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Modeling Population Health

Reflections on the Performativity of Epidemiological Techniques in the Age of Genomics

Risk reasoning has become the common-sense mode of knowledge production in the health sciences. Risk assessment techniques of modern epidemiology also co-shape the ways genomic data are translated into population health. Risk computations (e.g., in preventive medicine, clinical decision-support software, or web-based self-tests), loop results from epidemiological studies back into everyday life. Drawing from observations at various European research sites, I analyze how epidemiological techniques mediate and enact the linkages between genomics and public health. This article examines the epidemiological apparatus as a generative machine that is socially performative. The study design and its reshuffling of data and categories in risk modeling recombine old and new categories from census to genomics and realign genes/environment and nature/culture in novel and hybrid ways. In the Euro-American assemblage of risk reasoning and related profiling techniques, the individual and the population are no longer separate but intimately entangled. [epidemiology, risk, calculative techniques, performativity]

Like accounting in the world of business, practices of quantification are pervasive in the health sciences. Moreover, epidemiological statistics—odds ratios, relative risks, and predictive scores—circulate much beyond the medical sciences and public health. Risk figures fold into the very configurations of health matters, co-shaping the body politic in biomedical science, clinical practice, and everyday life: Clinicians who adhere to the evidence-based medicine movement view quantitative assessments as an antidote against hierarchical modes of decision-making. General practitioners consult prevention software to compute risk profiles for individual patients. Not only are risk calculations incorporated into decision support systems and used in consultation rooms, they also circulate broadly as publicly available self-tests for common diseases such as diabetes. Based on genomic markers of individual susceptibility, pharmacogenomics researchers aim at “personalizing” dosage of therapeutic agents. Although researchers emphasize the limitations, companies have picked up on genomic markers of difference, marketing commercial tests and genomics-informed nutrition recommendations. Beyond individual genetic testing, genomics has implications for broader public health policies.

Genomic techniques have spurred new debates over individual genetic difference—for example, how health interventions are conceptualized or whether regulatory politics assume sameness or difference among populations. They have changed contemporary knowledge systems in public health and human genetics far beyond an earlier focus on hereditary disease. At stake is the renegotiation of differences in individuals and groups and, often implicitly, reconceptualizations of nature and nurture as well as equality and justice. For instance,

government scientists envision regulatory politics that, informed by genomics, would result in differential exposure limits.

This article examines the on-going transformations in the body politic and the governmentality of population health as genomics-based data infrastructures reshape the “imperative of health” (Foucault 2000; Lupton 1995). In what ways do epidemiological techniques channel and mediate the uptake of genomic data? Does the availability of genomic data transform the societal agenda of public health science? Focusing on epidemiology as a relational “machine” at work in the biopolitical assemblage of population health, this article asks about the relationship between the methods apparatus, technical infrastructure, and content agendas in the age of genomics: What epistemological spaces—and ontological relations—do such epidemiological techniques bring about and afford? What do they render perceptible, and, on the other hand, what “regimes of imperceptibility” (Murphy 2004:281) do they enact?

Health policy-makers, governments, and international agencies intervene in and manage population health in indirect ways based on epidemiological quantifications. “Modern epidemiology” has been articulated as the study of “statistical distributions and determinants of health and disease in populations” (Last 1983:32–33), a definition also adopted by the World Health Organization (WHO). Epidemiological techniques have evolved as part of a cold war culture of technoscientific risk assessment and have become common-sense rationality in the health sciences. WHO, through standardized classifications and software, has chiefly promoted the epidemiological approach to standardize health statistics in a way that would be globally comparable. Exploring the performativity of epidemiological and biostatistical techniques means dealing with a ubiquitous practice that has no fixed boundaries or demarcations in terms of content, place, or subject matter. Rather, epidemiological tools can be characterized as highly mobile “theory-methods packages” (Fujimura 1996:16–17) that travel across contexts. They enable formal comparisons across different locales, while also channeling the modes of comparing that can be done.

The focus on performative aspects in this article is inspired by the notion of performativity that Donald MacKenzie (2006) and Michel Callon (2007) developed for economic modeling. Their analysis extends performativity beyond “speech acts” (Austin 1975 [1962]:20) to describe calculative devices in econometrics as performative in shaping actual markets. Building on this notion of performativity, Callon and Muniesa (2005) follow the ways calculative devices play out in economic experimentation and price setting. In a similar move, by focusing on the performativity of epidemiological risk modeling, I shift the perspective from viewing epidemiology as technique that *describes* matters of population health toward the *doing* of epidemiology as an infrastructure of knowledge production and generative machine of a particular, contingent social relationality.

With a performativity approach, we can further ask for the ways in which evidence-based medicine makes policy interventions and clinical practices isomorphic with the etiological formalizations in epidemiology. This allows us to rethink calculative devices as actants that are part of a generative infrastructural machine implicating policy-making and everyday life. In another twist, attention to the performative effects also evokes Judith Butler’s take on performativity as tactics of appropriation for political change (Butler 1990). This may open up the possibility of an account of the different strategic usages of epidemiological techniques. Can epidemiological methods in the age of genomics be made to perform differently toward articulations of social inequities?

Epistemological Foundations and Empirical Approach

This examination of epidemiological techniques as performative practices builds on the anthropological literature that engages with epidemiology as part of biomedicine (Frankenberg 1994; Trostle 2005; Trostle and Sommerfeld 1996), on scholarship on probability and prediction (Adams et al. 2009; Fortun 2008; Frankenberg 1994; Gigerenzer et al. 1990) as well as more recent reflections on anticipation (Adams et al. 2009; Fortun 2008). Having moved from working as a practitioner in epidemiology to science studies, I conducted interviews and participant observation in large-scale research projects ranging from environmental and nutritional epidemiology to cancer and cardiovascular research epidemiology. In part, my reflections on the emerging field of public health genomics are grounded in extended experience and participation in epidemiological research and can thus be seen as those of a “para-ethnographer,” as I make use of empirical materials generated in the “embedded ethnographic practice” (Holmes and Marcus 2006:36) of a practitioner. My observations largely refer to epidemiological research and teaching in Europe, particularly in Scandinavian and German contexts, with most of them being part of multicentered European studies or other international research platforms.

Hence, this article explores contemporary epidemiological techniques as a powerful assemblage of Euro-American rationality.¹ It focuses on the performativity of “modern epidemiology” and on the hybrids always created in the process of making things modern (Haraway 1997; Latour 1993). In following the battery of techniques that hold together the otherwise heterogeneous discipline, I take inspiration in anthropological scholarship on new technologies as “complex cultural objects” (Rapp 1999:306) implicated in the body politic and subject formation. Thus, my article centers on the epidemiological study itself, showing the pertinent set of methods as a powerful actant. This also takes up Leigh Star’s (1999) call for ethnographies of infrastructure that bring mundane tools such as medical questionnaires, classifications, and information technology to center stage. I deliberately focus on a rather abstract, technical object that involves a certain set of study designs and computational practices in their unfolding into social relations. In so doing, I expose the processual and generative aspects of epidemiological knowledge production.

Starting from a description of the social trajectories of epidemiological risk calculation in the age of genomics, the article presents three sections, each zooming in more closely on one platform² of methods performativity: (1) the work of study design and how quasi-experiments are conceived and brought to work; (2) the human–computer interface of statistical modeling; and (3) the data recombination taking place in genomic epidemiology. Together, these sections examine the mutual co-shaping and loops between content and methods as well as the implications for the on-going reconceptualization of interventions, health policies, clinical practices, and self-management in the age of genomic epidemiology.

Risk Estimates in Everyday Life and the Promise of Public Health Genomics

Contemporary health care systems use a host of technical tools that not only classify but also perform a particular mode of profiling. Using predictive numbers is not limited to genetics but part of a much broader mode of risk assessment as it evolved during the second half of the 20th century. In some European countries, citizens are enrolled into epidemiological data collecting as soon as they are in contact with the health care system—this holds in particular for the Nordic countries with their traditions of central population registers and registry research as key modes of

conducting health services research. The current European Union harmonization process prioritizes the development of comparable indicators and quantitative measures in different domains of policy and regulation, including public health. Risk management culture informs clinical practice and everyday life (e.g., through prevention tools and risk scores for decision making and web-based health tests). Statistical reasoning has entered not only policy-making but also everyday life.

A consultation room, a computer, an individual number for the probability of fatal disease event in the next 10 years, a physician and an astounded patient—“Is he crazy? How can he predict when I die while I am healthy? And how much earlier I might die, if I keep or change my habits?” The numbers in this case come from the software PRECARD®, also referred to as the Copenhagen risk score³—an “evidence-based prevention of cardiovascular disease,” as the CD cover reads. The software was developed during the 1990s to support decision-making concerned with prevention recommendations, and, by 2001, had entered one-third of all general practitioners’ consultation rooms in Denmark (Bauer 2008; Thomsen et al. 2001). Initiators of the software described the tool as an expert system, as a third party in the consultation room, which was present on a screen while physician and patient negotiate. In addition to its function in decision-making, the software was also meant as an educational tool. Consequently, patients find themselves in what they describe as bewildering conversations about how reduction of smoking or more exercising would translate into lower “risks of a fatal event” or gains in expected lifetime.

Technically, the software computes probabilities of cardiovascular disease such as stroke and myocardial infarction in extrapolations for 5 and 10 years. The 10 variables that are entered by the physician are divided into nonmodifiable factors (sex, diabetes, previous heart disease, familiar disposition, height) and modifiable risk factors (blood pressure, cholesterol levels, smoking, weight) that would become subject to preventive intervention. The numbers used for the risk computation derive from several Danish cohort studies of cardiovascular disease begun in the 1960s. Beyond the prediction as such, the tool computes estimates of the risk reduction gained with different lifestyle changes. For those computations, the algorithms use estimates for risk reduction confirmed in randomized trials. The expert system recommends the kind of lifestyle modification that would have the greatest effect, including preventive medication to lower blood pressure or cholesterol levels. Software development, in its early stages, was sponsored by a pharmaceutical company, and later by the public health system. Epitomizing the preemptive rationality guided by risk assessment, this not only works by optimizing lifestyle factors but also backs up practices of “prescribing by numbers” (Greene 2007) to reach the predictive optimum (e.g., for blood pressure or cholesterol levels).

Such risk scores for preventive medicine and risk communication tools are part of public outreach of epidemiological research centers. The German Diabetes Risk Score (available at <http://drs.dife.de/>) is designed to identify people with undiagnosed diabetes or at increased risk of diabetes (Holmberg et al. ; Schulze et al. 2007) Users can enter data for age, height, weight, waist circumference, history of hypertension, alcohol consumption, coffee consumption, physical activity, smoking, red meat intake, and consumption of whole-grain bread. The algorithm computes an individual prediction that can be interpreted as risk of developing type-2-diabetes in the next five years. The calculations of the tool are based on data from the German part of a European multicenter cohort study. The study that was begun in 1993 mainly investigates nutrition and cancer, but also includes chronic disease and so-called lifestyle risk factors. The tool draws on probabilities calculated from data on diabetes incidence rates among cohort members who had the same risk profile. In this way, the score recalibrates individual lives by actualizing

the collective disease experience. Prior to its release, the score was validated with databases other than the one from which it was created (i.e., it tested whether it would predict disease incidence for these other data sets). The tool comes as a side product and health gadget that invites the public to participate in its anticipatory practices. It synchronizes individual lives to an epidemiologically computed biopolitical optimum of population health.

The format of the score would principally allow one to take into account markers of genetic predisposition. Although the underlying epidemiological studies of both tools just presented have been used extensively for genomic epidemiology, so far DNA variation has not become part of those tools nor its successor versions. Developers of the cardiovascular prevention software confirmed that they did not include genetic information, except for the yes/no category of family history, because accounting for more (weak) risk factors would not significantly improve the prediction directed at modifiable factors. Therefore, even given some diagnostic relevance at the time of software development, genetic markers have not entered these tools. Most scientists do not consider genetic markers appropriate for a web-based prevention tool in the public domain. In the future, however, they expect genomic markers to improve these kinds of tools in the clinical context and in preventive medicine.

Although not included in those risk scores, commercial genetic testing is available for what is called “genomics-informed management of lifestyle risk.” With a website, a brochure, and a test kit, a Berlin-based company offers nutrigenetic tests and counseling. The company sells a personal metabolic profile based on up to 20 genetic polymorphisms. The brochures that advertise and describe the nutrigenetic test take up popularized versions of gene variation, such as “the stress gene” (company leaflet) to market genetic profiles as a means to personalize risk data. Marketed as a product to help lose weight, the website advertises the test as complementary to conventional nutrition counseling, yet improved by a personalized molecular profile that enables individually tailored nutrition recommendations.

Epidemiologists and nutrition scientists, however, caution that it is too early to derive recommendations based on genetic tests, as predictive capacities are still low. Although they hold that a combination of family history plus phenotypic lifestyle information (Joost 2005:A2610) allows much better prediction, they advocate more studies to improve the predictive capacity of nutrigenetic testing in the future. More generally, scientists hope to find genomic markers (or combinations of markers) that would further personalize risk assessment, medical treatment, and recommendations for preventive action. At the same time, researchers strategically mobilize the existence of commercial tests and consumer demands as rationales for the need for more research, especially because of the very large numbers needed for the study of multiple genomic markers.

Epidemiological assessments of predictive capacities, as well as guidelines for risk communication, are always approximate extrapolations that need continued revision. New self-tests and clinical software are being developed and updated to better translate the evidence base into an optimized practice and proactive self-management. Contemporary cultures of management and accountability, as Marilyn Strathern (2000) notes in *Audit Cultures*, are characterized by incessant remaking as well as constant improvement and optimization. With or without genomic data, computing risk projections mobilizes the collective past into probabilistic predictions of individual futures.

Risk figures computed via statistical modeling—odds ratios, relative risks, or absolute risks that are related to increase or decrease in risk per unit of exposure—travel from epidemiological studies to inform a wide range of practices. They imprint on the ways patients and nonpatients act in everyday life. In other words, these numbers co-shape lives, health beliefs

and practices, doctor–patient relationships, public health planning, resource allocation, and policy-making and regulation. As “immutable and combinable mobiles” (Latour 1987:227), they circulate beyond the context in which they originated. Yet, although enacted as new relations in everyday life, they carry the epistemic baggage from the original context in which they were created. It is the actual making of those risk estimates in the research process that I discuss in the remainder of this article. For each of these performativity platforms, I examine shifts associated with genomics about how epidemiological techniques fold into ways of knowing in public health in a broader sense. These performative platforms should neither be viewed as sequential nor entirely separated but as constitutive parts of the Euro-American risk assemblage.

Performativity Platform 1: Making Quasi-Experiments Work

What actually is epidemiology? What are the core procedures and practices in epidemiological research? When I started my first fellowship in epidemiology, senior colleagues introduced their discipline as being “mainly about methods.” An introductory textbook describes the working practice of epidemiology as “like common sense, but with a system” (Austin and Benson 1974:8). “Just methods” was a recurrent motif, as I proceeded with training and research. Training in epidemiology cultivates disinterested critique at the level of statistical techniques. Lecturers separated content from the actual biostatistical core of the discipline; some preferred to teach epidemiological techniques using “populations on Mars” as examples to avoid methods exercises being disturbed by content concerns. Professors of an advanced research course emphasized that epidemiologists were consulted as experts in methods—precisely because they had no commitments as to the subject matter—they would, unbiased by content-related agendas, base their judgments purely on statistical tests.

Although most epidemiologists agree that their discipline is an applied research area and largely an observational science, they point out that epidemiology is a science that chooses “designs that simulate experimentations” (Vineis 2003:80). Several textbooks frame this quasi-experimental approach of observational epidemiology by referring to John Snow’s study on cholera and water supplies in 19th-century London. This is recalled as the “grand experiment,” with the epidemiologist “taking advantage of situations that constitute a natural experiment” (e.g., Roberts 1978:187).

Modern analytic epidemiology follows up and evaluates differences not only between areas but between any population and group differentials by transforming them into natural experiments. In other words, group difference forms an empirical setting to be analyzed using standardized measures. Designing epidemiological projects is about bringing to work “quasi-experiments,” which, in a retrospective or prospective mode, enact health and disease in terms of patterns, variations, and trends as something conceivable and manageable at the population level. In the “epistemic culture” (Knorr-Cetina 1999) of epidemiology, statistical inference is based on statistical tests for hypothesized effects against random variation. The decision criteria to confirm or reject the significance of an association are based on cutpoints that define the significance level of confidence intervals, which is a mere convention of practice.

At the planning stage of an epidemiological study, much of its dimensions are still in play and allow transdisciplinary input. Meetings to develop new projects take place somewhat remote from the usual business and everyday routines. This is the rare space for conceptual discussions about causal relations between various exposures, other factors, and disease. Designing a study involves sketching out schemes, drawing, crossing out, and redrawing arrows on whiteboards.

Bringing together previous etiological studies, research agendas, and common-sense factors, arrow diagrams help systematize “webs of causation” (MacMahon et al. 1960:12–21). A more formalized visual method is the “directed acyclic graph” (DAG) (Shrier and Platt 2008:70, 71), with arrows that specify the relations between variables, distinguishing between main hypothesis, confounders, and effect modification. As guiding tools to transpose these interrelations into programming syntax, DAGs provide a grammar to convert the experimental constellation into a workable scheme for statistical analysis. In the age of genomics, epidemiologists include DNA variation in this causal web of potential determinants, treating genetic markers as statistical risk factors in the epidemiological model.

When I joined a European cancer epidemiology research cluster in the mid-1990s, the human genome project was about to be completed. Most epidemiologists, eager to incorporate genomics, anticipated major breakthroughs in understanding the causes of common diseases, focusing on “candidate genes” and single nucleotide polymorphisms (SNPs). The promise of genomic epidemiology, as a funding agency delegate put it at a meeting in 2000, was to open the black box between exposure and disease. It was with the hope for insights into mechanisms beyond mere probabilistic models that epidemiologists embraced genomics. They also saw a role for population-level designs in critically testing the influence of DNA sequence variation on specific diseases. With genomics, a host of new variables are generated, which methodologically requires very large population studies to obtain statistically robust results, particularly in conjunction with other risk factors in models of multiple causation.

New studies depend on data availability in existing infrastructures and their accessibility. Epidemiologists, in the age of genomics, look for studies that have retained blood samples and make new uses of these old samples. Recent projects and funding decisions also privilege large-scale biobanking endeavors for genomic epidemiology. To measure new variables from scratch that would track different steps in the complex pathways to embodiment is often considered too laborious, requiring additional work and funding. To manage the costs and secure statistical validity, the design phase also includes sample size calculations to maximize statistical validity and minimize study costs. In a trade-off between funding, validity, and complexity, the study design is optimized.

After completion of the design phase, the logistics for epidemiological fieldwork are tested. Data collecting often builds on routine data (i.e., from health registries or cause of death information). Logistics for a study include the development and validation of questionnaires and techniques for exposure measurement as well as medical screenings. Strategies and logistics of recruitment differ, depending on whether it is a clinical study or a survey in the general population. Planning the recruitment and logistics is part of the design phase; then the actual implementation is tested in pilot studies to identify problems and fine-tune procedures. Setting up large-scale population studies on cardiovascular risk in the 1970s, Danish researchers modeled the examination logistics (for tens of thousands of people) on the principle of a conveyor belt with consecutive stations for different measurements and examinations. Collecting data from study participants of an epidemiological study requires highly standardized protocols and staff able and willing to maintain the study. Interviewing and data processing are often considered as mere service work and delegated to nurses, technicians, or medical students once the rules are set. In clinical studies, specialized “study nurses” keep the logistics and observe the protocols for measurements, providing the required meticulous care for the data. The final “study handbook” and its specifications become a rigid regime for everyone contributing to the study.

When conceptualizing and implementing the study, epidemiologists iteratively calibrate and rescale real-world situations, transforming the latter into the quasi-experiment they set out to observe. What preoccupies researchers most is bias introduced with differential measurement. The “blinder” (the more disinterested) the interviewers are, the better for bias control in the positivist mode of epidemiological research. Getting rid of ambiguity and complexity is part of making the study work. In her ethnography on cytogenetic techniques in reproductive medicine, Rayna Rapp (1999:208) has described these processes of assigning complex things into fixed categories as “stabilization and disambiguation”; in scientific knowledge generation, these are necessary steps to reach a decision or diagnosis that can be worked with. Ambiguity regarding diagnoses and categories needs to be removed during the entire course of an epidemiological study; resolving such ambiguities in individual cases (e.g., for an unclear diagnosis) is done through “expert decisions,” with the PI having the final word. Then work must proceed—and what has been closed down is not to be reopened otherwise no result could be achieved. Similarly, final decisions about categorization of variables need to be closed down before statistical modeling for the actual quasi-experimental hypothesis testing can begin.

Performativity Platform 2: Computer Modeling and the Politics of Categorization

Interrogating the dataset via statistical hypotheses tests is the rationale of all data labor. After years of painstaking data collecting and validation, the final step—data analysis—comes as the reward, for it is only here that the empirical response to the hypothesis in a quasi-experiment is obtained. The screen and the software constitute the interface between the epidemiologist and her digitized simulated experiment—a human–computer *agencement*. Although the dataset seems detached, it is at the same time both a carefully crafted entity and part of an affective economy. Transposing a hypothesis into programming syntax involves iterative writing, compiling, and adapting the program to be run. Researchers can get caught up and absorbed until the data run works.

Large research centers may outsource the actual calculations to service companies, but the programming itself is key to the professional ethos of epidemiologists. Individual researchers would be known among colleagues as programming with virtuosity, meaning short and efficient syntax. “I do some programming every day (...) if one didn’t, one would lose the capacity, like a language,” senior epidemiologists take pride to tell their students. As a rule, curricula emphasize statistical analysis as the core of the discipline. Writing program syntax is laborious, but practitioners consider more user-friendly software with preprogrammed tools as dangerous, as these tools quickly produce numerical outputs; they can be used by anyone without requiring an understanding of inherent assumptions and limitations.

Effects of Statistical Modeling

Running a computer model is a powerful action, reshuffling the entire analysis file within seconds and producing an output with multiply adjusted risk estimates and confidence intervals. Pressing the submit button sets off the execution of a program, entangling the variables into a fact-generating procedure and thereby enacting an epistemic grid. Epidemiological study designs and analytic techniques formalize health science, decision analysis, and health economy in isomorphic ways: Biostatistical techniques are the same, whether the study is about social or biological variables or both, about humans or animals, local experiments or global econometric studies,

genetic haplotype pattern or socioeconomic status. General statistics handbooks relevant to epidemiological studies often explain programming syntax of mathematical procedures using examples from econometrics, marketing, animal experiments. In that sense, epidemiological practice is about performing the world in the data model and performing the data model in the world. Models can scale up and down between levels; they can draw together and recalibrate the space of policy, datascares, and the lab. One shift in perception that comes with these practices is a shift toward views of disease as patterns, variations, and trends for a population-whole, something that is measured at aggregate levels, and from there can be further stratified, by age and gender, lifestyle habits, and genetic susceptibility.

Bringing data from disparate contexts, scales, and histories into one modeling equation in the computation of population-level risk figures synchronizes, for example, the history of medical classification with late 20th-century notions of lifestyle and with the data output of PCR (polymerase chain reaction) and postgenomic technologies. What entered the model as just a single bureaucratic variable from a census or patient record or a single lab finding leaves the modeling procedure as a risk estimate at a certain significance level, a number that entangles and blends administrative categories with genotype information, in the very numerical risk estimates computed with the model.

Deciding which and how many variables to include and to adjust for in the statistical modeling is complicated. During analysis of an epidemiological data set on cancer mortality and radiation exposure, I puzzled about the consequences of the modeling decisions I had made: Should I adjust for gender or report gender-specific estimates? What kind of reification does the exclusion or inclusion of variables into the model produce? Should I leave out the variable ethnicity entirely or adjust for it just because the data are available in my case study? And what would ethnicity stand for in a model of disease causation—a proxy for social class, for exposure characteristics due to perhaps different dietary habits, or even for genetic difference? In what ways would the variables interact with each other? Grappling with these questions is part of epidemiological practice and managed by delimiting this discussion pragmatically to the phase of study design. Often, even in the design process, categorizations and groupings once set are kept simply for reasons of comparability and reference. Opening them up again once the analysis plan is closed down would mean undoing the achieved disambiguation, which makes it impossible to continue the research process.

Politics of Inclusion

In this sense, including “race” as a census category or “ethnicity” as difference categories in the calculations can make drugs ethnic, and exposures, genetics, and health racialized (Bauer 2006; Kahn 2004). However, statistical processing can afford a host of recombinations. Beyond modifying factors, there is a range of variables routinely adjusted for, such as age and gender. The status of variables such as socioeconomic status or ethnicity/race is more contested; often the latter are included routinely by default (Shim 2002), particularly in the United States, where the inclusion of minorities became mandatory for publicly funded studies in the 1990s (Epstein 2007; Lee et al. 2001). This was due to advocating diversity, instead of the previous “one size fits all” paradigm that implied that clinical research and health statistics should report results separately for both genders and for minority groups (Epstein 2007).

The use of census categories for this purpose has led to a proliferation of the categories race and ethnicity in biomedical research. The effects of this policy have been analyzed as

reification of biological notions of race in biomedical research (Duster 2005). At the same time, these minority categories are also mobilized as indicators of discrimination—as proxies for social inequities—to document the health effects of discrimination and thus work in various directions and agendas. Here, epidemiological techniques are invoked to work in a social medicine and public health agenda. Social epidemiologists make them perform (e.g., to document social inequality and the consequences of racism) (Krieger 2001). As Abu el-Haj (2007) notes, with respect to the inclusion of race in the biosciences, the entangled notions of race differ from those of “race science” and deterministic projects in eugenics. Following Abu el-Haj (2007), neoliberal risk reasoning and its mode of subject–citizen formation lead to exclusions by mechanisms that differ from those of biological determinism or reductionism.

Much of these discussions on race as an epidemiological variable refer to a specific North American assemblage of census data, identity politics, and notions of population diversity and subgroup categories. In contrast to the United States, race (or ethnicity) was not a routine administrative category in most European countries after World War II. Rather than focus on race, epidemiologists in Europe include variables such as migration background into study designs that strive to document social inequalities and effects of racism and discrimination (e.g., in the study of differences in mortality rates, health care utilization, or barriers to health care). Although many epidemiological concepts are rooted in behaviorism, asking questions such as why some are healthier than others, public health scientists use Antonovsky’s classic concept of public health in a decisively social framework. They strive to employ epidemiological tools to target the health of vulnerable groups, as outlined in the Ottawa Charter on health promotion.

However, moving from social disadvantage to vulnerability attributed to migrants as an entire population subgroup does perform a certain epidemiological categorization, producing similarities in and differences between groups. Also, the recent proliferation of ethnicity and race as group categories in epidemiological studies in Europe responds to globalized guidelines and multinational consortia. At times, these guidelines prompt epidemiologists in Europe to apply American census categories such as Caucasian to meet the demands of a global market of epidemiological knowledge generation to be citable and eligible to meta-analyses. Local studies in Germany or Scandinavia mostly use the categories of migrant rather than autochthonous when comparing these population groups (e.g., regarding differences in mortality rates and access or barriers to the health care system). In risk factor studies, these categories are sometimes used as proxies for social and lifestyle differences. Used as a proxy variable, migration history or ancestry becomes a boundary category of sorts that can be read as much as a social as a biological or genetic difference category.

Uncertainty

Running a statistical risk model enacts an almost literal performativity that plays out as iterative reshuffling of categories and connections. In inferential statistics, control of error and management of uncertainty are core goals of the design deliberations. Epidemiologists concentrate on managing uncertainty first and foremost by avoiding systematic error (bias). The possibility of unknown confounding due to an unaccounted factor that possibly distorts the association just found in the dataset makes observational studies less credible than randomized clinical trials that count as the gold standard, as they control confounding by randomization.

Genomics promised a methodological upgrade of observational studies: Genetic epidemiologists proposed that Mendelian randomization (random allocation of genes during

meiosis) would compensate for the fact that observational epidemiology cannot randomize the allocation of exposures (Ebrahim and Davey Smith 2008). Such studies would entail an inherently randomized variable for the study of gene–environment interaction (Davey Smith and Ebrahim 2003; Ebrahim and Davey Smith 2008). The appeal of genomic data to epidemiologists was thus also methodological: Not only would specifications of molecular pathways support statistical linkages between exposure and disease, Mendelian randomization promised an upgrade of observational designs in the evidence hierarchies.

Statistical hypotheses testing in epidemiological research is an exercise in the management of uncertainty. As epidemiological reasoning privileges disinterested methods, doing a scientifically sound study can outweigh content-related considerations. Rather than starting from a preconceived research question, researchers try to make work infrastructures already in place and take advantage of them, surfing them as research opportunities, much in the sense of what Hans-Jörg Rheinberger (1997) has described for the production of novelty in experimental systems. Compared to experimental systems of the laboratory, epidemiological research systems are more regulated and less flexible. In epidemiology, findings beyond the main hypothesis count as chance findings and hypothesis generating only. To count as evidence, they need to be proven in a confirmatory study.

Still, even in the regulated practice of epidemiology, novelty arises outside the standard approaches, sometimes when exploring a sidetrack among chance findings. Novelty can emerge in the on-going displacement, recombination, and blending of parameters from different contexts and their looping effects (Hacking 1995). In this way, modeling techniques channel, mobilize, and blend state administrative infrastructures, demography, biomarkers, and clinical records for genomic epidemiology. Surfing these new datascares of population health, knowledge production is constitutively locked in with loopings of the old and the new and constantly actualizes this relationship in emerging infrastructures. Such residual indeterminacy that is different from statistical uncertainty might be the driving force in how empirical constellations can be surfed to generate novel hypotheses.

Performativity Platform 3: Data Recombination in Genomic Epidemiology

Different Performances of Epidemiological Methods

Albeit epitomizing a contemporary node of the two poles of biopower (population and individual), epidemiological practices are heterogeneous. This plurality plays out in tensions between different subdisciplines, like genetic and social epidemiology, in the varied agendas that different actors pursue, and in the varied hopes and fears invested in the research process. Many epidemiologists perceive the trends to genomics and the individualization in risk factor epidemiology, as in contradiction to the original agenda of public health with its tradition in social medicine.

Since the mid-1990s, epidemiologists have criticized the neglect of conceptual frameworks within the discipline and raised concerns about its lack of theory and so-called disinterested perspective. In her seminal analyses of the conceptual frameworks in risk factor epidemiology, Nancy Krieger describes the different underlying concepts of disease causation in terms of the biomedical model, social production of disease, biopsychosocial, or eco-social frameworks, stressing the need for more theoretical work in epidemiology (Krieger 1994, 2001). This approach favors a more integrative practice of epidemiology that works toward an “ecosocial

framework” (Krieger 1994) or “eco-epidemiology” (Susser and Susser 1996). Robert Aronowitz (2008) has further pointed to the import of conceptual considerations, considering in particular the effects of “social framing” at work in any causal model, as the construction of variables itself causes effects in the actual studies.

Given the key role of risk reasoning in policy-making and resource allocation, any critique and advocacy in matters of health is confronted with a need to draw on or produce evidence in the epidemiological format in order to make an impact. Many social and environmental epidemiologists deploy epidemiological techniques to study social inequities and effects of racism or issues of environmental justice (Bolte et al. ; Mielck and Bloomfield 2001; Soskolne and Westra 2008).

Taking those different usages of epidemiology into account also expands my analysis of public health genomics: Some environmental health scientists and toxicologists draw on recent developments in (post)genomics to foster awareness about the environment, moving away from a narrow focus on heredity. For instance, toxicologist Steven Gilbert (2011) has described epigenomics as “biology of good,” as with epigenetics genes can be understood in their molecular, environmental, and social contexts.

Developers of the NGO platform toxipedia.org in the United States suggest an “ethics of epiprecaution” (www.toxipedia.org), alluding to epigenetics and the precautionary principle that has become a cornerstone of European Union science policy. They propose the terms “epiprotection” or “epiprevention” for the right of children “to reach and maintain their full genetic potential” (www.toxipedia.org). Although some of these strategies join the format of universalism yet with different conclusions, some of these tactics might be understood drawing on Butler’s (1990) relational notion of performative politics, a mode of appropriation of methods to rework the epidemiological research culture. In this context, though, the barriers to participation in this mode of research by unequally distributed resources need to be highlighted.

In public health, these (post)genomic toxicologists suggest precaution at the environmental (not individual) level as means to optimize environments for human health. This understanding of how environmental exposures leave imprints on exposed bodies that can be transmitted from generation to generation via epigenetic alterations (such as DNA methylation triggered by environmental conditions) brings the environment back to centerstage (Landecker 2011). This can take the shape of molecular enhancements as mass interventions in food environments, such as the folic acid supplementation of flour, practiced in the United States. Concepts of epigenetic heredity that link one’s grandparents’ nutrition and environment to the health of the here and now may even result in more determinism, justifying interventions into everyday lives in a novel mode. At the same time, activist scientists refer to genetic susceptibility studies to argue against any threshold that could be considered safe, refusing the logic of risk assessment.

In contrast to the toxicology and bioinformatics communities, established epidemiologists articulate reservations concerning genomics and epigenetics. Complicating the study by large amounts of variables and their multiple interactions pushes the limits of statistical validity, even for pooled analyses of several large studies. Epidemiological standards thus press for the reductions in the number of variables and for homogeneous study populations. Although epidemiological techniques can be a critical tool to challenge and retest what is considered evident, they always enact a powerful infrastructure of proving or disproving links between exposure and disease with a methodologically driven focus on few, strong risk factors. Thus, the textbook characterization of epidemiological research as “common sense but with a system”

(Austin and Benson 1974:8) is not neutral but a framework that privileges knowledge about few individual risk factors over complex structural, mutually interacting factors. Moreover, substantial resources are required to participate in that mode of knowledge generation. With the epigenetic study of regulatory mechanisms beyond DNA difference, the epistemic grids, the biopolitics, and enacted relations have broadened to pathways that modulate genome expression. Yet, the methodological grids and calculative devices of modern epidemiology enact regimes of profiling that again formalize the investigation of complex interactions in specific ways.

Public Health Genomics Redefined as Risk Communication

In 2011, the *Journal of Public Health Genomics* announced a shift from genomic association studies to systems biology and “genome-based health literacy” (Syurina et al. 2011:201). The authors embrace this vision as more “integrative and holistic,” guided by epigenomics and “personalized genome-based information” (Syurina et al. 2011:207). In this vein, systems biologists study molecular–physiological processes in silico and across species, using web-based platforms to store large datasets and manage data exchange between consortia.

A second pertinent shift stressed by proponents of public health genomics is the study of health literacy and education. In this risk communication spin of association studies, genomic epidemiology moves on from investigating the link between genetics and disease to association between attitudes to genomics and willingness to change lifestyle. Quantitative designs measure “the influence of health literacy and numeracy on genetic communication and the behavioral responses to genetic and genomic information” (Lea et al. 2011:279).

Epidemiology now investigates the associations between genomics literacy as a proxy for health literacy and behavior. This takes place in the very epistemic format of epidemiology (i.e., the study of distributions and determinants). In a recursive loop that uses the same statistical techniques, the hypothesis whether “attitude to genomics” is linked to the willingness to manage risk factors is tested. Thus, genomic epidemiology creates its own second-order application in the assessment and comparison of perceptions between different population groups. Public health genomics scientists identify underserved populations yet to be educated about genome-based risk prevention, creating urgency of action to target unmet needs. Here, the notion of methods has changed scale and now these techniques reformat and actualize other domains, such as science communication and the investigation of public acceptance.

Promissory beginnings are not new: More than a decade ago, “the beginning of something HuGE (Human Genome Epidemiology)” (Khoury and Little 2000:2) was announced in the millennium edition of the *American Journal of Epidemiology*. In 2005, public health scientists initiated a large-scale networking and concerted platform to make genome epidemiology happen. With the more generalized notion of omics technologies that describes the technological infrastructure of micro-array analyses beyond DNA, molecular epidemiology moved from the study of single DNA variants (single nucleotide polymorphisms, candidate genes) to genome-wide association studies envisioning quick results on genetic determinants of common disease. When those studies did not translate into gene-based understandings of disease, proteomics and systems biology emerge as next promissory level. This, in itself, is a performative feature that is characteristic of the economy of genomic knowledge generation on a global research market.

Significantly, the incorporation of omics into epidemiological research is altering notions of exposure and disease—the traditional units of epidemiological computations beyond that they become molecular. Although epidemiological techniques can flexibly scale up and down—

connecting molecular data to the population level—genomics has, in turn, altered the scale of the epidemiological practice. Terms such as the “exposome” (Vineis et al. 2009:8) of the human body or the “diseasomes” (Syurina et al. 2011:204) of entire human populations reflect the mobility of genomic reasoning in terms of a shift to patterns and arrays—a spectrum or range rather than an entity—through which statistical relations are mapped. That social scientists have also deployed software developed in genomics to map collaborations and institutional networks in terms of “sociomics” (McNally 2005) shows the mobility and extent to which omics have evolved into hybrid infrastructures in 21st-century knowledge production.

Conclusions

This article has highlighted performative features in the circulation and generation of epidemiological facts—starting from the trajectories of health risk figures, the enactment of quasi-experimental designs, and statistical modeling in the resulting datascares. It showed how epidemiological techniques contribute to the “burgeoning translation industry” (Franklin 1995:175) associated with genomics.

Probabilistic modeling and risk estimation epitomize particular biomedical configurations and bring into being specific social relations (Latour 2005). In their study of economic modeling, Callon and Muniesa (2005) have outlined three steps of the calculative process.

A first step relates to the detachment of entities and their arrangement in a single space. In epidemiological research practice, this corresponds to collecting and bringing together data from different domains into one database and then into a quantitative risk model.

A second step comprises the implementation of a common operating principle that enables comparison across a variety of calculative spaces. In epidemiology, such a comparative space is established via meta-analyses and systematic reviews of existing studies, which have become a research direction of their own.

The third step described by Callon and Muniesa (2005) is about producing new entities able to leave the calculative space without taking with it the whole methodological apparatus. In epidemiology, it is the risk estimates—and sometimes the assessment tools themselves—that travel to consumers, clinicians, and policy-makers who use them according to their own agendas. The design methods packages in epidemiology are flexible, powerful, and highly mobile across context and levels of analysis.

The risk computation that integrates genomic data into epidemiological modeling works as both risk calculus and prediction device. Adams et al. (2009) have characterized such predictive calculations as anticipatory regimes, proposing the pragmatist term of “abduction” for these ways of moving reasoning “from data gathered about the past to simulations or probabilistic anticipations of the future that in turn demand action in the present” (Adams et al. 2009:255). Abduction is different from induction (as in inference statistics) and deduction (from etiologic theory), as it displaces objects and methods. It is in the mode of abduction that epidemiology iteratively calibrates and synchronizes the world to designs and models. More than detecting etiologies, epidemiological techniques work as an engine, a generative machine that *produces* particular, contingent segmentations of health matters. It is the preliminary, preemptive management of uncertainty in epidemiological research that prompts incessant optimization at collective and individual levels.

The computer modeling with epidemiological datasets folds individual and population into each other: Over his or her life, an individual moves from one aggregate to the next, with a

different matrix of risk patterns present in each of them. Here, genetic markers provide yet another level of stratification that runs through these aggregates, enacting further segmentations along degrees of genetic susceptibility. From preventive medicine to science communication and securitization, the individual is entangled in the aggregate infrastructure of populational data practices. Epidemiological procedures, the creation of genomics infrastructures, and the proliferation of outcomes research as universalized approach contribute to stabilizing a particular configuration of populational subjectivity.

Gilles Deleuze (1992:5), no longer upholding notions of “the mass/individual pair,” coined the notion of “dividual” subjectivity for the suspensions of the individual in continuous networks and aggregates, markets, and banks in societies of control. It is in a different, aggregates-based mode of individuation that the individual in the society of control moves through statistical aggregated modeled as windows of differential susceptibility. In this way, public health genomics targets the entire life course performing in/dividuals as data points moving from fetal development and early childhood to adult life characterized by plasticity. Notions of “metabolic individuality” then emerge as a reassemblage of genetic disposition and exposure, including epigenetic transmissions of exposure of previous generations.

Although explanatory models rapidly change, a genomic infrastructure of knowledge production is being established that changes the ways knowledge is produced. For instance, studies in epigenomic epidemiology create a new version of the environment, formalized as the mediating background that triggers or silences gene activity into a quasi-experimental setting (Landecker 2011; Shostak 2005). With these evolving research platforms, the grids of im/perceptibility, understandings of body and identity, and indications and modes of intervening change. After a decade of research in genomic epidemiology, few associations between genomic markers and common disease at the population level have been identified. What remains is an infrastructure of automatized handling, microarrays and gene chips, platforms for databasing, and bioinformatics tools that will shape the postgenomic biomedical sciences. It is this infrastructure that has also left its impact in a few popular applications such as commercial ancestry testing. Exposing the performative effects of epidemiological techniques and evidence-based risk management not only helps us understand how genomics and its bio-socio-technical networks transform the science of public health, it also challenges the epistemic infrastructures that Euro-American risk reasoning and health knowledge are based on.

Notes

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1. Public health research in Western Europe has maintained close ties to international organizations and in particular to U.S. institutions. During the 1980s, West Germany ran an exchange program with Johns Hopkins University as it prepared for similar programs at German universities. Scandinavian countries with central population registries have played a leading role in epidemiology in Europe and maintained long-term trans-Atlantic collaborations.

2. The term “performativity platform” is inspired by the notion of biomedical platforms (Keating and Cambrosio 2003).

3. This early local prototype is, in many ways, comparable to other cardiovascular risk scores such as the Heartscore, Euroscore, or Framingham score.

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