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The Much Overlooked "Materials and Methods"

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Editorial

The ability of a scientist to interpret, understand, and reproduce another's work is dependent on the accuracy and detail provided in the "Materials and Methods" section of a scientific publication. This information is intended to provide insight into the resources used and details of how an experiment was performed. In recent years, these sections have undergone increased scrutiny with the rapid growth of scientific databases and their manual curation efforts. Last year, the Nucleic Acids Research (NAR) online Molecular Biology Database Collection included more than 1500 databases [1]. Biocurators manually review and scrutinize the published literature for inclusion into these biological databases. Teams of curation scientists dissect the methods sections of manuscripts, comparing their content to the text and figure legends. This level of scrutiny is required in order to assure the accuracy of data entered into each database, as well as to ensure complete understanding of the data that is manually annotated.

This close examination of Materials and Methods sections has brought several issues to light, such as oversights, inconsistencies, and an alarming number of errors. A recent article by Vasilevsky, et al., investigating the ability to accurately identify resources that were used in publications spanning several biomedical disciplines, quantified some of these issues [2]. The authors found that less than 50% of antibodies and cell lines used in these publications were identifiable based on the information reported in the publications. Even worse, DNA constructs were identifiable in only approximately 25% of the manuscripts they evaluated. At the Immune Epitope Database (IEDB), data from publications describing epitope specific immune receptors is manually curated [3]. Although these publications are about immune epitopes, the epitope sequence is provided in approximately 81% of the manuscripts. Determination of the epitope for a monoclonal antibody is a significant and publishable accomplishment, however, in manuscripts describing epitope specific antibodies, approximately 12% fail to adequately describe the antibody, either citing another reference or lacking sufficient information to identify the antibody. Without knowing what reagents were used in a published experiment, scientists cannot reproduce or truly comprehend results.

In light of these issues, several biological databases have begun a push toward better identification methods for resources, as well as improved journal standards. Several groups have begun initiatives to improve how authors describe the reagents used in scientific studies. The Resource Identification Initiative (www.force11.org/resource_identification_initiative) is a project that aims to promote the use of unique identifiers for research resources to improve resource identification, discovery, and reuse. The Resource Identification Portal (www.scicrunch.org/resources) is a searchable database that hosts stable identifiers for antibodies, model organisms, and tools (software, databases, and services).

Antibodies represent a great example of a very important and commonly used reagent that is often difficult to describe, identify, and locate. A lack of clearly defined naming convention creates difficulty in identifying specific author generated antibodies. For example, authors will often describe the same antibody using slightly different nomenclature, such as SA5.1 versus SA5-1. The arbitrary naming of antibodies also causes problems when two authors give very different antibodies the same name. It is also not uncommon for an author to refer by an antibody using the lab's "common name" for it rather than the one used by the vendor. These sorts of inconsistencies can be significant. For example, if the common name gives no hint that the typically mouse antibody had been humanized. If the author had referred to its vendor name and catalog number, it would have been possible to find such critical information. However, inclusion of just the vendor name and catalog number is not fail proof, as companies are bought and sold and many cease to operate. To address this issue, the Antibody Registry (AR) (www.antibodyregistry.org) was developed, as part of the Resource Identification Initiative, which assigns a stable and unique identifier [4]. By searching the AR, one can find these identifiers and report them alongside the mention of the antibody resource in a publication, as well as submit new antibodies to be assigned stable identifiers, regardless of vendor or developer. The success of the AR is still dependent upon the adoption by authors and journals, to both submit their antibodies to obtain AR identifiers and to require their use in publications.

Improved journal standards and author care regarding how reagents are described is another way to combat the lack of reproducibility. Unfortunately, in their recent study, Vasilevsky et al. found that regardless of the impact factor of the journal or the stringency of its reporting standards, the ability to uniquely identify the resources was lacking in all cases. Their findings suggest that journals that currently have stringent reporting guidelines are not strictly enforcing them. Standards have been proposed by a number of groups such as the Force11 (www.force11.org) initiative who formalized data citation principals. Nature Methods has recently adopted new editorial measures specifically to improve the consistency and quality of manuscripts [5]. In just this past month (June 2014), editors of approximately 40 journals came together at the National Institutes of Health to endorse new guidelines to improve reproducibility [6]. These initiatives and events are very promising for the future of reproducibility. However, authors, journal editors, and peer reviewers still need to do a better job writing and scrutinizing the methods sections of manuscripts to ensure that all resources and reagents are adequately and accurately described.

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