Editorial

Software Application Profiles: useful and novel software for epidemiological data analysis

Vincenzo Forgetta\(^1\) and J Brent Richards\(^1,2\)

\(^1\)Lady Davis Institute, Jewish General Hospital, Montreal, QC, Canada and \(^2\)Departments of Medicine, Human Genetics, Epidemiology and Biostatistics, McGill University, Montreal, QC, Canada

Ever wonder what new epidemiology-related software programs are out there? Are you frustrated by searching the internet for a software tool, only to find too many (or too few)? Do you have the best data visualizer on the planet and are itching to share it? Or, are you just an epi-software junkie looking for your fix?

Here at *IJE* we empathize with all these needs, and in response we have launched a new profile series, entitled the Software Application Profile (SAP).

To ensure accessibility to the epidemiology research community, SAP articles and accompanying software should follow the basic guidelines outlined below, with greater detail provided in the SAP Guide for Authors available on the *IJE* website [http://www.oxfordjournals.org/our_journals/ije/for_authors/general.html].

In addition to contributing novelty or significant utility, the software application should strive to satisfy established evaluation criteria, such as ease of access and installation, adequate user documentation, cross-platform compatibility and basic technical support. Eligible software applications include stand-alone applications (graphical or command line), web resources, and modules or libraries such as those for R or STATA.

Articles should be brief, between 1500 and 2000 words, and avoid overly technical jargon. Content should concisely describe how the software was built and provide a usage scenario that showcases sufficient functionality (more details in SAP Guide for Authors).

In this issue, we present the first article of the series by Oualkacha et al., which is an R package, RVPedigree, a suite of family-based rare variant association tests for normally and non-normally distributed quantitative traits. In addition to presenting a novel contribution to rare variant analysis, the authors have made significant efforts to include additional rare variant algorithms, as well as other features.
that expand accessibility and functionality, such as support for popular genotype data formats, computation of kinship matrix and support for parallel processing. All of these functionalities improve the utility of the software—something that we’ll look for in all SAP articles.

We look forward to receiving articles for peer review that introduce your epidemiological software application. Your efforts in building a novel and useful tool deserves to be shared with your peers, both as a recognition of your work and as a gift to all epidemiologists, biostatisticians and data analysts who need a tool to help them in their quest to improve human health.

Lastly, let’s also help Henry get ahead of the software curve!

SAP Editors: Vincenzo Forgetta and J. Brent Richards

References