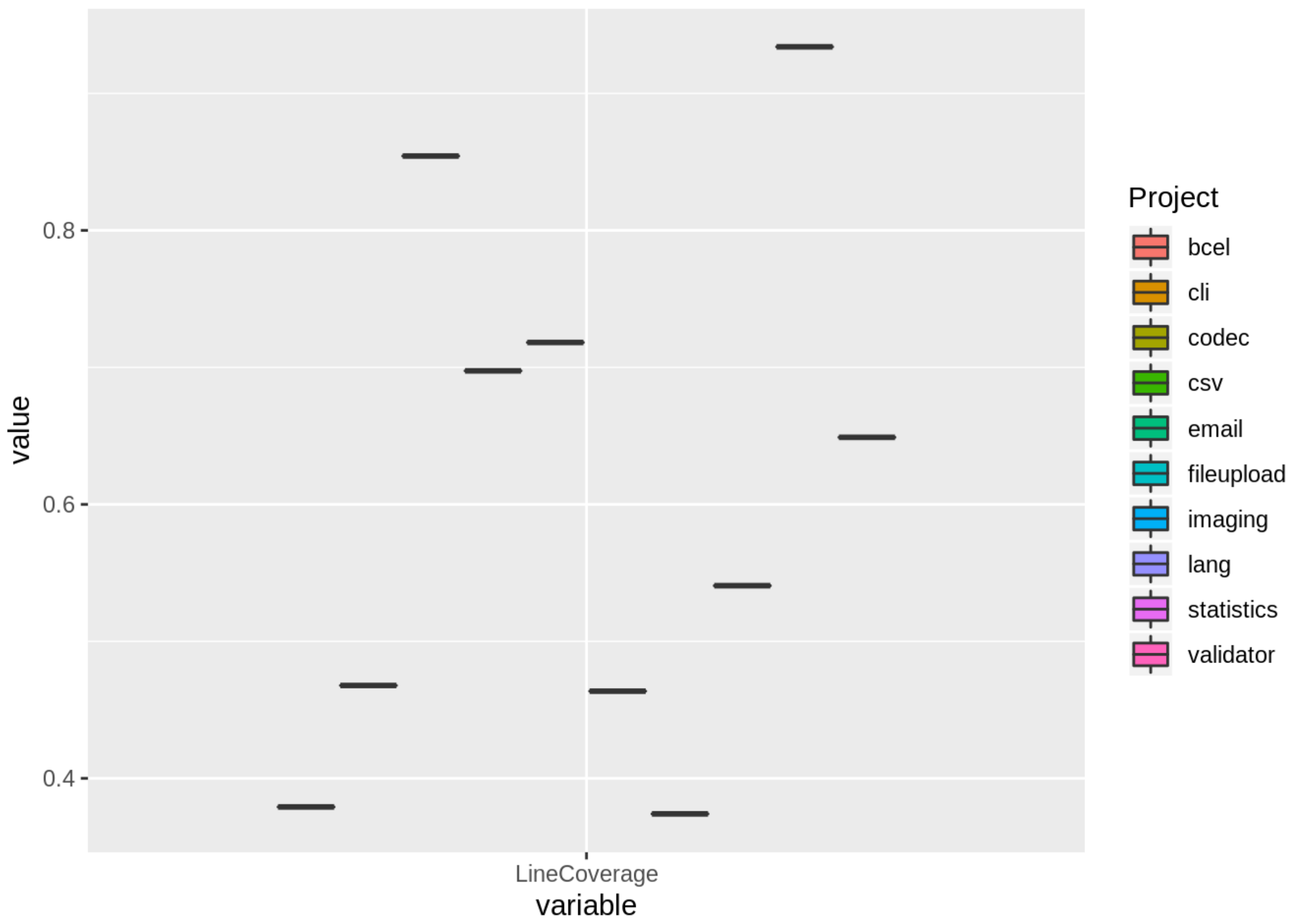


```
ggplot(data = pitEvo.mutationCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("MutationCoverage"))
```

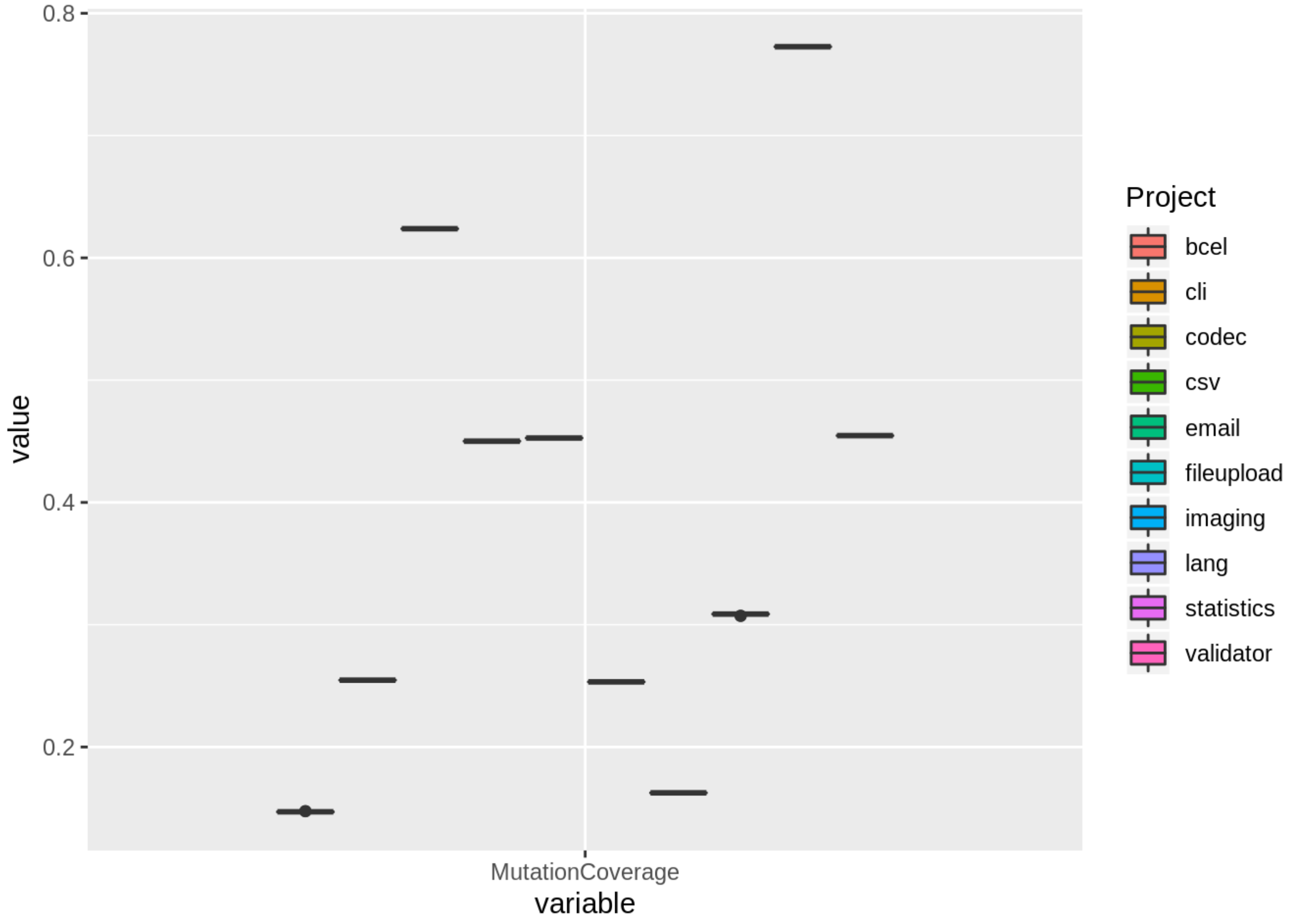


Randoop

```
ggplot(data = pitRandoop.lineCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("LineCoverage"))
```

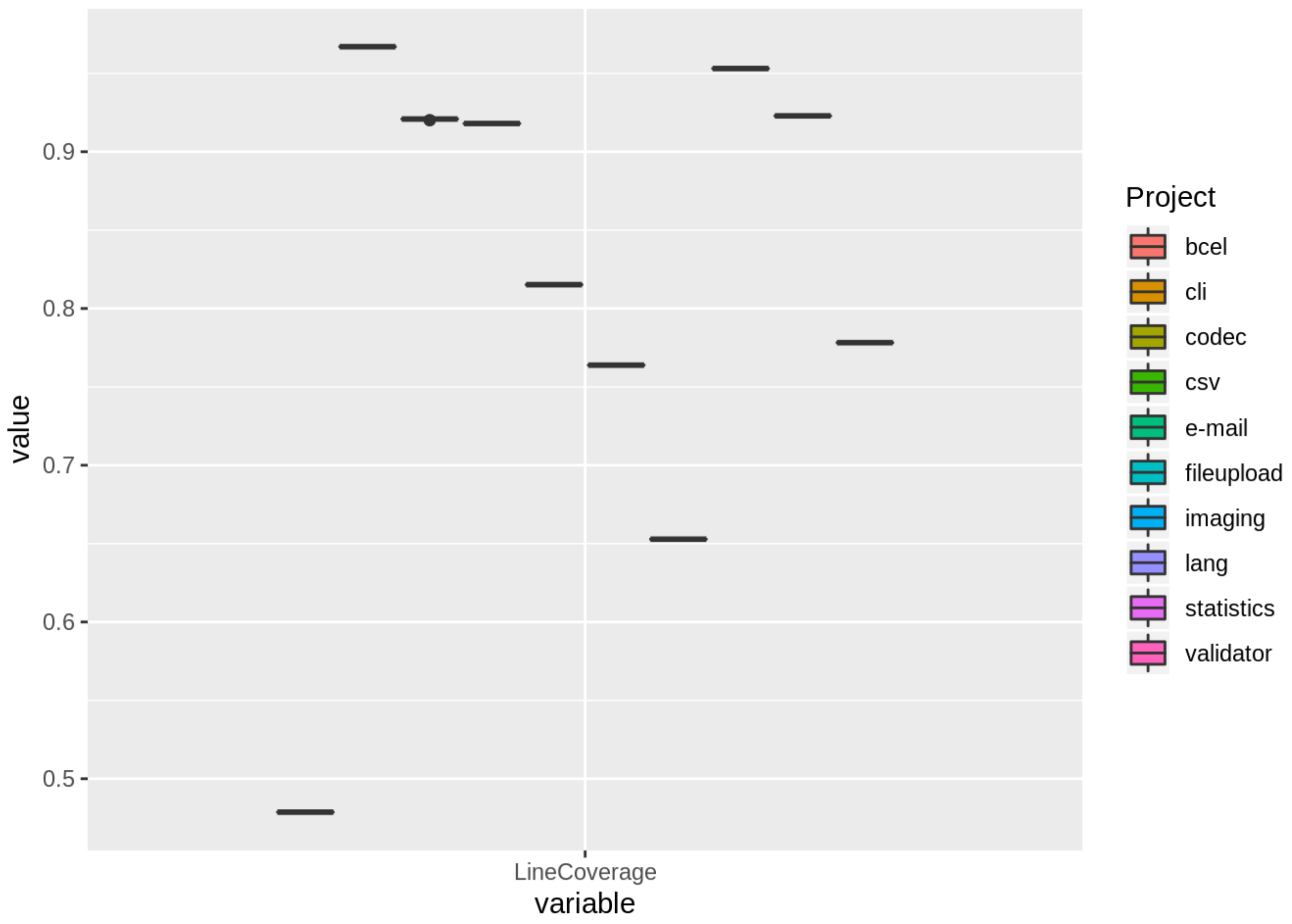


```
ggplot(data = pitRandoop.mutationCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("MutationCoverage"))
```

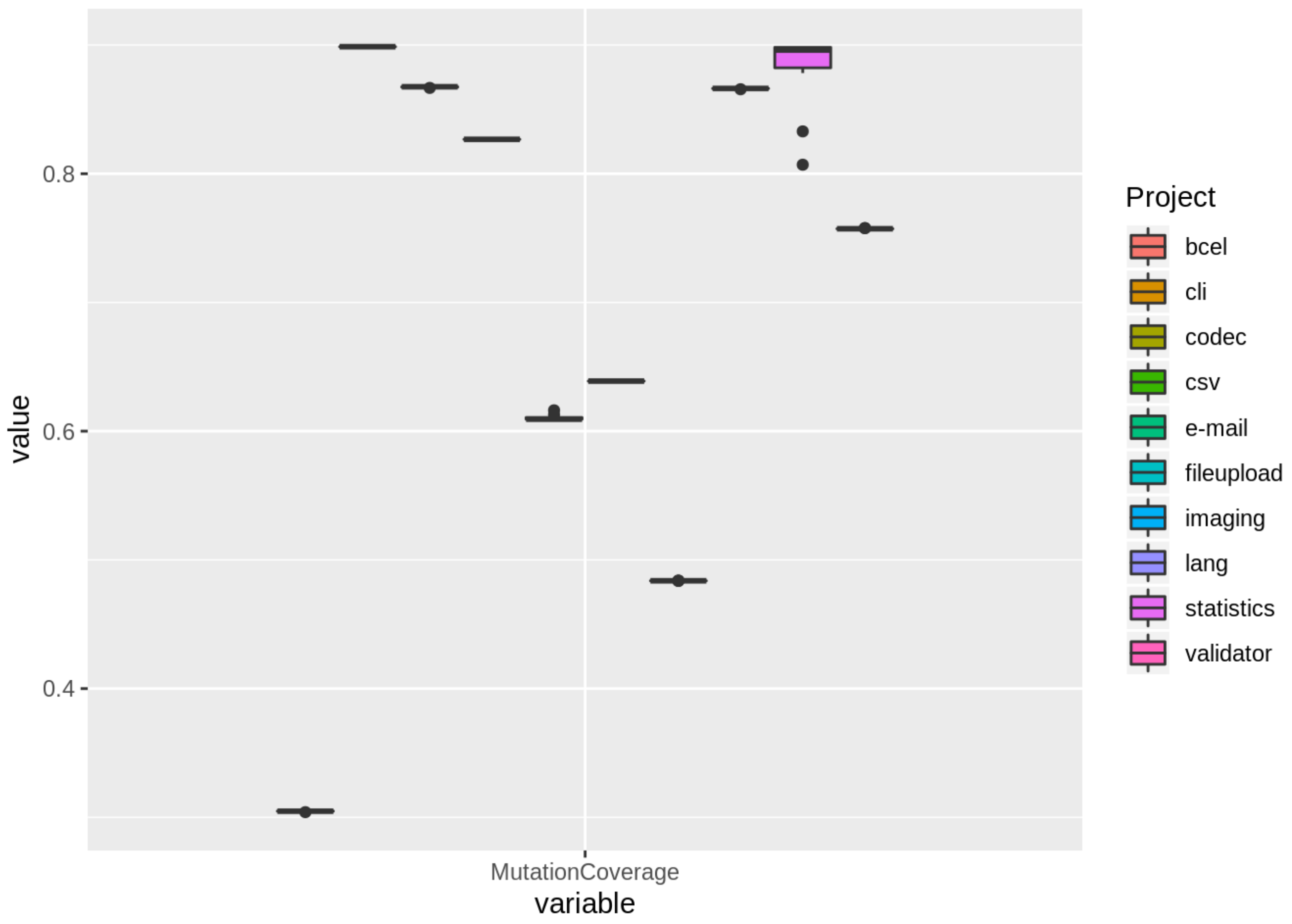


Manual

```
ggplot(data = pitManual.lineCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("LineCoverage"))
```



```
ggplot(data = pitManual.mutationCoverage, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=Project)) +
  scale_x_discrete(labels= c("MutationCoverage"))
```


0.8
0.6
0.4
value
MutationCoverage
variable
Project
bcel
cli
codec
csv
e-mail
fileupload
imaging
lang
statistics
validator