Both procedures used iodinated contrast media, iohexol (Omnipaque 350; GE Healthcare) in this case. The cause of the "floating gel" was an increase in serum density from residual contrast dye still present in the catheter used for the procedures (1). Laboratory tests should not be performed, even if the serum is extracted from beneath the gel barrier. The effect of residual dye is unknown, but laboratory results may be falsely low because of dilution with contrast media or be erroneous owing to interference with the assay itself (2, 3). This phenomenon can be avoided by properly flushing lines prior to sample collection (4) and/or waiting at least 1 half-life (approximately 20 min) before collecting a peripheral blood sample.

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**References**


**Handling False Positives in the Genomic Era**

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The genomic era is upon us, promising to individualize medicine and creating a buzz among scientists, physicians, and the general public alike. Although it is easy to become entwined in the excitement and anticipation of the impending medical revolution, scientists and clinicians must be vigilant about novel and unexpected scientific findings to prevent genomics from tarnishing its own reputation with a major blemish: false positives. A recent "Commentary" article in the journal *Nature* highlights the prevalence and negative impact of false-positive publications and discusses strategies to avoid reporting false positives as novel findings (1).

False positives are not new to the world of science; however, the ease with which a study can accidentally generate false positives has dramatically increased owing to the contemporary availability and production of massive and complex data sets. Generating such large amounts of data inevitably leads to greater numbers of tests performed, allowing apparently stronger signals to emerge by chance with greater frequency than our
minds might naturally expect. New statistical methods are constantly being developed to assist in distinguishing true signals from artifacts. New data sets and new technologies allow many of today’s large-scale studies to be “hypothesis-generating” rather than the typical “hypothesis-driven” studies of the past. Therefore, signals often emerge for novel pathways or genes previously not known to be coupled with the studied phenotype. If the investigator and available statistical methods fail to recognize a signal as spurious, the results may be misinterpreted as novel findings that provide the key to unlocking the door to a new mechanism or pathway. These “novel findings” can quickly navigate their way into publication in high-impact, peer-reviewed scientific journals. Furthermore, never before has the general public been so enamored with science and medicine, a fascination that can lead to such “novel findings” easily making their way into national headlines in the mainstream news media. The inevitable quick follow-up of such “novel findings” will inevitably lead, in time, to the recognition that they are little more than false positives. But the damage has already been done. Publishing with the perception of a novel finding that in fact is actually nothing more than a false positive may delay a research program substantially or even disrupt an entire scientific career, particularly if the spurious finding is chased by an unsuspecting and enthusiastic young investigator. If misinterpreted and reported sufficiently often, false positives could lead to an increased distrust of and a reduced confidence in genomic research among the public and scientific communities, ultimately slowing down the progression of science.

Investigators, editors, reviewers, and the scientific community can collectively reduce the impact of false positives. The implementation of rigorous quality-control measures by investigators can reduce artifacts at the experimental level and can identify them before additional experiments are performed. A data-analysis protocol that includes data visualization (e.g., creating a Manhattan plot to visualize $P$ value vs genomic position) aids the human eye in identifying spurious signals, compared with analyzing data presented only in a table. Prompt replication studies, particularly with a new sample set and different experimental platforms with different sources of error and bias, are critical, not only for increasing confidence and supporting truth but also for identifying and verifying false positives. Finally, investigators can engage in functional-validation studies. Although technically challenging, particularly with novel findings involving unknown genetic elements, functional validation not only demonstrates the biological relevance of the findings but also leads to hypotheses regarding the mechanism and function underlying the association. Scientific journals and editors can avoid publishing false-positive results through careful selection of highly qualified reviewers who are experts in the technology used and are therefore more likely to identify even subtle biases within the study design that could lead to false positives. Subsequent to publication, mechanisms for rapid dissemination of scientific results (i.e., in online media and discussion forums) will ultimately support ongoing dialogue and exchanges of opinions between scientists. These discussions should be highly encouraged.

Although we must exercise caution when interpreting novel findings in scientific publications, we must also be vigilant not to become stifled or crippled by the fear of false positives and end up hampering scientific progress. The genomic era is an exciting time and holds promise for a medical revolution, but we must ensure that we progress forward with certainty and not go off on a tangent of false findings.

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