Thematic Collection Article

Science, Technology, & Human Values
2024, Vol. 49(3) 555-577

DOI: 10.1177/01622439211035449
journals.sagepub.com/home/sth


When Extracting Is Not Subtracting: Accounting for Organism-technologies as Stakeholders in Microbial Resource Extraction through an Experiment in Discursive Biomimicry

Erika Amethyst Szymanski[1]

Abstract

This paper concerns how digitizing biological resources enables disentangling information technologies from biological bodies and, thus, from response-abilities among creatures from which they are derived. Extracting (digital) information from (biological) bodies makes it possible to stabilize, freeze, circulate, and control that information independently from creaturely activities—multiplying, not subtracting from the originating material. Such extractions tend to attenuate human interdependencies with other

[1]Colorado State University, Fort Collins, CO, USA

Corresponding Author:
Erika Amethyst Szymanski, Colorado State University, Williard O. Eddy Hall 345, 1773 Campus Delivery, Fort Collins, CO 80523, USA.
Email: erika.szymanski@colostate.edu

creatures even while expanding the scope of their utility as resources, to the effect of limiting those who have a stake in their development to humans alone. Where conventional natural resource extraction does violence to places and those interdependent with them, digital resource extractions may instead do violence to human capacities to recognize and act on multispecies interdependencies. Here, I argue that choosing to realize connections among organisms and organismal resources makes it possible to envision how creatures may be stakeholders in their own development, with joined ethical and epistemic consequences. I trace that possibility through a case study of the essential laboratory yeast *Saccharomyces cerevisiae* via the physical metaphor of snowflake yeast, an *S. cerevisiae* variant that maintains multicellular connections as it reproduces.

Keywords
microbes, extraction, multispecies, yeast, bioeconomy

Introduction

The phrase "resource extraction" tends to bring up images of such ecological atrocities as giant pits in the ground and long lines of scraped logs leaving scarred land. Extraction also tends to bring up critical perspectives on how extractivism entails violence to lands and people indigenous to them. Yet, in an era in which many resources are neither physical nor necessarily coupled to land, the question arises: to what extent do theorizations of natural resource extraction apply to "extracted" information resources?

Biodiversity is becoming Norway's "new oil," with deep fjords mined for new microbes—not for use as raw materials, but for genomes that might encode the next breakthrough antibiotic (see Delgado's article in this collection; Taffel 2021). Scientists from the United States and Europe go bioprospecting in exotic locations for novel microbial functions to funnel into drug discovery pipelines. Meanwhile, more familiar microbes are being exploited as "chassis," or physical housings for genetic parts, toward developing a theoretically endless array of products and applications designed to replace established technology with biotechnology.

In a (bio)economy in which fossil fuels are out and genes are in, such modes of generating value are readily slotted into established economic paradigms as evident equivalents for their predecessors (Birch 2017).

Bioengineers have been criticized as wanting to revolutionize production while changing nothing about consumption (Endy and Ginsberg 2020). Meanwhile, Birch and Tyfield (2013) have pointed to "the fetishization of all things 'bio'" (p. 301) through which bio-driven reconfigurations of actors are sometimes theorized without adequately considering how bio-based modes of value generation differ from their predecessors along basic economic lines. Their argument is that bio-assets and bio-commodities often invoke fundamentally different financial paradigms. We should similarly expect that biological materials made valuable as informational resources will involve different material paradigms, compared to biological materials made valuable as physical resources.

Information resources are decoupled from physical bodies, but information is never entirely disembodied (Hayles 1999). Rather than construing informational resources as *representative* of material things, we might instead consider them as re-mediations, abstractions in a different modality with different affordances. Through this lens, we might also ask how or even whether these medializations are connected. A material-semiotic response—consistent with the idea that information is never merely a one-to-one translation or representation—is that they are connected when those who enact them do the *work* to connect them, to associate them as being or being about "the same thing" (Mol 2002). That is, there are choices to be made.

My argument here is that doing the work to maintain connections among creatures and resources that bud from them allows that creatures might themselves have a stake in their own development. I further argue that discussions of how to responsibly develop digital resources *should* keep such possibilities open because this move opens a route toward realizing questions about the "goods" of technology development as more-than-human concerns (Latour 2004; Szymanski, Smith, and Calvert 2021). Making decisions with the interests and well-being of other creatures in mind requires listening to them—only possible if we first remember that decisions involve creatures to whom we can listen—and then cultivating communicative capabilities with them. Understanding bio-informational resource development as multiplying the practices through which we connect with them affords possibilities toward bringing other-than-human voices into conversations organized through Western worldviews, with ethical and epistemic consequences.

I mobilize "extraction" as an actor's category employed by social scientists. Conventional resource extraction diminishes the supply of a material at its origin and increases supplies of the resource derived from it. The same

does not hold for informational resources, wherein a microscopic quantity of the original material may suffice to generate any quantity of associated value. Joseph Millum (2010) observes that markets therefore apply to genetic resources in a qualitatively different way because the first person to sell an informational resource substantially reduces the value of the same information owned by others. Focusing on the originating material rather than the market system suggests an additional difference. Instead of subtracting, these extractions add. They displace and transform bio-remediations which add to the instantiations of a bio-informational thing, or what we might do the work to make coherent as an organism-technology.

The voice of the "bio" is notably absent in discussing whose interests count in the valuation and development of bio-resources, at least through Western lenses of responsible research and fair benefits-sharing (contrast Millum 2010 with Gudynas 2019). Other worldviews for organizing conversations about value—the Latin American concepts collectively known as buen vivir, for example (Gudynas 2011; 2019)—make multiple varieties of value legible, including those grounded in the perspectives of other-than-humans. These strategies could inform modes of accounting for social dimensions of information-based technologies, particularly given definitions of "society" not restricted to humans exclusively (Latimer and Miele 2013). However, those connections are unlikely or impossible if creatures are not connected with informational resources from which the "bio" has been distanced. In contrast, maintaining connections among organisms and the information technologies they promulgate ramifies conditions of possibility for accounting for more-than-human modes of knowledge and care, even within Western framings of "responsible" biotechnology development. We do different things with organisms than with technologies, so realizing something as an organism-technology has practical consequences.

Accomplishing this move requires choosing to hold onto living organisms as the context for biotechnology development wherein biological parts are defined in relation to biological wholes. I employ snowflake yeast, a form of the budding yeast *Saccharomyces cerevisiae* with a distinctive growth habit (Ratcliff et al. 2015), as a physical metaphor for how organism-technologies as assemblages may be traced. Budding yeast's development, when viewed as a "multicellular" snowflake, exemplifies how living things may simultaneously function as organisms, cells, technologies, physical and digital resources.

I begin by introducing snowflake yeast as a biological phenomenon. Thereafter, my argument is organized as a series of buds, inspired by the growth habits of budding snowflake yeast wherein each bud extends from

and remains connected to its parent, aggregating without necessarily proceeding in straight lines or a single direction. To be clear, I am adamantly not suggesting that humans should not manipulate yeast to extract value from it. Rather, I am suggesting that the myriad technologies derived from living things should not be cut apart to disentangle and commodify bioinformation resources at the expense of developing "simultaneously ethical and epistemic" (Candea 2013, 107) capacities for realizing multispecies interdependence in a bioeconomy-driven age (Calvert 2008; Frow 2013).

Snowflake Yeast

Budding yeasts, as a group, contrast with fission yeasts. Fission yeasts reproduce by splitting down the middle to form independent rod-shaped cells. Budding yeasts, in contrast, reproduce by pinching off bits of cytoplasm to form a small daughter cell that usually disconnects cleanly from the mother cell.[1] Some genetic mutations, however, lead to mother and daughter cells remaining connected, generation after generation, forming "snowflakes" that expand outward from a central progenitor (Ratcliff et al. 2015). Budding yeast does not bud in perfectly straight lines, and while buds reliably emerge from one and only one end of a cell, a yeast snowflake as a multicellular entity grows in multiple directions, occupying space as a clump rather than moving purposefully in one direction. Snowflake yeast are, in this way, an apt physical metaphor for how yeast has expanded and aggregated as yeast-based resources have been extracted. Snowflake yeast are a means of thinking through the shape of yeast development without imputing either a single progressive trajectory to where its development is going or any kind of subtraction upon the development of something new.

Where the initiative in this association lies is not straightforward, for yeast have domesticated humans as much as humans have domesticated yeast (Katz 2012).[2] Many humans have become adept at caring for yeast, and some—bakers, brewers, and winemakers, among others—have become uniquely attuned to yeast's needs. Such established human–yeast relations have continued to change through bioengineering and its neighboring biotechnologies. Employing yeast as a platform, a cell factory, and a chassis (as is often the case in metabolic engineering and synthetic biology) tends to position yeast as the thing being worked upon, not a thing doing work. Imagining yeast as a computer program (Szymanski 2018a), as in the synthetic yeast project discussed below, positions yeast as a source of information, not a source of physical material and physical labor as yeast are in

brewing and baking. These shifts have largely been enabled by genomics, whole-genome sequencing, and the apparatuses of control produced through the perception of comprehensive biological understanding they afford (Stevens 2013; Szymanski, Vermeulen, and Wong 2019). Simultaneously, yeast's "metabolic labor" (Beldo 2017) has done the heavy lifting not only in traditional food and beverage production but in other industrial fermentations to produce pharmaceuticals, biofuels, or alternative food proteins. Yeast genomes have been extracted from yeast bodies, and yeast-derived genetic parts from yeast genomes, to ramify additional value chains. One yeast-working repertoire (Leonelli and Ankeny 2015) buds from another.

As yeast is mobilized in different forms—as new buds emerge from parents—the results are additive, not subtractive. Digitizing yeast, relocating its genome from cells in Petri dishes to online databases, changes the shape of yeast and possibilities for working with it everywhere.[3] Simultaneously, these additions neither eliminate nor override the possibility of working with yeast in ways that do not depend on genomics, even as work with physical yeast bodies must be seen differently in relation to these developments. Separating "yeast" from yeast bodies expands the range of people who work with yeast. The same move makes it easier to reduce yeast solely to their instrumental value as defined through a particular use. Disconnecting yeast's value from yeast's creatureliness makes it easier to disconnect human goods (or, properly, the goods of specific humans) from other-than-human interdependencies. In contrast, retaining the conceptual morphology of the snowflake, so as to understand organism-technologies as assemblages of diverse morphological instances, enables holding onto human goods as necessarily entangled with other-than-human goods.

The central progenitor in this particular snowflake is called S288C. S288C is a standard laboratory strain of *S. cerevisiae* developed in the late 1950s in Berkeley, California, by Robert Mortimer, then a young medical physicist. Through Mortimer's willingness to share and the yeast's winning personality—reliable, easy to grow, undemanding—S288C became a cornerstone of the yeast genetics community and the foundation of its later digital instantiations (Langer 2016). S288C is itself a daughter of many mothers with a family tree that includes bakers and brewers' yeasts, yeasts found on discarded fruit in domestic orchards, and yeasts brought back on the rinds and peels of exotic produce from overseas trips—a good reminder that microbes in the laboratory always connect to microbes elsewhere.

Bud—Digitizing Yeast by Sequencing the Yeast Genome Enables Moving "Yeast" Online

When sequencing the complete genome of a eukaryote became a reasonable technical proposition in the 1980s, yeast was an obvious choice.[4] S288C had become a laboratory standard in the 1970s, fueled by Mortimer's "stock center," which provided uniform cultures to researchers, such that geographically and temporally distant yeast researchers could share resources and collate findings as if working on "the exact same cell" (Boone 2014, 436). Sharing strains and resources facilitated the expansion of a community working with that cell, plus collective resources that linked physical cells with shared tools: genetic maps, biochemical markers, modes of molecular manipulation, and specialized strains, among others. Such collective resources encouraged the conceptual and physical organization of an international "yeast community" oriented around what could be described as a single project: "the 'solution' of the organism" (Johnston 2000, 617).

Sequencing the yeast genome seemed possible not only because of the traction obtained by the standardized cell but—as in so many model organism communities—because of the existing coordination of yeast laboratories around common resources and the ethos of cooperation firmly established among them (Leonelli and Ankeny 2013). Extracting genome from cell was, however, compelling in different ways to different agendas. In the United States, yeast was seen as a pilot for the Human Genome Project—a means of developing technologies to sequence a much larger and more important genome with more speed and less expense. For the European Community's science directorate, where the project initially germinated, yeast genome sequencing became an ideal solution to the perceived problem that Europe was failing to compete with American and Japanese biotechnology. As a "capacity building exercise" (Parolini 2018) distributed among many European yeast laboratories, yeast could coordinate scientists across Europe and provide steady work to nurture nascent private sequencing companies, all while facilitating research–industry ties by developing an organism with clear economic value. And in Japan, yeast became tied to supporting a state-of-the-art sequencing center at RIKEN, Japan's largest biology research institute (Cook-Deegan 1994).

These three initially independent efforts became an intercontinental collaboration when leaders of the European project chose to prioritize completing a reference genome on time over completing a reference genome by themselves (Langer 2016). What resulted was a complete and remarkably high-quality reference genome for (more or less)[5] S288C and, through the

initiative of the American contributors, a digital database providing access to that sequence. From its release in 1996, the Stanford-based Saccharomyces Genome Database (SGD) has maintained the reference sequence and collated and curated a steadily expanding range of yeast genome-associated resources, all fully accessible, freely shared, and entirely online. Where the locus of yeast's collective physical resources had been Mortimer's physical repository of yeast strains, the locus of yeast's digital resources became the SGD.

Bud: Extracting the Genome from the Cell Enables "Yeast" to Live Apart from Yeast Bodies

Subsequent to publication of the reference genome sequence, "the yeast genome" came to index three distinct but connected phenomena: a physical set of molecules housed within cells, a digital text available online, and a historic event referenced as an important cultural touchstone in the scientific literature (Szymanski, Vermeulen, and Wong 2019). In contrast to working with a physical set of molecules, working with the digitized genome did not tie researchers to cells with any definite temporal or geographic location. The S288C reference sequence was compiled from fragments generated by nearly 600 (credited) individuals in ninety-four laboratories across nineteen countries using varied techniques from manual Sanger and Maxam-Gilbert sequencing to then-advanced automated ABI sequencers. Those fragments were generated from several different cosmid and yeast artificial chromosome (YAC) libraries built from distinct and geographically distant yeast cultures. Not until 2010, when researchers affiliated with the SGD "resequenced" S288C from a single colony growing in Palo Alto, could the reference genome be said to refer to any one physical yeast community (Engel et al. 2013). The reference sequence did not represent a set of physical molecules located in a yeast culture. It was a separate informational resource with a life of its own, lived apart from yeast cells, a "yeast" lineage that continued to replicate, expand, and diverge *in silico* through maintenance work and other activities of humans and software oriented around the sequence rather than any group of cells.

Bud: Extracting a Standardized Yeast Cell from Yeast Bodies Enables Yeast to Become a Universal Cell

Yeast is widely used as an explanatory model for human and other eukaryotic cells, but also sometimes stands in for whole organisms; in aging experiments, for example, prolonging the life of a single yeast cell is

sometimes interpreted in terms of prolonging human lives (e.g., Oliveira et al. 2017). The "yeast group" active at Cold Spring Harbor Laboratory through the 1970s and 1980s championed their organism as suitable for studying any biological question—including, in their later careers, handedness and hair growth patterns (Klar 2003). Ira Herskowitz, their contemporary at the University of California San Francisco, called yeast "the universal cell"—experimentally tractable, malleable, and able to model virtually any eukaryotic phenomenon (Herskowitz 1985).

Hannah Landecker (2007), in *Culturing Life*, traces how cells of human and other multicellular organisms have been separated from bodies to become technologies with distinct temporalities (e.g., through freezing) such that, through cell culture, many scientists can study "the same cell" in disparate times and places. Yeast may seem to already be single-celled, but laboratory yeast has likewise needed to be separated from the larger body in which it typically lives. Clonal populations have been extracted and isolated from yeast as it typically lives in heterogenous communities. S288C and other standardized laboratory strains must be *temporally* frozen, maintained as evolutionarily inert standards, to be aligned as "the same cell" across time and space. Standardized laboratory yeast has distinct capacities and characteristics; it becomes a different organism in comparison to yeast in the brewery or bakery (Borneman and Pretorius 2015). Simultaneously, each remains connected to and continues to influence the development of the other, as is evident, for example, in the lists of companies and trade organizations for which prominent yeast geneticists were asked to provide advice (Langer 2016; Ira Herskowitz Papers 1974-2003).

Landecker's work suggests mammalian cell culture as a necessary predicate to understanding yeast as the universal eukaryotic cell, insofar as cell culture enabled envisioning and manipulating cells as physically separate from whole organisms. By separating cells from bodies, yeast, human, and myriad other cells can be lined up, made equivalent to each other, and so used as models for one another. Similarly, by separating genomes from bodies, digitized genomes can be fixed in time, lined up, and compared as functional and structural equivalents.

Bud: Extracting Tools as Objects from Creatures as Living Things Distances Technologies from Organisms

Scientific uses of yeast as tools are often not organized around the "whole" yeast, and even whole yeast bodies do not yield the same fleshy reminders of their aliveness as mice, zebrafish, or other model organisms typically

studied intact. On the contrary, yeast is often employed as a container—a bag of chromosomes or genes that are themselves the objects of scientific interest, and which may or may not have originated in yeast. The SGD is organized around genes and around open reading frames, promoters, and other fragments of DNA that can be handled as if they were genes. Genes are the handles one holds while moving through the database's resources; cell type or strain becomes background, noticeable only if you look for it. Whole yeast cells appear in the guise of phenotypes—single-dimension, often binary behaviors invoked to characterize genes. The whole cell appears in the SGD logo where, evocatively, a budding yeast cell is the blank container within which the "SGD" resides.

Much scholarship around biotechnology and model organisms has addressed how organisms become technologies. Yeast, however, was already a human technology long before it began its career in laboratory science such that, for example, the boundaries that bio-objectification relies on being transgressed by biotechnology were less sharp and arguably absent in yeast's case even before biotechnology intervened (Holmberg, Schwennesen, and Webster 2011). Yeast is described in and outside of scientific communities as a friend of humanity and a pillar of civilization, an old tool being further refined, and a source of medical therapeutics such that scientists not only *can* but *should* continue to engineer yeast without meddling with "nature."

Yeast is both a tool itself and a source of other tools, which retain their yeastiness by virtue of name and lineage even when separated from yeast bodies. Yeast artificial chromosomes (YACs), for example, are constructed with telomeres, centromeres, and autonomous replicating sequences (ARS) from yeast, even while the backbone or starting point for the construct is a plasmid from bacteria (Murray and Szostak 1983). The DNA stored in the YAC—the reason for its construction—may originate anywhere and destined for many other cell types. Scientific activities to extract tools from yeast expand what "yeast" is and distance yeast resources from yeast bodies. This distancing makes it easier to work with yeast as a technology without also working with it as an organism.

Bud: Extracting Genomes from Organisms Enables Putting Them Back Again

Where the SGD takes yeast apart, the synthetic yeast project aims to put yeast back together.[6] The synthetic yeast project, or *Saccharomyces cerevisiae* 2.0, is the first effort in synthetic biology to construct a complete

eukaryotic genome[7] entirely from algorithmically redesigned, laboratory-synthesized DNA. In synthetic biology, yeast and other cells are most often "chassis" or "platforms" on or within which engineering takes place. The organism may be entirely absent from discussions concerned with engineering genetic pathways or circuits, and cellular responses to intracellular engineering are routinely construed as interruptions or "bugs" that need to be engineered away. The synthetic yeast project is a notable exception to this general pattern (Calvert and Szymanski 2020). This project is about re-placing a digital yeast genome: editing an informational text on a computer, transforming that *in silico* text into physical molecules, and convincing yeast to take up and incorporate those molecules into the physical genome it already contains. Yeast must be convinced to perform this final step of making the digital physical again, and their responses to redesigned DNA are the ultimate criteria by which the success of synthetic biologists' design work is assessed (Szymanski 2018b). Yeasts' capacity for action and response brings the liveliness of the tool back into the scientific picture, making yeast's creaturely characteristics impossible to ignore.

The synthetic yeast project revolves around chromosomes rather than "genetic parts" with defined functions, as do most synthetic biology projects oriented around specific applications. Yeast, however, has not always been characterized by the sixteen chromosomes now being redesigned. As late as 1986, Hershel Roman, a leading yeast geneticist at the University of Washington, reported that yeast might have sixteen or seventeen chromosomes—"the number hasn't been settled to everyone's satisfaction" (Roman 1986, 3). Chinese scientists mapping chromosome V in 1992 still reported the number as "about seventeen" (Zhu and Kuang 1992). Four years later, following the cooperative work of the yeast genome sequencing project, yeast's chromosome count was stably fixed at sixteen (Goffeau et al. 1996).

Fixing the chromosome count makes it possible to change it again, in that possessing a complete map of the yeast genome enables rearranging its geography. Among other changes, the synthetic yeast genome extracts all tRNA genes—essential for translating messenger RNA into chains of amino acids—from their typical locations scattered around the genome and consolidates them into a wholly new "neochromosome" (Richardson et al. 2017). Endeavoring to keep tRNA genes from moving has called for insulating them with DNA fragments extracted from other yeast species, which become part of *S. cerevisiae* through context and function when sequence alone would indicate a different parentage (Walker 2017). This plan

embodies a central design principle of the project, improving yeast genome stability so that the genome changes if and only if a scientist changes it.

To maintain the same chromosome count in the finished synthetic yeast cell, two of the smallest chromosomes will be linked to compensate for the addition of the neochromosome. At the project's outset, it remained an open question whether chromosome count matters to yeast in the same way that it matters to humans. It now appears that it does not, as viable yeasts have been constructed with the entire genome consolidated into a single giant chromosome (Shao et al. 2018). This example demonstrates how yeast might be considered users of redesigned DNA, whose responses about which designs support growth and survival must be taken into account before any additional applications can occur further downstream (Szymanski 2018b).

The synthetic yeast project envisions yeast as a computer program to be edited, refactored, and debugged (Szymanski 2018a). Its anticipated *end* users and stakeholders are biotech entrepreneurs, pharmaceutical companies, Silicon Valley start-ups, and scientific innovators. Looking down into the lab rather than outside it, however, we might see that yeast itself is a stakeholder with a "say" insofar as it is being asked to change and may refuse to do so. What is a resource to be mined (see: https://yeastmine.yeastgenome.org/yeastmine/begin.do), a participant to be involved, or a stakeholder who may accept or refuse a new technology? Responses to this question depend on where one draws the line between creature and technology or, alternately, where (as I suggest here) one does not.

Bud: Whose Labor Generates Value?

Jenny Bellon has worked as an expert in yeast mating at the Australian Wine Research Institute, constructing new yeast hybrids by mixing specimens of different yeast species in the same tube and waiting.[8] Rare yeast matings occur, rarely, when two cells whose genetic disparities mean that they would not ordinarily mate sit on top of each other for long enough. Bellon's work chiefly concerns developing precise experimental conditions that permit separating rare-mating progeny from cells which have not mated (Bellon et al. 2018). We might say that the yeast, whom Bellon sometimes describes as her children, do much of the work.

Yeast works across biotechnology. Crucially, while synthetic biologists have numerous options for linking bits of DNA, the most reliable strategy for difficult construction projects is assembly *in yeasto* (Mitchell et al. 2015). Yeast are experts at a construction technique called homologous

recombination, lining up matching sequences on separate DNA fragments and integrating them via a mechanism that scientists have yet to comprehensively describe or functionally mimic. Employing homologous recombination involves transforming yeast with appropriately designed sections of DNA—a simple procedure—and waiting; the scientist's primary work is identifying cells that have correctly assembled the DNA construct. In this process, yeast play the role of coworkers more than tools, being active participants in creating what *could* be called the surplus value extracted from their bodies: DNA sequences and resulting metabolic products that are far more valuable than the sugars on which yeast are fed.

Les Beldo (2017) has suggested that we consider the excess over and above what humans invest in obtaining value from animals and plants as the product of those creatures' "metabolic labor." Beldo uses this phrase to direct attention to the "exploitation at the center of human-animal relations of production" (p. 118) by making animal labor analogous to the exploited labor of working human classes. I wonder, however, what bringing other creatures into anthropogenic, anthropocentric conceptions of labor does for structuring multispecies relationships.

"Metabolic labor" usefully points to violence that occurs when animals are made to live for human use. Less helpfully, it constructs an equivalence between how human lives are understood to involve work and how animal lives are understood to involve work. In Beldo's example of the wretched Cornish rock broiler chicken, producing protein from grain becomes the work of the chicken. The analogy demands that work be separated from living when the process of living is exploited, such that thinking about the chicken as a creature needs to be separated from thinking about the chicken as an edible body.

Michael Pollan (2006) portrays a different view of living as labor in his stories about Polyface Farm, where the human-in-chief, Jack Salazar, says that cows and chickens do most of the work. Here, ascribing work is a way of assigning value to the life of the cow and the chicken—a view enabled, perhaps, by Salazar's obvious disinclination to distinguish his own life and work in a way that would enable a corporation to extract one from the other. The Cornish rock broiler chicken was developed entirely for the sake of being an edible body and is poorly suited to being a living creature. Salazar would have no use for this chicken that cannot walk well enough to perform a chicken's job at Polyface Farm—cleaning up the grubs from cow-trodden fields—and that can never satisfy Salazar's end goal for chickens, of living so as to express their creaturely distinctiveness. A Cornish rock broiler chicken cannot work for him because it cannot work well by living well.

Beldo identifies a prejudice against animal labor not being understood as labor. That prejudice could equally be understood in reverse, as a prejudice toward applying *labor* to all creatures with the presumption that they must be not only like humans, but like a narrow subset of humans. While the first error is a form of human exceptionalism, the second is a different form of human exceptionalism in the guise of human universalism—that what applies to a subset of human animals can and should be extended to understanding all other animals and that human experience is representative of animal experience.

Microbial life may be put to work, but to say that microbial labor is exploited speaks to a particular view of how microbes *should be* as much as to what humans *do with* them. Metabolic *labor* makes human relating with other species wholly about production and seems to offer the laboring animal the limited options of either passively complying or actively resisting. *Work* affords more diverse possibilities, beyond compliance or refusal, allowing that yeast may productively contribute new information in response to human demands (or requests, or invitations, or stories). Synthetic biologists may work on, with, in, or for yeast. Many examples of human working practices with sourdough starters, artisan winemaking, or craft brewing—multispecies working practices which at least sometimes exist outside of highly standardized industrial contexts oriented around maximizing surplus value—involve attitudes of seeking understanding, of care, and of living with and working with. These are not utopian practices. They involve death, loss, and frustration (e.g., Brice 2014). They also involve being responsive in the daily specificities of multispecies work.

Metabolic labor implies that we should not exploit the lives of other creatures. This position is impractical if plants are understood to be creatures and extracting value from bodies is understood to be exploitation. It is equally untenable with respect to microbes, some of whom—in their life and their death—indispensably contribute to the functional integrity of human bodies. The alternative suggested by Haraway (2008; 2016), Puig de la Bellacasa (2015), Krzwoszynska (2019), and others interested in *multispecies care*, is to ask how we may live well with other creatures, enabling more productive lines of thought about how the chicken and the human, or the yeast and the human, might have good lives together. There is no question that the miserable meat-production chickens Beldo describes do not live well. One compassionate response might be not to eat chicken and to advocate that others do the same. Another might be to raise delicious chickens that can live good chicken lives at farms where care is taken for all creatures—Salazar's approach.

Beldo (2017) acknowledges stretching the concept of labor to the extremes of what it can do, but argues that labor is the most apt term for animal vitality "within the existing vocabulary of capitalist production" (p. 125). This statement leaves wide open the possibility of developing more satisfactory alternatives *outside* the existing vocabulary of capitalist production. Rather than finding an analytic to apply to existing practice, I am more interested in opening up possibilities with respect to new practices, an interest made possible by the relatively open-to-experimentation fields with which I engage—synthetic biology, microbiomes, winemaking (all in contrast to factory farming)—and by an organism unlikely to incite ethical concerns (in contrast to chickens). This is, to me, a very good reason to work with creatures such as yeast because they afford such possibilities.

Bud: Yeast as a Good for Whom?

Whom and what are yeast good for? These are logical questions if we imagine yeast as a resource whose extraction and development will be good for some humans, but not for all equally. These questions also suggest that those important to extracting value from yeast are the users of yeast-based resources, eliding the possibility that yeast might itself be considered a stakeholder in its own development. The question that would seem to follow—what is good for yeast?—might also seem to advocate for an ethics of microbes (see Cockell 2004), or a utopian attitude toward more-than-human friendship. However, to suggest the possibility of caring for, about, and with microbes is not at all to suggest that this form of care resembles that appropriately applied to humans and other macrofauna—just as characterizing yeast and chickens as coworkers is not to suggest that we should bring them coffee or assign them human-appropriate offices. Living well means very different things for different creatures. Creatures may be seen as interested parties in the bioeconomic systems in which humans interpolate them *without* imagining that all creatures therefore occupy chairs of equal size and shape around some ideal imaginary multispecies table.

Being a stakeholder begins with having a voice. Having a voice requires being recognized as capable of communicating, inviting the possibility that others may listen. Humans do violence to their *own* capacity to learn from and be enriched by the voices of others when they make creatures tools and tools alone that can have no voice. By divorcing organism-derived technologies from organisms, we humans may cultivate capacities to forget our inevitable interdependences across more-than-human worlds and may attenuate capacities to be responsive to others in the daily specificities of our work.

In lieu of asking whose "good" yeast resource extraction serves, we might instead ask: what does it mean to live and work well with creatures who are simultaneously tools? Kelly Donati (2019) suggests multispecies conviviality—con-vivial, literally, to live with—as a strategy for considering what it is to eat well with creatures we also eat. Donati argues that creatures who are and who are not human should all have a voice in what it means to live well on a multispecies farm. For the sheep and dogs on whom she focuses, that means having space to express their needs to humans who consider the farm itself as an organism, the parts of which variously support the whole. Sheep, as farm animals who may be coworkers, technologies, and dinner, need to be accounted for as stakeholders whose voice matters in the sustainability of the farm system.

Working with yeast and other creatures as both creatures and tools need not be contradictory if yeast can be multiple and multiplied. On the contrary, improving human capacities to "listen" to other creatures' voices—to attend, to cultivate the capacity to respond, to become response-able—should also improve research outcomes. As has been noted by many multispecies scholars, being response-able to research organisms' participation as creatures travels with becoming open to observations beyond researchers' initial expectations, yielding both ethical and epistemic benefits (Candea 2013; Despret 2013; 2014). Questioning what it means to live and work and indeed eat well with creatures who are also tools and technologies is about locating perspectives from which humans may themselves be coworkers rather than always only controllers of other species, *even* when multispecies interactions are oriented around extracting value from living things for human benefit.

Conclusion

Because their material entanglements differ, critiques that appropriately apply to the extraction of material resources do not necessarily apply to the extraction of digital resources, not because the latter are not material, but because they are differently material. Digital resources are nevertheless subject to one of the same propensities as material resources—disentanglement from their origins—yet to different effect (Junka-Aikio and Cortes-Severino 2017). In the digital case, such disentanglements are liable to limit opportunities to realize (in both senses of the word) how biotechnical developments invoke more-than-human worlds. Cutting genome sequences and other digital resources away from creatures makes them wholly about the human choices made in their extraction, closing off consideration of

how these creatures may participate in their own development: to listen to, be response-able with, and learn from them. An understanding of the technology—the digital genome, for instance—might be mistaken for an understanding of the creature such that the creature's capacity to surprise, respond, or interrupt (Buller 2015) *beyond* the scope of the abstracted digital resource, is curtailed. Creaturely capacities to remind that they hold stakes in human well-being, and vice-versa, are similarly curtailed.

Extraction is about transformation, about *making* a resource. As Junka-Aikio and Cortes-Severino (2017) have observed in arguing for why cultural studies should attend to "extractivism," "the discursive construction of something as a 'resource' always entails . . . regulat[ing] how the relationship between nature and society is imagined and enacted" (p. 180)—or, we might say, how relationships among humans and other-than-humans are enacted. Doing the work to maintain connections among remedializations of creatures that become resources, I argue, may open up relationships that digital extractivism otherwise shuts down, leaving human societies more permeable to their more-than-human dimensions. In practical terms, envisioning organism-technologies enables the possibility of asking what it means to care for and to live well with tools that are also creatures. This framing differs substantially from envisioning laboring creatures from whom surplus value is extracted. While the latter suggests that creatures are exploited and that we have a moral obligation in the name of multispecies social justice to stop exploiting them, the former invites investigating what it means to live well with the variety of creatures upon whom our collective well-being depends.

Snowflake yeast interrupts yeast geneticists because it sticks to the walls and orifices of culture vessels; it refuses to lose its attachments and so gloms up equipment built with better-behaved cells in mind. I suggest that STS researchers should allow snowflake yeast to interrupt us for similar reasons. We do different things with creatures than with tools. They mandate different ethical concerns and raise different matters of care (Puig de la Bellacasa 2011) because creatures are concerned with their own interests while tools are built to serve the purposes of others. Creatures such as *S. cerevisiae* fit both descriptions: they have been constructed to serve specific purposes, and they have lives of their own. As yeast-based technologies are extracted from recognizably living yeast bodies, entanglements across the things we do with tools and the interests of other creatures become more difficult to see. That is an ethical problem, for the violence thereby enabled against other creatures and against humans in our many-faceted interdependences with them. It is also an epistemic problem, in that removing the

organism from the picture means that it can no longer interrupt, surprise, and challenge.

My larger point is that natural resource extractions raise different concerns when the concerning resources are chiefly informational, in contrast to conventional extractions of physical materials. How the materials of "digital" bio-extractions travel and form connections means that their loci of concern require re-examining apart from established extractivist critiques. Observers with critical eyes should not assume that theorizations of natural resource extraction apply to "extracted" information resources, any more than we should assume that no violence is done because different kinds of violence pertain.

Acknowledgments

I thank the Engineering Life and TRANSGENE research teams at the University of Edinburgh for their collegiality and intellectual support, along with participants in the workshop hosted by Ana Delgado at the University of Oslo that prompted this manuscript. I am grateful for feedback from Ana Delgado, Susanne Bauer, and the two anonymous reviewers, all of which led to substantial improvements.

Declaration of Conflicting Interests

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

Funding

The author(s) disclosed receipt of the following financial support for the research, authorship, and/or publication of this article: This article received funding from European Union Horizon 2020 (Grand ID: 678757), European Research Council (Grand ID: ERC 616510-ENLIFE), and The Biological and Biotechnological Sciences Research Council (Grant ID: BB/M005690/1, ERASynBio-IESY).

ORCID iD

Erika Amethyst Szymanski https://orcid.org/0000-0002-6321-8897

Notes

1. Yeast are always female, by disciplinary convention because they can all give rise to daughter cells.
2. See Larson and Fuller 2014, for a discussion of the multiple domestication pathways supported by archaeological and genetic evidence, including pathways initiated by creatures who are not human. See Baker et al. 2015, for a discussion of the likelihood that baker's and brewer's yeasts came into domestic relationships with humans on numerous, separate occasions.

3. For example, new yeast strains for producing beer and wine have been enabled by detailed studies of yeast genomics that map relationships among strains domesticated to particular purposes, and identify potential untapped reservoirs of genetic diversity (Gallone et al. 2016).
4. The research described in this and the following two sections came about through a European Research Council-funded project on the history of yeast, human, and pig genome sequencing (TRANSGENE: Medical translation in the history of modern genomics, led by Miguel Garcia-Sancho) during which I reviewed primary scientific literature, conducted oral history interviews, and visited several archives pertaining to significant yeast genomicists.
5. Though the reference sequence is "of" S288C, it was created through compiling sequence data from several closely related strains (Engel et al. 2013).
6. The research described in this and the following section stems from my work as a postdoctoral STS researcher with the synthetic yeast project, funded through a grant (BB/M005690/1, ERASynBio-IESY) from the Biological and Biotechnological Sciences Research Council co-led by a key synthetic biologist-member of the synthetic yeast consortium and a social scientist. I spent one or two days each week working with a synthetic yeast lab, conducted interviews of about twenty scientists contributing to the project, and participated in numerous conferences, workshops, and other events.
7. Eukaryotic genomes, in comparison to prokaryotic genomes belonging to bacteria and archaea, are (often much) larger and divided up into multiple chromosomes.
8. I visited with Bellon at the Australian Wine Research Institute to discuss her yeast mating work in November 2016.

References

Baker, Emily Clare, Bing Wang, Nicolas Bellora, David Peris, Amanda Beth Hulfachor, Justin A. Koshalek, Marie Adams, Diego Libkind, and Chris Todd Hittinger. 2015. "The Genome Sequence of Saccharomyces Eubayanus and the Domestication of Lager-brewing Yeasts." *Molecular Biology and Evolution* 32 (11): 2818-31.

Beldo, Les. 2017. "Metabolic Labor Broiler Chickens and the Exploitation of Vitality." *Environmental Humanities* 9 (1): 108-28.

Bellon, Jennifer R., Christopher M. Ford, Anthony R. Borneman, and Paul J. Chambers. 2018. "A Novel Approach to Isolating Improved Industrial Interspecific Wine Yeasts Using Chromosomal Mutations as Potential Markers for Increased Fitness." *Frontiers in Microbiology* 9 (July): 1442.

Birch, Kean. 2017. "Rethinking Value in the Bio-economy: Finance, Assetization, and the Management of Value." *Science, Technology, & Human Values* 42 (3): 460-90.

Birch, Kean, and David Tyfield. 2013. "Theorizing the Bioeconomy: Biovalue, Biocapital, Bioeconomics or . . . What?" *Science, Technology, & Human Values* 38 (3): 299-327.

Boone, Charles. 2014. "Yeast Systems Biology: Our Best Shot at Modeling a Cell." *Genetics* 198 (2): 435-37.

Borneman, Anthony R., and Isak S. Pretorius. 2015. "Genomic Insights into the Saccharomyces Sensu Stricto Complex." *Genetics* 199 (2): 281-91.

Brice, Jeremy. 2014. "Killing in More-than-human Spaces: Pasteurisation, Fungi, and the Metabolic Lives of Wine." *Environmental Humanities* 4 (1): 171-94.

Buller, Henry. 2015. "Animal Geographies II Methods." *Progress in Human Geography* 39 (3): 374-84.

Calvert, Jane. 2008. "The Commodification of Emergence: Systems Biology, Synthetic Biology and Intellectual Property." *BioSocieties* 3 (4): 383-98.

Calvert, Jane, and Erika Szymanski. 2020. "A Feeling for the (Micro)Organism? Yeastiness, Organism Agnosticism and Whole Genome Synthesis." *New Genetics and Society* 39 (4): 385-403.

Candea, Matei. 2013. "Habituating Meerkats and Redescribing Animal Behaviour Science." *Theory, Culture & Society* 30 (7–8): 105-28.

Cockell, Charles S. 2004. "The Rights of Microbes." *Interdisciplinary Science Reviews* 29 (2): 141-50.

Cook-Deegan, Robert. 1994. *The Gene Wars: Science, Politics, and the Human Genome*. New York: W. W. Norton.

Despret, Vinciane. 2013. "Responding Bodies and Partial Affinities in Human–Animal Worlds." *Theory, Culture & Society* 30 (7–8): 51-76.

Despret, Vinciane. 2014. *Domesticating Practices: The Case of Arabian Babblers*. New York: Routledge International Handbooks.

Donati, Kelly. 2019. "'Herding Is His Favourite Thing in the World': Convivial World-making on a Multispecies Farm." *Journal of Rural Studies* 66 (February): 119-29.

Endy, Drew, and Alexandra Daisy Ginsberg. 2020. "Must We Revolutionize Nothing?" Live online with Ferment TV by Gingko Bioworks, 1 July 2020. Accessed July 1, 2020. https://faberfutures.com/projects/ferment-tv/ferment-tv-05-must-we-revolutionize-nothing/.

Engel, Stacia R.Fred S. Dietrich, Dianna G. Fisk, Gail Binkley, Rama Balakrishnan, Maria C. Costanzo, Selina S. Dwight, et al. 2013. "The Reference Genome Sequence of Saccharomyces Cerevisiae: Then and Now." *G3: Genes|Genomes|-Genetics* 4 (3): 389-98.

Frow, Emma K. 2013. "Making Big Promises Come True? Articulating and Realizing Value in Synthetic Biology." *BioSocieties* 8 (4): 432-48.

Gallone, BrigidaJan Steensels, Troels Prahl, Leah Soriaga, Veerle Saels, Beatriz Herrera-Malaver, Adriaan Merlevede, et al. 2016. "Domestication and Divergence of Saccharomyces Cerevisiae Beer Yeasts." *Cell* 166 (6): 1397-410. e16.

Goffeau, A.B. G. Barrell, H. Bussey, R. W. Davis, B. Dujon, H. Feldmann, F. Galibert, et al. 1996. "Life with 6000 Genes." *Science* 274 (5287): 546-67.

Gudynas, Eduardo. 2011. "Buen Vivir: Today's Tomorrow." *Development* 54 (4): 441-47.

Gudynas, Eduardo. 2019. "Value, Growth, Development: South American Lessons for a New Ecopolitics." *Capitalism Nature Socialism* 30 (2): 234-43.

Haraway, Donna J. 2008. *When Species Meet*. Minneapolis: University of Minnesota Press.

Haraway, Donna J. 2016. *Staying with the Trouble: Making Kin in the Chthulucene*. Durham, NC: Duke University Press.

Hayles, N. Katherine. 1999. *How We Became Posthuman: Virtual Bodies in Cybernetics, Literature, and Informatics*. Chicago, IL: University of Chicago Press.

Herskowitz, Ira. 1985. "Cell Biology: Yeast as the Universal Cell." *Nature* 316 (6030): 678-79.

Holmberg, Tora, Nete Schwennesen, and Andrew Webster. 2011. "Bio-objects and the Bio-objectification Process." *Croatian Medical Journal* 52 (6): 740-42.

Ira Herskowitz Papers. 1974-2003. San Francisco, CA: University of California, San Francisco Library Archives & Special Collections.

Johnston, Mark. 2000. "The Yeast Genome: On the Road to the Golden Age." *Current Opinion in Genetics & Development* 10 (6): 617-23.

Junka-Aikio, Laura, and Catalina Cortes-Severino. 2017. "Cultural Studies of Extraction." *Cultural Studies* 31 (2–3): 175-84.

Katz, Sandor Elix. 2012. *The Art of Fermentation*. White River Junction, VT: Chelsea Green.

Klar, Amar J. S. 2003. "Human Handedness and Scalp Hair-whorl Direction Develop from a Common Genetic Mechanism." *Genetics* 165 (1): 269-76.

Krzywoszynska, Anna. 2019. "Caring for Soil Life in the Anthropocene: The Role of Attentiveness in More-than-human Ethics." *Transactions of the Institute of British Geographers* 44 (4): 661-75.

Landecker, Hannah. 2007. *Culturing Life: How Cells Became Technologies*. Cambridge, MA: Harvard University Press.

Langer, Erika Michelle. 2016. "Molecular Ferment: The Rise and Proliferation of Yeast Model Organism Research." *PhD diss*. San Francisco: University of California.

Larson, Greger, and Dorian Q. Fuller. 2014. "The Evolution of Animal Domestication." *Annual Review of Ecology, Evolution, and Systematics* 45 (1): 115-36.

Latimer, Joanna, and Mara Miele. 2013. "Naturecultures? Science, Affect and the Non-human." *Theory, Culture & Society* 30 (7–8): 5-31.

Latour, Bruno. 2004. "Why Has Critique Run Out of Steam? From Matters of Fact to Matters of Concern." *Critical Inquiry* 30 (2): 225-48.

Leonelli, Sabina, and Rachel A. Ankeny. 2013. "What Makes a Model Organism?" *Endeavour* 37 (4): 209-12.

Leonelli, Sabina, and Rachel A. Ankeny. 2015. "Repertoires: How to Transform a Project into a Research Community." *BioScience* 65 (7): 701-08.

Millum, Joseph. 2010. "How Should the Benefits of Bioprospecting Be Shared?" *The Hastings Center Report* 40 (1): 24-33.

Mitchell, Leslie A.James Chuang, Neta Agmon, Chachrit Khunsriraksakul, Nick A. Phillips, Yizhi Cai, David M. Truong, et al. 2015. "Versatile Genetic Assembly System (VEGAS) to Assemble Pathways for Expression in S. Cerevisiae." *Nucleic Acids Research* 43 (13): 6620-30.

Mol, Annemarie. 2002. *The Body Multiple: Ontology in Medical Practice*. Durham, NC: Duke University Press.

Murray, Andrew W., and Jack W. Szostak. 1983. "Construction of Artificial Chromosomes in Yeast." *Nature* 305 (5931): 189-93.

Oliveira, Ana V., Rita Vilaça, Cláudia N. Santos, Vítor Costa, and Regina Menezes. 2017. "Exploring the Power of Yeast to Model Aging and Age-related Neurodegenerative Disorders." *Biogerontology* 18 (1): 3-34.

Parolini, Giuditta. 2018. "Building Human and Industrial Capacity in European Biotechnology: The Yeast Genome Sequencing Project (1989–1996)." dx.doi: 10.14279/depositonce-6693.

Pollan, Michael. 2006. *The Omnivore's Dilemma: A Natural History of Four Meals*. New York: Penguin.

Puig de la Bellacasa, Maria. 2011. "Matters of Care in Technoscience: Assembling Neglected Things." *Social Studies of Science* 41 (1): 85-106.

Puig de la Bellacasa, Maria. 2015. "Making Time for Soil: Technoscientific Futurity and the Pace of Care." *Social Studies of Science* 45 (5): 691-716.

Ratcliff, William C., Johnathon D. Fankhauser, David W. Rogers, Duncan Greig, and Michael Travisano. 2015. "Origins of Multicellular Evolvability in Snowflake Yeast." *Nature Communications* 6:6102.

Richardson, Sarah M.Leslie A. Mitchell, Giovanni Stracquadanio, Kun Yang, Jessica S. Dymond, James E. DiCarlo, Dongwon Lee, et al. 2017. "Design of a Synthetic Yeast Genome." *Science* 355 (6329): 1040-44.

Roman, Herschel. 1986. "The Early Days of Yeast Genetics: A Personal Narrative." *Annual Review of Genetics* 20 (1): 1-14.

Shao, YangyangNing Lu, Zhenfang Wu, Chen Cai, Shanshan Wang, Ling-Li Zhang, Fan Zhou, et al. 2018. "Creating a Functional Single-chromosome Yeast." *Nature* 560 (7718): 331-35.

Stevens, Hallam. 2013. *Life Out of Sequence: A Data-driven History of Bioinformatics*. Chicago, IL: University of Chicago Press.

Szymanski, Erika Amethyst. 2018a. "Remaking Yeast: Metaphors as Scientific Tools in Saccharomyces Cerevisiae 2.0." *BioSocieties* 14 (7): 416-37.

Szymanski, Erika Amethyst. 2018b. "Who Are the Users of Synthetic DNA? Using Metaphors to Activate Microorganisms at the Center of Synthetic Biology." *Life Sciences, Society and Policy* 14 (1): 15.

Szymanski, Erika Amethyst, Robert D. J. Smith, and Jane Calvert. 2021. "Responsible Research and Innovation Meets Multispecies Studies: Why RRI Needs to Be a More-than-human Exercise." *Journal of Responsible Innovation*. doi: 10.1080/23299460.2021.1906040.

Szymanski, Erika Amethyst, Niki Vermeulen, and Mark Wong. 2019. "Yeast: One Cell, One Reference Sequence, Many Genomes?" *New Genetics and Society* 38 (4): 430-50.

Taffel, Sy. 2021. "Data and Oil: Metaphor, Materiality and Metabolic Rifts." *New Media & Society*. doi: 10.1177/14614448211017887.

Walker, Roy Scott Kamla. 2017. "De Novo Biological Engineering of a tRNA Neochromosome in Yeast." *PhD diss*. Edinburgh, UK: University of Edinburgh.

Zhu, Yiwen, and Darren Kuang. 1992. "Construction of the Physical Map of Yeast (Saccharomyces Cerevisiae) Chromosome V*." *Cell Research* 2 (1): 25-34.

Author Biography

Erika Szymanski is an assistant professor of rhetoric of science at Colorado State University. Her research concerns words as scientific tools, particularly as they participate in what microbes become through what humans do with them, with a current focus on genome synthesis and engineering microbiomes.