

The academic welfare state: making peer-review count

Diogo Verissimo and David L. Roberts

Durrell Institute of Conservation and Ecology, School of Anthropology and Conservation, Marlowe Building, University of Kent, Canterbury, Kent, CT2 7NR, UK

The peer-review process is a central pillar of academic publishing. However, the work that goes into ensuring the quality of published content is rarely recognised. Here we present a correction factor for the h-index, one of the most popular metrics for quantifying academic output, that will allow for the inclusion of peer-review effort in the evaluation of the outputs produced by an academic.

The peer-review process is a central pillar of academic publishing [1]. Traditionally, journal editors have relied on volunteer experts who ensure the quality of published content. However, as academia becomes more competitive, the number of papers submitted has risen, adding to the reviewer's burden [2,3]. This increase, together with the decrease in availability of reviewers, has led to the so called "tragedy of the reviewer commons" [4,5], resulting in a slow peer-review process that impacts knowledge advancement. This lack of availability to review may be a result of the lack of direct benefits to reviewers, which leaves this service largely unappreciated [1,2]. At most, peer-review activities feature on CVs as either a list, or simply a number, of journals an academic has reviewed for. A consensus has thus been built between editors and authors around the need to motivate academics to engage with the peer-review process [2,6–8].

Several incentive schemes have been discussed, from those that punish the slow [6], to those that financially compensate reviewers [2]. However, given the potential backlash against the former and conflicts of interest surrounding the latter, a more pragmatic option would be to explore the fact that much of academia is prestige-based, and design a metric that accounts for an academic's work as a reviewer [7,8]. This would increase the recognition of those who dedicate time to peer-review, providing an incentive to review more, but also putting pressure those who consider themselves 'too posh to peer-review' [5].

Currently one of the most popular metrics for quantifying academic output is the *h*-index [9]. However, this measure does not consider the other side of the publication process; peer-review. This could be incorporated through a correction factor (*c*) in the form of the ratio between an academic's published output (number of papers published, N_P) and their reviewed output (number of papers reviewed, N_R), as each academic can be assumed to have to review at least as much as they publish to keep the system sustain-

able (Eq. 1). The end result can then be multiplied by the academic's *h*-index, thus correcting for peer-review performance.

$$c = \frac{\sum(N_R)}{\sum(N_P)} \quad (1)$$

Although easy to interpret, this metric is somewhat simplistic. For example, it does not take into account that for every paper published, an average of 5 to 10 reviews are required, once rejections are considered [4]. As a result, reviewing effort will be greater than the number of peer-reviewed publications. By contrast, there are often several authors to a single paper, which means the burden of matching the reviewing effort needed to publish a paper should be divided among them. These aspects can be accommodated in the correction factor (*c'*) by dividing each paper published by the number of authors (N_a), and dividing the number of papers published by the average number of reviews (N_r) (Eq. 2). Thus correcting for the larger effort devoted to peer-review and for shared authorship.

$$c' = \frac{\sum(N_R/N_r)}{N_r \sum(N_P/N_a)} \quad (2)$$

Another aspect that may be considered is the impact of the journals a given academic has reviewed for, as academics often order journals on their CV from most to least prestigious. To account for this we can multiply each paper reviewed and published, by the 5-year *h*-index of the corresponding journal (h_j) [10] (Eq. 3). However, this may not be appropriate as the term, h_j , is not used when calculating an academic's *h*-index.

$$c'' = \frac{\sum((N_R/N_r)h_j)}{N_r \sum((N_P/N_a)h_j)} \quad (3)$$

One potential obstacle to the implementation of this correction factor, however, is the anonymity of the peer-review process. Even where records exist, the availability of data on a reviewer's achievements might be difficult to access, leaving it up to academics to self-report their performance. Nevertheless, there are already a number of journals, even in major publishers, that regularly release a list of their reviewers. Another possible issue is that, contrary to the number of papers published, the number of papers reviewed by an individual depends on the number of invitations that individual receives. This is out of the control of an academic. Nevertheless, the decreasing availability of reviewers suggests this may be less of an issue. This metric can therefore help provide more recognition and visibility to

those who selflessly invest in the advancement of knowledge often to the detriment of their own careers.

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More than tree dimensions: inter-lineage evolution's ecological importance

James O. McInerney

Department of Biology, National University of Ireland Maynooth, Co. Kildare, Ireland

Horizontal transfer of genes has sometimes been viewed as a nuisance for the work of understanding the evolutionary history of lineages. Recent work has shown that clever analysis of inter-lineage gene transfer is productive and has tremendous explanatory power, in particular, for niche adaptation. These studies alter our perception of what are the fundamental units of evolution and selection.

The shorthand version of evolution is that it occurs in lineages where offspring inherit sequences that are largely similar to their parents. The history of these lineages can be visualised using a phylogenetic tree. However, this narrative does not capture the entirety of the story and indeed, the benefits of abandoning this kind of thinking in favour of a more pluralistic account of evolution [1] are manifesting themselves at an increasingly fast rate. As a consequence of horizontal gene transfer (HGT) and a multitude of introgressive events [2], evolution can occur in any evolving entity and move laterally into a different evolving entity, meaning that evolution can occur outside lineages as well as inside. The widespread import of evolutionary elements is being reported for prokaryotes, viruses and other mobile genetic elements, though all of life is affected to some extent. One implication of introgression is that making a single unifying tree of prokaryotes is impossible [3].

While the importance of HGT has been increasingly appreciated, only recently have we seen an explicit move towards giving equal recognition to inter-lineage evolution and intra-lineage evolution [2]. Indeed it is being seen increasingly that inter-lineage evolution seems to have a particular importance for niche-adaptation [4,5]. This has led to a need to think about microbial evolution in ways

that do not involve trying to fit data onto phylogenetic trees and subsequently explaining these data by reference to the species trees. One recent study in particular [6] has demonstrated the benefits of an approach that steps outside of the boundaries of tree-thinking. The authors constructed a phylogenetic tree using 1,623 loci from 192 *Campylobacter* strains. These strains are common components of the gut microflora of several birds and mammals and frequently cause food poisoning in humans. On this resulting tree, they mapped MLST “clonal complexes” (strains that are identical when only seven housekeeping genes are genotyped) and ecological niche associations (in effect, the location from which the strain was isolated). A certain amount of correspondence was observed between the MLST data and the evolutionary tree constructed from the completed genomes. However, there were significant differences in host association and the branching pattern on this tree. Quite simply, in order to map host association on the tree, it was necessary to propose dozens of host-switchings. Rather than try to interpret the data solely with respect to this tree, the authors chose instead to carry out a genome-wide association study involving the selection of 30 bp “words” from the genomes and assessing whether there was an association between host and the presence or absence of particular words. This alternative analysis does not refer to a tree and in fact, it explicitly discards the tree by simulating the evolution of words on their tree and looking for significant associations that could not be caused by this tree. This is an explicit search for interesting evolutionary events that do not occur solely within a lineage, rather they can occur outside that lineage and can then be imported. What the authors found was indeed surprising. A seven-gene region was almost always seen to be present in strains that were isolated from cattle and was frequently absent from strains that were associated with chickens and wild birds. Three of the genes were associated with vitamin biosynthesis and