

Supplementary Figures for Revealing Subject-specific Temporal Patterns from Longitudinal Data

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1 Metabolomics

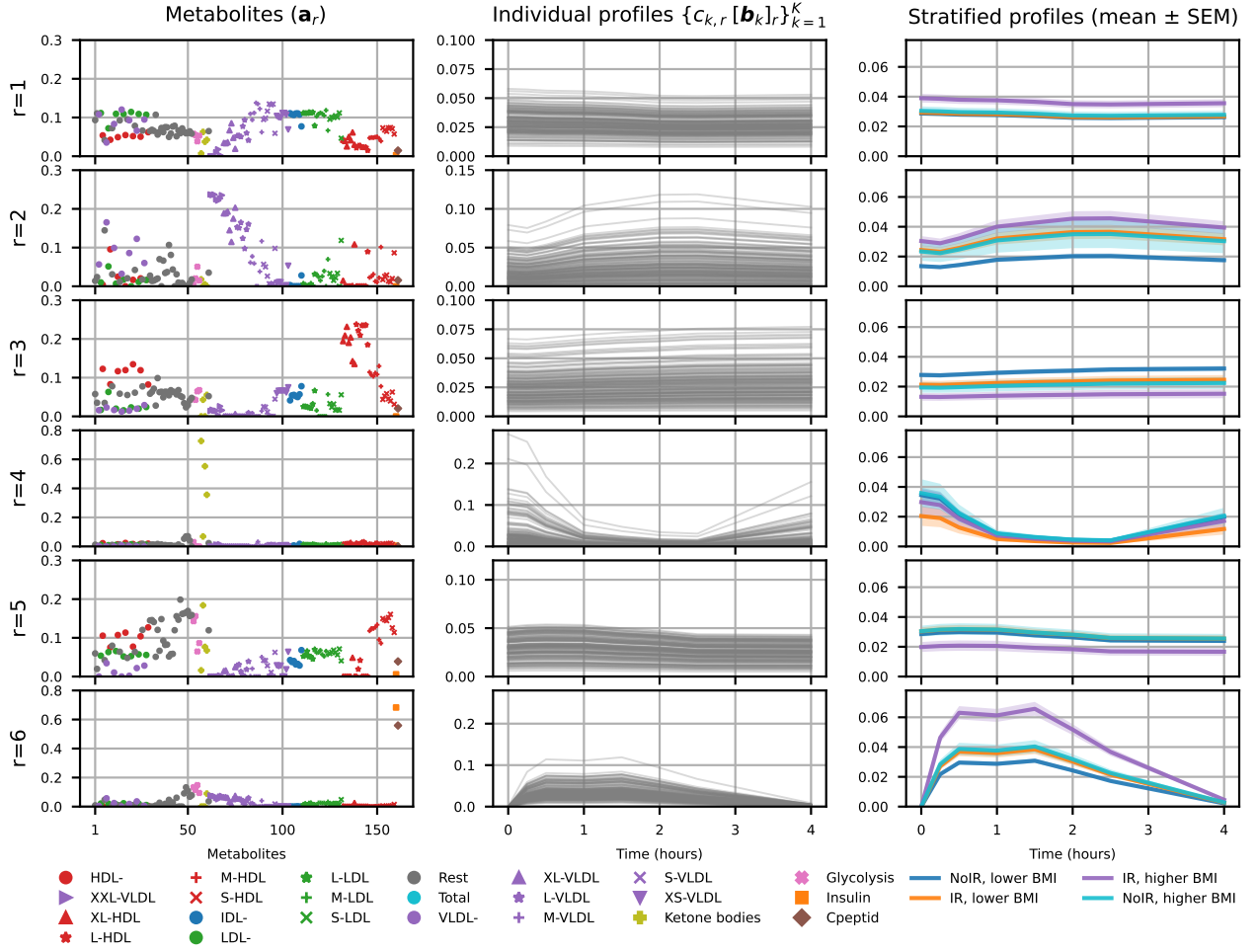


Figure S.1: Metabolomics. Components of a 6-component CP model (with nonnegativity constraints in all modes) of the metabolomics data from males. \mathbf{a}_r denotes the pattern in the metabolites mode, where metabolites are colored by lipoprotein classes. Different shapes are used for lipoprotein subclasses. Subject-specific time profiles scaled by the corresponding subject scores, i.e., $c_{k,r}[\mathbf{b}_k]_r$ for each component are shown in the middle column. The last column shows scaled subject-specific time profiles colored according to four BMI/IR groups.

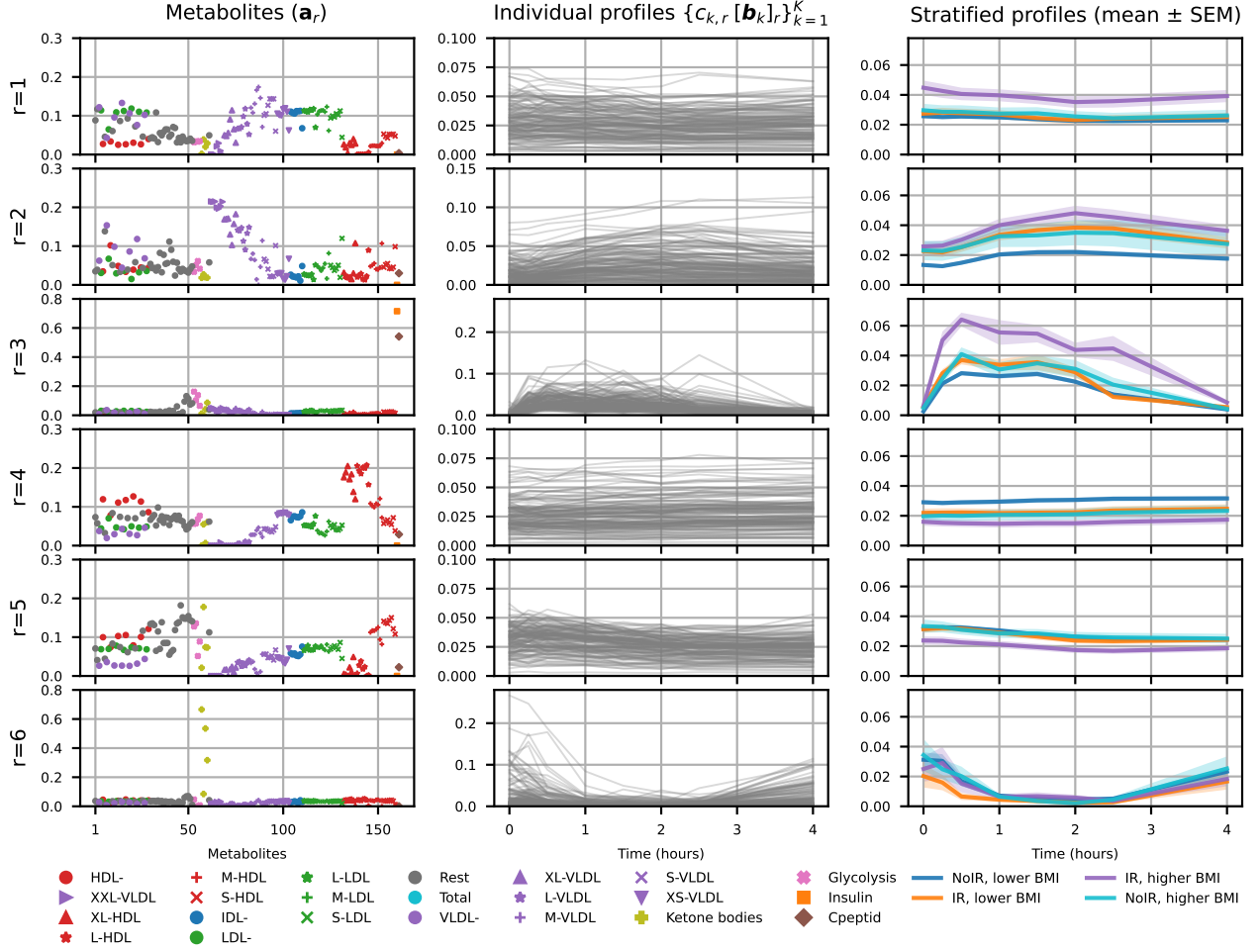


Figure S.2: Metabolomics. Components of a 6-component PARAFAC2 model (with nonnegativity constraints in all modes) of the metabolomics data from males. \mathbf{a}_r denotes the pattern in the metabolites mode, where metabolites are colored by lipoprotein classes. Different shapes are used for lipoprotein subclasses. Subject-specific time profiles scaled by the corresponding subject scores, i.e., $c_{k,r}[\mathbf{b}_k]_r$ for each component are shown in the middle column. The last column shows scaled subject-specific time profiles colored according to four BMI/IR groups.

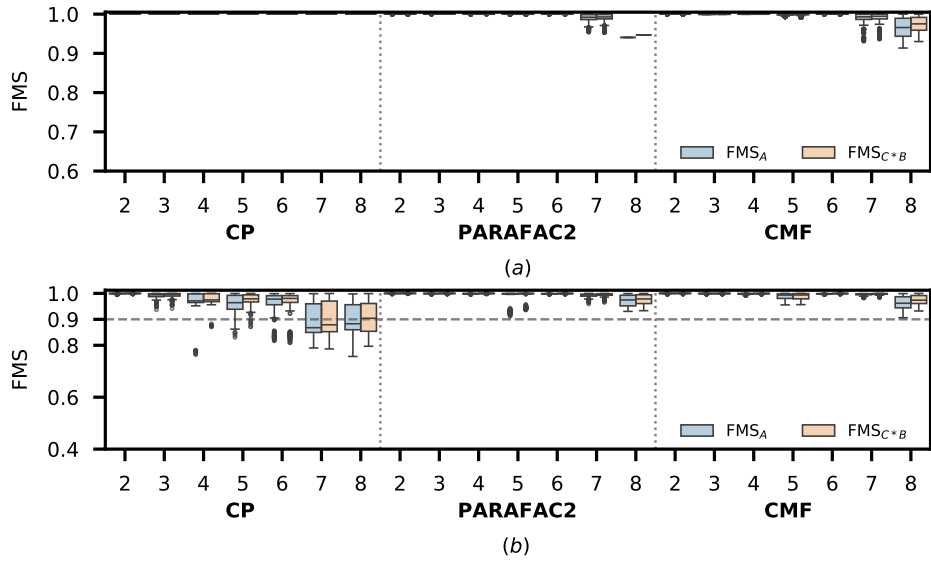


Figure S.3: (a) Reproducibility, and (b) Replicability of different models of the metabolomics data using different number of components (R) for the subset of the female subjects.

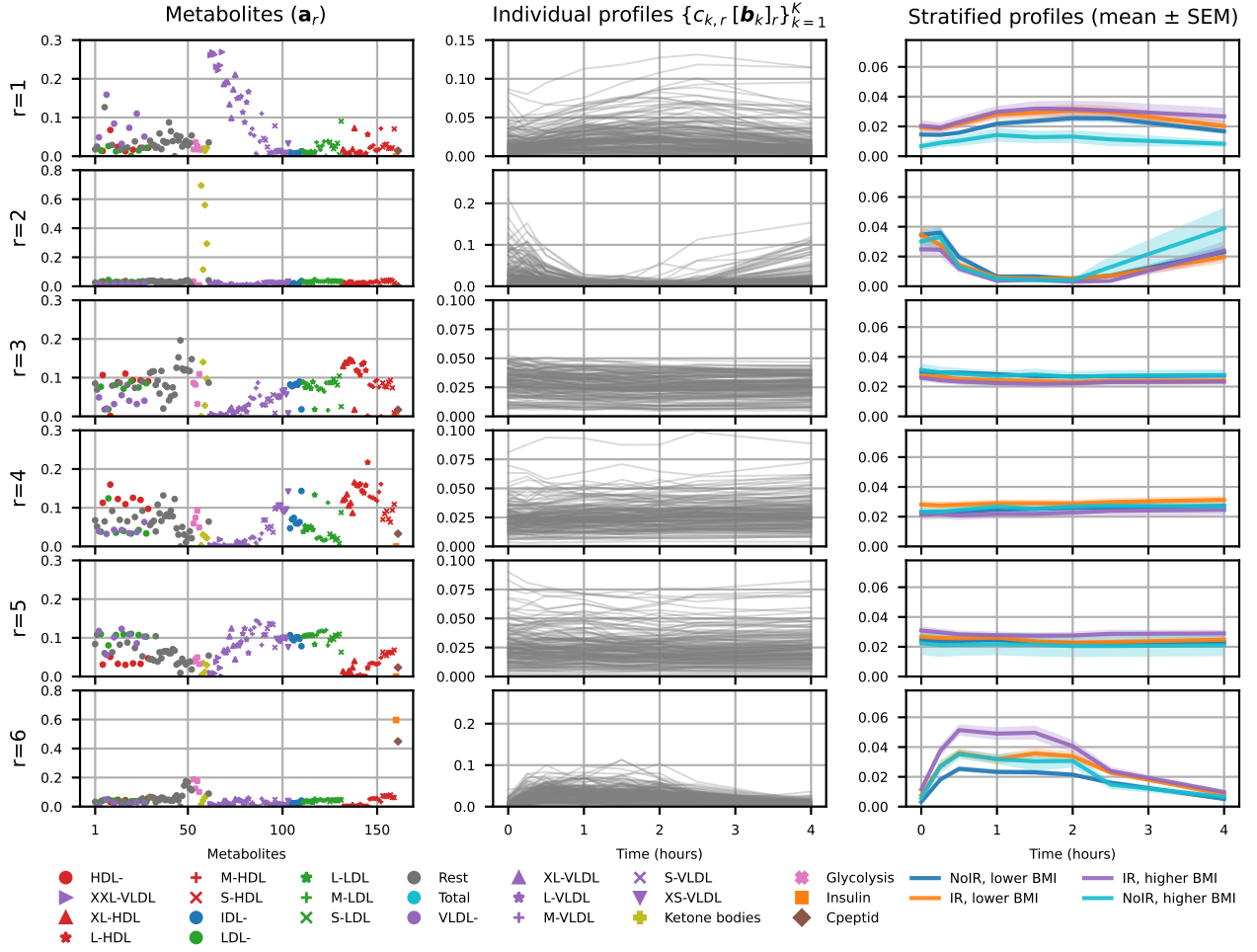


Figure S.4: Metabolomics. Components of a 6-component PARAFAC2 model (with nonnegativity constraints in all modes) of the metabolomics data from females. \mathbf{a}_r denotes the pattern in the metabolites mode, where metabolites are colored by lipoprotein classes. Different shapes are used for lipoprotein subclasses. Subject-specific time profiles scaled by the corresponding subject scores, i.e., $c_{k,r}[\mathbf{b}_k]_r$ for each component are shown in the middle column. The last column shows scaled subject-specific time profiles colored according to four BMI/IR groups.

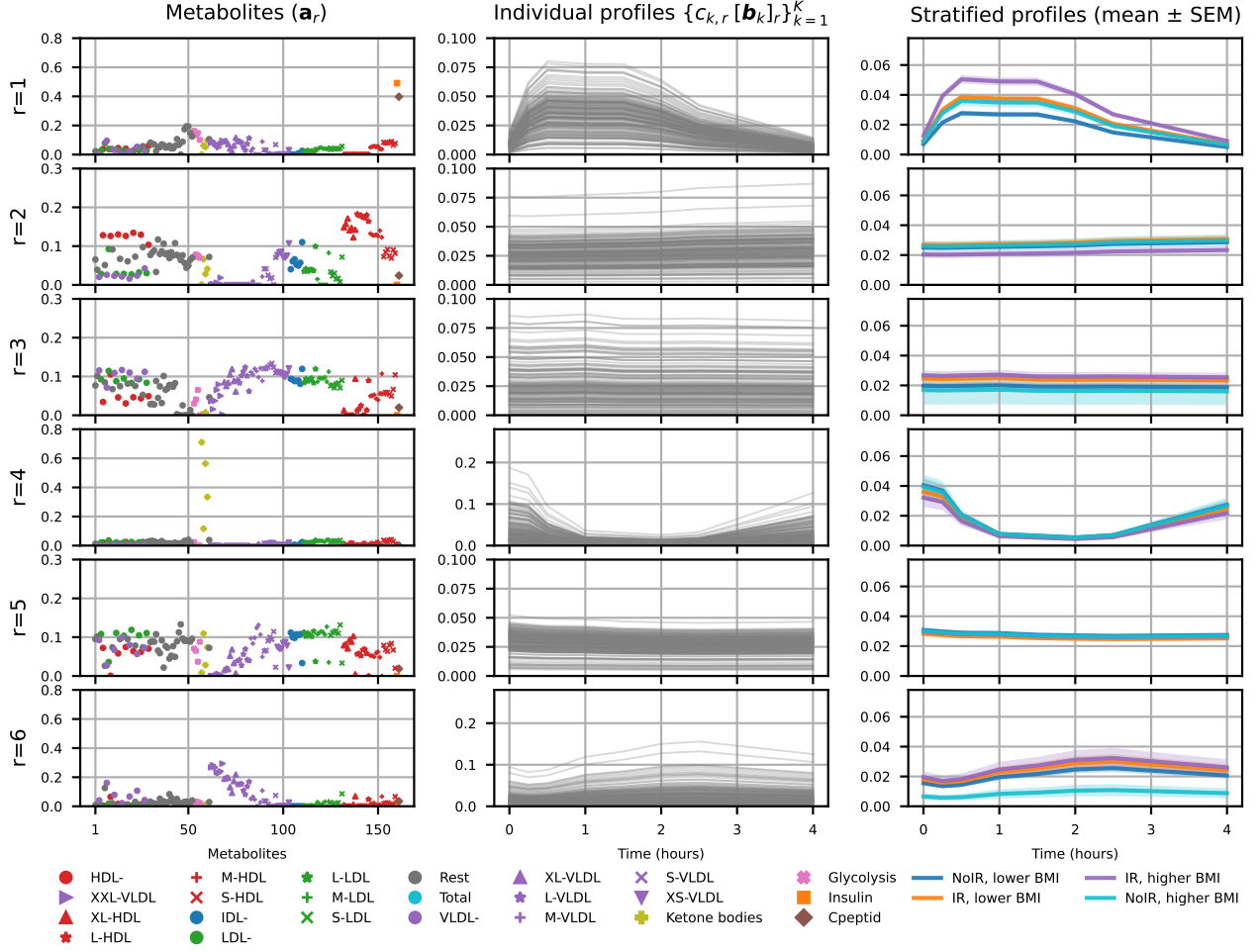


Figure S.5: Metabolomics. Components of a 6-component CP model (with nonnegativity constraints in all modes) of the metabolomics data from females. \mathbf{a}_r denotes the pattern in the metabolites mode, where metabolites are colored by lipoprotein classes. Different shapes are used for lipoprotein subclasses. Subject-specific time profiles scaled by the corresponding subject scores, i.e., $c_{k,r}[\mathbf{b}_k]_r$ for each component are shown in the middle column. The last column shows scaled subject-specific time profiles colored according to four BMI/IR groups.

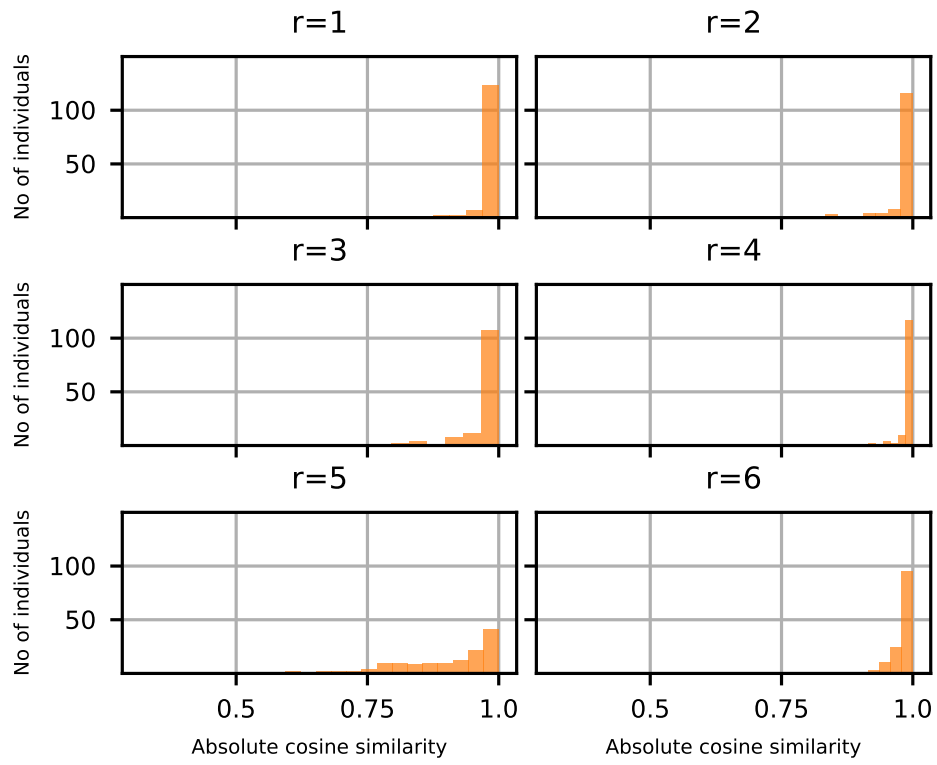


Figure S.6: Comparison of subject-specific time profiles ($c_{k,r}[\mathbf{b}_k]_r$) captured by CMF and PARAFAC2 for each component for metabolomics, where each histogram contains 140 data points, one for each male subject.

2 Sensitization

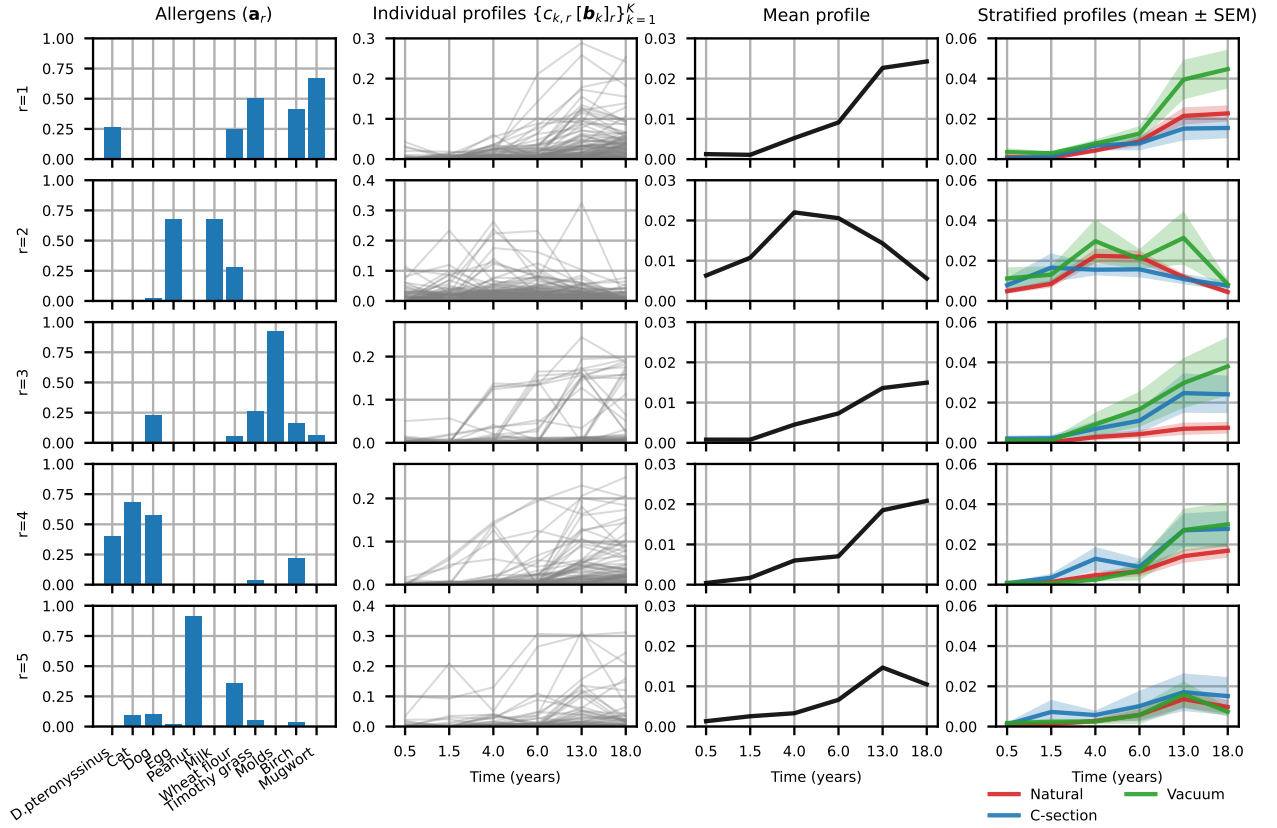


Figure S.7: Sensitization. Components of a 5-component PARAFAC2 model (with nonnegativity constraints in all modes) of the sensitization data. \mathbf{a}_r denotes the pattern in the allergens mode. Subject-specific time profiles scaled by the corresponding subject scores, i.e., $c_{k,r}[\mathbf{b}_k]_r$ are shown in the middle column. Mean of scaled subject-specific profiles are plotted in the third column while the last column shows mean (and standard error of mean) patterns of scaled subject-specific time profiles colored according to delivery/birth mode groups.

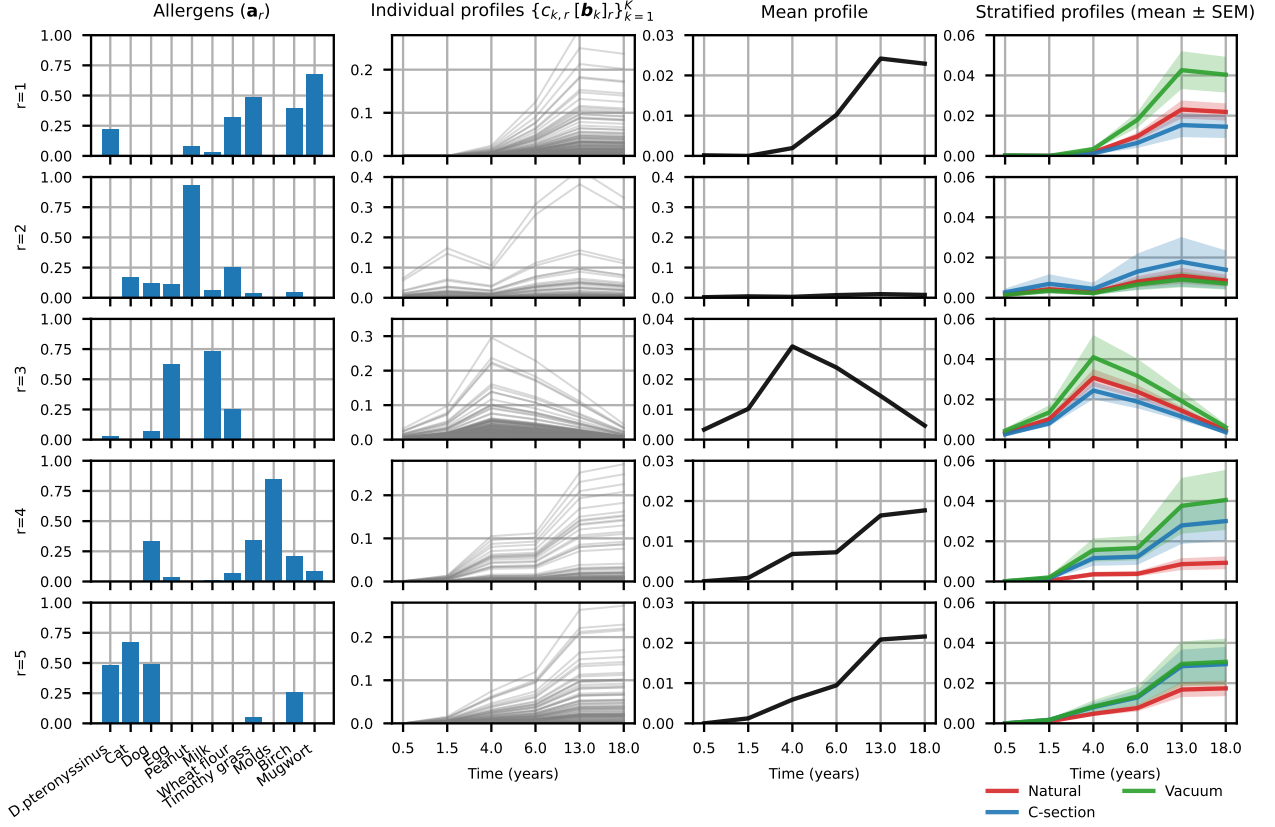


Figure S.8: Sensitization. Components of a 5-component CP model (with nonnegativity constraints in all modes) of the sensitization data. \mathbf{a}_r denotes the pattern in the allergens mode. Subject-specific time profiles scaled by the corresponding subject scores, i.e., $c_{k,r}[\mathbf{b}_k]_r$ are shown in the middle column. Mean of scaled subject-specific profiles are plotted in the third column while the last column shows mean (and standard error of mean) patterns of scaled subject-specific time profiles colored according to delivery/birth mode groups.

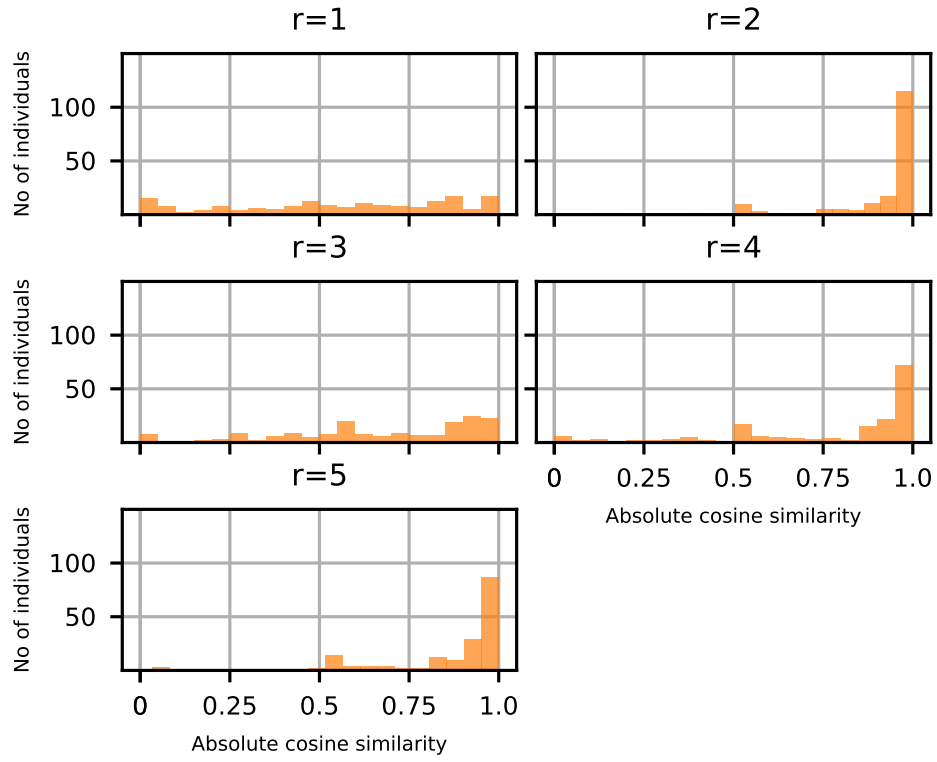


Figure S.9: Comparison of subject-specific time profiles ($c_{k,r}[\mathbf{b}_k]_r$) captured by CMF and PARAFAC2 for each component for metabolomics, where each histogram contains 176 data points, one for each subject.