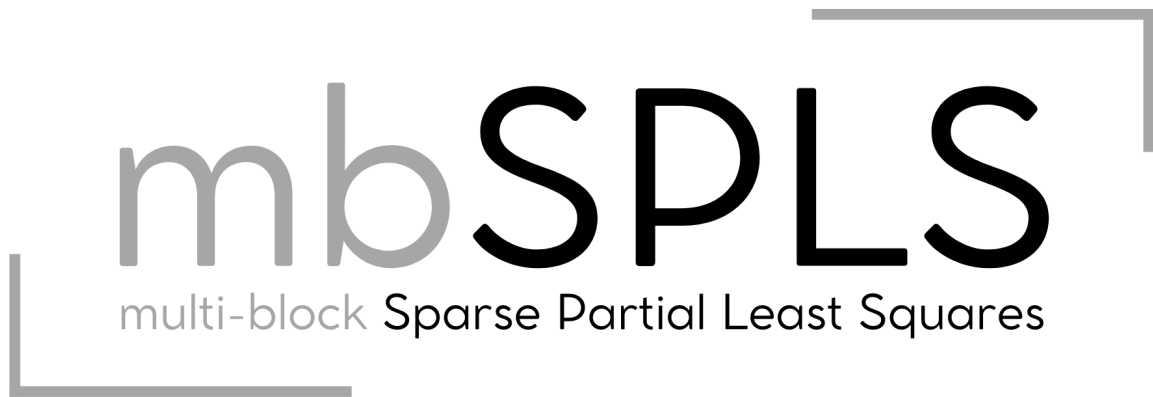


# MBSPLS Analysis Report



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19-Sep-2024

This report covers the results of the mb-sPLS analysis, including data preprocessing, model training, and validation steps.

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## Chapter 1. Input

### Input Parameters

name:

CW\_mbspls\_PRS\_BLOOD\_PROTEOMIC\_SOCIO\_5x5\_1000perm\_100boot\_fro\_matrixnorm\_grid\_search\_10\_10\_10\_10\_densities

Xs: [208x11 double; 208x19 double; 208x171 double; 208x8 double]

Xs\_names: [1x5 char; 1x7 char; 1x11 char; 1x7 char]

Xs\_feature\_names: [1x11 cell; 1x19 cell; 1x171 cell; 1x8 cell]

type\_correction: corrected

covariates: [208x10 double; []; []; []]

covariates\_names: [1x10 cell; []; []; []]

DiagNames: 208x1 cell

framework: 1

outer\_folds: 5

inner\_folds: 5

permutation\_testing: 1000

bootstrap\_testing: 100

correlation\_method: Spearman

optimization\_strategy: grid\_search

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## Chapter 2. Setup

### Setup Parameters

date: 18-Sep-2024

analysis\_folder: /data/core-psy-archive/projects/CW\_NfL/Analysis/  
PRS\_BLOOD\_PROTEOMIC\_SOCIO/18-Sep-2024

standalone\_version: MBSPLS\_DEV\_Aug2024\_correctionscale\_nosignflip\_R2022a

matlab\_version: R2022a

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## Chapter 3. Analysis Outputs