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Report on Bighorn Sheep Recovery Program

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December 28, 11

Floyd Rathbun
P.O.BOX 1612
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RE: Evaluation of Models and Documents Regarding Bighorn Sheep Wildlife-Livestock Interface and Risk of Disease.

Dear Floyd:

As agreed in emails that you and I exchanged on September 23 and 24, 2011, and in the email I received from Fred Fulstone and Marianne Leinassar on October 19, 2011, I have evaluated the following 8 documents and my report is attached with this letter sent to you by email:

1. Clifford et al. (2009) paper, published in Biological Conservation, **142**: 2559-2568.
2. Thurmond's review of Clifford et al.'s analyses
3. Baumer et al.'s model (unpublished extract of Risk Assessment by RAT Team)
4. Application of Baumer et al.'s model (your document # 11)
5. Thurmond's review of Baumer et al.'s model
6. Tigran Melkonyan of Clifford et al.'s analyses
7. Nancy East's review on modeling
8. Dr. Marie Bulgin's review of Clifford et al.'s analyses (confined to material on pp. 9-10)

As you will see from my report, I essentially concur with Professor Thurmond's and Tigran Melkonyan's criticism's of the Clifford study and Professor Thurmond's criticism of the Baumer assessment, although I disagree at times with Professor Thurmond's choice of words. I find Dr. Nancy East's review very unhelpful and think it will be of little use to you. Also Marie Bulgin's comments appear to be out of date (she makes the statement that "The Clifford paper was never published in a reviewed journal and overall, it would probably never be recommended for publication") and add nothing new to Professor Thurmond's criticisms.

I am not sure how your clients might want to use my expertise to further their interests, but of course they should feel free to use my attached report in any way they see fit. We can correspond further, should my services be of interest to them in the future.

Please mail a cheque for the agreed upon sum of $1000 for services rendered to my home address (2522 Hill Court, Berkeley, CA 94708-1910, SS# 523-15-3538).

Sincerely

Wayne M Getz

Wayne M. Getz
Professor of Environmental Science and Reseearch Biomathematician.

Attachment: 1 Report.

Evaluation of Models of the Wildlife-Livestock Interface and the Risk of Disease in Bighorn Sheep

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I. Introduction

Task: My task is to evaluate the applicability of mathematical modeling analyses set out in the following two documents determining grazing policies with regard to ranching domestic sheep on federal lands that are part of the range of endangered Sierra Nevada bighorn sheep.

1. Clifford et al. (2009), Assessing disease risk at the wildlife-livestock interface: a study of Sierra Nevada bighorn sheep. Biological Conservation, **142**: 2559-2568.
2. Baumer et al. (Feb, 2009). A process for identifying and managing risk of contact between Sierra Nevada bighorn sheep and domestic sheep. Unpublished (prepared by the Risk Assessment Team of the Sierra Nevada Bighorn Sheep Recovery Team, April 26-27, 2006)
3. Croft et al. (April 3, 2009) Application of analysis 2. above.

Context: Models are developed for many purposes, *inter alia* for prediction, design and assessment of management policies, explanation and understanding of the behavior of physical, biological and sociological processes. Models of ecological processes, including those involving the demography and epidemiology of animals and their pathogens, embody many simplifying assumptions and are described in terms of processes only evident at relatively low levels of temporal and spatial resolution. Thus models can always be criticized as inadequate if their purpose and context are not taken into account. If models built for the purposes of prediction, however, lack the statistical rigor that comes with validating the model in terms of their ability to predict data not used to fit the parameters of the model, then these models are of very little value in assessing the efficacy of management policies.

Conclusion: Both the Clifford et al. and Baumer et al. analyses fall into the "lack of statistical rigor" category and for this and other reasons outlined below cannot be used to predict the likelihood of diseases outbreaks in any of the Sierra Nevada bighorn sheep populations.

2. Clifford Et Al. Publication

In this publication, Clifford et al report results obtained from a model used to assess the risk of disease transmission from livestock to bighorn sheep in three Sierra Nevada populations (designated north, central and south) and evaluate the relative risks associated with land management alternatives. In the last paragraph of report (Section 4.2) they even claim that they have provided a "... quantitative and defensible tool ..." to accomplish this task. This claim is incorrect and it is very surprising that the reviewers of the manuscript allowed this statement to be included in the manuscript.

The claim is incorrect because the model has not been "defended" through a rigorous statistical evaluation of how well it is able to retrodict past events from empirical data (population abundance, disease outbreaks, incidence and prevalence) of known quality. Here I fully concur with the criticism's Thurmond articulates under his heading: *Use of 'Science' as a guise*. In particular, Thurmond criticizes the authors for claiming that they 'determined' distributions (or any of the model parameters for that matter) when in fact they only 'estimated' the values in some unspecified way. In truth, it always holds that one can never directly determine the parameters of population processes but only estimate them from data through the 'current best statistical practices.' Beyond this application of statistical methods, however, is model validation that requires one to fit model output to empirical data that has not been used to estimate model parameters. Thus Clifford et al. fail on two accounts in terms of the defensibility of their model as a predictive tool:

1. They do not use rigorous statistical methods to fit model parameters
2. They do not use rigorous statistical methods to validate model performance as a predictive tool.

The lack of statistical rigor does not preclude Clifford et al.'s model from having value in the context of explanation and understanding, or as a tool for evaluating ideas relating to management in a comparative sense (i.e. the model can be used to explore possible relative efficacies of different management options, though nothing definitive can be said about the absolution efficacy of any management policy). Often, reliable data are unavailable, but mathematical models can still prove useful in exploring the behavior of systems and gaining insights and understanding of systems that are too complex to otherwise comprehend. Sensitivity analysis, in particular, can be useful here and Clifford et al. employ this type of analysis to identify factors that play a critical role, and to understand how these factors influence outcomes. For example, Clifford et al. identify the rate of contact as a key factor (this of course is obvious and well known). However, I found their sensitivity analysis rather superficial and not very comprehensive.

Beyond the two statistical issues identified above is the question of the model itself. A poor model with good data will give poor statistical results and a good model with poor empirical data will also give poor statistical results. However, only good models can ultimately yield good statistical results if high quality data is available. In the absence of high quality data, however, good models are still needed if model analyses are to yield understanding and valid insights with regard the to the comparative performance of different management policies.

The real challenge in disease models is to properly characterize transmission, which requires both an understanding of the contact process and the various factors that influence the probability of transmission given contact. Many models treat transmission rather crudely under the assumption that the population is well mixed, with transmission being proportional to the product of the densities of susceptible and infected individuals. More sophisticated approaches treat transmission as a concatenation of two processes: a contact rate and the probability of transmission per contact. The notion of contact, however, is very problematic in being multidimensional—it has both distance and time components, and the probability of transmission per contact depends on how 'effective' the contact is. Specifically, the closer and longer period of time that two individuals are to one another, the greater the probability of transmission; though this probability is saturating rather than linear with regard to distance and time. Clifford et al. sweep all these difficulties under the rug with their assumption—rightly criticized by Thurmond, Melkonyan and Bulgin—that cohabitation of an area over an entire season is sufficient to say that all individuals in both the livestock and bighorn populations constitute a single well-mixed population. This is indeed a very strong assumption that needs justification, which Clifford et al. do provide, although I find their justification weak. Unlike Thurmond, however, I cannot say that it is "inexcusable for a scientist to make [this assumption] consciously." Scientists make these kinds of assumptions all the time. What this assumption essentially means is that in each time period the contact rate of domesticated and wild sheep is proportional to the number of individuals in each of the areas they occupy modified by the proportion of their areas that overlap. What seems to me to be more egregious in the contact rate calculation is, as Thurmond points out, "The fixed kernel method can be expected to inflate the size of the area beyond that which is real ...". I suspect that Clifford et al. might be unaware of how over-inflated the method they use can be. They method they used is particularly problematic and their exposition of their implementation of this method, as pointed out by Professor Thurmond, rather poor.

As an aside, I have considerable experience with methods for estimating home range size and the problem of over inflation. In this context, I refer you to two papers below (1 and 2) that I have written on the topic. I also have considerable experience on analyzing animal movement behavior and refer you to papers 3 to 7 below.

1. Getz W. M. and C. C. Wilmers, 2004. A local nearest-neighbor convex-hull construction of home ranges and utilization distributions. Ecography 27:489-505.
2. Getz, W.M, S. Fortmann-Roe, P. C. Cross, A. J. Lyons, S. J. Ryan, C.C. Wilmers, 2007. LoCoH: nonparametric kernel methods for constructing home ranges and utilization distributions. PLoS ONE 2(2): e207.
3. Nathan, R., W. M. Getz, E. Revilla, M. Holyoak, R. Kadmon, D. Saltz and P. E. Smouse, 2008. A movement ecology paradigm for unifying organismal movement research. PNAS 105(49):19052-19059.
4. Getz, W. M. and D. Saltz, 2008. A framework for generating and analyzing movement paths on ecological landscapes. PNAS 105(49): 19066-19071.
5. Boettiger, A., G. Wittemyer, R. Starfield, F. Volrath, I. Douglas-Hamilton, W. M. Getz, 2011. Inferring ecological and behavioral drivers of elephant movement using a linear filtering approach. Ecology 92: 1648-1657.
6. Nathan, R., O Spiegel, S. Fortmann-Roe, R. Harel, and W. M. Getz, in press. Tri-axial acceleration data in free-ranging animals identifies behavioral modes in the context of movement ecology. J. Exp. Biol.
7. Fortmann-Roe, S., R. Starfield and W. M. Getz, in press. Contingent Kernel Density Estimation. PLoS ONE.

Together with Thurmond and Melkonyan, I found the presentation of Clifford et al. rather opaque at times. It was often unclear what actual terms meant (e.g. at one point they talk about acutely infected individuals, which it seems to me is synonymous with their category of ‘infectious’ individuals but I could not be sure) and how they got particular results. They also used several unjustified *ad hoc* assumptions, with “the number of adequate contacts was reduced 100-fold …” being a particularly wooly example. I also thought that their choice of the discrete logistic model with carrying capacity given by a beta distribution as particularly poor. Since the population is very small, an individual-based model, using best current estimates of demographic parameters, would have been much better.

I could go on criticizing details of the Clifford et al. paper, but these details are completely superseded by the lack of statistical rigor in the paper, as well as a very poor treatment of the contact process associated with disease transmission.

III. Baumer Et Al. and Croft et al. Documents

I fully concur with Thurmond when he states that: “Description of the science and methodology (in Baumer et al.) was too limited and imprecise to be able to decipher what was done or to assess methods and results.” I would go a step further and state that this publication does not constitute a 'quantitative' study in even the most generous meaning of the term. Rather it is an outline of a how the authors would approach constructing a risk assessment model, should they decide build one. The Baumer et al. study is akin to staking out with pegs and string the locations of the trenches that must be dug to lay the foundations of a building: it does not even represent the foundational stage the building itself. Where this document may have some greater value, although it is outside my area of expertise, is in Section III; but I leave that to others to assess.

Given the preliminary nature of the Baumer et al. model, anything placed on top of it, such as the Croft et al. is likely to topple if it does not establish its own firm foundation. This was not done in the Croft et al. analysis and really remains to be done before the spirit of the Croft et al. prescription for assessment can be implemented. Of particular concern is the methodology used to construct the 'inverted cost surfaces' that are used to represent our best understanding of the likelihood of contacts between wild and domestic sheep. I think the Croft et al. document represents a sincere but premature effort to proscribe an approach to managing what is ultimately a very real risk of disease outbreaks in endangered bighorn sheep populations. More rigorous models and scientific underpinnings are needed. In particular, I think empirical data on the movements of both domestic and wild sheep using the same general locations are needed before a scientific assessment can be made of contact rates between these two species that are adequate for disease transmission. In closing, I refine (using capitalization for emphasis) a statement that I made above: Good models can ultimately yield good statistical results ONLY IF high quality data is available. The bottom line here is there is an urgent need to collect such data.

Review:
'A process for identifying and managing risk of contact between Sierra Nevada bighorn sheep and domestic sheep.' By Baumer, East, Echenique, Howorth, Leinassar, Papouchis, Stephenson, Weaver, Wilson

Reviewed by:
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May 25, 2009

Summary

Description of the science and methodology was too limited and imprecise to be able to decipher what was done or to assess all methods and results. Some specific comments are given below. As noted below, there were serious flaws in the regression model, its interpretation, and in it lack of validation. The authors also misused the model to predict erroneously habitat locations for bighorn sheep, based only on vegetation type etc., and ignored the fact that there are locations with the same vegetation type as locations in native bighorn sheep habitat but that have not been naturally inhabited by bighorn sheep. The authors use of the model in this way will provide spurious predictions for where big horn sheep might range and would expand the area of claimed 'hypothetical' big horn sheep habitat to include areas currently used by domestic sheep operations. This report does not represent good, or even mediocre, science; rather it appears to be an illegitimate attempt to apply some scientific tools, along with inappropriate assumptions, to artificially enlarge the range area considered to be inhabited by bighorn sheep.

Methods

Section II: Spatial Assessment of risk of contact between Sierra Nevada bighorn sheep and domestic sheep.

1. Construct bighorn sheep habitat suitability model
   A multivariate logistic regression model was used to predict preference of habitat by bighorn sheep. No specifics or assumptions were given for the model, and no results were presented indicating parameter estimates for the model. Consequently, one cannot assume the model was correctly constructed and results properly interpreted. Even if the model were constructed properly, the predictors (vegetation type, etc) would not be able to predict with perfect confidence the preference for habitat, as appears to have been assumed here. Typically, very good models might be able to explain 30% of the variation in habitat, if that. Also, there was no evidence that the model underwent any process for validation, which examines how accurate the model actually was. Validation should be completed and acceptable accuracy should be demonstrated before any model is applied or used in any way. Thus, it is not possible to make any conclusions as to whether the 'habitat' suitability surface, which is at the

crux of the work, was constructed properly, with appropriate assumptions, using a well-validated and accurate model. Even if all this were done well, it is unlikely that the habitat surface has an accuracy of more than 30-40%, if that.

2. Create resistance surface;
   This work cannot be assessed without the needed methodologic descriptions indicated above for no. 1. Very poorly done.

3. Identify source points for bighorn sheep movements
   The first sentence makes no sense. A likelihood (probability) of contact cannot be derived from the suitability of habitat. This is contrived and fallacious reasoning. Presence of a suitable habitat for bighorn sheep has little bearing on contact, even if the habitat model was perfect (which it is not). Although one could correctly argue that the probability of contact is low or nil for animals that do no co-habitate an area, one cannot say anything about the contact for animals that do co-habitate an area without knowledge (data) of specific contact characteristics. It is well known that many animal populations share the same habitat and have little or no contact with each other.
4. [Estimate] cost of movements for bighorn sheep on the landscape from source points. An obvious fatal flaw in the methodology here is that one will expect to find 'suitable habitat' that is not in bighorn sheep 'natural home range', which is the territory where the ewes tend to restrict themselves. The model will force ewes out of their home territory if there appears to be a predicted 'suitable' habitat elsewhere, which is contrary to the behavior of bighorn ewes. In fact, in times of starvation or diminished forages, ewes will stay in their preferred territory, rather than move to areas with feed, even if it means starvation and death.

   Generally, the word 'determined' is abused here, and demonstrates a lack of understanding and critical assessment. In these types of studies parameters are 'estimated'; one is seldom if ever able to 'determine'. The reason for raising this point is that modelers should recognize that no model is perfect, and most are downright misleading. To use the word 'determine' suggests the appropriate critical and validated thinking was not at work in developing these models and estimates.

A Review of the Document: 'Modeling risks of disease transmission from domestic sheep to bighorn sheep: implications for the persistence and restoration of an endangered endemic ungulate.'
Report title: 'Assessing risk of disease transmission at the wildlife-livestock interface: the case of Sierra Nevada bighorn sheep'
By Clifford, Schumaker, Stephensen, Bleich, Leoard-Cahn, Gonzales, Boyce, Mazet.

Reviewed by:
M C Thurmond DVM, PhD
Professor Emeritus
Veterinary Epidemiology
University of California
Davis, CA 95616
May 25, 2009

Summary of Review:

This study creates a hypothetical (modeled) situation of presumed contact between bighorn sheep and domestic sheep and applies standard spatial-temporal model to predict contact and mortality, given a set of assumptions. The authors failed to provide necessary and appropriate assumptions, biologic reasoning, or methodology to make conclusions about the risk, if any, of domestic sheep to the health or well being of bighorn sheep in the Sierra Nevada. Methods and assumptions can be expected to greatly overestimate the area bighorn sheep typical inhabit, which would result in larger overlapping areas of bighorn sheep and domestic sheep than actually exists. Highly inappropriate, if not egregious, assumptions were made about co-habitation of the two species and about animal-to-animal contact in the models. These assumptions would greatly over-estimate any contact and any transmission that would in reality ever take place between the two species. The authors ignored the possibility that respiratory disease in bighorn sheep could result from exposure to persistently infected bighorn sheep, which is a common phenomenon in other populations of animals, and not from domestic sheep. The scientific literature was not properly interpreted regarding transmission of respiratory disease from domestic sheep to bighorn sheep. Numerous biases, as illustrated by the systematic and insidious errors, of the study, did not reflect an impartial or objective treatment of the issue, as would be expected in a scientific inquiry. Methods and assumptions are seriously flawed, and thus conclusions have no scientific foundation. The authors did not apply best available or scientifically valid methods or data to the study. Much of the data and assumptions necessary for the model was contrived and without foundation, merit, or biological foundation. Biases imposed by the authors and serious and major flaws in the science preclude any conclusions from, or serious scientific consideration of, this study.

Introduction:

The authors present what appears to be their prejudicial position on the subject by stating 'The presence of domestic sheep within or adjacent to habitat occupied by Sierra Nevada bighorn sheep may threaten recovery and persistence of this unique subspecies, but the degree of risk has not been quantitatively evaluated.' (page 5). The bias of the authors, as revealed here, insinuated itself throughout the study. Authors seem not to be asking the question as to whether there is a risk, which is the fundamental question that still exists and, for the sake of scientific truth, should still be addressed. Rather, they presume there is a risk and they wish to make the case that the risk is by some measure sufficiently high to restrict domestic sheep to some areas. Interestingly, the authors acknowledge, however, that '--- direct contact between Sierra Nevada bighorn sheep and domestic sheep has not been documented in the past 30 years---.'. This lack of evidence for contact between the species is fundamental to the risk question and presents as a fundamental contradiction to their notion that domestic sheep may threaten bighorn sheep. The lack of evidence also does not support assumptions they made in their mathematical models about direct contact. The models were designed to operate as if direct contact would be very common and would occur with an extraordinary high probability (see further comments below).

Methods:

Derivation of transmission probabilities (page7)

There are several problems with the 'science', as described in this section. The use of fixed kernel method is somewhat archaic in that other methods, namely kriging and co-kriging, provide a more accurate estimate of spatial distributions. The fixed kernel method can be expected to inflate the size of the area beyond that which is real, which in this case would make it appear as if bighorn sheep have a wider distribution than in fact the actually have. Thus, the areas of overlap for bighorn sheep and domestic sheep, as estimated by the model, would be unrealistically large.

Imprecision in the writing makes it difficult to interpret results with a bandwidth of 0.8, which should have a unit of measure (miles, km, meters, etc). Such imprecision and failure to report something as simple as unitage begs the question of the quality of investigation pursued by the authors. If the bandwidth represents miles or kilometers, then the estimates could be further inflated than by use of the fixed kernel method alone. Peripheral movement of bighorn sheep outside their chosen 'home' territory of 0.8 mi, or even 0.8 km, would not likely be a common occurrence, especially for the majority of the population, which is female. Again, this 'adjustment' of the modeling would falsely enlarge even further the area estimated for bighorn sheep and would make it appear that there is a large amount of area that overlaps with domestic sheep.

The use of 100% volume contour also would result in a very large area for bighorn sheep, and likely overestimated the typical area for bighorn sheep because data points from which these estimates were obtained likely contained some points representing rare or unlikely excursions of bighorn sheep outside the normal bighorn habitat.

The authors noted that there is a patchyness and natural fragmentation to the population structure of Sierra bighorn sheep, as referenced (Wehausen 1980, Bleich et al. 1990). Their spatial model, however, ignores this fragmentation and patchyness and assumes a homogeneous, rather than patchy or fragmented distribution of bighorn sheep. This means that the model would behave as if a bighorn sheep would be just as likely to be in one area of the estimated habitat as in any other area. Clearly, this is not the case and to assume otherwise would not only misrepresent the distribution and biology of bighorn sheep but would also put an improper weight or emphasis on the number of bighorn sheep in areas of overlap with domestic sheep.

All these techniques and omissions would serve to make the area of bighorn sheep appear larger than it really is and would allow the model to 'pretend' that bighorn sheep would be equally likely to be in one spot at a given time as to be in a completely different spot at that time, when in fact they tend to be together in small groups in their preferred 'home' territory. Obviously, during rut, males stray outside their home territory, but do so in search of other bighorn sheep.

A major problem with the approach taken in this paper is the estimate authors contrived for the probability of overlap of the area they estimated for bighorn sheep and the areas where domestic sheep are allowed, and their illogical and inappropriate extension of this probability to the concept of transmission. They note that this probability is the proportion of domestic sheep allotment that overlaps with their estimated area for bighorn sheep, which, as noted above was estimated using methods that would likely result in a much larger area of bighorn sheep than is truly the case. They also assume that a domestic sheep, as an individual, will be equally likely to occupy one spot in the allotment area at any given time, as any other spot at that same time. Again, this assumption ignores the biology and management of domestic sheep that would result in bands of sheep grazing in selected areas, not randomly in all areas, and in some areas more than in others. As a consequence of this assumption, the model 'pretends' the domestic sheep are widely distributed as individuals throughout the allotment, not in flocks or bands. This assumption, along with the assumption that bighorn sheep also are not fragmented or patchy, helps the model simulate more possible 'contacts' between individual bighorn sheep and individual domestic sheep.

In a not uncommon slight-of-hand, the authors equate the proportion of overlap of bighorn sheep and domestic sheep with cohabitation (tope of page 9). This again is an extraordinary overextension of what is likely to be real, and a serious misrepresentation of biological and scientific reality. Certainly, if there truly were areas of overlap, one would expect some correlation with areas within the overlap that might be cohabitated by both species. This correlation might be in the order of magnitude of say 0.1% or 1%. It certainly is not 100%, which is what the authors have assumed for their model, in a somewhat hidden and devious way that the casual observer would not detect. If an area of overlap were considered 100% cohabitated, then one would expect to observe animals of both species together at any given location at any time within that overlap area. This assumption clearly is an onerous exaggeration of biological reality and is inexcusable for a scientist to make consciously.

In a further extension of their assumption about co-habitation, the authors commit a fatal flaw in their methods by assuming co-habitation is the same as contact between the two species: '--- we assumed that co-habitation was equivalent to contact between the two species'. This fallacious reasoning is responsible for the fatal biological and scientific flaw in the model, but to the author's advantage. Because of this assumption, the model is capable of predicting extensive disease contact for bighorn sheep and of predicting dire consequences for domestic sheep. One can cite many populations of animals and people that cohabitate in the same geographical space and that seldom, if ever, come into contact with each other. It is ludicrous to assume that just because two species share a geographic space they would necessarily have to contact each other. Humans share space with many bird species, for example, but seldom actually touch a bird. Such an egregious assumption also ignores basic and fundamental concepts of infectious disease epidemiology that specify conditions of contact (typically actual physical contact) that must be met before a disease agent is transmitted. This is known as 'effective contact' or 'adequate contact'. For example, even though one person may have had physical contact with a person shedding a cold virus, the cold virus may not have been transmitted sufficiently to cause disease. Each disease has its own characteristics for an effective contact; for some, 1 of 20 contacts (5%) might be 'effective', whereas for others 1 of 100 (1%) or more might be 'effective' and result in transmission. Effective contact also depends on the amount of agent shed (number of bacteria or viruses) by the infected animal and on the susceptibility of the contact animal. Thus, in order for transmission of an agent to take place, 1) the infected animal must be actively shedding sufficient numbers of the agent to cause an infection, 2) the recipient must come under close physical contact with the area of the infected animal (eg, nose) shedding the virus for a sufficiently long period of time for a sufficiently large dose of the agent to be transferred, and 3) the donor's immunity must be inadequate to protect against infection given the dose of the agent. Clearly, none of this common knowledge of infectious disease epidemiology was considered in this model.

In this study, the authors assumptions for effective contact were 100% (always became infected), 50% (became infected half the time), and 25% (became infected a quarter of the time), all of which were very excessive expectations and without any foundation in scientific data. Even under feedlot conditions, where animals are highly stressed and crowed and where infected animals shed large numbers of infectious agent, effective contact rates are typically in the order of magnitude of 10% or less. Assumptions of such inappropriately high effective contact rates would result in a strong bias favoring the spread of an agent from domestic sheep to bighorn sheep.

Model to predict impacts of a respiratory disease. (pages 10-12)
Some of the assumptions used in the disease transition state model are either invalid or overly stated. The authors have assumed in their model that a bighorn sheep experiencing persistent pasteurellosis could recover and become susceptible again. No citation or scientific evidence was presented for this as fact, and, given the scientific literature on pasteurellosis, it would be very unlikely that any animal could become newly infected again following a natural infection with the agent, if the animal truly had a persistent infection. Either the authors were not aware of the current state of knowledge and science surrounding pasteurellosis, or they chose to ignore it. Thus, the authors in fact did not '--- use the best available spatial, demographic, and disease data---', as claimed.

The authors also failed to consider the likelihood of intermittent shedding of agents causing respiratory disease in persistently infected bighorn sheep and the possibility, if not reasonable probability, that such a manifestation of infection would account for an initial case of respiratory disease in bighorn sheep, and not from exposure to a domestic sheep as they designed their model to assume. In many persistent infections, animals can experience an exacerbation of disease that results in renewed shedding of the agent and exposure of other animals. Such an event could follow conditions of nutritional or environmental stress, or experience with some other disease, which certainly would be expected for bighorn sheep. The author's complete omission of what would appear to be a likely scenario for respiratory disease in bighorn sheep is somewhat baffling, unless they were attempting to slant their findings so as to incriminate domestic sheep as the only culprit for respiratory disease in bighorn sheep. It is understandable that very little bighorn sheep data exist, but if the authors seemed willing to use expert opinion to provide contrived 'data' when no real data existed, then there would be no reason to not model respiratory disease in bighorn sheep as a result of exposure solely to a persistently infected bighorn sheep that was shedding the agent.

Generally, use of expert opinion, as was applied in this paper, would be considered inappropriate. Ethical guidelines dictated that it is appropriate to use expert opinion in epidemiological studies and modeling to provide parameter estimates only when the expert's view is completely independent both of the study and of the data being studied. Clearly, in the study by Clifford et al., one or more of the authors contributed expert opinion, while having a vested interest in the study and in the outcome of the study, and thus would have a serious conflict of interest.

Use of 'Science' as a guise:
Unscientific jargon and terminology and imprecision can be a harbinger for bad science. Here the authors claimed that they 'determined' distributions, when in fact the best one could hope for was a rough 'estimate'. Use of words like 'determined' indicate lack of scientific critical assessment and understanding of what methods actually can and cannot accomplish. It is seldom possible in science to absolutely 'determine' what is or is not fact or what might or might not happen. Rather, science, under carefully disciplined methods so as not to induce bias or prejudice, attempts to obtain 'estimates'. If, after repeated studies, each with a different approach or design aimed at the same general objective, the findings generally agree, then we can possess some degree of confidence in the conclusions.

Mathematical and statistical models can provide estimates based on the assumptions that are inputed into the model. These estimates are only as good or as believable as the assumptions that underlie the model. Thus, the science of modeling involves provision of accurate and precise assumptions that can be defended scientifically. Regrettably, for the reasons stated above, the authors have failed in this task. In this study, we have insight into how use of technical tools, such as models, can be used under the guise of 'science' to make claims and to coerce decisions toward one's own political agenda. Such an abuse of the term science is not only highly offensive to those who have strived to undertake high quality, unbiased science, it degenerates the findings we obtain from truly legitimate science, leaving us to wonder who can we trust and what can we believe.

Scientific references and cited papers.

A very unusual aspect of this work, compared to scientific efforts, is that most (27 of 45) of the documents cited are not from the peer-reviewed scientific literature. Rather, they are internal agency documents, monographs, or proceedings from meetings, none of which has undergone the necessary and critical scientific review to provide biological bases for the assumptions and rationale of this study. Typically, these types of citations would not be permitted in a scientific report, and many are not even available for critical independent analysis. Because those papers cited from proceedings and symposia were not of sufficient scientific quality to be submitted or to be published, one would beg the question why they were used at all by the authors. If the findings in these papers were so improper or inadequate as to prohibit publication, why would they be acceptable for use in this model? Again, the use of non validated information indicates the study was not based on the best available data; rather, it appears to suggest the study was based, in part at least, on the poorest available data.

The authors were specious in their proffered interpretation of what they refer to as 'pen transmission studies' (res) , wherein they claim 100% of bighorn sheep reported in other studies acquired respiratory disease after being co-housed with domestic sheep. What the authors failed to acknowledge was that some of the infections were induced by injection of the agent, which is hardly representative of natural exposure. For other infections, perhaps attributable to contact with sheep, disease was acquired only after several weeks of very close physical contact with numerous sheep under very confined and crowded conditions. Under experimental conditions like these, where several animals are forced into physical contact for several weeks in very close conditions, animals are known to become highly stressed, resulting in lowered immunity to infection and renewed shedding of infectious disease agents. These conditions hardly would mimic or represent what one might expect under range conditions from a brief, chance contact between a single bighorn sheep and a single domestic sheep, neither of which had experienced the stressful environment that would diminish immunity and allow a recrudescence of shedding. Nevertheless, the authors chose to assume such a ludicrous scenario of contact and exposure for their model by selecting model probabilities for transmission as high as 25, 50, and 100%. Again, the authors did not apply the best available data, or even mediocre reasoning, to their study.