Animating Mechanism:
Animations and the Propagation of Affect in the Lively Arts of Protein Modelling

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In the scientific literature, proteins are frequently figured as molecular machines; that is, as tiny mechanisms that operate in interlocking assemblages, and which act to build and maintain the body as a higher-order machine. Mechanical models parse living bodies in ways that seem, at first glance, to deaden lively processes. I build on feminist contributions to the science studies literature to show how, rather than spelling the "death of nature", mechanistic reasoning in the life sciences can become a site for feminist inquiry into modes of embodiment and the role of affect in the performance of scientific knowledge. I observe that researchers use their bodies kinaesthetically to manipulate and learn protein structures. Such forms of body-work enable modellers to animate their molecular mechanisms both onscreen and through elaborate gestures and affects. In this way molecular mechanisms are enlivened as they are propagated between researchers in pedagogical and professional contexts. I argue that this is not an extra-scientific phenomenon, but one intrinsic to the work of mechanistic modelling.

Keywords: molecular models, animations, affect

Introduction

During a series of interviews at a protein crystallography lab, a postdoctoral researcher demonstrated a molecular mechanism he had worked out for intercellular adhesion. This is a mechanism that operates between cells, and makes use of inter-locking proteins to maintain the structural integrity of developing tissues. His structural study of a group of cell surface proteins determined that these molecules are long and straight. One part of the protein is embedded in the cellular membrane, while the other extends out into the extra-cellular environment where it is available to bind to similar molecules on adjacent cells. The binding end of the protein has three short protrusions that give it a ratcheted structure. He hypothesized that this ratcheted structure provides a mecha-

nism to strengthen binding between adjacent cells.

We are in his lab, and I sit across from him as he tells me how his protein works. I am busy scribbling notes in my notebook as he talks with barely enough time watch how he is demonstrating the structure. "Here, take my hand", he says. With this, I look up. "As if we were shaking hands." I have to drop my notebook and pen in my lap, so that I can reach out my hand, apologetic for having been so distracted by my note taking. He wants to convey the strength of the associations made between molecules whose binding holds two adjacent cells together. We clasp hands in a firm handshake, but he leans back. I'm unprepared for this, and our hands slip apart. "How would we make our grip stronger?" he queries. "Suppose we are climbing a mountain, what kind of grip would we need?" Still holding hands, he eases me into an answer by gripping me at the wrist. I follow along, and clasp his wrist in turn. We both lean away. Our grasp is decidedly stronger. "Right", I confirm. Molecules binding at their first and second hooks would form a stronger bond. "And how would we make it even stronger?" He extends his grip further up my arm, clasping me at my elbow. I follow suit and we test the strength, mutually acknowledging the augmented stability of this third hold.

Ratcheting up the grip, from binding at the hands, to the wrists, to the elbows, he has sculpted a model for strong molecular association by using the physical intuition of his body. By enlisting my participation in this performance of his model he interrupts my note taking and redirects my ethnographic attention towards the *body-work* of modelling in structural biology. This crystallographer's body has become a key resource for him to be able to make arguments about molecular mechanisms. His body is invested in his interpretation of protein structures, and the forms and potential functions of these proteins animate his imagination. He in turn animates his hypothesis by entangling us both in this lively demonstration of his model. More than a pedagogical trick, I argue that this bodily intuition has formed the foundation for his scientific questions and committed him to several years worth of research into these intermolecular interactions. Despite little evidence to support his theory – that these proteins bind to each other using all three hooks – he still holds out hope that he might one day find the crystal structures that can validate this feeling he has for the strength of these molecular associations.

His animation of the mechanism seems at first to contradict the tropes and registers in which proteins are typically figured in the scientific literature. Proteins are frequently described as "molecular machines", "the machinery of life", "molecular devices and components" or even as "nature's robots" (e.g. Tanford and Reynolds, 2001). They are figured as the inanimate mechanical levers, hinges, locks, clamps, cogs, gears, springs, pumps, and motors that assemble, disassemble and reassemble in complex interlocking assemblages, and which act to build and maintain the body as a higher order machine (e.g. Hill and Rich, 1983; Bourne, 1986; Hoffman, 1991; Kreisberg *et al.*, 2002; Harrison, 2004; Chiu *et al.*, 2005). Protein modellers' pervasive mechanistic rhetoric could be read as an attempt to eradicate

vestiges of vitalism from biological explanations, to police rampant anthropomorphisms, and effectively reduce messy systems to deterministic logic. However, this crystallographer's performance forces me to take a closer look at the nature of mechanistic reasoning and machine metaphors in biology. As he performs them, mechanistic models are more than deterministic abstractions that explain away lively processes by reducing them to their physical and chemical properties.

In this paper, I aim to show how, rather than spelling the "death of nature" (see Merchant, 1983), mechanism in the life sciences might be an interesting site for feminist analyses of scientific practice. Rather than deadening life, these researchers' expressive performances show up what Donna Haraway has called the "unapologetic swerve of liveliness" that animates both bodies and knowledge in-the-making (1997: 137). I propose that with ethnographic attention to the expressive body-work of molecular modelling, the roles of embodiment, affect, and performance in scientific knowledge production can be made visible, and a more lively account of mechanism in biology can emerge.

The crystallographer described above enacts his model in ways that are exemplary of a kind of performativity that animates protein research more generally. In this paper I draw on three years of ethnographic research among protein crystallographers, biological engineers and other structural biologists who build and use models of protein molecules. I examine modes of learning and communication among these modellers in research and teaching contexts, paying special attention to how they use a variety of media, including their own bodies, to animate chemical and physical processes at the molecular scale. I have conducted ethnographic interviews with principal investigators, postdocs and graduate students in protein structure laboratories, as well as with instructors, teaching assistants and undergraduate students in teaching laboratories. In professional contexts, I observe researchers as they work with protein models at computer interfaces, and as they relay structural information to others in various sites, including at the laboratory bench, in weekly lab meetings, and during conference talks and poster sessions. In pedagogical contexts, I have observed semester-long graduate and undergraduate courses that teach concepts in protein structure, including lecture courses on biomolecular kinetics, protein folding, practical macromolecular crystallography, as well as a hands-on laboratory course in biological engineering.

With the development of methods that can document the body-work of protein modelling and communication among structural biologists, this study aims for an innovation in STS analyses of the performativity of scientific knowledge. Erving Goffman (2001) has suggested that ethnographers must "tune" their bodies "in" to the daily activities and practices of those they study. This would require subjecting one's own body to the rhythms of another's practices in order to gain a richer interpretation of the plays of affect, gesture and language among members in a particular group (Goffman, 2001: 154-155). In order to tune myself in to the subtle body-work and tacit practices of structural biologists, I draw on twenty-five years of train-

ing in classical ballet and contemporary dance, as well as three years of experience conducting research in molecular biology laboratories. These experiences afford a kind of "situated knowledge" (Haraway, 1991) through which I observe and interpret scientific practice. That is, they give me the skills to attend closely to others' corporeal techniques, and enable me to draw on my own affinity for movement in order to detect, recall, and relay researchers' subtle bodily affects, including the tempos, rhythms, and tones that propagate through their performances of scientific knowledge. As a situated knowledge practice, my analysis thus makes no attempt to mask the ways in which I *move with* and am *moved by* life scientists' lively practices.

Producing and Performing Protein Models

As much as biologists have fetishized the gene, historians and critics of the twentieth century life sciences have fixed on the rhetoric of text, code and information in genetics and genomics (see Doyle, 1997; Keller, 1995; Kay, 2000). But life scientists do more than manipulate words and DNA sequences. There is another history to tell, one in which the embodied nature of life science practice is perhaps more tangible. Here, I go beyond an analysis of texts and inscriptions in molecular biology to examine the production, performance and propagation of multi-dimensional models and animations of proteins in laboratories and classrooms. As James Griesemer has noted, accounts of models in the history of science require attention to "gestural as well as symbolic knowledge and the variety of means and modes of making, experiencing, and using models" (Griesemer, 2004: 435). Modelling practices thus defy analyses that focus exclusively on scientists' rhetoric, the technical production of models, or their representational status. The conceptualization and performance of models through researchers' bodies calls, rather, for an ethnographic examination of the *enactment* of models, and of modelling and theory-making in practice (on "enactment" see Mol, 2002; Barad, 2003). I examine how protein modelling practices can extend feminist theories of performativity in science, in particular the relations between modes of embodiment, learning and communication, and the role of affect in the propagation of scientific knowledge.

Feminist scholars have made major contributions to the literature on performance and performativity in science. This includes Judith Butler's (1993) analysis of the relationship between biological sex and gender performance in her extension of Austinian theories of performativity, and Donna Haraway's (1991; 1997) theory of "situated knowledges", which takes seriously the lively "material-semiotic" production and performance of scientific knowledge. Building on long-standing concerns in the science studies literature with human and nonhuman agencies in scientific practice, Karen Barad (1996; 2003) draws on both Butler and Haraway to propose a feminist theory of "agential realism" that can account for the "enactment" of scientific knowledge through the multiple material and conceptual agencies involved in its production. Barad's theory calls for an accounting of knowledge production at the scale of the "phenomena" that are produced in experi-

mental configurations, and so she pays particular attention to the specific configurations that are set up between the scientist, their apparatus for observation, and the things they observe.

In order to think through the dynamic relations between all agents in a laboratory configuration, Barad distinguishes *interaction* from *intra-action*. For her, interaction "presumes the prior existence of independent entities", and builds on a "Cartesian cut" that assumes an inherent distinction and division between subject and object in a given situation. Intra-action, on the other hand, "enacts an *agential cut*", that is, "a local resolution within the phenomenon" (Barad, 2003: 815). To elaborate her theory, Barad extends Neils Bohr's philosophy-physics and his treatment of the wave-particle duality of light, to account for the impossibility of separating an experimental object from the "agencies of observation" that draw it into view. Bohr was concerned with how different laboratory configurations could be used to enact distinct properties of light. Light could be detected in the form of either waves or particles, but never both forms at the same time. In Barad's framework of intra-action, light becomes one of two possible experimental objects – either a wave or a particle – through precise intra-actions between the scientist, their agencies for observation, and the substance subjected to experimentation. Thus, for her, laboratory observations refer not so much to the object as such, but to the phenomenon performed at the scale of the whole experimental configuration (Barad, 1996). For Barad, this means that "phenomena do not merely mark the epistemological inseparability of 'observer' and 'observed'; rather, *phenomena are the ontological inseparability of agentially intra-acting 'components'*" (Barad, 2003: 815, emphasis as in the original). Barad shows how subjects and objects precipitate out, as such, from their experimental configurations. In other words, the "agencies" which participate in experiments are themselves formed by each other in their intra-action. She is thus able to expand the frame for analysis of scientific experimentation to include the experimental configurations of objects and apparatuses, as well as the material and discursive agencies enacted by the scientist.[1]

Barad's notion of intra-action is particularly illuminating for understanding the production of the visual facts of science. That is, visualizations, like protein models, can be regarded as the products of intra-actions between scientists, their objects of analysis, and their visualization machinery – which includes the material and semiotic technologies they deploy to parse their data (on material-semiosis, see Haraway, 1997). I extend Barad's work to understand how, in the entangled configurations of the life science laboratory and classroom, knowledge is enacted through affect and feeling as well as through instruments and objects. So, while intra-actions can be seen to morph the object in order to produce experimental data, one must not assume that the human observer is left untouched. I aim to understand how, in their intra-actions with experimental objects and visualization media, scientists affect, and are affected by, scientific knowledge as they produce and perform it.

I investigate the intra-actions that produce structural knowledge of protein molecules. The primary objects, the

"epistemic things" in Hans-Jörg Rheinberger's (1997) terminology, are the proteinaceous substances being modelled. Yet, as invisible entities, molecules as such are inextricably bound up with the agencies of observation that draw them into view. In this case, these agencies include X-ray crystallographers' extensive assemblage of machines – including metaphors and interactive digital visualization media – collectively geared to produce and interpret atomic resolution models of proteins *as molecules*. Living substances are *made molecular* through these techniques and practices. The primary phenomena produced out of this intra-acting assemblage of human and nonhuman bodies and machines are then interactive computer graphic models of the atomic structures of proteins. However, as I examine below, these models are interactive (they can be handled, manipulated and modified), and so enable multiple sites of intra-action, not only for those who build them, but also for their extended users, including those who attempt to pull these models off the screen and communicate the fine details of protein structures to wider audiences. As this paper aims to show, such intra-actions produce another range of phenomena, including modes of animation that can bring mechanistic models to life.

After briefly describing the multiple sites of intra-action involved in producing and propagating protein models, this paper turns to examine ways that protein modellers animate their models and mechanistic theories, with a focus on situations where researchers use their own bodies to communicate protein structures and mechanisms. I explore how such temporally dynamic modes of animation enable researchers to communicate more than just the form of a molecular mechanism. They also relay a range of affects and sensibilities that enliven the model they perform. The paper then turns to examine how such molecular affects are propagated through forms of mimetic communication between researchers, shaping how knowledge of protein structures and mechanisms is relayed in both professional and pedagogical settings.

Sites of Intra-action in Protein Modelling

Crystallographic modelling is a fine example of intra-action in the production of visual facts in science. This visualization practice involves active and prolonged handling and manipulation of experimental data throughout what is an often-arduous process of constructing the model by hand (de Chadarevian, 2002) or onscreen (Myers, in press). Eric Francoeur and Jerome Segal (2004) have shown how a series of computer hardware and software innovations in the 1960s and 1970s enabled protein modellers to transition from building molecular models with physical materials to using interactive computer graphics systems for the display and analysis of structural data. Although modelling materials have changed dramatically between the early days of physical modelling with mechanical ball and stick parts (Francoeur, 1997), early computer graphics developers were able to preserve the materiality of physical models by engineering workstations interactive enough to give users the sensation that they were directly manipulating the

molecules onscreen with their hands (Langridge, 1974; 1981; Francoeur and Segal, 2004; Myers, in press).

Today, the field of protein crystallography has been reinvigorated with augmented computational power, faster interactive graphics capacity, and continually improved software, facilitating the production of atomic-resolution models, animations and simulations that amplify protein structures to human scale. Researchers also often use stereoscopic visualization aids that make use of 3D glasses and special graphics that make molecular models leap right off the screen. Through the time-consuming and physically engaging practice of building and using protein models and animations onscreen, otherwise invisible protein molecules are given body and fleshed out in time.

The human-computer interface that crystallographers use to build protein models offers an exceptional site to examine the intra-actions that shape knowledge of protein structures and mechanisms. Yet, once built, crystallographic protein models can travel: as digital objects, they become available to many other users. For example, once a crystallographer builds a protein model, she uploads the structural data into the Protein Data Bank (PDB), an online database. In so doing, she makes it available to a wider range of researchers, including biological engineers, predictive modellers, and drug designers who are always on the lookout for new protein structures. A curious researcher will download the coordinates of a protein structure and manipulate it onscreen. As I describe elsewhere (Myers, in press), these tools prosthetically couple the researcher to the model so that as they navigate through the intricate folds of the protein, zooming in on atomic details, and rotating it through virtual space, it becomes a tangible object (see also Francoeur and Segal, 2004). This practice constitutes a kind of body-work that enables the researcher to learn the structure by incorporating the form of the protein into their body as an "embodied model" (Myers, in press).

The intra-actions that produce molecular knowledge, however, do not end at the computer interface: the details of a molecular structure, and hypotheses about how it functions, must be communicated among researchers and their students. I examine sites of *social intra-action* to understand how, once acquired, structural knowledge of proteins is propagated. My observations of the pedagogical lives of models show that once a modeller learns the molecular structure through body-work at the computer interface, he or she may then be able to perform the model for others off-screen (see Myers, forthcoming). Indeed, researchers frequently enact molecular models through elaborate gestures and language in order to relay the specificities of molecular forms and movements. In addition to teachers' and students' lively performances of protein form in classrooms and teaching laboratories, researchers also readily enact their embodied knowledge of molecular structure. They do this in formal and informal research settings, including in weekly lab meetings, at conferences, and even as they chat with each other at the laboratory bench. Additionally, ethnographic interviews offer another site for researchers to express molecular knowledge through their bodies. In each of these sites, structural biologists may per-

form their knowledge of a protein alongside graphic renderings in order to elaborate a structure or its movements. In the absence of other visual media their moving bodies can also become effective stand-ins for the protein model. I argue that these performative modes of body-work are also intra-active in the sense that they require others who can *move with* and be *moved by* these molecular gestures – in both the physical and affective senses of the verb "to move" – in order for the details of the structure and hypotheses about molecular mechanisms to be relayed.

Modelling Biological Mechanisms

Mechanism has held a prominent place in the history of biological modelling and theory-making. This mode of reasoning builds on a long history of theories and metaphors that inscribe living bodies as machines (see for example Gieson, 1969; Hopwood, 1999; Keller, 1995; 2002; Lenoir, 1982; Pauly, 1996). Researchers working in the broad field of the life sciences have deployed mechanical theories of biological function at many scales of the organism, thus shaping the direction of such fields as embryology and development (see Hopwood, 1999) as well as cell biology (see Landecker, 2007). Mechanistic reasoning has also held sway in the field of biophysics, which includes the crystallographic studies of protein structures first initiated in the 1930s (see de Chadarevian, 2002; Law, 1973). Indeed, mechanistic explanations formed the foundation for what, in 1967, Gunter Stent called the "structural school" of molecular biology. Until the late 1950s, this school had dominated the field of what was then coming to be known as "molecular biology" (Stent, 1968: 391). Counter to the then nascent "informational school" that sought to reduce DNA to codes, the structural school approached biological molecules with the "idea that the physiological function of the cell" could be understood "only in terms of the three-dimensional configuration of its elements" (Stent, 1968: 391). This was a preoccupation that Stent saw reflecting a "down-to-earth view of the relation of physics to biology". In this view, "all biological phenomena, no matter what their complexity" could "ultimately be accounted for in terms of conventional physical laws" (Stent, 1968: 391).

The contributions of structural biology appeared to lose traction during the sequencing craze of the molecular genetics and genomics revolutions, which have dominated life science research agendas over the past forty years (Doyle, 1997; Kay, 2000). Twenty-first-century molecular biology is, however, in the midst of a protein structure revolution.[2] As protein modellers ramp up the pace of structure determination, making visible the forms and movements of a vast menagerie of proteins, they are producing a rich body of visual evidence that is fleshing out new understandings of biological molecules, and enabling new lines of inquiry. An important feature of this transition is that the nature of the substances that life science researchers investigate, and the kinds of the data they manipulate, are changing. Protein structure data defies the rhetoric of informatics, which, in the fields of genetics and genomics, has had the tendency to flatten life into code. By contrast, the practice of figuring life in structural biology has forced researchers to confront

the thickness and temporality of the substances that give body to cells.

In the contemporary structural biology literature, biological molecules are frequently figured as determinate, predictable, regulate-able machines that are reducible to their chemical and physical properties. Lecturing in a course on biomolecular kinetics for biological engineers-in-training, one protein modeller defines "mechanism" as the parsing of a living entity, such as a cell, into discrete, interconnected units. For him, a mechanism is an abstraction that severs a larger entity into parts and orders them by their functionality, affording an effective means for manipulation. As a biological engineer, he is invested in garnering as much mechanistic knowledge about his system as possible. He tells the class:

> You have to get a mechanistic understanding of everything. Because that's where the true power comes from. If you have a mechanistic understanding you really know how it works and you can change how it works. If you have kind of a philosophical understanding you can describe it after the fact. You can wrap some pretty words around it, but that understanding isn't sufficient to empower you to make the system do something different; that is, what you want it to do. So that's our mantra. The question is how deep into the mechanism do you need to know?

The "true power" that he invokes is that ability to engineer new kinds of molecular mechanisms that perform predictable functions in living systems. He desires a level of understanding that makes living processes tangible at the scale of intra- and inter-molecular forces and energies. The "mantra" frequently recited in this biological engineering course is "measure, model, manipulate, and make". He thus aims to build quantitative models that will enable intervention and re-engineering. In one sense, this biological engineer's designs on life serve as a not so subtle reminder of the ways that mechanistic thinking has historically alarmed feminist theorists concerned with the exploitation of nature (e.g. Merchant, 1983; Plumwood, 1993). I would, however, like to read his invocation for mechanistic knowledge more generously.

I want to draw attention to the kind of understanding that he gestures towards, even while he dismisses its merit. Though he is not convinced it will get you very far as an engineer, he does see that it is possible to "wrap some pretty words" around a model to aid in "describing" the mechanism, if only "after the fact". My fieldwork in his courses, and in group meetings among members of his laboratory show, however, that often a protein is first modelled as a lively body, before it becomes a mechanical object. Indeed, it is not only words, but bodies too, that get "wrapped" around the model as the mechanism is conceptualized and performed. My observations suggest that modelling molecules as complex molecular machines that take up space and move through time, has enlisted life scientists' own moving bodies as resources to "give body" (Hopwood, 1999) to the mechanisms they investigate, and to animate their theories.[3]

The development and application of a mechanical theory to a biological process is a practice that requires postulating an internal teleology of things; that is, relationships between the part and the whole, between structure and func-

tion, and between form and purpose. Determining how molecules work, how they perform their functions and interact with each other in the cell (with the assumption that they in fact perform a kind of work), is an act of interpretation – the researcher must form a hypothesis about an otherwise invisible process. The framework that structural biologists draw on to make such interpretations is clearly shaped by chemical and physical laws and theories. But it is also shaped by their experience working with models, and by analogies that produce metonymic shifts between the scale of human experience and that of molecular life. For example, a long history of "lock-and-key" metaphors, particularly prominent in research on antibody proteins (see Kay, 1993) has shaped the ways that structural biologists read mechanical function out of structure. Currently, the more pervasive analogies are those of "molecular machine" which are figured as the architectural and chemical "machinery" that "does work" in the cell and "drives" cellular life.[4]

I observe that in order to interpret the functions of molecules, protein modellers draw on their embodied experiences with human-scale mechanisms and machines (both within and beyond the laboratory) as sources of practical logic and reasoning. This practical knowledge shapes how they produce and also how they disseminate knowledge of protein structures and functions to others. Viewed from this perspective, mechanistic modelling appears to rely on researchers' dexterity with theories and language, as well as with their application of experiential knowledge. Thus, I propose that qualitative descriptions of protein mechanisms through both words and gestural forms are more than aesthetic flourishes of expressive scientists: they are integral to the very conception and development of mechanical models. Mechanistic reasoning is thus an intra-active, material-semiotic practice.

Animating Mechanisms

Mechanisms, or things that operate mechanically, have three-dimensional, temporal structures, in ways similar to living bodies. Mechanistic reasoning can be understood as a practice of ascribing form and teleology to an object, in such a way that accounts for how an object's shape changes and moves over time. A biological mechanism, by definition, involves some kind of movement or change: biological substances are transformed chemically and physically in the process of conducting work in the body. Animations or other moving images that pull entities into human time are very useful visual aids for playing through the temporal structures of mechanical objects and theories. They are also exceptional visualization tools in the life sciences, as they have the capacity to convey the pulsing rhythms, forms and movements of living substances, cells and tissues.

All kinds of animations have been developed in the history the life sciences. For example, embryologist Wilhelm Roux (1859-1924) employed everyday materials to create an animation that could defend mechanical theories of organismal development against Hans Driesch's vitalist theories. Roux animated the differential growth of cells in embryogenesis by incubating balls of dough containing varying quantities of

yeast, joining them together in cellular formations, and observing the patterns they formed as they rose (see Hopwood, 1999). Hannah Landecker (2005) identifies another form of animation, this one emerging in the early twentieth century. In its joining of biological and filmic techniques, microcinematography was a form of animation that brought cells to life on film screens. Today, protein crystallographers and protein folding researchers make use of the spatial and temporal possibilities of digital media to build and manipulate their protein models as time-based renderings onscreen. In the process they animate the molecular mechanisms they hypothesize and intuit. Such animations are proudly displayed and available to be downloaded from laboratory websites, frequently projected to awed audiences in conference presentations and in undergraduate classrooms, and they circulate widely through informal networks on the Internet.

Chris Kelty and Hannah Landecker (2004) have proposed a "theory of animation" that examines the relations between moving image technologies and the production of knowledge in the life sciences. For them, "media that represent the living organism over time, such as time-lapse microcinematography, not only demonstrate the life of the organism in question, they also *animate* it in relation to other, often dominant, modes of static representation" (Kelty and Landecker, 2004: 45). Kelty and Landecker are less interested in the ways that animations simulate liveliness than their "*status as images in relation to knowledge*" (Kelty and Landecker, 2004: 32, emphasis as in the original). They read animations as the playing of theories or models forward in time, that is, as the animation of otherwise static abstractions or ways of seeing that have already been systematized in scientific research. Thus, it is the theories themselves that are animated through time-based imaging technologies. Kelty and Landecker provide a crucial contribution to situating time-lapse imaging and animation within the history of theories and models in life science. To extend their work further, I foreground the ways that animations not only embed ways of seeing, but also, how, in pulling static models into time, animations refigure these ways of seeing and the very theories they enact. Animations perform knowledge, and in this, transform it.

A wide array of protein animations has been developed, some with high-end graphics, others with much simpler imagery. One of the more elaborate molecular animations currently circulating among life science researchers and students was developed for teaching core biological concepts to Harvard undergraduates. The project employed character animators and state of the art computer graphic animation systems in its aim to offer a glimpse into the "inner life of the cell".[5] Building directly on protein structure data, the creators see this as a "completely accurate rendering" (Marchant, 2006). However, this 3D flythrough set to ambient, orchestral music does more than just pull mechanical objects into time: these animations also provide glimpses into the scientists' and animators' molecular imaginations. As one reviewer comments, the molecules and organelles "move with bug-like authority, slithering, gliding and twisting through 3D space" (Marchant, 2006). Such renderings make clear the etymological relations among the terms *ani-*

mation, *animal*, and *animism*. A mechanism, like a protein, is not quite dead, and it is not quite alive. However, by pulling static molecular models into time, protein modellers enliven biological mechanisms though elaborate narratives, endowing them with animistic, even wily behaviours. Modellers use malleable media, and apply temporal structures and narrative forms such that their animations produce a liveliness that inflects molecular knowledge with a range of animistic affects.

Animations like this could be described fairly as "working conceptual hallucinations"; that is, "hybrid combinations of schematic, iconic and even fantastic features" (Gilbert and Mulkay quoted in Lynch, 1991: 209). I propose that such animations are renderings that combine researchers' practical knowledge with imagined forms: they are temporally dynamic tracings of researchers' physical intuitions – their *feeling for* – protein forms and movements. Animating media thus afford protein modellers a medium through which they can express their molecular imaginations and intuitions in time. I see these animations as pulling their users' and viewers' bodies into new understandings by entraining them to molecular temporalities and other ways of moving. In this sense, animations may be thought of as narratives that lure their users into new modes of embodiment through their play with time (see Stengers, 1999 on "lures"). I propose that it is through moving images and bodies that protein modellers are able to propagate their tacit knowledge of molecular structures and mechanisms. Entangled with this tacit knowledge is a range of affects that turn out to be central to how researchers learn and communicate molecular knowledge.

Embodied Animations and Molecular Affects

There are many viable media for animating life science data and hypotheses, including physical (e.g. rising dough), celluloid (e.g. film), and virtual (e.g. computer graphic) media. These are all malleable materials that can be used to pull abstract concepts – like mechanical theories – into space and time. Researchers bodies, it turns out, do just as well. With an interest in examining the role of affect in the performance of knowledge in science, I extend the study of animations beyond the visualization technologies and renderings produced onscreen, to include modes of animation that enliven the bodies and imaginations of scientists. The body-work involved in protein modelling and mechanistic reasoning demonstrates vividly what protein researchers must do with their bodies in order to bring molecular models and mechanisms to life. In many ways, they rely on gestures and affects to communicate structural knowledge of proteins amongst themselves and their colleagues, and to students and their wider publics. Through this ethnography, I hope to expand the category of what counts among practices to be tracked in analyses of the visual cultures of science.

In order to understand how embodied animations are enacted, I follow Kelty and Landecker (2004) to examine techniques in which lively substances are first fixed or frozen, and then re-animated. In this way I can track how static renderings are pulled into time through the animating media of researchers' bodies and imaginations. Protein

crystallography offers an illuminating example. Fit squarely within a tradition of biological imaging and modelling that fixes or freezes substances in order to bring them into view, crystallography produces static models of protein structures. To gather data on a protein structure, a crystallographer first crystallizes the protein, and then grows the crystals until they are large and organized enough to diffract X-rays. In order to visualize the structure of the molecules packed within each unit cell of the crystal, the crystal is dipped in liquid nitrogen just before it is subjected to X-ray diffraction. Cryofixation is widely used to dampen the highly energetic protein molecules whose forms vibrate rapidly, even within the ordered array of the crystal lattice. X-ray crystallography thus renders best-estimate models by averaging out the dynamic movements and subtle differences in conformation between all the molecules arrayed in the crystal. This technique produces a single structure, a static snapshot of the calculated average of all the protein molecules, frozen in time.

Edward, a crystallographer conducting postdoctoral research in a protein crystallography lab, tells me that this snapshot can be challenging to interpret for those not trained in the arts of protein visualization.[6] "Molecular biologists are notorious", he tells me. "The main criticism crystallographers have about molecular biologists is that they don't think about the structure as a *breathing entity*. [For them] it's just a rigid body." For non-experts who don't have a feel for the physics and chemistry of protein molecules, the structures available to download from the PDB don't convey how dynamic proteins "really are". During a second interview, we sit in front of his computer screen while he describes some of the challenges he faces using automated programs to predict how two proteins will bind to each other. Automated programs don't work so well, because, as he reminds me, "proteins are breathing entities". When I press him to explain what he means by this, he responds saying, "I don't know, sounds a bit romantic, doesn't it?"

The liveliness of the protein is a tangible concept for him: as he describes the protein he is currently working on, he holds his hands out in front of his body, as if holding a pulsing substance. The invisible object in his hands appears to breathe like lungs.[7] He knows how the protein moves in part from his close study of chemical laws and the physical properties of proteins. But he also has a tacit, kinaesthetic knowledge of the form of molecule that he did not learn from books – a knowledge he has gained from having spent tremendous effort and extended periods of time building and navigating through unique protein structures onscreen. In the process of building crystallographic models, working with X-ray diffraction data, and sculpting the model using interactive graphics, he has found a way to animate these static structures within his body and imagination.

Diane, who heads the protein crystallography lab where Edward works, has quite a vivid molecular imagination. She tells me that as she builds the model onscreen, she simultaneously builds up a detailed model of complex molecule in her "head", to the extent that it becomes available to her to rotate in her mind in three dimensions (see Myers, in press). She confesses, however, that this

is not easy to do:

> And I try now as an advisor, I try to get inside the structure and really try to understand it at that level. And I have for a few of them, but it is really time consuming, I mean, to sort of have the structure in your head in three dimensions, which is how I felt about some of the other structures that I actually did build myself.

Her ability to construct an embodied model of the protein is facilitated by the interface she has used to build the crystallographic model onscreen. Interactive computer graphics afford a kind of tangibility and manipulability that is similar in some ways to other modelling materials, including physical media (see Myers, in press; Francoeur and Segal, 2004). It is through the laborious work of modelling, manipulating the 3D graphic space on her computer screen, that she able to sculpt a fleshed out twin of the model, not just in her mind, but in her body. In the process of modelling the protein *in silico*, she cultivates an affective, kinaesthetic knowledge – a feeling for – the possible forms and movements of the protein *in vivo*.

She can do this with models that she has worked with and built herself, those with which she is intimately familiar. However, when presented with new structures and hypothetical mechanisms at conferences and in talks, she often finds the data difficult to grasp. "I would be at a meeting", she tells me, "and people would be discussing a mechanism, and I would kind of close my eyes and think about it and go, 'No. Too far away'". A mechanism is "too far away" for Diane if she can't interact with it or manipulate it onscreen. The physicality of handling and building molecular models, even through virtual technologies, enables her to learn the structure kinaesthetically. In this way, she can get "inside" the model. In many ways, however, the model also gets inside of her; and this is a key step if she is to acquire and use structural knowledge.

Once a structure is determined, its mechanism of function must be interpreted, and a hypothesis formed. In order to "think intelligently about structure", Diane must learn the structure intimately. Once the details of the model are embedded in her tissues, she has a way to feel her way around inside the protein and figure out how it works. Like Edward, Diane has a multi-sensory, kinaesthetic sense of how the protein moves:

> And you know, it's really this vision that you have of the active site, and sort of this sense of how tightly packed it is and how much flexibility there might be and where those regions of flexibility are. To have this sort of sense that you have. And you can think about it then *moving* in a way because you sort of know something about what the density was in each part, so that you know that that part is definitely mobile right in there, but that this part would not be mobile.

She emphasizes how difficult it is to express this multi-dimensional knowledge to others: "It's not something that is easy to communicate, because, you know you can't explain something in three dimensions to someone". Where words fail, her body becomes increasingly articulate. In interviews and while teaching Diane performs her embodied knowledge of the protein. Through expressive gestures and affects she conveys her feeling for the molecule's intra-molecular tensions and forces, its chemical attractions,

repulsions, affinities, and the possible ranges of motion across its chemical bonds. These are forces that she feels in her own body, to the extent that when students present her with half-built protein models whose configurations defy allowable bond angles and produce clashes between the radii of atoms, she winces audibly. Demonstrating the misshapen model by mimetically contorting her body, she tells me: "I feel the pain the molecule is in, because it just can't go like that!" Crystallographic models are thus inflected with affects, with modellers' feelings for the textures, tensions, forces and movements within and between proteins.

Some researchers are more reserved in their performance of their embodied models. At a scientific meeting, the same crystallographer who had enlisted my participation in performing his model of a cell adhesion molecule confessed to me that he had choreographed "a little dance" for one of the other molecules that he had modelled. "I hate dancing", he emphasized, "but there was just no other way to communicate the mechanism. I had to dance it". He declined to show me his "secret" dance when I asked, although he had performed it before for a small group of colleagues. Still other crystallographers, including Diane's most advanced graduate students and postdocs (those who have successfully built crystallographic models), talk excitedly about molecular movements they intuit, but can't otherwise see. They perform the vibrations of molecules captured within growing protein crystals, and wave their arms about to emulate the floppy ends of polypeptide chains that come out blurred in crystallographic snapshots. They also contort their bodies into sometimes-awkward configurations to demonstrate the conformational changes of the molecule and to show how it does its work mechanically and chemically in the cell.

As much as they are inflected with affect, I propose that embodied models, like those performed by Diane and Edward, can also be thought of, in Rheinberger's terminology, as "technical objects" that are employed in the investigation of "epistemic things". I have watched researchers fumble and correct the models they perform through their bodies, sometimes realizing mid-gesture that they have the structure wrong. They are quick to correct their own gestures and forms as a means to correct the model. In the process, they learn new things while they play through possible molecular configurations and movements with their own bodies. Not so much a kind of thought experiment, the body-work of reasoning in protein modelling could be considered as a kind of body experiment. Thus, I observe embodied models as tools readily available for researchers to use in their experimental practice. Like the crystallographer who ratcheted up his grip to demonstrate the binding of cell adhesion molecules, I see embodied models as "vehicles for materializing questions" (Rheinberger, 1997: 28); that is, as means that can propel scientists into new kinds of conceptual and corporeal understandings of their research objects.

Molecular Gestures and Mimetic Modelling

I have conducted ethnographic observations in the weekly group meetings of two laboratories. Members of one group

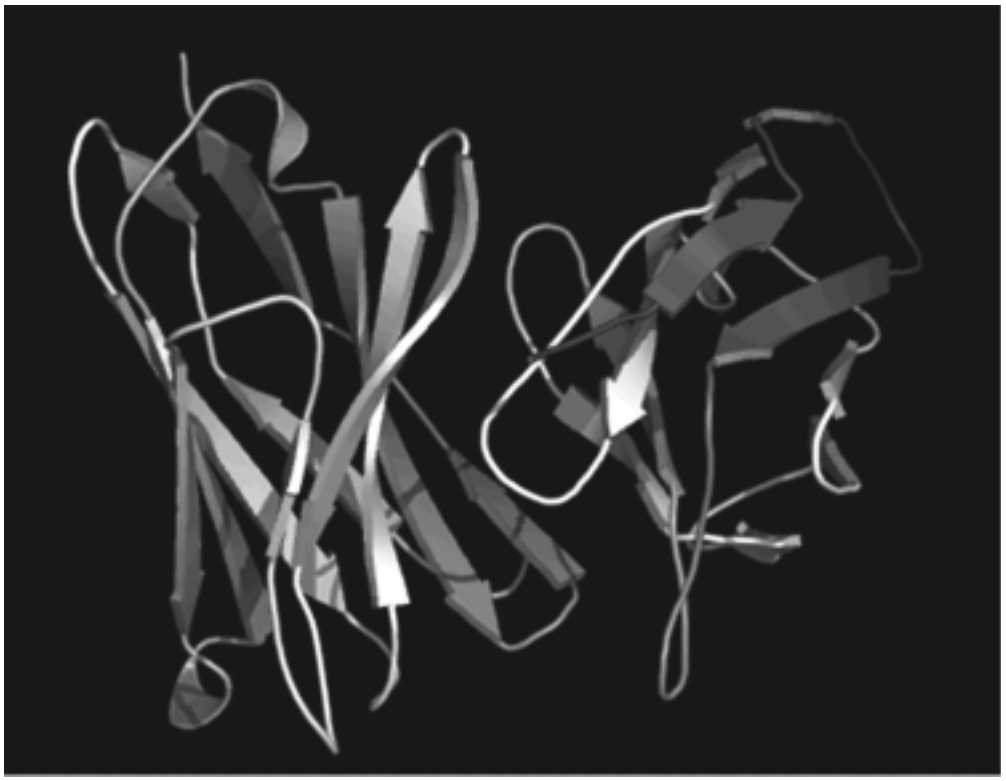
specialize in designing new protein structures. During one meeting, a PhD student presenting her recent progress was interrupted by a constant stream of questions from her colleagues who asked her to clarify the structure of the protein she is working on. Even with intricate computer graphic renderings of the molecule projected on the screen behind her, she was compelled to perform the structure. The protein she works on is complex: it forms a dimer, which means that it is made up of two similar molecules bound together. It also has intracellular and extra-cellular domains, with parts of the protein that must traverse the lipid bi-layer of the cell membrane. To communicate this intricate structure to the group, she proceeded to lift both her hands over her head and trace the winding backbones of the twinned molecules, one with each hand, following them as they traversed extra-cellular and intra-cellular spaces. Her gestures were large and sweeping, as if she were painting an accurate Ribbon diagram of the molecule for all her colleagues to see (see Figure 1).[8] Her elaborate choreography brought her arms from high up, over her head, down in front of her body, and all the way down to the ground. Her molecular dance ended with her fully bent over, hands touching the floor.

Questions still surfaced from the group, and she was asked to describe the mechanism that bound the molecules together. "I like to think of it this way", she said, and repeatedly crossed her arms at the forearms, fists clenched, demonstrating with the tension in her musculature the binding energy between the molecules. A visiting professor, still confused, leaned over the table, and repeated the gesture over and over as he asked questions, inquiring and confirming with her that this was indeed the form of the molecular interaction she was describing.

As this story suggests, researchers' bodies become animating media, both for figuring out how molecular mechanisms work, and for relaying knowledge about their structure. Scientists themselves become lively models through mimetic gestures that convey the form and movements of the molecule through the form and movements of their bodies. This *social intra-action* shows how bodily movement plays a role in how researchers learn and communicate structural knowledge to others. In the back and forth communication between the protein modeller and her interlocutors, her embodied model of the protein (itself a mimetic model)[9] is re-enacted in an intra-active exchange until shared understanding is acknowledged.

I see a kind of mimesis at play in protein modellers' entrainment to molecular movements, and in their teaching, learning and communication. This relay of forms and gestures can be seen as an intra-active process aimed at achieving mutual understanding. As the above examples show, such social intra-actions enable researchers to propagate their embodied models by communicating to other researchers and students through a kind of iconic and indexical "gymnastics" (Bourdieu, 1977: 1). Pierre Bourdieu has likened such performances to a kind of "mimesis" that is similar to a "rite or dance" in which there is "something ineffable", something that "communicates, so to speak, from body to body, i.e. on the hither side of words or concepts" (Bourdieu, 1977:1). It may be through

Figure 1: Two views of a protein model rendered as a Ribbon diagram. Note the arrows that indicate the direction of the folded polypeptide chain as it winds through the stucture. Used with permission from an anonymous ethnographic informant.



this mimetic, gestural language that biomolecules become intelligible, manipulable and workable as objects for the researcher, their colleagues and students.

Michael Taussig's (1993) multi-sensate theory of mimesis captures some of this movement and participation that I see at play in the communication of molecular knowledge.[10] Reading Benjamin, Taussig develops the notion of an "optical tactility", in which movement, sensation and perception are woven together. Mimesis has two layers for Taussig: it contains both an element of copy or imitation, as well as the "palpable, sensuous connection between the body of the perceiver and the perceived" (Taussig, 1993: 21). This mimetic faculty nourishes and sustains shared understanding and knowledge within a larger cultural milieu. On this, he suggests that the mimetic faculty is "the nature that culture uses to create second nature". It is "the faculty to copy, imitate, make models, explore difference, yield into and become Other"

(Taussig, 1993: xiii). To mime is thus to intra-actively build up a model of an other entity within one's own body – a model that can be shared with others.

For Taussig, "[to] ponder mimesis is to become sooner or later caught in sticky webs of copy and contact, image and bodily involvement of the perceiver in the image" (Taussig, 1993: 21). Mimesis involves perceptual and physical intra-actions between participating bodies. It is this intimate contact between scientist and substance – a contact mediated through prosthetic devices and visualizing machines – that is key for thinking through body-work of protein modelling, reasoning and communication. Moreover, it is through a kind of mimesis that a researcher's body and their model come to move toward a kind of resemblance, which is not so much a mirror-image reflection, but a kind of resonance. Self and other, modeller and model are thus not so readily separable from their relation: models and bodies become entangled in mimetic exchange. Below I investigate modes by which such resemblances are made to propagate.

Propagating Molecular Affects through Mimetic Transductions

Transduction is a term used widely in the field of structural biology. Proteins are figured as working machines that transduce force and energy within the cell (see for example Bourne, 1986; Harrison, 2004).[11] In this way, transduction is conceived as a mechanical process for moving and transforming signals between molecules; in a signalling network, molecules pass chemical energy and mechanical forces between them in a kind of contact-dance between molecular bodies. The specificity of the media through which the signal moves, in this case, the physics and chemistry of the protein, morphs the signal into different registers as it moves between molecules. Transduction is also an evocative term to describe the propagation of movements and affects in social intra-actions between scientists. Through their intra-actions with each other and with their models, protein modellers can be seen to transduce and so propagate the molecular affects and gestures they have cultivated in order to communicate their feeling for protein forms and mechanisms.

While teaching a class on protein folding, one researcher introduces Ribbon diagrams as representational conventions that show the direction of the polypeptide chain as it winds through the folded protein (see Figure 1). Taking up some confusion around a homework assignment, the professor goes over the details of the wording in "Question 2" which asks students to "draw, copy, or trace" a figure from the textbook. Obviously, some students had some trouble interpreting the meaning of "copy." He had to clarify: "This means *hand copy*! If you Xerox it, you don't assimilate it!" He demands the students get involved in the structures by tracing them: he tells the class that they have to "signal actively" to "get the notion". According to him, "you can't not learn something" if you actively get involved. He shows the class how to "look": "You have to trace them", he entreats, redirecting the students' attention to a human-scale model of a protein projected on the screen behind him. He reaches up and uses his hand to trace along the winding peptide backbone. As he follows the peptide, his

whole body gets swept up the fold. He effectively insists that his students participate bodily. In other words, they must *move with and be moved by* the model in order to learn the structure. In this way, protein models can entangle their users in participatory intra-actions that are geared towards learning (see also Myers, forthcoming).

To trace, that is, to hand-copy, is not to photo-copy. Tracing is a means to *transduce* the form of the polypeptide chain through one's body, not to delegate the task to a replicating machine. The aim here is not to replicate, but to emulate. Like the protein modeller who danced the Ribbon diagram of her molecule for her colleagues, the tracer's moving body, following the fold of the chain, emulates the form of the protein with their body, without producing a replica or a copy. In this way, the notion of transduction forces me to account for the specificity of the modelling media, and the kinds of bodies involved in these mimetic exchanges. Protein modellers communicate molecular forms within the range of motions available to their bodies: their contortions never actually look like the graphic models they project onscreen. Defying any simple theory of representation, embodied models and animations operate to emulate modellers' feeling for the tensions, forces, and movements of molecules. Thus protein modellers' embodied animations extend and expand assumptions about what counts as a model or scientific visualization in practice. Moreover, these animations require that theories of representation and communication in science account for the role of affect in propagating scientific knowledge.

I have observed this phenomenon of mimetic exchange among a wide range of protein researchers in a wide array of settings. It is, of course, difficult to gauge precisely whether my sampling is "representative" of the larger field. However, my aim is not to produce a portrait or caricature of these researchers, for the very reason that structural biologists' and biological engineers' professional identities are currently *in formation*: as these fields secure new footholds on the rapidly expanding terrain of twenty-first-century life science, what is representative of their practices is yet to be determined. Rather, this study is better positioned to track how new modes of embodiment can propagate among researchers in training as professional identities are being formed. My aim is to identify the tacit processes through which molecular gestures and affects are transduced, and thus how such practices can be made to propagate within and among communities of life scientists.

Conclusion

As I have tried to show in this paper, protein models are not the only phenomenon (in Barad's sense) produced in the protein modelling laboratory. Protein models are embodied and performed in ways that propagate more than structural information. Embodied animations transduce affects, emotions, and feelings that inflect knowledge about protein structure. Through their animated bodies, researchers perform their knowledge in a register that both feeds into and exceeds the discourse of mechanism in structural biology. In spite of their continuous attempts to police animistic language through mechanistic logic, I detect a surfacing of liveliness in structural

biologists' performances of their models. Molecular mechanisms are quickened, that is, enlivened through these intra-actions, recasting the trope of "molecular machines" within which proteins tend to be figured. I read structural biologists' excited gestures as symptomatic irruptions of an otherwise disavowed liveliness, performances that express their affective entanglements in knowledge making practices.

Going beyond Barad's call to account for the multiple agencies through which scientific knowledge is produced, this paper has aimed to document how such knowledge is inflected and transformed in its very performance. I propose that the intra-actions between participating bodies (human, nonhuman and machine) produce a second order phenomenon that could be called *intra-animacy*. This is not some immaterial "animism" that imbues matter with some external force, nor is it built up from a networked collection of individual agencies modelled on liberal notions of subjectivity. This liveliness is a phenomenon that is engendered through modellers' intra-actions with each other, and with their objects and machines. In turn, it animates their imaginations and narratives about the substances of life. I observe that this liveliness is performed as a range of affects and gestures that make visible structural biologists' intimate sensibilities with regards to molecular forms, their chemical affinities and physical movements. As I have shown, these performative affects are not an extra-scientific phenomenona, but one intrinsic to the conceptual and material work of protein modelling. As such, the mechanical theories of protein function that researchers produce can be seen to depend on this affective enlivening of mechanisms for the effective production and deployment of mechanistic theories.

Left to gather dust on the pages of elementary school textbooks or reduced to dead metaphors that fail to hail bodily participation, mechanistic models of protein function may indeed be "deanimations" of lively substances (see Haraway, 1998). If these models are disentangled from the intra-actions that produce and sustain them, they may appear deadening and inert. However, if these visualizations can be drawn back into Barad's expanded framing of experimental phenomena, and observed within the assemblages through which they are enacted, then the "machinery of life" can be seen to take on much livelier form. Enlivened models animate imaginations, techniques, experimental strategies, research questions and pedagogical interactions. Embodied animations are thus more than aesthetic flourishes: such modes of body-work are a crucial step in luring scientists and their students into new kinds of understanding. I suggest that it is protein modellers' capacity and willingness to *move with and be moved by* their models and animations – to mimetically transduce the intricate details of proteinaceous forms – which enables this liveliness to thrive.

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Notes

1 In a recent review of theories of agency in the STS literature, Lucy Suchman (2007) grapples with the legacy of actor network theory (ANT) and "its aftermath", including Barad's theory of "intra-action". Suchman locates Barad within a lineage of scholars concerned with the "mutual constitution" of human and nonhuman agencies in scientific practice. Suchman quotes Michel Callon to show that ANT's "network" is not one "connecting entities which are already there, but a network which configures ontologies. The agents, their dimensions, and what they are and do, all depend on the morphology of the relations in which they are involved" (Callon cited in Suchman, 2007). Yet, as Suchman's genealogy of theories of agency in STS makes clear, Barad's formulation is key for the development of a feminist account of power, knowledge and responsibility in science. Extending ANT to the embodiment and performativity of the scientists, Barad's agential realism poses the question: Where do scientists' bodies end and experimental instruments and objects begin? They do not simply interact, or mutually produce each other, but are profoundly *entangled*. It is the form of such entanglements – including the modes of embodiment and forms of knowledge performed – which remain within the purview of the scientist. This inseparability of objects and agents directs attention to issues raised in the feminist science studies literature of accountability in the production scientific knowledge.

For me, intra-action calls attention to intimate contact-dance between human and nonhuman bodies and machines in scientific practice. In this essay, I aim to show how such intra-actions depend on the *response-ability* of participating bodies. To *move with* and *be moved by* another within an intra-active practice also calls attention to the *responsibilities* involved in such entanglements. Thus, a theory of intra-action invests responsibility in the scientist's (and analyst's) act of circumscribing the phenomenon, locating subjects and objects, and producing and performing knowledge.

2 When the PDB was first founded in 1971, fewer than a dozen protein structures had been determined and deposited. By 2000, 13,635 structures were available for viewers to download onto their computers and view through interactive visualization software. As of November 2006, there were 40,132 searchable structures in the database (see http://rscb.org/pdb).

3 Here I take a cue from Nick Hopwood's (1999) treatment of the history of embryological modelling practices. He has documented how embodied knowledge contributed to late-nineteenth-century formulations of mechanism in structural studies of developing organisms. Hopwood describes embryologist Wilhelm His's (1831-1904) techniques for sculpting scale models of embryos in wax. In defence of a mechanical theory of embryological development, His developed a method for precisely reconstructing the form of embryos from the details derived from microscopic examination of tissue slices. Using "projective" drafting techniques and freehand wax sculpture, he worked the sectioned images into ex-

quisite three-dimensional form, a craft that demanded much artisanal skill. Hopwood sees His's commitment to modelling as "a passionate argument for doubly embodied knowledge" (Hopwood, 1999: 482). In Hopwood's reading, His's insight into the mechanical processes of embryogenesis was gained through the physicality of building models. His "had first to make his problem, to use his fingers", and it was by this method that he was able to "'to give body' to his [theoretical] views". In giving material form to the embryos he also "gave body" to his theory. His developed an embodied knowledge of the phenomenon in the practice of making models, such that that the problem of development became familiar to his body. As Hopwood argues, it was "the experience of modelling" that was "the most compelling evidence of the importance of mechanical principles in development" (Hopwood, 1999: 466). His thus learned the mechanical forces of embryogenesis by working with the physics of his body. Hopwood's study demonstrates that redirecting attention to the enactment of models reveals lively bodies and imaginations caught up in the work of theorizing mechanism in the life sciences.

4 One of the most pervasive metaphors currently at play among those who use the trope of "molecular machines" is that of the car and its parts: the cell is likened to a car, and looking into the cell compared to peering "under the hood" of a car. In this language, cells are made up of protein "components" and "devices", and figuring out how they all fit together and keep the cell "running" is the job of the biologist. The close ties between structural biology and mechanical engineering become very clear through these associations. See for example a video lecture of biophysicist Paul Wiggins produced by the Whitehead Institute, titled "Under the hood: A beginner's guide to the molecular motor" (see http://www.wi.mit.edu/news/video_gallery/index.html).

5 The animation is available to view online at http://www.studiodaily.com/main/technique/tprojects/6850.html.

6 All names of ethnographic research subjects have been changed to maintain anonymity.

7 Haemoglobin is one of the classical molecular structures that life science students learn, almost as a rite of passage into studies of molecular form and protein function. This is the molecule that carries oxygen in blood, and conveniently it is often taught and remembered as a "breathing molecule". In interviews, biochemistry students often re-enact the haemoglobin structure that they learn in class by making a gesture similar to Edwards', though the students' renderings are less articulated and nuanced. In a video interview accessible online, Max Perutz, who determined this large, complex structure in the 1960s through innovations in crystallographic techniques, can be seen animating the mechanism of haemoglobin, demonstrating with delight the form and movements of the protein as it captures and releases oxygen. See video interviews with Max Perutz online: "Face to Face with Max Perutz," Vega Science Trust. http://www.vega.org.uk/video/programme/1.

8 As Figure 1 demonstrates, and I show later in the paper, Ribbon diagrams, one of the most frequently used schema for rendering protein structures, have an instructive quality about them. Arrows in the model indicate the direction of the polypeptide backbone (from the first amino acid in the chain to the last) as it winds through the structure. As this protein modeller's performance indicates, these are not just visual guides for the eye, but are also useful for learning of forms kinaesthetically. Ribbon diagrams could be compared to the tracers and tailings of a rhythmic gymnast's ribbon if she were to trace the winding back bone of a protein as she dances. One animation available online treats a Ribbon diagram as if it were a rollercoaster, by taking the viewer on a rather dizzying ride along the strands of the Ribbon backbone of a protein model. See http://streaming.wi.mit.edu/?sub=protein_rollercoaster&vid=X11_001_220K_256x199.mov.

9 In this sense "mimetic models" are those that represent the form of the object in question. Galison (1997) develops this term in the contexts of the history of cloud chamber experiments in physics, while Daston (2003) uses it to explore the "extreme mimesis" achieved in the use of glass to craft highly accurate models of plant form.

10 Lucy Suchman (2007) also draws on both Taussig and Barad for a theory of mimesis in artificial intelligence simulations. Her insights resonate closely with my reading here.

11 The term transduction has at least three lineages in the history of science: one in acoustics and the other two in biology. It simultaneously refers to the "action or process of transducing a signal", such as sound through one medium to another, and "the transfer of genetic material from one cell to another by a virus or virus-like particle" (Oxford English Dictionary). Additionally, "signal transduction" is a concept frequently used in molecular biology to describe the transmission of extra-cellular signals into the cell and the propagation this signal as biophysical molecular events (see also Mackenzie, 2002). I incorporate each of these aspects of the term in my use here.

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