JIVE

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References

Ref.	Title	Details
(Lock et al. 2013)	Joint and individual variation explained (JIVE) for integrated analysis of multiple data types	The method, in details
(Jere et al. 2014)	Extracting commuting patterns in railway networks through matrix decompositions	An example
(O'Connell and Lock 2016)	R.JIVE for exploration of multi-source molecular data	The R package
(Palzer et al. 2022)	sJIVE: Supervised joint and individual variation explained	The supervised version

Installation

The package is called `r.jive` and is available on CRAN :
https://cran.r-project.org/package=r.jive

```
install.packages("r.jive")
## oooorrrrr......
pak::pak("jive")
```
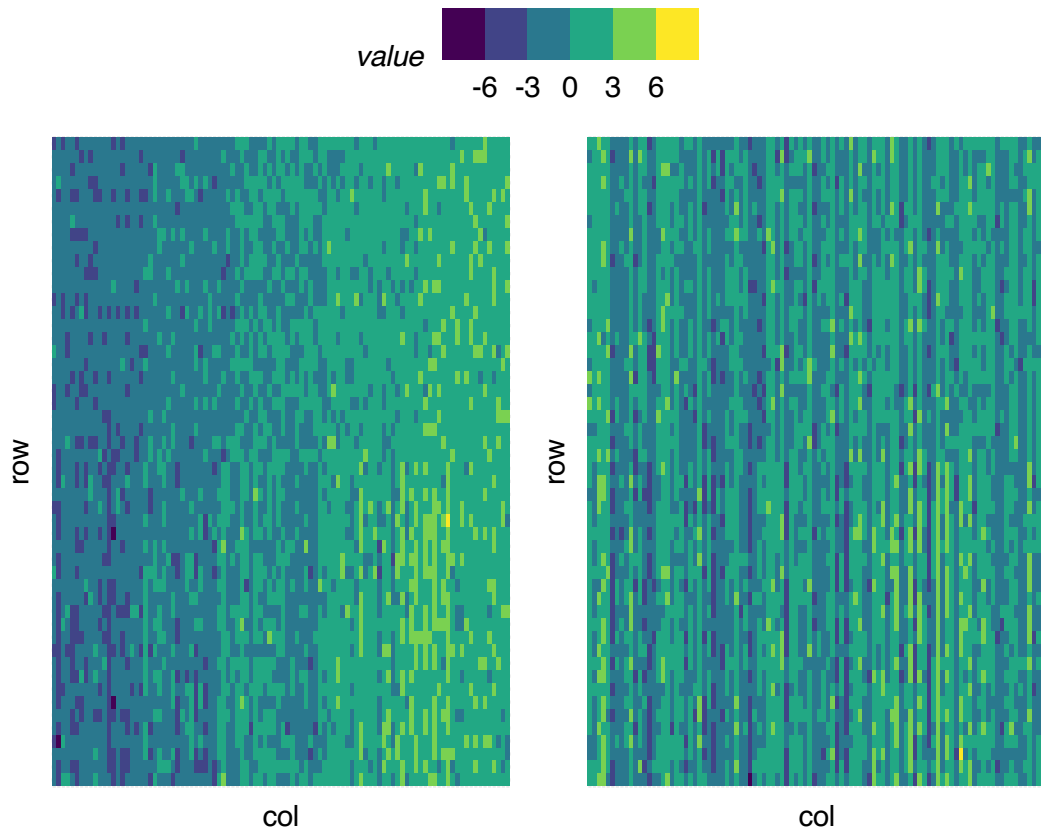
Examples from ?jive

The main function is called `jive`[1]:

```
library(r.jive)
set.seed(10)
data(SimData)
Results <- jive(SimData, showProgress =
FALSE)
```

What are those simulated data?

Load data that were simulated as in Section 2.4 of Lock et al., 2013, with rank 1 joint structure, and rank 1 individual structure for each dataset

Apply `jive` with default parameters

Focus on the four most important parameters:

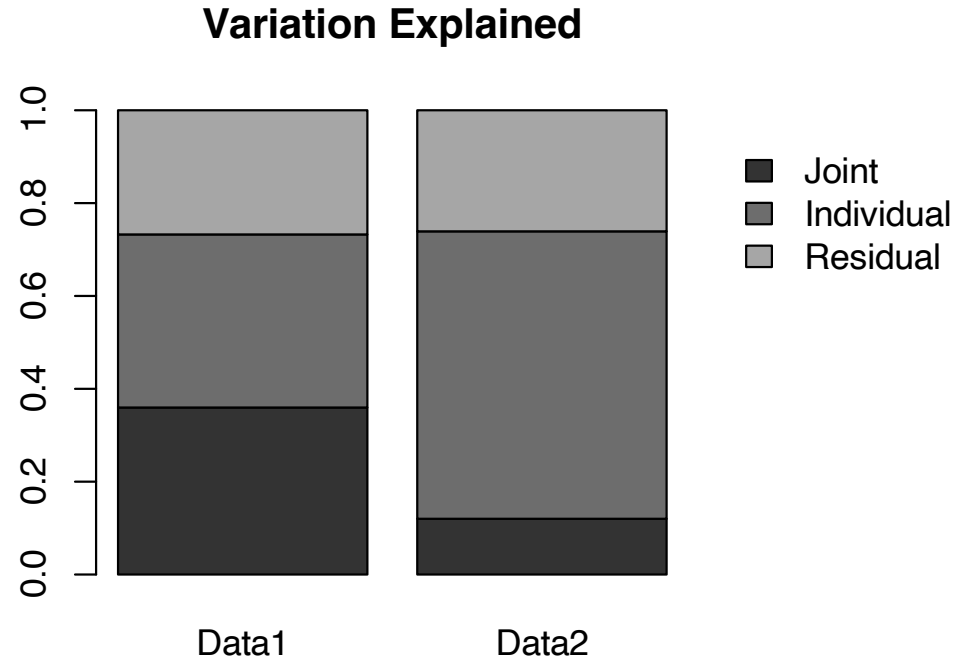| Parameter	Meaning	Default
`data`	list of data matrices	No default
`rankJ`	joint rank	1
`rankA`	specific rank	
`method`	rank selection	"perm"

Output

The output of `jive` is an S3 object of class "jive"

- `print` (not very clear what it is)
- `summary` (no surprise, but it helps understand `print`)
- `plot`, see `?plot.jive` for the different plots
- no `predict` :(

Summary of the results

```
summary(Results)
## $Method
## [1] "perm"
##
## $Ranks
##      Source  Rank
## [1,] "Joint" "1"
## [2,] "Data1" "1"
## [3,] "Data2" "1"
##
## $Variance
##            Data1 Data2
## Joint      0.360 0.120
## Individual 0.373 0.619
## Residual   0.267 0.261
```
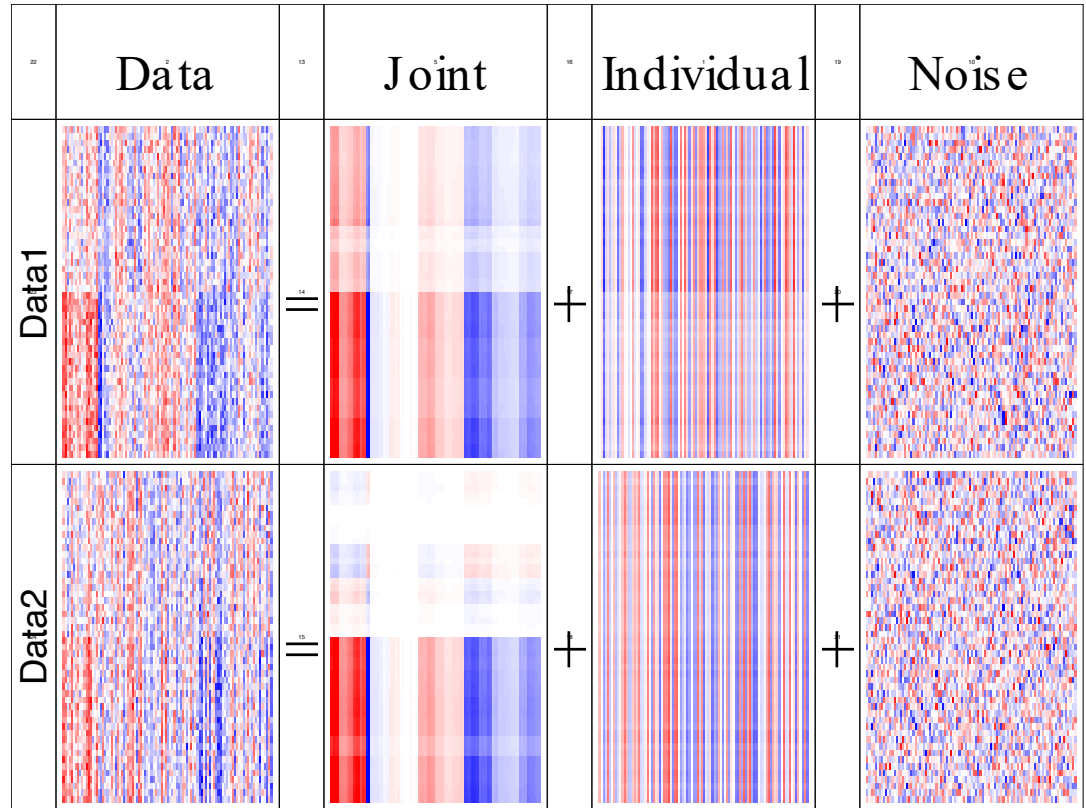
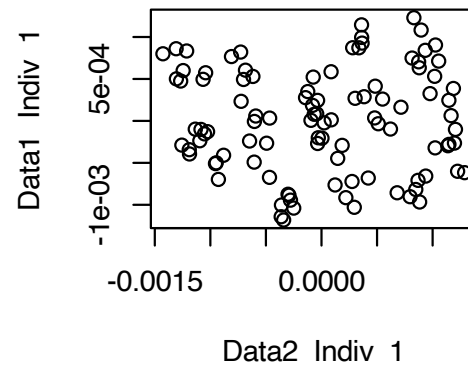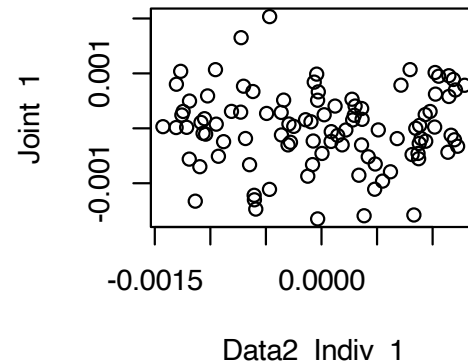## Plot "var" (default)

```
plot(Results, type = "var")
```
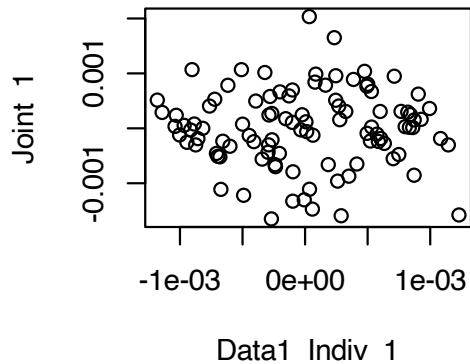

Variation Explained

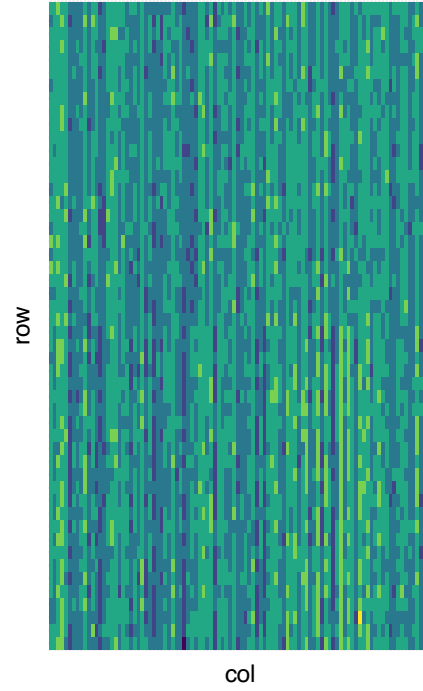# Plot "heat"

```
plot(Results, type =
"heat")
```
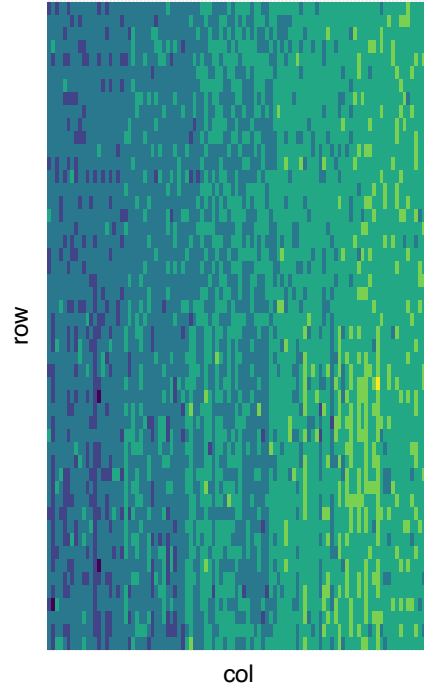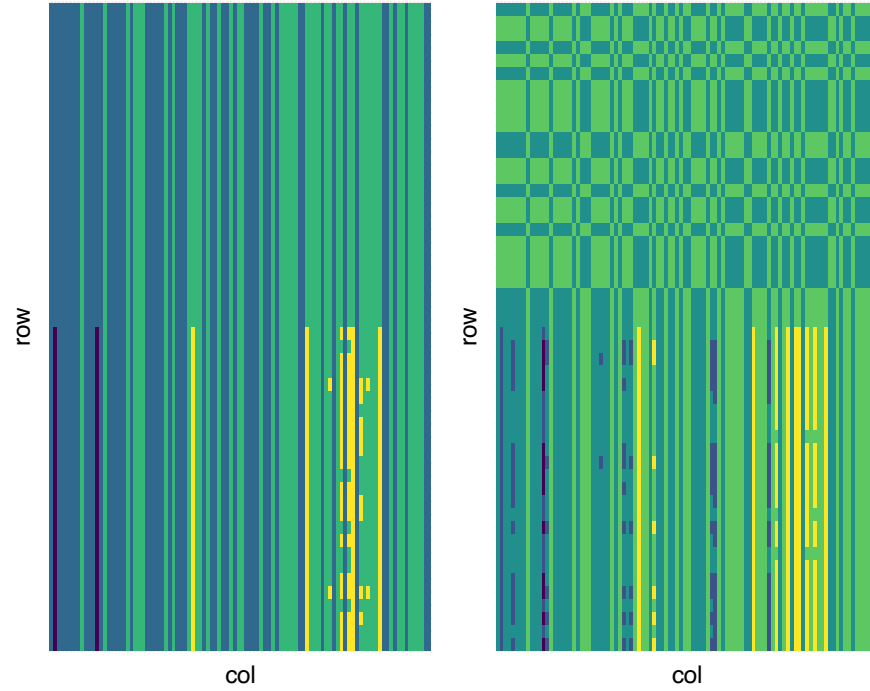
Plot "pca"

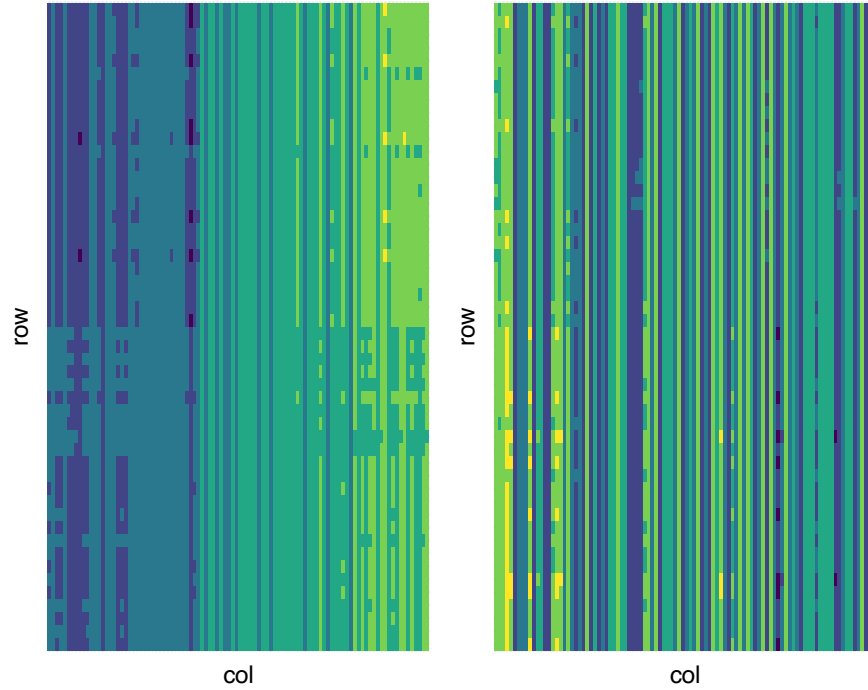See `?showPCA`

```
plot(Results, type =
"pca", 1, c(1, 1))
```

Data

Joint signal

Individual signal

HOW DOES IT WORK?

Just a touch of math...

$$\operatorname*{argmin}_{\mathbf{A},\mathbf{J}} \| \mathbf{X} - (\mathbf{J} + \mathbf{A}) \|_F^2$$

- $\mathbf{X}$ is the concatenation of all the blocks,
- orthogonality between joint ($\mathbf{J}$) and individual ($\mathbf{A}$) approximations
- $\mathbf{J}$ of lower rank r,
- $\mathbf{A}_k$ of lower rank r_k.

Choose the parameters

- Ranks:
  - with permutations (recommended)
  - with BIC (much faster)
  - just give them, if you are a medium
- number of permutations (100 by default) and $\alpha = 0.05$
- scale and center: super important!
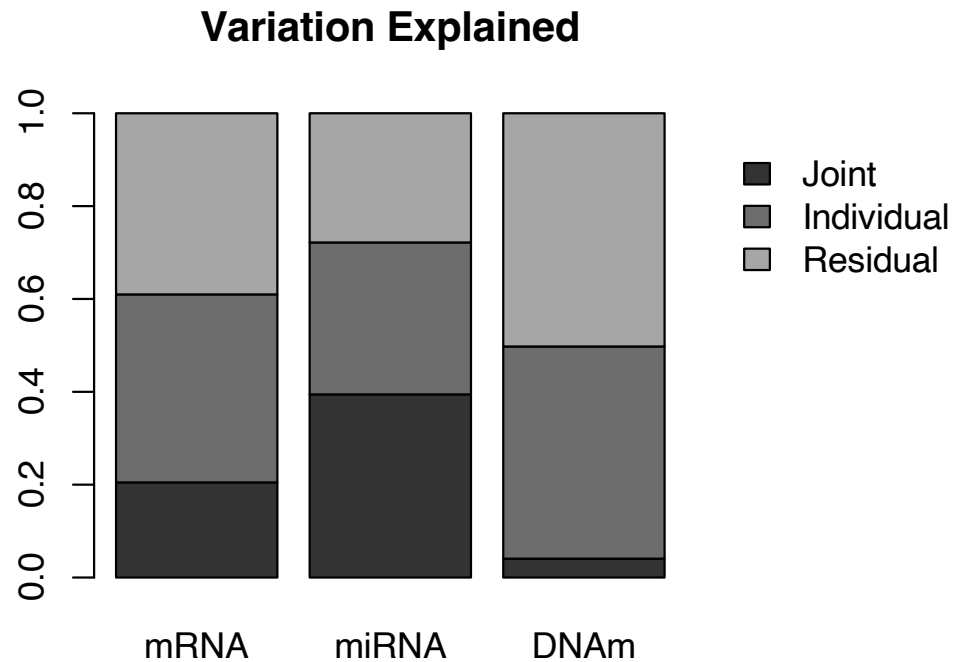- orthogonality: not even a choice

Application on MDD

See "Trame MDD" to load the data. CAUTION: rows = variables and columns = observations.

```
blocks.jive <- lapply(blocks, t)
set.seed(456)
res.jive <- jive(data = blocks.jive)
```
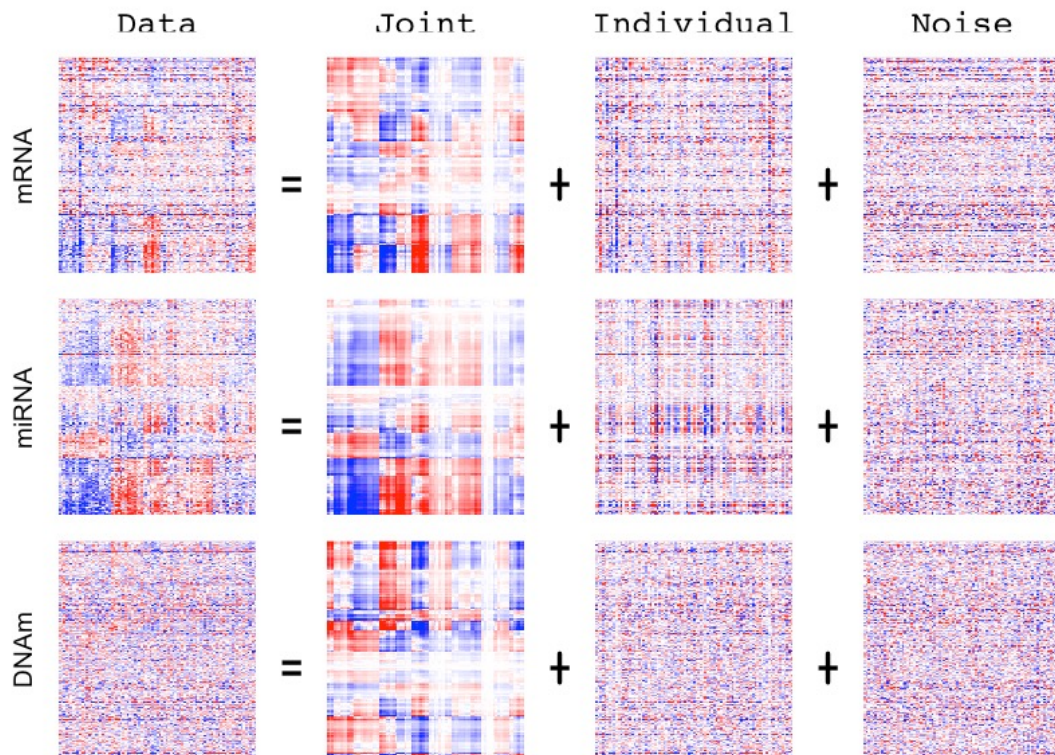
"Variation explained"

```
plot(res.jive)
```


Variation Explained

Legend: Joint, Individual, Residual

x-axis: mRNA, miRNA, DNAm

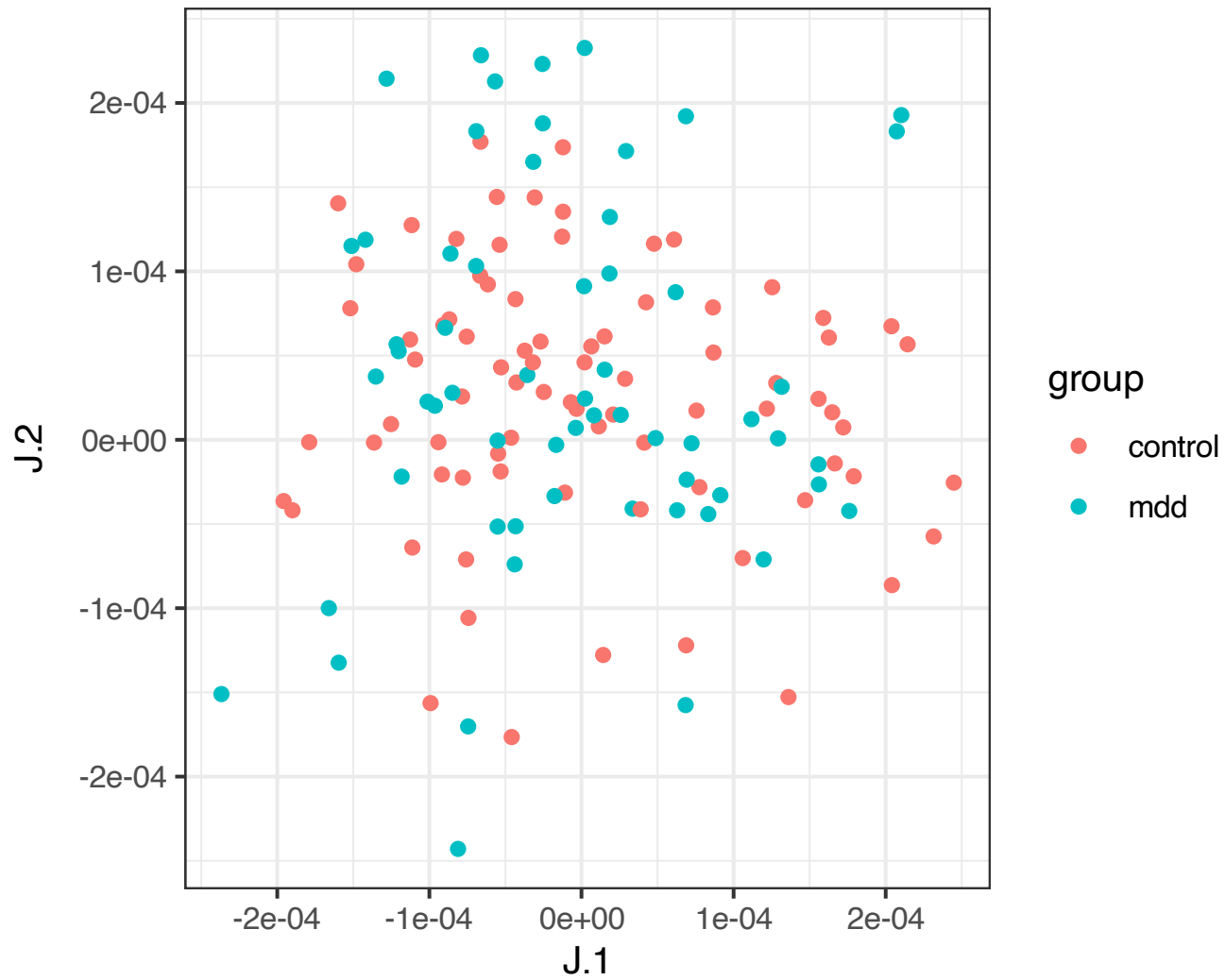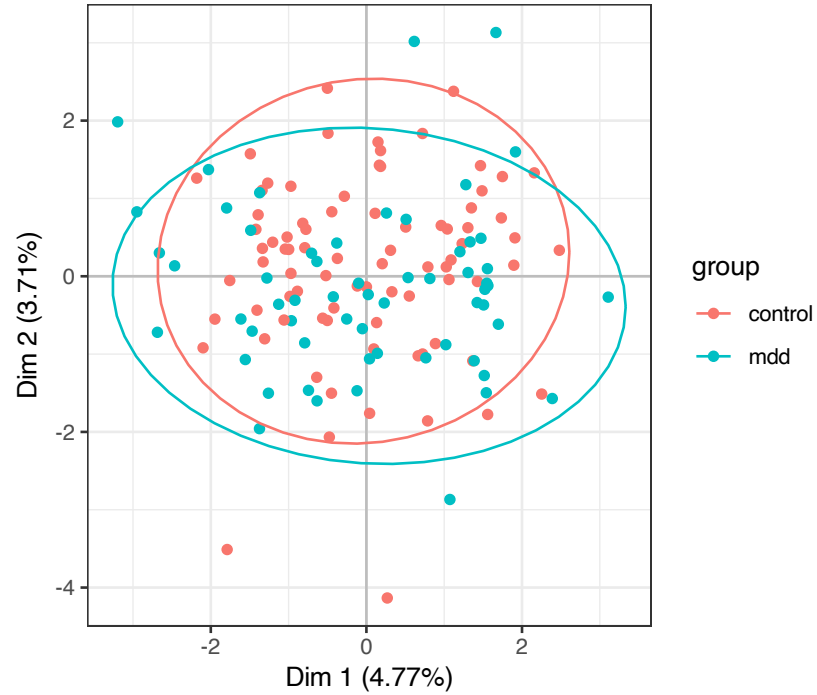# Heatmaps

```
plot.jive(res.jive, type =
"heat")
```
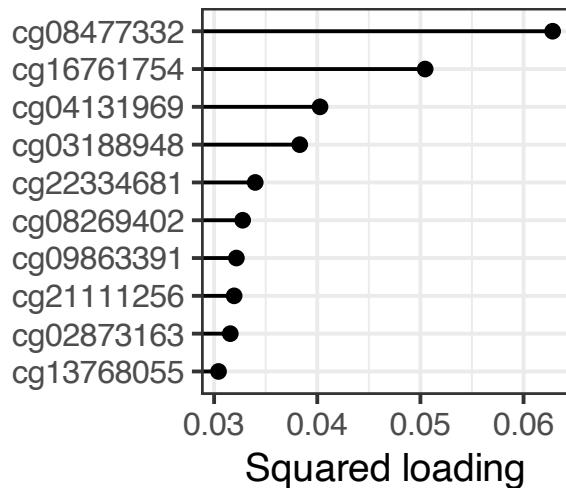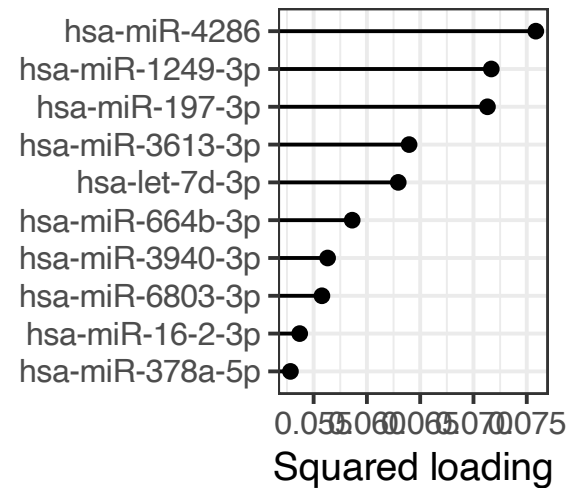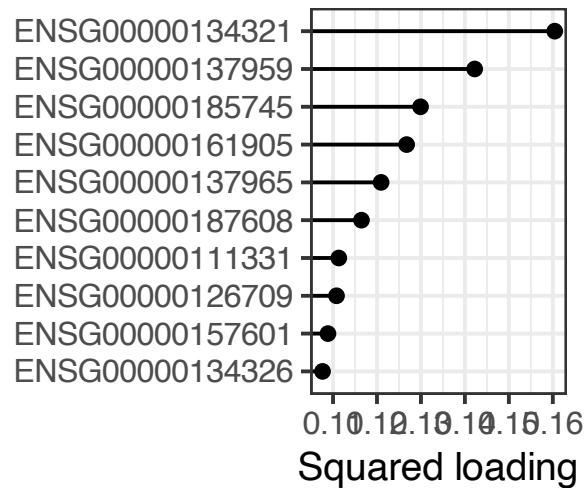
Joint structure

Individual structures

"Best" features

References

Jere, Shashank, Justin Dauwels, Muhammad Tayyab Asif, Nikola Mitro Vie, Andrzej Cichocki, and Patrick Jaillet. 2014. "Extracting Commuting Patterns in Railway Networks Through Matrix Decompositions." In *2014 13th International Conference on Control Automation Robotics & Vision (ICARCV)*, 541–46. https://doi.org/10.1109/ICARCV.2014.7064362.

Lock, Eric F., Katherine A. Hoadley, J. S. Marron, and Andrew B. Nobel. 2013. "Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Data Types." *The Annals of Applied Statistics* 7 (1): 523–42. https://doi.org/10.1214/12-AOAS597.

O'Connell, Michael J., and Eric F. Lock. 2016. "R.JIVE for Exploration of Multi-Source Molecular Data." *Bioinformatics* 32 (18): 2877–79. https://doi.org/10.1093/bioinformatics/btw324.

Palzer, Elise F., Christine H. Wendt, Russell P. Bowler, Craig P. Hersh, Sandra E. Safo, and Eric F. Lock. 2022. "sJIVE: Supervised Joint and Individual Variation Explained." *Computational Statistics & Data Analysis* 175: 107547. https://doi.org/10.1016/j.csda.2022.107547.

Your (quick) feedback

https://forms.gle/j6xTrzpMHh3WQVcb8