

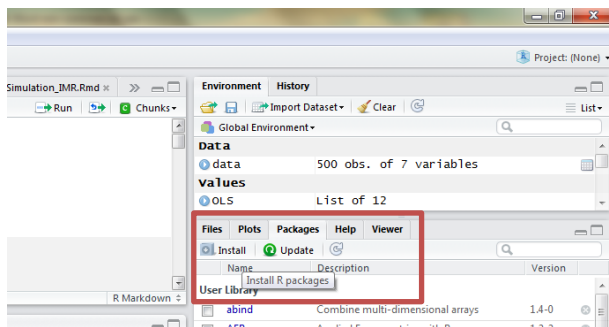
Optimalpostmatch package

The Optimalpostmatch package was designed to calculate the Hodges-Lehmann aligned rank test for matched sample from Optimal or Full matching algorithm. Hodges-Lehmann aligned rank test is one of the potential outcome analysis for an optimally or fully matched sample. The post-matching analysis for an optimally or fully matched sample is to estimate the Average Treatment Effect (ATE) by assessing the weighted average of the mean differences between treated and control participants of all matched sets within the sample. Then, Hodges-Lehmann aligned rank test is used as a significance test for the computed ATE.

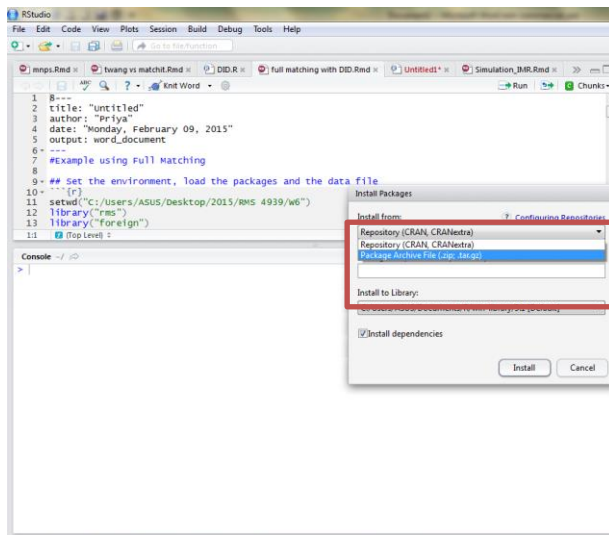
Following is the guideline in loading and operating the Optimalpostmatch package in Rstudio

Generally the R packages were installed from the CRAN repository. This repository contains only the published R packages. Since Optimalpostmatch is still in developmental phase, it will not be present in the CRAN repository. But, users can still load and use the package in their Rstudio. Following is the screenshot of steps on how to install package from alternative source.

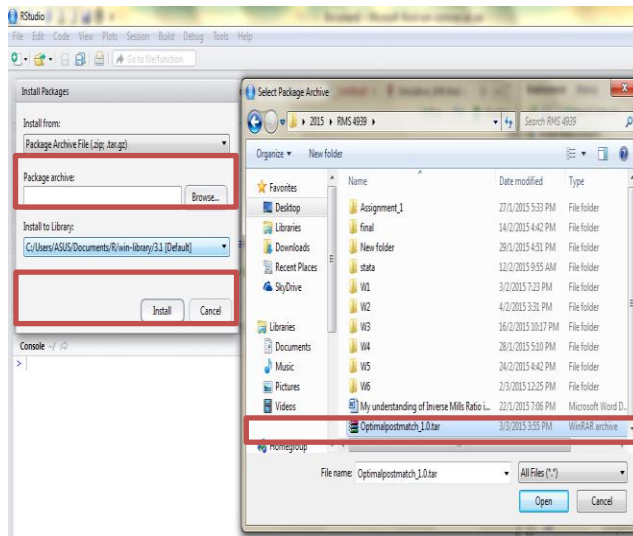
1. Open R Studio.
2. Select the Install Packages tab



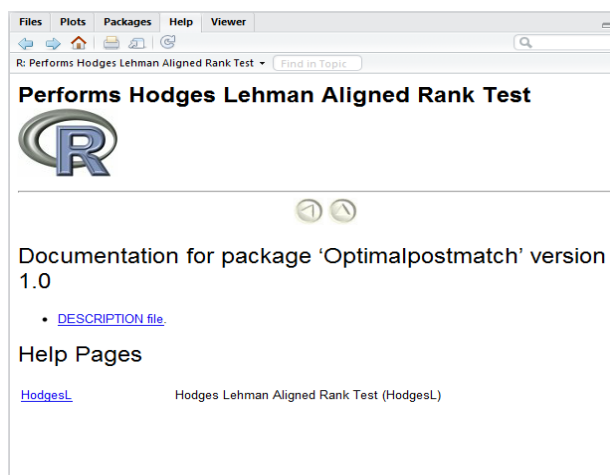
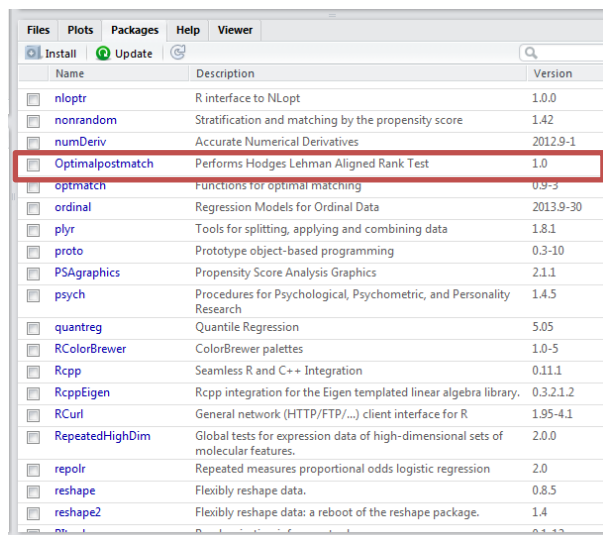
3. Under Install From: select Package Archive File .tar.gz



4. Browse to the Optimalpostmatch_1.0.tar.gz file on your hard drive (directory where the file is saved).
5. Select and install the package.



6. The package will appear under the pane on the bottom right of Rstudio (under packages).
7. Check the Optimalpostmatch package box and its ready to use.



Following is the steps in using the Optimalpostmatch package.

1. The first two arguments are used to rename the outcome and treatment variable in the matched dataset. **score09** and **treatm** are outcome and treatment variables in the dataset. The first two arguments rename the variables to **score** and **treat**.

```
names(match.data)[names(match.data)=="score09"]="score" ## Rename the outcome variable
names(match.data)[names(match.data)=="treatm"]="treat" ## Rename the treatment variable
```

2. Use the HodgesL function on the matched data obtained from full/optimal matching algorithm.

HodgesL (match.data)

```
63 ## Post matching analysis
64 {r}
65 library("optimalpostmatch")
66 names(match.data)[names(match.data)=="score09"]="score" #Rename the outcome
   variable
67 names(match.data)[names(match.data)=="treatm"]="treat" #Rename the treatment
   variable
68 HodgesL (match.data)
69
70
71
72
69:1 Chunk 5 R Markdown
```

```
Console C:/Users/ASUS/Desktop/2015/RMS 4939/final/
pretest  gender  african  hispanic  lses  age  cr08  absent
0.08040316 0.04955879 0.07640178 0.05827207 0.01308529 0.04830932 0.05469857 0.04674747
zip  hhincome
0.12947170 0.12345382
>
> ### 4. chi-square test after matching
> xbalance(treatm ~ pretest + african + lses + age + absent + cr08 + gender, data = match
.data, report = c("chisquare.test"))
---Overall Test---
      chisquare df p.value
unstrat    3.59  7  0.825
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> ## Post matching analysis
> library("optimalpostmatch")
> names(match.data)[names(match.data)=="score09"]="score" #Rename the outcome variable
> names(match.data)[names(match.data)=="treatm"]="treat" #Rename the treatment variable
> HodgesL (match.data)
$`z scores`
[1] -0.4116358

$p-value`
[1] "nonsignificant"
```