Philosophy of Science (2026), **00**, 1–10
doi:10.1017/psa.2026.10237

PSA PHILOSOPHY OF SCIENCE ASSOCIATION
PHILOSOPHY OF SCIENCE

SYMPOSIA PAPER

A challenge for adequacy-for-purpose views of data modeling

Jacqueline Mae Wallis

Department of Philosophy, University of Pennsylvania, USA
Email: jacqwa@sas.upenn.edu

(Received 24 April 2025 UTC; revised 08 June 2026 UTC; accepted 08 June 2026 UTC)

Abstract

Alisa Bokulich and Wendy Parker (2021) provide an account of data modeling they call the pragmatic-representational view (PR view). According to this view, data models are akin to theoretical models in that they should be evaluated based on their adequacy for particular purposes. In this paper, I present a challenge for the PR view. I argue that a separation between data generators and users can prevent adequacy-for-purpose from being a good evaluative tool. I analyze an example from microbiome bioinformatics to illustrate my critique of Bokulich and Parker's view and then propose a tripartite disambiguation of the term 'data model'.

1. Introduction

Data play a central role in the sciences, and philosophical attention to an array of data practices has been growing. Whereas much of the focus in the philosophy of data analyzes what I'll here call "downstream" practices (data management, data distribution, data analysis, etc.), there is a need to attend to "upstream" practices as well (experimental design, data generation, data processing, etc.). A recent contribution to the philosophy of upstream data practices is Alisa Bokulich and Wendy Parker's pragmatic-representational view (PR view) of data and data models (Bokulich and Parker 2021).

Work on data models draws from broader philosophical literature on modeling practices in the sciences. The PR view, for instance, advocates that data models, like theoretical models, be evaluated based on their adequacy or fitness for particular purposes (Parker 2020). In this paper, I present a challenge for the pragmatic aspect of the PR view. Using an example from microbiome bioinformatics, I will argue that a separation between data generators and data users can prevent adequacy-for-purpose from being a good evaluative tool. I then propose a novel tripartite disambiguation of the term 'data model'. Both contributions stem from what I will call the data generator–user gap. This paper thus nuances Bokulich and Parker's PR view and

© The Author(s), 2026. Published by Cambridge University Press on behalf of Philosophy of Science Association. This is an Open Access article, distributed under the terms of the Creative Commons Attribution licence (https://creativecommons.org/licenses/by/4.0/), which permits unrestricted re-use, distribution and reproduction, provided the original article is properly cited.

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

improves the prospects for using the philosophy of data to support better data generation and processing in the sciences.

2. The PR View of Data Models and Evaluation Via Adequacy Considerations

Data models are typically defined as processed versions of data (Frigg and Hartmann 2020; Bokulich and Watkins 2023; Antoniou 2021). Data modeling, then, is the correcting, converting, smoothing, organizing, rectifying, regimenting, or otherwise adjusting of "raw" data. In scientific research, data models and data modeling are meant to help data better function as evidence (Bokulich and Watkins 2023). Modern data is often generated via technologies that require at least some, but often significant, processing before the data are usable. Thus, data models are ubiquitous.

Here's how Bokulich and Parker define their pragmatic-representational view of data and data models:

> Pragmatic-representational view: Data are representations that are the product of a process of inquiry, and they should be evaluated in terms of their adequacy or fitness for particular purposes. (Bokulich and Parker 2021, 1)

The boldest contribution of Bokulich and Parker's PR view comes from the pragmatic aspect: the claim that data model evaluation should consider the model's adequacy or fitness for purpose. Evaluation based on adequacy considerations is widely acknowledged for cases of theoretical modeling in the sciences (Parker 2010, 2020; Jacquart 2016). Bokulich and Parker claim data models are similar: They ought to be evaluated according to "whether they can be used to achieve the particular epistemic or practical aims that interest their users" (2021, 10). Such a pragmatic view of data and data models is already acknowledged in some sciences (see, e.g., (Bokulich 2021)). Rather than evaluate data models based on how well they "mirror" the world, Bokulich and Parker argue, data modelers (should) evaluate whether a data model is adequate to achieve the user's purpose or fit for their specified task. Researchers may be able to choose among purposes or modify a data model so that it better fits the task at hand (Watkins 2024).

Notice here that Bokulich and Parker cite "users" of data and highlight whether data "can be used" in certain ways. They understand 'data models' to refer to "datasets or other entities—graphs, charts, equations, etc.—that are produced by processing other data or data models," and further say that "any instance of use of a dataset or data model will involve one or more *users*" (2021, 8, 11). They do not explicitly refer to those who *generate* the data in the first place and who may be more involved in upstream data processing procedures. While 'data model' is meant to refer to datasets (and other processed data entities), Bokulich and Parker also reference 'the context of data modeling' several times. Some such contexts will be upstream of data use, where those generating data are making decisions about how data ought to be processed. I attend to the distinction between data generators and users in my challenge to the PR view.

3. A Bioinformatics Data Model For Sequencing Bias Correction

In this section I analyze an example from microbiome sequencing bioinformatics to illustrate my challenge for adequacy-for-purpose views of data modeling. I chose a

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

research article titled "Consistent and correctable bias in metagenomic sequencing experiments," by Michael McLaren, Amy Willis, and Benjamin Callahan (2019).

From individual organisms to an environment, from healthcare to wastewater monitoring to agriculture, across all domains of life and from deep sea vents to the clouds, researchers use sequencing to produce data about the nucleic acid material in particular samples. Two prominent types of sequencing are known as marker-gene sequencing, where a taxonomically informative gene is targeted for measurement, and shotgun metagenomic sequencing, where all the genetic material in a sample is targeted. I will follow McLaren, Willis, and Callahan and refer to these methods jointly as 'MGS' (marker-gene and shotgun metagenomic sequencing). MGS is one of the main tools for microbiome science, the field which studies the microbes present in, on, and around organisms and their environments. Applying an MGS workflow to samples from a microbial community can identify thousands of different taxa and raise further questions about genes and functions.

Unfortunately, MGS pipelines are *biased*. That is, each step in an MGS experiment "preferentially measures (i.e. preserves, extracts, amplifies, sequences, or bioinformatically identifies) some taxa over others" (Brooks 2016; McLaren et al. 2019, 1; Sinha et al. 2017). In other words, the *measured* (output) abundances of various groups of organisms differ from the *actual* (input) abundances because protocols are better at measuring some targets than others. This experimental bias is widely recognized but rarely addressed systematically. In fact, McLaren, Willis, and Callahan note that a common approach in sequencing experiments is to assume, as long as all samples in a given experiment are processed using the same protocol, that these biases will just cancel out! They further comment that "almost every choice" in an MGS experiment has been implicated as contributing to bias (McLaren et al. 2019, 2; D'Amore et al. 2016; Hugerth and Andersson 2017; Sinha et al. 2017; Pollock et al. 2018). Such widespread MGS bias leads, they say, to quantitative incomparability between studies and (potentially) spurious biological conclusions.

McLaren, Willis, and Callahan's proposal for systematic bias correction is an example of data modeling. In the their model (which I'll call the MWC model), "bias manifests as a multiplication of the true relative abundances by taxon- and protocol-specific factors that are constant across samples of varying compositions" (McLaren et al. 2019, 2):

$$\boldsymbol{O} \sim \boldsymbol{A} \cdot \boldsymbol{B}^{(\boldsymbol{P})}$$

On the MWC model, a vector of the observed relative abundances $\boldsymbol{O}$ is compositionally equivalent to the product of the vectors of the actual relative abundances $\boldsymbol{A}$ and the protocol biases $\boldsymbol{B}^{(\boldsymbol{P})}$. Overall protocol biases are calculated by multiplying individual biases at each measurement step. These stepwise biases are taxon specific. During extraction, for instance, a particular taxon X may be measured four times more efficiently than another taxon Y but half as efficiently as another taxon Z. McLaren, Willis, and Callahan cite research suggesting that in actual experiments such bias mechanisms are indeed multiplicative.

McLaren, Willis, and Callahan emphasize that many MGS biases are linked to known biological, chemical, physical, and informatic features. Some microbial taxa, for example, have extra sturdy cell walls which reduce the efficiency of extraction (the cells don't break open as easily). Taxa that bind PCR primers especially well or

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

that have more copies of the marker gene may be overrepresented during amplification, etc.

One way my example differs from the cases considered by Bokulich and Parker is that McLaren, Willis, and Callahan discuss a data processing procedure (i.e., a data modeling context) but don't deal directly with data models as processed datasets (except for when they evaluate their model with some actual data). That being said, considering this bioinformatics data modeling example, how does the PR view fare?

4. The Data Generator–User Gap and Disambiguating 'Data Model'

I will now make two contributions. First, I argue that a gap between data generators and data users can prevent adequacy-for-purpose from being a good evaluative tool (§4.1). Second, I propose a novel tripartite disambiguation of the term 'data model' (§4.2).

4.1. The data generator–user gap

Here is my argument that in some contexts of data modeling, adequacy-for-purpose won't be a good evaluative tool.

P1: On the PR view, data models should be evaluated based on their adequacy for purpose.

P2: For adequacy-for-purpose to be a good evaluative tool, purposes should be specific, local, circumscribed, or at least particular.

P3: In some data modeling contexts, purposes are not specific, circumscribed, or very particular at all.

Conclusion: In some data modeling contexts, adequacy-for-purpose won't be a good evaluative tool.

Premise 1 comes from the PR view straightforwardly. I will draw support for premise 2 from the PR view in addition to broader literature on model evaluation and adequacy considerations. The specification of purposes, for instance, is an important task which requires "significant unpacking and reflection": "to judge a model's adequacy-for-purpose, the evaluator has to understand what the purpose is and what would count as achieving it" (Parker 2020, 461). I focus my critique on the claim that the purposes in data modeling contexts are particular. Bokulich and Parker write that the aims of data users are "typically rather specific and circumscribed" (2021, 10); Parker writes that "the purposes for which models are constructed and used are often rather circumscribed and local" (2020, 461). For theoretical models, this seems reasonable: "[B]y and large, the adequacy hypotheses put forward on behalf of models are highly local and highly specific. If they weren't so specific," writes Anna Alexandrova, "they would be either untestable or false" (2010, 300). This feature of model evaluation—that purposes should be circumscribed, local, specific—is supposedly true in data modeling as well as theoretical modeling.

Why the purpose has to be circumscribed, specific, and/or local is evident through Bokulich and Parker's use of a modeling *problem space*: a data model must stand "in a

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

suitable relationship" with a target T, user U, method W, background circumstances B, and goal (or purpose) P jointly (2021, 11–12). On my reading, because the problem space is constrained by T, U, W, and B, the specified goal, the purpose P, must be circumscribed. A less circumscribed purpose wouldn't jointly satisfy all the constraints in the problem space. The data model cannot be a solution unless the purpose P reflects the various constraints of the problem space. Intuitively, to evaluate a data model based on adequacy-for-purpose one must have some purpose in mind. Much more could be said about such purposes, but all I need to establish here (to support premise 2) is that purposes need to be *particular*, whether that be understood as being local, circumscribed, specific, etc.

Premise 3 is my main argumentative claim. I will defend it by arguing that a lack of specific/local/circumscribed purposes can happen when there is a gap or separation between data generators and data users. Thus, the source of the challenge to specifying particular data model purposes is what I will call the data generator–user gap. There are at least two ways to illustrate this gap, one which emphasizes scope and another which emphasizes iteration. I will use the problem space to demonstrate both senses of the data generator–user gap.

Sometimes the data generator–user gap is a gap in people. They might just be different groups of researchers. Microbiome science, for instance, is often called an observational field because so much of the research is "mere" description about which bugs are where and how many of them there are. One justification for funding such descriptive research is that others might use the data to achieve a downstream goal such as treating a disease. The data modeling problem space, then, might look like figure 1a. When those generating and processing the data are not the only users of that data, there can be a scope gap in their purposes. The purposes of the generator are more likely to be (but not always) global, general, and/or uncircumscribed (broader scope). This might be because they want the data to be usable for unknown others and unknown purposes. Downstream users usually have specific purposes (narrower scope). In figure 1a, the data generator must evaluate the data model. When there is a separation between the upstream data generator and the downstream data user, the generator must make decisions about data modeling without knowing the purpose(s) to which the data might be put. Call this the scope gap.

A second way to think about the data generator–user gap is in terms of data processing iteration (figure 1b). Bokulich and Parker note that the term 'raw data' is often used to contrast with data models or data products, and further that "in practice, such terminology frequently tracks not an absolute or intrinsic difference, but a relative one: datasets that are taken as input to a given study might be considered 'raw' data, even if they are the product of substantial prior processing" (2021, 8). As instruments themselves black box more and more computational processing, it makes sense that scientists tend to consider data to be raw whenever it is the input to their own contribution. Data generation pipelines may thus involve multiple iterations of data processing, where different researchers with different sets of expertise are responsible for sequentially modeling the data.

Here, the problem isn't that data generators' purposes aren't specific or particular, but that they can differ across iterations. Earlier data modelers might be concerned with correcting for particular instrument biases, whereas later ones might want

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

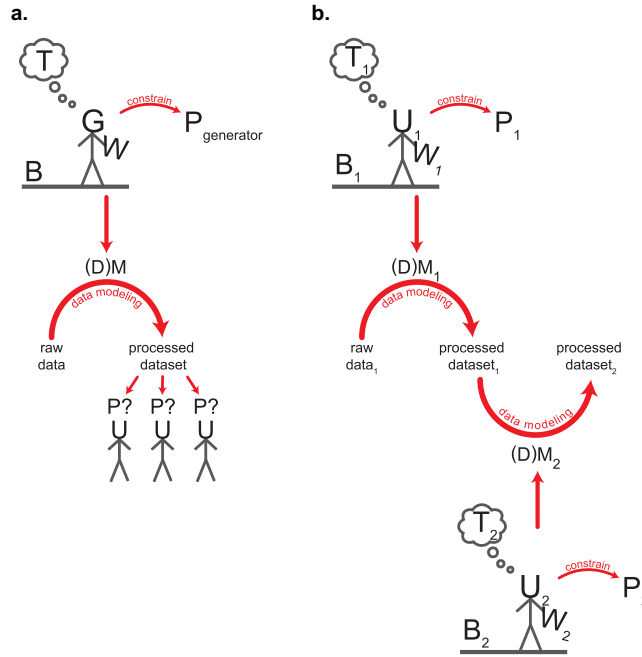


Figure 1. a. Scope gap. A data generator may have a broader purpose during data modeling, as compared to the specific, yet unknown, purposes of downstream users. b. Iteration gap. When data modeling occurs in an iterative pipeline, purposes might be of similar scope yet still differ. B = circumstances, T = target, G = data generator, U = user, W = method, P = purpose, (D)M = data model.

to adjust the data based on information gleaned from positive and negative experimental controls. Thus, when data modelers are part of an iterative pipeline, purposes might be of similarly narrow scope but still differ from each other. Modifications to data models or other decisions with regard to data model evaluation can then propagate down a pipeline, potentially becoming entrenched.

According to the PR view, McLaren, Willis, and Callahan should evaluate their data model with respect to a particular purpose. What might the purpose of the MWC model be? Let's use the problem space. The target of the data model seems easy enough to specify. The target is just whatever microbial community was or will be sampled for a given experiment. As McLaren, Willis, and Callahan deal with a few specific datasets in their manuscript, the targets would be whatever communities those samples came from. More generally, though, McLaren, Willis, and Callahan are not concerned with any particular microbial community. Instead, they attempt to provide a computational, data modeling solution for a problem that impacts use of MGS pipelines in microbiome research more broadly. Considered from this viewpoint, the target could be cashed out more generally as (micro)biological communities! As long as a microbial community is amenable to MGS methods, it could be considered a potential target for the data model that McLaren and colleagues propose.

Now to method and circumstances. These are also relatively straightforward. In fact, McLaren, Willis, and Callahan build their model from mechanistic understanding of the methods used for sequencing pipelines and the circumstances typically encountered in such experiments. I will note here, though, that McLaren and colleagues don't need to capture too much about how particular labs run their MGS

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

protocols; instead, the level that they address is rather a model of the general measurement process.

Now to the user(s). My argument in this paper is about a data generator–user gap, and now is when that separation is evident. Consider the following question: In the problem space of my bioinformatics example, who are the users? The identity of the user constrains the specification of the purpose or goal. So, who are they? The most obvious answer is the data modelers themselves: McLaren, Willis, and Callahan. They are developing the data model, exploring its features by applying it to real data, and arguing for its merits. They need to evaluate the data model, in order to know whether and how to advocate for its use (and to defend its worthiness to be published).

McLaren, Willis, and Callahan, however, produced a data model that is meant to aid *other users* in correcting their own data for this commonly ignored bias. So, it seems like the purpose should not be specified narrowly as correction of any particular dataset. The goal should be specified more broadly, otherwise it cannot satisfy the user constraint. But if the users are McLaren, Willis, and Callahan, then the purpose within the problem space, the one which should be considered for evaluating adequacy for purpose, needs to be theirs. Their purpose, however, is not circumscribed to their own uses. Thus, a separation between data generators and data users can prevent data modelers (like McLaren, Willis, and Callahan) from evaluating their data model based on adequacy-for-purpose alone.

In sum, because the PR view advocates evaluating data models in terms of adequacy- or fitness-for-purpose, evaluation requires specifying a particular purpose. I used an example from microbiome sequencing bioinformatics to illustrate the difficulty of such specification. Within the problem space for the MWC data model, an overly narrow purpose fails to capture the stated motivation for the project, and a more broadly specified purpose will make the evaluative task inaccessible to upstream data model generators.

4.2. A tripartite disambiguation of 'data model'

Questions about specifying the purpose of the MWC data model are sensitive to which entity is meant by the term 'data model'. I will now use the bioinformatics example to develop some distinctions in the meaning of 'data model' which have gone underemphasized in the literature. Table 1 summarizes how the three roles may impact data model evaluation.

In McLaren, Willis, and Callahan's manuscript, there seems to be three roles for data models. First, there is the data model qua model of the measurement process, illustrated in their manuscript as an idealized depiction of a sequencing experiment (McLaren et al. 2019, 3). The second role is the data model qua representation of a data processing procedure. This is the formal model itself, $\boldsymbol{O} \sim \boldsymbol{A} \cdot \boldsymbol{B}^{(P)}$, capturing the way bias may impact measurements across vector abundances. Correcting for bias using this model is a process that is applicable across experiments and datasets (thus there are general and specific instantiations). The third role is the data model qua processed or corrected dataset. Clearly, McLaren, Willis, and Callahan—and others attempting to create and evaluate data models that can play the second role—cannot be expected to evaluate their models with respect to the purposes of any subsequent data models playing the third role.

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

Table 1. Roles for data models versus features relevant for data model evaluation

	Features Relevant for Evaluation			
Role	Used for a purpose downstream of data generation?	Used to process "raw" data?	Models a data generating process?	Is also a model in the traditional sense?
Role 1. Data model as model of a measurement process	✗	✗	✓	✓
Role 2. Data model as representation of a data processing procedure	✗	✓	✓	✓
Role 3. Data model as processed dataset	✓	✗	✗	✗

When data models play roles 1 and 2, the generator–user gap is less problematic because these roles impact the design of the data processing procedure. Adequacy-for-purpose isn't a very helpful guide for data model evaluation, though, because downstream uses of the processed data are unknown (or at least less relevant). If a data model is playing role 3, however, then at least some contexts will feature a gap between the data generator and the data user. This makes the PR view, with its adequacy-for-purpose account of data model evaluation, less helpful to the data generator because it fails to distinguish between data models as datasets and data models as elements of an upstream data modeling context.

If a philosophical view of data models is meant to provide evaluative guidance to researchers, my analysis suggests that the PR view falls a bit short. An account of data model evaluation that can be useful to researchers like McLaren, Willis, and Callahan may need a more nuanced philosophy of data modeling as opposed to simply borrowing from the existing literature on pragmatic evaluation of theoretical models. Such an account could clarify these terminological problems in addition to providing better guidance for data model evaluation.

With respect to better evaluation, here is one lesson from the bioinformatics example. There have been many efforts to assess microbiome methods, including sequencing (e.g. (Golob et al. 2017; Quince et al. 2017; Knight et al. 2018; Sierra et al. 2020; Abellan-Schneyder et al. 2021)). The PR view suggests that having a better understanding of the purpose to which a dataset will be put could improve data model design. Here, though, I showed that less specific, less circumscribed purposes might also play a role. With respect to broader purposes, researchers might do well to facilitate more collaborations between those who do the bulk of the data generation (from sample collection through bioinformatic processing) and those who will be users of that data, as discussed by Sabina Leonelli (2016), for example. However, there are also benefits to be gained by better integrating teams within the data generation process itself. One of the strengths of the MWC data model is that it reflects, as the authors say, "properties of real experiments". Instead of imposing a bioinformatic model with dozens of parameters decoupled from actual experimentation, the MWC data model links model parameters to stages in the sequencing measurement process (or, more precisely, to aspects of a model of that process). Without an understanding

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

of the actual upstream measurement process, downstream computational folks cannot prioritize such parameter linking.

More communication between those working at the bench and those working in the cloud may allow each to adjust experimental design to account for measurement biases that accrue to distant stages in the pipeline. The MWC data model illustrates how bioinformatic data processing can correct for biases present in upstream steps of microbiome sequencing protocols, but it's also possible that adjustments to experimental design in the lab could help support more robust bioinformatic analysis in data processing steps.

5. Conclusion

In this paper I developed a challenge to Bokulich and Parker's pragmatic-representational view of data models. I argued that adequacy-for-purpose can fail as an evaluative tool. I claimed that this is because there can be a data generator–user gap that prevents specification of data model purposes. Said differently, because those generating data and data models are often separated from those using the data, a specific (local, circumscribed) purpose cannot always be identified. In many cases of data generation (where data models are needed) purposes will be decidedly less local, less circumscribed. Researchers may have the broad purpose of generating good data, whatever that means. However, these broad purposes are less amenable to data model evaluation on the pragmatic grounds advocated by the PR view. I then proposed a novel tripartite disambiguation of the term 'data model'.

Measuring the microbiome with MGS is a complex affair that can involve human participants and clinicians, benchwork in the lab, advanced biotech machinery, and extensive bioinformatics processing. This situation likely parallels other areas of modern science. Increasingly there are few people who deeply understand, in practice, how each step in a measurement pipeline works. This might create problems if researchers with different expertise cannot communicate adequately to correct each other's errors. What the MWC data model does, which I find particularly of note, is integrate bench portions of a research pipeline into the bioinformatics itself. My suggestion for future work is that a data model might be a better model if it can do such integration. That is, there can be multiple ways to address biases in a given research pipeline, and such upstream procedures should factor into data model evaluation.

Acknowledgments. This project benefitted from audiences at the 2023 ISHPSSB meeting in Toronto and the 2024 PSA in New Orleans. I'm also thankful for comments from Anya Plutynski, Gray Santana, Caleb Hazelwood, Aja Watkins, Marina DiMarco, Aline Potiron, and Vadim Keyser. Special thanks to Amy Willis for discussing her bioinformatics research with me.

Funding Statement. None to declare.

Declarations. None to declare.

References

Abellan-Schneyder, Isabel, Monica S. Matchado, Sandra Reitmeier, et al. 2021. "Primer, Pipelines, Parameters: Issues in 16S rRNA Gene Sequencing." *mSphere* 6 (1): e01202–20. https://doi.org/10.1128/mSphere.01202-20.

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press

Alexandrova, Anna. 2010. "Adequacy for Purpose: The Best Deal a Model Can Get." *The Modern Schoolman* 87 (3/4): 295–301. https://doi.org/10.5840/schoolman2010873/411.

Antoniou, Antonis. 2021. "What Is a Data Model?" *European Journal for Philosophy of Science* 11 (4): 101. https://doi.org/10.1007/s13194-021-00412-2.

Bokulich, Alisa. 2021. "Using Models to Correct Data: Paleodiversity and the Fossil Record." *Synthese* 198 (S24): 5919–40. https://doi.org/10.1007/s11229-018-1820-x.

Bokulich, Alisa, and Wendy Parker. 2021. "Data Models, Representation and Adequacy-for-Purpose." *European Journal for Philosophy of Science* 11 (31): 26. https://doi.org/10.1007/s13194-020-00345-2.

Bokulich, Alisa, and Aja Watkins. 2023. "Data Models." In *SAGE Encyclopedia of Theory in Science, Technology, Engineering, and Mathematics*, edited by James Mattingly. SAGE Publications, Inc. https://doi.org/10.4135/9781071872383.n55.

Brooks, J. Paul. 2016. "Challenges for Case-Control Studies with Microbiome Data." *Annals of Epidemiology* 26 (5): 336–41. https://doi.org/10.1016/j.annepidem.2016.03.009.

D'Amore, Rosalinda, Umer Zeeshan Ijaz, Melanie Schirmer, et al. 2016. "A Comprehensive Benchmarking Study of Protocols and Sequencing Platforms for 16S rRNA Community Profiling." *BMC Genomics* 17 (1): 55. https://doi.org/10.1186/s12864-015-2194-9.

Frigg, Roman, and Stephan Hartmann. 2020. "Models in Science." In *The Stanford Encyclopedia of Philosophy*, Spring 2020, edited by Edward N. Zalta. Metaphysics Research Lab, Stanford University. https://plato.stanford.edu/archives/spr2020/entries/models-science/.

Golob, Jonathan L., Elisa Margolis, Noah G. Hoffman, and David N. Fredricks. 2017. "Evaluating the Accuracy of Amplicon-Based Microbiome Computational Pipelines on Simulated Human Gut Microbial Communities." *BMC Bioinformatics* 18 (1): 283. https://doi.org/10.1186/s12859-017-1690-0.

Hugerth, Luisa W., and Anders F. Andersson. 2017. "Analysing Microbial Community Composition through Amplicon Sequencing: From Sampling to Hypothesis Testing." *Frontiers in Microbiology* 8: 1561. https://doi.org/10.3389/fmicb.2017.01561.

Jacquart, Melissa. 2016. "*Similarity, Adequacy, and Purpose: Understanding the Success of Scientific Models*." PhD diss., The University of Western Ontario. https://www.proquest.com/docview/2701138541.

Knight, Rob, Alison Vrbanac, Bryn C. Taylor, et al. 2018. "Best Practices for Analysing Microbiomes." *Nature Reviews Microbiology* 16: 410–22. https://doi.org/10.1038/s41579-018-0029-9.

Leonelli, Sabina. 2016. *Data-Centric Biology: A Philosophical Study*. University of Chicago Press.

McLaren, Michael R., Amy D. Willis, and Benjamin J. Callahan. 2019. "Consistent and Correctable Bias in Metagenomic Sequencing Experiments." *eLife* 8: e46923. https://doi.org/10.7554/eLife.46923.

Parker, Wendy S. 2010. "Scientific Models and Adequacy-for-Purpose." *The Modern Schoolman* 87 (3/4): 285–93. https://doi.org/10.5840/schoolman2010873/410.

Parker, Wendy S. 2020. "Model Evaluation: An Adequacy-for-Purpose View." *Philosophy of Science* 87 (3): 457–77. https://doi.org/10.1086/708691.

Pollock, Jolinda, Laura Glendinning, Trong Wisedchanwet, and Mick Watson. 2018. "The Madness of Microbiome: Attempting To Find Consensus 'Best Practice' for 16S Microbiome Studies." *Applied and Environmental Microbiology* 84 (7): e02627–17. https://doi.org/10.1128/AEM.02627-17.

Quince, Christopher, Alan W. Walker, Jared T. Simpson, Nicholas J. Loman, and Nicola Segata. 2017. "Shotgun Metagenomics, from Sampling to Analysis." *Nature Biotechnology* 35 (9): 833–44. https://doi.org/10.1038/nbt.3935.

Sierra, Maria A., Qianhao Li, Smruti Pushalkar, et al. 2020. "The Influences of Bioinformatics Tools and Reference Databases in Analyzing the Human Oral Microbial Community." *Genes* 11: 878. https://doi.org/10.3390/genes11080878.

Sinha, Rashmi, Galeb Abu-Ali, Emily Vogtmann, et al. 2017. "Assessment of Variation in Microbial Community Amplicon Sequencing by the Microbiome Quality Control (MBQC) Project Consortium." *Nature Biotechnology* 35 (11): 1077–86. https://doi.org/10.1038/nbt.3981.

Watkins, Aja. 2024. "The Adequacy of Purposes for Data: A Paleoecological Case Study." *Synthese* 203 (5): 159. https://doi.org/10.1007/s11229-024-04588-x.

Cite this article: Wallis, Jacqueline Mae. 2026. "A challenge for adequacy-for-purpose views of data modeling." *Philosophy of Science*. https://doi.org/10.1017/psa.2026.10237

https://doi.org/10.1017/psa.2026.10237 Published online by Cambridge University Press