

Statistical Integration of 'Omics Data Increases Biological Knowledge Extracted from Metabolomics Data: Application to Intestinal Exposure to the Mycotoxin Deoxynivalenol

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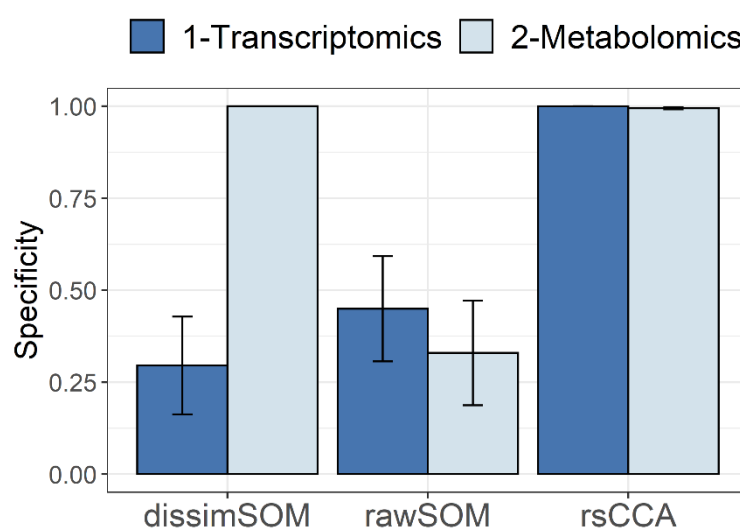


Figure S1. Average specificity of SOM (dissimilarity kernel-based and raw) and Robust Sparse CCA methods calculated for transcriptomic (middle blue bars) and metabolomic (light blue bars) blocks. One hundred Monte Carlo simulations.

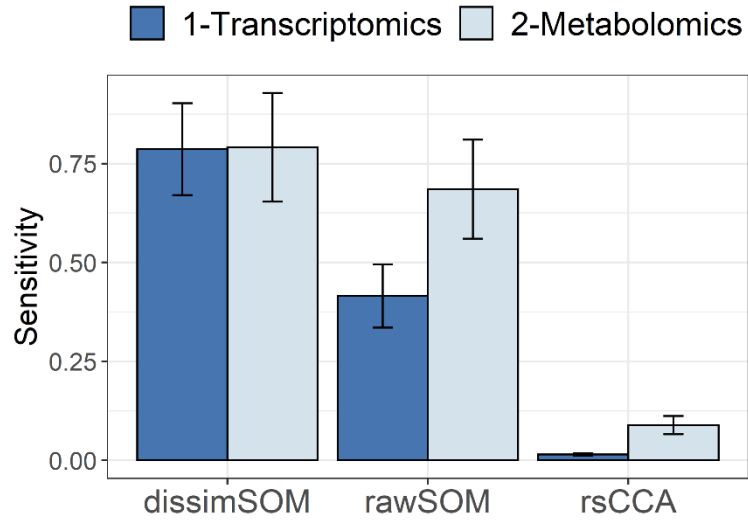


Figure S2. Average sensitivity of SOM (dissimilarity kernel-based and raw) and Robust Sparse CCA methods calculated for transcriptomic (middle blue bars) and metabolomic (light blue bars) blocks. One hundred Monte Carlo simulations.

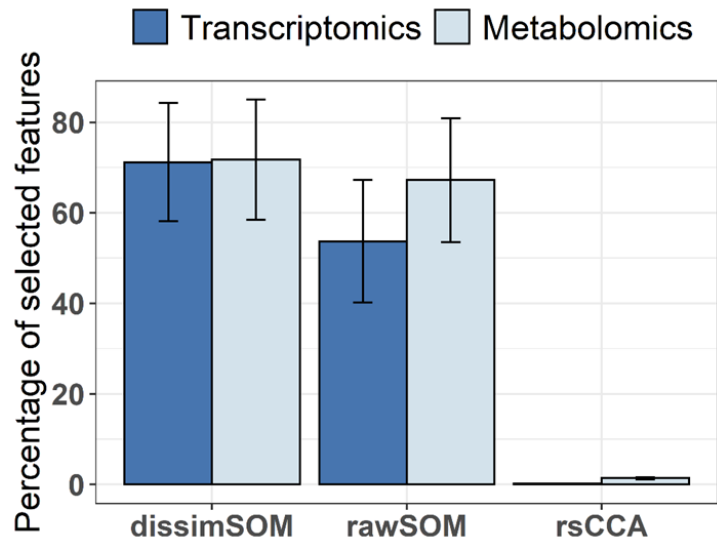


Figure S3. Average percentage of features selected by SOM (dissimilarity kernel-based and raw) and Robust Sparse CCA methods for transcriptomic (middle blue bars) and metabolomic (light blue bars) blocks. One hundred Monte Carlo simulations.