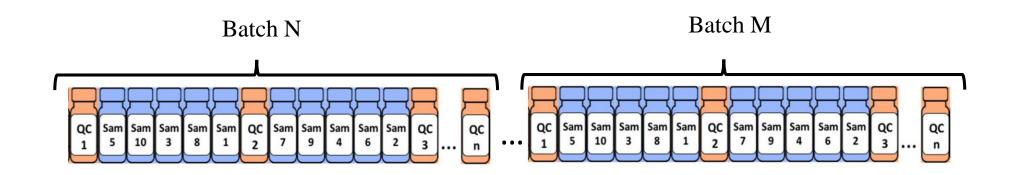
Application of gradient boosting machine for signal processing in LC-MS metabolomics

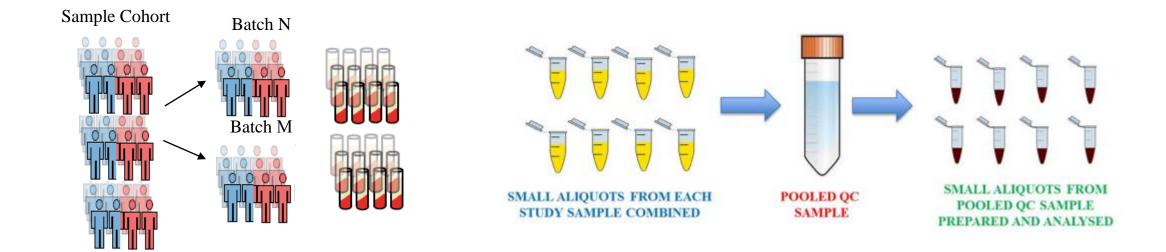
I. V. Plyushchenko*, I. A. Rodin

Chemistry Department, Lomonosov Moscow State University, Moscow 119991, Russia

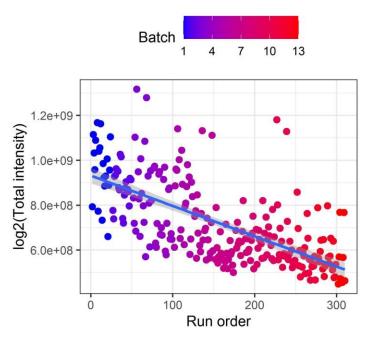
*e-mail: plyushchenko.ivan@gmail.com

Batch (Sequence) in LC-MS Untargeted Metabolomics

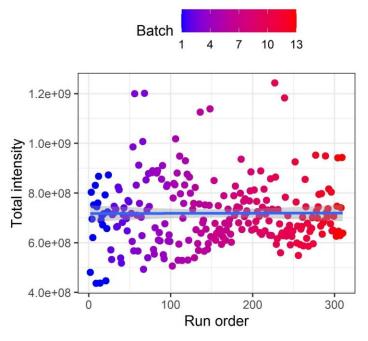




Signal Drift



Raw data



After correction

Signal Correction

$$M_i = f_{i,QC} (y_{i,QC} \sim x_{i,QC}) \qquad (1)$$

$$F_i = M_i(x_i) \tag{2}$$

$$I_i' = \frac{I_i}{F_i} 1000 \tag{3}$$

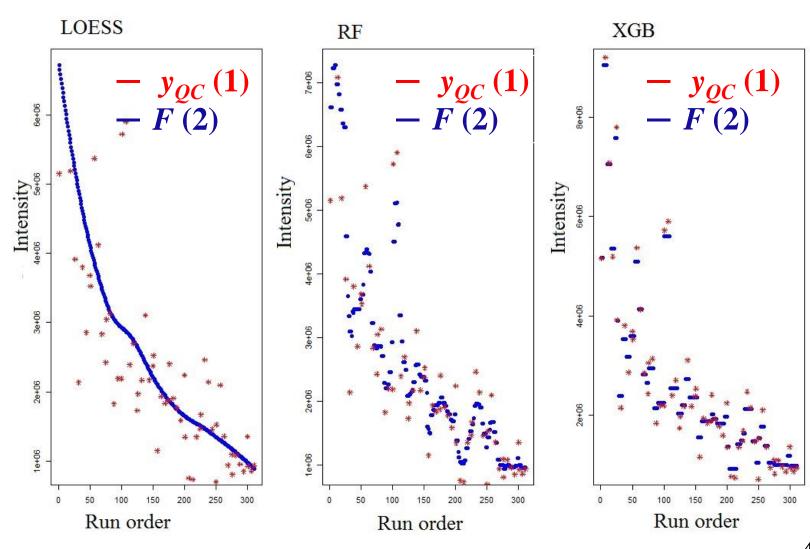
where i is the index of metabolite, QC is the index of QC samples (all study samples are denoted without this index),

M is a machine learning model, that is fitted by function f,

y is an intensity vector (dependent variable), x is a run order vector (independent variable),

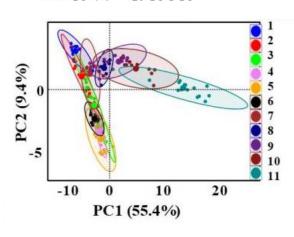
F is a vector of predicted values by the model M (correction factor),

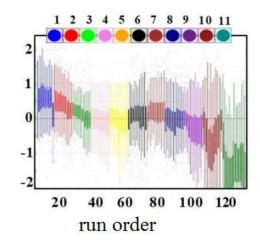
I' is a vector of corrected intensity values,I is a vector of original intensity values.

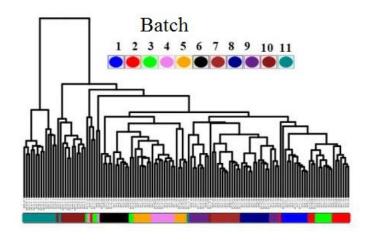


Batch Effect

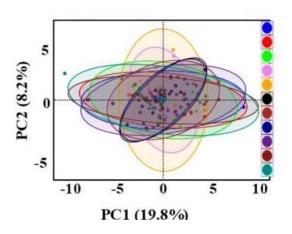
Raw data

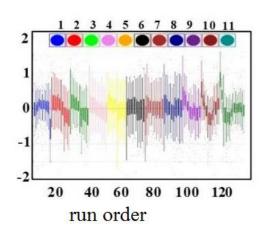


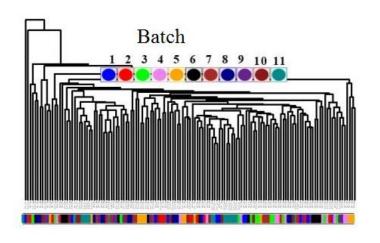




After correction



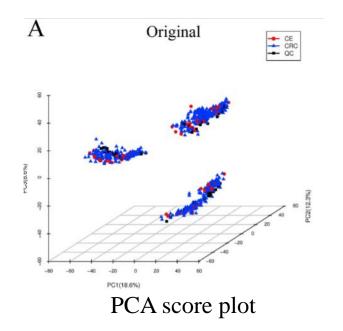




Test data

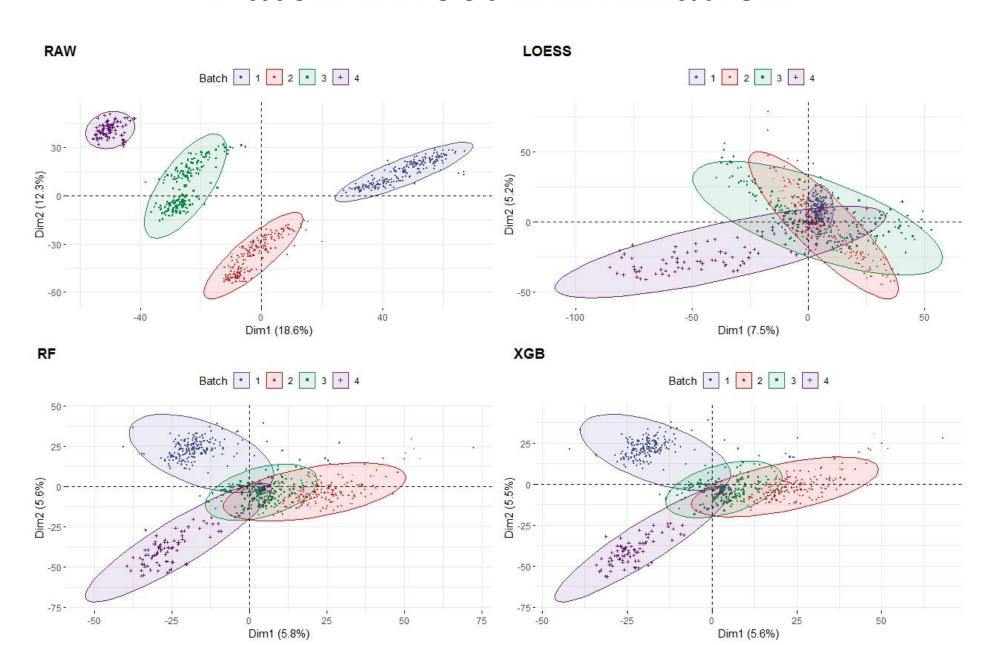
Amide [1] metabolomics dataset

Batch	Number of samples	Number of features
4	729	6969

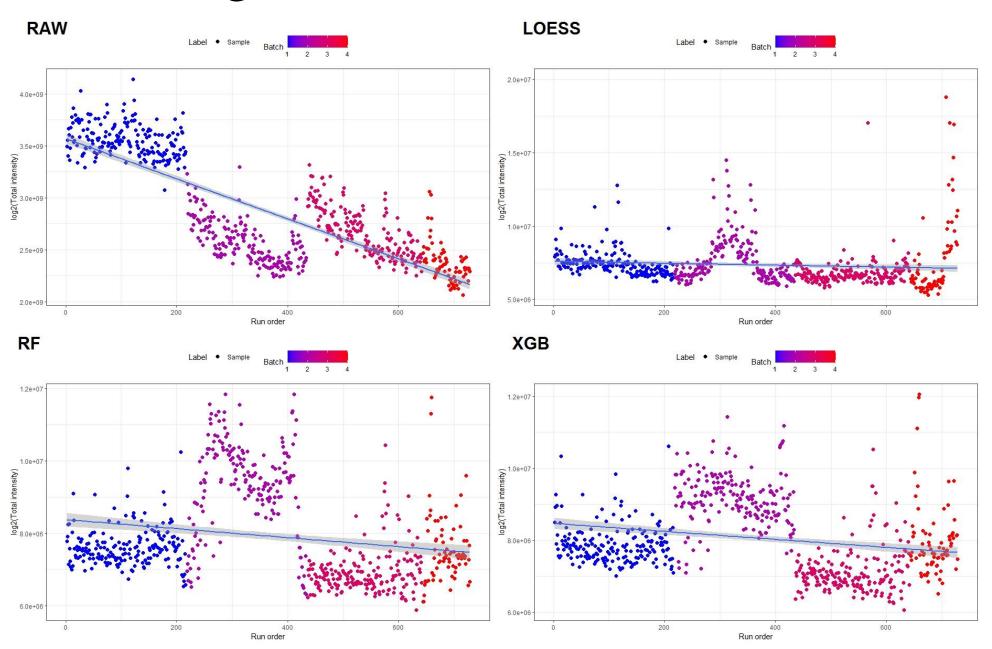


1. Deng K., Zhang F., Tan Q., Huang Y., Song W., Rong Z., Zhu Z.-J., Li K., Li Z. Anal. Chim. Acta. 1061 (2019), 60–69.

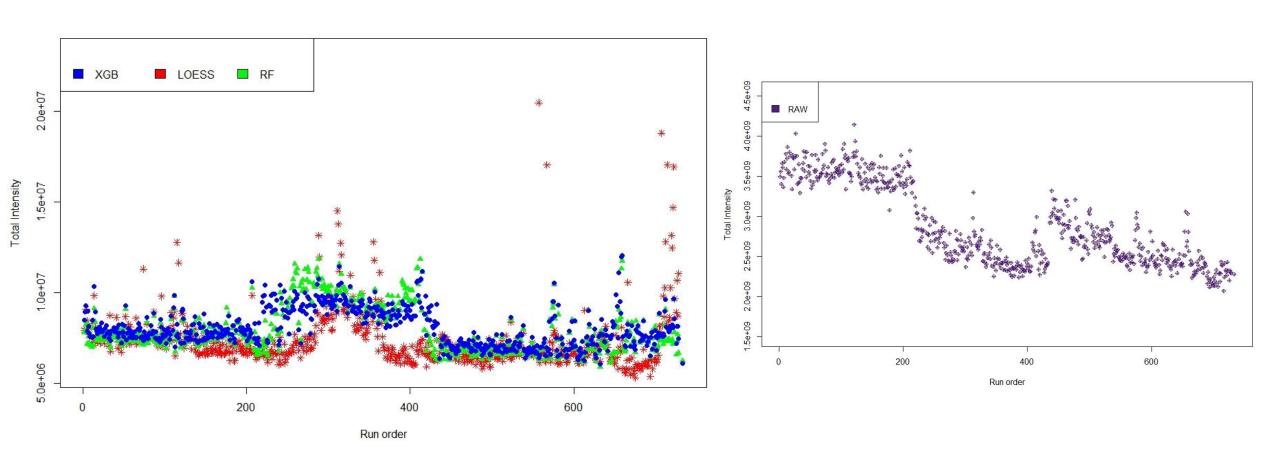
Batch Effect Elimination



Signal Drift Elimination



Signal Drift Elimination



Reference, code availability

Journal of Proteome Research (2021)

Omics Untargeted Key Script: R-Based Software Toolbox for Untargeted Metabolomics with Bladder Cancer Biomarkers Discovery Case Study

Plyushchenko, Ivan V.; Fedorova, Elizaveta S.; Potoldykova, Natalia V.; Polyakovskiy, Konstantin A.; Glukhov, Alexander I.; Rodin, Igor A.



QC-XGB:

https://github.com/plyush1993/OUKS/blob/5140dd 7af725e90abde166312d197409bb210239/Scripts%2 0(R)/4.%20Correction.R#L1005-L1272

