```
R version 4.4.0 (2024-04-24) -- "Puppy Cup"
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Platform: aarch64-apple-darwin20
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  Natural language support but running in an English locale
R is a collaborative project with many contributors. Type 'contributors()' for more information and 'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or 'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
[R.app GUI 1.80 (8376) aarch64-apple-darwin20]
[History restored from /Users/alperkaragol/.Rapp.history]
> setwd("/Users/alperkaragol/Desktop/Consurf/")
> # Set the path to your folder
> folder_path <- "/Users/alperkaragol/Desktop/Consurf/"</pre>
> # List all files in the folder with the pattern "pathogenicity_scores_"
> file_names <- list.files(path = folder_path, pattern = "*\\.txt$", full.names = TRUE)</pre>
> # Initialize an empty list to store the medians
> parcor <- list()</pre>
  # Loop through each file
> for (file_name in file_names) {
    # Extract the base name of the file
   base_name <- basename(file_name)</pre>
    # Extract the last three characters before the ".txt"
    vector_name <- substr(base_name, nchar(base_name) - 5, nchar(base_name) - 4)</pre>
    # Read the file into a vector
    file_vector <- scan(file_name, sep = ",", what = numeric())</pre>
   # Assign the vector to a variable with the extracted name
   assign(vector_name, file_vector)
+ print(vector_name)
+ }
Read 74679 items
[1] "A"
Read 74679 items
[1] "C"
Read 74679 items
[1] "CS"
Read 74679 items
[1] "D"
Read 74679 items
[1] "E"
Read 74679 items
[1] "F"
Read 74679 items
[1] "G"
Read 74679 items
[1] "H"
Read 74679 items
[1] "I"
Read 74679 items
[1] "K"
Read 74679 items
[1] "L"
Read 74679 items
[1] "M"
Read 74679 items
[1] "N"
Read 74679 items
[1] "P"
Read 74679 items
[1] "Q"
```

```
Read 74679 items
[1] "R"
Read 74679 items
[1] "S"
Read 74679 items
[1] "T"
Read 74679 items
[1] "V"
Read 74679 items
[1] "W"
Read 74679 items
[1] "Y"
> cor.test(I, T,alternative = "two.sided", method = "spearman", exact=FALSE )
      Spearman's rank correlation rho
data: I and T
S = 5.1912e+13, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to {\tt 0}
sample estimates:
       rho
0.2521385
> cor.test(A, T,alternative = "two.sided", method = "spearman", exact=FALSE )
      Spearman's rank correlation rho
data: A and T
S = 3.5986e+13, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
0.4815717
> cor.test(T, V,alternative = "two.sided", method = "spearman", exact=FALSE )
      Spearman's rank correlation rho
data: T and V
S = 4.7492e+13, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
        rho
0.3158177
> library(ppcor)
Loading required package: MASS
> pcor.test(I, T, CS, method = c("spearman"))
    estimate p.value statistic n gp Method
1 0.1786762 0 49.62527 74679 1 spearman

> pcor.test(A, T, CS, method = c("spearman"))

estimate p.value statistic n gp Method

1 0.3719073 0 109.4841 74679 1 spearman
> pcor.test(V, T, CS, method = c("spearman"))
estimate p.value statistic n gp Metho
                                              n gp Method
1 0.2192492 0 61.40815 74679 1 spearman > pcor.test(V, T, A, method = c("spearman")) estimate p.value statistic n gp Method
estimate p.value statistic n gp Method
1 0.182528 0 50.73151 74679 1 spearman
> pcor.test(I, T, A, method = c("spearman"))
estimate p.value statistic n gp Meth
                                             n gp Method
1 0.1835468 0 51.02452 74679 1 spearman > pcor.test(A, T, I, method = c("spearman"))
1 0.4554109 0 139.787 74679 1 spearman > pcor.test(V, T, I, method = c("spearman")) estimate p.value statistic
                    0 56.12645 74679 1 spearman
1 0.2011892
> pcor.test(I, T, V, method = c("spearman"))
estimate p.value statistic n gp Method
1 0.04392292 3.204824e-33 12.01437 74679 1 spearman
> pcor.test(A, T, V, method = c("spearman"))
    estimate p.value statistic n gp Method
1 0.4186155 0 125.9626 74679 1 spearman
```