

Tests for Tijana

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Do we need to transform the data?

If we want use Test for Association/Correlation Between Paired Samples (`cor.test` in R) for calculating the **Pearson coefficient** and **t - test** for determining the difference between patient and control group, we have to investigate if the data is close enough to normal. In that purpose a **D'Agostino - Pearson** normality test is used.

Table 1: D'Agostino - Pearson normality test.

	eGFR	ADC cortex	ADC medulla	ADC whole kidney	ADC CMD
p - value	0.0011694	0.0260224	5.14e-05	0.0003769	0.7733204

All the variables, except ADC CMD, have significant p - value (less then 0.05), so we **reject** the null hypothesis: **“Data is normally distributed”**. Before we conclude that the data needs to be transformed, using the residuals of linear regression model (LRM) will help us determine how well the data is described by the linear model. If the residuals are normally distributed with the mean 0, then LRM describes the data well enough even if the data does not satisfy the property of normal distribution. For the t - test the transformation of the data has to be done.

Table 2: D'Agostino - Pearson normality test for residuals.

	ADC cortex	ADC medulla	ADC whole kidney	ADC CMD
Residual mean	0.0000000	0.00e+00	0.0000000	0.0000000
p - value	0.0176107	3.85e-05	0.0001546	0.5560543

All the **residuals** are centered around 0 and all the p - values, except ADC CMD, are less than 0.05, so they are **not normally distributed around the mean** (in this case 0). This suggests that the transformation of the data is needed. If eGFR is **squared** and if for all dependent variables, except ADC CMD, **reciprocal value** is used then normality property of the data is satisfied.

Table 3: D'Agostino - Pearson normality test for transformed data.

	eGFR*eGFR	1/ADC cortex	1/ADC medulla	1/ADC whole kidney	ADC CMD
p - value	0.3000796	0.4614084	0.7432711	0.8134307	0.7733204

Now all the variables are close enough to **normal**, which p - value greater than 0.05 suggests. Let us see if the residuals have improved.

Table 4: D’Agostino - Pearson normality test for residuals of transformed data.

	1/ADC cortex	1/ADC medulla	1/ADC whole kidney	ADC CMD
Residual mean	0.0000000	0.0000000	0.0000000	0.0000000
p - value	0.8036011	0.6572567	0.7096842	0.5560543

All the p - values are now much greater than 0.05, so the **residuals are normaly distributed around 0**.

Pearson coefficient

After transforming the data, except ADC CMD, Pearson coefficient can be calculated (**df = 92**).

Table 5: Pearson coefficients with p - values after data transformation

	1/ADC cortex	1/ADC medulla	1/ADC whole kidney	ADC CMD
Pearson Coefficient	-0.2998056	-0.2510861	-0.3022892	0.0842358
p-value	0.0033282	0.0146451	0.0030645	0.4195481

All the coefficients, **except ADC CDM**, are **statistically significant**, meaning that they have p - values less than 0.05 (Pearson coefficient -0.2998056 for reciprocal transformed ADC cortex is highly statistically significant with p value of 0.0033282). For 1/ADC cortex and 1/ADC whole kidney p - values are less than 0.01 which is considered **highly significant**. Reciprocal transformation changes the sign of the Pearson coefficients, so let us confirm that by calculating the coefficients before transformation.

Table 6: Pearson coefficients with p - values before data transformation

	ADC cortex	ADC medulla	ADC whole kidney	ADC CMD
Pearson Coefficient	0.3024882	0.2542817	0.2985429	0.0908529
p-value	0.0030442	0.0133923	0.0034699	0.3838259

The difference of Pearson coefficients before and after data transformation is less than 1%, which indicates that by transforming the data **the strength of the linear relationship didn’t change only the direction of the slope did**.

Pearson coefficient for ADC CMD was not statistically significant (p - value greater than 0.05), meaning that there is no statistical evidence of linear relationship between eGFR and ADC CMD. Let us now calculate the **Spearman coefficient** for ADC CMD, to see if there is **monotonic relationship** between eGFR and ADC CMD. This coefficient can be calculated for data which is not normally distributed and it is not changed by data transformation like Pearson coefficient is.

Table 7: Spearman coefficient with p - value for ADC CMD

	ADC CMD
Spearman coefficient	0.1032984
p - value	0.3217985

The p - value 0.3217985 for Spearman coefficient 0.1032984 is **not statistically significant**, so there is **no statistical evidence of monotonic relationship**. Even though no statistical significant coefficient was found, **causality or some other type of relationship could still exist**.

T test for comparing the means of the patients and the control group

Data was collected from **84 patients** and **10 control - healthy individuals**.

Table 8: Comparison of variances with F test for patients and control group after transformation

	1/ADC cortex	1/ADC medulla	1/ADC whole kidney	ADC CMD
Num df	83	83	83	9
Denom df	9	9	9	83
F	1.61094713769377	2.5888830450246	2.68559194809279	1.58802809438613
p-value	0.447613459260643	0.122765687091866	0.109604955590782	0.264536501515841
Equal/Unequal	Equal variances	Equal variances	Equal variances	Equal variances

Notice that **numerator degrees of freedom (Num df)** and **denominator degrees of freedom (Denom df)** will change depending of the variances of the groups. We have to take care that the variance of the first group is greater from the variance of the second group, because F is calculated by dividing the variances.

Table 9: Critical F values

Num df	83	9
Denom df	9	83
Critical F lower	0.4402617	0.2926027
Critical F upper	3.4176039	2.2713763

So, if we look at the **Table 8.** and **Table 9.** for reciprocal transformed ADC cortex, with **numerator degrees of freedom 83** and **denominator degrees of freedom 9**, F value is **1.6109471** which is **lower** than upper critical F value **3.4176039** indicating that we **fail to reject the null hypothesis that: ‘Groups have the same variances’**. **P value** of **0.447613** also indicates that we **fail to reject the null hypothesis**.

Table 10: Comparison of means with t test (with equal variances and df = 92) for patients and control group after transformation

	1/ADC cortex	1/ADC medulla	1/ADC whole kidney	ADC CMD
t value	0.0310509907872609	1.22082647372431	0.669891329886053	1.53222216308377
p-value	0.975296137764459	0.22527137788787	0.504604993697292	0.128899244272177
Equal/Unequal	Equal means	Equal means	Equal means	Equal means

To **reject** the null hypothesis: " **Groups have equal means** " **p value** has to be **less than 0.05** and **t value greater** than critical value of **1.986086** or **less** than negative critical value **-1.986086**. For instance reciprocal transformed ADC cortex has t value 0.0310511 less than critical value 1.986086 and its p value 0.9752961 much greater than 0.05, so we fail to reject the null hypothesis.

T test for comparing the means of male and female group

Data was collected from **44 female** and **50 male**.

Table 11: Comparison of variances with F test for female and male group after transformation

	1/ADC cortex	1/ADC medulla	1/ADC whole kidney	ADC CMD
Num df	49	43	43	49
Denom df	43	49	49	43
F	1.20817211364376	1.41494592169965	1.05736980424442	1.06037179129772
p-value	0.529842680370616	0.239557472445604	0.845946499685994	0.848757103973593
Equal/Unequal	Equal variances	Equal variances	Equal variances	Equal variances

Table 12: Critical F values

Num df	43	49
Denom df	49	43
Critical F lower	0.55314	0.55944
Critical F upper	1.78751	1.80787

Look at the Table 11. and Table 12. for reciprocal transformed ADC cortex, with numerator degrees of freedom 49 and denominator degrees of freedom 43 , F value is 1.2081721 which is lower than upper critical F value 1.8078736 indicating that we fail to reject the null hypothesis that: 'Groups have the same variances' . P value of 0.5298427 also indicates that we fail to reject the null hypothesis.

Table 13: Comparison of means with t test (with equal variances and df = 92) for female and male group after transformation

	1/ADC cortex	1/ADC medulla	1/ADC whole kidney	ADC CMD
t value	1.85956118782433	1.40224001702787	1.76715838090193	-1.07166859303427
p-value	0.0661434542539402	0.164208820332678	0.0805177824747474	0.286672163074892
Equal/Unequal	Equal means	Equal means	Equal means	Equal means

To reject the null hypothesis: " Groups have equal means " p value has to be less than 0.05 and t value greater than critical value of 1.986086 or less then -1.986086 . For instance reciprocal transformed ADC cortex has t value 1.8595612 little less than critical value 1.986086 and its p value 0.06614345 little greater than 0.05, so we fail to reject the null hypothesis: 'Groups have the same means'.

Appendix





