

available filters and dramatically decreases clogging and breakage. This allows undesired components to be easily eliminated during blood diagnosis. Third, microscale electrophoresis using bacterial cellulose in a low-viscosity polymer matrix results in a dramatic improvement in separation and detection of analytes compared with current techniques. And finally, the unique light amplification properties of Nata de Coco^{6,7} provide a much greater level of detection sensitivity compared with other light amplification systems. All these properties allow optimized detection of genetic variation by virtue of better separation resolution and higher detection intensity of biomolecules⁷.

Our *in vitro* results using the methylthiazolydiphenyl-tetrazolium bromide (MTT) assay in the human leukemia cell line THP-1 also indicate that bacterial cellulose does not upregulate CD86 or CD54 expression, suggesting it is unlikely to be allergenic (Fig. 1e). Indeed, bacterial cellulose is already under clinical development as a scaffold for tissue-engineered products⁹.

Nata de Coco is just one of numerous nanomaterials found in nature that could be applied in innovative nanotechnology products and devices. Cellulose is the most abundant material in nature and, apart from bacteria, it can be derived from sources as diverse as wood, cotton, animals and plant cell walls. Other abundant natural materials that may be mined for nanomaterials include silk, collagen, chitin, chitosan and polylactic acid.

Recently, much of the emphasis in nanotechnology has been on synthetic materials, such as carbon nanotubes, nanoparticles (colloidal gold, quantum dots, latex and so on) and inorganic nanomaterials (ZnO, TiO₂, silica). For these synthetic nanomaterials to be applied as drug carriers, medical treatments, implants, tissue engineering constructs and cosmetics, extensive investigation will be necessary to establish their biocompatibility, safety, immunogenicity and allergenicity. Although advances in these areas are exciting and should continue to be funded and supported, we should not forget that many materials are available directly from the natural world with interesting properties on the nanoscale. These materials have a proven safety record in humans, biodegradable properties that make them environmentally friendly and in certain cases economic advantages over more sophisticated and expensive products and technologies.

Bacterial cellulose is just one attractive source of nanomaterials for use in medical and food applications. But the potential for naturally occurring nanomaterials is boundless. As we begin to use naturally occurring nanomaterials like Nata de Coco in applications beyond medical diagnostics, we will see that these natural nanomaterials are not just an alternative; rather, they may well be the preferred alternative.

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The author declares no competing financial interests.

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Systems biology standards—the community speaks

To the editor:

Your editorial 'Standard operating procedures' in the November issue (*Nat. Biotechnol.* **24**, 1299, 2006) highlights the impetus for standards development in biology. Such standards are particularly important in the area of systems biology, which aims to build models and quantitative simulations of complex biological systems. In particular, standards concerning modeling workflows, data formats and model publication are needed to facilitate collaboration and communication between modelers and experimenters from diverse scientific backgrounds. Various aspects of standardization have already been addressed, such as minimal requirements in the annotation of biochemical models (MIRIAM¹), compatibility of tools for kinetic modeling² and lessons that can be drawn from standards in high-throughput technologies³. Standardization is intensely debated in the systems biology community and plays a major role on the level of research politics: almost all systems biology projects that are currently funded by the European Commission (Brussels) promise to develop or define standards.

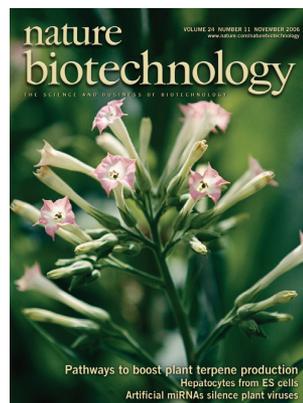
Here, we present the results of an online survey conducted to assess which *de facto* standards are already established in the

community and whether scientists would appreciate the enforcement of further standards (**Supplementary Results** online).

We have also explored the usage, advantages and shortcomings of existing methods and software tools. The 125 respondents from all over the world (75% modelers, 4% experimentalists or 21% both) cover various fields of systems biology research, including modeling of individual pathways, investigation of complex processes, development and application of computational methods and software development.

We provide here a concise summary of the most predominant opinions about standards (for a detailed evaluation of the survey, see **Supplementary Table 1** and **Supplementary Results** online).

About 80% of the respondents consider the creation of standards necessary or desirable: standards are expected to improve model reuse, expandability and integration, and allow for more productive collaboration. It was also pointed out that standards improve communication between software tools, free exchange of information and comparison between different studies; as a result, reimplementing of models becomes easier or dispensable, which reduces the duplication



of work and the possibility of implementation errors. Theoreticians and software developers need benchmark data as experimentally verified gold standards to apply and to improve their methods. Standards are also useful for educational purposes.

On the other hand, respondents also expressed the concern that standards should be flexible, not become too restrictive and not prevent alternatives or new developments. Those respondents who were against standards argued that biology is too complex to be standardized and obeying standards may cause practical difficulties.

The survey also revealed which tools and techniques are used for different applications (Supplementary Table 1 online); our findings may be instructive for several reasons: first, for researchers with an experimental background, they show the modeling and analysis methods suitable for particular biological problems; second, they provide modelers with an overview of the most popular software tools; and third, they can be exploited by tool developers seeking knowledge of the types of exchange formats and functionality most requested by users (see Supplementary Table 1 online). The survey displayed, for example, that although Systems Biology Markup Language (SBML) is widely recognized as standard format for systems biology models (60% of respondents said they were users), many respondents use either the storage format that comes with their favorite modeling tool/textual description or 'homemade' formats.

Another area that has received significant attention is standards for graphical notation. About 40% of the survey respondents draw graphical representations (e.g., wiring schemes or network graphs) according to a defined nomenclature. Often, the graphical functionality of the modeling tools is used. Tools that received particularly positive feedback included CellDesigner⁴ (convenience of drawing networks with this tool), the Molecular Interaction Map⁵ and Systems Biology Graphical Notation (an attempt to develop standards for graphical notation). MIRIAM was mentioned as a guideline for model publication.

Respondents expressed most strongly the need for standardization in the following fields: first, graphical representation of biochemical networks; second, experimental procedures; third, model encoding and model exchange; fourth, model analysis, validation procedures and computational protocols; fifth, spatial modeling; sixth, model publication; seventh, unified nomenclature across species (e.g., for molecules and enzymes); and eighth, parameter estimation and fitting procedures.

The need for publication and reproducibility of models was mentioned by several respondents. Fifty seven percent of those surveyed agreed that scientific journals should support development and establishment of standards. It was also suggested that journals should ask for the software tool that generated the results.

The large number of respondents and their elaborate and well-advised comments clearly indicate that many researchers in systems biology consider standardization an urgent issue. Eighty percent of the respondents favor standardization, but there is also consensus that standards should not be enforced at all costs; about half of the respondents state that standards should be enforced by journals. Efforts, and possibly the enforcement of standards, would be welcome especially in the following fields: first, graphical representation of biochemical networks; second, experimental conditions and scenarios; third, exchange formats for data and computational models; and fourth, nomenclature of cellular compounds and molecules.

Altogether, the results of our survey suggest five key goals for systems biology research going forward. First, as free availability and flexibility are the top criteria governing the choice of software tools, software developers should ensure that their tools are freely available, flexible, compatible to other tools and well documented. Second, to enable reuse and facilitate exchange of models, tool developers and tool users should develop standardized descriptions of model structures and parameters. Third, modelers should make their models available in a format that allows exchange and testing by others. This would be preferably SBML, which is accepted and appreciated by the majority of modelers; otherwise, at least the program code should be available. Journals have a role to play in enforcing this process—recommendations along these lines are already formalized in the

MIRIAM effort¹. Fourth, experimental biologists should store and provide their experimental data in numerical formats. And fifth, standards for graphical notation and unified nomenclature should be further developed.

In our opinion, standards have to be developed by scientists, in parallel with both tool development and modeling projects. Even so, the success of standards depends very much on science-related institutions, such as scientific journals, funding organizations and initiatives like the SBML consortium that support the acceptance and the necessary progression of standardization.

Note: Supplementary information is available on the Nature Biotechnology website.

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Incentivizing standards development and adoption

To the editor:

We read with great interest the editorial 'Standard operating procedures' (*Nat. Biotechnol.* **24**, 1299, 2006) and concur with your view that, traditionally, standards development has not been at the forefront of researchers' minds. However, as the biological sciences move away from the reductionist era and approach the age of

integrative translational medicine, the need for meaningful data sharing between disciplines and disease areas becomes ever more pressing.

The approach taken by the Microarray Gene Expression Data society is to be applauded and it is indeed the case that the domain experts are those best placed to develop the standards they will be expected to implement.