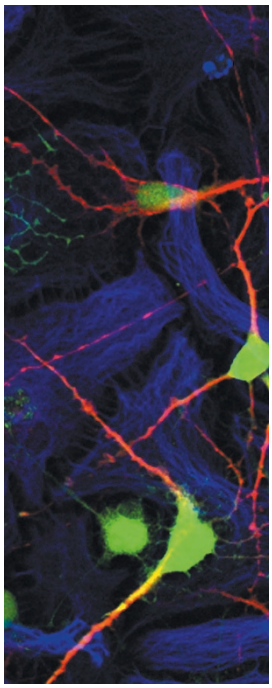
nature
cell biology

Signalling help



These days, signal transduction aficionados have a hard time. In the late 1970s, signalling emerged as a fully fledged field and since then, discoveries have been forthcoming at ever increasing rates. A mere decade ago, only a handful of papers was available for most of the limited set of players under study. Today, the number of researchers has mushroomed, and with them, the spectrum of model organisms and scientific approaches to the problem. As a result, the publication rate in this area has exploded: PubMed lists 6,770 papers for the keyword signalling in the 1970, up to 13,178 in the following decade, 89,167 in the 1990s and the new millennium has already seen 53,167 papers on the subject. Similar statistics apply to individual signalling proteins: the protein kinase family JNK/SAPK was covered by 1,593 papers in the 1990s and already 2,036 since 2000, while phosphoinositide 3-OH-kinase papers grew from 3,441 to 3,739 over the same period.

Tens of thousands of papers annually means that it is almost impossible to maintain up-to-date knowledge about individual signalling pathways, let alone to keep an overview over the field. The time is ripe to address this information overload. Platforms have to be developed to allow intelligent access to the information resource collected in the over 200,000 publications on the subject. To address this need, the Nature Publishing Group (this journal and *Nature* in particular), have formed a collaboration with the Alliance for Cellular Signalling (AfCS). The AfCS represents a sizeable group of leading scientists, formed with the aim of revolutionizing signalling research through 'big biology' approaches.

At the heart of this collaboration is the development of a comprehensive and free online resource, the Molecule Pages (MPs), a relational database of all significant published qualitative and quantitative information on signalling molecules. Although the emphasis is on mouse, orthologues far and wide will be covered. Importantly, the database aims to capture 'molecular states' and complex relationships between molecules, so that, for example, changes in a protein's functional interaction spectrum after activation are captured. This database will also allow entirely new insights to be gleaned through intelligent mining: the MP database was developed with the specific aim of allowing modelling of connections, and indeed whole pathways. An explicit goal is to filter the data to present only validated information. Thus, much of the data will be entered by leading researchers and every MP will be comprehensively peer reviewed by *Nature*. We regard an MP as a new fully fledged form of publication.

Owing to the complexity of multiple interconnected signalling networks, it is clear that the molecule-by-molecule approach followed by most individual laboratories will only yield part of the knowledge required for a comprehensive understanding of the exquisite specificity and sensitivity generated by the limited set of signalling molecules. Integrative large-scale approaches are now required to define all the components of signalling systems and to describe their complex overlapping physical and regulatory interactions. In this context, a second goal of the AfCS should be highlighted: the group has set up several laboratories with the long-term aim of mapping signalling pathways comprehensively in mouse B lymphocytes and cardiac myocytes.

A first version of the MP database, embedded in a new web-resource called the *Signalling Gateway*, will be launched this month. Furthermore, after validation, primary data from the AfCS laboratories will be released on the *Signalling Gateway* without restriction or delay. The site will be freely accessible at www.signaling-gateway.org. Further information on the project can be found on the existing *Signaling Update* (www.signaling-update.org), which will form part of the gateway, as well as a supplement in the December 12th issue of *Nature*. We hope that this site provides a useful tool to navigate the complex signalling landscape and that it will catalyse progress by pointing to facts and connections otherwise buried in the fast-growing mountain of information. We also hope that the interested reader will actively contribute to the project as an author or referee, or simply by providing feedback. This is an open project driven by the community for the community and it relies on active contribution to succeed. □