Improving Transparency, Falsifiability, and Rigour by Making Hypothesis Tests Machine Readable

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Abstract

Making scientific information machine-readable greatly facilitates its re-use. Many scientific articles have the goal to test a hypothesis, and making the tests of statistical predictions easier to find and access could be very beneficial. We propose an approach that can be used to make hypothesis tests machine readable. We believe there are two benefits to specifying a hypothesis test in a way that a computer can evaluate whether the statistical prediction is corroborated or not. First, hypothesis test will become more transparent, falsifiable, and rigorous. Second, scientists will benefit if information related to hypothesis tests in scientific articles is easily findable and re-usable, for example when performing meta-analyses, during peer review, and when examining meta-scientific research questions. We examine what a machine readable hypothesis test should look like, and demonstrate the feasibility of machine readable hypothesis tests in a real-life example.

Keywords: hypothesis testing, machine readability, metadata, scholarly communication
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In many scientific fields researchers rely on hypothesis tests to determine whether empirical observations corroborate predictions. In a well-specified hypothesis test, a theoretical hypothesis is used to derive predictions, which are operationalized when designing a specific study, and translated into a testable statistical hypothesis. Data is collected, and the statistical hypothesis is corroborated or not. Although this process sounds relatively straightforward, hypothesis tests are performed rather poorly in practice. First, statistical

hypotheses are stated verbally, but these verbal descriptions rarely sufficiently constrain flexibility in the data analysis. Second, there is a lack of transparency about which statistical tests in the results section are related to the predictions in the introduction section, and which pattern of results should be observed to conclude that a prediction is corroborated. Finally, researchers typically only implicitly specify what would lead them to act as if their prediction is confirmed (i.e., typically a *p*-value smaller than 0.05), and rarely specify what would lead them to act as if their prediction is falsified. By contrast, a well-specified hypothesis test states the statistical hypothesis for each prediction in a way that eliminates flexible implementations, clearly links predictions derived from the theoretical hypothesis to statistical tests, and gives unambiguous criteria to conclude the prediction is corroborated, falsified, or that the results are inconclusive.

We propose that the gold standard for well-specified hypothesis tests should be a statistical prediction that is machine readable. This means that a computer can evaluate whether a statistical prediction is corroborated (or not) based on clearly articulated evaluation criteria and the observed data. Computers do not handle ambiguity well, and making a hypothesis test machine readable guarantees that it is specified precisely. In this manuscript we demonstrate how hypothesis tests can be made machine readable. We believe that there are two broad arguments for a move to machine readable hypothesis tests. The first argument is that by specifying hypothesis tests in a format that can be read and evaluated by a machine, tests of predictions and the conclusions derived from these tests will become transparent, statistically falsifiable, and rigorous. This will help to alleviate poor practices in how scientists currently test hypotheses. The second argument is that the benefits of making data FAIR (findable, accessible, interoperable, and reusable) also apply to statistical predictions. If all aspects required to evaluate the test of a statistical prediction are machine-readable, we can easily reuse this information (e.g., when performing meta-analyses), and find and access this information (e.g., to answer meta-scientific questions about the proportion of statistical results in the scientific literature that corroborate the prediction).

Poor practices when testing predictions

As a concrete example of a typical hypothesis test in the published literature, DeBruine (2002) posited the theoretical prediction that people would exhibit higher levels of prosocial behavior towards those who physically resemble them, which follows from the idea that actions are influenced by an implicit evaluation of relatedness based on phenotypic similarity. Physical resemblance was manipulated by morphing face photographs with either the participant's own face (self morphs) or another person's face (other morphs). There were two versions of this manipulation: faces were morphed in shape only (n = 11) or in both shape and color (n = 13). Prosocial behavior was measured as the choice to trust or reciprocate trust in a monetary trust game where the first player could decide whether to trust the second player to split money and the second player, if trusted, could decide whether to reciprocate this trust by splitting the money equally or selfishly. The theoretical hypothesis was operationalized, and the operationalized prediction stated that people playing a trust game would trust and reciprocate more when playing with a person who was represented by a self morph than by an other morph. The statistical prediction was tested by counting the

number of trusting and reciprocating responses participants made to self and other morphs and then performing a t-test on these counts, separately analyzed for the shape morphs and the shape-colour morphs. The statistical results indicated that participants made more trust responses to self morphs than to other morphs for both morph types. However, there were no differences in how often they reciprocated their partners' trust. The conclusion drawn from this study was that these results show that facial resemblance can increase prosocial behaviour. It was noted that the fact that an effect was observed for the trust measure, but not for the reciprocation measure, could perhaps be explained by the different pay-off structures in the two-person bargaining game.

The first problem we can identify in this example is that it is not clear whether the operationalized prediction was confirmed if an effect was observed on both the trust measure and the reciprocation measure, or either of the two measures. From the conclusion the author draws we can infer that statistical prediction would be considered corroborated if the morphing manipulation had an effect on either the trust measure, or the reciprocation measure, or both. However, it is never clearly specified before the conclusion is reported which pattern of results would corroborate the prediction (e.g., if either, or both, of the tests were predicted to be statistically significant).

The second problem is that is is not clearly specified what would corroborate the hypothesis and what would statistically falsify the hypothesis. Although it is never explicitly stated, we can infer that the prediction would be corroborated when either of the two tests is significant at an alpha level of 0.05, without correcting for multiple comparisons. Furthermore, we can infer that a non-significant p-value is interpreted as the absence of any meaningful effect (even though this is a formally incorrect interpretation of a null hypothesis test). The third problem is that there is a range of options when analyzing the data (e.g., pooling the two types of morphs in one analysis, or reporting two separate analyses by morph version). As is often the case the testing statistical predictions, no unique analysis strategy follows unequivocally from the introduction and methods section, which can lead to flexibility in the data analysis.

What Does a Formalized Test of a Prediction Look Like?

If we want to make hypothesis tests machine readable, we need to capture all essential aspects of a hypothesis test in a machine readable data structure. A hypothesis test is a methodological procedure to evaluate a prediction that can be described on a conceptual level (e.g., people exhibit higher levels of prosocial behavior towards those who physically resemble them), an operationalized level (e.g., people playing a trust game make more trusting decisions when the person they play against is a self morph versus an other morph), and a statistical level (e.g., the average number of trust moves is statistically larger for games against self morphs than against other morphs in a dependent t-test).

We distinguish the following components of a statistical prediction: 1) a statistical test, 2) a test result, and 3) one or more criterion values that the test result is compared to. For example, our statistical prediction might be that we will observe a positive difference in the means between two measurements, which will be examined in a dependent t-test, from which we will determine the lower and upper 97.5% confidence interval around the

mean difference, which we will compare against a value of 0. Statistical hypotheses are probabilistic, and probabilistic hypotheses can be made falsifiable "by specifying certain rejection rules which may render statistically interpreted evidence 'inconsistent' with the probabilistic theory" (Lakatos, 1978). A hypothesis test thus requires researchers to specify when the observed results of a statistical test will lead them to act as if their prediction is consistent with the data, inconsistent with the data, or inconclusive (Neyman, Pearson, & Pearson, 1933).

As highlighted above, one limitation of current practice when testing hypotheses is that researchers often do not explicitly state what would corroborate or falsify their prediction. To be able to unambiguously evaluate a hypothesis, researchers need to specify the rules they will use to evaluate whether statistical results corroborate a prediction, falsify it, or when the results are inconclusive. For example, in a 2x2 design many different patterns of means across the four cells could be predicted (e.g., one of two main effects, or a specific pattern of the observed interaction effect), but the full pattern of possible results that would corroborate or falsify a prediction is seldom made explicit.

There are different approaches that can be used to statistically conclude that the prediction made in a study is falsified. In practice, corroborating or falsifying a statistical prediction in a single study is rarely sufficient to draw strong conclusions about a theory (Lakatos, 1978), and one should always keep random variation in mind when interpreting statistical results.

One approach to conclude a prediction is falsified is known as equivalence testing (Lakens, Scheel, & Isager, 2018). And equivalence test requires researchers to specify a smallest effect size of interest, and tests if the presence of an effect that is large enough to be deemed interesting can be statistically rejected. Continuing our example, we might conclude our prediction is corroborated when we can statistically conclude the observed mean difference is greater than zero, and not statistically smaller than the smallest effect size we care about. The prediction would be falsified if the effect is statistically smaller than the smallest effect size of interest, and inconclusive if we can neither conclude the effect is statistically greater than zero, nor statistically smaller than the smallest effect size we care about. If our statistical test is a dependent t-test, our test result is the upper and lower bound of a 97.5% confidence interval (i.e., a hypothesis test with a 2.5% alpha level), and our smallest effect size of interest is 0.2, we can conclude that we have corroborated our prediction if the lower bound of our 97.5% CI is larger than 0 and the upper bound is not smaller than 0.2. Our prediction is falsified if the upper bound of our 97.5% CI is smaller than 0.2, and our data is inconclusive in all other situations.

An important requirement to make statistical hypothesis machine readable is to identify the individual components that make it possible to evaluate a hypothesis test. Our example relies on *hypothesis* that is tested in an *analysis* that takes *data* as input and returns test *results*. Some of these tests results will be compared to *criteria*, used in the *evaluation* of the test result. For example, imagine a hypothesis predicts a certain difference in means between conditions. The data is analyzed with a Bayesian t-test (Dienes, 2019), and if the resulting Bayes factor is greater than some specified criterion (e.g., 6, used by the journal *Cortex*), the prediction is considered corroborated. If the Bayes factor is less than

142 the reciprocal of the criterion (e.g., 1/6), this is interpreted as evidence for the null model,
143 and the prediction is falsified. All other values are interpreted as inconclusive evidence.

Computationally Evaluating Hypotheses

145   If a prediction is machine readable, it is possible to automatically determine if a
146 prediction is corroborated by the data. We envision machine readable hypothesis tests as
147 part of a completely reproducible workflow. Computer scripts will load the raw data, and if
148 needed create the analytic data from the raw data (e.g., outlier removal, transformations,
149 computing sum scores according to pre-specified rules). The statistical test is automatically
150 performed on the analytic data, and the relevant test statistics are retrieved. These test
151 statistics are compared against pre-specified criteria, based on decision rules that evaluate
152 whether the prediction is corroborated, falsified, or inconclusive. All the information that is
153 required to perform these operations is stored in a structured meta-data file.

154   We provide an R script with a concrete example of a machine-readable statistical
155 prediction for the study by DeBruine (2002) described above. It is written using the R
156 package **scienceverse** and produces a JSON file, which is an open-standard file format that
157 can be used to transmit data. Because it is an open-standard file format, it can easily be
158 converted into any other data file format such as YAML or JATS, which in essence are all
159 nested lists. It can also be converted to a human-readable report, summarising the study
160 with verbal descriptions and a list containing the conclusion for each statistical prediction.

161   **Setting up a study.**   The top level list (Box 1) contains components describing
162 different aspects of the study, such as authors, hypotheses, materials, methods, data, and
163 analyses. In the future we might be able to describe all information in a scientific article
164 that we would like to be able to retrieve, but here we will focus on the aspects of the study
165 that are required to make statistical predictions machine readable. To achieve this, we need
166 a meta-data file that specifies the hypotheses, the analyses, and the evaluation criteria for
167 each prediction.

Box 1. The top-level structure of the machine-readable study description.

```
{
    "name": "Kinship and Prosocial Behaviour",
    "info": [],
    "authors": [],
    "hypotheses": [ ...Box 2... ],
    "methods": [],
    "data": [ ...Box 6... ],
    "analyses": [ ...Box 5... ]
}
```

168

169   **Hypotheses.**   A study could contain multiple hypotheses, but our example contains
170 only one. Each `hypothesis` (Box 2) consists of an `id` for referencing the hypothesis in other
171 components, a verbal human-readable `description`, one or more `criteria` to evaluate
172 analysis results, and rules to determine `corroboration` or `falsification` of the hypothesis.
173 If the data are available, these rules are automatically evaluated and a `conclusion` of

174 "corroborate", "falsify", or "inconclusive" is added.

```
Box 2. The hypothesis component.

    "hypotheses": [
        {
            "id": "self_pref",
            "description": "Cues of kinship will increase prosocial
                            behaviour. Cues of kinship will be
                            manipulated by morphed facial self-
                            resemblance. Prosocial behaviour will be
                            measured by responses in the trust game.
                            The prediction is that the number of
                            trusting AND/OR reciprocating moves will
                            be greater to self morphs than to other
                            morphs.",
            "criteria": [ ...Box3... ],
            "corroboration": { ...Box 4... },
            "falsification": { ...Box 4... },
            "conclusion": "corroborate"
        }
    ]
```

175

176   **Criteria.**   Each criterion (Box 3) needs an `id` to be able to reference them in the
177 evaluations and references a named `result` from an analysis with the id `analysis_id`.
178 An `operator` and a `comparator` are provided for each criterion to specify the method of
179 comparison (e.g., $>$, $<$, $=$, !=) and the comparison value (e.g., 0). For example, the first
180 criterion specifies that if the statistical result "conf.int[1]" from "trust_analysis" is "$>$" than
181 "0", then the criterion "trust_lowbound" evaluates to a `conclusion` of "true". In other words,
182 if we can statistically reject the null hypothesis (because the lower bound of the confidence
183 interval does not overlap with 0), this criterion of our statistical prediction is corroborated.
184 Although in essence this describes nothing more than what we do when we interpret test
185 results, this decision process is now captured and made explicit in machine-readable code.

Box 3. Criteria for evaluation.

```
"criteria": [
    {
        "id": "trust_lowbound",
        "analysis_id": "trust_analysis",
        "result": "conf.int[1]",
        "operator": ">",
        "comparator": 0,
        "conclusion": true
    },
    {
        "id": "trust_highbound",
        "analysis_id": "trust_analysis",
        "result": "conf.int[2]",
        "operator": ">",
        "comparator": 0.2,
        "conclusion": true
    },
    {
        "id": "recip_lowbound",
        "analysis_id": "recip_analysis",
        "result": "conf.int[1]",
        "operator": ">",
        "comparator": 0,
        "conclusion": false
    },
    {
        "id": "recip_highbound",
        "analysis_id": "recip_analysis",
        "result": "conf.int[2]",
        "operator": ">",
        "comparator": 0.2,
        "conclusion": true
    }
]
```

Hypothesis Evaluation. The `corroboration` and `falsification` sub-components (Box 4) describe rules to determine corroboration or falsification of a hypothesis from the criteria conclusions, and each consists of three elements. The `description` element contains verbal descriptions of the decision rules for concluding the hypothesis is corroborated or falsified. The `evaluation` element contains a logical version referencing the criteria `id`. For example, "`(trust_lowbound & trust_highbound) | (recip_lowbound & recip_highbound)`" means that the corroboration `result` will be set to "true" if the first two criteria are both true, or if the last two criteria are both true, while "`!trust_highbound & !recip_highbound`" means that the falsify conclusion will be

196 set to "true" if both of these criteria are false (note that an exclamation mark means "not").

Box 4. Corroboration and falsification rules.

```
"corroboration": {
    "description": "The hypothesis is corroborated if the
                    97.5% CI lower bound is greater than 0
                    and the 97.5% CI upper bound is greater
                    than 0.2 (the SESOI) for either the
                    trust or reciprocation moves.",
    "evaluation": "(trust_lowbound & trust_highbound) |
                    (recip_lowbound & recip_highbound)",
    "result": true
},
"falsification": {
    "description": "The hypothesis is falsified if the
                    97.5% CI upper bound is smaller than
                    0.2 (the SESOI) for both trust and
                    reciprocation.",
    "evaluation": "!trust_highbound & !recip_highbound",
    "result": false
}
```

197

198 **Analyses.** Each analysis is specified in the `analysis` component (Box 5). An
199 analysis consists of an `id` to reference the statistical test when evaluating the criteria and
200 the `code` used to run the analysis. Once data are attached and the analyses are run, a list
201 of named `results` is added to be referenced in the criteria. Each analysis can also contain
202 additional information, such as the software used to perform the analysis. The example
203 below specifies two *t*-tests, using the `t.test` function in R. In the working scienceverse
204 prototype used in this manuscript, short analyses can be added directly, while longer analysis
205 scripts that return a test result can be added by referencing to an external analysis script.

Box 5. The analysis component.

```
"analyses": [
    {
        "id": "trust",
        "func": "analysis_trust_func",
        "code": [
            "function () ",
            "{",
            "    t.test(kin$trust_self, kin$trust_other,
                        paired = TRUE, conf.level = 0.975)",
            "}"
        ],
        "software": "R version 3.6.2 (2019-12-12)",
        "results": { ...Box 7... }
    },
    {
        "id": "recip",
        "func": "analysis_recip_func",
        "code": [
            "function () ",
            "{",
            "    t.test(kin$recip_self, kin$recip_other,
                        paired = TRUE, conf.level = 0.975)",
            "}"
        ],
        "software": "R version 3.6.2 (2019-12-12)",
        "results": { ...Box 7... }
    }
]
```

Data. Each dataset can be specified in the `data` component (Box 6). A dataset consists of an `id` to reference the dataset in analyses and information about how to obtain the data (e.g., `doi`, `url`). The `codebook` contains descriptions of each column, but it is even possible to include the `data` file in this component. By storing the data underlying the reported analyses as nested lists in the same JSON file together with good meta-data, a reported analyses could be completely reproduced in the future with a single commond. Furthermore, it becomes very easy to perform additional analyses or sensitivity analyses on the data. Below, we present a data component with a codebook created by scienceverse using the Psych-DS 0.1.0 format, which is currently still in development. The descriptors for each column can be arbitrarily detailed, or follow other meta-data formats. For other software that helps researchers to create and share machine-readable codebooks, see Arslan (2019).

Box 6. The data component.

```
"data": [
    {
        "id": "kin",
        "codebook": {
            "@context": "https://schema.org/",
            "@type": "Dataset",
            "name": "kin",
            "schemaVersion": "Psych-DS 0.1.0",
            "url": "https://osf.io/ewfhs/",
            "variableMeasured": [
                {   "@type": "PropertyValue",
                    "name": "trust_self",
                    "description": "Number of trusting moves
                                    towards self-morphs",
                    "type": "int"
                },
                {   "@type": "PropertyValue",
                    "name": "trust_other",
                    "description": "Number of trusting moves
                                    towards self-morphs",
                    "type": "int"
                },
                {   "@type": "PropertyValue",
                    "name": "recip_self",
                    "description": "Number of reciprocating moves
                                    towards other-morphs",
                    "type": "int"
                },
                {   "@type": "PropertyValue",
                    "name": "recip_other",
                    "description": "Number of reciprocating moves
                                    towards other-morphs",
                    "type": "int"
                }
            ]
        },
        "data": {
            "trust_self": [1, 2, 2, 1, 1, 1, 1, 1, 2, 0, 2, 0,
                           1, 2, 2, 3, 2, 2, 1, 1, 2, 0, 0, 1],
            "trust_other": [1, 2, 2, 0, 1, 0, 0, 0, 1, 0, 1, 0,
                            1, 1, 1, 0, 1, 2, 2, 0, 0, 0, 2, 1],
            "recip_self": [0, 1, 3, 2, 1, 1, 1, 3, 3, 2, 3, 1,
                           1, 2, 3, 3, 3, 1, 1, 1, 3, 0, 3, 1],
            "recip_other": [1, 1, 2, 2, 3, 2, 1, 3, 3, 1, 3, 0,
                            1, 3, 3, 3, 3, 0, 3, 0, 1, 0, 3, 2]
        }
    }
]
```

²²⁰   **Automatic Evaluation.**   Now that the prediction is specified in a machine readable
²²¹ format, it is possible for the statistical prediction to be evaluated automatically. Auto-
²²² matic evaluation of machine readable hypotheses has at least two useful functions during
²²³ the peer review process. First, we foresee a future where researchers are required to
²²⁴ submit fully computationally reproducible analysis scripts with their submissions. This
²²⁵ will require editorial assistants or reviewers to check the computational reproducibility
²²⁶ of the reported results in a manuscript. Machine readable hypothesis tests would make
²²⁷ this check a matter of running a single function. For example, based on the information
²²⁸ specified in the analyses, criteria, and data components, the `study_analyze` function in
²²⁹ scienceverse demonstrates how it would be possible to read in the analytic data, perform
²³⁰ each analysis, and store the results. For example, the "trust_analysis" can be performed
²³¹ by running the analysis `t.test(x = kin$trust_self, y = kin$trust_other, paired =`
²³² `TRUE, conf.level = .975)` after the data is loaded as an object named "kin". We store
²³³ the result of this analysis (e.g., the t.test function in R returns a list of named numbers,
²³⁴ including "conf.int": [0.0213, 0.9787]). The criteria are then evaluated against the results of
²³⁵ the analyses. For example, because the first number in the "conf.int" result (0.0213) is larger
²³⁶ (">") than zero ("0"), we can store the conclusion that this criterion is "true" (see Box 3).

²³⁷   After the code has drawn conclusions about whether each criterion is met or not, based
²³⁸ on the results of the analyses, the evaluation rules can be used to determine whether the
²³⁹ prediction is corroborated, falsified, or neither (and thus the results are inconclusive). For
²⁴⁰ the prediction to be corroborated, the criteria for "trust_lowbound" and "trust_highbound"
²⁴¹ have to be met, and/or the criteria for "recip_lowbound" and "recip_highbound" have
²⁴² to be met. Since the conclusions for "trust_lowbound" and "trust_highbound" are both
²⁴³ true, the prediction is corroborated, and because it is not true that both upper bounds
²⁴⁴ for the confidence interval are smaller than 0.2, the prediction is not falsified. The overall
²⁴⁵ `conclusion` is therefore that our statistical prediction is corroborated. It will typically be
²⁴⁶ useful to return a human readable summary, which is presented in Figure 1 below. Such a
²⁴⁷ human-readable summary would allow editorial assistants or reviewers to quickly check the
²⁴⁸ computational reproducibility of the reported results.

Box 7. Results of data analysis.

```
"analyses": [
    {
        "id": "trust",
        ...
        "results": {
            "statistic": 2.5045,
            "parameter": 23,
            "p.value": 0.0198,
            "conf.int": [0.0213, 0.9787],
            "estimate": 0.5,
            "null.value": 0,
            "stderr": 0.1996,
            "alternative": "two.sided",
            "method": "Paired t-test",
            "data.name": "kin$trust_self and kin$trust_other"
        }
    },
    {
        "id": "recip",
        ...
        "results": {
            "statistic": -0.2138,
            "parameter": 23,
            "p.value": 0.8326,
            "conf.int": [-0.5089, 0.4256],
            "estimate": -0.0417,
            "null.value": 0,
            "stderr": 0.1949,
            "alternative": "two.sided",
            "method": "Paired t-test",
            "data.name": "kin$recip_self and kin$recip_other"
        }
    }
]
```

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Benefits of Machine Readability

We believe the benefits of making statistical predictions machine readable are worth the extra effort. First, machine-readable hypotheses remove ambiguity about what researchers predict and which criteria must be met to conclude a statistical hypothesis is corroborated. Predictions are explicitly linked to the tests that are performed to evalaute if the prediction is corroborated or not. The exact test is specified, which prevents flexibility in the data analysis. Furthermore, by specifying the criteria for corroboration or falsification explicitly prevents

Evaluation of Statistical Hypotheses

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Kinship and Prosocial Behaviour Postregistration

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Abstract

A reanalysis of data from DeBruine (2002) Facial Resemblance Enhances Trust, PRSLB.

Results

Hypothesis 1: self_pref

Cues of kinship will increase prosocial behaviour. Cues of kinship will be manipulated by morphed facial self-resemblance. Prosocial behaviour will be measured by responses in the trust game. The prediction is that the number of trusting AND/OR reciprocating moves will be greater to self morphs than to other morphs.

- `trust_lowbound` is confirmed if analysis trust yields `conf.int[1]>0`
  The result was conf.int[1] = 0.021 (TRUE)
- `trust_highbound` is confirmed if analysis trust yields `conf.int[2]>0.2`
  The result was conf.int[2] = 0.979 (TRUE)
- `recip_lowbound` is confirmed if analysis recip yields `conf.int[1]>0`
  The result was conf.int[1] = -0.509 (FALSE)
- `recip_highbound` is confirmed if analysis recip yields `conf.int[2]>0.2`
  The result was conf.int[2] = 0.426 (TRUE)

Corroboration (TRUE)

The hypothesis is corroborated if the 97.5% CI lower bound is greater than 0 and the 97.5% CI upper bound is greater than 0.2 (the SESOI) for either the trust or reciprocation moves.

```
(trust_lowbound & trust_highbound) | (recip_lowbound & recip_highbound)
```

Falsification (FALSE)

The hypothesis is falsified if the 97.5% CI upper bound is smaller than 0.2 (the SESOI) for both trust and reciprocation.

```
!trust_highbound & !recip_highbound
```

All criteria were met for corroboration.

Analyses

Analysis 1: trust

```
analysis_trust_func <- function ()
{
    t.test(kin$trust_self, kin$trust_other, paired = TRUE, conf.level = 0.975)
}
```

Analysis 2: recip

```
analysis_recip_func <- function ()
{
    t.test(kin$recip_self, kin$recip_other, paired = TRUE, conf.level = 0.975)
}
```

Figure 1. Example of machine readable output generated by scienceverse that shows the results and evaluation of the hypotheses.

future researchers who will replicate the study from having to infer which results would falsify the original finding. Although machine readable hypotheses might feel extremely rigid, it is possible to specify a range of sensitivity analyses across which the prediction should hold.

Another benefit of making statistical hypotheses machine readable is that many important aspects of the hypothesis test become accessible, findable, and usable. This will benefit researchers in the future. We can imagine a utopian future where meta-data files such as the example in Box 1 are accessible by browsing to a website that consists of the DOI, appended by /meta (e.g., https://doi.org/10.1098/rspb.2002.2034/meta/). Researchers can access these files to load all the information that is available about statistical predictions. For example, when a completely reproducible workflow is used, and data can be accessed as part of the JSON file, the meta-data file should be sufficient to easily calculate or access effect sizes from the performed statistical tests for meta-analyses.

While making hypothesis tests machine readable can obviously not ensure that statistical predictions are sensible or logically coherent, the process of writing a machine-readable statistical prediction could have a secondary benefit of providing a well-structured framework to think through and specify all important aspects of a statistical prediction. This might not be easy. Researchers might find it difficult to specify all required components in advance, or to specify the ranges of results that would corroborate or falsify a prediction. Sometimes a research idea is not yet well-specified enough to be tested in a confirmatory hypothesis test. Hypothesis tests are an extremely formalized procedure to make a decision whether a prediction is corroborated or not. If researchers realize they are actually not yet ready to make a falsifiable statistical prediction when creating a machine readable prediction, we would consider this a benefit as well, and we expect this to be a relatively common consequence of trying to formalize hypothesis tests.

Registered Reports as Use Case

We realize that several aspects of our proposal to make hypothesis tests machine readable sound futuristic. At the same time, we believe immediate use cases for machine readable hypothesis tests already exist in the form of the Registered Report publication format (Chambers, 2019). Registered Reports require researchers to clearly specify their statistical prediction, and are developed to reduce flexibility in the statistical analyses. After Stage 1 review based on the introduction, methods, and analysis plan, researchers can receive an "in principle acceptance". They then collect the data, and submit a Stage 2 Registered Report that includes the results and conclusion. Reviewers need to evaluate whether the analyses were conducted exactly as planned and whether conclusions follow from the predictions. This aspect of the peer review process is labor intensive and often still somewhat ambiguous, but could be automated if the statistical predictions were machine readable.

Scienceverse illustrates one possible workflow where after specifying the hypotheses at a Stage 1 submission, a machine readable html report can be produced with the `study_save` function. This report looks similar to Figure 1, without any of the lines containing coloured true or false evaluations of the predictions. When the data is collected, reviewers should be

able to use the JSON file generated at Stage 1, load the collected data with the `add_data`
function, run the preregistered analyses, and generate a human readable report as in Figure
1. This should make it realtively easy for reviewers to compare if planned and reported
analyses.

Conclusions

Technological innovation makes it possible to communicate scientific findings in digital
formats that allow for much easier re-use of scientific information contained in these digital
files compared to traditional journal articles. As we move towards a time where researchers
are expected to share their data in a way that is FAIR (findable, accessible, interoperable,
and reusable), we believe it is feasible and beneficial to make statistical predictions machine
readable as well. We see machine readable hypothesis tests as a logical development, with
immediate benefits for the rigour of hypothesis tests. Increasing the accessibility of essential
information related to hypothesis tests in scientific paper will also facilitate peer review,
especially of Registered Reports, and facilitate meta-scientific research. Making statistical
predictions machine readable will be an important next step towards a scientific literature
that can be accessed not just visually, but also computationally.

References

Arslan, R. C. (2019). How to automatically document data with the codebook package to facilitate data reuse. *Advances in Methods and Practices in Psychological Science*, *2*(2), 169–187. doi:10.1177/2515245919838783

Chambers, C. (2019). What's next for registered reports? *Nature*, *573*, 187–189. doi:10.1038/d41586-019-02674-6

DeBruine, L. M. (2002). Facial resemblance enhances trust. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, *269*, 1307–1312. doi:10.1098/rspb.2002.2034

Dienes, Z. (2019). How do I know what my theory predicts? *Advances in Methods and Practices in Psychological Science*, *2*(4), 364–377. doi:10.1177/2515245919876960

Lakatos, I. (1978). *The methodology of scientific research programmes: Volume 1: Philosophical papers.* Cambridge University Press.

Lakens, D., Scheel, A. M., & Isager, P. M. (2018). Equivalence testing for psychological research: A tutorial. *Advances in Methods and Practices in Psychological Science*, *1*(2), 259–269. doi:10.1177/2515245918770963

Neyman, J., Pearson, E. S., & Pearson, K. (1933). IX. On the problem of the most efficient tests of statistical hypotheses. *Philosophical Transactions of the Royal Society of London. Series A, Containing Papers of a Mathematical or Physical Character*, *231*(694-706), 289–337. doi:10.1098/rsta.1933.0009

Arslan, R. C. (2019). How to automatically document data with the codebook package to facilitate data reuse. *Advances in Methods and Practices in Psychological Science*, *2*(2), 169–187. doi:10.1177/2515245919838783

Chambers, C. (2019). What's next for registered reports? *Nature*, *573*, 187–189. doi:10.1038/d41586-019-02674-6

DeBruine, L. M. (2002). Facial resemblance enhances trust. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, *269*, 1307–1312. doi:10.1098/rspb.2002.2034

Dienes, Z. (2019). How do I know what my theory predicts? *Advances in Methods and Practices in Psychological Science*, *2*(4), 364–377. doi:10.1177/2515245919876960

Lakatos, I. (1978). *The methodology of scientific research programmes: Volume 1: Philosophical papers.* Cambridge University Press.

Lakens, D., Scheel, A. M., & Isager, P. M. (2018). Equivalence testing for psychological research: A tutorial. *Advances in Methods and Practices in Psychological Science*, *1*(2), 259–269. doi:10.1177/2515245918770963

Neyman, J., Pearson, E. S., & Pearson, K. (1933). IX. On the problem of the most efficient tests of statistical hypotheses. *Philosophical Transactions of the Royal Society of London. Series A, Containing Papers of a Mathematical or Physical Character*, *231*(694-706), 289–337. doi:10.1098/rsta.1933.0009