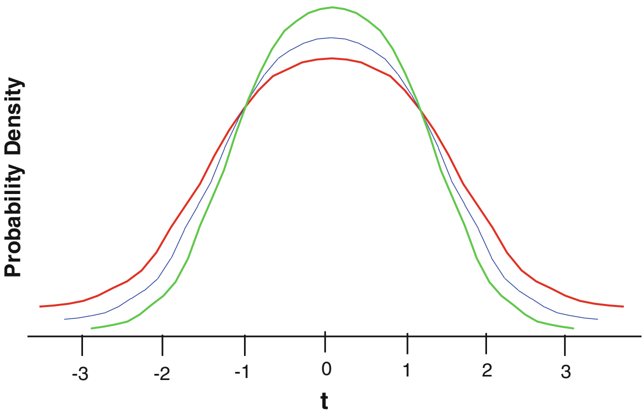
Chapter 4
Null-Hypothesis Testing with the T-Table

1 General Purpose

In the previous chapter we discussed that the patterns of Gaussian curve from biological data have a constant frequency distribution and that this phenomenon is used for making predictions from your data to future data. However, this is only entirely true with large samples like samples > 100. In practice many studies involve rather small samples and in order for your data from small samples to adequately fit a theoretical frequency distribution we have to replace the Gaussian normal distribution with multiple Gaussian t-distributions which are a little bit wider.

In the twenties the USA government employed wives of workless citizens in the Work Project Administration US. With the help of Monte Carlo Models, and a pocket calculator not yet available at that time, the numerical characteristics of the best fit Gaussian curves for any sample size was calculated. These characteristics were summarized in the famous t-table, which is still the basis of any statistical software program. This chapter is to assess how the t-table can be used for null-hypothesis testing.

T.J. Cleophas, A.H. Zwinderman, *Clinical Data Analysis on a Pocket Calculator*,
DOI 10.1007/978-3-319-27104-0_4



The above graph shows members of the family of t-distributions: with n = 5 the distribution is wide, with n = 10 and n = 100 this is increasingly less so. This chapter is to show how the t-table can be used for testing null-hypotheses of no effects in your data.

2 Schematic Overview of Type of Data File

Outcome
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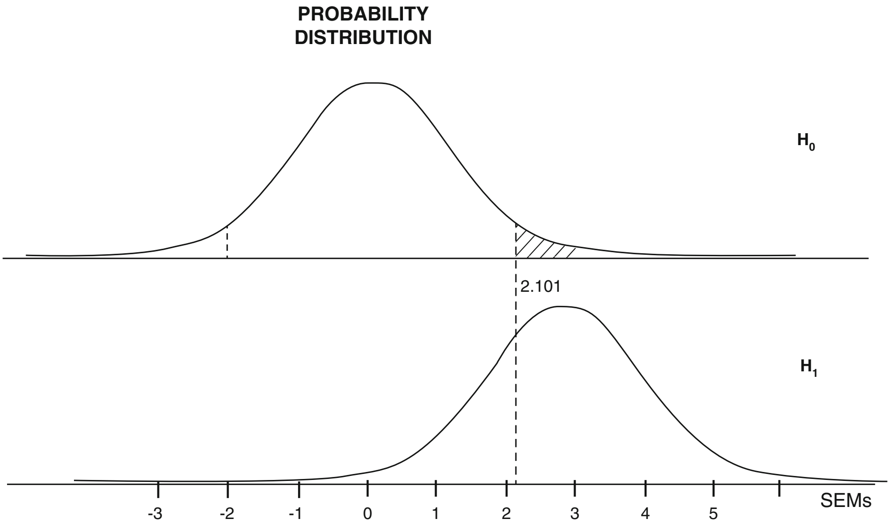
3 Primary Scientific Question

Is the result of our study significant different from the null-hypothesis? At what level of statistical significance?

4 Data Example



The above graph gives an example of experimental data is given with sample size (n) = 19 and mean result = 2.9 SEMs (SEM-units), and a t-distributed instead of normal frequency distribution. Any result larger than approximately 2 SEMs is statistically significantly different from 0 SEMs at $p < 0.05$. However, our mean of 2.9 SEMs is pretty far away in the <5 % tail, and, so, the chance of being so far away may be a lot smaller than 5 %. Our p-values may be a lot smaller than 0.05. The t-table can be more precise regarding the level of significance, and is given underneath.

5 T-Table

df	One-Tail = .4 Two-Tail = .8	.25 .5	.1 .2	.05 .1	.025 .05	.01 .02	.005 .01	.0025 .005	.001 .002	.0005 .001
1	0.325	1.000	3.078	6.314	12.706	31.821	63.657	127.32	318.31	636.62
2	0.289	0.816	1.886	2.920	4.303	6.965	9.925	14.089	22.327	31.598
3	0.277	0.765	1.638	2.353	3.182	4.541	5.841	7.453	10.214	12.924
4	0.271	0.741	1.533	2.132	2.776	3.747	4.604	5.598	7.173	8.610
5	0.267	0.727	1.476	2.015	2.571	3.365	4.032	4.773	5.893	6.869
6	0.265	0.718	1.440	1.943	2.447	3.143	3.707	4.317	5.208	5.959
7	0.263	0.711	1.415	1.895	2.365	2.998	3.499	4.029	4.785	5.408
8	0.262	0.706	1.397	1.860	2.306	2.896	3.355	3.833	4.501	5.041
9	0.261	0.703	1.383	1.833	2.262	2.821	3.250	3.690	4.297	4.781
10	0.260	0.700	1.372	1.812	2.228	2.764	3.169	3.581	4.144	4.587
11	0.260	0.697	1.363	1.796	2.201	2.718	3.106	3.497	4.025	4.437
12	0.259	0.695	1.356	1.782	2.179	2.681	3.055	3.428	3.930	4.318
13	0.259	0.694	1.350	1.771	2.160	2.650	3.012	3.372	3.852	4.221
14	0.258	0.692	1.345	1.761	2.145	2.624	2.977	3.326	3.787	4.140
15	0.258	0.691	1.341	1.753	2.131	2.602	2.947	3.286	3.733	4.073
16	0.258	0.690	1.337	1.746	2.120	2.583	2.921	3.252	3.686	4.015
17	0.257	0.689	1.333	1.740	2.110	2.567	2.898	3.222	3.646	3.965
18	0.257	0.688	1.330	1.734	2.101	2.552	2.878	3.197	3.610	3.922
19	0.257	0.688	1.328	1.729	2.093	2.539	2.861	3.174	3.579	3.883
20	0.257	0.687	1.325	1.725	2.086	2.528	2.845	3.153	3.552	3.850
21	0.257	0.686	1.323	1.721	2.080	2.518	2.831	3.135	3.527	3.819
22	0.256	0.686	1.321	1.717	2.074	2.508	2.819	3.119	3.505	3.792
23	0.256	0.685	1.319	1.714	2.069	2.500	2.807	3.104	3.485	3.767
24	0.256	0.685	1.318	1.711	2.064	2.492	2.797	3.091	3.467	3.745
25	0.256	0.684	1.316	1.708	2.060	2.485	2.787	3.078	3.450	3.725
26	0.256	0.684	1.315	1.706	2.056	2.479	2.779	3.067	3.435	3.707
27	0.256	0.684	1.314	1.703	2.052	2.473	2.771	3.057	3.421	3.690
28	0.256	0.683	1.313	1.701	2.048	2.467	2.763	3.047	3.408	3.674
29	0.256	0.683	1.311	1.699	2.045	2.462	2.756	3.038	3.396	3.659
30	0.256	0.683	1.310	1.697	2.042	2.457	2.750	3.030	3.385	3.646
40	0.255	0.681	1.303	1.684	2.021	2.423	2.704	2.971	3.307	3.551
60	0.254	0.679	1.296	1.671	2.000	2.390	2.660	2.915	3.232	3.460
120	0.254	0.677	1.289	1.658	1.980	2.358	2.617	2.860	3.160	3.373
∞	0.253	0.674	1.282	1.645	1.960	2.326	2.576	2.807	3.090	3.291

The t-table has a left-end column giving degrees of freedom (≈sample sizes), and two top rows with p-values (areas under the curve = p-values), one-tail meaning that only one end of the curve, two-tail meaning that both ends are assessed simultaneously. The t-table is, furthermore, full of t-values, that, with ∞ degrees of freedom, are equal to z-values (Chap. 36). The t-values are to be understood as mean results of studies, but not expressed in mmol/l, kilograms, but in so-called SEM-units (Standard error of the mean units), that are obtained by dividing your mean result by its own standard error. With many degrees of freedom (large samples) the curve will be a little bit narrower, and more in agreement with nature.

A t-value of 2.9 with 18° of freedom (19 patients and 1 group means we have 19–1 = 18° of freedom) indicates that we will need the row no. 18 of the table. The t-value 2.9 is left from 3.197 and right from 2.878. Now look right up to the second of the two upper rows: we are right from 0.01 and left from 0.005. The p-value equals <0.01.

6 Conclusion

In the previous chapter we discussed that the patterns of Gaussian curves from biological data have a constant frequency distribution and that this phenomenon is used for making predictions from your data to future data. However, this is only entirely true with large samples, like samples >100. In practice, many studies involve rather small samples, and in order for your data from small samples to adequately fit a theoretical frequency distribution we have to replace the Gaussian normal distribution with multiple Gaussian-like t-distributions which are a little bit wider. The t-table summarizes the numerical characteristics of these frequency distributions of any size. It helps us to predict precisely the chance and level of a statistically significant effect. E.g., a p value < 0.002 means that we have less than 0.2 % of finding such a result if there would be no effect in your data. In clinical term this indicates that your treatment was very efficaceous, and that the chance that this conclusion is erroneous will be less than 0.2 %, at least, if your null-hypothesis is true.

7 Note

More background, theoretical and mathematical information of null-hypothesis testing is given Statistics applied to clinical studies 5th edition, Chaps. 1–3, Springer Heidelberg Germany, 2012, from the same authors.