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Editorial

The only thing permanent is change

In seeking inspiration for this editorial, I decided to review *Genomics* Volume 1, Number 1 (September 1987). This turned out not to be an easy task because, instead of simply printing out some crisp PDF files or viewing the material online, I was forced to climb into my sport-utility vehicle and drive across town to the Health Sciences Library at the University of Washington. Once there, I found my way into the stacks and spent the afternoon excavating some history. Despite the inconvenience of actually having to go to a physical library, it was not at all an unpleasant experience because, buried deep within the building, neither my mobile phone nor my wireless e-mail device seemed to work. Thus, without distraction, I was able to lose myself “back in the day” when *Genomics* was a New Name, for a New Discipline, and a New Journal [1].

At first I thought I had found my theme for this editorial, that is, “how much things have changed,” using my trip to the library (instead of through cyberspace) as a metaphor for how far we have come. Certainly there have been tremendous technological advancements and data accumulation since the ink dried on the pages of the first production run of *Genomics*, but, somewhat to my surprise, the journal and its editors and contributors were remarkably prescient in identifying a number of concepts and themes that have stood the test of time through the Human Genome Project and into the current Genome Era. For example “bioinformatics” and “comparative genomics” were foundational topics for the journal even though these terms were not used at the time and, indeed, would not be coined or come into common use for another seven to eight years [2–5].

*Genomics*¹ was conceived as a new discipline “born from a marriage of molecular and cell biology with classical genetics and fostered by computational science” [1]. However, it has become much more than that and, indeed, the term is an icon of 21st-century biomedicine as evidenced by the epidemic proliferation of its semantic offspring (www.genomicglossaries.com/). *Genomics* as an approach, almost as a state of mind, has suffused so much of the biomedical landscape that it is challenging to practically define its scope for the purpose of specifying coherent topics and themes for a journal. Nevertheless, we want to provide guidance for our editors, contributors, and referees on this 16th anniversary of the first issue published in September 1987.

As we move forward into the future, we would like to emphasize the following areas that are, in many cases, a revival and elaboration of the foundational themes of the journal. We are interested in articles and reviews in the area of clinical genomics, which includes applications of genetics and genomics technologies to human disease, its etiologies, diagnosis, prevention,

¹ According to Tom Roderick of the Jackson Laboratories (personal communication), the term “genomics” was conceived during a small group discussion in a raw bar in Bethesda, Maryland, in 1986 following a large meeting at the National Institutes of Health. One of the founding editors, Frank Ruddle, had suggested the journal be called *Genome*, but Tom pointed out that this name had recently been taken when the *Canadian Journal of Genetics and Cytology* changed its name to *Genome* [6]. Tom then suggested they use the neologism “genomics” instead, an active word with the energetic ending “-ics,” a suffix with appropriate etymological connotations for the new field [1].

and treatment. We fully embrace the field of comparative genomics, which yields valuable insights into conserved and divergent aspects of function, regulation, and evolution. Bioinformatics and computational biology were innovative and groundbreaking aspects of *Genomics* in the beginning that we want to strongly reemphasize. This would include relevant topics from medical informatics, text mining, and data mining, particularly at the translational interface between clinical datasets and their research applications. We would like to see more functional genomics papers involving the use of large-scale and/or high-throughput methods to understand genome-scale function and regulation, including relationships to protein and RNA gene products and systems biology. Finally, we feel that it is very important to include significant advances in genomics technologies.

In addition to these topics, we would like to revive and emphasize some features that characterized *Genomics* in its earlier years. These include commentaries, book reviews, historical perspectives, tutorials, and mini and full review articles. We welcome your ideas, suggestions, and proposals in these areas. We are planning a special review issue to be published next year, and more information about this will be provided in the near future.

I thank those associate editors who have helped the journal over the years, some of whom have agreed to continue in this capacity, providing continuity and helping us to maintain the traditional strengths and high caliber of the journal. I also welcome the new associate editors, who bring new perspectives and energy and will work together to catalyze a renaissance of *Genomics*.

Finally, I extend my heartfelt appreciation to Dr. Victor McKusick, an inspiration to all, who honored me tremendously by inviting me to take his place as Editor-in-Chief of the journal. When Victor first telephoned me with this proposition of trying to fill his shoes, I was, at first, speechless. However, when I finally was able to respond I said: “Does this mean that I’ll be invited back to the Bar Harbor course?” Victor, with his characteristic wryness, replied: “Well, we’ll see.” Please help me in continuing the mission that Victor McKusick and Frank Ruddle began with the journal that both named and defined a new discipline: *Genomics*.

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