



## Editorial

### A Primer Series on -Omic Technologies for the Practice of Epidemiology

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Progress in genomics and other high throughput “-omic” technologies is promising to revolutionize the practice of epidemiology by providing new tools to measure exposures, susceptibility, and disease outcomes. New platforms of biomarker measurement are becoming increasingly available for epidemiologic studies. Examples include genomic, proteomic, metabolomic, noncoding RNA, epigenomic, mitochondrial DNA, telomerase, and microbiota studies. In addition, environmental measurements are becoming increasingly sophisticated, and the exposome holds promise with regard to measuring the impact of multiple exposures on health outcomes (1).

Omic technologies pose many challenges regarding the collection, analysis, validation, replication, and eventual utility of this information for medicine and public health (2). We should always be mindful of the potential pitfalls of adopting new technologies too soon. Because of this, the relationship between technologies and epidemiology is bidirectional. Although new omic technologies provide the tools to enhance epidemiologic research, epidemiology is needed to test and validate the application of these technologies for use in population settings (3).

Despite their tremendous appeal, it is premature to predict how new omic approaches will evolve over time. Likewise, we cannot anticipate what new platforms will be available and ready for research or clinical use, although our measurement capacity is likely to expand rapidly. What should be anticipated, however, is the need for an epidemiologic foundation for proper techniques for collection, sampling, processing, and storage of biologic specimens to be studied with these evolving technologies and development of principles for their optimal use, analysis, and validation in epidemiologic studies of all types. This need is particularly felt for cohort studies that collect biologic samples today but may assay those samples years if not decades into the future (1).

Analytic methods for omic technology platforms need to evolve and account for platform-specific peculiarities as well as study design issues. A greater challenge is how to integrate multiple platforms within the same analysis. As the possibilities for false leads increase exponentially with each new omic technology, methodologic work is essential in evaluating any technology’s analytic performance, reproducibility,

replication, disease associations, ethical and legal issues, and clinical use (2).

In order to inform our audience of the various omic fields, the *Journal* will publish a primer series for the epidemiologist interested in education about specific omic methods and technologies. Specifically, the series will inform epidemiologists how to read papers on the topics and what to do if they are interested in integrating emerging methods into their work.

In the present issue of the *Journal*, 2 articles represent the first installment of publications in this new series. Tzoulaki et al. (4) address the promise, design, and analysis of metabolomics studies in epidemiologic research. Nair et al. (5) review the study of microRNAs in human disease. What these articles have in common is that they address a series of questions and issues that are common to all of these technologies to educate the epidemiologist. What is the technology? What has been done in the field in the form of a synopsis of relevant original research publications, reviews, and meta-analyses? What are the main epidemiologic and statistical methods and software for design and analyses? What are the current methodological limitations of this technology in terms of measurement and statistical/analytical methods? What are the future prospects for this technology in the practice of epidemiology?

Proposed topics in this series will include, among others, epigenetics, the microbiome, proteomics, pathogen whole-genome sequencing, metagenomics, telomerases, and the exposome. We hope our readers will find these articles informative. We also invite prospective authors to submit articles to be considered for publication in the *Journal*’s series on the Practice of Epidemiology.

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## REFERENCES

1. Khoury MJ, Lam TK, Ioannidis JP, et al. Transforming epidemiology for 21st century medicine and public health. *Cancer Epidemiol Biomarkers Prev.* 2013;22(4):508–516.
2. Ioannidis JP, Khoury MJ. Improving validation practices in “omics” research. *Science.* 2011;334(6060):1230–1232.
3. Lam TK, Spitz M, Schully SD, et al. “Drivers” of translational cancer epidemiology in the 21st century: needs and opportunities. *Cancer Epidemiol Biomarkers Prev.* 2013;22(2):181–188.
4. Tzoulaki I, Ebbels T, Valdez A, et al. Design and analysis of metabolomics studies in epidemiological research: a primer in -omic technologies. *Am J Epidemiol.* 2014;180(2):129–139.
5. Nair VS, Pritchard CC, Tewari M, et al. Design and analysis for studying microRNAs in human disease: a primer in -omic technologies. *Am J Epidemiol.* 2014;180(2):140–152.