

Specious rules: an efficient and effective unifying method for removing misleading and uninformative patterns in association rule mining

Wilhelmiina Hämmäläinen¹

Geoffrey I. Webb²

¹Department of Computer Science, Aalto University, Finland wilhelmiina.hamalainen@aalto.fi

²Faculty of IT, Monash University, Melbourne, Australia geoff.webb@monash.edu

Abstract

We present theoretical analysis and a suite of tests and procedures for addressing a broad class of redundant and misleading association rules we call *specious rules*. Specious dependencies, also known as *spurious*, *apparent*, or *illusory associations*, refer to a well-known phenomenon where marginal dependencies are merely products of interactions with other variables and disappear when conditioned on those variables. The most extreme example is Yule-Simpson's paradox where two variables present positive dependence in the marginal contingency table but negative in all partial tables defined by different levels of a confounding factor. It is accepted wisdom that in data of any nontrivial dimensionality it is infeasible to control for all of the exponentially many possible confounds of this nature. In this paper, we consider the problem of specious dependencies in the context of statistical association rule mining. We define specious rules and show they offer a unifying framework which covers many types of previously proposed redundant or misleading association rules. After theoretical analysis, we introduce practical algorithms for detecting and pruning out specious association rules efficiently under many key goodness measures, including Mutual information and exact hypergeometric probabilities. We demonstrate that the procedure greatly reduces the number of associations discovered, providing an elegant and effective solution to the problem of association mining discovering large numbers of misleading and redundant rules.

Keywords: specious dependency, association rule, Yule-Simpson's paradox, mutual information, Birch's test

1 Introduction

Association rule mining is often a useful first step for any data mining task, because it reveals the statistical dependence structure of data. A major issue in association rule mining is that analyses often produce excessive numbers of rules. Even if rules are carefully pruned

with strict statistical measures, the results are likely to contain large numbers of redundant, unproductive, uninteresting or even misleading and paradoxical rules.

In this paper, we investigate the problem of *specious associations*, also known as spurious, apparent, illusory, or misleading associations (e.g., [13]). Specious associations refer to a well-known phenomenon where marginal dependencies appear as products of interactions with other variables and disappear when conditioned on those variables. The most extreme example is Yule-Simpson's paradox where two variables present positive dependence in the marginal contingency table but negative in all partial tables defined by different levels of a confounding factor. As far as we know, the problem has not previously been addressed in the context of association rule discovery, but there are approaches (e.g., [4, 5, 6, 12]) that prune out certain subtypes of specious rules, together with other search constraints.

We begin from basic definitions, tests and properties of specious rules. We show that specious rules offer a unifying framework that includes many previously proposed forms of redundant or misleading association rules as their special cases. Thus, their removal can drastically reduce the number of discovered associations. On the other hand, efficient detection of specious rules offers a solution to the oft-cited problem of misleading associations in traditional data analysis. We give new theoretical properties that help to identify specious dependencies efficiently, without testing all possible (exponentially many) confounding factors. Based on these, we introduce an efficient algorithm for detection and removal of specious dependencies. We report experiments on mining non-specious, statistical association rules with Mutual information, and draw final conclusions.

2 Definitions and concepts

2.1 Unconditional and conditional dependencies

According to a classical definition, two events

$X=x$ and $C=c$ are statistically independent, if $P(X=x, C=c) = P(X=x)P(C=c)$. Otherwise, they are considered dependent. A commonly used measure for this unconditional (or marginal) dependence is leverage $\delta(X=x, C=c) = P(X=x, C=c) - P(X=x)P(C=c)$. When X and C are (composed or single) binary variables, $\delta(X, C) = \delta(\neg X, \neg C) = -\delta(X, \neg C) = -\delta(\neg X, C)$, where X and C are used as shorthands for $X=1$ and $C=1$ and $\neg X$ and $\neg C$ as shorthands for $X=0$ and $C=0$ respectively. Therefore, the dependency can be represented by giving just one value pair, usually one expressing positive dependency.

In pattern discovery, statistical dependencies can be expressed as a type of association rules, which we call *statistical association rules* or *dependency rules* (see e.g., [4]). Such rules express always statistical dependencies but, unlike traditional association rules, do not have any minimum frequency requirements. Instead, there are requirements for the strength and/or significance of statistical dependencies. We concentrate on dependency rules of the form $X \rightarrow C=c$, $c \in \{0, 1\}$, where X is a set of positive valued binary attributes and C is a single binary attribute. Rule $X \rightarrow C=1$ (or simply $X \rightarrow C$) expresses a positive dependency between X and C while $X \rightarrow C=0$ (or $X \rightarrow \neg C$) expresses a negative dependency. We note that $X \rightarrow C$, $C \rightarrow X$, $\neg X \rightarrow \neg C$, and $\neg C \rightarrow \neg X$ express the same dependency.

When two dependency rules are compared, it is often useful to study the conditional dependence of one rule (e.g., $Q \rightarrow C$) on another with the same consequent attribute (e.g., $X \rightarrow C$). This is equivalent to studying conditional dependencies between Q and C given X or $\neg X$. Now Q and C are conditionally independent given $X=x$, $x \in \{0, 1\}$, if

$$P(X=x, Q, C) = \frac{P(X=x, Q)P(X=x, C)}{P(X=x)}.$$

Otherwise they are considered conditionally dependent. To measure the strength of the conditional dependence, we extend the leverage measure. *Conditional leverage* of $Q \rightarrow C$ given value X is

$$\delta_c(Q, C|X) = P(X, Q, C) - P(X, Q)P(C|X)$$

and given value $\neg X$ it is

$$\delta_c(Q, C|\neg X) = P(\neg X, Q, C) - P(\neg X, Q)P(C|\neg X).$$

The sign of the conditional leverage determines whether the given conditional dependency is positive or negative.

2.2 Specious dependency rules In this paper, we are interested in detecting and pruning out specious dependency rules. These are rules that occur only as side-products of other dependencies. Ultimately, specious

dependency rules are a phenomenon of the unknown population from which the sample data is drawn. Therefore, we give the definition in the population level and explain how statistical significance testing can be used to detect specious rules from sample data.

DEFINITION 1. (SPECIOUS DEPENDENCY RULE) *Let X and Q be sets of binary attributes and C a single binary attribute. Dependency rule $Q \rightarrow C=c$ ($c \in \{0, 1\}$) expressing positive dependency between Q and $C=c$ is specious if there is another rule $X \rightarrow C=c_x$ ($c_x \in \{0, 1\}$) such that $\delta_c(Q, C=c|X) \leq 0$ and $\delta_c(Q, C=c|\neg X) \leq 0$ in the population.*

Figure 1 shows four alternative ways that rule $X \rightarrow C=c$ or $X \rightarrow C \neq c$ can make $Q \rightarrow C=c$, $c \in \{0, 1\}$ specious. Note that in a and d, the specious rule is $Q \rightarrow C$ and in b and c, it is $Q \rightarrow \neg C$.

In the sample level, speciousness of $Q \rightarrow C=c$ can be detected by studying the conditional leverages $\delta_1 = \delta_c(Q, C|X)$ and $\delta_2 = \delta_c(Q, C|\neg X)$ and statistical significance of the conditional dependency. If both $\delta_1 \leq 0$ and $\delta_2 \leq 0$, then the observed dependency $Q \rightarrow C=c$ is completely due to variable X and either disappears or changes its direction when conditioned. However, sample data is only an incomplete presentation of the underlying population, and it is possible that both conditional leverages are weakly positive, even if the rule is specious. For detecting such specious rules, one has to test the significance of the observed deviations from conditional independence. If the deviations are not significant with a desired level, then the rule can be considered specious.

2.3 Statistical and information-theoretic tests

Birch's exact test [2] and Mutual information are two robust methods for evaluating significance of partial dependencies and detecting specious rules. Birch's exact test defines the exact hypergeometric probability that dependency $Q \rightarrow C=c$ is at least as strong as observed, if Q and C were actually conditionally independent given X (null hypothesis). In the original article, Birch gives only the hypergeometric point probability $P(n_{qc} | n, n_x, n_{xc}, n_{xq}, n_q, n_c)$ that the frequency of $QC=c$ is exactly n_{qc} , when data size (n) and frequencies of X , $(X, C=c)$, (X, Q) , Q and $C=c$ (n_x , n_{xc} , n_{xq} , n_q , and n_c) are fixed. The corresponding cumulative probability (p -value) is obtained by summing up all point probabilities where the dependency between Q and $C=c$ is at least as strong as observed (which is equivalent to $N_{qc} \geq n_{qc}$ under the null hypothesis of conditional independence). Now, the test for the speciousness of rule $Q \rightarrow C=c$, given $X \rightarrow C=c_x$ ($c_x = c$ or $c_x = 1 - c$) becomes

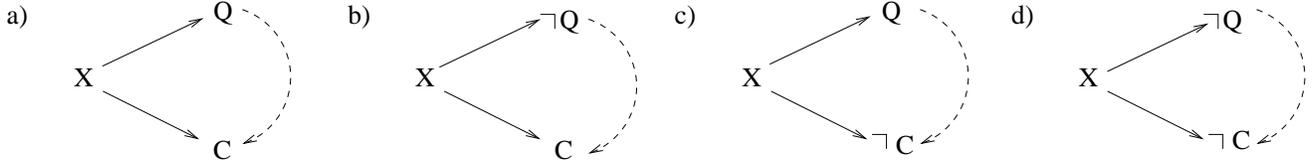


Figure 1: Four ways that $X \rightarrow C=c$ or $X \rightarrow C \neq c$ can make $Q \rightarrow C=c$, $c \in \{0, 1\}$ specious. The solid lines show genuine statistical dependencies, while the dotted lines show derived dependencies that arise as their side-products.

$$(2.1) \quad p_B = P(N_{qc} \geq n_{qc} \mid n, n_x, n_{xc}, n_{xq}, n_q, n_c) \\ = \frac{\sum_{i+j \geq n_{qc}} \binom{n_{xq}}{i} \binom{n_{x-q}}{n_{xc}-i} \binom{n_{-xq}}{j} \binom{n_{-x-q}}{n_{-xc}-j}}{\binom{n_x}{n_{xc}} \binom{n_{-x}}{n_{-xc}}}.$$

One problem is to select a threshold value $\alpha \in]0, 1]$ such that rules with $p_B > \alpha$ can be safely pruned out as specious (i.e., the null hypothesis of conditional independence is kept). A classical threshold in significance testing is $\alpha = 0.05$ but a smaller or larger value can be used to prune out more or less rules as specious.

A corresponding information-theoretic test for speciousness can be constructed using conditional Mutual information. With a short-hand notation $p_x = P(X)$ it is defined as

$$(2.2) \quad MI(Q \rightarrow C \mid X \rightarrow C) \\ = MI(Q \rightarrow C \mid X) + MI(Q \rightarrow C \mid \neg X) \\ = \log \frac{p_x^{p_x} p_{xqc}^{p_{xqc}} p_{xq-c}^{p_{xq-c}} p_{x-qc}^{p_{x-qc}} p_{x-q\bar{c}}^{p_{x-q\bar{c}}}}{p_{xq}^{p_{xq}} p_{x\bar{q}}^{p_{x\bar{q}}} p_{xc}^{p_{xc}} p_{x\bar{c}}^{p_{x\bar{c}}}} \\ + \log \frac{p_{\bar{x}}^{p_{\bar{x}}} p_{\bar{x}qc}^{p_{\bar{x}qc}} p_{\bar{x}q\bar{c}}^{p_{\bar{x}q\bar{c}}} p_{\bar{x}\bar{q}c}^{p_{\bar{x}\bar{q}c}} p_{\bar{x}\bar{q}\bar{c}}^{p_{\bar{x}\bar{q}\bar{c}}}}{p_{\bar{x}q}^{p_{\bar{x}q}} p_{\bar{x}\bar{q}}^{p_{\bar{x}\bar{q}}} p_{\bar{x}c}^{p_{\bar{x}c}} p_{\bar{x}\bar{c}}^{p_{\bar{x}\bar{c}}}}.$$

This measure is computationally easy to evaluate and it has also other attractive properties which help in the search. However, there is one drawback since MI is always non-negative and, therefore, negative and positive conditional dependence cannot be separated. As a solution, we have modified the measure such that the signs of terms are reversed in the case of negative conditional dependency (i.e., $MI(Q, C \mid X = x)$ becomes $-MI(Q, C \mid X = x)$ if $\delta_c(Q, C \mid X = x) < 0$). The modified (signed) measure is denoted MI_S . Once again, one should decide a minimum MI_S value which is required for non-speciousness.

Similarly, one can design a χ^2 -based test for speciousness (like Mantel-Haenszel's test and its variations that asymptotically approximate p_B), but it has

the same problem as MI in separating positive and negative conditional dependencies.

3 Relationship to redundancy, equivalence and Yule-Simpson's paradox

3.1 Speciousness of specialized and generalized rules Speciousness is closely related to the concepts of productivity [12] and redundancy [4] and the question of whether a more general rule $X \rightarrow C=c$ or its specialization $Q \rightarrow C=c$ is superfluous. There are two possible cases, where $X \rightarrow C=c$ makes $Q \rightarrow C=c$ specious and either $X \subset Q$ or $Q \subset X$ (where \subset denotes a proper subset). For simplicity, we represent the results only for positive consequence $C = 1$.

In the first case, rule $X \rightarrow C$ is a generalization of rule $Q \rightarrow C$, i.e., $X \subset Q$. In the next section we will show that this phenomenon can occur only if dependency $X \rightarrow C$ is more significant than $Q \rightarrow C$, with many types of significance measures. However, this means that $Q \rightarrow C$ is superfluous or redundant with respect to $X \rightarrow C$. Now $\delta_2 = 0$ and the speciousness depends on δ_1 , whether $\delta_1 \leq 0$ or $\delta_1 > 0$ but the deviation from zero is insignificant. If we mark $Q = XZ$ and the corresponding frequency by n_{xz} , the exact test for the speciousness of $XZ \rightarrow C$ given $X \rightarrow C$ reduces to

$$p_B = \frac{\sum_{i \geq n_{xzc}} \binom{n_{xz}}{i} \binom{n_{x-z}}{n_{xc}-i}}{\binom{n_x}{n_{xc}}}.$$

An interesting coincidence is that this is the same as the test for the significance of productivity in [12]. With mutual information, the test is simply $MI_S = MI(XZ \rightarrow C \mid X)$ (assuming $\delta_1 > 0$).

In the second case, rule $X \rightarrow C$ is a specialization of rule $Q \rightarrow C$, i.e., $Q \subset X$. Once again, it will turn out that $X \rightarrow C$ has to be more significant than $Q \rightarrow C$ to make it specious, given an appropriate significance measure (see Section 4). This means that one type of specious rules are generalizations of non-redundant rules (rules $X \rightarrow C$ which are better than any $Y \rightarrow C$, $X \subset Y$ with the given significance measure). Now $\delta_1 = 0$, and the speciousness depends solely on δ_2 . If we mark

$X = QZ$ and the corresponding frequency by n_{qz} , the exact test for the speciousness reduces to

$$p_B = \frac{\sum_{j \geq n_{qc}} \binom{n_{q-z}}{j} \binom{n-q}{n-qc-j}}{\binom{n-n_{qz}}{n_c-n_{qzc}}}.$$

With Mutual information, the equivalent test is $MI_S(Q \rightarrow C|QZ \rightarrow C) = MI(Q \rightarrow C|\neg(QZ)) = MI(\neg Q \rightarrow \neg C|\neg(QZ))$ (assuming $\delta_2 > 0$). This is the same as the significance of productivity of $\neg Q \rightarrow \neg C$ with respect to $\neg(QZ) \rightarrow \neg C$.

A further connection to redundancy testing occurs if we compare a rule $X \rightarrow C$ and its specialization $XZ \rightarrow C$ using speciousness tests. If $MI_S(X \rightarrow C|XZ \rightarrow C) = MI(\neg X \rightarrow \neg C|\neg(XZ))$ is too small, then $X \rightarrow C$ is specious, and if $MI_S(XZ \rightarrow C|X \rightarrow C) = MI(XZ \rightarrow C|X)$ is too small, then $XZ \rightarrow C$ is specious. Since both cannot occur simultaneously, only the rule with a smaller conditional MI value can be specious. It turns out that this is the same as comparing the unconditional MI values of rules. Thus, the test for redundancy in [4] (i.e., testing if $MI(XZ \rightarrow C) < MI(X \rightarrow C)$) is a special case of speciousness testing. It is also equivalent to comparing the significance of productivity of $XZ \rightarrow C$ with respect to $X \rightarrow C$ and of $\neg X \rightarrow \neg C$ with respect to $\neg(XZ) \rightarrow \neg C$.

3.2 Equivalent rules A special case of speciousness occurs when two sets of attributes, Q and X , cover the same set of elements, i.e., when $cov(X) = cov(Q)$. In this case, X and Q are called *equivalent* and they have exactly the same dependency rules. In this special case, speciousness of $Q \rightarrow C=c$ by $X \rightarrow C=c$ is of type a or c in Fig 1. On the other hand, if X and $\neg Q$ are equivalent, then X and Q have complement rules of the form $X \rightarrow C=c$ and $Q \rightarrow C \neq c$. This corresponds to cases b and d in Fig 1.

For a pair of equivalent rules, all conditional leverages (of $Q \rightarrow C=c$ given $X \rightarrow C=c$ or $X \rightarrow C \neq c$ and vice versa) are zero. This matches the definition of speciousness, even if one cannot consider them specious per se. Still, equivalent rules capture the same information and there is no need to report both, once the equivalence rule $X \rightarrow Q$ is reported. This type of speciousness has potentially important computational implications, because it enables radical pruning of the search space.

Equivalent rules are also related to the concepts of *closed item sets* and *minimal generators* [10]. An attribute set X is called closed, if for all $Y \supset X$ holds $P(Y) < P(X)$, and it is called a minimal generator if for all $Y \subset X$ holds $P(Y) > P(X)$. Now if X and Q are closed sets with the same minimal generator $Z = X \cap Q \neq \emptyset$, then $cov(X) = cov(Q) = cov(Z)$

and both $X \rightarrow C=c$ and $Q \rightarrow C=c$ are equivalent with $Z \rightarrow C=c$ and thus specious. However, this type of specious rules are also superfluous specializations explained in the previous subsection and are pruned as such. We recall that $Z = X \cap Q$ is not necessarily a generator at all (i.e., $P(X|Z) < 1$ and $P(X|Q) < 1$), even if X and Q were equivalent. In summary, all rules $Q \rightarrow C=c$ and $X \rightarrow C=c$, whose antecedents have the same minimal generator Z , are mutually equivalent and specious, but all mutually equivalent rules do not have the same minimal generator.

3.3 Yule-Simpson's paradox Speciousness is closely related to Yule-Simpson's paradox (see e.g., [1, 11]). The paradox refers to the situation where the unconditional dependency between Q and $C=c$ is positive, but becomes negative when conditioned on either X or $\neg X$. In a wider definition, disappearing dependences are also included here, i.e., there is marginal independence but conditional dependence or vice versa, like in the original definition by Yule [13]. In this sense, the core question of speciousness is whether Yule-Simpson's paradox occurs in the population. Assuming positive dependency $Q \rightarrow C=c$, the paradox can be expressed formally by three conditions

- (i) $P(C=c|Q) > P(C=c|\neg Q)$ i.e. $\delta_c(Q, C=c) > 0$;
- (ii) $P(C=c|Q, X) \leq P(C=c|\neg Q, X)$ i.e. $\delta_c(Q, C=c|X) \leq 0$;
- (iii) $P(C=c|Q, \neg X) \leq P(C=c|\neg Q, \neg X)$ i.e. $\delta_c(Q, C=c|\neg X) \leq 0$.

In this case, $Q \rightarrow C=c$ is specious by definition. However, it may easily go unnoticed in the traditional data analysis involving only pair-wise dependencies. Furthermore, it is possible that the confounding variable X is not present in the data.

A classical example demonstrates a specious dependency between a new treatment and recovery (see e.g., [9]). In the example, a positive marginal dependency between treatment and recovery is observed when the patients are considered as a whole. However, when the data is stratified by the sex of the patients, it turns out that the new treatment is negatively associated with recovery both for women and men. The explanation is that men were more often selected to have the new treatment and they also had a higher recovery rate.

One can easily show (by setting $\delta_1 \leq 0$ and $\delta_2 \leq 0$) that Yule-Simpson's paradox can occur only if

$$\delta(Q, C) \leq \frac{\delta(X, Q)\delta(X, C)}{P(X)P(\neg X)}.$$

This means that it can be avoided if either Q or C is independent from X . In the example of treatment and recovery, the paradox would have been avoided, if the same proportion of men and women had been allocated

to the new treatment, thus removing the dependency between the sex and treatment. However, this is seldom possible in retrospective studies or exploratory data analysis and examples of Yule-Simpson's paradox occur in real world data. One solution to the problem could be dependency rule analysis with speciousness detection. If dependency rules were searched from the treatment-recovery data, it would immediately be clear that the strongest and most significant dependencies are *Male* \rightarrow *Treatment* and *Male* \rightarrow *Recovery*, while *Treatment* \rightarrow *Recovery* is clearly weaker and relatively insignificant. Still, an exhaustive search would probably output it, together with many other specious rules, because they do not check interrelations of dependencies.

4 Detecting specious associations

4.1 Theoretical results Detecting specious dependency rules reduces to the following core problem: Given two rules, $r_1: Q \rightarrow C=c$ and $r_2: X \rightarrow C=c_x$, $c, c_x \in \{0, 1\}$, is r_1 specious by r_2 , r_2 by r_1 , or neither? In essence, this is the same as asking: How probable it is to observe at least as strong $Q \rightarrow C=c$, if Q and C were conditionally independent given dependency $X \rightarrow C=c_x$? If it is more probable than the opposite, observing as strong $X \rightarrow C=c_x$, given $Q \rightarrow C=c$, then at most r_1 can be specious. In the opposite case, at most r_2 can be specious. In both cases, it is also required that the probability is sufficiently high. There is also a special case, where the probabilities are equal. Then one cannot say that either rule is specious, because we cannot have a circular argument, where r_1 is made specious by r_2 and r_2 by r_1 . (Still, it suffices to report only one of the rules, if they are equivalent and the equivalence information is also reported.) Therefore, we can from now on assume that there are only three alternatives: either one of the rules is specious by the other or none of them is.

A brute-force approach for detecting specious rules would evaluate all possible rule pairs r_1 and r_2 . However, this is quite an intractable solution because the universe of all possible rules defined by k attributes is $\mathcal{O}(2^k)$. As a solution, we will show that when the rules are searched with appropriate goodness measures, then the speciousness of the best K rules (or all sufficiently good rules) can be checked exhaustively among those K rules, ignoring the rest. The foundation of this powerful result is the following observation on the relationship between marginal and conditional independence relations.

OBSERVATION 1. *Let us consider relationships of three binary variables X , Q , and C . Independence assumptions are presented by the following null hypotheses: H_{01} : X and C independent, H_{02} : Q and C independent,*

dent, H_{03} : Q and C conditionally independent given X , H_{04} : Q and C conditionally independent given $\neg X$, H_{05} : X and C conditionally independent given Q , H_{06} : X and C conditionally independent given $\neg Q$. Then the composed null hypotheses $(H_{01} \wedge H_{03} \wedge H_{04})$ and $(H_{02} \wedge H_{05} \wedge H_{06})$ are equivalent.

Proof. The proof is by showing that both composed null hypotheses describe the same data distribution. We recall that the distribution can be represented by triplet $(n_{xc}, n_{qc}, n_{xqc})$, when n , n_c , n_x , n_q , and n_{xq} are given.

Assuming $H_{01} \wedge H_{03} \wedge H_{04}$ means that $p_{xc} = p_x p_c$, $p_{xqc} = \frac{p_{xq} p_{xc}}{p_x} = p_{xq} p_c$, and $p_{\neg xqc} = \frac{p_{\neg xq} p_{\neg xc}}{p_{\neg x}} = p_{\neg xq} p_c$. Therefore, $p_{qc} = p_{xqc} + p_{\neg xqc} = (p_{xq} + p_{\neg xq}) p_c = p_q p_c$, and the triplet is $(p_x p_c, p_q p_c, p_{xq} p_c)$.

Assuming $H_{02} \wedge H_{05} \wedge H_{06}$ means that $p_{qc} = p_q p_c$, $p_{xqc} = \frac{p_{xq} p_{qc}}{p_q} = p_{xq} p_c$, and $p_{\neg xqc} = \frac{p_{\neg xq} p_{\neg qc}}{p_{\neg q}} = p_{\neg xq} p_c$. Therefore, $p_{xc} = p_{xqc} + p_{\neg xqc} = (p_{xq} + p_{\neg xq}) p_c = p_x p_c$, which leads to the same triplet $(p_x p_c, p_q p_c, p_{xq} p_c)$.

COROLLARY 4.1. *Let n , n_c , n_x , n_q , and n_{xq} be given. Then for the probability distributions of n_{xc} and n_{qc} given null hypotheses holds*

$$\begin{aligned} P(n_{xc}|H_{01})P(n_{qc}|n_{xc}, H_{03} \wedge H_{04}) &= \\ P(n_{xc}, n_{qc}|H_{01} \wedge H_{03} \wedge H_{04}) &= P(n_{xc}, n_{qc}|H_{02} \wedge H_{05} \wedge H_{06}) \\ &= P(n_{qc}|H_{02})P(n_{xc}|n_{qc}, H_{05} \wedge H_{06}) \end{aligned}$$

and thus

$$(4.3) \quad \frac{P(n_{xc} | H_{01})}{P(n_{qc} | H_{02})} = \frac{P(n_{xc} | n_{qc}, H_{05} \wedge H_{06})}{P(n_{qc} | n_{xc}, H_{03} \wedge H_{04})}.$$

Equation 4.3 means that for judging whether $P(n_{xc} | n_{qc}, H_{05} \wedge H_{06}) < P(n_{qc} | n_{xc}, H_{03} \wedge H_{04})$ (i.e., if r_2 could make r_1 specious), it suffices to check whether $P(n_{xc} | H_{01}) < P(n_{qc} | H_{02})$. This can be done by fixing the sampling model and estimating the point probabilities either directly or indirectly. However, it is not necessary to estimate the exact probabilities, because most goodness measures for statistical dependencies reflect the same distributions under the same null hypotheses. We will shortly show that for speciousness detection, it suffices that the goodness measure and its conditional counterpart are *order-homomorphic*, as defined in the following:

DEFINITION 2. *Let M be a goodness measure for dependency rules and M_c its conditional variant, such that $M(Q \rightarrow C=c)$ measures marginal dependence between Q and $C=c$ and $M_c(Q \rightarrow C=c|X \rightarrow C=c_x)$ measures conditional dependence between Q and $C=c$ given $X \rightarrow C=c_x$. M and M_c are called order-isomorphic, if for all rules r_1, r_2*

$$M_c(r_1|r_2) \leq M_c(r_2|r_1) \Leftrightarrow M(r_1) \leq M(r_2)$$

and order-homomorphic if for all rules r_1, r_2

$$M_c(r_1|r_2) \leq M_c(r_2|r_1) \Rightarrow M(r_1) \leq M(r_2).$$

Order-isomorphic measures M and M_c are called distance-preserving, if $M_c(r_1|r_2) - M_c(r_2|r_1) = M(r_1) - M(r_2)$ and ratio-preserving if $\frac{M_c(r_1|r_2)}{M_c(r_2|r_1)} = \frac{M(r_1)}{M(r_2)}$.

It turns out that many commonly used measures are order-homomorphic or even order-isomorphic. For example, exact hypergeometric point probabilities are ratio-preserving (P s in Eq. 4.3 are replaced by hypergeometric probabilities) and Mutual information and Log-likelihood ratio ($2MI$) are distance-preserving. For the χ^2 -measure, order-homomorphism may not hold exactly but asymptotically [7]. It is an open problem whether Fisher's p -value (cumulative hypergeometric probability) is order-homomorphic with Birch's p -value, like the corresponding point probabilities. If this could be proved, they would likely be the most robust measures for finding genuine rules.

Efficient speciousness detection is based on the following simple yet powerful theorem:

THEOREM 4.1. *Let (M, M_c) be a pair of order-homomorphic measures, where M is a marginal and M_c a conditional goodness measure for dependency rules. We assume that M and M_c are increasing (decreasing) by goodness, i.e., high (low) values indicate significant dependence. In addition, we assume that for any rule r_1 which is specious by another rule r_2 holds $M_c(r_1|r_2) < M_c(r_2|r_1)$ and $M_c(r_1|r_2) \leq \theta$ (for decreasing measures $M_c(r_1|r_2) > M_c(r_2|r_1)$ and $M_c(r_1|r_2) \geq \theta$), where θ is a predefined threshold. Then dependency rule r_1 can be made specious only by such r_2 for which $M(r_1) < M(r_2)$ ($M(r_1) > M(r_2)$).*

Proof. The proof follows directly from the definitions of speciousness and order-homomorphism.

This has an important consequence from an algorithmic point of view. For simplicity, we give the result only for increasing goodness measures.

COROLLARY 4.2. *Let R be a set of binary attributes and \mathcal{U} a universe of all possible rules $X \rightarrow C=c$, $C \in R$, $X \subseteq R \setminus \{C\}$, $c \in \{0, 1\}$. Let (M, M_c) be an order-homomorphic pair of increasing goodness measures and τ a minimum threshold for M (alternatively, M -value of the K th best rule). Further, let $\mathcal{R}_\tau = \{r \mid r \in \mathcal{U}, M(r) \geq \tau\}$ denote the set of all rules having sufficiently good M -value in the given data. Then, for detecting speciousness of any $r_1 \in \mathcal{R}_\tau$, it suffices to check $r_2 \in \mathcal{R}_\tau$, $r_2 \neq r_1$, having $M(r_2) \leq M(r_1)$. Furthermore, r_1 (or its reverse rule, with the antecedent and*

consequent reversed) and r_2 (or its reverse rule) should have the same attribute as the consequent.

In practice, this means that speciousness detection can be done in the post-processing phase, when only the best K rules or all sufficiently good rules are available. The only requirement is that the results set \mathcal{R} contains the best rules with the given measure or at least all non-specious rules. This is not guaranteed, if one has used any suboptimal pruning heuristics like minimum frequency thresholds, restrictions on the rule complexity, or exclusion of negative dependency rules ($X \rightarrow \neg C$). In the latter case, some specious rules may not be detected, even if the confounding factors were represented in the data.

4.2 Algorithm The simplest approach for speciousness detection is to search for the top- K (positive and negative) dependency rules with an order-homomorphic measure and then evaluate speciousness of each rule r_i with respect to better rules r_j in the post-processing phase. However, this approach typically results in a large number of specious rules, which are redundant specializations of more generic rules (Section 3.1). Therefore, it is desirable to prune out redundant rules during the actual search phase, which also accelerates the search remarkably (see e.g., [4]).

When the set of best non-redundant dependency rules has been discovered, the rest of the specious rules can be detected in the post-processing phase using Algorithm 1. In the algorithm, all three special cases of speciousness from Section 3 as well as the normal case are handled separately. One reason is that some special cases can be checked with less computation. For example, there is no need to evaluate frequency n_{xq} if the rules are equivalent or $X \subset Q$, assuming that n_x , n_{xc} , n_q , and n_{qc} are available. Birch's exact test is also computationally demanding and is preferably performed only when needed.

The first case covers equivalent rules which cannot be considered as specious per se. Still, they contain redundant information which only complicates understanding. If X and Q are equivalent, then each X 's rule has an equivalent Q 's rule; if X and $\neg Q$ are equivalent, then for each $X \rightarrow C=c$, there is $Q \rightarrow C \neq c$. Therefore, it is sufficient to report the equivalence information ($X \rightarrow Q$ or $X \rightarrow \neg Q$), unless it occurs as a dependency rule in the list (which happens when $|X| = 1$ or $|Q| = 1$).

The second case covers rules of the form $Q \subset X$, where $X \rightarrow C=c$ is a non-redundant specialization of $Q \rightarrow C=c$. The opposite case where $X \subset Q$ has already been handled during the search. Since $\delta_1 = 0$, one could simply check whether $\delta_2 \leq 0$. However, evaluating significance of speciousness detects also cases where δ_2

is weakly positive.

The third case corresponds to Yule-Simpson’s paradox, where both δ_1 and δ_2 are non-positive, and it is not necessary to evaluate the significance of speciousness at all. For example, if the measure is MI_S , then it is known that $MI_S \leq 0$. This case includes also a pathological special case which has to be checked separately. Namely, when $P(X) = P(C=c) = P(X, C=c)$, then all rules $Q \rightarrow C=c$ and $Q \rightarrow C \neq c$ have $\delta_1 = \delta_2 = 0$ and would be considered specious. This could potentially lose interesting dependencies and therefore, it is required that there remains rule $X \rightarrow Q$ or $X \rightarrow \neg Q$ containing the same information as $Q \rightarrow C=c$.

The fourth case is the normal case where the significance measure is always evaluated.

Algorithm 1 SpecDetect(\mathcal{R}, K, θ) for detecting specious rules among the top- K non-redundant dependency rules in an ordered list \mathcal{R} . Here, measure M_c is increasing by goodness and θ is its minimum threshold.

```

for  $i = K$  to 2 // in ascending order
  take rule  $r_i \in \mathcal{R} : Q \rightarrow C=c$ 
  for  $j = 1$  to  $i - 1$  // in descending order
    take rule  $r_j \in \mathcal{R} : X \rightarrow A = a$ 
    if  $(Q = X)$  or  $(Q = A)$  or  $(C = X)$  or  $(C = A)$ 
      reverse rules if needed
      resulting  $Q' \rightarrow C' = c$  and  $X' \rightarrow C' = a$ 
      if  $(c \neq a)$  and  $(\delta(X', Q') > 0)$ 
        take next  $r_j$ 
         $\delta_1 = \delta_c(Q, C=c|X')$ ;  $\delta_2 = \delta_c(Q, C=c|\neg X')$ 
        // Check four alternatives:
        if  $((Q' \text{ and } X') \text{ or } (Q' \text{ and } \neg X'))$  equivalent)
          report equivalence and prune out  $r_i$ 
        if  $((Q' \subset X') \text{ and } (c = a) \text{ and } (M_c(r_i|r_j) \leq \theta))$ 
          prune out  $r_i$ 
        if  $((\delta_1 \leq 0) \text{ and } (\delta_2 \leq 0))$ 
          if  $(n_x = n_{xc} = n_c)$  check pathological case
          else report Y-S paradox and prune our  $r_i$ 
        if  $(M_c(r_i|r_j) < \theta)$  // normal case
          report and prune out  $r_i$ 

```

5 Experiments

5.1 Test setting The main goal of the experiments was to explore the nature and extent of specious rules and how their pruning affects results. For this purpose we tested classical benchmark data sets with varying dimensions and densities from the UCI Machine Learning Repository [8] and the Frequent Itemset Mining Dataset Repository [3]. The test data is described in Table 1. All sets are real world data except T10I4D100K and T40I10D100K which are synthetic data sets simulating

Table 1: Description of data sets: Abbr=abbreviation, n =number of rows, k =number of attributes, $tlen$ =average transaction length.

Data	Abbr	n	k	$tlen$
Plants	Plants	22632	70	12.5
Chess	Chess	3196	75	37.0
Mushroom	Mush	8124	119	23.0
Accidents	Acc	340183	468	33.8
T10I4D100K	T1	100000	870	10.1
T40I10D100K	T4	100000	942	39.6
PumsbStar	PStar	49046	1934	50.5
Pumsb	Pumsb	49046	2113	74.0

market basket data.

In the experiments, we searched for the top-100 and top-1000 positive or negative dependency rules with Mutual information and analyzed the detected specious rules. The search was done with the Kingfisher program [4], which was extended with a special module for speciousness testing. The basic version of Kingfisher already prunes out redundant rules (a special case of specious rules) during the search and it was used as a baseline for comparison. No minimum frequency thresholds or other constraints were used, except with Accidents, which was computationally the most demanding data set. When the top-1000 rules were searched from Accidents, the complexity of rules was restricted to six attributes (max five attributes in the antecedent). For speciousness testing with MI_S , we used a cautious threshold $\theta = 0.5$. Larger thresholds were tried if no type 3 specious rules were detected. Birch’s p -value was calculated for checking that θ was not too large (i.e., none of the pruned partial dependencies were significant).

For each specious rule $Q \rightarrow C=c$, we recorded its subtype according to the first $X \rightarrow C=c$ or $X \rightarrow C \neq c$ that made it specious. The subtypes were the same as in Algorithm 1. In addition, we calculated several statistics for comparing specious (still non-redundant) and non-specious rules (their frequency, strength of dependency, rule complexity) and evaluating the degree of speciousness (conditional leverages, MI_S , Birch’s p , strength of the mediating rule $X \rightarrow Q = q$, $q \in \{0, 1\}$). Type 0 rules were excluded from statistics, because they are a special case, which cannot be considered specious per se.

5.2 Results Proportions of specious rules and their distribution to subtypes are given in Figure 2. Mean statistics characterizing non-equivalent specious rules in contrast to non-specious rules are given in Table 2.

Figure 2 shows that the proportion of specious

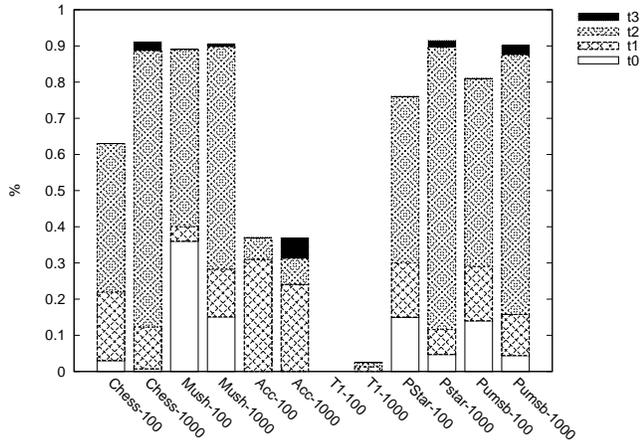


Figure 2: Proportion of specious rules and their subtypes among the top-100 and top-1000 rules. Sets Plants and T4 are excluded because they contained no specious rules.

rules varies greatly among the data sets. Chess, Mushroom, Accidents, PumsbStar and Pumsb contained a large proportion of specious rules, while Plants and T40I10D100K did not contain any and T10I4D100K only sparsely (none among the top-100 rules). Interestingly, Plants, T10I4D100K and T40I10D100K were the only sets of occurrence data, listing either U.S.A. states where plant species occurred or product items that occurred in market baskets. When the top-1000 rules were studied, over 90% of the 1000 best rules were specious in Chess, Mushroom, PumsbStar, and Pumsb. In these data sets, the most common subtype was 2 and even 78% of rules could express Yule-Simpson’s paradox. Accidents differed from these by having predominantly type 1 specious rules. Type 0 rules occurred most commonly in Mushroom. Type 3 rules were relatively rare and they did not occur among the top-100 rules at all. One explanation is the cautious threshold, and a larger threshold caught some type 3 rules among the top-100 rules in Pumsb and PumsbStar. Another explanation is that the same rule can be specious by many alternative rules and thus fall into different types. This was demonstrated by checking possible $X \rightarrow C=c$ and $X \rightarrow C \neq c$ rules in a reversed order, which resulted in some specious rules changing their type to 0.

Table 2 shows that non-specious rules were in general better than specious rules, excluding type 0 rules. They necessarily had larger MI , because a rule can become specious only by a better rule with the given goodness measure. However, non-specious rules had also larger frequency and leverage in all sets except Accidents. Among the top-100 rules, they had also

larger precision $p_{C|Q}$, but in the top-1000, the situation was slightly different (in PumsbStar and the T1 set, specious rules had higher precision). In addition, specious rules were on average more complex than non-specious rules. However, the difference was small in Accidents, where many specious rules were generalizations of non-specious rules. These results demonstrated that speciousness pruning produced simpler and better rules, which is itself desirable. We note that type 0 specious rules can well be better than non-specious rules (e.g., in the top-1000 Mushroom $avg(MI)=4297$) because they are often equivalent with the very best rules.

An analysis of conditional leverages revealed that on average, δ_1 was zero, but δ_2 was often negative. This means that in specious rules, Q and $C=c$ tended to be negatively associated given $\neg X$. The average MI_S values were always non-positive. Once again, Accidents differed from the others with extremely low MI_S . A likely reason is that Accidents was also the largest data set, with most frequent rules, which also tend to have large MI . On the other hand, Accidents had smallest conditional leverages (strong negative conditional dependencies) which led to sign reversal and low MI_S -values. The mediating rules $X \rightarrow Q = q$ were always strong, as expected, with $avg(\delta(X, Q = q)) > avg(\delta(Q, C=c))$. Still, X and Q had relatively few common attributes, except in Accidents, where type 1 was common. For the top-100 rules, the average p_B values were large ($p_B \approx 1.00$), except for Accidents $p_B \approx 0.91$. For the top-1000 rules, the p_B values were slightly smaller, p_B ranging from 0.99 (Mushroom) to 0.88 (Accidents). With the top-1000, the minimum p_B values were substantially smaller, ranging from 0.15 (Accidents) to 0.35 (T1), even if the maximum MI_S threshold was the same. Still, none of them was significant even in a traditional sense (where $\alpha = 0.05$ or $\alpha = 0.01$) and it is unlikely that any true dependencies had been pruned out as specious.

6 Conclusions

The problem of Yule-Simpson’s paradox and other specious dependencies have bothered statisticians and empirical scientists for more than a century. Still, no efficient method for detecting them has been known. In this research, we approached the problem from a new perspective, in the context of statistical association rule discovery. We showed that specious rules offer a unifying framework for many types of undesirable, redundant or misleading association rules. We introduced new theoretical properties that enable effective identification of possible confounding factors without testing all of the exponentially many possibilities. These results offer a remarkable improvement to cur-

Table 2: Mean values of statistics over all non-equivalent specious rules among the top-100 and top-1000 non-redundant rules with MI . Mean statistics for non-specious rules in parentheses.

Data	MI		fr		$p_{C Q}$		$p_{-C -Q}$		δ		$ Q $	
Top-100												
Plants	–	(8551)	–	(3535)	–	(0.86)	–	(0.95)	–	(0.120)	–	(1.3)
Chess	1338	(2159)	1287	(1819)	0.79	(0.93)	0.92	(0.98)	0.163	(0.176)	3.5	(1.2)
Mush	5622	(6483)	1771	(2350)	0.96	(0.99)	1.00	(0.98)	0.167	(0.206)	3.3	(0.6)
Acc	119793	(144940)	142478	(106631)	0.92	(0.95)	0.83	(0.89)	0.420	(0.317)	2.9	(2.3)
T1	–	(4339)	–	(730)	–	(0.89)	–	(0.99)	–	(0.007)	–	(1.4)
T4	–	(8064)	–	(1560)	–	(0.95)	–	(0.98)	–	(0.015)	–	(2.8)
PStar	46515	(46987)	23611	(24617)	0.99	(1.00)	0.99	(0.99)	0.245	(0.245)	2.3	(1.0)
Pumsb	47266	(47685)	23360	(24874)	0.99	(1.00)	1.00	(1.00)	0.247	(0.246)	2.6	(1.0)
Top-1000												
Plants	–	(6186)	–	(2799)	–	(0.81)	–	(0.93)	–	(0.095)	–	(1.6)
Chess	946	(1438)	1138	(1601)	0.67	(0.87)	0.89	(0.88)	0.129	(0.141)	3.8	(2.3)
Mush	3707	(4091)	1802	(2622)	0.89	(0.95)	0.92	(0.86)	0.144	(0.161)	3.0	(2.2)
Acc	36784	(43751)	110655	(88285)	0.76	(0.79)	0.63	(0.68)	0.326	(0.259)	2.6	(2.4)
T1	2604	(2950)	448	(473)	0.95	(0.89)	0.99	(0.99)	0.004	(0.005)	2.5	(1.6)
T4	–	(7449)	–	(1284)	–	(0.95)	–	(0.99)	–	(0.013)	–	(2.9)
PStar	39428	(42149)	16000	(21975)	0.98	(0.98)	0.99	(0.98)	0.203	(0.232)	3.9	(2.0)
Pumsb	41208	(41988)	19276	(21655)	0.98	(0.98)	0.99	(0.98)	0.225	(0.232)	3.8	(2.6)

rently known weak conditions. Then we showed how the properties can be implemented in the pattern discovery context, as an efficient generic algorithm that discovers the most significant, non-specious rules with any order-homomorphic significance measures. Preliminary experiments with Mutual information demonstrate that specious rules and Yule-Simpson’s paradox are indeed a common and serious problem in association rule discovery. However, with speciousness detection, association rules can reveal the real dependency structure of data and help to avoid misleading conclusions.

Acknowledgments

This research has been supported by the Academy of Finland under grant 307026 and by the Australian Research Council under grant DP140100087.

References

- [1] A. Alin. Simpsons paradox. *Wiley Interdisciplinary Reviews: Computational Statistics*, 2:247–250, 2010.
- [2] M. W. Birch. The detection of partial association, i: The 2 × 2 case. *J. Royal Statistical Society. Series B (Methodological)*, 26(2):313–324, 1964.
- [3] Frequent itemset mining dataset repository. Administered by B. Goethals. <http://fimi.ua.ac.be/data/>.
- [4] W. Hämmäläinen. Kingfisher: an efficient algorithm for searching for both positive and negative dependency

- rules with statistical significance measures. *Knowledge and Information Systems*, 32(2):383–414, 2012.
- [5] S. Huang and G.I. Webb. Pruning derivative partial rules during impact rule discovery. In *Proc. 9th Pacific-Asia Conf. Advances in Knowledge Discovery and Data Mining*, pp. 71–80. Springer, 2005.
- [6] Z. Jin, J. Li, L. Liu, T. D. Le, B.-Y. Sun, and R. Wang. Discovery of causal rules using partial association. In *Proc. 12th IEEE Int. Conf. Data Mining*, pp. 309–318. IEEE, 2012.
- [7] B. N. Lewis. On the analysis of interaction in multi-dimensional contingency tables. *J. Royal Statistical Society. Series A (General)*, 125(1):88–117, 1962.
- [8] M. Lichman. UCI machine learning repository, 2013.
- [9] D.V. Lindley and M.R. Novick. The role of exchangeability in inference. *Annals of Statistics*, 9:45–58, 1981.
- [10] N. Pasquier, Y. Bastide, R. Taouil, and L. Lakhal. Discovering frequent closed itemsets for association rules. In *Proc. 7th Int. Conf. Database Theory*, volume 1540 of *LNCS*, pp. 398–416. Springer-Verlag, 1999.
- [11] E. H. Simpson. The interpretation of interaction in contingency tables. *J. Royal Statistical Society. Series B (Methodological)*, 13(2):238–241, 1951.
- [12] G.I. Webb. Discovering significant patterns. *Machine Learning*, 68(1):1–33, 2007.
- [13] G.U. Yule. Notes on the theory of association of attributes in statistics. *Biometrika*, 2:121–134, 1903.