



100 YEARS AGO

The unfortunate fatal accident which occurred at the Fulham Public Baths on December 23 serves to show how dangerous an electric shock may be when the conditions are such that really good contact is made. In this case, two bathers were killed by standing up in their baths and putting their hands on a metal rail running along the top of the partition between the baths; on top of this rail ran the iron pipes containing the electric-supply leads. It seems that there was leakage, possibly in a faulty lampholder, to these pipes, which were insufficiently "earthed". The bathers therefore completed the earth through their bodies to the bath itself, and thus received a shock which, in spite of the fact that the pressure could only have been something like 170 volts, had fatal results on account of the very good contacts which existed. The circumstances of the case are altogether exceptional, and there is absolutely no need for users of electric light to take any alarm.

From *Nature* 8 January 1903.

50 YEARS AGO

Gregorio Ricci-Curbastro, inventor of the tensor calculus, was born at Lugo, in Italy, on January 12, 1853. The absolute differential calculus, as he himself called it, gained little attention until Einstein used it for the formulation of general relativity, even though it had reached a mature form by 1895, after some ten years of growth. It was so little thought of, indeed, that in 1901 Ricci was denied the Italian Royal Prize in mathematics on the ground that the calculus was "useful but not essential for the treatment of some mathematical questions". Nevertheless he himself retained a belief in its value... In 1912 Einstein's attention was directed to it by his colleague, Marcel Grossmann, and the outcome was the relativistic theory of gravitation published in 1916... The relativistic principle of covariance, namely, that the general laws of physics can be expressed in a form which is independent of the co-ordinate system, has a meaning only in so far as there exists a way of expressing them in such a form. The Ricci calculus provides a means of doing so... The tensor calculus is fully established as one of the main instruments of modern mathematics, and gives to its inventor a permanent place in the history of the subject.

From *Nature* 10 January 1953.

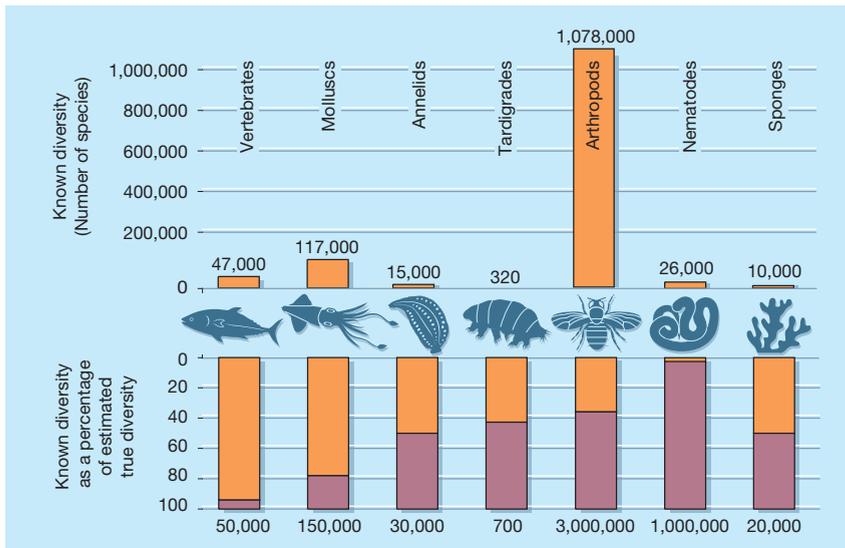


Figure 1 Known and estimated diversity of a selection of animal phyla. The histogram above each representative image indicates known diversity (in terms of number of species). That below represents known diversity as a percentage of estimated true diversity, shown by the number at the bottom. This graphic provides only a keyhole view of biodiversity and the task the systematist faces. It is confined to just a few phyla of the larger eukaryotes (loosely, organisms whose cells contain a nucleus), of which there are many more groups, including the plants and unicellular forms. And then there are the vast numbers of microscopic prokaryotes, consisting of the bacteria and archaea. Molecular barcoding methods may be the only way of charting unknown diversity.

using DNA sequences. All cellular organisms have the highly conserved small subunit ribosomal RNA (SSU) gene, which can be isolated specifically even from bulk samples of 'environmental DNA'. By surveying SSU gene sequences in a sample, it is possible to identify how many different taxa are present, and assess their relationships to previously described and sequenced groups. All environments sampled yield the same pattern: many of the constituent microorganisms come from major groups unknown to traditional microbiology, and the diversity of prokaryotes is probably 100 times higher than was previously expected^{6,9}. Similar SSU gene surveys of communities of eukaryotic microbes, such as marine picoplankton, also suggest that traditional, descriptive methods have sampled only the tip of diversity¹⁰⁻¹².

It is now accepted in bacteriology that taxa can be identified using sequence data, and rules of thumb for defining taxa based on sequence difference are developing¹³. The taxa so defined have been termed 'phylo-types'¹⁰ or 'molecular operational taxonomic units'¹⁴. Thus a DNA sequence can be used to both identify and classify an organism, much as a barcode identifies supermarket products.

Hebert *et al.*³ extend this idea to non-microbes, and propose that a database of DNA barcodes for identification of all animal taxa should be established. They test the use of the mitochondrially encoded cytochrome oxidase I (COI) gene in assigning specimens to different taxonomic levels — phylum, order and species. The COI gene

is a good target, as it is present in all animals, in many identical copies per cell, and is known to evolve relatively quickly. It carries sufficient 'signal' to allow differentiation between closely related taxa, and in a survey of moths collected around Guelph, Ontario, the authors show that the COI barcode can in most cases yield a reliable assignment to previously identified and sequenced species. Other insect specimens were correctly assigned to the superfamily level, and Hebert *et al.* claim that in general the approach can identify which phylum a sequence derives from.

This is indeed a promising approach. Many potential barcode sequences already exist in public databases: about 12,000 COI sequences, over 20,000 SSU gene sequences (from all organisms)¹⁵, and more than 50,000 sequences from the 'ribosomal internal transcribed spacer segment' (from higher eukaryotes). Plant systematists have also extensively surveyed the photosynthetic *rbcl* gene¹⁶. My group has used the SSU gene to successfully barcode soil nematode biodiversity¹³, and the large subunit ribosomal RNA gene has been used for identifying freshwater fauna¹⁷. It is not necessary to limit data collection to one gene, as sensitive amplification techniques allow the isolation of several sequences from one specimen. Given technological advance and genome-scale sequencing, sequencing of several barcode genes for large numbers of specimens could be achieved rapidly and cheaply.

A major unresolved issue is how closely these molecular taxa correspond to what