Uluslararası İleri Doğa Bilimleri ve Mühendislik Araştırmaları Dergisi
Sayı 8, S. 245-258, 3, 2024

Araştırma Makalesi

International Journal of Advanced Natural Sciences and Engineering Researches
Volume 8, pp. 245-258, 3, 2024

Research Article

https://as-proceeding.com/index.php/ijanser
ISSN: 2980-0811

A Statistical Approach to Real-time Reproductive Rate Estimates of the COVID-19 Pandemic Based on the Statistical Powers in terms of Different Sample Sizes, Effect Sizes and Standard Deviations for Independent/Paired Samples t-test

Neslihan İYİT [*1], Hediye Nagehan BÜYÜKBAYRAM [2]

*[*1] Selcuk University, Faculty of Science, Statistics Department, Konya, Turkiye, Corresponding Author e-mail: niyit@selcuk.edu.tr*
ORCID ID: 0000-0002-5727-6441
[2] Selcuk University, Faculty of Veterinary Medicine, Department of Biostatistics, Konya, Turkiye, e-mail: nbuyukbayram@gmail.com, ORCID ID: 0000-0002-6540-6007

(Received:17 March 2024, Accepted: 25 April 2024)

(2nd International Conference on Scientific and Innovative Studies ICSIS 2024, April 18-19, 2024)

ATIF/REFERENCE: İyit, N. & Büyükbayram, H. N. (2024). A Statistical Approach to Real-time Reproductive Rate Estimates of the COVID-19 Pandemic Based on the Statistical Powers in terms of Different Sample Sizes, Effect Sizes and Standard Deviations for Independent/Paired Samples t-test. *International Journal of Advanced Natural Sciences and Engineering Researches*, 8(3), 245-258.

Abstract – In this study, appropriate statistical powers for independent/paired samples t-test applications are tried to be determined using Monte Carlo simulation method in terms of different sample sizes, effect sizes and standard deviations. In the empirical part of this study, based on the Monte Carlo simulation method, firstly "independent samples t-test" is performed for testing the averages of real-time reproductive rate estimates of the COVID-19 Pandemic data between African and European Continents including 45 countries. And then "paired samples t-test" is performed for testing the averages of real-time reproductive rate estimates of the COVID-19 Pandemic data between December 2021 and January 2022 as the paired observations of 31 different countries taken from the European Continent.

As the principal results and major conclusions of this study, belonging to the independent samples t-test results, it is determined that the statistical power decreased as the standard deviation increased. The statistical power increased as the effect size widened at a fixed sample size and standard deviation value. Belonging to the paired samples t-test results, it is determined that the statistical power decreased as the significance level decreased. In addition, statistical powers for the paired samples t-test with fixed sample size and effect size are estimated to be higher than for the independent samples t-test. Also, statistical powers for the paired samples t-test with fixed sample size and effect size are found higher than for the independent samples t-test.

Keywords – Reproductive rate estimate of the COVID-19 pandemic, Monte Carlo simulation, independent/paired samples t-test, statistical power, sample size, effect size

1.Introduction

Statistical power calculation in the hypotheses tests is very important to draw statistically significant conclusions from the researches of interest in many fields [1,2]. Statistical power in a hypothesis test is the

probability of rejecting the null hypothesis and making correct decision if the null hypothesis is false so the alternative hypothesis is true [3]. Statistical power of a hypothesis test depends on the sample size, effect size, significance level, and standard deviation as the measure of variability of the interested population [4,5]. For more information about the relationships between statistical power, sample size, effect size, significance level, and standard deviation, see [6-12]. In hypothesis testing, after stating the null and the alternative hypotheses, significance level is determined. Test statistic, critical value, and related p-value is computed. And then decision will be made and conclusions will be drawn and interpreted from the empirical data [13-15].

Statistical power analysis is also vital for independent/paired samples t-tests as with all parametric tests. Lan and Lian [16], Kang [17], Dalmaijer et al. [18], Szucs and Ioannidis [19], Serdar et al. [20], Cheval et al. [21], Abt et al. [22], Sharma et al. [23], Lenzo et al. [24], Kelley [25] studied statistical power analysis in independent/paired samples t-tests in many fields such as human health, biometry, cluster analysis, neuroimaging, clinical studies, COVID-19 pandemic, sports science, nursing, healthcare, and education. In this study, appropriate statistical powers for independent/paired samples t-test applications will be tried to be determined using Monte Carlo simulation method in terms of different sample sizes, effect sizes and standard deviations. de Micheaux et al. [26], Muthén and Muthén [27], Onoz and Bayazit [28], Myers et al. [29], Kalos and Whitlock [30], Robert et al. [31], and Kroese et al. [32] studied Monte Carlo simulation method to determine statistical power of various hypotheses tests based on parametric and nonparametric methods.

Based on the Monte Carlo simulation method, in this study, "independent samples t-test" will be performed for testing the averages of real-time reproductive rate estimates of the COVID-19 Pandemic data between African and European Continents including 45 countries. Also "paired samples t-test" will be performed for testing the averages of real-time reproductive rate estimates of the COVID-19 Pandemic data between December 2021 and January 2022 as the paired observations of 31 different countries taken from the European Continent.

2.Material and Method

2.1.Materials

In this study, "independent samples t-test" for testing the averages of real-time reproductive rate estimates of COVID-19 pandemic between African and European Continents has actually been investigated. For this aim, in the material part of this study, 45 countries data [33] from African Continent and 45 countries data [33] from European Continent as equal sample sizes ($n_{African}=n_{European}=45$) in January 2022 given in Table 1 are randomly selected and taken into the study.

Table 1. Countries and continents for investigating the real-time reproductive rate estimates of the COVID-19 pandemic by independent samples t-test

Continents	**Countries**
African Region (AFR)	Algeria, Angola, Botswana, Burundi, Cameroon, Cape Verde, Comoros, Congo, Cote d'Ivoire, Democratic Republic of Congo, Djibouti, Egypt, Equatorial Guinea, Eritrea, Ethiopia, Gabon, Ghana, Guinea, Guinea-Bissau, Lesotho, Liberia, Libya, Madagascar, Malawi, Mali, Mauritania, Mauritius, Morocco, Mozambique, Namibia, Niger, Nigeria, Rwanda, Sao Tome and Principe, Senegal, Seychelles, Sierra Leone, South Africa, South Sudan, Sudan, Togo, Tunisia, Uganda, Zambia, Zimbabwe.
European Region (EUR)	Albania, Andorra, Austria, Belarus, Belgium, Bosnia and Herzegovina, Bulgaria, Croatia, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Kosovo, Latvia, Liechtenstein, Lithuania, Luxembourg, Malta, Moldova, Monaco, Montenegro, Netherlands, North Macedonia, Norway, Poland, Portugal, Romania, Russia, San Marino, Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Ukraine, United Kingdom.

Also in this study, "paired samples t-test" for testing the averages of the real-time reproductive rate estimates of the COVID-19 pandemic data belonging to the European Continent between December 2021 and January 2022 has actually been investigated. For this aim, n=31 countries data [33] from the European Continent are randomly selected and taken into the study as given in Table 2.

Table 2. Countries for investigating the European Continent's real-time reproductive rate estimates of the COVID-19 Pandemic by paired samples t-test

Continent	**Countries**
European Continent	Albania, Andorra, Belarus, Bosnia and Herzegovina, Bulgaria, Croatia, Cyprus, Denmark, Estonia, Finland, France, Greece, Iceland, Ireland, Italy, Kosovo, Latvia, Liechtenstein, Lithuania, Luxembourg, Monaco, Montenegro, North Macedonia, Norway, Portugal, Russia, San Marino, Spain, Sweden, Switzerland, United Kingdom.

2.2. Method

In the method part of this study, appropriate statistical powers for independent/paired samples t-test applications are tried to be determined using Monte Carlo simulation method in terms of different sample sizes, effect sizes and standard deviations. In the empirical part of this study, firstly "independent samples t-test" is performed for testing the averages of real-time reproductive rate estimates of COVID-19 Pandemic data between African and European Continents including 45 different countries. And then "paired samples t-test" is performed for testing the averages of real-time reproductive rate estimates of COVID-19 Pandemic data between December 2021 and January 2022 as the paired observations of 31 different countries taken from African and European Continents individually.

3.Results and Discussion

In the simulation part of this section, appropriate statistical powers for independent/paired samples t-test applications are tried to be determined using Monte Carlo simulation method in terms of different sample sizes, effect sizes and standard deviations.

For this aim, R-Studio program is used including Stats Package, Power calculations for one and two sample t-tests (pwr) library, and also Multivariate normal density and random deviates (mvtnorm) library.

In the emprical part of this section, firstly "independent samples t-test" is performed for testing the averages of real-time reproductive rate estimates of COVID-19 Pandemic data between African and European Continents. And then "paired samples t-test" is performed for testing the averages of real-time reproductive rate estimates of COVID-19 Pandemic data between December 2021 and January 2022 as the paired observations of 31 different countries taken from African and European Continents individually.

3.1. Results and discussion on determination of statistical powers in terms of different sample sizes, effect sizes and standard deviations for independent samples t-test using Monte Carlo Simulation Study

In the first simulation part of this study, 15.000 Monte Carlo trials are conducted in R-Studio and appropriate statistical powers $(1-\beta)$ are calculated for different standard deviations (σ), sample sizes (n), and effect sizes (d) determined by Cohen (1977, 1988) for the independent samples t-test as given in Table 3.

Table 3. Statistical powers for different standard deviations, sample sizes, and effect sizes in one/two-sided alternative hypotheses for independent samples t-test at α=0.05 significance level.

			Effect Size					
		Sample Size	d=0.2		d=0.5		d=0.8	
			One-Sided	Two-Sided	One-Sided	Two-Sided	One-Sided	Two-Sided
Standard Deviation	S. d =1	n= 50	1-β=0.274	1-β=0.180	1-β=0.804	1-β=0.711	1-β=0.982	1-β=0.966
		n= 100	1-β=0.431	1-β=0.315	1-β=0.960	1-β=0.928	1-β=0.999	1-β=0,998
		n= 250	1-β=0.734	1-β=0.629	1-β=0.994	1-β=0.998	1-β=0.999	1-β=0.999
		n=500	1-β=0.926	1-β=0.877	1-β=0.999	1-β=0.999	1-β=0.999	1-β=0.999
	S.d =1.5	n= 50	1-β=0.170	1-β=0.102	1-β=0.528	1-β=0.406	1-β=0.845	1-β=0.760
		n= 100	1-β=0.255	1-β=0.166	1-β=0.770	1-β=0.670	1-β=0.973	1-β=0.950
		n= 250	1-β=0.461	1-β=0.344	1-β=0.971	1-β=0.949	1-β=0.999	1-β=0.999
		n=500	1-β=0.693	1-β=0.584	1-β=0.998	1-β=0.997	1-β=0.999	1-β=0.999
	S.d =2	n= 50	1-β=0.130	1-β=0.075	1-β=0.365	1-β=0.256	1-β=0.655	1-β=0.534
		n= 100	1-β=0.183	1-β=0.112	1-β=0.572	1-β=0.450	1-β=0.877	1-β=0.807
		n= 250	1-β=0.318	1-β=0.216	1-β=0.873	1-β=0.801	1-β=0.993	1-β=0.986
		n=500	1-β=0.499	1-β=0.380	1-β=0.981	1-β=0.964	1-β=0.999	1-β=0.999
	S.d =2.5	n= 50	1-β=0.109	1-β=0.061	1-β=0.273	1-β=0.179	1-β=0.502	1-β=0.381
		n= 100	1-β=0.146	1-β=0.085	1-β=0.432	1-β=0.314	1-β=0.740	1-β=0.638
		n= 250	1-β=0.240	1-β=0.154	1-β=0.734	1-β=0.630	1-β=0.963	1-β=0.935
		n=500	1-β=0.373	1-β=0.264	1-β=0.926	1-β=0.878	1-β=0.998	1-β=0.995

According to Table 3, when the standard deviation is taken as $\sigma = 1.0$, the effect size is taken as d=0.2; for the sample sizes n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.274 and 0.180; 0.431 and 0.315; 0.734 and 0.629; 0.926 and 0.877 respectively. When $\sigma = 1.0$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.982 and 0.966; 0.999 and 0.998; 0.999 and 0.999; 0.999 and 0.999, respectively. When $\sigma = 1.5$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.170 and 0.102; 0.255 and 0.166; 0.461 and 0.344; 0.693 and 0.584, respectively. When $\sigma = 1.5$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.845 and 0.760;

0.973 and 0.950; 0.999 and 0.999; 0.999 and 0.999, respectively. When $\sigma = 2.0$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.130 and 0.075; 0.183 and 0.112; 0.318 and 0.216; 0.499 and 0.380, respectively. When $\sigma = 2.0$, and d=0.8; for n=50, 100, 250, and 500 in one/two sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.655 and 0.534; 0.877 and 0.807; 0.993 and 0.986; 0.999 and 0.999, respectively. When $\sigma = 2.5$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.109 and 0.061; 0.146 and 0.085; 0.240 and 0.154; 0.373 and 0.264, respectively. When $\sigma = 2.5$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.502 and 0.381; 0.740 and 0.638; 0.963 and 0.935; 0.998 and 0.995, respectively.

3.2. Results and discussion on determination of statistical powers in terms of different sample sizes, effect sizes and standard deviations for paired samples t-test using Monte Carlo Simulation Study

In the second simulation part of this study, 15.000 Monte Carlo trials are conducted in R-Studio and appropriate statistical powers $(1-\beta)$ are calculated for different standard deviations (σ), sample sizes (n), and effect sizes (d) determined by Cohen (1977, 1988) for the paired samples t-test as given in Table 4.

Table 4. Statistical powers for different standard deviations, sample sizes and effect sizes in one/two-sided alternative hypotheses for paired samples t-test at α=0.05 significance level.

			Effect Size					
		Sample Size	**d=0.2**		**d=0.5**		**d=0.8**	
			One-Sided	**Two-Sided**	**One-Sided**	**Two-Sided**	**One-Sided**	**Two-Sided**
Standard Deviation	**S. d =1**	**n= 50**	1-β=0.426	1-β=0.308	1-β=0.958	1-β=0.923	1-β=0.994	1-β=0.998
		n= 100	1-β=0.651	1-β=0.536	1-β=0.997	1-β=0.993	1-β=0.999	1-β=0,999
		n= 250	1-β=0.926	1-β=0.876	1-β=0.999	1-β=0.999	1-β=0.999	1-β=0.999
		n=500	1-β=0.993	1-β=0.986	1-β=0.999	1-β=0.999	1-β=0.999	1-β=0.999
	S.d =1.5	**n= 50**	1-β=0.252	1-β=0.162	1-β=0.763	1-β=0.658	1-β=0.972	1-β=0.947
		n= 100	1-β=0.396	1-β=0.285	1-β=0.943	1-β=0.901	1-β=0.998	1-β=0.997
		n= 250	1-β=0.692	1-β=0.580	1-β=0.998	1-β=0.997	1-β=0.999	1-β=0.999
		n=500	1-β=0.902	1-β=0.842	1-β=0.999	1-β=0.999	1-β=0.999	1-β=0.999
	S.d =2	**n= 50**	1-β=0.181	1-β=0.109	1-β=0.562	1-β=0.439	1-β=0.871	1-β=0.796
		n= 100	1-β=0.274	1-β=0.179	1-β=0.805	1-β=0.714	1-β=0.982	1-β=0.966
		n= 250	1-β=0.495	1-β=0.377	1-β=0.982	1-β=0.964	1-β=0.999	1-β=0.997
		n=500	1-β=0.736	1-β=0.631	1-β=0.999	1-β=0.998	1-β=0.999	1-β=0.998
	S.d =2.5	**n= 50**	1-β=0.144	1-β=0.084	1-β=0.425	1-β=0.309	1-β=0.734	1-β=0.624
		n= 100	1-β=0.209	1-β=0.130	1-β=0.653	1-β=0.538	1-β=0.929	1-β=0.879
		n= 250	1-β=0.374	1-β=0.262	1-β=0.925	1-β=0.877	1-β=0.998	1-β=0.995
		n=500	1-β=0.581	1-β=0.459	1-β=0.993	1-β=0.986	1-β=0.999	1-β=0.999

According to Table 4, when the standard deviation is taken as $\sigma = 1.0$, the effect size is taken as d=0.2; for the sample sizes n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.426 and 0.308; 0.651 and 0.536; 0.692 and 0.580; 0.902 and 0.842, respectively. When $\sigma = 1.0$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative

hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.994 and 0.998; 0.999 and 0.999; 0.999 and 0.999; 0.999 and 0.999, respectively. When $\sigma = 1.5$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.252 and 0.162; 0.396 and 0.285; 0.692 and 0.580; 0.902 and 0.842, respectively. When $\sigma = 1.5$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.972 and 0.947; 0.998 and 0.997; 0.999 and 0.999; 0.999 and 0.999, respectively. When $\sigma = 2.0$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.181 and 0.109; 0.274 and 0.179; 0.495 and 0.377; 0.736 and 0.631, respectively. When $\sigma = 2.0$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.871 and 0.796; 0.982 and 0.966; 0.999 and 0.997; 0.999 and 0.998, respectively. When $\sigma = 2.5$, and d=0.2; for the sample size n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.144 and 0.084; 0.209 and 0.130; 0.374 and 0.262; 0.581 and 0.459, respectively.

When $\sigma = 2.5$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.734 and 0.624; 0.929 and 0.879; 0.998 and 0.995; 0.999 and 0.999, respectively. For the sample size n=100 in one/two-sided alternative hypotheses, the statistical powers are estimated as 0.929 and 0.879, respectively. For the sample size n=250 in one/two-sided alternative hypotheses, the statistical powers are estimated as 0.998 and 0.995, respectively. For the sample size n=500 in one/two-sided alternative hypotheses, the statistical powers are estimated as 0.999 and 0.999, respectively.

3.3. Results and discussion on determination of statistical powers in terms of different sample sizes, effect sizes and significance levels for independent samples t-test using Monte Carlo Simulation Study

In the third simulation part of this study, 15.000 Monte Carlo trials are conducted in R-Studio and appropriate statistical powers $(1-\beta)$ are calculated for different significance levels (α), sample sizes (n), and effect sizes (d) determined by Cohen (1977, 1988) for the independent samples t-test as given in Table 5.

Table 5. Statistical powers for different significance levels, sample sizes and effect sizes in one/two-sided alternative hypotheses for independent samples t-test at $\sigma = 3.0$ standard deviation.

			Effect Size					
		Sample Size	d=0.2		d=0.5		d=0.8	
			One-Sided	Two-Sided	One-Sided	Two-Sided	One-Sided	Two-Sided
Significance Level	Alpha =0.10	n= 50	1-β=0.175	1-β=0.097	1-β=0.340	1-β=0.219	1-β=0.538	1-β=0.396
		n= 100	1-β=0.215	1-β=0.124	1-β=0.477	1-β=0.342	1-β=0.739	1-β=0,614
		n= 250	1-β=0.308	1-β=0.194	1-β=0.732	1-β=0.609	1-β=0.949	1-β=0.902
		n=500	1-β=0.427	1-β=0.294	1-β=0.908	1-β=0.839	1-β=0.995	1-β=0.989
	Alpha =0.05	n= 50	1-β=0.097	1-β=0.053	1-β=0.218	1-β=0.138	1-β=0.396	1-β=0.285
		n= 100	1-β=0.124	1-β=0.071	1-β=0.340	1-β=0.234	1-β=0.615	1-β=0.496
		n= 250	1-β=0.194	1-β=0.120	1-β=0.610	1-β=0.488	1-β=0.903	1-β=0.844
		n=500	1-β=0.295	1-β=0.198	1-β=0.841	1-β=0.762	1-β=0.989	1-β=0.977
	Alpha =0.01	n= 50	1-β=0.023	1-β=0.012	1-β=0.073	1-β=0.044	1-β=0.176	1-β=0.120
		n= 100	1-β=0.034	1-β=0.018	1-β=0.139	1-β=0.092	1-β=0.360	1-β=0.275
		n= 250	1-β=0.062	1-β=0.037	1-β=0.353	1-β=0.269	1-β=0.751	1-β=0.675
		n=500	1-β=0.113	1-β=0.073	1-β=0.645	1-β=0.556	1-β=0.955	1-β=0.930

According to Table 5, when the significance level is taken as $\alpha = 0.10$, the effect size is taken as d=0.2; for the sample sizes n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.175 and 0.097; 0.215 and 0.124; 0.308 and 0.194; 0.427 and 0.294, respectively. When $\alpha = 0.10$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.538 and 0.396; 0.739 and 0.614; 0.949 and 0.902; 0.995 and 0.989, respectively. When $\alpha = 0.05$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.097 and 0.053; 0.124 and 0.071; 0.194 and 0.120; 0.295 and 0.198, respectively. When $\alpha = 0.05$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.396 and 0.285; 0.615 and 0.496; 0.903 and 0.844; 0.989 and 0.977, respectively. When $\alpha = 0.01$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.023 and 0.012; 0.034 and 0.018; 0.062 and 0.037; 0.113 and 0.073, respectively. When $\alpha = 0.01$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.176 and 0.120; 0.360 and 0.275; 0.751 and 0.675; 0.955 and 0.930, respectively.

3.4. Results and discussion on determination of statistical powers in terms of different sample sizes, effect sizes and significance levels for paired samples t-test using Monte Carlo Simulation Study

In the fourth simulation part of this study, 15.000 Monte Carlo trials are conducted in R-Studio and appropriate statistical powers $(1-\beta)$ are calculated for different significance levels (α), sample sizes (n), and effect sizes (d) determined by Cohen (1977, 1988) for the paired samples t-test as given in Table 6.

Table 6. Statistical powers for different significance levels, sample sizes and effect sizes in one/two-sided alternative hypotheses for paired samples t-test at $\sigma = 3.0$ standard deviation.

			Effect Size					
		Sample Size	d=0.2		d=0.5		d=0.8	
			One-Sided	Two-Sided	One-Sided	Two-Sided	One-Sided	Two-Sided
Significance Level	Alpha =0.10	n= 50	1-β=0.214	1-β=0.124	1-β=0.473	1-β=0.335	1-β=0.735	1-β=0.609
		n= 100	1-β=0.278	1-β=0.172	1-β=0.664	1-β=0.529	1-β=0.910	1-β=0,844
		n= 250	1-β=0.427	1-β=0.292	1-β=0.908	1-β=0.838	1-β=0.995	1-β=0.989
		n=500	1-β=0.602	1-β=0.461	1-β=0.987	1-β=0.972	1-β=0.999	1-β=0.999
	Alpha =0.05	n= 50	1-β=0.123	1-β=0.071	1-β=0.334	1-β=0.228	1-β=0.607	1-β=0.483
		n= 100	1-β=0.171	1-β=0.103	1-β=0.528	1-β=0.406	1-β=0.844	1-β=0.762
		n= 250	1-β=0.294	1-β=0.196	1-β=0.837	1-β=0.758	1-β=0.989	1-β=0.977
		n=500	1-β=0.464	1-β=0.347	1-β=0.972	1-β=0.948	1-β=0.999	1-β=0.999
	Alpha =0.01	n= 50	1-β=0.032	1-β=0.018	1-β=0.134	1-β=0.087	1-β=0.345	1-β=0.257
		n= 100	1-β=0.051	1-β=0.031	1-β=0.275	1-β=0.201	1-β=0.645	1-β=0.553
		n= 250	1-β=0.112	1-β=0.072	1-β=0.640	1-β=0.550	1-β=0.953	1-β=0.929
		n=500	1-β=0.226	1-β=0.161	1-β=0.903	1-β=0.862	1-β=0.998	1-β=0.996

According to Table 6, when the significance level is taken as $\alpha = 0.10$, the effect size is taken as d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.214 and 0.124; 0.278 and 0.172; 0.427 and 0.292; 0.602 and 0.461, respectively. When $\alpha = 0.10$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.735 and 0.609; 0.910 and 0.844; 0.995 and 0.989; 0.999 and 0.999, respectively. When $\alpha = 0.05$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.123 and 0.071; 0.171 and 0.103; 0.294 and 0.196; 0.464 and 0.347, respectively. When $\alpha = 0.05$, d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.607 and 0.483; 0.844 and 0.762; 0.989 and 0.977; 0.999 and 0.999, respectively. When $\alpha = 0.01$, and d=0.2; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.032 and 0.018; 0.051 and 0.031; 0.112 and 0.072; 0.226 and 0.161, respectively. When $\alpha = 0.01$, and d=0.8; for n=50, 100, 250, and 500 in one/two-sided alternative hypotheses, the statistical powers $(1-\beta)$ are estimated as 0.345 and 0.257; 0.645 and 0.553; 0.953 and 0.929; 0.998 and 0.996, respectively.

3.5. Results and discussion on the empirical study for real-time reproductive rate estimates of the COVID-19 pandemic for independent samples t-test

In the first empirical part of this study, "independent samples t-test" for testing the averages of real-time reproductive rate estimates of the COVID-19 pandemic between African and European Continents has actually been investigated. For this aim, descriptive statistics belonging to 45 countries data [33] from African Continent and 45 countries data [33] from European Continent in equal sample sizes ($n_{African}=n_{European}=45$) in January 2022 given in Table 1 are given in Table 7.

Table 7. Descriptive statistics for the real-time reproductive rate estimates of the COVID-19 pandemic for both European and African Continents.

Continents	Sample Size (n)	Min.	Median	Mean ± Sd.	Max
African	45	0.76	1.02	1.064 ± 0.172	1.82
European	45	0.57	1.23	1.243 ± 0.202	1.83

Before performing independent samples t-test, "independence" assumption is satisfied by taking 45 different countries from two different continents as African and European given in Table 1. And also "normality" and "homogeneity of variance" are the other two important assumptions that must be satisfied before performing "independent samples t-test" to the COVID-19 pandemic reproductive rate data of the African and European continents. For this aim, hypotheses for checking the second assumption as the "normality" of the "independent samples t-test" are given as follows [34];

H_0: Randomly selected reproduction rate data for the African and European continents come from the normally distributed population.

H_1: Randomly selected reproduction rate data for the African and European countries do not come from the normally distributed population.

Table 8. Shapiro-Wilk goodness-of-fit test results for the African and European Continents real-time reproductive rate estimates of the COVID-19 Pandemic data.

Goodness-of-fit test statistics	Statistics value	df	p-value
[1]Shapiro – Wilk Test Statistic	0.989	45	0.697
[2]Shapiro – Wilk Test Statistic	0.981	45	0.673

1:for the African Continent; 2: for the European Continent

Using Shapiro-Wilk goodness-of-fit test, the "normality" assumption has been checked, and the null hypothesis given above for both reproduction rate data for the African, and European continents could not be rejected at $\alpha=0.05$ significance level ($p_{1,\text{Shapiro-Wilk}}=0.697>0.05$; $p_{2,\text{Shapiro-Wilk}}=0.673>0.05$). Then it is decided that the random samples of the COVID-19 pandemic reproduction rates of the randomly selected countries from the African, and European continents come from the normally distrubuted populations at $\alpha=0.05$ signifance level.

As checking the third assumption of the "independent samples t-test", hypotheses for the "homogeneity of variance" assumption are given as follows;

H_0: $\sigma^2_{\text{African}} = \sigma^2_{\text{European}}$

H_1: $\sigma^2_{\text{African}} \neq \sigma^2_{\text{European}}$

where $\sigma^2_{\text{African}}$ and $\sigma^2_{\text{European}}$ are the population variances of the real-time reproductive rate estimates of the COVID-19 pandemic belonging to the African, and European Continents, respectively.

Table 9. Levene homogeneity of variance test results for the African and European Continents real-time reproductive rate estimates of the COVID-19 pandemic data.

Homogeneity of variance test statistic	Statistic value	df	p-value
Levene Test Statistic	0.177	90	0.675

Using Levene homogeneity of variance test, the "homogeneity of variances" assumption has been checked, and the null hypothesis given above for the reproduction rate data for the African, and European continents could not be rejected at α=0.05 significance level (p-value=0.675>0.05). Then it is decided that the random samples of the COVID-19 pandemic reproduction rates of the randomly selected countries from the African, and European continents come from the homogeneous populations at α=0.05 signifance level.

The main hypotheses of the first part of the empirical study to compare averages of the real-time reproductive rate estimates of the COVID-19 pandemic between the African and European Continents by "independent samples t-test" are given as follows;

H_0: $\mu_{African} = \mu_{European}$

H_1: $\mu_{African} < \mu_{European}$

where in the alternative hypothesis, the main interest in on the average of the real-time reproductive rate estimates of the COVID-19 pandemic in the Africa Continent is smaller than the average of the real-time reproductive rate estimates of the COVID-19 pandemic in the European Continent in January 2022. Because inspite of the inadequate vaccine opportunities and poor health services, the low rate of cases and deaths in the Africa than the European countries surprises scientists. So while Africa does not have the vaccine opportunities and resources to fight the Covid-19 pandemic like Europe, it has been among the "least affected regions of the world" for months in the pandemic reports published by the World Health Organization (Njenga et al.; Okonji et al.; Musa et al.; Kong et al.)

Table 10. Independent samples t-test results for the COVID-19 pandemic reproduction rates data between the African and European Continents.

Continents	t- test value	p-value	Effect Size (d)	Power (*1-β*)
African- European	4.821	<0.00	0.5	0.834

Using "independent samples t-test", $|t-test\ statistic| = 4.821 > t_{88,0.950} = 1.664$ and $p-value = 0.000 < \alpha = 0.05$, the null hypothesis can be rejected at $\alpha = 0.05$ significance level. Then it is decided that, interestingly, the average of the reproduction rates of the randomly selected countries from the European continent is statistically higher than the average of the reproduction rates of the randomly selected countries from the African continent in January 2022, at the α=0.05 significance level.

Cohen (1962, 1977, 1988) reported that a statistical power of 0.80 represents a reasonable and realistic value in the scientific researches, and accordingly, the 4/1 ratio of α and β errors is appropriate. Then when the optimum medium effect size is choosen as d=0.5, based on Cohen's studies (1962, 1977,1988), by using G*Power [35], the statistical power of this one-sided alternative hypothesis given above is calculated as 0.834 for independent samples t-test.

3.6. Results and discussion on the empirical study for real-time reproductive rate estimates of the COVID-19 pandemic for paired samples t-test

Also in the second empirical part of this study, "paired samples t-test" for testing the averages of the real-time reproductive rate estimates of the COVID-19 pandemic data belonging to the European Continent between December 2021 and January 2022 has actually been investigated. For this aim, descriptive statistics belonging to randomly selected n=31 countries data [33] from the European Continent for December 2021 and January 2022 are given in Table 11.

Table 11. Descriptive statistics for the real-time reproductive rate estimates of the COVID-19 pandemic for the European Continent.

Continent	Time Periods	Sample Size (n)	Min.	Median	Mean ± Sd.	Max.
European	December 2021	31	0.92	1.18	1.194 ± 0.212	1.77
	January 2022	31	0.85	1.32	1.378 ± 0.28	2.07

Before performing paired samples t-test, "independence" assumption is again satisfied by taking 31 different countries from the European Continent given in Table 2. Here "independence" means that the measurements taken of a country do not affect the measurements taken of another country in the European Continent. In this test, each paired measurements as December 2021 and January 2022 are obtained from the same countries in the European Continent. The hypotheses for testing the "normality" assumption for the measured differences between these time periods belonging to the real-time reproductive rate estimates of the COVID-19 pandemic for this continent using Shapiro-Willk test is given as follows;

H_0: Measured differences between December 2021 and January 2022 belonging to the real-time reproductive rate estimates of the COVID-19 pandemic for the European Continent come from a normally distributed population.

H_1: Measured differences between December 2021 and January 2022 belonging to the real-time reproductive rate estimates of the COVID-19 pandemic for the European Continent do not come from a normally distributed population.

Table 12. Shapiro-Wilk goodness-of-fit test results for the European Continent's real-time reproductive rate estimates of the COVID-19 pandemic between December 2021 and January 2022

Goodness-of-fit test statistic	Statistic value	df	p-value
[1]Shapiro – Wilk Statistic	0.985	31	0.928

1: Real-time reproductive rate estimates of the COVID-19 pandemic measurements data between December 2021 and January 2022

By Shapiro-Wilk goodness-of-fit test, the "normality" assumption has been checked, and the null hypothesis given above for the real-time reproductive rate estimates of the COVID-19 pandemic measurement differences between December 2021 and January 2022 for the European continent could not be rejected at $\alpha=0.05$ significance level ($p_{Shapiro\text{-}Wilk}=0.928>0.05$). Then it can be decided that the measured differences between December 2021 and January 2022 belonging to the real-time reproductive rate estimates of the COVID-19 pandemic for the European Continent come from a normally distributed population at $\alpha=0.05$ significance level.

The main hypotheses of the second part of the empirical study to is to test the average of the measured differences between December 2021 and January 2022 belonging to the real-time reproductive rate estimates of the COVID-19 pandemic for the European Continent using "paired samples t-test" are given as follows;

H_0: $\mu_{d,European} = 0$

H_1: $\mu_{d,European} > 0$

where $d = \sum_{i=1}^{31} d_i \Big/ 31$ and d_i= real-time reproductive rate estimates of the COVID-19 pandemic in the European Continent between December 2021 and January 2022. $\mu_{d,European}$ is the mean difference between the real-time reproductive rate estimates of the COVID-19 pandemic between December 2021 and January 2022 belonging to the 31 countries of the European Continent given in Table 2.

In the alternative hypothesis given above, the main interest in on the mean difference of the real-time reproductive rate estimates of the COVID-19 pandemic in the European Continent between December 2021 and January 2022 is greater than zero.

Table 13. Paired samples t-test results for the real-time reproductive rate estimates of the COVID-19 pandemic measurements data of the European Continent between December 2021 and January 2022.

Continent	**Mean difference ± Std. deviation of mean difference**	**t-value**	**p-value**	**Effect Size (d)**	**Power (*1-β*)**
European	-0.184 ± 0.342	-2.996	0.005	0.5	0.879

Using paired samples t-test, $|t-test\ statistic| = 2.996 > t_{30,0.950} = 1.697$, and $p-value = 0.005 < \alpha = 0.05$, the null hypothesis can be rejected at $\alpha = 0.05$ significance level. Then it can be decided that the mean difference of the real-time reproductive rate estimates of the COVID-19 pandemic between December 2021 and January 2022 belonging to 31 countries in the European Continent is greater than zero at the α=0.05 signifance level.

When the optimum medium effect size is choosen as d=0.5, based on Cohen's studies (1962, 1977,1988), by using G*Power [35], the statistical power of this one-sided alternative hypothesis given above is calculated as 0.879 for paired samples t-test.

4.CONCLUSION

In this study, appropriate statistical powers for independent/paired samples t-test applications are tried to be determined using Monte Carlo simulation method in terms of different sample sizes, effect sizes and standard deviations. In the empirical part of this study, based on the Monte Carlo simulation method, firstly "independent samples t-test" is performed for testing the averages of real-time reproductive rate estimates of the COVID-19 Pandemic data between African and European Continents including 45 countries. And then "paired samples t-test" is performed for testing the averages of real-time reproductive rate estimates of the COVID-19 Pandemic data between December 2021 and January 2022 as the paired observations of 31 different countries taken from the European Continent.

As the main conclusions of this study, belonging to the independent samples t-test results, it is determined that the statistical power decreased as the standard deviation increased. The statistical power increased as the effect size widened at a fixed sample size and standard deviation value. Belonging to the paired samples t-test results, it is determined that the statistical power decreased as the significance level decreased. In addition, statistical powers for the paired samples t-test with fixed sample size and effect size are estimated to be higher than for the independent samples t-test. Also, statistical powers for the paired samples t-test with fixed sample size and effect size are found higher than for the independent samples t-test.

Acknowledgments: Neslihan İyit is the main author of this study. Nagehan Büyükbayram continues her P.Hd. degree under the supervision of the first author. The earlier version of this study is presented at the 2nd International Conference on Scientific and Innovative Studies (ICSIS) 2024 by the same authors.

Funding information: The authors state no funding involved.

Conflict of interest: The authors state no conflict of interest.

Ethical approval: The conducted research is not related to either human or animal use.

Data availability statement: All the data used in this study are public available in https://github.com/owid/covid-19-data/tree/master/public/data.

References

[1] Myors, B., Murphy, K. R., & Wolach, A. (2010). Statistical power analysis: A simple and general model for traditional and modern hypothesis tests. Routledge.

[2] Cohen, J. (2013). Statistical power analysis for the behavioral sciences. Routledge.

[3] Greenland, S., Senn, S. J., Rothman, K. J., Carlin, J. B., Poole, C., Goodman, S. N., & Altman, D. G. (2016). Statistical tests, P values, confidence intervals, and power: a guide to misinterpretations. European journal of epidemiology, 31(4), 337-350.

[4] İyit, N., Büyükbayram, H.N., and Tekin, M.E. (2022). A general overview for determination of sample size in parametric t-tests by a Monte-Carlo simulation study. Current Research in Science and Mathematics. March 2022, Ed.Assoc.Prof.Dr.Neslihan İyit, Gece Publishing, Ankara, Turkiye, pp.1-16.

[5] İyit, N., and Büyükbayram, H.N., (2024). Statistical determination of sample size in terms of different statistical powers and effect sizes in the biostatistical evaluation of life expectancy at birth data, Proceeding Book of 4th International Conference on Innovative Academic Studies (ICIAS), All Sciences Academy, 12-13 March 2024, Konya, Turkiye, pp.700-710.

[6] Nakagawa, S., & Cuthill, I. C. (2007). Effect size, confidence interval and statistical significance: a practical guide for biologists. Biological reviews, 82(4), 591-605.

[7] Ellis, P. D. (2010). The essential guide to effect sizes: Statistical power, meta-analysis, and the interpretation of research results. Cambridge University Press.

[8] Fritz, C. O., Morris, P. E., & Richler, J. J. (2012). Effect size estimates: current use, calculations, and interpretation. Journal of experimental psychology: General, 141(1), 2.

[9] Lenth, R. V. (2001). Some practical guidelines for effective sample size determination. The American Statistician, 55(3), 187-193.

[10] Suresh, K. P., & Chandrashekara, S. (2012). Sample size estimation and power analysis for clinical research studies. Journal of human reproductive sciences, 5(1), 7-13.

[11] Kraemer, H. C., & Blasey, C. (2015). How many subjects?: Statistical power analysis in research. Sage Publications.

[12] Krzywinski, M., & Altman, N. (2013). Points of significance: Power and sample size. Nature Methods, 10(12).

[13] Park, H. M. (2015). Hypothesis testing and statistical power of a test.

[14] Cohen, J. (2013). Statistical power analysis for the behavioral sciences. Routledge.

[15] Faul, F., Erdfelder, E., Lang, A. G., & Buchner, A. (2007). G* Power 3: A flexible statistical power analysis program for the social, behavioral, and biomedical sciences. Behavior research methods, 39(2), 175-191.

[16] Lan, L., & Lian, Z. (2010). Application of statistical power analysis–How to determine the right sample size in human health, comfort and productivity research. Building and Environment, 45(5), 1202-1213.

[17] Kang, H. (2021). Sample size determination and power analysis using the G* Power software. Journal of educational evaluation for health professions, 18.

[18] Dalmaijer, E. S., Nord, C. L., & Astle, D. E. (2022). Statistical power for cluster analysis. BMC bioinformatics, 23(1), 205.

[19] Szucs, D., & Ioannidis, J. P. (2020). Sample size evolution in neuroimaging research: An evaluation of highly-cited studies (1990–2012) and of latest practices (2017–2018) in high-impact journals. NeuroImage, 221, 117164.

[20] Serdar, C. C., Cihan, M., Yücel, D., & Serdar, M. A. (2021). Sample size, power and effect size revisited: simplified and practical approaches in pre-clinical, clinical and laboratory studies. Biochemia medica, 31(1), 27-53.

[21] Cheval, B., Sivaramakrishnan, H., Maltagliati, S., Fessler, L., Forestier, C., Sarrazin, P., ... & Boisgontier, M. P. (2021). Relationships between changes in self-reported physical activity, sedentary behaviour and health during the coronavirus (COVID-19) pandemic in France and Switzerland. Journal of sports sciences, 39(6), 699-704.

[22] Abt, G., Boreham, C., Davison, G., Jackson, R., Nevill, A., Wallace, E., & Williams, M. (2020). Power, precision, and sample size estimation in sport and exercise science research. Journal of Sports Sciences, 38(17), 1933-1935.

[23] Sharma, S. K., Mudgal, S. K., Thakur, K., & Gaur, R. (2020). How to calculate sample size for observational and experimental nursing research studies. National Journal of Physiology, Pharmacy and Pharmacology, 10(1), 1-8.

[24] Lenzo, V., Quattropani, M. C., Sardella, A., Martino, G., & Bonanno, G. A. (2021). Depression, anxiety, and stress among healthcare workers during the COVID-19 outbreak and relationships with expressive flexibility and context sensitivity. Frontiers in psychology, 12, 623033.

[25] Kelley, T. R., Knowles, J. G., Holland, J. D., & Han, J. (2020). Increasing high school teachers self-efficacy for integrated STEM instruction through a collaborative community of practice. International Journal of STEM Education, 7, 1-13.

[26] de Micheaux, P. L., & Tran, V. A. (2016). PoweR: A reproducible research tool to ease Monte Carlo power simulation studies for goodness-of-fit tests in R. Journal of Statistical Software, 69, 1-44.

[27] Muthén, L. K., & Muthén, B. O. (2002). How to use a Monte Carlo study to decide on sample size and determine power. Structural equation modeling, 9(4), 599-620.

[28] Onoz, B., & Bayazit, M. (2003). The power of statistical tests for trend detection. Turkish journal of engineering and environmental sciences, 27(4), 247-251.

[29] Myers, N. D., Ahn, S., & Jin, Y. (2011). Sample size and power estimates for a confirmatory factor analytic model in exercise and sport: A Monte Carlo approach. Research quarterly for exercise and sport, 82(3), 412-423.

[30] Kalos, M. H., & Whitlock, P. A. (2009). Monte carlo methods. John Wiley & Sons.

[31] Robert, C. P., Casella, G., & Casella, G. (2010). Introducing monte carlo methods with r (Vol. 18). New York: Springer.

[32] Kroese, D. P., Taimre, T., & Botev, Z. I. (2013). Handbook of monte carlo methods. John Wiley & Sons.

[33] owid/covid-19-data [Internet]. [cited 2024 February 23]. Available from https://github.com/owid/covid-19-data/tree/master/public/data

[34] Rochon, J., Gondan, M., & Kieser, M. (2012). To test or not to test: Preliminary assessment of normality when comparing two independent samples. BMC medical research methodology, 12, 1-11.

[35] Faul, F., Erdfelder, E., Lang, A. G., & Buchner, A. (2007). G* Power 3: A flexible statistical power analysis program for the social, behavioral, and biomedical sciences. Behavior research methods, 39(2), 175-191.