

MIGRATE Tutorial 1

A reminder: if you want to keep results (they are written by default into a file called `outfile` and `outfile.pdf`), save it using either `cp outfile yourfavoredfilename` or `mv outfile yourfavoredfilename` or change the name of the output file in the menu.

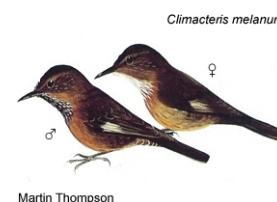
Datasets for MIGRATE

Download the migrate tutorials from the website at <http://www.peterbeerli.com/tutorials/migratetutorial.zip>. We will use a fragment of a large dataset of Australian treecreepers generated by Scott Edwards' group and also a simulated dataset using microsatellite markers. Once you unpack the zip directory you will this structure

```
tutorial0
tutorial1
tutorial2
windows
mac
```

The `tutorial1` directory contains these files

- `infile.treecreeper`: a two-population dataset with 2 loci.
- `infile.msat`: an example of a microsatellite data set (simulated data)
- `infile.1pop`: 1 population of the treecreeper data set, 2 loci.
- `infile.3pop`: 3 populations of the treecreepers, 2 loci.



For this tutorial, you will need to copy the content of the `windows` or `mac` directories into the `tutorial1` directory (pick the directory that matches your computer).

To start the program you will need to open a terminal window, on macs the program **Terminal.app** is located in **/Applications/Utilities**, on windows you can use the **Run...** command (on Windows 7 this is available in the menu, I am not sure where the command is located on Windows 8). if you have a mac running the latest OS (Yosemite 10.10) you can copy the application **migrateshell.app** and copy it into your **Applications** directory.

Instructions

1. Check where the data set `infile.treecreeper` is located (and remember the name of the folder).
2. use a text editor to look at the data; do you understand all parts?
3. Open a terminal window and change directory to the location of the migrate data.
4. Start MIGRATE from the commandline in the terminal.
5. Explore the menus, in particular the
 - S Search strategy,
 - I Input/Output formats!
6. Go to the Input/Output formats. Change the datafile name (first option) to `infile.treecreeper`, then go back to the main menu.
7. In the Strategy submenu:
 - Bayesian inference depends on a prior distributions to suggest new parameter values. Navigate to the prior settings (7 Prior distributions?, then 1 Set Theta prior distribution?, then 0 Set Uniform prior distribution). Confirm that the prior is uniform and set in the range of 0.000001 to 0.1 for Θ (Theta). Y will return to the previous menu.
 - Change the migration parameter M prior to the range of 0 to 2000. You need to specify 3 numbers for the uniform distribution : minimum maximum delta, the delta specifies the maximal jump the parameter value can do in a single step. Delta is best set around 1/10 of the difference of maximum and minimum.
 - Change the entry 10 Number of recorded steps in chain to 1000.
8. Back out to the main menu and WRITE the parameter file (W Write a parmfile in the main menu)
9. Start the run using Y (this should take about 5-20 seconds), inspect the feedback on the screen, it shows effective sample size, acceptance ratios (the default proposal mechanisms is slice sampling, we expect to see acceptance ratios of 1.0 for this).
10. Look at the output: there is a TEXT file and a PDF file. On Macs, you can open the PDF file from the commandline with `open filename`, on Linux use `acroread`, on windows old versions of acrobat reader will have no problem, but newer version have issues (Adobe in their wisdom decided that they stop to read older formats they deem insecure – but all other producers of PDF viewers can read the files just fine, for example in windows try Nitro PDF Reader [an overview about others can be found here: <http://www.makeuseof.com/tag/6-pdf-readers-windows/>]). Check out the figures with the posterior distribution. We expect smooth distributions that are unimodal, the color scheme indicates credibility intervals (50%, 95%, 99%).

11. Start MIGRATE again, but now change the number of sampled long steps to 50000 and then run (will take a couple of minutes).
12. **Write the value of the mode (output file: posterior distribution table) for the combined estimates (over all loci labeled All) of Θ_2 and $M_{1 \rightarrow 2}$ into the Excel worksheet on the computer in the front (towards the end of the demo we will look at the variance of your estimates.**

More fun with MIGRATE

- Copy the parmfile to parmfile.msat
- now start migrate-n using `migrate-n parmfile.msat`
- change the datatype to Brownian motion, and change the priors for theta and M so that the bounds are 0 and 100 with a delta of 10.
- run the program.
- Once several students have results we will discuss the results, in the meantime continue with the next items.
- Use replication (under Search strategy), for example run 3 replicates, this will not work fast on your computer, but with parallel MIGRATE (available for macs and linux) can run up to the number of cores/cpus faster than the version you currently use.
- Use the one-population dataset. In the Input/Output section turn on the **Event histogram** option (use the *All events, record every event, set the timeinterval to 0.001* and also turn on the **skyline plot**.
- More discussions and explanations of the outputs.

