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1	Risk factors	for bovine	respiratory	disease in	n Australian	feedlot cattle	Use of a
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- 2 causal diagram-informed approach to estimate effects of animal mixing and
- 3 movements before feedlot entry
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21 Abstract

22 A nationwide longitudinal study was conducted to investigate risk factors for bovine 23 respiratory disease (BRD) in cattle in Australian feedlots. After induction (processing), cattle 24 were placed in feedlot pens (cohorts) and monitored for occurrence of BRD over the first 50 25 days on feed. Data from a national cattle movement database were used to derive variables 26 describing mixing of animals with cattle from other farms, numbers of animals in groups 27 before arrival at the feedlot, exposure of animals to saleyards before arrival at the feedlot, and 28 the timing and duration of the animal's move to the vicinity of the feedlot. Total and direct 29 effects for each risk factor were estimated using a causal diagram-informed process to 30 determine covariates to include in four-level Bayesian logistic regression models. Mixing, 31 group size and timing of the animal's move to the feedlot were important predictors of BRD. 32 Animals not mixed with cattle from other farms prior to 12 days before induction and then 33 exposed to a high level of mixing (≥ 4 groups of animals mixed) had the highest risk of 34 developing BRD (OR 3.7) compared to animals mixed at least 4 weeks before induction with 35 less than 4 groups forming the cohort. Animals in groups formed at least 13 days before 36 induction comprising 100 or more (OR 0.5) or 50 to 99 (OR 0.8) were at reduced risk 37 compared to those in groups of less than 50 cattle. Animals moved to the vicinity of the 38 feedlot at least 27 days before induction were at reduced risk (OR 0.4) compared to cattle 39 undergoing short-haul transportation (<6 hours) to the feedlot within a day of induction, 40 while those experiencing longer transportation durations (6 hours or more) within a day of 41 induction were at slightly increased risk (OR 1.2). Knowledge of these risk factors could 42 potentially be used to inform management decisions to reduce the risk of BRD in feedlot 43 cattle.

44 Key words:

45 Bovine respiratory disease, feedlot, risk factors, total effects, causal diagram

46 **1. Introduction**

47 Bovine Respiratory Disease (BRD) describes a complex of diseases involving the 48 respiratory system in cattle. BRD is particularly common where cattle are kept in intensive or 49 confined conditions, such as in feedlots, and is a multifactorial disease; necessary factors 50 include pathogenic organisms, environmental stressors and immunological susceptibility 51 (Edwards, 2010). Previous research has identified market origin, number of cattle in the 52 animal's 'group', and comingling with cattle from other sources close to the time of feedlot 53 entry as risk factors for BRD. Increased risk of BRD has been demonstrated in groups 54 comprised of animals from multiple sources that were mixed at the feedlot compared to 55 predominately singled-sourced groups (Martin et al., 1982; Wilson et al., 1985; Martin and 56 Meek, 1986). Wide variation in incidence between source groups has been observed (Martin 57 et al., 1988) as well as evidence of clustering of fatal BRD cases within truckloads and/or 58 pens (Ribble et al., 1994). More recent studies agree that comingling of cattle from multiple 59 sources around the time of feedlot entry increases risk of BRD (O'Connor et al., 2005; Sanderson et al., 2008; Step et al., 2008). 60

61 Routine practice in North American sale barns involves comingling of cattle from multiple 62 farms immediately prior to sale (Macartney et al., 2003), which means that comingling and 63 market source are interlinked. Cattle identified as coming from a single source such as a 64 particular truckload or sale barn of origin may, in fact, have originated from several different 65 farms, leading to potentially important misclassification bias. While some prior studies have 66 reported that larger group size increases risk of BRD (Martin et al., 1982; Kilgore et al., 67 2005; O'Connor et al., 2005), 'groups' may have been assembled for varying lengths of time 68 and larger groups may be a proxy for a larger number of sources. In determining the effect of 69 the number of cattle in the animal's group, data indicating the date when the group was 70 formed were usually not available. These studies lacked sufficient data to separate the effects

of more refined individual factors, and to consider the effect of timing of exposure to comingling and auction sales relative to when cattle commenced being at risk of BRD at the feedlot.

While some North American studies returned equivocal results regarding the effect of transport distance on BRD risk (Cole et al., 1988; Ribble et al., 1995b; Schwartzkopf-Genswein et al., 2007), larger more recent studies suggest a positive association between distance transported and BRD incidence (Sanderson et al., 2008; Cernicchiaro et al., 2012).

78 Causal diagrams facilitate an informed approach to model building with postulated and 79 potential relationships defined based on a priori knowledge and plausible biological 80 pathways. Causal diagrams allow the separate estimation of total and direct effects, both of 81 which may be of interest to researchers and industry stakeholders (Dohoo et al., 2009). In a 82 causal diagram, the direct effect of an exposure is indicated by a single arrow directly linking 83 the exposure and outcome variables. An indirect effect of an exposure is indicated by a 84 pathway through a sequence of arrows passing through one or more intervening variables to 85 the outcome variable. The total effect of an exposure variable is the sum of the direct and all indirect effects of that exposure on the outcome. 86

Many factors associated with the assembly and movement of animals from their home property to the feedlot may affect the risk of BRD in the feedlot, and it was postulated that the effects of these factors depend on the timing of the animal's exposure. This paper describes the development of a causal diagram and subsequent analyses with the aim of evaluating the total and direct effects of risk factors relating to mixing of animals with cattle from other farms before the latest induction date for the animal's pen ('cohort closure'), numbers of animals in groups before induction, exposure of animals to saleyards before

arrival at the feedlot, and the timing and duration of the animal's move to the feedlot on therisk of BRD in Australian feedlot cattle.

96 2. Materials and methods

97 2.1. Overview of study design

98 A nationwide prospective longitudinal study was conducted in Australia to evaluate many 99 possible risk factors for BRD in feedlot cattle. Results for the subset of exposures relating to 100 animal mixing, group size, exposure to saleyards and timing and duration of the animal's 101 move to the feedlot are presented in this paper. Results for other exposures (e.g. animal entry 102 characteristics, season, pen features) will be reported separately. Managers of feedlots with a 103 minimum capacity of 1,000 cattle and the necessary resources to keep required records were 104 invited to participate. After arrival at the feedlot, cattle were inducted (animal identity and 105 other data recorded, and treatments applied), and enrolled in cohorts where a cohort consisted 106 of all animals placed together in a feedlot pen following induction. Each cohort consisted of 107 one of more 'group-13s' where a group-13 consisted of all animals that were together 13 days 108 before induction that then went into the same cohort. Cohorts were generally selected at the 109 convenience of the feedlot managers despite attempts to randomise the selection process. A 110 total of 35,160 animals were inducted into study cohorts from March 2009 to December 111 2011, of which 35,131 animals had sufficient data for inclusion in this study. The study 112 population had a nested hierarchical structure such that animals were clustered within 1,077 113 group-13s which, in turn, were clustered within 170 cohorts, which were clustered within 14 114 feedlots. The mean number of animals in a group-13 was 33 (range: 1 to 342) and the mean 115 number of animals per cohort was 207 (range: 17 to 395). The number of animals and cohorts 116 contributed per feedlot ranged from 466 animals in 3 cohorts to 6,114 animals in 22 cohorts. 117 Of the 14 participating feedlots, three routinely practiced 'pre-induction assembly'. This is a 118 management practice whereby animals from different farms are assembled on pasture close to

the feedlot for various periods of time prior to induction. Each animal was monitored from induction until it left the study cohort for any reason (i.e. removal to the hospital pen or another pen separate from the cohort, death or feedlot exit). Detailed data were recorded for each animal (e.g. identification number, arrival date, induction date, first day on feed, sex, dentition, breed, induction weight) and supplied as animal-level electronic files, while further data were supplied for animals that were hospitalised or died during the observation period.

125 2.2. National Livestock Identification System data

126 The Australian National Livestock Identification System (NLIS) requires that all cattle are 127 individually identified with a unique identification string that may be applied as an ear tag or 128 a rumen bolus, before they leave their farm of origin. Each farm, feedlot and saleyard is 129 identified by a unique Property Identification Code (PIC). The system relies on registered 130 users electronically scanning animals every time they are moved from one PIC location to 131 another ('transfers') and uploading this data to an online national electronic database. The 132 database records the PIC of issue (the animal's first lifetime PIC), and for each transfer, the 133 source and destination PIC, transfer date and transfer type. Transfer type distinguishes 134 between transfers to or from saleyards and 'point to point' (non-saleyard) transfers. NLIS 135 transfer data were obtained for 98.8% of study animals. Transfer data were simplified to 136 create a logical sequence from the PIC of issue to the feedlot for each animal. Multiple 137 transfers occurring within a 48 hour period (e.g. PIC A to a saleyard or intermediate PIC and 138 saleyard or intermediate PIC to PIC B) were consolidated to form a single record (PIC A to 139 PIC B) while the transfer detail was retained as a separate variable. Time intervals between 140 each transfer and the animal's induction date were used to determine the PIC at which the 141 animal was located at various time points prior to induction date. NLIS imputes some 142 transfers. For example, if an animal's record contains a transfer from PIC A to PIC B and 143 then a transfer from PIC C to PIC D, NLIS generates imputed transfers from B to 'unknown'

144 and 'unknown' to C, along with associated imputed transfer dates. These imputed transfers 145 were simplified and retained (PIC B to PIC C; imputed) but the imputed transfer dates were 146 changed to missing. It was usually possible to determine the location of these cattle at the 147 time points of interest by using the known transfer dates of other animals from the same 148 cohort that shared a common move sequence. For transfers to the feedlot PIC, we used the 149 arrival dates and tail tag numbers (identifying the most recent source PIC) supplied by the 150 feedlots, to validate the data supplied by NLIS. We also determined the total number of 151 lifetime transfers and the interval between transfers.

152 **2.3.** Case definition, exposure variables and causal diagrams

153 The unit of analysis was the individual animal. The outcome of interest was the 154 development of BRD during the first 50 days following induction. The case definition was 155 based on the clinical signs of disease recorded by feedlot staff in computerised hospital 156 records after suspected ill animals were removed from their cohort for examination and 157 treatment. Veterinarians servicing participating feedlots conducted regular training sessions 158 for feedlot staff on the diagnosis of BRD and seven of the fourteen participating feedlots 159 were serviced by the same veterinary group. Thus diagnosis of BRD was expected to be 160 relatively consistent across participating feedlots. All animals with clinical signs indicating 161 respiratory system involvement ("pneumonia", "respiratory", "BRD" and "IBR") were 162 classified as BRD cases by the research team.

All exposure variables were categorised for use in analyses, with definitions of categories based on prior hypotheses and distributions. Variables were derived from the NLIS data to determine each animal's PIC and the number of animals in its group at particular time points of interest. Each animal's time at risk began the day after induction into a study cohort; hence the induction date was designated "day 0". Days prior to this date were identified using

168 negative values, and time points of particular interest (days -91, -28, -13 and -2) were chosen 169 based on *a priori* hypotheses. It was hypothesised that the effects of mixing, group size, 170 exposure to a saleyard and timing of the animal's move to the feedlot on the risk of 171 developing BRD would differ depending on the timing of these events in relation to day 0. 172 Early studies describing the epidemic curves for BRD in feedlot calves indicated that the 173 majority of cases occurred in the first 4 weeks following arrival at the feedlot (Martin, 1983). 174 Assuming a similar epidemic curve would apply to animals exposed to stress and pathogens 175 through mixing, saleyard exposure or transport, we postulated that 28 days would be the 176 minimum amount of time required for the majority of susceptible animals in a group to 177 develop signs and recover from infection. More recently, researchers identified several 178 different temporal patterns in the cumulative incidence of BRD in feedlot populations 179 (Babcock et al., 2010). For the majority of cohorts in their study, the cumulative incidence of 180 BRD was more than 50% by 28 days. However, different patterns were identified and later 181 onset and more gradual rises in cumulative incidence were also observed. In all of these 182 patterns, the cumulative incidence was above 80% by day 90, and in 95% of cohorts it was 183 above 95% by day 90. Thus, day -91 was chosen to further evaluate the timing of mixing. At 184 the animal level, uncomplicated respiratory viral infections (e.g. with bovine herpesvirus type 185 1; (Ellis, 2009)) may resolve within 2 weeks, so day -13 was chosen as a comparative time 186 point to evaluate the effects of all exposures. Day -2 was only used to derive the variable 187 describing the timing and duration of transport to the feedlot so that transport within a day of 188 day 0 would be in a separate category to transport at earlier times.

Each animal's group was derived based on which cattle from its cohort were at the same PIC at each time point. For example, "group-28" identified the animal's group 28 days before induction. Changes in each animal's group between time points were used to describe mixing. Mixing before day -27, and between day -27 and day -13, were described as binary variables

193 (mixed or not mixed within period). Because the majority of animals were moved to the 194 vicinity of the feedlot within the 12 days prior to their induction, the amount of mixing 195 between day -12 and cohort closure (the latest induction date for the animal's pen) was 196 described by a categorical variable based on the number of group-13s forming the cohort (1, 197 2–3, 4–9 and \geq 10). These three variables were combined to form a single variable ('mixing 198 history') to describe the animal's lifetime mixing history. A further variable, ('mix first') 199 consisted of three categories which described the time interval of the earliest mixing event. 200 Numbers of animals in each animals group were also defined; for example, "group-28N" 201 indicated the number of animals in the animal's group-28.

202 Three binary saleyard variables were derived to describe whether or not animals had been 203 exposed to saleyards in the intervals before day -27, day -27 to day -13, and day -12 to 204 induction. The timing and duration of an animal's move to the feedlot was described by a 205 composite variable ('feedlot move timing') based on the number of days between arrival at the 206 feedlot vicinity and induction, and the estimated duration of transport for those animal's 207 arriving within 12 days before induction. The duration of transport was determined by 208 estimating the travel time between the source and feedlot PICs. Additional time was included 209 for transfers via saleyard or intermediate PICs or for driver rest periods for long-haul 210 transportation. The time interval between arrival at the vicinity of the feedlot and induction 211 ('Arrival day0') and other collapsed versions of variables described above were used in 212 analyses restricted to animals from the three feedlots routinely using pre-induction assembly.

Causal diagrams were constructed to describe postulated links between measured exposure variables and between exposure variables and occurrence of BRD in the first 50 days at risk. As this resulted in a very complex diagram, a simplified version (only including variables relevant to the assessment of the risk factors included in the analyses reported in this paper) is

shown in Figure 1. Figure 2 shows the causal diagram used to inform the analyses restricted to the three feedlots that routinely used pre-induction assembly. Additional variables included as potential confounders in either of these diagrams were cohort fill duration (all animals added to their cohort within a single day or over a longer period), total number of animals on feed in the animal's feedlot (average for the animal's induction month), number of animals in the animal's cohort, induction weight, breed and season in which the animal was inducted.

223 2.4. Data management and statistical modelling

The Stata® statistical software package (version 12) was used for all data management and preliminary analyses and MLwiN® (version 2.27) was used to fit final four-level models.

226 In estimating total effects, care needs to be taken to adjust appropriately for confounders, 227 including variables that become confounders through conditional associations (Dohoo et al., 228 2009). Various methods have been proposed for determining which covariates to fit when 229 estimating total effects, but they all have similar features (Greenland et al., 1999; Shrier and 230 Platt, 2008; Dohoo et al., 2009; Textor and Liskiewicz, 2011). The DAGitty® software 231 (Textor et al., 2011) was used to identify minimal sufficient adjustment sets to assess total 232 and direct effects of the exposure variable of interest on the occurrence of BRD. A sufficient 233 adjustment set is a set of variables that appropriately controls confounding of the association 234 between the exposure variable of interest and the outcome. When direct effects are required, 235 the sufficient adjustment set also includes all intervening variables between the exposure 236 variable of interest and the outcome. The causal diagram was reproduced within the 237 DAGitty® user interface. Each variable of interest was sequentially identified as the exposure 238 of interest, and the minimal sufficient adjustment sets for both total and direct effects as 239 defined by DAGitty® were noted.

240 The multilevel modelling software package MLwiN® (version 2.27) was used for 241 modelling. For each exposure of interest, a model containing covariates determined by the 242 minimal sufficient adjustment set for the total effects was fitted using second-order penalised 243 quasi-likelihood methods to produce starting values for the second model using Bayesian 244 Markov chain Monte Carlo (MCMC) methods. The process was then repeated using the 245 adjustment set for direct effects, where these were desired. For all models, random effects of 246 feedlot, cohort nested within feedlot and group-13 nested within cohort were included, and 247 Metropolis Hastings sampling methods were used. Gaussian prior distributions with 248 extremely large variances, the default for multilevel logistic models fitted in MLwiN® 249 (Browne, 2012), were used. After a burn-in of 1000 iterations, 10,000 further iterations were 250 run and diagnostic trajectory plots and summary statistics (Browne, 2012) assessed to 251 estimate the required chain length. Further iterations were run and models were reassessed 252 until convergence was achieved. Animal-level variables such as exposure to a saleyard prior 253 to day -27 displayed good mixing and low autocorrelation, while mixing history and feedlot 254 move timing displayed higher autocorrelation and were slower to converge. Consequently, 255 MCMC chains were run for between 50,000 and 300,000 iterations to obtain final posterior 256 parameter estimates of mean odds ratios (ORs) and 95% credible intervals.

257 **3. Results**

258 **3.1. Descriptive statistics**

Induction weights ranged from 196 to 756 kg; 20% of the study population were <400kg, 31% were 400–439kg, 34% were 440–479 kg and 15% were ≥480kg. The most common breeds in the study population were Angus (56%), tropical breeds or crosses (16%), British breed crosses (12%) and Hereford (6%). The study population comprised 92% steers and 8% heifers. An estimated 41% of animals had a single lifetime transfer (from the source property to the feedlot). For animals that had at least 2 lifetime transfers with known transfer dates,</p>

the transfer prior to the feedlot move occurred an average of 280 days (about 9 months) before induction, and 80% of these transfers occurred between 16 and 3 months before induction.

Of all suspected ill study animals removed from their cohort for examination and treatment, 77.3% (6,406/8,285) met the BRD case definition at first examination, comprising 18.2% (6,406/35,131) of the study population. The majority of animals that had BRD when first examined were examined during their first 50 days at risk, giving a 50-day BRD cumulative incidence of 17.6%. This cumulative incidence does not include BRD occurrences subsequent to diagnosis with another condition at the time of first examination.

Descriptive statistics for exposure variables of interest are shown in Table 1. The most common mixing history involved animals mixed prior to day -27 joining cohorts formed by 10 or more group-13s (labelled 'Yes, no, $\geq 10^{\circ}$; 22%) or 4–9 group-13s ('Yes, no, 4–9'; 16%). A high level of mixing within 12 days of induction was also common in animals not mixed prior to day -27 ('No, no, $\geq 10^{\circ}$; 15%; 'No, no, 4–9'; 10%). The majority (62%) of animals had been mixed prior to day -90 and 5% were mixed for the first time between days -90 and -28.

Smaller groups defined at day -13 (<50 animals) were the most common (39% of animals), but nearly a third of animals (33%) came from groups defined at day-13 with at least 100 animals. About a third (36%) of the study population had been exposed to saleyards prior to day -27, while relatively few had been through saleyards within 27 days of induction (3% between days -27 and -13 and 3% within 12 days of induction). Most cattle (76%) were moved to the feedlot within a day before induction, with 36% of these being transported for 6 hours or longer.

Those cattle that were moved to the vicinity of the feedlot prior to day -12 and mixed between day -27 and day -13 were mostly from the three feedlots that practiced pre-induction

assembly. The pre-induction assembly subset comprised 5,641 animals from 3 feedlots, 297 group-28s, 136 group-13s and 40 cohorts. The 50-day BRD cumulative incidence was 3.3% in this subset. As shown in Table 2, 31% of these animals arrived at the vicinity of the feedlot more than 27 days before induction and 31% arrived in the interval between days -27 and -13. More than half (57%) were in cohorts formed by four or more groups defined at day -28.

294

3.2. Multilevel logistic regression models

295 Estimated total effects of variables of interest on 50-day BRD cumulative incidence for 296 the whole study population are shown in Table 1. Mixing history had a marked effect. 297 Compared to the reference category of animals that had been mixed prior to day-27 from 298 cohorts formed by 2 or 3 group-13s ('Yes, no, 2-3'), a similar risk level was observed for 299 those not mixed between day -27 and cohort close ('Yes, no, no': OR 1.2), but risk was 300 substantially increased if more than 4 group-13s formed the cohort ('Yes, no, 4-9': OR 2.8; 301 'Yes, no, ≥ 10 ': OR 2.2). Risk was also markedly increased for animals not mixed before day 302 -27 ('No, no, no' and 'No, no, 2-3: OR:2.3), with the highest risk for animals subjected to a 303 high level of mixing between day -12 and cohort close ('No, no, 4-9' and 'No, no, \geq 10': OR 304 3.7). Based on the causal diagram (Fig. 1), direct and total effects for mixing history were 305 equivalent. Results from the analysis of the first mix timing variable indicated a similar 306 marked protective effect of prior mixing, both for animals first mixed before day -90 (OR 307 0.6) and for those first mixed between day -90 and day -28 (OR 0.6) compared to animals 308 first mixed between day -27 and cohort close. Estimated odds ratios for mixing between 309 days -27 and -13 were consistent with increased risk but estimates were imprecise. Subset 310 analysis (Table 2), used because mixing during this time interval was an uncommon practice 311 across the whole study population, showed a markedly increased risk for animals in cohorts formed by mixing 4 or more group -28s (OR:5.5) compared with less than four. 312

Animals in larger groups defined at day -13 were at reduced risk of BRD. Compared to animals from groups with less than 50 animals, animals from groups with 50 to 99 animals were at somewhat reduced risk (OR 0.8) and animals from groups with 100 or more animals were at markedly reduced risk (OR 0.5) of developing BRD (Table 1). The direct effects of the number of animals in the group-13 (Table 3) were of a similar magnitude to the total effects, indicating that these effects are not due to differences in mixing history, cohort fill duration or the number of animals in the cohort.

320 The total effect of exposure to saleyards varied with time of the exposure (Table 1), with 321 markedly increased risk associated with saleyard exposure closer to induction (exposed 322 between days -27 to -13: OR 1.9; days -12 to 0: OR 2.6) and modestly decreased risk for 323 saleyard transfers prior to day -27 (OR 0.8). However, there was no evidence for an important 324 direct effect of having been through a saleyard prior to day -27 after accounting for the 325 intervening variable, mixing history (OR 1.0, Table 3). The direct effects of salevard transfer 326 between days -27 and -13, and day -12 to induction were also much attenuated, after 327 accounting for mixing history and feedlot move timing as intervening variables, suggesting 328 that total effects of exposure to saleyards during these periods were probably largely due to 329 the effect of mixing. However, an important adverse direct effect of exposure to saleyards 330 between days -12 and induction was evident (OR 1.8) indicating that exposure within this 331 period has a negative effect over and above the effects of mixing and feedlot move timing.

Compared to animals undergoing transport of less than 6 hours within a day before induction, animals having longer transport times (6 hours or more) within a day of induction were at slightly increased risk (OR 1.2), while animals that moved to the vicinity of the feedlot at least 27 days before induction were at substantially reduced risk (OR 0.4). The direct effects of the feedlot move timing were generally similar to the total effects, with

337 greater differences in the estimates for exposure categories with very unbalanced 338 distributions across feedlots (Table 3). Subset analyses restricted to the three feedlots 339 practicing pre-induction assembly (Table 2) also provided evidence that animals arriving 340 prior to day -27 were at reduced risk compared to those arriving within 12 days before 341 induction.

342 **4. Discussion**

343 From this study, we identified important differences in the effects of risk factors relating to 344 animal mixing and moving depending on the timing of these events in relation to the animal's 345 induction at the feedlot. We found that there was a protective effect of mixing prior to 27 346 days before induction and an adverse effect of mixing 4 or more groups compared to less than 347 4 groups within 12 days of induction. Moving to the vicinity of the feedlot at least 27 days 348 prior to induction was protective and longer transport duration within a day of induction 349 slightly increased risk. The effect of saleyard exposure varied depending on the timing of 350 exposure, and the effect was largely mediated through mixing but saleyard exposure within 351 12 days of induction increased risk over and above the effect mediated through mixing and 352 the move to the feedlot. Being part of a larger group (more than 50 animals) established at 353 least 13 days prior to induction was protective.

Comingling of animals from multiple sources immediately prior to arrival at the feedlot has been consistently shown to be associated with increased risk of BRD (Martin et al., 1982; Ribble et al., 1995a; O'Connor et al., 2005; Sanderson et al., 2008; Step et al., 2008). Results from the current study demonstrated that the effect of comingling depends on prior mixing history; important differences were observed between categories of cattle with differing mixing histories. By utilising lifetime animal-level data we have been able to examine mixing history in a way that has not, to our knowledge, previously been described. Mixing prior to

361 27 days before induction was protective and comingling with cattle from less than 4 groups 362 within the 12 days preceding induction did not increase risk provided cattle had been mixed 363 prior to 27 days before feedlot entry. A high level of mixing (defined by the combination of 4 364 or more group-13s forming a cohort) close to induction markedly increased the risk of BRD.

365 Cattle transported for 6 hours or more within one day of induction were at slightly 366 increased risk of BRD compared to those undergoing shorter duration transport in this period, 367 which is consistent with findings from recent North American studies (Sanderson et al., 2008; 368 Cernicchiaro et al., 2012). To our knowledge, prior studies have not investigated the effect of 369 time interval between arrival at the vicinity of the feedlot and induction on BRD risk after 370 induction. Our results showed that cattle arriving at the feedlot vicinity more than 27 days 371 before induction were at reduced risk of BRD. We speculated that this may have been 372 overestimated as only three feedlots in the study moved cattle to the vicinity of the feedlot 373 prior to day -12 and there may have been uncontrolled confounding despite having fitted 374 feedlot as a random effect. However, results of analyses restricted to animals from these three 375 feedlots were consistent with a large protective effect, although the odds ratio estimate for 376 cattle moved prior to day -27 was imprecise. We postulated that the total effect of the feedlot 377 move timing was likely to be partially mediated through mixing (the intervening variable in 378 the causal diagram (Figure 1). Our results indicated that the timing of the move to the vicinity 379 of the feedlot was an important contributor to the risk of BRD over and above effects of 380 mixing.

In the current study, animals that were part of a larger group 13 days prior to induction were at reduced risk of BRD. A larger number of animals in a group has been associated with increased risk of BRD in prior studies, but this may be due to the effects of more comingling in larger groups (Martin et al., 1982; Martin, 1983; Martin and Meek, 1986). The

385 interpretation of the effects of 'group size' in prior research is problematic because the length 386 of time the group has been assembled was usually not able to be determined. The number of 387 animals in the cohort aligns more closely with group size investigated in other studies, but we 388 do not draw a conclusion about cohort size because it tended to be clustered by feedlot, 389 limiting the power to detect an effect and possibly leading to uncontrolled feedlot-level 390 confounding. We defined group size at a consistent time point for comparison of all study 391 animals, potentially avoiding misclassification bias if effects of group size depend on time 392 before induction when group size is assessed. However, group sizes were often stable for 393 extended periods of time before the move to the feedlot and for the majority of animals the 394 grouping structure did not change dramatically between 3 months and 13 days before 395 induction. Hence, our conclusion is that group size is very important, but the stability of 396 group sizes observed in our study means that the duration of time that the group is formed 397 should be considered alongside the effects of mixing history and feedlot move timing. As a 398 consequence of being in a larger group, fewer such groups are likely to be mixed to form a 399 cohort, but the similar effect in both total and direct effects models, indicates an important 400 effect over and above that mediated through mixing. Possible additional reasons for the 401 protective effect could relate to a lower level of stress associated with the disruption of their 402 social hierarchy, and if the group is of sufficient size, animals may be exposed to fewer novel 403 pathogens in the feedlot pen.

404 Conclusions are supported by secondary analyses. Although first mixing in the interval 405 from day -90 to day -28 occurred in only 5% of the full study population, it was associated 406 with a similar level of reduced risk as prior mixing before day -90. Because mixing from day 407 -28 to day -13 and moving to the feedlot prior to day -12, and to a lesser extent prior to day -408 2, were generally restricted to feedlots that practised pre-induction assembly, the analyses 409 restricted to these feedlots may be more appropriate for drawing inference about these

410 practices. Although consistent results indicative of a protective effect of moving animals to 411 the vicinity of the feedlot prior to day -27, and the harmful effect of mixing four or more 412 group-28s to form a cohort support our conclusions, further research is needed to better 413 understand the effects of mixing and moving associated with pre-induction assembly.

414 An important finding from this study is that the effects of exposure to saleyards differ 415 depending on the timing of exposure relative to induction. Our results show that cattle 416 exposed to saleyards more than 27 days before induction are at lower risk but this protective 417 effect is primarily mediated by factors other than the process of unloading, yarding, holding 418 then reloading at saleyards. This was demonstrated by separately estimating total and direct 419 effects. Similarly, the detrimental total effect of saleyard exposure within 27 days of 420 induction should be interpreted in combination with the much attenuated direct effect 421 estimates. Our results showed that saleyard exposure within 27 days of induction increased 422 risk of BRD but this is also due to factors other than the actual saleyard processes. However, 423 our results indicate that exposure to saleyards within 12 days prior to induction further 424 increased risk of BRD over and above effects of mixing and feedlot move timing.

425 There were several potential sources of bias in this study. Despite training of feedlot staff 426 by veterinarians, there may have been differences in detection and/or recording of clinical 427 signs between feedlots. Feedlot was fitted as a random effect in all models, and this will have 428 at least partially removed any confounding by feedlot. In using the PICs to determine whether 429 cattle were mixed, misclassification errors may have occurred in the classification of animals' 430 mixing histories and group sizes. Cattle with the same PIC were assumed to have mixed with 431 each other while on that farm when, in fact, some they may have been maintained on that 432 farm separately from other cattle. Similarly, cattle moved from multiple sources to a common 433 PIC were assumed to have been mixed on that new farm. However, these assumptions were

434 supported by additional data obtained from farms selling study cattle directly to feedlots 435 (about 30% of the study population) which indicated that 94% of study groups were mixed on 436 these farms. Under-recording of mixing and group sizes may also have occurred. Each 437 animal's groups were defined based only on the cattle entering the same cohort, and 438 additional animals may have been mixed with study animals prior to induction. Provided any 439 misclassification error patterns were the same across all true values of the variables, the 440 resulting misclassification biases for mixing history and group size variables would be 441 expected to be towards the null. The finding that cattle with a history of having being through 442 a saleyard or mixed prior to day -27 are at reduced risk would be expected to be largely 443 explained by the protective immunity expected to develop following exposure to viruses prior 444 to feedlot entry.

445 Beef cattle management practices in Australia differ from those in North America and 446 Europe in some key aspects. Cattle in Australia enter feedlots at an older average age, often 447 many months after weaning; and it is common for recently weaned cattle to be sold through 448 saleyards or weaner sales and then spend 6 months or more on an intermediate farm before 449 being sold to a feedlot (Walker et al., 2007). Accordingly, results of this study may not reflect 450 causal relationships in feedlot cattle in other countries. In addition, larger capacity feedlots 451 were more likely to participate in the study, so conclusions may not be generalizable to all 452 Australian feedlots. However, results should be generalizable to moderate to large feedlot 453 operations in Australia because feedlots from most major feedlot regions participated in the 454 study and enrolled cattle would be expected to be representative of the Australian feedlot 455 population as they came from throughout the wide geographical beef-cattle producing regions 456 and had a broad range of entry characteristics.

457 The use of a causal diagram and the determination and comparison of separate direct and 458 total effects provides informative estimates of effect from complex datasets. The adjusted 459 effects estimated in a multivariable model built using an automated model building process 460 may be direct, partial or total effects, and therefore do not necessarily reflect the total causal 461 effect of the exposure variable on the outcome variable (Westreich and Greenland, 2013). 462 This is because with automated model building processes, variable selection is not based on 463 whether variables may be potential confounders or intervening variables for particular 464 exposure-outcome relationships, so some variables that are important confounders may not be 465 included and intervening variables may be included in the model. However, the use of a 466 causal diagram to inform model building can result in uncontrolled confounding if the causal 467 diagram does not accurately capture causal pathways or important confounders are missing 468 from the diagram. It also relies on some assumptions about the directionality of associations 469 and this is not always clear.

470 **5. Conclusions**

471 The risk of BRD in feedlot cattle varied markedly with prior mixing history; there was a 472 protective effect of mixing prior to 27 days before induction and an adverse effect of mixing 473 4 or more groups compared to less than 4 groups within 12 days of induction. Moving to the 474 vicinity of the feedlot at least 27 days prior to induction was protective. Longer transport 475 duration (6 hours or more compared to less than 6 hours) within a day of induction slightly 476 increased risk of BRD. The effect of saleyard exposure varied depending on the timing of 477 exposure, and the effect was largely mediated through mixing but saleyard exposure within 478 12 days of induction increased risk. Being part of a larger group (more than 50 animals) 479 established at least 13 days prior to induction was protective. Management decisions 480 regarding these factors have the potential to markedly reduce the incidence of BRD in feedlot 481 cattle.

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- 562

563 564 Table 1. Distribution of variables and estimated odds ratios for their total effects on the occurrence of BRD by day 50 based on models derived from the causal diagram shown in Figure 1.

	Number of	Crude BRD 50-day	Adjusted	95% credible
Variable & category	animals (%)	cumulative incidence (%)	odds ratio	interval
Mixing history ^a	34.730			
No. no. no ^e	418 (1)	20.6	2.3	(0.4 - 7.4)
No no $2-3$	1 489 (4)	19.5	2.3	(1 3 - 3 8)
No. no. 4–9	3.334 (10)	30.3	3.7	(1.7-7.2)
No no ≥ 10	5 114 (15)	31.4	37	(1.7 - 7.4)
No ves ves	627 (2)	17.2	3.4	(1.7, 7.1)
No ves no ^e	407(1)	2.5	23	(0.5-6.9)
Ves no 2-3	3893(11)	57	Ref cat	(0.5 0.5)
Ves no 4-9	5 409 (16)	16.4	2.8	(1 3 - 5 4)
Ves no > 10	7 793 (22)	20.7	2.0	$(1.5 \ 5.4)$
$Ves ves ves^e$	946 (3)	13 7	2.2	(0.9-4.5)
Ves ves no ^e	1 958 (6)	3 3	2.2	(0.7 - 6.6)
Ves no no	3342(10)	3.5	1.2	(0.7-0.0) (0.5, 2.6)
1 es, 110, 110	5,542 (10)	5.4	1.2	(0.3-2.0)
Number of animals in				
group-13 ^b	35,131			
< 50	13,782 (39)	24.1	Ref. cat.	
50 to 99	9.783 (28)	21.3	0.8	(0.7 - 0.9)
> 100	11,566 (33)	69	0.5	(0.4 - 0.7)
_ 100	11,000 (00)		0.0	(0.1 0.7)
Saleyard transfer prior to				
day-27 ^b	34,730			
No	22,223 (64)	18.7	Ref. cat.	
Yes	12,507 (36)	15.7	0.8	(0.7 - 0.9)
Salavard transfer, between		· ·		
day 27 and day 13 ^b	35 131			
No	24 162 (07)	17.9	Pof out	
No	34,102(97)	11.0	1 0	(1, 2, 2, 7)
res	909 (3)	11.2	1.9	(1.3 - 2.7)
Salevard transfer between				
day-12 and day 0 ^b	35.131			
No	34,200 (97)	17.6	Ref. cat.	
Yes	931 (3)	21.4	2.6	(16 - 41)
105	<u> </u>	21.1	2.0	(1.0 1.1)
Feedlot move timing ^c	35,131			
Pre day-27 ^e	1,880 (5)	1.5	0.4	(0.2 - 0.8)
Day -27 to -13 ^e	2,000 (6)	4.6	1.0	(0.4 - 1.9)
Day -12 to -2: ≤ 6 hours	2.183 (6)	10.9	0.9	(0.6 - 1.2)
Day -12 to -2 : >6 hours	2.339 (7)	8.0	0.9	(0.5 - 1.4)
Day -1 to $0. \le 6$ hours	17 139 (49)	19.9	Ref cat	(*******)
Day -1 to 0; ≥ 6 hours	9,590 (27)	23.5	1.2	(1.0 - 1.5)
J	('')			()
First mix timing ^d	34,730			
Pre day -90	21,559 (62)	13.5	0.6	(0.5 - 0.7)
Day -90 to day -28	1,713 (5)	4.6	0.6	(0.4 - 0.9)
Day -27 to 0	11,458 (33)	27.4	Ref. cat.	

565 ^aMixing history: pre day-27, day-27 to day-13 and day-12 to cohort close; covariates include Fill, Weight, SY-

566 12_0, SY-27_13, SYpre-27, CohortN, Move_FL, Group-13N, N=34,726

567 ^bModels have no additional covariates as they have empty adjustment sets

568 Feedlot move time interval and transport duration (within 12 days); covariates: SY-12_0, SY-27_13, N=35,131

^dFirst mix timing describes the earliest time period that the animal was mixed with cattle from other PICs;

570 model derived from a variation of the causal diagram: covariates include Fill, Weight, SY-12 0, SY-27 13,

571 SYpre-27, CohortN, Move_FL, Group-13N, N=34,726

572 Categories where 7 or more feedlots have no observations

- 573 Table 2 Distribution of variables and estimated odds ratios for their total effects on the
- 574 occurrence of BRD by day 50 in the pre-induction assembly subset based on models derived
- 575 from the causal diagram shown in Figure. 2.

¥	N 1 C	G 1 DDD 50 1		
	Number of	Crude BRD 50-day		
	animals	cumulative	Adjusted	95% credible
Variable & category	(%)	incidence (%)	odds ratio	interval
Days between arrival at vicinity				
of feedlot and induction ^a	5,641			
> 27	1,747 (31)	1.5	0.6	(0.2 - 1.5)
27 to 13	1,723 (31)	5.3	1.2	(0.4 - 2.7)
12 to 0	2,171 (38)	3.3	Ref. cat.	
Number of animals in group-28 ^b	5,641			
< 50	1,962 (35)	5.3	Ref. cat.	
50 to 99	962 (17)	2.0	0.6	(0.2 - 1.2)
≥ 100	2,717 (48)	2.4	0.8	(0.3 - 1.8)
Number of group-28s forming				
cohort ^c	5,641			
< 4	2,421 (43)	2.1	Ref. cat.	
\geq 4	3,220 (57)	4.3	5.5	(1.0 - 18.7)

576 ^a Covariates: Breed, Induction weight, Season, SY-27_0 and SYpre_27. N=5,551

577 ^bCovariate: Arrival_day0. N=5,590

578 ^c Covariates: SY-27_0, Arrival_day0 and Group-28N. N=5,589

579 Table 3. Estimated odds ratios for direct effects of selected variables on the occurrence of BRD by day 50 based 580 on models derived from the causal diagram shown in Figure.1

Variable & category	Adjusted odds ratio	95% credible interval	
Number of animals in group-13 ^a			
< 50	Ref. cat.		
50 to 99	0.8	(0.7 - 1.0)	
\geq 100	0.6	(0.4 - 0.8)	
Saleyard transfer prior to day-27 ^b			
No	Ref. cat.		
Yes	1.0	(0.9 - 1.1)	
Saleyard transfer between day-27 and day-13 ^b			
No	Ref. cat.		
Yes	1.3	(0.8 - 2.0)	
Saleyard transfer between day-12 and day0 ^b			
No	Ref. cat.		
Yes	1.8	(1.0 - 2.9)	
Feedlot move timing ^b			
Pre day-27 ^c	0.6	(0.2 - 1.3)	
Day- 27 to -13 °	1.4	(0.6 - 3.0)	
Day-12 to -2 ; <6 hours	0.9	(0.6 - 1.3)	
Day-12 to -2 ; ≥ 6 hours	1.0	(0.6 - 1.5)	
Day-1 to 0; <6 hours	Ref. cat.		
Day-1 to $0, \geq 6$ hours	1.2	(1.0 - 1.5)	

581 582 ^aCovariates: Group-13N, CohortN, Fill, Weight, SY-12_0, SY-27_13, SYpre-27, FeedlotN, Mix and MoveFL.

N=34,726

^bModel: Mix, Move_FL, SY-12_0, SY-27_13, SYpre-27, CohortN, Group-13N, Fill and Weight. N=34,726 ^cCategories where 7 or more feedlots have no observations 583

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585



Figure 1: Causal diagram showing postulated causal paths linking variables related to
mixing history, group size, exposure to saleyards and timing of the move to the feedlot to
occurrence of bovine respiratory disease (BRD) in the first 50 days on feed.

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591

592 Figure 2: Causal diagram showing postulated causal paths linking variables related to the 593 interval between arrival and induction, group size and number of groups combined to 594 occurrence of bovine respiratory disease (BRD) in the first 50 days on feed in three feedlots 595 where pre-induction assembly was implemented routinely.