The way biologists conduct science has changed dramatically in recent decades, and this has and will continue to present significant challenges, argues ISCB President Professor Burkhard Rost.

What is the secret to the International Society for Computational Biology's (ISCB’s) success?

There is a very simple answer: passion. Intelligent Systems for Molecular Biology (ISMB), ISCB’s main activity, began as a meeting – and remained that way for a decade. In 1997, we decided to move it to the level of a society. In some sense the idea was to cement the future of the meeting but also to hire personnel and have a budget so that many of the things done by scientists would be done by professionals hired for that purpose.

In recent years, I believe what has made ISCB so successful has been that it opened itself up to input from people with a lot of passion and ideas. Everybody who has contributed has felt that there is something growing and that they have contributed. It’s not a rigid, closed circle with only some people in the know. Instead everybody can come, act, and create something important and new. In some sense, I feel proud that we have realised this. But ultimately the word is passion, meaning the passion of the scientist and of people who are very motivated and able.

Another secret to our success might lie in our change of focus. Scientists are extremely good at putting in a lot of work for a deadline, but too overloaded for continued investment of time. Societies are intrinsically structured around the idea that everybody contributes something every day, which is completely the opposite to the way scientists act. What we have done is rework the system to make it fit the people it represents.

Through what means does ISCB communicate the significance of computational biology to the larger scientific community, governments and the public?

The major way in which we do this is through our meetings. Our largest meeting is the ISMB conference, and then we have the ISMB European Conference on Computational Biology (ECCB), which is typically...
attended by about 2,000 people and is the main meeting in the field. Then there are regional meetings: ISCB Latin America and ISCB Africa are held once every two years, and ISCB Asia takes place every year. We also have focused meetings; for example, the next in Europe will be the Next Generation Sequencing (NGS) conference in June which will be held in Barcelona, Spain.

Has the field of computational biology evolved significantly over the course of your career?

20 years ago, a biologist asked a question and answered it more or less clearly in one experiment. However, over the last decade high-throughput biology has become dominant. Increasingly, experimental results no longer give you a clear answer, only a probability. This is where the line between computational and experimental biology is becoming blurred, and why handling data properly is becoming an important part of experimental biology now.

What specific challenges does the analysis of biological data pose?

In biology, data changes incredibly fast. To illustrate this, every time I want to develop a new drug or ask a certain question, my first step is to find out what is known, so I look up in databases what sequences are out there that have something to do with mine. These databases of protein sequences are growing rapidly. Computers may double in speed every 18 months, but biological databases are currently doubling in much less than a year. Currently, I’m managing a server that runs 1,000 queries a day and every day I can do less than the day before. There is no way that the growth of computers is going to solve this problem – we are fighting a losing battle.

The next issue is that if you go to the doctor five years from now, you will not receive the optimal treatment because our computers are not fast enough. This is a problem that already exists, it’s not hitting people today but it will hit them in a few years’ time.

How important will big data analysis be to advancing the field?

It’s immensely important. It becomes more central every day and that really has to do with the incredible advance of next-generation sequencing. Big data is growing faster than computers; the big data challenge is exploding in importance in life sciences. There are a few roles this will play into in the future, eg. for personalised health. Decisions within hospitals are about speed, requiring data to be handled rapidly. A solution is possible only if you can somehow collate the information together.

What progress has been made in this direction?

We are in a field where we are always behind, so the progress is amazing. If you look at other disciplines, the degree to which computational biologists are saving resources to do the best with the time they have is incredible.

Do you believe it is necessary for the advancement of computational biology that open access to publicly funded scientific and technical research literature becomes a reality?

ISCB is a member of the Federation of American Societies for Experimental Biology (FASEB) and we are the only member clearly supporting open access. One reason is we believe that big data challenges cannot be handled by single groups. We think that the only solution comes from sharing as much as we have and avoiding duplication of effort as much as possible.

Can you summarise your goals for ISCB in the coming years?

ISCB currently has 3,000 members. When I became President in 2007, we were hovering around 1,200, so we have more than doubled since then. If we doubled in membership again over the next five years, that would be great. I believe that it’s achievable, but it clearly requires a push. The field is ready for it as the demand for computational biology is high enough.

In many ways this is a personal view, but I believe the only way to do this is to become a federated society. There are many national societies that have numbers close to several thousand, and if they all joined, ISCB would be much larger. That would be my dream going forward, but it will not be easy to achieve.