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Editorial

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While much progress has been made over the last few decades on understanding the molecular mechanisms underpinning the process of aging by studying model organisms ranging from unicellular organisms to primates, work on human aging, despite its high medical and social relevance, has been hampered by the difficulty of demonstrating cause-and-effect relationships, and even more basally by the lack of appropriate methods or instruments to assess the aging process in humans in quantitative terms.

There is, however, a huge demand for such methods, as biogerontological research nowadays has to address the “human system” with high priority. The reason for this is of course the greying of society that is already quite prominent in almost all countries around the globe and is going to become even more prominent in the near future. This demographic change is bringing about major consequences for those who suffer from chronic disease and disability due to “unsuccessful” aging and severe medical, societal and economical consequences.

One major task for biogerontological research focused on human beings is the establishment of valid biomarkers of aging, as a basic requirement for analyzing human aging and the effects of upcoming interventions in quantitative terms. In its 7th Framework Program, the European Union has funded the Large-Scale Integrated Project European Study to Establish Biomarkers of Human Ageing (MARK-AGE) project (Grant Agreement #200880). The project was running from April 2008 through September 2013 and was coordinated by Prof. Alexander Bürkle (University of Konstanz, Germany).

The present Special Issue has two main objectives, *i.e.* (i) to describe the scientific background and the design of this project and (ii) to describe some methodological issues that can also be relevant for similar studies to be planned for the future. The first objective is discussed in the papers by Zampieri et al. (Reconfiguration of DNA methylation in ageing);

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Vanhooren et al. (Protein modification and maintenance systems as biomarkers of ageing); Jansen et al. (Quality control data of physiological and immunological biomarkers measured in serum and plasma); Sikora (Activation-induced and damage-induced cell death in aging human T cells); Gradinaru et al. (Oxidized LDL and NO synthesis—biomarkers of endothelial dysfunction and ageing); Malavolta et al. (Serum Copper to Zinc ratio: relationship with aging and health status); and Griffiths et al. (Novel ageing-biomarker discovery using data-intensive technologies). The second objective is discussed in Bürkle et al. (MARK-AGE Biomarkers of Ageing); Capri Miriam et al. (MARK-AGE population: from the human model to new insights); Moreno-Villanueva et al. (MARK-AGE Standard Operating Procedures [SOPs]: a successful effort); Moreno-Villanueva et al. (The MARK-AGE Phenotypic Database: Structure and strategy); Baur et al. (The MARK-AGE Extended Database: Data integration and pre-processing); Baur et al. (MARK-AGE data management: Cleaning, exploration and visualization of data); and Giampieri et al. (Statistical strategies and stochastic predictive models for the MARK-AGE data).

We hope that the present special issue of MAD will enable the reader to better understand the structure and potential of this big European study, whose more specific results will be published in another series of papers currently being prepared.