Package	Source	Version	Note
	1	R vers	ion
Base packages	CRAN	4.0.0	-
		Common p	purpose
data.table	CRAN	1.13.0	-
dplyr	CRAN	1.0.6	-
stringr	CRAN	1.4.0	-
doParallel	CRAN	1.0.15	-
BiocParallel	BC	1.22.0	-
ggplot2	CRAN	3.3.2	-
	T	Randomiz	zation
tuple	CRAN	0.4-02	-
randomizr	CRAN	0.20.0	-
	T	Integrat	tion
ipo	BC	1.14.0	-
Autotuner	BC	1.2.0	-
MetaboAnalystR	BC	3.0.2	-
xcms	BC	3.9.1	-
warpgroup	GH	0.1.0.9001	-
ncGTW	BC	1.2.0	-
	1	Correct	tion
pmp	BC	1.0.0	-
StatTarget	BC	1.20.0	This version allows to set high value in the CV cutoff
MetNormalizer	GH	1.3.02	-
batchCorr	GL	0.2.5	-
BatchCorrMetabolomics	GH	0.1.14	-
notame	GH	0.0.5	-
openxlsx	CRAN	4.1.5	-
pbapply	CRAN	1.4-3	-
caret	CRAN	6.0-86	-
rpart	CRAN	4.1-15	-
ipred	CRAN	0.9-9	-
catboost	GH	0.20	-
xgboost	CRAN	1.2.0.1	-
dbnorm	GH	0.2.2	-
ProteoMM	BC	1.6.0	-
WaveICA	GH	0.1.0	-
NormalizeMets	CRAN	0.25	-
RUVSeq	BC	1.22.0	-
edgeR	BC	3.12.1	This version allows to load RUVSeq
			package
tibble	CRAN	3.0.3	-
fpc	CRAN	2.2-7	-
FactoMineR	CRAN	2.3	-
cluster	CRAN	2.1.0	-
proBatch	BC	1.4.0	-
gPCA	CRAN	1.0	-
MetabolomicsBasics	CRAN	1.1	-
factoextra	CRAN	1.0.7	-

rafalib	CRAN	1.0.0	-			
RSEIS	CRAN	3.9-0	-			
ggsci	CRAN	2.9	-			
_ 66**		Annota	tion			
CAMERA	ВС	1.44.0	-			
RamClustR	GH	1.1.0	-			
xMSannotator	GH	1.3.2	From kuppal2 repo (https://github.com/kuppal2/xMSannotator). Fix for R 4.0 fun string 95 to n2<-as.data.frame(n1, stringsAsFactors = T). According to yufree repo (https://github.com/yufree/xMSannotator). Install manually (tar.gz), type = "source". Also see instruction from GH and SF.			
		Normaliz	ation			
affy	BC	1.66.0	-			
clusterSim	CRAN	0.49-1	-			
DiffCorr	CRAN	0.4.1	-			
lmm2met	GH	1.0	-			
MetabolomicsBasics	CRAN	1.1	-			
lme4	CRAN	1.1-23	-			
lmerTest	CRAN	3.1-2	-			
NormalizeMets	CRAN	0.25	-			
RColorBrewer	CRAN	1.1-2	-			
limma	BC	3.38.3	-			
	T-	Imputa	tion			
MetProc	CRAN	1.0.1	-			
impute	BC	1.62.0	-			
mice	CRAN	3.11.0	-			
missForest	CRAN	1.4	-			
StatTools	GL	0.0.915	-			
pcaMethods	BC	1.80.0	-			
imputeLCMD	CRAN	2.0	-			
imputeR	CRAN	2.2	-			
vegan	CRAN	2.5-6	-			
missMethods	CRAN	0.2.0	-			
Grouping						
corrr	CRAN	0.4.3.9000	-			
gplots	CRAN	3.0.4	-			
tidyverse	CRAN	1.3.0	-			
igraph	CRAN	1.2.6	-			
ggraph	CRAN	2.0.3	-			
robCompositions	CRAN	2.3.0	-			
compositions	CRAN	2.0-1	-			
gridExtra	CRAN	2.3	-			
stringi	CRAN	1.5.3	-			
notame	GH	0.0.5	-			
pmd	CRAN	0.1.9	-			
Statistics						
pcaMethods	BC	1.80.0	-			

caret CRAN 6.0-86 Other methods may require additional packages klaR CRAN 0.6-14 The klaR package should be exactly version 0.6-14 for RFS cwhmisc CRAN 6.6 The shapiro.wilk.test function should be used if some error with normality test in UVF. tuple CRAN 0.4-02 - pamr CRAN 1.56.1 For ML model in caret pls CRAN 2.7-3 For ML model in caret pls CRAN 0.9-29 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret randomForest CRAN 1.1 For multigroup Fold Change structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1-2 - <	OutlierDetection	CRAN	0.1.1	-	
klaR CRAN 0.6-14 The klaR package should be exactly version 0.6-14 for RFS cwhmisc CRAN 6.6 The shapiro, wilk test function should be used if some error with normality test in UVF. tuple CRAN 0.4-02 - pamr CRAN 1.56.1 For ML model in caret kernlab CRAN 2.7-3 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For ML model in caret ropls BC 1.0.1 For ML model in caret ropls BC 1.0.1 For	caret	CRAN	6.0-86	Other methods may require additional	
cwhmisc CRAN 6.6 The shapiro.wilk.test function should be used if some error with normality test in UVF. tuple CRAN 0.4-02 - pamr CRAN 1.56.1 For ML model in caret pls CRAN 2.7-3 For ML model in caret kernlab CRAN 0.9-29 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Ime4 CRAN 1.1-23 - Ime7fest CRAN 3.1-2 - Imma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 -				packages	
cwhmisc CRAN 6.6 The shapiro.wilk.test function should be used if some error with normality test in UVF. tuple CRAN 0.4-02 - pamr CRAN 1.56.1 For ML model in caret pls CRAN 2.7-3 For ML model in caret kernlab CRAN 0.9-29 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Ime4 CRAN 1.1-23 - Ime7fest CRAN 3.1-2 - limma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - patry CRAN 1.3-5 -	klaR	CRAN	0.6-14		
tuple CRAN 0.4-02 - pamr CRAN 1.56.1 For ML model in caret pls CRAN 2.7-3 For ML model in caret kernlab CRAN 0.9-29 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Imed CRAN 1.1-23 - ImerTest CRAN 1.1-23 - Imema BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 7.3-52 - pROC CRAN 1.14.4 - leaps CRAN 3.0	cwhmise	CRAN	6.6		
tuple CRAN 0.4-02 - pamr CRAN 1.56.1 For ML model in caret pls CRAN 2.7-3 For ML model in caret kernlab CRAN 0.9-29 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Ime4 CRAN 1.1-23 - Ime7Test CRAN 3.1-2 - Imma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 3.1 - reshape2 CRAN 3.0 - </td <td>CWIIIIISC</td> <td>CKAIN</td> <td>0.0</td> <td></td>	CWIIIIISC	CKAIN	0.0		
pamr CRAN 1.56.1 For ML model in caret pls CRAN 2.7-3 For ML model in caret kernlab CRAN 0.9-29 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - lme4 CRAN 1.1-23 - lme4 CRAN 1.1-23 - lme4 CRAN 3.1-2 - limma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.0-0 - party CRAN 1.0-2 - glmnet CRAN 1.6.2 - reshape2 CRAN 1.14.4 - leaps CRAN 3.0 - </td <td></td> <td></td> <td></td> <td></td>					
Pis	tuple	CRAN	0.4-02	-	
kernlab CRAN 0.9-29 For ML model in caret randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Ime4 CRAN 1.1-23 - ImerTest CRAN 3.1-2 - limma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 1.6.2 - reshape2 CRAN 1.14-2 - leaps CRAN 3.1 - gwQS CRAN 3.0 - vegan CRAN 1.4-13 - mairwiseAdo	pamr	CRAN	1.56.1	For ML model in caret	
randomForest CRAN 4.6-14 For ML model in caret ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Imed CRAN 1.1-23 - ImerTest CRAN 3.1-2 - Iimma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 0.00 - party CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 1.16-2 - reshape2 CRAN 1.4-4 - leaps CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp <td< td=""><td>pls</td><td>CRAN</td><td>2.7-3</td><td>For ML model in caret</td></td<>	pls	CRAN	2.7-3	For ML model in caret	
ropls BC 1.20.0 - structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Ime4 CRAN 1.1-23 - Ime7Est CRAN 3.1-2 - limma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 1.16-2 - reshape2 CRAN 1.14-4 - leaps CRAN 3.0.3 - wegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1	kernlab	CRAN	0.9-29	For ML model in caret	
structToolbox BC 1.0.1 For multigroup Fold Change MetabolomicsBasics CRAN 1.1 - Ime4 CRAN 1.1-23 - Ime7Test CRAN 3.1-2 - limma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 4.0-2 - pROC CRAN 1.16-2 - reshape2 CRAN 1.4-4 - leaps CRAN 3.0.3 - gwQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.	randomForest	CRAN	4.6-14	For ML model in caret	
MetabolomicsBasics CRAN 1.1 - Ime4 CRAN 1.1-23 - ImerTest CRAN 3.1-2 - Iimma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 1.16.2 - reshape2 CRAN 1.4.4 - leaps CRAN 3.1 - gWQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 -	ropls	BC	1.20.0	-	
Ime4	structToolbox	BC	1.0.1	For multigroup Fold Change	
ImerTest CRAN 3.1-2 - limma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 1.16.2 - reshape2 CRAN 1.4.4 - leaps CRAN 3.1 - gWQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 2.3 - dendextend CRAN 1.0.0 -	MetabolomicsBasics	CRAN	1.1	-	
limma BC 3.38.3 - NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 1.16.2 - reshape2 CRAN 1.4.4 - leaps CRAN 3.1 - gWQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 -				-	
NormalizeMets CRAN 0.25 - permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 1.16.2 - reshape2 CRAN 1.4.4 - leaps CRAN 3.1 - gWQS CRAN 3.0.3 - vegan CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.0.0 -				-	
permimp CRAN 1.0-0 - party CRAN 1.3-5 - glmnet CRAN 4.0-2 - MASS CRAN 7.3-52 - pROC CRAN 1.16.2 - reshape2 CRAN 1.4.4 - leaps CRAN 3.1 - gWQS CRAN 3.0.3 - vegan CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 3.9-0 -	limma	BC		-	
CRAN 1.3-5 -	NormalizeMets	CRAN	0.25	-	
Sample CRAN 4.0-2 -	permimp	CRAN	1.0-0	-	
MASS CRAN 7.3-52 - pROC CRAN 1.16.2 - reshape2 CRAN 1.4.4 - leaps CRAN 3.0.3 - gWQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	party	CRAN	1.3-5	-	
pROC CRAN 1.16.2 - reshape2 CRAN 1.4.4 - leaps CRAN 3.1 - gWQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 0.15 - Rtsne CRAN 3.0 -	glmnet	CRAN	4.0-2	-	
reshape2	MASS	CRAN	7.3-52	-	
leaps CRAN 3.1 - gWQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 3.0 -	pROC	CRAN	1.16.2	-	
gWQS CRAN 3.0.3 - vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	reshape2	CRAN	1.4.4	-	
vegan CRAN 2.5-6 - pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	leaps	CRAN	3.1	-	
pairwiseAdonis GH 0.0.1 - multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	gWQS	CRAN	3.0.3	-	
multcomp CRAN 1.4-13 - MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	vegan	CRAN	2.5-6	-	
MetStaT CRAN 1.0 - mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	pairwiseAdonis	GH	0.0.1	-	
mixOmics BC 6.12.1 - timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	multcomp	CRAN	1.4-13	-	
timecourse BC 1.60.0 - factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	MetStaT	CRAN	1.0	-	
factoextra CRAN 1.0.7 - FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	mixOmics	BC	6.12.1	-	
FactoMineR CRAN 2.3 - dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	timecourse	BC	1.60.0	-	
dendextend CRAN 1.13.4 - rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	factoextra	CRAN	1.0.7	-	
rafalib CRAN 1.0.0 - RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	FactoMineR	CRAN	2.3	-	
RSEIS CRAN 3.9-0 - ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	dendextend	CRAN	1.13.4	-	
ggsci CRAN 2.9 - pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	rafalib	CRAN	1.0.0	-	
pheatmap CRAN 1.0.12 - Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	RSEIS	CRAN	3.9-0	-	
Rtsne CRAN 0.15 - NbClust CRAN 3.0 -	ggsci	CRAN	2.9	-	
NbClust CRAN 3.0 -	pheatmap	CRAN	1.0.12	-	
	Rtsne	CRAN	0.15	-	
clustertend CRAN 1.4 -	NbClust	CRAN	3.0	-	
	clustertend	CRAN	1.4	-	

mclust	CRAN	5.4.6	-	
clValid	CRAN	0.6-9	-	
pvclust	CRAN	2.2-0	-	
fpc	CRAN	2.2-7	-	
Hmisc	CRAN	4.4-1	-	
corrplot	CRAN	0.84	-	
psych	CRAN	2.0.7	-	
pwr	CRAN	1.3-0	-	
effectsize	CRAN	0.3.2	-	
	ctly used packages:	105		
	attached packages:	179		
Total loaded packages:				429