

Computational stratification and subtyping on NAFLD liver lipidomics

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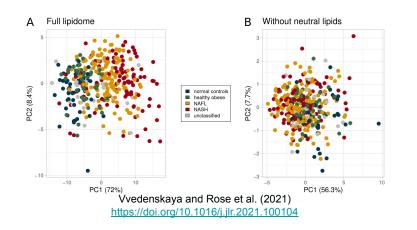
1st International Lipidomics Society annual conference and 7th Lipidomics Forum

bidt-Junior Research Group LipiTUM Chair of Experimental Bioinformatics TUM School of Life Sciences Weihenstephan Technical University of Munich Germany



Computational analysis of NAFLD liver lipidomics

- Liver lipidomics of 365 patients
- Quantified 316 lipid species
 - From 22 lipid classes

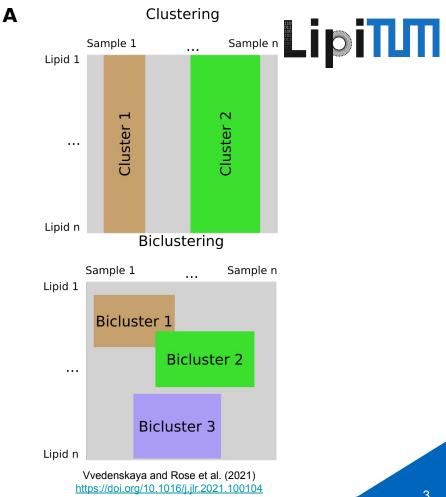


• How can we access the lipidome beyond neutral lipids?

- Novel workflow to access clinical (lipid-) omics data
 - Based on biclustering

Why biclustering?

- Clustering finds sample groups
 - Based on all features 0
 - Global similarity 0
- Biclustering extracts sample subgroups & molecular signatures
 - Disease phenotype usually manifested in Ο local pathway alterations
 - More suitable for disease subtyping Ο

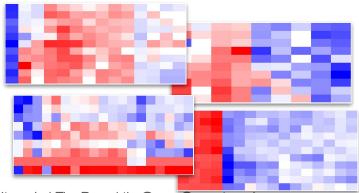


Application of biclustering in practice



- Many biclustering algorithms available
- Different objectives and heuristics
- Extensive parameterization necessary

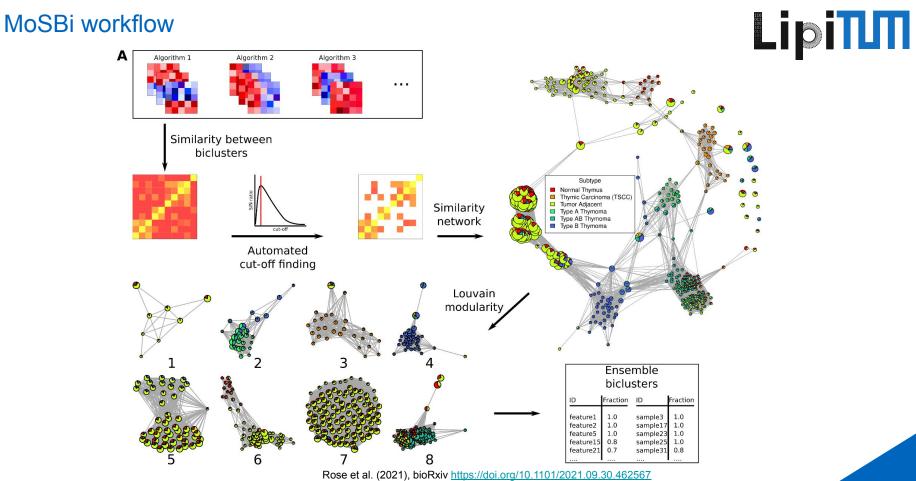
• Which algorithm should be used?



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Molecular signatures from Biclustering - MoSBi

- Ensemble biclustering method
 - Commonly used in machine learning
- Integrating the results of multiple biclustering algorithms
 - More robust predictions
 - Overcoming specificities of single algorithms

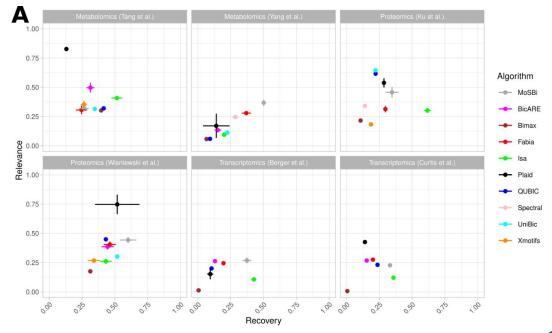


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MoSBi performance



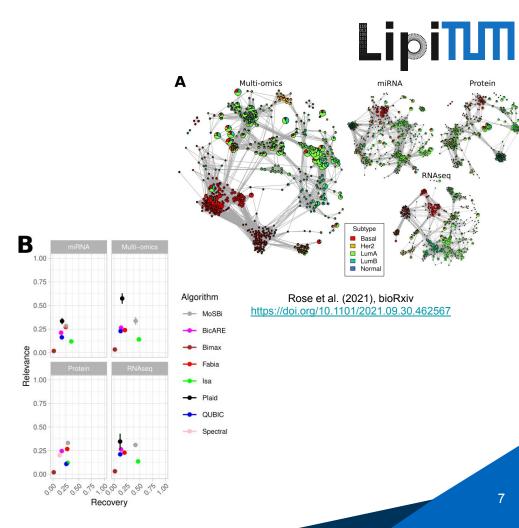
- Algorithm performance on cancer *omics* studies
 - Robust results of MoSBi
 - Heterogeneous outcomes of most algorithms
- Metrics:
 - Relevance: predicted biclusters correspond to known labels
 - Recovery: labels were recovered by predictions



Rose et al. (2021), bioRxiv https://doi.org/10.1101/2021.09.30.462567

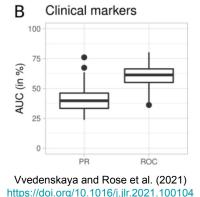
MoSBi in for multi-omics

- TCGA breast cancer data
- 484 samples with miRNA, RNAseq & Protein data
 - Analyzed independently and 0 combined

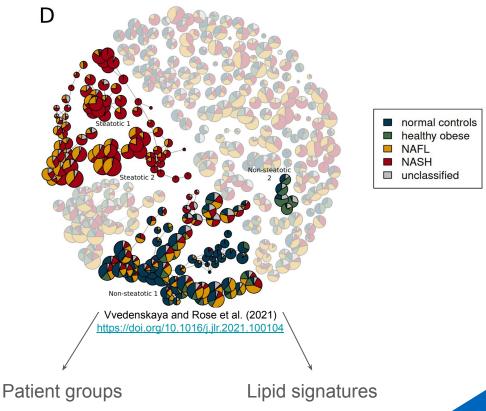


Back to non-alcoholic fatty liver disease





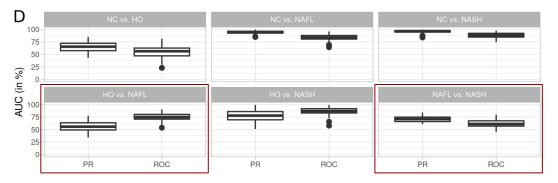
- Biclustering on clinical NAFL
 - lipidomics
- Network communities enriched of steatotic and non-steatotic samples

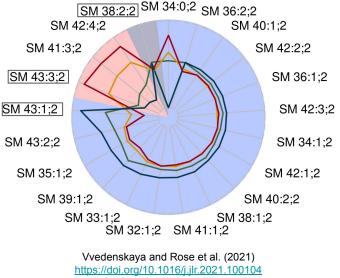


Lipid signatures



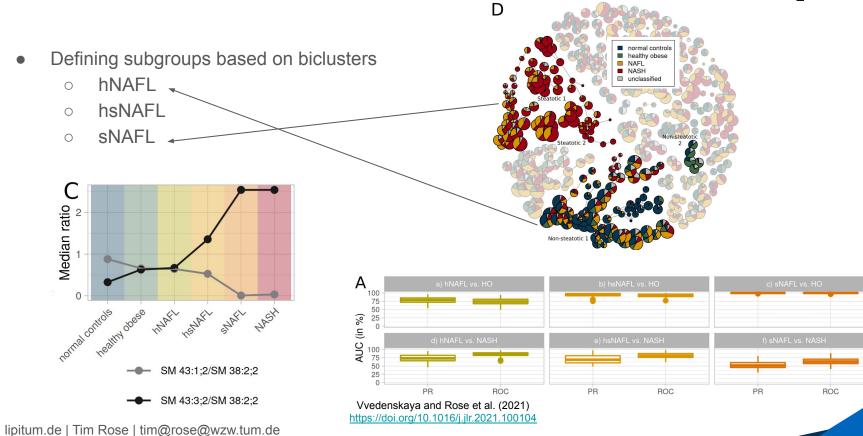
- Bi-directional SM changes
- SM ratios for disease classification
 - Problems with HO vs. NAFL & NAFL vs.
 NASH classifications





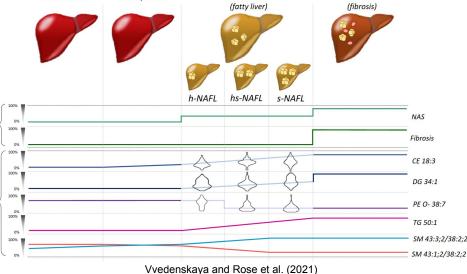
Subgrouping





Conclusion

- Novel biclustering-based stratification method
 - Available as web-app (<u>https://exbio.wzw.tum.de/mosbi/</u>) and R package
 Available as web-app (<u>https://exbio.wzw.tum.de/mosbi/</u>) and R
- Successful application in NAFLD liver lipidomics
- Identified NAFL subgroups with bi-directional SM alterations



NAFL

Healthy Obese

Normal control

Lipid markers

https://doi.org/10.1016/j.jlr.2021.100104



NASH

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Link to slides, workshop, web-app & publications: https://exbio.wzw.tum.de/ils2021



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CBG Max Planck Institute of Molecular Cell Biology and Genetics







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