Sweave Test Document for Heritability by Group

Joe's BG Temmmam

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Version: 2011V28;

19+ year-olds with amibiguous sibs and Null values recoded as .375.

> x <-rnorm(10)

[1] 0.57394270 -0.25282827 -0.97675737 -0.47666520 -0.83738334 1.49374929

[7] 0.85597354 -0.02435095 -1.17394356 1.51429415

	α	h^2	c^2	e^2	Mean	SD	Skew	.25	.375	.5	.75	1	Total N
Total	7160	0.710	0.050	0.240	-0.03	1.01	-0.03	2206	62	4864	0	28	7160
All FF	1782	0.850	0.040	0.120	-0.04	1.02	0.04	574	12	1186	0	10	1782
All MF	3558	0.650	0.060	0.290	0.01	1.02	-0.06	1110	26	2422	0	0	3558
All MM	1820	0.700	0.020	0.280	-0.07	0.99	-0.03	522	24	1256	0	18	1820

Table 1: Height

	Estimate	Std. Error	z value	$\Pr(> z)$
(Intercept)	3.0445	0.1709	17.81	0.0000
outcome2	-0.4543	0.2022	-2.25	0.0246
outcome3	-0.2930	0.1927	-1.52	0.1285
treatment2	0.0000	0.2000	0.00	1.0000
treatment3	0.0000	0.2000	0.00	1.0000

	Df	Deviance	Resid. Df	Resid. Dev
NULL			8	10.58
outcome	2	5.45	6	5.13
treatment	2	0.00	4	5.13

Now we look at Gaussian data:

One Sample t-test

t = 1.2594, df = 19, p-value = 0.2231

^{[7] 1.2815968 -1.2182136 -0.3996024 0.7517564 -0.5967970 -0.1962042} [13] 2.5385576 0.7041028 1.1901879 -0.4253724 -0.3238622 -1.0783299

^{[19] 2.0731882 -0.7840216}

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alternative hypothesis: true mean is not equal to 0 95 percent confidence interval: -0.1960511 \quad 0.7884443 sample estimates: mean of x 0.2961966
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Note that we can easily integrate some numbers into standard text: The third element of vector \mathbf{x} is 1.41387654617017, the p-value of the test is 0.22313.

Now we look at a summary of the famous iris data set, and we want to see the commands in the code chunks:

> data(iris) > summary(iris)

Sepal.	Length	Sepal.	Width	Petal.	Length	Petal.	Width
Min.	:4.300	Min.	:2.000	Min.	:1.000	Min.	:0.100
1st Qu.	:5.100	1st Qu.	:2.800	1st Qu.	:1.600	1st Qu.	:0.300
Median	:5.800	Median	:3.000	Median	:4.350	Median	:1.300
Mean	:5.843	Mean	:3.057	Mean	:3.758	Mean	:1.199
3rd Qu.	:6.400	3rd Qu.	:3.300	3rd Qu.	:5.100	3rd Qu.	:1.800
Max.	:7.900	Max.	:4.400	Max.	:6.900	Max.	:2.500

Species setosa :50 versicolor:50 virginica :50

> library(graphics) > pairs(iris)

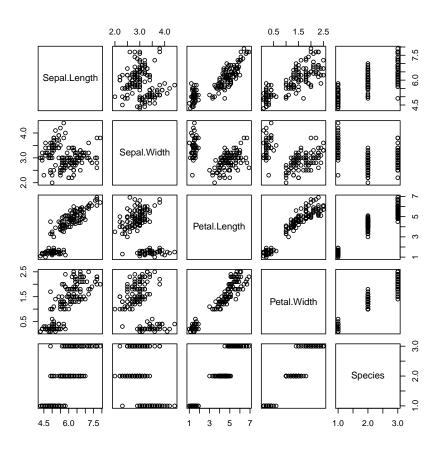


Figure 1: Pairs plot of the iris data.

> boxplot(Sepal.Length~Species, data=iris)

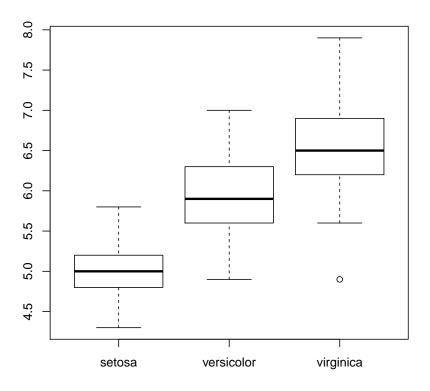


Figure 2: Boxplot of sepal length grouped by species.