How to Easily Calculate a P-Value from a Z-Score by Hand

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December 5, 2025

RECOMMENDED CITATION

stats writer (2025). *How to Easily Calculate a P-Value from a Z-Score by Hand*. PSYCHOLOGICAL SCALES. Retrieved from https://scales.arabpsychology.com/?p=105652

Determining the statistical significance of experimental results often hinges on calculating the p-value. While modern statistical software automates this process, understanding the underlying manual calculation using a Z-score is fundamental to grasping core statistical principles. This guide provides a detailed, step-by-step methodology for deriving the p-value manually from a calculated Z-score, emphasizing clarity and precision for different types of hypothesis tests.

The manual calculation process involves translating the Z-score--which represents how many standard deviations an observation is from the mean of the standard normal distribution--into a corresponding probability using a specialized statistical reference known as the Z-table. The exact procedure varies depending on whether you are conducting a left-tailed, right-tailed, or two-tailed hypothesis test.

For a foundational understanding, the process generally involves locating the Z-score in the table to find the cumulative probability (the area to the left of that score). Subsequent steps involve subtraction from one (for right-tailed tests) or multiplication by two (for two-tailed tests) to isolate the appropriate area that defines the P-value. It is crucial to master these adjustments, as incorrectly applying the conversion rules based on the type of test can lead to significant errors in statistical inference.

The Importance of the Standard Normal Distribution and Z-Scores

In practical statistical applications, particularly when analyzing data that follows a normal distribution, the Z-score serves as a standardized measure that allows comparison across different datasets. A Z-score standardizes any observed data point by transforming it into units of standard deviation away from the population mean. This standardization is critical because it links any normal distribution problem back to the universal standard normal distribution, which is characterized by a mean of zero and a standard deviation of one. By converting raw scores to Z-scores, we can utilize a single, universal table--the Z-table--to determine probabilities regardless of the original dataset's scale or unit of measurement.

The primary reason we calculate a p-value is to quantify the evidence against a null hypothesis in a hypothesis test. The P-value represents the probability of observing test results at least as extreme as the results actually observed, assuming the null hypothesis is true. If this probability is very low (typically below a predetermined significance level, often denoted as alpha, $\alpha = 0.05$), we reject the null hypothesis, concluding that the observed results are statistically significant and unlikely to be due to random chance alone. Understanding this link between the Z-score's position and the resulting probability area is essential for interpreting statistical conclusions correctly.

While statistical software often provides the corresponding P-value automatically once the Z-score is input, a manual approach requires reference to a Z-table. This table maps specific Z-score values to the cumulative probability, which is defined as the area under the curve to the left of that

Z-score. Understanding how to accurately read and interpret this table is the cornerstone of manually calculating the P-value for any standardized test statistic, ensuring that the critical region associated with the hypothesis test is correctly isolated.

General Procedure for Using a Z-Table

A Z-table typically organizes data by Z-score, listing the ones and tenths places down the left column and the hundredths place across the top row. To find the cumulative probability corresponding to a specific Z-score, for instance, 1.43, you first locate 1.4 in the vertical column and then trace horizontally until you intersect with the column labeled 0.03. The intersecting numerical value provides the cumulative probability, $P(Z \le z)$, which is the precise area under the standard normal distribution curve up to that specific standardized point.

It is absolutely critical to remember that the standard Z-table always provides the area to the left of the Z-score, representing the probability of observing a value less than or equal to the Z-score. This value directly equals the P-value only in the specific context of a left-tailed test involving a negative Z-score. This initial probability is the fundamental building block from which all other P-values are derived through simple arithmetic adjustments tailored to the directionality of the alternative hypothesis.

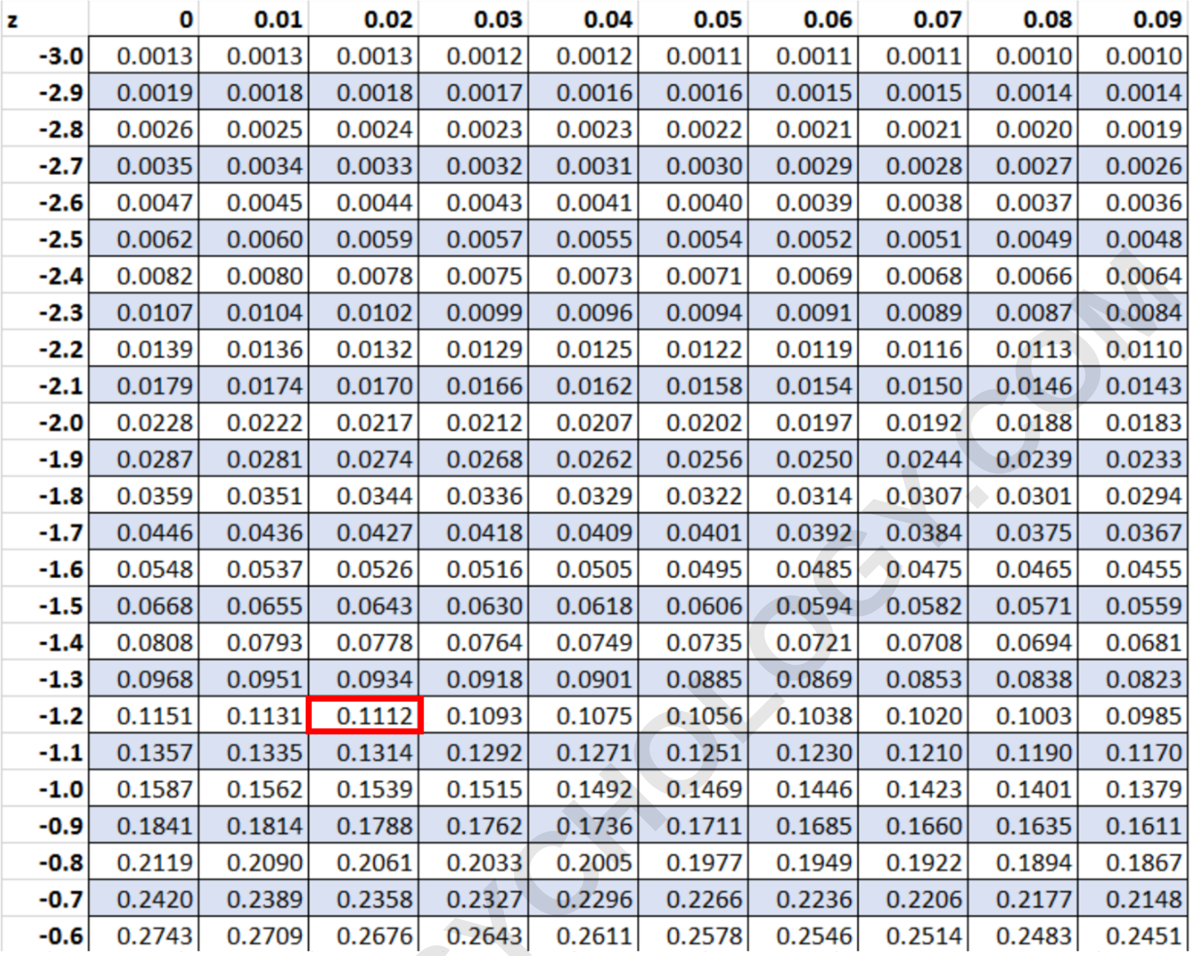
For scenarios involving right-tailed and two-tailed tests, adjustments must be made using fundamental probability rules, specifically recognizing that the total area under the probability density function curve must sum exactly to 1.0. For right-tailed tests, we subtract the Z-table value from 1 to find the area of the right tail. For two-tailed tests, we double the area of the relevant tail (either the left or the right tail), as the rejection region is split symmetrically across both extremes of the distribution.

Example 1: Calculating the P-Value for a Left-Tailed Test

Suppose we are conducting a left-tailed hypothesis test. In this statistical setting, we are testing whether the true population parameter is significantly less than a hypothesized value, meaning our entire critical or rejection region is concentrated in the left tail of the distribution. Let's assume our test statistic calculation yields a Z-score of **-1.22**. Our task is to determine the corresponding p-value to evaluate the statistical significance of this finding.

The procedure for a left-tailed test is the most direct when utilizing the conventional Z-table, especially when the Z-score is negative. Since the standard Z-table is designed to provide the cumulative probability--the area extending infinitely to the left of the Z-score--this value precisely corresponds to the area of the rejection region we are interested in. To find the probability associated with **-1.22**, we locate -1.2 in the left column of the negative Z-score table and trace it to the 0.02 column.

The relevant portion of the Z-table demonstrating this lookup is shown below:



z	0	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09
-3.0	0.0013	0.0013	0.0013	0.0012	0.0012	0.0011	0.0011	0.0011	0.0010	0.0010
-2.9	0.0019	0.0018	0.0018	0.0017	0.0016	0.0016	0.0015	0.0015	0.0014	0.0014
-2.8	0.0026	0.0025	0.0024	0.0023	0.0023	0.0022	0.0021	0.0021	0.0020	0.0019
-2.7	0.0035	0.0034	0.0033	0.0032	0.0031	0.0030	0.0029	0.0028	0.0027	0.0026
-2.6	0.0047	0.0045	0.0044	0.0043	0.0041	0.0040	0.0039	0.0038	0.0037	0.0036
-2.5	0.0062	0.0060	0.0059	0.0057	0.0055	0.0054	0.0052	0.0051	0.0049	0.0048
-2.4	0.0082	0.0080	0.0078	0.0075	0.0073	0.0071	0.0069	0.0068	0.0066	0.0064
-2.3	0.0107	0.0104	0.0102	0.0099	0.0096	0.0094	0.0091	0.0089	0.0087	0.0084
-2.2	0.0139	0.0136	0.0132	0.0129	0.0125	0.0122	0.0119	0.0116	0.0113	0.0110
-2.1	0.0179	0.0174	0.0170	0.0166	0.0162	0.0158	0.0154	0.0150	0.0146	0.0143
-2.0	0.0228	0.0222	0.0217	0.0212	0.0207	0.0202	0.0197	0.0192	0.0188	0.0183
-1.9	0.0287	0.0281	0.0274	0.0268	0.0262	0.0256	0.0250	0.0244	0.0239	0.0233
-1.8	0.0359	0.0351	0.0344	0.0336	0.0329	0.0322	0.0314	0.0307	0.0301	0.0294
-1.7	0.0446	0.0436	0.0427	0.0418	0.0409	0.0401	0.0392	0.0384	0.0375	0.0367
-1.6	0.0548	0.0537	0.0526	0.0516	0.0505	0.0495	0.0485	0.0475	0.0465	0.0455
-1.5	0.0668	0.0655	0.0643	0.0630	0.0618	0.0606	0.0594	0.0582	0.0571	0.0559
-1.4	0.0808	0.0793	0.0778	0.0764	0.0749	0.0735	0.0721	0.0708	0.0694	0.0681
-1.3	0.0968	0.0951	0.0934	0.0918	0.0901	0.0885	0.0869	0.0853	0.0838	0.0823
-1.2	0.1151	0.1131	0.1112	0.1093	0.1075	0.1056	0.1038	0.1020	0.1003	0.0985
-1.1	0.1357	0.1335	0.1314	0.1292	0.1271	0.1251	0.1230	0.1210	0.1190	0.1170
-1.0	0.1587	0.1562	0.1539	0.1515	0.1492	0.1469	0.1446	0.1423	0.1401	0.1379
-0.9	0.1841	0.1814	0.1788	0.1762	0.1736	0.1711	0.1685	0.1660	0.1635	0.1611
-0.8	0.2119	0.2090	0.2061	0.2033	0.2005	0.1977	0.1949	0.1922	0.1894	0.1867
-0.7	0.2420	0.2389	0.2358	0.2327	0.2296	0.2266	0.2236	0.2206	0.2177	0.2148
-0.6	0.2743	0.2709	0.2676	0.2643	0.2611	0.2578	0.2546	0.2514	0.2483	0.2451

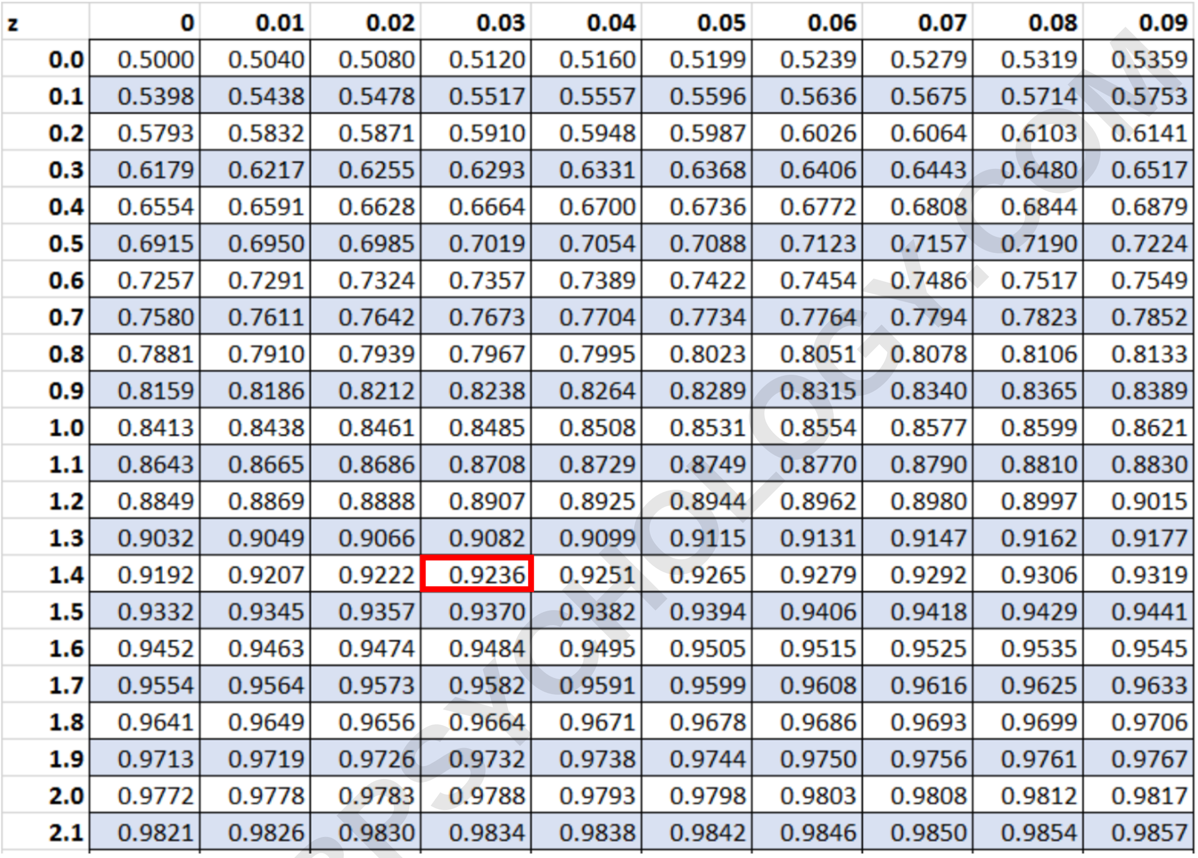
Upon consulting the table, the value corresponding to a Z-score of -1.22 is **0.1112**. Because this is a left-tailed test, this cumulative probability directly represents the area in the rejection region, meaning the resulting P-value is **0.1112**. If we were using a standard significance level of $\alpha = 0.05$, since 0.1112 is greater than 0.05, we would conclude that there is insufficient evidence to reject the null hypothesis.

Example 2: Calculating the P-Value for a Right-Tailed Test

Consider a contrasting statistical scenario where we are conducting a right-tailed hypothesis test. This test implies that we are investigating whether the population parameter is significantly greater than the null hypothesized value, thereby placing the critical region entirely in the right tail of the distribution. Assume our statistical analysis yields a positive Z-score of **1.43**. Our objective here is to find the area located to the right of this score, which represents the probability of observing a result this extreme or more extreme.

The initial step remains consistent with the previous example: we must use the Z-table to find the cumulative probability associated with 1.43. We look for 1.4 in the left column of the positive Z-score table and match it with the 0.03 column. This tabulated value represents P(Z < 1.43), the area to the left of the score. This value alone is not the P-value; it is the complement of the area we seek.

The relevant section of the Z-table used for this calculation is presented here:



z	0	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09
0.0	0.5000	0.5040	0.5080	0.5120	0.5160	0.5199	0.5239	0.5279	0.5319	0.5359
0.1	0.5398	0.5438	0.5478	0.5517	0.5557	0.5596	0.5636	0.5675	0.5714	0.5753
0.2	0.5793	0.5832	0.5871	0.5910	0.5948	0.5987	0.6026	0.6064	0.6103	0.6141
0.3	0.6179	0.6217	0.6255	0.6293	0.6331	0.6368	0.6406	0.6443	0.6480	0.6517
0.4	0.6554	0.6591	0.6628	0.6664	0.6700	0.6736	0.6772	0.6808	0.6844	0.6879
0.5	0.6915	0.6950	0.6985	0.7019	0.7054	0.7088	0.7123	0.7157	0.7190	0.7224
0.6	0.7257	0.7291	0.7324	0.7357	0.7389	0.7422	0.7454	0.7486	0.7517	0.7549
0.7	0.7580	0.7611	0.7642	0.7673	0.7704	0.7734	0.7764	0.7794	0.7823	0.7852
0.8	0.7881	0.7910	0.7939	0.7967	0.7995	0.8023	0.8051	0.8078	0.8106	0.8133
0.9	0.8159	0.8186	0.8212	0.8238	0.8264	0.8289	0.8315	0.8340	0.8365	0.8389
1.0	0.8413	0.8438	0.8461	0.8485	0.8508	0.8531	0.8554	0.8577	0.8599	0.8621
1.1	0.8643	0.8665	0.8686	0.8708	0.8729	0.8749	0.8770	0.8790	0.8810	0.8830
1.2	0.8849	0.8869	0.8888	0.8907	0.8925	0.8944	0.8962	0.8980	0.8997	0.9015
1.3	0.9032	0.9049	0.9066	0.9082	0.9099	0.9115	0.9131	0.9147	0.9162	0.9177
1.4	0.9192	0.9207	0.9222	0.9236	0.9251	0.9265	0.9279	0.9292	0.9306	0.9319
1.5	0.9332	0.9345	0.9357	0.9370	0.9382	0.9394	0.9406	0.9418	0.9429	0.9441
1.6	0.9452	0.9463	0.9474	0.9484	0.9495	0.9505	0.9515	0.9525	0.9535	0.9545
1.7	0.9554	0.9564	0.9573	0.9582	0.9591	0.9599	0.9608	0.9616	0.9625	0.9633
1.8	0.9641	0.9649	0.9656	0.9664	0.9671	0.9678	0.9686	0.9693	0.9699	0.9706
1.9	0.9713	0.9719	0.9726	0.9732	0.9738	0.9744	0.9750	0.9756	0.9761	0.9767
2.0	0.9772	0.9778	0.9783	0.9788	0.9793	0.9798	0.9803	0.9808	0.9812	0.9817
2.1	0.9821	0.9826	0.9830	0.9834	0.9838	0.9842	0.9846	0.9850	0.9854	0.9857

The cumulative probability P(Z < 1.43) is found to be **0.9236**. Since we are interested in the area in the right tail (the rejection region), we must utilize the principle that the total area under the standard normal distribution curve always equals 1.0. Therefore, the area to the right--which is our P-value--is calculated by subtracting the cumulative probability (the area to the left) from 1.0.

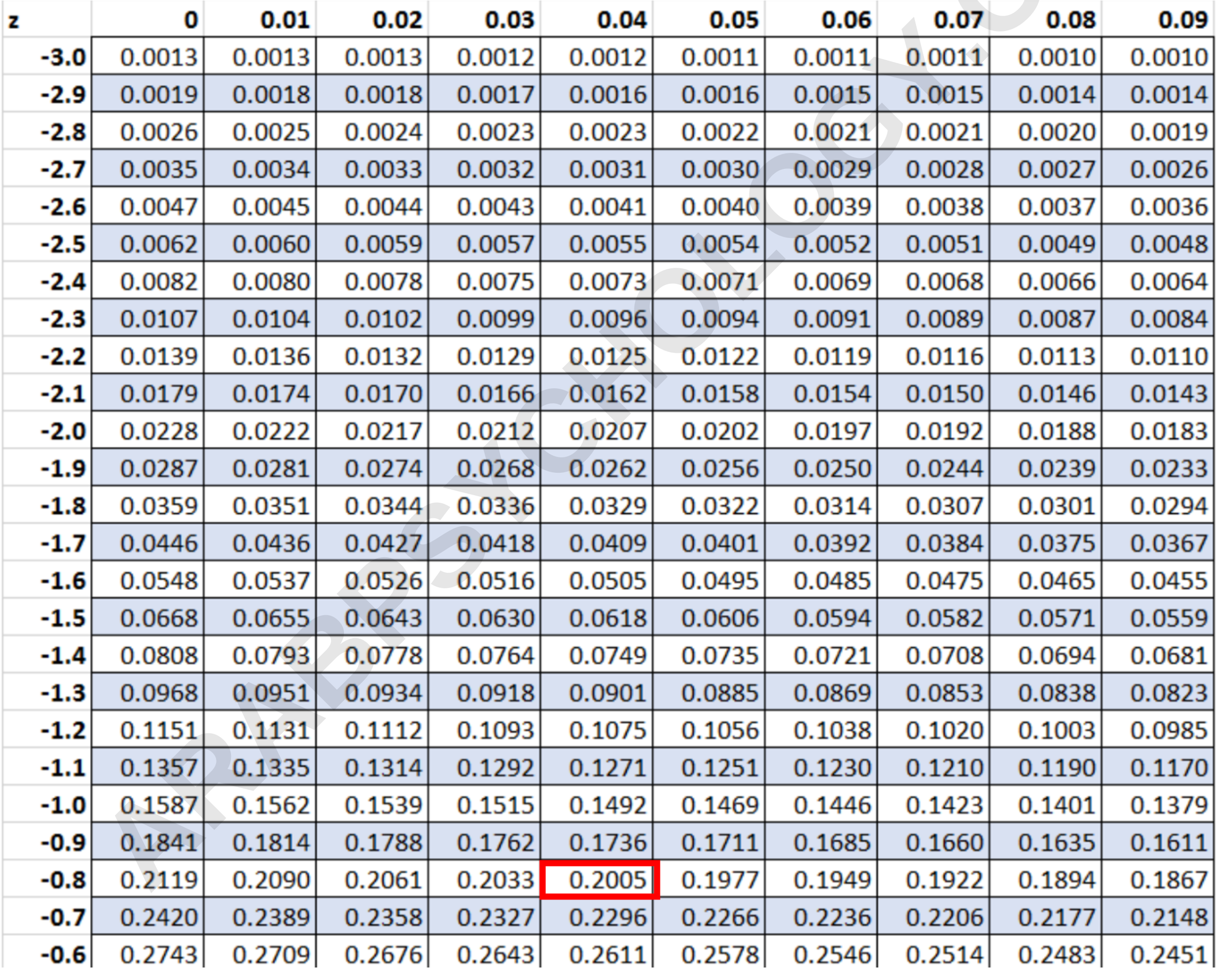
The final P-value calculation is performed as follows: 1 - 0.9236 = **0.0764**. This result, 0.0764, represents the probability of observing a Z-score of 1.43 or greater if the null hypothesis were true. Comparing this P-value to an alpha level of 0.05, we would again fail to reject the null hypothesis, as 0.0764 is larger than the critical threshold.

Example 3: Calculating the P-Value for a Two-Tailed Test

In a two-tailed hypothesis test, the alternative hypothesis posits that the population parameter is simply different from (not equal to) the hypothesized value. This necessitates splitting the critical region equally between both the extreme left and extreme right tails of the standard normal distribution. Suppose we obtain a Z-score of **-0.84**.

For a two-tailed test, the P-value must account for extreme results in both positive and negative directions. We first find the area corresponding to the calculated Z-score, **-0.84**, using the negative Z-table. We locate -0.8 in the left column and 0.04 in the top row. This gives us the area in the left tail: P(Z < -0.84), which represents the probability of observing a Z-score less than -0.84.

We refer to the following image representing the Z-table lookup used for determining the area of one tail:



z	0	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09
-3.0	0.0013	0.0013	0.0013	0.0012	0.0012	0.0011	0.0011	0.0011	0.0010	0.0010
-2.9	0.0019	0.0018	0.0018	0.0017	0.0016	0.0016	0.0015	0.0015	0.0014	0.0014
-2.8	0.0026	0.0025	0.0024	0.0023	0.0023	0.0022	0.0021	0.0021	0.0020	0.0019
-2.7	0.0035	0.0034	0.0033	0.0032	0.0031	0.0030	0.0029	0.0028	0.0027	0.0026
-2.6	0.0047	0.0045	0.0044	0.0043	0.0041	0.0040	0.0039	0.0038	0.0037	0.0036
-2.5	0.0062	0.0060	0.0059	0.0057	0.0055	0.0054	0.0052	0.0051	0.0049	0.0048
-2.4	0.0082	0.0080	0.0078	0.0075	0.0073	0.0071	0.0069	0.0068	0.0066	0.0064
-2.3	0.0107	0.0104	0.0102	0.0099	0.0096	0.0094	0.0091	0.0089	0.0087	0.0084
-2.2	0.0139	0.0136	0.0132	0.0129	0.0125	0.0122	0.0119	0.0116	0.0113	0.0110
-2.1	0.0179	0.0174	0.0170	0.0166	0.0162	0.0158	0.0154	0.0150	0.0146	0.0143
-2.0	0.0228	0.0222	0.0217	0.0212	0.0207	0.0202	0.0197	0.0192	0.0188	0.0183
-1.9	0.0287	0.0281	0.0274	0.0268	0.0262	0.0256	0.0250	0.0244	0.0239	0.0233
-1.8	0.0359	0.0351	0.0344	0.0336	0.0329	0.0322	0.0314	0.0307	0.0301	0.0294
-1.7	0.0446	0.0436	0.0427	0.0418	0.0409	0.0401	0.0392	0.0384	0.0375	0.0367
-1.6	0.0548	0.0537	0.0526	0.0516	0.0505	0.0495	0.0485	0.0475	0.0465	0.0455
-1.5	0.0668	0.0655	0.0643	0.0630	0.0618	0.0606	0.0594	0.0582	0.0571	0.0559
-1.4	0.0808	0.0793	0.0778	0.0764	0.0749	0.0735	0.0721	0.0708	0.0694	0.0681
-1.3	0.0968	0.0951	0.0934	0.0918	0.0901	0.0885	0.0869	0.0853	0.0838	0.0823
-1.2	0.1151	0.1131	0.1112	0.1093	0.1075	0.1056	0.1038	0.1020	0.1003	0.0985
-1.1	0.1357	0.1335	0.1314	0.1292	0.1271	0.1251	0.1230	0.1210	0.1190	0.1170
-1.0	0.1587	0.1562	0.1539	0.1515	0.1492	0.1469	0.1446	0.1423	0.1401	0.1379
-0.9	0.1841	0.1814	0.1788	0.1762	0.1736	0.1711	0.1685	0.1660	0.1635	0.1611
-0.8	0.2119	0.2090	0.2061	0.2033	0.2005	0.1977	0.1949	0.1922	0.1894	0.1867
-0.7	0.2420	0.2389	0.2358	0.2327	0.2296	0.2266	0.2236	0.2206	0.2177	0.2148
-0.6	0.2743	0.2709	0.2676	0.2643	0.2611	0.2578	0.2546	0.2514	0.2483	0.2451

The cumulative probability found for Z = -0.84 is **0.2005**. This value represents the area in one specific tail (the left tail, in this instance). Because the standard normal distribution is perfectly symmetrical around zero, the area in the opposite tail (P(Z > 0.84)) is also equal to 0.2005. To find the total P-value for the two-tailed test, we must sum the probabilities of both rejection regions, effectively doubling the area of the single tail we found.

Therefore, the final P-value is calculated by multiplying the area of the single tail by 2: 0.2005 * 2 = **0.401**. This substantial P-value indicates that there is very little statistical evidence to reject the null hypothesis at conventional significance levels, as results this close to the mean occur frequently under the null hypothesis assumption.

Summary of P-Value Calculation Rules

The precise technique used for calculating the P-value from the Z-table depends entirely on the alternative hypothesis defined in your study. It is imperative to correctly identify the type of test--left-tailed, right-tailed, or two-tailed--before applying the Z-table results. Failing to do so is a common source of error in manual statistical calculations.

Here is a concise summary detailing the rules derived from the preceding examples, ensuring accurate P-value determination based on the test type:

Left-Tailed Test (Ha: < value): The P-value is the direct cumulative probability (Area to the left) found in the Z-table, assuming a negative Z-score.

Right-Tailed Test (Ha: > value): The P-value is calculated by subtracting the Z-table cumulative probability from 1.0 (1 - Area to the left), which isolates the area in the right tail.

Two-Tailed Test (Ha: ≠ value): The P-value is calculated by finding the area of the relevant single tail (using the Z-table directly for the negative Z-score, or 1 minus the Z-table value for the positive Z-score) and multiplying that result by 2 to account for both tails.

Beyond Manual Calculation: Software Alternatives

While mastering the manual calculation provides crucial theoretical insight into the foundational mechanics of statistical testing and helps reinforce understanding of the standard normal distribution, in professional and academic practice, specialized statistical software is overwhelmingly utilized. Software packages offer significantly greater efficiency, precision (especially when interpolating non-tabulated Z-scores), and reliability when dealing with complex statistical models or high volumes of data.

R, Python (using libraries like SciPy), SPSS, and Excel all provide dedicated functions to calculate the exact P-value directly from a Z-score without relying on manual table lookups. Although the manual method is excellent for pedagogical purposes, researchers routinely depend on these technological tools to ensure accuracy and speed in their inference procedures.

The following tutorials explain how to calculate p-values from z-scores using various statistical software packages: