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Relational Presence

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What is a population but a method to know, aid, govern? Populations frame bioscientific research, including studies on the human microbiome. As microbial life transforms into data through genomic sequencing, computational modeling, and statistical aggregation, their tangled ecologies are pressed into clean(er) formats—fit for policy briefs and predictive models. Microbiome research, therefore, does not simply reflect microbial reality; it inscribes microbial life within systems of control and optimization, generating new populations that can be governed and intervened upon. Current human microbiome studies hypothesize that the transition from a subsistence economy to an industrial economy robs bodies of their capacities to metabolize efficiently, leading to health issues including inflammation, obesity, and metabolic disorders. Conceptual divisions of microbial populations into those from urban, industrialized, and (over)developed places (*dysbiotic* or "unhealthy" microbiome) against those from un(der)developed, pre-industrialized, and subsistence economies (*eubiotic* or "healthy" microbiome) make certain bodies (and their microbiota samples) more treasured for the extraction of bioinformation (Van Wichelen 2023). Subsequently, the microbial knowledge of "other" bodies is put to work to remedy these pathogenic instances, producing instances of epistemic colonialism and epistemic capitalism. Nothing new under the sun—for a biopolitical analysis.

Yet the datafication of microbes alters our concept of populations not just in degree but also in kind. Traditional epidemiology understands populations as human groups defined by geography, demographics, or social characteristics.

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Computational microbiomics, by contrast, abstracts microbial communities into universally comparable units—detached from their human and environmental contexts. This abstraction enables large-scale comparisons but risks erasing the lived realities of poverty, malnutrition, and colonial histories (Benezra 2016, 348; Radin 2017). Moreover, the increasing role of machine learning in genomic sequencing presents a methodological problem unique to its field: the so-called "small *n*, large *p* problem" (Alyass et al. 2015). Comparable to other omics research, the study of the human microbiome suffers from the issue where the number of parameters or microbial features (*p*) is much larger than the sample size (*n*). This matters as it presents difficulties for biomathematicians who are tasked to analyze and interpret omics data. In the case of microbiomics, non-industrialized populations are almost always underrepresented in omics studies, and with each added dimension (for instance, an increased model complexity) for a fixed sample size, the consistency of models decreases (Alyass et al. 2015, 6), with statistical and biopolitical implications.

While thousands of microbial species represent *p*, *n* is often represented by a handful of non-industrialized samples, leading not only to overgeneralization but to unstable comparisons, and arguably to what I term *hallucinatory populations*. Much like the hallucinations in AI-generated text and images, these populations lack real-world referents. They emerge from computational processes that struggle to encode complex social and historical contexts, revealing the blind spots where ideology hides behind precision. In the idealized eubiotic or dysbiotic microbiomes that sanitize histories of colonialism and capitalism, these hallucinations reveal deeper ideological investments (Žižek 2009). Here, computational microbiomics operates as a digitized biological rationale that sustains an ideological fantasy—one that naturalizes existing power relations while disavowing the material conditions that produce inequality. Much like Slavoj Žižek (2009) argues, the ideological works, not through the concealment of truth, but by refuting the material provisions core to differentiating knowledge from information. As microbial populations flicker with the authority of data, they carry phantom-like dimensions—emergent, not from a present world, but from algorithmic creations haunting bioscientific dashboards.

Datafication moves the analysis of populations beyond sovereign and disciplinary power, toward an understanding of how populations function as nodes of data-driven optimization (Halpern and Mitchell 2023). In this framework, populations, including microbial ones, become pre-emptive models—fluctuating risk landscapes that must be forecasted, managed, and adapted to an uncertain future. The uncertainty drives interventions, optimizing continuously while failing at the same time, justifying perpetual intervention. In the North (and for wealthy individuals in the South), such interventions are exhibited by the liberal state's support of "personalized" medicine, accompanied by grotesque performances of privileged biohackers—such as the American entrepreneur and anti-aging practitioner Bryan Johnson—whose affluence can buy them the full optimization of their gut's microbial life. In the South (and among marginalized communities in the North), we see public and global health interventions that practice modern and *depersonalized* medicine, chipping away at what remains of autonomy while negating subjects' singularity.

If computational microbiomics reduces lives to probabilities that may include *hallucinatory* ones, a feminist and postcolonial toolkit does the opposite: It insists on a relational presence, necessitating contextualization and radical collaboration between researchers and those researched. This entails not just a different method, but a different ethics of life.

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