Editorial: Omics research and bioinformatics – joined-up thinking or anarchy?

DNA makes RNA makes protein and cells are full of many other molecules – these are the subject matter of genomics, transcriptomics, proteomics and metabolomics, and no doubt lots of other omics too. Browsing in the library, one comes across a journal called Omics: A Journal of Integrative Biology. The articles in the current issue appear to apply individual omics, not joined-up omics. The first step in genomics is to characterise the DNA sequence and try to predict all the RNA and protein molecules it might encode: not too bad in bacteria, but fairly hopeless in higher organisms. Unlike the genome, you cannot get a sample of the entire transcriptome or proteome or metabolome: they depend on the conditions when you sample. Their complexity is largely unknown but might be expected to follow transcriptome < proteome < metabolome. The state of a biological system can be described in terms of the quantitative measurement of these constituents. This is easy to state but harder to implement, and is probably most advanced for the transcriptome (microarray data on gene expression).

Protein identification and quantification by mass spectroscopy are making a lot of progress. We have known about the contents of the metabolome for longer than the other two. So the experiment is to perturb the system, measure the response, model the result and predict what it means in terms of analysis of multiple interactions of gene products in biological networks. The perturbation method, which also exists in mathematics, can work well only with single, small perturbations. With large perturbations, systems become non-linear and impossible to analyse. This is the main reason that we are able to make only a few hypotheses and get only a few answers for each experiment. Even for linear systems, there is quite a challenge in terms of data storage and retrieval and statistical analysis, which are crucial for success.1 It can be argued that working with single genes and then single omes and their subsystems will lead to faster understanding than trying to analyse everything at once. In the plant world at least, there is a lot of enthusiasm for the joined-up thinking.

Martin Bishop
Editor, Briefings in Bioinformatics

Reference