Let's talk about Thurstone & Co.: An information-theoretical model for comparative judgments, and its statistical translation

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Abstract

This study revisits Thurstone's law of comparative judgment (CJ), focusing on two prominent issues of traditional approaches. First, it critiques the heavy reliance on Thurstone's Case V assumptions and, by extension, the Bradley-Terry-Luce (BTL) model when analyzing CJ data. Specifically, the study raises concerns about the assumptions of equal discriminal dispersions and zero correlation between the stimuli. While these assumptions simplify the trait measurement process, they may fail to capture the complexity of CJ data, potentially leading to unreliable and inaccurate trait estimates. Second, the study highlights the apparent disconnect between CJ's trait measurement and hypothesis testing processes. Although separating these processes simplifies the analysis of CJ data, it may also undermine the reliability of various statistical results derived from the measurement.

To address these issues, the study extends Thurstone's general form using a systematic and integrated approach based on Causal and Bayesian inference methods. This extension integrates core theoretical principles alongside key assessment design features relevant to CJ experiments, such as the selection of judges, stimuli, and comparisons. It then translates these elements into a probabilistic statistical model for analyzing dichotomous CJ data, overcoming the rigid assumptions of Case V and the BTL model.

Finally, the study emphasizes the relevance of this extension for contemporary empirical CJ research, particularly stressing the need for bespoke CJ models tailored to the specific assumptions of the experiments and data. It also lays the foundation for broader applications, encouraging researchers across the social sciences to adopt more robust and interpretable methodologies.

Keywords: causal inference, directed acyclic graphs, structural causal models, bayesian statistical methods, thurstonian model, comparative judgement, probability, statistical modeling

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1. Introduction

In *comparative judgment* (CJ) studies, judges assess a specific trait or attribute across different stimuli by performing pairwise comparisons (Thurstone, 1927b,a). Each comparison produces a dichotomous outcome, indicating which stimulus is perceived to have a higher trait level. For example, when assessing writing quality, judges compare pairs of written texts (the stimuli) to determine the relative writing quality each text exhibit (the trait) (Laming, 2004; Pollitt, 2012b; Whitehouse, 2012; van Daal et al., 2016; Lesterhuis, 2018a; Coertjens et al., 2017; Goossens and De Maeyer, 2018; Bouwer et al., 2023).

Numerous studies have documented the effectiveness of CJ in assessing traits and competencies over the past decade. These studies have highlighted three aspects of the method's effectiveness: its reliability, validity, and practical applicability. Research on reliability suggests that CJ requires a relatively modest number of pairwise comparisons (Verhavert et al., 2019; Crompvoets et al., 2022) to generate trait scores that are as precise and consistent as those generated by other assessment methods (Coertjens et al., 2017; Goossens and De Maeyer, 2018; Bouwer et al., 2023). In addition, the evidence suggests that the reliability and time efficiency of CJ are comparable, if not superior, to those of other assessment methods when employing adaptive comparison algorithms (Pollitt, 2012b; Verhavert et al., 2022; Mikhailiuk et al., 2021). Meanwhile, research on validity indicates the capacity of CJ scores to represent accurately the traits under measurement (Whitehouse, 2012; van Daal et al., 2016; Lesterhuis, 2018a; Bartholomew et al., 2018; Bouwer et al., 2023). Lastly, research on its practical applicability highlights CJ's versatility across both educational and non-educational contexts (Kimbell, 2012; Jones and Inglis, 2015; Bartholomew et al., 2018; Jones et al., 2019; Marshall et al., 2020; Bartholomew and Williams, 2020; Boonen et al., 2020).

Nevertheless, despite the increasing number of CJ studies, research in this domain remains unsystematic and fragmented, leaving several critical issues unresolved. This study identifies and discusses two prominent issues of traditional approaches that can undermine the reliability and validity of CJ's trait estimates (Perron and Gillespie, 2015, pp. 2). First, it critiques the heavy reliance on Thurstone's Case V assumptions (Thurstone, 1927a) and, by extension, the Bradley-Terry-Luce (BTL) model (Bradley and Terry, 1952; Luce, 1959) when analyzing CJ data. Specifically, the study raises concerns about the assumptions of equal discriminal dispersions and zero correlation between

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the stimuli. While these assumptions simplify statistical modeling, they may fail to capture the complexity of CJ data, potentially leading to unreliable and inaccurate trait estimates. Second, the study highlights the disconnect between CJ's trait measurement and hypothesis testing processes. Although separating these processes simplifies the analysis of CJ data, it may also undermine the reliability of various statistical results derived from the measurement.

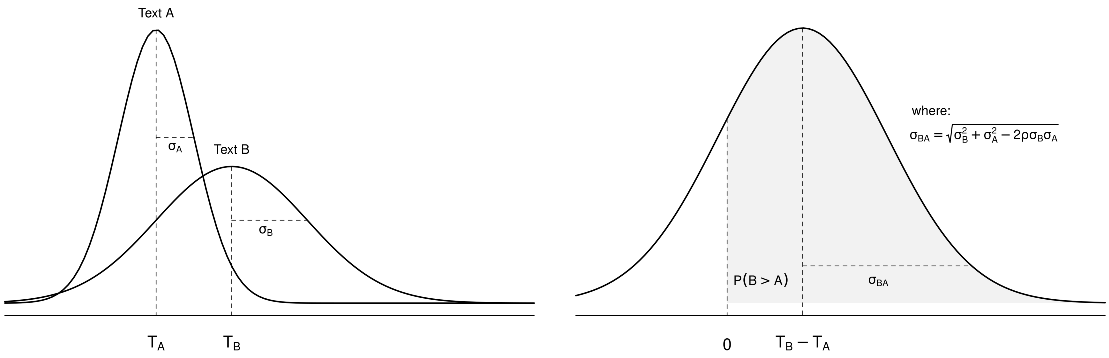
To address these issues, this study extends Thurstone's general form using a systematic and integrated approach based on Causal and Bayesian inference methods. In addition to improving statistical accuracy and strengthening measurement reliability and validity, the approach offers two key advantages. First, it clarifies the interactions among all actors and processes involved in CJ experiments. Second, it shifts the current comparative data analysis paradigm from passively accepting the BTL model assumptions to actively testing whether those assumptions fit the data under analysis.

As a result, the study divides its content into six main sections. Section 2 provides an overview of Thurstone's theory. Section 3 discusses the identified issues in detail. Section 4 extends Thurstone's general form to address these challenges. The extension integrates core theoretical principles alongside key assessment design features relevant to CJ experiments, such as the selection of judges, stimuli, and comparisons. Section 5 translates these theoretical and practical elements into a probabilistic statistical model to analyze dichotomous pairwise comparison data. Section 6 discusses the findings, limitations, and challenges and explores avenues for future research. Finally, Section 7 summarizes the study's conclusions.

2. Thurstone's theory

In its most general form, Thurstone's theory addresses pairwise comparisons wherein a single judge evaluates multiple stimuli (Thurstone, 1927a, pp. 267). The theory posits that two key factors determine the dichotomous outcome of these comparisons: the discriminal process of each stimulus and their discriminal difference. The *discriminal process* captures the psychological impact each stimulus exerts on the judge or, more simply, his perception of the stimulus trait. The theory assumes that the discriminal process for any given stimulus forms a Normal distribution along the trait continuum (Thurstone, 1927a, pp. 266). The mode (mean) of this distribution, known as the *modal discriminal process*, indicates the stimulus position on this continuum, while its dispersion, referred to as the *discriminal dispersion*, reflects variability in the perceived trait of the stimulus.

Figure 1a illustrates the hypothetical discriminal processes along a quality trait continuum for two written texts. The figure indicates that the modal discriminal process for Text B is positioned further along the continuum than that of Text A ($T_B > T_A$), suggesting that Text B exhibits higher quality. Additionally, the figure highlights that Text B has a broader distribution compared to Text A, which arises from its larger discriminal dispersion ($\sigma_B > \sigma_A$).



(a) Discriminal processes

(b) Discriminal difference

Figure 1: Hypothetical discriminal processes and discriminant difference along a quality trait continuum for two written texts.

However, since the individual discriminal processes of the stimuli are not directly observable, the theory introduces the *law of comparative judgment*. This law posits that in pairwise comparisons, a judge perceives the stimulus with a discriminal process positioned further along the trait continuum as possessing more of the trait (Bramley, 2008, pp. 251). This suggests that pairwise comparison outcomes depend on the relative distance between stimuli, not their absolute positions on the continuum. Indeed, the theory assumes that the difference between the underlying discriminal processes of the stimuli, referred to as the *discriminal difference*, determines the observed dichotomous outcome. Furthermore, the theory assumes that because the individual discriminal processes form a Normal distribution on the continuum, the discriminal difference will also conform to a Normal distribution (Andrich, 1978, pp. 452). In this distribution, the mode (mean) represents the relative separation between the stimuli, and its dispersion indicates the variability of that separation.

Figure 1b illustrates the distribution of the discriminal difference for the hypothetical texts depicted in Figure 1a. The figure indicates that the judge perceives Text B as having significantly higher quality than Text A. Two key observations support this conclusion: the positive difference between their modal discriminal processes ($T_B - T_A > 0$) and the probability area where the discriminal difference distinctly favors Text B over Text A, represented by the shaded gray area denoted

Table 1: Thurstones cases and their asumptions

Assumption	**General form**	**Thurstone's**					**BTL model**
		Case I	**Case II**	**Case III**	**Case IV**	**Case V**	
Discriminal process (distribution)	Normal	Normal	Normal	Normal	Normal	Normal	Logistic
Discriminal dispersion (between stimuli)	Different	Different	Different	Different	Similar	Equal	Equal
Correlation (between stimuli)	One per pair	Constant	Constant	Zero	Zero	Zero	Zero
How many judges compare?	Single	Single	Multiple	Multiple	Multiple	Multiple	Multiple

as $P(B > A)$. As a result, the dichotomous outcome of this comparison is more likely to favor Text B over Text A.

3. Two Prominent Issues in Traditional CJ Practice

Thurstone noted from the outset that his general form, described in Section 2, led to a *trait scaling problem*. Specifically, the model required estimating more "unknown" parameters than the number of available pairwise comparisons (Thurstone, 1927a, pp. 267). For instance, in a CJ experiment with five texts, the general form would require estimating 20 parameters: five modal discriminal processes, five discriminal dispersions, and 10 correlations –one per comparison (see Table 1). However, a single judge could only provide $\binom{5}{2} = 10$ unique comparisons, an insufficient data set to estimate the required parameters.

To address this issue and facilitate the practical implementation of the theory, Thurstone developed five cases derived from this general form, each progressively incorporating additional simplifying assumptions into the model. In Case I, Thurstone postulated that pairs of stimuli would maintain a constant correlation across all comparisons. In Case II, he allowed multiple judges to undertake comparisons instead of confining evaluations to a single judge. In Case III, he posited that there was no correlation between stimuli. In Case IV, he assumed that the stimuli exhibited similar dispersions. Finally, in Case V, he replaced this assumption with the condition that stimuli had equal discriminal dispersions. Table 1 summarizes the assumptions of the general form and the five cases. For a detailed discussion of these cases and their progression, refer to Thurstone (1927a) and Bramley (2008, pp. 248–253).

However, Thurstone designed Case V to provide a "rather coarse scaling" of traits (Thurstone, 1927a, pp. 269), prioritizing statistical simplicity over precise trait measurement. He cautioned that its use "should not be made without (an) experimental test" (Thurstone, 1927a, pp. 270), as it imposes the most extensive set of simplifying assumptions among all the proposed cases (Bramley, 2008, pp. 253; Kelly et al., 2022, pp. 677) (see Table 1). Therefore, it is surprising that, despite these limitations, CJ research has predominantly relied on Case V to measure different traits, raising significant concerns about the reliability and validity of such measurements in contexts where the case's assumptions may not hold (Kelly et al., 2022, pp. 677).

Furthermore, since Thurstone's primary goal was to define a psychological scale and "allocate the compared stimuli on this continuum" (Thurstone, 1927a, pp. 269), he did not provide specific guidance on how to use the measurement scores from Case V to conduct hypothesis tests related to the measured traits. Although the CJ practice has circumvented this issue by using the point estimates of the scores or their transformations for such analyses, a fundamental question remains: Is this method appropriate for addressing these inquiries?

Thus, this section discusses these two prominent issues. Specifically, Section 3.1 examines the heavy reliance on Thurstone's Case V assumptions in the statistical analysis of CJ data. Conversely, Section 3.2 focuses on the apparent disconnect between the approaches to trait measurement and hypothesis testing in CJ.

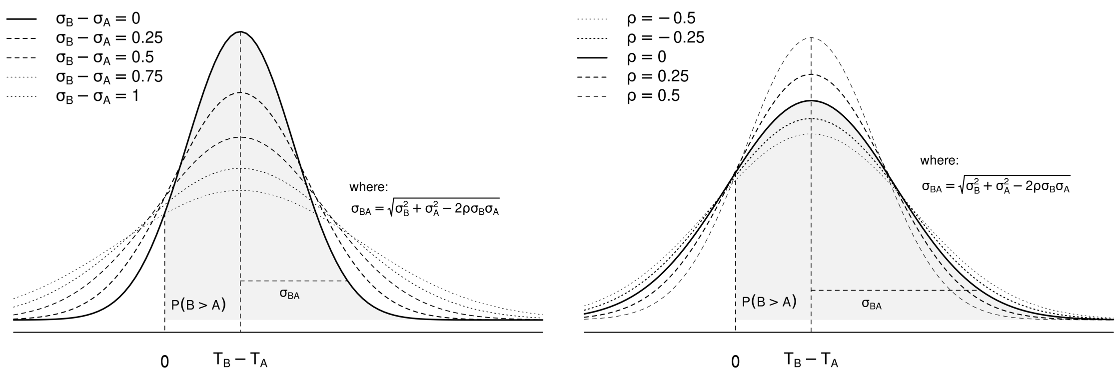
3.1. The Case V and the statistical analysis of CJ data

As previously discussed, Case V remains the most widely used model in CJ literature. This preference primarily stems from the BTL model, which provides a simplified statistical representation of the case. The BTL model mirrors the assumptions of Case V, with one notable distinction: while Case V assumes a Normal distribution for the stimuli' discriminal processes, the BTL model uses the more mathematically tractable Logistic distribution (Andrich, 1978; Bramley, 2008, pp. 254) (see Table 1). However, this substitution has minimal impact on the model's estimation or interpretation because the discriminal process scale is arbitrary up to a non-monotonic transformation (van der Linden, 2017a, pp. 16; McElreath, 2021). Furthermore, this limited impact is supported by the fact that the Normal and Logistic distributions exhibit analogous statistical properties, differing only by a scaling factor of approximately 1.7.

However, Thurstone acknowledged that some assumptions of Case V could be problematic when researchers assess complex traits or heterogeneous stimuli (Thurstone, 1927b, pp. 376). Thus, given that modern CJ applications often involve such traits and stimuli, two key assumptions of Case V, and by extension, the BTL model, may not always hold in theory or practice. These assumptions are the equal dispersion and zero correlation between stimuli.

3.1.1. The assumption of equal dispersions between stimuli

According to the theory, discrepancies in the discriminal dispersions of stimuli shape the distribution of the discriminal difference, directly influencing the outcome of pairwise comparisons. A thought experiment can help illustrate this idea. In this experiment, researchers observe the discriminal processes for two texts, similar to those shown in Figure 1a. Additionally, the discriminal dispersion for Text A remains constant, and the texts are uncorrelated ($\rho = 0$). Figure 2a demonstrates that an increase in the uncertainty associated with the perception of Text B relative to Text A ($\sigma_B - \sigma_A$), broadens the distribution of their discriminal difference. This broadening affects the probability area where the discriminal difference distinctly favors Text B over Text A, expressed as $P(B > A)$, ultimately influencing the comparison outcome. Additionally, the figure reveals that when the discriminal dispersions of the texts are equal, as in the BTL model ($\sigma_B - \sigma_A = 0$), the discriminal difference is more narrow than when the dispersions differ. As a result, the discriminal difference is more likely to favor Text B over Text A, as it is represented by the shaded gray area.



(a) Discrepancies in the dispersions of stimuli

(b) Correlation between stimuli

Figure 2: The effect of dispersion discrepancies and stimuli correlation on the distribution of the discriminal difference.

In experimental practice, however, the thought experiment occurs in reverse. Researchers first observe the comparison outcome and then use the BTL model to infer the discriminal difference between stimuli and their respective discriminal processes (Thurstone, 1927b, pp. 373). Consequently, the outcome's ability to reflect *true* differences between stimuli largely depends on the validity of the model's assumptions (Kohler et al., 2019, pp. 150), in this case, the assumption of equal dispersions. For instance, when the assumption accurately captures the complexity of the data, the BTL model estimates a discriminal difference distribution that accurately represents the *true* discriminal difference between the texts. This scenario is illustrated in Figure 2a, when the model's discriminal difference distribution aligns with the *true* discriminal difference distribution, represented by the thick continuous line corresponding to $\sigma_B - \sigma_A = 0$. The accuracy of this discriminal difference then ensures reliable estimates for the texts' discriminal processes.

Notably, while the assumption of equal dispersions simplifies the trait measurement process, evidence from the CJ literature suggests that the BTL model may fail to capture the complexity of modern CJ data. Specifically, the assumption of equal dispersions may not hold when researchers assess complex traits or heterogeneous stimuli (Thurstone, 1927b, pp. 376; Bramley, 2008, pp. 273; Kelly et al., 2022, pp. 678), as these traits and stimuli can introduce judgment discrepancies due to their unique characteristics (van Daal et al., 2016; Lesterhuis, 2018b; Chambers and Cunningham, 2022). Indeed, the CJ literature may already provide evidence of such discrepancies, particularly in the form of "misfit" statistics. For instance, *misfit texts* are those whose comparisons result in more judgment discrepancies than those involving other texts (Pollitt, 2004, pp. 11; Pollitt, 2012b, pp. 290).

These discrepancies may arise from two possible causes. First, the discriminal processes of misfit texts may substantially overlap with those of non-misfit texts. Second, misfit texts may represent outlying observations with characteristics that make them difficult to compare and position on the trait scale. Regarding the first cause, the overlap can occur when misfit texts have equal dispersion and share the same trait space as non-misfit texts or when they exhibit larger discriminal dispersions. Although the BTL model can distinguish the first scenario, it is inherently agnostic to the second. Figure 1a illustrates how an increased discriminal dispersion can widen the overlap between two texts, leading to more judgment discrepancies. In the figure, text B has a broader discriminal dispersion than text A, expanding the overlap between their discriminal processes, a space where judges struggle to determine which text possesses more of the trait.

When the assumption of equal dispersions between stimuli does not hold, significant statistical and measurement issues can arise Specifically, the BTL model may overestimate the trait's reliability, that is, the degree to which the outcome accurately reflects the *true* discriminal differences between stimuli. This overestimation, in turn, results in spurious conclusions about these differences (McElreath, 2020, pp. 370) and, by extension, about the underlying discriminal processes of stimuli. Figure 2a also illustrates this scenario when the model's discriminal difference distribution aligns with the thick continuous line for $\sigma_B - \sigma_A = 0$, while the *true* discriminal difference follows any discontinuous line where $\sigma_B - \sigma_A \neq 0$.

Finally, regarding the second cause, if researchers recognize that misfit statistics may represent outlying observations, the conventional CJ practice of excluding stimuli based on these statistics

(Pollitt, 2012a,b; van Daal et al., 2016; Goossens and De Maeyer, 2018), may unintentionally discard valuable information, introducing bias into the trait estimates (Zimmerman, 1994; McElreath, 2020, chap. 12). The direction and magnitude of these biases remain unpredictable, as they depend on which stimuli researchers exclude from the analysis.

3.1.2. The assumption of zero correlation between stimuli

The correlation ρ measures how much the judges' perception of a specific trait in one stimulus depends on their perception of the same trait in another. As with the discriminal dispersions, this correlation shapes the distribution of the discriminal difference, directly impacting the outcomes of pairwise comparisons. A similar thought experiment, as the one depicted in Section 3.1.1, can illustrate this idea. The experiment only assumes that the discriminal dispersions for both texts remain constant. Figure 2b reveals that as the correlation between the texts increases, the distribution of their discriminal difference becomes narrower. This narrowing affects the area under the curve where the discriminal difference distinctly favors Text B over Text A, denoted as $P(B > A)$, thus influencing the comparison outcome. Furthermore, the figure shows that when two texts are independent or uncorrelated ($\rho = 0$), their discriminal difference is less narrow compared to scenarios where the texts are positively correlated. As a result, the discriminal difference is less likely to favor Text B over Text A, as it is represented by the shaded gray area.

As outlined in the previous section, researchers approach this process in reverse. They begin by observing the outcomes and using the BTL model to estimate the stimuli' discriminal differences and discriminal processes. Given that the BTL model assumes independent discriminal processes across comparisons, if this assumption holds in the data, the model estimates a discriminal difference distribution that accurately reflects the *true* discriminal difference between the texts. Once more, the accuracy of the discriminal difference ensures reliable estimates for the discriminal processes of the texts.

Thurstone assumed that stimuli were uncorrelated because judges' biases, arising from two opposing and equally weighted effects occurring during the pairwise comparisons, canceled each other out (Thurstone, 1927a, pp. 268). Andrich (1978) provided a mathematical demonstration of this cancellation using the BTL model under the assumption of discriminal processes with additive biases. However, evidence from the CJ literature indicates that the assumption of zero correlation does not hold in practice in at least two scenarios: when intricate aspects of multidimensional, complex traits or heterogeneous stimuli influence judges' perceptions or when additional hierarchical structures are relevant to the stimuli.

In the first scenario, research on text quality suggests that when judges evaluate multidimensional, complex traits or heterogeneous stimuli, they often rely on various intricate characteristics of the stimuli to form their judgments (van Daal et al., 2016; Lesterhuis, 2018b; Chambers and Cunningham, 2022). These additional relevant characteristics, when assessed, are unlikely to be equally weighted or opposing. As a result, they may exert an uneven influence on judges' perceptions, creating biases that resist cancellation. For example, this could occur when a judge assessing the argumentative quality of a text places more weight on its grammatical accuracy than other judges, thereby favoring texts with fewer errors but weaker arguments. Furthermore, since the discriminal difference of the stimuli becomes an observable outcome only through the judges' perceptions, these biases could introduce dependencies between the stimuli (van der Linden, 2017b, pp. 346). While direct evidence for this particular scenario is lacking, studies such as Pollitt and Elliott (2003) demonstrate the presence of such biases, supporting the notion that the factors influencing pairwise comparisons may not always cancel out.

In the second scenario, the shared context or inherent connections introduced by additional hierarchical structures may create dependencies between stimuli, a statistical phenomenon known as clustering (Everitt and Skrondal, 2010). Although the CJ literature acknowledges the existence of such hierarchical structures, the statistical approaches to account for this additional source of dependence have been insufficient. For instance, when CJ data incorporates multiple samples of stimuli from the same individuals, researchers frequently rely on (averaged) point estimates of the BTL scores to conduct subsequent analyses and tests at the individual level (Bramley and Vitello, 2019; Boonen et al., 2020; Bouwer et al., 2023; van Daal et al., 2017; Jones et al., 2019; Gijsen et al., 2021). However, this approach can introduce additional statistical and measurement issues, which we discuss in greater detail in Section 3.2.

Thus, erroneously assuming zero correlation between stimuli can also lead to significant statistical and measurement issues. Specifically, neglecting judges' biases or relevant hierarchical structures can create dimensional mismatches in the model, leading to the over- or underestimation of trait reliability (Ackerman, 1989; Hoyle, 2023, pp. 341, 482). These inaccuracies can result in spurious conclusions about the discriminal differences (McElreath, 2020, pp. 370) and, by extension, the underlying discriminal processes of the stimuli. This issue is illustrated in Figure 2b when the discriminal difference distribution of the BTL model follows the thick continuous line ($\rho = 0$), while the *true* discriminal difference follows any discontinuous line where ($\rho \neq 0$).

Finally, as discussed in the previous section, removing judges based on misfit statistics risks discarding valuable information and even introduce bias into the trait estimates (Zimmerman, 1994; McElreath, 2020, chap. 12). The direction and magnitude of these biases remain unpredictable because they depend on which judges researchers exclude from the analysis. *Misfit judges* are those whose evaluations deviate substantially from the shared consensus due to the unique characteristics of either the stimuli or the judges themselves (Pollitt, 2012a, pp. 164-165; Pollitt, 2012b, pp. 289-290; van Daal et al., 2016, pp. 4; Goossens and De Maeyer, 2018, pp. 20).

3.2. The disconnect between trait measurement and hypothesis testing

Building on the previous section, it is clear that, researchers typically rely on the BTL model to measure a trait and place the compared stimuli along its continuum (Thurstone, 1927a, pp. 269). Additionally, the CJ literature shows that researchers frequently use point estimates of BTL scores or their transformations to conduct further analyses or hypothesis tests. For example, researchers have used these scores to identify 'misfit' judges and stimuli (Pollitt, 2012b; van Daal et al., 2016; Goossens and De Maeyer, 2018), detect biases in judges' ratings (Pollitt and Elliott, 2003; Pollitt, 2012b), calculate correlations with other assessment methods (Goossens and De Maeyer, 2018; Bouwer et al., 2023), or test hypotheses related to the underlying trait of interest (Casalicchio et al., 2015; Bramley and Vitello, 2019; Boonen et al., 2020; Bouwer et al., 2023; van Daal et al., 2017; Jones et al., 2019; Gijsen et al., 2021).

Nevertheless, while separating the trait measurement and hypothesis testing processes simplifies the analysis of CJ data, the statistical literature cautions against relying solely on the point estimates of BTL scores to conduct further analyses or hypothesis tests, as this practice can undermine the resulting statistical conclusions. A key consideration is that BTL scores are parameter estimates that inherently carry uncertainty (measurement error). Ignoring this uncertainty can bias the analysis and reduce the precision of hypothesis tests. The direction and magnitude of such biases are often unpredictable. Results may be attenuated, exaggerated, or remain unaffected depending on the degree of uncertainty in the scores and the actual effects being tested (Kline, 2023, pp. 25; Hoyle, 2023, pp. 137). Furthermore, the reduced precision in hypothesis tests diminishes their statistical power, increasing the likelihood of committing type-I or type-II errors (McElreath, 2020). Figure 3 illustrates these issues, demonstrating how neglecting measurement error by relying only on outcome averages can reduce the precision of a predictor's estimated effect.

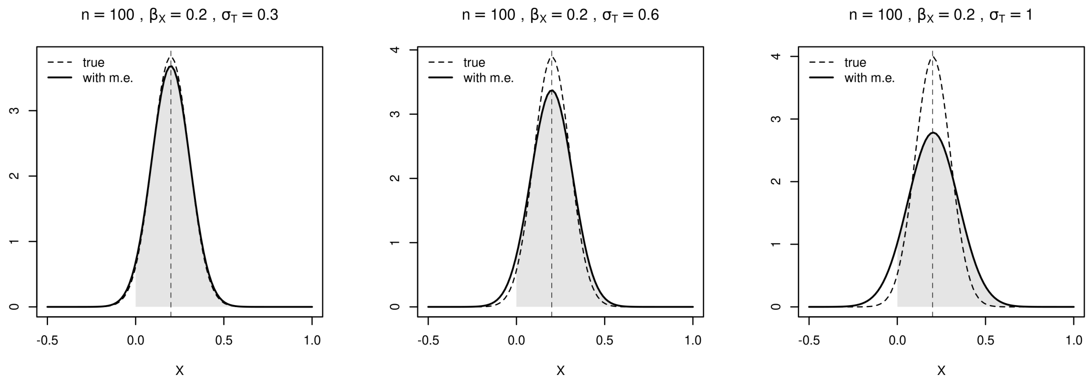


Figure 3: The effect of outcome uncertainty on the estimation of an effect β linked to the predictor. Uncertainty increases from left to right.

In aggregate, the heavy reliance on Thurstone's Case V assumptions in the statistical analysis of comparative data can compromise the reliability of trait estimates. This overreliance may also undermine their validity (Perron and Gillespie, 2015, pp. 2), particularly when coupled with the disconnect between the trait measurement and hypothesis testing processes. However, the structural approach to causal inference can address these issues by offering a systematic and integrated framework that strengthens measurement reliability and validity while enhancing the statistical accuracy of hypothesis tests.

4. Extending Thurstone's general form

The *structural approach* to causal inference provides a formal framework for identifying causes and estimating their effects using data. The approach uses structural causal models (SCMs) and directed acyclic graphs (DAGs) (Pearl, 2009; Pearl et al., 2016; Gross et al., 2018; Neal, 2020) to formally and graphically represent the assumed causal structure of a system, such as the one found in CJ experiments. Essentially, SCMs and DAGs function as *conceptual models* on which identification analysis rests (Schuessler and Selb, 2023, pp. 4). *Identification analysis* helps researchers to determine whether an estimator can accurately compute an estimand based solely on its (causal) assumptions, regardless of random variability (Schuessler and Selb, 2023, pp. 4). Here, *estimands* represent the specific quantities researchers aim to determine (Everitt and Skrondal, 2010). *Estimators* denote the methods or functions that transform data into an estimate, while *estimates* are the numerical values approximating the estimand (Neal, 2020; Everitt and Skrondal, 2010).

A motivating example that will appear in the rest of the document clarifies these concepts. In this example, researchers aim to determine: "To what extent do different teaching methods influence students' ability to produce high-quality written texts?" To investigate this, a researcher designs a CJ experiment by randomly assigning students (individuals) to two groups, each receiving a different teaching method. Judges then compare pairs of students' written texts (stimuli) to produce a dichotomous outcome reflecting the relative quality of each text (trait). Based on this setup, researchers can reformulate the research question as the estimand: "*On average*, is there a difference in the ability to produce high-quality written texts between the two groups of students?". Following current CJ practices, researchers then rely on estimates from the BTL model, or its transformations, to approximate this estimand.

However, Section 3 presents compelling evidence that Thurstone's Case V, and by extension the BTL model, suffers from several statistical and measurement limitations. These limitations hinder the model's ability to identify various estimands relevant to CJ inquiries, including the one described in the example. Identification is crucial because it is a necessary condition for ensuring consistent estimators. *Consistency* refers to the property of an estimator whose estimates converge to the "true" value of the estimand as the data size approaches infinity (Everitt and Skrondal, 2010). Without identification, consistency cannot be achieved, even with "infinite" and error-free data. Thus, deriving meaningful insights from finite data becomes impossible (Schuessler and Selb, 2023, pp. 5).

Luckily, SCMs and DAGs support identification analysis through two key advantages. First, regardless of complexity, they can represent various causal structures using only five fundamental building blocks (Neal, 2020; McElreath, 2020). This feature allows researchers to decompose complex structures into manageable components, facilitating their analysis (McElreath, 2020). Second, they depict causal relationships in a non-parametric way. This flexibility enables feasible identification strategies without requiring specification of the types of variables, the functional forms relating them, or the parameters of those functional forms (Pearl et al., 2016, pp. 35).

Thus, this section addresses the issues identified in Section 3 by extending Thurstone's general form using the structural approach to Causal inference. Specifically, it combines the core theoretical principles outlined in Section 2 with key assessment design features relevant to CJ experiments, such as the selection of judges, stimuli, and comparisons. In addition to improving statistical accuracy and strengthening measurement reliability and validity, the approach offers two key advantages. First, it clarifies the interactions among all actors and processes involved in CJ experiments. Second, it shifts the current comparative data analysis paradigm from passively accepting the model assumptions to actively testing whether those assumptions fit the data under analysis.

Accordingly, Section 4.1 incorporates the theoretical principles into what we refer to as the *conceptual-population model*. This model assumes that researchers have access to a *conceptual population* of comparative data, that is, data representing all repeated judgments made by every available judge for each pair of stimuli produced by each pair of individuals in the population. Conversely, Section 4.2 integrates the assessment design features into what we refer to as the *sample-comparison model*. This model assumes a more realistic scenario where researchers only have access to a sample of judges, individuals, stimuli, and comparisons from the conceptual population.

4.1. The conceptual-population model

In the conceptual-population model, we assume an idealized scenario where researchers have access to a *conceptual population* of comparative data –data representing all repeated judgments made by each judge for every stimulus pair produced by each pair of individuals in the population. This assumption allows us to integrate Thurstone's theoretical principles and propose innovations to address some of the issues raised in Section 3.

4.1.1. Integrating the first theoretical principles

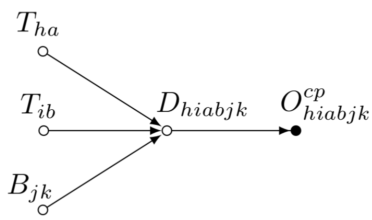
Before incorporating the theoretical principles into the *conceptual-population model*, it is essential to further define SCMs. SCMs are formal mathematical models characterized by a set of *endogenous* variables V, a set of *exogenous* variables E, and a set of functions F (Pearl, 2009; Cinelli et al., 2020). Endogenous variables are those whose causal mechanisms a researcher chooses to model (Neal, 2020). In contrast, exogenous variables represent *errors* or *disturbances* arising from omitted factors that the investigator chooses not to model explicitly (Pearl, 2009, pp. 27,68). Lastly, the functions, referred to as *structural equations*, express the endogenous variables as non-parametric functions of other endogenous and exogenous variables. These functions use the symbol ':=' to denote the asymmetrical causal dependence between variables and the symbol ' $\perp$ ' to represent *d-separation*, a concept akin to (conditional) independence.

SCM 4a illustrates the first theoretical principles of the conceptual-population model designed to examine the impact of different teaching methods on students' writing ability. This SCM outlines the relationship between the conceptual-population outcome (O^{cp}_{hiabjk}) and several related variables. The subscripts h and i label the students who authored the texts (individuals), while the indices a and b represent the compared texts (stimuli). The index j refers to the judge, and k represents the judgment index, accounting for experimental conditions where judges perform the same judgment multiple times, i.e., a *repeated measures design* (Lawson, 2015, pp. 366-376). Notably, the indexing system facilitates comparisons between texts written by the same student ($h = i$, $a \neq b$) and between texts written by distinct students ($h \neq i$, where $a = b$ is possible). However, it excludes cases where judges compare a student's text to itself ($h = i$, $a = b$), as such comparison lacks practical relevance within the CJ framework.

In line with Thurstone's theory, SCM 4a depicts the texts' discriminal processes (T_{ha}, T_{ib}) and their discriminal difference (D_{hiabjk}) (see Section 2). Additionally, based on the arguments developed in Section 3.1.2 and the recommendations of Andrich (1978) and Wainer et al. (1978), the SCM incorporates the judges' biases (B_{kj}). Together with the outcome, these variables constitute the preliminary set of endogenous variables, $V = \{O_{hiabjk}, D_{hiabjk}, T_{ha}, T_{ib}, B_{kj}\}$. Finally, the SCM presents the preliminary set of structural equations, $F = \{f_O, f_D\}$, which define the non-parametric dependencies among these variables.

$$O^{cp}_{hiabjk} := f_O(D_{hiabjk})$$
$$D_{hiabjk} := f_D(T_{ha}, T_{ib}, B_{jk})$$

(a) SCM



(b) DAG

Figure 4: Conceptual-population model, scalar form.

Notably, every SCM has an associated DAG (Pearl et al., 2016; Cinelli et al., 2020). A DAG is a *graph* consisting of nodes connected by edges, where nodes represent random variables. The term *directed* indicates that edges or arrows extend from one node to another, indicating the direction of causal influence. The absence of an edge implies no direct relationship between the nodes. The term *acyclic* means that the causal influences do not form loops, ensuring the influences do not cycle back on themselves (McElreath, 2020). DAGs conventionally depict observed variables as solid black circles and unobserved (latent) variables as open circles (Morgan and Winship, 2014). They also display conditioned variables by surrounding them with a square. Here, *conditioning* refers to restricting the statistical analysis to a subset of the population defined by the values of the given variable (Neal, 2020, pp. 32). Although DAGs often omit exogenous variables for simplicity, this section includes exogenous variables to improve clarity and reveal potential issues related to conditioning and confounding (Cinelli et al., 2020).

Figure 4b displays the DAG corresponding to SCM 4a, illustrating the expected causal relationships outlined in Thurstone's theory. The graph shows that the discriminal processes of the texts (T_{ha}, T_{ib}) influence their discriminal difference (D_{hiabjk}), which in turn determines the outcome (O^{cp}_{hiabjk}). It also highlights the influence of judges' biases (B_{kj}) on the discriminal difference. Additionally, the DAG differentiates between observed endogenous variables, such as the outcome (solid black circle), and latent endogenous variables, including the texts' discriminal processes, their discriminal difference, and the judges' biases (open circles).

4.1.2. *The* conceptual population *data structure*

Although specifying a system's data structure is not mandatory when using SCMs and DAGs, defining one in this case can improve clarity and facilitate the description of the system. Thus, to re-express the scalar form of the CJ system shown in Figure 4 into an equivalent vectorized form, we first define the vectors I and J, along with the matrices IA and JK, as follows:

$$I = \begin{bmatrix} 1 \\ 2 \\ \vdots \\ h \\ \vdots \\ i \\ \vdots \\ n_I \end{bmatrix} ; \; J = \begin{bmatrix} 1 \\ 2 \\ \vdots \\ j \\ \vdots \\ n_J \end{bmatrix} ; \; IA = \begin{bmatrix} 1 & 1 \\ 1 & 2 \\ \vdots & \vdots \\ 1 & n_A - 1 \\ 1 & n_A \\ \vdots & \vdots \\ h & a \\ \vdots & \vdots \\ i & b \\ \vdots & \vdots \\ n_I & n_A - 1 \\ n_I & n_A \end{bmatrix} ; \; JK = \begin{bmatrix} 1 & 1 \\ 1 & 2 \\ \vdots & \vdots \\ 1 & n_K - 1 \\ 1 & n_K \\ \vdots & \vdots \\ j & k \\ \vdots & \vdots \\ n_J & n_K - 1 \\ n_J & n_K \end{bmatrix} \tag{1}$$

Here, each element of I represents a unique individual h or i, where n_I denotes the total number of individuals. Similarly, each element of J corresponds to a unique judge j, with n_J indicating the total number of judges. Moreover, each row of IA represents a unique pairing of individuals h, i with stimuli a, b. As a result, the matrix IA contains $(n_I \cdot n_A)$ rows and 2 columns, where n_A specifies the number of stimuli available per individual. Likewise, each row of JK associates a judge j with a judgment index k. Consequently, the matrix JK has $(n_J \cdot n_K)$ rows and 2 columns, where n_K indicates the number of judgments each judge makes.

Additionally, we construct the matrix R to map each row of the IA matrix with a corresponding row from the JK matrix. Thus, this matrix has n rows and 6 columns, where $n = \binom{n_I \cdot n_A}{2} \cdot n_J \cdot n_K$. Here, the term $\binom{n_I \cdot n_A}{2}$ represents the binomial coefficient, which quantifies the total number of unique comparisons possible between every pair of stimuli generated by each pair of individuals in the population. Whe define the matrix as follows:

$$R = \begin{bmatrix} 1 & 1 & 1 & 2 & 1 & 1 \\ 1 & 1 & 1 & 2 & 1 & 2 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & 1 & 1 & 2 & 1 & n_K - 1 \\ 1 & 1 & 1 & 2 & 1 & n_K \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ h & i & a & b & j & k \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ n_I & n_I & n_A - 1 & n_A & n_J & 1 \\ n_I & n_I & n_A - 1 & n_A & n_J & 2 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ n_I & n_I & n_A - 1 & n_A & n_J & n_K - 1 \\ n_I & n_I & n_A - 1 & n_A & n_J & n_K \end{bmatrix} \tag{2}$$

It is easier to visualize the structure of these vectors and matrices by considering an example where $n_I = 5$, $n_A = 2$, $n_J = 3$, and $n_K = 3$. In this simple case, the vectors and matrices described in equations (1) and (2) take the following form:

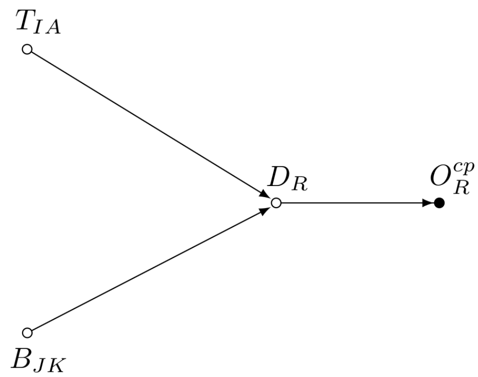
$$I = \begin{bmatrix} 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{bmatrix} ; \; J = \begin{bmatrix} 1 \\ 2 \\ 3 \end{bmatrix} ; \; IA = \begin{bmatrix} 1 & 1 \\ 1 & 2 \\ 2 & 1 \\ 2 & 2 \\ 3 & 1 \\ 3 & 2 \\ 4 & 1 \\ 4 & 2 \\ 5 & 1 \\ 5 & 2 \end{bmatrix} ; \; JK = \begin{bmatrix} 1 & 1 \\ 1 & 2 \\ 1 & 3 \\ 2 & 1 \\ 2 & 2 \\ 2 & 3 \\ 3 & 1 \\ 3 & 2 \\ 3 & 3 \end{bmatrix} ; \; R = \begin{bmatrix} 1 & 1 & 1 & 2 & 1 & 1 \\ 1 & 1 & 1 & 2 & 1 & 2 \\ 1 & 1 & 1 & 2 & 1 & 3 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & 1 & 5 & 1 & 1 & 1 \\ 1 & 1 & 5 & 1 & 1 & 2 \\ 1 & 1 & 5 & 1 & 1 & 3 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & 1 & 5 & 1 & 3 & 1 \\ 1 & 1 & 5 & 1 & 3 & 2 \\ 1 & 1 & 5 & 1 & 3 & 3 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 5 & 1 & 5 & 2 & 3 & 1 \\ 5 & 1 & 5 & 2 & 3 & 2 \\ 5 & 1 & 5 & 2 & 3 & 3 \end{bmatrix}$$

Now, using equations (1) and (2), we can re-express SCM 4a and DAG 4b in an equivalent vectorized form, as shown in Figure 5. In this depiction, the outcome O_R^{cp}, the texts' discriminal difference D_R, their discriminal processes T_{IA}, and the judges' biases B_{JK} are represented as vectors rather than scalar values. These vectors capture all the observations from the conceptual population. Specifically, O_R^{cp} and D_R are observed and latent vectors of length n, respectively. Moreover, T_{IA} and B_{JK} are latent vectors of lengths $(n_I \cdot n_A)$ and $(n_J \cdot n_K)$, respectively.

$$O_R^{cp} := f_O(D_R)$$

$$D_R := f_D(T_{IA}, B_{JK})$$

(a) SCM



(b) DAG

Figure 5: Conceptual-population model, vectorized form.

4.1.3. Integrating hierarchical structural components

The conceptual-population model integrates two *hierarchical structural components* to examine how different teaching methods influence students' writing ability. This approach builds on the principles of Structural Equation Modeling (SEM) (Hoyle, 2023, pp. 138) and Item Response Theory (IRT) (Fox, 2010, chap. 6; van der Linden, 2017a, chap. 24). Each structural component defines how observed or latent variables affect the primary latent variable of interest (Everitt and Skrondal, 2010). Their hierarchical nature enables researchers to test hypotheses while accounting for uncertainties associated with trait estimation (see Section 3.2), particularly when stimuli exhibit a hierarchical structure (see Section 3.1.2).

The top branch of DAG 6b depicts the first component. This component describes how the students' writing-quality trait (T_I) and a set of *relevant* text-related variables (X_{IA}) (e.g., text length) causally influence the texts' written-quality trait (T_{IA}). The DAG also highlights the idiosyncratic errors (e_{IA}), which capture variations in the texts' trait that neither the students' trait nor other relevant text-related variables can explain. In this structure, T_I and e_{IA} are latent vectors of length n_I and $(n_I \cdot n_A)$, respectively. Additionally, X_{IA} is an observed matrix with a dimension of $(n_I \cdot n_A)$ rows and q_{IA} columns (variables).

Additionally, the DAG's top branch illustrates how a set of *relevant* student-related variables (X_I), such as the teaching method, causally influence the students' writing-quality trait (T_I). The DAG also includes the idiosyncratic errors (e_I), which capture variations in the students' traits that the relevant student-related variables cannot explain. Here, e_I is a latent vector of length n_I, and X_I can be an observed matrix with n_I rows and q_I columns (variables).

Here, *relevant* refers to variables that satisfy the *backdoor criterion* (Neal, 2020, pp 37), that is, they belong to a *sufficient adjustment set* (Pearl, 2009; Pearl et al., 2016; Morgan and Winship, 2014). A *sufficient* set (potentially empty) blocks all non-causal paths between a predictor and an outcome without opening new ones (Pearl, 2009).

$$O_R^{cp} := f_O(D_R)$$

$$D_R := f_D(T_{IA}, B_{JK})$$

$$T_{IA} := f_T(T_I, X_{IA}, e_{IA})$$

$$T_I := f_T(X_I, e_I)$$

$$B_{JK} := f_B(B_J, Z_{JK}, e_{JK})$$

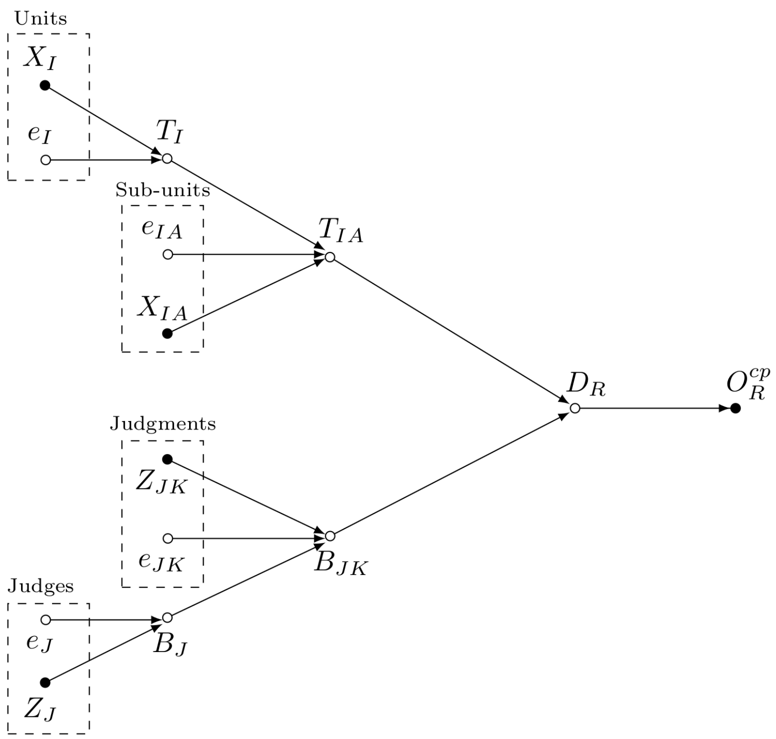
$$B_J := f_B(Z_J, e_J)$$

$$e_I \perp \{e_J, e_{IA}, e_{JK}\}$$

$$e_J \perp \{e_{IA}, e_{JK}\}$$

$$e_{IA} \perp e_{JK}$$

(a) SCM



(b) DAG

Figure 6: Conceptual-population model, final vectorized form.

Similarly, the bottom branch of DAG 6b depicts the second component. This component describes how the judges' bias (B_J) and a set of *relevant* judgment-related variables (Z_{JK}) (e.g., the number of judgments a judge makes) causally influence the biases associated with each text B_{JK}. The DAG also highlights the idiosyncratic errors (e_{JK}), which capture variations in the texts' bias that neither the judges' bias nor other relevant judgment-related variables can explain. In this description, B_J and e_{JK} are latent vectors of length n_J and $(n_J \cdot n_K)$, respectively. Additionally, Z_{JK} is an observed matrix with a dimension of $(n_J \cdot n_K)$ rows and q_{JK} columns.

Moreover, the DAG's bottom branch describes how a set of *relevant* judge-related variables (Z_J), such as judgment expertise, causally influence the judges' bias (B_J). The DAG also accounts for idiosyncratic errors (e_J), capturing the variations in the judges' bias that relevant judge-related variables cannot explain. Here, e_J is a latent vector of length n_J, and Z_J is an observed matrix with n_J rows and q_J columns.

Notably, all variables and functions shown in SCM 6a and DAG 6b define the set of endogenous variables V, structural equations F, and exogenous variables E for the conceptual-population model. Additionally, the figures demonstrate that all exogenous variables are independent of one another, as indicated by the relationships $e_{IA} \perp \{e_I, e_{JK}, e_J\}$, $e_I \perp \{e_{JK}, e_J\}$ and $e_{JK} \perp e_J$.

Overall, the conceptual-population model extends Thurstone's general form by introducing key innovations to address the limitations discussed in Section 3.1.2 and Section 3.2. These enhancements include accounting for judges' biases and integrating hierarchical structural components. Nevertheless, despite its promise of enhancing measurement accuracy and precision, the model still depends on the unrealistic assumption that researchers have access to a *conceptual population* of comparative data, encompassing all repeated judgments from every judge for each pair of stimuli produced by every individual in the population. Since researchers rarely meet this assumption in practice, they must consider a more realistic scenario. The extensions to the conceptual-population model, derived from this realistic scenario, are concisely described in the sample-comparison model.

4.2. The sample-comparison model

In the sample-comparison model, we assume a more realistic scenario than the conceptual-population model. Specifically, we assume researchers have access to a data sample consisting of a limited number of judgments (n_K^s) from a sample of judges (n_J^s) and a specific number of texts (n_A^s) from a sample of students (n_I^s), drawn from the conceptual population. Additionally, we assume that judges do not make *all possible comparisons* allowed by the sample, but rather only n_C comparisons.

4.2.1. The sample mechanism

To facilitate the interpretation of the sample-comparison model, we first define the data sample using several binary vector variables: S_I, S_J, S_{IA}, S_{JK}, and S as follows.

$$S_I = \begin{bmatrix} i_{(1)} \\ i_{(2)} \\ \vdots \\ i_{(h)} \\ \vdots \\ i_{(i)} \\ \vdots \\ i_{(nI)} \end{bmatrix} ;\ S_J = \begin{bmatrix} j_{(1)} \\ j_{(2)} \\ \vdots \\ j_{(j)} \\ \vdots \\ j_{(nJ)} \end{bmatrix} ;\ S_{IA} = \begin{bmatrix} ia_{(1)} \\ ia_{(2)} \\ \vdots \\ ia_{(ia)} \\ \vdots \\ ia_{(nI \cdot nA)} \end{bmatrix} ;\ S_{JK} = \begin{bmatrix} jk_{(1)} \\ jk_{(2)} \\ \vdots \\ jk_{(jk)} \\ \vdots \\ jk_{(nJ \cdot nK)} \end{bmatrix} ;\ S = \begin{bmatrix} s_{(1)} \\ s_{(2)} \\ \vdots \\ s_{(s)} \\ \vdots \\ s_{(n)} \end{bmatrix} \tag{3}$$

Each element of the vectors S_I and S_J is a binary value that indicates the presence (1) or absence (0) of data in the I and J vectors, as defined in equation (1). Therefore, the vector S_I contains n_I elements, and the vector S_J contains n_J elements. For example, we define each element of the vector S_I as in equation (4), and we apply a similar definition to S_J.

$$i_{(i)} = \begin{cases} 1 & \text{if the data for the } i \text{ element of } I \text{ is observed} \\ 0 & \text{if the data for the } i \text{ element of } I \text{ is missing} \end{cases} \tag{4}$$

Each element of the vectors S_{IA} and S_{JK} is defined like $i_{(i)}$ with vector I, but applied to data in the matrices IA and JK, as defined in equation (1). Therefore, the vector S_{IA} contains $n_I \cdot n_A$ elements, and the vector S_{JK} contains $n_J \cdot n_K$ elements. For example, we define each element of the vector S_{IA} as in equation (5), and we apply a similar definition to S_{JK}.

$$ia_{(ia)} = \begin{cases} 1 & \text{if the data for the } i, a \text{ elements of } IA \text{ are observed} \\ 0 & \text{if the data for the } i, a \text{ elements of } IA \text{ are missing} \end{cases} \tag{5}$$

The equation shows that the observed values in the S_I and S_J vectors determine the binary values in the S_{IA} and S_{JK} vectors, through the IA and JK matrices, respectively. Specifically, researchers cannot observe stimuli and judgments for individuals and judges they did not sample initially.

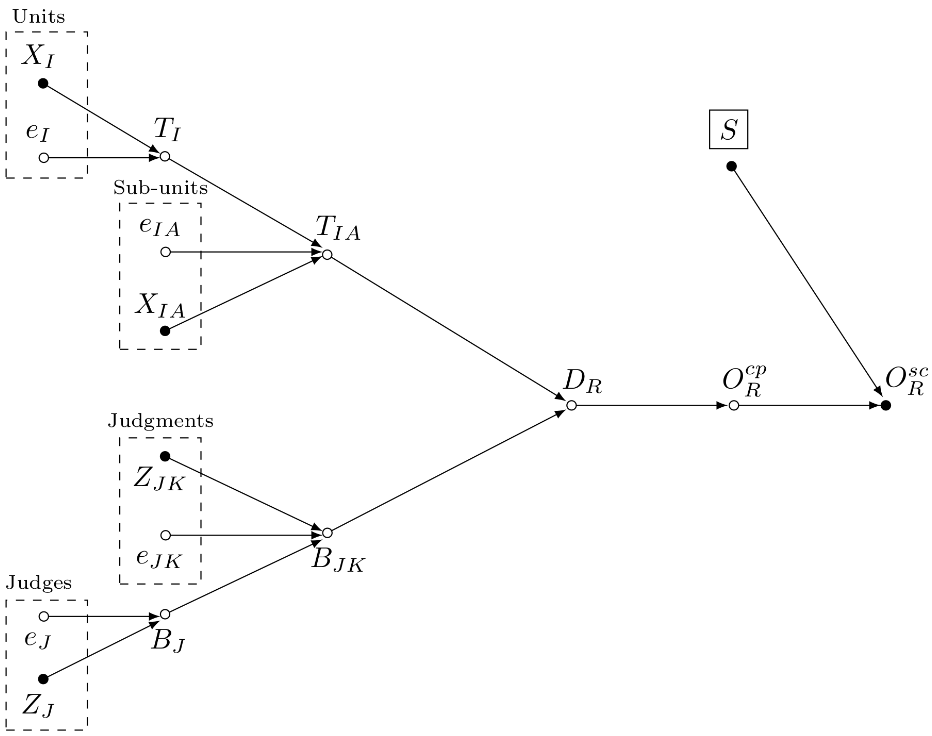
Finally, the vector S in equation (3) contains $n = \binom{n_I \cdot n_A}{2} \cdot n_J \cdot n_K$ elements, with each element defined in equation (6). This equation shows that the observed values in S_{IA} and S_{JK} determine the binary values in S through the R matrix. Specifically, researchers can only observe a subset of judges' comparisons for a subset of stimuli generated by a subset of individuals.

$$s_{(s)} = \begin{cases} 1 & \text{if the data for the } i, a \text{ with the } h, b \text{ and the } j, k \text{ elements of } R \text{ are observed} \\ 0 & \text{if the data for the } i, a \text{ with the } h, b \text{ and the } j, k \text{ elements of } R \text{ are missing} \end{cases} \tag{6}$$

With the definition of S, we can now integrate the sample mechanism into the conceptual-population model. Figure 7 illustrates this model. Following the convention of McElreath (2020, pp. 499-516) and Deffner et al. (2022, pp. 6), the DAG 7b depicts the conceptual-population outcome O_R^{cp} as an unobserved variable, emphasizing the researchers' inability to access such an outcome due to the sampling mechanism. Additionally, the DAG depicts the conditioned *sample design* variable S causally influencing the sample-comparison outcome O_R^{sc}. This variable shows that the sample-comparison outcome is a subset drawn from the conceptual-population outcome O_R^{cp}.

$$
\begin{aligned}
O_R^{sc} &:= f_S(O_R^{cp}, S) \\
O_R^{cp} &:= f_O(D_R) \\
D_R &:= f_D(T_{IA}, B_{JK}) \\
T_{IA} &:= f_T(T_I, X_{IA}, e_{IA}) \\
T_I &:= f_T(X_I, e_I) \\
B_{JK} &:= f_B(B_J, Z_{JK}, e_{JK}) \\
B_J &:= f_B(Z_J, e_J) \\
e_I &\perp \{e_J, e_{IA}, e_{JK}\} \\
e_J &\perp \{e_{IA}, e_{JK}\} \\
e_{IA} &\perp e_{JK}
\end{aligned}
$$

(a) SCM



(b) DAG

Figure 7: Sample-comparison model including sampling mechanism

Notice,

4.2.2. The comparison mechanism

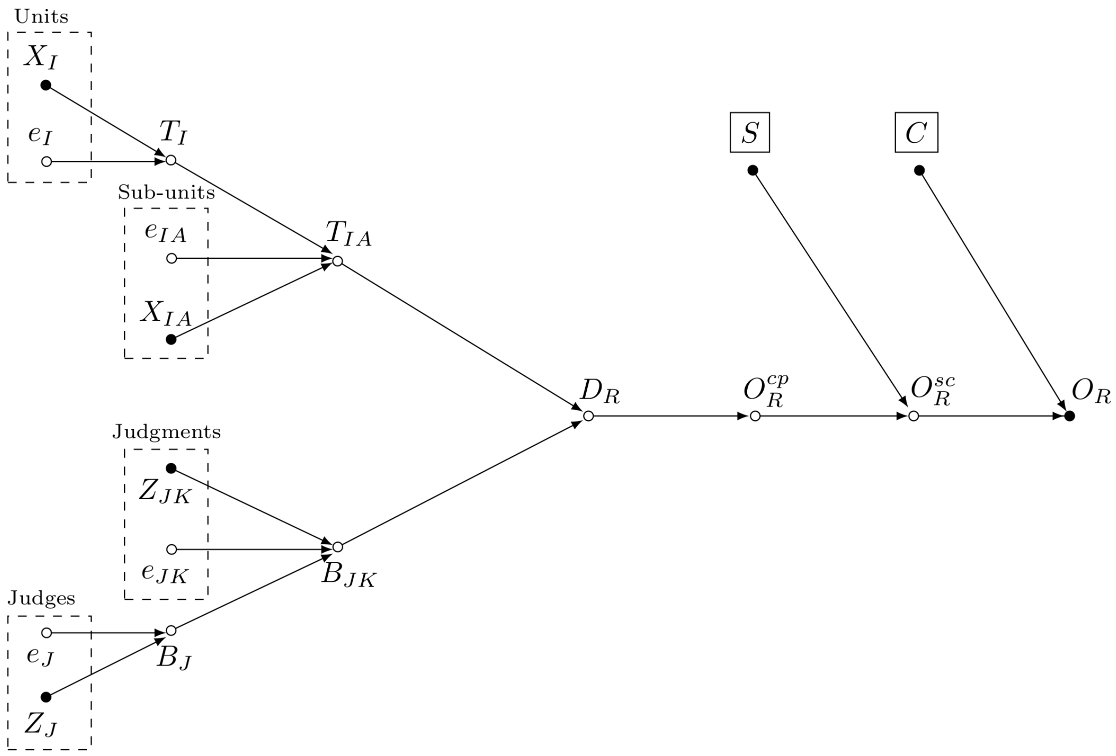
Conversely, we make the scenario depicted in Section 4.2.1 more realistic by integrating the comparison mechanism, that is, we assume that researchers do not have access to *all comparisons* from the sample, but rather a sufficient number of comparisons (n_C) so that a proportion, $P(B > A)$, may be determined for each pair of stimuli (Thurstone, 1927a, pp. 267). Figure 8 illustrates this model, incorporating both the sample and comparison mechanisms.

Following the convention of McElreath (2020, pp. 499-516), the DAG 8b depicts the sample-comparison outcome O_R^{sc} as an unobserved variable, emphasizing the researchers' inability to access such an outcome due to the comparison mechanism. Moreover, the DAG shows the conditioned *comparison design* variable C, which causally influence the observed outcome O_R. This variable reflects how this observed outcome is a sample drawn from the sample-comparison outcome O_R^{sp}. Specifically, the variable is a vector $C = \{c_1, \dots, c_n\}$, where n corresponds to the number of rows in the matrix R (refer to Section 4.1.2), and each c_i is a binary variable indicating the presence (1) or absence (0) of data in the corresponding positions of the sample-comparison outcome O_R^{sp}. Specifically,

$$c_i = \begin{cases} 1 & \text{if the data for the } i^{th} \text{ element of } O_R^{sp} \text{ is observed} \\ 0 & \text{if the data for the } i^{th} \text{ element of } O_R^{sp} \text{ is missing} \end{cases}$$

$$
\begin{aligned}
O_R &:= f_C(O_R^{sc}, C) \\
O_R^{sc} &:= f_S(O_R^{cp}, S) \\
O_R^{cp} &:= f_O(D_R) \\
D_R &:= f_D(T_{IA}, B_{JK}) \\
T_{IA} &:= f_T(T_I, X_{IA}, e_{IA}) \\
T_I &:= f_T(X_I, e_I) \\
B_{JK} &:= f_B(B_J, Z_{JK}, e_{JK}) \\
B_J &:= f_B(Z_J, e_J) \\
e_I &\perp \{e_J, e_{IA}, e_{JK}\} \\
e_J &\perp \{e_{IA}, e_{JK}\} \\
e_{IA} &\perp e_{JK}
\end{aligned}
$$

(a) SCM



(b) DAG

Figure 8: Sample-comparison model including sample and comparison mechanisms

Notice,

5. Abandoning the BTL model

$$
\begin{aligned}
O_R &= O_R^{sc} \odot C \\
O_R^{sc} &= O_R^{cp} \odot S \\
O_R^{cp} &\overset{iid}{\sim} \text{Bernoulli}\left[\text{inv\_logit}(D_R)\right] \\
D_R &= (T_{IA}[R_1, P_1] - T_{IA}[R_2, P_2]) + B_{JK}[U, V] \\
T_{IA} &= T_I + \beta_{XA} X_{IA} + e_{IA} \\
T_I &= \beta_{XI} X_I + e_I \\
B_{JK} &= B_J + \beta_{ZK} Z_{JK} + e_{JK} \\
B_J &= \beta_{ZJ} Z_J + e_J \\
e_I &\overset{iid}{\sim} \text{Normal}(0, 1) \\
e_J &\overset{iid}{\sim} \text{Normal}(0, 1) \\
e_{IA} &\overset{iid}{\sim} \text{Normal}(0, p_{IA}) \\
e_{JK} &\overset{iid}{\sim} \text{Normal}(0, p_{JK})
\end{aligned}
$$

(a) Statistical model

$$
\begin{aligned}
O_R &:= f_C(O_R^{sc}, C) \\
O_R^{sc} &:= f_S(O_R^{cp}, S) \\
O_R^{cp} &:= f_O(D_R) \\
D_R &:= f_D(T_{IA}, B_{JK}) \\
T_{IA} &:= f_T(T_I, X_A, e_{IA}) \\
T_I &:= f_T(X_I, e_I) \\
B_{JK} &:= f_B(B_J, Z_K, e_{JK}) \\
B_J &:= f_B(Z_J, e_J) \\
e_I &\perp \{e_J, e_{IA}, e_{JK}\} \\
e_J &\perp \{e_{IA}, e_{JK}\} \\
e_{IA} &\perp e_{JK}
\end{aligned}
$$

(b) SCM

Figure 9: Sample-comparison model, including sample and comparison mechanisms and assuming equal discriminal dispersions for the student's traits

$$O_R = O_R^{sc} \odot C$$

$$O_R^{sc} = O_R^{cp} \odot S$$

$$O_R^{cp} \overset{iid}{\sim} \text{Bernoulli}\left[\text{inv\_logit}(D_R)\right]$$

$$D_R = (T_{IA}[R_1, P_1] - T_{IA}[R_2, P_2]) + B_{JK}[U, V]$$

$$T_{IA} = T_I + \beta_{XA} X_{IA} + e_{IA}$$

$$T_I = \beta_{XI} X_I + e_I$$

$$B_{JK} = B_J + \beta_{ZK} Z_{JK} + e_{JK}$$

$$B_J = \beta_{ZJ} Z_J + e_J$$

$$e_I \overset{iid}{\sim} \text{Normal}(0, s_{XI})$$

$$e_J \overset{iid}{\sim} \text{Normal}(0, s_{ZJ})$$

$$e_{IA} \overset{iid}{\sim} \text{Normal}(0, p_{IA})$$

$$e_{JK} \overset{iid}{\sim} \text{Normal}(0, p_{JK})$$

Contraints:

$$\sum_{g=1}^{G_{XI}} s_{XI}/G_{XI} = 1; \quad \sum_{g=1}^{G_{ZJ}} s_{ZJ}/G_{ZJ} = 1$$

(a) Statistical model

$$O_R := f_C(O_R^{sc}, C)$$

$$O_R^{sc} := f_S(O_R^{cp}, S)$$

$$O_R^{cp} := f_O(D_R)$$

$$D_R := f_D(T_{IA}, B_{JK})$$

$$T_{IA} := f_T(T_I, X_A, e_{IA})$$

$$T_I := f_T(X_I, e_I)$$

$$B_{JK} := f_B(B_J, Z_K, e_{JK})$$

$$B_J := f_B(Z_J, e_J)$$

$$e_I := f_e(X_I)$$

$$e_J := f_e(Z_J)$$

$$e_{IA} \perp e_{JK}$$

(b) SCM

Figure 10: Sample-comparison model, including sample and comparison mechanisms and assuming different discriminal dispersions for the student's traits

6. Discussion

6.1. Findings

6.2. Limitations and further research

7. Conclusion

Declarations

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Consent to participate: Not applicable

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8. Appendix

8.1. Statistical and Causal inference

This section introduces fundamental statistical and causal inference concepts necessary for understanding the core theoretical principles described in this document. It does not, however, offer a comprehensive overview of causal inference methods. Readers seeking more in-depth understanding may wish to explore introductory papers such as Pearl (2010), Rohrer (2018), Pearl (2019), and Cinelli et al. (2020). They may also find it helpful to consult introductory books like Pearl and Mackenzie (2018), Neal (2020), and McElreath (2020). For more advanced study, readers may refer to seminal intermediate papers such as Neyman (1923), Rubin (1974), Spirtes et al. (1991), and Sekhon (2009), as well as books such as Pearl (2009), Morgan and Winship (2014), and Hernán and Robins (2020).

8.1.1. Empirical research and randomized experiments

Empirical research uses evidence from observation and experimentation to address real-world challenges. In this context, researchers typically formulate their research questions as *estimands* or *targets of inference*, i.e., the specific quantities they seek to determine (Everitt and Skrondal, 2010). For instance, researchers might be interested in answering the following question: "To what extent do different teaching methods (T) influence students' ability to produce high-quality written texts (Y)?" To investigate this, researchers could randomly assign students to two groups, each exposed to a different teaching method ($T_i = \{1, 2\}$). Then, they would perform pairwise comparisons, generating a dichotomous outcome ($Y_i = \{0, 1\}$) showing which student exhibits more of the ability. In this scenario, the research question can be rephrased as the estimand, "*On average*, is there a difference in the ability to produce high-quality written texts between the two groups of students?" and this estimand can be mathematically represented by the random associational quantity in Equation 7, where $E[\cdot]$ denotes the expected value.

$$E[Y_i \mid T_i = 1] - E[Y_i \mid T_i = 2] \tag{7}$$

Researchers then proceed to identify the estimands. *Identification* determines whether an estimator can accurately compute the estimand based solely on its assumptions, regardless of random variability (Schuessler and Selb, 2023, pp. 4). An *estimator* refers to a method or function that transforms data into an estimate (Neal, 2020). *Estimates* are numerical values that approximate the estimand derived through the process of *estimation*, which integrates data with an estimator (Everitt and Skrondal, 2010). The Identification-Estimation flowchart (McElreath, 2020; Neal, 2020), shown in Figure 11, visually represents the transition from estimands to estimates.

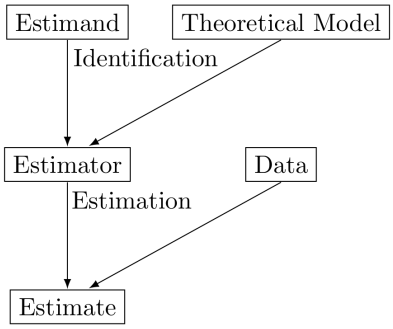


Figure 11: Identification-Estimation flowchart. Extracted and slightly modified from Neal (2020, pp. 32)

Identification is a necessary condition to ensure *consistent* estimators. An estimator achieves *consistency* when it converges to the "true" value of an estimand as the data size approaches infinity (Everitt and Skrondal, 2010). Without identification, researchers cannot achieve consistency, even with "infinite" and error-free data. As a result, deriving meaningful insights about an estimand from finite data becomes impossible (Schuessler and Selb, 2023, pp. 5). Therefore, to ensure accurate and reliable estimates, researchers prioritize estimators with desirable identification properties. For instance, the Z-test is a widely used estimator for comparing group proportions, yielding accurate estimates when its underlying assumptions are satisfied (Kanji, 2006). Furthermore, researchers can interpret estimates from the Z-test as causal, provided the data is collected through a randomized experiment.

Randomized experiments are widely recognized as the gold standard in evidence-based science (Hariton and Locascio, 2018; Hansson, 2014). This recognition stems from their ability to enable researchers interpret associational estimates as causal. They achieve this by ensuring data, and by extension an estimator, satisfies several key identification properties, such as common support, no interference, and consistency (Morgan and Winship, 2014; Neal, 2020). The most critical property, however, is the elimination of confounding. *Confounding* occurs when an external variable X simultaneously influences the outcome Y and the variable of interest T, resulting in spurious associations (Everitt and Skrondal, 2010). Randomization addresses this issue by decoupling the association between the intervention allocation T from any other variable X (Morgan and Winship, 2014; Neal, 2020).

Nevertheless, researchers often face constraints that limit their ability to conduct randomized experiments. These constraints include ethical concerns, such as the assignment of individuals to potentially harmful interventions, and practical limitations, such as the infeasibility of, for example, assigning individuals to genetic modifications or physical impairments (Neal, 2020). In these cases, causal inference offers a valuable alternative for generating causal estimates and understanding the mechanisms underlying specific data. In addition, the framework can provide significant theoretical insights that can enhance the design of experimental and observational studies (McElreath, 2020).

8.1.2. Identification under causal inference

Unlike classical statistical modeling, which focuses primarily on summarizing data and inferring associations, the *causal inference* framework is designed to identify causes and estimate their effects using data (Shaughnessy et al., 2010; Neal, 2020). The framework uses rigorous mathematical techniques to address the *fundamental problem of causality* (Pearl, 2009; Pearl et al., 2016; Morgan and Winship, 2014). This problem revolves around the question, "What would have happened 'in the world' under different circumstances?" This question introduces the concept of counterfactuals, which are instrumental in defining and identifying causal effects.

Counterfactuals are hypothetical scenarios that are *contrary to fact*, where alternative outcomes resulting from a given cause are neither observed nor observable (Neal, 2020; Counterfactual, 2024). The structural approach to causal inference (Pearl, 2009; Pearl et al., 2016) provides a formal framework for defining counterfactuals. For instance, in the scenario described in Section 8.1.1, the approach begins by defining the *individual causal effect* (ICE) as the difference between each student's potential outcomes, as in Equation 8.

$$\tau_i = Y_i \mid do(T_i = 1) - Y_i \mid do(T_i = 2) \tag{8}$$

where $do(T_i = t)$ represents the intervention operator, $Y_i \mid do(T_i = 1)$ represents the potential outcome under intervention $T_i = 1$, and $Y_i \mid do(T_i = 1)$ represents the potential outcome under intervention $T_i = 2$. Here, an *intervention* involves assigning a constant value to the treatment variable for each student's potential outcomes. Note that if a student is assigned to intervention $T_i = 1$, the potential outcome under $T_i = 2$ becomes a counterfactual, as it is no longer observed nor observable. To address this challenge, the structural approach extends the ICE to the *average causal effect* (ACE, Equation 9), representing the average difference between the students' observed potential outcomes and their counterfactual counterparts.

$$\tau = E[\tau_i]$$
$$= E[Y_i \mid do(T_i = 1)] - E[Y_i \mid do(T_i = 2)] \tag{9}$$

Even though counterfactuals are unobservable, researchers can still identify the ACE from associational estimates by leveraging the structural approach. The approach identifies the ACE by statistically conditioning data on a *sufficient adjustment set* of variables X (Pearl, 2009; Pearl et al., 2016; Morgan and Winship, 2014). This *sufficient* set (potentially empty) must block all non-causal paths between T to Y without opening new ones. When such a set exists, then T and Y are *d-separated* by X ($T \perp Y \mid X$) (Pearl, 2009), and X satisfies the *backdoor criterion* (Neal, 2020, pp 37). Here, *conditioning* describes the process of restricting the focus to the subset of the population defined by the conditioning variable (Neal, 2020, pp. 32) (see Equation 10).

Conditioning on a sufficient adjustment set enables researchers to estimate the ACE, even when the data comes from an observational study. This process is feasible because such conditioning ensures that the ACE estimator satisfies several critical properties, including confounding elimination (Morgan and Winship, 2014). Naturally, the validity of claims about the causal effects of T on Y now hinges on the assumption that X serves as a sufficient adjustment set. However, as Kohler et al. (2019, pp. 150) noted, drawing conclusions about the real world from observed data inevitably requires assumptions. This requirement holds true for both observational and experimental data.

For instance, if researchers cannot conduct the randomized experiments described in Section 8.1.1 and must instead rely on observational data, they can still identify the ACE as long as an observed variable X, such as the socio-economic status of the school, satisfies the backdoor criterion. Under these circumstances, researchers first identify the *conditional average causal effect* (CACE, Equation 10)

$$CACE_t = E[Y_i \mid T_i = t, X] \tag{10}$$

From the CACE, researchers can identify the ACE from associational quantities as in Equation 11. This identification process is commonly known as the *backdoor adjustment*. Here, $E_X[\cdot]$ represents the marginal expected value over X (Morgan and Winship, 2014).

$$
\begin{aligned}
\tau &= E[Y_i \mid do(T_i = 1)] - E[Y_i \mid do(T_i = 2)] \\
&= E_X[CACE_1 - CACE_2] \\
&= E_X\left[E[Y_i \mid T_i = 1, X] - E[Y_i \mid T_i = 2, X]\right]
\end{aligned}
\tag{11}
$$

Notably, the approach extends the ACE identification for a continuous variable T as in Equation 12, ensuring broad applicability across different causal scenarios (Neal, 2020, pp. 45)

$$
\begin{aligned}
\tau &= E[Y_i \mid do(T_i = t)] \\
&= dE_X\left[E[Y_i \mid T_i = t, X]\right]/dt
\end{aligned}
\tag{12}
$$

8.1.3. Diving into the specifics

The structural approach to causal inference uses SCMs and DAGs to formally and graphically represent the presumed causal structure underlying the ACE (Pearl, 2009; Pearl et al., 2016; Gross et al., 2018; Neal, 2020). Essentially, these tools serve as *conceptual (theoretical) models* on which identification analysis rests (Schuessler and Selb, 2023, pp. 4). Thus, using these tools, researchers can determine which statistical models can identify (ACE, CACE, or other), assuming the depicted causal structure is correct (McElreath, 2020), thus enabling valid causal inference. Figure 11 shows the role of theoretical models in the inference process.

SCMs and DAGs support identification analysis through two key advantages. First, regardless of complexity, they can represent various causal structures using only five fundamental building blocks (Neal, 2020; McElreath, 2020). This feature allows researchers to decompose complex structures into manageable components, facilitating their analysis (McElreath, 2020). Second, they depict causal relationships in a non-parametric and fully interactive way. This flexibility enables feasible ACE identification strategies without defining the variables' data types, the functional form between them, or their parameters (Pearl et al., 2016, pp. 35).

Thus, Section 8.1.3.1 and Section 8.1.3.2 elaborate on the first advantage, while Section 8.1.3.2 and Section 8.1.3.3 do so for the second. Finally, Section 8.1.3.4 explains how researchers use SCMs and DAGs alongside Bayesian inference methods in the estimation process.

8.1.3.1. The five fundamental block for SCMs and DAGs.

Figures 12, 13, 14, 15, and 16 display the five fundamental building blocks for SCMs and DAGs. The left panels of the figures show the formal mathematical models, represented by the SCMs, defined in terms of a set of *endogenous* variables $V = \{X_1, X_2, X_3\}$, a set of *exogenous* variables $E = \{e_{X1}, e_{X2}, e_{X3}\}$, and a set of functions $F = \{f_{X1}, f_{X2}, f_{X3}\}$ (Pearl, 2009; Cinelli et al., 2020). Endogenous variables are those whose causal mechanisms a researcher chooses to model (Neal, 2020). In contrast, exogenous variables represent *errors* or *disturbances* arising from omitted factors that the investigator chooses not to model explicitly (Pearl, 2009, pp. 27,68). Lastly, the functions, referred to as *structural equations*, express the endogenous variables as non-parametric functions of other variables. These functions use the symbol ':=' to denote the asymmetrical causal dependence of the variables and the symbol ' $\perp$ ' to represent *d-separation*, a concept akin to (conditional) independence.

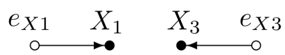
Notably, every SCM has an associated DAG (Pearl et al., 2016; Cinelli et al., 2020). The right panels of the figures display these DAGs. A DAG is a graph consisting of nodes connected by edges, where the nodes represent random variables. The term *directed* means that the edges extend from one node to another, with arrows indicating the direction of causal influence. The term *acyclic* implies that the causal influences do not form loops, ensuring the influences do not cycle back on themselves (McElreath, 2020). DAGs represent observed variables as solid black circles, while they use open circles for unobserved (latent) variables (Morgan and Winship, 2014). Although the *standard representation* of DAGs typically omits exogenous variables for simplicity, the *magnified representation* depicted in the figures offers one key advantage: including exogenous variables can help researchers highlight potential issues related to conditioning and confounding (Cinelli et al., 2020).

$$X_1 := f_{X1}(e_{X1})$$

$$X_3 := f_{X3}(e_{X3})$$

$$e_{X1} \perp e_{X3}$$

(a) SCM



(b) DAG

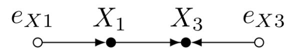
Figure 12: Two unconnected nodes

$$X_1 := f_{X1}(e_{X1})$$

$$X_3 := f_{X3}(X_1, e_{X3})$$

$$e_{X1} \perp e_{X3}$$

(a) SCM



(b) DAG

Figure 13: Two connected nodes or descendant

$$X_1 := f_{X1}(e_{X1})$$

$$X_2 := f_{X2}(X_1, e_{X2})$$

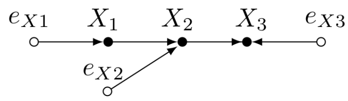
$$X_3 := f_{X3}(X_2, e_{X3})$$

$$e_{X1} \perp e_{X2}$$

$$e_{X1} \perp e_{X3}$$

$$e_{X2} \perp e_{X3}$$

(a) SCM



(b) DAG

Figure 14: Chain or mediator

$$X_1 := f_{X1}(X_2, e_{X1})$$

$$X_2 := f_{X2}(e_{X2})$$

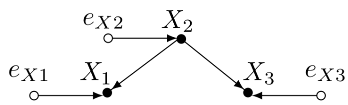
$$X_3 := f_{X3}(X_2, e_{X3})$$

$$e_{X1} \perp e_{X2}$$

$$e_{X1} \perp e_{X3}$$

$$e_{X2} \perp e_{X3}$$

(a) SCM



(b) DAG

Figure 15: Fork or confounder

$$X_1 := f_{X1}(e_{X1})$$

$$X_2 := f_{X2}(X_1, X_3, e_{X2})$$

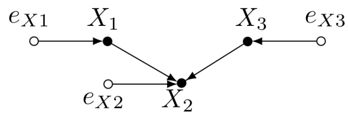
$$X_3 := f_{X3}(e_{X3})$$

$$e_{X1} \perp e_{X2}$$

$$e_{X1} \perp e_{X3}$$

$$e_{X2} \perp e_{X3}$$

(a) SCM



(b) DAG

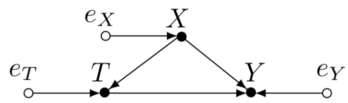
Figure 16: Collider or inmorality

A careful examination of these building blocks highlights the theoretical assumptions underlying their observed variables. SCM 12a and DAG 12b depict two unconnected nodes, representing a scenario where variables X_1 and X_3 are independent or not causally related. SCM 13a and DAG 13b illustrate two connected nodes, representing a scenario where a *parent* node X_1 exerts a causal influence on a *child* node X_3. In this setup, X_3 is considered a *descendant* of X_1. Additionally, X_1 and X_3 are described as *adjacent* because there is a *direct path* connecting them. SCM 14a and DAG 14b depict a *chain*, where X_1 influences X_2, and X_2 influences X_3. In this configuration, X_1 is a parent node of X_2, which is a parent node of X_3. This structure creates a *directed path* between X_1 and X_3. Consequently, X_1 is an *ancestor* of X_3, and X_2 fully *mediates* the relationship between the two. SCM 15a and DAG 15b illustrate a *fork*, where variables X_1 and X_3 are both influenced by X_2. Here, X_2 is a parent node that *confounds* the relationship between X_1 and X_3. Finally, SCM 16a and DAG 16b show a *collider*, where variables X_1 and X_3 are concurrent causes of X_2. In this configuration, X_1 and X_3 are not causally related to each other but both influence X_2 (an *inmorality*). Notably, all building blocks assume the errors are independent of each other and from all other variables in the graph, as evidenced by the pairwise relations $e_{X1} \perp e_{X2}$, $e_{X1} \perp e_{X3}$, and $e_{X2} \perp e_{X3}$.

Researchers can then use these building blocks to represent the scenario outlined in Section 8.1.2. SCM 17a and DAG 17b depict the plausible causal structure for this example. In this context, the variable X (socio-economic status of the school) is thought to be a confounder in the relationship between the teaching method T and the outcome Y. The figures display multiple descendant relationships such as $X \to T$, $X \to Y$, and $T \to Y$. They also highlight unconnected node pairs, evident from the relationships $e_T \perp e_X$, $e_T \perp e_Y$, and $e_X \perp e_Y$. Additional, the figures show one fork, $X \to \{T, Y\}$, and two colliders: $\{X, e_T\} \to T$ and $\{X, T, e_Y\} \to Y$.

$$
\begin{aligned}
X &:= f_X(e_X) \\
T &:= f_T(X, e_T) \\
Y &:= f_Y(T, X, e_Y) \\
e_T &\perp e_X \\
e_T &\perp e_Y \\
e_X &\perp e_Y
\end{aligned}
$$

(a) SCM



(b) DAG

Figure 17: Plausible causal structure the scenario outlined in Section 8.1.2.

8.1.3.2. The probabilistic implications of these blocks.

Beyond their graphical capabilities, SCMs and DAGs can encode the probabilistic information embedded within a causal structure. They achieve this encoding by relying on three fundamental assumptions: the local Markov, the minimality, the causal edges assumption. The *local Markov assumption* encodes probabilistic independencies between variables by declaring that nodes in a graph are independent of all its non-descendants, given its parents (Neal, 2020, pp. 20). Meanwhile, the *minimality assumption* encodes probabilistic dependencies among variables by stating that every pair of adjacent nodes exhibits a dependency (Neal, 2020, pp. 21). Finally, the *causal edges assumption* encodes causal relationships between variables by declaring that each parent node acts as a direct cause of its children (Neal, 2020, pp. 22). Figure 18 illustrates how these assumptions influence the statistical and causal interpretations of graphs.

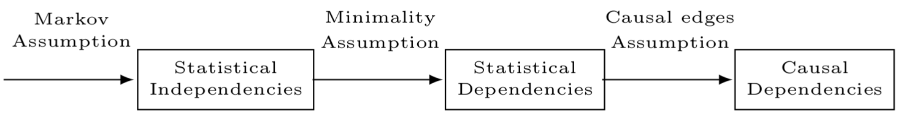


Figure 18: The flow of association and causation in graphs. Extracted and slightly modified from Neal (2020, pp. 31)

A notable implication of the assumptions underlying the probabilistic encoding is that any conceptual model described by an SCM and DAG can represent the joint distribution of variables more efficiently (Pearl et al., 2016, pp. 29). This expression takes the form of a product of conditional probability distributions (CPDs) of the type $P(child \mid parents)$. This property is formally known as the *Bayesian Network factorization* (BNF, Equation 13) (Pearl et al., 2016, pp. 29; Neal, 2020, pp. 21). In this expression, $pa(X_i)$ denotes the set of variables that are the parents of X_i.

$$\begin{aligned} P(X_1, X_2, \dots, X_P) &= X_1 \cdot \prod_{p=2}^{P} P(X_i \mid X_{i-1}, \dots, X_1) \quad \text{(by chain rule)} \\ &= X_1 \cdot \prod_{p=2}^{P} P(X_i \mid pa(X_i)) \qquad\qquad \text{(by BNF)} \end{aligned} \tag{13}$$

This encoding enables researchers with conceptual (theoretical) knowledge in the form of an SCM and DAG to predict patterns of (in)dependencies in the data. As highlighted by Pearl et al. (2016, pp. 35), these predictions depend solely on the structure of these conceptual models without requiring the quantitative details of the equations or the distributions of the errors. Moreover, once researchers observe empirical data, the patterns of (in)dependencies in the data can provide significant insights into the validity of the proposed conceptual model.

The five fundamental building blocks described in Section 8.1.3.1 clearly illustrate which (in)dependencies can SMCs and DAGs predict. For instance, applying the BNF to the causal structure shown in the SCM 12a and DAG 12b enables researchers to express the joint probability distribution of the observed variables as $P(X_1, X_3) = P(X_1)P(X_3)$, supporting the theoretical assumption that the observed variables X_1 and X_3 are unconditionally independent ($X_1 \perp X_3$) (Neal, 2020, pp. 24). Conversely, when X_3 is unconditionally dependent on X_1 ($X_1 \not\perp X_3$), as depicted in the SCM 13a and DAG 13b, the BNF express their joint probability distribution as $P(X_1, X_3) = P(X_3 \mid X_1)P(X_1)$. Notably, these descriptions demonstrate the clear correspondence between the structural equations illustrated in Section 8.1.3.1 and the CPDs.

Beyond the insights gained from two-node structures, researchers can uncover more nuanced patterns of(in)dependencies from chains, forks, and colliders. These (in)dependencies apply to any data set generated by a causal model with those structures, regardless of the specific functions attached to the SCM (Pearl et al., 2016, pp. 36). For instance, applying the BNF to the chain structure depicted in the SCM 14a and DAG 14b allow researchers to represent the joint distribution for the observed variables as $P(X_1, X_2, X_3) = P(X_1)P(X_2 \mid X_1)P(X_3 \mid X_2)$. This expression implies that X_1 and X_3 are unconditionally dependent ($X_1 \not\perp X_3$), but conditionally independent when controlling for X_2 ($X_1 \perp X_3 \mid X_2$). Moreover, in the fork structure shown in the SCM 15a and DAG 15b, researchers can express the joint distribution of the observed variables as $P(X_1, X_2, X_3) = P(X_1 \mid X_2)P(X_2)P(X_3 \mid X_2)$. Similar to the chain structure, this expression allows researchers to further infer that X_1 and X_3 are unconditionally dependent ($X_1 \not\perp X_3$), but conditionally independent when controlling for X_2 ($X_1 \perp X_3 \mid X_2$). Finally, researchers analyzing the collider structure illustrated in the SCM 16a and DAG 16b can express the joint distribution of the observed variables as $P(X_1, X_2, X_3) = P(X_1)P(X_2 \mid X_1, X_3)P(X_3)$. This representation allows researchers to infer that X_1 and X_3 are unconditionally independent ($X_1 \perp X_3$), but conditionally dependent when controlling for X_2 ($X_1 \not\perp X_3 \mid X_2$). The authors Pearl et al. (2016, pp. 37, 40, 41) and Neal (2020, pp. 25–26) provide the mathematical proofs for these conclusions.

Using these additional probabilistic insights, researchers can revisit the scenario in Section 8.1.2. In this context, applying the BNF to the SCM 19a structure, enables the representation of the joint probability distribution of the observed variables as $P(Y, T, X) = P(Y \mid T, X)P(T \mid X)P(X)$. From this expression, researchers can infer that the outcome Y is unconditionally dependent on the teaching method T ($Y \not\perp T$). This dependency arises from two key structures: a direct causal path from the teaching method T to the outcome Y, represented by the two-connected-nodes structure $T \rightarrow Y$ (black path in DAG 19b), and a confounding non-causal path from the teaching method T to the outcome Y through the socio-economic status of the school X, represented by the fork structure $T \leftarrow X \rightarrow Y$ (gray path in DAG 19b).

$$X := x$$

$$T := f_T(x, e_T)$$

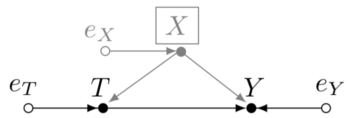
$$Y := f_Y(T, x, e_Y)$$

$$e_T \perp e_X$$

$$e_T \perp e_Y$$

$$e_X \perp e_Y$$

(a) SCM



(b) Conditioned DAG

Figure 19: Plausible causal structure the scenario outlined in Section 8.1.2.

8.1.3.3. From probability to causality.

The structural approach to causal inference translates probabilistic insights into actionable strategies seeking to identify the ACE from associational quantities. The approach achieves this by relying on the *modularity assumption*, which posits that intervening on a node alters only the causal mechanism of that node, leaving others unchanged (Neal, 2020, pp. 34).

The modularity assumption underpins the concepts of manipulated graphs and Truncated Factorization, which are essential for representing interventions $P(Y_i \mid do(T_i = t))$ within SCMs and DAGs. *Manipulated graphs* simulate physical interventions by removing specific edges from a DAG, while preserving the remaining structure unchanged (Neal, 2020, pp. 34). In parallel, *Truncated Factorization* (TF) achieves a similar simulation by removing specific functions from the conceptual model and replacing them with constants, while keeping the rest of the structure unchanged (Pearl, 2010). The probabilistic implications of this factorization are formalized in Equation 14, where S represents the subset of variables X_p directly influenced by the intervention, while an example illustrating these concepts follows below.

$$P(X_1, X_2, \dots, X_P \mid do(S)) = \begin{cases} \prod P(X_p \mid pa(X_p)) & \text{if } p \notin S \\ 1 & \text{otherwise} \end{cases} \tag{14}$$

Using the TF, researchers can define the *backdoor adjustment* to identify the ACE. This adjustment states that if a variable $X_p \in S$ serves as a *sufficient adjustment set* for the effect of X_a on X_b, then the ACE can be identified using Equation 15. The sufficient adjustment set (potentially empty) must block all non-causal paths between X_a and X_b without introducing new paths. If such a set exists, then X_a and X_b are *d-separated* by X_p ($X_a \perp X_b \mid X_p$) (Pearl, 2009), and X_p satisfies the *backdoor criterion* (Neal, 2020, pp. 37).

$$P(X_a \mid do(X_b = x)) = \sum_{Xp} P(X_a \mid X_b = x, X_p) P(X_p) \tag{15}$$

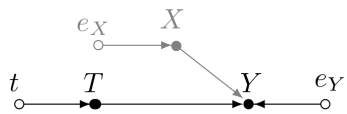
Ultimately, the backdoor adjustment enables researchers to express the ACE as:

$$\begin{aligned} \tau &= E[X_a \mid do(X_b = 1)] - E[X_a \mid do(X_b = 2)] \\ &= E_{Xp}\left[E[X_a \mid do(X_b = 1), X_p] - E[X_a \mid do(X_b = 2), X_p]\right] \\ &= \sum_{Xp} X_a \cdot P(X_a \mid X_b = 1, X_p) \cdot P(X_p) - \sum_{Xp} X_a \cdot P(X_a \mid X_b = 2, X_p) \cdot P(X_p) \end{aligned} \tag{16}$$

With these new insights, researchers revisiting the scenario in Section 8.1.3.2 can infer that the socio-economic status of the school, X, satisfies the backdoor criterion, assuming the causal structure depicted by the SCM 19a and DAG 19b is correct. This means that X serves as a sufficient adjustment set, as it effectively blocks all confounding non-causal paths introduced by the fork structure. Nevertheless, since Y remains dependent on T even after conditioning ($Y \not\perp T \mid X$), this dependency can only be attributed to the direct causal effect $T \to Y$. Notably, for the purpose of identification, the conditioned DAG 19b is equivalent to the manipulated DAG 20b, because X satisfies the backdoor criterion.

$$
\begin{aligned}
X &:= f_X(e_X) \\
T &:= t \\
Y &:= f_Y(t, X, e_Y) \\
e_T &\perp e_X \\
e_T &\perp e_Y \\
e_X &\perp e_Y
\end{aligned}
$$

(a) SCM



(b) Manipulated DAG

Figure 20: Plausible causal structure the scenario outlined in Section 8.1.3.2.

Researchers can then apply the *backdoor adjustment* to identify the ACE of T on Y. They achieve this by first identifying the CACE of T on Y by conditioning on X, and then marginalizing this effect over X to obtain the ACE. This process is expressed in Equation 17 (see Section 8.1.2).

$$
\begin{aligned}
\tau &= E[Y_i \mid do(T_i = 1)] - E[Y_i \mid do(T_i = 2)] \\
&= E_X \left[E[Y_i \mid T_i = 1, X] - E[Y_i \mid T_i = 2, X] \right] \\
&= \sum_X Y_i \cdot P(Y_i \mid T_i = 1, X) \cdot P(X) - \sum_X Y_i \cdot P(Y_i \mid T_i = 2, X) \cdot P(X)
\end{aligned}
\tag{17}
$$

8.1.3.4. The estimation process.

Ultimately, researchers can use Bayesian inference methods to estimate the ACE. The approach begins by defining two probability distributions: the likelihood of the data, $P(X_1, X_2, \ldots, X_P|\theta)$, and the prior distribution, $P(\theta)$ (Everitt and Skrondal, 2010), where X_P represents a random variable, and θ represents a one-dimensional parameter space for simplicity. After observing empirical data, researchers can update the priors to posterior distributions using Bayes' rule in Equation 18:

$$
P(\theta \mid X_1, X_2, \ldots, X_P) = \frac{P(X_1, X_2, \ldots, X_P \mid \theta) \cdot P(\theta)}{P(X_1, X_2, \ldots, X_P)} \tag{18}
$$

Given that the denominator on the right-hand side of Equation 18 serves as a normalizing constant independent of the parameter θ, researchers can simplify the posterior updating process into three steps. First, they integrate new empirical data through the likelihood. Second, they update the parameters' priors to a posterior distribution according to Equation 19. Ultimately, they normalize these results to obtain a valid probability distribution.

$$P(\theta \mid X_1, X_2, \ldots, X_P) \propto P(X_1, X_2, \ldots, X_P \mid \theta) \cdot P(\theta) \tag{19}$$

Temporarily setting aside the definition of prior distributions $P(\theta)$, note that the posterior updating process depends heavily on the assumptions underlying the likelihood of the data. However, as the number of random variables, P, increases, this joint distribution quickly becomes intractable (Neal, 2020). This intractability is evident from Equation 20, where the likelihood distribution is expressed by multiple chained CPDs.

$$P(X_1, X_2, \ldots, X_P \mid \theta) = P(X_1 \mid \theta) \prod_{p=2}^{P} P(X_i \mid X_{i-1}, \ldots, X_1, \theta) \tag{20}$$

Nevertheless, researchers can manage the complexity of the likelihood by assuming specific local (in)dependencies among variables. SCMs and DAGs provide a formal framework to represent these assumptions, as detailed in Section 8.1.3.2. These assumptions improve model tractability and simplify the estimation process by enabling the derivation of the BNF of the likelihood (Equation 21). With this simplified structure, any probabilistic programming language can model the system and compute the parameter's posterior distribution using Equation 18.

$$P(X_1, X_2, \ldots, X_P \mid \theta) = P(X_1 \mid \theta) \prod_{p=2}^{P} P(X_i \mid pa(X_i), \theta) \tag{21}$$

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