

FLOW, PROCESS, FOLD: INTERSECTIONS IN BIOINFORMATICS AND CONTEMPORARY ARCHITECTURE

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This paper traces shared terms — metaphors — in two registers of discourse, bioinformatics and architecture, with the goal of teasing out the mutually informing contexts of each.

We are becoming immersed in a growing repertoire of computer-based media for creating, distributing, and interacting with digitized versions of the world. Computer-mediated communication has already been significant in biology and medicine. In this essay we want to juxtapose several developments — not all of them integrally connected — in fields of computational biology, bioinformatics, robotics, and computer-aided design, which are significant for other areas in which computers have begun to mediate processes of work and creativity. We are particularly concerned with architects' engagement with information technology in their own work. Oft-noted features of the growth of computer-mediated forms of work and communication — particularly evident in the biomedical areas with which we are concerned — are the acceleration of nearly every aspect of design and production, along with the high degree of both modularity and adaptability of processes. IT workers have responded to the explosion of data created by digital technology by generating dynamic systems for facilitating the information flow, replacing static forms with fluid architectures for extracting meaning.

We want to suggest ways in which some architects are using information technology to address critical contemporary issues of philosophical, ethical, and social concern. Many have found philosophical resonance in the writings of Deleuze and Guattari, particularly in their effort to displace key modernist notions of difference as other, lack, or negative, with difference as a positive source. Equally powerful are Deleuze and Guattari's rejection of positions stressing reductionism and organic unity; in place of totalizing unity, they advocate locality, situatedness, rhizomic strategies, "bodies without organs," and machinic assemblages.

The architects we explore have engaged with computer technology on many planes. They have sought to engage the digital communications revolution in the material expression of the buildings they construct. They have also embraced computer-mediated design and production as an opening for a new critical discourse, a new line of flight, at once a new critical language and phenomenology.

BIOINFORMATICS: A NEW BIOLOGY FOR THE INFORMATION AGE

One of the most interesting developments in recent biology is an inexorable shift — almost in spite of the rhetoric of the practitioners themselves — toward a disunified model of science. It's not that biological scientists have given up their search for laws of nature. Hardly. But in the past two decades a new biology has arisen: a highly context-specific, yet mathematically exact form of local science that might be described as a *science of the particular*. Similar trends can be seen in areas of medicine such as surgery, where surgical planning and simulation are being tailored to the specific patient as opposed to a generic plan selected from a medical atlas. Similarly the goal of pharmacogenetics, a new postgenomic field, is to target drug design for the individual.

What makes this possible? Computing technology, particularly broadband web and simulation technology. How? Take work on protein structure as an example. Rather than telling the familiar story of Jacob and Monod's theoretical work and how it propelled biology into the Information Age, a media-sensitive account would look at the contributions of information technology itself. About the same time as Jacob and Monod's work, new developments in computer architectures and algorithms for generating models of chemical structure and simulations of chemical interactions allowed computational experiments to interact with and draw together theory and laboratory experiment in completely novel ways.

Such a claim suggests that notions of theorizing have radically shifted in many areas of science, not least biology. For decades many biologists aspired to theoretical constructs modeled along the lines of the physical sciences. Like physicists, they have searched for the holy grail of a grand unifying theory, preferably reducible to fundamental laws of physics and chemistry. For those wanting to view molecular biology as an extension of physics and chemistry, a key step was provided by the work of Christian B. Anfinsen. Anfinsen's Nobel Prize-winning work on protein folding established that all the information required to fold proteins into their final (native) state is contained in the linear sequence of amino acids themselves.¹ But how is the tertiary structure, the final folded state of molecules encoded in that primary sequence? It is this structural code that biologists have needed to determine in order to understand the genetic message.

Anfinsen's work suggested that it is reasonable to suppose that the native fold of a protein can be predicted computationally using information about its chemical composition alone, and that finding the global minimum of a protein's potential energy function should be tantamount to



Step by step animation of alpha shape visualizations of the molecule gramicidin by Duke University computer scientist Herbert Edelsbrunner. Alpha Shapes software was designed by Edelsbrunner to combine the Computational Geometry Algorithms Library (CGAL) with visualization and interaction tools in order provide new means for generating visualizations. The project derives its direction from new methods (new geometric and topological insights and algorithms) and application problems (from biochemistry and pharmacy). Source: <http://biogeometry.cs.duke.edu/gallery/animation/>.

identifying the protein's native fold.² Unfortunately, the task of finding the global minimum of one of these functions has not proven easy, because the potential energy surface of a protein contains many local minima. Some computational biologists have argued that even more is possibly at stake here than just the computational complexity of the task. It may be impossible in principle to fold proteins without the assistance of "chaperones" or the rapid formation of local interactions which then determine the further folding of the peptide. This suggests local amino acid sequences, possibly the result of evolutionary adaptation, which form stable interactions and serve as nucleation points in the folding process. Indeed, Cyrus Levinthal, the author of this hypothesis (known as Levinthal's paradox), argued that the conformation space--the set of all possible configurations a molecule can assume in folding from its starting uncoiled state to its native fold--for even the average sized protein molecule is exponentially large. For example, each bond connecting amino acids can have several possible states (e.g. three for this example), so that a protein of 101 amino acids could exist in $3^{100} = 5 \times 10^{47}$ configurations. Even if the protein is able to sample new configurations at the rate of 10^{13} per second, or 3×10^{20} per year, it will take 10^{27} years to try them all. Proteins actually fold in a time scale of seconds or less. Levinthal concluded that random searches are not the way proteins fold.³

Computer modeling and the introduction of tools from artificial intelligence (AI) and expert systems in biochemistry during the 1960s and 1970s seemed to offer a way out of the dark wood of protein folding and at the same time promised the theoretical unification of biology. But what has actually emerged is something quite different. We would describe it as a disunified but more effective biology.

Models, whether physical or virtual, have always played crucial roles in understanding the structure of biological molecules. Think of Watson and Crick's discovery of DNA, for example, for which making a physical model was the key step. In biology as in architecture, geometry is everything; for the functional properties of a molecule depend not only on the interlinkage of its chemical constituents but also on the way in which the molecule is configured and folded in three dimensions. Much of biochemistry has focused on understanding the relationship between biological function and molecular conformational structure. Model building is the sine qua non of this enterprise.

A milestone in the making of physical 3D models of molecules was Kendrew's construction of myoglobin. An attempt to build a physical model from a Fourier map of the electron densities derived from x-ray crystallographic sources, Kendrew's model was a room-filling forest of brass rods and wires. It was obvious that such 3D representations would only become really useful when it was possible to manipulate them at will—to size and scale them arbitrarily from actual x-ray crystallographic and electron density map data. Proponents of the



field of computer graphics and computer-aided design, newly minted at MIT in Ivan Sutherland's 1963 dissertation, argued that computer representations of molecular structure would allow these manipulations.

Computer modeling, requiring the specification of codes to produce these models from known data, was at first embraced because it promised molecular biologists, particularly the biophysicists among them, a unified theory; it would move the field toward such a goal by providing a framework from which would emerge a fully mathematized and thus fully scientific theoretical biology.⁴

Cyrus Levinthal at MIT first illustrated the method for representing molecular structure in computer graphics by adapting Sutherland's CAD program to biochemistry. Levinthal reasoned that since protein chains are formed by linking molecules of a single class, amino acids, it should be relatively easy to specify the linkage process in a form mathematically suitable for a digital computer.⁵

But there was a hitch: in an ideal world dominated by a powerful central theory one would like, for example, to use the inputs of xyz coordinates of the atoms, types of bond, etc., to calculate the pairwise interaction of atoms in the amino acid chain, predict the conformation of the protein molecule, and check this prediction against its corresponding xray crystallographic image. However, as we have noted in our discussion above of Levinthal's paradox, the parameters used as input in the computer program do not provide much limitation on the number of molecular conformations. Other sorts of input are needed to filter among the myriad possible structures. Perhaps the most important of these is energy minimization: the basic physical hypothesis is that, like water running downhill, a large protein molecular string will fold to reach the lowest energy level. Such minimization calculations could not be done, as Levinthal noted, because the necessary formula could not in the state of molecular biological theory of 1965 be written down and manipulated with a finite amount of labor. Levinthal's solution to this problem was a computer visualization generated in real-time interaction between human and machine. The computer became in effect both a microscope for examining molecules and a laboratory for quantitative experiment, all in the service of producing a general theory of protein folding. Levinthal emphasized that interactivity facilitated through visualization was a crucial component of his model-building program, CHEMGRAF,⁶ where the user could *observe* the result of the calculations and to be able to halt the minimization process at any step, either to terminate it completely or to alter the conformation and then resume it.⁷ CHEMGRAF was thus a first step toward decentering the importance of theorizing in biology and elevating the emphasis on visualization, haptic interaction, and experimental tinkering as a method of investigation. It would take an explosion in molecular biological data to complete the redefinition of biology as information science.



The measures taken by Levinthal to avoid computationally intensive techniques illustrate the wide variety of simplifications that have typically been introduced into molecular dynamics computations, such as constructing models that hold fixed certain parameters or ignoring others deemed not to be essential for purposes of approximation. Other approaches have used time averaging or ensemble averaging to calculate properties such as the global free energy of the protein. Another approach has been to construct simulations using randomized Monte Carlo methods for generating successive configurations and averaging over all samples that are generated. While both molecular dynamics and Monte Carlo methods are theoretically capable of treating the protein-folding problem, they too require very large amounts of computation time for molecules with many degrees of freedom.

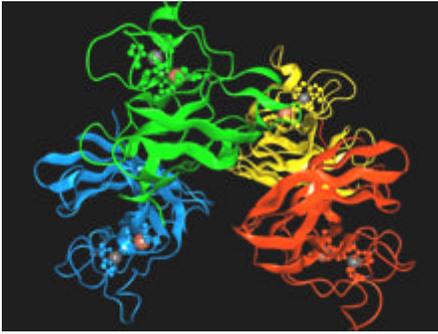


Figure 1. A vector ribbon diagram of the molecule superoxide dismutase from the Brookhaven Protein Databank. Source: www.accelrys.com/support/life/images/2sod.jpg

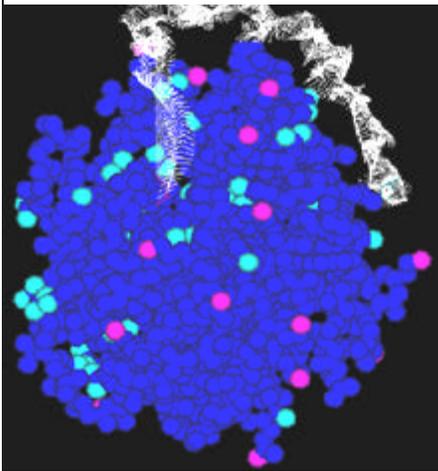


Figure 2. Bruttig and Latombe's time-lapse image of plausible binding motions for a flexible ligand (in white) and a protein structure (in blue), as mapped according to their conformational probabilistic roadmap technique. Source: robotics.stanford.edu/~latombe/projects/#F.

Characteristic of the trend in contemporary science away from reductionist theories is to draw upon strategies and methods from completely different domains, in effect to cut the Gordian knot in one area by adapting tools from another. One such approach to protein folding relevant to our architectural concerns later in this paper is the use of algorithms based on robot motion planning by Latombe, Brutlag and colleagues in order to improve the speed and efficiency of protein folding simulation methods.⁸ In this context, similar to the elements of a robot navigating a local terrain, Latombe, et al. model molecules as sequences of vectors (**figure 1**), where each vector is an element of secondary structure, such as an alpha-helix or beta-sheet, etc[see text box]. The set of all its 3D placements is the molecule's conformational space, over which the energy field is defined (**figure 2**). Instead of inducing the motion of the robot through actuators, Latombe et al. examine the possible motions of the robot induced by the energy landscape of its immediate environment and generate a network of pathways called a probabilistic conformational roadmap, a graph whose nodes and edges are respectively low-energy conformations and short weighted pathways. The weight of a pathway measures the difficulty for the molecule to move along it. The power of a probabilistic conformational roadmap derives from its ability to encode compactly a huge number of energetically

favorable folding pathways, each defined as a sequence of contiguous local

pathways. Instead of simulating the entire set of potential fold configurations, the motion planning technique guesses several possible intermediate configurations of the protein and obtains a distribution of energetically favorable intermediate configurations (**figure 3**) to which a “difficulty weight” is assigned representing the energy barriers along the path.

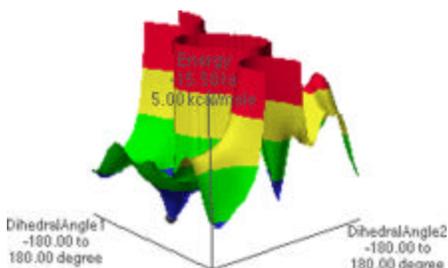


Figure 3. A side angle view of a Ramachandran plot conformational energy map for a peptide analogue which contains a single amino acid residue, alanine, flanked by two peptide bonds and capped at each end with methyl groups. Source: www.molecules.org/experiments/Bevilacqua/Bevilacqua.html.

A PARADIGM SHIFT IN BIOLOGY

The type of modeling represented by Levinthal's work as well as the recent work on motion planning depends crucially on high-quality crystallographic data, and these have proven difficult to obtain in the quantity desired to drive the field rapidly forward.⁹ But simultaneously another stream of work flooded the biological knowledge base. The development of restriction enzymes, recombinant DNA techniques, gene-cloning techniques, and PCR (polymerase chain reaction) produced a deluge of data on DNA, RNA, and protein sequences.¹⁰ Since the mid-

1980s, sequence data has been growing at an exponential rate, doubling over 15 months, reaching a figure of ten million base pairs a day. Such an explosion of data encouraged the development of a second approach to determining protein structure and function; namely, prediction from sequence data alone.

The field of bioinformatics has taken a different approach to this problem than the "bottom-up" brute force energetics approaches. Rather than deriving structure and function directly from the physical properties of amino acids and the first principles of protein folding dynamics, the bioinformatics approach involves comparing new sequences with preexisting ones and discovering structure and function by homology to known structures. The approach is eclectic, heterogeneous and multiple: Rather than proceeding linearly from genetic information to molecular structure to function in the spirit of the old "central dogma"--"DNA produces RNA, produces protein, produces function"--bioinformatics draws on bits and pieces of pattern in one domain and maps them comparatively in another domain through sophisticated probabilistic methods of data analysis, pattern matching, machine learning and robotics. We are not suggesting that scientists in the field of bioinformatics reject energetic or thermodynamic accounts of protein folding; far from it. But in their search for methods that save computing cycles, they have followed a bootstrapping approach in which the statistical and knowledge-base methods of bioinformatics have assisted in refining the structures input into large all-atom energetics calculations for ab initio structure prediction.¹¹ In the new paradigm, both approaches inform one another.

What we are calling the “bioinformatics” approach identifies the function and structure of unknown proteins by applying search algorithms to existing

protein libraries in order to determine sequence similarity, percentages of matching residues, and the statistical significance of each database sequence. A database of proteins for which structural and sequence information is available is used to predict structural features for proteins of neighboring sequences. From proteins of known structures, a comparison of sequence and 3D geometry makes it possible to derive rules or parameters that will subsequently permit the determination of the probability for a given fragment to arrange into a particular regular structure. As for tertiary structures, they also allow the researcher to define sequence templates for families of protein structures that adopt a common fold. If a sequence of an unknown structure can be matched with a template, a model of the fold can be built by analogy. Schematically, for predicting structures

To elucidate the structure and function of proteins bioinformatics focuses its computational tools on secondary and tertiary structure. Secondary structure consists of local folding regularities maintained by hydrogen bonds and traditionally divided into three major classes: alpha-helices, beta-sheets, and coils representing all the rest. In alpha-helices, backbone hydrogen bonds link residues i and $i+4$, whereas in beta-sheets, hydrogen bonds link two sequence segments, in either parallel or antiparallel fashion. The secondary structure can be sensitive to single amino acid changes and depends on both local and long-range interactions. A key tool used in elucidating structure-function relationships is a search for sequences that correspond to small conserved regions of proteins, modular structures known as motifs.¹ Motifs are key patterns of amino acids that form the building blocks in the secondary structure of proteins. The sequence patterns defined by motifs are powerful probes for searching databases of known structure and function to determine the structure and function of an unknown gene or protein. Several different kinds of motifs are related to secondary and tertiary structure--the final folded structure of protein. Secondary structure consists of patterns of repeating polypeptide structure within an α -helix, β -sheet, and reverse turns. At the next level supersecondary structure refers to a few common motifs of interconnected elements of secondary structure. Segments of α -helix and β -strand often combine in specific larger structural motifs. One example is the α -helix-turn-helix motif found in DNA-binding proteins. This motif contains 22 amino acids in length that enable it to bind to DNA. Another motif at the supersecondary level is known as the Rossmann fold, in which three α -helices alternate with three parallel β strands. This has turned out to be a general fold for binding mono- or dinucleotides, and is the most common fold observed in globular proteins.¹ In addition to searching for motifs, another principal strategy for determining structure-function relations are various sequence alignment methods. Among these are consensus sequences, weight matrices, and profiles, all of which employ a battery of different probabilistic methods for teasing out structure similarity.

of unknown proteins, model building in bioinformatics proceeds through three main alternative approaches:

1. Starting from the sequence knowledge
2. Assembling fragments from different, known homologous structures
3. Carrying out limited structural changes from a known neighboring protein.

In order to keep pace with the flood of data emerging from automated sequencing since the 1990s, genome researchers have looked increasingly to artificial intelligence, machine learning, and as we noted above, even robotics in developing automated methods for discovering protein motifs and folding patterns from sequence data. The power of these methods is their ability both to represent structural features rather than strictly evolutionary steps and to discover motifs from sequences automatically. Indeed, a central axiom of the field is that massively automated methods are the *only* ways to get at the structure of large genomes and make sense of medically relevant sequence information. The methods developed in the field of machine learning such as perceptrons, genetic algorithms, neural networks, Bayesian networks, hidden Markov models, minimal length encoding, and context-free grammars have been used singly and in combination to extract conserved residues, discover pairs of correlated residues, and find higher order relationships between residues as well.¹²

FLOW AND FOLD

The results of automated sequencing of genes and proteins, combined with the necessity of devising novel informatics techniques for extracting meaning from this data, has radically transformed the theoretical enterprise of biology. The “central dogma” emerging from the work of Watson, Crick, Monod, and Jacob in the late 1960s, may be schematized as follows:

DNA → RNA → Protein → Function

The fundamental dogma of this new biology reformulates the central dogma of Jacob-Monod in terms of “information flow” (**figure 4**):¹³

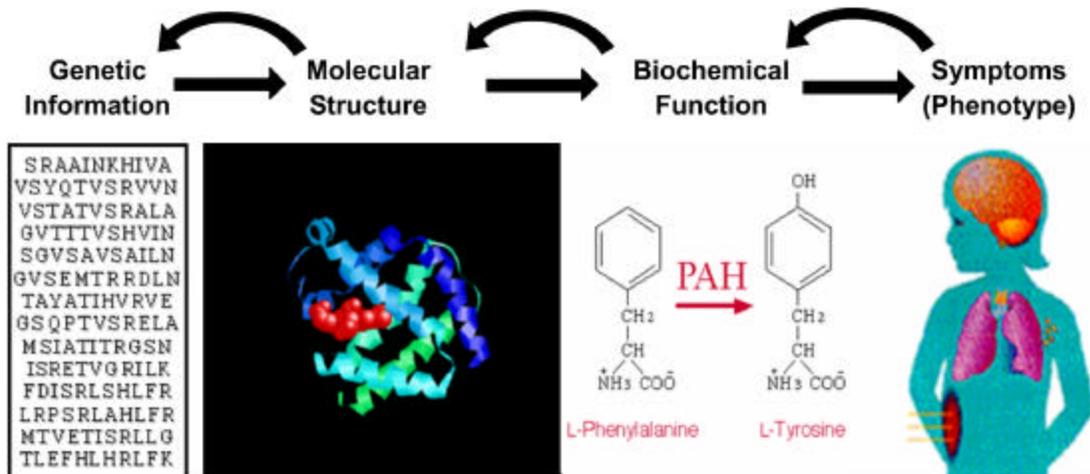


Figure 4. The “central dogma of DNA” as revised by the bioinformatics paradigm. Source: Doug Brutlag.

Genomics, computational biology, and bioinformatics have restructured the playing field of biology, bringing a substantially modified toolkit to the repertoire of molecular biology skills developed in the 1970s. The new biology is a data-bound rather than observational science. To understand the data, the tools of information science have not become mere handmaidens to theory; they have fundamentally changed the picture of biological theory itself. As a result, disciplinarily, biology has become an information science, while institutionally it has become “Big Science.”¹⁴ Along with biochemistry components, new skills are now required to sift through the data, including machine learning, robotics, databases, statistics and probability, artificial intelligence, information theory, algorithms, and graph theory.¹⁵

A 1985 NIH report sums up the difference between a unified biology and the information-technology-infused, heterogeneous, multiple, data-driven, and enfolded state of biology. Contrasting this biology with theoretical physics, “which consists of a small number of postulates and the procedures and apparatus for deriving predictions from those postulates,” NIH writers view contemporary biology as an interconnected assemblage of different strata from DNA to protein to organismic and behavioral biology, each with its own unique set of laws and processes.¹⁶ Rather than a unified theory, the field’s critical questions can often only be answered by relating one biological level to another through the techniques of informatics.¹⁷

SHARED METAPHORS

Our account of the impact of computing on biology has argued that biology as it was once practiced has been remade by the steady introduction of computational tools, computer-mediated forms of communication, and an entire material infrastructure of genetic and cellular tagging, labeling, sequencing, and processing that turned the world of biological flows and folds into digital information. As a result, the practitioners of biology in silico have a different relationship to their research objects than their predecessors. The first generation of computational biologists looked to computers as tools for data storage and retrieval, and for assistance in carrying out lengthy redundant computations—but not as the site for experiment and design work. Genomics researchers, by contrast, find themselves immersed in distributed increasingly automated computational environments for the identification, manipulation, and design of their research objects. In a certain sense, the ontology of the domain has shifted.

The architects we are interested in discussing have been similarly affected by engagement with computers, and they have looked to computational biology for metaphors to articulate the new directions in which they want to take architectural practice. The architects we are calling “post-architects” all share an interest in engaging with the computer in their architectural practice, not just as a useful tool for implementing designs, or as a new medium for expression, but as a new material agency that can challenge the foundations of traditional design practice and propel architecture in a new direction, a new line of flight. In addition to their interests in computers and computational biology, what characterizes post-architects in our account is their agreement on what they take to be limitations of “postmodern architecture” and on a new program that can move beyond them. For our post-architects the writings of Gilles Deleuze are particularly salient in this new enterprise. Our purpose will be to show how these different concerns—architectural computing fused with metaphors from computational biology—co-mingle with the philosophical positions articulated by Deleuze to inspire this new architecture.

Peter Eisenman has provided one of the clearest statements of the motivation post-architects share for engaging computational media. In a recent essay entitled “Visions Unfolding: Architecture in the Age of Electronic Media,” Eisenman points to a crisis in the current state of his art: “During the fifty years since the Second World War, a paradigm shift has taken place that should have profoundly affected architecture: this was the shift from the mechanical paradigm to the electronic one.”¹⁸ Updating Walter Benjamin’s “The Work of Art in the Age of Mechanical Reproduction,” Eisenman argues for a necessary distinction between the mechanically reproduced and the electronically mediated. Mechanical reproduction has always required a human subject to mediate and interpret the process of reproduction itself: photographs are differentially printed according to the specific visual characteristics desired by the photographer. In this way, Eisenman contends, “the photograph can be said to remain in the control of human vision.”¹⁹

Electronic media, on the other hand, are not subject to human intervention or interpretation because they are not produced according to a visible mechanical logic. Rather, electronic media are themselves *processes of mediation* that are hidden from the user and controlled by the internal wirings of an entirely other logic – that of the digital. Eisenman asserts that electronic media’s elision of the human discursive function in the process of production places it outside the control of human vision. By *vision*, Eisenman means the process linking “seeing to thinking, the eye to the mind”²⁰ that perpetually aligns the production of content with the desires of an anthropomorphizing subject. Electronic media, because they do not pass through the intermediary of human vision, are capable of disrupting how we experience reality itself: “For reality always demanded that our vision be interpretive.”²¹

Eisenman wonders how, when every other cultural practice has been fundamentally transformed by the shift to electronic media, architecture has remained largely unchanged. As we have argued, the field of biology no longer exists as it was once envisioned: bioinformatics *is* the electronic mediation of biology, remaking the field right down to the central dogma of molecular biology. Why has architecture resisted such a transformation? Eisenman answers that architecture has remained stolidly rooted in the mechanical paradigm because “architecture was the visible manifestation of the overcoming of natural forces such as gravity and weather by mechanical means.”²² As a result, architecture has not only centered on designing structures that shelter, but in doing so has produced designs intended *to look as though* they will securely shelter – that is, the mechanics of their design is immediately interpretable by human vision. Such continuing recourse to the “mechanics of vision” in architecture has resisted an ability to *think architecture* in ways more commensurate with the new paradigm of electronic mediation.

Realizing the limitations inherent in an architecture dominated by the mechanics of vision, architects such as Peter Eisenman, Neil Denari, and Greg Lynn have discarded the eye-mind connection in favor of the transformative powers of electronic media and openness toward the systems of metaphor that such media enable, encourage, and engender. Neil Denari foregrounds such an openness by wondering:

[W]ould it be possible today to describe certain architectural propositions without the lush and open-ended (technical) language of the life sciences? It seems that almost no architect is completely immune to the models offered by the soft systems of molecular biology, especially as they are transposed through forms of communication (media-based languages, etc.) that are themselves compounding the possible theoretical positions for architecture. [My] works...while less indebted to the formal models of biological systems, do nonetheless employ the conceptual and abstract terminologies of such systems. After more than a decade ... of rapid absorption into the discourse of architecture, concepts and fields such as entropy, cybernetics, self-organizing systems, neural networks, and complexity have helped construct new formations of meaning, geometry, and space.²³

Greg Lynn extends this sentiment in pointing to the further transformative potential for a merger of new media, the tools of computational biology, and architecture:

In their search for systems that can simulate the appearance of life, the special effects and animation industry has developed a useful set of tools for these investigations; as contemporary animation software utilizes a combination of deformable surfaces and physical forces. The convergence of computer aided technological processes and biological models of growth, development and transformation can be investigated using animation rather than conventional architectural design software. Rather than being designed as stationary inert forms, space is highly plastic, flexible, and mutable in its dynamic evolution through motion and transformation. In animation simulations, form is not only defined by its internal parameters, as it is also effected by a mosaic of other fluctuating external, invisible forces and gradients including: gravity, wind, turbulence, magnetism and swarms of moving particles. These gradient field effects are used as abstract analogies for; pedestrian and automotive movement, environmental forces such as wind and sun, urban views and alignments, and intensities of use and occupation in time.²⁴

NEW ARCHITECTURE AND COMPUTER-AIDED DESIGN

The strongest buttress of the eye-mind complex has been architectural theory itself, especially as espoused by modernism. In its search for unity, harmony, and simplicity in design, modernism aspired to remake every site in the image of man as monument to human ingenuity and Western ideals of beauty, proportion, and progress. Modernism encompassed each site within its totalizing logic, viewing local particularities as obstacles to the realization of the architect's vision. One way to dismantle the eye-mind link is to reject such generalized theories in favor of increased attention to the indigenous differences in each site. Just as the new biology has moved away from sweeping—but unuseful—theoretical generalizations, architects have begun to discard the totalizing tenets of modernism and embrace more context-specific practices of building.

Such a shift in focus is not, however, an entirely recent phenomenon. Inspired by the post-structuralist writings of Jacques Derrida, architectural deconstruction, or *deconstructivism*, emerged in the 1970s and 1980s as a “postmodern” antidote to the hegemonic narratives of modernism. Intending to subvert the homogenizing anthropocentrism of modernism, deconstructivist architects sought to expose the contradictions and flaws inherent in the process of building itself.²⁵ As a common technique, deconstructivist architects disrupted traditional architectural regimes by identifying “repressed” styles within the local context of a site, then forcefully combining the repressed motifs in a single building without any concern for overall unity or design. Exemplary of deconstructivist architecture is the Frank Gehry House in Los Angeles, which according to Greg Lynn, represents

materials already present within, yet repressed by, the suburban neighborhood: sheds, chain-link fences, exposed plywood, trailers, boats and recreational vehicles...The house is seen to provoke conflict within the neighborhood due to its public representation of hidden aspects of its context. The Gehry House violates the neighborhood from within.²⁶

Deconstructivism engaged in dispersed guerilla warfare against the modernist tradition of architecture by tactically dismantling localized contexts from within. In order to expose the inherent superficiality of modernism, deconstructivist architects deracinated the modernist motifs, styles, and materials from their underlying semiotic regimes and recombined them in a free-floating currency of signs.

But by the early 1990s many architects had begun to feel that postmodernism had trapped itself as a negative reaction against modernism.²⁷ Rather than freeing architects from the self-aggrandizing styles and forms of traditional modernism, deconstructivism appeared to be a superficial reshuffling of styles permanently bound within the same rhetoric it struggled to resist. Eisenman diagnosed this persistent problem in postmodernism: “[D]espite repeated changes in style from Renaissance through Post Modernism and despite many attempts to the contrary, the seeing human subject – monocular and anthropocentric – remains the primary discursive term of architecture.”²⁸ Architecture, according to Eisenman, still had to move outside its self-inscribed circle of discourse. His remedy for the problem was to form a new collaboration, a human-machine assemblage that would de-center the architectural design process.

Eisenman, of course, was not the only former devotee of postmodernism²⁹ to turn to computers for new approaches to design. Frank Gehry also turned to computer-aided design (CAD) in search of new directions. Gehry’s buildings of the 1990s, especially the Experience Music Project (Seattle), Guggenheim Bilbao, and the planned Walt Disney Concert Hall (Los Angeles) are rife with imagery of flow, folds, and biological metaphor. But in our view, Gehry’s work does not represent the embrace of the machinic assemblages and de-centering practices of post-architecture. Computers, as we will show below, do not in and of themselves enable the architect to break free of traditional assumptions. If anything, they can reify those assumptions in software code and firmware in ways difficult to escape. To appreciate the ways in which the group we are calling post-architects have used computers in breaking free of these constraints, we consider briefly the history of computer-aided design.

Computer-aided design entered our story at the very beginning of the field. Sketchpad, the first CAD program was the basis of Levinthal’s early molecular design program, CHEMGRAF. But architects were no less receptive to CAD than early molecular biologists were to molecular graphics and computational modeling. Indeed, the reactions of the two groups were often parallel. As initially conceived, architectural CAD programs were mainly used as tools to augment the existing design techniques of architecture.³⁰ Architects did not design using CAD programs; rather they used the traditional drafting tools of architecture to design buildings as they always had. After completing original designs, architects tended to use CAD programs to produce slick, full-color design layouts to entice clients and to store digitally their designs. Similarly, the word in the lab corridors among molecular biologists was that molecular graphics produced pretty pictures rather than serving as aids to discovery.³¹ Though CAD programs were electronic

media from the start, architects used them more as high-tech additions to an older toolkit for mechanical reproduction.

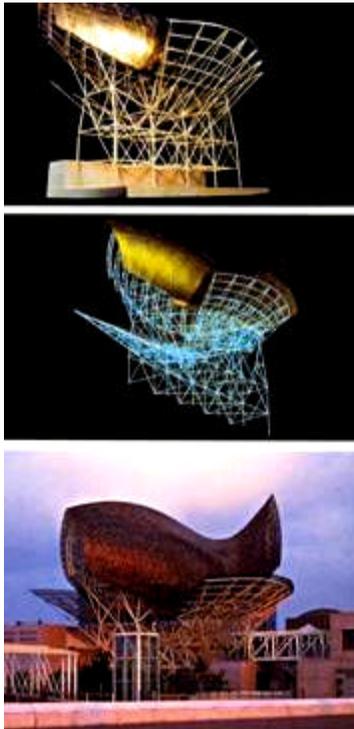
Part of the initial resistance to designing in CAD stemmed from the fact that initial CAD programs were not immersive design environments. In fact, only recently did CAD programs such as AutoCAD become truly three-dimensional, in a real-time volume-rendering sense. Early PC CAD programs were actually 2D graphing systems that automatically extended shapes to a single fixed vanishing point, then projected a vertical “thickness” to the 2D forms in order to approximate solid volumes. This 2½D approach, as it is called, created the semblance of geometric solids; however, the perspective of the solid was mapped only to the vanishing point from the position at which the shape was originally drawn. Therefore, if you rotated the 2½D shape around its vertical axis, the shape would appear to recede in reference to the original vanishing point, even though the rotation of the object should also rotate the vanishing point and change the perspectival projection in 3D space. Only recently have most architectural CAD programs been completely overhauled to provide true 3D volumetric rendering that plots solids dynamically in real-time from an underlying data tree representation of the object: an innovation coded into bioinformatics media from the beginning.

The design tools presented in CAD also limited the extent of potential collaboration between the designer and the medium. Since early CAD programs were used to reproduce traditional design processes, architectural CAD programs were coded to integrate the same traditional rectilinear drafting techniques into a set of computer tools: the protractor, compass, straightedge, T-square, and French curve were all automated as tool options within the program’s own architecture. As such, early CAD programs provided no real advantage over traditional drafting techniques; in fact they were often less intuitive. It is important to understand the precise capabilities and limitations of early architectural CAD programs because, as William J. Mitchell observes, “Architects tend to draw what they can build, and build what they can draw.”³² Rather than providing a means for interactive collaboration as in CHEMGRAF, CAD programs reified a system of traditional design processes and significantly limited the ability to think outside of them. Coloring outside the lines is not only stylistically inadvisable in CAD programs; it is technologically impossible because there is no tool to allow it. Again, as Mitchell notes: “By greatly enhancing the efficiency of traditional drafting practices, these systems further marginalized alternative practices.”³³ In architectural CAD programs, the template for an ideal conventionalized architecture – the traditional paradigm of the mechanics of vision – is coded into the program itself. Subsequent releases and offshoots of these early programs preserved or exaggerated these initial limitations.

In the 1990s computer-aided design, linked with computer-aided manufacturing and a new repertoire of malleable building materials encouraged many architects to express fascination with the soft, anexact forms of bioinformatics; but this appreciation at times masked the radical potential of the technology underpinning these capabilities. In his article for the celebration of the



Figures 5 & 6. Photographs depicting Frank Gehry's design process for the 1995-2000 Experience Music Project (above) and the 1989-92 Fish Sculpture for the 1992 Barcelona Olympic games (below). In the top image, the physical model is being digitally scanned into CATIA to produce the completed building in Seattle below it. Below: model, CATIA design, and finished model for Gehry's Fish Sculpture. Source: William Mitchell, "Roll Over Euclid: How Frank Gehry Designs and Builds," in *Frank Gehry, Architect*. Edited by J. Fiona Ragheb. (New York: Guggenheim Museum, 2001),



Guggenheim Bilbao, for instance, Mitchell focuses on Frank Gehry's building process as a means of generating soft, pliant forms and circumventing the built-in limitations of CAD. According to Mitchell, Gehry's process begins by freely sculpting a physical model of his desired design. Gehry then inputs the three-dimensional structure of his physical models into the robust CATIA program (the CAD/CAM environment used by Boeing to design the 777, the first airplane to be entirely designed in CAD/CAM) (**figures 5 & 6**). Mitchell describes this process as follows:

In Gehry's office, the process begins with the use of a very accurate three-dimensional digitizer to capture vertex, edge, and surface coordinates from a large-scale physical model. Using CATIA, mathematical curves and surfaces are then fitted as closely as possible to these digitized points. Rapid-prototyping devices, such as computer-controlled three-dimensional deposition printers and multi-axis milling machines, are then used to "build back" physical models for visual inspection and comparison with the original. The process iterates, with adjustments as necessary to the digital model, until the design team is satisfied.³⁴

In this way, Mitchell views Gehry's iterative multimedia process as "far more revolutionary" in its ability to transcend the limitations of traditional CAD functionality alone.³⁵

However, despite Gehry's apparent ability to both utilize and transcend the functionality of CATIA, he is in fact doing nothing revolutionary with CAD. To be sure, he begins with three-dimensional rather than two-dimensional models. Nevertheless, as with previous CAD architectural implementations, Gehry has recourse to a metaphysics of presence in privileging *real* materials. His high valuation of the "direct tactility of the physical model and the speed, freshness, and energy of the freehand gesture"³⁶ smacks of a Pollock-esque modernism in which the artist spilled his singular genius onto canvas. Professor of digital architecture Dennis Dollens argues that Gehry's design process combines the "warps and wefts of one experiment with the splines [vector lines] and lofts of another and arrives at a third transformative structure,"³⁷ a work process paralleling that of the post-architects. However, with due respect to Dollens, Gehry does not engage in a transformative repetition of form through CATIA; rather, he subjects

each CATIA prototype to a process of “visual inspection and comparison with the original” and thus privileges the original physical form. He produces no “third transformative structure” but only a progressive digital approximation of the physical model: a form that for all its anexact smoothness stems directly from the anthropomorphic ideals of Gehry himself. Gehry uses CATIA solely to rapidly prototype and apply his design to an automated process of highly specific mechanical production,³⁸ not to draw upon the powers of its electronic mediation to decenter his interpretive function as architect. Dollens reports that Gehry’s approach enables his initial drawings and models to “be enhanced digitally, allowing him to take such advantage of electronic production while not being seduced by technology.”³⁹ Such a fear of the “seductive” powers of technology reveals Gehry’s unwillingness to subject his artistic genius to an equally powerful process of electronic mediation: an attitude binding him to the modernist architects he intends to oppose.

An alternative approach – that of Eisenman, Lynn, and Denari, the group we are calling “post-architects” – is to use electronic media to interact with anexact forms on their own terms and within an equally mediated space. If traditional CAD software is circumscribed within the mechanics of vision, why not change the software to the types of robust, high-powered programs of bioinformatics? Peter Eisenman observes: “What we need is the kind of software that the people who model complex biological and physical data in complex research institutions employ that can be used as models for architecture.”⁴⁰ Through the increasing use of rigorous modeling applications such as Alias | Wavefront’s Maya, Discreet’s 3D Studio Max, and SOFTIMAGE | 3D, architects are beginning to acquire such media. Utilizing NURBS-based strategies for generating vectorial topologies, these new modeling programs enable new ways of thinking about form and space. According to Lynn, the newer media offer “perhaps the first opportunity for architects to draw and sketch using calculus...by supplanting the traditional tools of exactitude and stasis with tools of gradients, flexible envelopes, temporal flows and forces.”⁴¹ Architects can now work on a similar level as that of bioinformaticists: a level where complex algorithms can model the affective space of each site, thereby allowing them to *think architecture* in the language of Deleuze through a *process of collaboration* with the outside logic of the electronic media. Eisenman has endorsed such a process of collaboration:

I am certain of the need to reassess architecture within a digitized process, i.e. that there is no beginning, there is no truth, there is no origin, and there is no *a priori* given. In other words, there is no longer the necessity to begin from a rectangle, a circle, or a square. The notions of the Cartesian absolute as *a priori* truth already invested with beauty and goodness no longer exist or no longer are taken as truthful or necessarily beautiful, or the only necessarily youthful and beautiful. If this is the case, then one has to find other matrices of form-making. And the human hand/mind relationship is not able to conceptualize this because all it can do is draw from the inventory of what it is possible to do with the human hand. That inventory of the possible is limited through knowledge and experience; the computer is not limited by the same knowledge and experience. The computer has no experience or knowledge of the images that it makes.⁴²

In fostering a collaboration in which electronic media present their own reciprocal subjectivity, architects have succeeded in displacing their own discursive function. The result of this folding together of the desire of the architect with the computational/graphical power of electronic media is a cyborg assemblage that allows for an expanded opening onto greater degrees of creative freedom.

FINDING THE FOLD: REBSTOCK PARK

One of the first to articulate the post-architectural style was Peter Eisenman. In 1992 Eisenman submitted a proposal for the redevelopment of Rebstock Park, a 250-acre site on the perimeter of Frankfurt. First developed in the mid-19th century by Ernst May, the original architecture of Rebstock Park employed the once fashionable suburban solution of the *Siedlung*: mass-produced blocks of housing and commercial areas repetitively and densely staggered across large peripheries of development without interpenetrating streets or alleyways. Though *Siedlungen* were simple, cost-efficient, and immediate solutions to the problems of urban expansion at the time, as the larger urban fabric of Frankfurt developed, the unvascularized space between the cellular series of buildings gradually degenerated into a necrotic zone of stagnant urbanism. In Eisenman's words: "Now all the open space was in a sense left over; the 'ground' became a wasteland."⁴³

Rebstock Park posed an interesting challenge to Eisenman in that the carefully gridded homogeneity of the site left little to deconstruct. Ironically, it was the mechanical regularity of the grid itself – the interstitial spaces of difference *between* the cloned buildings – that became the strongest element of Rebstock Park, with the potential to infect and subvert the architectural plan as a whole. In many ways, the site had already been deconstructed by the urban framework itself: its most apparent flaws had been laid bare in its development within its surrounding context.

In contrast to his earlier attempts to draw inspiration from the works of Derrida, Eisenman now disenchanted with deconstructivism found resonance for his new direction in the works of Gilles Deleuze, a contemporary French philosopher whose works escaped the standard bounds of philosophy just as architects tried to move beyond the traditional trappings of architecture. Rather than seeing the semiotic slippages opened up by deconstruction as unbridgeable lacks or absences (*différance*), Deleuze views differences as positive elements: *lines of flight* capable of cutting across disciplines and opening new possibilities. Difference for Deleuze is expressed as diffuse and dispersed leaks from outside the perimeters of traditional thought; it can erupt inward, propagate, and transform the entire process of thinking. For some architects, Deleuze offers a means for *thinking architecture* as a positive program centered on and generated by just such an unfolding of difference: the inhuman, irrational element capable of de-centering or *deterritorializing* the anthropomorphic subject. Greg Lynn describes this new disciplinary shift: "Where complexity and contradiction arose previously from inherent contextual conflicts, attempts are presently being made to fold specific locations, materials and programs into architecture smoothly while maintaining their individual identity."⁴⁴ As with bioinformatics, a new fold of

architects—whom we call “post-architects”—filters out redundant patterns of data within a specific locus in order to isolate the unpredictable variants, in accordance with the basic tenet of informatics: an increase in information can grow only out of an increase in difference.

Eisenman’s approach to Rebstock Park was Deleuzian: rather than erase or cover up the corrupted grid, Eisenman decided to push it to its limits, to nurture it through a process of repetition until it erupted into a new singularity that transformed the totality of the site.

Eisenman’s desire to subvert the stability of the grid led him to the work of René Thom, a French mathematician who had studied the dynamics of unexpected events within stable mathematical systems.⁴⁵ Thom’s work, commonly known as catastrophe theory, is often demonstrated by a series of mathematical diagrams known as the “butterfly cusp” in which, according to Eisenman,

a catastrophe begins with a stable condition, moves through the radical moment of change, and then returns to a stable condition. Isolated in their original sequence these figures are the residual inscriptions of a condition that is impossible to represent in a single frame of time or space.⁴⁶

Intrigued by the notion that the highly mechanical grid held within it the potential for a momentary buckling of traditional form, Eisenman used Thom’s “ideas of ‘event’ and ‘catastrophe’ [to] circumscribe the project for Rebstock and formalize, as indices of a mathematical process, the urban context of Frankfurt”⁴⁷ – a city traditionally known for its well-regulated financial stability yet nonetheless caught in the two largest cultural disruptions of the 20th century.

In order to trigger a new shape for Rebstock, Eisenman first mapped the local geography of the site using a 7x7 orthogonal grid, choosing the number seven arbitrarily, simply to represent the seven drawings of Thom’s butterfly cusp series. Eisenman then overlaid and shaped this grid to the Rebstock groundplain “in an attempt to establish both spatial and temporal modulation.”⁴⁸ As a second step, Eisenman superimposed another unmodulated 7x7 orthogonal grid over the modulated landscape grid and connected the translated vertices between the two “to produce a warped surface which first appears to separate the two grids rather than connect them.”⁴⁹ In a second study of the two grids, Eisenman again connected each vertex of the orthogonal grid to its corresponding vertex of the landscape grid *as well as the vertex directly below it (figure 7)*. The result of this second translation was that

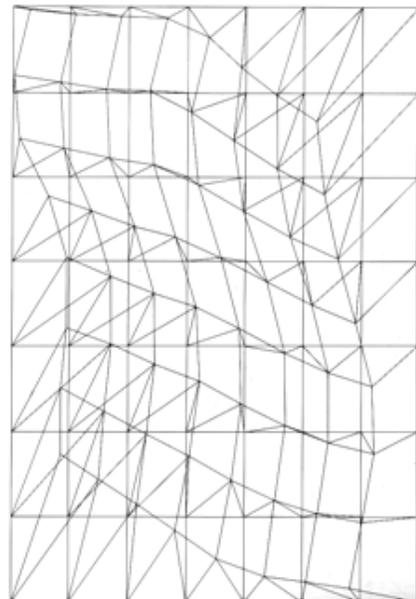


Figure 7. Diagram of Peter Eisenman’s creation of the Rebstock Park fold, displaying how the fold emerged when each vertex of the seven-square butterfly cusp grid was attached to the corresponding and adjacent vertices of the modulated groundplain grid. Source: Peter Eisenman, *Unfolding Frankfurt* (Berlin: Ernst and Sohn, 1991), 25.

“another warped, netlike structure/surface appears which suggests not an oppositional relationship between the two figures, but rather a construct of perpetual mediation – the fold.”⁵⁰ The topology of the fold became the primary logic for Eisenman's new plan for Rebstock. Eisenman then orthogonally projected the original *Siedlung* footprint onto the disrupted, multidimensional surface of the fold such that the uniformly repeated blocks of the *Siedlung* were distorted in accordance with their position in the fold, each building disrupted and disrupting within the productive transformation of the grid (**figure 8**).

By focusing on and iterating the wasted space of the grid, which threatened to overwhelm the rational plan of the *Siedlung*, Eisenman provoked a catastrophe – an intrusion of external forces in the unexpected form of the fold – that transformed Rebstock Park from the *outside* according to a new and other logic – what Eisenman calls an “ur-logic” that operates outside that of the subject. In *The Fold: Leibniz and the Baroque*, Deleuze develops Leibniz's notion of the fold as resembling “a sheet of paper divided into infinite folds or separated into bending movements, each one determined by the consistent or conspiring surroundings.”⁵¹ Deleuze's “consistent or conspiring surroundings” are the possibilities of the outside – the potentials for change inherent in the local particularities of the environment – that intrude upon and influence the anthropomorphic form of the grid. Eisenman himself borrows Deleuze's metaphor of folded paper in comparing the fold to origami: “Deleuze's idea of folding is more radical than origami, because it contains no narrative, linear sequence; rather, in terms of traditional vision, it contains a quality of the unseen.”⁵² The grid is therefore inflected by *what cannot be seen* by the subject: the virtual field of possibilities indigenous to each site.

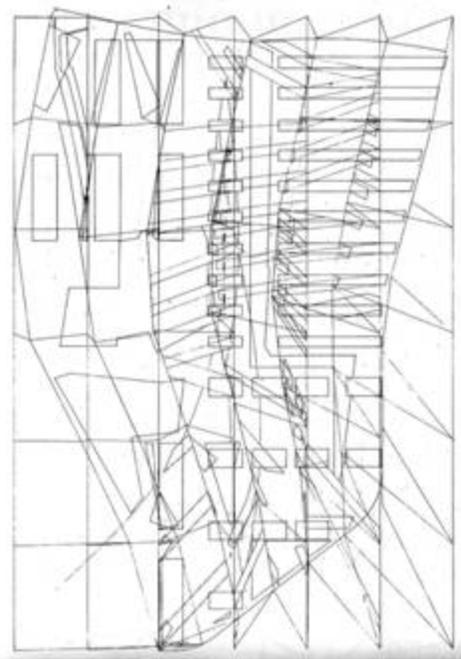


Figure 8. Eisenman's projection of the original *Siedlung* footprint onto the east-west orientation of the fold. Source: Peter Eisenman, *Unfolding Frankfurt* (Berlin: Ernst and Sohn, 1991), 35.

INCORPORATING THE AFFECTIVE

While such talk of the *unseen*, the *virtual*, and the *outside* might suggest a revitalized form of mysticism, neither Deleuze nor Eisenman intends such a connotation. Rather, they imply quite the opposite: that the outside, in its multiplicity of possibilities, flouts completely human ability to know, see, or imagine, and that is precisely its power. The outside is not so much mystical as rigorously computational. In explaining his notion of probabilistic conformational roadmaps in robot motion-planning and ligand-folding, Jean-Claude Latombe describes a similar phenomenon:

The traditional framework of robot motion planning is based on manipulating a robot through a workspace while avoiding collisions with the obstacles in this space. Our application of motion planning, on the other hand, is aimed at determining potential paths that a robot (or ligand) may naturally take based on the energy distribution of its workspace. Hence, instead of inducing the motion of the robot through actuators, we examine *the possible motions of the robot induced by the energy landscape of its immediate environment*.⁵³

Latombe's distinction between the two approaches to motion planning is an important one in that it foregrounds Deleuze's distinction between *effective* and *affective* space. Effective space is rational space functioning according to a discernible logic, as in the first method for motion planning. Effective space is negotiated by a binary logical process, such as colliding/not colliding with obstacles. In effective space, actions are directed from the inside-out: the subject is able to adapt by exerting itself within the space. As a result, interactions within effective space are *extensive*, concerned with conditions of quantity than quality.

Affective space, on the other hand, does not operate according to a knowable or predictable logic and can only be inferred in excess of its effective conditions. Rather than allowing an extensive, outward response to the space, affective space induces an *affect* within the subject: an *intensive*, outside-in inflection in response to specific forces inherent in the site. Subjects do not logically *adapt to* an affective space; rather they are qualitatively changed and *adapted by the space*. In the case of ligand-binding, the second method of motion-planning not only takes into account the navigation of the effective space of the molecular environment but also considers the affective space: whether or not the energetic forces in the environment reconfigure the structure of the ligand into a different molecular conformation.⁵⁴ The probabilistic conformational roadmap can therefore be considered an extrapolated mapping of the affective space in regards to energy minimization.

An understanding of effective and affective space allows us to revisit Eisenman's development of the Rebstock fold within the larger history of architecture. The unifying figure of traditional modernism was that of the anthropomorphic, rectilinear grid, often the nine-square grid of the skyscraper that acted as the basic diagram for the ultimate monument to modernism. In modernist building, the grid was imposed *on a site*: the ground was cleared as a *tabula rasa* and the architecture *extended* upward with a will toward overcoming its environmental conditions. Modernism therefore viewed spaces as only effective, conceiving of contextual conditions as physical, knowable, and mechanical phenomena to be rationally overcome.

Deconstructivism aimed to disrupt the grid through its conception of the *diagonal*, a transgressive cutting across that mimicked its dismantling of modernism. The diagonal subverted the effective space of modernism by revealing the diagonals—the hidden or suppressed directionals—inherent in all grids and all modernist agendas. The slant drove a critical wedge in modernism by exposing its hidden attempts to surmount the effective space of local context—but it could not bring affective spaces to bear upon architecture.

With Rebstock, however, the grid became the object of affective space. Eisenman allowed the differential forces at play in the site to inflect his seven-square grid to produce the fold. In this way, differences within the site could be incorporated within the grid to produce a context-specific architecture. Greg Lynn, Eisenman's colleague and former student, achieved a similar result in his Stranded Sears Tower project. As with most modernist skyscrapers, the Sears Tower is constructed along the guidelines of the nine-square grid and consists of nine interconnected structural tubes that mutually reinforce one another in a unified overcoming of gravity. In his project, Lynn played with the possibility of undoing the unity of the nine tubes in order to allow each tube to be differentially inflected by the affective space of its surrounding environment. Lynn described his project:

The Stranded Sears Tower attempts to generate a multiplicitous urban monument that internalizes influences by external forces while maintaining an interior structure that is provisional rather than essential...The iconic status of the existing Sears Tower arises from its disassociation from its context. The building establishes itself as a discrete and unified object within a continuous and homogeneous urban fabric. My project, by contrast, affiliates the structure of the tower with the heterogeneous particularities of its site while preserving aspects of its monumentality: laying the structure into its context and entangling its monolithic mass with local contextual forces allows a new monumentality to emerge from the old forms.⁵⁵



Figure 9 Longitudinal sectional perspective of Neil Denari's 1998 Multisection Office Block project. The "laminar structure" of Denari's localized worldsheet serves as a single continuously folded structure that mediates between previous binaries such as "inside/outside" and "vertical/horizontal." Source: Neil Denari, *Gyrscopic Horizons*. (New York: Princeton Architectural Press, 1999), 103.

Neil Denari also employs techniques of folding to produce what he calls a "localized worldsheet," consisting of "a single curving sheet...that bends into itself, creating envelopes or internal surfaces that merge seamlessly with the exterior."⁵⁶ In projects such as his Vertical Smoothhouse of 1997, Denari used his localized worldsheets to transgress traditional binarisms of architecture such as inner/outer (**figure 9**). In all three projects, the final architectural form was produced by the interaction of outside forces with more traditional forms of modernism in the affective space of the site, thereby displacing the architect subject as the anthropomorphic interpreter of form.

Eisenman describes this process of decentering: "When the environment is inscribed or folded in such a way, the individual no longer remains the discursive function; the individual is no longer required to understand or interpret space."⁵⁷

One should note that the architectures developed within such affective spaces are not only products of affect but are also integrated within the affective

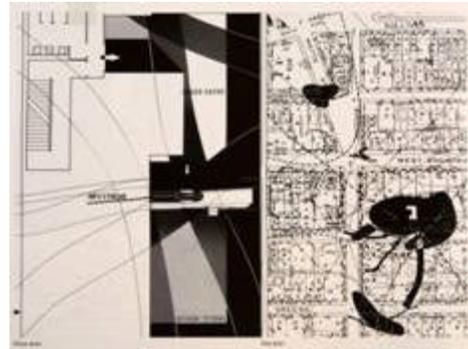
space itself as yet another external force. In other words, affectively produced architectures are affective spaces themselves that displace their spectators' subjectivity. Since the smooth surfaces of folded architecture are not reducible to generalized concepts or idealized forms, they resist their viewers' interpretation: they are forms in and of themselves rather than microcosms of a grander vision. In this way, affective architecture resists subjugation by the optical – that is, the mind-eye reading of the observer. Eisenman describes this power of the fold to resist the optical whole:

Once the environment becomes affective, inscribed within another logic or an ur-logic, one which is no longer translatable into the vision of the mind, then reason becomes detached from vision... This begins to produce an environment that "looks back" – that is, the environment seems to have an order than we can perceive, even though it does not seem to mean anything.⁵⁸

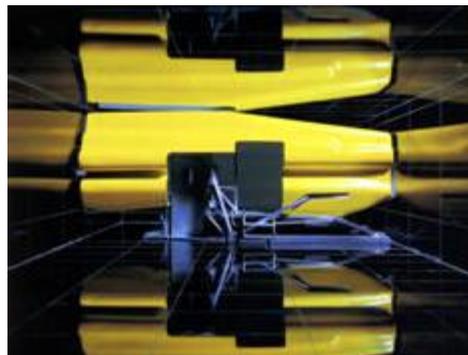
Such an ability to "look back," or what Eisenman calls *reciprocal subjectivity*, endows architecture with a new power to deterritorialize the viewer – a *haptic* rather than *optic* ability to induce an affective change rather than effect an interpretation for rapid visual consumption. The fold is therefore one strategy for moving beyond the mechanics of vision in favor of a new relationship to built space: a performative encounter with the other, the outside. Taken as a larger field of movement, the fold represents a dramatic turn away from traditional forms and theories of architecture toward a Deleuzian ontology as a positive building program.

FURTHER VECTORS FOR MOVEMENT

While the three projects mentioned above – Eisenman's Rebstock Park, Lynn's Stranded Sears Tower, and Denari's Virtual Smoothhouse – index a similar move away from previous practices of building, they all nonetheless retain connections to modernism in their use of modernist forms as initial objects of inflection and in their relatively static methods of determining local forces. Though Eisenman's development of the Rebstock fold as the "in-between" of the gridded groundplan and the seven-square grid allows an unpredictable form to emerge from the outside, the "forces" it seeks to internalize in the grid are not so much dynamic forces as



Above: Floor plan and local site plan for Neil Denari's 1993 Details Design Studio project, in which Denari mapped the local flows of information. The project was designed to act as a functional "wall" that would divide act as an architectural interface between the clerical and design spaces of the Details company. **Below:** Final design for the Details Design Studio project. The undulating sheet of Denari's design is a physical model of information and personnel flows around and through the office space. "The project creates an information cipher that passes through the space, becoming reified in form within the room itself." Source: Neil Denari, *Gyroscopic Horizons*. (New York: Princeton Architectural Press, 1999), 150-152.



static geographies. Similarly, Lynn's Stranded Sears Tower maps each independent tube to relatively static influences, such as "adjacent buildings, landforms, sidewalks, bridges, tunnels, roads and river's edge."⁵⁹ What is missing from both Eisenman's and Lynn's experiments is an ability to *generate new form* rather than merely inflecting older modernist diagrams within a context of temporally and spatially *dynamic forces* rather than local static geometries.

As his own answer to this challenge, Lynn has developed a new theory and practice of architecture known as *animate design*. In animated design, Lynn considers "Force is an initial condition, the cause of both motion and the particular inflections of a form...so that architecture can be modeled as a participant immersed within dynamic flows."⁶⁰ To implement such a system, Lynn maps the flows of local forces over time – wind and weather patterns, traffic flows, information and energy channels, animal migration patterns – in order to model the affective space of the site. Lynn then inserts a form to the force-field

model of the space that represents the constraints of building – differently for the number of rooms and arranged the tensions space. Once have reached pattern, Lynn then envelope within a single *blob* that is by each of the **12**). The "folded, pliant, surface

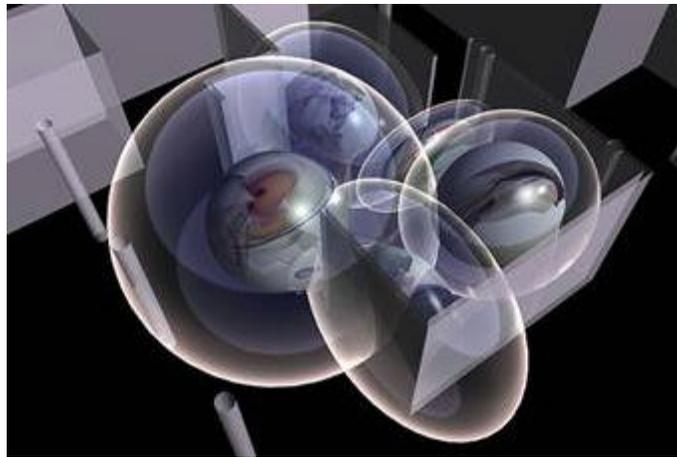


Figure 12. Generation of blob surface from the five project nodes for Greg Lynn's 1995 Artists Space installation. In order to generate a continuous surface between the five different projects to be displayed, Lynn allowed five globular spheres to interact within the local forces of the gallery space, then joined the five spaces by generating a topological surface that flowed amongst the surface of each node. Source: Greg Lynn FORM website, <http://www.basilisk.com/aspace/imajj/glowblobs.jpeg>.

and mediates between each of the forms "in order to incorporate their contexts with minimal resistance."⁶¹

In order to move beyond the inert lines and points of Euclidean geometry, Lynn has adopted a topological or NURBS (Non-Uniform Rational Bézier Spline) approach in which surfaces are defined as vector flows whose paths are inflected by the distributed forces within the space. These splines literally seek the path of least resistance among the network of forces in order to establish a distributed field of equilibrium in a manner analogous to Latombe's probabilistic conformational roadmaps. Just as bioinformaticists use PCR to map the energetics vectors within a space in order to predict the folding patterns of proteins or ligands induced by the space, Lynn submits the forms of his internal building constraints to the vectorial forces inherent in each site in order to

space that internal the desired such as five sized spheres and types of required – and be inflected in response to within the the forms a stable will usually the forms membrane or itself inflected forms (**figure** resulting and supple" complies with

produce a new form that complies with the affective space while still retaining its identity.

To many observers, Lynn's desire for his architecture to accommodate the dynamic forces of its environment is a fool's quest since architecture is innately static – at least any architecture that is intended to serve as a permanent protective shelter.⁶² Though it may be possible to create a computer model in which a pliant surface dynamically adapts itself to a flux of forces, it is much more difficult to *build* such structures with physical materials. Lynn's only option, according to his critics, is to take his structures from a single frozen image within a larger simulation; such an architecture, they say, is no more animate than more traditional modes of building.

However, it is problematic to assume that a fixed form can derive only from a fixed image. A single fixed form can evolve from a composite of multiple possible configurations of the same form over time. In order to dismiss reductive readings of his process, Lynn describes such a composite form in the shape of a boat hull:

Although the form of a boat hull is designed to anticipate motion, there is no expectation that its shape will change. An ethics of motion neither implies nor precludes literal motion. Form can be shaped by the collaboration between an envelope and the active context in which it is situated. While physical form can be defined in terms of static coordinates, the virtual force of the environment in which it is designed contributes to its shape. The particular form of a hull stores multiple vectors of motion and flow from the space in which it was designed. A boat hull does not change its shape when it changes its direction, obviously, but variable points of sail are incorporated into its surface. In this way, topology allows for not just the incorporation of a single moment but rather a multiplicity of vectors, and therefore, a multiplicity of times, in a single continuous surface.⁶³

As with the boat hull, the resultant forms of Lynn's architecture are fashioned in response to a virtual multiplicity of forces, thereby enabling Lynn to successfully generate new forms from the active fluctuation of forces within a given locus. Architectural forms cannot physically fold once they have been built; however, they can index a virtual process of continuous folding. As an affective space, Lynn's animate forms operate according to what Eisenman calls an "excessive condition"⁶⁴ – the field of possibilities in the process of folding are indexed in their excess in the actualized physical form.

An early example of Lynn's use of animate design is his March 1995 entry for competition to design a protective roof and lighting scheme for the underside of the bus ramps leading into the New York City Port Authority Bus Terminal (**figures 13 & 14**). Lynn summarized his design process for the Port Authority Gateway as follows:

The site was modeled using forces that simulate the movement and flow of pedestrians, cars, and buses across the site, each with differing speeds and intensities of movement along Ninth Avenue, 42nd and 43rd streets, and the four elevated bus ramps emerging from below the Hudson River. These various forces of movement established a gradient field of attraction across the site. To discover the shape of this invisible field of attraction, we introduced geometric particles that change their position and shape according to the

influence of the forces. From the particles studies, we captured a series of phase portraits of the cycles of movement over a period of time. These phase portraits are swept with a secondary structure of tubular frames linking the ramps, existing buildings and the Port Authority Bus Terminal. Eleven tensile surfaces are stretched across these tubes as an enclosure and projection surface.⁶⁵

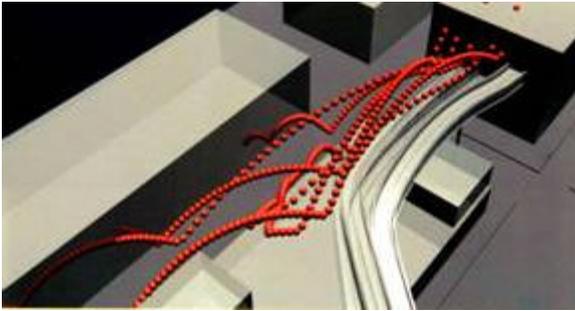


Figure 13. Particle phase portrait study for Greg Lynn's 1995 submission to the New York City Port Authority Gateway competition. In this study, Lynn used an animation sweep technique to capture the movements of geometric particles introduced to an invisible field of local forces. Source: Greg Lynn, *Animate Form* (New York: Princeton Architectural Press, 1999), 108.



Figure 14. Final design submission to the Port Authority Gateway competition. Lynn developed the tubular framework design from the phase portraits then attached translucent tensile fabric to the frame. The fabric functioned to diffuse ambient light and act as a projection screen for information. Source: Greg Lynn, *Animate Form*, 112-113.

Lynn's modeling practices recall the techniques used by environmental scientists in generating dynamic visualizations of massive flows of weather data. But there are close parallels to modeling practices in bioinformatics as well. For instance, Lynn's "gradient field of attraction" bears a striking resemblance to the mapping of molecular energy landscapes. Equally analogous is the means by which Lynn's possible vector flows of particles cross through the field of attraction, just as bioinformaticists "represent the protein as a sequence of vectors, each representing an SSE [secondary structure element]"⁶⁶ which folds in accordance with its particular molecular energy landscape. Increasingly, at the outer limits of experimental explorations in each field, architecture and bioinformatics have begun to fold back upon each other.

CONCLUSION: THE DIGITAL OUTSIDE

Biology had to take a leap into molecular biology, or dispersed life regroup in the genetic code. Dispersed work had to regroup in third-generation machines, cybernetics and information technology. What would be the forces in play, with which the forces within man would then enter into a relation? It would no longer involve raising to infinity or finitude but an unlimited finity, thereby evoking every situation of force in which a finite number of components yields a practically unlimited diversity of combinations. It would be neither the fold nor the unfold that would constitute the active mechanism, but something like the *Superfold*, as borne out by the foldings proper to the chains of the genetic code, and the potential of silicon in third-generation machines, as well as by the contours of a sentence in modern literature, when literature 'merely turns back on itself in an endless reflexivity'.⁶⁷

Gilles Deleuze, *Foucault*.

We have pointed to multiple points of articulation between current developments in bioinformatics and architecture. In our view they are not merely the result of random coincidences between two disparate fields. Articulated in the

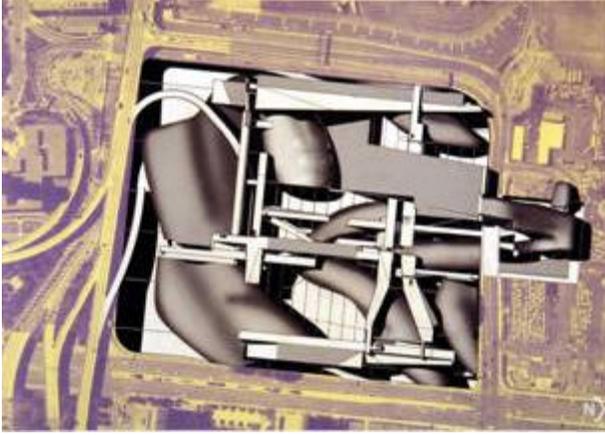


Figure 15. Overhead siteplan for Neil Denari's Museum of the Twentieth Century project submission from 1993. Denari's image demonstrates the generation of form from the integration of external traffic flows. "What I am really trying to create is an architecture that generates difference out of the repetitive conditions that surround us in the everyday zones that occur from place to place." (Denari, interview by Peter Zellner, "City of Sorts," *21C* (1997, issue 24), 69. Image source: Neil Denari, *Gyroscopic Horizons*. (New York: Princeton Architectural Press, 1999), 81.

recent work of Eisenman, Denari, and Lynn, we find a concern to address what they called a crisis of the mechanics of vision: architecture could not move beyond its own circular process of logic and theory—beyond its own language game—without some force from the outside to move it. They located that external force, we have argued, in the highly automated massively parallel stacked multiple alignment algorithms, neural networks, and Markov Chains that practitioners of bioinformatics draw upon in processing the flow of sequence data into the dynamic folds of protein. When merged with immersive computer design environments, these new machinic assemblages

enable architects to *think architecture* in Deleuze's terms: *thinking architecture* ceases to be a solely human practice.

The overlap produced by the similar technological desires of bioinformaticists and architects indexes just one fold in a much larger multiplicity. Building on the work of Michel Foucault, Deleuze conceived of the *outside* as an affective space external to the larger epistemic areas of discourse at any given time: a network of hidden forces that inflects, stratifies, and organizes the systems of discourse it subtends. Foucault's lifework was to map the margins of such networks throughout different periods of history; his metaphor of the Panopticon presents one such diagram of the space of the outside. We have attempted in this paper to map a small section of a similar diagram of the outside for our particular historical location. In our diagram, the outside is inscribed in the fluid lines of flight of electronic media that cut across and inflect not only architecture and bioinformatics, but also disciplines as diverse as genetics, robotics, psychology, astronomy, physics, philosophy, and engineering. All of these fields either have been or are being remade from the outside by electronic media, and in none of them is *thinking* any longer a solely human practice. Perhaps it never was.

Endnotes

¹ C.B. Anfinsen, "Principles that govern the folding of protein chains," *Science* Vol. 181(96)(1973), pp. 223-230.

C.B. Anfinsen and H.H. Scheraga, "Experimental and theoretical aspects of protein folding," *Advances in Protein Chemistry*, Vol. 29 (1975), p. 205-300.

CB Anfinsen, "The formation and stabilization of protein structure," *Biochemistry Journal*, Vol. 128(4)(1972), pp. 737-49.

² C.J. Epstein, R.F. Goldberger, and C.B. Anfinsen, "The Genetic control of tertiary protein structure: Studies with model systems," *Cold Spring Harbor Symposium on Quantitative Biology*, vol. 28(1963), pp. 439-449.

³ Cyrus Levinthal, "How to fold graciously," in J. T. P. DeBrunner and E. Munck, eds., *Mossbauer Spectroscopy in Biological Systems: Proceedings of a meeting held at Allerton House, Monticello, Illinois*. Urbana, Illinois, University of Illinois Press, 1969, pp. 22-24.

⁴ Anthony G. Oettinger, "The Uses of Computers in Science," *Scientific American*, Vol. 215, no. 3, 1966, pp. 161-172, quoted from p. 161.

⁵ See Cyrus Levinthal, "Molecular Model-Building by Computer," *Scientific American*, Vol. 214, no. 6, 1966, pp. 42-52.

⁶ Cyrus Levinthal, "Molecular Model-Building by Computer," pp. 48-49.

I therefore decided to develop programs that would make use of a man-computer combination to do a kind of model-building that neither a man nor a computer could accomplish alone. This approach implies that one must be able to obtain information from the computer and introduce changes in the way the program is running in a span of time that is appropriate to human operation. This in turn suggests that the output of the computer must be presented not in numbers but in visual form.

⁷ Lou Katz and Cyrus Levinthal, "Interactive Computer Graphics and the Representation of Complex Biological Structures," *Annual Reviews in Biophysics and Bioengineering*, 1(1972): 465-504.

⁸ J. C. Latombe, *Robot Motion Planning*, Boston: Kluwer Academic Publishers, 1991. M. S. Apaydin, A. P. Singh, D. L. Brutlag, and J. C. Latombe, "Capturing Molecular Energy Landscapes with Probabilistic Conformational Roadmaps," in *International Conference on Robotics and Automotons 2001*. (in press)

⁹ The Protein Data Bank (PDB) was established in 1971 as a computer-based archival resource for macromolecular structures. But two decades later in April 1990 only 535 atomic coordinate entries were recorded for macromolecules, and in 1999, following a period of rapid improvement in technology for obtaining crystallographic data, the Biological Macromolecule Crystallization Database (BMCD) of the Protein Data Bank contained entries for a meager 5400 protein molecules.

¹⁰ Indeed more than 140,000 genes were cloned and sequenced in the twenty years from 1974 to 1994, of which more than 20 percent were human genes.¹⁰ By the early 1990s at the beginning of the Human Genome Initiative, the NIH GenBank database (release 70) contained more than 74,000 sequences, while the Swiss Protein database (Swiss-Prot) included nearly 23,000 sequences. Protein databases were doubling in size every 12 months, and some were predicting that as a result of technological impact of the Human Genome Initiative by the year 2000 ten million base pairs a day would be sequenced, predictions that have been more than borne out.

¹¹ See for instance Ram Samudrala, Yu Xia, Enoch Huang, and Michael Levitt, "Ab Initio Protein Structure Prediction Using a Combined Hierarchical Approach," *PROTEINS: Structure, Function, and Genetics* Suppl 3(1999), pp. 194-198. For evidence on this point see the entries in the Critical Assessment of Protein Prediction competition hosted at the Lawrence Livermore National Laboratory hosted since 1994.

¹² See especially the papers in L. Hunter, ed., *Artificial Intelligence and Molecular Biology*, Menlo Park, CA, AAAI Press, 1993.

¹³ Douglas L. Brutlag, "Understanding the Human Genome," in P. Leder, D.A. Clayton, and E. Rubenstein, eds., *Scientific American: Introduction to Molecular Medicine*, New York; Scientific American, Inc., 1994, pp. 153-168. Walter Gilbert characterizes the situation sharply:

The next tenfold increase in the amount of information in the databases will divide the world into haves and have-nots, unless each of us connects to that information and learns how to sift through it for the parts we need

¹⁵ These are the disciplines graduate students and postdocs in molecular biology in Brutlag's lab at Stanford are expected to work with. Source: Douglas Brutlag, "Department Review: Bioinformatics Group, Department of Biochemistry, Stanford University, 1998," personal communication.

¹⁶ New disciplinary requirements were imposed on the biologist who wanted to interpret and use the matrix of biological knowledge:

The development of the matrix and the extraction of biological generalizations from it are going to require a new kind of scientist, a person familiar enough with the subject being studied to read the literature critically, yet expert enough in information science to be innovative in developing methods of classification and search. This implies the development of a new kind of theory geared explicitly to biology with its particular theory structure. It will be tied to the use of computers, which will be required to deal with the vast amount and complexity of the information, but it will be designed to search for general laws and structures that will make general biology much more easily accessible to the biomedical scientist. *Ibid.*, p. 67.

¹⁷ *Ibid.*, pp. 26-27.

¹⁸ Peter Eisenman, "Visions unfolding: architecture in the age of electronic media," in Luca Galofaro, *Digital Eisenman: An Office of the Electronic Era*. (Basel: Birkhäuser Publishers for Architecture, 1999), p. 84.

¹⁹ *Ibid.*

²⁰ *Ibid.*, 85.

²¹ *Ibid.*, 84.

²² *Ibid.*

²³ Denari, *Gyroscopic Horizons*. (New York: Princeton Architectural Press, 1999), 11n3.

²⁴ Gregg Lynn 1995 <http://www.basilisk.com/aspace/formview.html>

²⁵ In *Deconstructivist Architecture* Mark Wigley described a deconstructive architect as "not one who dismantles buildings, but one who locates the inherent dilemmas within buildings – the structural flaws," 133.

²⁶ Lynn, "The Folded, the Pliant, and the Supple," *Folds, bodies & blobs*, 115.

²⁷ The Marxist literary critic Frederick Jameson, in his essay entitled "Postmodernism, or The Cultural Logic of Late Capitalism", diagnosed postmodernism as a "depthless" and "schizophrenic" logic doomed to operate only through an ahistorical "pastiche" of past styles.

²⁸ Eisenman, "Visions unfolding", 85.

²⁹ For Eisenman's early embrace of postmodern approaches, see Peter Eisenman, "Cardboard Architecture: House 1 (1967), in Peter Eisenman, Michael Graves, Charles Gwathmey, John Hedjuk, Richard Meier, Collin Rowe, and Kenneth Frampton, *Five Architects*, (New York: Oxford University Press, 1975), pp. 15-23, and Eisenman, "Cardboard Architecture: House II (1969)," *Five Architects*, pp. 25-37.

³⁰ Kathryn Henderson, *On Line and On Paper: Visual Representations, Visual Culture, and Computer Graphics in Design Engineering*, (Cambridge: MIT Press, 1999), 99.

³¹ Stephen S. Hall, "Protein Images Update Natural History," *Science*, Vol. 267, 3 February 1995, pp. 620-624.

³² William J. Mitchell, "Roll Over Euclid: How Frank Gehry Designs and Builds," in J. Fiona Ragheb, ed., *Frank Gehry, Architect* (New York: The Solomon R. Guggenheim Foundation, 2001), pp. 352-363. Quoted from p. 354.

³³ *ibid.*, p. 354.

³⁴ *ibid.*, p. 358.

³⁵ *ibid.*, p. 363.

³⁶ *ibid.*, p. 357.

³⁷ Dennis Dollens, "Fish, Snake, Gehry & Guggenheim," www.sitesarch.org/reviews/GehryBil.html.

³⁸ Gehry's describes the impressive degree to which CAD/CAM applications allow mass-customization of building materials by listing the project's components:

Number of aluminum and stainless steel shingles: over 21,000. There are over 3,000 panels, each composed of an average of seven metal shingles. Each is uniquely shaped; there are no repeating patterns. The panels that sheath EMP were milled in Germany, colored in England, shaped, cut and assembled in Kansas City, and brought to Seattle to be attached. The gold-colored stainless steel panels have a special beaded-glass finish that reflects and changes with varying light and weather conditions. (*Experience Music Project: The Building*, (Seattle: EMP, 2000), 30).

³⁹ Dennis Dollens, "Fish, Snake, Gehry & Guggenheim," www.sitesarch.org/reviews/GehryBil.html.

⁴⁰ Selim Koder, "Interview with Peter Eisenman," from *"Intelligente Ambiente"*, *Ars Electronica* (1992), http://xarch.tu-graz.ac.at/home/rurban/course/intelligent_ambiente/interview_eisenman.en.html.

⁴¹ Lynn, *Animate Form* (New York: Princeton Architectural Press, 1999), 17.

⁴² Selim Koder, "Interview with Peter Eisenman," from *"Intelligente Ambiente"*, *Ars Electronica* (1992), http://xarch.tu-graz.ac.at/home/rurban/course/intelligent_ambiente/interview_eisenman.en.html.

⁴³ Eisenman, *Unfolding Frankfurt*, 10.

⁴⁴ Lynn, "The Folded, the Pliant, and the Supple," *Folds, bodies & blobs*, 117.

⁴⁵ On René Thom, see Thom's *Structural Stability and Morphogenesis an Outline of a General Theory of Models*. Translated from the French edition, as updated by the author, by D.H. Fowler. (Cambridge: Perseus Books, 1989).

⁴⁶ Eisenman, *Unfolding Frankfurt* (Berlin: Ernst & Sohn Verlag für Architektur und technischen Wissenschaften, 1991) p. 10

⁴⁷ Eisenman, *Unfolding Frankfurt*, p. 10.

⁴⁸ John Rajchman, "Perplications: On the Space and Time of Rebstockpark," in Peter Eisenman, *Unfolding Frankfurt*, p. 23.

⁴⁹ *Ibid.*, p. 25.

⁵⁰ *Ibid.*, p. 25.

⁵¹ Gilles Deleuze, *The Fold: Leibniz and the Baroque*, 6. Deleuze is referencing Leibniz's statement in *Pacidus Philalethi* (C, 614-15):

The division of the continuous must not be taken as of sand dividing into grains, but as that of a sheet of paper or of a tunic in folds, in such a way that an infinite number of folds can be produced, some smaller than others, but without the body ever dissolving into points or minima.

⁵² Eisenman, "Visions unfolding," 87.

⁵³ Amit P. Singh, Jean-Claude Latombe, Douglas L. Brutlag, "A Motion Planning Approach to Flexible Ligand Binding," *Proc. 7th Int. Conf. on Intelligent Systems for Molecular Biology (ISMB)*, (AAAI Press: Menlo Park, CA, 1999), 253. Emphasis added.

⁵⁴ *Ibid.*, 254.

⁵⁵ Greg Lynn, "Multiplicitous and inorganic bodies," *Folds, bodies & blobs*, 53.

⁵⁶ Denari, *Gyroscopic Horizons*, 83.

⁵⁷ Eisenman, "Visions unfolding," 88.

⁵⁸ *Ibid.*

⁵⁹ Greg Lynn, "Multiplicitous and inorganic bodies," 56.

⁶⁰ Lynn, *Animate Form*, 11.

⁶¹ Lynn, "The Folded, the Pliant, and the Supple," 117.

⁶² As an example of this view, see Alicia Imperiale's "Time Frozen / Time Liberated?" in *New Flatness: Surface Tension in Digital Architecture* (Basel: Birkhäuser – Publishers for Architecture, 2000), 74-8.

⁶³ Lynn, *AF*, 10.

⁶⁴ Eisenman, "Visions unfolding," 87.

⁶⁵ Lynn, *Animate Form*, 103.

⁶⁶ PCR paper, 6.

⁶⁷ Gilles Deleuze, *Foucault*. Translated by Seán Hand. (Minneapolis: University of Minnesota Press, 1988), p. 131.