

Analysis of transcriptomics and metabolomics data

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Parameters:

```
.years1 = 18  
.years2 = 19  
.bins1 = 1  
.bins2 = 2  
.bins3 = 3  
.bins4 = 4  
.bins5 = 5  
.bins6 = 6  
.bins7 = 7  
.ver = V3
```

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1 Task

Analysis of transcriptomics and metabolomics data with canonical correlation.
Main ideas are from package **mixOmics**.

Final document in folder /reports:

```
> fileName(outputFile)
```

```
[1] "60_Trans-x-Meta_18-19-1-2-3-4-5-6-7-V3"
```

2 Information from pISA

Data directory

```
> .inroot
```

```
[1] "../..input"
```

Results directory

```
> .oroot
```

```
[1] "../..output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3"
```

```
project:      _p_VinskaTrta
```

```
Investigation: _I_EnViRoS
```

```
Study:        _S_01_Integ
```

```
Assay:         _A_01_Desc-R
```

3 Data

Priporočljivo je najprej prebrati phenodata in feature-data, potem pa podatke. To omogoča izbor spremenljivk in vzorcev takoj za tem, ko podatke preberemo.

```
> cat(knit_child(file.path("../doc", "10a_Read-Data.Rnw"), quiet=TRUE))
```

Entered 10a-ReadData.Rnw

3.1 Phenodata

Two incomplete lines in original phenodata were manually completed. Sample ids (ID) were parsed in Excel to form factors of interest: variety, year and day.

```
> (pfn <- getDesc(.adesc
+      , "Phenodata"))
[1] "Phenodata_20201109.txt"
> dir(file.path(.iroot), pattern = pfn)
[1] "Phenodata_20201109.txt"
> phdata <- read.table(file.path(.iroot, pfn)
+      , header = TRUE
+      , sep = "\t"
+      , stringsAsFactors = FALSE
+      )
> rownames(phdata) <- phdata[,1]
> my.summary(phdata)
```

ID	Variety	Date	variety
C18_11d_WS1: 1	Cabernet Volos:134	21.06.2018: 20	C:134
C18_11d_WS2: 1	Fleurtaï :136	26.06.2019: 20	F:136
C18_11d_WS3: 1		7.08.2018 : 20	
C18_11d_WS4: 1		8.07.2019 : 20	
C18_11d_WW1: 1		1.08.2018 : 16	
C18_11d_WW2: 1		18.07.2019: 16	
(Other) :264		(Other) :158	

year	day	treat	rep	project.name
18:136	34 : 36	WS:135	1 :48	EnViro:270
19:134	49 : 24	WW:135	2 :48	
	20 : 20		3 :48	
	22 : 20		4 :48	
	67 : 20		NA's:78	
	44 : 16			
	(Other):134			

species	plant.name	tissue	health.status
Vitis vinifera:270	grapevine:270	: 78	water stress:134
		leaf:192	well watered:136

plant.number	growth.location	growth.conditions
:78	Udine:270	outside:270
R1:48		
R2:48		
R3:48		
R4:48		

several leaves ground together and stored at -80oC; an aliquot was received f

```

Metabolites.Order                                Metabolites.File.Name
2          : 2                                : 80
3          : 2          1019Cabernet Volos_6_12_WS1.D: 1
4          : 2          1019Cabernet Volos_6_12_WS2.D: 1
5          : 2          1019Cabernet Volos_6_12_WW1.D: 1
6          : 2          1019Cabernet Volos_6_12_WW2.D: 1
(Other):180          1019Cabernet Volos_6_21_WS1.D: 1
NA's      : 80          (Other)                :185

          Metabolites.File Transcripts.ID
          : 80                :190
Cabernet Volos08_07WS: 4      C1_S1 : 1
Cabernet Volos08_07WW: 4      C1_S2 : 1
Cabernet Volos08_08WS: 4      C1_S3 : 1
Cabernet Volos08_08WW: 4      C1_S4 : 1
Cabernet Volos18_07WS: 4      C1_W1 : 1
(Other)                :170      (Other) : 75

> dim(phdata)
[1] 270 21

> names(phdata)
[1] "ID"                "Variety"
[3] "Date"              "variety"
[5] "year"              "day"
[7] "treat"              "rep"
[9] "project.name"       "species"
[11] "plant.name"         "tissue"
[13] "health.status"      "plant.number"
[15] "growth.location"    "growth.conditions"
[17] "sampling"            "Metabolites.Order"
[19] "Metabolites.File.Name" "Metabolites.File"
[21] "Transcripts.ID"

```

3.2 Declare factor types

In 2018, day 11 is present only for C and day 10 only for F. The two day points coincide and are changed to a common value 11.

```

> for(yr in levels(phdata$year)){
+   cat("\n\nYear:", yr, "\n")
+   print(
+     with(phdata[phdata$year==yr, ], ftable(treat, variety, factor(day)))
+   )
+ }
> phdata[phdata$day==10, "day"] <- 11

```

Factors

```

> factors <- colnames(phdata)[4:8]
> factors
[1] "variety" "year"      "day"      "treat"    "rep"
> for (varname in factors)
+ phdata[,varname] <- factor(phdata[,varname])
> #
> # Change the order of levels for treatment
> phdata$treat <- factor(phdata$treat, levels=c("WW", "WS"))
> str(phdata[,factors])
'data.frame':      270 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 26 levels "3","11","14",...: 2 2 2 2 2 2 2 2 4 4 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...

```

Date of sampling might be useful as well

```

> library(lubridate)
Warning: package 'lubridate' was built under R version 4.0.3

```

Attaching package: 'lubridate'

The following objects are masked from 'package:BiocGenerics':

```
intersect, setdiff, union
```

The following objects are masked from 'package:base':

```
date, intersect, setdiff, union
```

```

> phdata$date <- as_date(phdata$Date, format="%d.%m.%Y")
> table(data.frame(phdata$date, "Count"=1))

```

	Count
phdata.date	1
2018-06-04	4
2018-06-11	8
2018-06-12	8
2018-06-15	4
2018-06-21	20
2018-06-29	4
2018-07-04	4
2018-07-05	16
2018-07-10	4
2018-07-16	4
2018-07-20	16
2018-07-23	4
2018-07-31	4
2018-08-01	16
2018-08-07	20
2019-06-18	4
2019-06-26	20
2019-07-08	20
2019-07-12	4
2019-07-17	4

```

2019-07-18 16
2019-07-21 8
2019-07-22 2
2019-07-23 8
2019-07-29 16
2019-07-30 4
2019-08-06 4
2019-08-08 16
2019-08-12 4
2019-08-19 4

```

3.3 Select samples

Check for assay specific sample selection column (assay name)

```

> .aName
[1] "_A_01_Desc-R"
> selectId <- substr(gsub("-", ".", .aName), 2, nchar(.aName))
> #selectId <- .vzorci
> selectId
[1] "A_01_Desc.R"
> #
> if(selectId %in% names(phdata)){
+ pdata <- phdata[!is.na(phdata[, selectId]), ]
+ cat("Sample selection column found (", selectId, ")\n",
+ nrow(pdata), "samples will be used.\n")
+ } else {
+ pdata <- phdata
+ cat("No sample selection column found,\n",
+ nrow(pdata), "samples will be used.\n")
+ }
No sample selection column found,
 270 samples will be used.
> dim(pdata)
[1] 270 22

```

Table of sample conditions

```

> head(pdata[, factors])
      variety year day treat rep
C18_11d_WS1      C   18  11    WS   1
C18_11d_WS2      C   18  11    WS   2
C18_11d_WS3      C   18  11    WS   3
C18_11d_WS4      C   18  11    WS   4
C18_11d_WW1      C   18  11    WW   1
C18_11d_WW2      C   18  11    WW   2
> for(yr in levels(pdata$year)){
+ cat("\n\nYear: ", yr, "\n")
+ print(
+ with(pdata[pdata$year==yr, ], ftable(treat, variety, factor(day)))
+ )
+ }

```

Year: 18

		3	11	14	20	28	33	34	39	45	49	52	60	61	67
treat	variety														
WW	C	1	4	1	5	1	1	4	1	1	4	1	1	4	5
	F	1	4	1	5	1	1	4	1	1	4	1	1	4	5
WS	C	1	4	1	5	1	1	4	1	1	4	1	1	4	5
	F	1	4	1	5	1	1	4	1	1	4	1	1	4	5

Year: 19

		14	22	34	38	43	44	47	48	49	55	56	63	65	69	76
treat	variety															
WW	C	1	5	5	1	1	4	0	0	4	4	1	1	4	1	1
	F	1	5	5	1	1	4	4	1	0	4	1	1	4	1	1
WS	C	1	5	5	1	1	4	0	0	4	4	1	1	4	1	1
	F	1	5	5	1	1	4	4	1	0	4	1	1	4	1	1

> my.summary(pdata)

ID	Variety	Date	variety	
C18_11d_WS1: 1	Cabernet Volos:134	21.06.2018: 20	C:134	
C18_11d_WS2: 1	Fleurtai :136	26.06.2019: 20	F:136	
C18_11d_WS3: 1		7.08.2018 : 20		
C18_11d_WS4: 1		8.07.2019 : 20		
C18_11d_WW1: 1		1.08.2018 : 16		
C18_11d_WW2: 1		18.07.2019: 16		
(Other) :264		(Other) :158		
year	day	treat	rep	project.name
18:136	34 : 36	WW:135	1 :48	EnViros:270
19:134	49 : 24	WS:135	2 :48	
	20 : 20		3 :48	
	22 : 20		4 :48	
	67 : 20		NA's:78	
	11 : 16			
	(Other):134			
species	plant.name	tissue	health.status	
Vitis vinifera:270	grapevine:270	: 78	water stress:134	
		leaf:192	well watered:136	

plant.number	growth.location	growth.conditions
:78	Udine:270	outside:270
R1:48		
R2:48		
R3:48		
R4:48		

several leaves ground together and stored at -80°C ; an aliquot was received f

Metabolites.Order	Metabolites.File.Name
2 : 2	: 80
3 : 2	1019Cabernet Volos_6_12_WS1.D: 1
4 : 2	1019Cabernet Volos_6_12_WS2.D: 1
5 : 2	1019Cabernet Volos_6_12_WW1.D: 1
6 : 2	1019Cabernet Volos_6_12_WW2.D: 1
(Other):180	1019Cabernet Volos_6_21_WS1.D: 1
NA's : 80	(Other):185

Metabolites.File	Transcripts.ID	date
: 80	:190	2018-06-21: 20
Cabernet Volos08_07WS: 4	C1_S1 : 1	2018-08-07: 20
Cabernet Volos08_07WW: 4	C1_S2 : 1	2019-06-26: 20
Cabernet Volos08_08WS: 4	C1_S3 : 1	2019-07-08: 20
Cabernet Volos08_08WW: 4	C1_S4 : 1	2018-07-05: 16
Cabernet Volos18_07WS: 4	C1_W1 : 1	2018-07-20: 16
(Other):170	(Other): 75	(Other):158

For separate yearly analyses, it will be handy to have two, separate phenodata objects.

```
> dim(pdata)
[1] 270 22
> table(pdata$year)

18 19
136 134
> pdata18 <- pdata[pdata$year==18,]
> dim(pdata18)
[1] 136 22
> pdata18[1:5,1:6]
      ID      Variety      Date variety year day
C18_11d_WS1 C18_11d_WS1 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WS2 C18_11d_WS2 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WS3 C18_11d_WS3 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WS4 C18_11d_WS4 Cabernet Volos 12.06.2018      C    18 11
C18_11d_WW1 C18_11d_WW1 Cabernet Volos 12.06.2018      C    18 11
> #
> pdata19 <- pdata[pdata$year==19,]
> dim(pdata19)
[1] 134 22
> pdata19[1:5,1:6]
      ID      Variety      Date variety year day
C19_22d_WS1 C19_22d_WS1 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WS2 C19_22d_WS2 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WS3 C19_22d_WS3 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WS4 C19_22d_WS4 Cabernet Volos 26.06.2019      C    19 22
C19_22d_WW1 C19_22d_WW1 Cabernet Volos 26.06.2019      C    19 22
```

3.4 Featuredata

```
> (ffn <- getDesc(.adesc, "Featuredata"))
[1] "Transcripts1819-02.txt"
> if(ffn=="") {
+ cat("No feature data declared in the assay metadata file.\\\\"")
+ fdata <- NULL
+ }

> fdata <- read.table(file.path(.iroot, ffn)
+ , sep = "\t"
+ , header = TRUE
+ , na.strings = c("", "-", "NA")
+ , stringsAsFactors = FALSE
+ , quote = "\"",
+ # , row.names = 1
+ )
> if(interactive()) my.summary(fdata)
> #"
```

Some genes are listed more than once. Is it OK? Column geneID can not be used as row names.

```
> tbl <- table(fdata$geneID)
> tbl[tbl>3]
named integer(0)
> tbl[tbl==3]
```

```
Vitvi01g01443 Vitvi03g00845 Vitvi04g02157 Vitvi05g01641 Vitvi06g01689
      3          3          3          3          3
Vitvi07g01861 Vitvi08g01514 Vitvi08g01692 Vitvi08g02189 Vitvi12g01199
      3          3          3          3          3
Vitvi16g00114 Vitvi17g01011 Vitvi19g00061 Vitvi19g01931 Vitvi19g01936
      3          3          3          3          3
Vitvi19g01964
      3
```

```
> tbl[tbl==2]
```

```
Vitvi00g00711 Vitvi00g00822 Vitvi00g00983 Vitvi00g01149 Vitvi00g01320
      2          2          2          2          2
Vitvi00g01329 Vitvi00g01996 Vitvi00g01999 Vitvi00g02041 Vitvi01g00036
      2          2          2          2          2
Vitvi01g00137 Vitvi01g00165 Vitvi01g00274 Vitvi01g00301 Vitvi01g00348
      2          2          2          2          2
Vitvi01g00373 Vitvi01g00397 Vitvi01g00398 Vitvi01g00417 Vitvi01g00478
      2          2          2          2          2
Vitvi01g00553 Vitvi01g00625 Vitvi01g00681 Vitvi01g00696 Vitvi01g00793
      2          2          2          2          2
Vitvi01g00814 Vitvi01g00828 Vitvi01g00861 Vitvi01g00885 Vitvi01g00993
      2          2          2          2          2
Vitvi01g01351 Vitvi01g01436 Vitvi01g01632 Vitvi01g01645 Vitvi01g01671
      2          2          2          2          2
```

Vitvi01g01773	Vitvi01g01814	Vitvi01g01956	Vitvi01g01982	Vitvi01g02258
2	2	2	2	2
Vitvi01g02269	Vitvi02g00007	Vitvi02g00023	Vitvi02g00085	Vitvi02g00187
2	2	2	2	2
Vitvi02g00220	Vitvi02g00222	Vitvi02g00278	Vitvi02g00380	Vitvi02g00387
2	2	2	2	2
Vitvi02g00485	Vitvi02g00561	Vitvi02g00739	Vitvi02g01143	Vitvi02g01273
2	2	2	2	2
Vitvi02g01365	Vitvi02g01416	Vitvi02g01458	Vitvi02g01751	Vitvi03g00042
2	2	2	2	2
Vitvi03g00059	Vitvi03g00097	Vitvi03g00121	Vitvi03g00167	Vitvi03g00273
2	2	2	2	2
Vitvi03g00278	Vitvi03g00375	Vitvi03g00432	Vitvi03g00442	Vitvi03g00464
2	2	2	2	2
Vitvi03g00521	Vitvi03g00532	Vitvi03g00537	Vitvi03g00541	Vitvi03g00757
2	2	2	2	2
Vitvi03g00785	Vitvi03g00804	Vitvi03g00855	Vitvi03g00900	Vitvi03g00936
2	2	2	2	2
Vitvi03g01059	Vitvi03g01228	Vitvi03g01320	Vitvi04g00092	Vitvi04g00112
2	2	2	2	2
Vitvi04g00113	Vitvi04g00127	Vitvi04g00199	Vitvi04g00205	Vitvi04g00227
2	2	2	2	2
Vitvi04g00279	Vitvi04g00314	Vitvi04g00371	Vitvi04g00450	Vitvi04g00483
2	2	2	2	2
Vitvi04g00520	Vitvi04g00888	Vitvi04g01149	Vitvi04g01257	Vitvi04g01359
2	2	2	2	2
Vitvi04g01462	Vitvi04g01469	Vitvi04g01474	Vitvi04g01560	Vitvi04g01624
2	2	2	2	2
Vitvi04g01633	Vitvi04g01668	Vitvi04g01671	Vitvi04g01694	Vitvi04g01695
2	2	2	2	2
Vitvi04g01709	Vitvi04g01746	Vitvi04g01763	Vitvi04g02022	Vitvi04g02037
2	2	2	2	2
Vitvi04g02038	Vitvi04g02099	Vitvi04g02114	Vitvi04g02185	Vitvi05g00115
2	2	2	2	2
Vitvi05g00132	Vitvi05g00144	Vitvi05g00210	Vitvi05g00239	Vitvi05g00390
2	2	2	2	2
Vitvi05g00409	Vitvi05g00418	Vitvi05g00436	Vitvi05g00443	Vitvi05g00503
2	2	2	2	2
Vitvi05g00541	Vitvi05g00556	Vitvi05g00652	Vitvi05g00737	Vitvi05g00790
2	2	2	2	2
Vitvi05g00953	Vitvi05g00991	Vitvi05g01068	Vitvi05g01130	Vitvi05g01255
2	2	2	2	2
Vitvi05g01369	Vitvi05g01562	Vitvi05g01570	Vitvi05g01603	Vitvi05g01634
2	2	2	2	2
Vitvi05g02135	Vitvi06g00022	Vitvi06g00089	Vitvi06g00200	Vitvi06g00201
2	2	2	2	2
Vitvi06g00212	Vitvi06g00213	Vitvi06g00215	Vitvi06g00243	Vitvi06g00259
2	2	2	2	2
Vitvi06g00319	Vitvi06g00337	Vitvi06g00356	Vitvi06g00365	Vitvi06g00414
2	2	2	2	2
Vitvi06g00439	Vitvi06g00443	Vitvi06g00454	Vitvi06g00472	Vitvi06g00512
2	2	2	2	2
Vitvi06g00525	Vitvi06g00533	Vitvi06g00652	Vitvi06g00668	Vitvi06g00701

2	2	2	2	2
Vitvi06g00789	Vitvi06g01242	Vitvi06g01279	Vitvi06g01469	Vitvi06g01486
2	2	2	2	2
Vitvi06g01604	Vitvi06g01690	Vitvi06g01693	Vitvi06g01718	Vitvi06g01739
2	2	2	2	2
Vitvi06g01836	Vitvi07g00067	Vitvi07g00078	Vitvi07g00080	Vitvi07g00205
2	2	2	2	2
Vitvi07g00316	Vitvi07g00406	Vitvi07g00416	Vitvi07g00464	Vitvi07g00594
2	2	2	2	2
Vitvi07g00630	Vitvi07g00636	Vitvi07g00708	Vitvi07g00908	Vitvi07g00916
2	2	2	2	2
Vitvi07g01028	Vitvi07g01205	Vitvi07g01306	Vitvi07g01340	Vitvi07g01364
2	2	2	2	2
Vitvi07g01402	Vitvi07g01441	Vitvi07g01524	Vitvi07g01569	Vitvi07g01737
2	2	2	2	2
Vitvi07g01749	Vitvi07g01817	Vitvi07g01903	Vitvi07g01937	Vitvi07g01973
2	2	2	2	2
Vitvi07g01983	Vitvi07g01996	Vitvi07g02049	Vitvi07g02102	Vitvi07g02119
2	2	2	2	2
Vitvi07g02123	Vitvi07g02135	Vitvi07g02302	Vitvi07g02394	Vitvi07g02412
2	2	2	2	2
Vitvi07g02447	Vitvi07g02491	Vitvi07g02523	Vitvi07g02528	Vitvi07g02557
2	2	2	2	2
Vitvi07g02631	Vitvi07g02863	Vitvi07g03034	Vitvi07g03040	Vitvi07g03070
2	2	2	2	2
Vitvi07g03110	Vitvi08g00215	Vitvi08g00703	Vitvi08g00740	Vitvi08g00744
2	2	2	2	2
Vitvi08g00799	Vitvi08g00853	Vitvi08g00935	Vitvi08g00961	Vitvi08g00981
2	2	2	2	2
Vitvi08g00983	Vitvi08g00999	Vitvi08g01042	Vitvi08g01082	Vitvi08g01108
2	2	2	2	2
Vitvi08g01206	Vitvi08g01241	Vitvi08g01243	Vitvi08g01302	Vitvi08g01346
2	2	2	2	2
Vitvi08g01376	Vitvi08g01395	Vitvi08g01417	Vitvi08g01506	Vitvi08g01513
2	2	2	2	2
Vitvi08g01519	Vitvi08g01766	Vitvi08g01833	Vitvi08g01864	Vitvi08g01884
2	2	2	2	2
Vitvi08g01931	Vitvi08g01959	Vitvi08g02249	Vitvi08g02367	Vitvi08g02413
2	2	2	2	2
Vitvi09g00067	Vitvi09g00156	Vitvi09g00233	Vitvi09g00239	Vitvi09g00243
2	2	2	2	2
Vitvi09g00249	Vitvi09g00253	Vitvi09g00258	Vitvi09g00277	Vitvi09g00292
2	2	2	2	2
Vitvi09g00297	Vitvi09g00446	Vitvi09g00490	Vitvi09g00653	Vitvi09g00675
2	2	2	2	2
Vitvi09g00816	Vitvi09g00861	Vitvi09g01320	Vitvi09g01500	Vitvi09g01555
2	2	2	2	2
Vitvi09g01556	Vitvi09g01557	Vitvi09g01559	Vitvi09g01930	Vitvi09g01933
2	2	2	2	2
Vitvi09g02012	Vitvi10g00078	Vitvi10g00087	Vitvi10g00125	Vitvi10g00154
2	2	2	2	2
Vitvi10g00219	Vitvi10g00290	Vitvi10g00303	Vitvi10g00316	Vitvi10g00317
2	2	2	2	2

Vitvi10g00336	Vitvi10g00365	Vitvi10g00457	Vitvi10g00554	Vitvi10g00582
2	2	2	2	2
Vitvi10g00605	Vitvi10g00635	Vitvi10g00662	Vitvi10g00663	Vitvi10g00784
2	2	2	2	2
Vitvi10g01029	Vitvi10g01098	Vitvi10g02139	Vitvi10g02141	Vitvi10g02143
2	2	2	2	2
Vitvi10g02151	Vitvi10g02152	Vitvi10g02155	Vitvi10g02157	Vitvi10g02322
2	2	2	2	2
Vitvi10g02324	Vitvi10g02368	Vitvi10g02370	Vitvi10g02408	Vitvi11g00001
2	2	2	2	2
Vitvi11g00068	Vitvi11g00102	Vitvi11g00136	Vitvi11g00137	Vitvi11g00198
2	2	2	2	2
Vitvi11g00270	Vitvi11g00339	Vitvi11g00360	Vitvi11g00480	Vitvi11g00517
2	2	2	2	2
Vitvi11g00597	Vitvi11g00614	Vitvi11g00692	Vitvi11g00724	Vitvi11g00812
2	2	2	2	2
Vitvi11g00865	Vitvi11g01141	Vitvi11g01176	Vitvi12g00021	Vitvi12g00032
2	2	2	2	2
Vitvi12g00089	Vitvi12g00121	Vitvi12g00157	Vitvi12g00220	Vitvi12g00229
2	2	2	2	2
Vitvi12g00284	Vitvi12g00596	Vitvi12g00598	Vitvi12g00606	Vitvi12g00615
2	2	2	2	2
Vitvi12g00628	Vitvi12g00646	Vitvi12g00689	Vitvi12g00691	Vitvi12g00694
2	2	2	2	2
Vitvi12g00837	Vitvi12g01277	Vitvi12g01467	Vitvi12g01780	Vitvi12g01840
2	2	2	2	2
Vitvi12g01863	Vitvi12g01897	Vitvi12g01952	Vitvi12g02074	Vitvi12g02434
2	2	2	2	2
Vitvi12g02435	Vitvi12g02440	Vitvi13g00019	Vitvi13g00031	Vitvi13g00053
2	2	2	2	2
Vitvi13g00095	Vitvi13g00096	Vitvi13g00111	Vitvi13g00149	Vitvi13g00288
2	2	2	2	2
Vitvi13g00328	Vitvi13g00332	Vitvi13g00334	Vitvi13g00344	Vitvi13g00510
2	2	2	2	2
Vitvi13g00627	Vitvi13g00628	Vitvi13g00636	Vitvi13g00637	Vitvi13g00700
2	2	2	2	2
Vitvi13g00744	Vitvi13g01070	Vitvi13g01077	Vitvi13g01233	Vitvi13g01272
2	2	2	2	2
Vitvi13g01327	Vitvi13g01364	Vitvi13g01839	Vitvi13g01854	Vitvi13g02272
2	2	2	2	2
Vitvi14g00020	Vitvi14g00025	Vitvi14g00053	Vitvi14g00160	Vitvi14g00185
2	2	2	2	2
Vitvi14g00237	Vitvi14g00281	Vitvi14g00327	Vitvi14g00380	Vitvi14g00383
2	2	2	2	2
Vitvi14g00397	Vitvi14g00404	Vitvi14g00439	Vitvi14g00484	Vitvi14g00535
2	2	2	2	2
Vitvi14g00562	Vitvi14g00627	Vitvi14g00654	Vitvi14g00658	Vitvi14g00763
2	2	2	2	2
Vitvi14g00841	Vitvi14g01061	Vitvi14g01128	Vitvi14g01280	Vitvi14g01294
2	2	2	2	2
Vitvi14g01321	Vitvi14g01472	Vitvi14g01520	Vitvi14g01596	Vitvi14g01678
2	2	2	2	2
Vitvi14g01746	Vitvi14g01758	Vitvi14g01809	Vitvi14g01983	Vitvi14g02002

2	2	2	2	2
Vitvi14g02027	Vitvi14g02478	Vitvi14g02644	Vitvi14g02869	Vitvi15g00225
2	2	2	2	2
Vitvi15g00526	Vitvi15g00563	Vitvi15g00690	Vitvi15g00827	Vitvi15g00840
2	2	2	2	2
Vitvi15g00878	Vitvi15g00908	Vitvi15g00974	Vitvi15g01077	Vitvi15g01403
2	2	2	2	2
Vitvi15g01468	Vitvi15g01491	Vitvi15g01537	Vitvi15g01539	Vitvi16g00018
2	2	2	2	2
Vitvi16g00048	Vitvi16g00095	Vitvi16g00461	Vitvi16g00796	Vitvi16g00857
2	2	2	2	2
Vitvi16g00935	Vitvi16g00949	Vitvi16g00982	Vitvi16g01025	Vitvi16g01083
2	2	2	2	2
Vitvi16g01089	Vitvi16g01211	Vitvi16g01323	Vitvi16g01326	Vitvi16g01348
2	2	2	2	2
Vitvi16g01358	Vitvi16g01371	Vitvi16g01375	Vitvi16g01391	Vitvi17g00038
2	2	2	2	2
Vitvi17g00161	Vitvi17g00210	Vitvi17g00222	Vitvi17g00225	Vitvi17g00240
2	2	2	2	2
Vitvi17g00253	Vitvi17g00263	Vitvi17g00277	Vitvi17g00287	Vitvi17g00299
2	2	2	2	2
Vitvi17g00428	Vitvi17g00468	Vitvi17g00519	Vitvi17g00548	Vitvi17g00603
2	2	2	2	2
Vitvi17g00614	Vitvi17g00869	Vitvi17g00905	Vitvi17g01148	Vitvi17g01183
2	2	2	2	2
Vitvi17g01348	Vitvi17g01399	Vitvi17g01407	Vitvi18g00056	Vitvi18g00132
2	2	2	2	2
Vitvi18g00177	Vitvi18g00234	Vitvi18g00310	Vitvi18g00358	Vitvi18g00444
2	2	2	2	2
Vitvi18g00507	Vitvi18g00517	Vitvi18g00534	Vitvi18g00579	Vitvi18g00743
2	2	2	2	2
Vitvi18g00762	Vitvi18g00784	Vitvi18g00838	Vitvi18g00909	Vitvi18g00960
2	2	2	2	2
Vitvi18g00966	Vitvi18g01002	Vitvi18g01004	Vitvi18g01019	Vitvi18g01095
2	2	2	2	2
Vitvi18g01103	Vitvi18g01223	Vitvi18g01226	Vitvi18g01242	Vitvi18g01299
2	2	2	2	2
Vitvi18g01309	Vitvi18g01430	Vitvi18g01436	Vitvi18g01634	Vitvi18g01677
2	2	2	2	2
Vitvi18g02066	Vitvi18g02228	Vitvi18g02237	Vitvi18g02378	Vitvi18g03244
2	2	2	2	2
Vitvi19g00015	Vitvi19g00020	Vitvi19g00094	Vitvi19g00138	Vitvi19g00155
2	2	2	2	2
Vitvi19g00197	Vitvi19g00226	Vitvi19g00337	Vitvi19g00339	Vitvi19g00341
2	2	2	2	2
Vitvi19g00353	Vitvi19g00421	Vitvi19g00531	Vitvi19g00539	Vitvi19g00552
2	2	2	2	2
Vitvi19g00602	Vitvi19g00612	Vitvi19g00621	Vitvi19g00675	Vitvi19g00706
2	2	2	2	2
Vitvi19g00745	Vitvi19g00782	Vitvi19g00904	Vitvi19g00928	Vitvi19g01352
2	2	2	2	2
Vitvi19g01464	Vitvi19g01552	Vitvi19g01690	Vitvi19g01692	Vitvi19g01725
2	2	2	2	2

Vitvi19g01864	Vitvi19g01933	Vitvi19g01937	Vitvi19g01940	Vitvi19g01952
2	2	2	2	2
Vitvi19g01957	Vitvi19g01959	Vitvi19g01963	Vitvi19g01965	Vitvi19g01966
2	2	2	2	2
Vitvi19g01969	Vitvi19g01970	Vitvi19g02001	Vitvi19g02292	
2	2	2	2	

A glimpse into feature data (or NULL if nonexistent)

```
> fdata[1:6,]
```

	YEAR	geneID	BINCODE	NAME
1	2018	Vitvi15g01736	26.9	misc.glutathione S transferases
2	2018	Vitvi07g02832	35.2	not assigned.unknown
3	2018	Vitvi07g02830	35.2	not assigned.unknown
4	2018	Vitvi07g02812	35.2	not assigned.unknown
5	2018	Vitvi07g02811	35.2	not assigned.unknown
6	2018	Vitvi09g02033	35.2	not assigned.unknown

```
1          glutathione S-transferase tau 7 | Chr2:12618111-12618871
2 Disease resistance protein (TIR-NBS-LRR class) family | Chr4:7197325-7201393
3
4
5
```

```
6 Disease resistance protein (CC-NBS-LRR class) family | Chr1:4145374-4147680
```

```
> cat(gsub("\\| ", " |\\n\\|\\t", fdata$DESCRIPTION[1:6]), sep="\n\n")
```

```
glutathione S-transferase tau 7 |
      Chr2:12618111-12618871 REVERSE LENGTH=227 |
      201606
```

```
Disease resistance protein (TIR-NBS-LRR class) family |
      Chr4:7197325-7201393 REVERSE LENGTH=1219 |
      201606
```

```
NA
```

```
Tir-nbs-lrr, resistance protein
```

```
NA
```

```
Disease resistance protein (CC-NBS-LRR class) family |
      Chr1:4145374-4147680 FORWARD LENGTH=768 |
      201606
```

```
> fd <- (apply(fdata[1:6, c(2:5)], 1, paste, collapse="\n\t"))
```

```
> cat(gsub("\\| ", " |\\n\\|\\t", fd[1:6]), sep="\n\n")
```

```
Vitvi15g01736
      26.9
      misc.glutathione S transferases
      glutathione S-transferase tau 7 |
      Chr2:12618111-12618871 REVERSE LENGTH=227 |
      201606
```

```
Vitvi07g02832
      35.2
```

```

not assigned.unknown
Disease resistance protein (TIR-NBS-LRR class) family |
Chr4:7197325-7201393 REVERSE LENGTH=1219 |
201606

Vitvi07g02830
35.2
not assigned.unknown
NA

Vitvi07g02812
35.2
not assigned.unknown
Tir-nbs-lrr, resistance protein

Vitvi07g02811
35.2
not assigned.unknown
NA

Vitvi09g02033
35.2
not assigned.unknown
Disease resistance protein (CC-NBS-LRR class) family |
Chr1:4145374-4147680 FORWARD LENGTH=768 |
201606

> cat.feature <- function(x,...) {
+ #x <- t(apply(x,1, FUN=function(x) paste(names(x),x,sep=":\t") ))
+ #cat(x)
+ fd <- (apply(x,1,paste,collapse="\n\t"))
+ cat(gsub(" \\| ", " |\\n\\|\\t", fd), sep="\n\n")
+ }
> cat.feature(fdata[1,2:5])
Vitvi15g01736
26.9
misc.glutathione S transferases
glutathione S-transferase tau 7 |
Chr2:12618111-12618871 REVERSE LENGTH=227 |
201606
> cat.feature(fdata[1:2,2:5])
Vitvi15g01736
26.9
misc.glutathione S transferases
glutathione S-transferase tau 7 |
Chr2:12618111-12618871 REVERSE LENGTH=227 |
201606

Vitvi07g02832
35.2
not assigned.unknown
Disease resistance protein (TIR-NBS-LRR class) family |
Chr4:7197325-7201393 REVERSE LENGTH=1219 |
201606

```

3.5 Transcripts measurements

Normalised transcript measurements for each year are available in two separate files. The first few lines contain factor values and are commented out (by a hash). The first effective line is the table header line with sample ids.

3.5.1 Normalized values

Data for year 2018:

```
> (t18fn <- getDesc(.adesc, "Transcript data 18"))
[1] "/input/Transcripts 2018.txt"
> td <- read.table(file.path(.aroot, t18fn),
+   header = TRUE,
+   sep = "\t",
+   row.names = 1
+   )
> head(td)
```

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Vitvi15g01736	4.6646023	4.109897	4.4482203	4.013955
Vitvi07g02832	-2.4786650	-1.601359	-1.4274193	-2.066419
Vitvi07g02830	-1.8506337	-2.218030	-1.0648492	-1.580992
Vitvi07g02812	-0.5805446	-1.266940	-0.3278837	-1.019113
Vitvi07g02811	2.2762225	1.823447	1.9550503	1.648742
Vitvi09g02033	-1.6901691	-2.218030	-2.6498117	-1.449747
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Vitvi15g01736	4.717536	4.154237	4.475261	4.466465
Vitvi07g02832	-2.608485	-1.801183	-1.886474	-3.583384
Vitvi07g02830	-1.544354	-1.405255	-1.755229	-1.381750
Vitvi07g02812	-0.858463	-0.434401	-1.234397	-1.047331
Vitvi07g02811	2.086902	2.105707	2.134837	1.908469
Vitvi09g02033	-2.608485	-1.961648	-3.108866	-4.320350
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Vitvi15g01736	4.400333	4.641164	4.4191231	4.534438
Vitvi07g02832	-5.683146	-2.452000	-4.4274120	-1.876949
Vitvi07g02830	-2.513221	-2.452000	-4.4274120	-2.263972
Vitvi07g02812	-2.875791	-2.693008	-2.5529429	-3.157057
Vitvi07g02811	1.414886	1.409803	0.3970164	1.273993
Vitvi09g02033	-2.513221	-3.345084	-2.1054839	-1.716484
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Vitvi15g01736	4.924801	5.085690	5.3397350	5.263629
Vitvi07g02832	-2.827859	-3.130016	-4.6322874	-3.196388
Vitvi07g02830	-3.190429	-1.545054	-2.1297871	-3.196388
Vitvi07g02812	-2.827859	-1.182484	-3.4098950	-2.303303
Vitvi07g02811	1.517916	1.357250	0.9626591	1.344985
Vitvi09g02033	-4.412821	-3.130016	-2.3103594	-4.418780
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Vitvi15g01736	2.05871733	2.2895026	2.9234830	2.575657
Vitvi07g02832	-5.85417200	-4.4786818	-4.4659691	-2.468738
Vitvi07g02830	-2.15373228	-3.2562893	-3.7290035	-2.709746
Vitvi07g02812	-1.21031581	-2.3632045	-2.3504919	-2.999252
Vitvi07g02811	0.02847105	0.5362686	0.9824914	1.231702
Vitvi09g02033	-4.26920950	-3.7417162	-2.5915000	-3.847249

	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770
Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450

```
> dim(td)
```

```
[1] 16005    48
```

```
> t18 <- td
```

```
> (t19fn <- getDesc(.adesc, "Transcript data 19"))
```

```
[1] "/input/Transcripts 2019.txt"
```

```
> td <- read.table(file.path(.aroot, t19fn),
+   header = TRUE,
+   sep = "\t",
+   row.names = 1
+   )
> head(td)
```

	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi15g01736	5.42	5.35	4.68	4.92
Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Vitvi15g01736	5.84	5.83	4.56	5.23

Vitvi07g02832	2.54	3.14	3.01	2.16
Vitvi07g02830	1.13	2.25	2.18	1.90
Vitvi07g02812	0.99	0.84	0.85	0.22
Vitvi07g02811	2.91	3.10	3.18	2.61
Vitvi09g02033	1.21	1.67	2.52	2.21
	F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4
Vitvi15g01736	5.44	6.13	5.96	6.16
Vitvi07g02832	3.84	3.05	3.89	4.02
Vitvi07g02830	2.74	2.79	2.90	2.88
Vitvi07g02812	1.03	0.93	1.49	1.29
Vitvi07g02811	3.32	2.89	3.35	3.26
Vitvi09g02033	1.99	1.14	1.65	1.29

```
> dim(td)
```

```
[1] 15562    32
```

```
> t19 <- td
```

```
> dim(t18)-dim(t19)
```

```
[1] 443  16
```

Data for year 2018 have more genes than data for year 2019.

```
> allNames <- unique(c(rownames(t18), rownames(t19)))
```

```
> length(allNames)
```

```
[1] 16325
```

```
> sum(allNames %in% rownames(t18))
```

```
[1] 16005
```

```
> sum(allNames %in% rownames(t19))
```

```
[1] 15562
```

```
> tbl <- table(gene.in.18=allNames %in% rownames(t18),
+              gene.in.19=allNames %in% rownames(t19))
> tbl
```

	gene.in.19	
gene.in.18	FALSE	TRUE
FALSE	0	320
TRUE	763	15242

We have complete yearly data on 15242 genes. At the meeting on Nov. 19 we decided to use only the genes in the intersection. This will allow us to use the combined set of data.

3.5.2 Keep genes in the intersection

```
> gene.keep <- (allNames %in% rownames(t18)) & (allNames %in% rownames(t19))
> sum(gene.keep)
[1] 15242
> t18 <- t18[allNames[gene.keep], ]
> t19 <- t19[allNames[gene.keep], ]
> all(rownames(t18) == rownames(t19))
[1] TRUE
> dim(t18)
[1] 15242    48
> dim(t19)
[1] 15242    32
```

Order rows of yearly phenodata according to the sequence of samples (columns) in the measurements.

Year 2018

```
> dim(pdata18)
[1] 136  22
> dim(t18)
[1] 15242    48
> pdata18 <- pdata18[colnames(t18), ]
> dim(pdata18)
[1] 48 22
> dim(t18)
[1] 15242    48
> pdata18[, 4:8]
```

	variety	year	day	treat	rep
C18_11d_WS1	C	18	11	WS	1
C18_11d_WS2	C	18	11	WS	2
C18_11d_WS3	C	18	11	WS	3
C18_11d_WS4	C	18	11	WS	4
C18_11d_WW1	C	18	11	WW	1
C18_11d_WW2	C	18	11	WW	2
C18_11d_WW3	C	18	11	WW	3
C18_11d_WW4	C	18	11	WW	4
C18_34d_WS1	C	18	34	WS	1
C18_34d_WS2	C	18	34	WS	2
C18_34d_WS3	C	18	34	WS	3
C18_34d_WS4	C	18	34	WS	4
C18_34d_WW1	C	18	34	WW	1
C18_34d_WW2	C	18	34	WW	2
C18_34d_WW3	C	18	34	WW	3
C18_34d_WW4	C	18	34	WW	4
C18_67d_WS1	C	18	67	WS	1
C18_67d_WS2	C	18	67	WS	2
C18_67d_WS3	C	18	67	WS	3
C18_67d_WS4	C	18	67	WS	4
C18_67d_WW1	C	18	67	WW	1
C18_67d_WW2	C	18	67	WW	2

C18_67d_WW3	C	18	67	WW	3
C18_67d_WW4	C	18	67	WW	4
F18_10d_WS1	F	18	11	WS	1
F18_10d_WS2	F	18	11	WS	2
F18_10d_WS3	F	18	11	WS	3
F18_10d_WS4	F	18	11	WS	4
F18_10d_WW1	F	18	11	WW	1
F18_10d_WW2	F	18	11	WW	2
F18_10d_WW3	F	18	11	WW	3
F18_10d_WW4	F	18	11	WW	4
F18_34d_WS1	F	18	34	WS	1
F18_34d_WS2	F	18	34	WS	2
F18_34d_WS3	F	18	34	WS	3
F18_34d_WS4	F	18	34	WS	4
F18_34d_WW1	F	18	34	WW	1
F18_34d_WW2	F	18	34	WW	2
F18_34d_WW3	F	18	34	WW	3
F18_34d_WW4	F	18	34	WW	4
F18_67d_WS1	F	18	67	WS	1
F18_67d_WS2	F	18	67	WS	2
F18_67d_WS3	F	18	67	WS	3
F18_67d_WS4	F	18	67	WS	4
F18_67d_WW1	F	18	67	WW	1
F18_67d_WW2	F	18	67	WW	2
F18_67d_WW3	F	18	67	WW	3
F18_67d_WW4	F	18	67	WW	4

```
> all(rownames(pdata18)==colnames(t18))
```

```
[1] TRUE
```

Get rid of unused factors

```
> str(pdata18[,factors])
```

```
'data.frame':      48 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 26 levels "3","11","14",...: 2 2 2 2 2 2 2 2 8 8 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

```
> for (var in factors) pdata18[,var] <- factor(pdata18[,var])
```

```
> str(pdata18[,factors])
```

```
'data.frame':      48 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 1 level "18": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 3 levels "11","34","67": 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

Year 2019

```
> dim(pdata19)
```

```
[1] 134  22
```

```
> dim(t19)
```

```
[1] 15242  32
```

```
> pdata19 <- pdata19[colnames(t19),]
> dim(pdata19)
[1] 32 22
> dim(t19)
[1] 15242 32
> pdata19[,4:9]
```

	variety	year	day	treat	rep	project.name
C19_22d_WS1	C	19	22	WS	1	EnViros
C19_22d_WS2	C	19	22	WS	2	EnViros
C19_22d_WS3	C	19	22	WS	3	EnViros
C19_22d_WS4	C	19	22	WS	4	EnViros
C19_22d_WW1	C	19	22	WW	1	EnViros
C19_22d_WW2	C	19	22	WW	2	EnViros
C19_22d_WW3	C	19	22	WW	3	EnViros
C19_22d_WW4	C	19	22	WW	4	EnViros
C19_44d_WS1	C	19	44	WS	1	EnViros
C19_44d_WS2	C	19	44	WS	2	EnViros
C19_44d_WS3	C	19	44	WS	3	EnViros
C19_44d_WS4	C	19	44	WS	4	EnViros
C19_44d_WW1	C	19	44	WW	1	EnViros
C19_44d_WW2	C	19	44	WW	2	EnViros
C19_44d_WW3	C	19	44	WW	3	EnViros
C19_44d_WW4	C	19	44	WW	4	EnViros
F19_22d_WS1	F	19	22	WS	1	EnViros
F19_22d_WS2	F	19	22	WS	2	EnViros
F19_22d_WS3	F	19	22	WS	3	EnViros
F19_22d_WS4	F	19	22	WS	4	EnViros
F19_22d_WW1	F	19	22	WW	1	EnViros
F19_22d_WW2	F	19	22	WW	2	EnViros
F19_22d_WW3	F	19	22	WW	3	EnViros
F19_22d_WW4	F	19	22	WW	4	EnViros
F19_44d_WS1	F	19	44	WS	1	EnViros
F19_44d_WS2	F	19	44	WS	2	EnViros
F19_44d_WS3	F	19	44	WS	3	EnViros
F19_44d_WS4	F	19	44	WS	4	EnViros
F19_44d_WW1	F	19	44	WW	1	EnViros
F19_44d_WW2	F	19	44	WW	2	EnViros
F19_44d_WW3	F	19	44	WW	3	EnViros
F19_44d_WW4	F	19	44	WW	4	EnViros

```
> all(rownames(pdata19)==colnames(t19))
[1] TRUE
```

Get rid of unused factors levels

```
> str(pdata19[,factors])
```

```
'data.frame':      32 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 2 2 2 2 2 2 2 2 2 2 2 ...
 $ day    : Factor w/ 26 levels "3","11","14",...: 5 5 5 5 5 5 5 5 12 12 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...
```

```

> for (var in factors) pdata19[,var] <- factor(pdata19[,var])
> str(pdata19[,factors])

'data.frame':      32 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 1 level "19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 2 levels "22","44": 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...

> t1819 <- data.frame(t18, t19)
> pdata1819 <- rbind(pdata18, pdata19)
> str(pdata1819[,factors])

'data.frame':      80 obs. of  5 variables:
 $ variety: Factor w/ 2 levels "C","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ year   : Factor w/ 2 levels "18","19": 1 1 1 1 1 1 1 1 1 1 ...
 $ day    : Factor w/ 5 levels "11","34","67",..: 1 1 1 1 1 1 1 1 2 2 ...
 $ treat  : Factor w/ 2 levels "WW","WS": 2 2 2 2 1 1 1 1 2 2 ...
 $ rep    : Factor w/ 4 levels "1","2","3","4": 1 2 3 4 1 2 3 4 1 2 ...

> catln("Sample names ",
+ c("different", "OK")[1+all(rownames(pdata1819)==colnames(t1819))])
Sample names  OK

```

3.6 Metabolite measurements

Normalised transcript measurements for each year are available in two separate files. The first few lines contains variable names

```
> if(.ver==1){  
+ (mfn18 <- getMeta(.adesc, "Metabolite data 18"))  
+ (mfn19 <- getMeta(.adesc, "Metabolite data 19"))  
+ } else {  
+ (mfn18 <- getMeta(.adesc, "Metabolite data 18-2"))  
+ (mfn19 <- getMeta(.adesc, "Metabolite data 19-2"))  
+ }  
[1] "/input/Metabolites_2019-Nor2W_ISTD.txt"
```

Read the metabolomics data

```
> m18 <- read.table(file.path(.aroot, mfn18), sep="\t", header=TRUE)  
> dim(m18)  
[1] 96 60  
> m19 <- read.table(file.path(.aroot, mfn19), sep="\t", header=TRUE)  
> dim(m19)  
[1] 96 60
```

Check consistency of column names

```
> ok <- all(colnames(m18)==colnames(m19))  
> if(ok) {catln("Column names match")} else {  
+   catln("Column names do not match")}
```

Column names match

```
> cbind(names18=colnames(m18), names19=colnames(m19))  
      names18      names19  
[1,] "ID"      "ID"  
[2,] "Variety"  "Variety"  
[3,] "Date"     "Date"  
[4,] "Treat"    "Treat"  
[5,] "Rep"      "Rep"  
[6,] "Alanine"  "Alanine"  
[7,] "Arabinose" "Arabinose"  
[8,] "Ascorbic.acid" "Ascorbic.acid"  
[9,] "Aspartic.acid" "Aspartic.acid"  
[10,] "GABA"     "GABA"  
[11,] "Trans.Caffeic.acid" "Trans.Caffeic.acid"  
[12,] "Catechin" "Catechin"  
[13,] "Citric.acid" "Citric.acid"  
[14,] "Erythronic.acid" "Erythronic.acid"  
[15,] "Ethanolamine" "Ethanolamine"  
[16,] "Fructose"   "Fructose"  
[17,] "Fructose.6.phosphate" "Fructose.6.phosphate"  
[18,] "Fumaric.acid" "Fumaric.acid"  
[19,] "Galactinol"  "Galactinol"  
[20,] "Galactose"   "Galactose"  
[21,] "Gallic.acid" "Gallic.acid"  
[22,] "Gluconic.acid" "Gluconic.acid"
```

[23,]	"Glucopyranose..H2O."	"Glucopyranose..H2O."
[24,]	"Glucose"	"Glucose"
[25,]	"Glutamic.acid"	"Glutamic.acid"
[26,]	"Glyceric.acid"	"Glyceric.acid"
[27,]	"Glycine"	"Glycine"
[28,]	"Hydroquinone"	"Hydroquinone"
[29,]	"Myo.Inostol"	"Myo.Inostol"
[30,]	"Isoleucine"	"Isoleucine"
[31,]	"Leucine"	"Leucine"
[32,]	"Lyxonic.acid"	"Lyxonic.acid"
[33,]	"Maleic.acid"	"Maleic.acid"
[34,]	"Malic.acid"	"Malic.acid"
[35,]	"Malonic.acid"	"Malonic.acid"
[36,]	"Mannose.6.phosphate"	"Mannose.6.phosphate"
[37,]	"Melibiose"	"Melibiose"
[38,]	"Phenylalanine"	"Phenylalanine"
[39,]	"Phosphoric.acid"	"Phosphoric.acid"
[40,]	"Proline"	"Proline"
[41,]	"Putrescine"	"Putrescine"
[42,]	"Pyroglutamic.acid"	"Pyroglutamic.acid"
[43,]	"Quinic.acid"	"Quinic.acid"
[44,]	"X3.caffeoylquinic.acid"	"X3.caffeoylquinic.acid"
[45,]	"Raffinose"	"Raffinose"
[46,]	"Rhamnose"	"Rhamnose"
[47,]	"Ribonic.acid"	"Ribonic.acid"
[48,]	"Ribose"	"Ribose"
[49,]	"Serine"	"Serine"
[50,]	"Shikimic.acid"	"Shikimic.acid"
[51,]	"Succinic.acid"	"Succinic.acid"
[52,]	"Sucrose"	"Sucrose"
[53,]	"Tartaric.acid"	"Tartaric.acid"
[54,]	"Threitol"	"Threitol"
[55,]	"Threonic.acid"	"Threonic.acid"
[56,]	"Threonolactone"	"Threonolactone"
[57,]	"Threonine"	"Threonine"
[58,]	"Uracil"	"Uracil"
[59,]	"Valine"	"Valine"
[60,]	"Xylose"	"Xylose"

Use first column as row names

```
> rownames(m18) <- m18[,1]
> rownames(m19) <- m19[,1]
```

Delete samples with missing values

```
> x <- m18
> num_id <- 6:ncol(x)
> dim(x)
[1] 96 60

> x <- x[apply(!is.na(x[,num_id]),1,all),]
> dim(x)
[1] 96 60
```

```

> m18 <- x

> x <- m19
> num_id <- 6:ncol(x)
> dim(x)
[1] 96 60
> x <- x[apply(!is.na(x[, num_id]), 1, all), ]
> dim(x)
[1] 94 60
> m19 <- x

```

Both years together

```

> m1819 <- rbind(m18, m19)
> dim(m1819)
[1] 190 60
> colnames(m1819)[1:7]
[1] "ID" "Variety" "Date" "Treat" "Rep"
[6] "Alanine" "Arabinose"
> rownames(m1819) <- m1819[, 1]
> head(rownames(m1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> length(rownames(m1819))
[1] 190

```

At some point, we will not need the first five descriptive columns.
Intersection of transcriptomics and metabolomics samples

```

> dim(m1819)
[1] 190 60
> dim(t1819)
[1] 15242 80
> head(colnames(t1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> head(rownames(m1819))
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2"
> sum(colnames(t1819) %in% rownames(m1819))
[1] 80
> sum(rownames(m1819) %in% colnames(t1819))
[1] 80
> all(sort(colnames(t1819)[(colnames(t1819) %in% rownames(m1819))]) ==
+ sort(rownames(m1819)[(rownames(m1819) %in% colnames(t1819))]))
[1] TRUE

> m_num_id <- 6:ncol(m1819)
> colnames(m1819)[-m_num_id]
[1] "ID" "Variety" "Date" "Treat" "Rep"

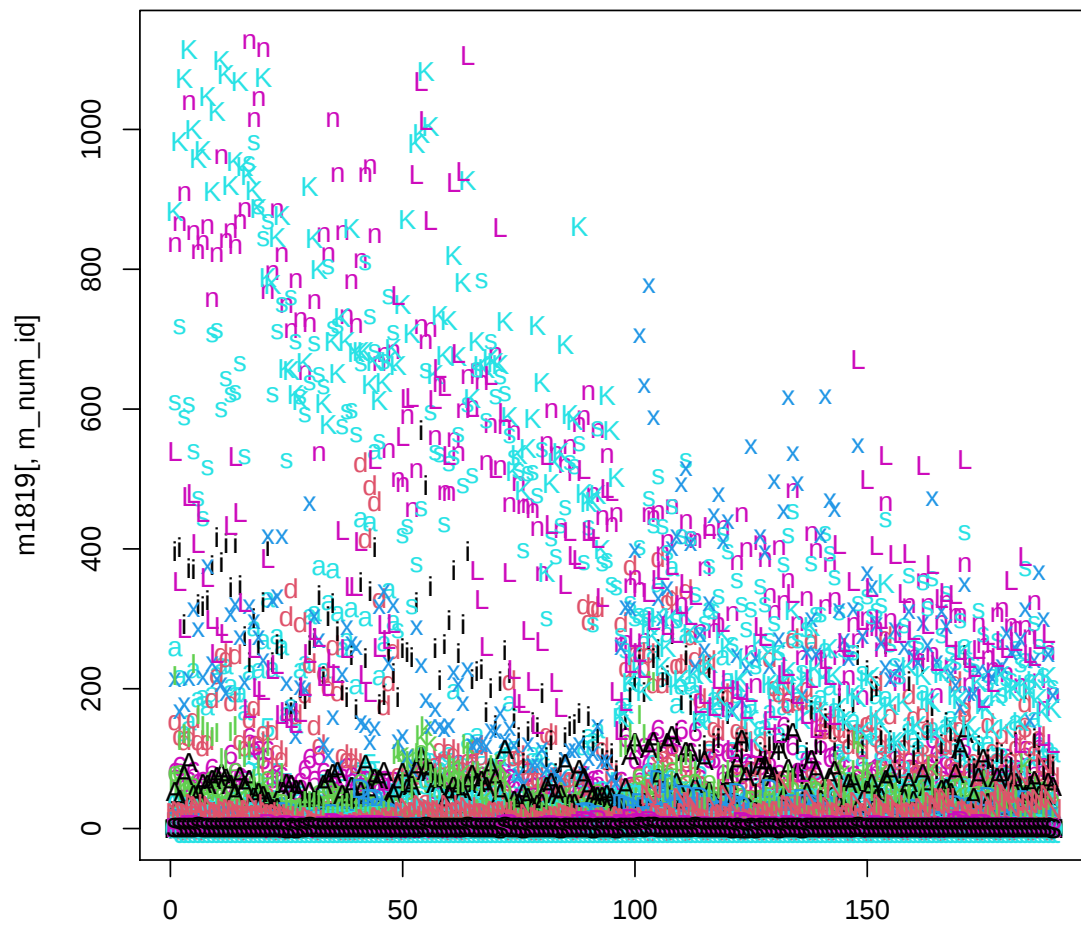
```

We end up with 80 samples

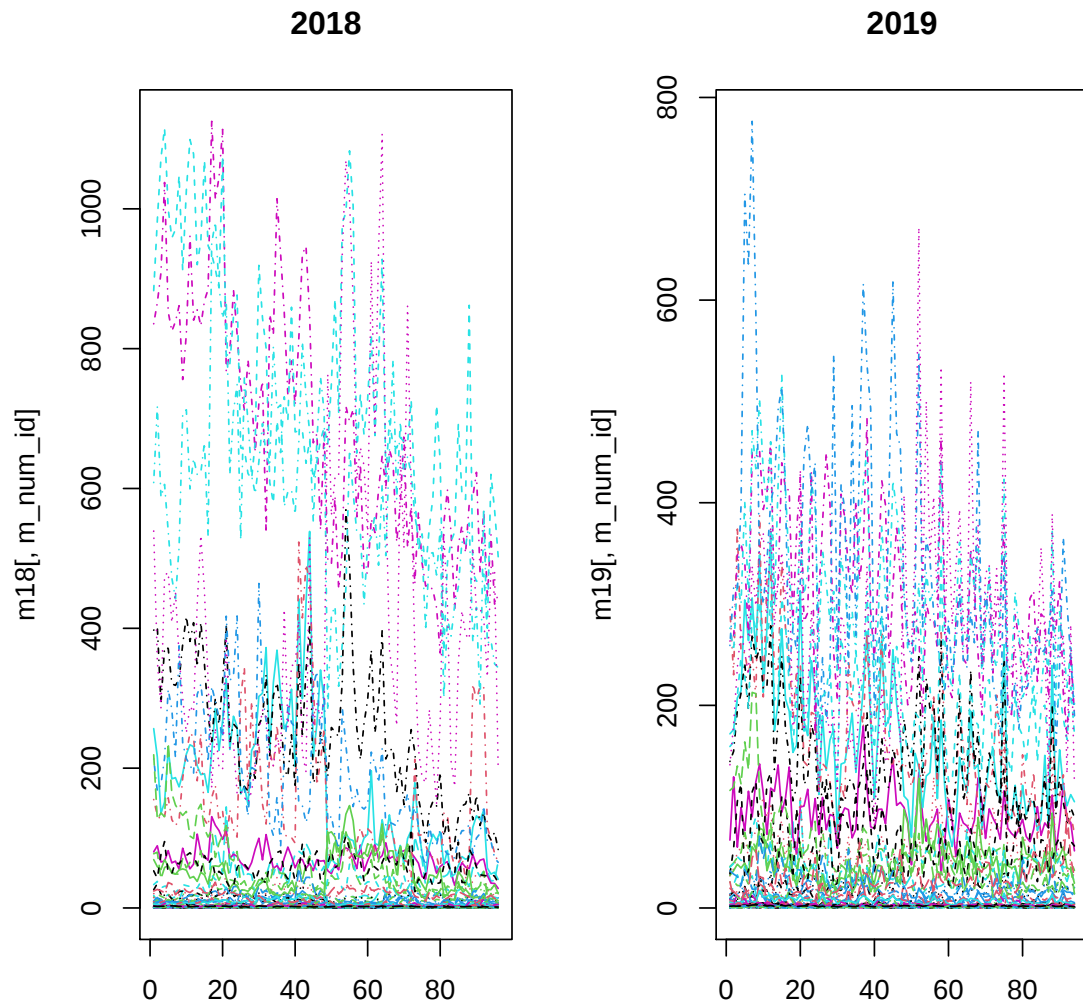
Phenodata for metabolomics data will be prepared when needed from the total phenodata. Selection of needed metabolomics data will be finalized in data analysis scripts.

3.7 Visualize metabolites

```
> matplot(m1819[,m_num_id])
```



```
> par(mfrow=c(1,2))  
> matplot(m18[,m_num_id], main="2018", type="l")  
> matplot(m19[,m_num_id], main="2019", type="l")
```



Median standardization of samples

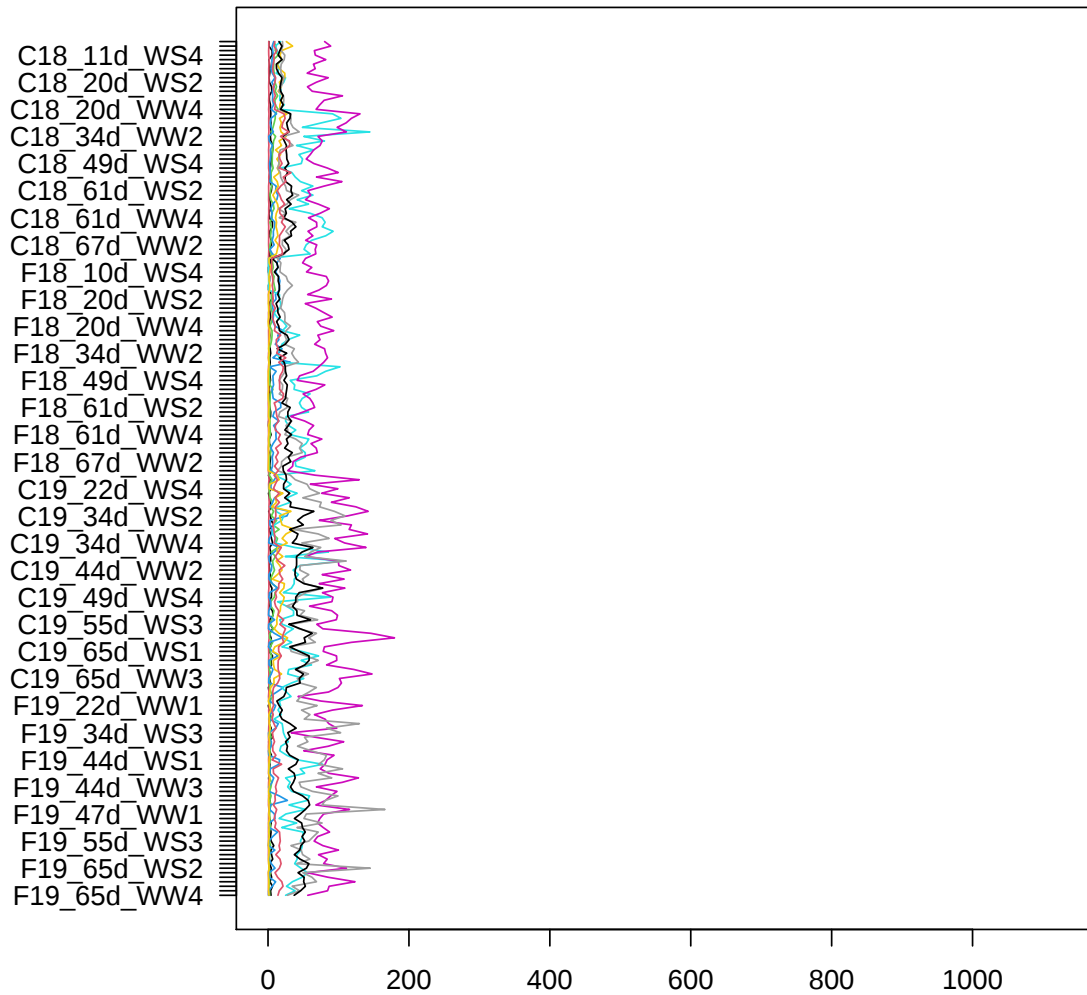
```
> my.parallel <- function(x, m=1:ncol(x), ...){
+ m <- m[m<ncol(x)]
+ par(mar=c(4,8,3,1))
+ xlim <- range(x,na.rm=TRUE)
+ n1 <- nrow(x)
+ plot(0,0,xlim=xlim,ylim=c(n1,1) , type="n", axes=FALSE, ann=FALSE)
+ title(paste(range(m),collapse=":"))
+ axis(1)
+ axis(2,at=1:n1,labels=rownames(x), las=2)
+ box()
+ for(i in m)
+   lines(x[,i],1:n1 , col=i)
+
+ }
> #
> #my.parallel(x)
```

```

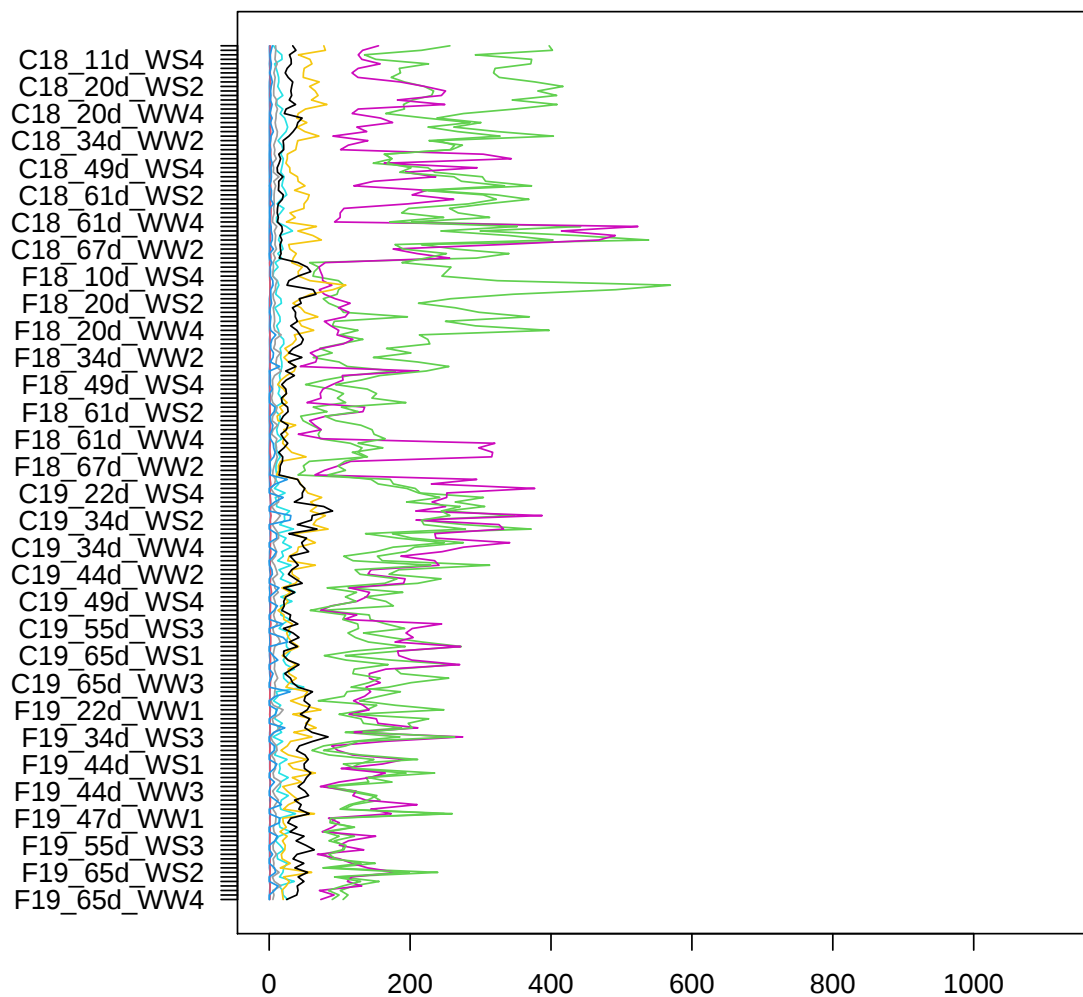
> x <- m1819[,m_num_id]
> for(k in seq(1,ncol(x),10)) {
+   if(interactive()) windows()
+   my.parallel( x, k:(k+9))
+ }

```

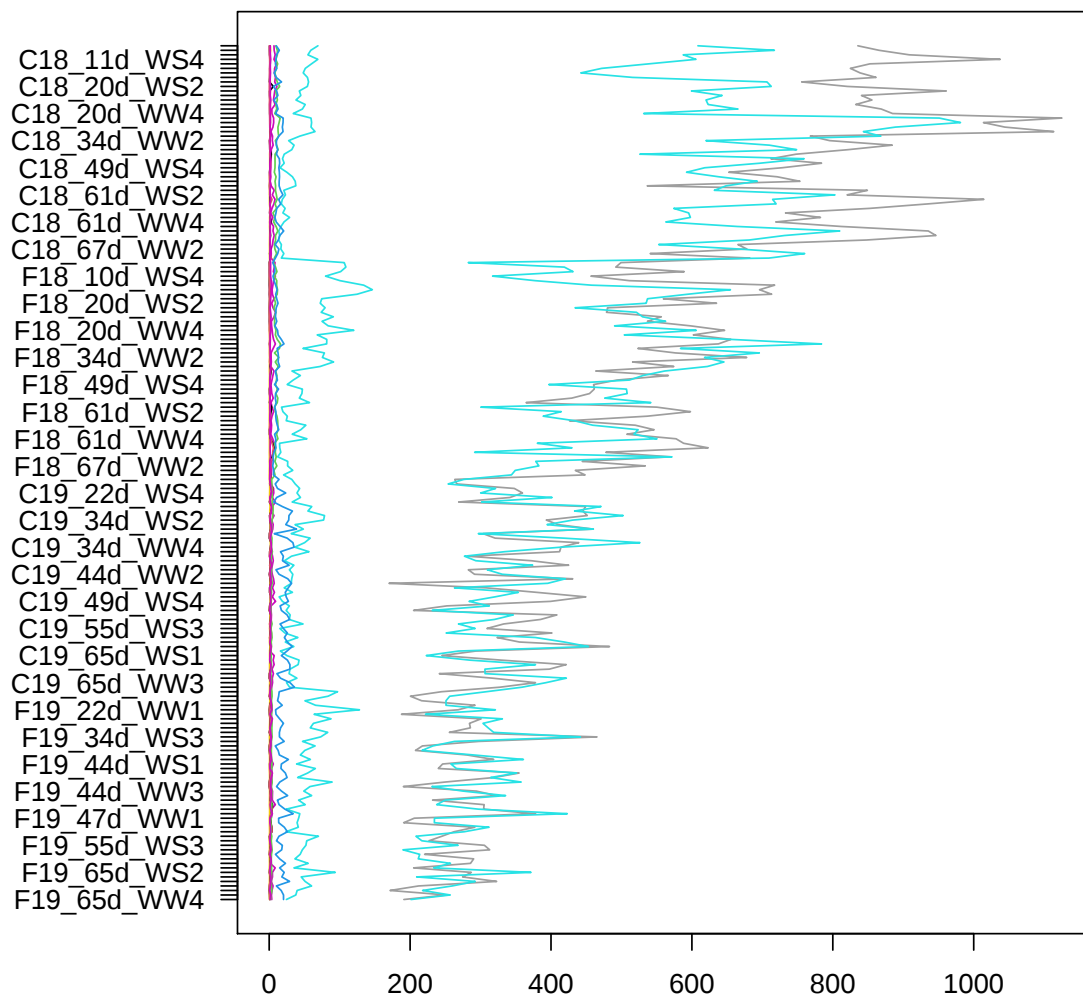
1:10



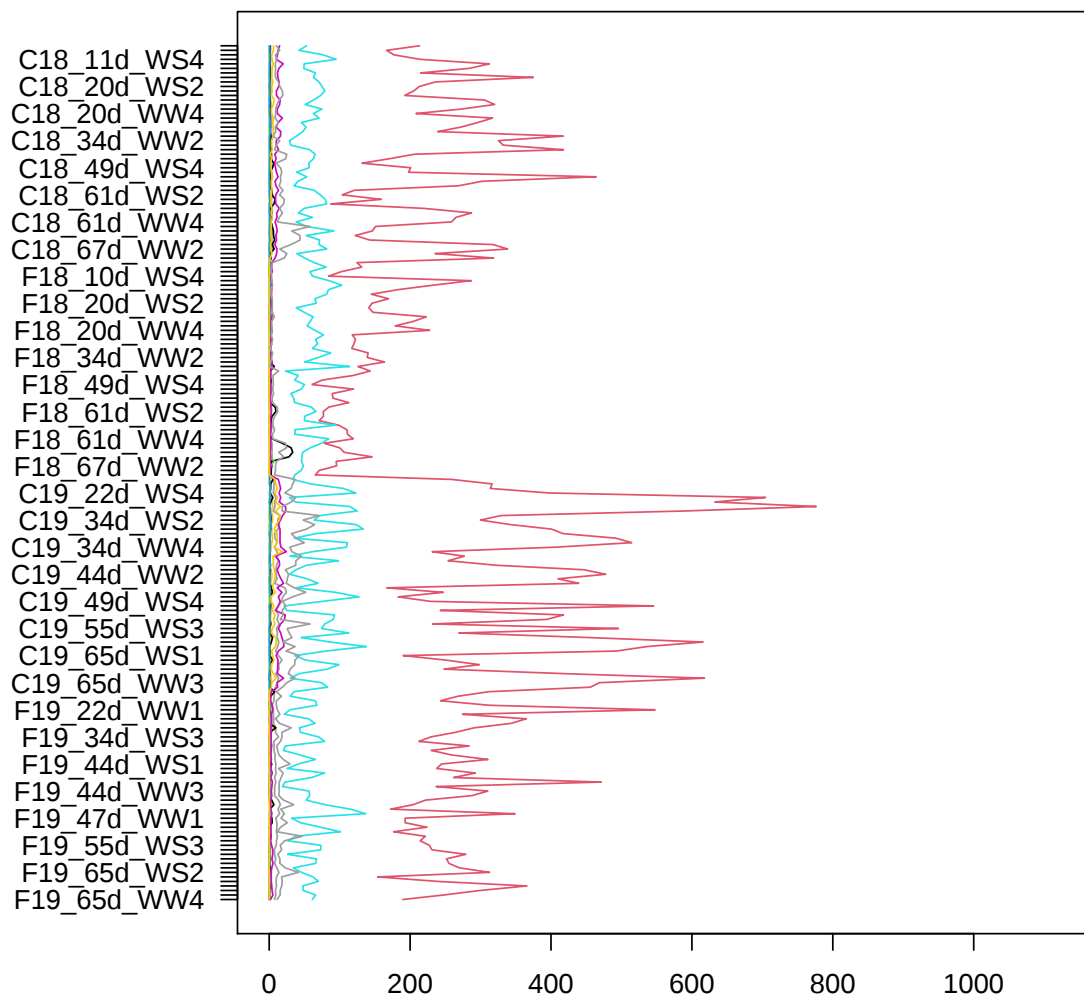
11:20



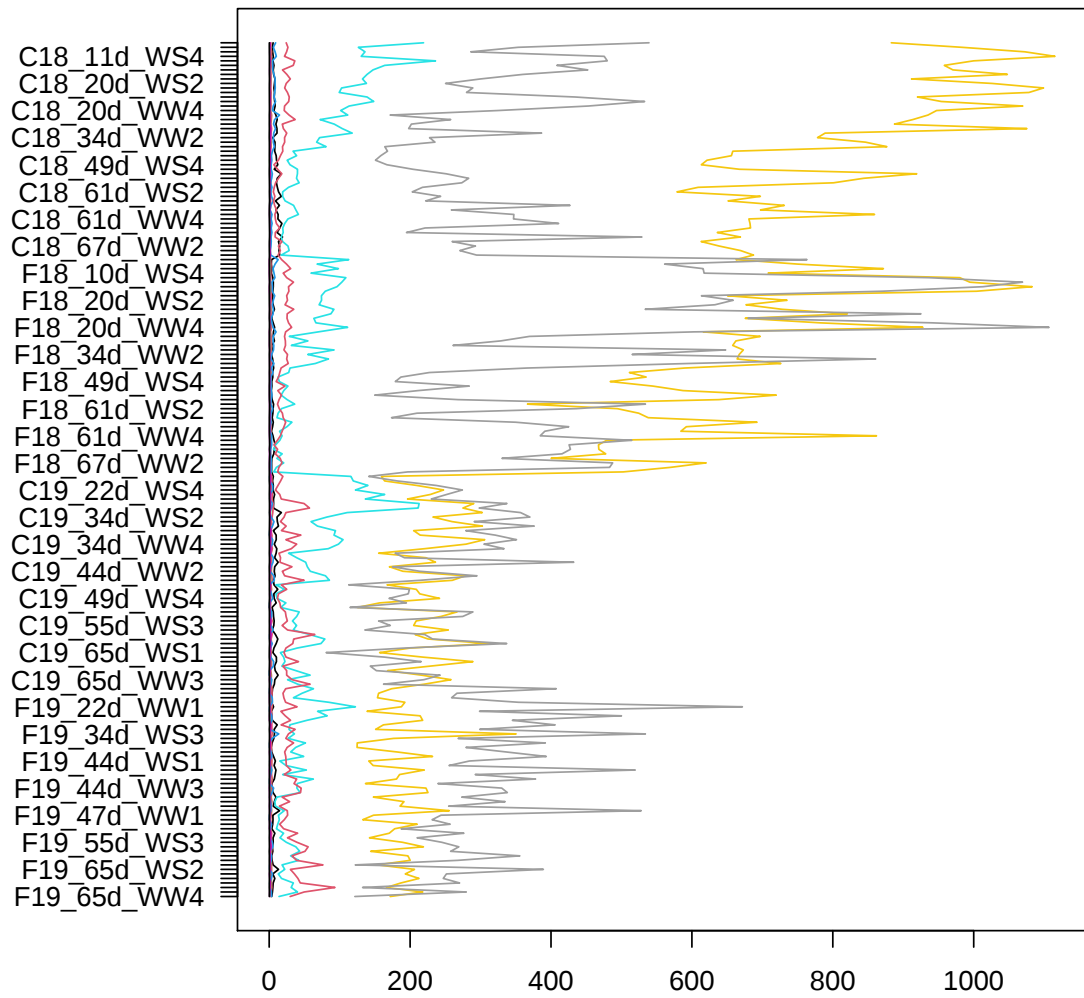
21:30



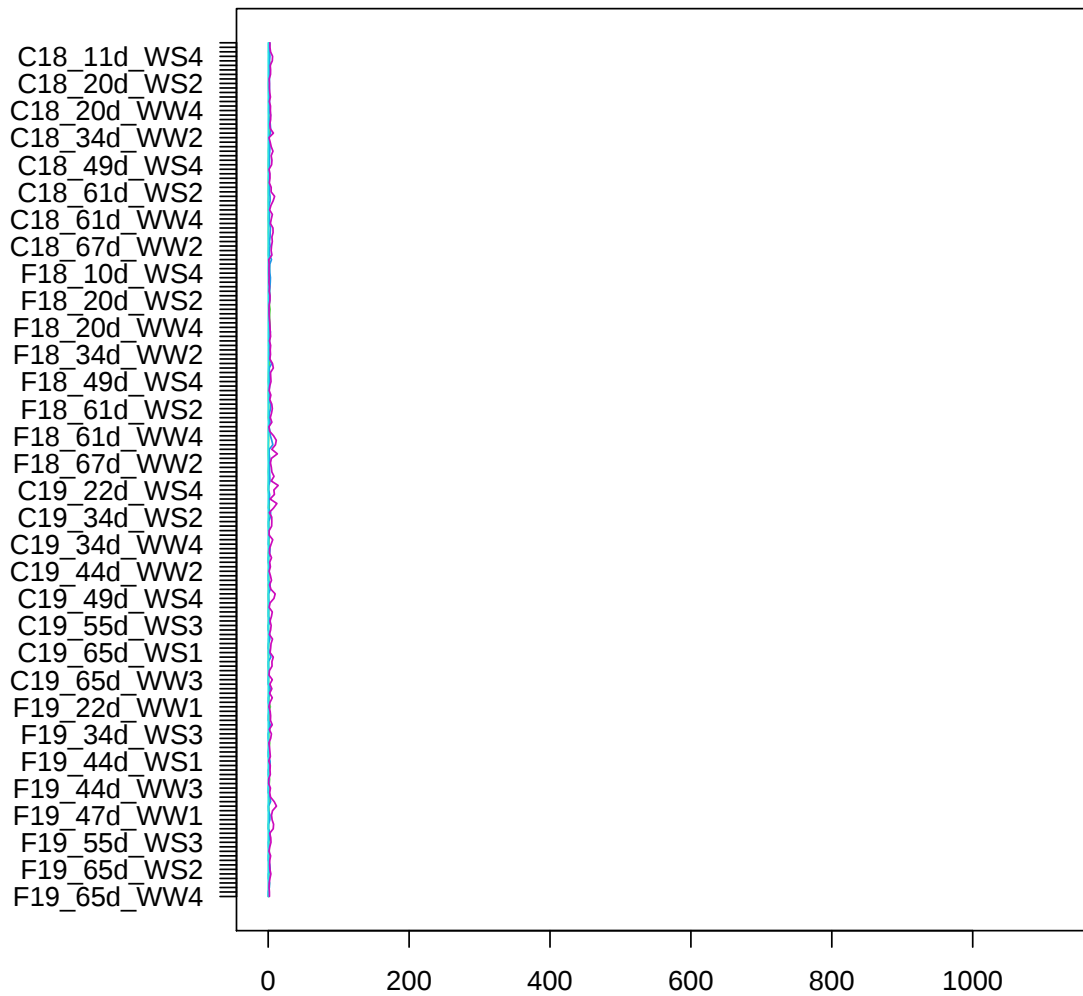
31:40



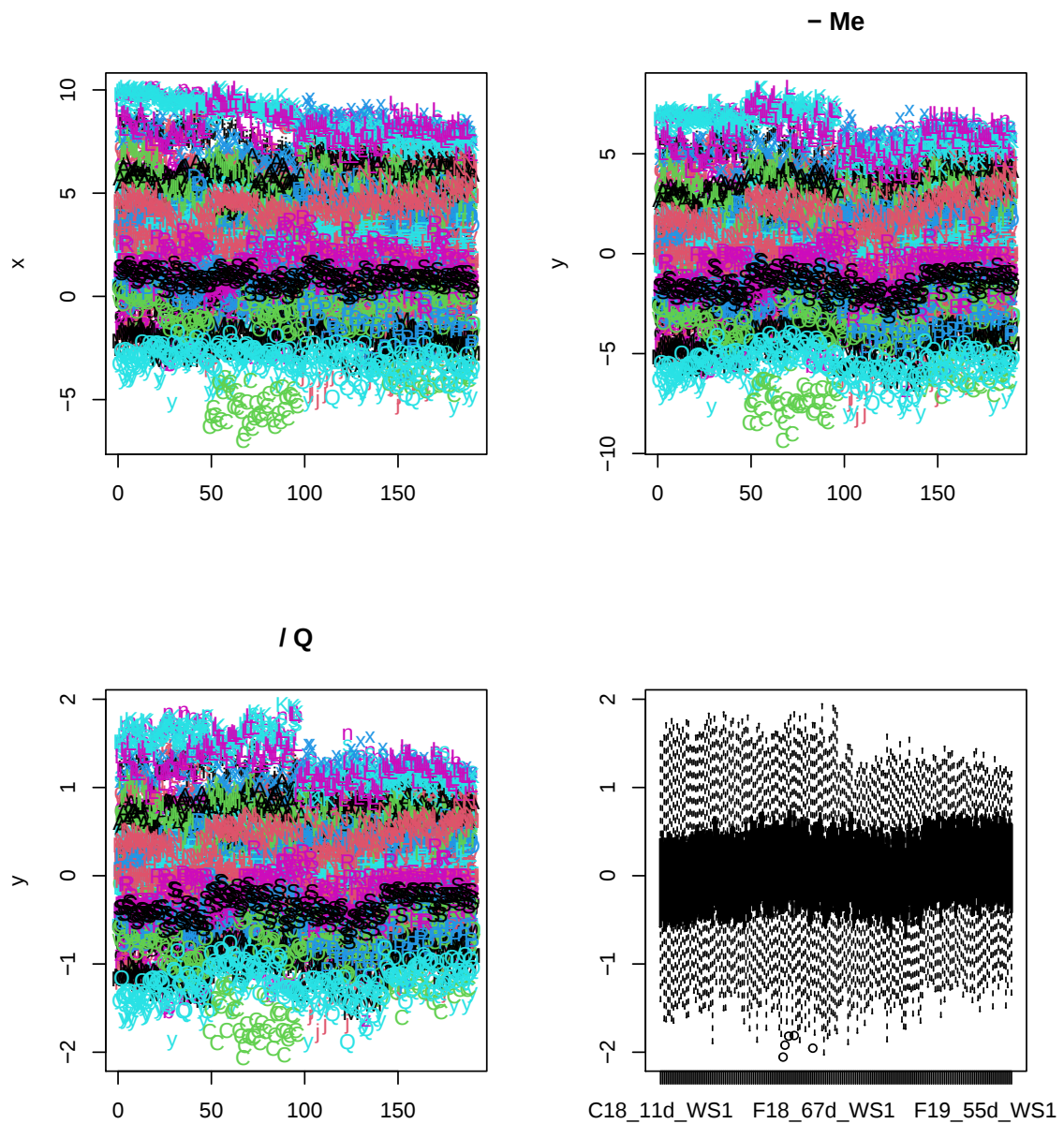
41:50



51:54

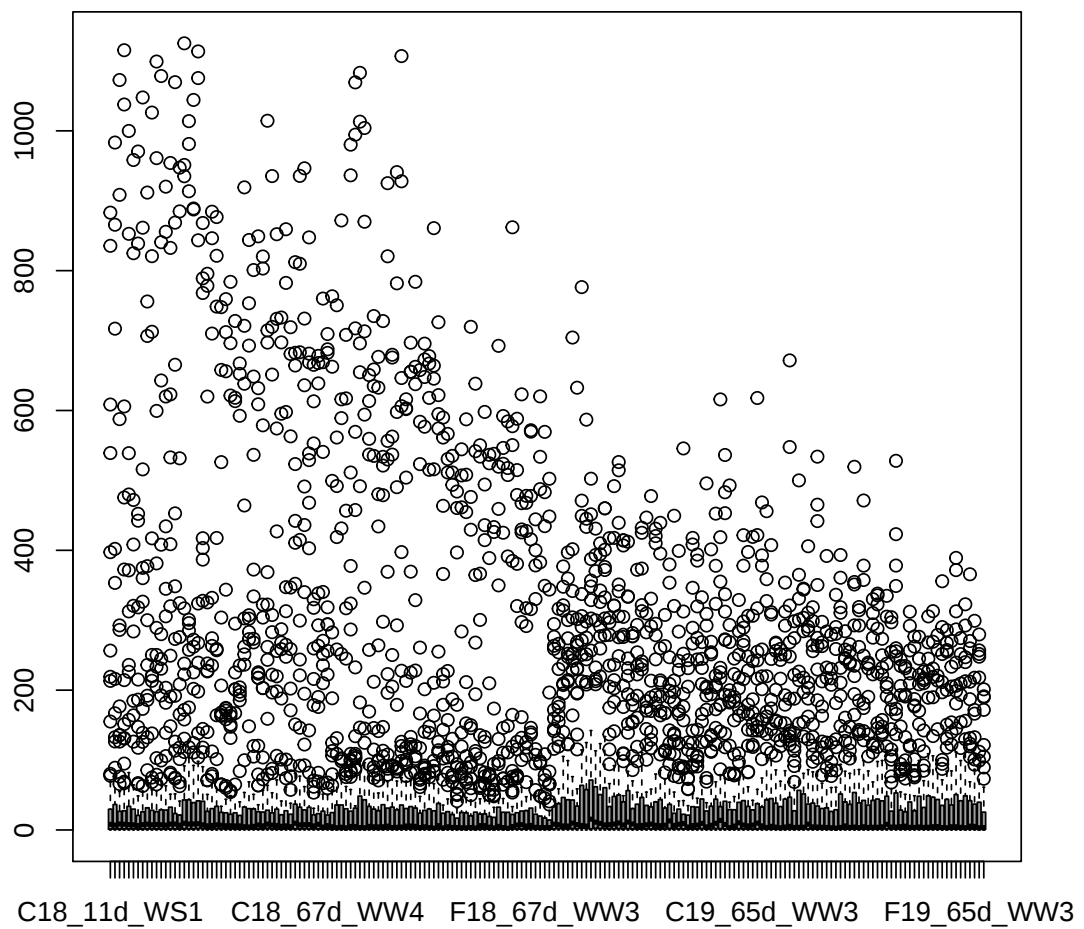


```
> par(mfrow=c(2,2))
> x <- log2(m1819[,m_num_id])
> matplot(x)
> dim(x)
[1] 190 55
> Me <- apply(x,1,median, na.rm=TRUE)
> Q <- apply(x,1,function(x) diff(quantile(x, probs=c(0.25,0.75), na.rm=TRUE)))
> y <- sweep(x,1,Me)
> matplot(y, main="- Me")
> y <- sweep(y,1,Q, "/")
> matplot(y, main="/ Q")
> boxplot(t(y))
```



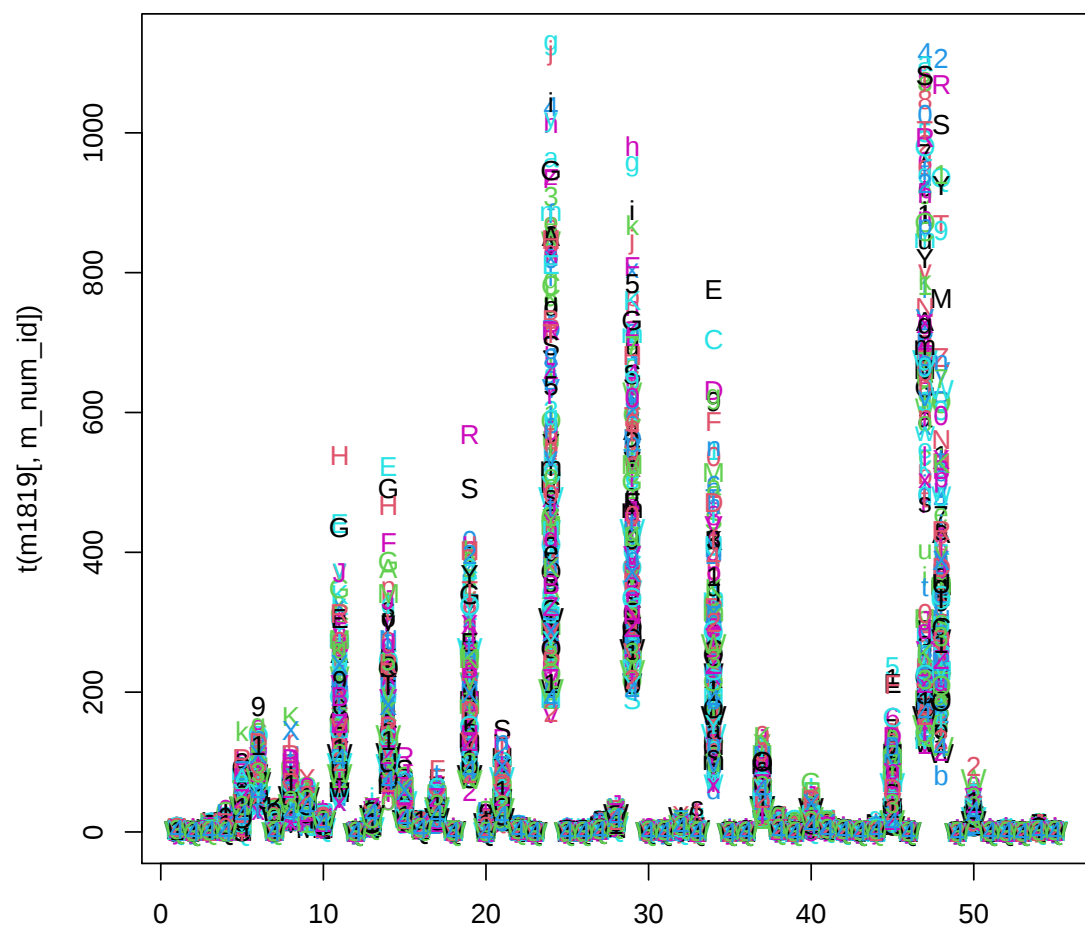
Data are highly skewed with marked differences between years

```
> boxplot(t(m1819[,m_num_id]), col=8)
```

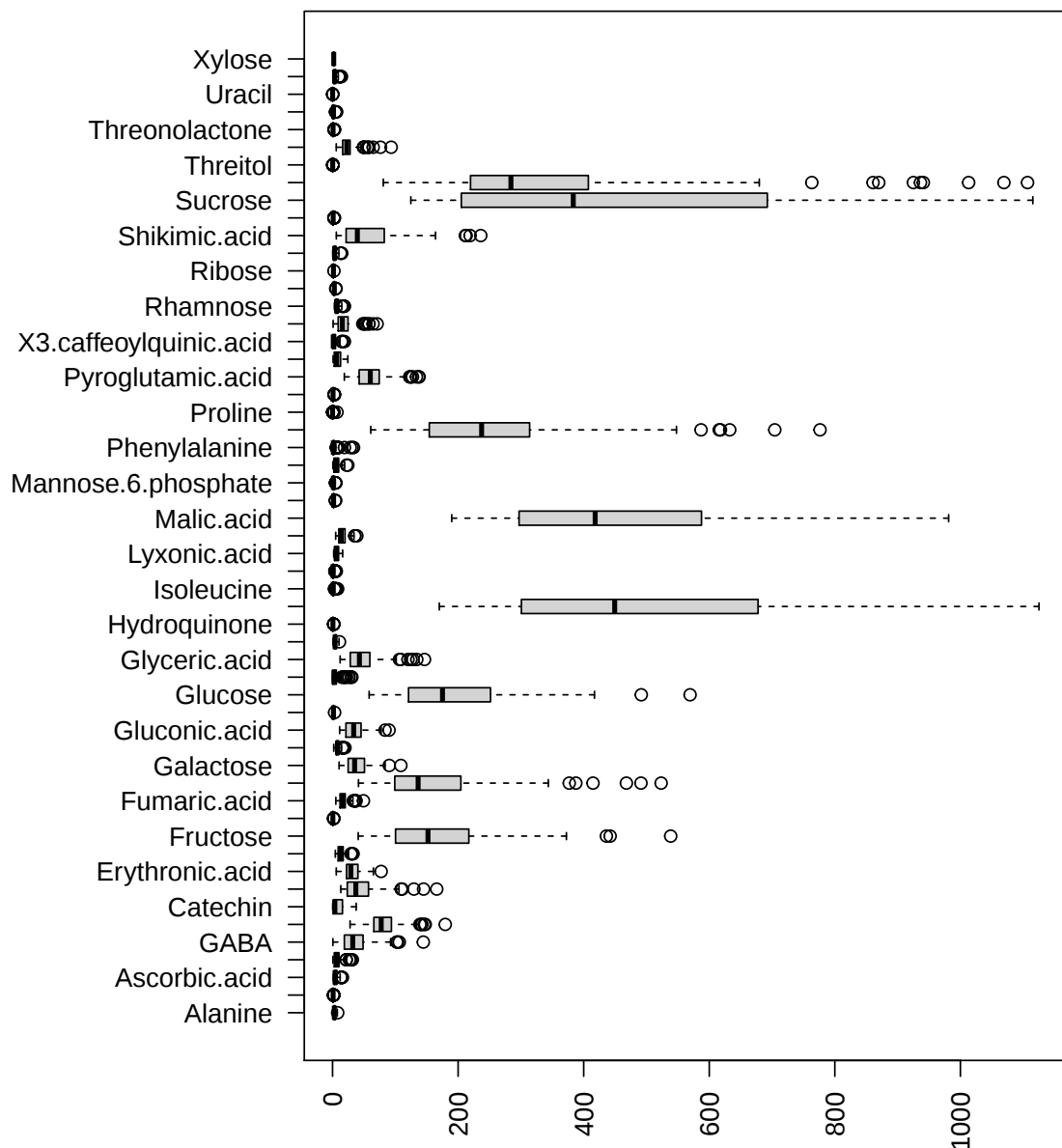


```
> matplot(t(m1819[,m_num_id]))
```

```
Warning in matplot(t(m1819[, m_num_id])): default 'pch' is smaller than number
```



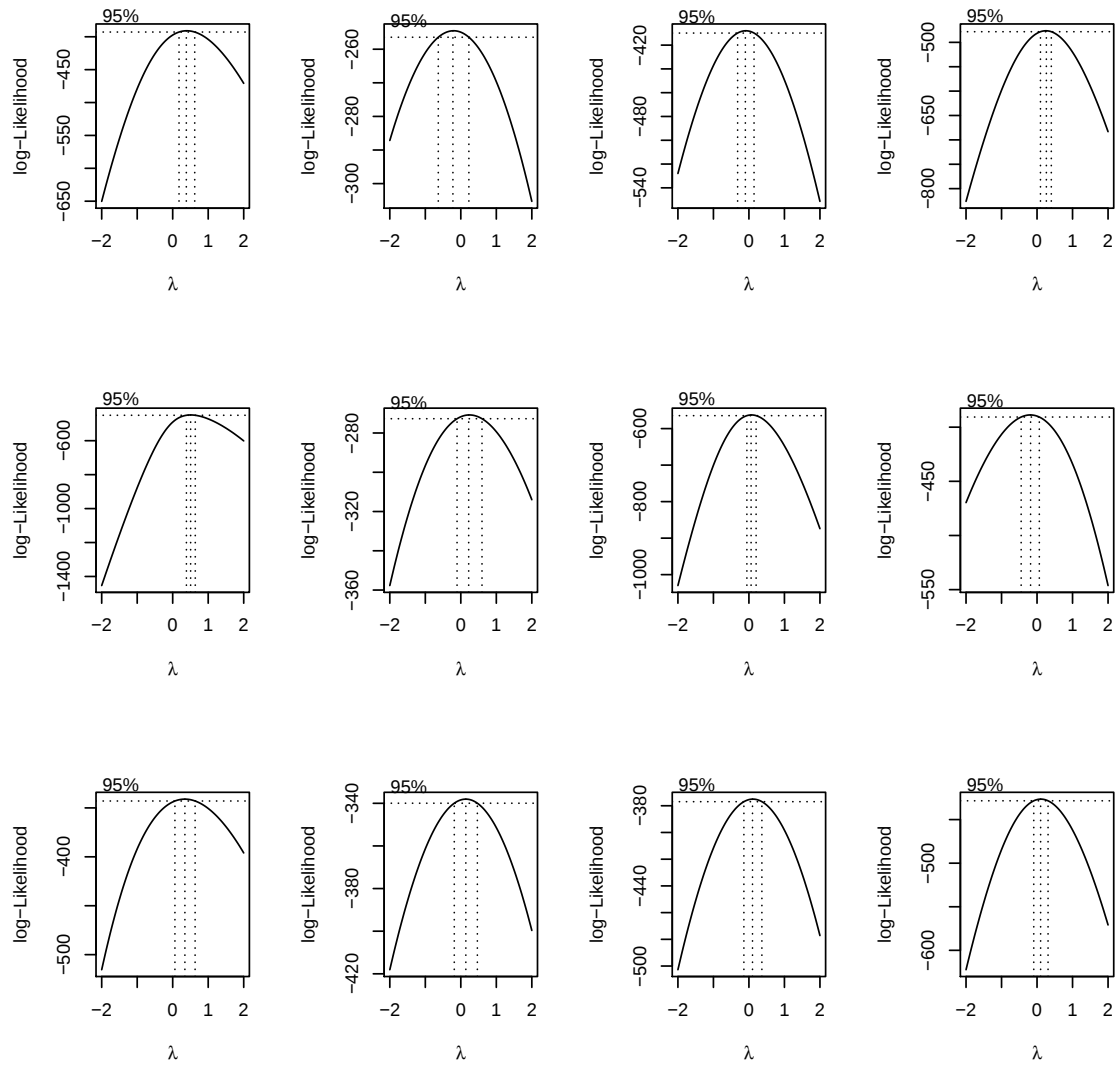
```
> par(mar=c(4,10,3,1))
> boxplot(m1819[,m_num_id], horizontal=TRUE, las=2)
```



Box-Cox transformation

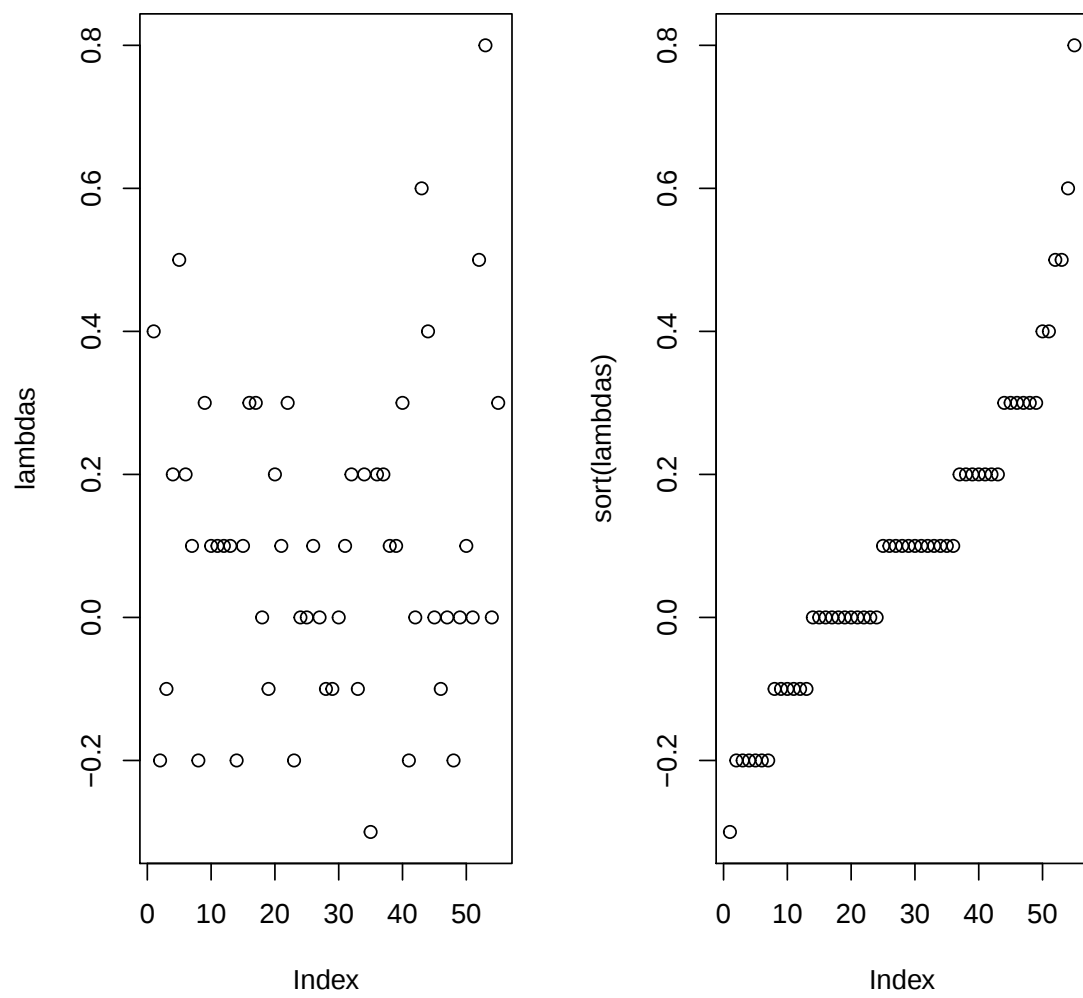
```
> library(MASS)
> par(mfrow=c(3,2))
> my.boxcox <- function(x, plotit=FALSE,...) {
+   require(MASS)
+   bc <- boxcox(x ~1, plotit=plotit, ...)
+   bc$x[which.max(bc$y)]
+ }

> par(mfrow=c(3,4))
> apply(m1819[,m_num_id[1:12]], 2, my.boxcox, plotit=TRUE)
```

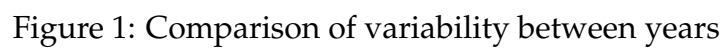


Alanine	0.38383838	Arabinose	-0.22222222	Ascorbic.acid	-0.10101010
Aspartic.acid	0.26262626	GABA	0.50505051	Trans.Caffeic.acid	0.22222222
Catechin	0.06060606	Citric.acid	-0.18181818	Erythronic.acid	0.34343434
Ethanolamine	0.14141414	Fructose	0.10101010	Fructose.6.phosphate	0.10101010

```
> lambdas <- apply(m1819[,m_num_id ], 2, my.boxcox )
> par(mfrow=c(1,2))
> plot(lambdas)
> plot(sort(lambdas))
```

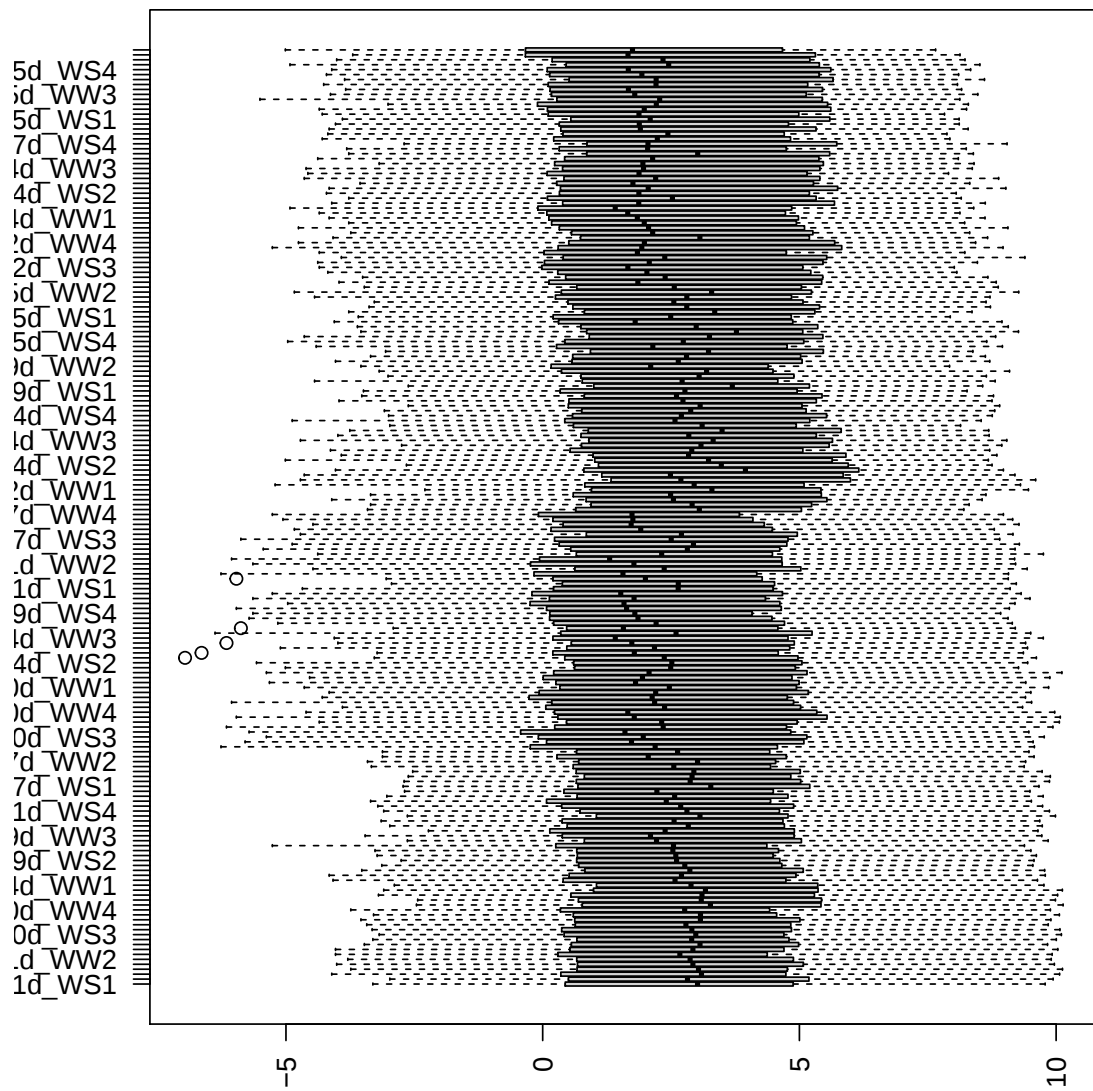


It seems that logarithm is adequate.



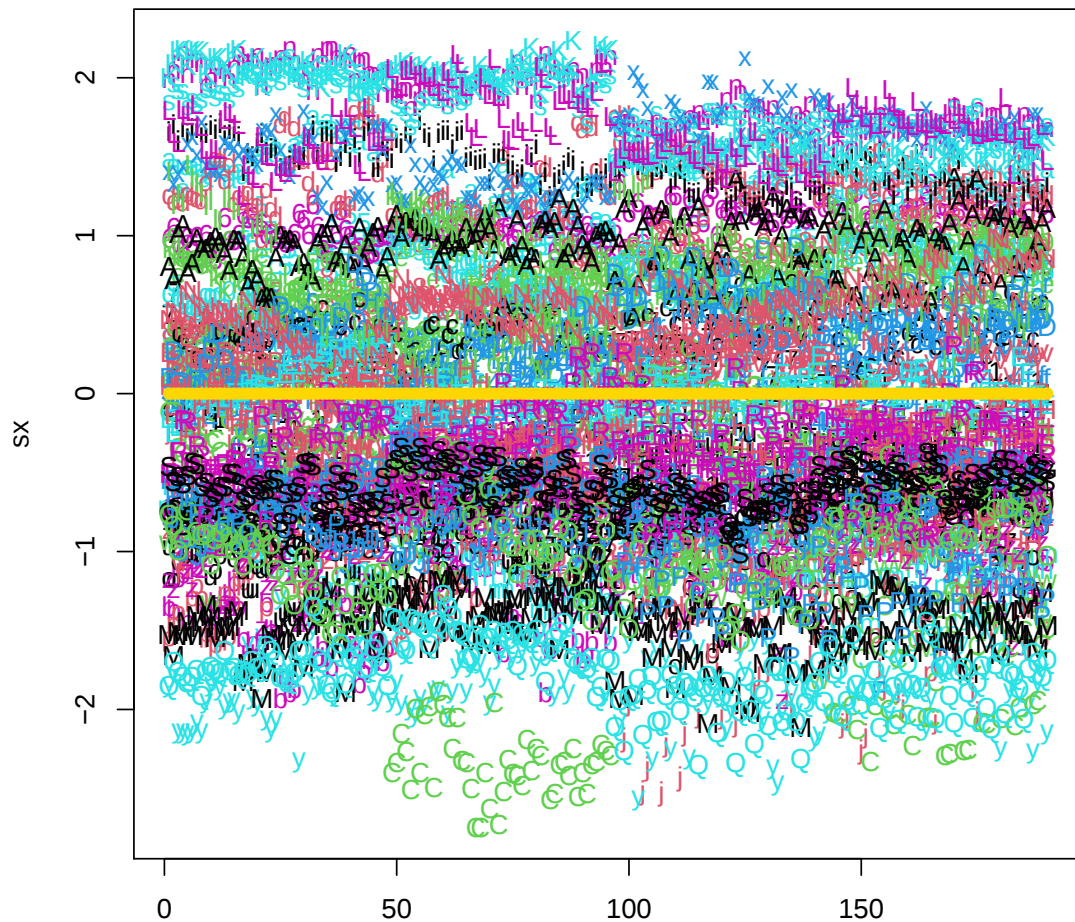
Data are highly skewed with marked differences between years

47



For CCA standardized values are needed
Standardization across samples

```
> x <- t(log2(m1819[,m_num_id]))
> dim(x)
[1] 55 190
> sx <- t(scale(x))
> matplot(sx)
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```

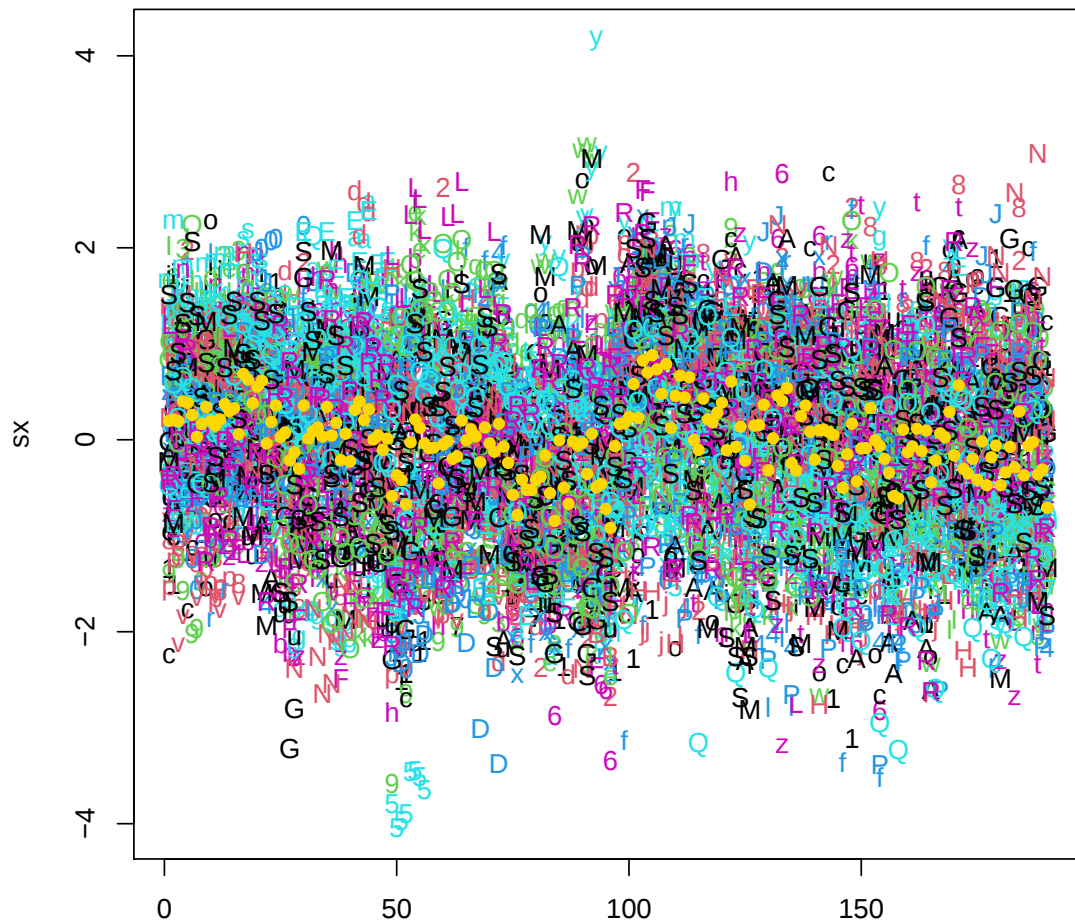


```
> head(apply(sx, 1, mean, na.rm=TRUE))
  C18_11d_WS1  C18_11d_WS2  C18_11d_WS3  C18_11d_WS4  C18_11d_WW1
-3.184006e-17 -1.833682e-17 -6.796765e-17  1.422868e-17  6.904002e-17
  C18_11d_WW2
-5.304607e-17

> head(apply(sx, 1, sd, na.rm=TRUE))
C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4 C18_11d_WW1
          1          1          1          1          1
C18_11d_WW2
          1
```

Standardization across variables

```
> x <- log2(m1819[,m_num_id])
> sx <- scale(x)
> matplot(sx)
> points(1:nrow(sx), apply(sx,1,mean, na.rm=TRUE), col="gold", pch=16)
```



```
> head(apply(sx,2,mean, na.rm=TRUE))
      Alanine      Arabinose      Ascorbic.acid
1.531806e-17  1.355995e-17  4.655907e-17
Aspartic.acid      GABA Trans.Caffeic.acid
-6.557711e-17  3.110716e-16  2.505785e-16
```

```
> head(apply(sx,2,sd, na.rm=TRUE))
      Alanine      Arabinose      Ascorbic.acid
           1           1           1
Aspartic.acid      GABA Trans.Caffeic.acid
           1           1           1
```

```
> x <- log2(m18[,m_num_id])
> sx <- scale(x)
> sm18 <- sx
> matplot(t(sm18), ylim=c(-4,4))
```

2018

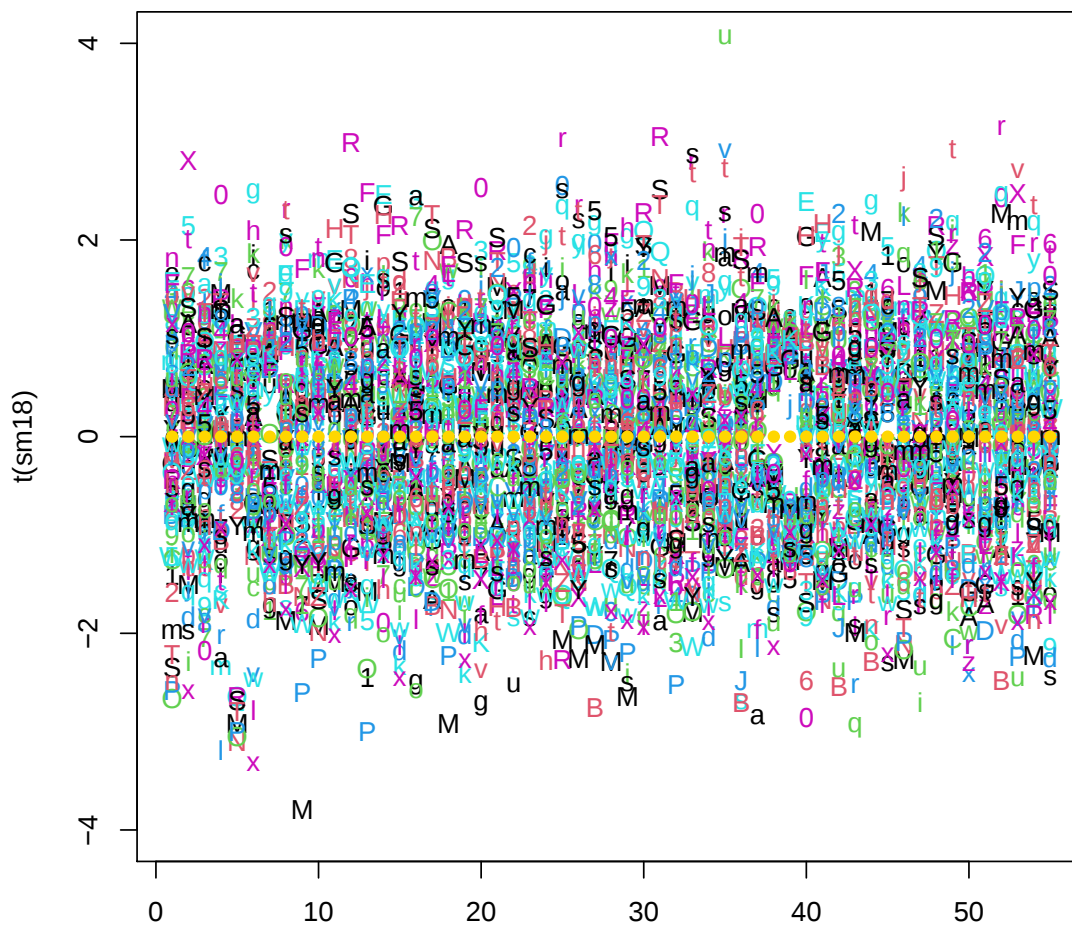


Figure 2: Plot of standardized data 2018 (log2).

Warning in matplot(t(sm18), ylim = c(-4, 4)): default 'pch' is smaller than nu

```
> title("2018")
> points(1:ncol(sx), apply(sx,2,mean, na.rm=TRUE), col="gold", pch=16)
> head(apply(sx,2,mean, na.rm=TRUE))
```

Alanine	Arabinose	Ascorbic.acid
5.585561e-17	-8.097635e-18	1.017456e-16
Aspartic.acid	GABA	Trans.Caffeic.acid
2.398684e-16	1.168222e-16	-1.130547e-15

```
> head(apply(sx,2,sd, na.rm=TRUE))
```

Alanine	Arabinose	Ascorbic.acid
1	1	1
Aspartic.acid	GABA	Trans.Caffeic.acid
1	1	1

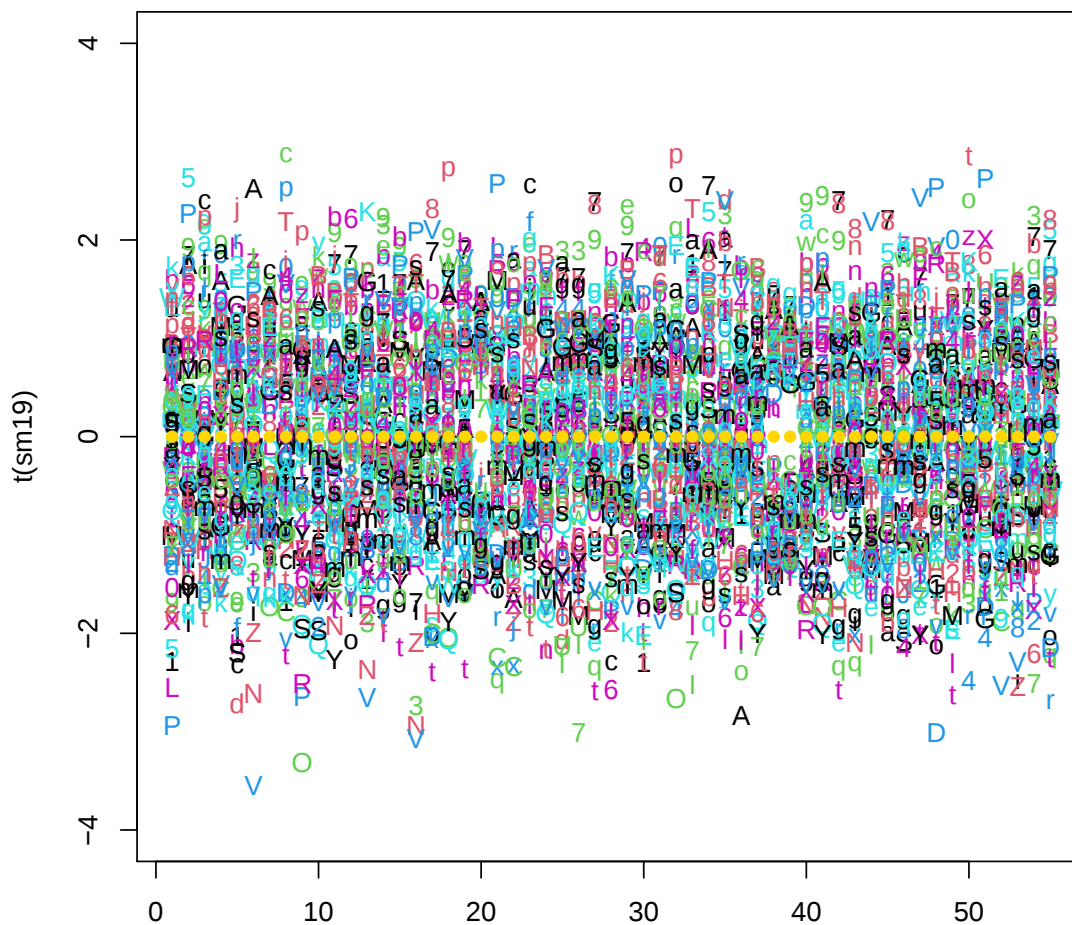


Figure 3: Plot of standardized data 2019 (log2).

```
> x <- log2(m19[,m_num_id])
> sx <- scale(x)
> sm19 <- sx
> matplot(t(sm19), ylim=c(-4,4))
Warning in matplot(t(sm19), ylim = c(-4, 4)): default 'pch' is smaller than nu
> title("2019")
> points(1:ncol(sx), apply(sx,2,mean, na.rm=TRUE), col="gold", pch=16)
> head(apply(sx,2,mean, na.rm=TRUE))
```

Alanine	Arabinose	Ascorbic.acid
7.181686e-18	-2.255141e-17	6.650427e-17
Aspartic.acid	GABA	Trans.Caffeic.acid
-5.090675e-17	7.660638e-17	7.454743e-16

```
> head(apply(sx,2,sd, na.rm=TRUE))
```

Alanine	Arabinose	Ascorbic.acid
1	1	1
Aspartic.acid	GABA	Trans.Caffeic.acid
1	1	1

```

> par(mar=c(4,10,3,1))
> sx <- sm18
> boxplot(sx, horizontal=TRUE, las=2, main="2018", ylim=range(sm1819))
Error in boxplot.default(groups, ...): object 'sm1819' not found
> points( apply(sx,2,mean, na.rm=TRUE),1:ncol(sx), col="gold", pch=16)
Error in plot.xy(xy.coords(x, y), type = type, ...): plot.new has not been cal

> par(mar=c(4,10,3,1))
> sx <- sm19
> boxplot(sx, horizontal=TRUE, las=2, main="2019", ylim=range(sm1819))
Error in boxplot.default(groups, ...): object 'sm1819' not found
> points( apply(sx,2,mean, na.rm=TRUE),1:ncol(sx), col="gold", pch=16)
Error in plot.xy(xy.coords(x, y), type = type, ...): plot.new has not been cal

> sm1819 <- rbind(sm18,sm19)
> dim(sm1819)
[1] 190  55
> matplot(t(sm1819))
Warning in matplot(t(sm1819)): default 'pch' is smaller than number of columns
> title("2018, 2019")
> sx <- sm1819
> points(1:ncol(sx), apply(sx,2,mean, na.rm=TRUE), col="gold", pch=16)
> head(apply(sx,2,mean, na.rm=TRUE))
      Alanine      Arabinose      Ascorbic.acid
3.168495e-17 -1.489408e-17  8.393380e-17
Aspartic.acid      GABA Trans.Caffeic.acid
9.599184e-17  9.681283e-17 -2.025261e-16

> head(apply(sx,2,sd, na.rm=TRUE))
      Alanine      Arabinose      Ascorbic.acid
0.997351      0.997351      0.997351
Aspartic.acid      GABA Trans.Caffeic.acid
0.997351      0.997351      0.997351

```

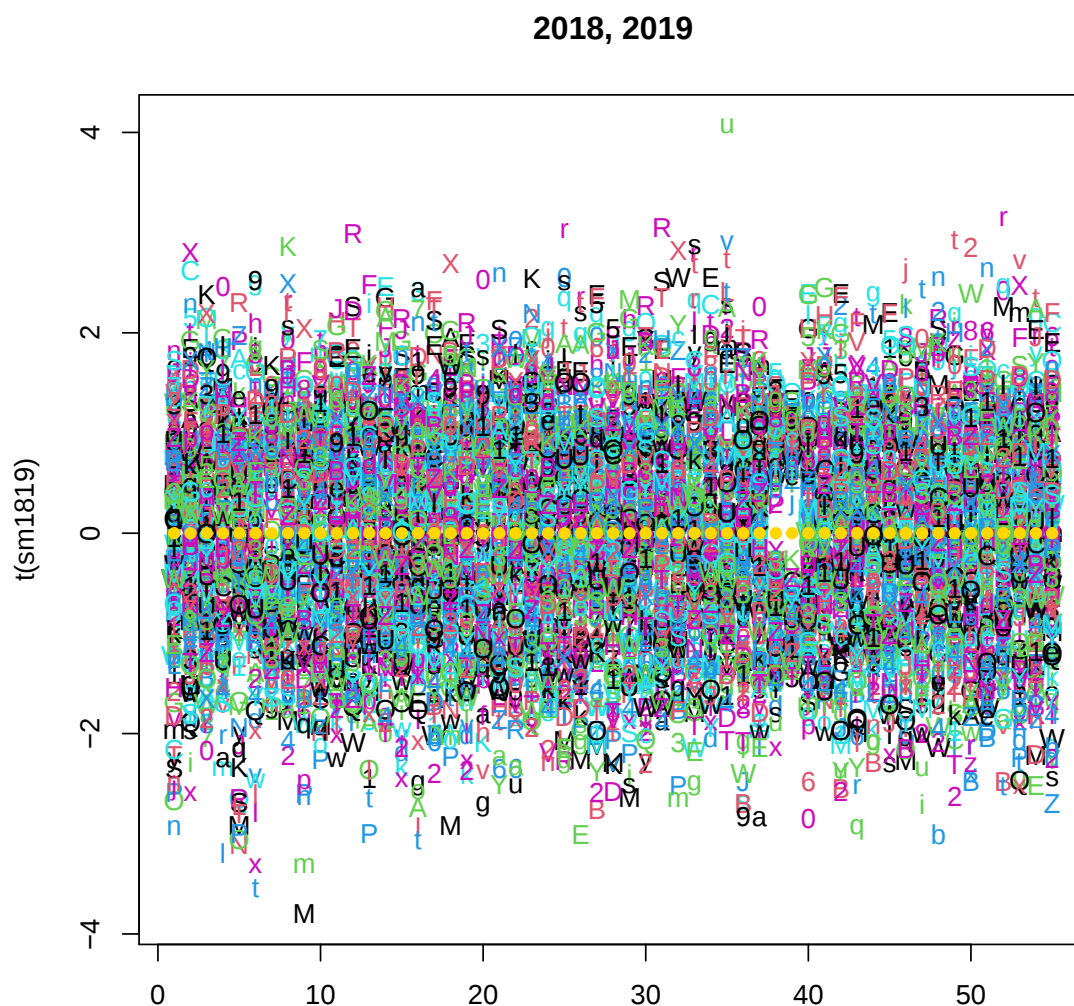


Figure 4: Plot of standardized data 2018, 2019 (log2).

3.9 Featuredata for metabolites

Rows in featuredata and columns of metabolite data ARE in the same order.

```
> (fmfn <- getMeta(.adesc, "Featuredata metabolites"))
[1] "Featuredata_metabolites_210127.txt"
> mfdata <- read.table(file.path(.iroot, fmfn), sep="\t", header=TRUE)
> cbind(colnames(sm1819), make.names(mfdata[,1]), mfdata[,1])

      [,1]                [,2]
[1,] "Alanine"           "Alanine"
[2,] "Arabinose"         "Arabinose"
[3,] "Ascorbic.acid"     "Ascorbic.acid"
[4,] "Aspartic.acid"     "Aspartic.acid"
[5,] "GABA"              "GABA"
[6,] "Trans.Caffeic.acid" "Trans.Caffeic.acid"
[7,] "Catechin"          "Catechin"
[8,] "Citric.acid"       "Citric.acid"
[9,] "Erythronic.acid"   "Erythronic.acid"
```

[10,]	"Ethanolamine"	"Ethanolamine"
[11,]	"Fructose"	"Fructose"
[12,]	"Fructose.6.phosphate"	"Fructose.6.phosphate"
[13,]	"Fumaric.acid"	"Fumaric.acid"
[14,]	"Galactinol"	"Galactinol"
[15,]	"Galactose"	"Galactose"
[16,]	"Gallic.acid"	"Gallic.acid"
[17,]	"Gluconic.acid"	"Gluconic.acid"
[18,]	"Glucopyranose..H2O."	"Glucopyranose..H2O."
[19,]	"Glucose"	"Glucose"
[20,]	"Glutamic.acid"	"Glutamic.acid"
[21,]	"Glyceric.acid"	"Glyceric.acid"
[22,]	"Glycine"	"Glycine"
[23,]	"Hydroquinone"	"Hydroquinone"
[24,]	"Myo.Inostol"	"Myo.Inostol"
[25,]	"Isoleucine"	"Isoleucine"
[26,]	"Leucine"	"Leucine"
[27,]	"Lyxonic.acid"	"Lyxonic.acid"
[28,]	"Maleic.acid"	"Maleic.acid"
[29,]	"Malic.acid"	"Malic.acid"
[30,]	"Malonic.acid"	"Malonic.acid"
[31,]	"Mannose.6.phosphate"	"Mannose.6.phosphate"
[32,]	"Melibiose"	"Melibiose"
[33,]	"Phenylalanine"	"Phenylalanine"
[34,]	"Phosphoric.acid"	"Phosphoric.acid"
[35,]	"Proline"	"Proline"
[36,]	"Putrescine"	"Putrescine"
[37,]	"Pyroglutamic.acid"	"Pyroglutamic.acid"
[38,]	"Quinic.acid"	"Quinic.acid"
[39,]	"X3.caffeoylquinic.acid"	"X3.caffeoylquinic.acid"
[40,]	"Raffinose"	"Raffinose"
[41,]	"Rhamnose"	"Rhamnose"
[42,]	"Ribonic.acid"	"Ribonic.acid"
[43,]	"Ribose"	"Ribose"
[44,]	"Serine"	"Serine"
[45,]	"Shikimic.acid"	"Shikimic.acid"
[46,]	"Succinic.acid"	"Succinic.acid"
[47,]	"Sucrose"	"Sucrose"
[48,]	"Tartaric.acid"	"Tartaric.acid"
[49,]	"Threitol"	"Threitol"
[50,]	"Threonic.acid"	"Threonic.acid"
[51,]	"Threonolactone"	"Threonolactone"
[52,]	"Threonine"	"Threonine"
[53,]	"Uracil"	"Uracil"
[54,]	"Valine"	"Valine"
[55,]	"Xylose"	"Xylose"
	[, 3]	
[1,]	"Alanine"	
[2,]	"Arabinose"	
[3,]	"Ascorbic acid"	
[4,]	"Aspartic acid"	
[5,]	"GABA"	
[6,]	"Trans-Caffeic acid"	

```

[7,] "Catechin"
[8,] "Citric acid"
[9,] "Erythronic acid"
[10,] "Ethanolamine"
[11,] "Fructose"
[12,] "Fructose-6-phosphate"
[13,] "Fumaric acid"
[14,] "Galactinol"
[15,] "Galactose"
[16,] "Gallic acid"
[17,] "Gluconic acid"
[18,] "Glucopyranose[-H2O]"
[19,] "Glucose"
[20,] "Glutamic acid"
[21,] "Glyceric acid"
[22,] "Glycine"
[23,] "Hydroquinone"
[24,] "Myo-Inositol"
[25,] "Isoleucine"
[26,] "Leucine"
[27,] "Lyxonic acid"
[28,] "Maleic acid"
[29,] "Malic acid"
[30,] "Malonic acid"
[31,] "Mannose-6-phosphate"
[32,] "Melibiose"
[33,] "Phenylalanine"
[34,] "Phosphoric acid"
[35,] "Proline"
[36,] "Putrescine"
[37,] "Pyroglutamic acid"
[38,] "Quinic acid"
[39,] "3-caffeoylquinic acid"
[40,] "Raffinose"
[41,] "Rhamnose"
[42,] "Ribonic acid"
[43,] "Ribose"
[44,] "Serine"
[45,] "Shikimic acid"
[46,] "Succinic acid"
[47,] "Sucrose"
[48,] "Tartaric acid"
[49,] "Threitol"
[50,] "Threonic acid"
[51,] "Threonolactone"
[52,] "Threonine"
[53,] "Uracil"
[54,] "Valine"
[55,] "Xylose"

> all(colnames(sm1819) == make.names(mfdata[,1]))
[1] TRUE

```

```

> rownames(mfdata) <- make.names(mfdata[,1])
> # to be sure, that the fdata rows are in the same order as data
> mfdata <- mfdata[colnames(sm1819),]
> head(mfdata)

```

	Metabolite	Bin
Alanine	Alanine	5.1001
Arabinose	Arabinose	10.6.1001
Ascorbic.acid	Ascorbic acid	17.5.1001
Aspartic.acid	Aspartic acid	13.1.1.2.1001
GABA	GABA	22.1002
Trans.Caffeic.acid	Trans-Caffeic acid	16.2.1.1006

Alanine	
Arabinose	cell wall
Ascorbic.acid	hormone metabol
Aspartic.acid	amino acid metabolism.synthesis.central amino acid metaboli
GABA	pol
Trans.Caffeic.acid	secondary metabolism.phenylpropanoids.lignin

3.10 Interesting bins

For Canonical Correlation Analysis (CCA) we will need to restrict the number of genes (and metabolites) to those that are of more interest. The Mapman bins of interest are provided in the file (at the investigation layer).

List of bins for metabolite and transcripts:

```
> (bfn <- getMeta(.adesc, "Interesting bins"))
[1] "Bin_selection_2.txt"
> bindata <- read.table(file.path(.iroot, bfn), sep="\t", header=TRUE, dec="$")
> head(bindata)
  bin description
1   2 major CHO metabolism
2   3 minor CHO metabolism
3   8 TCA / organic transformation
4  10 cell wall
5  13 amino acid metabolism
6  16 secondary metabolism
> str(bindata)
'data.frame':      8 obs. of  2 variables:
 $ bin      : chr  "2" "3" "8" "10" ...
 $ description: chr  "major CHO metabolism" "minor CHO metabolism" "TCA / orga
```

At some point, the transcripts and metabolites that correspond to the bins of interest (including the sub-bins) will be selected. Let us try to find them for the first bin:

```
> bindata$bin
[1] "2" "3" "8" "10" "13" "16" "27.3" "35"
> paste0("^", bindata$bin[1], "\\.")
[1] "^2\\."
> ind <- grep(paste0("^", bindata$bin[1], "\\."), fdata$BINCODE)
> ind
[1] 449 478 502 503 514 982 1128 1604 1654 1839 1904
[12] 2102 2191 2368 2495 2496 2497 3842 3973 4049 4398 4444
[23] 4544 5112 5424 5514 5714 5870 6003 6641 6913 7102 7367
[34] 7400 7507 7737 7987 8541 8807 8810 8952 9215 9405 9614
[45] 9783 10279 10410 10468 11168 11217 11324 11658 11967 12036 12225
[56] 12418 12547 12609 12663 13007 13181 13182 13252 13509 13868 14410
[67] 14612 14713 14740 14975 15363 15451 15526 15644 15665 15833 15871
[78] 16263 16349 16362 16622 16930
> fdata[ind, 2:3]
```

	geneID	BINCODE
449	Vitvi02g01845	2.2.1.3
478	Vitvi01g00025	2.2.1.1
502	Vitvi01g00052	2.2.2.6
503	Vitvi01g00053	2.2.2.6
514	Vitvi01g00064	2.2.2.2
982	Vitvi01g00681	2.2.2.3
1128	Vitvi01g00932	2.2.2.1.1
1604	Vitvi02g00184	2.2.2.1.2
1654	Vitvi02g00250	2.1.2.2
1839	Vitvi02g00512	2.2.1.3
1904	Vitvi02g00605	2.2.2.1.2
2102	Vitvi02g01232	2.2.2.1.2
2191	Vitvi03g00088	2.2.1.3.1
2368	Vitvi03g00304	2.1.2.1
2495	Vitvi03g00500	2.2.2.1.1
2496	Vitvi03g01571	2.2.2.1.1
2497	Vitvi03g01572	2.2.2.1.1
3842	Vitvi05g00164	2.2.1.3.1
3973	Vitvi05g00357	2.2.2.1.2
4049	Vitvi05g00442	2.1.2.1
4398	Vitvi05g01193	2.1.1.1
4444	Vitvi05g01324	2.2.2.3
4544	Vitvi05g01516	2.2.1.1
5112	Vitvi06g00583	2.2.2.2
5424	Vitvi06g01272	2.2.1.4
5514	Vitvi06g01427	2.2.1.3.1
5714	Vitvi07g00167	2.1.2.4
5870	Vitvi07g00353	2.2.1.5
6003	Vitvi07g00544	2.1.2.1
6641	Vitvi07g01830	2.2.2.4
6913	Vitvi08g00225	2.1.1.2
7102	Vitvi08g00930	2.2.2.4
7367	Vitvi08g01307	2.2.1.1
7400	Vitvi08g01353	2.2.2.4
7507	Vitvi08g01497	2.1.2.3
7737	Vitvi08g01815	2.1.2.60
7987	Vitvi09g00193	2.2.1.3
8541	Vitvi10g00094	2.1.2.2
8807	Vitvi10g00494	2.2.2.2
8810	Vitvi10g00499	2.2.2.6
8952	Vitvi10g00739	2.1.2.2
9215	Vitvi11g00030	2.2.1.5
9405	Vitvi11g00260	2.2.1.4
9614	Vitvi11g00542	2.1.1.1
9783	Vitvi11g00903	2.1.2.2
10279	Vitvi12g00558	2.2.2.1.2
10410	Vitvi12g00770	2.1.2.1
10468	Vitvi12g01618	2.1.1.2
11168	Vitvi13g00692	2.2.2.9
11217	Vitvi13g00792	2.2.1.3.1
11324	Vitvi13g01242	2.2.2.10
11658	Vitvi14g00070	2.2.1.3.1

```

11967 Vitvil4g00608      2.1.2
12036 Vitvil4g00950      2.2.1.1
12225 Vitvil4g01406 2.2.2.1.1
12418 Vitvil4g01692      2.2.1.99
12547 Vitvil4g01873      2.1.2.1
12609 Vitvil4g01968      2.1.2.2
12663 Vitvil4g02032      2.2.2.2
13007 Vitvil5g00885      2.1.2.2
13181 Vitvil5g01127 2.2.2.1.2
13182 Vitvil5g01128 2.2.2.1.2
13252 Vitvil6g00033      2.2.2.6
13509 Vitvil6g00895      2.2.1.1
13868 Vitvil6g01405      2.1.2.2
14410 Vitvil7g00738      2.1.2.1
14612 Vitvil7g01221      2.2.1.5
14713 Vitvil8g00111      2.1.2.3
14740 Vitvil8g00144 2.2.2.1.1
14975 Vitvil8g00454      2.1.2.4
15363 Vitvil8g02758      2.1.2.1
15451 Vitvil8g01114      2.2.1.4
15526 Vitvil8g01242      2.1.2
15644 Vitvil8g01657      2.1.1.3
15665 Vitvil8g01682 2.2.1.3.1
15833 Vitvil8g02365      2.1.1.1
15871 Vitvil8g02417      2.2.1.1
16263 Vitvil9g00538      2.1.2.3
16349 Vitvil9g00678 2.2.2.1.2
16362 Vitvil9g00704      2.2.1.99
16622 Vitvil10g02394      2.1.2.2
16930 Vitvil9g02064 2.2.2.1.2

```

```
> bindata$bin
```

```
[1] "2"      "3"      "8"      "10"     "13"     "16"     "27.3"  "35"
```

```
> paste0("^", "26.9", "$")
```

```
[1] "^26.9$"
```

```
> ind <- grep(paste0("^", "26.9", "$"), fdata$BINCODE)
```

```
> ind
```

```

[1]      1    590   1709   3285   3293   4238   4239   4240   4241   4311   4315
[12]  4940   5088   5806   5807   5809   6075   7120   7239   7242   7348   7349
[23]  9989   9990  10683  10689  10862  12705  12710  12903  13263  13264  13269
[34] 14299  14747  14797  16444  16446  16449  16457  16458  16459  16460  16461
[45] 16462  16463  16729  16933

```

```
> fdata[ind, 2:3]
```

	geneID	BINCODE
1	Vitvil5g01736	26.9
590	Vitvi01g00149	26.9
1709	Vitvi02g00335	26.9
3285	Vitvi04g00880	26.9
3293	Vitvi04g00908	26.9
4238	Vitvi05g01959	26.9
4239	Vitvi05g01961	26.9

4240	Vitvi05g01962	26.9
4241	Vitvi05g01963	26.9
4311	Vitvi05g02001	26.9
4315	Vitvi05g00910	26.9
4940	Vitvi06g00372	26.9
5088	Vitvi06g01724	26.9
5806	Vitvi07g00283	26.9
5807	Vitvi07g00285	26.9
5809	Vitvi07g00286	26.9
6075	Vitvi07g00674	26.9
7120	Vitvi08g00957	26.9
7239	Vitvi08g01129	26.9
7242	Vitvi08g01137	26.9
7348	Vitvi08g02226	26.9
7349	Vitvi08g02228	26.9
9989	Vitvil12g00080	26.9
9990	Vitvil12g00081	26.9
10683	Vitvil12g02153	26.9
10689	Vitvil12g02159	26.9
10862	Vitvil13g00208	26.9
12705	Vitvil15g00172	26.9
12710	Vitvil15g00231	26.9
12903	Vitvil15g00746	26.9
13263	Vitvil16g01498	26.9
13264	Vitvil16g01499	26.9
13269	Vitvil16g01501	26.9
14299	Vitvil17g01467	26.9
14747	Vitvil18g00152	26.9
14797	Vitvil18g00219	26.9
16444	Vitvil19g02145	26.9
16446	Vitvil19g02150	26.9
16449	Vitvil19g01048	26.9
16457	Vitvil19g02189	26.9
16458	Vitvil19g02192	26.9
16459	Vitvil19g01305	26.9
16460	Vitvil19g01311	26.9
16461	Vitvil19g01326	26.9
16462	Vitvil19g02197	26.9
16463	Vitvil19g01338	26.9
16729	Vitvi07g02188	26.9
16933	Vitvil19g01328	26.9

```

> xx <- "27.3"
> bindata$bin
[1] "2"      "3"      "8"      "10"     "13"     "16"     "27.3"  "35"
> paste0("^",xx,"$")
[1] "^27.3$"
> ind1 <- grep(paste0("^",xx,"$"),fdata$BINCODE)
> ind1
[1] 1421 3631 4719 8064 11915 13247 13534 14400 14799 14801
> fdata[ind1,2:3]

```

```

      geneID BINCODE
1421 Vitvi01g01749    27.3
3631 Vitvi04g01606    27.3
4719 Vitvi06g00072    27.3
8064 Vitvi09g00288    27.3
11915 Vitvi14g00482    27.3
13247 Vitvi16g00026    27.3
13534 Vitvi16g00956    27.3
14400 Vitvi17g00725    27.3
14799 Vitvi18g00222    27.3
14801 Vitvi18g00224    27.3

```

```
> bindata$bin
```

```
[1] "2"      "3"      "8"      "10"     "13"     "16"     "27.3"  "35"
```

```
> paste0("^",xx,"\\.")
```

```
[1] "^27.3\\."
```

```
> ind2 <- grep(paste0("^",xx,"\\."),fdata$BINCODE)
```

```
> ind2
```

```

 [1]      20      23      73      83      86      96     107     111     195     223
[11]     226     265     293     309     316     337     343     345     377     415
[21]     512     513     519     545     577     610     633     651     655     660
[31]     662     677     688     690     737     738     754     765     779     814
[41]     816     838     839     841     862     893     894     909     958     979
[51]    1029    1066    1080    1086    1090    1098    1117    1119    1129    1130
[61]    1131    1132    1139    1141    1144    1151    1176    1177    1186    1198
[71]    1199    1203    1215    1226    1231    1243    1268    1269    1270    1284
[81]    1286    1287    1296    1308    1364    1365    1374    1382    1391    1408
[91]    1411    1413    1425    1427    1437    1454    1464    1482    1485    1516
[101]    1534    1552    1557    1583    1586    1601    1614    1617    1618    1642
[111]    1647    1650    1667    1669    1680    1699    1704    1706    1718    1727
[121]    1736    1745    1751    1765    1775    1778    1780    1803    1805    1809
[131]    1838    1923    1929    1937    1942    1948    1961    1966    1972    1977
[141]    1992    2002    2003    2004    2013    2053    2088    2125    2135    2137
[151]    2144    2152    2155    2156    2161    2170    2172    2173    2178    2198
[161]    2214    2226    2232    2249    2250    2293    2308    2316    2338    2343
[171]    2346    2359    2360    2380    2383    2387    2390    2400    2403    2428
[181]    2444    2461    2473    2484    2508    2509    2541    2555    2578    2579
[191]    2592    2594    2644    2646    2662    2681    2706    2727    2752    2765
[201]    2770    2781    2802    2803    2804    2807    2828    2829    2841    2843
[211]    2854    2876    2888    2896    2928    2931    2940    2941    2942    2956
[221]    2966    2994    3023    3024    3025    3046    3054    3061    3064    3081
[231]    3082    3095    3105    3127    3139    3140    3142    3152    3166    3191
[241]    3217    3221    3222    3223    3224    3232    3252    3258    3259    3274
[251]    3283    3295    3304    3353    3357    3358    3362    3374    3387    3388
[261]    3389    3390    3391    3411    3416    3449    3451    3453    3504    3506
[271]    3510    3515    3528    3540    3546    3564    3571    3572    3613    3617
[281]    3621    3622    3626    3630    3650    3659    3667    3668    3669    3687
[291]    3696    3704    3745    3772    3774    3785    3791    3799    3824    3882
[301]    3907    3911    3913    3915    3950    3951    3953    3954    3983    4039
[311]    4056    4084    4115    4158    4162    4163    4176    4195    4210    4235
[321]    4263    4279    4286    4293    4320    4352    4353    4358    4359    4370
[331]    4478    4482    4484    4547    4555    4573    4585    4607    4631    4654
[341]    4678    4686    4712    4735    4762    4789    4790    4795    4799    4801

```

[351]	4806	4813	4826	4830	4846	4847	4848	4849	4850	4863
[361]	4864	4867	4879	4886	4889	4893	4896	4897	4898	4913
[371]	4921	4932	4938	4942	4945	4952	4967	5006	5021	5027
[381]	5032	5040	5042	5053	5060	5104	5119	5130	5142	5150
[391]	5163	5200	5246	5247	5287	5288	5293	5301	5312	5316
[401]	5323	5336	5353	5370	5373	5399	5403	5419	5431	5454
[411]	5464	5469	5470	5481	5490	5491	5495	5513	5527	5537
[421]	5547	5563	5564	5578	5586	5593	5594	5605	5617	5618
[431]	5621	5623	5624	5640	5641	5677	5687	5695	5703	5712
[441]	5724	5741	5744	5780	5789	5794	5797	5827	5872	5879
[451]	5899	5922	5923	5924	5927	5936	5938	5947	5973	5983
[461]	5984	5985	5988	5994	6007	6014	6045	6049	6061	6062
[471]	6064	6073	6087	6120	6121	6131	6138	6151	6161	6162
[481]	6178	6180	6315	6325	6326	6385	6394	6408	6421	6467
[491]	6474	6501	6539	6541	6553	6561	6564	6568	6580	6586
[501]	6593	6612	6622	6633	6634	6652	6663	6671	6673	6675
[511]	6680	6711	6712	6718	6754	6762	6775	6776	6780	6788
[521]	6789	6794	6795	6799	6845	6849	6862	6880	6893	6900
[531]	6909	6923	6928	6933	6939	6949	6951	6969	6978	6980
[541]	7010	7046	7053	7066	7067	7075	7082	7099	7116	7124
[551]	7125	7131	7148	7151	7157	7167	7180	7187	7201	7241
[561]	7249	7253	7260	7284	7295	7297	7306	7310	7313	7327
[571]	7341	7358	7364	7387	7407	7416	7431	7501	7518	7524
[581]	7532	7553	7571	7589	7592	7595	7598	7609	7637	7665
[591]	7666	7668	7671	7674	7716	7722	7743	7748	7751	7752
[601]	7758	7759	7760	7764	7768	7774	7778	7779	7786	7790
[611]	7793	7803	7818	7821	7828	7875	7876	7880	7887	7925
[621]	7927	7932	7939	7940	7962	7985	8001	8007	8010	8017
[631]	8020	8059	8072	8075	8079	8098	8101	8117	8138	8139
[641]	8146	8157	8158	8220	8231	8333	8345	8405	8431	8438
[651]	8461	8476	8478	8482	8504	8519	8525	8563	8574	8599
[661]	8603	8622	8625	8628	8656	8657	8666	8672	8673	8676
[671]	8677	8691	8696	8699	8702	8726	8729	8733	8745	8760
[681]	8787	8788	8794	8797	8809	8816	8828	8858	8872	8883
[691]	8893	8914	8923	8948	8960	8998	9009	9013	9014	9039
[701]	9040	9047	9072	9073	9084	9092	9094	9120	9121	9124
[711]	9125	9126	9148	9149	9158	9166	9174	9202	9209	9210
[721]	9211	9226	9265	9271	9272	9282	9285	9287	9294	9309
[731]	9318	9321	9325	9331	9337	9339	9354	9358	9373	9381
[741]	9382	9383	9391	9446	9448	9455	9460	9472	9489	9493
[751]	9508	9513	9517	9539	9543	9544	9587	9588	9593	9607
[761]	9633	9661	9683	9703	9712	9775	9788	9807	9813	9829
[771]	9840	9842	9844	9846	9851	9872	9895	9898	9902	9933
[781]	9968	9981	9988	10000	10006	10023	10062	10073	10074	10076
[791]	10097	10108	10123	10145	10154	10164	10183	10199	10200	10216
[801]	10217	10218	10233	10262	10267	10268	10269	10278	10283	10286
[811]	10313	10318	10319	10348	10349	10371	10391	10401	10411	10471
[821]	10485	10573	10596	10598	10600	10617	10650	10651	10663	10671
[831]	10679	10681	10696	10726	10739	10745	10747	10758	10762	10764
[841]	10789	10790	10824	10829	10843	10848	10857	10867	10914	10918
[851]	10945	10951	10954	10955	10996	11035	11042	11048	11057	11058
[861]	11060	11062	11063	11071	11080	11085	11108	11113	11114	11126
[871]	11127	11128	11141	11157	11171	11172	11227	11265	11266	11282

```

[881] 11293 11298 11316 11319 11326 11337 11360 11366 11378 11395
[891] 11397 11403 11406 11407 11408 11412 11459 11460 11491 11514
[901] 11528 11534 11544 11551 11558 11579 11581 11584 11619 11626
[911] 11631 11638 11639 11681 11707 11759 11761 11763 11770 11805
[921] 11807 11830 11870 11891 11896 11910 11912 11916 11918 11928
[931] 11944 11947 11954 11968 11971 11975 11996 11998 12012 12015
[941] 12032 12033 12045 12052 12072 12108 12132 12162 12177 12185
[951] 12218 12240 12267 12278 12288 12293 12294 12297 12312 12317
[961] 12349 12355 12360 12361 12367 12377 12378 12383 12385 12388
[971] 12437 12461 12486 12487 12507 12518 12540 12544 12565 12566
[981] 12587 12591 12602 12603 12612 12622 12623 12665 12676 12680
[991] 12707 12733 12759 12810 12820 12842 12843 12878 12889 12898
[1001] 12914 12918 12919 12939 12941 12960 12982 12983 12984 12985
[1011] 12986 12990 13001 13018 13020 13025 13034 13039 13041 13048
[1021] 13049 13052 13053 13065 13066 13082 13083 13102 13125 13152
[1031] 13155 13159 13160 13163 13173 13180 13184 13201 13206 13236
[1041] 13245 13250 13255 13278 13282 13299 13303 13305 13336 13348
[1051] 13354 13376 13421 13432 13457 13489 13511 13521 13544 13561
[1061] 13572 13592 13593 13603 13628 13674 13696 13697 13698 13761
[1071] 13787 13798 13799 13810 13813 13815 13821 13845 13872 13880
[1081] 13896 13905 13906 13912 13928 13940 13944 13958 13983 13991
[1091] 13995 13997 14024 14051 14083 14103 14111 14113 14125 14137
[1101] 14154 14155 14172 14199 14203 14225 14229 14232 14243 14251
[1111] 14253 14267 14291 14293 14302 14313 14317 14323 14330 14349
[1121] 14350 14357 14358 14364 14376 14401 14406 14423 14425 14428
[1131] 14442 14451 14459 14489 14497 14503 14515 14556 14557 14566
[1141] 14568 14570 14609 14611 14616 14641 14650 14653 14660 14662
[1151] 14677 14691 14694 14696 14701 14745 14750 14770 14783 14789
[1161] 14798 14812 14815 14822 14824 14848 14873 14885 14889 14896
[1171] 14909 14926 14930 14950 14961 14972 15000 15021 15025 15033
[1181] 15043 15044 15046 15057 15059 15067 15068 15103 15106 15113
[1191] 15132 15164 15171 15176 15180 15188 15197 15202 15203 15246
[1201] 15248 15253 15265 15268 15291 15292 15304 15312 15319 15348
[1211] 15373 15386 15404 15406 15407 15409 15418 15419 15426 15431
[1221] 15448 15449 15476 15483 15490 15507 15511 15516 15525 15558
[1231] 15588 15618 15619 15620 15621 15625 15633 15635 15640 15641
[1241] 15650 15734 15775 15853 15854 15862 15881 15889 15904 15926
[1251] 15967 15977 15979 15988 15990 15993 16009 16073 16074 16087
[1261] 16107 16153 16166 16174 16180 16228 16231 16250 16257 16264
[1271] 16275 16285 16289 16294 16296 16312 16313 16317 16329 16344
[1281] 16352 16403 16423 16428 16496 16524 16525 16526 16556 16560
[1291] 16564 16593 16594 16600 16604 16608 16641 16651 16667 16678
[1301] 16682 16686 16746 16753 16755 16786 16793 16838 16862 16871
[1311] 16882 16909 16919 16935

```

```
> head(sort(fdata[ind2,3]))
```

```
[1] "27.3.1" "27.3.1" "27.3.1" "27.3.10" "27.3.10" "27.3.10"
```

```
> ind <- c(ind1,ind2)
```

```
> table(fdata[ind,3])
```

```

 27.3  27.3.1 27.3.10 27.3.11 27.3.12 27.3.13 27.3.14 27.3.15
   10      3      5     73      20       2       7       5
27.3.16 27.3.17 27.3.18 27.3.19 27.3.2 27.3.20 27.3.21 27.3.22

```

```

      5      4      3      2      6      7      14      41
27.3.23 27.3.24 27.3.25 27.3.26 27.3.27 27.3.29 27.3.3 27.3.30
      15      12      90      15      44      11      34      21
27.3.32 27.3.34 27.3.35 27.3.36 27.3.37 27.3.38 27.3.39 27.3.4
      46      10      55      10      8      2      3      18
27.3.40 27.3.41 27.3.42 27.3.44 27.3.46 27.3.47 27.3.48 27.3.49
      18      2      4      27      5      2      7      2
  27.3.5 27.3.50 27.3.51 27.3.52 27.3.53 27.3.54 27.3.55 27.3.57
      18      27      3      11      1      12      12      21
27.3.58 27.3.59 27.3.6 27.3.60 27.3.61 27.3.62 27.3.63 27.3.64
      4      10      78      5      2      10      13      3
27.3.65 27.3.66 27.3.67 27.3.68 27.3.69 27.3.7 27.3.70 27.3.71
      3      2      117      10      28      21      3      11
27.3.72 27.3.73 27.3.75 27.3.8 27.3.80 27.3.81 27.3.82 27.3.84
      1      7      2      20      7      2      2      4
27.3.85 27.3.86 27.3.9 27.3.99
      6      3      12      165

```

```
> length(ind)
```

```
[1] 1324
```

```
> #@ function to find a bin and sub-bins
```

```
> in_bins <- function(x, bincodes) {
```

```
+   in1 <- grep(paste0("^", x, "\\."), bincodes)
```

```
+   in2 <- grep(paste0("^", x, "$"), bincodes)
```

```
+   in3 <- c(in2, in1)
```

```
+   return(in3)
```

```
+ }
```

```
> in_bins("2", c("2", "2.1", "2.1.1", "22", "22.2.1"))
```

```
[1] 1 2 3
```

3.10.1 Genes in bins of interest

Find genes in sub-bins

```
> intgenes1 <- sapply(bindata$bin, function(x) fdata$geneID[grep(paste0("^", x,
> str(intgenes1)
```

```
List of 8
```

```
$ 2 : chr [1:82] "Vitvi02g01845" "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g0
```

```
$ 3 : chr [1:84] "Vitvi02g01701" "Vitvi10g02295" "Vitvi00g01259" "Vitvi01g0
```

```
$ 8 : chr [1:56] "Vitvi07g03070" "Vitvi01g00274" "Vitvi01g00698" "Vitvi01g0
```

```
$ 10 : chr [1:201] "Vitvi02g01716" "Vitvi07g02990" "Vitvi10g02284" "Vitvi10g
```

```
$ 13 : chr [1:187] "Vitvi07g03049" "Vitvi00g00869" "Vitvi02g01749" "Vitvi01g
```

```
$ 16 : chr [1:237] "Vitvi02g01683" "Vitvi02g01722" "Vitvi10g02185" "Vitvi07g
```

```
$ 27.3: chr [1:1314] "Vitvi02g01753" "Vitvi02g01762" "Vitvi02g01795" "Vitvi02
```

```
$ 35 : chr [1:6244] "Vitvi07g02832" "Vitvi07g02830" "Vitvi07g02812" "Vitvi07
```

Find genes in bins (no dot at the end)

```
> intgenes2 <- sapply(bindata$bin, function(x) fdata$geneID[grep(paste0("^",
> str(intgenes2)
```

List of 8

```
$ 2 : chr(0)
$ 3 : chr(0)
$ 8 : chr(0)
$ 10 : chr(0)
$ 13 : chr [1:8] "Vitvi01g01704" "Vitvi02g00467" "Vitvi04g00506" "Vitvi07g01
$ 16 : chr "Vitvi08g01337"
$ 27.3: chr [1:10] "Vitvi01g01749" "Vitvi04g01606" "Vitvi06g00072" "Vitvi09g0
$ 35 : chr(0)
```

Combine two sets

```
> intgenes <- Map(c, intgenes1, intgenes2)
> str(intgenes)
```

List of 8

```
$ 2 : chr [1:82] "Vitvi02g01845" "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g0
$ 3 : chr [1:84] "Vitvi02g01701" "Vitvi10g02295" "Vitvi00g01259" "Vitvi01g0
$ 8 : chr [1:56] "Vitvi07g03070" "Vitvi01g00274" "Vitvi01g00698" "Vitvi01g0
$ 10 : chr [1:201] "Vitvi02g01716" "Vitvi07g02990" "Vitvi10g02284" "Vitvi10g
$ 13 : chr [1:195] "Vitvi07g03049" "Vitvi00g00869" "Vitvi02g01749" "Vitvi01g
$ 16 : chr [1:238] "Vitvi02g01683" "Vitvi02g01722" "Vitvi10g02185" "Vitvi07g
$ 27.3: chr [1:1324] "Vitvi02g01753" "Vitvi02g01762" "Vitvi02g01795" "Vitvi02
$ 35 : chr [1:6244] "Vitvi07g02832" "Vitvi07g02830" "Vitvi07g02812" "Vitvi07
```

```
> # unlist(intgenes)table(fdata$BINCODE)
> head(fdata[fdata[, "geneID"]%in% unlist(intgenes),2:3], 10)
```

	geneID	BINCODE
2	Vitvi07g02832	35.2
3	Vitvi07g02830	35.2
4	Vitvi07g02812	35.2
5	Vitvi07g02811	35.2
6	Vitvi09g02033	35.2
7	Vitvi09g02034	35.2
8	Vitvi08g02428	35.2
10	Vitvi07g02753	35.2
16	Vitvi07g03006	35.2
20	Vitvi02g01753	27.3.30

```
> tail(fdata[fdata[, "geneID"]%in% unlist(intgenes),2:3], 10)
```

	geneID	BINCODE
16919	Vitvi18g01322	27.3.21
16921	Vitvi18g01950	35.2
16922	Vitvi18g03096	35.2
16927	Vitvi19g01926	35.2
16928	Vitvi19g01994	35.2
16929	Vitvi19g02044	35.2
16930	Vitvi19g02064	2.2.2.1.2
16932	Vitvi19g01155	35.2
16934	Vitvi19g01515	35.2
16935	Vitvi19g01589	27.3.37

```
> length(unique(unlist(intgenes)))
```

```
[1] 8338
```

```

> nn <- t(t(sapply(intgenes, length)))
> nn
      [,1]
2       82
3       84
8       56
10      201
13      195
16      238
27.3   1324
35     6244

```

Number of interesting genes: 8338.

3.10.2 Metabolites in bins of interest

```

> intmtbs <- sapply(bindata$bin, function(x) rownames(mfdata)[in_bins(x, mfdata$Bin)])
> str(intmtbs)
List of 8
 $ 2    : chr [1:3] "Fructose" "Glucose" "Sucrose"
 $ 3    : chr [1:7] "Erythronic.acid" "Galactinol" "Galactose" "Myo.Inositol" ...
 $ 8    : chr [1:2] "Fumaric.acid" "Succinic.acid"
 $ 10   : chr [1:5] "Arabinose" "Melibiose" "Rhamnose" "Ribonic.acid" ...
 $ 13   : chr [1:8] "Aspartic.acid" "Isoleucine" "Leucine" "Phenylalanine" ...
 $ 16   : chr [1:6] "Trans.Caffeic.acid" "Catechin" "Gallic.acid" "Hydroquinone"
 $ 27.3 : chr(0)
 $ 35   : chr [1:8] "Gluconic.acid" "Glucopyranose..H2O." "Lyxonic.acid" "Maleic.acid"

> x <- "2"
> mfdata$Bin[grepl("^", x), mfdata$Bin]
[1] "22.1002"      "2.2.1.1001" "2.2.1.1002" "21.1009"      "22.1003"
[6] "21.1010"      "2.1.1.1006" "21.1011"     "23.2.1002"

> mfdata$Bin[in_bins(x, mfdata$Bin)]
[1] "2.2.1.1001" "2.2.1.1002" "2.1.1.1006"

> nn <- t(t(sapply(intmtbs, length)))
> nn
      [,1]
2       3
3       7
8       2
10      5
13      8
16      6
27.3    0
35      8

> # unlist(intmtbs)
> head(mfdata[unlist(intmtbs), 2:3], 10)

```

	Bin
Fructose	2.2.1.1001
Glucose	2.2.1.1002
Sucrose	2.1.1.1006
Erythronic.acid	3.99.1007
Galactinol	3.1.1001
Galactose	3.99.1010
Myo.Inostol	3.4.1001
Raffinose	3.1.1002
Threitol	3.3.1011
Xylose	3.99.1027

	Description
Fructose	major CHO metabolism.degradation.sucrose.fructose
Glucose	major CHO metabolism.degradation.sucrose.glucose
Sucrose	major CHO metabolism.synthesis.sucrose.sucrose
Erythronic.acid	minor CHO metabolism.misc.erythronic acid
Galactinol	minor CHO metabolism.raffinose family.galactinol
Galactose	minor CHO metabolism.misc.galactose
Myo.Inostol	minor CHO metabolism.myo-inositol.inositol
Raffinose	minor CHO metabolism.raffinose family.raffinose
Threitol	minor CHO metabolism.sugar alcohols.threitol
Xylose	minor CHO metabolism.misc.xylose

```
> tail(mfdata[unlist(intmtbs),2:3], 10)
```

	Bin
Quinic.acid	16.2.99.1044
X3.caffeoylquinic.acid	16.2.99.1008
Gluconic.acid	35.1.1012
Glucopyranose..H2O.	35.1.1038
Lyxonic.acid	35.1.1023
Maleic.acid	35.1.1024
Malonic.acid	35.1.1036
Phosphoric.acid	35.1.1035
Tartaric.acid	35.1.1037
Threonolactone	35.1.1034

Quinic.acid	secondary metabolism.phenylpropanoids.unspecified
X3.caffeoylquinic.acid	secondary metabolism.phenylpropanoids.unspecified.3-caf
Gluconic.acid	not assigned.no ontolo
Glucopyranose..H2O.	not assigned.no ontology.g
Lyxonic.acid	not assigned.no ontology.
Maleic.acid	not assigned.no onto
Malonic.acid	not assigned.no ontology.
Phosphoric.acid	not assigned.no ontology.pho
Tartaric.acid	not assigned.no ontology.t
Threonolactone	not assigned.no ontology.th

```
> length(unique(unlist(intmtbs)))
```

```
[1] 39
```

3.11 Created objects overview

```
> #if(!exists("addObject")) {
> addObject <- function(x=NULL, desc="", x0=my.objects) {
+ if(is.null(x)) x0 <- data.frame(name="", description="", class="", nrow=NA,
+ nr <- length(x)
+ nc <- ncol(x)
+ if( is.data.frame(x) | is.matrix(x) | is.array(x) ) {
+   nr <- nrow(x)
+   nc <- ncol(x)
+ }
+ if(is.null(nc)) nc <- NA
+ x0 <- rbind(x0, c(deparse(substitute(x)), desc, class(x)[1], nr, nc))
+ x0 <- x0[x0$name!="", ]
+ }
+ rownames(x0) <- 1:nrow(x0)
+ return(x0)
+ }
> #}

> (my.objects <- addObject())
  name description class nrow ncol
1              NA    NA

> (my.objects <- addObject(t18, "Transcripts for 2018"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48

> (my.objects <- addObject(t19, "Transcripts for 2019"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32

> (my.objects <- addObject(t1819, "Transcripts for 18/19"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
3 t1819 Transcripts for 18/19 data.frame 15242   80

> (my.objects <- addObject(pdata18, "Phenodata for 2018"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
3 t1819 Transcripts for 18/19 data.frame 15242   80
4 pdata18 Phenodata for 2018 data.frame    48   22

> (my.objects <- addObject(pdata19, "Phenodata for 2019"))
  name      description      class  nrow ncol
1  t18 Transcripts for 2018 data.frame 15242   48
2  t19 Transcripts for 2019 data.frame 15242   32
3 t1819 Transcripts for 18/19 data.frame 15242   80
4 pdata18 Phenodata for 2018 data.frame    48   22
5 pdata19 Phenodata for 2019 data.frame    32   22

> (my.objects <- addObject(pdata1819, "Phenodata for 2018/19"))
```

```

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819 Transcripts for 18/19 data.frame 15242  80
4      pdata18 Phenodata for 2018 data.frame  48  22
5      pdata19 Phenodata for 2019 data.frame  32  22
6      pdata1819 Phenodata for 2018/19 data.frame  80  22
> (my.objects <- addObject(fdata,"Trans. featuredata 18/19"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819 Transcripts for 18/19 data.frame 15242  80
4      pdata18 Phenodata for 2018 data.frame  48  22
5      pdata19 Phenodata for 2019 data.frame  32  22
6      pdata1819 Phenodata for 2018/19 data.frame  80  22
7      fdata Trans. featuredata 18/19 data.frame 16936  5
> (my.objects <- addObject(m18,"Metabolites for 2018"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819 Transcripts for 18/19 data.frame 15242  80
4      pdata18 Phenodata for 2018 data.frame  48  22
5      pdata19 Phenodata for 2019 data.frame  32  22
6      pdata1819 Phenodata for 2018/19 data.frame  80  22
7      fdata Trans. featuredata 18/19 data.frame 16936  5
8      m18  Metabolites for 2018 data.frame  96  60
> (my.objects <- addObject(m19,"Metabolites for 2019"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819 Transcripts for 18/19 data.frame 15242  80
4      pdata18 Phenodata for 2018 data.frame  48  22
5      pdata19 Phenodata for 2019 data.frame  32  22
6      pdata1819 Phenodata for 2018/19 data.frame  80  22
7      fdata Trans. featuredata 18/19 data.frame 16936  5
8      m18  Metabolites for 2018 data.frame  96  60
9      m19  Metabolites for 2019 data.frame  94  60
> (my.objects <- addObject(m1819,"Metabolites for 18/19"))

      name      description      class  nrow ncol
1      t18  Transcripts for 2018 data.frame 15242  48
2      t19  Transcripts for 2019 data.frame 15242  32
3      t1819 Transcripts for 18/19 data.frame 15242  80
4      pdata18 Phenodata for 2018 data.frame  48  22
5      pdata19 Phenodata for 2019 data.frame  32  22
6      pdata1819 Phenodata for 2018/19 data.frame  80  22
7      fdata Trans. featuredata 18/19 data.frame 16936  5
8      m18  Metabolites for 2018 data.frame  96  60
9      m19  Metabolites for 2019 data.frame  94  60
10     m1819 Metabolites for 18/19 data.frame  190  60
> (my.objects <- addObject(sm18,"Standardized metabolites 18"))

```

	name	description	class	nrow	ncol
1	t18	Transcripts for 2018	data.frame	15242	48
2	t19	Transcripts for 2019	data.frame	15242	32
3	t1819	Transcripts for 18/19	data.frame	15242	80
4	pdata18	Phenodata for 2018	data.frame	48	22
5	pdata19	Phenodata for 2019	data.frame	32	22
6	pdata1819	Phenodata for 2018/19	data.frame	80	22
7	fdata	Trans. featuredata 18/19	data.frame	16936	5
8	m18	Metabolites for 2018	data.frame	96	60
9	m19	Metabolites for 2019	data.frame	94	60
10	m1819	Metabolites for 18/19	data.frame	190	60
11	sm18	Standardized metabolites 18	matrix	96	55

```
> (my.objects <- addObject(sm19,"Standardized metabolites 19"))
```

	name	description	class	nrow	ncol
1	t18	Transcripts for 2018	data.frame	15242	48
2	t19	Transcripts for 2019	data.frame	15242	32
3	t1819	Transcripts for 18/19	data.frame	15242	80
4	pdata18	Phenodata for 2018	data.frame	48	22
5	pdata19	Phenodata for 2019	data.frame	32	22
6	pdata1819	Phenodata for 2018/19	data.frame	80	22
7	fdata	Trans. featuredata 18/19	data.frame	16936	5
8	m18	Metabolites for 2018	data.frame	96	60
9	m19	Metabolites for 2019	data.frame	94	60
10	m1819	Metabolites for 18/19	data.frame	190	60
11	sm18	Standardized metabolites 18	matrix	96	55
12	sm19	Standardized metabolites 19	matrix	94	55

```
> (my.objects <- addObject(sm1819,"Standardized metabolites 18/19"))
```

	name	description	class	nrow	ncol
1	t18	Transcripts for 2018	data.frame	15242	48
2	t19	Transcripts for 2019	data.frame	15242	32
3	t1819	Transcripts for 18/19	data.frame	15242	80
4	pdata18	Phenodata for 2018	data.frame	48	22
5	pdata19	Phenodata for 2019	data.frame	32	22
6	pdata1819	Phenodata for 2018/19	data.frame	80	22
7	fdata	Trans. featuredata 18/19	data.frame	16936	5
8	m18	Metabolites for 2018	data.frame	96	60
9	m19	Metabolites for 2019	data.frame	94	60
10	m1819	Metabolites for 18/19	data.frame	190	60
11	sm18	Standardized metabolites 18	matrix	96	55
12	sm19	Standardized metabolites 19	matrix	94	55
13	sm1819	Standardized metabolites 18/19	matrix	190	55

```
> (my.objects <- addObject(mfdata,"Metabolites featuredata 18/19"))
```

	name	description	class	nrow	ncol
1	t18	Transcripts for 2018	data.frame	15242	48
2	t19	Transcripts for 2019	data.frame	15242	32
3	t1819	Transcripts for 18/19	data.frame	15242	80
4	pdata18	Phenodata for 2018	data.frame	48	22
5	pdata19	Phenodata for 2019	data.frame	32	22
6	pdata1819	Phenodata for 2018/19	data.frame	80	22
7	fdata	Trans. featuredata 18/19	data.frame	16936	5
8	m18	Metabolites for 2018	data.frame	96	60
9	m19	Metabolites for 2019	data.frame	94	60

```

10      m1819      Metabolites for 18/19 data.frame 190 60
11      sm18      Standardized metabolites 18      matrix 96 55
12      sm19      Standardized metabolites 19      matrix 94 55
13      sm1819 Standardized metabolites 18/19      matrix 190 55
14      mldata      Metabolites featuredata 18/19 data.frame 55 3

```

```
> (my.objects <- addObject(intgenes, "Names of genes in bins"))
```

```

      name      description      class  nrow ncol
1      t18      Transcripts for 2018 data.frame 15242 48
2      t19      Transcripts for 2019 data.frame 15242 32
3      t1819      Transcripts for 18/19 data.frame 15242 80
4      pdata18      Phenodata for 2018 data.frame 48 22
5      pdata19      Phenodata for 2019 data.frame 32 22
6      pdata1819      Phenodata for 2018/19 data.frame 80 22
7      fdata      Trans. featuredata 18/19 data.frame 16936 5
8      m18      Metabolites for 2018 data.frame 96 60
9      m19      Metabolites for 2019 data.frame 94 60
10     m1819      Metabolites for 18/19 data.frame 190 60
11     sm18      Standardized metabolites 18      matrix 96 55
12     sm19      Standardized metabolites 19      matrix 94 55
13     sm1819 Standardized metabolites 18/19      matrix 190 55
14     mldata      Metabolites featuredata 18/19 data.frame 55 3
15     intgenes      Names of genes in bins      list 8 <NA>

```

```
> (my.objects <- addObject(intmtbs, "Names of metabolites in bins"))
```

```

      name      description      class  nrow ncol
1      t18      Transcripts for 2018 data.frame 15242 48
2      t19      Transcripts for 2019 data.frame 15242 32
3      t1819      Transcripts for 18/19 data.frame 15242 80
4      pdata18      Phenodata for 2018 data.frame 48 22
5      pdata19      Phenodata for 2019 data.frame 32 22
6      pdata1819      Phenodata for 2018/19 data.frame 80 22
7      fdata      Trans. featuredata 18/19 data.frame 16936 5
8      m18      Metabolites for 2018 data.frame 96 60
9      m19      Metabolites for 2019 data.frame 94 60
10     m1819      Metabolites for 18/19 data.frame 190 60
11     sm18      Standardized metabolites 18      matrix 96 55
12     sm19      Standardized metabolites 19      matrix 94 55
13     sm1819 Standardized metabolites 18/19      matrix 190 55
14     mldata      Metabolites featuredata 18/19 data.frame 55 3
15     intgenes      Names of genes in bins      list 8 <NA>
16     intmtbs      Names of metabolites in bins      list 8 <NA>

```

```
> my.objects
```

```

      name      description      class  nrow ncol
1      t18      Transcripts for 2018 data.frame 15242 48
2      t19      Transcripts for 2019 data.frame 15242 32
3      t1819      Transcripts for 18/19 data.frame 15242 80
4      pdata18      Phenodata for 2018 data.frame 48 22
5      pdata19      Phenodata for 2019 data.frame 32 22
6      pdata1819      Phenodata for 2018/19 data.frame 80 22
7      fdata      Trans. featuredata 18/19 data.frame 16936 5
8      m18      Metabolites for 2018 data.frame 96 60

```

9	m19	Metabolites for 2019	data.frame	94	60
10	m1819	Metabolites for 18/19	data.frame	190	60
11	sm18	Standardized metabolites 18	matrix	96	55
12	sm19	Standardized metabolites 19	matrix	94	55
13	sm1819	Standardized metabolites 18/19	matrix	190	55
14	mldata	Metabolites featuredata 18/19	data.frame	55	3
15	intgenes	Names of genes in bins	list	8	<NA>
16	intmtbs	Names of metabolites in bins	list	8	<NA>

List of data objects:

```
> my.objects
```

	name	description	class	nrow	ncol
1	t18	Transcripts for 2018	data.frame	15242	48
2	t19	Transcripts for 2019	data.frame	15242	32
3	t1819	Transcripts for 18/19	data.frame	15242	80
4	pdata18	Phenodata for 2018	data.frame	48	22
5	pdata19	Phenodata for 2019	data.frame	32	22
6	pdata1819	Phenodata for 2018/19	data.frame	80	22
7	fdata	Trans. featuredata 18/19	data.frame	16936	5
8	m18	Metabolites for 2018	data.frame	96	60
9	m19	Metabolites for 2019	data.frame	94	60
10	m1819	Metabolites for 18/19	data.frame	190	60
11	sm18	Standardized metabolites 18	matrix	96	55
12	sm19	Standardized metabolites 19	matrix	94	55
13	sm1819	Standardized metabolites 18/19	matrix	190	55
14	mldata	Metabolites featuredata 18/19	data.frame	55	3
15	intgenes	Names of genes in bins	list	8	<NA>
16	intmtbs	Names of metabolites in bins	list	8	<NA>

List of interesting genes, based on typification on 50* reports (key: Transcript stats. Typification is extracted from the file in the relevant output directory. To allow manual curation, the info is extracted from the Type column.

```
> tsfn <- getMeta(.adesc, "Transcript stats")
> stat4 <- read.table(file.path(.aroot, tsfn), sep="\t", header=TRUE)
> colnames(stat4)
```

```
[1] "X" "A" "Coef.mc"
[4] "Coef.c" "Coef.mf.mc" "Coef.f.c"
[7] "Kcoef.f" "t.mc" "t.c"
[10] "t.mf.mc" "t.f.c" "P.value.mc"
[13] "P.value.c" "P.value.mf.mc" "P.value.f.c"
[16] "P.value.adj.mc" "P.value.adj.c" "P.value.adj.mf.mc"
[19] "P.value.adj.f.c" "F" "F.p.value"
[22] "Type" "interestingC" "interestingFC"
[25] "geneID" "BINCODE" "NAME"
[28] "DESCRIPTION"
```

```
> rownames(stat4) <- stat4[,1]
> head(stat4)
```

		X	A	Coef.mc	Coef.c	
Vitvi03g00325	Vitvi03g00325	2.29529737	3.1923214	5.400429		
Vitvi17g00601	Vitvi17g00601	-0.09054575	-1.1866150	4.512791		
Vitvi05g00011	Vitvi05g00011	3.00782492	2.7136299	4.101024		
Vitvi13g02005	Vitvi13g02005	2.33061623	2.9484215	4.078080		
Vitvi02g00695	Vitvi02g00695	-0.45420732	-0.8399601	4.047520		
Vitvi14g01381	Vitvi14g01381	-0.72321946	-1.1530667	3.935431		
		Coef.mf.mc	Coef.f.c	Koef.f	t.mc	t.c
Vitvi03g00325		-1.7940481	-0.29162541	5.108803	4.801209	2.919406
Vitvi17g00601		2.1921385	-0.33971975	4.173071	-2.341540	3.200805
Vitvi05g00011		0.5883901	0.03610049	4.137125	8.336348	4.528348
Vitvi13g02005		-1.2356105	1.22197743	5.300058	3.618330	1.798857
Vitvi02g00695		0.7715056	-1.08372917	2.963791	-1.857328	3.216927
Vitvi14g01381		0.8596946	0.58827898	4.523710	-1.546481	1.897163
		t.mf.mc	t.f.c	P.value.mc	P.value.c	
Vitvi03g00325		-1.9079328	-0.10592036	9.103982e-05	0.0080809276	
Vitvi17g00601		3.0587557	-0.16189100	2.892715e-02	0.0042173372	
Vitvi05g00011		1.2781316	0.02678234	3.604890e-08	0.0001755321	
Vitvi13g02005		-1.0722232	0.36215284	1.571115e-03	0.0861338096	
Vitvi02g00695		1.2062964	-0.57870975	7.705364e-02	0.0040613495	
Vitvi14g01381		0.8153037	0.19053890	1.366212e-01	0.0713562714	
		P.value.mf.mc	P.value.f.c	P.value.adj.mc	P.value.adj.c	
Vitvi03g00325		0.069880852	0.9166302	1.006038e-04	0.28511458	
Vitvi17g00601		0.005867102	0.8729075	3.029669e-02	0.23762225	
Vitvi05g00011		0.214866433	0.9788810	4.329163e-08	0.07644173	
Vitvi13g02005		0.295539873	0.7207826	1.694639e-03	0.58897413	
Vitvi02g00695		0.240844889	0.5688147	7.988693e-02	0.23288283	
Vitvi14g01381		0.423862612	0.8506793	1.407775e-01	0.56306208	
		P.value.adj.mf.mc	P.value.adj.f.c	F		
Vitvi03g00325		0.29606841	0.9999488	9.550446		
Vitvi17g00601		0.05151288	0.9999488	37.060841		
Vitvi05g00011		0.56223076	0.9999488	84.152716		
Vitvi13g02005		0.66176271	0.9999488	6.968467		
Vitvi02g00695		0.59836313	0.9999488	35.455608		
Vitvi14g01381		0.76054331	0.9999488	19.816526		
		F.p.value	Type	interestingC	interestingFC	
Vitvi03g00325		1.356555e-04	Type5	*		
Vitvi17g00601		2.421190e-09	Type5	*		
Vitvi05g00011		8.630059e-13	Type1	*		
Vitvi13g02005		9.348733e-04	Type1.4			
Vitvi02g00695		3.642503e-09		*		
Vitvi14g01381		5.922355e-07	Type1			
		geneID	BINCODE			
Vitvi03g00325	Vitvi03g00325	27.3.25				
Vitvi17g00601	Vitvi17g00601	17.6.3				
Vitvi05g00011	Vitvi05g00011	35.2				
Vitvi13g02005	Vitvi13g02005	29.5.1				
Vitvi02g00695	Vitvi02g00695	20.1				
Vitvi14g01381	Vitvi14g01381	35.2				
Vitvi03g00325	RNA.regulation of transcription.MYB domain transcription factor					
Vitvi17g00601	hormone metabolism.gibberelin.induced-regulated-responsive-act					
Vitvi05g00011	not assigned.u					

```

Vitvi13g02005 protein.degradation.subt
Vitvi02g00695 stress.
Vitvi14g01381 not assigned.u

Vitvi03g00325 RAD-like
Vitvi17g00601 Gibberellin-regulated family prote
Vitvi05g00011 Pollen Ole e 1 allergen and extensin family pro
Vitvi13g02005 Subtilisin-like serine endopeptidase family prote
Vitvi02g00695 Polyketide cyclase/dehydrase and lipid transport superfamily pro
Vitvi14g01381

```

Select interesting genes

```

> filter <- unlist(intgenes) #stat4$Type!="
> length(filter)
[1] 8424
> statig <- stat4[filter,]
> dim(statig)
[1] 8424 28

> (my.objects <- addObject(stat4,"Statistics from transcript analysis (50*.Rnw)
name description class
1 t18 Transcripts for 2018 data.frame
2 t19 Transcripts for 2019 data.frame
3 t1819 Transcripts for 18/19 data.frame
4 pdata18 Phenodata for 2018 data.frame
5 pdata19 Phenodata for 2019 data.frame
6 pdata1819 Phenodata for 2018/19 data.frame
7 fdata Trans. featuredata 18/19 data.frame
8 m18 Metabolites for 2018 data.frame
9 m19 Metabolites for 2019 data.frame
10 m1819 Metabolites for 18/19 data.frame
11 sm18 Standardized metabolites 18 matrix
12 sm19 Standardized metabolites 19 matrix
13 sm1819 Standardized metabolites 18/19 matrix
14 mfddata Metabolites featuredata 18/19 data.frame
15 intgenes Names of genes in bins list
16 intmtbs Names of metabolites in bins list
17 stat4 Statistics from transcript analysis (50*.Rnw) data.frame
nrow ncol
1 15242 48
2 15242 32
3 15242 80
4 48 22
5 32 22
6 80 22
7 16936 5
8 96 60
9 94 60
10 190 60
11 96 55
12 94 55
13 190 55
14 55 3
15 8 <NA>
16 8 <NA>
17 15242 28

```

```
> (my.objects <- addObject(statig, "Statistics for interesting genes"))
```

	name	description	class
1	t18	Transcripts for 2018	data.frame
2	t19	Transcripts for 2019	data.frame
3	t1819	Transcripts for 18/19	data.frame
4	pdata18	Phenodata for 2018	data.frame
5	pdata19	Phenodata for 2019	data.frame
6	pdata1819	Phenodata for 2018/19	data.frame
7	fdata	Trans. featuredata 18/19	data.frame
8	m18	Metabolites for 2018	data.frame
9	m19	Metabolites for 2019	data.frame
10	m1819	Metabolites for 18/19	data.frame
11	sm18	Standardized metabolites 18	matrix
12	sm19	Standardized metabolites 19	matrix
13	sm1819	Standardized metabolites 18/19	matrix
14	mfddata	Metabolites featuredata 18/19	data.frame
15	intgenes	Names of genes in bins	list
16	intmtbs	Names of metabolites in bins	list
17	stat4	Statistics from transcript analysis (50*.Rnw)	data.frame
18	statig	Statistics for interesting genes	data.frame

	nrow	ncol
1	15242	48
2	15242	32
3	15242	80
4	48	22
5	32	22
6	80	22
7	16936	5
8	96	60
9	94	60
10	190	60
11	96	55
12	94	55
13	190	55
14	55	3
15	8	<NA>
16	8	<NA>
17	15242	28
18	8424	28

How many interesting genes are in the interesting bins?

```
> filter <- rownames(statig) %in% unlist(intgenes)
```

```
> sum(filter)
```

```
[1] 7617
```

```
> rownames(statig)[filter]
```

```
[1] "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g00053" "Vitvi01g00064"
[5] "Vitvi01g00681" "Vitvi01g00932" "Vitvi02g00184" "Vitvi02g00250"
[9] "Vitvi02g00512" "Vitvi02g00605" "Vitvi02g01232" "Vitvi03g00088"
[13] "Vitvi03g00304" "Vitvi03g01571" "Vitvi03g01572" "Vitvi05g00164"
[17] "Vitvi05g00357" "Vitvi05g00442" "Vitvi05g01193" "Vitvi05g01324"
[21] "Vitvi05g01516" "Vitvi06g00583" "Vitvi06g01272" "Vitvi06g01427"
```

[25]	"Vitvi07g00167"	"Vitvi07g00353"	"Vitvi07g00544"	"Vitvi07g01830"
[29]	"Vitvi08g00225"	"Vitvi08g00930"	"Vitvi08g01307"	"Vitvi08g01353"
[33]	"Vitvi08g01497"	"Vitvi08g01815"	"Vitvi09g00193"	"Vitvi10g00094"
[37]	"Vitvi10g00494"	"Vitvi10g00499"	"Vitvi10g00739"	"Vitvi11g00030"
[41]	"Vitvi11g00260"	"Vitvi11g00542"	"Vitvi11g00903"	"Vitvi12g00558"
[45]	"Vitvi12g00770"	"Vitvi12g01618"	"Vitvi13g00692"	"Vitvi13g00792"
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[53]	"Vitvi14g01406"	"Vitvi14g01692"	"Vitvi14g01873"	"Vitvi14g01968"
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[61]	"Vitvi16g00033"	"Vitvi16g00895"	"Vitvi16g01405"	"Vitvi17g00738"
[65]	"Vitvi18g00111"	"Vitvi18g00144"	"Vitvi18g00454"	"Vitvi18g02758"
[69]	"Vitvi18g01114"	"Vitvi18g01242"	"Vitvi18g01657"	"Vitvi18g01682"
[73]	"Vitvi18g02365"	"Vitvi18g02417"	"Vitvi19g00538"	"Vitvi19g00678"
[77]	"Vitvi19g00704"	"Vitvi02g01701"	"Vitvi10g02295"	"Vitvi00g01259"
[81]	"Vitvi01g00140"	"Vitvi01g00509"	"Vitvi01g00714"	"Vitvi01g00793"
[85]	"Vitvi01g01440"	"Vitvi02g00191"	"Vitvi02g00514"	"Vitvi02g00729"
[89]	"Vitvi03g00029"	"Vitvi03g00056"	"Vitvi03g00063"	"Vitvi03g00287"
[93]	"Vitvi04g00117"	"Vitvi04g01318"	"Vitvi04g01689"	"Vitvi05g00149"
[97]	"Vitvi05g00170"	"Vitvi05g00436"	"Vitvi05g00752"	"Vitvi06g00121"
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> head(statig[filter, c("Type", "BINCODE", "DESCRIPTION")])
```

	Type	BINCODE
Vitvi01g00025		2.2.1.1
Vitvi01g00052		2.2.2.6
Vitvi01g00053		2.2.2.6
Vitvi01g00064	Type3.F	2.2.2.2
Vitvi01g00681		35.2

Vitvi01g00932	2.2.2.1.1	
Vitvi01g00025		fructokinase-like protein Chr1:2
Vitvi01g00052	Glucose-6-phosphate/phosphate translocator-like protein	Chr5:1
Vitvi01g00053	Glucose-6-phosphate/phosphate translocator-like protein	Chr5:1
Vitvi01g00064		Glycosyl transferase%2C family 35 Chr3:1
Vitvi01g00681		phosphoglucan%2C water dikinase Chr4:12
Vitvi01g00932		alpha-amylase-like 3 Chr1:2

3.12 Data overview

```
> x <- my.objects
> x$name[1]

[1] "t18"

> for(i in 1:nrow(x)){
+ cat("\n\n----- ", x[i,1], ": ", x[i,2], " -----")
+ print(x[i,])
+ cat("\n")
+ print(head(eval(as.name(x[i,1]))))
+ }
```

```
----- t18: Transcripts for 2018 -----
```

name	description	class	nrow	ncol
1 t18	Transcripts for 2018	data.frame	15242	48
	C18_11d_WS1 C18_11d_WS2 C18_11d_WS3 C18_11d_WS4			
Vitvi15g01736	4.6646023 4.109897 4.4482203 4.013955			
Vitvi07g02832	-2.4786650 -1.601359 -1.4274193 -2.066419			
Vitvi07g02830	-1.8506337 -2.218030 -1.0648492 -1.580992			
Vitvi07g02812	-0.5805446 -1.266940 -0.3278837 -1.019113			
Vitvi07g02811	2.2762225 1.823447 1.9550503 1.648742			
Vitvi09g02033	-1.6901691 -2.218030 -2.6498117 -1.449747			
	C18_11d_WW1 C18_11d_WW2 C18_11d_WW3 C18_11d_WW4			
Vitvi15g01736	4.717536 4.154237 4.475261 4.466465			
Vitvi07g02832	-2.608485 -1.801183 -1.886474 -3.583384			
Vitvi07g02830	-1.544354 -1.405255 -1.755229 -1.381750			
Vitvi07g02812	-0.858463 -0.434401 -1.234397 -1.047331			
Vitvi07g02811	2.086902 2.105707 2.134837 1.908469			
Vitvi09g02033	-2.608485 -1.961648 -3.108866 -4.320350			
	C18_34d_WS1 C18_34d_WS2 C18_34d_WS3 C18_34d_WS4			
Vitvi15g01736	4.400333 4.641164 4.4191231 4.534438			
Vitvi07g02832	-5.683146 -2.452000 -4.4274120 -1.876949			
Vitvi07g02830	-2.513221 -2.452000 -4.4274120 -2.263972			
Vitvi07g02812	-2.875791 -2.693008 -2.5529429 -3.157057			
Vitvi07g02811	1.414886 1.409803 0.3970164 1.273993			
Vitvi09g02033	-2.513221 -3.345084 -2.1054839 -1.716484			
	C18_34d_WW1 C18_34d_WW2 C18_34d_WW3 C18_34d_WW4			
Vitvi15g01736	4.924801 5.085690 5.3397350 5.263629			
Vitvi07g02832	-2.827859 -3.130016 -4.6322874 -3.196388			
Vitvi07g02830	-3.190429 -1.545054 -2.1297871 -3.196388			
Vitvi07g02812	-2.827859 -1.182484 -3.4098950 -2.303303			
Vitvi07g02811	1.517916 1.357250 0.9626591 1.344985			
Vitvi09g02033	-4.412821 -3.130016 -2.3103594 -4.418780			
	C18_67d_WS1 C18_67d_WS2 C18_67d_WS3 C18_67d_WS4			
Vitvi15g01736	2.05871733 2.2895026 2.9234830 2.575657			
Vitvi07g02832	-5.85417200 -4.4786818 -4.4659691 -2.468738			
Vitvi07g02830	-2.15373228 -3.2562893 -3.7290035 -2.709746			
Vitvi07g02812	-1.21031581 -2.3632045 -2.3504919 -2.999252			
Vitvi07g02811	0.02847105 0.5362686 0.9824914 1.231702			
Vitvi09g02033	-4.26920950 -3.7417162 -2.5915000 -3.847249			

	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770
Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450

----- t19: Transcripts for 2019 -----

name	description	class	nrow	ncol
2	t19 Transcripts for 2019	data.frame	15242	32
	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi15g01736	5.42	5.35	4.68	4.92
Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
	F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
	F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4
Vitvi15g01736	5.84	5.83	4.56	5.23
Vitvi07g02832	2.54	3.14	3.01	2.16
Vitvi07g02830	1.13	2.25	2.18	1.90
Vitvi07g02812	0.99	0.84	0.85	0.22
Vitvi07g02811	2.91	3.10	3.18	2.61
Vitvi09g02033	1.21	1.67	2.52	2.21
	F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4

Vitvi15g01736	5.44	6.13	5.96	6.16
Vitvi07g02832	3.84	3.05	3.89	4.02
Vitvi07g02830	2.74	2.79	2.90	2.88
Vitvi07g02812	1.03	0.93	1.49	1.29
Vitvi07g02811	3.32	2.89	3.35	3.26
Vitvi09g02033	1.99	1.14	1.65	1.29

----- t1819: Transcripts for 18/19 -----

name	description	class	nrow	ncol
3 t1819	Transcripts for 18/19	data.frame	15242	80

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Vitvi15g01736	4.6646023	4.109897	4.4482203	4.013955
Vitvi07g02832	-2.4786650	-1.601359	-1.4274193	-2.066419
Vitvi07g02830	-1.8506337	-2.218030	-1.0648492	-1.580992
Vitvi07g02812	-0.5805446	-1.266940	-0.3278837	-1.019113
Vitvi07g02811	2.2762225	1.823447	1.9550503	1.648742
Vitvi09g02033	-1.6901691	-2.218030	-2.6498117	-1.449747
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Vitvi15g01736	4.717536	4.154237	4.475261	4.466465
Vitvi07g02832	-2.608485	-1.801183	-1.886474	-3.583384
Vitvi07g02830	-1.544354	-1.405255	-1.755229	-1.381750
Vitvi07g02812	-0.858463	-0.434401	-1.234397	-1.047331
Vitvi07g02811	2.086902	2.105707	2.134837	1.908469
Vitvi09g02033	-2.608485	-1.961648	-3.108866	-4.320350
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Vitvi15g01736	4.400333	4.641164	4.4191231	4.534438
Vitvi07g02832	-5.683146	-2.452000	-4.4274120	-1.876949
Vitvi07g02830	-2.513221	-2.452000	-4.4274120	-2.263972
Vitvi07g02812	-2.875791	-2.693008	-2.5529429	-3.157057
Vitvi07g02811	1.414886	1.409803	0.3970164	1.273993
Vitvi09g02033	-2.513221	-3.345084	-2.1054839	-1.716484
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Vitvi15g01736	4.924801	5.085690	5.3397350	5.263629
Vitvi07g02832	-2.827859	-3.130016	-4.6322874	-3.196388
Vitvi07g02830	-3.190429	-1.545054	-2.1297871	-3.196388
Vitvi07g02812	-2.827859	-1.182484	-3.4098950	-2.303303
Vitvi07g02811	1.517916	1.357250	0.9626591	1.344985
Vitvi09g02033	-4.412821	-3.130016	-2.3103594	-4.418780
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Vitvi15g01736	2.05871733	2.2895026	2.9234830	2.575657
Vitvi07g02832	-5.85417200	-4.4786818	-4.4659691	-2.468738
Vitvi07g02830	-2.15373228	-3.2562893	-3.7290035	-2.709746
Vitvi07g02812	-1.21031581	-2.3632045	-2.3504919	-2.999252
Vitvi07g02811	0.02847105	0.5362686	0.9824914	1.231702
Vitvi09g02033	-4.26920950	-3.7417162	-2.5915000	-3.847249
	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi15g01736	3.891121	3.040087	4.216897	3.763086
Vitvi07g02832	-2.726982	-4.610965	-2.436913	-3.355855
Vitvi07g02830	-2.726982	-3.873999	-1.493496	-2.075747
Vitvi07g02812	-1.672534	-3.388572	-2.230462	-2.462770

Vitvi07g02811	1.436764	1.552266	1.811015	1.352490
Vitvi09g02033	-2.520531	-2.736495	-3.815424	-2.993285
F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4	
Vitvi15g01736	4.8591409	4.8669435	4.9805904	4.9453953
Vitvi07g02832	2.8881443	2.7032394	2.2757651	2.0553154
Vitvi07g02830	2.8426117	2.4130023	2.2135368	2.0169691
Vitvi07g02812	0.8222302	0.9363895	0.7209384	0.3104447
Vitvi07g02811	3.5853480	3.5007015	3.2965509	3.2141610
Vitvi09g02033	1.0793880	1.0850336	0.6285743	0.8579324
F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4	
Vitvi15g01736	5.705006	4.619238	4.808548	5.276124
Vitvi07g02832	2.747538	3.349854	2.537311	2.621336
Vitvi07g02830	2.287722	3.464855	1.989824	2.321031
Vitvi07g02812	1.073767	1.384521	1.472076	1.016877
Vitvi07g02811	3.818074	4.000053	3.198197	3.501954
Vitvi09g02033	1.073767	1.566041	1.237985	1.268416
F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4	
Vitvi15g01736	4.0647184	3.8504580	5.1418322	4.6269091
Vitvi07g02832	2.2592790	2.1761360	2.3686660	1.2127920
Vitvi07g02830	2.1186455	1.9359657	2.6356368	1.5129655
Vitvi07g02812	0.4316833	-0.6220298	-0.5985972	-0.2055206
Vitvi07g02811	2.9490282	2.7595613	3.1300210	2.4602029
Vitvi09g02033	1.5459405	1.3699329	1.4288835	1.4477479
F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4	
Vitvi15g01736	4.0961725	4.80222138	4.3291524	4.4419027
Vitvi07g02832	1.8816574	1.82887526	1.7895023	1.6490200
Vitvi07g02830	2.1414534	1.62149541	2.1153419	2.1541121
Vitvi07g02812	0.1031253	-0.09471163	0.3053805	0.2855497
Vitvi07g02811	3.0025984	2.73213947	2.8750439	3.0458304
Vitvi09g02033	1.7460934	1.45938991	2.0072243	1.2444445
F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4	
Vitvi15g01736	1.5831276	1.7408584	2.97840555	4.1664059
Vitvi07g02832	1.3093668	1.9241330	2.01456521	2.9813855
Vitvi07g02830	0.8382242	1.4203666	2.18501915	2.8731326
Vitvi07g02812	0.1974739	0.4558154	-0.03878421	-0.0111843
Vitvi07g02811	1.8823168	2.5341865	2.65708760	2.9461961
Vitvi09g02033	1.6066824	1.5040245	1.25520700	0.9986635
F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4	
Vitvi15g01736	3.5580430	3.569471	4.4112089	4.3597440
Vitvi07g02832	2.5563386	2.180583	2.6637430	2.7538173
Vitvi07g02830	2.0265816	2.154972	2.7552617	2.3663511
Vitvi07g02812	0.6773148	0.106805	-0.2413317	-0.1063251
Vitvi07g02811	3.0678390	2.949349	2.9761917	2.9625700
Vitvi09g02033	1.7205680	1.541742	1.6527997	1.3320450
C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4	
Vitvi15g01736	3.18	3.50	3.19	3.61
Vitvi07g02832	-5.05	-3.02	-0.80	-0.02
Vitvi07g02830	-5.05	-5.35	-2.39	-3.99
Vitvi07g02812	-1.35	-0.95	-0.15	0.26
Vitvi07g02811	2.09	2.29	2.34	2.63
Vitvi09g02033	-5.05	-3.76	-2.39	-2.76
C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4	
Vitvi15g01736	5.42	5.35	4.68	4.92

Vitvi07g02832	-1.36	-2.10	-1.15	-3.81
Vitvi07g02830	-2.28	-1.81	-2.07	-2.59
Vitvi07g02812	-1.36	0.16	-0.29	-0.75
Vitvi07g02811	2.85	3.16	3.09	2.89
Vitvi09g02033	-5.45	-3.68	-1.78	-3.81
C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4	
Vitvi15g01736	5.13	5.19	5.71	5.29
Vitvi07g02832	-3.13	-1.28	-3.18	-2.29
Vitvi07g02830	-3.87	-5.53	-5.50	-2.29
Vitvi07g02812	-0.10	-1.01	-0.29	-0.04
Vitvi07g02811	2.11	1.92	2.40	2.29
Vitvi09g02033	-3.87	-3.95	-2.69	-2.00
C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4	
Vitvi15g01736	6.19	5.62	5.62	6.19
Vitvi07g02832	-5.54	-5.31	-3.73	-1.81
Vitvi07g02830	-3.22	-5.31	-3.73	-2.05
Vitvi07g02812	-0.59	-0.45	-1.07	-0.55
Vitvi07g02811	2.44	2.13	2.08	2.26
Vitvi09g02033	-3.22	-3.72	-3.73	-3.18
F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4	
Vitvi15g01736	3.03	3.93	4.24	2.85
Vitvi07g02832	3.35	3.23	3.02	2.98
Vitvi07g02830	2.28	2.39	1.75	1.35
Vitvi07g02812	2.19	1.04	0.89	1.56
Vitvi07g02811	3.84	3.72	3.01	3.43
Vitvi09g02033	2.70	1.61	1.94	2.47
F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4	
Vitvi15g01736	5.00	4.97	4.47	5.51
Vitvi07g02832	3.18	3.04	2.81	3.05
Vitvi07g02830	2.59	2.07	1.81	2.20
Vitvi07g02812	1.72	1.08	1.42	1.35
Vitvi07g02811	3.79	3.43	3.24	3.33
Vitvi09g02033	2.24	1.90	2.08	1.25
F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4	
Vitvi15g01736	5.84	5.83	4.56	5.23
Vitvi07g02832	2.54	3.14	3.01	2.16
Vitvi07g02830	1.13	2.25	2.18	1.90
Vitvi07g02812	0.99	0.84	0.85	0.22
Vitvi07g02811	2.91	3.10	3.18	2.61
Vitvi09g02033	1.21	1.67	2.52	2.21
F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4	
Vitvi15g01736	5.44	6.13	5.96	6.16
Vitvi07g02832	3.84	3.05	3.89	4.02
Vitvi07g02830	2.74	2.79	2.90	2.88
Vitvi07g02812	1.03	0.93	1.49	1.29
Vitvi07g02811	3.32	2.89	3.35	3.26
Vitvi09g02033	1.99	1.14	1.65	1.29

----- pdata18: Phenodata for 2018 -----

name	description	class	nrow	ncol
4	pdata18 Phenodata for 2018	data.frame	48	22

	ID	Variety	Date	variety	year	day
C18_11d_WS1	C18_11d_WS1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS2	C18_11d_WS2	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS3	C18_11d_WS3	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS4	C18_11d_WS4	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW1	C18_11d_WW1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW2	C18_11d_WW2	Cabernet Volos	12.06.2018	C	18	11
	treat	rep	project.name	species	plant.name	tissue
C18_11d_WS1	WS	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS2	WS	2	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS3	WS	3	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS4	WS	4	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW1	WW	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW2	WW	2	EnViros Vitis	vinifera	grapevine	leaf
	health.status	plant.number	growth.location			
C18_11d_WS1	water stress		R1	Udine		
C18_11d_WS2	water stress		R2	Udine		
C18_11d_WS3	water stress		R3	Udine		
C18_11d_WS4	water stress		R4	Udine		
C18_11d_WW1	well watered		R1	Udine		
C18_11d_WW2	well watered		R2	Udine		
	growth.conditions					
C18_11d_WS1	outside					
C18_11d_WS2	outside					
C18_11d_WS3	outside					
C18_11d_WS4	outside					
C18_11d_WW1	outside					
C18_11d_WW2	outside					
C18_11d_WS1	several leaves ground together and stored at -80oC;	an aliquot was				
C18_11d_WS2	several leaves ground together and stored at -80oC;	an aliquot was				
C18_11d_WS3	several leaves ground together and stored at -80oC;	an aliquot was				
C18_11d_WS4	several leaves ground together and stored at -80oC;	an aliquot was				
C18_11d_WW1	several leaves ground together and stored at -80oC;	an aliquot was				
C18_11d_WW2	several leaves ground together and stored at -80oC;	an aliquot was				
	Metabolites.Order	Metabolites.File.Name				
C18_11d_WS1	2	1019Cabernet Volos_6_12_WS1.D				
C18_11d_WS2	4	1019Cabernet Volos_6_12_WS2.D				
C18_11d_WS3	102	1219Cabernet Volos_6_12_WS3.D				
C18_11d_WS4	100	1219Cabernet Volos_6_12_WS4.D				
C18_11d_WW1	6	1019Cabernet Volos_6_12_WW1.D				
C18_11d_WW2	8	1019Cabernet Volos_6_12_WW2.D				
	Metabolites.File	Transcripts.ID	date			
C18_11d_WS1	Cabernet Volos6_12WS	C1_S1	2018-06-12			
C18_11d_WS2	Cabernet Volos6_12WS	C1_S2	2018-06-12			
C18_11d_WS3	Cabernet Volos6_12WS	C1_S3	2018-06-12			
C18_11d_WS4	Cabernet Volos6_12WS	C1_S4	2018-06-12			
C18_11d_WW1	Cabernet Volos6_12WW	C1_W1	2018-06-12			
C18_11d_WW2	Cabernet Volos6_12WW	C1_W2	2018-06-12			

----- pdata19: Phenodata for 2019 -----

name	description	class	nrow	ncol
5 pdata19	Phenodata for 2019	data.frame	32	22

	ID	Variety	Date	variety	year	day
C19_22d_WS1	C19_22d_WS1	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WS2	C19_22d_WS2	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WS3	C19_22d_WS3	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WS4	C19_22d_WS4	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WW1	C19_22d_WW1	Cabernet Volos	26.06.2019	C	19	22
C19_22d_WW2	C19_22d_WW2	Cabernet Volos	26.06.2019	C	19	22

	treat	rep	project.name	species	plant.name	tissue
C19_22d_WS1	WS	1	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WS2	WS	2	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WS3	WS	3	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WS4	WS	4	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WW1	WW	1	EnViros Vitis	vinifera	grapevine	leaf
C19_22d_WW2	WW	2	EnViros Vitis	vinifera	grapevine	leaf

	health.status	plant.number	growth.location
C19_22d_WS1	water stress	R1	Udine
C19_22d_WS2	water stress	R2	Udine
C19_22d_WS3	water stress	R3	Udine
C19_22d_WS4	water stress	R4	Udine
C19_22d_WW1	well watered	R1	Udine
C19_22d_WW2	well watered	R2	Udine

	growth.conditions
C19_22d_WS1	outside
C19_22d_WS2	outside
C19_22d_WS3	outside
C19_22d_WS4	outside
C19_22d_WW1	outside
C19_22d_WW2	outside

C19_22d_WS1	several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WS2	several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WS3	several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WS4	several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WW1	several leaves ground together and stored at -80oC; an aliquot was
C19_22d_WW2	several leaves ground together and stored at -80oC; an aliquot was

	Metabolites.Order	Metabolites.File.Name
C19_22d_WS1	2	11120Cabernet_Volos_26_06_2019WS_1.D
C19_22d_WS2	27	11120Cabernet_Volos_26_06_2019WS_2.D
C19_22d_WS3	53	11420Cabernet_Volos_26_06_2019WS_3.D
C19_22d_WS4	79	11420Cabernet_Volos_26_06_2019WS_4.D
C19_22d_WW1	3	11120Cabernet_Volos_26_06_2019WW_1.D
C19_22d_WW2	28	11120Cabernet_Volos_26_06_2019WW_2.D

	Metabolites.File	Transcripts.ID	date
C19_22d_WS1	Cabernet Volos26_06WS	C1S1	2019-06-26
C19_22d_WS2	Cabernet Volos26_06WS	C1S2	2019-06-26
C19_22d_WS3	Cabernet Volos26_06WS	C1S3	2019-06-26
C19_22d_WS4	Cabernet Volos26_06WS	C1S4	2019-06-26
C19_22d_WW1	Cabernet Volos26_06WW	C1W1	2019-06-26
C19_22d_WW2	Cabernet Volos26_06WW	C1W2	2019-06-26

----- pdata1819: Phenodata for 2018/19 -----

	name	description	class	nrow	ncol
6	pdata1819	Phenodata for 2018/19	data.frame	80	22

	ID	Variety	Date	variety	year	day
C18_11d_WS1	C18_11d_WS1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS2	C18_11d_WS2	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS3	C18_11d_WS3	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WS4	C18_11d_WS4	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW1	C18_11d_WW1	Cabernet Volos	12.06.2018	C	18	11
C18_11d_WW2	C18_11d_WW2	Cabernet Volos	12.06.2018	C	18	11

	treat	rep	project.name	species	plant.name	tissue
C18_11d_WS1	WS	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS2	WS	2	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS3	WS	3	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WS4	WS	4	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW1	WW	1	EnViros Vitis	vinifera	grapevine	leaf
C18_11d_WW2	WW	2	EnViros Vitis	vinifera	grapevine	leaf

	health.status	plant.number	growth.location
C18_11d_WS1	water stress	R1	Udine
C18_11d_WS2	water stress	R2	Udine
C18_11d_WS3	water stress	R3	Udine
C18_11d_WS4	water stress	R4	Udine
C18_11d_WW1	well watered	R1	Udine
C18_11d_WW2	well watered	R2	Udine

	growth.conditions
C18_11d_WS1	outside
C18_11d_WS2	outside
C18_11d_WS3	outside
C18_11d_WS4	outside
C18_11d_WW1	outside
C18_11d_WW2	outside

C18_11d_WS1	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS2	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS3	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WS4	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW1	several leaves ground together and stored at -80oC; an aliquot was
C18_11d_WW2	several leaves ground together and stored at -80oC; an aliquot was

	Metabolites.Order	Metabolites.File.Name
C18_11d_WS1	2	1019Cabernet Volos_6_12_WS1.D
C18_11d_WS2	4	1019Cabernet Volos_6_12_WS2.D
C18_11d_WS3	102	1219Cabernet Volos_6_12_WS3.D
C18_11d_WS4	100	1219Cabernet Volos_6_12_WS4.D
C18_11d_WW1	6	1019Cabernet Volos_6_12_WW1.D
C18_11d_WW2	8	1019Cabernet Volos_6_12_WW2.D

	Metabolites.File	Transcripts.ID	date
C18_11d_WS1	Cabernet Volos6_12WS	C1_S1	2018-06-12
C18_11d_WS2	Cabernet Volos6_12WS	C1_S2	2018-06-12
C18_11d_WS3	Cabernet Volos6_12WS	C1_S3	2018-06-12

C18_11d_WS4	Cabernet Volos6_12WS	C1_S4	2018-06-12
C18_11d_WW1	Cabernet Volos6_12WW	C1_W1	2018-06-12
C18_11d_WW2	Cabernet Volos6_12WW	C1_W2	2018-06-12

----- fdata: Trans. featuredata 18/19 -----

name	description	class	nrow	ncol
7 fdata	Trans. featuredata 18/19	data.frame	16936	5

YEAR	geneID	BINCODE	NAME
1 2018	Vitvi15g01736	26.9	misc.glutathione S transferases
2 2018	Vitvi07g02832	35.2	not assigned.unknown
3 2018	Vitvi07g02830	35.2	not assigned.unknown
4 2018	Vitvi07g02812	35.2	not assigned.unknown
5 2018	Vitvi07g02811	35.2	not assigned.unknown
6 2018	Vitvi09g02033	35.2	not assigned.unknown

1	glutathione S-transferase tau 7 Chr2:12618111-1261887
2	Disease resistance protein (TIR-NBS-LRR class) family Chr4:7197325-7201393
3	
4	
5	
6	Disease resistance protein (CC-NBS-LRR class) family Chr1:4145374-414768

----- m18: Metabolites for 2018 -----

name	description	class	nrow	ncol
8 m18	Metabolites for 2018	data.frame	96	60

	ID	Variety	Date	Treat	Rep	Alanine
C18_11d_WS1	C18_11d_WS1	Cabernet Volos	12.06.2018	WS	1	1.223
C18_11d_WS2	C18_11d_WS2	Cabernet Volos	12.06.2018	WS	2	1.112
C18_11d_WS3	C18_11d_WS3	Cabernet Volos	12.06.2018	WS	3	5.831
C18_11d_WS4	C18_11d_WS4	Cabernet Volos	12.06.2018	WS	4	5.902
C18_11d_WW1	C18_11d_WW1	Cabernet Volos	12.06.2018	WW	1	1.356
C18_11d_WW2	C18_11d_WW2	Cabernet Volos	12.06.2018	WW	2	2.092
	Arabinose	Ascorbic.acid	Aspartic.acid	GABA		
C18_11d_WS1	1.066	8.117	8.089	17.886		
C18_11d_WS2	1.160	11.133	5.949	10.234		
C18_11d_WS3	0.879	10.096	6.678	13.095		
C18_11d_WS4	1.018	14.431	7.517	15.499		
C18_11d_WW1	1.601	7.691	5.486	19.291		
C18_11d_WW2	1.339	8.210	5.679	13.753		
	Trans.Caffeic.acid	Catechin	Citric.acid	Erythronic.acid		
C18_11d_WS1	80.287	25.947	20.514	15.557		
C18_11d_WS2	88.974	34.903	20.895	19.794		
C18_11d_WS3	65.787	19.247	18.653	16.739		
C18_11d_WS4	67.085	17.094	23.812	14.426		
C18_11d_WW1	81.970	19.296	22.901	19.993		
C18_11d_WW2	64.485	12.899	18.695	11.829		
	Ethanolamine	Fructose	Fructose.6.phosphate	Fumaric.acid		

C18_11d_WS1	9.651	256.529		0.340	6.264
C18_11d_WS2	8.394	216.117		0.342	10.383
C18_11d_WS3	12.476	135.301		0.543	17.822
C18_11d_WS4	8.195	151.369		0.715	18.262
C18_11d_WW1	8.609	226.207		0.328	7.599
C18_11d_WW2	7.318	184.706		0.810	9.945
Galactinol Galactose Gallic.acid Gluconic.acid					
C18_11d_WS1	155.122	77.573	9.195	33.393	
C18_11d_WS2	132.623	79.791	9.302	37.969	
C18_11d_WS3	126.392	41.544	8.744	28.773	
C18_11d_WS4	131.486	57.803	8.224	31.098	
C18_11d_WW1	157.545	60.714	11.427	31.330	
C18_11d_WW2	126.285	49.702	8.332	25.503	
Glucopyranose..H2O. Glucose Glutamic.acid Glyceric.acid					
C18_11d_WS1		1.312	397.334	4.505	69.173
C18_11d_WS2		1.502	402.054	2.890	59.053
C18_11d_WS3		1.659	292.569	1.305	54.919
C18_11d_WS4		1.394	372.552	1.841	69.051
C18_11d_WW1		1.692	371.347	3.031	60.075
C18_11d_WW2		1.416	320.623	2.389	51.259
Glycine Hydroquinone Myo.Inostol Isoleucine Leucine					
C18_11d_WS1	6.807	1.477	835.518	0.505	0.201
C18_11d_WS2	7.061	2.023	865.686	0.521	0.263
C18_11d_WS3	8.531	0.927	908.430	0.672	0.312
C18_11d_WS4	6.743	1.597	1037.661	1.360	0.715
C18_11d_WW1	10.307	1.011	852.664	1.458	0.767
C18_11d_WW2	7.696	1.462	824.958	0.868	0.453
Lyxonic.acid Maleic.acid Malic.acid Malonic.acid					
C18_11d_WS1	9.430	10.029	608.498	1.522	
C18_11d_WS2	11.522	14.427	717.038	1.356	
C18_11d_WS3	11.563	10.359	587.634	1.714	
C18_11d_WS4	9.272	9.856	605.796	2.119	
C18_11d_WW1	12.048	8.792	538.940	1.562	
C18_11d_WW2	9.964	10.932	471.971	1.542	
Mannose.6.phosphate Melibiose Phenylalanine					
C18_11d_WS1		0.808	2.083	0.875	
C18_11d_WS2		0.989	1.985	1.125	
C18_11d_WS3		1.251	0.641	0.967	
C18_11d_WS4		1.583	0.833	1.847	
C18_11d_WW1		0.822	1.783	1.043	
C18_11d_WW2		1.803	1.494	1.626	
Phosphoric.acid Proline Putrescine Pyroglutamic.acid					
C18_11d_WS1	213.244	0.101	0.497		53.123
C18_11d_WS2	166.889	0.127	0.450		42.267
C18_11d_WS3	176.720	0.058	0.970		76.347
C18_11d_WS4	214.354	0.075	1.013		94.950
C18_11d_WW1	312.643	0.062	0.658		49.663
C18_11d_WW2	283.940	0.072	0.530		49.167
Quinic.acid X3.caffeoylquinic.acid Raffinose Rhamnose					
C18_11d_WS1	14.818		6.213	10.251	5.533
C18_11d_WS2	12.661		6.165	14.986	4.578
C18_11d_WS3	11.718		3.530	8.977	4.821
C18_11d_WS4	10.058		3.844	10.579	5.764

C18_11d_WW1	19.851		5.759	8.697	5.336
C18_11d_WW2	13.756		4.197	9.104	6.794
	Ribonic.acid	Ribose	Serine	Shikimic.acid	Succinic.acid
C18_11d_WS1	2.474	1.384	9.146	219.107	1.280
C18_11d_WS2	2.305	1.479	5.915	126.574	1.294
C18_11d_WS3	3.371	1.514	8.361	135.991	0.831
C18_11d_WS4	2.660	1.398	10.141	130.577	0.962
C18_11d_WW1	3.265	1.638	4.650	236.070	1.399
C18_11d_WW2	2.962	1.489	5.005	163.985	1.083
	Sucrose	Tartaric.acid	Threitol	Threonic.acid	
C18_11d_WS1	882.997	539.120	0.225	24.147	
C18_11d_WS2	983.233	353.426	0.177	26.607	
C18_11d_WS3	1072.681	286.172	0.254	24.718	
C18_11d_WS4	1115.331	475.558	0.301	21.698	
C18_11d_WW1	999.836	479.856	0.325	36.390	
C18_11d_WW2	958.282	408.288	0.280	34.171	
	Threonolactone	Threonine	Uracil	Valine	Xylose
C18_11d_WS1	1.328	2.239	0.104	2.450	2.720
C18_11d_WS2	1.176	1.813	0.162	2.512	2.244
C18_11d_WS3	0.805	2.015	0.140	3.369	2.349
C18_11d_WS4	1.170	2.495	0.167	6.216	2.529
C18_11d_WW1	1.598	1.840	0.132	5.816	2.663
C18_11d_WW2	3.032	1.927	0.159	2.902	3.113

----- m19: Metabolites for 2019 -----

name	description	class	nrow	ncol
9	m19 Metabolites for 2019	data.frame	94	60

	ID	Variety	Date	Treat	Rep	Alanine
C19_22d_WS1	C19_22d_WS1	Cabernet Volos	26.06.2019	WS	1	0.650
C19_22d_WS2	C19_22d_WS2	Cabernet Volos	26.06.2019	WS	2	2.649
C19_22d_WS3	C19_22d_WS3	Cabernet Volos	26.06.2019	WS	3	2.419
C19_22d_WS4	C19_22d_WS4	Cabernet Volos	26.06.2019	WS	4	3.827
C19_22d_WW1	C19_22d_WW1	Cabernet Volos	26.06.2019	WW	1	0.706
C19_22d_WW2	C19_22d_WW2	Cabernet Volos	26.06.2019	WW	2	1.942
	Arabinose	Ascorbic.acid	Aspartic.acid	GABA		
C19_22d_WS1	1.247	1.904	13.274	9.180		
C19_22d_WS2	1.398	5.727	8.869	23.178		
C19_22d_WS3	0.867	2.017	4.596	32.755		
C19_22d_WS4	1.017	1.504	3.410	22.873		
C19_22d_WW1	2.004	2.132	19.741	41.313		
C19_22d_WW2	1.480	2.928	9.350	26.870		
	Trans.Caffeic.acid	Catechin	Citric.acid	Erythronic.acid		
C19_22d_WS1	66.990	12.883	31.709			25.538
C19_22d_WS2	129.414	15.800	38.657			26.195
C19_22d_WS3	60.016	2.537	55.403			22.170
C19_22d_WS4	99.206	1.855	59.210			22.071
C19_22d_WW1	76.202	21.185	73.021			30.835
C19_22d_WW2	115.259	10.126	49.305			23.633
	Ethanolamine	Fructose	Fructose.6.phosphate	Fumaric.acid		
C19_22d_WS1	8.599	171.867	0.479			9.047

C19_22d_WS2	13.501	176.185		0.622	13.445
C19_22d_WS3	10.279	207.331		0.677	7.430
C19_22d_WS4	7.624	214.450		0.835	22.531
C19_22d_WW1	15.707	304.063		1.565	8.710
C19_22d_WW2	10.127	264.016		2.103	10.704
Galactinol Galactose Gallic.acid Gluconic.acid					
C19_22d_WS1	294.569	40.947	9.181	40.217	
C19_22d_WS2	230.193	44.573	7.518	43.984	
C19_22d_WS3	376.973	49.802	2.261	50.658	
C19_22d_WS4	252.079	54.842	6.406	46.994	
C19_22d_WW1	252.012	74.540	13.647	47.091	
C19_22d_WW2	231.162	58.764	13.311	35.647	
Glucopyranose..H2O. Glucose Glutamic.acid Glyceric.acid					
C19_22d_WS1		1.387	144.629	25.802	32.106
C19_22d_WS2		2.251	154.731	9.139	36.908
C19_22d_WS3		1.533	195.323	0.067	43.242
C19_22d_WS4		1.432	212.122	0.098	39.413
C19_22d_WW1		1.613	242.088	19.923	44.391
C19_22d_WW2		1.781	195.095	7.727	32.590
Glycine Hydroquinone Myo.Inositol Isoleucine Leucine					
C19_22d_WS1	2.568	0.423	263.471	2.020	2.045
C19_22d_WS2	2.829	0.695	266.187	0.774	0.771
C19_22d_WS3	6.176	0.765	347.932	5.260	5.348
C19_22d_WS4	6.483	0.624	359.609	3.221	3.221
C19_22d_WW1	4.499	0.566	341.821	1.856	1.861
C19_22d_WW2	8.703	0.689	269.005	0.421	0.422
Lyxonic.acid Maleic.acid Malic.acid Malonic.acid					
C19_22d_WS1	3.493	13.987	276.263	0.675	
C19_22d_WS2	3.858	8.553	254.016	1.878	
C19_22d_WS3	3.424	11.835	321.350	2.306	
C19_22d_WS4	3.790	23.523	300.204	3.114	
C19_22d_WW1	4.531	10.645	401.581	0.993	
C19_22d_WW2	4.055	6.472	301.624	1.665	
Mannose.6.phosphate Melibiose Phenylalanine					
C19_22d_WS1		1.205	6.724	5.377	
C19_22d_WS2		1.543	6.853	2.096	
C19_22d_WS3		1.894	6.738	1.931	
C19_22d_WS4		2.067	5.623	1.046	
C19_22d_WW1		3.565	9.824	5.229	
C19_22d_WW2		4.117	7.431	2.159	
Phosphoric.acid Proline Putrescine Pyroglutamic.acid					
C19_22d_WS1	259.108	0.464	0.485	33.695	
C19_22d_WS2	316.404	0.098	0.839	58.816	
C19_22d_WS3	313.879	1.147	1.458	105.150	
C19_22d_WS4	396.911	0.229	1.515	122.998	
C19_22d_WW1	704.345	0.572	1.817	28.799	
C19_22d_WW2	632.581	0.027	0.355	37.222	
Quinic.acid X3.caffeoylquinic.acid Raffinose Rhamnose					
C19_22d_WS1	13.034		8.122	36.599	5.873
C19_22d_WS2	14.606		9.279	33.422	4.772
C19_22d_WS3	16.247		11.758	31.000	5.841
C19_22d_WS4	14.022		8.011	22.234	5.517
C19_22d_WW1	16.332		11.727	37.581	7.723

C19_22d_WW2	14.347			9.076	31.426	6.132
	Ribonic.acid	Ribose	Serine	Shikimic.acid	Succinic.acid	
C19_22d_WS1	3.493	1.288	0.655	116.010		2.085
C19_22d_WS2	3.837	1.557	0.877	119.361		1.965
C19_22d_WS3	3.424	1.244	4.975	140.147		1.277
C19_22d_WS4	3.790	1.327	4.954	122.447		0.986
C19_22d_WW1	4.535	1.718	1.314	163.920		2.240
C19_22d_WW2	4.026	1.751	0.751	136.498		1.704
	Sucrose	Tartaric.acid	Threitol	Threonic.acid		
C19_22d_WS1	159.355	141.312	0.174	19.457		
C19_22d_WS2	163.889	181.688	0.138	16.222		
C19_22d_WS3	209.538	237.050	0.400	12.469		
C19_22d_WS4	247.484	274.167	0.296	8.828		
C19_22d_WW1	228.772	251.925	0.204	14.991		
C19_22d_WW2	196.369	230.069	0.290	17.121		
	Threonolactone	Threonine	Uracil	Valine	Xylose	
C19_22d_WS1	0.744	2.224	0.094	8.289	1.756	
C19_22d_WS2	0.637	2.497	0.134	4.267	2.012	
C19_22d_WS3	0.413	0.791	0.058	14.206	1.704	
C19_22d_WS4	0.284	0.630	0.109	8.056	1.939	
C19_22d_WW1	0.914	2.013	0.205	8.808	3.059	
C19_22d_WW2	0.912	1.596	0.150	2.664	2.215	

----- m1819: Metabolites for 18/19 -----

name	description	class	nrow	ncol
10 m1819	Metabolites for 18/19	data.frame	190	60

	ID	Variety	Date	Treat	Rep	Alanine
C18_11d_WS1	C18_11d_WS1	Cabernet Volos	12.06.2018	WS	1	1.223
C18_11d_WS2	C18_11d_WS2	Cabernet Volos	12.06.2018	WS	2	1.112
C18_11d_WS3	C18_11d_WS3	Cabernet Volos	12.06.2018	WS	3	5.831
C18_11d_WS4	C18_11d_WS4	Cabernet Volos	12.06.2018	WS	4	5.902
C18_11d_WW1	C18_11d_WW1	Cabernet Volos	12.06.2018	WW	1	1.356
C18_11d_WW2	C18_11d_WW2	Cabernet Volos	12.06.2018	WW	2	2.092
	Arabinose	Ascorbic.acid	Aspartic.acid	GABA		
C18_11d_WS1	1.066	8.117	8.089	17.886		
C18_11d_WS2	1.160	11.133	5.949	10.234		
C18_11d_WS3	0.879	10.096	6.678	13.095		
C18_11d_WS4	1.018	14.431	7.517	15.499		
C18_11d_WW1	1.601	7.691	5.486	19.291		
C18_11d_WW2	1.339	8.210	5.679	13.753		
	Trans.Caffeic.acid	Catechin	Citric.acid	Erythronic.acid		
C18_11d_WS1	80.287	25.947	20.514			15.557
C18_11d_WS2	88.974	34.903	20.895			19.794
C18_11d_WS3	65.787	19.247	18.653			16.739
C18_11d_WS4	67.085	17.094	23.812			14.426
C18_11d_WW1	81.970	19.296	22.901			19.993
C18_11d_WW2	64.485	12.899	18.695			11.829
	Ethanolamine	Fructose	Fructose.6.phosphate	Fumaric.acid		
C18_11d_WS1	9.651	256.529	0.340			6.264
C18_11d_WS2	8.394	216.117	0.342			10.383

C18_11d_WS3	12.476	135.301		0.543	17.822
C18_11d_WS4	8.195	151.369		0.715	18.262
C18_11d_WW1	8.609	226.207		0.328	7.599
C18_11d_WW2	7.318	184.706		0.810	9.945
Galactinol Galactose Gallic.acid Gluconic.acid					
C18_11d_WS1	155.122	77.573	9.195	33.393	
C18_11d_WS2	132.623	79.791	9.302	37.969	
C18_11d_WS3	126.392	41.544	8.744	28.773	
C18_11d_WS4	131.486	57.803	8.224	31.098	
C18_11d_WW1	157.545	60.714	11.427	31.330	
C18_11d_WW2	126.285	49.702	8.332	25.503	
Glucopyranose..H2O. Glucose Glutamic.acid Glyceric.acid					
C18_11d_WS1		1.312	397.334	4.505	69.173
C18_11d_WS2		1.502	402.054	2.890	59.053
C18_11d_WS3		1.659	292.569	1.305	54.919
C18_11d_WS4		1.394	372.552	1.841	69.051
C18_11d_WW1		1.692	371.347	3.031	60.075
C18_11d_WW2		1.416	320.623	2.389	51.259
Glycine Hydroquinone Myo.Inostol Isoleucine Leucine					
C18_11d_WS1	6.807	1.477	835.518	0.505	0.201
C18_11d_WS2	7.061	2.023	865.686	0.521	0.263
C18_11d_WS3	8.531	0.927	908.430	0.672	0.312
C18_11d_WS4	6.743	1.597	1037.661	1.360	0.715
C18_11d_WW1	10.307	1.011	852.664	1.458	0.767
C18_11d_WW2	7.696	1.462	824.958	0.868	0.453
Lyxonic.acid Maleic.acid Malic.acid Malonic.acid					
C18_11d_WS1	9.430	10.029	608.498		1.522
C18_11d_WS2	11.522	14.427	717.038		1.356
C18_11d_WS3	11.563	10.359	587.634		1.714
C18_11d_WS4	9.272	9.856	605.796		2.119
C18_11d_WW1	12.048	8.792	538.940		1.562
C18_11d_WW2	9.964	10.932	471.971		1.542
Mannose.6.phosphate Melibiose Phenylalanine					
C18_11d_WS1		0.808	2.083	0.875	
C18_11d_WS2		0.989	1.985	1.125	
C18_11d_WS3		1.251	0.641	0.967	
C18_11d_WS4		1.583	0.833	1.847	
C18_11d_WW1		0.822	1.783	1.043	
C18_11d_WW2		1.803	1.494	1.626	
Phosphoric.acid Proline Putrescine Pyroglutamic.acid					
C18_11d_WS1	213.244	0.101	0.497		53.123
C18_11d_WS2	166.889	0.127	0.450		42.267
C18_11d_WS3	176.720	0.058	0.970		76.347
C18_11d_WS4	214.354	0.075	1.013		94.950
C18_11d_WW1	312.643	0.062	0.658		49.663
C18_11d_WW2	283.940	0.072	0.530		49.167
Quinic.acid X3.caffeoylquinic.acid Raffinose Rhamnose					
C18_11d_WS1	14.818		6.213	10.251	5.533
C18_11d_WS2	12.661		6.165	14.986	4.578
C18_11d_WS3	11.718		3.530	8.977	4.821
C18_11d_WS4	10.058		3.844	10.579	5.764
C18_11d_WW1	19.851		5.759	8.697	5.336
C18_11d_WW2	13.756		4.197	9.104	6.794

	Ribonic.acid	Ribose	Serine	Shikimic.acid	Succinic.acid
C18_11d_WS1	2.474	1.384	9.146	219.107	1.280
C18_11d_WS2	2.305	1.479	5.915	126.574	1.294
C18_11d_WS3	3.371	1.514	8.361	135.991	0.831
C18_11d_WS4	2.660	1.398	10.141	130.577	0.962
C18_11d_WW1	3.265	1.638	4.650	236.070	1.399
C18_11d_WW2	2.962	1.489	5.005	163.985	1.083
	Sucrose	Tartaric.acid	Threitol	Threonic.acid	
C18_11d_WS1	882.997	539.120	0.225	24.147	
C18_11d_WS2	983.233	353.426	0.177	26.607	
C18_11d_WS3	1072.681	286.172	0.254	24.718	
C18_11d_WS4	1115.331	475.558	0.301	21.698	
C18_11d_WW1	999.836	479.856	0.325	36.390	
C18_11d_WW2	958.282	408.288	0.280	34.171	
	Threonolactone	Threonine	Uracil	Valine	Xylose
C18_11d_WS1	1.328	2.239	0.104	2.450	2.720
C18_11d_WS2	1.176	1.813	0.162	2.512	2.244
C18_11d_WS3	0.805	2.015	0.140	3.369	2.349
C18_11d_WS4	1.170	2.495	0.167	6.216	2.529
C18_11d_WW1	1.598	1.840	0.132	5.816	2.663
C18_11d_WW2	3.032	1.927	0.159	2.902	3.113

----- sm18: Standardized metabolites 18 -----

name	description	class	nrow	ncol
11 sm18	Standardized metabolites 18 matrix		96	55

	Alanine	Arabinose	Ascorbic.acid	Aspartic.acid
C18_11d_WS1	-1.4062900	0.65468542	0.8810975	0.17362695
C18_11d_WS2	-1.5802391	0.96453480	1.4020301	-0.34308903
C18_11d_WS3	1.4491728	-0.05253557	1.2408231	-0.14870734
C18_11d_WS4	1.4712993	0.48575419	1.8298271	0.05030402
C18_11d_WW1	-1.2175587	2.14593351	0.7922128	-0.47933609
C18_11d_WW2	-0.4248767	1.49069835	0.8998807	-0.42119453
	GABA	Trans.Caffeic.acid	Catechin	Citric.acid
C18_11d_WS1	-0.2865262	0.6433701	1.2842804	-0.45074790
C18_11d_WS2	-0.7398570	1.0291864	1.4800244	-0.39186847
C18_11d_WS3	-0.5396917	-0.1046505	1.0870947	-0.75502850
C18_11d_WS4	-0.4028365	-0.0312767	1.0087832	0.02625003
C18_11d_WW1	-0.2251239	0.7212781	1.0887732	-0.09856208
C18_11d_WW2	-0.4998831	-0.1797194	0.8229012	-0.74783230
	Erythronic.acid	Ethanolamine	Fructose	
C18_11d_WS1	-0.9872651	-0.62799456	0.92588792	
C18_11d_WS2	-0.2904856	-0.92055331	0.65059273	
C18_11d_WS3	-0.7754247	-0.08972082	-0.10150358	
C18_11d_WS4	-1.2056083	-0.97085522	0.07871419	
C18_11d_WW1	-0.2615480	-0.86753000	0.72387326	
C18_11d_WW2	-1.7797622	-1.20815529	0.39837062	
	Fructose.6.phosphate	Fumaric.acid	Galactinol	Galactose
C18_11d_WS1	0.13294745	-2.4447847	0.31909535	1.4804393
C18_11d_WS2	0.14300253	-0.9484950	0.04264797	1.5359128
C18_11d_WS3	0.93556084	0.6511680	-0.04224784	0.2516422

C18_11d_WS4	1.40731402	0.7233805	0.02745826	0.9015674
C18_11d_WW1	0.07134611	-1.8727471	0.34643857	0.9982504
C18_11d_WW2	1.62118662	-1.0761093	-0.04374197	0.6044452
	Gallic.acid	Gluconic.acid	Glucopyranose..H2O.	Glucose
C18_11d_WS1	0.5398335	0.70666638	-0.3989666	1.2857497
C18_11d_WS2	0.5750503	0.99736367	0.0559675	1.3127487
C18_11d_WS3	0.3867488	0.36959942	0.3903860	0.5859735
C18_11d_WS4	0.2001235	0.54549323	-0.1950386	1.1385120
C18_11d_WW1	1.2013335	0.56231750	0.4566399	1.1311052
C18_11d_WW2	0.2398368	0.09651817	-0.1423663	0.7953175
	Glutamic.acid	Glyceric.acid	Glycine	Hydroquinone
C18_11d_WS1	0.91195762	0.8579279	0.8620770	1.5633506
C18_11d_WS2	0.31554078	0.6101076	0.9417316	2.1487235
C18_11d_WS3	-0.75260462	0.4963996	1.3529285	0.6965274
C18_11d_WS4	-0.29030226	0.8551622	0.8415377	1.7087108
C18_11d_WW1	0.37953934	0.6369905	1.7641183	0.8579428
C18_11d_WW2	0.05976519	0.3883441	1.1289664	1.5443555
	Myo.Inositol	Isoleucine	Leucine	Lyxonic.acid
C18_11d_WS1	0.8774455	-0.9989703	-1.34356895	-0.1334790
C18_11d_WS2	1.0121331	-0.9538992	-1.05082043	0.7791878
C18_11d_WS3	1.1951407	-0.5861411	-0.86478360	0.7953679
C18_11d_WS4	1.7001916	0.4325397	0.03821471	-0.2104462
C18_11d_WW1	0.9545803	0.5330824	0.11465979	0.9825287
C18_11d_WW2	0.8291475	-0.2163238	-0.45874662	0.1174265
	Maleic.acid	Malic.acid	Malonic.acid	Mannose.6.phosphate
C18_11d_WS1	-0.19963359	0.3021843	-0.036274507	0.1155221
C18_11d_WS2	0.89926101	0.9313804	-0.426704977	0.4663541
C18_11d_WS3	-0.10179395	0.1684395	0.365374977	0.8742404
C18_11d_WS4	-0.25221947	0.2851244	1.082482659	1.2827765
C18_11d_WW1	-0.59745773	-0.1631500	0.051428417	0.1453378
C18_11d_WW2	0.06091111	-0.6717914	0.007861343	1.5086377
	Melibiose	Phenylalanine	Phosphoric.acid	Proline
C18_11d_WS1	0.02733171	-0.726244206	0.51989190	-0.30749780
C18_11d_WS2	-0.05942391	-0.479127289	0.02008297	-0.07176952
C18_11d_WS3	-2.09435345	-0.627939396	0.13679833	-0.87830641
C18_11d_WS4	-1.62267429	0.008371749	0.53047870	-0.61378593
C18_11d_WW1	-0.25263209	-0.553545093	1.30011632	-0.80967552
C18_11d_WW2	-0.57099288	-0.116939413	1.10374948	-0.65579511
	Putrescine	Pyroglutamic.acid	Quinic.acid	
C18_11d_WS1	-0.8493213	-0.1955665	1.2477133	
C18_11d_WS2	-1.0496524	-0.9317976	1.0576983	
C18_11d_WS3	0.4991721	0.9724628	0.9642101	
C18_11d_WS4	0.5866417	1.6747440	0.7797010	
C18_11d_WW1	-0.2834413	-0.4124706	1.6009038	
C18_11d_WW2	-0.7196820	-0.4447971	1.1578881	
	X3.caffeoylquinic.acid	Raffinose	Rhamnose	
C18_11d_WS1	1.1811104	0.19679395	-0.40506566	
C18_11d_WS2	1.1780489	0.68033760	-0.80168442	
C18_11d_WS3	0.9579504	0.02780822	-0.69341921	
C18_11d_WS4	0.9915877	0.23689895	-0.31944532	
C18_11d_WW1	1.1511581	-0.01254122	-0.48095691	
C18_11d_WW2	1.0262675	0.04569641	0.02471514	
	Ribonic.acid	Ribose	Serine	Shikimic.acid

C18_11d_WS1	0.2273135	0.3777505	1.4663727	1.842062
C18_11d_WS2	-0.1399435	0.7163120	0.6428656	1.208321
C18_11d_WS3	1.8331155	0.8355890	1.2968085	1.291200
C18_11d_WS4	0.6035722	0.4290780	1.6615050	1.244280
C18_11d_WW1	1.6672807	1.2370428	0.1881974	1.928182
C18_11d_WW2	1.1617515	0.7506767	0.3272109	1.507384
	Succinic.acid	Sucrose	Tartaric.acid	Threitol
C18_11d_WS1	1.0191164	0.8091671	0.80383281	-0.344894916
C18_11d_WS2	1.0481215	1.2386381	-0.02639419	-1.014381129
C18_11d_WS3	-0.1327153	1.5864121	-0.44140757	-0.006640386
C18_11d_WS4	0.2575998	1.7421454	0.55718283	0.467051519
C18_11d_WW1	1.2561500	1.3055212	0.57487253	0.681093763
C18_11d_WW2	0.5734997	1.1359717	0.25731610	0.265269687
	Threonic.acid	Threonolactone	Threonine	Uracil
C18_11d_WS1	0.6942373	0.7373110	0.36528745	-1.61372948
C18_11d_WS2	0.9085691	0.5499635	-0.17611986	0.14921803
C18_11d_WS3	0.7458717	-0.0342207	0.09487384	-0.43134589
C18_11d_WS4	0.4579763	0.5420799	0.64301038	0.27013071
C18_11d_WW1	1.6003394	1.0225643	-0.13819726	-0.66539698
C18_11d_WW2	1.4613386	2.0096905	-0.01968125	0.07486595
	Valine	Xylose		
C18_11d_WS1	-0.4085276	1.4230608		
C18_11d_WS2	-0.3672574	0.6553803		
C18_11d_WS3	0.1174862	0.8378696		
C18_11d_WS4	1.1289800	1.1325131		
C18_11d_WW1	1.0191397	1.3385454		
C18_11d_WW2	-0.1289273	1.9616131		

----- sm19: Standardized metabolites 19 -----

	name	description	class	nrow	ncol
12	sm19	Standardized metabolites 19 matrix		94	55

	Alanine	Arabinose	Ascorbic.acid	Aspartic.acid
C19_22d_WS1	-2.28752579	0.9403623	-1.0540962	1.19124789
C19_22d_WS2	-0.06158371	1.3475393	0.7376079	0.81046676
C19_22d_WS3	-0.20548609	-0.3543774	-0.9602929	0.18971227
C19_22d_WS4	0.52129329	0.2140697	-1.4377884	-0.09213435
C19_22d_WW1	-2.15659140	2.6303296	-0.8700772	1.56602830
C19_22d_WW2	-0.55346391	1.5505880	-0.3538981	0.86033887
	GABA	Trans.Caffeic.acid	Catechin	Citric.acid
C19_22d_WS1	-2.0323860	-0.9938474	0.8527101	-1.67638583
C19_22d_WS2	-0.3918826	1.3562354	1.0099922	-1.13237150
C19_22d_WS3	0.2207130	-1.3861940	-0.3994714	-0.14414860
C19_22d_WS4	-0.4153454	0.4075340	-0.6407469	0.03832698
C19_22d_WW1	0.6318617	-0.5340035	1.2359988	0.61399827
C19_22d_WW2	-0.1300775	0.9428225	0.6671459	-0.46432938
	Erythronic.acid	Ethanolamine	Fructose	
C19_22d_WS1	-1.2175885	-0.8712792	0.3243023	
C19_22d_WS2	-1.1427103	0.3226974	0.3859147	
C19_22d_WS3	-1.6344947	-0.3989557	0.7901026	
C19_22d_WS4	-1.6476877	-1.1897965	0.8739289	

C19_22d_WW1	-0.6619705	0.7232572	1.7408895	
C19_22d_WW2	-1.4461156	-0.4383860	1.3902271	
	Fructose.6.phosphate	Fumaric.acid	Galactinol	Galactose
C19_22d_WS1	-1.0652443	-1.4534293	1.5571772	0.4683739
C19_22d_WS2	-0.4847639	-0.5767557	0.9578989	0.6541628
C19_22d_WS3	-0.2964892	-1.8891556	2.1566137	0.8970506
C19_22d_WS4	0.1696035	0.5657048	1.1786215	1.1081328
C19_22d_WW1	1.5654996	-1.5374322	1.1779755	1.7800830
C19_22d_WW2	2.2220611	-1.0812628	0.9681075	1.2593768
	Gallic.acid	Gluconic.acid	Glucopyranose..H2O.	Glucose
C19_22d_WS1	0.38412015	-0.04805977	-0.13373660	0.1559991
C19_22d_WS2	-0.06029156	0.21531208	1.45539795	0.3433414
C19_22d_WS3	-2.73227043	0.63086345	0.19471396	0.9897702
C19_22d_WS4	-0.41625748	0.41002269	-0.02895331	1.2187082
C19_22d_WW1	1.26563058	0.41608799	0.36165480	1.5853658
C19_22d_WW2	1.21019151	-0.40287935	0.68680964	0.9865293
	Glutamic.acid	Glyceric.acid	Glycine	Hydroquinone
C19_22d_WS1	1.3756550	-0.61528670	-0.3501976	-0.81473630
C19_22d_WS2	0.9432323	-0.29358237	-0.1811938	0.20506160
C19_22d_WS3	-1.1047691	0.07197092	1.1819767	0.40215335
C19_22d_WS4	-0.9463344	-0.14202072	1.2666787	-0.01625995
C19_22d_WW1	1.2679235	0.13249760	0.6288225	-0.21662199
C19_22d_WW2	0.8733089	-0.58075280	1.7808429	0.18725389
	Myo.Inostol	Isoleucine	Leucine	Lyxonic.acid
C19_22d_WS1	-0.4931878	0.7338915	0.7841428	0.2695410
C19_22d_WS2	-0.4534582	-0.4293295	-0.3383337	0.7268966
C19_22d_WS3	0.5839990	1.8943873	1.8903485	0.1777297
C19_22d_WS4	0.7118769	1.2996823	1.3069034	0.6450647
C19_22d_WW1	0.5153543	0.6312162	0.6756495	1.4668247
C19_22d_WW2	-0.4126627	-1.1677270	-1.0318469	0.9560705
	Maleic.acid	Malic.acid	Malonic.acid	Mannose.6.phosphate
C19_22d_WS1	-0.6769811	-0.39537009	-2.29900049	-1.28178172
C19_22d_WS2	-1.8886366	-0.75158295	-0.05142714	-0.72979540
C19_22d_WS3	-1.0885482	0.24605349	0.39953074	-0.27221438
C19_22d_WS4	0.6036622	-0.04275143	1.05934681	-0.07707658
C19_22d_WW1	-1.3496060	1.19169284	-1.45111020	1.13978918
C19_22d_WW2	-2.5754485	-0.02272957	-0.31584733	1.46118311
	Melibiose	Phenylalanine	Phosphoric.acid	Proline
C19_22d_WS1	-1.19839159	1.7579976	-0.49055772	1.2703159
C19_22d_WS2	-1.13893131	0.7985530	0.06340232	-0.4298909
C19_22d_WS3	-1.19188360	0.7150507	0.04118480	2.2599005
C19_22d_WS4	-1.75790301	0.0906991	0.69200184	0.4981703
C19_22d_WW1	-0.01206706	1.7295732	2.28242786	1.4991228
C19_22d_WW2	-0.88556830	0.8287126	1.98444974	-1.8394764
	Putrescine	Pyroglutamic.acid	Quinic.acid	
C19_22d_WS1	-0.7934654	-1.00153451	0.7740780	
C19_22d_WS2	-0.0272814	0.07758864	0.9081317	
C19_22d_WS3	0.7452612	1.20302833	1.0334794	
C19_22d_WS4	0.7988737	1.50673669	0.8600945	
C19_22d_WW1	1.0529879	-1.30568571	1.0396224	
C19_22d_WW2	-1.2296812	-0.80868919	0.8870690	
	X3.caffeoylquinic.acid	Raffinose	Rhamnose	
C19_22d_WS1		1.025430	0.99176797	-0.2947308

C19_22d_WS2	1.085933	0.80097838	-0.8228022
C19_22d_WS3	1.193502	0.64292196	-0.3086284
C19_22d_WS4	1.019179	-0.05539435	-0.4537915
C19_22d_WW1	1.192302	1.04739905	0.4018280
C19_22d_WW2	1.075884	0.67159794	-0.1849566
	Ribonic.acid	Ribose	Serine Shikimic.acid
C19_22d_WS1	0.2760324	-0.8349973	-1.1566697 1.426647
C19_22d_WS2	0.7094154	0.2034611	-0.8346685 1.463366
C19_22d_WS3	0.1839781	-1.0253033	1.0801758 1.670380
C19_22d_WS4	0.6525500	-0.6716752	1.0755091 1.496282
C19_22d_WW1	1.4805564	0.7422078	-0.3886066 1.872425
C19_22d_WW2	0.9312634	0.8463777	-1.0057807 1.636361
	Succinic.acid	Sucrose	Tartaric.acid Threitol
C19_22d_WS1	1.3480820	-0.95919968	-1.54420625 -0.7789986
C19_22d_WS2	1.2161849	-0.83820682	-0.88559872 -1.3855780
C19_22d_WS3	0.2572087	0.22149378	-0.18857488 1.3992531
C19_22d_WS4	-0.3182332	0.93930471	0.19263210 0.6113202
C19_22d_WW1	1.5076382	0.60023924	-0.02908515 -0.3627575
C19_22d_WW2	0.8990756	-0.05844232	-0.26690897 0.5577319
	Threonic.acid	Threonolactone	Threonine Uracil
C19_22d_WS1	-0.6908467	-0.1584903	1.056815676 -0.2000785
C19_22d_WS2	-1.1014968	-0.4615778	1.174635680 0.5903944
C19_22d_WS3	-1.6957130	-1.3074161	0.004860347 -1.2766167
C19_22d_WS4	-2.4755504	-2.0383825	-0.226722381 0.1300120
C19_22d_WW1	-1.2797199	0.2432078	0.955380406 1.5383291
C19_22d_WW2	-0.9796887	0.2389318	0.719170159 0.8418766
	Valine	Xylose	
C19_22d_WS1	1.4318730	-0.2215267	
C19_22d_WS2	0.4298923	0.3488749	
C19_22d_WS3	2.2448056	-0.3475185	
C19_22d_WS4	1.3888491	0.1939763	
C19_22d_WW1	1.5235141	2.1048705	
C19_22d_WW2	-0.2809546	0.7517590	

----- sm1819: Standardized metabolites 18/19 -----

name	description	class	nrow	ncol
13 sm1819	Standardized metabolites 18/19 matrix		190	55

	Alanine	Arabinose	Ascorbic.acid	Aspartic.acid
C18_11d_WS1	-1.4062900	0.65468542	0.8810975	0.17362695
C18_11d_WS2	-1.5802391	0.96453480	1.4020301	-0.34308903
C18_11d_WS3	1.4491728	-0.05253557	1.2408231	-0.14870734
C18_11d_WS4	1.4712993	0.48575419	1.8298271	0.05030402
C18_11d_WW1	-1.2175587	2.14593351	0.7922128	-0.47933609
C18_11d_WW2	-0.4248767	1.49069835	0.8998807	-0.42119453
	GABA	Trans.Caffeic.acid	Catechin	Citric.acid
C18_11d_WS1	-0.2865262	0.6433701	1.2842804	-0.45074790
C18_11d_WS2	-0.7398570	1.0291864	1.4800244	-0.39186847
C18_11d_WS3	-0.5396917	-0.1046505	1.0870947	-0.75502850
C18_11d_WS4	-0.4028365	-0.0312767	1.0087832	0.02625003
C18_11d_WW1	-0.2251239	0.7212781	1.0887732	-0.09856208

C18_11d_WW2	-0.4998831	-0.1797194	0.8229012	-0.74783230
	Erythronic.acid	Ethanolamine	Fructose	
C18_11d_WS1	-0.9872651	-0.62799456	0.92588792	
C18_11d_WS2	-0.2904856	-0.92055331	0.65059273	
C18_11d_WS3	-0.7754247	-0.08972082	-0.10150358	
C18_11d_WS4	-1.2056083	-0.97085522	0.07871419	
C18_11d_WW1	-0.2615480	-0.86753000	0.72387326	
C18_11d_WW2	-1.7797622	-1.20815529	0.39837062	
	Fructose.6.phosphate	Fumaric.acid	Galactinol	Galactose
C18_11d_WS1	0.13294745	-2.4447847	0.31909535	1.4804393
C18_11d_WS2	0.14300253	-0.9484950	0.04264797	1.5359128
C18_11d_WS3	0.93556084	0.6511680	-0.04224784	0.2516422
C18_11d_WS4	1.40731402	0.7233805	0.02745826	0.9015674
C18_11d_WW1	0.07134611	-1.8727471	0.34643857	0.9982504
C18_11d_WW2	1.62118662	-1.0761093	-0.04374197	0.6044452
	Gallic.acid	Gluconic.acid	Glucopyranose..H2O.	Glucose
C18_11d_WS1	0.5398335	0.70666638	-0.3989666	1.2857497
C18_11d_WS2	0.5750503	0.99736367	0.0559675	1.3127487
C18_11d_WS3	0.3867488	0.36959942	0.3903860	0.5859735
C18_11d_WS4	0.2001235	0.54549323	-0.1950386	1.1385120
C18_11d_WW1	1.2013335	0.56231750	0.4566399	1.1311052
C18_11d_WW2	0.2398368	0.09651817	-0.1423663	0.7953175
	Glutamic.acid	Glyceric.acid	Glycine	Hydroquinone
C18_11d_WS1	0.91195762	0.8579279	0.8620770	1.5633506
C18_11d_WS2	0.31554078	0.6101076	0.9417316	2.1487235
C18_11d_WS3	-0.75260462	0.4963996	1.3529285	0.6965274
C18_11d_WS4	-0.29030226	0.8551622	0.8415377	1.7087108
C18_11d_WW1	0.37953934	0.6369905	1.7641183	0.8579428
C18_11d_WW2	0.05976519	0.3883441	1.1289664	1.5443555
	Myo.Inostol	Isoleucine	Leucine	Lyxonic.acid
C18_11d_WS1	0.8774455	-0.9989703	-1.34356895	-0.1334790
C18_11d_WS2	1.0121331	-0.9538992	-1.05082043	0.7791878
C18_11d_WS3	1.1951407	-0.5861411	-0.86478360	0.7953679
C18_11d_WS4	1.7001916	0.4325397	0.03821471	-0.2104462
C18_11d_WW1	0.9545803	0.5330824	0.11465979	0.9825287
C18_11d_WW2	0.8291475	-0.2163238	-0.45874662	0.1174265
	Maleic.acid	Malic.acid	Malonic.acid	Mannose.6.phosphate
C18_11d_WS1	-0.19963359	0.3021843	-0.036274507	0.1155221
C18_11d_WS2	0.89926101	0.9313804	-0.426704977	0.4663541
C18_11d_WS3	-0.10179395	0.1684395	0.365374977	0.8742404
C18_11d_WS4	-0.25221947	0.2851244	1.082482659	1.2827765
C18_11d_WW1	-0.59745773	-0.1631500	0.051428417	0.1453378
C18_11d_WW2	0.06091111	-0.6717914	0.007861343	1.5086377
	Melibiose	Phenylalanine	Phosphoric.acid	Proline
C18_11d_WS1	0.02733171	-0.726244206	0.51989190	-0.30749780
C18_11d_WS2	-0.05942391	-0.479127289	0.02008297	-0.07176952
C18_11d_WS3	-2.09435345	-0.627939396	0.13679833	-0.87830641
C18_11d_WS4	-1.62267429	0.008371749	0.53047870	-0.61378593
C18_11d_WW1	-0.25263209	-0.553545093	1.30011632	-0.80967552
C18_11d_WW2	-0.57099288	-0.116939413	1.10374948	-0.65579511
	Putrescine	Pyroglutamic.acid	Quinic.acid	
C18_11d_WS1	-0.8493213	-0.1955665	1.2477133	
C18_11d_WS2	-1.0496524	-0.9317976	1.0576983	

C18_11d_WS3	0.4991721		0.9724628	0.9642101
C18_11d_WS4	0.5866417		1.6747440	0.7797010
C18_11d_WW1	-0.2834413		-0.4124706	1.6009038
C18_11d_WW2	-0.7196820		-0.4447971	1.1578881
	X3.caffeoylquinic.acid		Raffinose	Rhamnose
C18_11d_WS1		1.1811104	0.19679395	-0.40506566
C18_11d_WS2		1.1780489	0.68033760	-0.80168442
C18_11d_WS3		0.9579504	0.02780822	-0.69341921
C18_11d_WS4		0.9915877	0.23689895	-0.31944532
C18_11d_WW1		1.1511581	-0.01254122	-0.48095691
C18_11d_WW2		1.0262675	0.04569641	0.02471514
	Ribonic.acid	Ribose	Serine	Shikimic.acid
C18_11d_WS1	0.2273135	0.3777505	1.4663727	1.842062
C18_11d_WS2	-0.1399435	0.7163120	0.6428656	1.208321
C18_11d_WS3	1.8331155	0.8355890	1.2968085	1.291200
C18_11d_WS4	0.6035722	0.4290780	1.6615050	1.244280
C18_11d_WW1	1.6672807	1.2370428	0.1881974	1.928182
C18_11d_WW2	1.1617515	0.7506767	0.3272109	1.507384
	Succinic.acid	Sucrose	Tartaric.acid	Threitol
C18_11d_WS1	1.0191164	0.8091671	0.80383281	-0.344894916
C18_11d_WS2	1.0481215	1.2386381	-0.02639419	-1.014381129
C18_11d_WS3	-0.1327153	1.5864121	-0.44140757	-0.006640386
C18_11d_WS4	0.2575998	1.7421454	0.55718283	0.467051519
C18_11d_WW1	1.2561500	1.3055212	0.57487253	0.681093763
C18_11d_WW2	0.5734997	1.1359717	0.25731610	0.265269687
	Threonic.acid	Threonolactone	Threonine	Uracil
C18_11d_WS1	0.6942373	0.7373110	0.36528745	-1.61372948
C18_11d_WS2	0.9085691	0.5499635	-0.17611986	0.14921803
C18_11d_WS3	0.7458717	-0.0342207	0.09487384	-0.43134589
C18_11d_WS4	0.4579763	0.5420799	0.64301038	0.27013071
C18_11d_WW1	1.6003394	1.0225643	-0.13819726	-0.66539698
C18_11d_WW2	1.4613386	2.0096905	-0.01968125	0.07486595
	Valine	Xylose		
C18_11d_WS1	-0.4085276	1.4230608		
C18_11d_WS2	-0.3672574	0.6553803		
C18_11d_WS3	0.1174862	0.8378696		
C18_11d_WS4	1.1289800	1.1325131		
C18_11d_WW1	1.0191397	1.3385454		
C18_11d_WW2	-0.1289273	1.9616131		

----- mldata: Metabolites featuredata 18/19 -----

name	description	class	nrow	ncol
14 mldata	Metabolites featuredata 18/19	data.frame	55	3

	Metabolite	Bin
Alanine	Alanine	5.1001
Arabinose	Arabinose	10.6.1001
Ascorbic.acid	Ascorbic acid	17.5.1001
Aspartic.acid	Aspartic acid	13.1.1.2.1001
GABA	GABA	22.1002
Trans.Caffeic.acid	Trans-Caffeic acid	16.2.1.1006

Alanine		
Arabinose		cell wall
Ascorbic.acid		hormone metabol
Aspartic.acid	amino acid metabolism.synthesis.central	amino acid metaboli
GABA		pol
Trans.Caffeic.acid	secondary metabolism.phenylpropanoids.lignin	

----- intgenes: Names of genes in bins -----

	name	description	class	nrow	ncol
15	intgenes	Names of genes in bins	list	8	<NA>

\$`2`

```
[1] "Vitvi02g01845" "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g00053"
[5] "Vitvi01g00064" "Vitvi01g00681"
```

\$`3`

```
[1] "Vitvi02g01701" "Vitvi10g02295" "Vitvi00g01259" "Vitvi01g00140"
[5] "Vitvi01g00509" "Vitvi01g00714"
```

\$`8`

```
[1] "Vitvi07g03070" "Vitvi01g00274" "Vitvi01g00698" "Vitvi01g00735"
[5] "Vitvi01g00861" "Vitvi01g01724"
```

\$`10`

```
[1] "Vitvi02g01716" "Vitvi07g02990" "Vitvi10g02284" "Vitvi10g02279"
[5] "Vitvi07g02943" "Vitvi00g02116"
```

\$`13`

```
[1] "Vitvi07g03049" "Vitvi00g00869" "Vitvi02g01749" "Vitvi01g00035"
[5] "Vitvi01g00113" "Vitvi01g00502"
```

\$`16`

```
[1] "Vitvi02g01683" "Vitvi02g01722" "Vitvi10g02185" "Vitvi07g03081"
[5] "Vitvi10g02269" "Vitvi07g03083"
```

\$`27.3`

```
[1] "Vitvi02g01753" "Vitvi02g01762" "Vitvi02g01795" "Vitvi02g01721"
[5] "Vitvi02g01717" "Vitvi02g01790"
```

\$`35`

```
[1] "Vitvi07g02832" "Vitvi07g02830" "Vitvi07g02812" "Vitvi07g02811"
[5] "Vitvi09g02033" "Vitvi09g02034"
```

----- intmtbs: Names of metabolites in bins -----

	name	description	class	nrow	ncol
16	intmtbs	Names of metabolites in bins	list	8	<NA>

```

$`2`
[1] "Fructose" "Glucose" "Sucrose"

$`3`
[1] "Erythronic.acid" "Galactinol" "Galactose"
[4] "Myo.Inositol" "Raffinose" "Threitol"

$`8`
[1] "Fumaric.acid" "Succinic.acid"

$`10`
[1] "Arabinose" "Melibiose" "Rhamnose" "Ribonic.acid"
[5] "Ribose"

$`13`
[1] "Aspartic.acid" "Isoleucine" "Leucine" "Phenylalanine"
[5] "Proline" "Shikimic.acid"

$`16`
[1] "Trans.Caffeic.acid" "Catechin"
[3] "Gallic.acid" "Hydroquinone"
[5] "Quinic.acid" "X3.caffeoylquinic.acid"

$`27.3`
character(0)

$`35`
[1] "Gluconic.acid" "Glucopyranose..H2O." "Lyxonic.acid"
[4] "Maleic.acid" "Malonic.acid" "Phosphoric.acid"

```

```

----- stat4: Statistics from transcript analysis (50*.Rnw) -----

```

```

      name                description      class
17 stat4 Statistics from transcript analysis (50*.Rnw) data.frame
      nrow ncol
17 15242    28

```

		X	A	Coef.mc	Coef.c	
Vitvi03g00325	Vitvi03g00325	2.29529737	3.1923214	5.400429		
Vitvi17g00601	Vitvi17g00601	-0.09054575	-1.1866150	4.512791		
Vitvi05g00011	Vitvi05g00011	3.00782492	2.7136299	4.101024		
Vitvi13g02005	Vitvi13g02005	2.33061623	2.9484215	4.078080		
Vitvi02g00695	Vitvi02g00695	-0.45420732	-0.8399601	4.047520		
Vitvi14g01381	Vitvi14g01381	-0.72321946	-1.1530667	3.935431		
		Coef.mf.mc	Coef.f.c	Koef.f	t.mc	t.c
Vitvi03g00325		-1.7940481	-0.29162541	5.108803	4.801209	2.919406
Vitvi17g00601		2.1921385	-0.33971975	4.173071	-2.341540	3.200805
Vitvi05g00011		0.5883901	0.03610049	4.137125	8.336348	4.528348
Vitvi13g02005		-1.2356105	1.22197743	5.300058	3.618330	1.798857
Vitvi02g00695		0.7715056	-1.08372917	2.963791	-1.857328	3.216927
Vitvi14g01381		0.8596946	0.58827898	4.523710	-1.546481	1.897163

	t.mf.mc	t.f.c	P.value.mc	P.value.c
Vitvi03g00325	-1.9079328	-0.10592036	9.103982e-05	0.0080809276
Vitvi17g00601	3.0587557	-0.16189100	2.892715e-02	0.0042173372
Vitvi05g00011	1.2781316	0.02678234	3.604890e-08	0.0001755321
Vitvi13g02005	-1.0722232	0.36215284	1.571115e-03	0.0861338096
Vitvi02g00695	1.2062964	-0.57870975	7.705364e-02	0.0040613495
Vitvi14g01381	0.8153037	0.19053890	1.366212e-01	0.0713562714
	P.value.mf.mc	P.value.f.c	P.value.adj.mc	P.value.adj.c
Vitvi03g00325	0.069880852	0.9166302	1.006038e-04	0.28511458
Vitvi17g00601	0.005867102	0.8729075	3.029669e-02	0.23762225
Vitvi05g00011	0.214866433	0.9788810	4.329163e-08	0.07644173
Vitvi13g02005	0.295539873	0.7207826	1.694639e-03	0.58897413
Vitvi02g00695	0.240844889	0.5688147	7.988693e-02	0.23288283
Vitvi14g01381	0.423862612	0.8506793	1.407775e-01	0.56306208
	P.value.adj.mf.mc	P.value.adj.f.c	F	
Vitvi03g00325	0.29606841	0.9999488	9.550446	
Vitvi17g00601	0.05151288	0.9999488	37.060841	
Vitvi05g00011	0.56223076	0.9999488	84.152716	
Vitvi13g02005	0.66176271	0.9999488	6.968467	
Vitvi02g00695	0.59836313	0.9999488	35.455608	
Vitvi14g01381	0.76054331	0.9999488	19.816526	
	F.p.value	Type	interestingC	interestingFC
Vitvi03g00325	1.356555e-04	Type5	*	
Vitvi17g00601	2.421190e-09	Type5	*	
Vitvi05g00011	8.630059e-13	Type1	*	
Vitvi13g02005	9.348733e-04	Type1.4		
Vitvi02g00695	3.642503e-09		*	
Vitvi14g01381	5.922355e-07	Type1		
	geneID	BINCODE		
Vitvi03g00325	Vitvi03g00325	27.3.25		
Vitvi17g00601	Vitvi17g00601	17.6.3		
Vitvi05g00011	Vitvi05g00011	35.2		
Vitvi13g02005	Vitvi13g02005	29.5.1		
Vitvi02g00695	Vitvi02g00695	20.1		
Vitvi14g01381	Vitvi14g01381	35.2		
Vitvi03g00325	RNA.regulation of transcription.MYB domain transcription factor			
Vitvi17g00601	hormone metabolism.gibberelin.induced-regulated-responsive-act			
Vitvi05g00011	not assigned.u			
Vitvi13g02005	protein.degradation.subt			
Vitvi02g00695	stress.			
Vitvi14g01381	not assigned.u			
Vitvi03g00325	RAD-like			
Vitvi17g00601	Gibberellin-regulated family prote			
Vitvi05g00011	Pollen Ole e 1 allergen and extensin family pro			
Vitvi13g02005	Subtilisin-like serine endopeptidase family prote			
Vitvi02g00695	Polyketide cyclase/dehydrase and lipid transport superfamily pro			
Vitvi14g01381				

----- statig: Statistics for interesting genes -----

name		description	class	nrow	ncol
18 statig	Statistics for interesting genes	data.frame	8424	28	
		X	A	Coef.mc	Coef.c
NA	<NA>	NA	NA	NA	NA
Vitvi01g00025	Vitvi01g00025	3.057806	3.114662	-1.26413832	-0.1137121
Vitvi01g00052	Vitvi01g00052	3.349527	3.259138	-0.78711296	0.1807789
Vitvi01g00053	Vitvi01g00053	4.631552	4.893533	0.19949344	-0.5239621
Vitvi01g00064	Vitvi01g00064	1.833567	2.504210	-0.03291293	-1.3412870
Vitvi01g00681	Vitvi01g00681	7.031147	7.124845	-0.23932641	-0.1873968
		Coef.f.c	Koef.f	t.mc	t.c
NA	NA	NA	NA	NA	NA
Vitvi01g00025	0.8379419	-0.4261964	21.759123	-3.17429440	-0.5617227
Vitvi01g00052	1.0025864	0.2154735	14.324978	-1.24351347	0.5618546
Vitvi01g00053	-0.8385976	-0.6391041	16.427027	0.24070623	-1.2437164
Vitvi01g00064	2.0300614	1.9971485	6.239789	-0.02947731	-2.3632291
Vitvi01g00681	0.1691963	-0.0701301	52.405974	-0.63272966	-0.9746584
		t.f.c	P.value.mc	P.value.c	P.value.mf.mc
NA	NA	NA	NA	NA	NA
Vitvi01g00025	1.4136908	4.211606e-16	0.004486561	0.58012959	
Vitvi01g00052	1.0641997	1.868977e-12	0.227103309	0.58004129	
Vitvi01g00053	-0.6798298	1.255313e-13	0.812069388	0.22703005	
Vitvi01g00064	1.2215701	3.137274e-06	0.976756560	0.02762602	
Vitvi01g00681	0.3005428	3.998197e-24	0.533600377	0.34059797	
		P.value.f.c	P.value.adj.mc	P.value.adj.c	
NA	NA	NA	NA	NA	
Vitvi01g00025	0.1718074	8.299069e-16	0.2416402		
Vitvi01g00052	0.2990763	2.640125e-12	0.7466585		
Vitvi01g00053	0.5038863	1.914305e-13	0.9594257		
Vitvi01g00064	0.2351312	3.580556e-06	0.9965809		
Vitvi01g00681	0.7666578	1.819120e-22	0.8804002		
		P.value.adj.mf.mc	P.value.adj.f.c	F	
NA	NA	NA	NA	NA	
Vitvi01g00025	0.8515913	0.9999488	1305.9897		
Vitvi01g00052	0.8515913	0.9999488	553.7057		
Vitvi01g00053	0.5797790	0.9999488	599.6382		
Vitvi01g00064	0.1599574	0.9999488	51.0410		
Vitvi01g00681	0.7000202	0.9999488	6549.1885		
		F.p.value	Type	interestingC	interestingFC
NA	NA	<NA>	<NA>	<NA>	<NA>
Vitvi01g00025	2.882747e-25			*	
Vitvi01g00052	2.674051e-21				
Vitvi01g00053	1.147679e-21				
Vitvi01g00064	1.179244e-10	Type3.F			
Vitvi01g00681	9.309219e-33				
		geneID	BINCODE		
NA	<NA>	<NA>			
Vitvi01g00025	Vitvi01g00025	2.2.1.1			
Vitvi01g00052	Vitvi01g00052	2.2.2.6			
Vitvi01g00053	Vitvi01g00053	2.2.2.6			
Vitvi01g00064	Vitvi01g00064	2.2.2.2			
Vitvi01g00681	Vitvi01g00681	35.2			

NAME

NA		<NA>
Vitvi01g00025	major CHO metabolism.degradation.sucrose.fructokinase	
Vitvi01g00052	major CHO metabolism.degradation.starch.transporter	
Vitvi01g00053	major CHO metabolism.degradation.starch.transporter	
Vitvi01g00064	major CHO metabolism.degradation.starch.starch phosphorylase	
Vitvi01g00681		not assigned.unknown

NA		
Vitvi01g00025	fructokinase-like protein	Chr1:2
Vitvi01g00052	Glucose-6-phosphate/phosphate translocator-like protein	Chr5:1
Vitvi01g00053	Glucose-6-phosphate/phosphate translocator-like protein	Chr5:1
Vitvi01g00064	Glycosyl transferase%2C family 35	Chr3:1
Vitvi01g00681	phosphoglucan%2C water dikinase	Chr4:12

Factor for days within the year

```
> pdata1819$day <- factor(as.character(pdata1819$day))
```

4 Preparation of data for mixOmics

Data for **mixOmics** analysis should follow the traditional mathematical orientation: samples in rows, variables in columns. The matrices must have appropriate dimensions. Due to different ranges and variability in years 2018 and 2019, we will analyze them separately.

4.0.1 Selection of samples, transcripts and metaboloms

```
> .years <- addArgs[grep("years", names(addArgs))]
```

Common samples in the given year (18, 19).

```
> table(pdata1819$year)
```

```
18 19
```

```
48 32
```

```
> select_year <- pdata1819$year %in% .years
```

```
> sum(select_year)
```

```
[1] 80
```

```
> rownames(pdata1819)[select_year]
```

```
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1" "C18_11d_WW2" "C18_11d_WW3" "C18_11d_WW4"
[9] "C18_34d_WS1" "C18_34d_WS2" "C18_34d_WS3" "C18_34d_WS4"
[13] "C18_34d_WW1" "C18_34d_WW2" "C18_34d_WW3" "C18_34d_WW4"
[17] "C18_67d_WS1" "C18_67d_WS2" "C18_67d_WS3" "C18_67d_WS4"
[21] "C18_67d_WW1" "C18_67d_WW2" "C18_67d_WW3" "C18_67d_WW4"
[25] "F18_10d_WS1" "F18_10d_WS2" "F18_10d_WS3" "F18_10d_WS4"
[29] "F18_10d_WW1" "F18_10d_WW2" "F18_10d_WW3" "F18_10d_WW4"
[33] "F18_34d_WS1" "F18_34d_WS2" "F18_34d_WS3" "F18_34d_WS4"
[37] "F18_34d_WW1" "F18_34d_WW2" "F18_34d_WW3" "F18_34d_WW4"
[41] "F18_67d_WS1" "F18_67d_WS2" "F18_67d_WS3" "F18_67d_WS4"
[45] "F18_67d_WW1" "F18_67d_WW2" "F18_67d_WW3" "F18_67d_WW4"
[49] "C19_22d_WS1" "C19_22d_WS2" "C19_22d_WS3" "C19_22d_WS4"
[53] "C19_22d_WW1" "C19_22d_WW2" "C19_22d_WW3" "C19_22d_WW4"
[57] "C19_44d_WS1" "C19_44d_WS2" "C19_44d_WS3" "C19_44d_WS4"
[61] "C19_44d_WW1" "C19_44d_WW2" "C19_44d_WW3" "C19_44d_WW4"
[65] "F19_22d_WS1" "F19_22d_WS2" "F19_22d_WS3" "F19_22d_WS4"
[69] "F19_22d_WW1" "F19_22d_WW2" "F19_22d_WW3" "F19_22d_WW4"
[73] "F19_44d_WS1" "F19_44d_WS2" "F19_44d_WS3" "F19_44d_WS4"
[77] "F19_44d_WW1" "F19_44d_WW2" "F19_44d_WW3" "F19_44d_WW4"
```

Name of sample, gene and metabolite names to consider

Samples

```
> sampleNames <- rownames(pdata1819)[select_year]
```

```
> head(sampleNames)
```

```
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
```

```
[5] "C18_11d_WW1" "C18_11d_WW2"
```

4.0.2 Transcripts matrix: T

Exclude bin 35 for now

```
> intgenesAll <- intgenes
> intgenes <- intgenes[names(intgenes)!="35"]
> names(intgenes)
[1] "2"      "3"      "8"      "10"     "13"     "16"     "27.3"
```

Actually, start with small set of genes, keep just bin 1

```
> names(intgenesAll)
[1] "2"      "3"      "8"      "10"     "13"     "16"     "27.3" "35"
> keepbins <- names(intgenesAll)[.bins]
> intgenes <- intgenesAll[names(intgenesAll)%in% keepbins]
> names(intgenes)
[1] "2"      "3"      "8"      "10"     "13"     "16"     "27.3"

> geneNames <- unlist(intgenes)
> # any doublets
> which(table(geneNames)>1)
Vitvi14g02644 Vitvi18g01242
          1650           2037
> geneNames <- unique(geneNames)
> length(geneNames)
[1] 2178
> # keep genes that are measured
> geneNames <- geneNames[geneNames %in% rownames(t1819)]
> length(geneNames)
[1] 2049
> head(geneNames)
[1] "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g00053" "Vitvi01g00064"
[5] "Vitvi01g00681" "Vitvi01g00932"

> T <- t1819[geneNames, sampleNames]
> head(T)
```

	C18_11d_WS1	C18_11d_WS2	C18_11d_WS3	C18_11d_WS4
Vitvi01g00025	2.525428	2.478706	2.651938	2.423295
Vitvi01g00052	3.372516	3.221593	3.540013	3.532502
Vitvi01g00053	4.733444	4.558951	5.010778	4.990309
Vitvi01g00064	3.204010	2.826364	3.435292	2.918474
Vitvi01g00681	7.006432	7.112737	7.282731	7.034244
Vitvi01g00932	3.902681	3.862343	4.236901	3.985243
	C18_11d_WW1	C18_11d_WW2	C18_11d_WW3	C18_11d_WW4
Vitvi01g00025	2.535710	2.212984	2.361454	2.516753
Vitvi01g00052	2.550469	3.315024	3.315533	3.221392
Vitvi01g00053	4.392540	4.709945	4.821214	4.843719
Vitvi01g00064	2.690307	2.970480	2.995004	3.004581
Vitvi01g00681	6.930850	7.044802	7.057018	7.024871
Vitvi01g00932	3.950284	3.816622	4.079860	3.807215
	C18_34d_WS1	C18_34d_WS2	C18_34d_WS3	C18_34d_WS4
Vitvi01g00025	2.578949	2.311085	2.583815	3.010003
Vitvi01g00052	2.253492	2.757454	2.656510	2.128346
Vitvi01g00053	4.594141	4.939657	4.431605	4.583447
Vitvi01g00064	2.511611	2.502197	2.142444	2.499113
Vitvi01g00681	6.891684	6.678274	6.859723	6.453177
Vitvi01g00932	3.745214	3.507557	4.022424	3.898226
	C18_34d_WW1	C18_34d_WW2	C18_34d_WW3	C18_34d_WW4
Vitvi01g00025	2.726730	2.745623	2.401136	2.614643
Vitvi01g00052	2.245390	1.684681	2.286576	2.679252
Vitvi01g00053	4.304855	4.545437	4.485788	5.121025
Vitvi01g00064	1.681696	2.702874	2.612473	2.295465
Vitvi01g00681	6.164293	6.536588	6.699936	6.371025
Vitvi01g00932	3.644268	3.104288	3.549279	3.684507
	C18_67d_WS1	C18_67d_WS2	C18_67d_WS3	C18_67d_WS4
Vitvi01g00025	3.954792	3.662574	3.702285	3.724124
Vitvi01g00052	2.688860	3.005134	3.291143	3.271692
Vitvi01g00053	3.690792	3.716075	3.626788	3.145972
Vitvi01g00064	1.753158	1.724258	2.113975	1.452874
Vitvi01g00681	6.959409	6.936884	6.836479	6.531912
Vitvi01g00932	4.848866	4.516614	4.411571	4.418600
	C18_67d_WW1	C18_67d_WW2	C18_67d_WW3	C18_67d_WW4
Vitvi01g00025	3.017593	3.1550122	3.098662	3.0632025
Vitvi01g00052	2.482471	2.3852736	2.784489	1.8757093
Vitvi01g00053	3.362112	3.5472244	3.706569	3.0389141
Vitvi01g00064	1.373478	0.9839821	1.378348	0.3759491
Vitvi01g00681	6.877357	6.8713393	6.813021	6.9990242
Vitvi01g00932	3.631923	3.8305964	3.678031	3.6617490
	F18_10d_WS1	F18_10d_WS2	F18_10d_WS3	F18_10d_WS4
Vitvi01g00025	3.190328	3.545382	3.811687	3.705025
Vitvi01g00052	4.033268	4.005980	3.479549	3.335980
Vitvi01g00053	3.076932	3.454593	3.492709	3.455495
Vitvi01g00064	4.645416	4.820738	4.626337	4.620433
Vitvi01g00681	7.047604	7.072526	7.152525	7.190802
Vitvi01g00932	4.871946	4.880086	4.918555	4.949219
	F18_10d_WW1	F18_10d_WW2	F18_10d_WW3	F18_10d_WW4
Vitvi01g00025	3.005951	2.755574	3.247298	2.969490
Vitvi01g00052	3.375932	3.188418	3.082239	3.253917
Vitvi01g00053	2.789974	2.822546	2.923977	2.733084

Vitvi01g00064	4.350841	4.319612	4.355473	4.429152
Vitvi01g00681	7.162528	6.908959	7.144751	6.976919
Vitvi01g00932	5.124985	4.787164	5.143878	5.115840
	F18_34d_WS1	F18_34d_WS2	F18_34d_WS3	F18_34d_WS4
Vitvi01g00025	2.16706262	2.1668879	2.1549196	2.638828
Vitvi01g00052	2.91541049	2.7158399	3.0016969	3.377254
Vitvi01g00053	4.34490150	4.3929206	5.2173197	5.025046
Vitvi01g00064	-0.09883144	0.8748018	0.3448193	1.496935
Vitvi01g00681	6.67898485	6.9279474	6.5777358	6.979445
Vitvi01g00932	3.10628299	3.2370563	3.5527121	3.244341
	F18_34d_WW1	F18_34d_WW2	F18_34d_WW3	F18_34d_WW4
Vitvi01g00025	1.9572744	1.85282095	2.254265	2.4787012
Vitvi01g00052	3.1387492	3.54087695	3.032267	2.9261602
Vitvi01g00053	4.4869625	4.99342458	4.780498	4.4272837
Vitvi01g00064	-0.2468172	-0.09471163	1.035023	0.9078483
Vitvi01g00681	6.3819679	6.48666832	6.767507	6.4394005
Vitvi01g00932	2.8977411	3.17830687	3.446615	3.6090979
	F18_67d_WS1	F18_67d_WS2	F18_67d_WS3	F18_67d_WS4
Vitvi01g00025	3.8714193	3.411367	3.4349493	2.83516476
Vitvi01g00052	2.4624461	2.732211	2.4752948	2.28683118
Vitvi01g00053	3.4543547	3.180826	3.0074054	3.94746773
Vitvi01g00064	0.1012586	-1.021232	-0.2978714	-0.05126174
Vitvi01g00681	6.9261259	6.723329	6.9402200	6.59279764
Vitvi01g00932	3.5053725	3.597451	2.9236761	2.42469999
	F18_67d_WW1	F18_67d_WW2	F18_67d_WW3	F18_67d_WW4
Vitvi01g00025	2.979030	3.007746	2.5105281	2.5763134
Vitvi01g00052	2.450210	2.047726	2.0475561	2.4108593
Vitvi01g00053	2.911310	2.969079	3.5205958	3.5941147
Vitvi01g00064	-2.261285	-1.478158	-0.4146633	-0.4869291
Vitvi01g00681	6.744527	6.736881	6.3439143	6.5238761
Vitvi01g00932	2.705269	2.491469	2.2928427	2.2889762
	C19_22d_WS1	C19_22d_WS2	C19_22d_WS3	C19_22d_WS4
Vitvi01g00025	4.46	3.49	3.98	3.50
Vitvi01g00052	4.55	4.48	4.50	5.00
Vitvi01g00053	4.97	5.18	5.32	5.84
Vitvi01g00064	3.24	2.66	2.92	2.62
Vitvi01g00681	8.22	7.92	8.21	7.77
Vitvi01g00932	4.76	4.20	4.54	4.17
	C19_22d_WW1	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Vitvi01g00025	3.52	3.70	3.06	3.32
Vitvi01g00052	3.75	4.17	4.14	4.09
Vitvi01g00053	5.48	5.79	5.51	5.32
Vitvi01g00064	2.13	2.66	2.23	2.01
Vitvi01g00681	7.33	7.72	7.67	7.29
Vitvi01g00932	4.15	4.12	4.38	4.40
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3	C19_44d_WS4
Vitvi01g00025	3.80	3.96	4.00	3.86
Vitvi01g00052	3.86	3.92	4.24	4.10
Vitvi01g00053	6.40	6.29	6.27	6.24
Vitvi01g00064	3.51	3.66	3.74	3.51
Vitvi01g00681	7.31	7.43	7.50	6.99
Vitvi01g00932	4.22	4.34	4.59	4.13
	C19_44d_WW1	C19_44d_WW2	C19_44d_WW3	C19_44d_WW4

Vitvi01g00025	3.05	2.87	2.84	3.12
Vitvi01g00052	3.19	2.72	3.37	3.74
Vitvi01g00053	6.04	5.82	6.12	6.25
Vitvi01g00064	2.24	3.21	3.05	2.63
Vitvi01g00681	7.24	7.59	7.50	7.33
Vitvi01g00932	3.89	4.07	4.35	4.21
F19_22d_WS1	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4	
Vitvi01g00025	3.56	3.18	3.65	3.46
Vitvi01g00052	3.80	4.10	5.15	2.77
Vitvi01g00053	4.82	4.69	6.12	3.96
Vitvi01g00064	0.26	-0.48	1.59	-0.95
Vitvi01g00681	7.82	7.42	7.18	8.01
Vitvi01g00932	3.70	3.63	3.57	3.39
F19_22d_WW1	F19_22d_WW2	F19_22d_WW3	F19_22d_WW4	
Vitvi01g00025	3.19	3.63	3.17	3.75
Vitvi01g00052	4.51	4.81	4.50	4.50
Vitvi01g00053	5.06	5.51	5.55	5.48
Vitvi01g00064	-0.03	1.93	0.78	1.30
Vitvi01g00681	6.79	7.17	7.07	7.28
Vitvi01g00932	3.12	3.37	3.36	3.43
F19_44d_WS1	F19_44d_WS2	F19_44d_WS3	F19_44d_WS4	
Vitvi01g00025	3.39	2.90	3.37	3.27
Vitvi01g00052	4.75	4.36	3.44	3.44
Vitvi01g00053	5.66	5.64	5.38	5.40
Vitvi01g00064	1.38	1.51	2.05	0.75
Vitvi01g00681	6.45	6.96	7.04	6.91
Vitvi01g00932	3.92	3.68	3.65	3.80
F19_44d_WW1	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4	
Vitvi01g00025	2.58	2.80	2.93	2.68
Vitvi01g00052	3.77	4.55	3.99	3.84
Vitvi01g00053	5.29	5.71	5.85	5.66
Vitvi01g00064	0.52	0.42	0.60	0.41
Vitvi01g00681	7.09	6.76	7.21	6.91
Vitvi01g00932	3.86	3.43	3.93	3.37

```
> T <- t(T)
```

```
> dim(T)
```

```
[1] 80 2049
```

4.0.3 Metabolites matrix: M

```
> metabNames <- unlist(intmtbs)
> # any doublets
> which(table(metabNames) > 1)

named integer(0)

> metabNames <- unique(metabNames)
> length(metabNames)

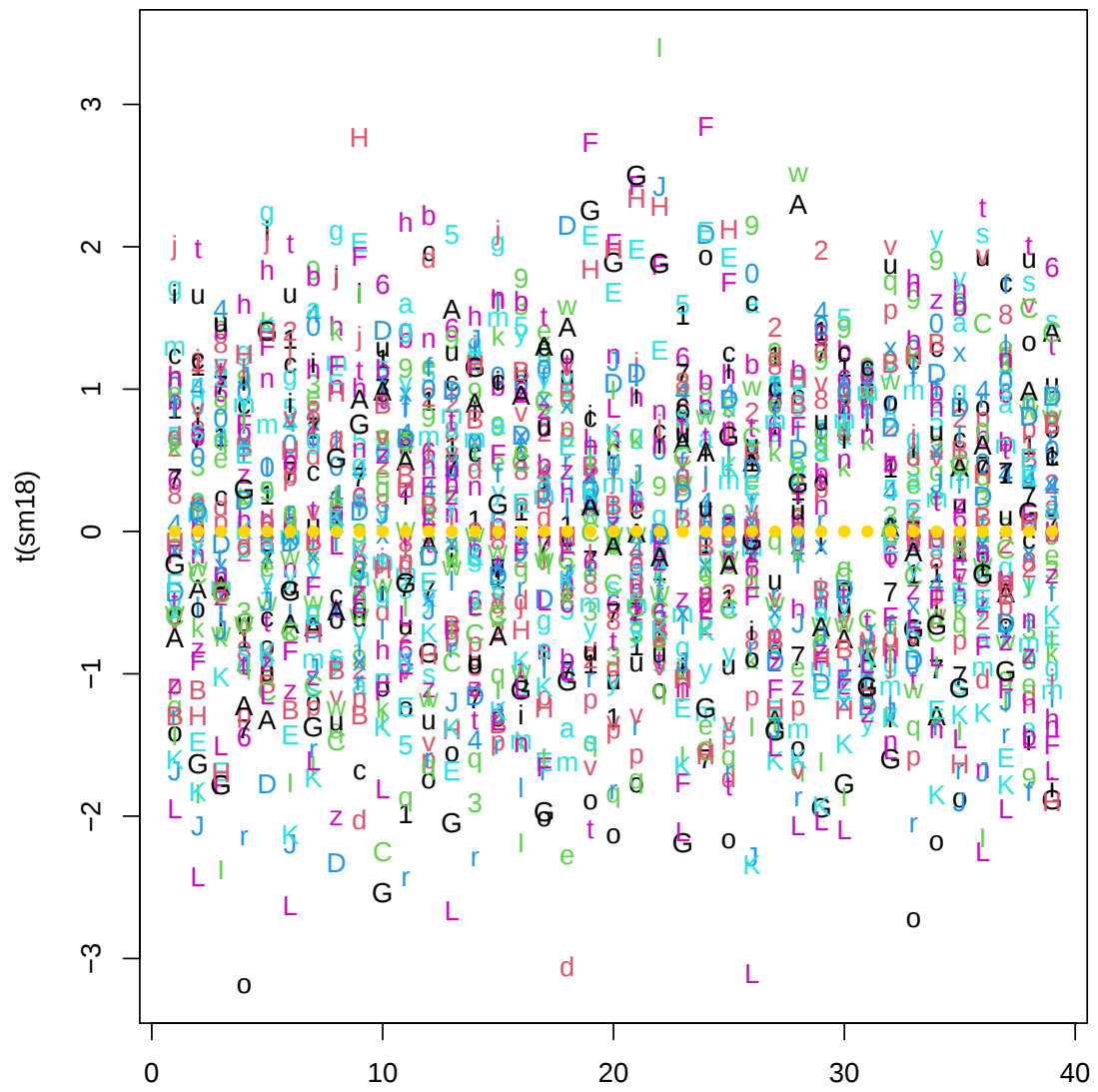
[1] 39
```

Standardization across log transformed variables variables, separately for each year.

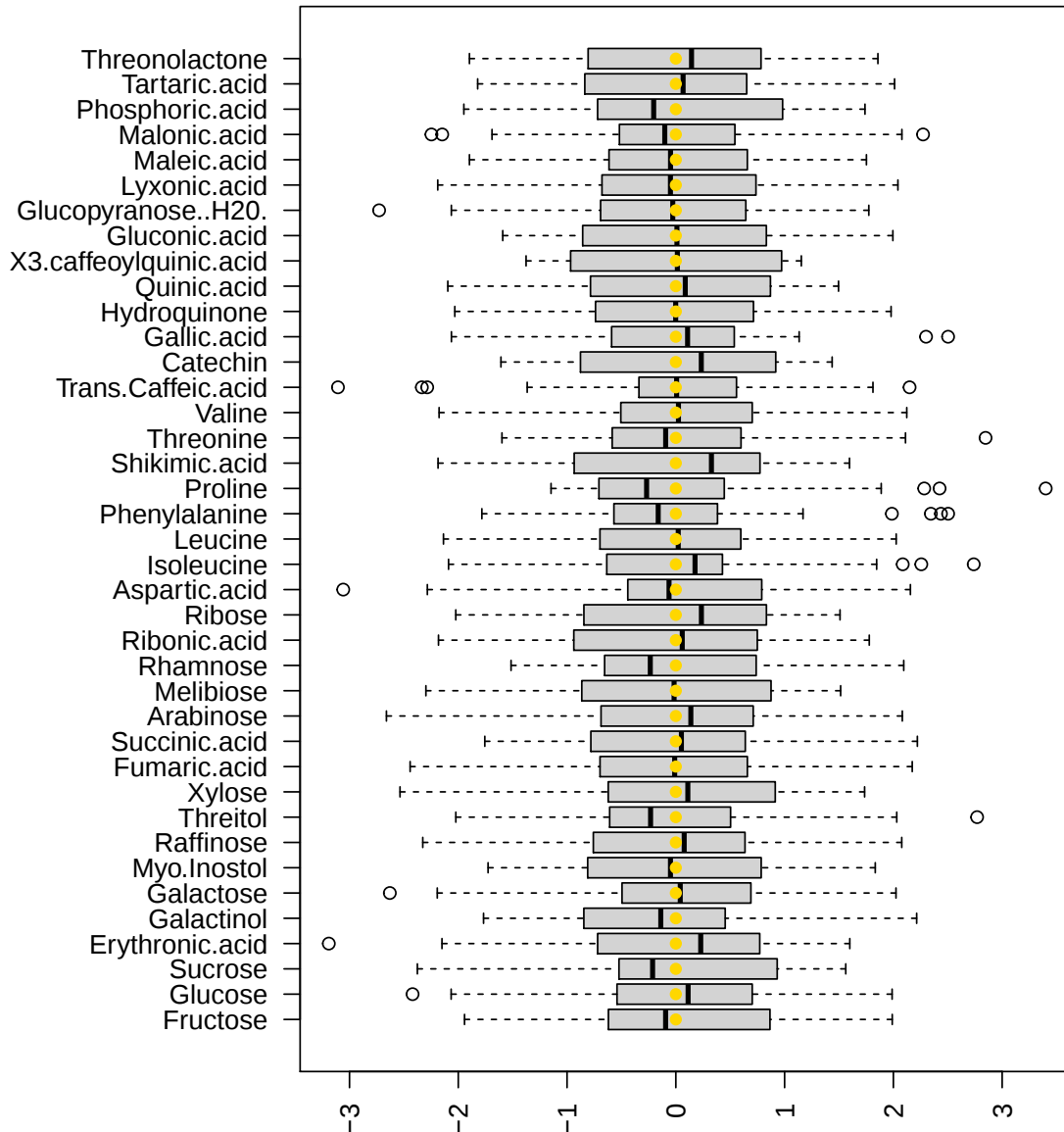
```
> if(18 %in% .years){
+ x <- log2(m18[,m_num_id])
+ dim(x)
+ x <- x[sampleNames,metabNames]
+ dim(x)
+ sx <- scale(x)
+ sm18 <- sx
+ matplot(t(sm18))
+ title("2018")
+ points(1:ncol(sx), apply(sx,2,mean, na.rm=TRUE), col="gold", pch=16)
+ head(apply(sx,2,mean, na.rm=TRUE))
+ head(apply(sx,2,sd, na.rm=TRUE))
+
+ par(mar=c(4,10,3,1))
+ boxplot(sm18, horizontal=TRUE, las=2, main="2018")
+ points( apply(sm18,2,mean, na.rm=TRUE), 1:ncol(sm18), col="gold", pch=16)
+ }
```

Warning in matplot(t(sm18)): default 'pch' is smaller than number of columns a

2018



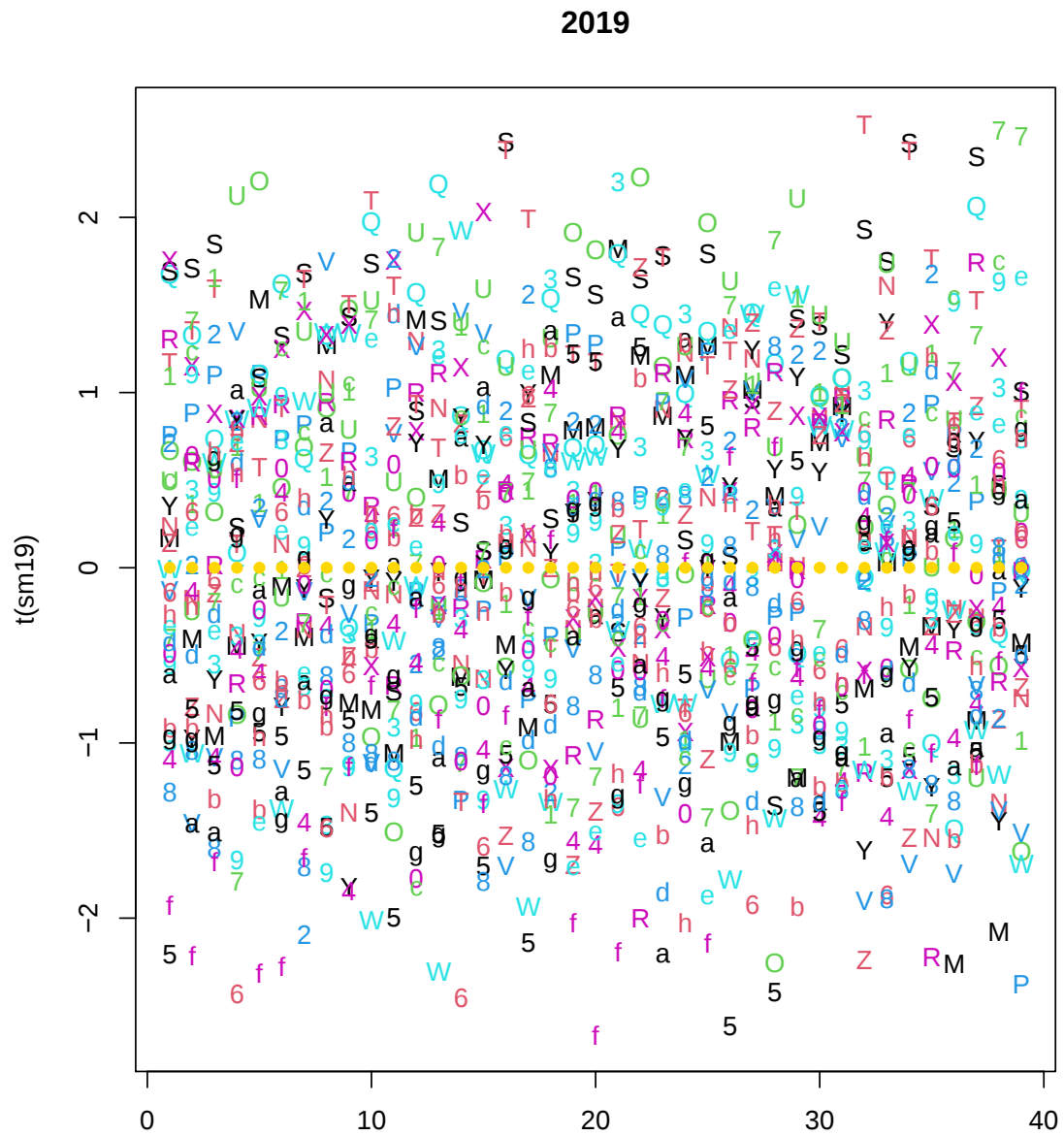
2018



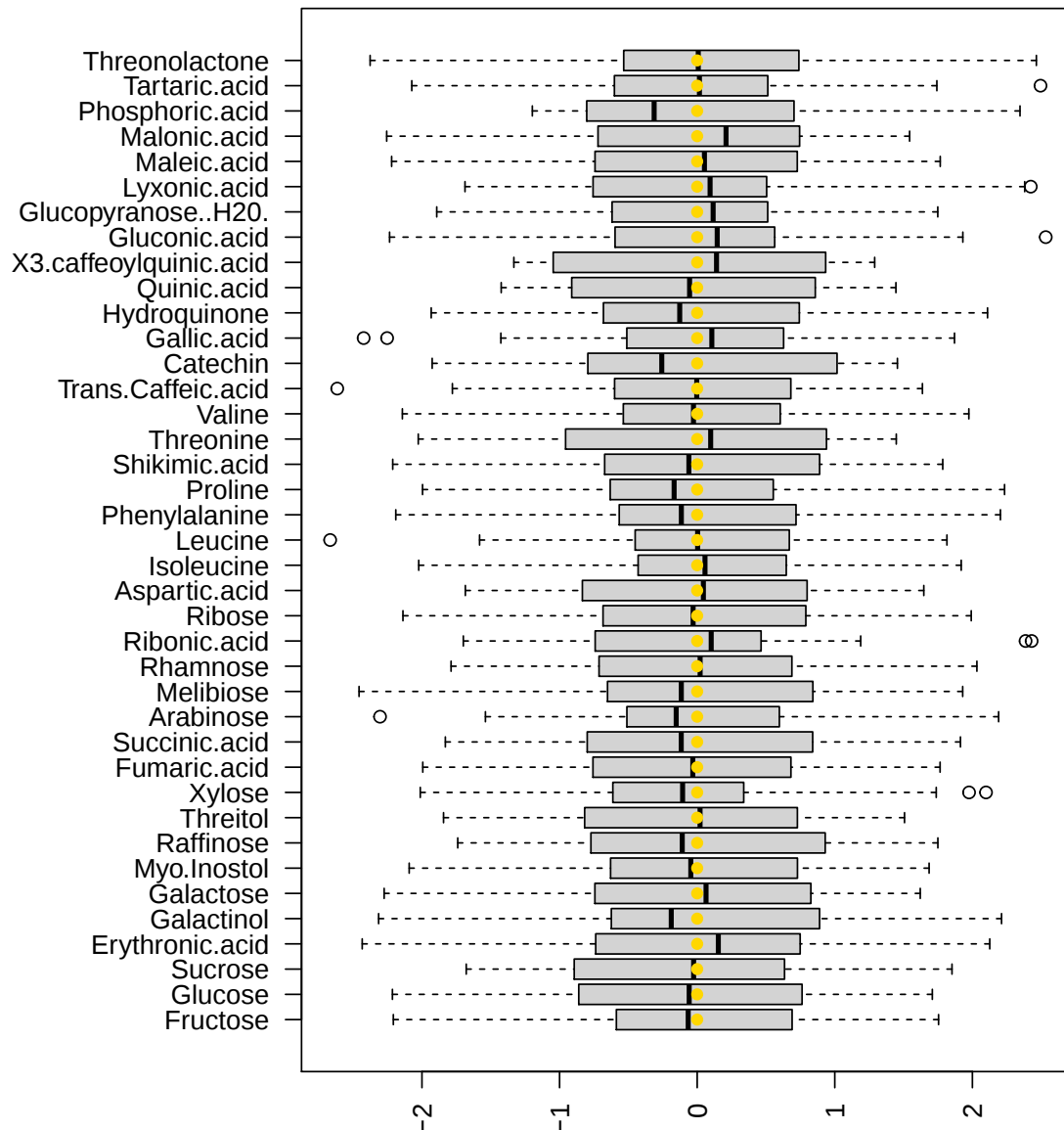
```
> if(19 %in% .years){
+ x <- log2(m19[,m_num_id])
+ dim(x)
+ x <- x[sampleNames,metabNames]
+ dim(x)
+ sx <- scale(x)
+ sm19 <- sx
+ matplot(t(sm19))
+ title("2019")
+ points(1:ncol(sx), apply(sx,2,mean, na.rm=TRUE), col="gold", pch=16)
+ head(apply(sx,2,mean, na.rm=TRUE))
+ head(apply(sx,2,sd, na.rm=TRUE))
+ par(mar=c(4,10,3,1))
+ boxplot(sm19, horizontal=TRUE, las=2, main="2019")
+ points( apply(sm19,2,mean, na.rm=TRUE),1:ncol(sm19), col="gold", pch=16)
```

+ }

Warning in `matplot(t(sm19))`: default 'pch' is smaller than number of columns a

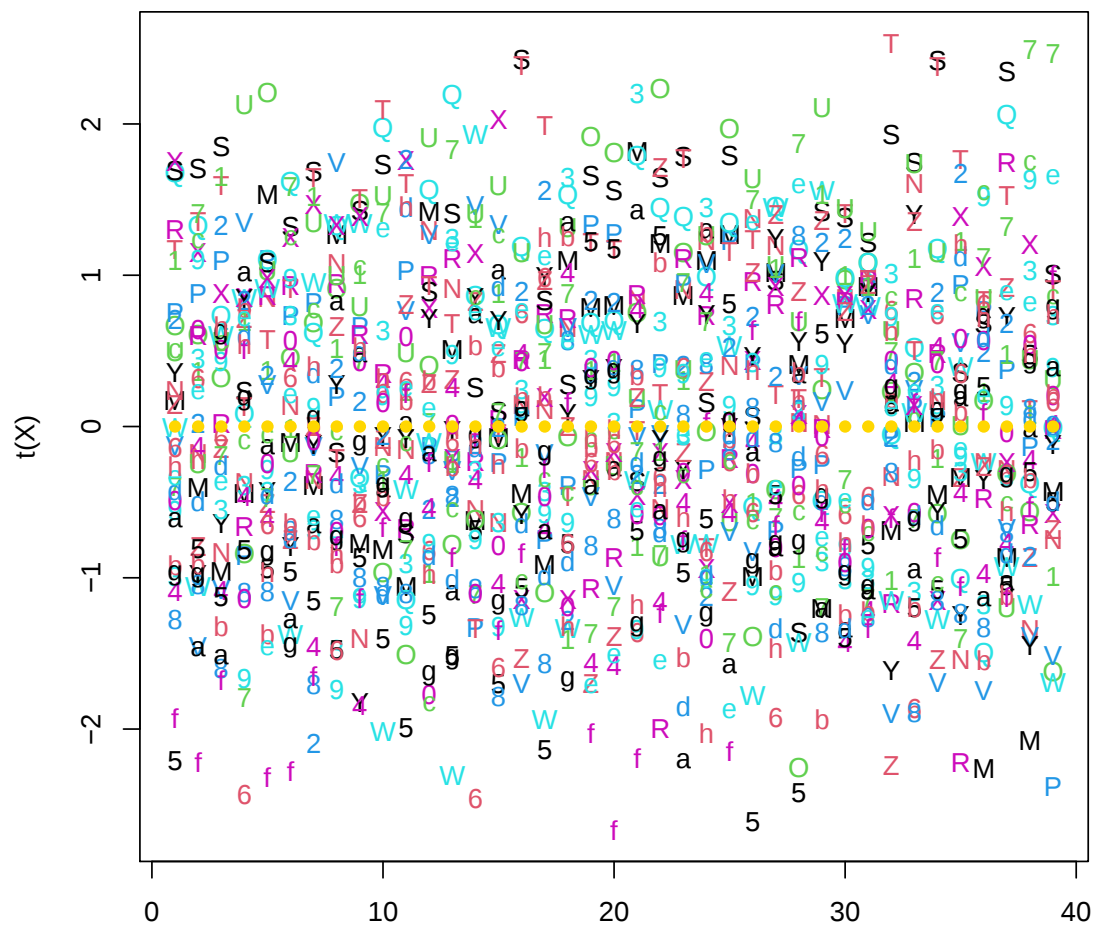


2019



```
> if( 18 %in% .years) X<- sm18
> if( 19 %in% .years) X <- sm19
> if( sum(.years) > 20) X <- rbind(sm18,sm19)
Error in sum(.years): invalid 'type' (character) of argument
> dim(X)
[1] 80 39
> matplot(t(X))
Warning in matplot(t(X)): default 'pch' is smaller than number of columns and
> title(paste(.years))
> sx <- X
> points(1:ncol(sx), apply(sx,2,mean, na.rm=TRUE), col="gold", pch=16)
```

18
19



```
> head(apply(sx,2,mean, na.rm=TRUE))
```

Fructose	Glucose	Sucrose	Erythronic.acid
4.056712e-16	3.809886e-16	-1.003266e-15	-1.726050e-16
Galactinol	Galactose		
-1.168499e-16	-2.731122e-16		

```
> head(apply(sx,2,sd, na.rm=TRUE))
```

Fructose	Glucose	Sucrose	Erythronic.acid
1	1	1	1
Galactinol	Galactose		
1	1		

```
> head(X)[,1:4]
```

	Fructose	Glucose	Sucrose	Erythronic.acid
NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA
NA.2	NA	NA	NA	NA
NA.3	NA	NA	NA	NA
NA.4	NA	NA	NA	NA
NA.5	NA	NA	NA	NA

```
> M <- X[sampleNames,metabNames]
```

```
Error in X[sampleNames, metabNames]: subscript out of bounds
```

```
> head(M)
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```
> head(apply(sx, 2, mean, na.rm=TRUE))
```

Fructose	Glucose	Sucrose	Erythronic.acid
4.056712e-16	3.809886e-16	-1.003266e-15	-1.726050e-16
Galactinol	Galactose		
-1.168499e-16	-2.731122e-16		

```
> head(apply(sx, 2, sd, na.rm=TRUE))
```

Fructose	Glucose	Sucrose	Erythronic.acid
1	1	1	1
Galactinol	Galactose		
1	1		

```
> dim(M)
```

```
Error in eval(expr, envir, enclos): object 'M' not found
```

```
> range(M)
```

```
Error in eval(expr, envir, enclos): object 'M' not found
```

```
> boxplot(M)
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```
> points(1:ncol(M), apply(M, 2, mean), pch=16, col="gold")
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```
> matplot(t(M))
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```
> points(1:ncol(M), apply(M, 2, mean), pch=16, col="gold")
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

Standardize transcripts

```
> range(T)
```

```
[1] -6.427422 13.360000
```

```
> T <- scale(T)
```

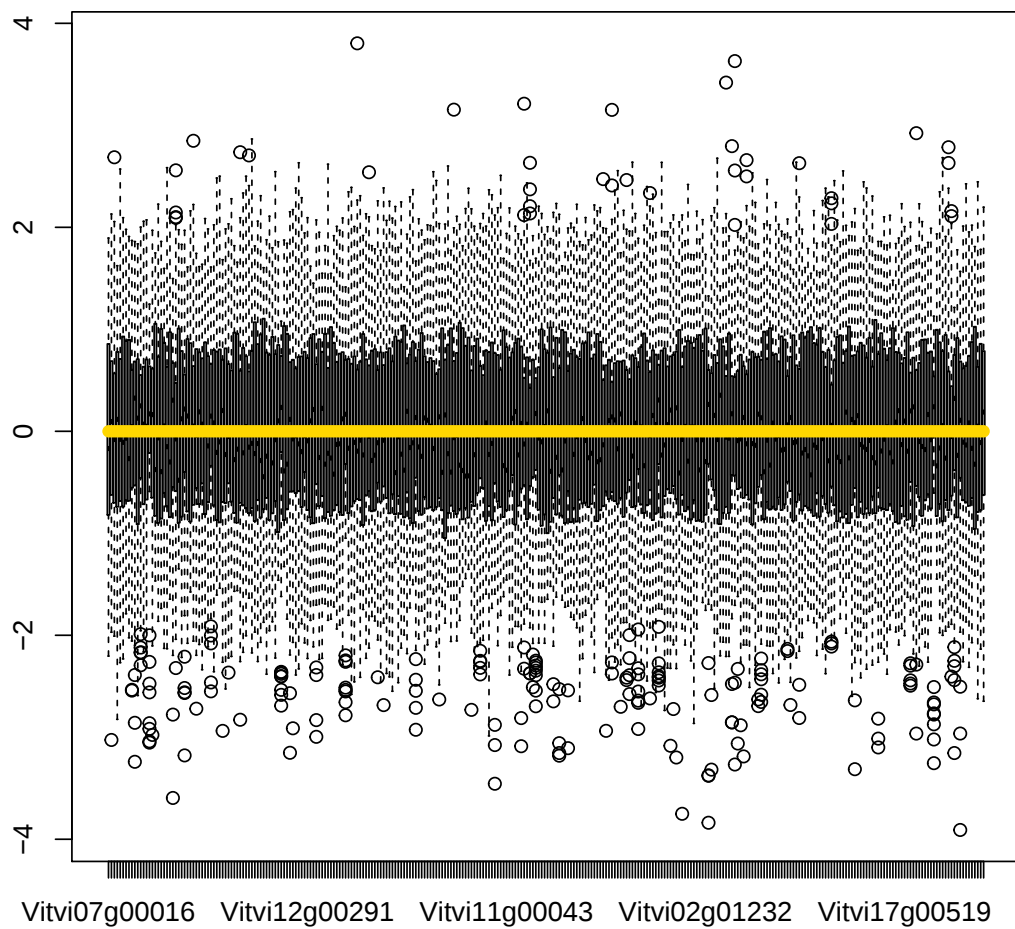
```
> range(T)
```

```
[1] -5.274539 4.739938
```

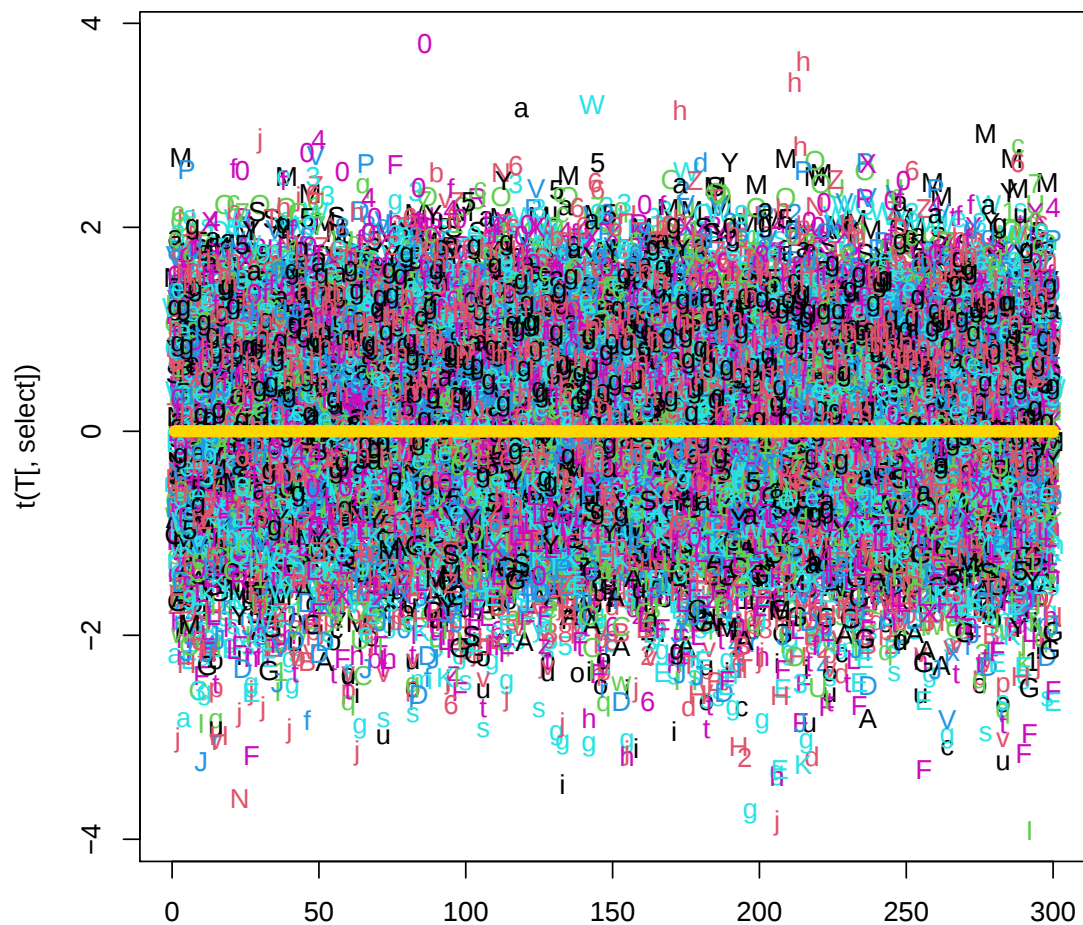
```
> select <- sample(1:ncol(T), min(ncol(T), 300))
```

```
> boxplot(T[, select])
```

```
> points(1:ncol(T[, select]), apply(T[, select], 2, mean), pch=16, col="gold")
```



```
> matplot(t(T[,select]))
Warning in matplot(t(T[, select])): default 'pch' is smaller than number of co
> points(1:ncol(T[,select]),apply(T[,select], 2, mean), pch=16, col="gold")
```



Check orientation, dimension names and dimensions:

```
> all(dimnames(M)[[1]]==dimnames(T)[[1]])
Error in eval(expr, envir, enclos): object 'M' not found
> dimnames(M[1:5,1:5])
Error in eval(expr, envir, enclos): object 'M' not found
> dimnames(T[1:5,1:5])
[[1]]
[1] "C18_11d_WS1" "C18_11d_WS2" "C18_11d_WS3" "C18_11d_WS4"
[5] "C18_11d_WW1"

[[2]]
[1] "Vitvi01g00025" "Vitvi01g00052" "Vitvi01g00053" "Vitvi01g00064"
[5] "Vitvi01g00681"
> dim(M)
Error in eval(expr, envir, enclos): object 'M' not found
> dim(T)
[1] 80 2049
```

Graphical overview of data

```
> library(gplots)
```

```
Warning: package 'gplots' was built under R version 4.0.3
```

```
Attaching package: 'gplots'
```

```
The following object is masked from 'package:stats':
```

```
lowess
```

```
> lhei <- c(1,8)
```

```
> lwid <- c(1,6)
```

```
> heatmap.2(t(M),lhei=lhei,lwid=lwid,trace="none", margins=c(7,7),cexCol=0.75)
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```
> ## nf <- layout(matrix(c(1,2,3,4),2,2,byrow = TRUE), c(1,3), c(1,6), TRUE)
```

```
> ## layout.show(nf)
```

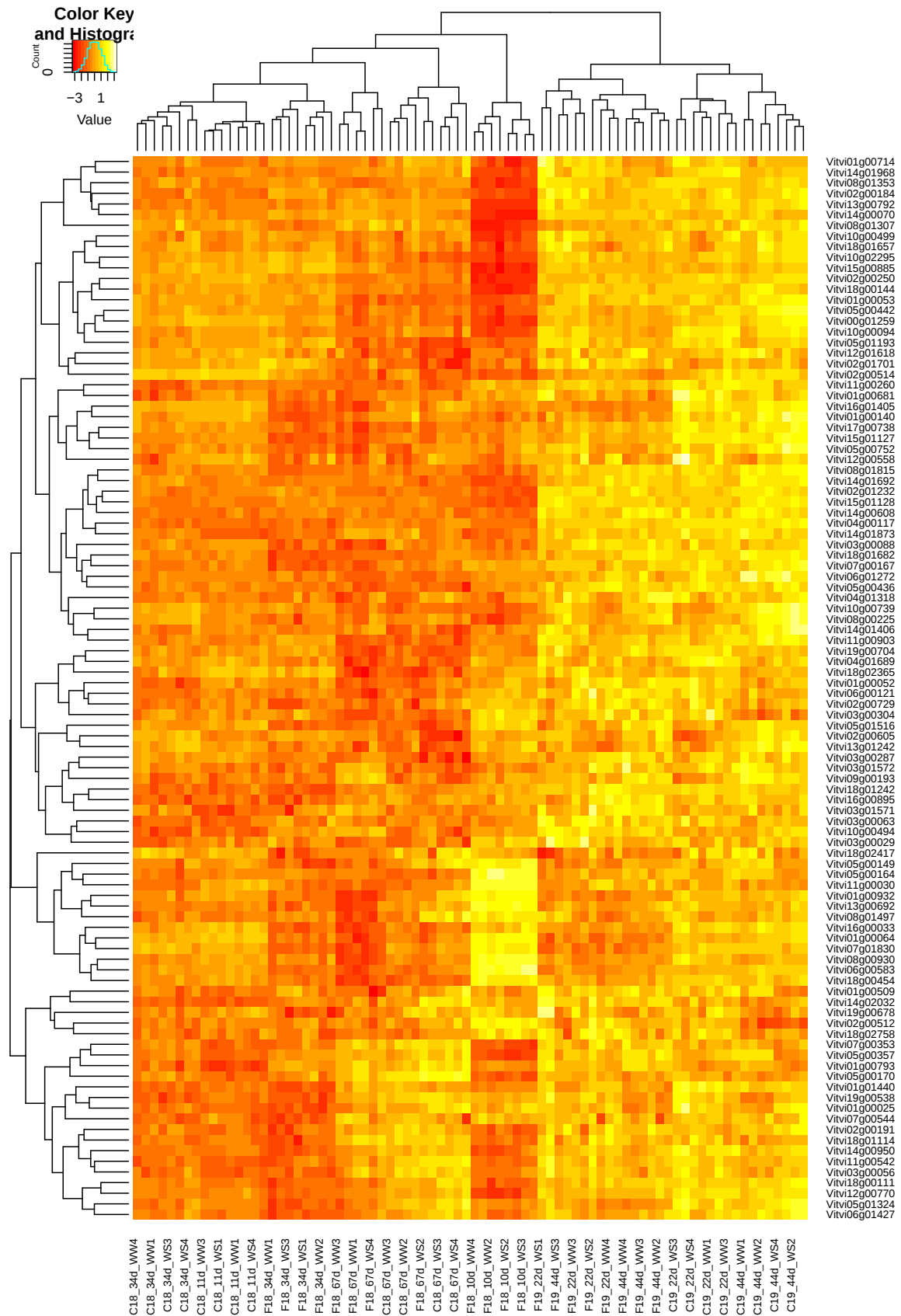
```
> ## lmat <- matrix(c(4,3,2,1),2,2,byrow = TRUE)
```

```
> ## lwid <- c(1,3)
```

```
> lhei <- c(1,8)
```

```
> lwid <- c(1,6)
```

```
> heatmap.2(t(T[,1:min(ncol(T),100)]), lhei=lhei, lwid=lwid,trace="none", marg
```



```
> cat(knit_child(file.path("../doc/", "60b_mixomics.Rnw"), quiet=TRUE))
```

5 Canonical correlation - rCCA

Dimensionality of the problem requires regularized Canonical correlation analysis (rCCA). We will follow the methods implemented in the package **mixOmics**. For explanation see <http://mixomics.org/methods/rcca/>. Quotes below are from this page.

Functions in mixOmics objects are named X and Y, so we will use the same convention and rename by alphabet order:

- X is transcripts/genes data (so far M)
- Y is metabolites data (so far T)

```
> X <- M
Error in eval(expr, envir, enclos): object 'M' not found
> dim(X)
[1] 80 39
> Y <- T
> dim(Y)
[1] 80 2049

> library(mixOmics)
```

Correlation plots

```
> library(CCA)
Warning: package 'CCA' was built under R version 4.0.3
Loading required package: fda
Warning: package 'fda' was built under R version 4.0.3
Loading required package: splines
Loading required package: Matrix

Attaching package: 'Matrix'
The following object is masked from 'package:spam':

    det

Loading required package: fds
Warning: package 'fds' was built under R version 4.0.3
Loading required package: rainbow
Warning: package 'rainbow' was built under R version 4.0.3
Loading required package: pcaPP
Warning: package 'pcaPP' was built under R version 4.0.3
Loading required package: RCurl
Warning: package 'RCurl' was built under R version 4.0.3

Attaching package: 'fda'
```

The following object is masked from 'package:lattice':

melanoma

The following object is masked from 'package:graphics':

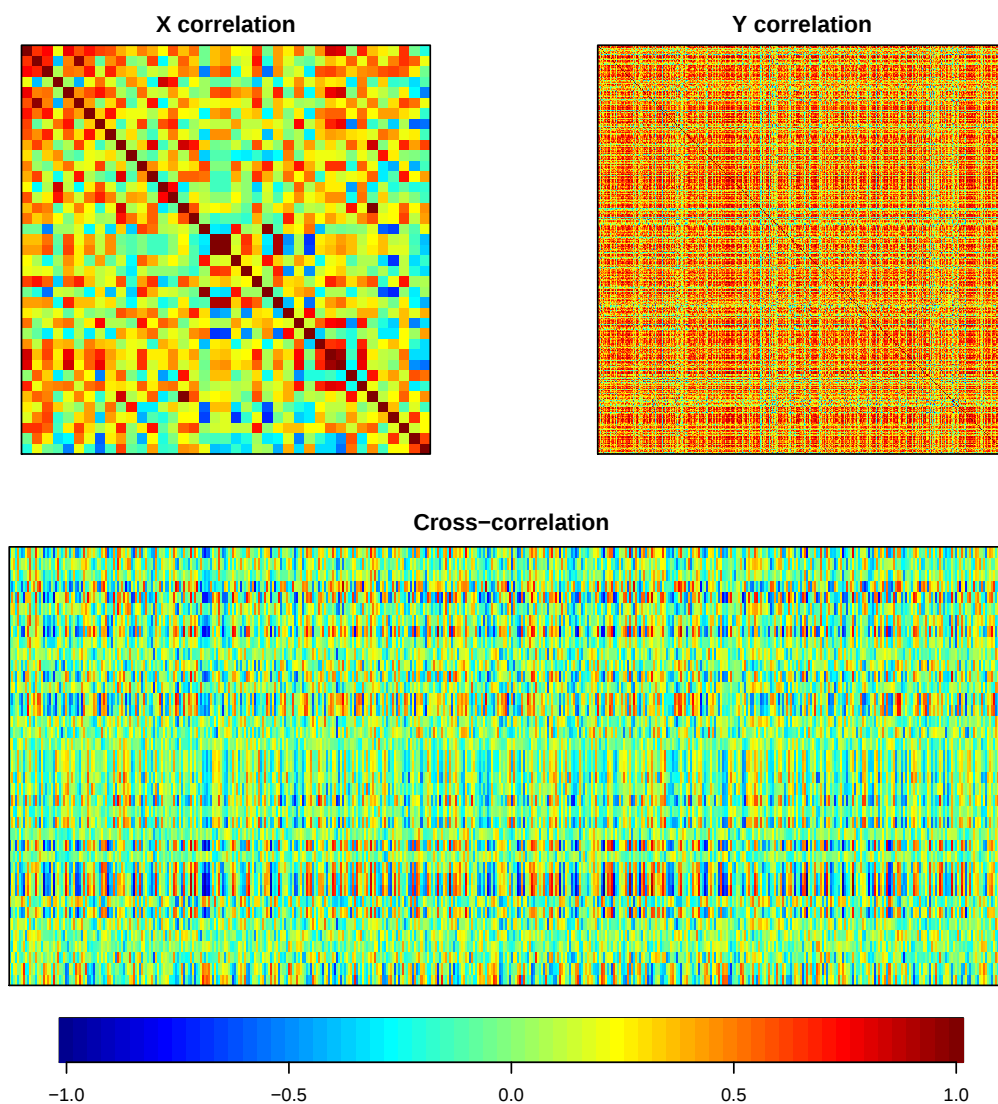
matplot

Attaching package: 'CCA'

The following object is masked from 'package:mixOmics':

rcc

```
> correl <- matcor(X, Y[, sample(1:ncol(Y), min(ncol(Y), 500))])  
> img.matcor(correl, type = 2)
```



```
> detach(unload=TRUE)
```

Note: function `rcc()` is in namespaces of packages **CCA** and **mixOmics** - we want to use the latter one.

```
> bla <- getAnywhere(rcc)  
> str(bla)
```

```

List of 5
 $ name      : chr "rcc"
 $ objs      :List of 2
  ..$ package:mixOmics:function (X, Y, ncomp = 2, method = c("ridge", "shrinkage"), lambda1 = 0, lambda2 = 0)
  ..$ :function (X, Y, ncomp = 2, method = c("ridge", "shrinkage"), lambda1 = 0, lambda2 = 0)
 $ where     : chr [1:2] "package:mixOmics" "namespace:mixOmics"
 $ visible: logi [1:2] TRUE FALSE
 $ dups      : logi [1:2] FALSE TRUE
 - attr(*, "class")= chr "getAnywhere"

```

Check co-linearity of covariance matrices
Metabolites

```

> covX <- cov(X)
> det(covX)
[1] NaN
> det(cor(X))
[1] NaN
> heatmap(covX)
Error in hclustfun(distfun(x)): NA/NaN/Inf in foreign function call (arg 10)

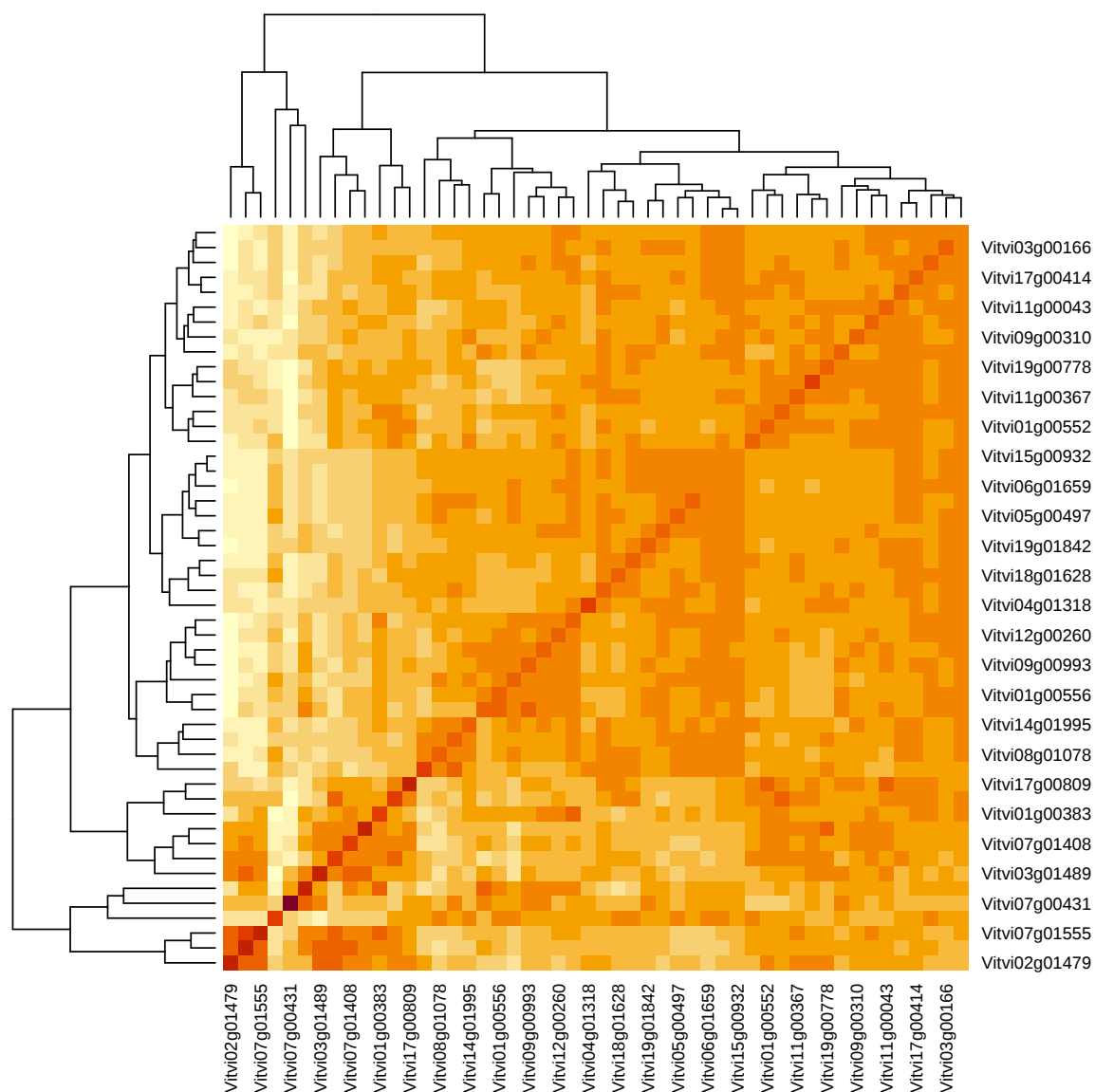
```

Transcripts, small submatrix, determinant almost zero

```

> covY <- cov(Y[, sample(1:ncol(Y), min(50, ncol(Y)))])
> det(covY)
[1] 4.979671e-49
> corY <- cor(Y[, sample(1:ncol(Y), min(50, ncol(Y)))])
> det(corY)
[1] 3.69194e-48
> heatmap(covY)

```



5.0.1 Estimation of penalisation parameters

Before running rCCA, we need to tune the regularization parameters λ_1 and λ_2 . We can use the cross-validation procedure (CV), or the shrinkage method which may output different results. The shrinkage estimate method = "shrinkage" can be used to bypass tune.rcc to choose the shrinkage parameters, see ?rcc.

```
> system.time(mt.shrink <- rcc(M,T, ncomp=3, method = 'shrinkage'))
```

```
Error: object 'M' not found.
```

```
Timing stopped at: 0 0 0
```

```
> plot(mt.shrink, scree.type="barplot")
```

```
Error in plot(mt.shrink, scree.type = "barplot"): object 'mt.shrink' not found
```

```
> dotplot(mt.shrink$cor, xlab="Canonical correlation",pch=16, cex=1.5)
```

```
Error in dotplot(mt.shrink$cor, xlab = "Canonical correlation", pch = 16, : ob
```

Parameters λ :

```
> mt.shrink$lambda
```

```
Error in eval(expr, envir, enclos): object 'mt.shrink' not found
```

```
> det(covX)
```

```
[1] NaN
```

```
> det(covX+diag(mt.shrink$lambda[1],nrow(covX)))
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

```
> det(covY)
```

```
[1] 4.979671e-49
```

```
> det(covY+diag(mt.shrink$lambda[2],nrow(covY)))
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

Cross-validation

```
> if(FALSE) {
```

```
+ grid1 <- seq(0, 0.2, length = 10)
```

```
+ grid2 <- seq(0.0001, 1, length = 10)
```

```
+ system.time(cv <- tune.rcc(X, Y,
```

```
+ grid1 = grid1, grid2 = grid2, validation = "loo"))
```

```
+ #
```

```
+ 
```

```
+ image(cv$mat, xlim=range(cv$grid1), ylim=range(cv$grid2))
```

```
+ points(mt.shrink$lambda[1],mt.shrink$lambda[2],pch=16,col=4,cex=2)
```

```
+ points(cv$opt.lambda1,cv$opt.lambda2,pch=16,col=6,cex=2)
```

```
+ legend("topright",col=c(4,6),pch=c(16,16),cex=1.5, legend=c("shrink","CV"),
```

```
+ 
```

```
+ #
```

```
+ 
```

```
+ cv$opt.lambda1
```

```
+ cv$opt.lambda2
```

```
+ 
```

```
+ 
```

```
+ # Analysis
```

```
+ 
```

```
+ system.time(mt.cv <- rcc(X,Y, ncomp = 3, lambda1 = cv$opt.lambda1, lambda2 =
```

```
+ }
```

5.1 Comparison

Function to omit printing small values

```
> print.blank <- function(x, eps=0, zero.print=".", shrink=TRUE, maxln=50, ...
+ nr <- nrow(x)
+ if( shrink ) x <- x[apply(x,1,function(y) any(abs(y) > eps)),]
+ x <- x[1:min(maxln,nrow(x)),]
+ print.table(local({x[abs(x)<eps] <- 0; x}),zero.print=zero.print)
+ if(maxln < nr) cat("\n", maxln, "/", nr, "rows printed\n")
+ }
> #print.blank(rbind(x,x),eps=0.1)
```

Concatenate names and bin ids. mt.shrink has original names, used for printout of the network.

```
> mt <- mt.shrink
Error in eval(expr, envir, enclos): object 'mt.shrink' not found
> filter <- match(mt$names$colnames$X, rownames(mfdata))
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> table(filter)
filter
FALSE TRUE
 807 7617
> binm <- mfdata$Bin[filter]
> head(cbind(mt$names$colnames$X, binm, mfdata[filter, 1:2]))
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> mt$names$colnames$X=paste( mt$names$colnames$X, binm, sep=" | ")
Error in eval(quote(list(...)), env): object 'mt' not found
> #
> filter <- match(mt$names$colnames$Y, fdata$geneID)
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> bing <- fdata$BINCODE[filter]
> head(cbind(mt$names$colnames$Y, bing, fdata[filter, 2:3]))
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> mt$names$colnames$Y=paste( mt$names$colnames$Y, bing , sep=" | ")
Error in eval(quote(list(...)), env): object 'mt' not found
> head(mt$names$colnames$Y)
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> #
> dimnames(mt$loadings$X) <- list(mt$names$colnames$X, paste0("Comp", 1:ncol(m
Error in eval(expr, envir, enclos): object 'mt' not found
> dimnames(mt$loadings$Y) <- list(mt$names$colnames$Y, paste0("Comp", 1:ncol(m
Error in eval(expr, envir, enclos): object 'mt' not found
```

5.1.1 Loadings

Metabolites

Genes with absolute nonzero loadings above the third quartile are listed
Shrink

```
> x <- cbind(mt$loadings$X)
Error in cbind(mt$loadings$X): object 'mt' not found

> quantile(abs(x))
Error in quantile.default(abs(x)): missing values and NaN's not allowed if 'na
> (eps <- quantile(abs(x), 0.75))
Error in quantile.default(abs(x), 0.75): missing values and NaN's not allowed
> print.blank(x, eps=eps)
Error in FUN(newX[, i], ...): object 'eps' not found

> nettip <- "txt"
> suffix <- paste(addArgs, collapse="-")
> (netfn <- gsub("\\.", "_", paste0("loadings-metabolite-", suffix)))
[1] "loadings-metabolite-18-19-1-2-3-4-5-6-7-V3"

> pth <- .oroot
> (netpath <- file.path(pth, paste(netfn, nettip, sep=".")))
[1] "../..output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/loadings-metabolite-1
> my.write.table(cbind(mt$loadings$X), file=netpath,
+   label="Loadings for metabolites"
+   )
Error in cbind(mt$loadings$X): object 'mt' not found
```

Transcripts

Shrink

```
> y <- cbind(mt$loadings$Y)
Error in cbind(mt$loadings$Y): object 'mt' not found

> quantile(abs(y))
Error in `[.data.frame`(x, order(x, na.last = na.last, decreasing = decreasing
> (eps <- quantile(abs(y), 0.75))
Error in `[.data.frame`(x, order(x, na.last = na.last, decreasing = decreasing
> print.blank(y, eps=eps)
Error in FUN(newX[, i], ...): object 'eps' not found

> nettip <- "txt"
> suffix <- paste(addArgs, collapse="-")
> (netfn<- gsub("\\.", "_", paste0("loadings-genes-", suffix)))
[1] "loadings-genes-18-19-1-2-3-4-5-6-7-V3"

> pth <- .oroot
> (netpath<- file.path(pth, paste(netfn, nettip, sep=".")))
[1] "../..output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/loadings-genes-18-19-
> my.write.table(cbind(mt$loadings$Y), file=netpath,
+   label="Loadings for genes"
+   )
Error in cbind(mt$loadings$Y): object 'mt' not found
```

Upper 5%

```
> y <- cbind(mt$loadings$Y)
Error in cbind(mt$loadings$Y): object 'mt' not found
> quantile(abs(y))
Error in `[.data.frame`(x, order(x, na.last = na.last, decreasing = decreasing
> (eps <- quantile(abs(y), 0.95))
Error in `[.data.frame`(x, order(x, na.last = na.last, decreasing = decreasing
> print.blank(y, eps=eps)
Error in FUN(newX[, i], ...): object 'eps' not found
```

5.2 Summary

```
> mt$explained_variance
Error in eval(expr, envir, enclos): object 'mt' not found
```

5.3 Plots

```
> variety <- factor(substr(mt$names$sample, 1, 1))
Error in substr(mt$names$sample, 1, 1): object 'mt' not found
> status <- as.numeric(factor(substr(mt$names$sample, 10, 10)))
Error in substr(mt$names$sample, 10, 10): object 'mt' not found
> day <- as.numeric(factor(substr(mt$names$sample, 5, 5)))
Error in substr(mt$names$sample, 5, 5): object 'mt' not found

> my.plotIndiv <- function(x, comp=c(1,2), col=c(4,2), pch=c(16,1), grid=TRUE,
+   variety <- factor(substr(x$names$sample, 1, 1))
+   statusf <- factor(substr(x$names$sample, 10, 10))
+ status <- as.numeric(statusf)
+ dayf <- factor(substr(x$names$sample, 5, 5))
+ day2 <- substr(x$names$sample, 5, 6)
+ day2[day2=="11"] <- "10"
+ day2 <- factor(day2)
+ day <- as.numeric(day2)
+ #
+ cols <- col[as.numeric(variety)]
+ pchs <- pch[status]
+ cexs <- day/2
+
+ #
+ if(missing(title)) title <- x$names$data
+ #
+ if(length(comp)==2 & !shift){
+   par(mfrow=c(1,2), mar=c(5,3,2,0.5))
+   for(i in 1:2){
+     xy <- x$variates[[i]][,comp]
+     xlab <- paste("Variate", comp[1])
+     ylab <- paste("Variate", comp[2])
+     plot(xy[,1], xy[,2], type="n", xlab="", ylab="", axes=FALSE, ann=FALSE, asp=
+     title(title[i])
+     if(grid) abline(h=seq(-4,4,0.5), v=seq(-4,4,0.5), col="grey90", lwd=0.1)
+     box()
+     axis(1, cex.axis=0.75)
+     axis(2, las=2, cex.axis=0.75)
+     if(i ==1) mtext(ylab, 2, line=1.5)
+     if(i ==1) {
+ legend( par("usr")[1]*1.3, par("usr")[3]*1.2
+       , pch=c(NA, NA, unique(pchs), 1, 1, 1)
+       , text.col=c(unique(cols), 1, 1, 1, 1, 1)
+       , pt.cex=c(rep(1,4), unique(cexs))
+       , legend=c(levels(variety), levels(statusf), levels(day2))
+       , bty="n"
+       , xpd=TRUE
+       , horiz=TRUE
+       )
+       ncexs <- length(levels(day2))
+       legend("topleft",
+       , pch=1
```

```

+         , text.col=1
+         , pt.cex=sort(unique(cexs))
+         , legend=levels(day2)
+         , bty="n"
+         , xpd=TRUE
+         , horiz=FALSE
+     )
+ }
+
+     mtext(xlab,1,line=-4,outer=TRUE, adj=0.55)
+
+     points(xy[,1],xy[,2],cex=cexs,pch=pchs,col=cols, ...)
+ }
+ }
+ #
+ if(length(comp)==3 & shift){
+     par(mfrow=c(1,2), mar=c(5.5,3,2,0.5))
+     for(i in 1:2){
+         xy <- x$variates[[i]][,comp]
+         xlab <- paste("Variate",comp[1])
+         ylab <- paste("Variate",comp[2])
+         plot(xy[,1],xy[,2],type="n",xlab="",ylab="",axes=FALSE,ann=FALSE, asp=
+         title(title[i])
+         if(grid) abline(h=seq(-4,4,0.5),v=seq(-4,4,0.5),col="grey90",lwd=0.1)
+         box()
+         axis(1,cex.axis=0.75)
+         axis(2, las=2,cex.axis=0.75)
+         if(i ==1) mtext(ylab,2,line=1.5)
+         if(i ==1) {
+ #             legend("topright"
+ legend( par("usr")[1]*1.3,par("usr")[3]*1.2
+         , pch=c(NA,NA,unique(pchs),1,1,1)
+         , text.col=c(unique(cols),1,1,1,1,1)
+         , pt.cex=c(rep(1,4),unique(cexs))
+         , legend=c(levels(variety),levels(statusf), levels(day2))
+         , bty="n"
+         , xpd=TRUE
+         , horiz=TRUE
+         )
+     }
+     mtext(xlab,1,line=-4,outer=TRUE, adj=0.55)
+
+     points(xy[,1],xy[,2],cex=cexs,pch=pchs,col=cols, ...)
+     segments(xy[,1],xy[,2],xy[,1],xy[,3],col=cols)
+ }
+ }
+
+ #
+ if(length(comp)==2 & shift){
+     par(mfrow=c(1,1), mar=c(6,4,2,0.5))
+     xy <- x$variates[[1]][,comp]
+     xy2 <- x$variates[[2]][,comp]

```

```

+       xlab <- paste("Variate",comp[1])
+       ylab <- paste("Variate",comp[2])
+       plot(xy[,1],xy[,2],type="n",xlab="",ylab="",axes=FALSE,ann=FALSE, asp=
+       title(title[i])
+       if(grid) abline(h=seq(-4,4,0.5),v=seq(-4,4,0.5),col="grey90",lwd=0.1)
+       box()
+       axis(1,cex.axis=0.75)
+       axis(2, las=2,cex.axis=0.75)
+       mtext(ylab,2,line=2)
+       if(1 ==1) {
+       legend( par("usr")[1]*1.05,par("usr")[3]*1.3
+       , pch=c(NA,NA,unique(pchs),1,1,1)
+       , text.col=c(unique(cols),1,1,1,1,1)
+       , pt.cex=c(rep(1,4),unique(cexs))
+       , legend=c(levels(variety),levels(statusf), levels(day2))
+       , bty="n"
+       , xpd=TRUE
+       , horiz=TRUE
+       )
+       }
+       mtext(xlab,1,line=-3,outer=TRUE)
+       legend("topright",pch=c(1,NA),lwd=c(NA,2),legend=c("M","T"),bty="n")
+
+       points(xy[,1],xy[,2],cex=cexs,pch=pchs,col=cols,...)
+       segments(xy[,1],xy[,2],xy2[,1],xy2[,2],col=cols)
+   }
+
+
+
+
+ #
+ if(length(comp)==3 & !shift){
+   par(mfrow=c(1,2), mar=c(5,3,2,0.5))
+   for(i in 1:2){
+     persp.xyz(x$variates[[i]],cex=cexs,pch=pchs,col=cols,...)
+     title(title[i])
+   }
+ }
+ }
+ }
+ }
> my.plotIndiv(mt, comp=1:2)
Error in substr(x$names$sample, 1, 1): object 'mt' not found

```

@

```

> # cabernet blue
> my.plotIndiv(mt, comp=1:2, shift=TRUE)
Error in substr(x$names$sample, 1, 1): object 'mt' not found
> my.plotIndiv(mt, comp=1:3, shift=TRUE)
Error in substr(x$names$sample, 1, 1): object 'mt' not found
> my.plotIndiv(mt, comp=1:3,side="", phi=45, theta=40)
Error in substr(x$names$sample, 1, 1): object 'mt' not found

```

```
Error in data.frame(x$variates[[1]][, comp]): object 'mt' not found
```

```
> stereo(mt, turn=-40, elevation=30)
```

```
Error in data.frame(x$variates[[1]][, comp]): object 'mt' not found
```

```
> plotIndiv(mt, comp=c(1,2)
+ , group=variety
+ , col.per.group=c(4,2)
+ )
```

```
Error in plotIndiv(mt, comp = c(1, 2), group = variety, col.per.group = c(4, :
```

```
> plotIndiv(mt, comp=c(1,2)
+ , ind.names=FALSE
+ , group=variety
+ , col.per.group=c(4,2)
+ , pch=c(16,1)[status]
+ #, cex=c(1,1.5,2)[day]
+ #, star=TRUE
+ #, style="graphics"
+ )
```

```
Error in plotIndiv(mt, comp = c(1, 2), ind.names = FALSE, group = variety, : c
```

```
> my.plotIndiv(mt, comp=c(1,2)
+ )
Error in substr(x$names$sample, 1, 1): object 'mt' not found
```

```
> my.plotIndiv(mt, comp=c(1,3)
+ )
Error in substr(x$names$sample, 1, 1): object 'mt' not found
```

```
> my.plotIndiv(mt, comp=c(2,3)
+ )
Error in substr(x$names$sample, 1, 1): object 'mt' not found
```

```
> plotVar(mt)
Error in plotVar(mt): object 'mt' not found
```

```
> if(interactive()) graphics.off()
```

First three components, interactive 3d rgl image

```
> #plotVar(mt, style="3d")
```

```
> plotVar(mt, cutoff=0.6, cex=c(1.5,1)*3, style="ggplot2")
```

```
Error in plotVar(mt, cutoff = 0.6, cex = c(1.5, 1) * 3, style = "ggplot2"): ob
```

```
> plotVar(mt, cutoff=0.6, cex=c(1.5,1)*0.7, style="graphics")
Error in plotVar(mt, cutoff = 0.6, cex = c(1.5, 1) * 0.7, style = "graphics"):

> plotVar(mt, cutoff=0.6, cex=c(1.5,1)*0.7, style="lattice")
Error in plotVar(mt, cutoff = 0.6, cex = c(1.5, 1) * 0.7, style = "lattice"):

> plotVar(mt, cutoff=0.6, cex=c(1.5,1)*0.7, style="lattice", overlap=FALSE)
Error in plotVar(mt, cutoff = 0.6, cex = c(1.5, 1) * 0.7, style = "lattice", :
```

Additional plots

```
> cim(mt, margins=c(10,10), xlab="Genes", ylab="Metabolites"  
+ )
```

```
Error in cim(mt, margins = c(10, 10), xlab = "Genes", ylab = "Metabolites"): o
```

Select rectangles to zoom

```
> if(interactive()) cim(mt, margins=c(6,8), xlab="Genes", ylab="Metabolites",
```

```
> cim(cor(M,T), margins=c(6,8), xlab="Genes", ylab="Metabolites")  
Error in is.data.frame(x): object 'M' not found
```

6 Relevance network

Customized network function

```
> cutoff <- 0.7
```

6.1 Network with high cutoff: 0.7

```
> cutoff
[1] 0.7

> nettip <- "pdf"
> suffix <- paste(addArgs, collapse="-")
> (netfn<- gsub("\\.", "_", paste0("network-", cutoff, "_", suffix)))
[1] "network-0_7_18-19-1-2-3-4-5-6-7-V3"

> pth <- .oroot
> (netpath<- file.path(pth, paste(netfn, nettip, sep=". ")))
[1] "../..output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/network-0_7_18-19-1-2-3-4-5-6-7-V3.pdf"

> #jpeg(netpath)
> net <- my.network(mt, cutoff=cutoff, lwd=4
+   , shape.node=c("rectangle", "rectangle")
+   , color.node=c( 2, 4)
+   , show.edge.labels=TRUE
+   # , interactive=interactive()
+   , name.save=file.path(pth, netfn)
+   , save=nettip
+   , main=paste0("Bins :", suffix, paste("\ncutoff =", cutoff))
+ )

Warning: package 'igraph' was built under R version 4.0.3

Attaching package: 'igraph'

The following objects are masked from 'package:lubridate':

    %--%, union

The following objects are masked from 'package:BiocGenerics':

    normalize, path, union

The following objects are masked from 'package:stats':

    decompose, spectrum

The following object is masked from 'package:base':

    union

Error: object 'mt' not found.

> #dev.off()
```

```

> str(net)
Error in str(net): object 'net' not found

> sapply(net$gR, print)
Error in h(simpleError(msg, call)): error in evaluating the argument 'X' in se

> library(igraph)
> nettip <- "gml"
> (netfn<- gsub("\\.", "_", paste0("network-", cutoff, "_", suffix)))
[1] "network-0_7_18-19-1-2-3-4-5-6-7-V3"
> (netpath <- file.path(.oroot, paste(netfn, nettip, sep=". ")))
[1] ".././output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/network-0_7_18-19-1-2
> write.graph(net$gR, file=netpath, format=nettip)
Error in "igraph" %in% class(graph): object 'net' not found

> #jpeg(netpath)
> net <- my.network(mt.shrink, cutoff=cutoff, lwd=4
+   , shape.node=c("rectangle", "rectangle")
+   , color.node=c( 2, 4)
+   , show.edge.labels=TRUE
+ #   , interactive=interactive()
+   , name.save=file.path(pth, netfn)
+   , save=nettip
+   , main=paste0("Bins :", suffix, paste("\ncutoff =", cutoff))
+ )
Error: object 'mt.shrink' not found.
> #dev.off()
> #sapply(net$gR, print)

```

Extract edges from the graph and prepare the data.frame with names, bin codes, descriptions ...

```

> edg <- matrix(unlist(sapply(attr(E(net$gR), "vnames"), strsplit, split="\\|")),
Error in h(simpleError(msg, call)): error in evaluating the argument 'X' in se
> colnames(edg)=c("Metabolite", "geneID")
Error in colnames(edg) = c("Metabolite", "geneID"): object 'edg' not found
> medg <- mldata[edg[,1], 1:3 ]
Error in `[.data.frame` (mldata, edg[, 1], 1:3): object 'edg' not found
> tedg <- fdata[match(edg[,2], fdata$geneID), -1]
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> edges <- data.frame(edg, weight=E(net$gR)$weight, medg, tedg )
Error in data.frame(edg, weight = E(net$gR)$weight, medg, tedg): object 'edg'
> str(edges)
function (...)
> dim(edges)
NULL

```

Export edges file

```

> cutoff <- 0.5

```

6.2 Network with low cutoff: 0.5

```
> cutoff
[1] 0.5
> nettip <- "pdf"
> suffix <- paste(addArgs, collapse="-")
> (netfn<- gsub("\\.", " ", paste0("network-", cutoff, "_", suffix)))
[1] "network-0_5_18-19-1-2-3-4-5-6-7-V3"
> pth <- ".oroot"
> (netpath<- file.path(pth, paste(netfn, nettip, sep=".")))
[1] ".././output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/network-0_5_18-19-1-2-3-4-5-6-7-V3"

> #
> net <- my.network(mt, cutoff=cutoff, lwd=4,
+   shape.node=c("rectangle", "rectangle"),
+   color.node=c( 2, 4)
+   , name.save=file.path(pth, netfn)
+   , save=nettip
+   , main=paste0("Bins :", suffix, paste("\ncutoff =", cutoff))
+ )
Error: object 'mt' not found.
```

To prepare the edges table, we will use cutoff 0.5. For visual inspection, filter on column weight can be used.

```
> #
> cutoff
[1] 0.5
> net <- my.network(mt.shrink, cutoff=cutoff,
+   shape.node=c("rectangle", "rectangle"),
+   color.node=c( 2, 4),
+   show.edge.labels=TRUE
+ )
Error: object 'mt.shrink' not found.
> str(net)
Error in str(net): object 'net' not found
```

Extract edges from the graph and prepare the data.frame with names, bin codes, descriptions ...

```
> edg <- matrix(unlist(sapply(attr(E(net$gR), "vnames"), strsplit, split="\\|")),
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> colnames(edg)=c("Metabolite", "geneID")
Error in colnames(edg) = c("Metabolite", "geneID"): object 'edg' not found
> medg <- mdata[edg[,1], 1:3]
Error in [.data.frame(mdata, edg[,1], 1:3): object 'edg' not found
> tedg <- fdata[match(edg[,2], fdata$geneID), -1]
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> edges <- data.frame(edg, weight=E(net$gR)$weight, medg, tedg)
Error in data.frame(edg, weight = E(net$gR)$weight, medg, tedg): object 'edg'
> str(edges)
function (..)
> dim(edges)
NULL
```

Add CCA loadings for metabolite and gene:

```
> head(edg)
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
> loadings <- cbind(
+   mt.shrink$loadings$X[edg[,1], ],
+   mt.shrink$loadings$Y[edg[,2], ]
Error in cbind(mt.shrink$loadings$X[edg[,1], ], mt.shrink$loadings$Y[edg[,2], ]):
> colnames(loadings) <-
+ c(paste0("M.comp", 1:3), paste0("G.comp", 1:3))
Error in colnames<-(*tmp*, value = c("M.comp1", "M.comp2", "M.comp3", : att
> head(loadings)

1 function (x, ...)
2 x$loadings
> edges <- data.frame(edges, loadings)
> head(edges)
Error in xj[i]: object of type 'closure' is not subsettable
```

6.3 Weight distribution

```
> metabolites <- unique(edges$Metabolite)
> metabolites

NULL

> transcripts <- unique(edges$geneID)
> length(transcripts)

[1] 0

> append <- FALSE
> out <- ""
> for(mtb in metabolites){
+   out <- paste(out, knit_child(file.path("../doc/", "60ba_weights_statistics.Rm
+ }
```

6.4 Export edges file

```
> nettip <- "txt"
> suffix <- paste(addArgs, collapse="-")
> pth <- .oroot
> (netfn<- gsub("\\.", "_", paste0("edges_table-", cutoff, "_", suffix)))

[1] "edges_table-0_5_18-19-1-2-3-4-5-6-7-V3"

> (netpath <- file.path(.oroot, paste(netfn, nettip, sep=".")))

[1] "../..output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/edges_table-0_5_18-19-1-2-3-4-5-6-7-V3.txt"

> my.write.table(edges, file=netpath,
+   label=paste("Edges table, cutoff =", cutoff)
+   )
```

Warning in write.table(x, file = file, col.names = col.names, sep = sep, : app

```
Object: edges \\
Label: Edges table, cutoff = 0.5 \\
File :\\
\\href{run:D:\\DEJAVNOSTI\\OMIKE\\pISA-projects\\_p_VinskaTrta\\_I_EnViRoS\\_S_
```

```

> plot(
+   mt.shrink$loadings$X[,1],
+   mt.shrink$loadings$X[,2])
+   m <- nrow(mt.shrink$loadings$Y)
+   segments(
+ rep( 0, m),rep(0,m),
+   mt.shrink$loadings$Y[,1]*3,
+   mt.shrink$loadings$Y[,2]*3, col=4)
+ )
+ m <- nrow(mt.shrink$loadings$X)
+ segments(
+ rep( 0, m),rep(0,m),
+   mt.shrink$loadings$X[,1],
+   mt.shrink$loadings$X[,2], col=2)
+ )
Error: <text>:9:2: unexpected ')'
8:   mt.shrink$loadings$Y[,2]*3, col=4)
9:   )
   ^

```

```

> par(mfrow=c(2,2))
> with(edges, plot(G.comp1, M.comp1))
Error in plot(G.comp1, M.comp1): object 'G.comp1' not found
> with(edges, plot(G.comp2, M.comp2))
Error in plot(G.comp2, M.comp2): object 'G.comp2' not found
> with(edges, plot(G.comp3, M.comp3))
Error in plot(G.comp3, M.comp3): object 'G.comp3' not found

```

```

> names(net)
Error in eval(expr, envir, enclos): object 'net' not found
> heatmap(net$M)
Error in heatmap(net$M): object 'net' not found

> rw <- apply(net$M,1,function(x, eps=0.1) any(abs(x)>= eps))
Error in apply(net$M, 1, function(x, eps = 0.1) any(abs(x) >= eps)): object 'n
> cl <- apply(net$M,2,function(x, eps=0.1) any(abs(x)>= eps))
Error in apply(net$M, 2, function(x, eps = 0.1) any(abs(x) >= eps)): object 'n
> x <- net$M
Error in eval(expr, envir, enclos): object 'net' not found
> x <- x[rw,cl]
Error in `[.data.frame`(x, rw, cl): object 'cl' not found
> print.blank(t(x))

```

	NA	NA.1	NA.2	NA.3	NA.4	NA.5	NA.6	NA.7	NA.8
Fructose									
Glucose									
Sucrose									
Erythronic.acid									
Galactinol									
Galactose									
Myo.Inostol									
Raffinose									
Threitol									
Xylose									
Fumaric.acid									
Succinic.acid									
Arabinose									
Melibiose									
Rhamnose									
Ribonic.acid									
Ribose									
Aspartic.acid									
Isoleucine									
Leucine									
Phenylalanine									
Proline									
Shikimic.acid									
Threonine									
Valine									
Trans.Caffeic.acid									
Catechin									
Gallic.acid									
Hydroquinone									
Quinic.acid									
X3.caffeoylquinic.acid									
Gluconic.acid									
Glucopyranose..H2O.									
Lyxonic.acid									
Maleic.acid									

Malonic.acid
Phosphoric.acid
Tartaric.acid
Threonolactone

NA.9 NA.10 NA.11 NA.12 NA.13 NA.14 NA.15 NA.16

Fructose
Glucose
Sucrose
Erythronic.acid
Galactinol
Galactose
Myo.Inostol
Raffinose
Threitol
Xylose
Fumaric.acid
Succinic.acid
Arabinose
Melibiose
Rhamnose
Ribonic.acid
Ribose
Aspartic.acid
Isoleucine
Leucine
Phenylalanine
Proline
Shikimic.acid
Threonine
Valine
Trans.Caffeic.acid
Catechin
Gallic.acid
Hydroquinone
Quinic.acid
X3.caffeoylquinic.acid
Gluconic.acid
Glucopyranose..H2O.
Lyxonic.acid
Maleic.acid
Malonic.acid
Phosphoric.acid
Tartaric.acid
Threonolactone

NA.17 NA.18 NA.19 NA.20 NA.21 NA.22 NA.23

Fructose
Glucose
Sucrose
Erythronic.acid
Galactinol
Galactose
Myo.Inostol
Raffinose

Threitol
 Xylose
 Fumaric.acid
 Succinic.acid
 Arabinose
 Melibiose
 Rhamnose
 Ribonic.acid
 Ribose
 Aspartic.acid
 Isoleucine
 Leucine
 Phenylalanine
 Proline
 Shikimic.acid
 Threonine
 Valine
 Trans.Caffeic.acid
 Catechin
 Gallic.acid
 Hydroquinone
 Quinic.acid
 X3.caffeoylquinic.acid
 Gluconic.acid
 Glucopyranose..H2O.
 Lyxonic.acid
 Maleic.acid
 Malonic.acid
 Phosphoric.acid
 Tartaric.acid
 Threonolactone

NA.24 NA.25 NA.26 NA.27 NA.28 NA.29 NA.30

Fructose
 Glucose
 Sucrose
 Erythronic.acid
 Galactinol
 Galactose
 Myo.Inositol
 Raffinose
 Threitol
 Xylose
 Fumaric.acid
 Succinic.acid
 Arabinose
 Melibiose
 Rhamnose
 Ribonic.acid
 Ribose
 Aspartic.acid
 Isoleucine
 Leucine
 Phenylalanine

Proline
 Shikimic.acid
 Threonine
 Valine
 Trans.Caffeic.acid
 Catechin
 Gallic.acid
 Hydroquinone
 Quinic.acid
 X3.caffeoylquinic.acid
 Gluconic.acid
 Glucopyranose..H2O.
 Lyxonic.acid
 Maleic.acid
 Malonic.acid
 Phosphoric.acid
 Tartaric.acid
 Threonolactone

NA.31 NA.32 NA.33 NA.34 NA.35 NA.36 NA.37

Fructose
 Glucose
 Sucrose
 Erythronic.acid
 Galactinol
 Galactose
 Myo.Inositol
 Raffinose
 Threitol
 Xylose
 Fumaric.acid
 Succinic.acid
 Arabinose
 Melibiose
 Rhamnose
 Ribonic.acid
 Ribose
 Aspartic.acid
 Isoleucine
 Leucine
 Phenylalanine
 Proline
 Shikimic.acid
 Threonine
 Valine
 Trans.Caffeic.acid
 Catechin
 Gallic.acid
 Hydroquinone
 Quinic.acid
 X3.caffeoylquinic.acid
 Gluconic.acid
 Glucopyranose..H2O.
 Lyxonic.acid

Maleic.acid
Malonic.acid
Phosphoric.acid
Tartaric.acid
Threonolactone

NA.38 NA.39 NA.40 NA.41 NA.42 NA.43 NA.44

Fructose
Glucose
Sucrose
Erythronic.acid
Galactinol
Galactose
Myo.Inostol
Raffinose
Threitol
Xylose
Fumaric.acid
Succinic.acid
Arabinose
Melibiose
Rhamnose
Ribonic.acid
Ribose
Aspartic.acid
Isoleucine
Leucine
Phenylalanine
Proline
Shikimic.acid
Threonine
Valine
Trans.Caffeic.acid
Catechin
Gallic.acid
Hydroquinone
Quinic.acid
X3.caffeoylquinic.acid
Gluconic.acid
Glucopyranose..H2O.
Lyxonic.acid
Maleic.acid
Malonic.acid
Phosphoric.acid
Tartaric.acid
Threonolactone

NA.45	NA.46	NA.47	C19_22d_WS1	C19_22d_WS2
Fructose			7.425148751	7.460947291
Glucose			7.176213050	7.273618456
Sucrose			7.316100476	7.356575216
Erythronic.acid			4.674573640	4.711219557
Galactinol			8.202461801	7.846700153
Galactose			5.355685851	5.478098160
Myo.Inostol			8.041500364	8.056296305

Raffinose	5.193732325	5.062726163	
Threitol	-2.522840789	-2.857259828	
Xylose	0.812292845	1.008630305	
Fumaric.acid	3.177439471	3.748997850	
Succinic.acid	1.060047384	0.974529312	
Arabinose	0.318461465	0.483364361	
Melibiose	2.749319725	2.776735687	
Rhamnose	2.554097638	2.254594043	
Ribonic.acid	1.804466643	1.939978765	
Ribose	0.365132593	0.638768944	
Aspartic.acid	3.730531274	3.148771447	
Isoleucine	1.014355293	-0.369594529	
Leucine	1.032100843	-0.375197235	
Phenylalanine	2.426801472	1.067638717	
Proline	-1.107803290	-3.351074441	
Shikimic.acid	6.858105360	6.899187717	
Threonine	1.153156788	1.320195821	
Valine	3.051198063	2.093222111	
Trans.Caffeic.acid	6.065873847	7.015849886	
Catechin	3.687396681	3.981852653	
Gallic.acid	3.198651301	2.910348915	
Hydroquinone	-1.241270432	-0.524915117	
Quinic.acid	3.704207995	3.868489231	
X3.caffeoylquinic.acid	3.021835027	3.213969334	
Gluconic.acid	5.329733562	5.458906907	
Glucopyranose..H2O.	0.471967788	1.170566057	
Lyxonic.acid	1.804466643	1.947853143	
Maleic.acid	3.806014654	3.096430540	
Malonic.acid	-0.567040593	0.909197063	
Phosphoric.acid	8.017409749	8.305624028	
Tartaric.acid	7.142740172	7.505319326	
Threonolactone	-0.426625474	-0.650634722	
	C19_22d_WS3	C19_22d_WS4	C19_22d_WW1
Fructose	7.695792033	7.744497506	8.248226462
Glucose	7.609718032	7.728750446	7.919387758
Sucrose	7.711068092	7.951191447	7.837766677
Erythronic.acid	4.470536865	4.464080092	4.946496941
Galactinol	8.558317387	7.977732126	7.977348622
Galactose	5.638131776	5.777209280	6.219942914
Myo.Inostol	8.442661562	8.490285318	8.417097222
Raffinose	4.954196310	4.474695614	5.231931551
Threitol	-1.321928095	-1.756330919	-2.293358943
Xylose	0.768925336	0.955312803	1.613060107
Fumaric.acid	2.893362211	4.493839441	3.122672719
Succinic.acid	0.352758525	-0.020340448	1.163498732
Arabinose	-0.205896101	0.024319679	1.002882509
Melibiose	2.752320428	2.491340047	3.296310561
Rhamnose	2.546215385	2.463883980	2.949161371
Ribonic.acid	1.775682702	1.922197848	2.181102551
Ribose	0.314986485	0.408168371	0.780730036
Aspartic.acid	2.200378798	1.769771739	4.303123168
Isoleucine	2.395062800	1.687508661	0.892196710
Leucine	2.418999465	1.687508661	0.896078055

Phenylalanine	0.949348164	0.064882852	2.386535070
Proline	0.197865391	-2.126580497	-0.805912948
Shikimic.acid	7.130797052	6.936013618	7.356848079
Threonine	-0.338250400	-0.666576266	1.009347172
Valine	3.828428485	3.010063683	3.138814469
Trans.Caffeic.acid	5.907275263	6.632355473	6.251756958
Catechin	1.343123519	0.891419187	4.404971224
Gallic.acid	1.176960992	2.679423798	3.770511935
Hydroquinone	-0.386468347	-0.680382066	-0.821126042
Quinic.acid	4.022101445	3.809620235	4.029629568
X3.caffeoylquinic.acid	3.555570778	3.001982343	3.551762085
Gluconic.acid	5.662718215	5.554404666	5.557379454
Glucopyranose..H2O.	0.616357697	0.518031493	0.689746438
Lyxonic.acid	1.775682702	1.922197848	2.179829491
Maleic.acid	3.564987801	4.556000161	3.412104045
Malonic.acid	1.205392513	1.638768944	-0.010134377
Phosphoric.acid	8.294064699	8.632671736	9.460138448
Tartaric.acid	7.889047583	8.098911122	7.976850486
Threonolactone	-1.275786313	-1.816037165	-0.129733930
	C19_22d_WW2	C19_22d_WW3	C19_22d_WW4
Fructose	8.044481553	8.257095502	7.973232415
Glucose	7.608032994	8.082612120	7.931612150
Sucrose	7.617423385	8.181967193	8.103156648
Erythronic.acid	4.562730873	5.022722894	4.972049271
Galactinol	7.852760447	7.968234784	7.700890490
Galactose	5.876860697	6.071376549	5.866091967
Myo.Inostol	8.071489178	8.811413229	8.798196359
Raffinose	4.973886748	4.221335776	4.197393640
Threitol	-1.785875195	-1.347398782	-1.307572802
Xylose	1.147306699	1.544485386	1.648465443
Fumaric.acid	3.420078116	3.400947728	4.859224162
Succinic.acid	0.768925336	0.695102986	0.723340120
Arabinose	0.565597176	0.685267407	0.390667686
Melibiose	2.893556369	3.074334166	2.488257913
Rhamnose	2.616357697	2.644317778	2.568275372
Ribonic.acid	2.009347172	2.468583317	2.458382004
Ribose	0.808179084	0.831066511	1.141432791
Aspartic.acid	3.224966365	2.650994269	1.674912553
Isoleucine	-1.248107862	2.080316560	1.539531071
Leucine	-1.244685096	2.072448850	1.539531071
Phenylalanine	1.110363243	-0.606034724	-0.136061550
Proline	-5.210896782	-0.550042516	-2.373327247
Shikimic.acid	7.092736002	7.733272983	7.724411531
Threonine	0.674460652	-0.083141235	-1.343732465
Valine	1.413594082	3.630754919	2.927517246
Trans.Caffeic.acid	6.848735598	6.491067415	6.961611753
Catechin	3.339992484	3.600507645	2.365132593
Gallic.acid	3.734547054	1.857184806	3.030159483
Hydroquinone	-0.537424112	0.309176187	-0.340075442
Quinic.acid	3.842677192	4.531942833	4.560714954
X3.caffeoylquinic.acid	3.182056609	4.009436756	3.176163174
Gluconic.acid	5.155708762	6.274876633	6.492317890
Glucopyranose..H2O.	0.832687516	1.231432408	0.679874148

Lyxonic.acid	2.019701914	2.468583317	2.458382004
Maleic.acid	2.694211608	4.213425053	5.044219237
Malonic.acid	0.735522177	1.579180148	1.688404188
Phosphoric.acid	9.305106414	9.600739924	9.196970898
Tartaric.acid	7.845922795	8.398589796	8.219492848
Threonolactone	-0.132894270	0.597411988	0.525066592
	C19_44d_WS1	C19_44d_WS2	C19_44d_WS3
Fructose	7.601852483	7.262527119	7.327112471
Glucose	7.243716678	6.724773037	6.894866256
Sucrose	7.785308600	7.279889112	7.797745816
Erythronic.acid	5.995710629	5.595891494	5.336783245
Galactinol	7.938550450	7.546199948	7.876001168
Galactose	5.323153865	4.833294924	4.719840555
Myo.Inostol	8.687326689	8.137995268	8.539713289
Raffinose	5.011048305	5.515226746	5.242831124
Threitol	-1.689659879	-2.251538767	-1.395928676
Xylose	1.484395963	0.725086725	0.466757616
Fumaric.acid	4.154048466	4.330056381	3.582676423
Succinic.acid	1.403267722	0.956056652	.
Arabinose	0.021479727	-0.005782353	-0.826232932
Melibiose	3.493903472	3.514627273	3.685828047
Rhamnose	3.436694888	3.301587647	2.939038470
Ribonic.acid	2.173127433	1.512985335	1.614003045
Ribose	0.788268083	0.561692721	0.090853430
Aspartic.acid	4.011495639	3.150072197	0.523060062
Isoleucine	-0.418889825	-0.502259911	0.798257933
Leucine	-0.418889825	-1.498178735	0.805705185
Phenylalanine	0.154453593	-0.194294815	-0.590744853
Proline	-3.756330919	-2.727379545	-2.514573173
Shikimic.acid	6.389962535	4.781254786	5.287656979
Threonine	1.367930141	1.121678557	-1.311148256
Valine	0.949348164	0.881273061	2.240924865
Trans.Caffeic.acid	7.120383047	6.132330066	5.749668341
Catechin	3.761710784	3.684033231	4.396022448
Gallic.acid	3.411697404	3.145351386	1.804053559
Hydroquinone	0.715454127	-0.434402824	0.392866916
Quinic.acid	4.605079434	3.105678078	3.825175049
X3.caffeoylquinic.acid	4.241840184	2.404358195	2.577247536
Gluconic.acid	5.807664038	4.893119476	5.162975338
Glucopyranose..H2O.	1.225891862	0.567545448	0.500802053
Lyxonic.acid	2.174406419	1.518031493	1.614003045
Maleic.acid	4.006657082	4.330199833	4.237487238
Malonic.acid	1.695993813	-0.194294815	0.904580435
Phosphoric.acid	7.854251289	8.113710916	7.988894828
Tartaric.acid	8.381296353	7.482340089	7.584556686
Threonolactone	0.101650076	-1.197599960	-1.325539348
	C19_44d_WS4	C19_44d_WW1	C19_44d_WW2
Fructose	8.289746876	7.525473828	7.410705735
Glucose	7.843688694	6.930406189	7.010086069
Sucrose	7.882826431	7.414778242	7.567560658
Erythronic.acid	5.342056884	5.339208663	5.270117753
Galactinol	7.913559645	7.174306539	7.130807346
Galactose	6.033775373	5.011987545	5.034655924

Myo. Inostol	8.731519297	8.142883095	8.186852116
Raffinose	5.233964732	4.525505149	4.782985108
Threitol	-1.369594529	-3.083141235	-2.380821784
Xylose	0.884402553	1.027154052	1.020768865
Fumaric.acid	4.952752894	3.794207895	4.355650617
Succinic.acid	0.615416297	0.567545448	0.270229907
Arabinose	0.027154052	0.101650076	0.237563718
Melibiose	3.398897571	3.292487292	3.281549893
Rhamnose	3.669933836	2.962734091	2.846794159
Ribonic.acid	1.642470537	1.771885579	1.552377071
Ribose	0.659924558	0.874993639	0.867105730
Aspartic.acid	0.774839760	2.398076692	2.284217983
Isoleucine	-0.296899300	0.439357178	-2.011587974
Leucine	-0.296899300	0.458382004	-1.965784285
Phenylalanine	-0.729770093	0.843179890	0.169925001
Proline	-2.878321443	-2.766111940	-0.463947100
Shikimic.acid	5.694239472	5.758862790	5.864879462
Threonine	-1.526992432	0.677169939	0.100304906
Valine	1.086104371	1.641083553	0.439357178
Trans.Caffeic.acid	6.639622888	6.651496633	6.872631791
Catechin	3.541638734	4.058922543	4.319256637
Gallic.acid	2.947479146	3.313390985	3.565353457
Hydroquinone	-0.017417053	0.112366523	0.276198865
Quinic.acid	3.885671972	3.494927567	3.756703086
X3.caffeoylquinic.acid	2.513238062	2.882838656	3.066950244
Gluconic.acid	5.366252264	4.997427908	4.771040414
Glucopyranose..H2O.	0.521050737	1.078609835	1.057970069
Lyxonic.acid	1.642470537	1.778208576	1.551885103
Maleic.acid	4.824156844	3.267236142	3.807354922
Malonic.acid	1.853197255	0.823749360	0.888304895
Phosphoric.acid	8.329271626	8.803646814	8.899734542
Tartaric.acid	8.755852316	7.452455415	7.738335504
Threonolactone	-0.529072743	-0.205896101	-0.606034724
	C19_44d_WW3	C19_44d_WW4	F19_22d_WS1
Fructose	7.931027030	7.719628395	6.787445525
Glucose	7.504826931	7.356804072	7.541019153
Sucrose	8.121916804	8.022062595	7.441740749
Erythronic.acid	5.257651841	5.330701802	4.700939026
Galactinol	7.591918729	7.576454113	7.170185465
Galactose	5.401801101	5.225660543	5.773574423
Myo. Inostol	8.751142325	7.409933966	7.934404450
Raffinose	4.687004682	4.594667973	3.346956889
Threitol	-1.573466862	-2.023269779	-2.314732593
Xylose	0.942608336	1.028569152	1.227741076
Fumaric.acid	3.989865623	4.957311029	3.270229907
Succinic.acid	-0.603840511	-0.311148256	-0.020340448
Arabinose	0.012926174	-0.080087911	0.617298483
Melibiose	3.483106345	2.934893874	2.870463362
Rhamnose	3.057276965	2.587124922	2.252476214
Ribonic.acid	1.859174456	2.113367121	1.962363932
Ribose	0.726831217	1.025737561	0.492622329
Aspartic.acid	0.428678410	0.595503661	4.450221496
Isoleucine	0.507921465	1.075874867	0.596458140

Leucine	0.513995979	1.055889758	-0.032093630
Phenylalanine	-1.207561070	-0.539519530	2.960326357
Proline	-2.867752202	-3.145605322	-1.775959726
Shikimic.acid	6.320123598	6.417768144	5.973932655
Threonine	-1.586405918	-1.775959726	1.606442228
Valine	1.690640579	2.222186307	2.385154897
Trans.Caffeic.acid	6.263560293	6.754767273	6.632544512
Catechin	3.736929526	2.565109697	1.929790998
Gallic.acid	2.223113589	2.971221642	2.962549023
Hydroquinone	0.376290383	0.186500558	-1.061902439
Quinic.acid	4.055195654	4.353252707	1.552868871
X3.caffeoylquinic.acid	3.023077888	2.606442228	-3.506352666
Gluconic.acid	5.210622644	5.551423731	5.942725616
Glucopyranose..H2O.	0.950841638	0.588804567	-0.024736678
Lyxonic.acid	1.859174456	2.113367121	1.970117398
Maleic.acid	4.722739236	4.990773378	3.828123787
Malonic.acid	1.241230036	1.434561512	0.217851097
Phosphoric.acid	8.679708801	8.779184195	8.282907715
Tartaric.acid	8.204478222	7.741075923	8.670489843
Threonolactone	-0.826232932	-0.187707155	0.402722177
	F19_22d_WS2	F19_22d_WS3	F19_22d_WS4
Fructose	6.733422135	6.123024654	7.254376731
Glucose	7.291428588	7.002274958	7.485716625
Sucrose	7.278932599	7.264020286	7.589875819
Erythronic.acid	4.662889079	4.481815574	3.648925559
Galactinol	7.082085157	6.904399798	7.058500501
Galactose	5.622842522	4.926189234	5.568822573
Myo.Inostol	7.647537575	7.757663354	8.191138197
Raffinose	4.118858038	3.341701164	3.338424415
Threitol	-3.095419565	-2.573466862	-2.434402824
Xylose	1.128953220	0.642470537	1.107687869
Fumaric.acid	3.645932176	2.585923977	4.032806145
Succinic.acid	-0.304006187	-0.795859283	-0.502259911
Arabinose	0.216610069	-0.506352666	0.071762669
Melibiose	2.848397600	2.727702673	2.075874867
Rhamnose	2.039138394	1.687060688	1.745452483
Ribonic.acid	2.017921908	1.659011171	2.079292767
Ribose	0.427606173	0.035623910	0.871843649
Aspartic.acid	3.627023106	1.260025656	1.260627908
Isoleucine	-1.841662973	1.544485386	-0.232768963
Leucine	-2.231074664	1.544485386	-0.220950447
Phenylalanine	0.986956963	-1.055891201	-2.000000000
Proline	-4.132894270	-1.046921047	-3.083141235
Shikimic.acid	5.546894460	5.105049443	6.403421120
Threonine	0.868686765	-1.098505545	-1.384583703
Valine	1.018634174	2.543990720	1.392317423
Trans.Caffeic.acid	6.423309237	5.413932513	6.233849723
Catechin	1.240008965	1.273814245	-1.139235797
Gallic.acid	2.916285546	1.047538389	2.544238074
Hydroquinone	-0.899695094	-0.169744676	-0.643856190
Quinic.acid	1.040541794	1.076559095	2.084404483
X3.caffeoylquinic.acid	-4.184424571	-2.717856771	-1.648371671
Gluconic.acid	5.682826084	5.629968543	5.854344805

Glucopyranose..H2O.	-0.168122759	-0.072482754	-0.367731785
Lyxonic.acid	2.029982866	1.659011171	2.079292767
Maleic.acid	3.744806934	3.565840854	4.209843231
Malonic.acid	0.370722275	1.271425676	1.665847521
Phosphoric.acid	8.065776932	7.926224822	8.286807237
Tartaric.acid	8.057915932	8.016440604	8.466790238
Threonolactone	-0.114035243	-0.475936324	-0.004334590
	F19_22d_WW1	F19_22d_WW2	F19_22d_WW3
Fructose	7.112575038	6.630696684	7.025704346
Glucose	7.954516227	6.900866808	7.823290804
Sucrose	7.552008111	7.117840468	7.743521700
Erythronic.acid	3.980482356	4.336783245	4.044219237
Galactinol	7.149869032	6.825314996	7.248904798
Galactose	6.201045686	5.063244062	5.898982227
Myo.Inostol	8.068106476	7.552884237	8.232780657
Raffinose	3.534933133	3.924289952	3.166233395
Threitol	-1.878321443	-2.643856190	-2.717856771
Xylose	1.452595435	0.740711733	1.103665483
Fumaric.acid	3.331131922	3.145677455	3.012926174
Succinic.acid	0.088141597	-0.058893689	-0.469929258
Arabinose	0.856786546	-0.074000581	0.305678743
Melibiose	2.569248030	2.583519084	2.703322227
Rhamnose	2.639232163	1.640620928	1.886355044
Ribonic.acid	2.005759269	1.631802755	1.930169608
Ribose	0.739848103	0.189033824	0.453122447
Aspartic.acid	3.442412752	3.029806228	1.447314700
Isoleucine	-1.612637459	-0.907792562	0.293958979
Leucine	-1.698997744	-0.902389203	0.295135249
Phenylalanine	-0.329159664	0.423309237	-1.971430848
Proline	-3.736965594	-3.522840789	-2.164884385
Shikimic.acid	6.934799540	6.102364188	6.364362316
Threonine	0.611644543	0.244887059	-1.621488377
Valine	0.069014678	1.466757616	1.797012978
Trans.Caffeic.acid	7.064872076	6.514863937	6.041155352
Catechin	1.037030731	1.844787350	0.190298792
Gallic.acid	4.304511042	3.844586516	2.102993993
Hydroquinone	-1.241270432	-1.340075442	-0.291592017
Quinic.acid	2.377679059	1.660381035	1.815985227
X3.caffeoylquinic.acid	-3.921390165	-4.351074441	-3.224317298
Gluconic.acid	5.756516293	5.468811367	5.840161067
Glucopyranose..H2O.	0.187767747	-0.378944497	0.306845500
Lyxonic.acid	2.008630305	1.642470537	1.930169608
Maleic.acid	3.177279996	3.272769732	3.886940276
Malonic.acid	1.895690390	0.108357178	2.184915004
Phosphoric.acid	9.097334261	8.100157702	8.511590589
Tartaric.acid	9.391548639	8.221828758	8.965813138
Threonolactone	1.635057830	-0.118726939	0.157043710
	F19_22d_WW4	F19_44d_WS1	F19_44d_WS2
Fructose	7.062391587	6.992983641	6.829786149
Glucose	7.623844919	6.717429670	6.957055596
Sucrose	7.767257526	7.142535972	7.205011221
Erythronic.acid	4.315566230	5.419437764	5.303378929
Galactinol	7.270314017	7.327274183	6.675011387

Galactose	5.692427198	4.762774013	5.085382163
Myo.Inostol	8.151153569	7.943569750	7.906962729
Raffinose	3.869772723	4.888694550	3.727920455
Threitol	-1.883635243	-1.857259828	-2.380821784
Xylose	1.090175950	0.925239905	0.913033000
Fumaric.acid	4.217153150	3.853297078	3.954568571
Succinic.acid	-1.164884385	-0.055891201	0.280956314
Arabinose	0.117695043	-0.334607229	0.004321606
Melibiose	2.573374526	3.247319935	3.173447286
Rhamnose	2.170886478	3.131918679	2.796390097
Ribonic.acid	2.004681156	1.933194920	1.873419503
Ribose	0.483364361	0.422233001	0.661749600
Aspartic.acid	0.715454127	4.048933645	3.933194920
Isoleucine	0.534061602	-0.432454552	-0.115597447
Leucine	0.533064922	-0.450084446	-0.463947100
Phenylalanine	-0.910501849	1.869476634	0.370722275
Proline	-3.411195433	-3.380821784	-1.268816758
Shikimic.acid	5.739037979	3.915520901	4.571737477
Threonine	-2.145605322	1.408711861	1.392317423
Valine	1.676267408	-0.104697379	1.557777671
Trans.Caffeic.acid	6.337889456	6.390753656	6.339422474
Catechin	0.703100700	0.694211608	0.457331625
Gallic.acid	2.589523817	3.139469495	3.157367148
Hydroquinone	-0.571321590	-1.248107862	-1.675765438
Quinic.acid	1.694211608	1.138159145	1.263635404
X3.caffeoylquinic.acid	-2.365871442	-3.775959726	-4.210896782
Gluconic.acid	5.735143041	5.630958725	5.643971601
Glucopyranose..H2O.	0.205392513	0.035623910	-0.069451881
Lyxonic.acid	2.004681156	1.934327778	1.873813198
Maleic.acid	4.343834172	4.112283109	4.061603409
Malonic.acid	1.494671612	0.246104010	-0.046921047
Phosphoric.acid	8.425043819	7.933991554	7.893307599
Tartaric.acid	8.431313730	8.151209393	7.995710629
Threonolactone	0.021479727	0.149259365	0.028569152
	F19_44d_WS3	F19_44d_WS4	F19_44d_WW1
Fructose	7.602305433	7.101366434	7.144474708
Glucose	7.875939753	7.136909109	7.446223140
Sucrose	7.782015335	7.531693361	7.497556483
Erythronic.acid	4.848597904	5.212686057	5.268621531
Galactinol	7.364090870	7.160758876	6.630827710
Galactose	6.033709310	5.035755858	5.509505834
Myo.Inostol	8.470402643	8.317041717	7.962022607
Raffinose	4.307938479	4.085254677	3.844285211
Threitol	-1.552156356	-1.846843212	-2.708396442
Xylose	0.970117398	0.725959235	1.417920008
Fumaric.acid	3.771674334	4.759741743	3.999458888
Succinic.acid	-1.204233052	-0.520769439	0.147957881
Arabinose	-0.112474729	-0.300448367	0.602171791
Melibiose	3.291014101	2.928086020	3.253232939
Rhamnose	3.260326813	3.083894126	2.863740264
Ribonic.acid	1.668119125	1.757450016	2.083043129
Ribose	0.513995979	0.344828497	0.906120953
Aspartic.acid	1.699107385	1.106348320	3.018456141

Isoleucine	-0.054392297	0.484395963	-2.035046947
Leucine	-0.112474729	0.483364361	-2.139235797
Phenylalanine	-0.666576266	-0.428565884	-0.867752202
Proline	-2.539519530	-3.556393349	-4.643856190
Shikimic.acid	5.719539415	4.259875054	5.968712867
Threonine	-1.727379545	-1.595096878	0.279768422
Valine	1.389566812	1.591200673	-0.430508908
Trans.Caffeic.acid	6.211479514	6.433543714	7.004433975
Catechin	0.212880566	-0.164884385	1.348798960
Gallic.acid	2.452331857	2.735738782	4.092968509
Hydroquinone	-1.032093630	-0.821126042	-0.971430848
Quinic.acid	2.160920188	1.151858817	2.200064862
X3.caffeoylquinic.acid	-2.481968507	-1.741782610	-4.351074441
Gluconic.acid	5.883767424	5.727239777	5.620410461
Glucopyranose..H2O.	0.478195258	0.199122642	0.558757430
Lyxonic.acid	1.668119125	1.757450016	2.083043129
Maleic.acid	4.519730595	4.667267692	3.910540801
Malonic.acid	2.204766751	1.510455622	1.222186307
Phosphoric.acid	8.192963450	8.032282712	8.880367177
Tartaric.acid	9.020854965	8.191977113	8.562616408
Threonolactone	0.490570130	-0.473931188	1.055195654
	F19_44d_WW2	F19_44d_WW3	F19_44d_WW4
Fructose	6.277724444	6.792907397	7.186203399
Glucose	6.398350370	6.919387758	7.256623861
Sucrose	7.094658343	7.798212563	7.816004434
Erythronic.acid	5.164705840	4.989229854	5.180426378
Galactinol	6.182950466	6.949850050	6.891674358
Galactose	4.267760499	4.675703040	5.059355278
Myo.Inositol	7.573336653	8.200015803	8.334014002
Raffinose	3.807045740	3.828530037	3.771251752
Threitol	-2.717856771	-2.177881725	-1.831357964
Xylose	0.853596506	0.929033479	1.137503524
Fumaric.acid	3.983130425	3.440819347	4.763730250
Succinic.acid	-0.090802937	-1.077041036	-0.610433188
Arabinose	-0.239566125	-0.514573173	0.105678078
Melibiose	2.948787713	2.948040106	2.935836874
Rhamnose	1.876173114	1.963474124	2.458644479
Ribonic.acid	1.711935357	1.929412288	1.951587795
Ribose	0.534061602	0.556797247	0.944108799
Aspartic.acid	2.496462350	0.063502942	0.547943311
Isoleucine	-2.411195433	0.435095152	-0.043943348
Leucine	-3.717856771	0.411426246	-0.090802937
Phenylalanine	-3.145605322	-1.937878288	-1.732164608
Proline	-4.237863830	-2.954557029	-3.171368418
Shikimic.acid	5.314914001	5.296604239	5.458283564
Threonine	-0.254977851	-1.948975997	-2.965784285
Valine	-0.722610301	1.674008609	1.118359726
Trans.Caffeic.acid	6.718567124	6.100578245	6.613369576
Catechin	0.950095094	0.728573603	-0.382701517
Gallic.acid	3.412646055	2.296016823	3.016496320
Hydroquinone	-0.867752202	-0.816037165	-0.775959726
Quinic.acid	1.810237431	1.585923977	1.863542051
X3.caffeoylquinic.acid	-4.573466862	-3.717856771	-2.286304185

Gluconic.acid	5.358818205	5.666074843	5.806066226
Glucopyranose..H2O.	0.526068812	0.181420640	0.359521170
Lyxonic.acid	1.708849377	1.929412288	1.951587795
Maleic.acid	3.381560255	4.128458384	4.711990404
Malonic.acid	1.144046370	1.598365205	1.604545816
Phosphoric.acid	7.889430952	8.277385049	8.170125362
Tartaric.acid	7.903556525	8.366772440	8.401007480
Threonolactone	0.593592806	0.429749851	0.407080775

```
> sapply(net$gR, print)
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'X' in se
```

6.5 Save network with igraph

```
> library(igraph)
```

```
> nettip <- "gml"
```

```
> (netfn<- gsub("\\.", "_", paste0("network-", cutoff, "_", suffix)))
```

```
[1] "network-0_5_18-19-1-2-3-4-5-6-7-V3"
```

```
> (netpath <- file.path(.oroot, paste(netfn, nettip, sep=". ")))
```

```
[1] "../..output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/network-0_5_18-19-1-2
```

```
> write.graph(net$gR, file=netpath, format=nettip)
```

```
Error in "igraph" %in% class(graph): object 'net' not found
```

```
> net1 <- read.graph(file=netpath, format=nettip)
```

```
Error in read.graph.gml(file, ...): At rinterface.c:5028 : Cannot read GML fil
```

```
> if(interactive()) tkplot(net1)
```

```
> subnet <- function(net, i=1:2){
```

```
+ n <- list(net[[i]])
```

```
+ class(n) <- class(net)
```

```
+ return(n)
```

```
+ }
```

```
> net2 <- subnet(net1, 1)
```

```
Error in subnet(net1, 1): object 'net1' not found
```

```
> class(net2)
```

```
Error in eval(expr, envir, enclos): object 'net2' not found
```

```
> tkplot(net2)
```

```
Error in "igraph" %in% class(graph): object 'net2' not found
```

Save correlation matrix (M) used for network construction.

```
> (Mfn <- file.path(.oroot, "network-M.txt"))
```

```
[1] "../..output/60_Trans-x-Meta-18-19-1-2-3-4-5-6-7-V3/network-M.txt"
```

```
> my.write.table(t(net$M), file=Mfn, label="Correlation matrix (M) used for ne
```

```
Error in h(simpleError(msg, call)): error in evaluating the argument 'x' in se
```

A Metadata files

A.1 Project metadata

Table 1: Project metadata

Item	Value
project:	_p_VinskaTrta
Short Name:	VinskaTrta
Title:	Vine related research
Description:	*
pISA projects path:	D:/DEJAVNOSTI/OMIKE/pISA-projects
Local pISA-tree organisation:	NIB
pISA project creation date:	2020-11-13
pISA project creator:	AB
Project funding code:	*
Project coordinator:	Marusa Pompe Novak
Project partners:	*
Project start date:	*
Project end date:	*
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.2 Investigation metadata

Table 2: Investigation metadata

Item	Value
Investigation:	_I_EnViRoS
Short Name:	EnViRoS
Title:	Integration of data from different platforms
Description:	*
Phenodata:	./phenodata_20201113.txt
pISA Investigation creation date:	2020-11-13
pISA Investigation creator:	AB
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.3 Study metadata

Table 3: Study metadata

Item	Value
Study:	_S_01_Integ
Short Name:	01_Integ
Title:	*
Description:	*
Raw Data:	
pISA Study creation date:	2020-11-13
pISA Study creator:	AB
Principal investigator:	*
License:	CC BY 4.0
Sharing permission:	Private
Upload to FAIRDOMHub:	Yes

A.4 Assay metadata

Table 4: Assay metadata

Item	Value
Assay:	_A_01_Desc-R
Short Name:	01_Desc-R
Assay Class:	DRY
Assay Type:	R
Title:	Data overview and descriptive statistical presentation
Description:	First we will organize the data and perform preliminary data analyses to overview what we have.
pISA Assay creation date:	2020-11-13
pISA Assay creator:	Andrej Blejec
Analyst:	Andrej Blejec
Phenodata:	Phenodata_20201109.txt
Featuredata:	Transcripts1819-02.txt
Featuredata metabolites:	Featuredata_metabolites_210127.txt
Transcript data 18:	/input/Transcripts 2018.txt
Transcript data 19:	/input/Transcripts 2019.txt
Metabolite data 18:	/input/Metabolites_2018_raw_-data.txt
Metabolite data 19:	/input/Metabolites_2019_raw_-data.txt
Metabolite data 18-2:	/input/Metabolites_2018-Nor2W_-ISTD.txt
Metabolite data 19-2:	/input/Metabolites_2019-Nor2W_-ISTD.txt
Water potential data:	/input/Stem water potential 2018 2019.txt
Interesting bins:	Bin_selection_2.txt
Transcript stats:	/output/50_Expression-water-stress-0.05-1.5-0.5-1-1/lm-fit-means-swpXvariety-statistics.txt
Note:	Metabolites version 2 are normalized in more consistent way

B SessionInfo

Windows 10 x64 (build 19042)

- R version 4.0.2 (2020-06-22), x86_64-w64-mingw32
- Locale: LC_COLLATE=Slovenian_Slovenia.1250, LC_CTYPE=Slovenian_Slovenia.1250, LC_NUMERIC=C, LC_TIME=Slovenian_Slovenia.1250
- Running under: Windows 10 x64 (build 19042)
- Matrix products: default
- Base packages: base, datasets, graphics, grDevices, grid, methods, parallel, splines, stats, utils
- Other packages: amisc 0.1.0, Biobase 2.50.0, BiocGenerics 0.36.0, dotCall64 1.0-0, fda 5.1.9, fds 1.8, fields 11.6, Formula 1.2-4, ggplot2 3.3.3, gplots 3.1.1, Hmisc 4.4-1, igraph 1.2.6, knitr 1.30, lattice 0.20-41, lubridate 1.7.9.2, MASS 7.3-51.6, Matrix 1.2-18, mixOmics 6.14.0, pcaPP 1.9-73, rainbow 3.6, RCurl 1.98-1.2, reshape2 1.4.4, spam 2.6-0, survival 3.2-7, xtable 1.8-4
- Loaded via a namespace (and not attached): backports 1.2.0, base64enc 0.1-3, bitops 1.0-6, caTools 1.18.1, checkmate 2.0.0, cluster 2.1.0, colorspace 1.4-1, compiler 4.0.2, corpcor 1.6.9, crayon 1.3.4, data.table 1.13.2, digest 0.6.27, dplyr 1.0.2, ellipse 0.4.2, ellipsis 0.3.1, evaluate 0.14, foreign 0.8-80, generics 0.1.0, ggrepel 0.9.0, glue 1.4.2, gridExtra 2.3, gtable 0.3.0, gtools 3.8.2, hdrclde 3.4, highr 0.8, htmlTable 2.1.0, htmltools 0.5.0, htmlwidgets 1.5.3, jpeg 0.1-8.1, KernSmooth 2.23-17, ks 1.12.0, latticeExtra 0.6-29, lifecycle 0.2.0, magrittr 2.0.1, maps 3.3.0, matrixStats 0.57.0, mclust 5.4.7, munsell 0.5.0, mvtnorm 1.1-1, nnet 7.3-14, pillar 1.4.7, pkgconfig 2.0.3, plyr 1.8.6, png 0.1-7, purrr 0.3.4, R6 2.5.0, rARPACK 0.11-0, RColorBrewer 1.1-2, Rcpp 1.0.5, rlang 0.4.10, rpart 4.1-15, RSpectra 0.16-0, rstudioapi 0.13, scales 1.1.1, stringi 1.5.3, stringr 1.4.0, tibble 3.0.4, tidyr 1.1.2, tidyselect 1.1.0, tools 4.0.2, vctrs 0.3.6, withr 2.3.0, xfun 0.19

Analysis project path: [\[link\]](#)

Local

D:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Network

O:

DEJAVNOSTI

OMIKE

pISA-projects

_p_VinskaTrta

_I_EnViRoS

_S_01_Integ

_A_01_Desc-R

other

Main file : [../doc/60_Trans-x-Meta.Rnw](#)

Main file : [../scripts/60_Trans-x-Meta.Rnw](#)

Project file: [\[link\]](#)

View as vignette

Source files can be viewed by pasting this code to R console:

```
projectName <-"other"
mainFile <-"60_Trans-x-Meta"
commandArgs()
library(tkWidgets)
openPDF(file.path(dirname(getwd()), "doc",
paste(mainFile, "PDF", sep=".")
viewVignette("viewVignette", projectName,
file.path("../doc", paste(mainFile, "Rnw", sep=".")))
```