If you are a data scientist or researcher, you will certainly be interested in reproducible research. R package `rrtable` makes it possible to make reports with HTML, LaTex, MS word or MS Powerpoint formats from a table of R codes.

**Package Installation**

You can install R package `rrtable` with the following command.

**Package Loading**

You can load the `rrtable` package with the following R command.

**Sample Data**

Sample data sampleData3 is included in rrtable package. You can see the sampleData3 by folllowing R command.

Or you can make a table of this data

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3[9,]) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
|  |  |  | df2flextable2(sampleData3) |  |

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
| title |  | R package `rrtable` |  |  |
| subtitle |  | Reproducible Research with a Table of R codes |  |  |
| author |  | Keon-Woong Moon |  |  |
|  |  | If you are a data scientist or researcher, you will certainly be interested in reproducible research. R package `rrtable` makes it possible to make reports with HTML, LaTex, MS word or MS Powerpoint formats from a table of R codes. |  |  |
| header2 | Package Installation | You can install R package `rrtable` with the following command. | if(!require(devtools)){ install.packages("devtools") } | echo=TRUE,eval=FALSE |
| devtools::install\_github("cardiomoon/rrtable") |
| header2 | Package Loading | You can load the `rrtable` package with the following R command. | require(rrtable) | echo=TRUE |
| header2 | Sample Data | Sample data sampleData3 is included in rrtable package. You can see the sampleData3 by folllowing R command. | str(sampleData3) | echo=TRUE |
|  |  | Or you can make a table of this data | df2flextable2(sampleData3[9,]) |  |
|  |  |  | df2flextable2(sampleData3) |  |
| header3 | mytable object | You can add mytable object with the following R code. | df2flextable2(sampleData3[11,]) | echo=FALSE |
| mytable |  |  | mytable(Dx~.,data=acs) |  |
| header3 | Plot | You can insert a plot into your document. | df2flextable2(sampleData3[13,]) | echo=FALSE |
| plot |  |  | plot(iris) |  |
| header3 | ggplot | You can insert a ggplot into a document | df2flextable2(sampleData3[15,]) | echo=FALSE |
| ggplot |  |  | ggplot(iris,aes(x=Sepal.Length,y=Sepal.Width,color=Species))+geom\_point() |  |
| header3 | R code | You can insert the result of R code. For example, you can insert the result of regression analysis. | df2flextable2(sampleData3[17,]) | echo=FALSE |
| Rcode |  |  | fit=lm(mpg~wt\*hp,data=mtcars) |  |
| summary(fit) |
| header3 | Two ggplots | You can insert two parallel ggplots with the following code. | df2flextable2(sampleData3[19,]) | echo=FALSE |
| 2ggplots |  |  | ggplot(iris,aes(Sepal.Length,Sepal.Width))+geom\_point() |  |
| ggplot(iris,aes(Sepal.Length,Sepal.Width,colour=Species))+geom\_point()+guides(colour=FALSE) |
| header3 | Two plots | You can insert two parallel plots with the following code. | df2flextable2(sampleData3[21,]) | echo=FALSE |
| 2plots |  |  | hist(rnorm(1000)) |  |
| plot(1:10) |
| header2 | HTML Report | You can get report with HTML format(this file) by following R command. | data2HTML(sampleData3) | echo=TRUE,eval=FALSE |

**mytable object**

You can add mytable object with the following R code.

**mytable object**

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3[11,]) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
| mytable |  |  | mytable(Dx~.,data=acs) |  |

|  |  |
| --- | --- |
|  | mytable(Dx~.,data=acs) |

| Dx | NSTEMI | STEMI | Unstable.Angina | p |
| --- | --- | --- | --- | --- |
| (N=153) | (N=304) | (N=400) |
| age | 64.3 ± 12.3 | 62.1 ± 12.1 | 63.8 ± 11.0 | 0.073 |
| sex |  | | | 0.012 |
| - Female | 50 (32.7%) | 84 (27.6%) | 153 (38.2%) |
| - Male | 103 (67.3%) | 220 (72.4%) | 247 (61.8%) |
| cardiogenicShock |  | | | < 0.001 |
| - No | 149 (97.4%) | 256 (84.2%) | 400 (100.0%) |
| - Yes | 4 ( 2.6%) | 48 (15.8%) | 0 ( 0.0%) |
| entry |  | | | 0.001 |
| - Femoral | 58 (37.9%) | 133 (43.8%) | 121 (30.2%) |
| - Radial | 95 (62.1%) | 171 (56.2%) | 279 (69.8%) |
| EF | 55.0 ± 9.3 | 52.4 ± 9.5 | 59.2 ± 8.7 | < 0.001 |
| height | 163.3 ± 8.2 | 165.1 ± 8.2 | 161.7 ± 9.7 | < 0.001 |
| weight | 64.3 ± 10.2 | 65.7 ± 11.6 | 64.5 ± 11.6 | 0.361 |
| BMI | 24.1 ± 3.2 | 24.0 ± 3.3 | 24.6 ± 3.4 | 0.064 |
| obesity |  | | | 0.186 |
| - No | 106 (69.3%) | 209 (68.8%) | 252 (63.0%) |
| - Yes | 47 (30.7%) | 95 (31.2%) | 148 (37.0%) |
| TC | 193.7 ± 53.6 | 183.2 ± 43.4 | 183.5 ± 48.3 | 0.057 |
| LDLC | 126.1 ± 44.7 | 116.7 ± 39.5 | 112.9 ± 40.4 | 0.004 |
| HDLC | 38.9 ± 11.9 | 38.5 ± 11.0 | 37.8 ± 10.9 | 0.501 |
| TG | 130.1 ± 88.5 | 106.5 ± 72.0 | 137.4 ± 101.6 | < 0.001 |
| DM |  | | | 0.209 |
| - No | 96 (62.7%) | 208 (68.4%) | 249 (62.2%) |
| - Yes | 57 (37.3%) | 96 (31.6%) | 151 (37.8%) |
| HBP |  | | | 0.002 |
| - No | 62 (40.5%) | 150 (49.3%) | 144 (36.0%) |
| - Yes | 91 (59.5%) | 154 (50.7%) | 256 (64.0%) |
| smoking |  | | | < 0.001 |
| - Ex-smoker | 42 (27.5%) | 66 (21.7%) | 96 (24.0%) |
| - Never | 50 (32.7%) | 97 (31.9%) | 185 (46.2%) |
| - Smoker | 61 (39.9%) | 141 (46.4%) | 119 (29.8%) |

**Plot**

You can insert a plot into your document.

**Plot**

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3[13,]) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
| plot |  |  | plot(iris) |  |

|  |  |
| --- | --- |
|  | plot(iris) |

**ggplot**

You can insert a ggplot into a document

**ggplot**

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3[15,]) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
| ggplot |  |  | ggplot(iris,aes(x=Sepal.Length,y=Sepal.Width,color=Species))+geom\_point() |  |

|  |  |
| --- | --- |
|  | ggplot(iris,aes(x=Sepal.Length,y=Sepal.Width,color=Species))+geom\_point() |

**R code**

You can insert the result of R code. For example, you can insert the result of regression analysis.

**R code**

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3[17,]) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
| Rcode |  |  | fit=lm(mpg~wt\*hp,data=mtcars) |  |
| summary(fit) |

|  |  |
| --- | --- |
|  | fit=lm(mpg~wt\*hp,data=mtcars);summary(fit) |
|  |  |
|  | Call: |
|  | lm(formula = mpg ~ wt \* hp, data = mtcars) |
|  |  |
|  | Residuals: |
|  | Min 1Q Median 3Q Max |
|  | -3.0632 -1.6491 -0.7362 1.4211 4.5513 |
|  |  |
|  | Coefficients: |
|  | Estimate Std. Error t value Pr(>|t|) |
|  | (Intercept) 49.80842 3.60516 13.816 5.01e-14 \*\*\* |
|  | wt -8.21662 1.26971 -6.471 5.20e-07 \*\*\* |
|  | hp -0.12010 0.02470 -4.863 4.04e-05 \*\*\* |
|  | wt:hp 0.02785 0.00742 3.753 0.000811 \*\*\* |
|  | --- |
|  | Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 |
|  |  |
|  | Residual standard error: 2.153 on 28 degrees of freedom |
|  | Multiple R-squared: 0.8848, Adjusted R-squared: 0.8724 |
|  | F-statistic: 71.66 on 3 and 28 DF, p-value: 2.981e-13 |
|  |  |
|  |  |

**Two ggplots**

You can insert two parallel ggplots with the following code.

**Two ggplots**

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3[19,]) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
| 2ggplots |  |  | ggplot(iris,aes(Sepal.Length,Sepal.Width))+geom\_point() |  |
| ggplot(iris,aes(Sepal.Length,Sepal.Width,colour=Species))+geom\_point()+guides(colour=FALSE) |

|  |  |
| --- | --- |
|  | ggplot(iris,aes(Sepal.Length,Sepal.Width))+geom\_point() |
|  | ggplot(iris,aes(Sepal.Length,Sepal.Width,colour=Species))+geom\_point()+guides(colo |
|  | ur=FALSE) |

**Two plots**

You can insert two parallel plots with the following code.

**Two plots**

|  |  |
| --- | --- |
|  | df2flextable2(sampleData3[21,]) |

| **type** | **title** | **text** | **code** | **option** |
| --- | --- | --- | --- | --- |
| 2plots |  |  | hist(rnorm(1000)) |  |
| plot(1:10) |

|  |  |
| --- | --- |
|  | hist(rnorm(1000)) |
|  | plot(1:10) |

**HTML Report**

You can get report with HTML format(this file) by following R command.