Synthese
DOI 10.1007/s11229-016-1018-z

Holistic modeling: an objection to Weisberg's weighted feature-matching account

Wei Fang[1]

Received: 27 July 2015 / Accepted: 6 January 2016

Abstract Michael Weisberg's account of scientific models concentrates on the ways in which models are similar to their targets. He intends not merely to explain what similarity consists in, but also to capture similarity judgments made by scientists. In order to scrutinize whether his account fulfills this goal, I outline one common way in which scientists judge whether a model is similar enough to its target, namely maximum likelihood estimation method (MLE). Then I consider whether Weisberg's account could capture the judgments involved in this practice. I argue that his account fails for three reasons. First, his account is simply too abstract to capture what is going on in MLE. Second, it implies an atomistic conception of similarity, while MLE operates in a holistic manner. Third, Weisberg's atomistic conception of similarity can be traced back to a problematic *set-theoretic* approach to the structure of models. Finally, I tentatively suggest how these problems might be solved by a *holistic* approach in which models and targets are compared in a *non-set-theoretic* fashion.

Keywords Weisberg · Weighted feature-matching account · Similarity · Model · Set-theoretic · Holistic · Scientific representation

1 Introduction

There is increasing interest in the philosophy of modeling literature in the problem of the relationship between scientific models and the world (this problem sometimes is also expressed as the problem of how to use models to represent the world). In particular, the similarity account has attracted much recent attention. Among defenders

✉ Wei Fang
fangwei_jiner@163.com

[1] Department of Philosophy, University of Sydney, Sydney, NSW 2000, Australia

Published online: 21 January 2016

of this view, Giere (1988, 1999a, 1999b, 2004, 2010), Godfrey-Smith (2006) and Weisberg (2012, 2013) have made the most substantial contributions.

Despite famous criticisms of the notion of similarity in general by Quine (1969) and Goodman (1972), Giere developed an early version of the similarity account of the relationship between models and the world, which claimed that:

> The appropriate relationship, I suggest, is *similarity*. Hypotheses, then, claim a *similarity* between models and real systems. But since anything is similar to anything else in some respects and to some degree, claims of similarity are vacuous without at least an implicit specification of relevant *respects and degrees*. The general form of a theoretical hypothesis is thus: Such-and-such identifiable real system is similar to a designated model in indicated respects and degrees. (Giere 1988, p. 81; author's emphasis)

Godfrey-Smith (2006) expresses more or less the same idea:

> Many of the special features of model-based science come from the role played by resemblance relations between model system and target. Philosophers tend to distrust resemblance relations because they are seen as vague, context-sensitive, and slippery. Here, those features of resemblance are indeed important, but they are not necessarily problematic. They are the source of both distinctive strengths and weaknesses of model-based science. (733)

However, because neither Giere nor Godfrey-Smith specify clearly what aspects should be counted and what degrees should be tolerated when building and testing models, some (Suárez 2003) find the early version untenable.

Giere (2004, 2010) developed a more sophisticated account, according to which scientific representation is a four-place activity:

> Shifting the focus to scientific practice suggests that we should begin with the activity of *representing*, which, if thought of as a relationship at all, should have several more places. One place, of course, goes to the agents, the scientists who do the representing. Since scientists are *intentional* agents with goals and purposes, I propose explicitly to provide a space for purposes in my understanding of representational practices in science. So we are looking at a relationship with roughly the following form: *S* uses *X* to represent *W* for purposes *P*." (2004, p. 743; author's emphasis)

Hence, apart from models and the target systems, the activity of scientific representation should also incorporate factors such as the role played by scientists, and the intentions those scientists have with regard to modelling. Incorporating these factors is partly because similarity is a symmetric relationship in which if A is similar to B then B is also similar to A, whereas scientific representation is an asymmetric process where we only claim that the model represents the world and thus is similar to the world in certain aspects, but not vice versa. When including intentions, the modeling process is naturally asymmetric as the scientists only aim to use the model to represent the target.

In next section, I will consider how Weisberg, following Giere and Godfrey-Smith, develops an even more sophisticated similarity account of models. A case study drawn from biological modelling will be described in Sect. 3. Section 4 will discuss whether Weisberg's account could capture the judgments involved in the case study, and the last section will tentatively suggest an alternative to Weisberg's account.

2 The weighted feature-matching account

It is important to note in advance that Weisberg says that his account is "intended to be sensitive to *how scientists represent the world with models* and to how their representational goals and ideals shape the standards of fidelity that they apply to models". (2013, p. 135; my emphasis) In particular, it aims to answer questions about "what similarity supervenes on, how it depends on context, *how similarity judgments are to be evaluated*". (*Ibid.*, 143; my emphasis) Elsewhere, he claims his account could let us "*capture the similarity judgments made by scientists*" (*Ibid.*, 155; my emphasis). In a word, it attempts to not just generally spell out *what* the notion of similarity means, but more importantly aims to *capture* similarity judgments made by scientists[1] given how they choose a feature set, a weighting function, and assign values to weighting parameters.[2]

Weisberg (2012, 2013) calls his approach to similarity the *weighted feature-matching* account. He borrows the basic ideas from psychologist Amos Tversky's *contrast* account of similarity, which claims that the similarity of objects a and b depends on the features they share and the features that they do not. In light of this, Weisberg proposes his own account of similarity:

$$\mathrm{S}(\mathrm{m}, \mathrm{t}) = \frac{\theta \mathrm{f}(\mathrm{M_a} \cap \mathrm{T_a}) + \rho \mathrm{f}(\mathrm{M_m} \cap \mathrm{T_m})}{\theta \mathrm{f}(\mathrm{M_a} \cap \mathrm{T_a}) + \rho \mathrm{f}(\mathrm{M_m} \cap \mathrm{T_m}) + \alpha \mathrm{f}(\mathrm{M_a} - \mathrm{T_a}) + \beta \mathrm{f}(\mathrm{M_m} - \mathrm{T_m}) + \gamma \mathrm{f}(\mathrm{T_a} - \mathrm{M_a}) + \delta \mathrm{f}(\mathrm{T_m} - \mathrm{M_m})} \quad (1)$$

where $f(x)$ refers to the weighting function, $\alpha, \beta, \gamma, \delta, \theta$, and ρ denote weighting terms (parameters), subscripts a and m stand for attributes and mechanisms, and M denotes the model and T the target. $(M_a \cap T_a)$ stands for attributes shared by the model and the target, $(M_a - T_a)$ represents attributes that the model has while the target does not, and $(T_a - M_a)$ attributes that the target has while the model does not. The same story

[1] Parker expresses a similar interpretation of Weisberg's account, claiming that "Ultimately, however, Weisberg's account seems best characterized as an account of what underwrites scientists' *judgments* of the *extent* to which models and targets are similar". (2015, 271; author's emphasis).

[2] Weisberg's account can be more strongly interpreted as aiming to "capture *how* similarity judgments are made by scientists", for his similarity equation and its associated interpretation (as I will describe below) includes the way in which features are *selected* and *weighted* differently by scientists. This clearly involves the "how" problem: how do scientists select and weight these features so as to make appropriate similarity judgments? But to be charitable, in this paper I simply interpret his account as attempting to "capture similarity judgments made by scientists". The latter interpretation is weaker than the former because it merely interprets Weisberg's account as *describing* similarity judgments rather than the process by which they are made.

goes for mechanisms m. Attributes and mechanisms as a whole are called features of the model and the target.

Then an interpretation for this equation is given. First, there must be a feature set Δ, and the set of features of the model and the set of features of the target are defined as sets of features in Δ. Primarily illuminated by Giere's "four-place activity" account, Weisberg claims that the elements of Δ are determined by a combination of context, conceptualization of the target, and the theoretical goals of the scientist; that is, "There is no context-free answer to this question, but part of the answer lies in the modeler's intended scope. The modeler's intended scope takes into account the research question of interest, the context of research, and the community's prior practice." (*Ibid*., 149) What is more, the contents of Δ might change through time as science develops, which in turn might result in a reevaluation of the established model-world relationship. (*Ibid*., 149)

Second, consider the values of weighting parameters $\alpha, \beta, \gamma, \delta, \theta$, and ρ. On Weisberg's account, different kinds of modeling require different weighting parameters. For example, if what interests us is the *minimal modeling* which concerns merely the mechanism responsible for bringing about the phenomenon of interest, the goal of this modeling is written as:[3]

$$\frac{|\mathrm{M_m} \cap \mathrm{T_m}|}{|\mathrm{M_m} \cap \mathrm{T_m}| + |\mathrm{M_a} - \mathrm{T_a}| + |\mathrm{M_m} - \mathrm{T_m}|} \rightarrow 1 \tag{2}$$

where $M_m \cap T_m$ has a high value while $|M_a - T_a|$ and $|M_m - T_m|$ have low values. (*Ibid*., 151)

Finally consider the weighting function $f(x)$, telling us the relative importance of each feature in the set Δ. In Weisberg's view, scientists in most cases have in their mind some subset of the features in Δ, which they regard as especially important. Hence some features are weighted more heavily, and others would simply be equally weighted. According to Weisberg, the background theory determines which features in Δ should be weighted more heavily. In cases where the background theory is not rich enough to make these determinations, deciding which features should be weighted more heavily is in part an empirical problem.

This is Weisberg's account in abstract form. Before plunging into the next section's discussion, let us briefly consider how Weisberg's account *would* work in practice. Imagine in the real world there is a causal process between the number of functional copies of a gene (G) and the rate (E) at which some enzyme is produced.[4] Based on empirical data, scientists build a model (see Fig. 1):[5]

After building this model, scientists attempt to test whether the model captures the target—or, to use Weisberg's terminology, whether the model is maximally similar

[3] Weisberg also describes three other kinds of modelling practice which require different weighting parameters: hyperaccurate, how-possibly and mechanistic modeling. For details please see Weisberg (2013, pp. 150–152).

[4] Assume there is such a data set regarding the variables in the model. Note this extremely simple case should be regarded as a textbook example used merely for introductory purpose.

[5] This model is borrowed from Shipley (2002, pp. 47–48), though slightly different from the original one.

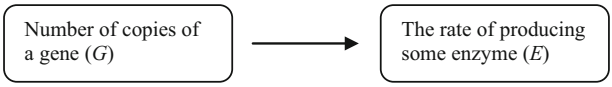

Fig. 1 A biological model of a causal process

to the target. Suppose for the moment that Weisberg's account can be applied to this simple case.[6] This modeling falls into the category of minimal modeling[7], where scientists are interested in the mechanism responsible for bringing about the phenomenon of interest. Therefore we can apply Eq. (2) to this case, where the only mechanism involved is a causal process between G and E. Adding back those simplifications about weighting functions and weighting terms to (2), we obtain equation (3):

$$\mathrm{S}\ (\mathrm{m},\ \mathrm{t}) = \frac{\rho \mathrm{f}\,(\mathrm{M_m} \cap \mathrm{T_m})}{\rho \mathrm{f}\,(\mathrm{M_m} \cap \mathrm{T_m}) + \alpha \mathrm{f}(\mathrm{M_a} - \mathrm{T_a}) + \beta \mathrm{f}(\mathrm{M_m} - \mathrm{T_m})} \tag{3}$$

For simplicity, we stipulate $\rho = \alpha = \beta = 1$. Since minimal modelling concerns only the mechanism responsible for bringing about the phenomenon, we weight $(M_m \cap T_m)$ very heavily and $(M_a - T_a)$ and $(M_m - T_m)$ lightly, e.g., the values of weighting functions for them are 0.81, 0.05 and 0.09 respectively. Thus we finally achieve a similarity value of 0.85, which is very near the maximal similarity value 1.00. Therefore, if the testing process is correct, scientists then can conclude, at least from Weisberg's perspective, that their model is good enough.[8]

3 The maximum likelihood estimation method

In fact, even with a toy model like the one described above, it seems not perfectly straightforward how Weisberg's account could really apply. This is partly because Weisberg does not give us any specific example about his account's application, and partly because its applicability is still in dispute (I will argue this in Sect. 4).

In contrast, the toy model can be readily treated by many scientific testing methods, and *maximum likelihood estimation* (MLE) is the often-used one I will elaborate in this section.[9] In preparation, let me first briefly outline the basics of this method, and then use this method to test a more complicated model drawn from scientific practice, namely the *leaf gas-exchange model*.

[6] I will argue extensively in Sect. 4 that the applicability of Weisberg's account is in fact in dispute.

[7] Because we have already assumed that there is a causal mechanism between the two variables and that is just what the modellers aim to capture.

[8] This model is drawn from Shipley (2002, chapter 3). Also, the following discussion about the maximum likelihood estimation method is based on Shipley (2002).

[9] Though, for the limit of space, I will not demonstrate the claim that the toy model can be readily treated by many scientific testing methods, the following elaboration of the MLE regarding a more complicated model should lend support to this claim.

The essence of the MLE lies in the comparison between the *predicted* and the *observed* variance and covariance matrices. Specifically, we first specify the causal structure of the model under investigation, and then translate it into a statistical model in the form of structural equation(s).[10] After this, we use certain covariance algebra to derive the *predicted* variance and/or covariance[11] between variables in the model. The covariance of variables *A* and *B* is expressed as: *Cov(A, B)*. Note that the *predicted* variance and/or covariance is derived purely from the structural equations without appealing to empirical data. If we have also collected empirical data about the target system on which the model is built, we can derive the *observed* variance and/or covariance between variables.

The next step is to obtain the maximum likelihood estimates of the free parameter(s)[12] of the model by minimising the difference between the observed and predicted variances and/or covariances.[13] The typical way to do this is to choose values for parameters in the predicted covariance, so as to make it as numerically close as possible to the observed covariance. The process of choosing values for parameters is roughly like playing the game of 20 questions: Is it organic or inorganic? Is it a fruit or vegetable? Is it an apple or banana? Is it green or red? ...

After fixing the values of parameters, we then calculate the number of degrees of freedom in the model, which is given by function: $v(v+1)/2-(p+q)$, where v is the number of variables, p is the number of free parameters, and q is the number of free variances of exogenous variables (including the error variables) (Shipley 2002, p. 114). Finally, based on the values of parameters and the number of degrees of freedom, we are able to calculate the probability of having observed the measured minimum difference between the predicted and the observed covariance,[14] and conclude whether our model is good enough in terms of a certain acceptability criterion (say above 0.05 is good enough).[15]

[10] Variables on the right side of the equation are causes and on the left side are effects. 'ε' is an error variable representing other unmodelled cause of the variable E, or pure randomness.

[11] The variance is the expected square of the deviation around a variable's expected value, defined as: $E=[(X_i-\mu_X)^2]$, where μ_X is X_i's expected value. Simply put, it is the measure of distance between the expected and the measured values of a variable. The covariance is simply a generalization of the variance. If we have two different random variables (X, Y) measured on the same observational units, then the covariance between them is defined as: $E[(X_i-\mu_X)(Y_i-\mu_Y)]$, in which $(X_i-\mu_X)$ and $(Y_i-\mu_Y)$ mean deviations of X and Y from its mean μ_X and μ_Y respectively. (Shipley 2002, p. 74)

[12] A free parameter is one that can be adjusted to make the model fit the data.

[13] This is typically done by using the maximum likelihood chi-squared statistic. For details see Shipley (2002, pp. 110–114).

[14] The maximum likelihood estimates (typically using the maximum likelihood chi-squared statistic) guarantee that, by iteratively choosing values for free parameters, the numerical values of the predicted covariance matrix become as close as possible to the actual covariances measured in the data. In essence, to increase the fit as close as possible is also to decrease the difference as much as possible. Hence at a certain point we obtain a minimum difference. The next step is to calculate the probability of having observed such a minimum difference. The value of probability can be calculated by some commercial computer programs, given certain maximum likelihood estimates and degrees of freedom.

[15] In scientific testing the acceptability criterion of 0.05 (or other values depending on different fields of study) is also called the *significance level* or *P value*, used by scientists to determine whether the null hypothesis should be rejected in favor of alternative hypothesis. In short, the significance level indicates whether there is a relationship between various variables represented in the model under testing, or whether

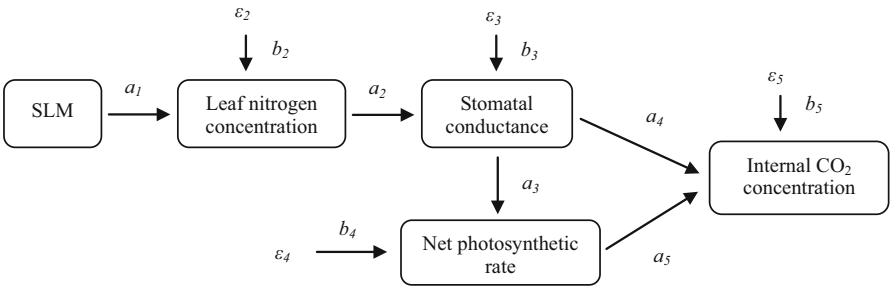

Fig. 2 The proposed path model relating leaf morphology and leaf gas exchange. The letters with subscripts show the free parameters whose maximum likelihood estimates must be obtained

Now, let us consider a more complicated model and its testing using the method sketched above (i.e., MLE). Shipley and Lechowicz (2000) proposed a path model about the leaf gas-exchange based on five variables[16]: specific leaf mass (SLM: leaf dry mass divided by leaf area, g/m^2), leaf organic nitrogen concentration ($mmol/m^2$), stomatal conductance to water ($mmol/m^2$ per s), net photosynthetic rate ($\mu mol/m^2$ per s) and internal CO_2 concentration ($\mu l/l$). This model is expressed in Fig. 2[17].

In Fig. 2, directed lines represent causal relations, and square boxes are causal relata. a_x and b_y are free parameters, and ε_n denotes an error variable representing other unmodelled causes of the variable into which it points.

Now suppose we intend to evaluate whether this model is scientifically acceptable. Having specified the causal structure, the next step is to translate it into an observational (i.e., statistical) model in the form of a set of structural equations[18] (for technical details, see *Appendix 1*, *Box 1*). The third step is to derive the predicted variance and covariance between each pair of variables in the model using covariance algebra. Following the algebra, we finally obtain a table showing the variances and covariances between each pair of variables (see *Appendix 1, Box 2*).

The fourth step is to estimate the free parameters by minimising the difference between the observed and predicted variances and covariances[19]. As described above, the typical way to do this is roughly like playing the game of 20 questions. More

Footnote 15 continued
the result can be explained by the null hypothesis. For example, if the probability is less than or equal to the significance level, then the null hypothesis is rejected and then the outcome is said to be *statistically significant*. An outcome is said to be statistically significant only if it can enable the rejection of the null hypothesis. On the other hand, if the probability is larger than the significance level, then the null hypothesis cannot be rejected.

16 There are reasons why we choose this model but not others. First, it is definitely a mathematical model and falls into the category of minimal modeling according to Weisberg's terminology. Second, it is neither too complicated nor too simple to grasp. Third, and most important, it is a good exemplar in the discourse of causal modeling and related testing methods.

17 The figure is also drawn from Shipley (2002, p. 131), with only small modifications.

18 In most structural equations, the causal relations are assumed to be additively linear (Shipley 2002, p. 105), so we here follow this assumption. It also should be noted that since causal relations are asymmetric while these equations are symmetric, this translation is only a partial translation.

19 See footnote 13.

specifically, "We start with an initial guess of the values of the free parameters and calculate the likelihood of the data given the current parameter values. We then see whether we can modify our guess of the values of the free parameters in such a way as to improve the likelihood. We continue with this process until we find values such that any change to them will do worse than the present values." (Shipley 2002, pp. 110–111)

Fortunately, many computer programs can perform this somewhat time-consuming process[20], so for simplicity we here just follow the final outcome of this process. The final maximum likelihood value reached is 4.72, the magnitude of which indicates the difference between the predicted and the observed covariance matrices[21]. In general, the larger the maximum likelihood value, the further the predicted covariance matrix deviates from the observed covariance matrix. (Shipley 2002, p. 119)

Finally, to determine whether the model fits the empirical data well, we have to calculate the probability of having observed the measured minimum difference, assuming that the observed and predicted covariances are identical except for random sampling variation[22]. To achieve this, we first calculate the degree of freedom in the model. In our model, we have 5 variables, 5 error variables and 5 free parameters, so the degree of freedom is 5. Given the final maximum likelihood value (i.e. 4.72) and the degrees of freedom (i.e. 5), we arrive at the conclusion that the probability of having observed the measured minimum difference between the predicted and observed covariance matrices is 0.45[23]. According to one commonly used interpretation in the biological modelling[24], if the calculated probability is small enough (e.g. below 0.05) then one can conclude that the model is wrong, whereas if the probability is big enough (e.g. above 0.05) then one can conclude that the model is sufficiently consistent with the data (or not inconsistent enough to reject), thus is acceptable (Shipley 2002, p. 115). Therefore, since our probability is sufficiently larger than 0.05, we conclude that the leaf gas-exchange model is good enough.

4 Can Weisberg's account capture how the gas-exchange model is assessed?

We mentioned above that Weisberg's account attempts to not just generally explain *what* the representational relation between models and the world is, but more importantly to capture similarity judgments made by scientists. Our question hence is to what extent Weisberg's account, intended to capture similarity judgments made by scientists, could *capture* the relevant judgment involved in the leaf gas-exchange modelling discussed above.

[20] See Shipley (2002, pp. 110–114) for more details about these techniques.

[21] This difference can be calculated using some formula. For more details, see Shipley (2002, pp. 113–114).

[22] See footnote 14.

[23] See Shipley (2002) for more details about the calculations of this value.

[24] There might be other interpretations which set different threshold values for the acceptable probability, but our case discussed in this paper is neutral on exactly which value is actually chosen.

To answer this question, we first need to identify which aspect of how the leaf gas-exchange model was assessed involves a similarity judgment. Given that MLE seems to involve the *comparison* of predicted with observed data, let us suppose, for Weisberg's argument, that the MLE can be thought of as a sort of similarity judgment. However, we shall see in the following that even if MLE is understood as a sort of similarity judgment, Weisberg's account still fails to capture that judgment. In what follows I will first raise a less important concern, and then move on to develop two crucial, interconnected arguments.

4.1 Weisberg's account is too abstract

My first concern is that his account is too abstract to shed light on how the practice of selecting and weighting features (i.e. the "move-back-and-forth practice") can be actually made by scientists.

Needless to say, it is basic practice in modelling that scientists move back and forth to adjust the weights of features based on their intuitions about the similarity, and/or change the model based on similarity values achieved. But the trouble is that this practice is not instantiated in Weisberg's account, for his account only claims that scientists can decide which features should be included in the similarity calculation and how importantly they should be weighted respectively, given certain background theory or theories. He does mention that when the background theory is not rich enough, deciding which features should be weighted more heavily is in part an empirical problem. But the problem remains: how could his account cash out this "move-back-and-forth" issue when the background theory is not rich enough? No clear image emerges. Nevertheless, the empirical issue of selecting and weighting features stands at the core of modelling practice. Hence, as an account of capturing similarity judgments made by scientists, merely mentioning that "this is an empirical problem" falls short of casting light on what is really going on in science.

By contrast, the "move-back-and-forth" practice is perfectly exemplified by the MLE. We concluded in last section that the probability of having observed the measured minimum difference is 0.45, which is sufficiently larger than the threshold value 0.05. Hence we claimed that our model is good enough. If, on the other hand, the probability is not 0.45 but 0.045, smaller than the threshold value, we should conclude instead that our model is not good enough and there must be features the model misses or misrepresents. If this is the case, we should modify the model slightly by adding or subtracting more features to/from the model. We practice this again and again until we reach an acceptable probability value.

In words, because of its abstractness, Weisberg's account simply fails to shed light on how the process of selecting and weighting features can be actually exercised by scientists. This might not constitute a serious problem because, he might argue, the practice could be integrated into his account someday. I agree, but two serious problems make this integration superfluous.

4.2 Weisberg's account is *atomistic* in nature

The first serious problem is that his account is *atomistic* in spirit[25], while the MLE is *holistic*. To show this, let us take a closer look at his similarity Eq. (1). The numerator invites us to weight features shared, and the denominator asks us to weight all features involved (including three feature subsets: features shared, features possessed by the model but not the target, and features possessed by the target but not the model). Each feature is weighted independently and only once, with it falling into one of the three feature subsets. The boundary between features is clear-cut, without involving overlapping, correlation, covariance or any other relationship. Each feature's weight is simply added together to obtain the overall sum of weights of the numerator or denominator. And the final value of the similarity measure is the ratio of the overall sum of weights of the numerator to the overall sum of weights of the denominator.

But it is evident that this is not what we find in MLE. Consider the leaf gas-exchange model: when testing this model, we are interested in exploring whether the predicted covariance matrix of the model *as a whole* fits the observed covariance matrix using the MLE, rather than weighting whether each individual feature, or each individual covariance predicted by the model, *matches* each individual feature or covariance of the observed data (remember that in the testing we choose values for free parameters for the whole predicted covariance matrix and see how the matrix as a whole fits the observed matrix). In other words, the final measure of fit concerns not simply the sum of each feature's measure of weight, nor the ratio between the sums of weights of the numerator and the denominator. Put slightly differently, the essence of testing, at least in our model, is not based on weighting each feature independently and then adding them together, but on the *holistic* relationship between the predicted data and the observed data *as a whole*.

Three possible responses are on offer. First, Weisberg might launch a rescue by his notion of *fidelity criteria*. In fact, Weisberg does discuss the fit between the output (i.e. predictions) or internal causal structure of the model, on the one hand, and their counterparts in the real world phenomenon, on the other. For example, he says "dynamical fidelity criteria[26] tell us how close the output of the model must be to the output of the real world phenomenon. [. . .] These criteria deal only with the output of the model, that is, its predictions about how a real-world phenomenon will behave." (2013, p. 41) And the representational fidelity criteria "specify how closely the model's internal structure must match the causal structure of the real-world phenomenon to be considered an adequate representation". (*Ibid*., 41) When discussing the representa-

[25] Parker recently made a similar point, asking "can feature weights really be assigned independently?" She says that "In his account of model-world similarity, Weisberg deviates from Tversky in restricting the weighting function such that it assigns weights to features independently of which other features are shared", and that "Weisberg's restriction seems to go too far, however. For surely the perceived significance of a feature 'shared' by a model and a target sometimes does depend on which other features are 'shared"'. (Parker 2015, pp. 273–274).

[26] For Weisberg, fidelity criteria "describe how similar the model must be to the world in order to be considered an adequate representation. There are two types of fidelity criteria: *dynamical fidelity criteria* and *representational fidelity criteria*." (2013, p. 41).

tional ideal of MAXOUT[27] he also says that "This ideal says that the theorist should maximize the precision and accuracy of the model's output." (*Ibid.*, 109) These points suggest that sometimes to judge whether a model is adequate, modellers primarily pay attention to the overall fit of outputs or causal structures of the model to the target. That is, they focus on how *similar* the output or causal structure of the model is to their real world phenomenon. Interestingly, this is just what the MLE implies, for it concerns the overall fit between the predicted and observed covariance matrices.

But, unfortunately, there seems no way to integrate these ideas into Weisberg's account of similarity between model and target. His formula simply does not (and perhaps cannot) incorporate a *holistic* comparison of either outputs or causal structures between the model and the target. The formula essentially depends on assessing the (weighted) contribution of each feature independently. This is largely due to his understanding of the structures of models, a crucial point we shall consider in our last argument.

The second possible response may be that Weisberg's similarity account may be compatible with our holistic diagnostic. Suppose, for example, that MLE reveals that the model for leaf gas-exchange is wrong. Presumably it is wrong because modellers in constructing it incorrectly identified or weighted certain features of the model. Fixing the model to make it sufficiently similar to its target might require adding or subtracting features *separately*, or weighting them differently. In doing so, the argument goes, an atomistic approach to similarity is employed. But, as we shall see in the last argument, since each individual feature of the model or target cannot be weighted independently without affecting the weighing of other features, adding or subtracting features (or weighting them differently) cannot keep other features (and perhaps relations between them) intact; that is, it must result in the re-weighting of many other features, and perhaps (if it is a causal model) the re-weighting of many relations between these features. Again, this is clearly a holistic issue.

The last possible response might involve the distinction between different representational strategies[28], or representational ideals in Weisberg's terminology[29]. Weisberg might rightly point out that the holistic character of MLE presupposes the upholding of the representational strategy of *precision* (Weisberg's own terminology is MAXOUT; see footnote 27) whereby modellers are only interested in the precision of predicted outcomes, though unrealistic assumptions are always made. This is true in the MLE, where scientists make a number of unrealistic assumptions, for instance, that the causal relations involved are additively linear, that all error variables are unit normal variables, and so on. Despite these unrealistic assumptions, the predictions based on the MLE can be made very precise.

[27] MAXOUT is a representational ideal which guarantees that models are useful for predicting but gives no guarantee that the models are useful for explaining. (2013, p. 109).

[28] The discussion surrounding representational strategies started from Levins (1966), who claimed that there are three types of representational strategies (i.e. realism, precision and generality) among which tradeoffs exist, and continued well into this century by Orzack and Sober (1993), Taylor (2000), Odenbaugh (2003, 2006), Orzack (2005), Weisberg (2006), Matthewson and Weisberg (2009), etc.

[29] Weisberg himself also distinguishes various different representational ideals: completeness, simplicity, 1-causal, maxout, and P-general. For details please see his (2013, chapter 6, section 2).

This is also true in the modelling practice of many other domains, economics for example. Alan Musgrave says that "Economic theorists often make assumptions which seem to be quite obviously false. For example, an economist may assume that goods are infinitely divisible, that consumers have a perfect knowledge of them, that transport costs are nil, that the government's budget is balanced, even that there is no government". (1981, p. 377) This basic fact aroused the famous *Friedman twist* in economics, where Friedman claimed that "an economic theory should not be criticized for containing 'unreal assumptions': the only legitimate way to criticize an economic theory is to point out that its predictions are at variance with the facts." (*Ibid*., 377)

Thus the representational strategy of precision is in itself unproblematic. But the worry is that, Weisberg might argue, this strategy is just one among many, and focusing solely on it might stretch it too far. Admittedly, our considerations discussed so far might just amount to tilting at windmills, for perhaps his account holds an entirely different representational strategy, *realism* for example. Indeed, it should be accepted that his account bears a closer relationship to the strategy of realism than to generality and precision (or other strategies), for it turns heavily on the one-by-one manner of feature-matching. Note that his account requires that a model be *maximally similar* to its target in important respects and to substantive degrees. But if Weisberg's objection proceeds in this way, its functioning as a general account of model-world relationship might be greatly undermined, for it might turn out that it only covers a small portion of the modelling practice where the representational strategy of realism is employed, and in particular it fails to cover the MLE in which precision is deployed. It is not too bad since covering a bit is better than containing nothing. But we shall see in the next argument, even the hope of maintaining this small portion is at risk.

In summary, it turns out that the similarity account is *atomistic* in nature while the "similarity judgment" in MLE is made in a *holistic* manner. Further, his considerations about "fidelity criteria" offer no help. Weisberg might rescue his account by claiming either that his account is compatible with MLE, or that his account exemplifies the representational strategy of realism while the MLE the precision. But neither is convincing, for the former is simply untrue and the latter defeats itself. Perhaps it is not an accident that his account shows an atomistic flavor, the reason of which I shall explore in the next argument.

4.3 Weisberg's account assumes a *set-theoretic* approach

The second concern discussed above can be traced back to a deeper one, i.e. Weisberg's understanding of the structure of models. Weisberg's basic claim is that models are *interpreted structures*. (2013, p. 15) Corresponding to his three different kinds of models, Weisberg distinguishes three distinct structures: concrete, mathematical and computational structures. Of direct relevance to the discussion here is the mathematical structure, for the gas-exchange model clearly falls into the category of mathematical models. He states that in many cases of modeling these mathematical structures are *trajectories in state spaces*, but in other cases other kinds of mathematical structures

can also be deployed. (2013, p. 29) It is worth noting here that the trajectory (or state space) view of structures of models stems from the semantic view of models.[30]

Interestingly, though Weisberg rejects the semantic view about the model-world relation (Weisberg 2013, pp. 137–142), not only does he expressly uphold the semantic view on the *structure* of models, his similarity account of the *model-world relation* also assumes a set-theoretic approach that resembles the one found in the semantic view.[31] Given that the adequacy of semantic view on the nature (i.e. structures) of models has been challenged by many authors (Downs 1992; Frigg 2006; Godfrey-Smith 2006; Odenbaugh 2008), and my argument in this paper concentrates solely on the model-world relation rather than the nature of models, in what follows I will only consider the point that Weisberg's similarity account on the model-world relation assumes an inappropriate set-theoretic approach. Let us demonstrate this.

It can be proved that Weisberg's similarity measure is equivalent to the *Jaccard similarity coefficient* between two sets (see *Box 1* below)[32]. Box 1 should make it intuitively clear that Weisberg's account says just what the Jaccard similarity coefficient says—that the degree of similarity between two things depends on the ratio of elements shared to the total elements of these two things. The full demonstration can be found in *Appendix 2*.

Box 1. The Jaccard Similarity Coefficient (JSC)

The Jaccard index, also known as the Jaccard similarity coefficient, is a statistic used for comparing the similarity and diversity of sample sets. For two non-empty finite sets X and Y, the Jaccard coefficient is the number of elements in the intersection X ∩ Y of X and Y:

$J(X, Y) = |X \cap Y| / |X \cup Y|$ (If X and Y are both empty, we define $J(X, Y) = 1$.)

It measures the probability that an element of at least one of two sets is an element of both, and is thus a reasonable measure of similarity or 'overlap' between the two. (Levandowsky and Winter 1971, p. 34)

This approach to similarity assumes a *set-theoretic* way of describing objects (models and targets) in which features are independent of each other, just as elements of a set are independent of each other. That is, it views both the model and the target as a set of independent elements, the similarity between which consists in the ratio of the number of elements shared to the number of total elements. However, as my second argument (and MLE practice) shows, modellers, at least in many forms of mathematical modelling, do not engage in set-theoretic descriptions and comparisons

[30] The semantic view about models (or more generally about theories) has two versions, one is the set-theoretic predicate approach developed by Suppes (1957, 1960, 1962, 1967), Sneed (1971) and Stegmuller (1976), and the other is the state space approach developed by van Fraassen (1970, 1972, 1974) and Suppe (1974, 1977).

[31] The semantic view of models, as Weisberg himself criticizes, takes mathematical models to be more or less equivalent to logicians' models, and thus accounts for the model-world relation by tools (typically *set theory*) appropriate for logicians' models. In particular, it takes model-world relation to be an isomorphism relationship (or some weakened versions), i.e. a mapping between two *sets* that preserves structure and relations. (Weisberg 2013, pp. 137–138).

[32] I thank Arnaud Pocheville for letting me notice this.

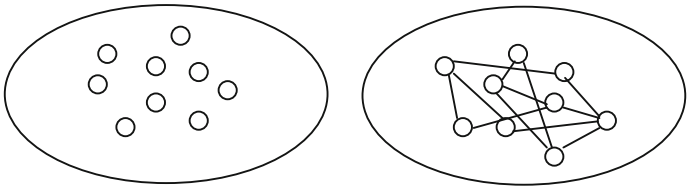

Fig. 3 Set-theoretic and non-set-theoretic ways of describing objects. The former assumes that features of the object are independent while the latter assumes that they are interconnected

of their models with their targets. *Rather, they judge their models as wholes*; *models are not bags of features*. This is because models are *organized structures*[33] where features bear strong relationships (in contrast with elements of a set) to one another, rather than *aggregative structures,* as Weisberg's account assumes, where features are independent. The difference between set-theoretic and non-set-theoretic ways of describing objects can be brought out by a simple figure (see Fig. 3).

Figure 3 reveals that if features are interconnected with one another, then it is simply misleading to assess the fit between the model and the target in a set-theoretic way, for this inevitably severs the interconnections among features[34]. This can also be shown by taking a closer look at the structural equations (described in *Appendix 1*, *Box 1*) derived from the leaf gas-exchange model (or more precisely, derived from the causal structure of the model). Consider, for example, the variable "net photosynthetic rate" (X_4), whose relationship with other variables in the model is described as follows:

$$\mathrm{X_4} = \mathrm{a_3X_3} + \mathrm{b_4\varepsilon_4} \tag{4}$$

where X_3 is the variable "stomatal conductance", ε_4 an error variable, and a_3 and b_4 two free parameters. Equation (4) shows that the value of X_4 depends on both the values of X_3 and ε_4, and their parameters a_3 and b_4. (Similarly, the value of X_3 in turn depends on the values of X_2 and ε_3, and their parameters a_2 and b_3. And so on and on.) According to Weisberg's account, "net photosynthetic rate" and "stomatal conductance" are two attributes shared by the model and the target. Now suppose, because of certain reasons, we weight the attribute "stomatal conductance" very highly. If so, and other things being equal, we must also weight the attribute "net photosynthetic rate" very highly, for the latter additively relies on the former. And if we weight "net photosynthetic rate" very highly, we must also, for the same reason, weight "internal CO_2 concentration" (X_5) very highly. And so on and on until we weight all attributes very highly. The same story also holds for mechanisms. Mechanisms here mean causal relations between variables. For example, if we weight the causal relation from X_1 to X_2 very highly, we must also weight the causal relation from X_2 to X_3 very highly, for the latter is simply the causal result of the former.

[33] I will say more about my conception of structures in the next section.

[34] A proponent of similarity view can reply that the whole structure composed of various interconnected elements can be thought of as a single feature, and the similarity judgment is just made about the similarity of this single feature between the model and the target. But this way of reply makes Weisberg's view descend into a version of holistic approach that he rejects.

The reverse is also true: if we weight the causal relation from X_2 to X_3 very highly, we must also weight the causal relation from X_1 to X_2 very highly, for the latter is simply the cause of the former. The story goes until we weight all causal relations very highly. The tricky thing here is that the structural equation describes a causal network, in which each variable bears direct or indirect causal relations on others.[35] In short, contrary to the set-theoretic approach, a feature cannot be weighted independently without affecting the weighing of others; we are weighting an overall causal network (i.e. structure), rather than any individual feature in the network. This in turn explains the point discussed in Sect. 4.2 that the act of adding or subtracting features can only be properly understood in a holistic manner.

The difference (between the set-theoretic and non-set-theoretic) both echoes and further explains my second concern regarding Weisberg's account, in which I claimed that his account is *atomistic*, while the MLE is *holistic*. I hope it now becomes clear that this difference has a deep root in distinct understandings of the structure of models. For if we embrace the set-theoretic approach which can be derived from the Jaccard similarity index (as we did in the *Appendix 2*), and thereby assume that features in models are independent of each other, then an atomistic account ensues. Obviously, an atomistic understanding about features precisely corresponds to, and can be explained by, a set-theoretic conception about structures (remember that Weisberg expressly embraces the semantic theory's view of model structures).

This difference also partly explains why Weisberg rejects the holistic approach to similarity, stating that his "notion of similarity begins from an everyday notion, but rejects the idea that similarity is a strictly holistic relation of resemblance". (2013, p. 155) For if similarity is a holistic relation of resemblance in which features bear relationships to one another, similarity judgments cannot be simply made in a set-theoretic way as Weisberg does. In other words, in order to maintain his set-theoretic account, a holistic approach must be rejected. This does not mean that no similarity account can be made consistent with the holistic approach in the end, but only that Weisberg's version of similarity account is as a matter of fact inconsistent with the holistic approach.

So, as I suggested in the previous section, the possibility of tailoring Weisberg's account to cover holistic model assessment can be blocked, and even the hope of maintaining the similarity account for the small portion of modelling practice involving the representational strategy of realism is at risk (for its assuming of the set-theoretic approach makes it inconsistent with most—if not all—mathematical modelling).

In sum, given these considerations I am inclined to conclude that Weisberg's account fails to capture those similarity judgments made by scientists, for these judgments are simply not what his account suggests. Its failure might at first blush be due to its atomistic conception of features, but the bedrock underlying it is its set-theoretic conception about the structures of models. Its failure, however, might hint at the

[35] In cases where no causal relation (direct or indirect) holds between two variables, the situation could be slightly different, for weighting one would not affect weighting the other. For example, if there is no causal relation between X_3 and X_4 in the leaf gas-exchange model, then weighting the causal relation between X_3 and X_5 would not affect weighting the one between X_4 and X_5. But the general claim still applies here, for many (if not most) variables in the model still bear causal relations on one another.

direction where a new perspective is called for. This is what I will outline in the next section.

5 A tentative approach: Holistic fit between models and targets

Given the failure of Weisberg's similarity account, I claim that a *non-set-theoretic* approach is called for.[36] More specifically, this approach will replace Weisberg's set-theoretic based similarity account with a *holistic account of fit*, suggesting that (1) a *holistic approach* in science is more central and pervasive than Weisberg envisions, and (2) *holistic testing* is a comparison of models and targets in a *non-set-theoretic* way using various testing methods (for various purposes), and (3) this is typically done by the comparison of the predicted data drawn from the model and the observed data drawn from the target *as a whole*. These points should become clear if we consider the modelling literature in science. For example, Johnson and Omland (2004, p. 102) in a paper summarizing recent developments in ecology and evolution modelling say that

> Once a set of candidate models is specified, each model must be fit to the observed data. At an early stage of the analysis, one can examine the goodness-of-fit of the most heavily parameterized (i.e. global) model in the candidate set. Such goodness-of-fit can be assessed using conventional statistical tests (e.g. χ^2 tests or G tests) or a PARAMETRIC BOOTSTRAP procedure […]. If the global model provides a reasonable fit to the data, then the analysis proceeds by fitting each of the models in the candidate set to the observed data using the method of MAXIMUM LIKELIHOOD or the method of LEAST SQUARES (authors' emphasis).

If I understand the modelling practice cited above correctly, it seems that it proceeds in a holistic manner without implying set-theoretic elements. More specifically, it is fairly clear that both the maximum likelihood and the least squares method commonly used in modelling practice are holistic testing methods[37], whereby predicted and observed data are compared *as a whole* so as to make judgments about models. These are not the only ways of testing the goodness-of-fit of models, but they are nonetheless very important and pervasive in science. This alternative approach succeeds in avoiding those problems plaguing Weisberg' account, for it is holistic, non-set-theoretic.

[36] A whole body of literature falls into this category of non-set-theoretic approach, such as the "mediating models movement" led by Morgan and Morrison (1999), Hughes's "denotation-demonstration-interpretation" account (1997), Suárez's "inferential account" (2004, 2015a, 2015b), etc. Suárez, in some sense, even anticipates the "anti-set-theoretic" criticism developed in this article, as he claims, when criticizing the Tversky-Weisberg similarity account, that "the idea of context-relative description presupposes that some antecedent notion of representation is already in place, since it assumes that sources and targets are *represented as having particular sets of features* in context" (Suárez 2015a, 8; my emphasis).

[37] Least squares is a method of fitting a model to data by minimizing the squared differences between observed and predicted values (Johnson and Omland 2004, p. 102). Whether or not the least squares method is a holistic approach is less obvious but it is at least not set-theoretic, for any change in a parameter of the predicted curve will possibly affect all the deviations to be squared (i.e. the distance of each point to the curve).

Admittedly, the complete account of it remains to be done, but it is a move in the right direction.

A word is needed on my conception of the structure of models. Some may raise the issue that since the notion of structure is also employed in my holistic view of the model-world relation, I owe them an account of what the nature of structures is. My answer is twofold. First, the ontological problem of the nature of structures does not arise in modelling practice, the absence of which does not affect the operation of the latter. Second, even if such an account is required, a *deflationist view* (Downs 1992; Suárez 2004, 2015a, b; Godfrey-Smith 2006; Odenbaugh 2014) is sufficient for us to understand the modelling practice, which states only that structures (or means of representation), of various kinds (e.g. concrete objects, equations, graphs, pictures, etc.), are important inferential tools in modelling practice.[38] Scientists use them, combined with interpretations of them, to achieve various goals such as understanding, predicting, intervening, etc.

This is the basic idea, and there are several qualifications. First, unlike Weisberg, I do not aim to develop an *all-encompassing* account covering all kinds of modelling practices.[39] Rather, I only claim that the holistic approach is central and pervasive in science, though without committing that it is the only approach. Hence it opens the gate for further investigation on this topic. Second, due to its importance and pervasiveness in scientific modelling, it would be worth developing a full-fledged version of the holistic approach, though this is surely beyond this paper's scope. Key issues like how a holistic approach could be specified in detail still remain unclear at this stage. Also, how Weisberg's considerations about different kinds of *fidelity criteria* and *representational ideals* could be integrated into this approach also remains to be seen. Third, it should be noted that this approach is not necessarily inconsistent with the basic intuition shared by many authors: models are similar to their targets in certain respects and to certain degrees. For a holistic approach also concerns the respects and degrees to which a model is similar (or fit) to its target, though clearly in a holistic manner. Perhaps it is fair to say that the notion of similarity functions mainly *heuristically* in the process of constructing models—the context of discovery—

[38] Suárez's use-based inferential account is especially pertinent, expressing that "*A* represents *B* if (i) the representational force of *A* points towards *B*, and (ii) *A* allows competent and informed agents to draw specific inferences regarding *B*" (2004, p. 773). Note that the reference to the presence of agents and purposes of inquiry is crucial for this account: "First, the establishing and maintaining of representational force in (i) requires some agent's intended uses to be in place; and these will be driven by pragmatic considerations. Second, the type and level of competence and information required in (ii) for an agent to draw inferences regarding *B* on the basis of reasoning about *A* is a pragmatic skill that depends on the aim and context of the particular inquiry" (2004, p. 773). This account is deflationist because it construes representation as *means*, rather than *constituents*, of inference-making, implying that representation can be fulfilled by any means of inference (such as induction, deduction, abduction, etc.), without committing to any constitutive relationship (such as similarity, isomorphism, partial isomorphism, homomorphism, etc.) between the target and the model.

[39] Though my account is developed using a mathematical model as an example, I do not think it cannot be applied to concrete models. It will be worth developing another article to support this claim, but let me just mention several points relevant to our current purpose. First, I agree (with Weisberg) that concrete models are concrete structures (plus certain construal). Second, these concrete structures, like their mathematical counterparts, are *organized entities* in which elements bear relationships to each other. Third, I think a set-theoretic approach of comparison (or similarity) cannot capture these organized entities.

where scientists only single out certain aspects of the world to which certain degrees of importance are assigned. In the process of testing models—that is, the context of justification–however, similarity might not find a position.

6 Conclusion

In this paper I have argued that Weisberg's *weighted feature-matching* account of similarity is not as plausible as it seems. To achieve this, I first discussed a biological model (i.e. the leaf gas-exchange model) and then examined how to use the maximum likelihood estimation to evaluate the goodness of the model. After that, I considered the problem of whether Weisberg's account could accommodate this case study. We saw that it failed as an account of capturing similarity judgments made by scientists. First, his account is simply too abstract. Second and more seriously, it implies an atomistic conception of features while our case operates in a holistic manner. Third and most importantly, the atomistic conception of features can be traced back to a set-theoretic view of the structures of models, where elements of a set are independent of each other. Finally, I tentatively suggested a *holistic* alternative, where elements of the structures bear strong relationships to each other.

Acknowledgments I am grateful to a number of friends and colleagues for feedback on early drafts of this work, including Pierrick Bourrat, Mark Colyvan, Paul Griffiths, Qiaoying Lu, John Matthewson and Arnaud Pocheville. Special thanks is due to Paul Griffiths and Arnaud Pocheville, who gave me extremely useful help and encouragement over the course of developing this work. Thanks to the National Social Science Fund of China (Grant Number: 14ZDB018).

Compliance with ethical standards

Conflict of Interest the author declares that he or she has no conflict of interest.

Funding This study was funded by the National Social Science Fund of China (Grant Number: 14ZDB018).

Appendix 1: The leaf gas-exchange model

Box 1. The structural equations for the leaf gas-exchange model

SLM $(X_1) = N(0, \sigma_1)$[a]	$\varepsilon_2 = N(0, \sigma_2)$
Leaf nitrogen concentration $(X_2) = a_1X_1 + b_2\varepsilon_2$	$\varepsilon_3 = N(0, \sigma_3)$
Stomatal conductance $(X_3) = a_2X_2 + b_3\varepsilon_3$	$\varepsilon_4 = N(0, \sigma_4)$
Net photosynthetic rate $(X_4) = a_3X_3 + b_4\varepsilon_4$	$\varepsilon_5 = N(0, \sigma_5)$
Internal CO_2 concentration $(X_5) = a_4X_3 + a_5X_4 + b_5\varepsilon_5$	

$\mathrm{Cov}(X_1, \varepsilon_2) = \mathrm{Cov}(X_1, \varepsilon_3) = \mathrm{Cov}(X_1, \varepsilon_4) = \mathrm{Cov}(X_1, \varepsilon_5) = \mathrm{Cov}(X_2, \varepsilon_3) = \mathrm{Cov}(X_2, \varepsilon_4) = \mathrm{Cov}(X_2, \varepsilon_5) = \mathrm{Cov}(X_3, \varepsilon_4) = \mathrm{Cov}(X_3, \varepsilon_5) = \mathrm{Cov}(X_4, \varepsilon_5) = \mathrm{Cov}(\varepsilon_2, \varepsilon_3) = \mathrm{Cov}(\varepsilon_2, \varepsilon_4) = \mathrm{Cov}(\varepsilon_2, \varepsilon_5) = \mathrm{Cov}(\varepsilon_3, \varepsilon_4) = \mathrm{Cov}(\varepsilon_3, \varepsilon_5) = \mathrm{Cov}(\varepsilon_4, \varepsilon_5) = 0$

Since some variables are causally independent of one another (e.g. X_1 and ε_4, X_2 and ε_5, and so on), the covariance between them is simply zero

[a] $N(0, \sigma)$ means 'a normally distributed random variable with a population mean of zero and a population standard deviation of σ'. Because our interest is in the causal relations between variables but not the mean values of the variables themselves, all variables are 'centered' by subtracting the mean value of each variable. This treatment ensures that the mean of each transformed variable is zero and thus the intercepts are zero. Besides, since we assume that all error variables (ε) are unit normal variables, so they are with a zero mean and a standard deviation of 1. (Shipley 2002, pp. 105–106)

Box 2. Predicted population variances and covariances for variables described in *Box 1*

	X1	X2	X3	X4	X5
X_1	$\mathrm{Var}(X_1)$	$a_1\mathrm{Var}(X_1)$	$a_1a_2\mathrm{Var}(X_1)$	$a_1a_2a_3\mathrm{Var}(X_1)$	$(a_1a_2a_4 + a_1a_2a_3a_5)\mathrm{Var}(X_1)$
X_2		$\mathrm{Var}(X_2)$	$a_1^2a_2\mathrm{Var}(X_1)$ $+a_2b_2^2\mathrm{Var}(\varepsilon_2)$	$a_1^2a_2a_3\mathrm{Var}(X_1)$ $+a_2a_3b_2^2\mathrm{Var}(\varepsilon_2)$	$(a_1^2a_2a_4 + a_1^2a_2a_3a_5)\mathrm{Var}(X_1)$ $+(a_2a_4b_2^2 + a_2a_3a_5b_2^2)\mathrm{Var}(\varepsilon_2)$
X_3			$\mathrm{Var}(X_3)$	$a_1^2a_2^2a_3\mathrm{Var}(X_1)$ $+a_3b_3^2\mathrm{Var}(\varepsilon_3)$	$(a_1^2a_2^2a_4 + a_1^2a_2^2a_3a_5)\mathrm{Var}(X_1)$ $+(a_4b_3^2 + a_3a_5b_3^2)\mathrm{Var}(\varepsilon_3)$
X_4				$\mathrm{Var}(X_4)$	$a_1^2a_2^2a_3^2a_5\mathrm{Var}(X_1) + a_3a_4\mathrm{Var}(X_3)$ $+a_3^2a_5b_3^2\mathrm{Var}(\varepsilon_3) + a_5b_4^2\mathrm{Var}(\varepsilon_4)$
X_5					$\mathrm{Var}(X_5)$

(This table and the associated calculations are made by myself, though guided by Shipley (2002))

Appendix 2: Derivation of Weisberg's similarity account from the JSC[40]

One can show that Weisberg's similarity index is the weighted average of the similarity coefficients upon mechanisms and attributes. The demonstration goes as follows:

$$J(A, B) = \frac{(A \cap B)}{(A \cup B)}$$

$$W(M_m, T_m) = \frac{(M_m \cap T_m)}{(M_m \cup T_m)} = J(M_m, T_m)$$

[40] I thank Arnaud Pocheville for giving me this demonstration.

$$
\begin{aligned}
W(M_a, T_a) &= \frac{(M_a \cap T_a)}{(M_a \cup T_a)} = J(M_a, T_a) \\
W(M, T) &= \frac{(M_m \cup T_m) J(M_m, T_m) + (M_a \cup T_a) J(M_a, T_a)}{(M_m \cup T_m) + (M_a \cup T_a)} \\
\ldots &= \frac{(M_m \cup T_m) \frac{(M_m \cap T_m)}{(M_m \cup T_m)} + (M_a \cup T_a) \frac{(M_a \cap T_a)}{(M_a \cup T_a)}}{(M_m \cup T_m) + (M_a \cup T_a)} \\
\ldots &= \frac{(M_m \cap T_m) + (M_a \cap T_a)}{(M_m \cup T_m) + (M_a \cup T_a)}
\end{aligned}
$$

The last equation is just Weisberg's formula. If the sets of mechanisms and attributes are disjoint (which in fact is an assumption made by Weisberg), that is, if $M_m \cap M_a = T_m \cap T_a = M_m \cap T_a = T_m \cap M_a = \emptyset$, then Weisberg's similarity index is the Jaccard similarity index on the union of mechanisms and attributes:

$$
\begin{aligned}
W(M, T) &= \frac{(M_m \cap T_m) + (M_a \cap T_a)}{(M_m \cup T_m) + (M_a \cup T_a)} = \frac{((M_m \cup M_a) \cap (T_m \cup T_a))}{((M_m \cup M_a) \cup (T_m \cup T_a))} \\
&= J(M_m \cup M_a, T_m \cup T_a)
\end{aligned}
$$

Proof of this equation follows directly from:

$$|A \cup B| = |A| + |B| - |A \cap B|$$

Let us prove the numerator:

$$
\begin{aligned}
((M_m \cup M_a) \cap (T_m \cup T_a)) &= ((M_m \cap T_m) \cup (M_a \cap T_m) \cup (M_m \cap T_a) \cup (M_a \cap T_a)) \\
\ldots &= ((M_m \cap T_m) \cup (M_a \cap T_a)) \\
\ldots &= ((M_m \cap T_m)) + ((M_a \cap T_a)) \\
&\quad -((M_m \cap T_m) \cap (M_a \cap T_a)) \\
\ldots &= ((M_m \cap T_m)) + ((M_a \cap T_a))
\end{aligned}
$$

The denominator:

$$
\begin{aligned}
((M_m \cup M_a) \cup (T_m \cup T_a)) &= (M_m \cup T_m) + (M_a \cup T_a) + ((M_m \cup T_m) \cap (M_a \cup T_a)) \\
\ldots &= (M_m \cup T_m) + (M_a \cup T_a)
\end{aligned}
$$

This means that if attributes and mechanisms are disjoint, similarity on mechanisms and attributes can be thought of somehow as independent. If mechanisms and attributes were not disjoint, however, elements in the intersection would be counted twice in the average and the Weisberg's similarity index would be simply wrong.

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