Omics data integration with the O2PLS R-package

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O2PLS Method

- ► Trygg & Wold, 2003
- Decomposition:

$$X = TW^{\top} + T_{\perp}W_{\perp}^{\top} + E$$
$$Y = UC^{\top} + U_{\perp}C_{\perp}^{\top} + F$$

- ▶ Joint part: U = TB + H
- ▶ Find W and C such that T and U have high covariance.
- W and C corrected for independent latent variation specific for X and Y.
- n joint components, nx X-specific components, ny Y-specific components

O2PLS R package: Overview

- ▶ Input data X and Y, rows are **the same** subjects
- Number of components n, nx and ny.
 - ► Main fitting function o2m(X, Y, n, nx, ny)
 - Simultaneous estimation of all components per part
 - Stripped version is also present: stripped = TRUE
 - Automatic switching to high dimensional mode with p_thresh = 3000
 - ► Output: list of class o2m
- print/plot/summary/predict/loadings: see help("___.o2m", "O2PLS")
- ► For a complete overview: ?02PLS

Data to be analyzed

- ► DILGOM population study
- Gene expression (p = 6272)
- ► Metabolites (*q* = 137)
- ightharpoonup N = 191 participants

Data analysis

- Install from Github with devtools:
- devtools::install_github("selbouhaddani/02PLS",
 ref = "Upgrade")
- ▶ library(O2PLS)
- Fit O2PLS: X = RNA, Y = Metabolites
- ▶ Low dimensional mode, since q < 3000.

```
fit <-o2m(X, Y, n = 1, nx = 8, ny = 1)
```

▶ Number of components chosen with cross-validation, see paper



Inspecting the results

fit

- > O2PLS fit
- > with 1 joint components
- > and 8 orthogonal components in X
- > and 1 orthogonal components in Y
- > Elapsed time: 1.41 sec

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Some timings (i5 laptop) with stripped = TRUE

Problem size	Timing Low D	Timing High D
1000 vars	3 sec	15 sec
5000 vars	300 sec	130 sec

Summarizing the results

[TRUNCATED...]

```
summary(fit)
*** Summary of the O2PLS fit ***
- Call: o2m(X = X, Y = Y, n = 1, nx = 8, ny = 1)

    Modeled variation

-- Total variation:
in X: 116016.8
in Y: 2516.821
-- Joint, Orthogonal and Noise as proportions:
          data X data Y
Joint 0.013 0.522
Orthogonal 0.490 0.069
Noise 0.497 0.410
```

Plotting the loadings

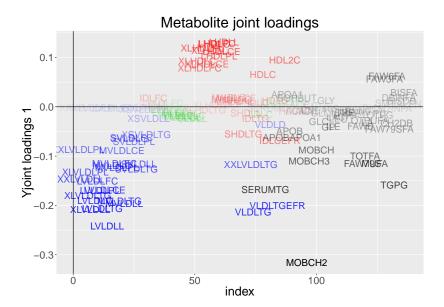
- Plot the loadings: plot(fit, loading_name, i, j, use_ggplot2, label, ...)
- Returns ggplot2 object
- Example: some fancy extra's:

```
alp <- loadings(fit, "Yjoint", 1) %>% abs %>% sqrt
```

cols contains labeling {VLDL, LDL, HDL, other}

```
plot(fit, "Yj", i=1, label = "colnames",
    size = 6, alpha = alp/max(alp), col = cols) +
    theme(text = element_text(size = 22)) +
    ggtitle("Metabolite joint loadings")
```

Previous code results in:



Summary

- O2PLS package for omics data analysis
- ▶ Install via Github: selbouhaddani/O2PLS, branch Upgrade
- Overview of Package: ?02PLS
- ▶ Main function: o2m, see also ?o2m

Future work

- ► Release on CRAN + Vignette!
- ▶ Upgrade (automated and parallelized) cross-validation
- Enhancing plots of loadings/scores

Remarks

- Acknowledgments
 - Geurt Jongbloed, TU Delft
 - Szymon Kielbasa, LUMC
- Try it out in your research!
- Please cite if you use it:

```
citation("O2PLS")
```

```
el Bouhaddani, S., Houwing-duistermaat, J., Jongbloed, G., Salo, P., Perola, M., & Uh, H.-W. (2016).

Evaluation of O2PLS in Omics data integration.

BMC Bioinformatics BMTL Supplement
doi:10.1186/s12859-015-0854-z
```

- ▶ The name *O2PLS* is a registered trademark
- Alternatives:
 - ► A. o2plsR
 - ▶ B. TwOpls
 - ► C. o2pls4Omics
 - ▶ D. OMICSpls

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- Thank you!