

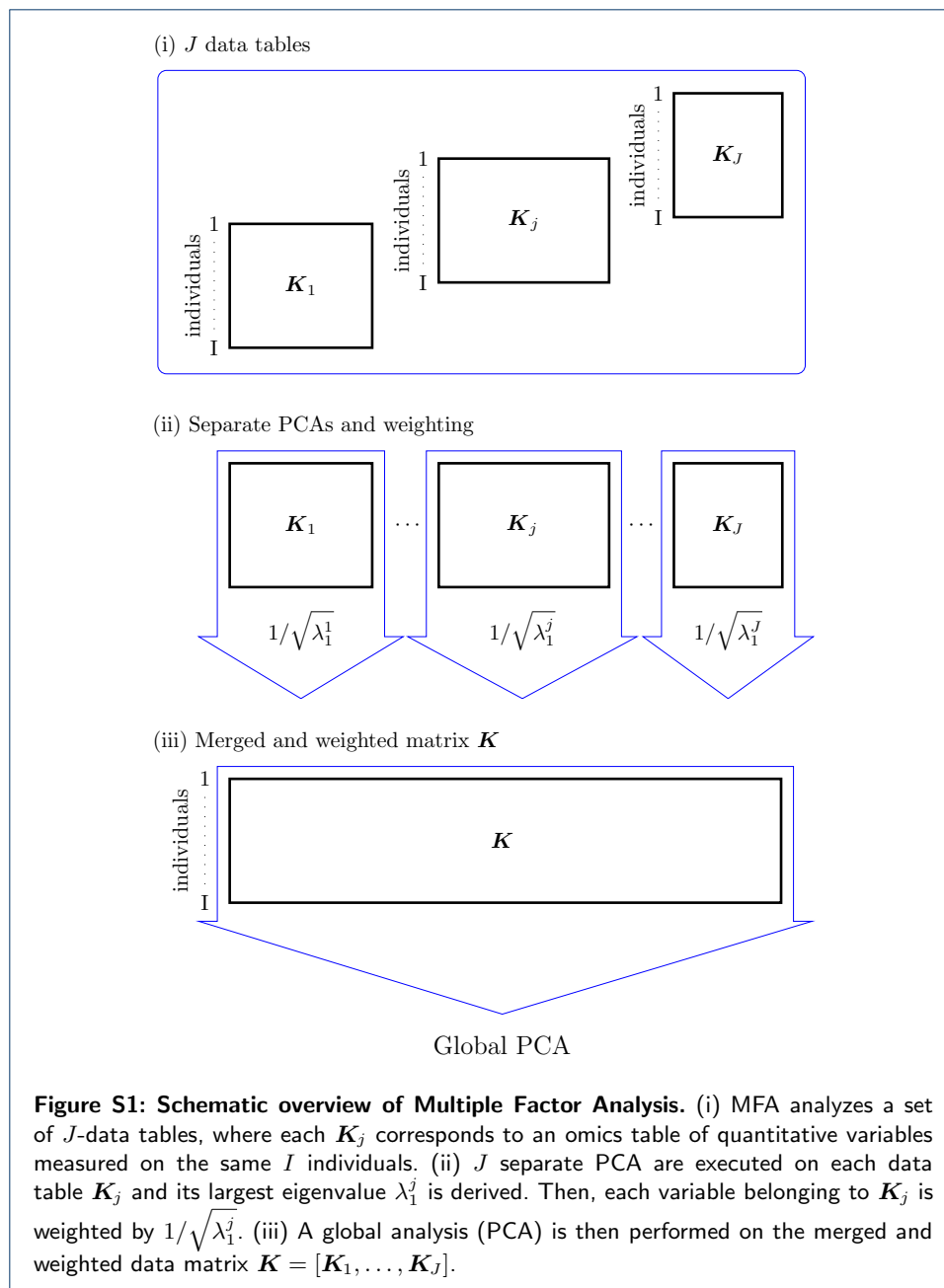
Supplementary figures

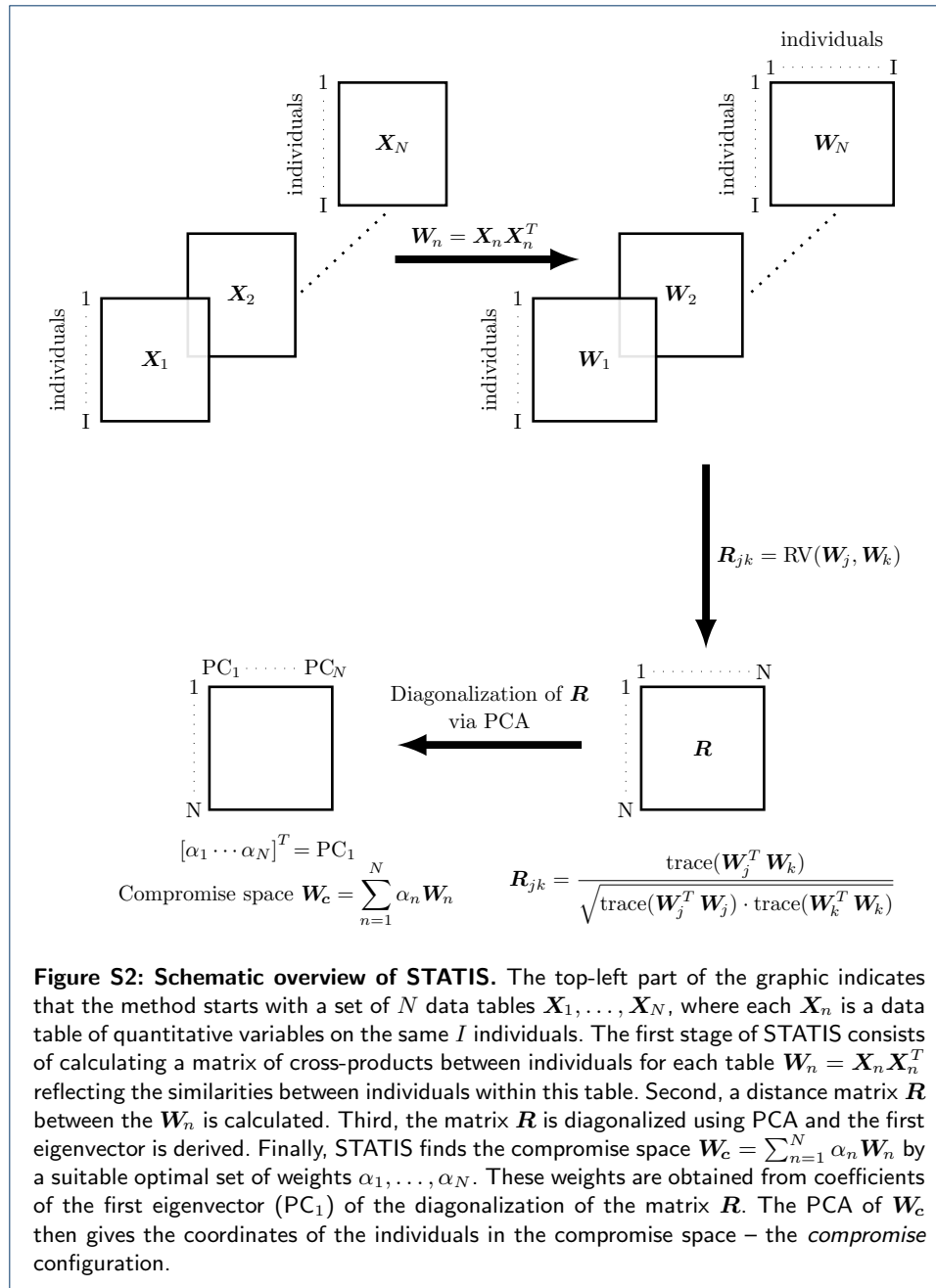
Handling Missing Rows in Multi-Omics Data Integration: Multiple Imputation in Multiple Factor Analysis Framework

Valentin Voillet^{1,2,3}, Philippe Besse⁴, Laurence Liaubet^{1,2,3}, Magali San Cristobal^{1,2,3,4} and Ignacio González⁵

Author details

¹ INRA, UMR1388 Génétique, Physiologie et Systèmes d'Élevage, F-31326, Castanet-Tolosan, France. ² Université de Toulouse INPT ENSAT, UMR1388 Génétique, Physiologie et Systèmes d'Élevage, F-31326, Castanet-Tolosan, France. ³ Université de Toulouse INPT ENVT, UMR1388 Génétique, Physiologie et Systèmes d'Élevage, F-31076, Toulouse, France. ⁴ Université de Toulouse INSA, UMR5219 Institut de Mathématiques, F-31077, Toulouse, France. ⁵ INRA, UMR875 Mathématiques et Informatiques Appliquées, F-31326, Castanet-Tolosan, France.





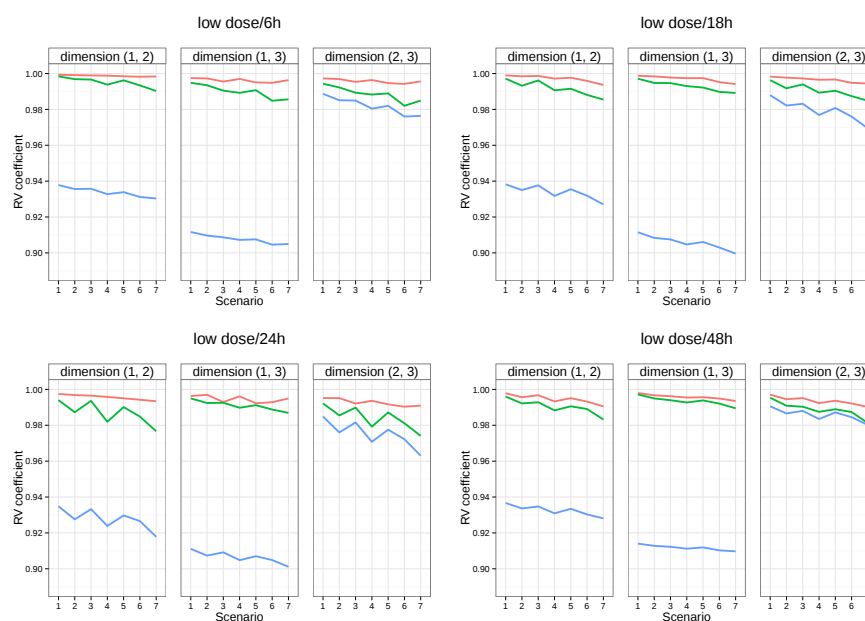


Figure S3: Performance on liver toxicity data with missing individuals in the low-dose treatment. Average RV coefficient between the configuration obtained by MFA on the complete dataset and either MI-MFA (red line), RI-MFA (green line) or MVI-MFA (blue line) on the incomplete dataset. Results are given for all of the first three two-dimensional possible configurations as a function of the scenarios presented in Table 1. The discrete RV values are joined by lines for ease of understanding.