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# Multiblock omics data fusion using the Consensus OPLS R package



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## Introduction

Omic 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



Check here MATLAB in-house scripts available at [GitHub Unige](#) with demo\_data [5]

R package available in [CRAN](#) New features



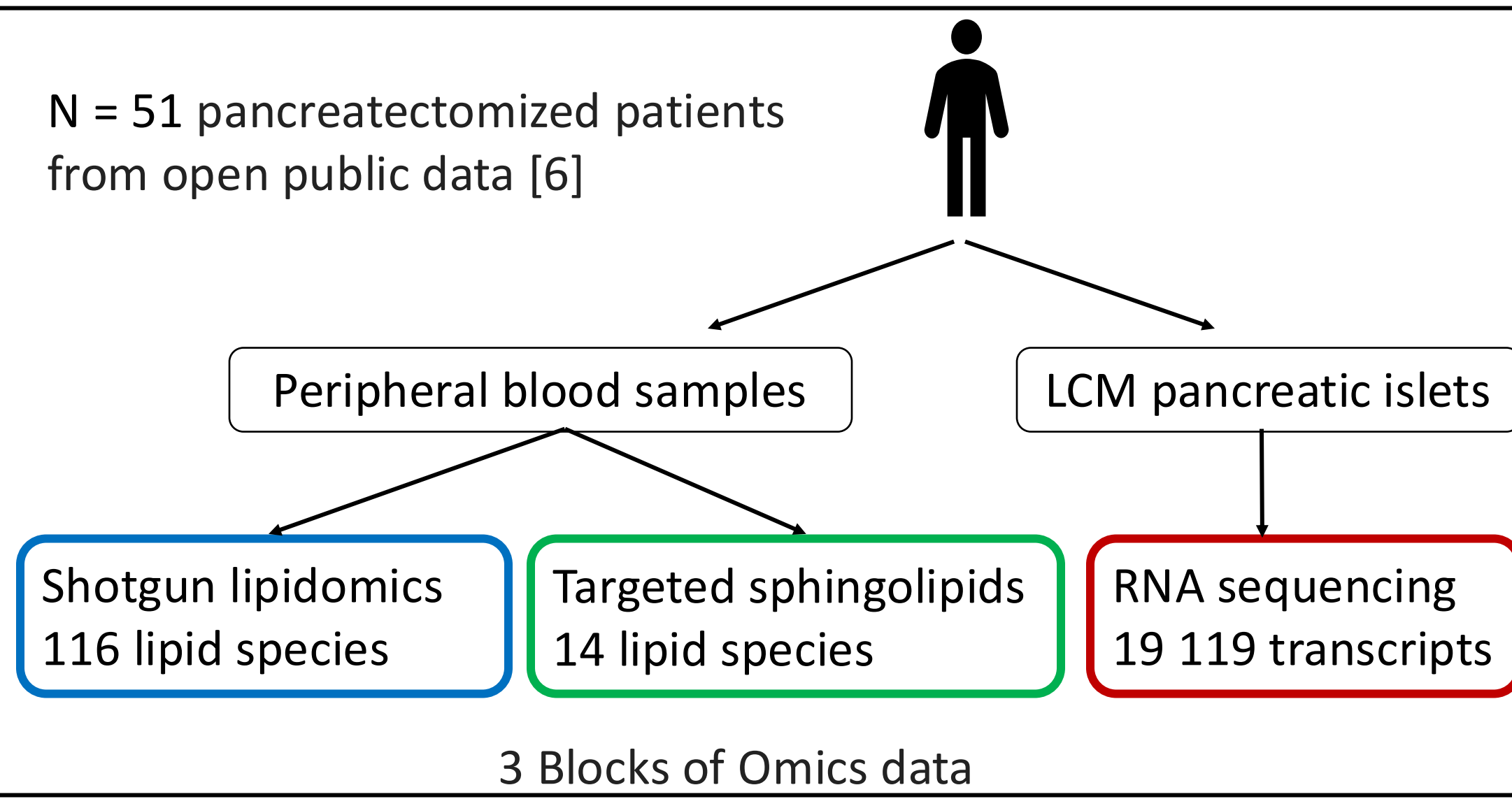
## Upgrades

Kernels non-linear  
Multiple predictive components

Variable Importance in Projection (VIP)  
Prediction of new samples

Parallel computing

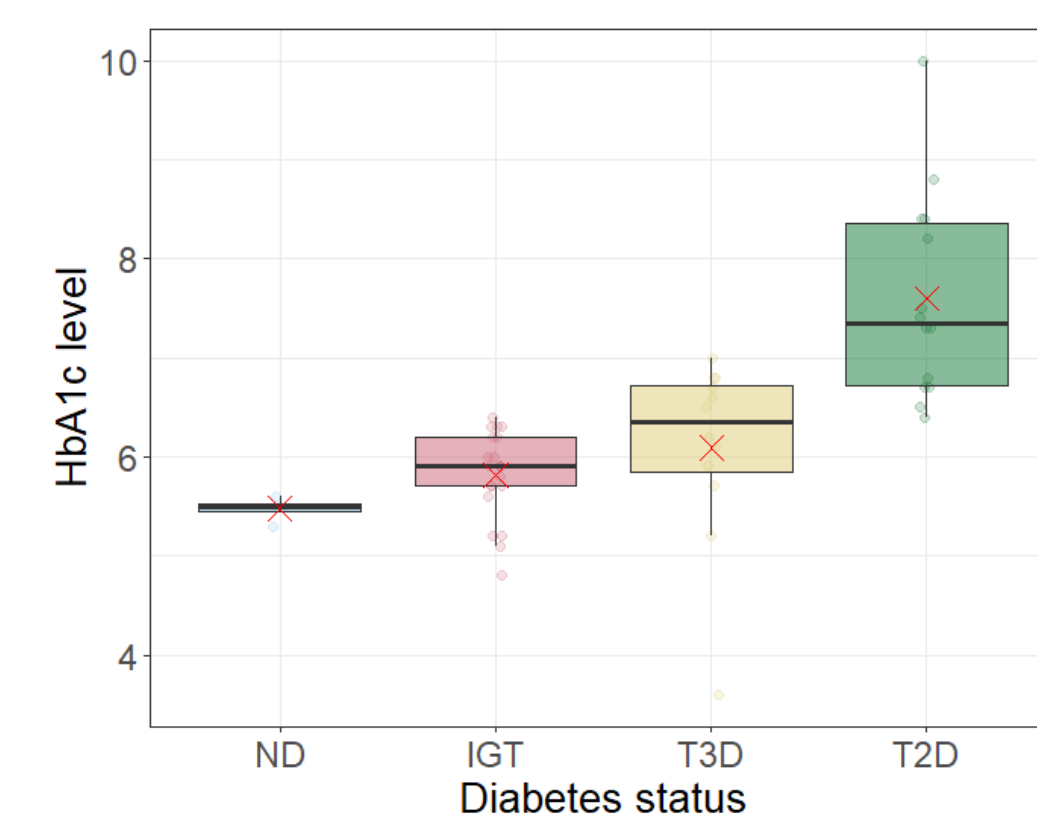
N = 51 pancreatomectomized patients from open public data [6]



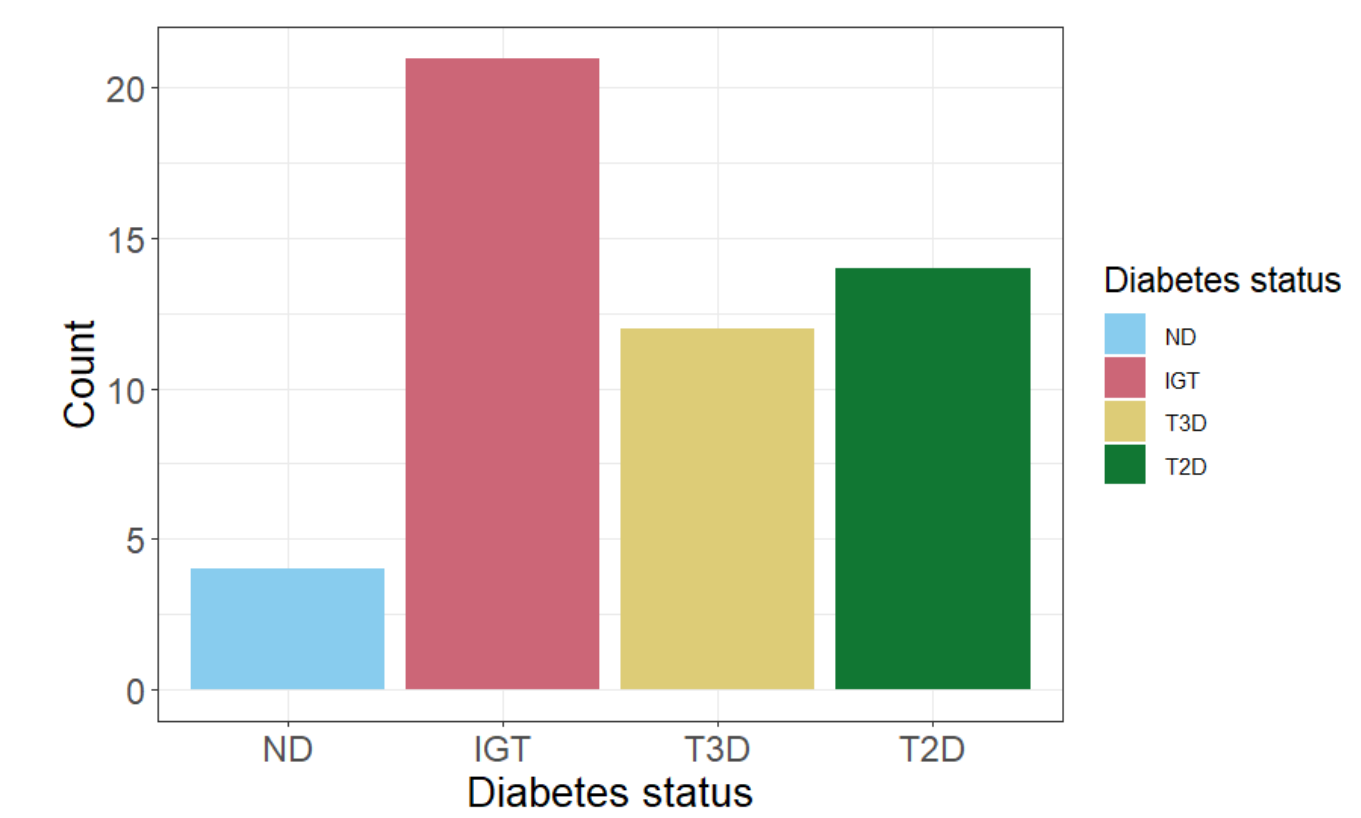
3 Blocks of Omics data

## Use case

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).



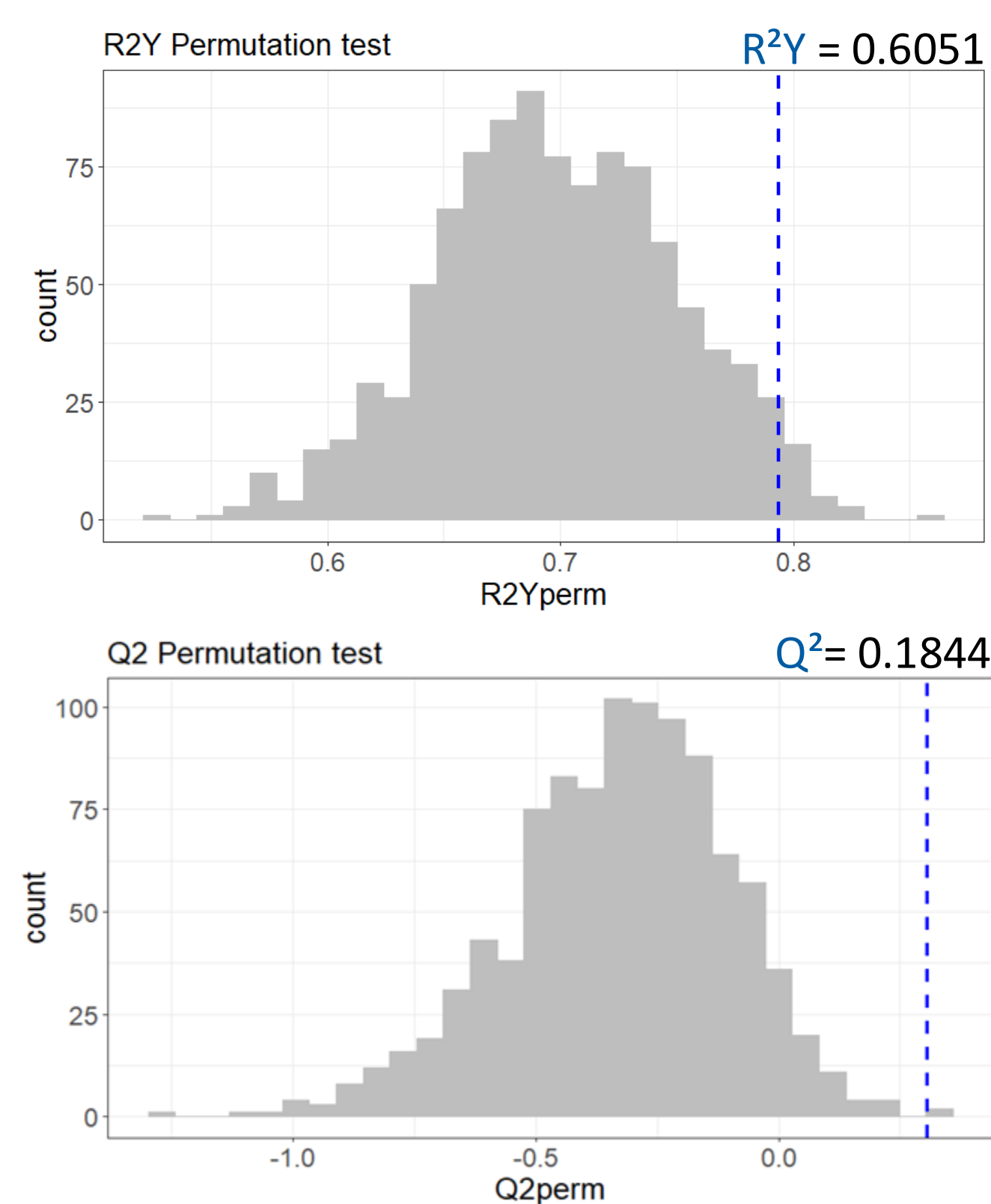
## Results and discussion

### Model computation

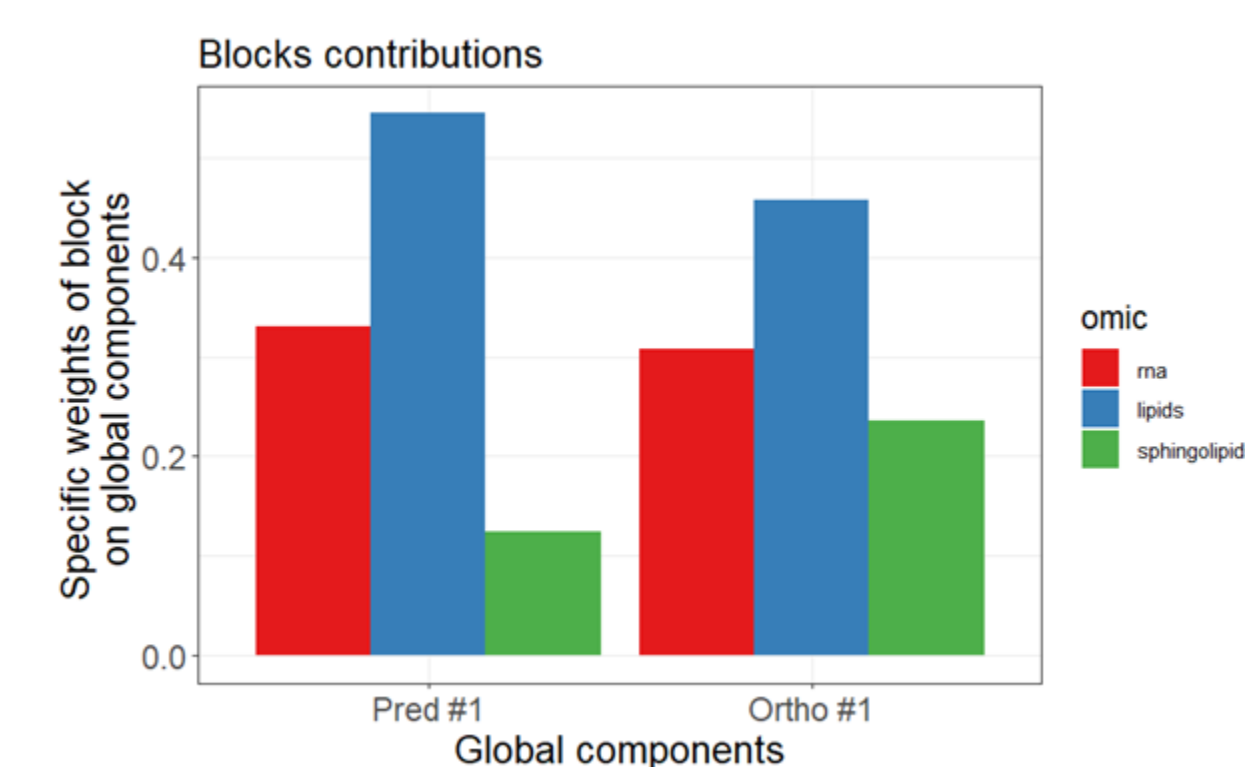
```
COPLS_results <- ConsensusOPLS(
  data = my_data_with_3_blocks_of_omics_data,
  y = response_HbA1c_variable,
  maxComp = 1, #one predictive component
  maxOrthoComp = 1, #one orthogonal component
  modelType = "reg", #regression model
  nperm = 1000, #number of permutations
  cvType = "nfold", #type of cross-validation
  nfold = 5, #number of subjects = leave-one-out
  kernelParams = list(type = "p",
    params = c(order = 1)),
  mc.cores = 1 #how many cores for parallelization
)
```

### Quality assessment

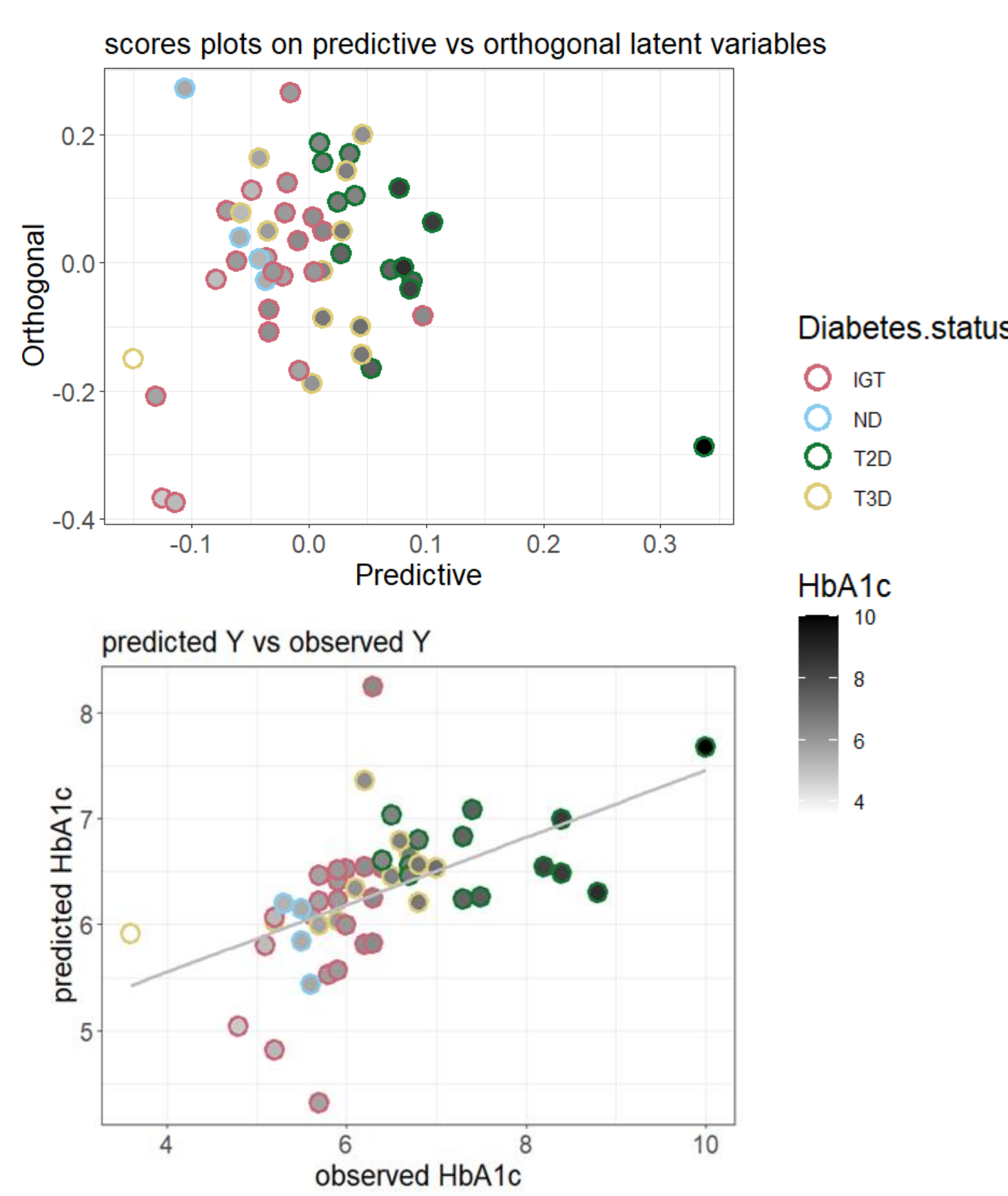
1000 models are computed with permuted Y values. The results of the optimal model are significantly different from the results of the permuted models.



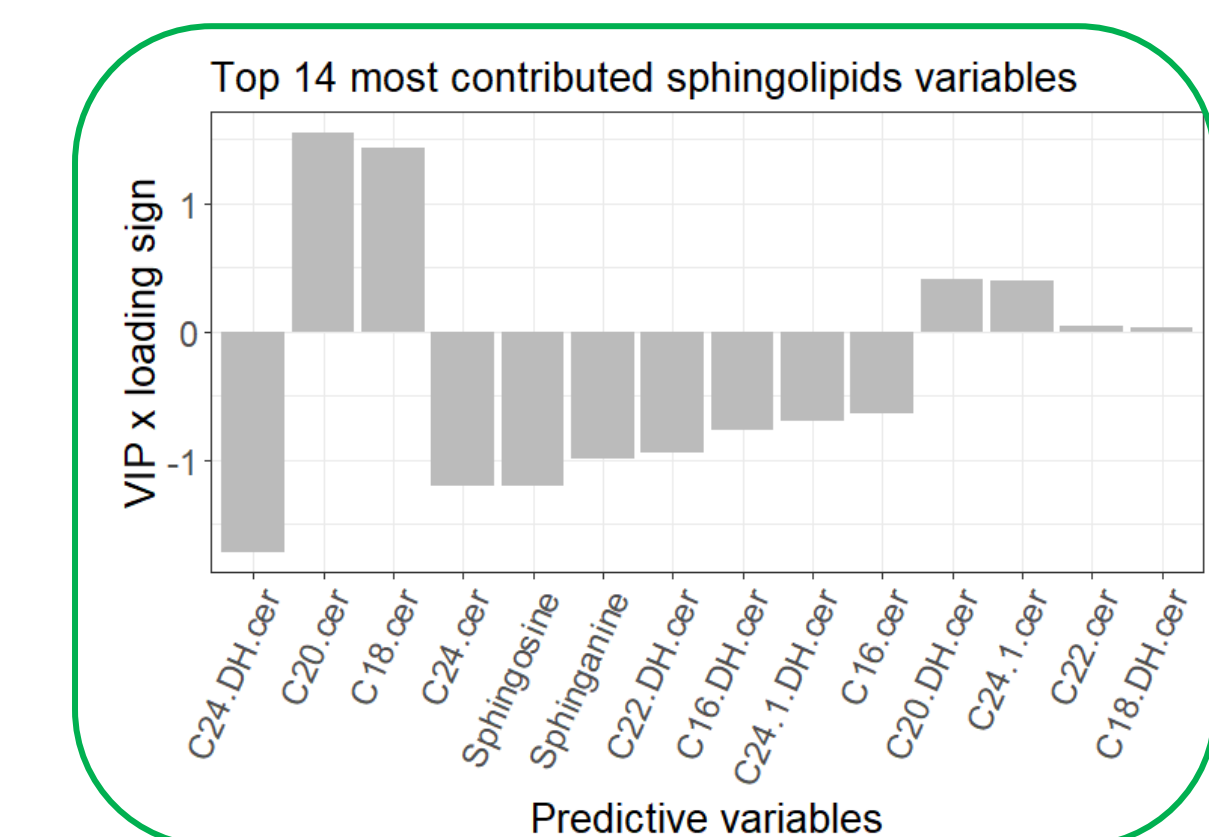
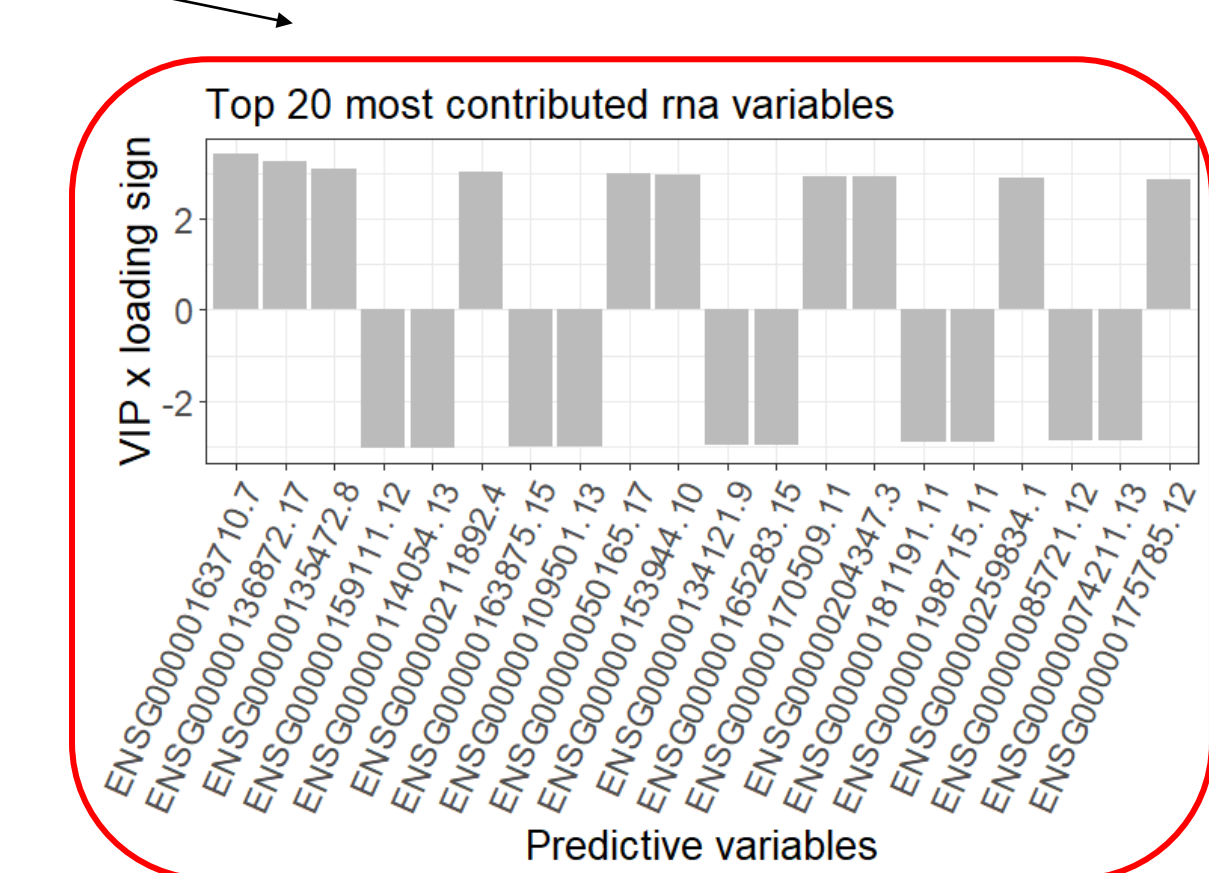
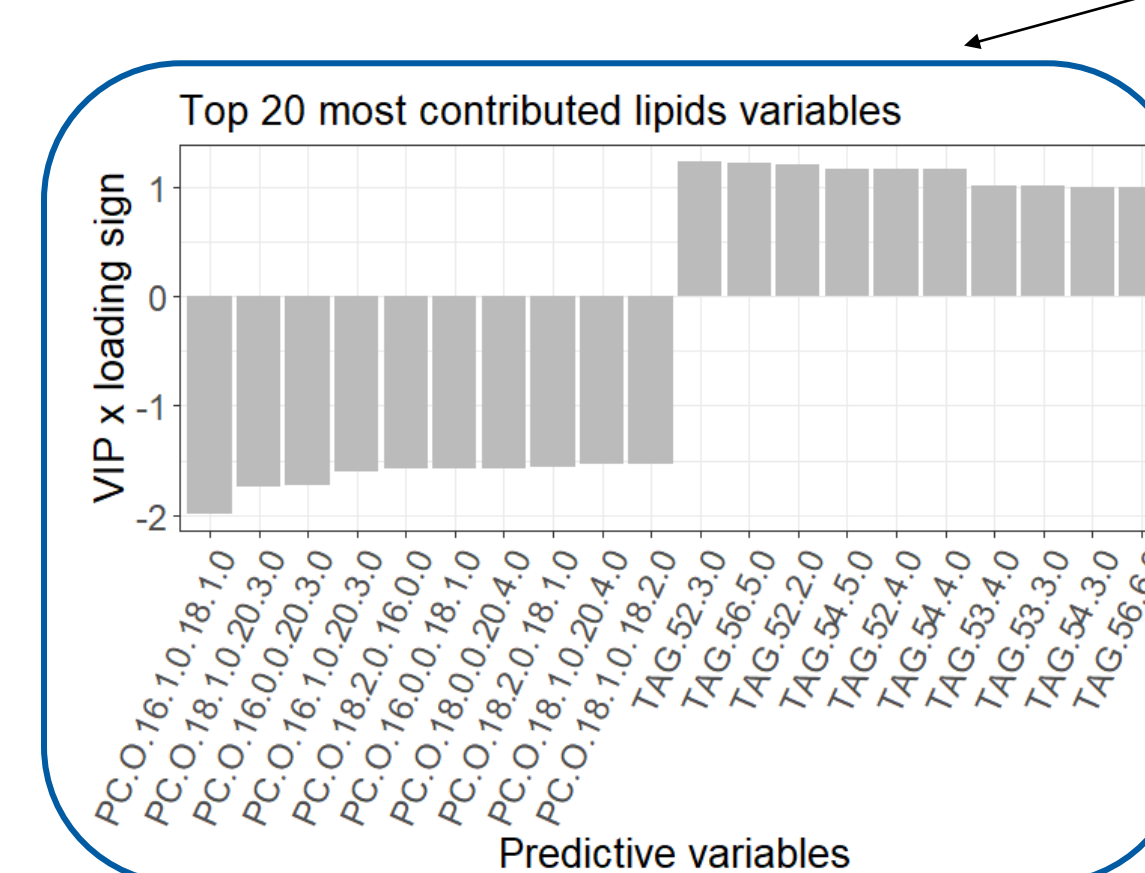
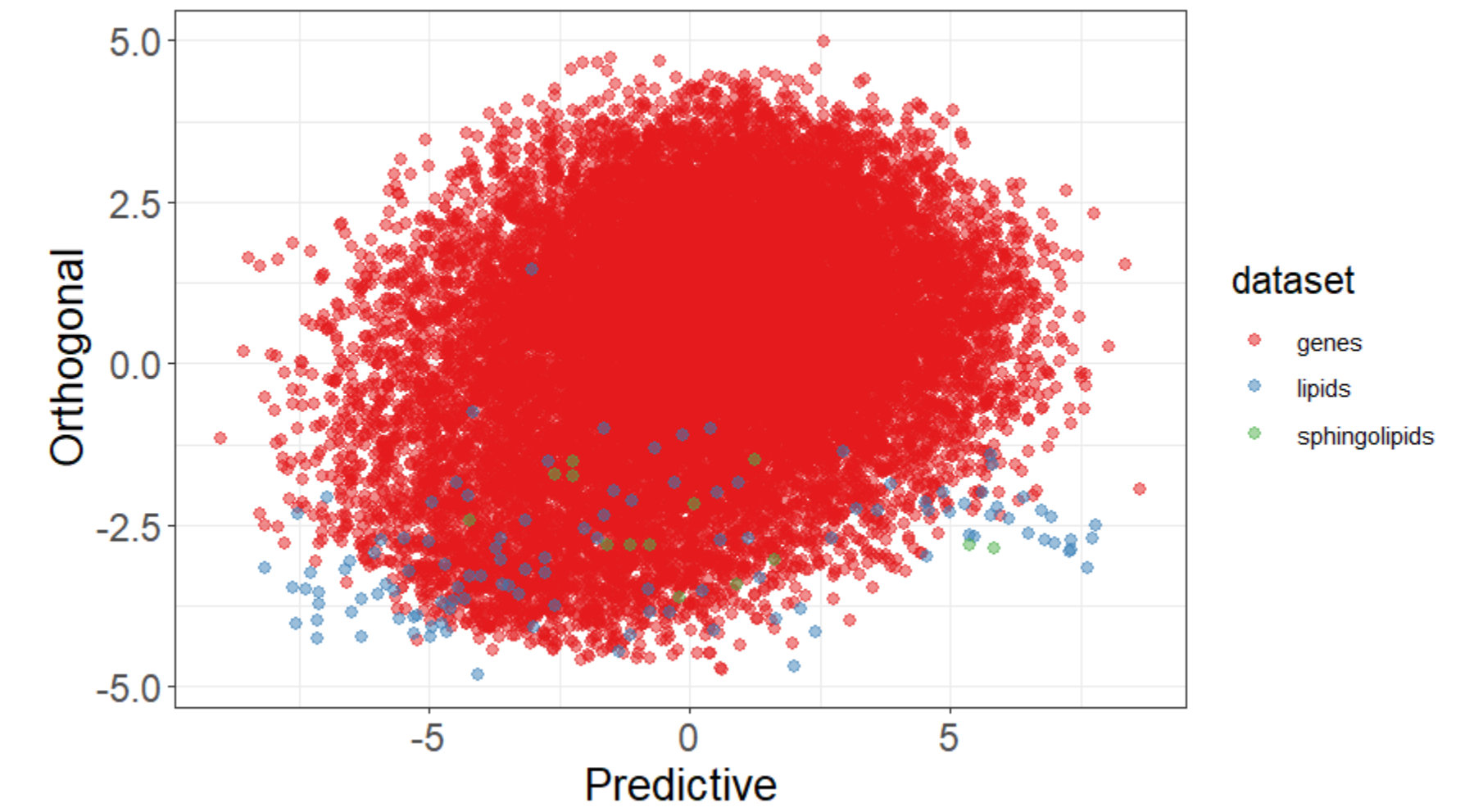
### Regression Analysis (ConsensusOPLS-reg) of HbA1c levels



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



### Loadings plots on predictive vs orthogonal latent variables



## 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

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