

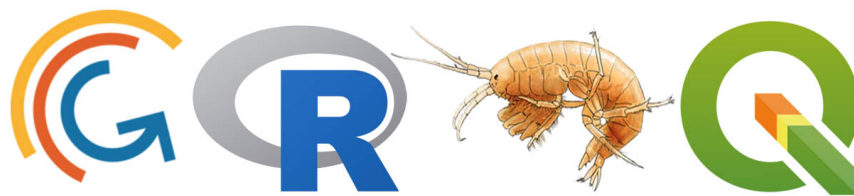


Multi-agent simulation with Gama and R Practical Training Manual

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Prerequisite: to have acquired basic notions in R (e.g. workspace, package, data.frame, list, for loop, function, etc.) and GIS (e.g. shapefile, attribute table, etc.) and corresponding skills.

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Chapter 1

Model presentation

1.1 Ecological bases

This model has been inspired by earlier works carried out by GDRI EHEDE researchers (Li et al., 2015; Clauzel et al., 2015; Li et al., 2017).

In brief, after Li et al. (2015), the black-and-white snub-nosed monkey *Rhinopithecus bieti* is endemic to Yunnan and Tibet, China, and categorized as "endangered" in the IUCN Red List. Surveys have shown that the monkeys live in 15 isolated groups, 12 of them in Yunnan, in a narrow range of the Three Parallel Rivers region, one of the most ecologically important areas of China, the rugged terrain of which makes it difficult to carry out surveys. The species is threatened by habitat alteration, poaching and economic activities such as farming and collection of timber. The areas between populations are damaged by logging, grazing, mining, agriculture and firewood collection. Because of this habitat fragmentation the monkeys may incur a high energy cost if they travel long distances between habitat patches. Fragmentation may subsequently prevent genetic exchange between populations, making the species more vulnerable to extinction. Where required, reserve managers need to establish habitat corridors to facilitate exchange between populations, identifying priority areas for restoration to increase landscape connectivity.

"Snubbies" is a nickname given to the species.

1.2 Geography and data

Tab. 1.1 describes the 5 habitat types defined by Li et al. (2017) and fig. 1.1 shows the study area and the location of the monkey groups with their ID number.

- The shapefile `source2P` corresponds to this map, and the predefined style file `source2P.qml` can be used in QGIS for a better display. The attribute `DN` gives the habitat types of Tab. 1.1.

- The shapefile `source2P_envconv` is the concave polygon of `source2P`
- The shapefile `groups` gives the geographical limit of each monkey group. The group ID number, the name of the area and a population size estimate are given as attributes.

Table 1.1: Habitat quality and composition after Li et al. (2017)

ID	habitat type	Land cover	Altitude	Cost value
1	Optimal	Armand pine and hemlock, fir-spruce forest, coniferous broad-leaved mixed forest	2250-4730	1
2	Suboptimal	Sclerophyllous evergreen broad-leaved forest, shrub-dominated land	1220-5240	10
3	Suitable	Cold coniferous forest, sub-alpine meadow, broad-leaved forest	1310-4950	70
4	Unfavourable	Warm coniferous forest (Yunnan pine forest), hot dry savanna, sparse shrub grass	1200-5490	90
5	Highly unfavourable	Cropland, settlements, water body, barren land	1215-5410	100

1.3 Model purpose

Here we want to build a multi-agent model to simulate and explore the effect of habitat and life-history trait parameters (real values known or unknown) on snubby dispersion.

1.4 Model parameters

1.4.1 Input parameters

step 1 hour (the iteration time resolution)

maximum speed the maximum speed (km/day) that can sustain a snubby in a favourable habitat

maximum survival [0,1] the maximum survival in a favourable habitat. The end user give it per year (s_y), but this should be converted to the scale of the step (here hour), using the following formula: $s_h = e^{\frac{\ln s_y}{365 \times 24}}$

disperser proportion the proportion of snubbies who evade their group and wander outside. The end user give it per year (p_y), but this should be converted to the scale of the step (hour): $p_h = e^{\frac{\ln p_y}{365 \times 24}}$

habitat viscosity $[0,1]$ the resistance of a given habitat. Multiplies the maximum speed to give the speed really sustained in this habitat.

habitat security $[0,1]$ the security of a given habitat. Multiplies the maximum survival to give the actual survival in this habitat.

habitat dislike $[0,0.5]$ the probability for a snubby to move into a habitat of lesser quality.

habitat preference $[0.5,1]$ the probability for a snubby to move into a habitat of better quality.

1.4.2 During simulation

When one snubby dies, one snubby is created in its aboriginal group.

1.4.3 Output parameters

Bitmap Bitmap of snubby distribution (framerate: 6 months).

Shapefile Shapefile of snubby distribution with their individual attributes (framerate: 1 year).

group composition and wanderers Snubby number in each group and outside, split by group origin.

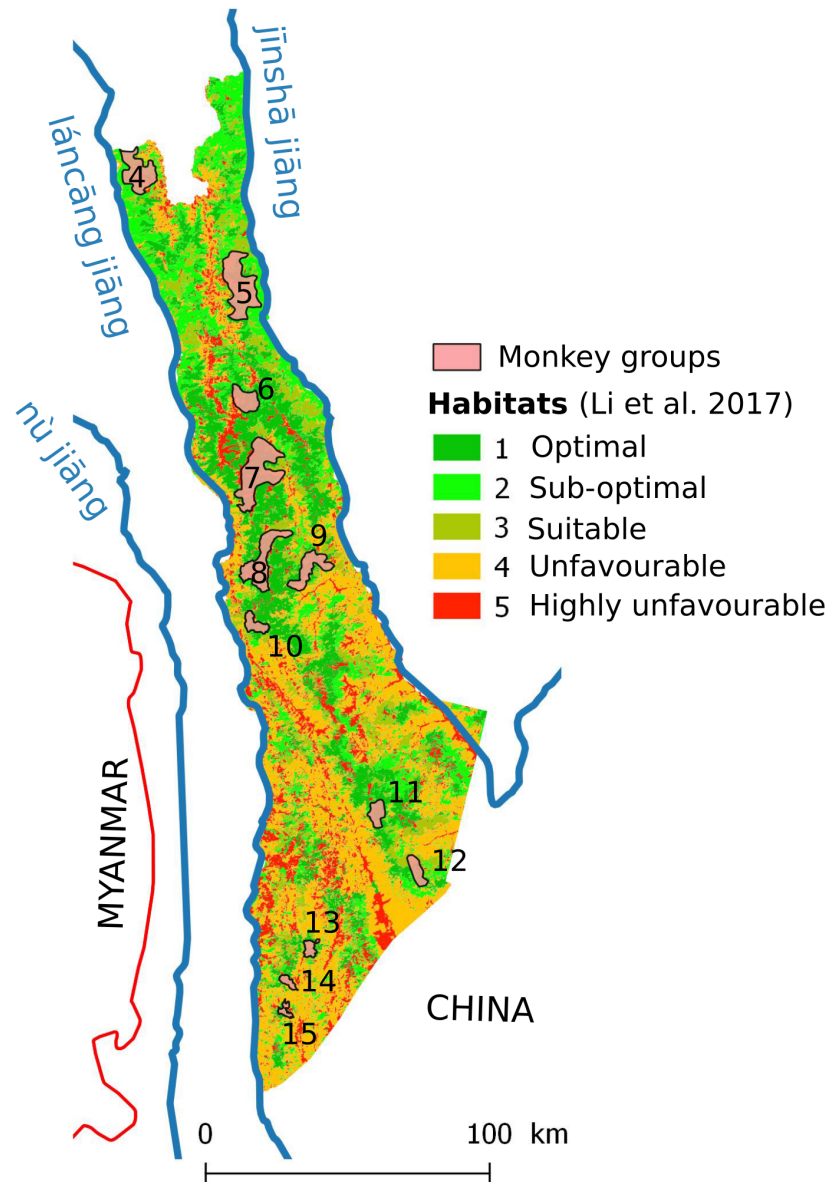


Figure 1.1: Study area. Numbers on the map are the group IDs.

Chapter 2

Gama model

2.1 Principle

See:

- Grignard et al. (2013)
- <https://gama-platform.github.io>
- <https://github.com/gama-platform/gama/wiki/Overview>
- <https://github.com/gama-platform/gama/wiki>
- <https://github.com/gama-platform/gama/wiki/Download>

2.2 Gama in practice

See practical training on November 6-7, 2018.



Chapter 3

Preparing experiments and analyzing results in R

Most likely, for full size research, you will carry out simulations on intensive computing systems with hundreds of cores available in parallel, to run thousands of experiments. Intensive computing systems generally use UNIX and simulations can be run in shell scripts using `gama-headless.bat` as an entry point. R can be run on such a platform as well and be used for simulations. Here, for teaching purpose, this training manual presents how to do it in R on Windows using a personal computer. Your computer has likely no more than 2-4 CPU, and it is advisable not to allocate more than two to the job (we will see later how to do it). In this context, running a large number of simulations or to simulate on a large number of time steps can be time consuming.

3.1 Installing gamar

`gamar` is a R package available at <https://github.com/choisy/gamar>.

With the `library(devtools)`, if not already installed, it can be installed on line as following:

```
1 library(devtools)
2 devtools::install_github("choisy/gamar")
3 library(gamar)
```

First, one declares the path to the program `Gama.exe`. Here below an example, but the path you are going to write must be adapted to your own computer:

```
1 defpath("C:/Program Files/GAMA1.7RC2.Windows.64bits")
```

3.2 Preparing experiments

3.2.1 Reading the model

Now, one must read the model (here `snubbies.gaml`) and extract informations that will be used by R. The path to the model must be declared explicitly (here `snubbies.gaml` is in the folder "U:/Users/pgiraud02/gama_workspace/snubbies/models"). Again this to adapt to your own computer.

```
1 experiment1 <- getmodelparameter("U:/Users/pgiraud02/gama_
  workspace/snubbies/models/snubbies.gaml", "run")
2 experiment1
```

For convenience, we have prepared some home-made functions to ease readings and parameter handling. They are in the file `HomeFunctions.r`. One sources it, and get a `data.frame` with attributes:

```
1 source("Homefunctions.r")
2 ex1<-expe2df(experiment1)
3 ex1
4 attributes(ex1)
```

3.2.2 Preparing the simulations

The duration of each simulation is stored in a variable, here named `simulation_duration` and the number of experiments to run in the variable `B`

```
1 simulation_duration <- 2 * 365 * 24 # two years (step is one
  hour)
2 B<-2 # number of simulations
```

Now, a `data.frame` must be prepared with each row the parameter values of each experiment. Note that parameters can be explored randomly allocating values between limits. See for instance the function `runif` in R (but many others are available).

```
1 ?runif
```

Values can be defined quite flexibly and the value(s) of a given parameter can be used as a function of another. See example below.

```

1 simuls<-data.frame(
2 v_max=0.3472222,
3 s_max=0.5,
4 explorer_snubbies=runif(B,0.1,0.5),
5 viscosity_factor_habitat_1=1,
6 viscosity_factor_habitat_2=0.9,
7 viscosity_factor_habitat_3=0.5,
8 viscosity_factor_habitat_4=0.1,
9 viscosit_factor_habitat_5=0,
10 security_factor_habitat_1=1,
11 security_factor_habitat_2=0.9,
12 security_factor_habitat_3=0.5,
13 security_factor_habitat_4=0.1,
14 security_factor_habitat_5=0
15 )
16
17 simuls

```

Then, experiments can be prepared. This will end up by the creation of one variable `experimentplan` and as many XML files as experiments (e.g. the number of row of `simuls`). Pay attention about the unusual way to specify the path with `setmodelpath`, with a slash `"/U:/..."` at the beginning. This is a provisory way to get around a bug of `gama-headless` running on Windows.

```

1 for (i in 1:nrow(simuls))
2 {
3 local_experiment <- experiment1
4 local_experiment <- setparametervalue(local_experiment,"
5 simulation_id",i)
6 local_experiment <- setparametervalue(local_experiment,"max_
7 snubby_survival_init",simuls[i,"s_max"])
8 local_experiment <- setparametervalue(local_experiment,"max_
9 snubby_speed",simuls[i,"v_max"])
10 local_experiment <- setparametervalue(local_experiment,"max_
11 snubby_survival_init",simuls[i,"s_max"])
12 local_experiment <- setparametervalue(local_experiment,"
13 explorer_snubbies_init",simuls[i,"explorer_snubbies"])
14 local_experiment <- setparametervalue(local_experiment,"
15 viscosity_init_habitat_1",simuls[i,"viscosity_factor_
16 habitat_1"])
17 }

```

```

10 local_experiment <- setparametervalue(local_experiment, "
    viscosity_init_habitat_2",simuls[i,"viscosity_factor_
    habitat_2"])
11 local_experiment <- setparametervalue(local_experiment, "
    viscosity_init_habitat_3",simuls[i,"viscosity_factor_
    habitat_3"])
12 local_experiment <- setparametervalue(local_experiment, "
    viscosity_init_habitat_4",simuls[i,"viscosity_factor_
    habitat_4"])
13 local_experiment <- setparametervalue(local_experiment, "
    viscosity_init_habitat_5",simuls[i,"viscosity_factor_
    habitat_5"])
14 local_experiment <- setparametervalue(local_experiment, "
    security_init_habitat_1",simuls[i,"security_factor_habitat_
    1"])
15 local_experiment <- setparametervalue(local_experiment, "
    security_init_habitat_2",simuls[i,"security_factor_habitat_
    2"])
16 local_experiment <- setparametervalue(local_experiment, "
    security_init_habitat_3",simuls[i,"security_factor_habitat_
    3"])
17 local_experiment <- setparametervalue(local_experiment, "
    security_init_habitat_4",simuls[i,"security_factor_habitat_
    4"])
18 local_experiment <- setparametervalue(local_experiment, "
    security_init_habitat_5",simuls[i,"security_factor_habitat_
    5"])
19
20 local_experiment <- setfinalstep(local_experiment,simulation_
    duration)
21 local_experiment <- setoutputframerate(local_experiment, "
    simulation_id",24)
22 local_experiment <- setoutputframerate(local_experiment, "
    number_of_dispersers",24)
23 local_experiment <- setoutputframerate(local_experiment, "
    reading_map",30*24) # save the corresponding bit map every
    30 days
24 local_experiment <- setsimulationid(local_experiment,i)
25 local_experiment <- setmodelpath(local_experiment,"/U:/Users/
    pgiraud02/gama_workspace/snubbies/models/snubbies.gaml")

```



```

26
27 local_experiment <- setseed(local_experiment,1)
28
29 if(i<2)
30 {
31
32 experimentplan <- addtoexperimentplan(simulation = local_
    experiment)
33 }
34 else
35 {
36 experimentplan <- addtoexperimentplan(simulation = local_
    experiment,experimentplan = experimentplan)
37 }
38 outFile <- paste0("./input_",formatC(i,width=nchar(nrow(simuls
    )),flag="0"),".xml")
39
40 writemodelparameterfile(experimentplan,outFile)
41 }

```

The variable of interest is `experimentplan`. However here, additionally, XML files are saved on the disk with `writemodelparameterfile`. This can be useful if simulations are run not from R on intensive computing systems and UNIX platforms. There, running simulations with a UNIX shell script is system dependent and will use those XML files (in this case, see with the IT manager how to proceed). Here, with this R script, XML files have been written in the workspace. You can see them either using Windows Explorer or from R with the following command:

```
1 dir()
```

3.3 Running simulations

Simulations are run very simply then. We add some code lines to get the duration of the simulations at the end.

```

1 t0<-Sys.time() # store the start time
2 runexpplan(experimentplan,hpc=2) # run the simulations on 2
  CPU
3 t1<-Sys.time() # store the end time

```

```
4 t1 - t0
```

3.4 Reading results

3.4.1 XML

Simulations results are stored in the folder `./workgamar`. There one finds:

- as many files as experiments, named `run_1.xml`, `run_2.xml`, etc. Those files just describe the values of the input parameters. No point to read them, all useful information is in the data.frame `simuls` (see above 3.2.2).
- a folder named `out_run_1` (or `out_run_2`, `out_run_3`, etc. depending on the number of runs executed before). One finds the following inside:
 - a folder named `snapshot` containing bitmaps. Note the file name gives the number of the experiment and the step. E.g. `reading_map0-10.png` means experiment #1 (the experiment numbers are incremented from 0), step 10.
 - text files `console-outputs-0.txt`, `console-outputs-1.txt`, etc. corresponding to the console outputs of experiment #1, #2, etc. They are not of much interest when everything goes smoothly, but useful to identify where a simulation has crashed, should it happen.
 - xml files `simulation-outputs0.xml`, `simulation-outputs01.xml`, etc. corresponding to the outputs of experiment #1, #2, etc.

One needs some R code to read the XML file. Here we use a home-made function `readNamesXMLOutputs` to read variable names (it as been sourced before see 3.2.1)

```
1 library(XML)
2
3 path<-"./workgamar/out_run_1/" # the path to the XML files
4 outs<-dir(path,pattern="*.xml") # one reads them
5 outs<-outs[order(as.numeric(substr(outs,19,nchar(outs)-4)))] #
   to get the files in the right order whatever the number of
   digit (to avoid this order: 1,11,12,13,...,2, 20, 21,...)
6
7 outs<-paste0(path,outs) # now the full path with file names
8 outs
9
```

```

10 mycolnames<-readNamesXMLOutputs(outs[1]) # one uses a home
    made function to extract the variables names from one of
    the XML files
11
12 results<-rep(list(NA),length(outs)) # one prepares an empty
    list to store the readings
13 for(i in 1:length(outs)) {
14   results[[i]]<-xmlToDataFrame(outs[i]) # we read the XML
    file into a data.frame
15   names(results[[i]])<-mycolnames # one gives names to columns
16 }
17
18 names(results)<-outs # one gives a name to each experiments
19
20 head(results[[1]])

```

3.4.2 CSV

In the folder `outputs` one finds CSV files whose names look like that: `transfer_2019_7200.csv`. They are the files which store monkey distribution in the groups at each selected time step.

```

1 myfiles<-dir("./outputs",full.names = TRUE)
2 trans<-rep(list(NA),length(myfiles))
3 for(i in 1:length(myfiles)) trans[[i]]<-read.csv(myfiles[i],
    header=F)

```

Each file is in a list.

First, let us extract the first simulation of the 10th saving.

```

1 tabt<-trans[[10]][1:13,]
2 colnames(tabt)<-paste0("G",tabt[1,])
3 rownames(tabt)<-paste0("G",tabt[1,])
4 tabt<-tabt[-1,-1]
5 tabt
6
7 > tabt
8      G6  G5  G15  G13  G14  G4  G12  G11  G9  G8  G7  G10
9 G6   48   0   0   0   0   0   0   0   0   0   0
10 G5    1 300   0   0   0   0   0   1   0   0   0
11 G15   0   0  98   2   1   0   0   0   0   0   0

```

12	G13	0	0	0	116	0	0	0	2	1	0	0	0
13	G14	0	0	2	2	98	0	0	0	0	0	0	0
14	G4	0	0	0	0	0	80	0	0	0	0	0	0
15	G12	0	0	0	0	0	0	50	3	1	0	0	0
16	G11	0	0	0	0	1	0	0	243	1	1	0	0
17	G9	0	0	0	0	0	0	0	2	885	0	0	0
18	G8	0	0	0	0	0	0	0	0	5	197	0	1
19	G7	1	0	0	0	0	0	0	0	2	2	100	0
20	G10	0	0	0	0	0	0	0	0	4	0	0	29

The first column gives the current distribution of individuals of the G6 group. 48 stayed in their group, 1 left for G5 and 1 for G7.

The sum of the first row, gives the current total number of individuals in a group. G6 has lost 2 individuals, so the sum of the row is 48. But G5 has gained 2 individuals, one from G6, the other from G9, but did not lose any, hence the size of the group is $1+300+1=302$ (the sum of the row). The total number of individual in each group is easy to obtain:

```
1 rowSums(tabt)
```

3.4.3 Shapefile

In R one can use the package `rgdal`.

```
1 library(rgdal)
2 snub<-readOGR("U:/Users/pgiraud02/gama_workspace/snubbies/
  outputs","snubby_2019_4392")
3 head(snub@data)
4 plot(snub)
5 plot(snub[snub@data$origin!=snub@data$current,],col="red",fg="
  red",add=TRUE)
6
7 groups<-readOGR("U:/Users/pgiraud02/gama_workspace/snubbies/
  includes/groups","groups")
8 plot(groups)
9 plot(snub[snub@data$origin!=snub@data$current,],col="red",fg="
  red",add=TRUE)
```

The shapefile can be read from any GIS as well.

In both cases monkey location is given as a circle polygon (of class `SpatialPolygonsDataFrame` in R), which might not be optimal for display.

In R one can easily extract the centroid of each polygon:

```
1 snubpts<-getSpatialPolygonsLabelPoints(snub)
2 plot(snubpts,pch=1,cex=0.5)
3 plot(snubpts[snub@data$origin!=snub@data$current,],pch=19,col=
  "red",fg="red",add=TRUE)
```

One can extract the geographical coordinates alone into a matrix as well:

```
1 snubmat<-coordinates(snub)
```

3.5 Analysing results

To come soon...

Bibliography

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