

RE: [EXTERNAL] reminder - genetics data

Jerod Merkle <jmerkle@uwyo.edu>

Sun 12/18/2022 10:56 AM

To: Geremia, Chris J <Chris_Geremia@nps.gov>

Hey Ger,

I started working on network - genetics data a bit today. And another question arose regarding the match between genetics and GPS data... I think I might be missing some GPS data. There are 42 individuals in your genetics data that don't seem to have GPS data in my records. According to your VGL Bison Sample Key, many are animals captured a long time ago, and many have NA in the Date and Year columns. I am using a cleaned GPS dataset you sent me many years ago and then I'm merging it with Molly's more recent data. Anyway, maybe that old dataset you sent me was a subset? Here are the Animal IDs I am missing (note that I replaced the YELL-, Yell-, or YNP with BI, but the numbers should be right):

```
> genIDs[genIDs %in% d$id == FALSE]
```

```
[1] "BI001" "BI002" "BI003" "BI004" "BI005" "BI006" "BI007" "BI008" "BI009"  
[10] "BI010" "BI011" "BI012" "BI013" "BI014" "BI015" "BI016" "BI018" "BI021"  
[19] "BI022" "BI023" "BI024" "BI027" "BI045" "BI049" "BI052" "BI057" "BI060"  
[28] "BI061" "BI062" "BI063" "BI068" "BI069" "BI088" "BI090" "BI108" "BI115"  
[37] "BI145" "BI153" "BI356" "BI368" "BI373" "BI930423"
```

Any thoughts here?

Thanks,

Jerod

From: Geremia, Chris J <Chris_Geremia@nps.gov>

Sent: Friday, September 9, 2022 11:06 AM

To: Jerod Merkle <jmerkle@uwyo.edu>

Subject: Re: [EXTERNAL] reminder - genetics data

Jer,

That is correct.

Here is the master excel spreadsheet of the genetics bank data. The columns "Eartag" and "Animal Status" identify the radiomarked bison. Please take a look at this in addition to checking with me about some of these unknowns.

Ger

From: Jerod Merkle <jmerkle@uwyo.edu>

Sent: Friday, September 9, 2022 10:47 AM

To: Geremia, Chris J <Chris_Geremia@nps.gov>

Subject: RE: [EXTERNAL] reminder - genetics data

Hi Ger,

One quick question. There are some ids in the gps data that do not have genetics data (see list below). Can you confirm this (assuming blood wasn't taken, or whatever)? I just want to make sure there isn't a funny error somewhere. Thanks.

```
[1] "033" "038" "064" "066" "067" "070" "071" "072"
```

[9] "075" "080" "095" "096" "301" "3225" "360" "583"

Jerod

From: Geremia, Chris J <Chris_Geremia@nps.gov>
Sent: Wednesday, September 7, 2022 3:12 PM
To: Jerod Merkle <jmerkle@uwyo.edu>
Subject: Re: [EXTERNAL] reminder - genetics data

Hey Jer,

There are 156 collared bison in this analysis.
Relatedness based off of microsats at 52 loci.
I estimated pairwise relatedness measures for 7 common indices:

COMMAND	NAME AND/OR REFERENCE	COLUMN IN RESULT FILE
dyadml	dyadic likelihood estimator, Milligan (2003)	11
lynchli	Li <i>et al.</i> (1993)	7
lynchrd	Lynch and Ritland (1999)	8
quellergt	Queller and Goodnight (1989)	10
ritland	Ritland (1996)	9
trioml	triadic likelihood estimator, Wang (2007)	5
wang	Wang (2002)	6

Each row in the output file shows is a single pairwise comparison. Columns show the 2 individuals being compared (ind1.id, ind2.id) and the value of each of the indices:

```
pair.no ind1.id ind2.id group trioml wang lynchli lynchrd ritland quellergt dyadml
1 1 Yell-025 Yell-041 YeYe 0 -0.1775 -0.1537 -0.0724 -0.0845 -0.1216 0
```

Pairwise relatedness increases with the value. Reference values are 0.50 - parent/offspring, 0.50 - full sibling, 0.25 - half sibling, and 0.00 - unrelated. But point estimates show a bit of variation.

I simulated parent offspring, full and half siblings, and unrelated individuals from our allele frequencies. Each estimator did a pretty good job of identifying those individuals. The correlation coefficient of relatedness values for estimated and simulated values were: dysaml (0.95), lynchli (0.93), lynchrd (0.90), quellergt(0.95), ritland(0.81), trioml(0.96), and wang (0.93). It seems like you could use any of the indices based on this simulation analysis, let's hope ritland estimator doesn't provide the best fit.

I will work on grouping the animals and building some dendrograms or dapc plots.

Good luck.

I will try to keep our numerous research projects on the table and keep progress rolling on my side.
Ger

From: Geremia, Chris J <Chris_Geremia@nps.gov>
Sent: Wednesday, September 7, 2022 8:21 AM
To: Jerod Merkle <jmerkle@uwyo.edu>
Subject: Re: [EXTERNAL] reminder - genetics data

On it this am. Sorry again for the delay.

From: Jerod Merkle <jmerkle@uwyo.edu>
Sent: Tuesday, September 6, 2022 9:16 AM
To: Geremia, Chris J <Chris_Geremia@nps.gov>
Subject: RE: [EXTERNAL] reminder - genetics data

No worries. If you can get it to me within the next week or two, that would still work. Thanks!
Jerod

From: Geremia, Chris J <Chris_Geremia@nps.gov>
Sent: Friday, September 2, 2022 8:11 PM
To: Jerod Merkle <jmerkle@uwyo.edu>
Subject: Re: [EXTERNAL] reminder - genetics data

Hey Jer,

It's Friday evening 9/2, and I just sat down to run the genetic analyses. For whatever reason the networks are down and I can't tackle. I'm heading out for the weekend and will be back Tues evening. 10 year anniversary. I will work on it then.

I'm sorry. It's been a rather bad time. I realize you need this now. My sincerest apologies. Starting next week I am around and can really buckle down on the things we spoke about.

Ger

From: Jerod Merkle <jmerkle@uwyo.edu>
Sent: Friday, August 26, 2022 9:06 AM
To: Geremia, Chris J <Chris_Geremia@nps.gov>
Subject: RE: [EXTERNAL] reminder - genetics data

That'll work. Thanks!

From: Geremia, Chris J <Chris_Geremia@nps.gov>
Sent: Thursday, August 25, 2022 1:34 PM
To: Jerod Merkle <jmerkle@uwyo.edu>
Subject: Re: [EXTERNAL] reminder - genetics data

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Hi Jer,

I remember you needed this soon. I think it's going to be early next week when I can get you the relatedness. Sorry for the delay.

Ger

From: Jerod Merkle <jmerkle@uwyo.edu>
Sent: Monday, August 22, 2022 7:57 AM
To: Geremia, Chris J <Chris_Geremia@nps.gov>
Subject: [EXTERNAL] reminder - genetics data

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Hey Ger,

So wonderful to visit with you two weeks ago! Looking forward to working on all the projects we discussed. In the meantime, have you looked at the genetics data? If so, could you send over the matrix of index of relatedness among the pairs of individuals? I'm at the point in the other analysis where I can pop them in and assess how relatedness affects movement/sociality.

Thank you,
Jerod