Optimalpostmatch package

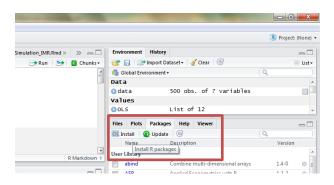
The Optimalpostmatch package was designed to calculate the Hodges-Lehmann aligned rank test for matched sample from Optimal or Full matching algorithm. Hodges-Lehmann aligned rank test is one of the potential outcome analysis for an optimally or fully matched sample. The post-matching analysis for an 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

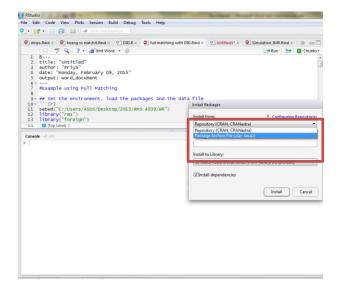
Generally the R packages were installed from the CRAN repository. This repository contains only the published R packages. Since Optimalpostmatch is still in developmental phase, it will not be present in the CRAN repository. But, users can still load and use the package in their Rstudio. Following is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

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isole -/ 🛱	Documents	🔒 W4	28/1/2015 5:10 PM	File folder	
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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.

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	Name	Description	Version
	nloptr	R interface to NLopt	1.0.0
	nonrandom	Stratification and matching by the propensity score	1.42
	numDeriv	Accurate Numerical Derivatives	2012.9-1
	Optimalpostmatch	Performs Hodges Lehman Aligned Rank Test	1.0
	optmatch	Functions for optimal matching	0.9-3
	ordinal	Regression Models for Ordinal Data	2013.9-30
	plyr	Tools for splitting, applying and combining data	1.8.1
	proto	Prototype object-based programming	0.3-10
	PSAgraphics	Propensity Score Analysis Graphics	2.1.1
	psych	Procedures for Psychological, Psychometric, and Personality Research	1.4.5
	quantreg	Quantile Regression	5.05
	RColorBrewer	ColorBrewer palettes	1.0-5
	Rcpp	Seamless R and C++ Integration	0.11.1
	RcppEigen	Rcpp integration for the Eigen templated linear algebra library.	0.3.2.1.2
	RCurl	General network (HTTP/FTP/) client interface for R	1.95-4.1
	RepeatedHighDim	Global tests for expression data of high-dimensional sets of molecular features.	2.0.0
	repolr	Repeated measures proportional odds logistic regression	2.0
1	reshape	Flexibly reshape data.	0.8.5
	reshape2	Flexibly reshape data: a reboot of the reshape package.	1.4
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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)

<pre>63 * ### Post matching analysis 64 * ```{r} 55 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 * ```</pre>
70 71 72 69:1 C Chunk 5 \$ =
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
<pre>> ### 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) S'z scores' [1] -0.4116358 S'p-value' [1] "nonsignificant"</pre>