

# Method Comparison

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This script runs the CD and ADMM algorithms and compares the results using identical random sample inputs.

```
#set parameters for simulation
rho <- 0.9
n <- 200
p <- 4

#create covariance matrix
cov_matrix <- matrix(0, nrow = p, ncol = p)
for (i in 1:p) {
  for (j in 1:p) {
    cov_matrix[i, j] <- rho^abs(i - j)
  }
}

#simulate data
set.seed(100) # for reproducibility
X <- MASS::mvrnorm(n = n, mu = rep(0, p), Sigma = cov_matrix)

#set b
b <- c(1, rep(0, p - 1))

#lambda value
lambda_value <- 0.01

#ADMM and CD algorithms and compare their results
result_admm <- cg_admm(X, b, lambda_value)
re <- cg_cd(X, b, lambda_value)
result_cd_cpp <- cg_cd_cpp(X, b, lambda_value)

print(re)
```

```
## $u
##           [,1]
## [1,] 5.705206
## [2,] 0.000000
## [3,] 0.000000
## [4,] 0.000000
print(result_admm)
```

```
## $u
##           [,1]
```

```
## [1,] 3.8217697
## [2,] -0.9483531
## [3,] -3.9735019
## [4,] 12.7479771
##
## $objective_value
## [1,]
## [1,] 152.5081
print(result_cd_cpp)

## [1,]
## [1,] 1.138682
## [2,] 0.000000
## [3,] 0.000000
## [4,] 0.000000
```