

Box 2 Cross-functional individuals

In the course of compiling this survey, several investigators remarked that it tends to be easier for computer scientists to learn biology than for biologists to learn computer science. Even so, it is hard to believe that learning the central dogma and the Krebs cycle will enable your typical programmer-turned-computational-biologist to stumble upon a project that yields important novel biological insights. So what characterizes successful computational biologists?

George Church, whose laboratory at Harvard Medical School (Cambridge, MA, USA) has a history of producing bleeding-edge research in many cross-disciplinary domains, including computational biology, says, “Individuals in my lab tend to be curious and somewhat dissatisfied with the way things are. They are comfortable in two domains simultaneously. This has allowed us to go after problems in the space between traditional research projects.” A former Church lab member, Greg Porreca, articulates this idea further: “I’ve found that many advances in computational biology start with simple solutions written by cross-functional individuals to accomplish simple tasks. Bigger problems are hard to address with those rudimentary algorithms, so folks with classical training in computer science step in and devise highly optimized solutions that are faster and more flexible.”

An overarching theme that also emerges from this survey suggests that tools for computational analyses permeate biological research according to three stages: first, a cross-functional individual sees a problem and devises a solution good enough to demonstrate the feasibility of a type of analysis; second, robust tools are created, often utilizing the specialized knowledge of formally trained computer scientists; and third, the tools reach biologists focused on understanding specific phenomena, who incorporate the tools into everyday use. These stages echo existing broader literature on disruptive innovations¹ and technology-adoption life cycles^{2,3}, which may suggest how breakthroughs in computational biology can be nurtured.

1. Christiansen, C.M. & Bower, J.L. Disruptive technologies: catching the wave. *Harvard Business Review* (1995).
2. Moore, G.A. *Crossing the Chasm: Marketing and Selling High-Tech Products to Mainstream Customers* (HarperBusiness, 1999).
3. Rogers, E.M. *Diffusion of Innovations* (Free Press, 2003).

discover how to incentivize individuals in such a way that they support scientific discovery. One possibility is being tested by InnoCentive (partnering with Nature Publishing Group; <http://www.innocentive.com/>), which allows participants to pose scientific problems and offer cash prizes to other participants who provide a solution.

As in real life, different types of social interactions may justify different social networks, such as LinkedIn (<http://www.linkedin.com/>) for professional networking, which has thrived, even in the shadow of more general-purpose larger networks like Facebook. Several research-oriented efforts have been started, such as Sage Bionetworks (<http://sagebase.org/>), whose CEO, Stephen Friend, predicted earlier this year the coming obsolescence of “hunter-gatherer approaches,

where large groups collect massive clinical and genomic information and expect that they as the data generator will be the data analyzer” (<http://www.xconomy.com/national/2010/01/06/five-biotechnologies-that-will-fade-away-this-decade/>). The two studies discussed above demonstrate successful applications of alternative paradigms for data analysis and data generation. When recruiting expertise to create these kinds of platforms, says Su, “it’s hard to find people who have really traversed both computer science and biology. Discovery-oriented computational biologists with experience working on collaborative projects involving experimental scientists are particularly valuable.”

1. Cooper, S. *Nature* **466**, 756–760 (2010).
2. Eriksson, N. *PLoS Genet.* **6**, e1000993 (2010).