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EDITORIAL

EJHG to follow variation nomenclature and stimulate data reporting

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With the advent of next generation sequencing, basic, translational and clinical scientists in the biomedical field are confronted with a data deluge of unprecedented proportions. While in the past genetic data often were imprecise because of modest resolution of the technology, today the reverse is almost true. DNA data have become precise to the base pair. Indeed, more information is often obtained than one knows how to interpret.

In this situation, the least which journals, databases and other data sources can do to counteract confusion, is to be more stringent in nomenclature, in order to avoid ambiguity and degradation of the quality of high precision data. *EJHG* has decided to adapt its editorial policy, changing it from stimulating authors to follow existing nomenclature, to actively assess and sanction the nomenclature compliance of manuscripts to be published.

A second field where genetics journals may assist is in the improvement of the availability of annotation. It is well known that much data does not make it into the published literature, but also much of the data that does make it into the literature is not deposited in databases, while very suitable databases do exist. In time this leads to loss of information or of the traceability thereof. To address this issue, *EJHG* will also assess the data presented in manuscripts for their deposition in the appropriate databases.

As of this issue the instructions to authors will reflect these more stringent policies, which we expect to increasingly become common policy in biomedical sciences.

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