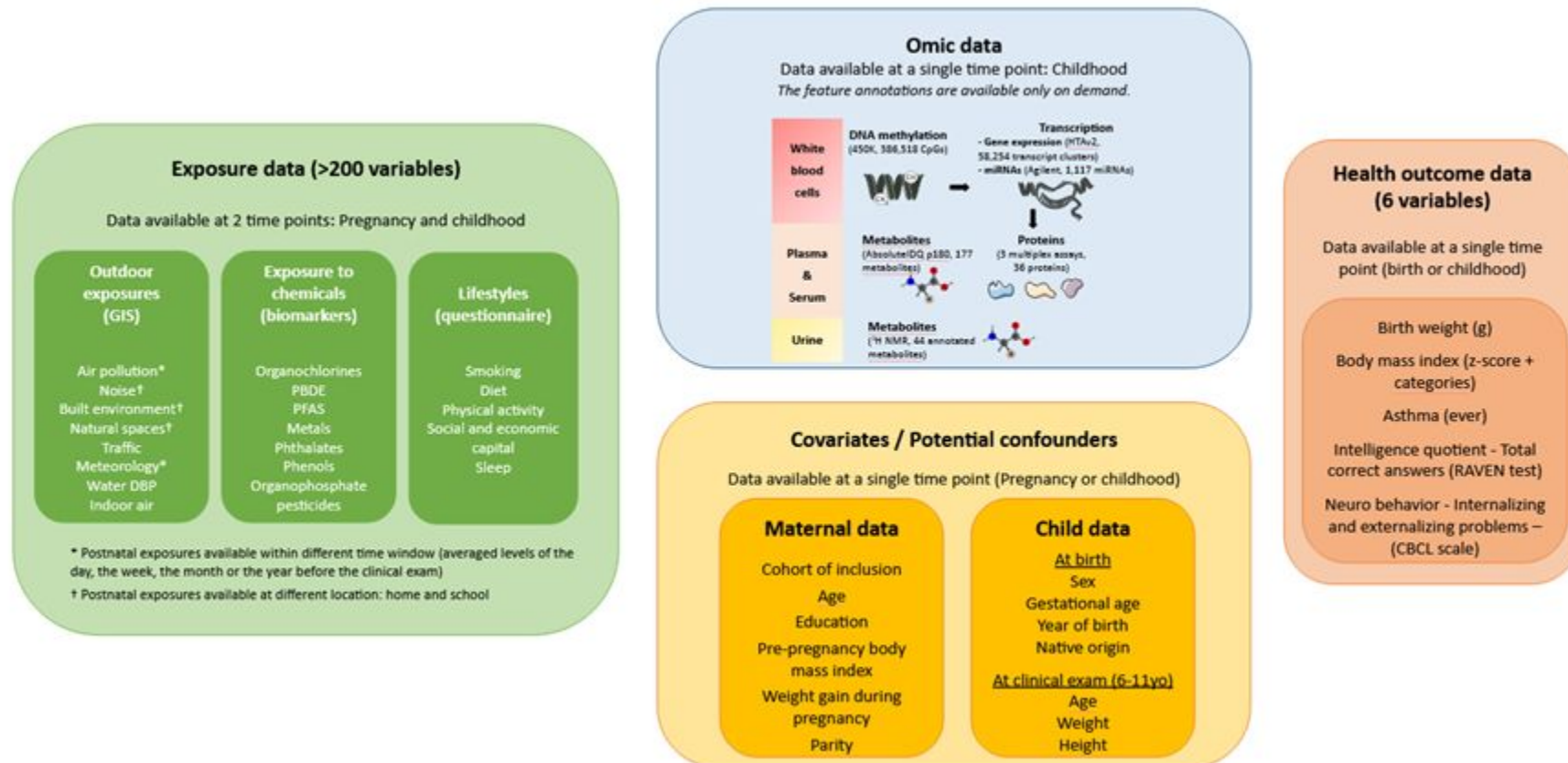


Data description:



The data provided were simulated following the structure of the HELIX subcohort database.

An overview of available data is shown in the figure.

Two sets of datasets are available: 1 with complete case data and 1 including missing data. Each set is composed by:

- 1 dataset for exposures: exposome

- 1 dataset for covariates: covariates
- 1 dataset for outcomes: phenotype
- OMIC (coming soon)

To facilitate the analysis, exposure variables were transformed to approach normal distribution.

You can refer to the [codebook](#) for variable description (variable name, domain, type of variable, transformation, ...)

Health outcome data:

- 2 continuous variables: Birthweight and child BMI z-score
- 2 count variables: Intelligence quotient and Neuro behavior
- 2 categorical variables: Asthma (two categories) and child BMI (4 categories, that can be combined if needed)

Challenge examples:

Challenge 1: Combined effects of exposures

- Determine if there are particular combinations of exposures (“cocktail effects”), high-order interactions or exposure patterns that are particularly harmful or beneficial for one or several health outcomes.
- Handle the multicenter design of the study (i.e. center may be a strong determinant of exposure patterns).
- Control for potential confounders.

Challenge 2: Using omics data to improve inference on the link between exposome and health.

- Incorporate the different omics layers into the analysis linking the exposome and one or more health outcomes.
- Show how the extra information available in the omics data can improve the inference of an analysis using only exposome and health (e.g. improvement in statistical power, ...).
- Control for potential confounders and multicenter design.

Challenge 3: Multi-omics analysis

- Incorporate different layers of omics data (including exposome as one of the layers) to find patterns that can explain variations in one or more health outcomes.
- Control for potential confounders and multicenter design.
- Maximize power in a context of moderate sample size.

Challenge 4: Causal structure in the exposome

- Define hypothesised causal relationships between the different exposures and one health outcome, and incorporate this information into the analysis.
- Compare this approach with *agnostic* analyses that perform variable selection treating all exposures in the same way.
- Illustrate how one can answer a large number of causal questions referring to different exposures using causal inference techniques for high-dimensional data
- Incorporation of mediation analysis and high-dimensional mediation analysis is a welcome addition.

Challenge 5: Visualization techniques

- Tools to visualize the complex relationships between the different components of the analysis, with the main aim of illustrating determinants of health effects.
- Strong interest in visualizing the magnitude and direction of the associations.
- Incorporate multiple data types.
- Find the right balance between complexity and clarity.