What is design in synthetic biology? From techniques to reflexive meta-materials

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Abstract

Claims concerning the role of design figure heavily in the recent emergence of synthetic biology. This paper argues that there can be no straightforward application of engineering design principles to biotechnological problems. The design practices appearing in synthetic biology embody wide-ranging and heterogeneous re-organisation of techniques of working with biological substances in networked assemblages. This paper analyses the function of design in synthetic biology via the concepts of 'meta-technique' and 'meta-material.' These two terms suggest how existing biological techniques and materials are being intensively re-organised. The notion of design as a meta-technique shows how synthetic biology draws highly reflexively from digital cultures for practices of collaboration, standardisation and a sense of ongoing change. The notion of biological substance as meta-material suggests a way of thinking about the dynamism of living things infused by models, constructs and work-processes. Design in synthetic biology has important implications for how we think about biotechnology and biomedicine more generally. Synthetic biology design software, as well as the several hundred scientific papers and patents published between 2004-2009, indicate an alteration of biological substance in train. Existing critical accounts of biotechnology and genomic medicine contend that species differences and evolutionary histories undergo a flattening or lateralization in molecular biology and genomics. By contrast, analysis of design practices appearing in synthetic biology suggests a different set of topological operations are taking shape in synthetic biology. Effects of depth and verticality appear at critical design conjunctions in synthetic biology, and these meta-stable effects intensify public, economic and lived responses.

Keywords: synthetic biology, design, technique, materiality, emergence, new media

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Say that it was desirable to make molecular biology widely available, accessible and popular. How could molecular biology as a set of laboratory techniques for working with biological substance be reorganised to allow greatly increased development of biotechnologies in areas ranging across food, energy, health-care and climate change? One practical response to this question in the last few years takes the form of synthetic biology.[1] Synthetic biology can be seen as another participant alongside genomics, systems biology, stem cells, assisted reproduction technologies and recombinant DNA biotechnologies in an ongoing systematic change in the mode of existence of biological substance. The proponents of synthetic biology advocate 'engineering design principles' – abstraction, modularity or 'decoupling', and standards (e.g. (Forster & Church, 2007; Kitney, 2007; Marshall, 2008; Weiss, 2007)) – whose application might re-fashion molecular biology as biological engineering. In their highly cited survey of 'the new engineering discipline of synthetic biology,' Adrianantoadro and co-authors invoke the canonical engineering principles of standardisation, decoupling and

1 Synthetic biology epitomises another of what Kaushik Sunder Rajan, following Michael Fischer, has described as 'new emergences in the life sciences' (Sunder Rajan, 2006, 279-280). Whatever else synthetic biology might do, it has rapidly enrolled large numbers of scientists, and garnered substantial funding. While it is difficult to directly convey a sense of the intense interest in synthetic biology, the sheer variety of projects, laboratories, institutions, publications, conferences and companies co-signing and investing in synthetic biology only a few years after its announcement should give us pause for thought. How has it managed to take shape so quickly? What sensations, performances or contagions have occurred? One index of this rapidity can be found in publications and patents. Several hundred scientific papers with keyword 'synthetic biology' have appeared since 2000 (approx 370 in February 2009). Just over one hundred patents have been awarded with the same keyword (approx 115 in February 2009). The choice of a single keyword 'synthetic biology' to compile a body of relevant literature is deliberatively restrictive. Additional keywords such as 'synthetic genome,' 'biological engineering,' 'cellular engineering,' 'synthetic cell', or 'DNA synthesis,' let alone 'protein engineering' or 'metabolic engineering,' would have widened the sample of papers and patents in relevant ways, but made the resulting set of publications and patents difficult to handle. The results of simple web searches would have added several hundred thousand extra items labelled 'synthetic biology' to the analysis. Symptomatically, the most cited paper in the synthetic biology literature currently (March 2009) is a paper entitled 'Accurate multiplex gene synthesis from programmable DNA microchips' (Tian et al., 2004).

abstraction and attempt to apply them to biology (Andrianantoandro, Basu, Karig, & Weiss, 2006). They are not alone in this. Nearly all of the major figures associated with synthetic biology cite design principles in their scientific publications, in public lectures and in patent applications, and these principles organise the structure of workshops, conferences and publications.

On the basis of these principles, many descriptions of synthetic biology divide it into three related, partially overlapping classes (Balmer & Martin, 2008) (Lentzos, Bennett, Boeke, Endy, & Rabinow, 2008) (Rinie van Est, 2007) and (O'Malley, Powell, Davies, & Calvert, 2008):

1. device-based standardised construction
2. mid-range problem-focused re-engineering of microbes as biotechnologies
3. whole genome engineering or cellular 'chassis' production

(Some analysts include other categories such as artificial cells or artificial DNA – they too belong to synthetic biology, but for the sake of brevity, I leave them aside here.) These design approaches are loosely aligned with three North American public scientific personae: Drew Endy, Jay Keasling and J. Craig Venter respectively.[2] Associated with each of these researchers are different discursive, media, collaborative, institutional, commercial, legal and technical arrangements that I leave aside. The most coherent and transnationally extended instance of synthetic biology is probably the annual iGEM undergraduate synthetic biology competitions held at MIT, Massachussets, a competition that serves also to publicise the development of standards and libraries for biological parts or BioBricks. The most

2 As Paul Rabinow observes, these three examples probably represent the spectrum of what it might mean to transform biology into a enterprise under the rubric of synthetic biology (Lentzos et al., 2008, 315-316).

commercially and practically promising synthetic biology project would most likely be Keasling's work on the anti-malarial compound artemisinin (Hale, Keasling, Renninger, & Diagana, 2007). Finally, the most publicly visible events in synthetic biology in the few brief years of its existence (post-2003) are perhaps the publication associated with Craig Venter of the first synthesis of an entire genome, an artificial genome labelled JCVI1.0 (Daniel G. Gibson, 2008, 1216) cf. (Gibson et al., 2008), a lightly re-designed version of the 'minimal genome' contained in the bacteria *mycoplasma genitalium*.

This personified classification of synthetic biology design principles has been adopted and reiterated by policy analysts, funding bodies, science journalists and social scientists. Yet it tends to take at face value the fundamental claim that *design* can be conducted according to *principles*. The notion of design invoked in almost every discussion of synthetic biology, whether is it is technical, scientific, policy-oriented or for a popular audience, invokes principles. Actual design techniques and the practices of design are seldom discussed. The fact that design is also a melange of techniques and practices, spanning a highly variable set of techniques, materials, abstractions and sensations, and often standing on shifting ground is barely recognised. This oblivion of the grounding of design techniques in software, documents, databases, diagrams, and many textual, graphical and calculative devices skews analysis of synthetic biology in particular ways.[3]

3 This over-estimation of principles also appears in analyses of synthetic biology. In their work, Maureen O'Malley and co-authors view the prospect of design in synthetic biology quite pessimistically. They argue that synthetic biology in its present incarnations tends to simplify complexity, variability and contextual richness in the interests of instrumental management. They suggest that any engineering of the biological substances entails significant limitations:

> This drive towards simplicity appears to sacrifice the possibility of attaining a deep understanding of contextual influences on parts, their evolved variability and the relationship of context and variation to functional properties. (O'Malley et al., 2008,61)

and conclude:

> If synthetic biology's future is to be more than a modest contributor to 'analytic' biology, it needs to develop broader engineering principles that do more than mimic those of non-biological engineering. Uncritical acceptance of the strongly programmatic statements being made about the field is unlikely to further such advances. (O'Malley et al., 2008,63)

While sharing their scepticism about 'strongly programmatic statements,' I would suggest that the

This paper seeks to problematise design in synthetic biology. The paper departs from the question of how *techniques* are re-organised under the rubric of *design* in synthetic biology. From the perspective of laboratory techniques, synthetic biology offers little novelty. The rapid emergence of synthetic biology can be read as another symptom of the 'end' of molecular biology as a twentieth century life sciences discipline (Rheinberger, 2008, 304). While many working biologists remain sceptical or adopt pragmatic attitudes to the advent of synthetic biology (treating it as a useful funding possibility and a potential vector of science popularization), this paper questions an assumption that seems to be mostly quickly taken for granted by both its supporters and opponents: that synthetic biology brings an engineering design process to biotechnology. Arguably, the practices of design figuring in synthetic biology are more heterogeneous than the frequent reiteration of this assumption and its associated principles would lead us to believe. Certainly, design principles can be found in the introductory pages of many engineering textbooks, especially those associated with software, electrical and electronic engineering (e.g. (Abelson, Sussman, & Sussman, 1996) has been cited by several synthetic biologists). However, the widespread affirmation of these engineering design principles does not answer the question of how such principles practically, materially and semiotically reorganise the techniques of molecular biology (cloning,

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advent of synthetic biology as a program based on engineering design principles calls for more analysis rather than dismissal. Indeed, we need to look for practical forms of mimicry already in operation, and ask what is being imitated, how and with what consequences for the temporality and plasticity of biological substance. Evelyn Fox-Keller already commented in *The Century of the Gene* on the need for more sophisticated engineering approaches in biology. She recommended that biology should borrow more from engineering:

> Engineers have developed a conceptual toolkit for the design of systems -like airplanes, for example, or computers- in which reliability is the first and foremost criterion. As such, their approach might be said to be directly complementary to that geneticists, and I suggest that the latter might profitably borrow some of the concepts and terms developed in the study of dynamic stability to enlarge their own conceptual toolkits (Keller, 2000, 147).

Perhaps neither the 'broader engineering principles' that O'Malley and co-authors call for, nor the 'conceptual toolkit' that Keller supports, animate synthetic biology. Rather, the question is how techniques of molecular biology and genomics are re-deployed in design processes. This undertaking borrows existing forms of design work and modelling, it interpellates engineering subjectivities (a key aim of the IGEM competition), and invests in software development, infrastructure and logistics for biological substances (a dimension strongly highlighted in the synthetic genome work).

sequencing, mutagenesis, RNA interference, etc). The rather flat and neatly packaged descriptions of synthetic biology that depart from broad and abstract engineering design principles engender an unambivalent sense of the direction and aspirations of synthetic biology. These descriptions cover over a multitude of heterogeneous dynamics and connections. Above all, they offer little understanding of the credibility and desirability of synthetic biology. Arguably, the very term 'design' does important work here. It is freighted with many resonances and values in relation to products, architecture, fashion and services. When design permeates biotechnology, it brings with it collective imaginings of 'human capability.' Under the guise of design, many practices and sensibilities drawn from disjoint spaces can begin to impose themselves on biotechnology. From a perspective that is critical of design, we might regard synthetic biology as a place where transformations in biological existence can be seen in train. If so, the examples of gene design software, standards for biological parts, biological chassis and platform design I discuss below all display the imprint of wider design imaginings on techniques of working with biological substance.

Critical work on design principles suggests that they lead very troubled lives in practice (Flusser, 1999), (Margolin, 2002), (Suchman, 2005) (Suchman, 2001). While design principles attempt to organise and solidify a loose federation of related activities and actors, they also smooth over the uneven, shifting connections between diverse practices that use textual, graphical, symbolic materials and systems of collaboration, modelling, and transactions drawn from digital media cultures, computer science, electronic circuit design, etc. Invocations of design principles function as outward-facing simplifications of a much more intensive process concerned with the development of what we might term 'meta-technique.' A meta-technique organises, groups, assembles and sorts other techniques, practices, methods, protocols, touches, services, and infrastructures into specific

arrangements. At the same time, a meta-technique engenders processes of reflection and subjectification (for instance, by raising the question of who can design what). The invocation of design in synthetic biology epitomises a meta-technique because it must both practically work with the specificities of many different materials, technologies, subjectivities (consumer, researcher, designer, engineer, scientist, citizen, student, investor, regulator), and reflect on forms of value (aesthetic, economic, moral-ethical) that underpin subject positions. Meta-technique in synthetic biology displays several facets. These include the engineering of heterologous biological substances as 'meta-materials' using constructs such as pathways and networks, and the reflexive translocation of media and digital cultures' ways of organizing work, doing design, collaboration and circulation into modes of biological existence. Both the projects of the 'minimal genome' (as presented in (Glass et al., 2006), the second most highly cited paper in synthetic biology to date, (Daniel G. Gibson, 2008, 1216) (Gibson et al., 2008) and the patent (J. C. Venter, Smith, & Hutchinson III, 2007)) and the popular standard part-based approaches exemplified in in IGEM and BioBricks.

The discussion below has two main sections. Firstly I briefly discuss why techniques help situate the 'synthetic' character of synthetic biology more precisely than any general design principles. This section of the paper relies on the notion of meta-technique to conceptualise the problem of subsuming extant biological techniques in a design process. Secondly, I argue that design as a meta-technique (and hence biological substance as meta-material) entails a transcontextual movement between biology and network cultures. Here the paper examines borrowings of conventions, patterns of collaboration, and above all design practices from information and network cultures. The 'sheer intensity' of synthetic biology, this argument implies, derives from such transcontextual movements. This section discusses the implications of design for the mode of existence of biological substance in broader

biopolitical frames.

Techniques in synthetic biology: rapid emergence, familiarity and metastability

Synthetic biology is sometimes presented as the inevitable consequence of an acceleration in research afforded by faster and cheaper commercial DNA synthesis (Garfinkel, Drew Endy, Gerald L. Epstein, & Friedman, 2007,1). Certainly, cheaper and faster DNA synthesis is pivotal in the synthetic biology enterprise. Once long stretches of genetic material can be synthesised quickly and cheaply, then biologists and engineers can envisage new forms of experiment and prototyping, and can henceforth, in principle, discover and innovate more rapidly. DNA synthesis is a quite substantial biotechnology growth industry. Sponsorship of high-profile synthetic biology events such as IGEM (the annual international Genetically Engineered Machine competition) and conferences such as SB4.0 advertises the fact that DNA synthesis firms (e.g. DNA2.0, GeneArt, Integrated DNA and Coda Genomics) can construct and deliver sequences of DNA, saving much time and effort for researchers. They offer 'an immediate and easy path from sequence databases and DNA manipulation software to physical reality' (DNA2.0, 2009,39). A customer enters a DNA (or sometimes amino acid) sequence into a web-based form and the gene synthesis service will deliver it in a few days or weeks (e.g. (GeneArt, 2009)). Reliance on such services weaves synthetic biology tightly into digital economies, with all their network infrastructures and transactional arrangements.[4]

The utility of larger pieces of DNA made quickly on demand by commercial providers presupposes design and modelling techniques. How does sequence design get done in a web service context? For instance, the design tool *Gene Designer* is a software application that

4 In the last ten years, the web has been heavily reconfigured as a service platform (as contrasted with the more common idea of the web as 'new media'). 'Web services' embody a contemporary form of attachment to complex, dynamic, distributed products.

runs on PCs, and it links gene design directly to a web-based DNA synthesis company. It was first described in an academic paper (Villalobos, Ness, Gustafsson, Minshull, & Govindarajan, 2006), and is widely and freely distributed by the DNA synthesis company DNA2.0, one of the major suppliers of DNA for synthetic biology. Hardly any of the DNA synthesis companies are simply offering to synthesise a sequence of DNA. They all offer to design or help design a sequence of DNA for some purpose. Design appears in several forms. The example of *Gene Designer* (see Figure 1) illustrates some of the borrowings from software cultures.

[FIGURE 1 ABOUT HERE]

The design promise of *Gene Designer* is stated clearly on the first page of the manual that comes with the software:

> *Gene Designer* from DNA2.0 Inc. is tool [*sic*] for molecular biologist and synthetic biologist. This software enables the user to:
>
> Design large and small DNA fragemnts [*sic*].
>
> Optimize expression in desired hosts using codon optimization
>
> . Build and Manupulate [*sic*] DNA from building blocks such as promoters and ORFS.
>
> (DNA2.0, 2009, 1)

Gene Designer offers a palette of sequence elements, some proprietary to DNA2.0, others more generic, that can be dragged and dropped onto an iconic view of what will become a sequence. The process of design here, as in many other domains of new media work, consists in choosing elements from menus, dragging them and arranging them on screen. The list of

the elements contained in the 'Design Toolbox' section of the screen include regulatory elements, codon elements, 'drug resistance cassettes,' and reporter proteins. 'Custom objects' based on any DNA sequence can easily be added. In fact, a typical design project begins by finding a DNA sequence of interest in an online database such as GenBank, pasting it in a new ORF (Open Reading Frame) or by finding a protein or enzyme amino acid sequence of interest and pasting it in a new amino acid (AA) sequence object that will be reversed translated back into DNA sequence. One might find a gene from a microbial database that conferences resistance to some antibiotics or find a protein that could be biotechnologically or biomedically useful. In either case, the specific sequence would need to be flanked by various generic promotor, regulator, stop and stop sequences. The actual codons that comprise the synthetic DNA construct can then be 'optimised' by the software to confer optimum expression of the target protein construct in the chosen host.

Once a design has been assembled using these components, it can be checked for errors, optimised in various ways, checked for completeness, then 'quoted' (an estimate of the cost of synthesis) or 'ordered' directly. This small software application resembles the kind of design software found in the software and electronics industries, but also in graphic, media and industrial design. In the layers of graphic abstraction and on-screen manipulation, it differs from earlier 'gene design' software, even that of just a few years earlier such as *Gene Design*, a web-based software application that first became available in 2006 (sricha11, 2009). Already, research prototypes for synthetic biology IDEs (Integrated Development Environments) have started to appear. Software applications such as Genocad (GenoCad, 2009), SynBioss (Hill, Tomshine, Weeding, Sotiropoulos, & Kaznessis, 2008) and Clotha {IGem 2008 Berkeley Team, 2008 #120} borrow visually and architecturally from software development environments such as Eclipse {Eclipse.org, 2009 #118} or software such as

AutoCAD for 2D and 3D design {AutoDesk Inc., 2009 #119}. Like software development design platforms, or the engineering design software used for electronic circuits design (EDA – Electronic Design Automation), the objects, models, components and processes that need to be assembled have been heavily de-contextualised in this software. While in *Gene Designer* everything on the palette of components is still ultimately a DNA sequence, the classification and iconic rendering of the sequences as small icons that can be dragged and dropped onto a 'new object' tends to [word missing here?] how and by whom new sequences are put together. It is hardly worth saying that the distribution of such tools for personal computers or on the web means that design work can be carried out quickly and often, without access to specialised resources.

Design software of this kind may seem rather superficial. I would argue that the evident superficiality of the software is precisely what differentiates the practices of design in synthetic biology from antecedent technical practices in genetic engineering and molecular biology. There is a certain deliberate superficiality to the design practices embodied in browsing lists of components, cutting and pasting, dragging and dropping components, checking for codon optimization and errors, and then ordering the DNA construct via a commercial web service. Their very arrangement on screen as colourful iconic components connected by arrows and lines renders them superficial in a literal sense. The design surfaces that such software unfurls can be seen as propagating shallow understandings of context, simplifications of cellular or extra-cellular interactions, and even a reductionist understanding of the dynamics of genome transcription. However, each component of the 'Design Toolbox' running down the left hand side of the screen embodies a technique of combining, separating, connecting, sorting, signalling, expressing, or reporting drawn from the last four or five decades of molecular biology. For instance, there is a set of components called 'recombinases'.

The different components in this set include the sequence for enzymes such as Cre (Cyclic Recombinase) recombinase (1029 bases) and corresponding sequences for recognition sites such as loxP (Locus of Chromosomal Crossover in bacteriophage P1 -34 bases). Together the two Cre-LoxP components help deal with difficult topological manipulations of tissue in organisms. They offer the possibility of designing a construct that could perform 'site specific recombination' using Cre-Lox recombination, a technique patented by Dupont in the 1980s [TBA – EP1988111596A], itself drawing on research done in the 1970s [refs in patent]. Subsequently, during the 1990s, Cre-Lox site-specific recombination was adapted for use in model organisms such as mice (Akagi et al., 1997), and the technique has been useful in tissue-specific research into complex cancer and immune systems. Much more detailed analysis would be needed to see how this particular technique – Cre-Lox recombination – is being used in current synthetic biology work. For present purposes, the important point is that the technique is itself one limited attempt to deal with context, interactions, and variabilities encountered in assessing 'role of genes in complex processes such as tumorigenesis, embryonic development and functioning of the immune system' (Akagi et al., 1997). Almost every entry in the 'Design Toolbox' enfolds a similarly complex weave of techniques, patents, research efforts and responses to specific experimental problems (for instance, mouse models have been developed to help explore the dynamics of sporadic cancer (Willimsky & Blankenstein, 2007)). It is as if the history of molecular biology as technical accomplishments is re-rendered as an expanding set of menu options.

It would be perhaps worthwhile analysing some of the other design software (and perhaps constructing a wider genealogy of software in biology) in use in synthetic biology. The software can be regarded as an index of the topological transformations assembled and concatenated when biology is re-factored as a design process. In other words, the proliferation

of synthetic biology design software and design environments signify an effort to re-materialise biological substance as a meta-material subject to meta-techniques. Not only synthetic biology, but also other related efforts in tissue engineering and stem cell science could be said to participate in the project of constructing meta-materials, materials whose properties are subject to ongoing transformation and re-organisation.[5] While commodities with more or less fixed use-values and exchange values may emerge from the design process, the process itself is of much greater interest. The design process itself embodies the possibility of ongoing synthesis, ongoing invention of new things. At the same time, as the built-in network connection between the *Gene Designer* software and the DNA2.0 ecommerce service indicates, this highly open temporality, in which new things can appear at any time, is deeply linked to flows of transactions, value and hence the life of capital.

In analysing the rapid emergence of synthetic biology, it is important to acknowledge a vague sense of familiarity that accompanies it. Many of the reactions and expectations concerning synthetic biology are reminiscent of discussions and regulation of recombinant DNA technologies in the 1970s and 1980s (see (Wheale, McNally, & Athene Trust., 1990) for a list of issues at that time). There are many threads that any analysis of the relatively recent and rapid (re-)appearance of synthetic biology could take up. While there are cases of life science work that rate higher in public awareness and debate (stem-cells, PGD, personalized genomics, biofuels, genetic diversity, tissue engineering, etc) or that directly raise more salient ethical, social, economic and legal issues, the rapidity and heterogeneity of synthetic biology make it a particularly compelling instance of the rapid, provisional reorganisation of labour, life and language analysed in much recent literature on biomedical and life sciences

5 Melinda Cooper, for instance, has recently argued that stem-cell based tissue engineering not only adopts embryogenesis as its pivotal process, but promises to engineer indefinite transformation. (Cooper, 2008). Again, I would suggest that attention to actual techniques of reprogramming. Analysis of the design of constructs for cellular reprogramming would be a worthwhile counterpoint to the seemingly ineluctable potency attributed to stem-cells.

(Helmreich, 2009; Rose, 2006; Waldby & Mitchell, 2006). Specific questions of commodification and intellectual property have figured in some work already being done on synthetic biology (Calvert, 2008; Kumar & Rai, 2007; Pottage, 2006; Rai & Boyle, 2007), and they could be developed further. While acknowledging its familiarity, Alain Pottage justifiably, I think, suggested several years ago that '[w]hat is significant about synthetic biology is not (just) that it suspends evolutionary genealogies, but that it collects biological elements into digital media and modes of organization' (Pottage, 2006, 146).[6] (The act of *collecting* is particularly significant in this context, as I argue below.)

Meta-technique, lateralization and contemporary biological substance

For several reasons, the techniques of synthetic biology offer a way to analyse it without making pre-judgments as to its relevance or importance. In synthetic biology, *techniques* exist in a rather unstable state. They are at once generic, transportable, wide-ranging, and hybrid.

Firstly, and more generally, techniques, as we know from Michel Foucault's treatment of them in relation to formation of self (Foucault, Gros, Ewald, & Fontana, 2005), have no necessary connection to epistemological regimes, knowledge and truth. Techniques can be somewhat agnostic or generic in relation to knowledges, values, subjectivities, selfhood or personhood and even embodiment. There is something at once eminently superficial and yet precise and concrete about techniques. Because they have a fairly low-profile, techniques can lead a particularly polyphase existence. Less universal and abstract than concepts or mathematical functions, less fragile than the nested, interwoven structures of technologies, techniques move

6 Epistemological tensions in synthetic biology have been discussed in other work (O'Malley et al., 2008). More widely, questions of risk and safety stand front-stage in the policy work (Emergence, 2008; ETC Group, 2007; EU NEST High-Level Expert Group, 2005; Garfinkel et al., 2007). Finally, synthetic biology's rather expansive promises, advanced in patent claims, in scientific publications and in public forums in the last five years (2004-9) could and should be critically analysed from the perspective of recent work on global biocapital and bioeconomies (Cooper, 2008; Fortun, 2008; Rajan, 2003; Thacker, 2005). This paper takes some preliminary steps in that direction.

through a series of more or less temporary embodiments in individuals, groups, pedagogical systems, devices and institutions.

Secondly, techniques in the sciences of the living displays a long history of surprise transpositions and reorderings. In her account of how cells became standard platforms for biological work in both biological research and medicine, Hannah Landecker advocates close attention to technique:

> Keeping an eye on practices, protocols, methods, technique, touch, or infrastructure provides access to the ways in which work on some life (nematodes, insects, yeast) reshapes human life by introducing systematic change into biological existence. Perhaps more importantly, this methodological focus on genres of technique and infrastructures of research allows room for the vast realms of contemporary biological practical and biotechnological intervention that are not based directly on human matter or health or reproduction (Landecker, 2007, 234).

The cases she discusses drawn from twentieth century tissue culture are directly relevant to synthetic biology. However, the effect of her methodical emphasis on technique is to undercut epochal questions of 'how biotechnology changes what it is to be human' (222). Arguably, biological existence at any point in recent history can be better grasped from the perspective of technique and practice rather than from relatively abstract concepts of life, gene, heredity, reproduction or sovereignty. If synthetic biology does attempt to 'introduce systematic change into biological existence,' it draws heavily on existing techniques of living substance. In this respect, its practices, protocols, techniques, touch or infrastructures would be worth exploring in their own right. Landecker's methodological emphasis on practices and techniques is premised on the fact that 'technologies of living substance' (1), as exemplified in tissue culture

techniques of artificial parthogenesis, immortalisation, and cell fusion, have frequently short-circuited metaphysical debates about body, difference, time, vitality and substance. While it is too early to say how deep, wide-ranging or surprising such short-circuiting might be in the domain of synthetic biology, it is possible to detect in current efforts some unmistakeable traits. The techniques of modelling, synthesis, assembly, exchange and distribution loosely coalescing in synthetic biology are all oriented by highly valorised notions of *design.*

Thirdly, accounts of biotechnology have usually agreed that the advent of recombinant DNA or genetic engineering technique (Cooper, 2008, 31-3; Wheale et al., 1990, 3-4) decoupled biological substance from evolutionary processes. This suggests a different status for biological techniques derived from molecular biology as they move into synthetic biology.[7] Existing modes of production of standardised products, materials and services were challenged by technical intervention into nuclear DNA. These techniques defined

7 Molecular biology has for the last fifty years or so proliferated a set of procedures that have percolated into many different facets of work on living things. Following Hans-Jörg Rheinberger's account in 'What Happened to Molecular Biology', we could say that molecular biology has become a set of techniques that function as general procedures for problems concerning the living:

> Today, it appears rather that molecular biology has wound its way, in the form of a wide variety of molecular biological procedures, into all of the life sciences, in particular cell biology, developmental biology, evolutionary biology and, most significantly, the molecular study of disease. As a result, the history of classical molecular biology as a discipline has itself been relegated to the realms of history (Rheinberger, 2008, 306).

The key point is that molecular biology, according to Rheinberger, takes the form of 'wide variety' of procedures. The 'low-level' physical techniques associated with earlier molecular biology techniques include x-ray crystallography, chromatography, and electrophoresis. The shift to model organisms of yeasts, bacteria and viruses rather than insects or plants later employs biological macromolecules such as enzymes as *in vivo* technical implements for searching, cutting, copying, and splicing genetic material. The procedures or techniques of molecular biology have incrementally built up in increasingly nested and convoluted biotechnical systems. Latterly, both the results and deployment of all these individual techniques are arrayed and concatenated in large-scale information-technology heavy automated and networked coordination of techniques. This process of arraying and concatenating culminated in what seemed at the time gigantic technical feats of whole genome sequencing in the 1990s. Today, they are being rapidly recapitulated in large-scale high-throughput sequencing efforts of metagenomics and personalized genomics. Each addition to the set of techniques has tended to precipitate new layer of organisation of those techniques. At the kernel of these transformations, we find recurrent transpositions of techniques and technical elements between *in vitro* and *in vivo* settings. Rheinberger describes how these transpositions between living and non-living allows molecular biology as procedure or technique to move crabwise across many different life science settings. Changes in experimental systems inevitably trigger disciplinary, institutional, regulatory and commercial reorientations. If today, synthetic biology appears in the wake of genomics (in the same way that genomics came in the wake of molecular biology and recombinant DNA), then we would need to ask what shifts in experimental system or assemblage does it signal? What new layering or folding of the topology of experimental-technical mode of existence of life is taking shape?

biotechnology in terms of transfers of genetic material (as in bacterial recombination), borrowings (e.g. enzymes and other molecular constructs derived from extremophiles) and 'abnormal' transgenic events (transduction, horizontal gene transfer, etc). Coupled with its challenge to Fordist modes of production, biotechnology de-stabilised Darwinian and neo-Darwinian theories of evolution. A common trope for this dimension of biotechnology is *lateralization* or *flattening* (or alternately, 'de-standardisation' (Cooper, 2008)[8]). Versions of this argument can be found, for instance, in (Franklin, Lury, & Stacey, 2000) and (Parisi, 2007), as well as (Rose, 2006).[9] Nikolas Rose, for instance, writes:

> [I]n the interventions that proliferate in this flattened world, almost any vital element can, in principle, be freed from its ties to cell, organ, organism, or species, set free to circulate and to be combined with any other, provided certain conditions are met (Rose, 2006, 16).

The transfers and transpositions effected in biotechnology occur as 'intensive movement'[10] freed from reference to external biological reference points such as species differences, attributes of specific organisms, ecological or physiological contexts, or social and economic reference points such as nations, publics, citizens, consumers or institutions. However, there are good reasons to be cautious in seeing synthetic biology as another confirmation of the 'lateralization of evolutionary descent' view. Lateralization is highly conditional, as the last

8 From the perspective of those accounts of biotechnology that equate lateralization with de-standardisation (Cooper, 2008), the arrival of standardisation projects in the form of synthetic biology appears distinctly anomalous. (In fact, as I will argue below, in synthetic biology, standardisation has no necessary connection with standardised commodities. It has much more connection, I would argue, with the reorganisation of collaborative work than with making the same things many times. Hence, a version of the de-standardisation thesis might still stand.) Furthermore, synthetic biology's whole invocation of design explicitly responds to biotechnology's failure to deliver on the promise of full lateralization, in either the more abstract or economic versions. Flattening of organismic differences has hindered as well as enabled change and invention.

9 This trope, it should be noted, also commonly figures in descriptions of economic globalization such as Thomas Friedman's *The World is Flat,* (Friedman, 2005).[where it is just as misleading! See the Atlantic article a year or so ago entitled, The World is Spiky.]

10 As the cultural theorist Brian Massumi describes, intensity is a movement in process that 'cannot be determinately indexed to anything outside of itself' (Massumi, 2002,7). The fairly colloquial term 'sheer intensity' expresses something of this recursive, movement, that follows no proper line, a kind of movement that seems slippery because it is so steep.

part of Rose's formulation suggests: 'provided certain conditions are met.' For a start, there is never any complete lateralization, only partial lateralizations alongside resurgences of linearity or verticality (Pottage, 2006, 143-144). In any case, the visual-spatial metaphor of flattening is perhaps insufficiently topological to capture the subductions and foldings that accompany any lateral movement.

Finally, in synthetic biology, the contingencies of biological substance as produced by molecular biology and genomics intersect with design practices. Aspirations to design embodied in synthetic biology owe much to adjacent technological cultures associated with digital microelectronics and software engineering as well as to other engineering disciplines. However, of necessity, its techniques and materials come from contemporary life sciences, particularly the techniques and procedures developed in molecular biology and genomics. Since design processes are not well-established in the life sciences, they must be borrowed from other design-focused disciplines. Design techniques have, to date, been widely developed in industrial engineering, in service design, in media production, in software and hardware, in transport and infrastructure, in fashion and consumer goods, in architecture, urban spaces and landscapes (Doordan, 1995) (Margolin, 2002). Various forms of engineering design already stand in close proximity to synthetic biology: bioprocess engineering and biochemical engineering use mathematical models, calculations and experimental apparatus to design bioreactors or production processes that yield flows of biomolecules or organic chemicals. However, most of these bioengineering design focus on the non-living elements of biotechnology. (For instance, a bioreactor is a designed technical element of a biochemical plant, but the yeast or microbes that inhabit it are at the moment not products of design as such.) In its concern with design, synthetic biology subsumes the techniques of molecular biology, genomics and biotechnology into a meta-technical design process.

Pathways, platforms and chassis as meta-materials

Jane Calvert has recently suggested that just as systems biology seeks to understand 'emergence,' synthetic biology in turn aims to control it (Calvert, 2008, 394). She goes on to argue that this renders the products of synthetic biology ready for commodification. (For an explicit formulation of control over emergence, we could turn to the European Union-funded synthetic biology network: (Emergence, 2008)). Certainly synthetic biology engineers emergence, and no doubt the prospect of new commodities dazzles many synthetic biology enterprises, investors and spectators. But any attempt to control emergence using techniques drawn from other engineering processes is bound to initiate other kinds of emergence. To be more specific, I would argue that, the superficial, generic, disruptive, intensive and trans-contextual character of design meta-techniques imbue synthetic biology with some profound instabilities. They materialize biological substance as meta-materials, materials whose properties are intensified or potentialised in ways that cannot be indexed directly either to life or to mechanism.

A meta-material typically takes the form of a construct such as 'pathway,' 'platform' or 'chassis' elicited from existing biological substances. For instance, a relatively early synthetic biology paper authored by Chan, Kosuri and Endy entitled 'Refactoring Bacteriophage T7' (Leon Y Chan, Sriram Kosuri, & Drew Endy, 2005) applies the software design technique of *refactoring* to a relatively small viral genome. The paper reports, '[h]ere, we converted the genome of a natural biological system, bacteriophage T7, to a more structured design' (L. Y. Chan, S. Kosuri, & D. Endy, 2005). In software design, the term 'refactoring' refers to

> a disciplined technique for restructuring an existing body of code, altering its internal structure without changing its external behavior. Its heart is a series of small behavior-preserving transformations. Each transformation (called a 'refactoring') does little, but a

sequence of transformations can produce a significant restructuring' (Fowler, 2008).

Refactoring is an example of a design meta-technique that takes existing technical objects or practices and reorganises them. In Chan, Kosuri and Endy's work, the result of the re-factoring process is T7.1, a refactored version of the bacterial virus or bacteriophage T7 first discovered in the 1940s. A very small genome is treated as a body of code amenable to small transformations that render it more usable by others, and for other purposes. In this case, individual functional genetic elements were separated out by endonuclease restriction sites (Leon Y Chan et al., 2005,3). In one respect this reduces the scope of emergence. But in others, it allows a specific biological substance to participate more widely in processes of design, modification, standardisation and experimentation. Many synthetic biology projects can be seen as 're-factoring' processes that support emergence rather than control it. While constraining some 'emergent phenomena' in biological systems is of crucial interest to synthetic biology as a constructive engineering project, triggering emergence at the level of organization or collaborative processes is highly valorised. From the standpoint of the design techniques unfolding in synthetic biology, the question is not so much whether emergence is controlled or not, but what almagam of techniques render biological substance susceptible to design. If emergence itself becomes designable, then temporalities can be inhabited differently.

One index of a meta-material is the presence of increasingly large heterologous constructs within biological substance. Recombinant DNA techniques had already treated individual biomolecules such as enzymes as technical elements inside the cell rather than outside it (see (Watson, 2007, 75-106)). However, the scale of the constructs in synthetics means that is of a different order. In the oft-cited work of Jay Keasling's group (Martin, Pitera, Withers, Newman, & Keasling, 2003), the authors describe how they engineered a new metabolic pathway in the

standard biological model organism, *E.coli*, to produce a precursor chemical compound, amorphadiene, for the anti-malarial drug, artemisinin, a drug currently derived from plant sources such as Chinese wormwood. In their work, Martin and co-authors added a complete metabolic pathway to *e.coli* rather than modifying existing metabolic pathways. As they say, 'we chose to bypass this pathway [the DXP pathway that produces the precursor, amorphadiene] by engineering the expression of the *S. Cerevisiae* mevalonate pathway in *E.coli'* (Martin et al., 2003, 797). The engineered pathway is 'heterologous', or as software designers might say, 'orthogonal' to the existing metabolic pathways in *E.coli* because there is little correspondence between the existing and added structures. If the introduced pathway crisscrossed existing pathways in *E.coli.*, it might encounter 'unknown physiological control elements' (797). Hence, whatever else it aims to do, one index of design in the context of synthetic biology will be to generate increasingly extensive heterologies.

If design as meta-technique widens the scope of variation and substitution, then the limit case might a purely heterologous construct, a biological substance that has become generic meta-material, capable of indefinite variations and modifications. In a paper in *Science* January 2008 entitled 'Complete Chemical Synthesis, Assembly, and Cloning of a Mycoplasma genitalium Genome', Daniel Gibson and co-authors including J. Craig Venter and Hamilton O. Smith described the design and assembly of a complete bacterial synthetic genome at the J. Craig Venter Institute using a combination of *in vitro* and *in vivo* methods (Daniel G. Gibson, 2008).[11] The key achievement of this well-publicised paper was synthesis of an entire genome.

11 The minimal genome synthesised by Daniel Gibson and others and announced in 2008 is meant to pre-emptively eliminate undesirable emergent phenomena associated with cellular environments for the production of genomes. The 'complete chemical synthesis' suggests that the genome can be purified of unwanted biological dependencies on cells. However, there are several grounds on which this claim to 'complete … synthesis' and hence the control of emergence falls short. It still 'suffers' from unwanted dependencies on the specificities of living substance. For instance, while DNA synthesis services can readily supply DNA in 20kb lengths, the assembly of the fragments into a whole genome, even the minimal 592kb genome of *m. genitalium,* still relies on other organisms, and in particular, yeast (Gibson et al., 2008).

While the genome in question is one of the most compact microbial genomes known (582, 970 base pairs), it has not been synthesised before. Given that sequencing a complete genome was a major accomplishment 20 years ago, synthesising whole genomes is significant. In order to manage the synthesis process, the genome itself had to be viewed from the perspective of design and construction. The architecture of the *M. genitalium* genome had already been the target of the question 'How few parts would it take to construct a cell?' (Glass et al., 2006, 425) in a paper published by the same research group almost ten years earlier (Hutchison et al., 1999). In the 2008 papers, the process of designing rather than analyzing the genome's architecture becomes the key objective. More specifically, since it is possibly the largest 'chemically synthesized molecule of defined structure' (1219), the process of synthesis itself is the main focus of design. Here the concept of meta-techniques again highlights how design process brings together several different modes of production.[12]

Additional operations attach to designed whole genomes. Somewhat trivially, they include 'watermarking' of the sequences with the scientists' names. More significantly, the

12 The bacterial genome was divided into 101 'cassettes' (6 kB lengths of DNA) that were synthesized commercially by DNA synthesis services. This is highlighted in the paper in both text and images:

> Synthesis of DNA the size of our cassettes has become a commodity, so we opted to outsource their production, principally to Blue Heron Technology, but also to DNA2.0 and GENEART. The main challenges in this project were the assembly and cloning of synthetic DNA molecules larger than those previously reported. (Daniel G. Gibson, 2008, 1216)

The availability of cheap, web-based DNA synthesis services is a key component of synbio, and highlighted by many different commentators, both affirmatively and negatively. A hierarchical process of building 1/8, ¼, ½ and finally a full, exact genome is described heavily in terms of efficiency of speed. Hence, although the process of assembling a complete genome does not yield any new understanding of living systems, or any particular product, it lays down a process for synthesis of designed genomes that combines readily available commercial services, speed and exactness.

In the second, and third stages, the 101 small DNA cassettes supplied by the commercial DNA synthesis services were joined using in vitro recombination via Bacterial Artificial Chromosomes in *e.coli.* In the fourth stage, quarter-size pieces of the genome were joined using in vivo in yeast. In a much accelerated version of the assembly process described in a paper published almost a year later (Gibson et al., 2008), only the first stage was done in vitro. The entire genome was then synthesised in yeast in a single step. Twenty five fragments were added into yeast and the entire genome was synthesised by yeast. The authors speculate that it might also be possible for yeast to assemble the 101 cassettes directly in a single step to yield the complete *mycoplasma g.* genome (20408). As the authors conclude:

> Thus, large DNA molecules can be assembled much more rapidly from synthetic or naturally occurring subfragments than with any other system described previously. Our methods should accelerate research projects, particularly in the emerging field of synthetic biology (Gibson et al., 2008, 20409).

streamlined construction process needs to be set against the framework of the patent application that precedes them by several years and whose publication date is just weeks after this paper. The most relevant U.S. and European patent is simply titled ‘Synthetic Genomes’ (C. Venter, J. & Smith, 2008). The outstanding claims here in terms of design meta-techniques include the possibility of 'millions of genomes':

> [0011] According to one exemplary embodiment and method, a synthetic version of the Mycoplasma genitalium genome having 482 protein- coding genes and 43 RNA genes comprising a 580-kilobase circular chromosome is assembled from gene cassettes. Each cassette may be made from chemically synthesized oligonucleotides. Several versions of each cassette may be made such that combinatorial assembly into a complete chromosome results in millions of different genomes. These genomes may be tested for functionality by "genome transplantation," replacement of a cell's resident chromosome by the synthetic genome. (C. Venter, J. & Smith, 2008,3)

Read together, the papers and the patents envisage a combinatorial explosion. Note that the patent claim is not just for 'combinations' but 'combinatorial assembly' of 'millions of [cassette-based] different genomes.' Viewed in this way, the *Science* paper articulates the design of a process (‘synthesis’), while the patents more abstractly delineate combinatorial

assembly for many possible purposes: '[r]ational methods may be used to design the synthetic genome ... Synthetic genomes of the invention may be introduced into vesicles ... to generate synthetic cells. Synthetic genomes of synthetic cells may be used for a variety of purposes' (J. C. Venter et al., 2007, 1). Together, the papers in *Science* and the patent *decouple* the making of materials from the manifold uses to which these materials are put. This decoupling clears space for design to inhabit. '"[D]ecoupling" the design of engineered genetic material from the actual construction of the material' is the first 'benefit' of 'synthetic genomics' (Garfinkel et al., 2007, 10). When biological substance such as a whole genome becomes a meta-material, it displays cuts and joins that allow further processes of design to begin to attach and multiply.

Reflecting network media in biological meta-materials

The term 'rational design' often appears in synthetic biology. It highlights an underlying apprehension of 'irrational' or incomprehensible excess.[13] Excess or surplus could be understood in terms described by Eugene Thacker in *Global Genome* as constitutive of biotechnology more generally (Thacker, 2005). Thacker's argument (based on Marx and Bataille) is too complex to be discussed here in any detail, but his conclusions are immediately relevant: '[t]here is never too much data, only the production of an excess that serves to trigger further development of tools for the management of this excess' (Thacker, 2005, 128). Like Melinda Cooper's notion of life as surplus value (and in fact, sharing some of the same theoretical resources), Thacker's understanding of biotechnology as haunted by excess information resounds strongly in the context of the advent of synthetic biology. Synthetic biology appears in 2000 (Rawls, 2000), and is named as such at just around the time

13 As Alain Pottage has argued in his analysis of Craig Venter's sampling and sequencing ocean microbe voyages in the research vessel *Sorcerer II*, synthetic biology goes hand in hand with the corralling of an abundance ('combinatorial' in scale) of genomes to be used as resources (Pottage, 2006).

when the mismatch between the output of genomic information and the practical development of new biotechnologies seems most pronounced. However inviting it might be to see synthetic biology as a response to a surplus intrinsic to life itself, the situation is more complicated. I would argue here that we can better understand how synthetic biology intensifies and re-structures molecular biology by exploring its intersection with the highly invested collaborative techniques and practices of digital media and network cultures. This intersection, no doubt, is a complex, multiple event or site. Rather than presuming that in synthetic biology there is either something radically new or just a re-packaging of existing practices, we could ask how existing practices from previously disparate domains come into conjunction. Again, the concept of meta-technique offers one of moving continuously rather than jumping straight from molecular biology's techniques to design or engineering principles. If one were to approach synthetic biology in terms of its network-cultural practices, we might be able to see how some of the effects of rapid emergence and sheer intensity arise.

In synthetic biology, the flows and borrowings from network media display several distinctly reflexive layers. They include the explicit use of documents called RFCs (Request for Comments) first developed by the Internet Engineering Task Force (IETF) to enrol participants in developing standards in the late 1960s; the proliferation of computer-assisted design (CAD) software for synthetic biology (e.g. GeneDesign discussed above), a move that mirrors the automation of design in electronics and software engineering of the 1970s; the institution of 'registries' or libraries for biological parts, a shift reminiscent of the boom in registries and libraries in object-oriented software design of the 1980s; the borrowing of conceptual constructs such as 'virtual machine' and above all 'network' from software and communication engineering of the 1980s and early 1990s; the adoption of web-based collaborative platforms such as Wikis; and the proliferation of eCommerce-style form-based

websites to facilitate both design and purchasing of synthetic biology products, both modes typical of the late 1990s and early 2000s.[14]

Substantial practical efforts are being made to locate synthetic biology within web and network cultures, and to mold synthetic biology in the direct image of the web-network ethos of sharing, openness, collaboration and display. *OpenWetWare* is perhaps the leading example of this. This publicly editable MediaWiki promotes sharing of practical information about techniques, protocols, materials and resources in 'biology and biological engineering' between several thousand registered users (OpenWetWare, 2009). The BioBricks Foundation, discussed more below, is contained within it, as are the web pages for the highly publicised annual iGEM synthetic biology competition. These efforts capitalise on the internet as an infrastructure built through co-operative work, and regard web-enabled software platforms as a key transformative element of life science research.[15] Networks and software are not only the practical tools of communication, coordination and control. Here they represent the potential for ongoing transformation and dynamism effected through flexible and fluctuating flows of imitation, invention, contagion and talent. The advent of design for biological

14 Importantly, network culture displays an inconsistent but significant affective investment in bioscience and biotechnology research. One of the most explicit post-Fordist network media design discourses over the last five years carries the label 'Web2.0.' This term designates a shift in the design of services offered by websites, and the roles afforded to users of websites. In this shift, visitors to websites, in some way or other, become the producers of content for the website. The tremendous growth and popularity of websites such as FaceBook, Flickr, YouTube starting in 2000 is often described as a reorganisation of modes of production and consumption in which the practices of consumption becomes inextricably interwoven with the production of services and goods (Harrison & Barthel, 2009). Web2.0 has been explicitly constructed as a full-blown commercial incarnation of the ideas of openness, collaboration and sharing that animated the growth of internet cultures over the last two to three decades. Since Web2.0 is both a way of re-configuring production and a challenge to existing or familiar ways of work, Web2.0 has an unstable political-economical existence. Synthetic biology has relatively high visibility in the field of awareness associated with Web2.0. The doyen of Web2.0, the computer book publisher Tim O'Reilly, has written about and sponsored meetings on synthetic biology (in the same way that Microsoft funds synthetic biology conferences). He recently stated of synthetic biology:

> So don't follow the money. Follow the excitement. The people inventing the future are doing so just because it's fun. (O'Reilly, 2009)

Many proclamations in blogs, websites and publications associated with network cultures such as *Wired* magazine signal a similar affective interest in synthetic biology, seeing it as akin somehow to the growth of the internet, and even as the successor to network cultures as site of radical invention. [TBA -refs?]

15 These efforts are not confined to synthetic biology since, for instance, 'open bionetworks' for disease research or for medical treatment have also begun to appear (Sage, 2009).

substance is hard to imagine without reference to the network processes that a synthetic biology wiki such as *OpenWetWare* encapsulates. The spread of synthetic biology is *partly* animated by the same wave of speculative-affective attachment to digital media and information networking that drives social networking websites such as *FaceBook* or *MySpaces*. Although little discussed in the current scientific, policy and social science research on synthetic biology, network cultures have a strong practical presence in synthetic biology. Again, as in the argument concerning meta-materials, I would argue that what is at stake here is not so much the reduction of complexity, or the suppression of troubling forms of emergence, but the elaboration of a meta-technique that renders change open-ended and potently recursive. The most important strand of this dimension of the meta-technical configuration of synthetic biology is probably the upsurge of standard-making efforts and the development of mechanisms of collaboration, copying, sharing and circulation of standard-based constructs in synthetic biology.

Standards for biological parts have been very visibly associated with synthetic biology for several years now, most visibly in the form of the oft-mentioned BioBricks stored at the Registry of Standard Biological Parts (Canton, Labno, & Endy, 2008; Shetty, Endy, & Knight, 2008) and mandated for use in the annual IGEM competition. The principal spokesperson for standard biological parts, Drew Endy, has published widely and delivered many public presentations promoting BioBricks, and more importantly, the need for standards (Baker et al., 2006; Endy, 2005, 2006, 2008; Endy & Siegel, 2007). As a matter of course, almost all discussion of synthetic biology make some reference to standard biological parts. However, discussions of the genesis of these standards as design artefacts is much more scarce.[16] In some senses it is very early to analyse the advent of any technical standard in synthetic biology. Compared to some technical standards (for instance, many of the standards used in everyday digital media such network protocols or video formats), the scale and intricacy of the BioBrick standards can seem trivial. The first standard for BioBricks, BBFRFC10, written by Tom Knight of MIT dates from only a few years ago and can be read very quickly since it only contains six paragraphs. This excerpt of the first three conveys the simplicity of the BioBrick standard:

16 (Peccoud et al., 2008) reports an analysis of how different parts stored in the Registry of Standard Biological Parts are actually related to other in practice.

```
       Draft Standard for Biobrick Biological Parts

               Tom Knight
               3 May 2007

This standard defines the required sequence properties for a
Biobrick(tm) standard biological part. It does not define any
functional characteristics of the parts, nor does it motivate any
aspect of these standards. All sequences defined herein are specified
in the 5' to 3' direction.

0. A Biobrick compatible standard biological part consists of a DNA
  fragment potentially conveying informational or functional
  properties to a composite structure assembled from multiple parts.
  The current assembly process requires certain sequence properties
  for the part and the surrounding DNA.


1. Allowed sequences within Biobrick parts include any DNA sequence
  which does not contain the following subsequences:

  EcoRI site:  GAATTC
  XbaI site:  TCTAGA
  SpeI site:  ACTAGT
  PstI site:  CTGCAG
```

(Knight, 2007)

The excerpt shows how lightly the standard is defined. A 'BioBrick compatible standard compatible biological part only needs to contain some 'informational' or 'functional DNA.' It must start and end with explicitly specified sequences, and must be supplied in plasmids that meet certain requirements (antibiotic resistance markers) or specific bacterial strains (*E.coli.* K-12). It cannot contain certain subsequences that would be recognised by the specific restriction enzymes used to cut strands of DNA. Biological substance that complies with the standard can function as a part to be used by designers in producing biological constructs. Such parts can be controlled by software or design automation tools, and therefore require no special techniques or unusual equipment.

These attributes are not specific to synthetic biology since any biologist working with recombinant DNA techniques needs to be aware of, for instance, subsequences recognised by

the restriction enzymes she or he uses. Moreover, if six paragraphs comprise the entirety of the technical standard for a BioBrick, it is not surprising that synthetic biology would be accused of reductive treatments of biological complexity. From the perspective of meta-technique, there is another way to view this. We might expect that standards in this most intricate of engineering domains, life, would entail incredibly complex specifications. Indeed, contemporary technical standards in other fields (for instance Institute of Electrical and Electronic Engineering IEEE standards for video formats) often run to hundreds of pages. I would argue that the content of the standard is much less important in this case than the problem of soliciting collective engagement with the very idea of a biological part. The key issue here is not so much what is designed by who designs what. The form of draft standard directly copies the important internet standard documents called RFCs (Request for Comments). These were written by members of the ARPANET Network Working Group beginning in 1969 to define the protocols of the internet (Abbate, 2000,74). (The 5500 or so RFCs can be viewed at Internet Engineering Task Force repository (IETF Secretariat, 2008)). In its stylistic conventions (choice of font, use of paragraph numbering, and general style of expression), the BioBrick draft standard adheres closely to the internet RFCs. These documents epitomise deliberately informal, yet technically precise collaborative production of technical standards for information networks. Over three decades, they anchored a distributed, constantly growing and modulating entity (the internet) to a process of design that remained mostly pragmatic. There are less than ten actually written RFCs at the time of writing (see (BioBricks Foundation, 2009)). If their existence suggests an attempt to model synthetic biology on the cultural-technical processes that produce communication protocols for the internet, then we would need to ask: who today in synthetic biology designs what? The role of RFCs in synthetic biology remains to be seen. Nonetheless, the rapid growth of the iGEM

competition and the Registry of Standard Biological Parts suggest that the question of who designs what attracts wide interest and the investment of substantial amounts of work.

Conclusion: design as intensification

Cooper, Sunder Rajan and Thacker all cogently argue that biotechnology and contemporary neoliberal capital have been co-produced. Sunder Rajan writes: 'understanding biocapital involves analyzing the relationship between materiality and modes of abstraction that underlie the coemergences of new forms of life science with market regimes for the conduct of such science.(Sunder Rajan, 2006, 113,33).) The shared tenor of their argument is that the variable substance of biotechnology – life at every scale from the microbial to the ecosystem, and at extreme limits (physical, spatial and temporal), from the most objective dimensions of biochemical and physical properties through to the most sensitive, nuanced expectations and sensibilities concerning selfhood, memory, illness and mortality – exudes potential resources and new limits for the growth of capital. How do the concepts of meta-technique and meta-material add here? What does analysis of the role of design in the rapid emergence of synthetic biology contribute? Is synthetic biology's rapid emergence just one among several others – genome sequencing, genome-wide association studies, stem cells and tissue engineering, personalised genomic medicine, etc – that have magnetised public interest in life sciences in recent years?

This paper has argued that to date the problematic presence of design in synthetic biology has been downplayed. The scientific and engineering literature invokes highly abstract and de-contextualised notions of design embodied in principles. In social science research, much of the discussion actually takes these principles at face value, and then argues that any application of engineering design principles to biology tends to impoverish or diminish life

itself by simplifying or de-contextualising. In contrast to these complementary positions, I would argue that there are good reasons to think that the inevitable simplifications that occur during standardisation, model development, and use of design tools at the same time allow an intensification and contestation to occur. As critical accounts of design have argued for several decades now, practices of design display much greater heterogeneity than the abstract principles of abstraction, modularity, and de-coupling can convey. The mobilisation of design in biotechnology means following or making new pathways of coordinated and more or less shared practice. The key cases of design software, of chassis or platform design, of standard-making efforts in synthetic biology all display extensive borrowings from adjacent information, network and software cultures. It is more important, I would suggest, at this point, to track those borrowings and to understand what is carried across and what is not. From this perspective, an emphasis on technique and procedures is particularly useful since it brings into view and at the same time questions the de-coupling between thinking and making, between designing and producing, that design aspirations inevitably rely on.

Seen from the perspective of recent critical work on biotechnology and capital, the injection of design into biotechnology enlarges the processes that capture surpluses associated with biological substances. However, synthetic biology throws up new conjunctions and complications for current critical accounts of biocapital. In the last decade or so, a common vein of thought running through work on biotechnology held that recombinant DNA technologies flatten or lateralize species and evolutionary differences. Versions of the 'lateralization thesis' run across much of the biosociality-influenced literature. Indeed, arguments about biotechnological excess (Thacker, 2005), surplus life (Cooper, 2008), genomic commodification (Parry, 2004) and hype-fetishism (Sunder Rajan, 2006) all to some extent rely on the lateralization thesis. While synthetic biology also imagines a hyper-

flattened terrain of inter-species difference, the design processes taking shape there in some ways resist flattening. The notion of meta-technique seeks to convey the uneven materials, practices and indeed subjects that must coalesce before biology can be engineered. The flatness sometimes implied in notions of biocapital contrasts with the topological boundaries, forms of closure, compaction, discreteness and path-dependent connections that arise in design work. The notion of metamaterials and meta-techniques seeks to articulate the curiously composite status of the biological substance likely to result.

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Figure 1