Multiblock omics data fusion using the Consensus OPLS R package

Céline Bougel, van Du T. Tran, Julien Boccard, Marie Tremblay-Franco, Florence Mehl

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Introduction

Omics approaches have proven their value in providing a broad monitoring of biological systems. However, despite the wealth of data generated by modern analytical platforms, the analysis of a single dataset is still limited and insufficient to reveal the full biochemical complexity of biological samples. The fusion of information from several data sources constitutes therefore a relevant approach to assessing biochemical events more comprehensively.

However, inherent problems encountered when analysing single tables are amplified with the generation of multi-block datasets. Finding the relationships between data layers of increasing complexity constitutes a challenging task. Here we propose an extension to the versatile methodology combining the strength of established data analysis strategies, multiblock approaches with Orthogonal Partial Least Squares Discriminant analysis (OPLS-DA) framework [1], to offer an efficient tool as an R package for the fusion of Omics data obtained from multiple sources.

Multi-Omics Data Integration

	ConsensusOPLS [1]	KPCA [2]	DIABLO [3]	MOFA [4]
R Package	ConsensusOPLS	kernlab	mixOmics	MOFA2
Aim	Multi-block and multivariate relationship modeling	Dimensionality reduction	Multi-block and multivariate relationship modeling	Identification of common factors
Approach	Consensus Kernel-based OPLS	Kernel-based PCA	Latent projections for integrating multiple omics datasets	Bayesian model to discover shared latent factors
Model type	Supervised (regression or classification)	Unsupervised	Supervised (classification)	Unsupervised
Non-linearity	Yes in kernel	Yes in kernel	No	No
Parameters	Kernel, Cross-validation type	Kernel	Design matrix	Bayesian inference

MATLAB in-house scripts available at GitHub Unige with demo_data [5] — Check here

R package available in CRAN New features — Check here

Upgrades

Kernels non-linear

Multiple predictive components

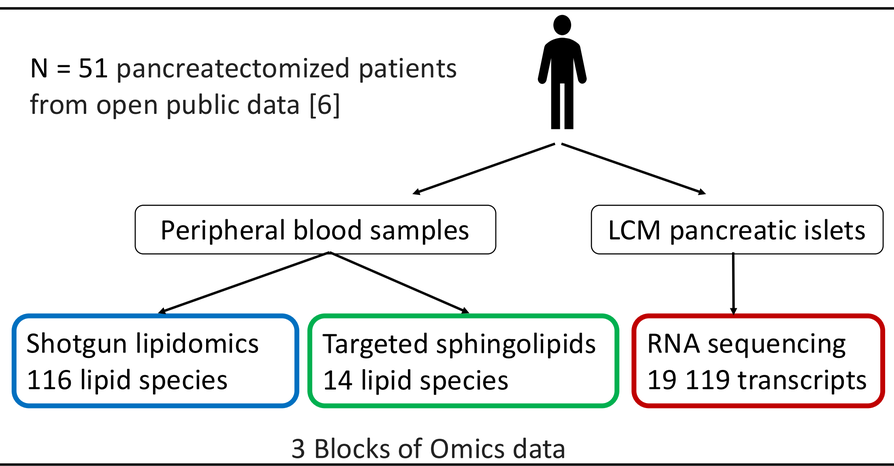
Variable Importance in Projection (VIP)

Prediction of new samples

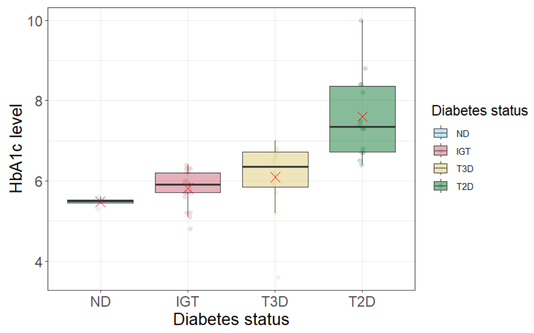
Parallel computing

Use case

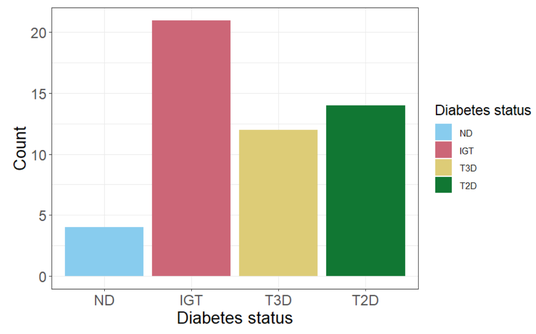
N = 51 pancreatectomized patients from open public data [6]



4 groups of patients based on glycemic values at fasting and at the 2-hour timepoint of an oral glucose tolerance test, using the thresholds defined in the guidelines of the American Diabetes Association :



Non-diabetic (ND);
impaired glucose tolerance (IGT);
type 2 diabetes (T2D);
type 3c diabetes (T3D).



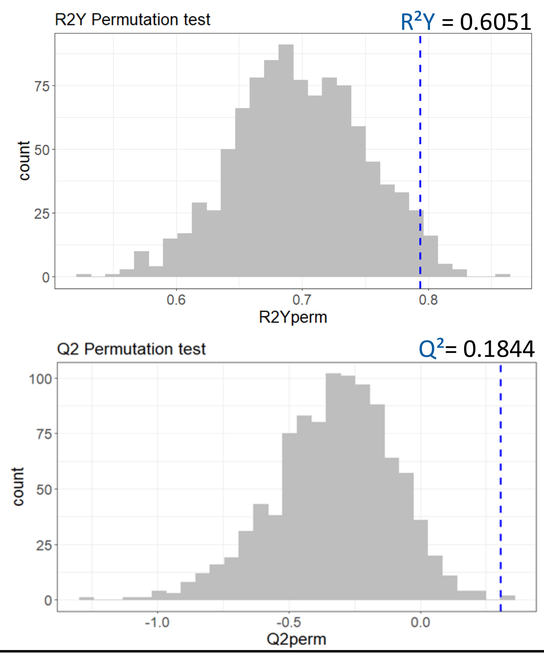
Results and discussion

Model computation

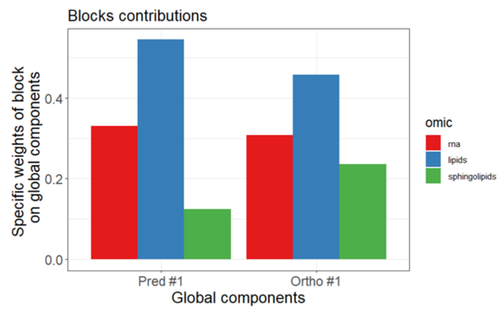
```
COPLS_results <- ConsensusOPLS(
      data         = my_data_with_3_blocs_of_omics_data,
      Y            = response_HbA1c_variable,
      maxPcomp     = 1,        #one predictive component
      maxOcomp     = 1,        #one orthogonal component
      modelType    = "reg",    #regression model
      nperm        = 1000,     #number of permutations
      cvType       = "nfold", #type of cross-validation
      nfold        = 51,       # number of subjects = leave-one-out
      kernelParams = list(type = "p",
                          params = c(order = 1)),
                          #linear polynomial kernel
      mc.cores     = 1         #How many cores for parallelization
)
```

Quality assessment

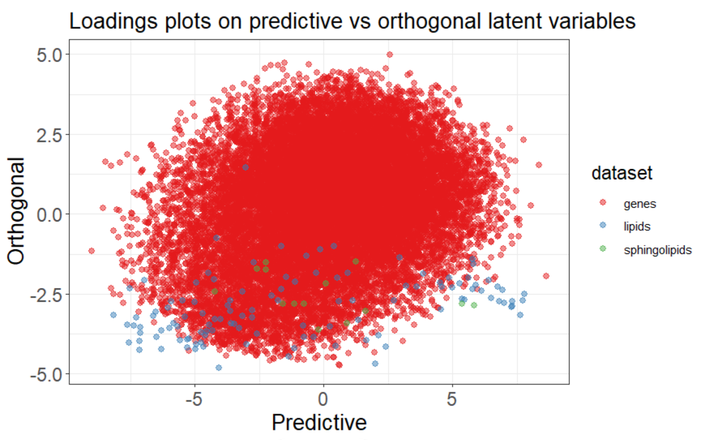
1000 models are computed with pemuted Y values. The results of the optimal model are significantly different from the results of the permuted models.

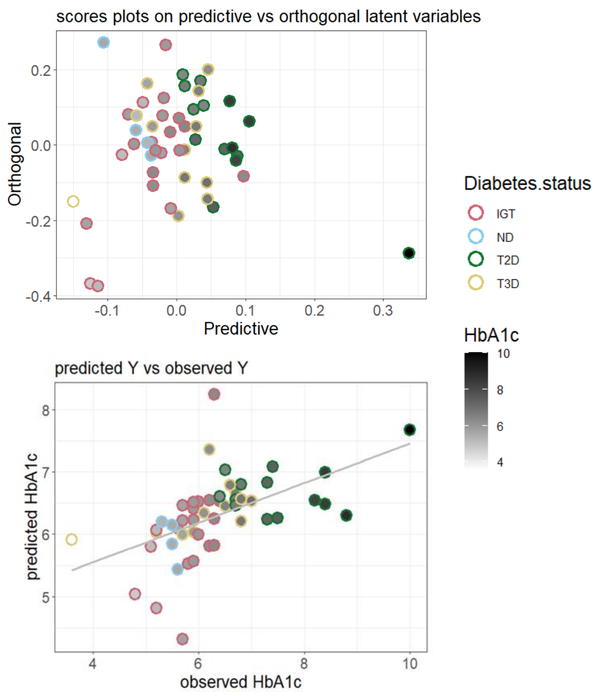


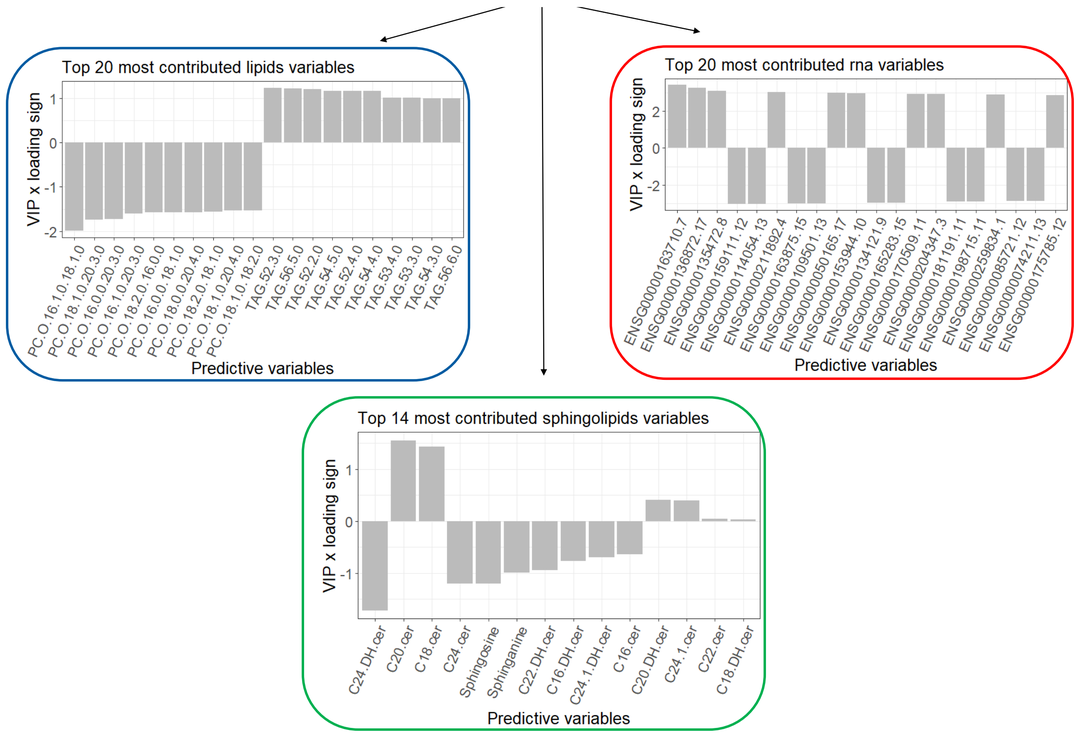
Regression Analysis (ConsensusOPLS-reg) of HbA1c levels



The 3 omics contribute to the modelization of HbA1c levels. The untargeted lipidomics dataset brings the largest part of the information.







Conclusions

The **ConsensusOPLS R package** proposes a **free**, **open-source,** and **easy-to-use software** for the Consensus OPLS method, which was demonstrated as a **relevant and widely applicable** method for the **horizontal integration of omics data**, with multiple functionality upgrades.

References

The **ConsensusOPLS R package** is available at https://CRAN.R-project.org/package=ConsensusOPLS.

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