Eurocat

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Special Report:

Special Report:

Using Capture-Recapture Methods to Ascertain Completeness of a Register: Case Study and Methodological Considerations

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This report has been prepared as one of a series of EUROCAT publications addressing the measurement of data quality in congenital anomaly registers. It uses as a case study a register of Anophthalmia/microphthalmia in England, which is not a member of EUROCAT. For further information about publications related to capture-recapture analysis in EUROCAT registries, contact eurocat@ulster.ac.uk.

Summary

We used capture-recapture methods to estimate the completeness of a register of congenital malformations of the eye. Given five primary sources of cases, we used loglinear models, along with simpler methods on collapsed data. Primary choice of model was based on minimum Bayes Information Criterion (BIC). Our optimal model estimated a total of 577 cases, which given 382 found implies 67.2% completeness (95%CI 55.7-76.4). However, there was evidence that true uncertainty is greater than that reflected in confidence interval. Completeness was much higher for severe cases (the focus of the register: 85.4%; CI 76.9-92.1) and those surviving for more than one year (83.7%; CI 74.0-93.2). Cases were also more completely ascertained in less densely populated areas – a likely partial cause of the excess case rate found previously in rural areas. We found application of the methods challenging, and requiring close collaboration between epidemiologists responsible for data collection and the statistician. We conclude that application of these methods has had some but limited use in informing interpretation of these data, but possibly not worth its considerable cost.

Background

A register of congenital anomalies of the eye – anopththalmia and microphthalmia –among births in England 1988-94, was assembled as the basis for a study of geographical variation and clustering (Dolk 1998). Investigators were aware that the register was likely to be incomplete, but unsure by how much. The study we report here, suggested by a DH reviewer, uses capture-recapture methods to make estimates of the number of cases missed by the register, including by specific subgroups (such as those with severe or mild anomalies).

Completeness of the registry is of interest because: (a) a large number of missed cases would increase the possibility of selection bias in studies carried out using registry data; (b) knowledge of the absolute prevalence of this anomaly would help comparisons between places; (c) identification of sub-groups more or less completely ascertained would allow improved ascertainment in the future and focused analyses less subject to selection bias. We also sought through this exercise to gain insight on the potentials and limitations of capture-recapture methods in public health more generally, about which there has been controversy (Anonymous 1995a and 1995b, Cormack 1999, Hook and Regal 1999).

Project Aims

- To assess the completeness of case ascertainment in the Anopththalmia Register by use of capture-recapture methods
- To assess differences in the completeness of ascertainment of different case types, according to severity, associated abnormalities and survival
- To consider the implications of the results for the use and interpretation of data from the Anophthalmia register
- To consider the implications of the results for the use of capture-recapture methodology as a tool in assessing the completeness of registers.

Methods

The register

The register sought to cover all births in England between 1988-94 (4,570,350 live and stillbirths, and 4,538,790 live births). Cases could be live births, stillbirths or terminations of pregnancy following prenatal diagnosis of congenital anomaly.

The register was established as a two stage process with data collection starting in 1994. In the first stage of case ascertainment we sent requests to multiple sources of information for notification of cases, asking for minimal identification details including name, postcode, whether the child had anophthalmos or microphthalmos, and the names of clinicians involved in the care of the child. The sources were:

1. Databases kept by national referral centres. (Moorfields and the National Artificial Eye Service).
2. Pediatricians. (Including pediatric surgeons and specialist clinicians.)

3. Medical genetics departments.
4. Districts (request sent to Director of public health in each district).
5. Other national (parents, miscellaneous clinicians, pathologists, death certificates)
6. Regional registers (Oxford, North-West Thames, Northern – covering approx 25% of the population)

All of these primary sources except the last had the potential to identify cases across England.

In the second stage notifications received were followed up, primarily by enquiry to treating ophthalmologists, to identify further details and to clarify whether the case met the detailed criteria for inclusion in the register. At the same time the ophthalmologists were asked to provide details of any cases under their care not identified by the stage one sources. We refer to the ophthalmologists as a supplementary source. There was no opportunity for overlap between cases identified by ophthalmologists and by other sources.

Cases were classified into mild and severe, according whether axial length was less than 15 mm at birth. Since there is no standard cut off point between mild microphthalmos and the normal eye, we anticipated that mild microphthalmos would be less completely reported. This has been discussed in more detail elsewhere (Busby, Dolk et al. 1998; Dolk, Busby et al. 1998)

At the time of undertaking this analysis, the register included 414 non-chromosomal cases. This is fewer than the 449 reported on by Dolk et al (Dolk, Busby et al. 1998), because information received since that report showed that 35 cases originally included did not in fact meet the criteria for inclusion (15 were chromosomal, 11 were holo/a-prosencephaly, and 9 did not have anophthalmia at all).

Statistical methods

"Capture-recapture" methods seek to identify the number of cases missing from a register and hence the total in a population from information on the numbers of cases ascertained from more than one source. The term comes from studies of wild animals, of which some are caught and tagged ("captured") and then in another exercise others are caught. From the numbers of tagged animals "recaptured" it is possible to infer, under assumptions, the total number in the wild. The use of the method for epidemiological studies such as this has quite recently been reviewed (Hook and Regal 1995).

At its crudest the method assumes complete independence of sources (that a case is found from source A makes it no more or less likely to be found from source B). For example, suppose source A find 150 cases and source B finds 200 cases, with 100 of cases common to both. We can describe the data thus:

		Found by source A	
		Yes	No
Found by source B	Yes	100	100
	No	50	*X*

If identification by sources A and B are independent, then because 50% of cases found by B are not found by A, we expect that 50% of those not found by B will also not be found by A. To make this true the number of cases found by neither source (x) would have to be 50. This is our estimate of missing cases, and the estimated total number is thus 50+50+100+100 =300.

Unfortunately the assumption of independence of sources is unreasonable in most circumstances – certainly for the anophthalmia register. If there are more than two sources, it is possible by using log-linear models to allow for some dependence between the sources. With three sources pair-wise dependence can be accommodated, with four sources up to 3-way dependence can be accommodated, and so on. Assuming maximum dependence allowable, however, leads to estimates with very wide confidence intervals. Thus, it is necessary to seek a compromise between this model and the usually implausible complete independence. Estimates can be sensitive to just how this compromise is made (model choice).

A quite extensive literature explores various approaches to model choice, along with other issues in capture-recapture analysis. We have informed our approach by the review cited above (Hook and Regal 1995), and several contributions to a published debate (Chang, LaPorte et al. 1999; Cormack 1999; McGilchrist 1999), in particular tried to follow the fifteen recommendations proposed by Hook and Regal in that debate (Hook and Regal 1999; Hook and Regal 2000). Specifically, we fitted a wide range of models as follows:

- the five models equivalent to collapsing to two groups of sources: one Vs all others
- five main effects only (i.e. assuming independent sources),
- each two-way interaction individually (ten models)
- all ten two-way interactions together
- all ten two-way and ten three-way interactions together
- The twenty models identified by by entering each two-and three-way interaction in order of incremental significance (forward selection).

From these we emphasise estimates from the model which minimised Bayes' information criterion (BIC – Draper variant), but report also report that which minimises Akaike's information criterion (AIC), and the range of estimates from other models. We also fitted other models to investigate sensitivity to the approach chosen.

Results

Because live births comprised the great majority of cases identified (382/414), and it was expected that identification of cases ("catchability") would be quite different in live births and others (stillbirths, terminations, and 3 unknown whether born live), we confined our main analysis to these 382 cases.

Table 1 shows the proportion of these cases identified by each of the five primary sources (315 cases) in total), and additionally by the regional registers (25) and ophthalmologists(42). Because the registers were not national and the ophthalmologists were a supplementary source (consulted only in the second stage) the formal capture-recapture analysis was confined to the 315 identified by the five primary sources. The additional 67 cases were nevertheless discounted from the estimated numbers of missing cases in calculation of percentages found, as described

below. A table of numbers of cases identified by each combination of sources is given in Appendix table A1.

Following Hook and Regal (1995), we begin by estimating missing cases by collapsing the data to two groups of sources (Appendix Table A2), which gave estimates from 131-172. We also made estimates considering only overlaps between pairs of sources, which ranged from 0 to 167. These simple estimates are underestimates if identification by one source is positively associated with identification by another, as often found in data of these sort ((Hook and Regal 1995)), and confirmed by loglinear analyses of our data.

To avoid the expected bias in the two-source estimates, our main estimate is from the 5-source log-linear model, with model choice by minimum BIC. This estimated 262(95% CI 185-371) cases missing from primary sources, thus a total of 577 (500-686). Adding the 42 cases found by the opthalmologists and the 25 found in the three registries to the 315 found from the primary sources gives a national ascertainment rate of 382/577=66.2% (95%CI 55.7-76.4). The optimal model by BIC was that including all terms significant at $p<0.10$. This comprised, as well as main source effects, interactions between sources 1-2, 2-3, 3-4, 1-2-3, and 1-2-5.

The confidence intervals above do not reflect uncertainty in model choice. The AIC resulted in the same model, but the full range of 5-source loglinear analyses (Appendix Table A3) gave estimates ranging from 135 (95%CI 101-180) to 483(95%CI 276-846). The former model included only the interaction for sources 4 and 5, and the latter was the model with all two-way interactions. Both performed poorly by BIC and AIC. The lowest and highest confidence limits (39 and 2146) were both for the model including all interactions up to 3-way, which again performed poorly by BIC. Models with BICs and AICs within 5 of the optimal gave estimates of missing cases ranging from 190 to 315, with 95% confidence limits ranging from 140 to 480.

Considering subgroups separately

We used loglinear analyses to estimate missing and total cases in subgroups. For each sub-group we used the same approach as described for the whole group above, but combined source groups with the “other” category so as to avoid any group reporting less than ten cases, as we found such minor sources led to very imprecise estimates. Results are summarised in table 2. Note that severity was not ascertained for 42 cases, and survival for 15. Because the registry was set up to study mainly “severe” cases we repeated each analysis restricting to this group.

Not surprisingly, estimated ascertainment was much more complete in severe (85.4%) than mild cases (35.0%), and in those that survived above one year (although the estimate for those dying was very imprecise, even by the optimistic nominal CI). The greater ascertainment of surviving cases was also apparent when restricting attention to severe cases. There was little difference in estimated completeness in births with and without other major abnormalities.

Cases were divided by population density of ward of residence into “more dense” (quintiles 1-2) and “less dense” (other). Estimated completeness of case finding was considerably higher in less than more densely populated wards (93.2% Vs 58.9%). This was also so for severe cases (100% Vs 79.5%). There was little difference overall in completeness in more and less deprived areas, defined similarly using Carstairs index of deprivation in wards (“less deprived”=quintiles 1-3. “more deprived”=other), although severe cases were somewhat better ascertained in less deprived wards.

As well as being of interest in their own right, summing these sub-group estimates (“total known” on table) provides alternative estimates to total ascertainment, although because there

were some cases with missing values in the subgroup-defining variables, these suffer from additional source of uncertainty. Completeness estimated by this method was higher with stratification into all groups except severe/mild. Uncertainty in these estimates (not calculated formally) is likely to be somewhat greater then for the unstratified estimate, which required fewer parameters to be estimated.

Special analysis in registry regions

A special analysis of the cases found by registries in their regions allowed us to make an independent estimate of cases missing there. In these regions, the registers identified 48 cases while 52 were identified by the primary national sources, with an overlap of 23 (77 in total). An assumption that the registers were independent of other sources in ascertaining cases leads to an estimate of 25X29/23=32 (95% CI 16-62)) cases in regions covered by registries found by neither the registries nor the primary national ascertainment. This is out of an estimated total of 77+32=109, thus 29.4% (32/109) are estimated as missed by the primary sources and the registries. As a further eight cases were supplemented by the opthalmologists in stage 2, this reduces to 24/109=22.0% missed, or 78.0% (95%CI 61.2-91.4) completeness of ascertainment. Similar calculations lead to estimates of completeness of ascertainment of severe cases in regions covered by registries of 89.4%(70.0-100).

To take the experience in registry areas as an alternative indicator of the number missing elsewhere and hence across the country, we need to assume that the proportion of total estimated cases found by primary national sources in registry areas (52/109=47.7%) applies elsewhere, where 262 cases were found by primary national sources (315-53). This yields an estimate of a further 287 missed by primary sources, or 287-34-1=252 missed after subtracting those 34 supplemented by ophthalmologists, and 1 supplemented by the registries (presumably by someone who had moved from a registry region). Adding this to the estimate for the registry areas, we estimate a total missing of 252+24=276, out of an estimated total (found and missed) of 382+276=658 hence a completeness of 58.1% (382/658). This estimate of completeness is slightly lower than that estimated from the loglinear analysis of the primary national sources reported above (66.2%). Although we have not calculated a formal uncertainty interval, the small number of cases in the registry areas would suggest considerable uncertainty.

Sensitivity to source grouping

We considered the sensitivity of results to specification of source groups by reanalysing the 315 cases found by the five primary sources after collapsing these five to 4,3, or 2 groups of sources, in all possible ways (10, 25, and 15 respectively). Recall that five-source minimum-BIC estimate of cases missed by primary sources was 262. Two source estimates ranged from 131 to 203 (median 159). As discussed above, two-source estimates are expected to be spuriously low. Four source estimates ranged from 168 to 360 (median 216). However, the three-source estimates were more variable , some being very high (range 132-1171, median 168). The high estimates were from combinations for which the minimum BIC criterion selected the “saturated” model with all two-way interactions (5/25 of the total source combinations). Nominal confidence intervals in these estimates were very wide (eg 204-1278 for the lowest of them – 511). Estimates from three source groups based on minimum AIC were even more variable, and high on average (median 585), with 16/25 selected models including all two-way interactions. The variability of three-source estimates, especially by AIC, was reduced by adding 1 to counts

of “2 hit” cells, as a correction to known biases in “saturated” models (Hook and Regal 1995). (BIC: 3/25 models saturated, 130-997 median 155; AIC: 12/25; 130-997, median 248.)

Simpler approaches

A more informal estimate was made (Busby; submitted PhD thesis) based on comparing survival in these cases to that in registries more exhaustively ascertained. Survival in our data was about 70%. In registries with prospective or other more exhaustive ascertainment survival rates ranged from 50-64% ((Clementi, Turolla et al. 1992)Vrijheid personal communication). Under the assumption that surviving cases are fairly completely ascertained in all registers, and survival rates in a complete register are 50%, we can calculate that the UK anophthalmia register must be missing 30% of non-surviving cases.

Simpler approaches also identified the more and less completely ascertained subgroups. For example, the proportion of cases identified by at least two sources provided very similar rankings of subgroups as did our “best” estimate of proportion of cases found (Spearman correlation 0.97; proportions identified by >1 source for total group and first 10 sub-groups mentioned in table 2: 53.7,46.6,60.7, 71.7,49.2,54.4,52.9,57.1,40.3,51.4,50.7). However, this and other simpler approaches depend on assumptions which will may not be met more generally.

Discussion

The estimated 66% overall completeness of the overall registry is very similar to the more informal one (70%) described above. The better ascertainment of severe cases (81.4%) and those that survived (83.7%) confirmed expectation. The slightly poorer ascertainment of cases with other abnormality present was less expected. However, a likely reason for this is the low proportion of those with major abnormalities who survived one year (70.1% Vs 97.8%).

Uncertainty

How far should these estimates be trusted? Even by the spuriously narrow nominal confidence intervals, they are subject to considerable uncertainty. To include the additional uncertainty from model choice we look at the range of estimates made from different models. The highest upper confidence limits of cases missing from primary sources (with the exception of those from models with very large numbers of interaction terms, and the anomalous estimates from three source groups –discussed below) were about 500, which gives a lower bound of about 45% completeness. At the other extreme, few estimates gave lower confidence limits below 100, which (on discounting the 67 found by supplementary sources) gives an upper bound of about 95% completeness. Thus a more cautious uncertainty interval informed by these results is 45%-95%.

The higher completeness of severe and longer surviving cases seems unlikely to be an artifact, especially given the plausibility of these findings. However, true uncertainty in the higher completeness in these subgroups is greater than suggested by the nominal confidence intervals. Similar reasoning to that above for cases overall suggest a cautious uncertainty interval of around 55-95%.

Implications

The implication of there being this order of missing cases depends on the use to which the register is put. Clearly if rates of anophalmia as identified by this register are to be compared with those in other registers, relative completeness of this and the other registers must be considered. Even quite large differences (say up to 20%) would be rather plausibly explained by variations in completeness. For severe anophthalmia, comparisons would be more secure. The primary motivation behind the creation of this register, however, was to compare rates in subgroups within it, and to investigate whether there was local clustering. For these purposes the critical question is whether completeness varies across the sub-groups to be compared, and geographically. More complete ascertainment in wards of lower population density, suggested in these analyses, would cause a spurious excess risk in less populous areas. An excess in areas of very low population density was indeed found (Dolk, Busby et al. 1998), although its specific pattern did not closely follow what would be expected from an artifact due to differential ascertainment. The excess was greater for severe than mild anophalmia, although the difference in ascertainment was greatest for mild cases. The excess was predominantly in the quintile of lowest population density, but to preserves sufficient numbers for capture-recapture analysis, we could only compare completeness in two groups, comprising the three lowest and two highest quintiles. Nevertheless, the finding of variability in completeness by population density does diminish the evidence for a truly higher risk in rural areas.

The usefulness of capture-recapture methods to evaluate completeness of disease registers

Some authors (Anonymous 1995b; Anonymous 1995a) are enthusiastic over the potential of capture-recapture methods in public health, suggesting in particular that they can provide information on disease rates without costly exhaustive surveys. However others (Cormack 1999) question whether, given the substantial uncertainties around capture-recapture estimates, they are can provide useful results. The uncertainty surrounding the estimates we made is indeed considerable, perhaps improving little on what informed investigators would have guessed from informal arguments. Nevertheless, the strongly suggestive findings of greater completeness for severe and surviving cases, though not unexpected, do reassure investigators using these data, and consumers of their research, that problems due to missing cases are likely to be minor in these groups.

For the uses to which this register has been put, and surely quite frequently in epidemiology, the main concern was whether there were differences in completeness over groups to be compared. The standard methods we used did allow this, but it may be that methods more focussed on such comparisons would have allowed clearer conclusions. For example overall log-linear models with an indicator for subgroup would enable inference on differences in completeness in sub-groups. With some but not total overlap of parameters in sub-groups greater power could be achieved. We found little guidance in the extant literature on the application such models in this context.

The striking difference between results for three source-group models using BIC for model choice compared to those using AIC gives cause for some concern. Our choice of BIC was based on Hook and Regal's comment ((Hook and Regal 1995)) that BIC had preferable theoretical properties.

We did not find learning to use the method a trivial undertaking. It took an experienced epidemiological statistician about a month to become familiar with the methods and write

software (in STATA) to apply them. (This process would have been shortened if we had found extant specialist software.) To identify an appropriate way to apply the methods to these data required repeated discussions between the epidemiologist who knew detail of the data collection, and the statistician. The cost of making the estimates was thus considerable.

Conclusions

- The anophthalmia register identified severe cases and those which survived a year quite completely (>80% found), but mild cases and those which died sooner much less so.
- There was some evidence for more complete ascertainment in wards of lower population density, which would explain some though not all the rural excess noted by Dolk et al 1998.
- The capture-recapture approach yielded useful though uncertain estimates at the cost of considerable effort. Some of the key conclusions were also suggested by simpler approaches.

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Table 1. Proportions of cases identified by each source group

Source	Numbers (%)				
PRIMARY	All	Severe	Mild	With other abnormality	Survived 1 year
National referral centres	85(25.3)	75(34.1)	10(8.6)	42(22.5)	85(30.3)
Pediatricians	114(33.9)	88(40.0)	26(22.4)	74(39.6)	93(30.9)
Medical genetics departments	38(11.3)	32(14.5)	6(5.2)	29(15.5)	31(11.4)
Districts	92(27.4)	61(27.7)	31(26.7)	45(24.2)	83(29.0)
Other	103(30.7)	88(40.0)	13(12.9)	64(34.2)	77(27.0)
TOTAL PRIMARY	315(82.5)	201(90.1)	80(68.4)	167(86.5)	251(81.8)
ADDITIONAL					
Opthalmologists*	42(11.0)	13(5.8)	25(21.4)	8(4.1)	1(0.3)
Regional registries*	25(6.5)	9(4.0)	12(10.3)	18(9.3)	6(1.0)
TOTAL	382(100)	223(100)	117(100)	193(100)	307(100)

* cases identified in addition to those from source listed above them.

Table 2. Estimates of missing and total cases in sub-groups

Group	Found				Estimated missing from primary sources (nominal 95%CI)	Estimated total	Percent found
	Total	Primarys ources	Supplementary sources				
			ophthal	regional registry			
	a	b	c	d	e	g=b+e	f=a/g
All	382	315	42	25	262(185-371)	577	66.2(55.7-76.4)
By severity							
Severe	223	201	13	9	60(41-89)	261	85.4(76.9-92.1)
Mild	117	80	25	12	254(114-565)	334	35.0(18.1-60.3)
total known	340	281			314	595	57.1
By survival							
died in 1 year	60	53	1	6	56(0-143)	109	55.0(30.6-100)
survived 1 year	307	251	39		116(82-164)	367	83.7(74.0-93.2)
total known	367	304			112	476	77.1
By presence of other abnormality							
Present	193	167	8	18	91(59-142)	258	74.8(62.5-85.4)
Absent	189	148	34	7	92(59-143)	240	78.8(64.9-91.3)
total	382	315	42	25	183	489	76.7
By population density							
Higher	231	192	26	13	200(129-310)	392	58.9(46.0-72.0)
Lower	124	99	14	11	34(19-64)	133	93.2(79.5-100)
total	382	291	40	24	234	525	67.6
by SES							
more deprived	148	118	20	10	70(44-110)	188	78.7(64.9-91.4)
less deprived	205	171	20	14	77(57-117)	248	82.7(71.2-89.9)
					147	437	81.0
Severe only: By survival							
died in 1 year	46	40	1	5	30(11,81)	70	65.7(38.0,90.2)
survived 1 year	174	159	11	4	37(24,58)	196	88.8(80.2,95.1)
total known	220	199	12	9		266	82.7
By presence of other abnormality							
Present	131	121	2	8	69(38,124)	190	68.9(53.5,82.4)
Absent	92	80	11	1	37(19,72)	117	78.6(60.5,92.9)
total	223	201	13	9	106	307	72.0
By population density							
Higher	128	119	6	3	67(39,113)	186	68.8(55.2,81.0)
Lower	83	72	6	5	11(6,22)	83	100(88.3,100)
total	211	191	12	8	78	269	78.4
by SES							
more deprived	88	78	7	3	38(20,71)	116	75.9(59.1-89.8)
less deprived	122	112	5	5	26(15,164)	138	88.4(78.2,96.1)

Appendix Supplementary tables

Table A1/ Full data listing:

	hosps	ped	genetics	distrs	other	count
1.	0	0	0	0	0	(missing)
2.	0	0	0	0	1	55
3.	0	0	0	1	0	42
4.	0	0	0	1	1	8
5.	0	0	1	0	0	14
6.	0	0	1	0	1	2
7.	0	0	1	1	0	3
8.	0	0	1	1	1	0
9.	0	1	0	0	0	55
10.	0	1	0	0	1	11
11.	0	1	0	1	0	10
12.	0	1	0	1	1	6
13.	0	1	1	0	0	7
14.	0	1	1	0	1	2
15.	0	1	1	1	0	2
16.	0	1	1	1	1	2
17.	1	0	0	0	0	39
18.	1	0	0	0	1	12
19.	1	0	0	1	0	14
20.	1	0	0	1	1	4
21.	1	0	1	0	0	1
22.	1	0	1	0	1	0
23.	1	0	1	1	0	2
24.	1	0	1	1	1	0
25.	1	1	0	0	0	5
26.	1	1	0	0	1	8
27.	1	1	0	1	0	1
28.	1	1	0	1	1	2
29.	1	1	1	0	0	2
30.	1	1	1	0	1	4
31.	1	1	1	1	0	0
32.	1	1	1	1	1	2
total						315

Table A1(a) Distribution of number of sources indentifying cases.

nhits	Freq.	Percent	Cum.
1	205	65.08	65.08
2	73	23.17	88.25
3	27	8.57	96.83
4	8	2.54	99.37
5	2	0.63	100.00
Total	315	100.00	

Table A2 Estimates obtained by collapsing data to two sources, one source Vs all others combined.

Source*	Estimated cases (95%CI) missing	total
hosp	150(98-30)	465
ped	168(114-48)	483
genetics	131(69-51)	446
distrs	163(107-48)	478
other	172(117-53)	487

Table A3. Five-source estimates

Model*	deviance	df	AIC	BIC(D)	estimated cases missing (95%CI)	total
(main effects only)	55.6	25	5.6	-42.3	138(106-180)	453
i12	55.5	24	7.5	-38.5	136(102-181)	451
i13	55.0	24	7.0	-38.9	141(108-186)	456
i23	43.8	24	-4.2	-50.1	156(118-205)	471
i14	54.1	24	6.1	-39.9	147(110-194)	462
i24	55.5	24	7.5	-38.4	137(102-182)	452
i34	55.1	24	7.1	-38.8	141(107-185)	456
i15	51.9	24	3.9	-42.0	154(115-205)	469
i25	53.1	24	5.1	-40.8	153(114-205)	468
i35	55.5	24	7.5	-38.5	140(106-184)	455
i45	55.4	24	7.4	-38.6	135(101-180)	450
all two-way	19.2	15	-10.8	-39.5	483(276-846)	798
all 2 and 3-way	3.1	5	-6.9	-16.5	290(39-2146)	605
Adding variables sequentially by forward selection						
+ i235	42.5	24	-5.5	-51.5	158(120-208)	473
+ i125	30.2	23	-15.8	-59.9	190(142-255)	505
+ i23	24.7	22	-19.3	-61.4	203(150-274)	518
+ i245	20.5	21	-21.5	-61.7	227(165-313)	542
+ i14	16.9	20	-23.1	-61.4	253(180-354)	568
+ i124	11.7	19	-26.3	-62.7	262(185-371)	577
+ i123	9.8	18	-26.2	-60.7	265(187-374)	580
+ i15	7.9	17	-26.1	-58.7	291(200-423)	606
+ i34	6.1	16	-25.9	-56.5	307(209-451)	622
+ i35	5.0	15	-25.0	-53.7	293(198-434)	608
+ i24	4.3	14	-23.7	-50.5	315(205-483)	630
+ i12	3.9	13	-22.1	-47.0	291(178-476)	606
+ i134	3.8	12	-20.2	-43.2	291(178-476)	606
+ i13	3.5	11	-18.5	-39.5	280(167-469)	595
+ i345	3.4	10	-16.6	-35.8	287(169-486)	602
+ i135	3.2	9	-14.8	-32.0	292(170-499)	607
+ i145	3.1	8	-12.9	-28.2	292(171-500)	607
+ i234	3.1	7	-10.9	-24.3	293(170-508)	608
+ i45	3.1	6	-8.9	-20.4	291(147-575)	606
+ i25	3.1	5	-6.9	-16.5	290(39-2146)	605

* interaction terms indicated by “i” followed by source numbers, for example i245 is the 3-way interaction between sources 2, 4, and 5.