CrossMark

Introduction to Mammalian Genome special issue: Informatics and Integrative Genomics—Part 1

Ann-Marie Mallon[1]

Last year, we celebrated 25 years of the Mouse Genome Informatics (MGI) resource from the Jackson Laboratory. The development of MGI and other global bioinformatics resources and analytical methodologies has accelerated over this 25-year period in a vast array of scientific disciplines and across many research groups. Informatics and integrative genomics is a huge field, driving forward new areas of insight in many aspects of mouse genetics and functional genomics. In this special issue, we are focusing on reviewing the breadth of work in the larger global bioinformatics infrastructure that underpins this area.

The special issue is broken into two parts, with Part 1 reflecting on the 25 years of MGI. Part 1 begins with a historical perspective of MGI by Janan Eppig and colleagues reviewing how MGI has changed over the last quarter of a century and what plans are in place for the future. The review by Susan Bello et al. describes the Allele, Phenotype, and Disease data within MGI and plans in place to improve access and analysis. The use of mouse phenotype data to drive translational research into human disease has expanded rapidly, and this review describes methods implemented in MGI to enable researchers to identify novel human disease genes. Underlying all of the MGI data is the mouse reference genome and gene set. The article by Yunzia Zhu et al. focuses on the process of building this unified mouse gene catalog. Following on from this, Mary Dolan et al. describe how the mouse gene catalog is associated with orthologous human genes to enable comparative genomics.

The review of the MGI Gene Expression Database (GXD) by Constance Smith et.al describes an integral part of the MGI resource which enables users to access a vast array of gene expression data in the context of other genetic-, functional-, phenotypic-, and disease-orientated data. Data accessibility is a key component of bioinformatics, and Howie Motenko et al. describe a new tool MouseMine, which is built on the InterMine framework to provide a new data warehouse for accessing mouse data from MGI.

The special issue will continue in Part 2, to cover a vast array of other bioinformatics aspects from global mouse infrastructures, to underpinning resources for the reference populations, complex trait analysis, mutagenesis, and embryonic imaging to a final section on integrative genomics which will focus on cross-species applications.

✉ Ann-Marie Mallon
    a.mallon@har.mrc.ac.uk

[1] MRC Mammalian Genetics Unit, MRC Harwell, Harwell
     Science and Innovation Campus, Harwell OX11 0RD, UK