Your license will expire in 25 days.

**General Linear Model**

|  |  |  |
| --- | --- | --- |
| **Notes** | | |
| Output Created | | 06-AUG-2024 08:31:05 |
| Comments | |  |
| Input | Active Dataset | DataSet2 |
| Filter | <none> |
| Weight | <none> |
| Split File | <none> |
| N of Rows in Working Data File | 81 |
| Missing Value Handling | Definition of Missing | User-defined missing values are treated as missing. |
| Cases Used | Statistics are based on all cases with valid data for all variables in the model. |
| Syntax | | GLM avsomaareamm2 avnoprocesses BY GENOTYPE1WT2A53T REGION1SN2VTA3CP /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /POSTHOC=GENOTYPE1WT2A53T REGION1SN2VTA3CP(LSD) /EMMEANS=TABLES(GENOTYPE1WT2A53T) COMPARE ADJ(LSD) /EMMEANS=TABLES(REGION1SN2VTA3CP) COMPARE ADJ(LSD) /EMMEANS=TABLES(GENOTYPE1WT2A53T\*REGION1SN2VTA3CP) /CRITERIA=ALPHA(.05) /DESIGN= GENOTYPE1WT2A53T REGION1SN2VTA3CP GENOTYPE1WT2A53T\*REGION1SN2VTA3CP. |
| Resources | Processor Time | 00:00:00.05 |
| Elapsed Time | 00:00:00.00 |

[DataSet2]

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| **Warnings** |
| Post hoc tests are not performed for GENOTYPE [1 = WT; 2= A53T] because there are fewer than three groups. |

|  |  |  |
| --- | --- | --- |
| **Between-Subjects Factors** | | |
|  | | N |
| GENOTYPE [1 = WT; 2= A53T] | 1 | 12 |
| 2 | 15 |
| REGION[1=SN; 2=VTA; 3=CP] | 1 | 9 |
| 2 | 9 |
| 3 | 9 |

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Multivariate Tests**a | | | | | | |
| Effect | | Value | F | Hypothesis df | Error df | Sig. |
| Intercept | Pillai's Trace | .985 | 635.355b | 2.000 | 20.000 | <.001 |
| Wilks' Lambda | .015 | 635.355b | 2.000 | 20.000 | <.001 |
| Hotelling's Trace | 63.536 | 635.355b | 2.000 | 20.000 | <.001 |
| Roy's Largest Root | 63.536 | 635.355b | 2.000 | 20.000 | <.001 |
| GENOTYPE1WT2A53T | Pillai's Trace | .689 | 22.194b | 2.000 | 20.000 | <.001 |
| Wilks' Lambda | .311 | 22.194b | 2.000 | 20.000 | <.001 |
| Hotelling's Trace | 2.219 | 22.194b | 2.000 | 20.000 | <.001 |
| Roy's Largest Root | 2.219 | 22.194b | 2.000 | 20.000 | <.001 |
| REGION1SN2VTA3CP | Pillai's Trace | .045 | .244 | 4.000 | 42.000 | .912 |
| Wilks' Lambda | .955 | .234b | 4.000 | 40.000 | .918 |
| Hotelling's Trace | .047 | .224 | 4.000 | 38.000 | .923 |
| Roy's Largest Root | .044 | .459c | 2.000 | 21.000 | .638 |
| GENOTYPE1WT2A53T \* REGION1SN2VTA3CP | Pillai's Trace | .148 | .839 | 4.000 | 42.000 | .509 |
| Wilks' Lambda | .852 | .831b | 4.000 | 40.000 | .513 |
| Hotelling's Trace | .173 | .821 | 4.000 | 38.000 | .520 |
| Roy's Largest Root | .171 | 1.791c | 2.000 | 21.000 | .191 |
| a. Design: Intercept + GENOTYPE1WT2A53T + REGION1SN2VTA3CP + GENOTYPE1WT2A53T \* REGION1SN2VTA3CP | | | | | | |
| b. Exact statistic | | | | | | |
| c. The statistic is an upper bound on F that yields a lower bound on the significance level. | | | | | | |

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| --- | --- | --- | --- | --- | --- | --- |
| **Tests of Between-Subjects Effects** | | | | | | |
| Source | Dependent Variable | Type III Sum of Squares | df | Mean Square | F | Sig. |
| Corrected Model | av soma area (mm2) | .472a | 5 | .094 | 5.050 | .003 |
| av no processes | 8.145b | 5 | 1.629 | 5.475 | .002 |
| Intercept | av soma area (mm2) | 3.024 | 1 | 3.024 | 161.671 | <.001 |
| av no processes | 354.518 | 1 | 354.518 | 1191.514 | <.001 |
| GENOTYPE1WT2A53T | av soma area (mm2) | .389 | 1 | .389 | 20.824 | <.001 |
| av no processes | 7.978 | 1 | 7.978 | 26.815 | <.001 |
| REGION1SN2VTA3CP | av soma area (mm2) | .012 | 2 | .006 | .322 | .728 |
| av no processes | .098 | 2 | .049 | .165 | .849 |
| GENOTYPE1WT2A53T \* REGION1SN2VTA3CP | av soma area (mm2) | .064 | 2 | .032 | 1.704 | .206 |
| av no processes | .056 | 2 | .028 | .094 | .911 |
| Error | av soma area (mm2) | .393 | 21 | .019 |  |  |
| av no processes | 6.248 | 21 | .298 |  |  |
| Total | av soma area (mm2) | 4.176 | 27 |  |  |  |
| av no processes | 385.409 | 27 |  |  |  |
| Corrected Total | av soma area (mm2) | .865 | 26 |  |  |  |
| av no processes | 14.393 | 26 |  |  |  |
| a. R Squared = .546 (Adjusted R Squared = .438) | | | | | | |
| b. R Squared = .566 (Adjusted R Squared = .463) | | | | | | |

**Estimated Marginal Means**

**1. GENOTYPE [1 = WT; 2= A53T]**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Estimates** | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | Mean | Std. Error | 95% Confidence Interval | |
| Lower Bound | Upper Bound |
| av soma area (mm2) | 1 | .216 | .039 | .134 | .298 |
| 2 | .458 | .035 | .384 | .531 |
| av no processes | 1 | 3.099 | .157 | 2.772 | 3.427 |
| 2 | 4.193 | .141 | 3.900 | 4.486 |

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| --- | --- | --- | --- | --- | --- |
| **Pairwise Comparisons** | | | | | |
| Dependent Variable | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | Mean Difference (I-J) | Std. Error | Sig.b |
|
| av soma area (mm2) | 1 | 2 | -.242\* | .053 | <.001 |
| 2 | 1 | .242\* | .053 | <.001 |
| av no processes | 1 | 2 | -1.094\* | .211 | <.001 |
| 2 | 1 | 1.094\* | .211 | <.001 |

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| --- | --- | --- | --- | --- | --- |
| **Pairwise Comparisons** | | | | | |
| Dependent Variable | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | 95% Confidence Interval for Differenceb | | |
| Lower Bound | Upper Bound | |
| av soma area (mm2) | 1 | 2 | -.352 | -.132 | |
| 2 | 1 | .132 | .352 | |
| av no processes | 1 | 2 | -1.533 | -.655 | |
| 2 | 1 | .655 | 1.533 | |
|  |  |  |  |  |  | |
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| Based on estimated marginal means |
| \*. The mean difference is significant at the .05 level. |
| b. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments). |

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| --- | --- | --- | --- | --- | --- |
| **Multivariate Tests** | | | | | |
|  | Value | F | Hypothesis df | Error df | Sig. |
| Pillai's trace | .689 | 22.194a | 2.000 | 20.000 | <.001 |
| Wilks' lambda | .311 | 22.194a | 2.000 | 20.000 | <.001 |
| Hotelling's trace | 2.219 | 22.194a | 2.000 | 20.000 | <.001 |
| Roy's largest root | 2.219 | 22.194a | 2.000 | 20.000 | <.001 |
| Each F tests the multivariate effect of GENOTYPE [1 = WT; 2= A53T]. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | |
| a. Exact statistic | | | | | |

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| --- | --- | --- | --- | --- | --- | --- |
| **Univariate Tests** | | | | | | |
| Dependent Variable | | Sum of Squares | df | Mean Square | F | Sig. |
| av soma area (mm2) | Contrast | .389 | 1 | .389 | 20.824 | <.001 |
| Error | .393 | 21 | .019 |  |  |
| av no processes | Contrast | 7.978 | 1 | 7.978 | 26.815 | <.001 |
| Error | 6.248 | 21 | .298 |  |  |
| The F tests the effect of GENOTYPE [1 = WT; 2= A53T]. This test is based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | | |

**2. REGION[1=SN; 2=VTA; 3=CP]**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Estimates** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | Mean | Std. Error | 95% Confidence Interval | |
| Lower Bound | Upper Bound |
| av soma area (mm2) | 1 | .333 | .046 | .238 | .429 |
| 2 | .313 | .046 | .217 | .408 |
| 3 | .364 | .046 | .269 | .460 |
| av no processes | 1 | 3.703 | .183 | 3.322 | 4.083 |
| 2 | 3.674 | .183 | 3.294 | 4.054 |
| 3 | 3.562 | .183 | 3.181 | 3.942 |

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| **Pairwise Comparisons** | | | | | |
| Dependent Variable | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | Mean Difference (I-J) | Std. Error | Sig.a |
|
| av soma area (mm2) | 1 | 2 | .021 | .065 | .755 |
| 3 | -.031 | .065 | .636 |
| 2 | 1 | -.021 | .065 | .755 |
| 3 | -.052 | .065 | .435 |
| 3 | 1 | .031 | .065 | .636 |
| 2 | .052 | .065 | .435 |
| av no processes | 1 | 2 | .029 | .259 | .913 |
| 3 | .141 | .259 | .592 |
| 2 | 1 | -.029 | .259 | .913 |
| 3 | .112 | .259 | .669 |
| 3 | 1 | -.141 | .259 | .592 |
| 2 | -.112 | .259 | .669 |

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| --- | --- | --- | --- | --- | --- |
| **Pairwise Comparisons** | | | | | |
| Dependent Variable | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval for Differencea | | |
| Lower Bound | Upper Bound | |
| av soma area (mm2) | 1 | 2 | -.114 | .155 | |
| 3 | -.166 | .104 | |
| 2 | 1 | -.155 | .114 | |
| 3 | -.187 | .083 | |
| 3 | 1 | -.104 | .166 | |
| 2 | -.083 | .187 | |
| av no processes | 1 | 2 | -.509 | .567 | |
| 3 | -.397 | .679 | |
| 2 | 1 | -.567 | .509 | |
| 3 | -.426 | .650 | |
| 3 | 1 | -.679 | .397 | |
| 2 | -.650 | .426 | |
|  |  |  |  |  |  | |
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| --- |
| Based on estimated marginal means |
| a. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments). |

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| **Multivariate Tests** | | | | | |
|  | Value | F | Hypothesis df | Error df | Sig. |
| Pillai's trace | .045 | .244 | 4.000 | 42.000 | .912 |
| Wilks' lambda | .955 | .234a | 4.000 | 40.000 | .918 |
| Hotelling's trace | .047 | .224 | 4.000 | 38.000 | .923 |
| Roy's largest root | .044 | .459b | 2.000 | 21.000 | .638 |
| Each F tests the multivariate effect of REGION[1=SN; 2=VTA; 3=CP]. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | |
| a. Exact statistic | | | | | |
| b. The statistic is an upper bound on F that yields a lower bound on the significance level. | | | | | |

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| **Univariate Tests** | | | | | | |
| Dependent Variable | | Sum of Squares | df | Mean Square | F | Sig. |
| av soma area (mm2) | Contrast | .012 | 2 | .006 | .322 | .728 |
| Error | .393 | 21 | .019 |  |  |
| av no processes | Contrast | .098 | 2 | .049 | .165 | .849 |
| Error | 6.248 | 21 | .298 |  |  |
| The F tests the effect of REGION[1=SN; 2=VTA; 3=CP]. This test is based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | | |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **3. GENOTYPE [1 = WT; 2= A53T] \* REGION[1=SN; 2=VTA; 3=CP]** | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | Mean | Std. Error | 95% Confidence Interval |
| Lower Bound |
| av soma area (mm2) | 1 | 1 | .238 | .068 | .096 |
| 2 | .235 | .068 | .092 |
| 3 | .175 | .068 | .033 |
| 2 | 1 | .428 | .061 | .301 |
| 2 | .391 | .061 | .264 |
| 3 | .554 | .061 | .426 |
| av no processes | 1 | 1 | 3.166 | .273 | 2.599 |
| 2 | 3.067 | .273 | 2.499 |
| 3 | 3.065 | .273 | 2.498 |
| 2 | 1 | 4.239 | .244 | 3.732 |
| 2 | 4.281 | .244 | 3.774 |
| 3 | 4.059 | .244 | 3.551 |

|  |  |  |  |
| --- | --- | --- | --- |
| **3. GENOTYPE [1 = WT; 2= A53T] \* REGION[1=SN; 2=VTA; 3=CP]** | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval |
| Upper Bound |
| av soma area (mm2) | 1 | 1 | .380 |
| 2 | .377 |
| 3 | .317 |
| 2 | 1 | .556 |
| 2 | .518 |
| 3 | .681 |
| av no processes | 1 | 1 | 3.733 |
| 2 | 3.634 |
| 3 | 3.632 |
| 2 | 1 | 4.747 |
| 2 | 4.789 |
| 3 | 4.566 |

**Post Hoc Tests**

**REGION[1=SN; 2=VTA; 3=CP]**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Multiple Comparisons** | | | | | |
| LSD | | | | | |
| Dependent Variable | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | Mean Difference (I-J) | Std. Error | Sig. |
|
| av soma area (mm2) | 1 | 2 | .022443832518306 | .064468582924032 | .731 |
| 3 | -.041588594508454 | .064468582924032 | .526 |
| 2 | 1 | -.022443832518306 | .064468582924032 | .731 |
| 3 | -.064032427026759 | .064468582924032 | .332 |
| 3 | 1 | .041588594508454 | .064468582924032 | .526 |
| 2 | .064032427026759 | .064468582924032 | .332 |
| av no processes | 1 | 2 | .020776496369892 | .257136429605512 | .936 |
| 3 | .145155185944660 | .257136429605512 | .578 |
| 2 | 1 | -.020776496369892 | .257136429605512 | .936 |
| 3 | .124378689574768 | .257136429605512 | .634 |
| 3 | 1 | -.145155185944660 | .257136429605512 | .578 |
| 2 | -.124378689574768 | .257136429605512 | .634 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Multiple Comparisons** | | | | |
| LSD | | | | |
| Dependent Variable | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval | |
| Lower Bound | Upper Bound |
| av soma area (mm2) | 1 | 2 | -.111625925080479 | .156513590117091 |
| 3 | -.175658352107239 | .092481163090331 |
| 2 | 1 | -.156513590117091 | .111625925080479 |
| 3 | -.198102184625544 | .070037330572026 |
| 3 | 1 | -.092481163090331 | .175658352107239 |
| 2 | -.070037330572026 | .198102184625544 |
| av no processes | 1 | 2 | -.513967982621549 | .555520975361333 |
| 3 | -.389589293046781 | .679899664936101 |
| 2 | 1 | -.555520975361333 | .513967982621549 |
| 3 | -.410365789416673 | .659123168566209 |
| 3 | 1 | -.679899664936101 | .389589293046781 |
| 2 | -.659123168566209 | .410365789416673 |
|  |  |  |  |  |  |

|  |
| --- |
| Based on observed means. The error term is Mean Square(Error) = .298. |

**Explore**

|  |  |  |
| --- | --- | --- |
| **Notes** | | |
| Output Created | | 06-AUG-2024 08:35:06 |
| Comments | |  |
| Input | Active Dataset | DataSet2 |
| Filter | <none> |
| Weight | <none> |
| Split File | <none> |
| N of Rows in Working Data File | 81 |
| Missing Value Handling | Definition of Missing | User-defined missing values for dependent variables are treated as missing. |
| Cases Used | Statistics are based on cases with no missing values for any dependent variable or factor used. |
| Syntax | | EXAMINE VARIABLES=avsomaareamm2 BY GENOTYPE1WT2A53T /PLOT=BOXPLOT /STATISTICS=NONE /NOTOTAL. |
| Resources | Processor Time | 00:00:00.25 |
| Elapsed Time | 00:00:00.00 |

**GENOTYPE [1 = WT; 2= A53T]**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Case Processing Summary** | | | | | | | |
|  | GENOTYPE [1 = WT; 2= A53T] | Cases | | | | | |
| Valid | | Missing | | Total | |
| N | Percent | N | Percent | N | Percent |
| av soma area (mm2) | 1 | 12 | 33.3% | 24 | 66.7% | 36 | 100.0% |
| 2 | 15 | 33.3% | 30 | 66.7% | 45 | 100.0% |

**av soma area (mm2)**

img.eps

**Explore**

|  |  |  |
| --- | --- | --- |
| **Notes** | | |
| Output Created | | 06-AUG-2024 08:35:57 |
| Comments | |  |
| Input | Active Dataset | DataSet2 |
| Filter | <none> |
| Weight | <none> |
| Split File | <none> |
| N of Rows in Working Data File | 81 |
| Missing Value Handling | Definition of Missing | User-defined missing values for dependent variables are treated as missing. |
| Cases Used | Statistics are based on cases with no missing values for any dependent variable or factor used. |
| Syntax | | EXAMINE VARIABLES=avnoprocesses BY GENOTYPE1WT2A53T /PLOT=BOXPLOT /STATISTICS=NONE /NOTOTAL. |
| Resources | Processor Time | 00:00:00.20 |
| Elapsed Time | 00:00:00.00 |

**GENOTYPE [1 = WT; 2= A53T]**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Case Processing Summary** | | | | | | | |
|  | GENOTYPE [1 = WT; 2= A53T] | Cases | | | | | |
| Valid | | Missing | | Total | |
| N | Percent | N | Percent | N | Percent |
| av no processes | 1 | 12 | 33.3% | 24 | 66.7% | 36 | 100.0% |
| 2 | 15 | 33.3% | 30 | 66.7% | 45 | 100.0% |

**av no processes**

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