

Statistically Speaking

An Introduction to Bayesian Data Analysis for Correlations

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Introduction

Bayesian approaches to data analysis can be a good alternative or supplement to traditional hypothesis testing. Unlike *P* values, simple Bayesian analyses can provide a direct measure of the strength of evidence both for and against a study hypothesis, which can be helpful for researchers for interpreting and making decisions about their results. This article provides an introduction to Bayesian methods for exploring the relationship between 2 quantitative variables, illustrated with a dataset from the literature and analyzed with free, easy-to-use software.

Background

In recent years, statistical experts have increasingly warned researchers in the medical sciences and other fields about problems stemming from the misuse and misinterpretation of null hypothesis significance testing and *P* values [1]. For example, many researchers mistakenly interpret the *P* value to be the probability that the study's results were due to random chance or believe the 95% confidence interval to be the range of values that has a 95% chance of containing the true population parameter. One oft-suggested alternative that can sidestep some of these problems is a Bayesian approach to data analysis, which provides researchers with results in a form that can be more intuitive and less prone to misinterpretation than *P* values [2].

Although researchers are increasingly adopting Bayesian methodologies in many fields, lack of training in both the methods and its software packages has perhaps discouraged widespread use. To help overcome this problem, researchers at the University of Amsterdam have developed a free, open-source statistical software program called JASP that allows researchers to use a graphical interface to analyze data with both classical hypothesis testing and its Bayesian analogs [3]. Although still in preliminary release at the time of writing, the software provides enough power for many

types of analyses and is increasingly being used by educators as an alternative to other data analysis software, such as SPSS, R, and WinBUGS. This article will use JASP version 0.8.3.1 to illustrate the advantages of a Bayesian analysis of correlation and to compare the results to information provided from traditional methods.

The example data used here consist of 2 measurements taken from 24 overweight/obese adolescents: waist circumference (cm), and total area of visceral fat (cm²) as obtained from magnetic resonance images. The data were retrieved from the supporting information of an article by Eloi et al [4] on the investigation of magnetic resonance imaging as a tool for quantifying abdominal fat. A scatterplot of the data suggests a moderate, positive relationship between waist circumference and total visceral fat area (Figure 1).

For a traditional correlation analysis, we can use JASP or any standard statistical software. Table 1 shows the correlation table output from JASP through its "Regression → Correlation Matrix" menu selection. The observed correlation coefficient for Pearson *r* was 0.46, suggesting a moderate effect for the relationship between the 2 variables. In a classical 2-sided hypothesis test, this correlation coefficient is statistically significant at the .05 level (*P* = .023), with a 95% confidence interval of (0.074, 0.730).

Because this article will be comparing Bayesian results with traditional results, a quick refresher about the interpretation of these results might help cast the Bayesian results herein in sharper contrast. Recall that a *P* value tells us how likely it would be to observe results at least as extreme as what we saw in our study if the null hypothesis is true (ie, that the true population correlation coefficient is equal to zero; $H_0: \rho = 0$). From our example *P* value of .023, we can say that if in fact there no correlation existed between visceral fat area and waist circumference, we would see a sample displaying such a strong linear pattern as ours (or even stronger) only about 2.3% of the time, which is a fairly rare occurrence. In

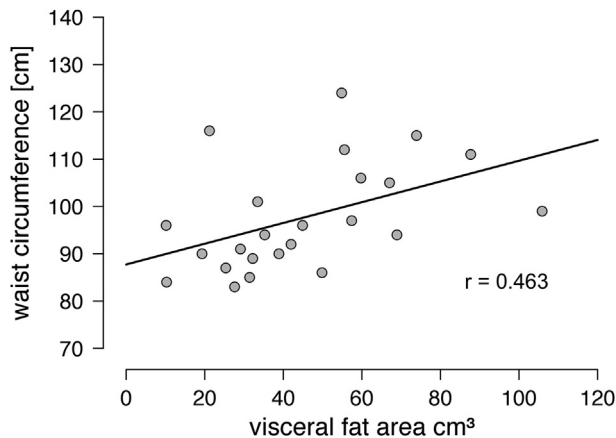


Figure 1. Scatterplot of waist circumference and visceral fat area. Data from Eloi et al [4].

other words, if we were to take random samples from a null situation with no correlation, we would still get sample correlations as at least as high as ours about one time out of 50. Note that this does not imply that the probability that these results were due to random chance is 2.3%, nor does it imply that there is a 97.7% probability that our hypothesis is true, nor even that the evidence favors the alternative hypothesis H_1 over H_0 .

Recall also that a 95% confidence interval is interpreted the range of values produced by a method which, if the study were to be exactly repeated many times, would contain the true population parameter 95% of the time. Note that this does not mean that there is a 95% chance that the true population correlation lies within these range of values.

Bayesian Analysis

We can use JASP to do a Bayesian analysis of the same data using the "Regression → Bayesian Correlation Pairs" menu selection with the default options. Table 2 and Figure 2 show some results from this analysis.

The Bayesian Pearson correlation coefficient was calculated to be 0.46, the same as the classical value found previously. The other results may look strange to researchers accustomed to traditional hypothesis testing, but they succinctly summarize a great deal of information, as described to follow [5].

Table 1
Traditional Pearson correlation

	r	P Value	95% Confidence Interval	
			Lower	Upper
Visceral fat area, cm^3 – waist circumference, cm	0.463	.023	0.074	0.730

Table 2
Bayesian Pearson correlation

	r	BF_{10}	95% Credible Interval	
			Lower	Upper
Visceral fat area, cm^3 – waist circumference, cm	0.463	2.953	0.062	0.708

BF_{10} and BF_{01} : Strength of Evidence for the Hypothesis

BF_{10} and BF_{01} in Table 2 and Figure 2 are Bayesian results not found in traditional hypothesis testing. They are both forms of what is known as the Bayes factor (BF), a measure that compares 2 things: the likelihood of the data under the alternative hypothesis and the likelihood of the data under the null hypothesis. It essentially answers the question, "How much more consistent are these data with the hypothesis that the effect in the population is *something* rather than *nothing*?"

BF_{10} is the form of the BF that gives likelihood of the data under the null hypothesis divided by the likelihood of the data under the alternative, so that BF_{10} values greater than 1 signal more evidence in favor of the alternative and values less than 1 signal more evidence in favor of the null. In our example, the BF_{10} is 2.95, which means that our analysis found the data to be about 3 times more likely under the alternative hypothesis than under the null. This can be considered "anecdotal/borderline-moderate" evidence for the study hypothesis that the 2 variables are correlated. (See Table 3 for a list of common labels for the strength of evidence in BFs [6].) The BF_{01} is simply $1/\text{BF}_{10}$, that is, the likelihood of the data under the null compared to the alternative. As they both contain

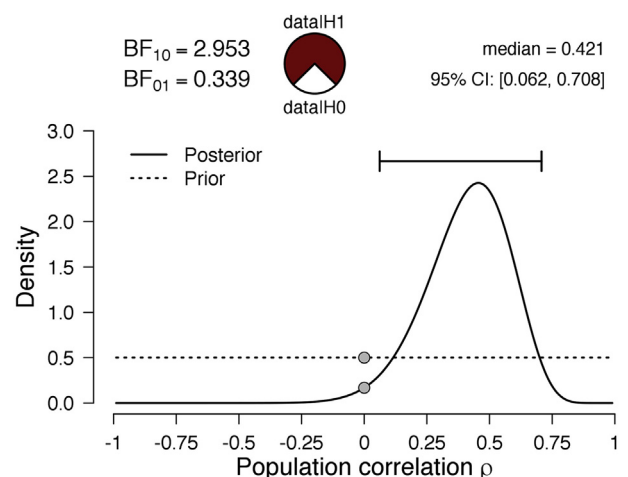


Figure 2. Graphical results from the Bayesian analysis in JASP showing the prior and posterior distributions of the true population correlation.

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