

This DietContent_JonahVentures.txt file was generated on 2021-11-03 by Lee Hecker

GENERAL INFORMATION

1. Title of Dataset: DietContent_JonahVentures.xlsx
2. Author Information
 - A. Principal Investigator Contact Information
Name: Lee Hecker
Institution: University of Alberta
Address: 751 General Services Building, Edmonton,
Alberta
Email: lhecker@ualberta.ca
3. Date of data collection (single date, range, approximate date):
2019/12/16
4. Geographic location of data collection: Ronald Lake, Alberta
(57.975336, -111.7049353)
5. Information about funding sources that supported the collection of the data: Primary funding from Natural Sciences and Engineering Research Council of Canada. Supporting funding from the Alberta Conservation Association, Northern Scientific Training Program, and University of Alberta Northern Research Awards.

SHARING/ACCESS INFORMATION

1. Links to publications that cite or use the data: <https://onlinelibrary.wiley.com/doi/epdf/10.1002/ece3.8298>
2. Was data derived from another source? yes/no
 - A. If yes, list source(s): Jonah Ventures (https://jonahventures.com/?gclid=Cj0KCQjw5oiMBhDtARIsAJi0qk0QIVzqVIT8-ecURAYm71vN0JabPS9pG8IaILKYDb7LWNnur68s8w8aAhNhEALw_wcB)
3. Recommended citation for this dataset:
Hecker, L.J., M.A. Edwards, and S.E. Nielsen. 2021. Assessing the nutritional consequences of switching foraging behavior in wood bison. Ecology & Evolution. DOI: 10.1002/ece3.8298

DATA-SPECIFIC INFORMATION:

1. Number of variables: 100
2. Number of cases/rows: 314

3. Variable List:

ESVID - Unique identifier for each taxonomic unit

PrimerID - The kind of primary used in eDNA analyses

ClientID - Identifier for the client

Domain - Plant Domain

Phylum - Plant Phylum

Order - Plant Order

Family - Plant Family

Genus - Plant Genus

Species - Plant Species

Common - Plant common name

ID - Confidence of each read

Number of Species - Number of potential species the read could be

Sequ - DNA sequence of identified in the sample

Spring1 - Summer10a

The number of reads of a particular DNA sequence found in each fecal sample. Those labeled with an "a" are duplicates of the same fecal sample.

ReadSum - the total number of DNA sequence read within a sample