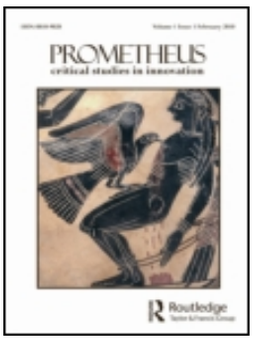

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RESPONSE

Thoughts on the *Manchester Manifesto*

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George Church is a professor at Harvard University and founder of the personal genome project. He has patents in the fields of genome reading and writing, automation and instrumentation, and advocates open source and transparency; for example, by developing the open access next generation sequencing platform (Polonator.org) and the open access human genome plus trait dataset (PersonalGenomes.org).

One major omission from the *Manchester Manifesto* and this proposition paper is that the alternative to the patent system is probably not open access: it is more likely to be trade secrets. While the *Manifesto* mentions the term 'patent' many times, 'trade secret' and 'copyright' are not mentioned at all. It is often the case, as the *Manifesto* declares, that patents might be 'incomplete and need an expert to decipher', but in practice, there are many such experts who do just this: they decipher patents and are free to publish versions that are accessible to, and can be understood by, a wide audience. If any particular patent is truly too incomplete or obfuscated, then it will not stand up in court, and the trade secret route might have been safer for the inventor. The easiest route to the open access the *Manifesto* proposes might apply to government-funded research, but even here it is probable that a significant fraction of the funded research community would develop methods for stopping just short of an enabling discovery, and then switching to stealth mode with private – not government – funding. A more likely route to open access would be to encourage organizations that promote or profit (at least in part) from open access, open source methods. Prominent examples are Linux, Google Code, MediaWiki, TropicalDisease.org, Open Source Drug Discovery (OSDD.org), CreativeCommons.org, One Laptop per Child (OLPC), BioBricks, Polonator.org, OpenCola and GitHub.

Ironically, a data type that is crucial for both industrialized and developing nations, and yet is among the least open deals with integrating human genomes, environments and traits (GET). The general lack of open access for GET data is occasionally ascribed to privacy complexities, but in reality, trade secrecy, academic priority seeking and copyrights play large roles, and access is often limited to collaborators – a practice that could result in coercion to collaborate and/or biases against researchers in developing nations. Ironically again, most international

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government funding is directed towards projects with little open access, such as the HapMap and 1000 genomes projects (where attempts to provide shareable trait data have been blocked), and genome-wide association studies (GWAS) data, which are difficult for most people worldwide to access. Nevertheless, fully open access community genomics resources, such as PersonalGenomes.org and Evidence.personalgenomes.org, have been made available under a worldwide creative commons license (Lunshof *et al*., 2008; 2010), demonstrating that such a system is feasible, with little or no peer-reviewed evidence to the contrary. Not only are the raw GET data from the personal genomes project publicly available, but so too are cell lines and genome interpretation software, and they are already represented in many journal articles. Commercial adoption of these resources has also been swift, in part because the creative commons license explicitly requires shareability. Progress toward standards and consensus (needed for Food and Drug Administration approval) is readily traceable, as is curation and critique – analogous to Wikipedia, but decidedly non-anonymous and transparent.

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