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Who are the Guardians of Truth and Integrity?[*]

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Abstract

On October 9th, Brain Health Alliance (BHA, a 501c3 not-for-profit organization) hosted Guardians 2023, our 2nd annual conference entitled “Who are the Guardians of Truth and Integrity?” The Guardians conferences focus on the global impact of information cyberwars on citizens of planet Earth. Internationally in media of many forms, information has been warped and twisted, resulting in disease, death, and destruction around the globe. To combat the spread of lies and extremified propaganda, the Guardians conferences strive to promote better understanding and awareness about the harm caused by information wars, and to advance learning and knowledge about how to support truth and integrity through technological and sociological research and education for communications in science, engineering, and medicine.

Keywords

Research integrity, citational justice, publishing ethics, scientific truth, GWAS, fake stuff, academic ghosting, FAIR Metrics.

Contents

Guardians 2023 Program

Guardians 2023 was held on October 9th as a half-day online event with 3 invited speakers:

- Dr. Nan Laird, Harvard University, Boston MA
- Dr. Walter Scheirer, University of Notre Dame, Notre Dame IN
- Dr. Alicia Andrzejewski, William & Mary, Williamsburg VA

who gave insightful presentations related to truth, integrity, information, and communication relevant to the current state of affairs for scientific research in today’s world. The workshop began with recognition of Dr. Anthony Fauci as our 2023 Guardian of Truth and Integrity.

Opening Remarks

- 09:00 Julie Neidich, BHAVI 2023 Guardian: Anthony S. Fauci (2023 Guardian slides and video)

Invited Talks

- 09:15 Julian Hecker and Nan Laird, Fallacies and Pitfalls in Genome-Wide Association Studies (JH slides, NL slides, JH+NL video)
- 10:15 Walter Scheirer, Photoshop Fantasies: Why is there so much fake stuff on the Internet? (WS slides, WS video)
- 11:15 Alicia Andrzejewski, Academic Ghosting: Towards an Academy of Truth-Telling (AA slides, AA video)

Technical Talks

- 12:30 Daniel Kristanto, Multiverse in Functional Magnetic Resonance Imaging Analysis (DK slides, DK video)
- 13:00 Koby Taswell, Consistent Bibliographic Data Formats with the BabbleNewt Project (KT slides, KT video)
- 13:30 Adam Craig, Managing Lexical-Semantic Hybrid Records of FAIR Metrics Analyses with the NPDS Cyberinfrastructure (AC slides, AC video)

Closing Remarks

- 14:00 Carl Taswell, Reproducibility, Reliability, and Integrity in Scholarly Research: What Accountability for Willful Disregard? (CT slides, CT video)

All slides and recordings of the talks are also available at www.BHAVI.us/BhaviHome/Symposia/202310.

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[*] All talks at Guardians 2023 were presented virtually and are available online.

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2023 Guardian: Anthony S. Fauci

2023 Guardian — BHA recognized Anthony S. Fauci, MD, as the BHAVI 2023 Guardian of Truth and Integrity. Throughout his career, Dr. Fauci has worked tirelessly to improve societal health through research in infectious diseases such as HIV, SARS, H1N1, and many more. During his time as the Director of the NIH National Institute of Allergy and Infectious Diseases, Dr. Fauci provided exemplary leadership in support of integrity in medical scientific research. His dedication to truth, honesty, and integrity proved crucial in the fight against the global COVID-19 pandemic during which Dr. Fauci and many other physician/scientists would have otherwise been swallowed by the sea of fake information that made it more difficult to save lives. For his lifetime of service and dedication to saving lives through integrity in clinical research, BHA honored Dr. Fauci as the 2023 Guardian of Truth and Intergity.

Julian Hecker and Nan Laird

Hecker, Craig, et al. 2023 — This talk and the associated slides, video, and article review common ways researchers misinterpret genome-wide association study (GWAS) results and how to avoid these fallacies and pitfalls. The authors review several relevant statistical methods, but one of the most important defenses against drawing wrong conclusions requires maintaining the appropriate mindset: Finding statistically significant associations between genetic variants and a phenotype of interest is not the end, but the beginning of a scientific journey.

Valid statistical methods do serve a purpose: Because a GWAS can consist of over a million statistical tests of association between the trait of interest and individual variants of all the genes in the genome, the likelihood is high that some tests will produce p-values less than 0.05 by random chance (DerSimonian and Laird 2015). Analysts need to address this bias by using statistical methods that correct the p-values with a stricter threshold of significance, such as the Bonferroni false discovery rate correction (Tam et al. 2019) or the versatile gene-based association study (VEGAS) methodology (Hecker, Maaser, et al. 2017). Even these corrections do not guarantee that subsequent studies will be able to replicate the results. The winner's curse is a statistical effect that leads to overestimation of the effect sizes of genetic variants that passed the significance threshold in GWAS (Zhong and Prentice 2010), which can lead researchers to underestimate the sample sizes they need for the next study to have the desired power. Several methods, including bootstrap resampling and empirical Bayesian estimation, can provide corrected estimates of effect sizes (Forde et al. 2023).

However strong the statistical association between the genetic variant and the trait variant, it does not tell us that the genotype causes the phenotype. As genes pass from one generation to the next, recombination, mutation, selection, and genetic drift act on them in complex ways, leading some pairs of genetic variants at different places in the genome to co-occur more or less often than one would expect, a situation known as linkage disequilibrium (LD, Slatkin 2008). Simple proximity of two genes to one another on the genome can lead to LD, creating statistical associations between genes without any causal relationship to the trait of interest simply because proximity causes them to be co-inherited more often (Lappalainen and MacArthur 2021). To account for this disconnect between correlation and causation, researchers use a category of methods called fine mapping to incorporate knowledge about the structure of the genome and rates of co-inheritance to identify which GWAS hit in a neighborhood with multiple such hits is most likely to be a causal variant (Schaid et al. 2018).

In addition to spatial proximity on the genome, natural selection and genetic drift can cause two genes to co-occur at higher or lower than overall average rates in a sector of the population with shared ancestry. This LD due to population stratification can lead the GWAS results to tag both genes as significantly associated with a trait that occurs at higher or lower rates in this same sector of the population, even when only one gene has any effect on it (Derks et al. 2022). While it is possible to correct for this association to some extent by including principal components of genetic ancestry as statistical covariates in the GWAS analysis (Price et al. 2006), it may be more effective to design the study to avoid introducing the effect in the first place. One way is with a family-based study design instead of a study that tests for associations throughout the general population (Derks et al. 2022). Examples include the transmission disequilibrium test (TDT, Schaid 1998) and family-based association test (FBAT, Abecasis et al. 2000).

The need for statistical corrections and additional analyses described above can make achieving the needed statistical power challenging. As an alternative to conducting a single sufficiently large study, researchers can use meta-analysis to combine results from multiple studies (Mikolajewicz and Komarova 2019; Steel et al. 2021; Abdellaoui et al. 2023). However, the predominance of study participants of European ancestry in past studies can bias results and limit the ability to generalize results to the rest of the population (Derks et al. 2022). Furthermore, the analysts need to check the metadata of the studies to ensure that the study designs are similar enough to allow comparison (Mikolajewicz and Komarova 2019; Steel et al. 2021).

Following the steps described above can help researchers to better identify a statistically promising association between a genetic variant and a phenotype, but they still cannot prove a causal association or reveal the mechanisms of cause and effect. GWAS hits often occur in non-coding regions of the genome with obscure regulatory functions (Abdellaoui et al. 2023; Aguet et al. 2023). Catalogues of known functional elements, such as the Encyclopedia of DNA Elements (ENCODE) (Moore et al. 2020) and GENCODE (Frankish et al. 2020), can help researchers leverage existing knowledge from other experimental methods (Kichaev et al. 2019). One important class of methods is quantitative trait locus (QTL) analyses, which involve searching for associations between locations on the genome, the QTLs, and various measurable features. These include associations between molecular QTLs and molecular phenotypes, including DNA methylation and production of specific metabolites (Lappalainen and MacArthur 2021; Aguet et al. 2023). They also include expression QTLs, which associate with downstream differences in the expression levels of other genes, as well as loci where both kinds of effects colocalize (Rheenen et al. 2021). These methods can extend to comprehensive post-GWAS analyses, particularly transcriptome-wide association studies (TWAS) and proteome-wide association studies (PWAS) (Gedik et al. 2023). Combining these locus-focused methods with information indicating similarity of annotations from single-cell gene expression, protein-protein interaction, and pathway participation features can lead to even more accurate identification of causal variants (Weeks et al. 2023). In this way, statistical data analysis and biological activity functional testing achieve a kind of synergy wherein statistical methods like GWAS identify candidates for study through lower-throughput laboratory experiments, which in turn provide knowledge of mechanisms of interaction that advanced statistical methods can use to more effectively find and prioritize subsequent candidate variants (Gallagher and Chen-Plotkin 2018).

Walter Scheirer

Photoshop Fantasies — In the past decade, the world has witnessed an increasing trend in fake posts, news, and online information. Recent estimates approximate that less than 60% of all web traffic is human with a majority of social media accounts operated by bots driven by automated algorithms (Read 2018). Elections and politics have been adversely impacted by fake information touted as fact with debates over what is fact or fiction becoming increasingly prevalent. When everything from deep fakes to memes recasts real life into fictional fantasies, how much can we trust the information we consume online?

Though fake information is rampant these days, modified images have been central to the history of propaganda, art, and entertainment. Authoritarian regimes such as the Chinese Communist Party under Mao Zedong used photo editing to rewrite history (Jaubert 1989). One significant example of this was removing the Gang of Four from images of Mao Zedong's funeral in an attempt to erase them from history. Although actions to rewrite history are often malicious at worst, misguided at best, picture editing in and of itself is not a purely evil act.

Since the first edited pictures in the 1840s, various methods have been employed to change the original image to something different, such as removing figures from a picture, cropping the edges to remove context, face swapping with cutouts, adding props, and more. Early photographers and artists used these techniques to improve the subject's appearance or add a sense of whimsy to the image by including fantastical figures. Some edited photography was obviously intended as a joke, such as an image of farmers cutting corn the size of logs. However, this intentional humor has not been the case for all edited images. Disputes only arise when an obviously impossible image is portrayed and contextualized deceptively as capturing and conveying truth, rather than recognizing the edited image as just that, ie, an image that has been altered no longer representing the truth.

Moving forward into the future of the digital age, photo editing techniques naturally lent themselves to digital picture editing with the creation of various image filters that would later become the foundations of software programs such as Adobe Photoshop. This change paved the way for cleaner removal or duplication of objects within an image as well as face swaps and other digital effects. Building from computer based signal processing for picture editing, AI became the next major step, enabling an interested layperson to engage in the art, without themselves having practiced the skills needed for photo-editing.

Today, with the internet as the 'frontier of the imagination', photoshop battles, AI-generated art, and edited memes have become the norm. By understanding the history, as a community, we can better learn to handle debates over truth and reality in the present and prepare for new futures as generated images become more widespread than in the past. For further discussion of this topic, see the book entitled "A History of Fake Things on the Internet" by Walter Scheirer 2023.

Alicia Andrzejewski

Academic Ghosting — Despite the respected image and prestige of those persons participating in academia, there exists a much darker underbelly to the institution. Universities may refuse or otherwise fail to protect their faculty professors and teachers from harassment by students and vice versa. Discussion of neurodivergence and/or mental illness has been heavily stigmatized, leaving faculty members with behavioral health challenges without support by their colleagues, mentors, and supporting staff. Ghosting whether by the institution during the hiring process and/or by colleagues and mentors while at work has become endemic to the academic system.

Ghosting can be defined as the act of disappearing from someone's life without a word. A pattern once rampant within online dating, it has now reared its ugly head within academia. During hiring, many aspiring faculty send in applications, yet never hear back from the hiring committee, the HR department, or administrative staff. Although being ghosted during hiring can be upsetting and leave highly talented individuals in the dark, some members of HR departments claim that they do so to not sour the individual on the institution should there be a later attempt to hire that individual. This perspective seems illogical since an interested academic on the job market could also be soured on the institution by not hearing back with an update in the first place.

Ghosting can be even more devastating when the ghoster is a mentor or colleague of the ghostee. Outside of a student's own skills, successful completion of Ph.D. degrees are dependent on the faculty mentor's timely participation in advising the student and helping organize the thesis review committee. Despite a mentor's crucial role, it is not uncommon for mentors to ghost a student, while still clearly being a part of the institution, often leading to great emotional, career, and financial damage to the student. Sadly, those who have successfully made it to the position of faculty professor are also not necessary safe from being targeted because colleagues ghost others for seemingly no apparent reason. It can be completely insidious with a slow decay in communication over time, or more obvious with an abrupt shift from constant and friendly communication to absolutely nothing at all.

Ghosting within academia may represent a lack of motivation to face tough conversations which simply must happen for the health of both individuals and the organization as a whole. Without addressing these problems within academia, the community will only become more unstable and the problems will likely worsen. Unfortunately, clear methods to fix the concerns are not immediately apparent. For ghosting during hiring, some hiring committee leaders have taken it upon themselves to personally email each and every applicant. But this task may impose a great cost in time and cannot be applied similarly to some of the other ghosting problems within academia. However, the best way forward to start is at least to begin the conversation and to spread awareness of the problems caused by academic ghosting. For more information and discussion, see articles in the Chronicle of Higher Education (Andrzejewski 2022; Andrzejewski 2023a; Andrzejewski 2023b) as well as an episode of the Academic Life podcast hosted by Dr. Christina Gessler featuring Dr. Andrzejewski (Gessler and Andrzejewski 2023).

Daniel Kristanto

Kristanto et al. 2023 — When conducting research, each choice made about methodology can impact to the results. These selections range from the actual experimental methods to the data processing methods performed, including statistical analysis of the results. To optimize across these various methods, a researcher can perform 'multiverse analysis', which considers the various branching paths of possible methodologies, ie, of different methodologic data processing pipelines.

This paradigm can be applied to functional magnetic resonance imaging (fMRI) assessment of human brain networks. To begin, a systematic literature review of 252 papers was conducted to determine the posssible forking methodological paths. Some common methods used were structural pre-processing, functional pre-processing, noise removal, functional connectivity definition, and graph analysis. Then using active machine learning, a smaller set of optimal paths can be deduced. Both study results and an online interactive web application where viewers can see the various possible pipelines are discussed.

Koby Taswell

S. K. Taswell, Anand, et al. 2023 — Appropriate reference citation serves as the foundation for ensuring research integrity, but managing a large number of resources can become burdensome. To address this concern, numerous organizations and research groups have developed a variety of automated tools for reference citation management associated with metadata formats to store the bibliographic data. Once properly stored in bibliography data files, citations can be used for references in documents or in other operations such as automated citation analysis for plagiarism detection.

BibTeX and BibLaTeX are widely used reference citation formats, common to the mathematics, computer science, and engineering communities for use with TeX and LaTeX document typesetting. Despite their decades-long history and wide recognition within these communities, they remain error prone due to format inconsistencies combined with various issues of instability and difficulty when debugging large-scale bibliographies. The BabbleNewt Project aims to address these deficiencies by providing a new format that can be easily converted to and from past versions of BibTeX and BibLaTeX while supporting migration to a more robust, fast, simple, and consistent JSON-like interoperable format.

Adam Craig

Craig, Athreya, et al. 2023b — Citation metrics that rate a publication more highly based on how many other works cite it create a perverse incentive to avoid citing potential rivals (S. K. Taswell, Triggle, et al. 2020). The FAIR Metrics, with FAIR an acronym for Fair Attribution to Indexed Reports and Fair Acknowledgment of Information Records, as defined in Craig, Ambati, Dutta, Mehrotra, et al. 2019, solves this problem directly by quantifying how fairly a publication cites previously published work, thus providing alternative metrics to incentivize fairness with citational justice (C. Taswell 2022). The 4 FAIR Metric counts measure the numbers of claims misquoted from or misattributed to prior work, quoted from prior work, presented as novel, or plagiarized from other sources. These counts are used to calculate the corresponding 4 FAIR Metric ratios which provide summary scores, each emphasizing a different aspect of citation practice. Unlike commonly used lexical plagiarism detection tools, the FAIR Metrics depend on entity equivalences between the concepts and ideas expressed in documents, not just lexical similarity between documents. Demonstration with a human analyst evaluating the FAIR Metrics on example texts provides a prototype workflow for use of the FAIR Metrics that enables human-performed peer review to be more objective and that serves as a standard for comparison of results from future automated algorithms.

This work extends the preliminary version of an analysis presented at eScience 2023 (Craig, Athreya, et al. 2023a), which described the successful application of a human-performed FAIR Metrics evaluation workflow to 5 reports and a brief description of methods for publishing semantic descriptions of the evaluation with the PDP-DREAM Ontology. Both the original workflow proposed in Craig, Ambati, Dutta, Mehrotra, et al. 2019 and that of Craig, Athreya, et al. 2023a focus on comparison of claims between one test document and one comparison document. This extended version Craig, Athreya, et al. 2023b of Craig, Athreya, et al. 2023a elaborates on the structure of these RDF description records and analyses 4 more example pairs. In a change from the earlier procedures, analysts were required to evaluate scores in comparison to all references cited by the test and comparison documents. This approach provides a more robust way to evaluate allegations of plagiarism via the creation of a RDF document clarifying which claims from the test document match claims that may or may not be referenced in other documents.

The authors selected 9 example test-comparison pairs for evaluation. One case was selected as a negative control representing a known pair of documents without plagiarism. Seven cases were selected as known plagiarism from the Retraction Watch database with differing forms and extents of plagiarism. The last case was selected as reported plagiarism based on the comparison documented in detail in Craig, Ambati, Dutta, Kowshik, et al. 2019. For each test document, a designated comparison document was chosen for evaluation. In general, FAIR Metrics ratio scores for test-comparison pairs of known plagiarism were lower than the negative control case, with the most extreme instances of known plagiarism having the lowest scores.

In the case of reported but not-yet-retracted plagiarism, which compared Wilkinson et al. 2016 to C. Taswell 2007, the FAIR Metrics analysis confirms this reported plagiarism as paraphrasing plagiarism, classifying the FAIR Principles claims wrongly misrepresented as novel by Wilkinson et al. 2016 instead as plagiarized from C. Taswell 2007. Overall, the FAIR Metrics scores found for Wilkinson et al. 2016 align with those of the extreme examples of plagiarism, thus confirming the plagiarism by Wilkinson et al. 2016 of C. Taswell 2007.

Carl Taswell

C. Taswell 2023 — As each year passes in the current era of information wars, the importance of maintaining reproducibility, reliability, validity, and integrity in scholarly research only grows greater, but there are not yet enforceable safeguards that have been adopted. In the long term, as a community of researchers, we should consider licensing analogous to that required in the professions of medicine, law and education. In the short term, the current situation leaves many questions unanswered. What steps can be taken now to respond to complaints from victims of plagiarism, misconduct, and fraud? Which organizations will remain committed not only to talking about preventing plagiarism, misconduct, and fraud but also sanctioning these violations of professional conduct when they occur? How can we not only heal from but also cure and prevent the problems of grooming, gaslighting, and ghosting in academia? Guardians 2024 will continue this conversation with the website open for submissions beginning on 9 January 2024.

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