Veterinary Epidemiologic Research - 2nd Edition

Errata

Updated: 7 February 2018

First printing (Nov. 2009)

After commencing shipping of the 2nd Edition of Veterinary Epidemiologic Research, we discovered that some of the lines in some of the Figures are printed very faintly (and in some cases are almost invisible). This was a surprise as the Figures had all printed perfectly well when the galley proofs were examined. In total, 20 figures are affected to some degree. To obtain a 2 page sheet with all of these figures printed correctly, go to: www.upei.ca/ver/errata

In addition, the following errors were fixed with the 2nd printing Errors listed for the 2nd printing had not been detected at the time of the 1st printing so also apply to this printing.

Page	***Location***	***Description***
49	last paragraph of Ex. 2.5	should say "Consequently, you would require 1,370 (685*2) animals with 685 being ..."
252	near the end of the 2nd paragraph	" … all cases of uterine cancer ..."
253	2nd line	" … the sample OR will be more than the source population OR. "
290	Equation 13.8	insert "=" sign before Σ
291	1st row of top table	replace 118 with 18
296	Title of Example 13.10	"Detection of ..."
368	Fig 15.1	Add arrow between twins and retained placenta (to agree with what is stated in text)
610	Fig 23.1 caption	Fig. 23.1 Profile plot (left) and mean plot (right) for growth of salmon; fish with jaw deformities shown with dashed lines.
620	2nd last matrix element	σ_{34}

Second printing (Jan 2010)

The following are the errors in the 2nd Edition of Veterinary Epidemiologic Research that have been identified as of the date shown above.

Page	***Location***	***Description***
11	7th line	*Histophilus somni* (Hs)
13	Example 1.2	switch the 0s and 1s in the BRSV column and the values in the "Number Diseased" column then become 720, 0 1680, 1120, 0, 0, 2520, 0
45	4th last line in Ex 2.4	$(0.0191/0.0080)^2=5.7$
62	3rd paragraph	delete this paragraph (it has already been stated)
95	Fig 5.2 caption	replace "reduced major axis" with "std. dev. ratio line"
138	Eq 6.3 last line	$=(a_1*b_0)/(a_0*b_1)$

138	Eq 6.4 last line	$=(a_1*b_0)/(a_0*b_1)$
153	Fig 7.1	replace Exploratory with Explanatory
231	Eq 11.1	should be $VE_d = \frac{(I_{nv} - I_v)}{I_{nv}}$
234	Ex 11.10 - last equation	replace "29-12" with "29-10.5"
276	first bullet point	replace with "in case-control studies, it is not possible to estimate the effect of the matched factor(s) on the outcome because its distribution has been forced to be identical in the outcome groups. We can, however, investigate whether the matching factor acts as an effect modifier (*ie* if it produces interaction with the exposure of interest). "
283	Ex 13.4, 7th last line	" ...risk of -brd- in non-exposed ... "
332	Eq 14.9	numerator of F-statistic is incorrect, replace with $F_{\text{group}} = \frac{\left(\frac{\text{SSE}_{\text{red}} - \text{SSE}_{\text{full}}}{\text{df E}_{\text{red}} - \text{df E}_{\text{full}}}\right)}{\text{MSE}_{\text{full}}} \sim F([\text{df E}_{\text{red}} - \text{df E}_{\text{full}}], \text{df E}_{\text{full}}) \text{ under } H_0$
338	Ex 14.7	The constant in the column based on hierarchical coding is not what we would expect with 0/1 coding of these variables. The Stata "add-on" program -xi3- was used to create these hierarchical variables and it codes them so that so that the sum of all values within each of the new hierarchical variables equals 0. This has no impact on the coefficients but changes the constant.
340	3rd paragraph	delete this paragraph (it has already been stated)
346	Ex 14.12, last line	23+6+1=30
357	Eq 14.18 last line	replace dfE with dfE-1 , and replace 0.017 with 0.019
358	2nd line after Eq 14.20	add a set of () " … or $2\sqrt{((k+1)/n)}$
363	1st sentence of paragraph 3	replace sentence with "With an AR1 structure, correlations have an exponential decay over time (the structure of the decay is more complex for AR2, AR3 *etc*). "
370	last line pgph 1, last line on page	references top 13.12.8 and 13.12.7 should be 13.11.8 and 13.11.7 respectively
371	first word in Example 15.1	replace "Three" with "Four"
371	Ex 15.1, 3rd line of last pgph	replace (0.63-0.73) with (0.72 - 0.87)
373	Fig 15.2	caption should be "Fig 15.2 Multiple correspondence analysis of risk factors for milk bacteria counts (case-control)"
376	last line 1st pgph	Fig 15.3
377	lines 6 and 13	references are to Fig 15.6 and 15.5 respectively
381	Ex 15.4 - last line of 3rd table	the two powers are -.5 and 0
407	Ex 16.4, 2nd last line	change 30% to 40%

420	Ex 16.12, top table	last column should be labeled “leverage”
423	Ex 16.14, 1st line of last pgph	change “set 1” to “set 23”
437	1st pgph	“ … log odd of being at or above … of being below ...”
463	Ex 18.7, 4th last line	change “higher” to “lower”
489	Ex 19.6	last equation is for L_2 (not L_1), 3rd last line should start with “The product of ...”
504	5th last line	“19.17” (not 19.16)
515	Ex 19.22, last line	“19.21” (not 19.22)
556	2nd line	replace Eq 21.2 with Eq. 21.3
573	14th line from bottom	replace 3.84 with 1.92
574	Ex 21.10	There was an error in the Stata program code which generated this example. to correct the code, replace line 275 of the -do- file with: xi: xtmixed y shsize heifer i.season sdim ||herdid: , var ml A revised Example is attached at the end of this Errata
583	3rd line	replace $\pm 1.96\sigma h$ with $\pm 1.96\sigma_h$
583	2nd paragraph - last line	“& Skrondal (2008), Section 6.2.2”
589	4th line	replace Eq. 22.8 with Eq. 22.2
589	1st line of Section 22.4.3	“Section 22.3”
615	6th - 7th line	“repeated measures ANOVA approach”
628	Ex 23.7 - last line 2nd pgph	replace 2.121 with 2.141
628	Ex 23.7 - 12th line from bottom	replace “latent class” with “latent variable”
632	Ex 23.9 - last line in table	add # to the values 21084.62 and 21101.43 (to reference to footnote)
659	Ex. 24.8, 5th line	switch u_j and u_j^*
670	7th line	replace “area” with “areal”
677	Ex. 25.6 - heading	replace 65th with 75th
Ch 29	throughout	year of publication text by Rothman, Greenland and Lash should be 2008 (not 1998)

A number of references were missed when generating the chapter specific reference lists. They are shown here.

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Example 21.10 Box-Cox analysis for somatic cell count data

data=scc40_2level

The data contain n=2,178 observations and the mean (natural) logarithmic cell count is 4.757. The following table and graph give a Box-Cox analysis:

λ	1	0.5	0.33	0.25	0
ln(L) for $Y^{(\lambda)}$	-17247.28	-9807.27	-7585.75	-6532.35	-3604.68
pl(λ) from(21.15)	-17247.28	-140987.63	-14493.24	-14302.89	-13965.84
λ	-0.10	-0.25	-0.33	-0.5	-1
ln(L) for $Y^{(\lambda)}$	-2530.05	-1014.68	-219.64	1282.26	5236.52
pl(λ) from(21.15)	-13926.84	-13965.57	-14033.58	-14258.82	-15484.91

The table and figure indicate the optimal value of λ to be close to, and slightly less than, zero, but a

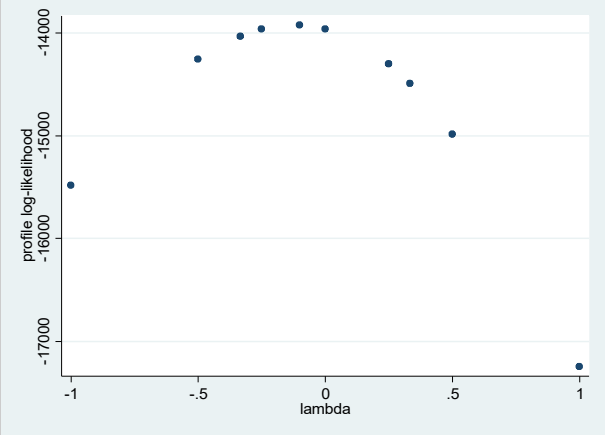

Fig. 21.5: Profile-likelihood function for Box-Cox analysis of SCC data

95% CI for λ does not include zero; the large number of lowest-level observations causes the CI to be very narrow. With the optimal transformation so close to the log-transformation, the Box-Cox analysis supports our choice of analysing the log somatic cell counts, in the sense that no power transformation improves the compliance with model assumptions substantially. Analysis of the power transformed (λ=-0.10) SCC values instead of -lnscc- reduced the skewness of the cow-level residuals, but did not substantially change the inference (results not shown).

Third printing (2015)

The following are the errors in the 3rd printing of the 2nd Edition of Veterinary Epidemiologic Research that have been identified as of the date shown above.

Page	***Location***	***Description***
13	Example 1.2	change the values in the "Number Diseased" column to 720, 0 1680, 1120, 0, 0, 2520, 0
357	2nd line	should read " … small percentage (0.3%) of … "