

Adapting commons regimes for biological information

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I should first precise that I am not a biologist nor a biotech specialist. My interest for the issues addressed by this panel comes from 2 sides: my company is a provider of services for the public debate by citizens of policy issues, and among these issues public health and the impact of R&D orientation in the biotech domain are prominent; I am also an analyst and promoter of information commons at large, and one of the key issues there is how to adapt the commons regimes to the situation in various domains (software, various media, biology, ...) or subdomains (genome, seeds, cells, immunology, biomedical nanotech, ...).

The key difference between domains lies in the relation between information and other entities. In the field of software, models of computation and universal machines make it possible to abstract information and its processing from execution environments. Of course a particular information processing can still be motivated by the wish to obtain some effects when projecting back the resulting information in an interpretation domain for presentation to a human being or for control of some physical process. However, there is a whole range of activities in which one can consider information processing per se, abstracting it from carriers and interpretation domains. When information is used to represent media contents, one is not far from the same situation, but a new dimension is introduced by the existence – installed prior to digital networked media – of physical carriers that have an economy of their own.

Let's now look at biology. The modelling and isolation of information layers in many areas of biology (genetics of course, but also proteomics, immunology, neurosciences, physiology of perception, cellular processes, physiology of development) is fully part of what gave birth to the information era. However, there are huge differences between these various fields with regard to how much one can or not consider information separately from the environment in which it interacts with other biological constructs. DNA sequences are closest to pure information (the relationship between information representing a DNA sequence and the DNA molecule itself is a pure transcription: sequencing or synthesis), but their expression in a real organism is dependent on an environment that can not be taken for granted as much as for software. When one considers evolutionary processes, this dependency on context, systems, architectures and history at many scales becomes even more important².

Some may say that also for software, real products and services are not reducible to the software itself. However we are speaking here of a much more radical difference. First, while you can combine software code or components in extremely diverse ways in order to obtain a huge variety of functions in many different domains, only a very limited part of the combinations that can be done in the biological information domain work at all (in a real-life

1 Talk at *Open source biotech* panel in Wizards of OS 4, Berlin, September 2006

2 The reader can further explore this complexity by reading a small opus by Henri Atlan (in French): "La fin du 'tout génétique' ?": Vers de nouveaux paradigmes en biologie, INRA, Paris, 1998 or a very large one by Stephen Jay Gould: "The Structure of Evolutionary Theory", Belknap Press, 2002.

biological situation) and produce useful results. Enough to produce huge diversity in nature, but only under strong feedback from the cell, organism, population and environment. Second, biological information is actually scarce in terms of the values it can take. This is one of the reasons why granting property-like monopolies for biological information has such extreme consequences (for software it is only from the accumulation of patents or from patents on some essential algorithms that one obtains similar disasters).

The result of these properties is that while it is of course needed to put pure genomic information under a commons regime, it is far from sufficient for obtaining the benefits that we are likely to expect from such a regime. For one thing, we will get these benefits only if some higher-level biological entities also are under some form of commons regime: cell lines, seeds, for instance. For another, we will also need to attach governance mechanisms to the biological commons. Biological entities are not pure information, which has a bearing on the relationship between the commons and economic activities and the governance mechanisms requirements. This calls for the choice of adapted commons regimes, that are also made necessary by ethical issues of a different nature than those encountered for, say, software.

It turns out that there were quite a few rights regimes in history that tried to address at least partly these issues, and which the norm setters have worked hard on destroying from the 1930s to recently. The 19th century English plant variety certificates achieved a disjunction between production of a variety (which they submitted to an exclusive right) and derived innovation (which remained free). This has been progressively weakened by restrictions about derived innovation in the UPOV conventions. The restriction of drug-related patents to their production processes, when and where it was in place, achieved the objective of leaving the molecules, that are connected to the biological scarcity of drug targets, in the commons, while accepting temporary monopolies for their synthesis or extraction technology. We all know where we stand now on this. We have thus some wisdom from the past, but it is clear that new mechanisms are also needed.

James Love (who speaks in this panel) has proposed with Tim Hubbard to create a disjunction between the market for innovation for drugs and the market for producing drugs, which is clearly a very useful step carefully adapted to these “mixed” industries that have both a physical and informational nature, and takes in account the need for a significant upfront investment.

In other biological domains, such as seeds and plant varieties, organisations such as Suman Sahai's Gene Campaign, or Semences Paysannes in France have created commons regimes that give a specific role in terms of governance to the community producing the entities that are made part of the commons. A difficult issue is how to connect or not the issue of fair returns for these communities with the definition of the usage rights for the entities that they have cared for or helped produce. This issue came prominent in the debates on genetic resources and traditional knowledge. My own feeling (inspired by the examples quoted above) is that rather than using property-like mechanisms and the related contracts for the access and usage rights, one must look at new approaches combining universality of rights of access and usage (with appropriate limits on this usage), disclosure rules, conditions on governance, and direct or indirect remuneration.

When biological information and new biological entities are extracted or produced mostly by scientific and technical communities, there are complex issues of governance of their usage. These issues are exemplified in the growing exchange of synthetic biology compounds (components of synthetic “cell-like” biological “machinery”). One will need at the same time a self-governance of the scientific communities and an external societal governance process, with a dialogue between the 2. This is also true for large databases of individual biologic information that raise huge ethical and political risks, in particular when they are connected to massively applicable biometry, and also raise serious risks in terms of the economic balance for health systems.

I would like to leave it here, with more open questions than true answers, for a deeper discussion to take place.

More info:

- On general information commons issues including for biological information : Philippe Aigrain, Cause commune; l'information entre bien commun et propriété, Editions Fayard, Collection Transversales, 2005, downloadable under a CC license at <http://www.causecommune.org>, in French, soon available also in Italian and Arabic. In English, see Philippe Aigrain, Positive Intellectual Rights and Information Exchanges, initially drafted in May 2000, revised in July 2001, final version published in [Rishab Ayier Ghosh, ed., CODE, MIT Press, 2005](#). Former version is on-line at the Free / Open Source research community, <http://freesoftware.mit.edu/papers/aigrain.pdf>
- Articles on biology and biotech issues from the Transversales Sciences Culture site (in French), <http://grit-transversales.org/recherche.php3?recherche=biologie&Submit=Go>
- Specifically on commons approaches in biology: K. Ravi Srinivas: The Case for Biolinuxes and other pro-commons initiatives, The Sarai Reader 2, 2002, pages 321-328, <http://www.sarai.net/journal/02PDF/10infopol/09biolinux.pdf>
- On rights regime in the seed domain: Suman Sahai / Gene Campaign, farmer rights and IPR, <http://www.genecampaign.org/We%20stand%20for/Farmers%20rights&IPR.html>.