Downloaded from http://bioinformatics.oxfordjournals.org/ at :: on August 30, 2016

15 years of "Bioinformatics"

As we look forward to the year ahead, we also want to look back and acknowledge the outstanding contribution of our Editors and Associate Editors over the past year.

Bioinformatics remains the main reference publication in the field of Bioinformatics and Computational Biology as evidenced by high citations and a 10% increase in submissions - from around 2000 papers in 2012 to 2200 papers in 2013. During 2013 more than 700 papers were published in Bioinformatics, and for 160 of these the authors selected Open Access publication.

Our model of Editorial rotation always makes the end of the year a sad time as we say goodbye to some of our Associate Editors. This year Mario Albrecht and Martin Bishop end their terms as Associate Editors, our sincere thanks go to both of them. Martin has been with the journal since its inception and has handled in excess of 5000 manuscripts during his time as an editor. The journal is deeply indebted to him for his contribution.

The beginning of a new year is also a great time to welcome new Associate Editors who bring their own ideas and renewed enthusiasm. This year we welcome Robert F. Murphy, who will focus on the areas of biological imaging and information extraction.

2013 was a special year for Bioinformatics since it marked the 15th anniversary of the establishment of the journal in its current form - with the name and current editorial organization. On this occasion we want to recognize the exceptional contributions of all our past Associate Editors, Editors and editorial assistants. In particular, we want to highlight the outstanding work done by past Editors Alex Bateman, Martin Bishop, Christos Ouzounis, Chris Sander and Gary Stormo in organizing and consolidating our journal during critical times in its history. In recognition of their immense contributions we have appointed Alex, Martin, Christos, Chris and Gary as our first 'Honorary Editors'. Their advice will certainly prepare us better for the many scientific and editorial challenges that the field of bioinformatics is facing.