

## Fwd: Meta paper

Mike Russell <Mike.Russell@gov.ab.ca>

To: Robert Serrouya <serrouya@ualberta.ca>

Cc: Clayton Lamb <ctlamb@ualberta.ca>, Barry Nobert <Barry.Nobert@gov.ab.ca>, Dave Hervieux <Dave.Hervieux@gov.ab.ca>

Thu, Feb 18, 2021 at 2:59 PM

Hi Rob and Clayton,

I was about to send this before Clayton's question about the censoring, so added that to my bullets to reduce the number of e-mails.

Attached are the CMR/SECR reports for NAR and RPC (sorry they are pretty raw still). I didn't have an ALP report but I put the estimates in the table below. As discussed, not for distribution. I'm not sure how helpful this will be, but it might be useful.

### Censoring individuals for which it is unclear if the event occurred before or after May 1<sup>st</sup>:

It is a rare occurrence but because we have such a large dataset it does occur. It was more of an issue with VHF collars that would be relocated infrequently. If they were noted alive in January but not found on our April survey, but found dead in the summer we cannot determine if their death occurred in one lambda year or the next. While I'm sure there are ways to incorporate a probability approach to assign the known fate to one lambda year or another, we instead censored them from their last observed alive date to avoid negative bias in our survival estimates.

### Minimum total counts:

I also tabulated the total counts for adult cows, adult bulls and calves from our spring composition surveys in the same spreadsheet that we provided to you last fall. There are a few early years that we don't have the group observations for, so these are blank. As discussed, our composition surveys count a large portion of each population but are biased to the collared cows. Sightability is wickered when these caribou live in the trees, and in some years a large proportion do. There is also bias in this because all populations have transitioned from significant migration into the forested foothills, to an alternative strategy of staying in the mountains. It isn't a wild hypothesis to propose that there may be a correlative trend in sightability error due to this. Anyway, these counts should not be used for estimates of abundance or trend. I'm not sure the best approach for the IPM but correcting for average group size and active collars will likely be necessary due to the bias in our survey approach.

### DNA:

- Based on a rough assessment from the DNA MR estimate, our sampling fraction was reasonably high in recent years (see last column below).
- We found very few uncollared groups on our transect surveys for DNA, and also during alpine flights along contours during multiple other surveys (composition extra flying, WMU440 moose, rut survey in Narraway).
- CMR assumes closure with no mortality in adults and calves throughout the winter, so there is negative bias in the MR estimates and therefore the sampling fraction will also be negatively biased.
- I used the number of calves counted and assumed a 50:50 sex ratio in the calves to estimate the sampling fraction for adult caribou (subtracted ½ calves from SECR estimate).
- I'm not sure how consistent this sampling fraction would be across the dataset but I expect it varied with the number of active collars. We have had a pretty good and well distributed collar sample in RPC and ALP in most years though. Our collar sample in Narraway really declined because we ran out of cows to collar, but the trend in total count is a pretty good representation of the decline/crash that began ~2010. Our survey efforts increased dramatically in recent years as we tried to account for the possibility we were missing groups... we weren't ☹
- I recognize the sex ratio in ALP is a bit of a surprise. It is interesting that the sampling fraction for males in RPC comparison is similar.

Local Population	Survey Date	Type	Group	N	SE	95% CI	Estimated Minimum Sampling Fraction on Composition Surveys
A La Peche	2017-18	SECR	Males	81	4.2	76-93	0.32
			Females	71	2.5	68-80	0.88
			Total	152	4.9	142-162	0.63
Narraway	2018-19	CMR-Prelim	Males	18	6.1	11-25	0.58
			Females	38	3.4	27-51	0.68
			Total	56	--	--	0.68

Redrock-Prairie Creek	2018-19	CMR-Prelim	Males	63	7	80-102	0.33
			Females	90	5.7	50-78	0.76
			Total	153	--	--	0.65

**From:** Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>  
**Sent:** Wednesday, February 17, 2021 1:02 PM  
**To:** Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)>  
**Subject:** Re: Meta paper

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250-814-4632

On Wed, Feb 17, 2021 at 11:17 AM Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)> wrote:

Thanks Clayton.

Yes agree. That's a similar process we explored and eventually had Dan include a frequentist approach for the app. Most of the differences between the 2 methods were small. Unfortunately, our biggest challenge is explaining the situation with clarity in the boardrooms. Juggling Bayesian theory, priors/imputation and fluid ever-changing estimates to non-scientists would eat up too much oxygen in the conservation discussion, even if they might be better estimates. Also the trends in the estimates are robust and speak for themselves, so fancy sometimes hinders. So I guess that's a longer way of saying I agree ☺

Attached are two tables that explain how the survival estimate is calculated. Nick DeCesare developed this workflow in 2012 and we have been using it since. Barry is working on adjusting Dan's script that automates many of these aspects, but the precise development of the life history tables remains the most difficult aspect to automate (due to a very complex telemetry database, with multiple data sources, sampling intervals and determination of fate outcomes/censor events).

Two tabs in the attached excel workbook include:

Life\_History – We update these tables manually for all collared individuals each year. It is a monthly life history events table with all events (capture/censor/death/alive) assigned to month that they fall within. This is an annual estimate (May 01-April 30). We censor individuals that we can't precisely determine if they died before, or after, the April 30<sup>th</sup> threshold.

KM\_Survival – Pretty straight forward. Use the resulting monthly estimates of at-risk sample and all events to calculate a 12-month mean estimate of KM-S-hat and variance. The km variance column is the Greenwood formula that we use for the estimate.

We then use PopTools (no longer supported) to bootstrap the estimates. Barry has created an R script to replicate this and the outputs are comparable. Barry would you mind sending along?

**From:** Clayton Lamb <[ctlamb@ualberta.ca](mailto:ctlamb@ualberta.ca)>  
**Sent:** Saturday, February 13, 2021 9:11 AM  
**To:** Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)>  
**Cc:** Barry Nobert <[Barry.Nobert@gov.ab.ca](mailto:Barry.Nobert@gov.ab.ca)>; Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>  
**Subject:** Re: Meta paper

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Thanks all,

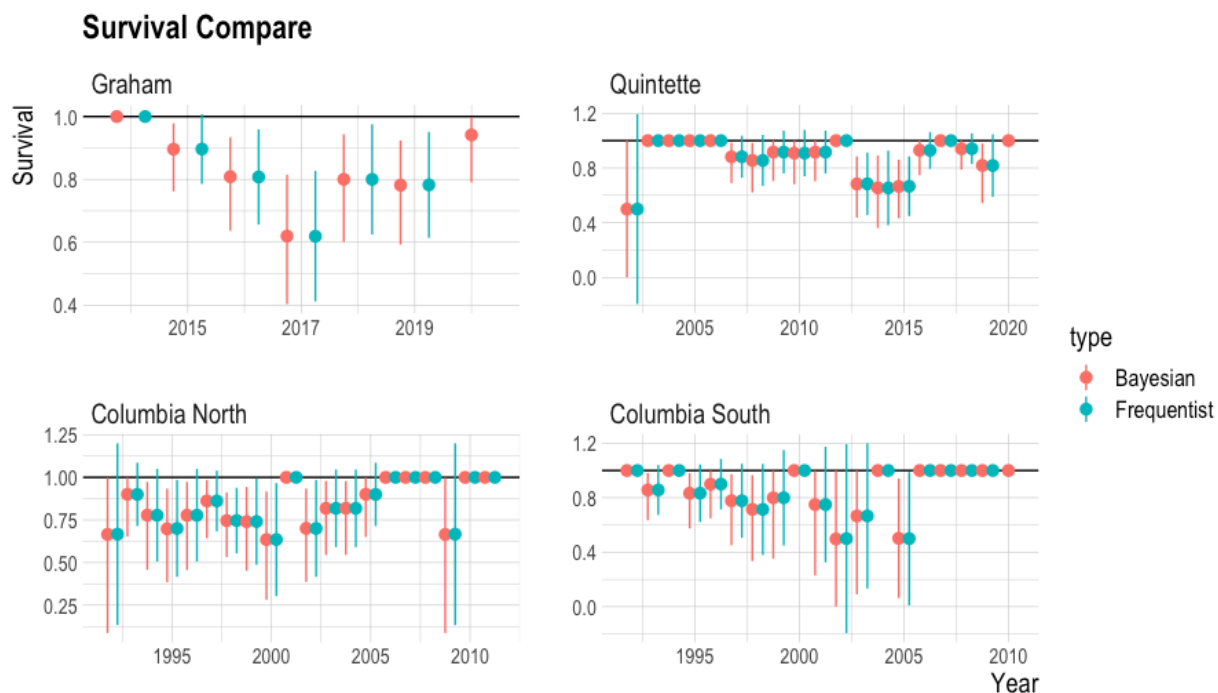
Any methods/equations for how you calculate survival, and the R script for bootstrapping errors would be very helpful, Mike. I'd like to have the survival estimates and errors as comparable between BC and AB as possible. So I would happily use the AB method for our data.

A note on the Eacker app- I dug into the underlying code a few months ago and pulled out the key pieces so I could run the "Eacker" bayesian survival estimates outside the app. The app basically uses frequentist survival estimates, and they only are different when a prior is shared between herds. Some very small differences in error bands, but that was it. I ended up opting to just use frequentist survival approaches as they were similar, simpler, and also essentially what the Eacker app was using anyways. Our GitHub for this work is not public yet so I can't show you the code easily, but here is a screenshot of the plot comparing the two types of estimates for 4 herds.

Best,  
Clayton

--  
Clayton Lamb, PhD (he/him)

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On Feb 11, 2021, at 4:50 PM, Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)> wrote:

We calculate survival no problem, in R, but we wanted to do it as closely the same way as you guys. We have 1500 raw caribou records (indiv caribou) in BC for the IPM - it's impressive. I'll bring in Clayton here to this thread.

On Thu, Feb 11, 2021 at 3:37 PM Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)> wrote:

Hi Rob,

Our KM survival analysis wasn't calculated in R for these data but the bootstrapping of the estimates was. We are looking to transition as much of our workflow to R as possible, but we are still working out the issues and QAQC of this method.

Are you looking to calculate survival for a different dataset?

I attached the code for the Shiny App that Dan Eacker developed that includes a KM-analysis in R. We haven't adopted this script for our reporting of vital rates yet. Barry has been doing some great work to iron out the outstanding issues and is your best bet if you have questions.

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**From:** Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>  
**Sent:** Thursday, February 11, 2021 3:07 PM  
**To:** Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)>  
**Subject:** Fwd: Meta paper

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Hey Mike, do you do your survival calculations in R?

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**From:** Clayton Lamb <[ctlamb@ualberta.ca](mailto:ctlamb@ualberta.ca)>  
**Date:** Thu, Feb 11, 2021 at 2:02 PM  
**Subject:** Re: Meta paper  
**To:** Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>

Wonder if they do this in R? Would just replicate on our side if I got the code or the formula

Best,  
Clayton

--  
Clayton Lamb, PhD (he/him)

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On Feb 11, 2021, at 2:59 PM, Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)> wrote:

"mortality estimates represent the KM based on staggered entry design (Pollock '89) for our collared sample of female cows."

----- Forwarded message -----  
**From:** Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)>  
**Date:** Thu, Nov 12, 2020 at 11:27 AM  
**Subject:** RE: Meta paper  
**To:** Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>  
**Cc:** Dave Hervieux <[Dave.Hervieux@gov.ab.ca](mailto:Dave.Hervieux@gov.ab.ca)>, Troy Hegel <[Troy.Hegel@gov.ab.ca](mailto:Troy.Hegel@gov.ab.ca)>, Barry Nobert <[Barry.Nobert@gov.ab.ca](mailto:Barry.Nobert@gov.ab.ca)>

Hi Rob – Had a chance to review the treatment categories with Dave today (Table below and also in the spreadsheet). Let me know if you have any questions about the attached vital rate estimates. Sorry to be redundant but, as before, the methods follow CJZ Hervieux et al (2013) "Widespread declines" paper. The recruitment and Lambda estimates are based on the recruitment of females (i.e. female calves only, Hatter and Bergerud 1991) and the mortality estimates represent the KM based on staggered entry design (Pollock '89) for our collared sample of female cows.

We haven't had a chance to discuss again, but a couple things that will be important for interpretation:

- **Lag effects** - I can't remember if we discussed, but if not already accounting for it, the analysis should account for lag effects of control efforts relative to vital rates (maybe more delayed on adult survival, more immediate for recruitment)? My minimal understanding is that IPMs typically use priors that take this into account, but would be good to hear how the models address this.
- **Cumulative effects across years** - Similarly, the annual vital rates are likely not independent of control efforts in previous years and the cumulative implementation of control treatments may be important. This may be addressed in the IPM, but we should remember to consider its effect.
- **Geographic scope effect** - We've spoken about it a few times, but the range-specific analysis may be misleading without the larger geographic extent of the control efforts. For example, until 2013 very few wolves were removed outside of the caribou ranges. In 2014 the control efforts not only expanded into the summer range of the ALP pop, but also the intensity and geographic extent of removals increased in the Lower foothills and central mixedwood subregions outside of the ranges, in the north and east of all 3 of the SMC ranges. In many ways, the story is that all 3 of these populations are likely responding to the wolf removals that occurred not only in the boundaries of the ranges themselves, but also the more productive areas that likely act as a source (metapop) for wolf recolonization adjacent to and between these three ranges. Our df might not be 3 here, post-2013. We do not expect wolf removals within the range boundaries alone to result in the response in caribou rates that these data represent. I'm not sure how to address this in the model, but certainly we need to be aware of this and speak to it in the manuscript.
- Narraway declined rapidly and it was difficult to maintain an adequate sample due to the reduced population here. As a result, our Narraway estimates are based on small sample sizes since 2013, before the implementation of predator control. The sample remains representative of the small remnant population (high sampling fraction), but the estimates are based on a smaller sample; the robustness of which may be disproportionately weaker than the other 2 populations for these years.
- Year in the attached table refers to the end of the caribou year. For example 2016 = estimates of female vital rates between May 1, 2015 and April 30, 2016.

Table with wolf control treatment categories, specified by winter period and coinciding with caribou year (May 1 to Apr 30), for each of the SMC populations.

Pop'n	No wolf control		Wolf Control in Winter Range Only		Wolf control in both Winter and Summer Ranges	
	Start	End	Start	End	Start	End
NARR	2002/03	2014/15	2015/16	2016/17	2017/18	2019/20
RRPC	1994/95	2013/14	2014/15 <sup>1</sup>	2014/15 <sup>1</sup>	2015/16	2019/20
ALAP	1998/99	2004/05	2005/06	2012/13	2013/14 <sup>2</sup>	2019/20

<sup>1</sup> There were a few opportunistic removals in summer range during 2014/15 in RPC, but considered minimal

<sup>2</sup> Removals did not occur in the ALP summer range until March of 2013/14

Classification: Protected A

**From:** Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>  
**Sent:** Thursday, October 29, 2020 5:29 PM  
**To:** Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)>  
**Subject:** Re: Meta paper

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Hi Mike

How's it coming along? No huge worries but we're getting ready to data crunch

thanks

On Fri, Oct 16, 2020 at 8:53 AM Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)> wrote:

Hi Rob – Just a heads-up that I haven't forgotten about this, am almost finished. Will have this early next week. No later.

Classification: Protected A

**From:** Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>  
**Sent:** Wednesday, October 07, 2020 10:12 AM  
**To:** Mike Russell <[Mike.Russell@gov.ab.ca](mailto:Mike.Russell@gov.ab.ca)>  
**Subject:** Fwd: Meta paper

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**From:** Robin Steenweg <[Robin.Steenweg@gov.ab.ca](mailto:Robin.Steenweg@gov.ab.ca)>  
**Date:** Fri, Jan 12, 2018 at 9:49 AM  
**Subject:** RE: Meta paper  
**To:** Robert Serrouya <[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)>, Dave Hervieux <[Dave.Hervieux@gov.ab.ca](mailto:Dave.Hervieux@gov.ab.ca)>

Hi Rob,

Attached are the annual lambda values, and confidence intervals for Little Smoky, ALP, and RRPC caribou populations. I've included beside each lambda value for each year for each population, the treatment (i.e. No wolf control, vs wolf control).

Please let me know if this all looks good. Hopefully writing is going well?

Robin

**From:** Robert Serrouya [mailto:[serrouya@ualberta.ca](mailto:serrouya@ualberta.ca)]  
**Sent:** December-04-17 11:20 AM  
**To:** Robin Steenweg; Dave Hervieux  
**Subject:** Meta paper

Hi Dave and Robin

Dave- Thanks for the chat last week about the meta paper that looks at lambda responses to treatments across broad areas.

Attached is the spreadsheet with the relevant data. I'm just starting to fill it in (ie it's a template) and I am asking the relevant P.I.s to fill in as well. Let's keep all; this confidential for now

Many columns will not be relevant for Alberta because of the different method of measuring lambda. I've already filled in the LSM & RPC because it is published. Could you please fill in the relevant before and after data for the other nearby ranges? Years for start and end will be important.

also, as we discussed, it would be easiest if some ranges were lumped? ie those subject to the same treatment with a similar response?

I may also call you to help with "outlining the treatment polygons properly" with a GIS shapefile. I'm sure Robin can help with this.

Current suggested author list is:

Me (Rev, and general concept)

Bruce (Rev, many places)

Dale (Quintette, Peace wolf control, Graham, etc)

Dave (LSM, all Alberta ranges)

Robin (Parsnip, and new ranges being treated in Alberta)

Doug (Parsnip, Kennedy feeding trials)

Chris Ritchie (Transplant)

Stan (All)

Target journal (likely to fail): Science

Title: Using adaptive management to save endangered species

I'm happy to follow up with any phone calls as needed.

Cheers

--

Rob Serrouya

University of Alberta | ABMI | Caribou Monitoring Unit

Resources for Woodland Caribou Science and Recovery:

<https://cmu.abmi.ca/>

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<2020\_10\_Serrouya\_SMC\_Vital\_Rates.xlsx>

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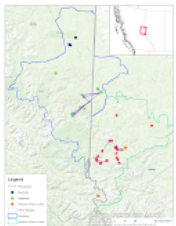
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#### 4 attachments



**RRPC - Narraway.png**  
8423K

 **RPC-Narraway\_Tables.pdf**  
186K

 **RPC-Narraway Summary.docx**  
29K

 **2020\_10\_Serrouya\_SMC\_Vital\_Rates\_w\_TotalCnt.xlsx**  
31K