## What ID is, beyond what it is not

**To the editor:** Although your recent editorial[1], "An intelligently designed response" was apposite, an important omission was apparent. Yes, debunking intelligent design (ID) by scientific reasoning requires good lay communication skills. Yes, merely (correctly) dismissing ID as nonsense will only fuel charges of scientific arrogance. And yes, the point about the nature of science has to be made because doing so makes palpable that ID is not science. However, the advice to avoid a religious discussion is questionable—particularly as so doing does not necessarily entail an atheistic rant.

As well as emphasizing what ID is not, we also need to consider what it is. ID proponents eschew its association with literalist creationism but couple religious conservatism with a technology-friendly modernity. In the UK, we have a Christian organization, absurdly named 'Truth in Science', which has distributed glossy paraphernalia to the science departments of secondary schools and sixth form colleges, advocating ID inclusion in science lessons. Despite contravening the national curriculum, this marketing ploy has apparently proven effective in persuading a number of schools that it has scientific credentials. ID appeals to fundamentalists of other religions. Harun Yahya, the pseudonymous vehicle for Muslim creationist propaganda, has distributed a lavish, 800-page tome to schools and universities, scientists and museums in France and the US. Thus, referring to religion is both unavoidable and necessary to understand the strategy at work here. ID is nothing more than sexed-up creationism for the media age, a realization necessary for an effective refutation of its scientific posturing.

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1. Anonymous. *Nat. Methods* **4,** 983 (2007).

*Please visit methagora for further discussion on this topic.*

## Reannotation of array probes at NCBI's GEO database

**To the editor:** The Gene Expression Omnibus (GEO) database[1] hosted by the National Center for Biotechnology Information (NCBI) is the largest public archive for microarray data. Many factors contribute to the value and reusability of archived microarray data, including accurate probe annotation. As outlined by others[2–4], this issue presents particular challenges, primarily because microarrays are labeled using many different annotation conventions and because probe-to-gene assignments continually evolve.

Chen and colleagues[5] recently stated that GEO is experiencing only linear growth in citations despite exponential data growth, and claimed the reason for this imbalance is out-of-date probe annotation. It is not clear that exponential growth in any database should necessarily lead to an exponential increase in citation rates. Should we really expect citation rates to GenBank to keep pace with the exponential growth rates for DNA sequence data? Regardless, our numbers do not support the assertions in Chen *et al.*[5] and instead show very similar rates of growth for GEO data and third-party citations (**Supplementary Fig. 1** online).

Chen and colleagues also raised a fair point that for GEO data to be accurately evaluated, probe annotations should be repeatedly synchronized with latest gene mappings. They suggested that this task could be facilitated by implementing standardized column headers in microarray tables. We agree with both points. In fact, a standardized header system has been in place at GEO for several years (**Supplementary Table 1** and **Supplementary Discussion** online) and is the basis of our internal reannotation pipeline. These standard column headers enable us to provide up-to-date annotation for genes within the Entrez GEO Profiles database (http://www.ncbi.nlm.nih.gov/sites/entrez?db=geo). Annotation tables are freely available for download (ftp://ftp.ncbi.nih.gov/pub/geo/DATA/annotation/) and, when possible, include several auxiliary annotation categories, including chromosomal position and gene ontology terms.

GEO recognizes that accurate probe annotation is fundamental to data reuse, and we thank Chen and colleagues for raising this point. We will continue to make considerable efforts to acquire sufficient probe sequence tracking information from submitters. Our annotation procedures continue to be refined: we are working to implement a probe sequence mapping procedure, to increase the fraction of curated arrays and to reannotate more frequently.

*Note: Supplementary information is available on the Nature Methods website.*

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