Package	Source	Version	Note				
<u> </u>	l	R vers	ion				
Base packages	CRAN	4.0.0	-				
1 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	-				
Randomization							
tuple	CRAN	0.4-02	-				
randomizr	CRAN	0.20.0	-				
Integration							
ipo	BC	1.14.0	-				
Autotuner	BC	1.2.0	-				
MetaboAnalystR	GH	3.0.2	-				
xcms	BC	3.9.1	-				
warpgroup	GH	0.1.0.9001	-				
ncGTW	BC	1.2.0	-				
		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	-				
pcpr2	GH	0.0.0.1	-				
MetabolomicsBasics	CRAN	1.1	-				

factoextra	CRAN	1.0.7	_				
rafalib	CRAN	1.0.7	-				
RSEIS	CRAN	3.9-0	-				
	CRAN	2.9	-				
ggsci CRAN 2.9 - Annotation							
CAMERA	BC	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.				
mWISE	GH	0.1.0	Forked from b2slab/mWISE to plyush1993/mWISE and depends were manually changed to R (>= 4.0).				
metID	GH	1.1.0	Databases from				
			(https://github.com/jaspershen/demoData/tree/master/inst/ms2_databada)				
			should be copied in "ms2_database" folder in metID library folder.				
tidyverse	CRAN	1.3.0	-				
batchCorr	GL	0.2.5	_				
		Normaliz	zation				
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	-				
mgcv	CRAN	1.8-32	-				
gamm4	CRAN	0.2-6	-				
gpboost	CRAN	0.6.7	-				
NormalizeMets	CRAN	0.25	-				
RColorBrewer	CRAN	1.1-2	-				
limma	BC	3.38.3	-				
	1	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	-				
OutlierDetection	CRAN	0.1.1	Require spatstat package version 1.64-1 (CRAN)				
ClassDiscovery	CRAN	3.3.13	-				
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				
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	-				
tdfdr	CRAN	0.1	-				
MetabolomicsBasics	CRAN	1.1	-				
lme4	CRAN	1.1-23	_				
lmerTest	CRAN	3.1-2	-				
mgcv	CRAN	1.8-32	-				
gamm4	CRAN	0.2-6	_				
drc	CRAN	3.0-1	-				
DRomics	CRAN	2.2-0	-				
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	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	-	
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	-	
	y used packages:	118		