# READ ME

This README_file_SimulationModel_RL.pdf file was generated on 2023-02-27 by Roxane Lassis

## 1. GENERAL INFORMATION

**1.1. Title of Dataset:** Code files and initial metapopulation file used for model construction and simulation analyses for article "Genetic rescue from protected areas is modulated by migration, hunting rate and timing of harvest".

**1.2. Authors Information:**

 **A.** Principal Investigator Contact Information

  Name: Roxane Lassis

  Institution: Département de biologie et Centre d'Études Nordiques, Université de Sherbrooke

  Adress: Sherbrooke, QC, Canada J1K 2R1

  Email: roxane.lassis@usherbrooke.ca

 **B.** Co-investigator Contact Information

  Name: Fanie Pelletier

  Institution: Département de biologie et Centre d'Études Nordiques, Université de Sherbrooke

  Adress: Sherbrooke, QC, Canada J1K 2R1

 **C.** Co-investigator Contact Information

  Name: Joanie Van de Walle

  Institution: Biology Department, Woods Hole Oceanographic Institution

  Adress: Woods Hole, MA, USA 02543

 **D.** Co-investigator Contact Information

  Name: Marco Festa-Bianchet

  Institution: Département de biologie et Centre d'Études Nordiques, Université de Sherbrooke

  Adress: Sherbrooke, QC, Canada J1K 2R1

**1.3. Date of code implementation:** 2021-2022

**1.4. Geographic location of data collection used to parametrize the model:** Alberta, Canada.

# 2. FILE OVERVIEW

## 2.1. File List:

Files of scripts the stochastic individual-based metapopulation model we developed to evaluate the potential for migration from protected areas to mitigate the evolutionary consequences of selective harvest. Model simulations were run to track horn length through time in a metapopulation including large protected and trophy-hunted populations connected through male breeding migrations, under multiple scenarios of male breeding migration rates and harvest regulations. Example of initial metapopulation used to run the model is also provided.

SimulationRuns.R

Simulation design and runs of the simulation model that, at each annual time step, cycles over all individuals and computed horn growth, breeding, migration and survival rates. The model considers four main annual processes that included several sub-processes: 1) Development, including ageing and horn growth, 2) Breeding, including yearling production, siring success, and offspring phenotype attribution, 3) Breeding migration, and 4) Survival, including both harvest and natural mortality. Population sub-processes are ordered within each time step to approximate the sequence of events over a bighorn sheep annual cycle: ageing and yearling production in spring; horn growth in summer; male breeding migration, harvest mortality and siring probability in autumn, and natural mortality over winter. The simulation model uses 29 parameters to model the effects on these sub-processes of individual characteristics such as age, sex and horn length, and environmental variables such as population density and hunting rate.

GenerateInitPopulations.R

Create metapopulations gathering initial protected and exploited populations to use as start metapopulation for each simulation with the script "SimulationRuns.R".

SimulationFunctions.R

Definition of model functions used in scripts "GenerateInitPopulations.R" and "SimulationRuns.R" that simulate life-history and demographic processes of development, breeding, migration and survival.

Init_pop_1.xlsx

Example of initial metapopulation file generated with the script "GenerateInitPopulations.R" and can be used to run the model with the script "SimulationRuns.R".

**2.2. Relationship between files:** To run model simulations, use the script "SimulationRuns.R" where scenarios and model parameters are defined. This script requires an imput file of the initial metapopulation, that can be produced with "GenerateInitPopulations.R". Example of used initial metapopulation is provided in file "Init_pop_1.xlsx". Scripts "SimulationRuns.R" and "GenerateInitPopulations.R" require the model functions defined in script "SimulationFunctions.R".

Folder architecture for the scripts:

1) General folder of the simulation model

"[...]/SimulationModel/"

2) Folder of the scripts to run the simulation model

"[...]/SimulationModel/Scripts/"

"[...]/SimulationModel/Scripts/Run_Model/SimulationRuns.R"

"[...]/SimulationModel/Scripts/Run_Model/GenerateInitPopulations.R"

"[...]/SimulationModel/Scripts/Run_Model/SimulationFunctions.R"

3) Folder of the initial metapopulation files generated by "GenerateInitPopulations.R"

"[...]/SimulationModel/Inits/ "

"[...]/SimulationModel/Inits/Init_pop_1.xlsx"

4) Folder of the output results after model simulation generated by "SimulationRuns.R"

"[...]/SimulationModel/Outputs/"

NB. Above put your folder address instead of "[...]"

**2.3. Additional related data and files that were not included in the current files:** Data from long-term studies in Ram Mountain and Sheep River Provincial Park, Alberta, Canada, used to parametrize the simulation model.

**2.4. Are there multiple versions of the code?** No

# 3. METHODOLOGICAL INFORMATION

**3.1. Description of methods used for model implementation:** Individual-based modelling to simulate a biological system consisting of a protected and a trophy-hunted bighorn population, *Ovis canadensis*, connected through male breeding migrations.

**3.2. Methods for model parametrization:** Estimation of model parameters and initial conditions is based on data from the province of Alberta that includes protected and hunted areas, and more specifically from the Ram Mountain and Sheep River populations of bighorn sheep in Alberta, Canada, with detailed knowledge of life history and population dynamics from decades of monitoring marked individuals.

**3.3. Software-specific information needed to run provided scripts:** Code implementation, model simulations and analyses were conducted in the open-source statistical programming language R (R Core Team, 2021).

**3.4. People involved with model implementation:** Roxane Lassis, Fanie Pelletier, Joanie Van de Walle and Marco Festa-Bianchet.