$test_tex$

Contents

descr(iris)

Warning: The `validate` argument of `as_tibble()` is deprecated as of tibble 2.0.0.
Please use the `.name_repair` argument instead.

Variables	Total (N=150)	p
Sepal.Lengtl	h	
N	150	$< 0.001^{\text{tt}1}$
mean	5.8	
sd	0.83	
median	5.8	
Q1 - Q3	5.1 - 6.4	
\min - \max	4.3 - 7.9	
Sepal.Width	1	
N	150	$< 0.001^{\text{tt1}}$
mean	3.1	
sd	0.44	
median	3	
Q1 - Q3	2.8 - 3.3	
\min - \max	2 - 4.4	
Petal.Lengtl	1	
N	150	$< 0.001^{\text{tt1}}$
mean	3.8	
sd	1.8	
median	4.3	
Q1 - Q3	1.6 - 5.1	
\min - \max	1 - 6.9	
Petal.Width	L	
N	150	$< 0.001^{\text{tt1}}$
mean	1.2	
sd	0.76	
median	1.3	
Q1 - Q3	0.3 - 1.8	
min - max	0.1 - 2.5	
Species		
setosa	50 (33%)	$> 0.999^{\rm chi1}$
versicolor	50 (33%)	
virginica	50 (33%)	
tt1 Students o	ne-sample t-	-test
chil Cl.	1 1	

^{chi1} Chi-squared goodness-of-fit test

```
descr(
  iris,
  "Species",
  group_labels = list(setosa = "My custom group label"),
  var_options = list(Sepal.Length = list(label = "My custom variable label"))
)
```

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Variables	My custom group label (N=50)	versicolor (N=50)	virginica (N=50)	$ \begin{array}{c} \text{Total} \\ \text{(N=150)} \end{array} $	p
Sepal.Length	1				
N S	50	50	50	150	$< 0.001^{\rm F}$
mean	5	5.9	6.6	5.8	
sd	0.35	0.52	0.64	0.83	
median	5	5.9	6.5	5.8	
Q1 - Q3	4.8 - 5.2	5.6 - 6.3	6.2 - 6.9	5.1 - 6.4	
\min - \max	4.3 - 5.8	4.9 - 7	4.9 - 7.9	4.3 - 7.9	
Sepal.Width					
N	50	50	50	150	$< 0.001^{\rm F}$
mean	3.4	2.8	3	3.1	
sd	0.38	0.31	0.32	0.44	
median	3.4	2.8	3	3	
Q1 - Q3	3.2 - 3.7	2.5 - 3	2.8 - 3.2	2.8 - 3.3	
min - max	2.3 - 4.4	2 - 3.4	2.2 - 3.8	2 - 4.4	
Petal.Length	l				
N	50	50	50	150	$< 0.001^{\mathrm{F}}$
mean	1.5	4.3	5.6	3.8	
sd	0.17	0.47	0.55	1.8	
median	1.5	4.3	5.5	4.3	
Q1 - Q3	1.4 - 1.6	4 - 4.6	5.1 - 5.9	1.6 - 5.1	
\min - \max	1 - 1.9	3 - 5.1	4.5 - 6.9	1 - 6.9	
Petal.Width					
N	50	50	50	150	$< 0.001^{\rm F}$
mean	0.25	1.3	2	1.2	
sd	0.11	0.2	0.27	0.76	
median	0.2	1.3	2	1.3	
Q1 - Q3	0.2 - 0.3	1.2 - 1.5	1.8 - 2.3	0.3 - 1.8	
min - max	0.1 - 0.6	1 - 1.8	1.4 - 2.5	0.1 - 2.5	

F F-test (ANOVA)

```
descr(iris) %>% capture.output(print(.)) %>% knitr::raw_latex()
```

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chi1 Chi-squared goodness-of-fit test

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