Molecular Representations: REFLECTIONS ON MICROARRAYS AND PROSTATE CANCER

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Abstract:

In this article the author debates the concept of representation and its changes related to the emergence of genetics through the example of the microarray. The microarray is discussed in the context of its uses to define a molecular biomarker for prostate cancer. The contrast between the current research with microarrays and the traditional accepted form of defining prostate cancer, the Gleason score, is used to define the difference between an analogical body and a digital body. This difference hinges on the fact that the Gleason score was a form of representing the prostate anatomy and defining cancer on the basis of physiological differences and visual observation. The shift to a molecular representation stems from the wish to determine markers for disease in the DNA itself. The uniqueness of microarray technology is that it leads to a questioning of the concept of representation, as it allows for the process of naming disease to be conjugated with technologies of intervention.

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MOLECULARIZING THE BODY

Recent investigations of science and scientific practice from an anthropological, or otherwise social scientific point of view have analyzed the idea of a “molecularization” of life and the body from a number of different perspectives . These works begin to delineate a change from physiologically-based classifications, which name and give meaning to the body based on outer appearance and macro-structures, to classificatory practices increasingly based on molecular or genetic characteristics. This paper adds to this concept by discussing the concept of molecular representation through the example of prostate cancer.

Through an analysis of the distinction between physiological and the molecular representations of prostate cancer in science, my goal is to better define the molecular itself. Molecular forms of representation can be described, aside from their relationship to molecular biology (the DNA molecule), by a shift from physiology to information, from visual to numerical, and from diagnostics to manipulation. Representation as it is usually understood, whereby something (e.g. a concept) stands for something else (e.g. the body), does not accurately describe this relationship, as the concepts that are used to *represent* aspects of the body and disease become at the same time forms of manipulating and interfering in that same body.

Current literature on molecularization has analyzed the complex ways through which the adoption of new technologies that operate on the molecular scale are having an impact on social dynamics, including: understandings of health and disease , the development of new drugs and treatments , racial identities and forms of classification , and the ethical and political challenges emerging from molecularization of “life itself” . Recently artists have also begun exploring the potential of the molecular as a medium for expression, suggesting that such technologies produce not only new metaphors about life that circulate in society, but are novel ways of interacting with nature that problematize our traditional understandings of what representing and interacting with the world means, and thus should themselves be continually investigated by artists and scholars.

The practices of building new life forms, such as the much debated fluorescent bunny Alba or the semi-living sculptures of Australian artists Oron Catts and Ionat Zurr are phenomena related to “molecularization” that, while not pertaining to health or the body directly, ultimately make explicit the importance of discussing representation in new ways in the context of our current abilities to manipulate living matter through biotechnologies, and even inanimate matter through nanotechnologies. While some have called for the obliteration of the representation concept , in this paper I want to analyze it in terms of its established premises about what it means to describe the body and its features, and how that defines our relationship to its meaning and materiality.

We have yet to fully explore the myriad theoretical challenges posed by these new technologies, which have to do also with the ways our own Western worldview operates, separating matter from meaning and conceiving of the body as a fixed biological support for representations, thus limiting the scope of what questions can be asked of the process of molecularization. The present article does not intend to outline all of these challenges nor does it intend to solve the problem, which is the object of intense debate among all involved in social studies of science.

My intentions are more limited: to explore, through a very localized example of a specific debate on how prostate cancer is being investigated, some broader theoretical questions of interest that arise from a comparison between two specific ways of “enframing” [1] the biological body: one physiological, or

analogical, and one molecular, or *digital*. The use of the concepts of analogical and digital can be misleading, insofar as they limit the ways we conceive of the relationship between these new molecular-scale technologies and the body. The metaphor of DNA as an informational molecule has been present in other debates on biotechnology and genetics , yet the aim here is to focus less on information and more on the issue of representation. I wish to make this apparent duality (analog and digital) less clear-cut and more problematic, at least as it has been used before to describe the intersections of bodies and technologies , contextualizing the way which it can be productive to think about a molecular framework of representation.

Another goal is to escape the conundrum brought about by ideas of a dematerialized and fully informational body. Such a theoretical stance would not be able to grasp the complexity of the impact molecularization is having and will continue to have in our relationships to our biology, our identities and how we represent ourselves. A “digital body” evokes ideas of complete control, an image also used by scientists when describing the impact of genetics . My aim is to discuss how *matter* is important in these molecular representational practices, which do more than just create and manipulate meaning, but operate on a level where naming and labeling also serve to manipulate and embody in a very material sense. To this end the microarray [2] will serve as the starting point of the discussion, being an object where these issues start to become material.

MOLECULAR REPRESENTATIONS

My argument stems from ethnographic observations conducted in two major scientific institutions in the State of Sao Paulo, Brazil: the University of Sao Paulo (USP) and the Ludwig Center for Cancer Research, Sao Paulo branch [3]. This paper’s discussion is drawn mainly from the scientific papers that were used in the context of the cancer research, which describe a state-of-the-art search for a molecular biomarker for prostate cancer, the specific aim of the research being developed collaboratively between the two institutions aforementioned. These papers come from different countries and institutions, and inform not only Brazilian scientists, but laboratories all over the world working on similar problems. Molecularization is not limited to national borders or to one specific area of science, as current research suggests.

My focus will not be on the ethnographic description of how that specific group of scientists practiced the molecularization of the prostate, but on the issue of molecularization itself as an artifact of knowledge, and as a novel way of conceptualizing nature. What does it mean to frame the search for molecular biomarkers as part of this more general process of molecularization? What issues can be raised concerning the relationships between scientific classifications and how they enable the body (or nature) to exist in specific ways ?

I will analyze the microarray as it relates to how the prostate (and prostate cancer) is being translated into molecular terms. This translation, more than a change in a visual or descriptive modality, represents a paradigm shift in terms of representational elements and in how that representation is coupled with the will to manipulate the body. Although this coupling of representation with manipulation is perhaps typical of what defines the modern , the molecular can be analyzed in terms of the way it enables it in different and novels ways. In contrast to Nikolas Rose and his ethical and philosophical debates on molecularization in terms of a “politics of life itself,” my focus will be on the relationship between the materiality of the body and the practices of representation being developed. Representation in molecular terms becomes a search for reconstruction, undermining the duality between naming and intervening .

My argument is based on a comparison between the Gleason score and microarray data, both methods of naming prostate cancer and evaluating a tumor's characteristics. The Gleason score, which relies on a visual form of classification that correlates forms and shapes with function, is a very established biomarker, having been incorporated into the medical establishment and its routines. The microarray is an emerging technology that is still disputed in terms of its use and application , but is regarded as extremely promising. There are no firmly established molecular biomarkers for prostate cancer to date, and yet the use of the microarray for prostate cancer research is one of the most important avenues for cancer research today .

Microarrays are at the same time a way of seeing genic expression, a way of translating this into data which can then be processed by computers as well as a potential for drastically changing how we classify and approach the treatment of cancer and other diseases. This molecular classification is much more than just descriptive: because of the specificity of the molecular realm in the cell, genetically-based classification schemes enable new ways of interacting with and recreating the structures being described . This suggests the need to reevaluate what representation means in science and art as we shift to adopting molecular technologies into our practices and understandings of biology, life and the body.

Specifically related to health, microarrays allow for a rationalization of early therapeutic developments by helping to establish "signatures" or targets usable in diagnosis. Chips have the potential to transform individuals into "patients-in-waiting" and "consumers-in-waiting" : patients-in-waiting because genomic representations of life carry an added legitimacy as foretellers of one's biological future; and consumers-in-waiting since these newly established conditions make individuals susceptible to new treatment protocols, drugs, tests, etc.

This idea of describing while at the same time recreating the body is an aspect of what Paul Rabinow has called "biosociality." Rabinow's concept is closely tied to the management of risk: surveillance is replaced with a constant management of populations according to a perceived predisposition to pathologies described in genetic terms. Having one or more genes associated with a known disease constitutes an embodied risk before any symptoms manifest themselves, shifting our understanding of health and disease.

In addition Rabinow points to the constant management of the self in order to produce an efficient and adaptable subject. We are moving away from the surveillance of individuals and groups known to be dangerous, and heading towards the naming and managing of risk factors that reconstruct individuals and groups in different ways, decontextualizing them from social, historical, or embodied factors and experiences. The molecularization of prostate cancer, in this sense, is currently the most advanced technology available to operate this decontextualization in the specific realm of this disease. It permits the rendering of the body in terms of complex data sets, which can be viewed and manipulated in a multitude of modalities (visual, computational, biotechnological). The ability to name a gene or group of genes as "biomarkers" for prostate cancer, thus, operates not only a change in representation (cancer is classified in genetic terms), but shifts how we experience the disease (early detection, constant management), and even our bodies. The ability to localize such pathologies changes subjective experiences of one's body and of having the disease itself.

ANALOGICAL BODY, DIGITAL BODY: FROM GLEASON TESTING TO MICROARRAYS

Some of the questions that have to be posed to this scientifically enabled instrumentalization of the DNA are: how is the body enframed by technology? How do specific technologies create forms of perceiving and relating to the body that are unique? How does the body fit and adapt, in all its complexity, to the limitations intrinsic to each technology? Does the body integrate seamlessly with the machine-human complexes that compose contemporary science or does its complexity pose a problem to these systems? What does the current research with microarrays have to do with our representations of the body?

DNA has two basic functions according to the currently accepted model: replication, which is responsible for heredity and transcription of genes, the process that generates “messages” . The RNA that results from transcription can be messenger RNA (mRNA), ribosomal RNA (rRNA) or transport RNA (tRNA). These three kinds of RNA together are responsible for the process of translation, which results in a polypeptide (a protein or part of one). These polypeptides are the functional and active parts of the cell.

The microarray is a technique for measuring gene expression in a comparative fashion, using the amount of mRNA that was produced by each gene. This way, a measure is obtained of how active a given gene is in a cellular/physiological condition as compared to another. Instead of counting the mRNA strands, a chip is produced, and over its surface immobilized DNA sequences are placed, which will then be tested. The RNA is extracted during a particular circumstance that is meant to be analyzed (e.g. when a particular drug is put in contact with some cells) and marked by fluorescent molecules, which are then spread over the surface of the chip.

Each mRNA sequence will attach itself to a specific place on the chip (a specific DNA sequence relative to a specific gene), according to the principle that complementary nucleotide chains unite in a stable manner. After this process is completed, the chip is analyzed and the light coming from each spot on the chip is measured. Through contrast we can have a measurement of the activity of each gene as compared to a control situation. This type of testing only works by contrast; therefore two distinct sets of mRNA are always used, derived from two distinct contexts. [4] Sometimes several conditions can be compared virtually if all real experiments are carried out using a single reference condition as the counterpart for the condition of interest:

The importance of cancer-related microarray research has grown exponentially, as shown by Mohr et al. (2002). According to the authors, the number of MEDLINE citations with the words ‘microarray’ and ‘microarray+cancer’ has exploded since 1998. They grow from zero to about one hundred and seventy in 1999, three-hundred and fifty in 2000 and seven hundred in 2001. Approximately 25% of that total are in cancer related papers. Some of the most promising applications for microarrays are in the creation of molecular profiles for individuals, through analysis of SNPs (single nucleotide polymorphisms). These molecular fingerprints could help in the understanding, for example, of the different reactions presented by different people to the same drugs and treatments, as described by the emerging field of pharmacogenomics.

For Mohr et al., the study of microarrays can lead to the discovery of molecular markers for cancer:

> Microarray-based expression comparison indicates a panel of up- or down-regulated genes that reveals a relevant molecular fingerprint of the cellular state and provides a large body of candidate molecular markers of the disease. Combined with knowledge of the clinical

> importance of disease process, global transcript analysis could have powerful application in cancer diagnosis and patient management. (Mohr et al., 2002:3169)

The use of the term “molecular fingerprint” is suggestive of the archeological connections (in a Foucauldian sense) between the ongoing process of translation of the body into molecular and genetic terms and the nineteenth century’s establishment of disciplines such as criminal anthropology, which were searching for biological markers for personality traits. This was done through the measuring of the cranium and analysis of bodily proportions in order to determine whether a person was a homosexual, “degenerate”, mentally disabled, or had any potential diseases. The actual use of fingerprinting, discovered at the time, imposed itself as an objective way of marking the individual. A molecular fingerprint, beyond marking the individual from all others, allows for a potential manipulation of those same molecular characteristics, thus displacing the classificatory logic we inherited from the nineteenth century.

This archeological relationship can be better understood if we compare contemporary research on cancer and microarrays with more traditional Gleason testing for prostate tumor malignancy. This test, used worldwide, is based on the visual observation of morphological characteristics of the cell by a pathologist using an optic microscope. Researchers are now trying to establish molecular markers that will allow for a more 'objective' classification of tumors based on genetic elements, allowing for a more specific targeting of tumors during treatments.

> Molecular classification of cancer: Unfortunately, the morphologic appearance of tumor, previously used as one of the cancer markers, presents serious limitations for the identification and classification of cancer. Two tumors with a similar histological appearance can have very different clinical behavior. This variability reflects the molecular heterogeneity of tumor. Since perturbation in the transcriptional program accounts greatly for the biological diversity of tumor, gene expression profiling can help to disclose genes whose expression could be considered ideal for molecular classification of cancer. Within each molecular portrait, it will be relevant to individualize specific markers with different ‘taxonomic value’. (Mohr et al., 2002:3170).

The search for biological markers for prostate cancer is not specific to the post-genomic context, and has existed before genomic research. PSA testing (Prostate Specific Antigen) is a well established biomarker for prostate cancer. With the Gleason test, a method was established to grade tumors according to malignancy, facilitating treatment and prognosis.

The Gleason test is performed by microscopic analysis of cross-sections of cancerous tissue taken from the prostate. The test evaluates the capacity of cancer cells to imitate the architecture and patterns of normal cells, analyzing especially if those cells form glands that are characteristic of this tissue. The ability of the tumor to “imitate” normal tissue and its gland architecture is called differentiation. Experience has shown that a tumor with a highly differentiated architecture (that is, one which closely imitates normal tissue) will probably behave like normal tissue – and in doing so will be less malignant and less aggressive. A Gleason score of one means highly differentiated tissue, while a score of five indicates little differentiation, therefore more malignancy.

While some authors are enthusiastic about the potential of these techniques, others are less optimistic and

raise several questions for the widespread use of molecular markers for the diagnosis and treatment of cancer. Even among those papers that expressed a more favorable view there were different levels of optimism, which denotes a field still undefined and rich in polemic.

Asmann et al. , for example, argue in favor of the potential of the CRISP-3 gene (cysteine-rich secretory protein 3) as a molecular biomarker for prostate cancer. In their research, the authors tried to identify (in a total of six hundred genes expressed in the prostate) nine that were expressed differently in tumors. The results obtained through microarrays were compared with results from Gleason testing, thus making a direct comparison of data coming from both methodologies. In their comparison, the authors emphasize the non-specific nature of the PSA test, and the necessity to find better classification tools which could enable better diagnosis and treatment. The paper explicitly compares both ways of classifying cancer and argues in favor of data-based classifications as more objective and more specific.

Although biomarkers are being developed for prostate cancer, experiments have not shown conclusive results beyond statistical models that suggest a group of genes or a single gene as potential biomarker. Singh et al. are more cautious in their research, and suggest a group of genes as potentially correlated with characteristics and behaviors of tumors. According to the authors, until the present there were not any single genes that were highly correlated with prostate cancer (they do not cite in this article the CRISP-3 gene). For these authors, the lack of specificity and certainty in the results coming from the experiments with gene expression does not allow for a complete substitution of histological exams such as the Gleason score. At the same time they suggest the combined use of different methods in order to increase the certainty of diagnosis:

> Our analysis revealed global gene expression differences that were sufficiently robust to distinguish tumor from normal in both training and validation sets. While the level of accuracy (86% - 92%) is not sufficient to replace histological examination, these molecular markers may be useful adjuncts to morphology-based diagnostics. In addition, while certain genes differentially expressed between normal and tumor prostate specimens in microarray experiments have been correlated with outcome in large data sets (...), in our data such differentially expressed genes were not highly correlated with outcome. (Singh, Febbo et al., 2002:206)

Another paper critical to the possibilities of mathematical modeling of biological processes suggests that the present interest in numerical models for cellular processes stems from a renewal of the technology and a new wave of raw empirical data (such as those from the Human Genome Initiative), but its impetus to actually explain those processes is limited. According to the paper, models have been successful in physics and engineering, but the enormous complexity of biological processes and the lack of sufficient empirical data impose limits to this same success in the life sciences. The authors assert that this type of modeling is necessarily limited, making reference to the contemporary belief that the interactions between molecular components can be understood with mathematical models or computer simulations to the extent of building the capacity of reproducing them:

> On the one hand, the cell is not a well-stirred reactor. It is a highly heterogeneous and compartmentalized structure, in which phenomena like molecular crowding or channeling are

> present (...), and in which the discrete nature of the molecular components cannot be neglected (...). On the other hand, so few details about the actual in vivo processes are known that it is very difficult to proceed without numerous, and often arbitrary, assumptions about the nature of the nonlinearities and the values of the parameters governing the reactions. Understanding these limitations, and ways to overcome them, will become increasingly important in order to fully integrate modeling into experimental biology. (Vilar, Guet et al., 2003:471).

The specialized debate on the subject of mathematical and computational modeling of biological processes can be said to include optimists and pessimists, and all kinds of opinions in between. The conflicts around the possibility of modeling biological processes, and how to best make use of current modeling tools, is a feature of scientific discourse since its inception . The mathematization of our representations of nature and the body has a long history, and the current disputes around biological modeling can be traced back to the hydraulic automatons of seventeenth century European courts, in terms of a history of how scientific knowledge has imagined the possibility of explaining and reproducing the workings of the body .

More recently, the rise of molecular biology as the dominant explanation of life and biology has established DNA as the material basis for heredity, and much has been written on how the Human Genome Initiative and molecular biology has changed our concept of life . Yet seeing the gene or “the book of life” as a metaphor and analyzing the changing meanings life takes does not address the central and most particular feature of molecular representations: that of enabling the overcoming of the duality between naming and manipulating the body through biotechnologies. The materiality of the body becomes a medium of expression or “biomedia” in ways not captured by more common theories of genetics and biotechnology. Thus my goal is to debate the specificity of the practices of representation themselves as a way to grasp this shift from a duality between meaning/materiality to the current forms of representing the body in a molecular fashion.

Current research on science and the body indicates that the impetus to model is connected to the recreating of the body in specific ways that need to be critically explored. The idea of authoring the body is useful when trying to grasp what is to be understood from the ethnographic study of molecular representational practices: more than studying worldviews or meanings of biology, what is increasingly at stake are the ways through which our bodies will be accessed, maintained, regulated, cured, understood, made known and experienced materially.

CONCLUSION: CONFUSING MODELS AND BODIES

The microarray is a materialization of an emerging project for shifting representations of the prostate, from physiological to data-based forms. While such data-based representations are grounded on a deeper wish to name structures within the body through the same elements that enable control and manipulation, the contested nature of the field points to the difficulties inherent to (and so often overlooked by theorists) the complete “instrumentalizing” of the biology of living beings associated by new molecular representations.

Just like other biotechnologies (cloning, gene therapy, stem cell research, transgenic organisms, among others), microarray data have proved to be inexact and “noisy” insofar as research presents them as a way to establish objective classifications of genetically based phenomena. This noise present in the attempts to reduce the body to information has not been adequately taken into account by analyses of the social processes of reconstructing these bodily representations, which are in many senses also tied to projects of

reshaping the body, even if not so seamlessly as some would like that process to be. Practices outside the laboratories, such as the clinical implementation of molecular classifications of disease , present a vehicle where further research can assess how the trends discussed herein are being materialized throughout society.

The search for a molecular biomarker for prostate cancer is contextualized in the desire to establish a tool for naming cancer in a very different way than is traditionally done, a way to abandon the subjectivity of the human eye in favor of the “machine objectivity” of DNA testing and molecular biomarkers. Studies suggest that this translation of the body into molecular terms is occurring in other fields, also in the same conflictual and processual manner .

Another way to approach this issue is to look at Michel Foucault’s analysis of classification and knowledge . According to Foucault, the *episteme* underlying the classical scientific epistemology was that of the *máthêsis*, or the search for measure and order. In contrast to previous periods, where knowledge of nature was constructed mainly by a listing of all known things, from the seventeenth century on, with the advent of scientific thought, it became imperative to organize, make connections, classify and give order to all knowledge collected. In this sense mathematics was the universal language of ‘objectivity’, enabling the description of those relations between natural objects .

Thus, the *episteme* of classical science, according to this interpretation, motivated and gave sense to the construction of models, be they mathematical or otherwise, that could in theory *describe* the truth of all nature in an *analogical* fashion. Language did not confuse itself with materiality, and truth was an abstract representation of nature derived through the scientific method. Currently this difference seems to be collapsing, and thus my use of the term ‘digital’ to describe this new reality. The description of the body, for example, in ‘linguistic’ terms by use of genetics does not simply yield a theoretical representation of the truth of the organic body, but also provides the tools with which to manipulate and change the very material reality it seeks to explain.

Just as in digital information, which allows the manipulation and total addressability of the elements (pixels) of a given system , as well as the multiple actualization of that information (in the form of sound, image, form, etc.), the ongoing translation of the body into ‘informational terms’ (more specifically genetic terms) is built on the quest to open up ways of manipulating the body and its processes. The description of genetic information and its relationship to the body’s functioning is part of a project to build techniques of intervention, correction and improvement of that same body.

Such claims have to be contextualized, first of all, in terms of where they are produced and what needs they serve. For the purposes of this paper, what is at stake is the fragility of these claims when interpreted in terms of the actual process of construction of the molecular representation of prostate cancer. The process of translating pathological classifications (Gleason score) with molecular and information-based categories tests the limits imposed by the material body and its complexity. Those limits will further constrain the development of these technologies, which should be the object of further ethnographic research.

The complexity of the body in the face of our will to manipulate it becomes easier to understand when we interpret molecular representational practices in a certain history of the body as medium of expression. In

many of the works of what we know as “body art”, the aspect of the body’s materiality comes to the fore as a counterpoint to our treatment of it as malleable. Bodily fluids (e.g. blood), the inextricable associations between the material and the emotional (e.g. the pain when cutting into flesh), the fragility of our embodied constitution (e.g. in self-harm performances such as those of Bob Flanagan) are all elements that emerge from experimentation of the body-as-medium. Some recent experiments with artificial life and art have also demonstrated the aesthetic limitations of attempts to envision a virtual realm that is a complete reproduction of reality, raising questions about how the theme of control over life and biology cannot be ignored in favor of discourses that merely glorify technology’s control over our bodies.

Current experimentation with molecular technologies as means for enabling biology to become a medium for expression also can be seen as yet another chapter in this history of the “body as medium,” and begin to raise issues of how we will exist in a world where new life forms are one among the many modes of expression we have at our disposal . When discussing his fluorescent bunny experiment Eduardo Kac makes explicit his concern with how such new life forms will be accepted into the world, how we will care for them and interact with them in an ethical manner . The theme of subverting scientific techniques for aesthetic purposes, a crucial aspect of the Tissue Culture and Art Project, can also be interpreted as a performative attempt to interact with the “biotechnological establishment” and make explicit meanings that remain invisible in its more conventional forms of expression. Catts and Zurr’s “semi-living sculptures” can be read, beyond the semi-living objects themselves, as performances of creating new living beings which, because of their attempt at being purely aesthetic experiments, reveal some of the instrumentalizing meanings embedded in laboratory practices.

The microarray is thus a way to start a debate on contemporary scientific representations of bodily matter, its meanings and its effects. Representation is a question in itself only in art and in science , and the specificity of scientific representations has been defined as their supposed power to describe the inner workings of an object, opening it up to the active manipulation of its principles. While this has been debated in terms of scientific visual cultures , it is only recently that a debate on biological matter as representation is becoming more relevant. That is the deeper goal of this essay: to offer molecular representations as a theoretical delineation of this ontological turn involving bodies, technologies and “representations.” The need to think beyond the visual, or beyond a separation of meanings/matter does not stem from theoretical reasons only, but from the fact that “hybrids” and “cyborgs” are increasingly a part of how we interact with ourselves, our world and each other.

The microarray is more than a “immutable mobile,” or an “inscription” : it effectively bridges the realms of scientific description and the manipulation of matter , a bridge that tends to become wider and more easily crossable in the near future. Beyond the intellectual and epistemological challenges inherent in this discussion, what matters most is defining more precisely the processes through which our present and future worlds and bodies are being actively (re)constructed. Such practices are not neutral, and a greater comprehension of the means through which they takes place will enable more productive discussions on what kind of present and future worlds and bodies we hope to inhabit.

Notes:

[1] The term “enframed” might suggest to the reader a reference to Heidegger’s analysis of technology,

which is not the case here. At least in this paper, the term serves as more of an image that seeks to explain a certain translation of the body from analogical to digital terms, as discussed in the pages that follow.

[2] A DNA microarray, also known as genome chip, DNA chip, or gene array is a collection of microscopic DNA spots, usually representing single genes, arrayed on a solid surface.

[3] The field research mentioned occurred between May and August of 2004. In this four month period several visits to USP were made, to the Mathematics and Statistics Institute (IME), where a Ph.D. program in Bioinformatics was created and where several research projects in that field are ongoing. Inside USP visits were also made to the Chemistry Institute, where important research in prostate cancer was being carried out under the supervision of Professor Sergio Verjovski-Almeida. Interviews were also conducted with several researchers of the Ludwig Institute for Cancer Research and from the Cancer Hospital A. C. Camargo (both institutions are housed in the same building and work very closely). In those institutions researchers from the medical field and from Bioinformatics were interviewed. Both institutions mentioned (USP and the Ludwig/Cancer Hospital) worked at the time in a collaborative fashion in sequencing projects and post-genomic work, with expression of genes related to tumors of the prostate.

[4] For more information see *Nature Genetics* 21, supplement, pp. 1-60, 1999. [http://www.nature.com/cgi-taf/DynaPage.taf?file=/ng/journal/v21/n1s/index.html].