Special Issue on
Computational and Statistical Approaches for the Analysis and Modelling of Individual Phenotypes

CALL FOR PAPERS

A major need in medicine is to develop personalized diagnostics and/or treatments tailored on different individuals. However, humans exhibit great phenotypic diversity which originates from the complex interplay of genetic, epigenetic, and environmental factors, and this diversity affects both disease manifestation and response to therapy. Nonetheless, variability among samples collected from the same individual is at least twofold lower than the variability among different individuals. This is what is observed, for instance, in the case of the metabolic phenotype in healthy individuals and makes, in principle, personalized medicine possible.

Statistical and computational characterization of individual and interindividual variability is thus pivotal to the deployment of systems and personalized medicine approaches which will allow both higher sensitivity and specificity of personalized assays and substantial new insights on health and disease.

This comprises, but is not limited to, problems like the modelling of the individual response to drug treatment or modelling the differences among different disease phenotypes, onset, and progression such as those observed in cancer therapy.

In this special issue we aim to collect results from cutting-edge research on the problem of modelling individual phenotypes using computational and statistical methods. We welcome multidisciplinary approaches, combining different data types and *a priori* biological knowledge, integrating experimental and clinical data and annotations and interactions between elements, often embedded into network and multinetwork structures. In particular we encourage submission describing methodologies for the definition of personalized diagnostics and treatments.

Both theoretical and applicative contributions will be considered, including the proposal of novel methods or meta-analyses of existing data. We support reproducible biomedical research and we encourage contributors to detail the analytical and computational pipelines and to submit both data and the computer code implementing their algorithms for analysis.

Potential topics include but are not limited to the following:

- Modelling of individual phenotypes
- Patient groups stratification through relevant individual phenotypic signatures for personalized medicine applications
- Single sample analysis and profiling
- Single sample network inference
- Data integration at the individual level
- Effect of cofactors (*e.g.*, age and ageing, gender, nutrition, and lifestyle) on the individual phenotype
- Analysis and modelling of the individual response to drug and intervention treatments
- Characterization of individual functional/biochemical pathways

Authors can submit their manuscripts through the Manuscript Tracking System at https://mts.hindawi.com/submit/journals/cmmm/csaa/.

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