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| Institute of Zoology, CAS & Oxford University |
| Erin, Give the application a name |
| Overview document |

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| Erin Saupe & Huijie Qiao  2018-11-27 |

1. Generating the configuration files (in JSON format) and running commands for the simulations.

The script was written in Java. All the scripts in Java can be downloaded via a subversion repository (svn://mmweb.animal.net.cn/NicheBreadth/trunk). The function for step No.1 can be found in the following location.

**package** org.ioz.niche.breadth.r2016\_r12

**class** GenerateJson

**public** **void** generateSpeciesJson()

**public** **void** generateScenarioJson()

**public** **void** generateCommand()

**Json format of the configuration of virtual species:**

{

"id" : 1,

//should be the same length as the environmental layers defined in the scenario configuration file

"niche\_breadth" : [[v1\_min, v1\_max], [v2\_min, v2\_max], […], [vn\_min, vn\_max]],

//

"dispersal\_ability" : [0.3,0.7,0.9,0,1.0],

"dispersal\_speed" : 100,

"dispersal\_method" : 2,

"number\_of\_path" : -1,

"speciation\_years" : 10000,

"species\_extinction\_threshold" : 0,

"species\_extinction\_time\_steps" : 1,

"species\_extinction\_threahold\_percentage" : 0.8,

"group\_extinction\_threshold" : 0,

"initial\_seeds" : [[124.5, 54.5]]

}

**Json format of the configuration of virtual scenario:**

{

"environments" : ["path\_to\_env\_layer\_1", "path\_to\_env\_layer\_2", "…", "path\_to\_env\_layer\_n"],

"total\_years" : 120000,

"mask" : "path\_to\_mask\_layer",

//connect the species configuration via the “species\_id”.

"species" : ["species\_id"],

"burn\_in\_year" : 0

}

**Command to launch the simulation application:**

> ./NB\_Icesheet base\_folder scenario\_configuration Results\_folder 800 0 0

1. Launching the simulations by running the commands generated in step No.1.

The simulation application was written in C++. The source code is open accessed. Everyone can use it under GNU Public License. The latest source code can be downloaded via svn://mmweb.animal.net.cn/nb\_icesheet/trunk. More details about the code is in its documentation.

The simulations’ results were saved in a batch of log files in plain text, GIS raster (GTIFF) or NEXUS tree formats.

**The output directory structure generated by the simulation application:**

├── Map\_Folder //a folder to save the distribution year by year

│   ├── 100.csv

│   ├── 200.csv

│   ├── xxx.csv

│   └── 120000.csv

├── Phylogram.html //An HTML file to show the speciation tree in browser

├── runtime.log //A log file to save the runtime information.

├── seeds.csv //Seed point of the simualtion

├── stats

│   └── stat.csv //The number of speciation and extinction in the simulation

├── suitable.tif //suitable area (potential distribution) of the virtual species in the simulation.

└── tree.new // the speciation tree in NEXUS format.

1. Analyzing the log files, extract the useful information and import them into the database.

The scripts were written in Java. All the functions are in the following package and classes.

**package** org.ioz.niche.breadth.r2016\_r12

**class** HandleResult

**class** MeanLat\_By\_Continent\_NB

**class** MeanLat\_By\_Continent

**class** MoreMetrics

**class** Speciation\_Convex\_Stat

**class** Speciation\_Extinction\_Lat

**class** overAllFunctions

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| --- | --- | --- |
| Class | Function | Database Table |
| MoreMetrics | allMetricsNoNicheBreadth() | Biome |
| MoreMetrics | allMetricsNoNicheBreadth() | Continent |
| MoreMetrics | Continent2 () | Continent2 |
| HandleResult | generateConvexMaps() | Convex |
| HandleResult | generateConvexMaps() | Convex\_with\_year |
| MoreMetrics | allMetricsNoNicheBreadth() | Distribution |
| HandleResult | generateOriginMaps() | Diversity |
| HandleResult | generateOriginMaps() | Extinction |
| HandleResult | generateExtinctionTable() | Extinction\_with\_year |
| HandleResult | detectSpeciationExtinctionTemp2Prec\_Origin() | Extinction\_in\_combined\_environments |
| MoreMetrics | allMetricsNoNicheBreadth() | Lat |
| MoreMetrics | allMetricsNoNicheBreadth() | Lon |
| MoreMetrics | nicheBreadth() | Niche\_breadth |
| HandleResult | generateOriginMaps() | Origin |
| Speciation\_Convex\_Stat | calculate\_convex\_speciation() | Speciation\_Convex |
| Speciation\_Convex\_Stat | calculate\_convex\_speciation() | Speciation\_Convex\_E |
| Speciation\_Extinction\_Lat | speciation\_extinction\_by\_others() | Speciation\_Extinction\_BIOME |
| Speciation\_Extinction\_Lat | speciation\_extinction\_by\_others() | Speciation\_Extinction\_Continent |
| Speciation\_Extinction\_Lat | speciation\_extinction\_by\_others() | Speciation\_Extinction\_Continent2 |
| Speciation\_Extinction\_Lat | speciation\_extinction\_by\_lat() | Speciation\_Extinction\_Lat |
| Speciation\_Extinction\_Lat | speciation\_extinction\_by\_others() | Speciation\_Extinction\_TT |
| HandleResult | detectSpeciationExtinctionTemp2Prec\_XXX() | Speciation\_extinction\_in\_combined  \_environments\_XXX |
| HandleResult | insertResult\_removeUnfinished() | Simulations |
| MoreMetrics | allMetricsNoNicheBreadth() | Temperate\_Tropic |
| overAllFunctions | insertTree | Tree |

1. Extracting the required data from the database, analyzing the data tables, and creating the figures for the manuscripts.

Using R scripts for each figures.