

Using the IMfig program.

IMfig is a program for generating a figure of an isolation-with-migration model from the output file generated by running the IMA2 program. IMfig generates an eps (encapsulated post script) file which can then be printed or converted to a PDF file. Examples of the figures generated by IMfig are given in Hey (in press) and later in this document.

This kind of figure represents an estimate of history as a fat phylogenetic tree made up of boxes (for sampled and ancestral populations), horizontal lines (for splitting times) and curved arrows (for migration). Time is represented as depth on the vertical axis, with the sampled populations/species at the top of each figure at the most recent time. Population size is represented as width along the horizontal axis. Each population is represented by a box, the height of which refers to how long it has lasted and the width of which refers to its effective size. The confidence interval for a populations size is given both by a double headed arrow extending from the right margin of that population's box and by faint boxes representing the lower and higher 95% Highest Posterior Density (HPD) intervals. Similarly 95% HPD intervals for splitting times are given by dashed lines and doubled-headed arrows. Migration arrows are printed depending on the users wishes. One option only prints arrows if 2NM values are statistically significant by the test of Nielsen and Wakeley (2001) with asterisks: "*" for $p < 0.05$; "***" for $p < 0.01$, and "****" for $p < 0.001$.

The source code for IMfig is a Python script, and execution requires that Python be installed (<http://www.python.org/>). The program was written with Python version 2.5.4 but it is quite possible that it will work with other versions of Python 2.x. Users are also recommended to use an eps file viewer. Getting the settings right for a particular figure can take a fair bit of playing around and may ultimately require several runs of IMfig. The program runs quickly, but the process of getting the best settings proceeds much more easily if you can view the eps files generated during the process rather than printing them all. There are many programs for viewing eps files; one that is easy to use and free is GSview (<http://pages.cs.wisc.edu/~ghost/>).

Running IMfig

Recent generations of Macintosh computers come with python preinstalled so it should be pretty easy to run **IMfig** in a terminal window. Similarly linux/unix users should be able to figure things out without too much trouble. For Microsoft windows, users can follow these steps:

- Install the python interpreter for version 2.5.4 (<http://www.python.org/>).
- copy the `imfig.py` file and the output file generated by the **IMa2** program to the same folder.
- open a command prompt window and use the 'cd' command to move to that folder.
- Set system path so that it includes the path to the python interpreter. This can be done by typing and entering the following at the prompt in the command prompt window:
`path=%path%;xxx` where xxx is the full path of the folder where the python interpreter is. It might be something like `C:\Program Files\Python25` but you will have to check..
- Enter the python command. For example if your **IMa2** output file is called `my_results.out` and you want the eps file to be named `my_results.eps` then enter the following at the command prompt:

```
python imfig.py -imy_results.out -omy_results.eps
```
- Open `my_results.eps` in GSview or some other eps file viewer.

Generating an IMa2 output file suitable for IMfig

The file that is read by **IMfig** should be an output file generated using a regular run of **IMa2**, or an L-mode run in which one or more genealogy (*.ti) files saved from prior runs are analyzed. **IMfig** extracts information from the phylogenetic tree in the original data file used by **IMa2** and from the following tables in the **IMa2** output file:

- Marginal Peak Locations and Probabilities
- MARGINAL DISTRIBUTION VALUES AND HISTOGRAMS OF POPULATION SIZE AND MIGRATION PARAMETERS
- MARGINAL DISTRIBUTION VALUES AND HISTOGRAMS OF PARAMETERS IN MCMC
- MARGINAL DISTRIBUTION VALUES IN DEMOGRAPHIC UNITS

The last table (for demographic units) will be skipped by **IMfig** if the `-d` option is used on the command line. Doing an **IMa2** analysis in demographic units requires that **IMa2** be run using demographic units, which requires in turn some information on mutation rates and generation times (see **IMa2** documentation).

Command line options:

Just running the program without any flags should cause the following text to appear on the screen:

```
IMfig program. Copyright 2009 Jody Hey
IMfig command line terms:
-a include ancestral population #'s in plot
-b adjust width spacing of population boxes, values > 0, default = 1
-c color, blue for pop size, red for migration (default grayscale)
-d do not use demographic scale information even if in input file
-f font. Default=Arial. Use postscript fonts available on the computer
  e.g. Arial, Helvetica, Times-roman, Courier
-g global plot scale sets the size of the plot, max = 1, default = 1
-h arrow width, default = 1
-i input file name
-m migration (2Nm) arrow option:
  -ma : arrow printed for all 2Nm > 0
  -ms : arrows only when 2Nm is statistically significant (default)
  -m# : '#' is a number, arrows printed when 2Nm >= # (e.g. -m0.1)
-o output file name, e.g. -o myoutputfile.eps, default= im_eps_file.eps
-p fontsize(default is 14 for full scale, default follows global scale)
-s print square, rather than landscape
-t relative height of oldest time point, values between 0 and 1
  default value = 1/# sampled populations
-x adjust width of plot, >1 means wider, <1 means narrower
-y adjust height of splittimes, relative to bottom of figure, max = 1.
```

The `-i` (input file) and `-o` (output file) flags are required to generate a figure. All other flags are optional. Several flags affect the size/shape of the plot. If you need to generate multiple figures in which the height and width of the figures are on the same scale (e.g. so that ½ inch of height corresponds to a certain length of time) then you can use the `-t` and/or the `-y` options. Similarly

to have a unit distance on the horizontal axis mean the same thing (e.g. ½ inch corresponds to a certain effective population size) for different figures, you can play around with the `-x` option. If you use `-g` to make the plot bigger or smaller you may also need to adjust the font size (`-f`) and the arrow head size (`-h`).

Examples:

On the next several pages are shown results using an **IMa2** output file from an analysis of a 3 population model. On each page is given a command line, a brief description and the resulting figure. The pages are shown in landscape orientation because this is the default for IMfig output files.

Command Line Flag	Page #
default – no optional flags	5
-a	6
-b	7
-c	8
-d	9
-f	10
-g	11
-h	12
-ma	13
-m#	14
-p	15
-s	16
-t	17
-x	18
-y	19

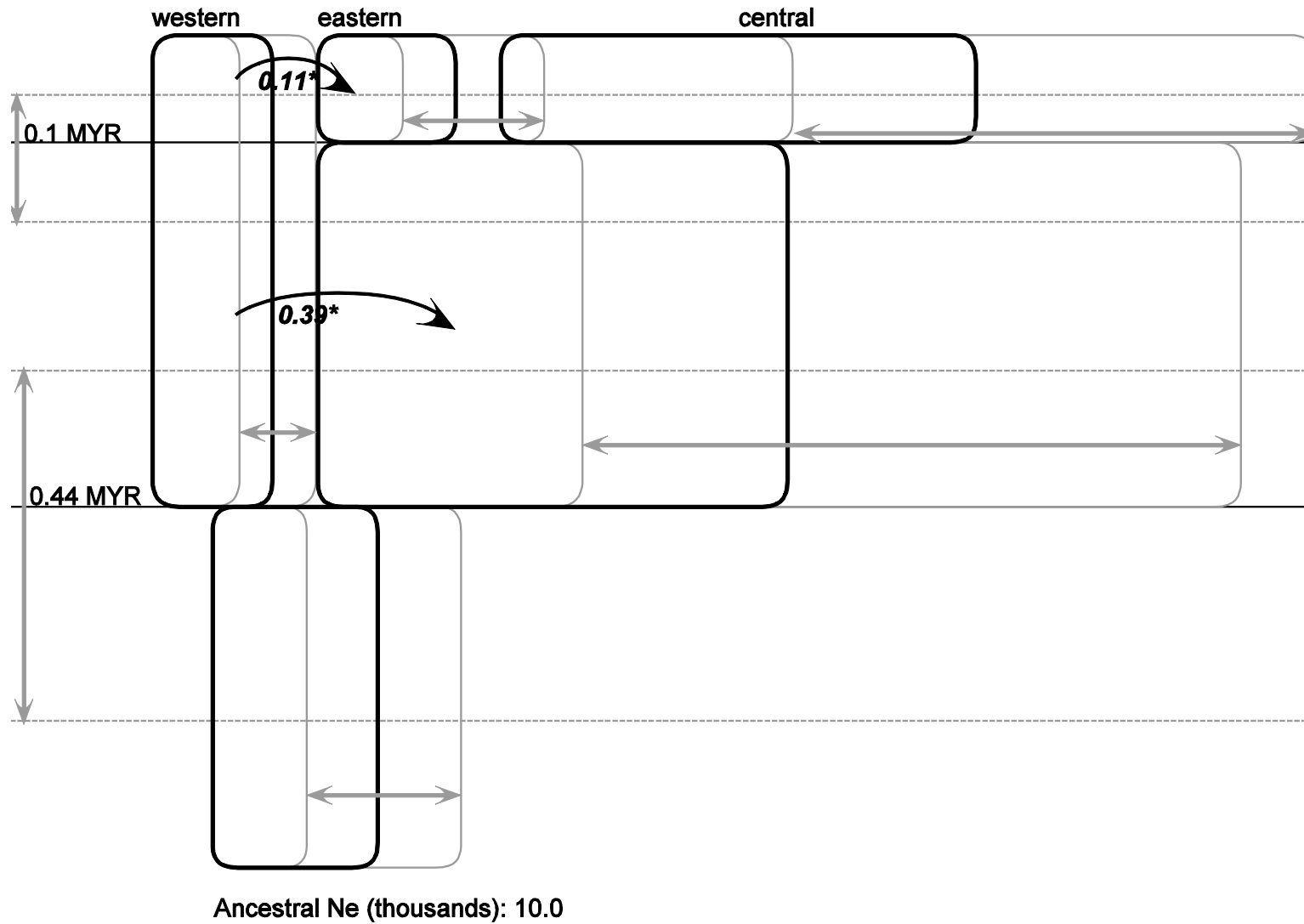
References:

Hey, J. *in press*. The Divergence of Chimpanzee Species and Subspecies as Revealed in Multi-population Isolation-with-Migration Analyses. *Molecular Biology and Evolution*.

Nielsen, R., and J. Wakeley. 2001. Distinguishing migration from isolation. A Markov chain Monte Carlo approach. *Genetics* 158:885-896.

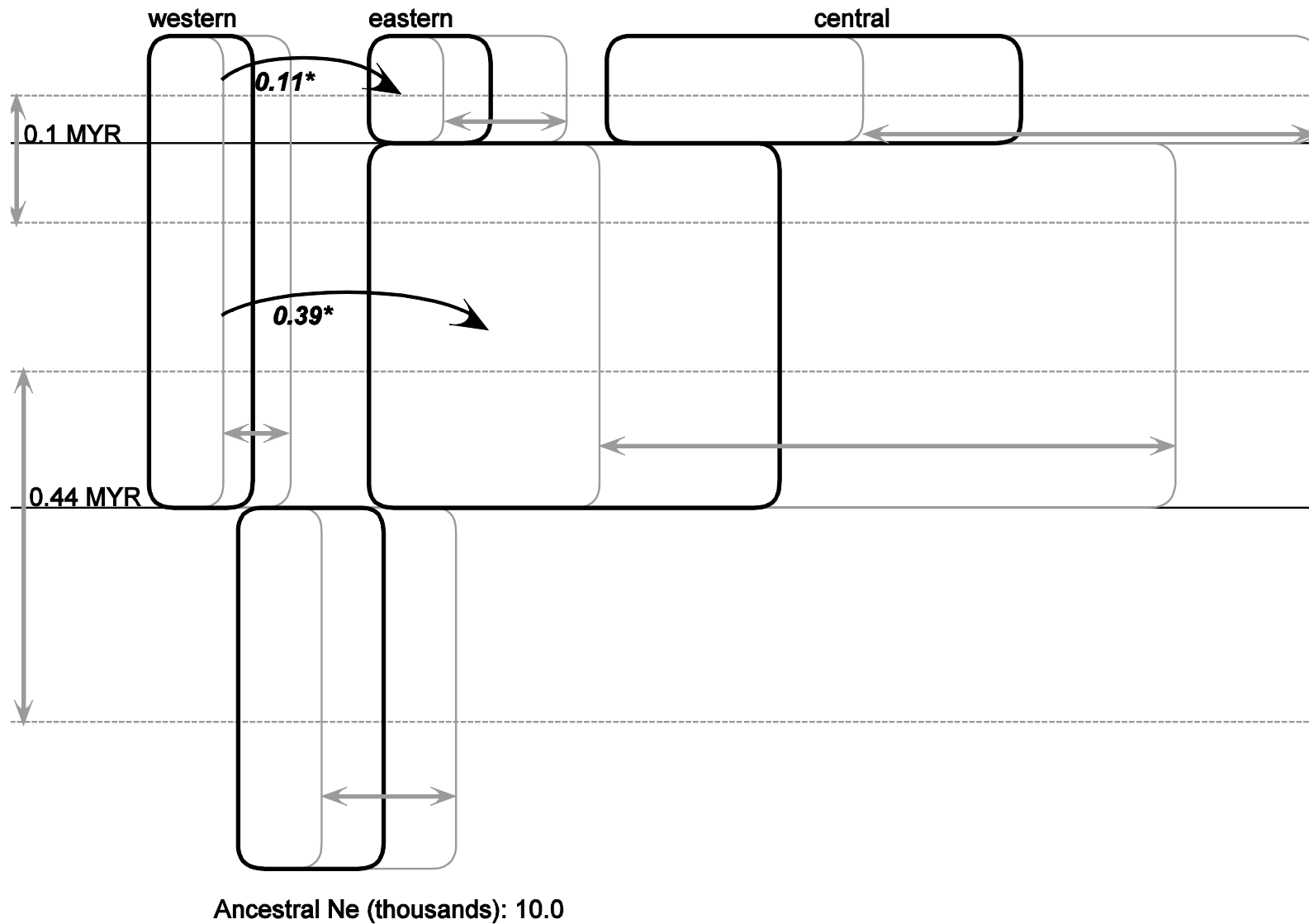
Default settings

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example.eps`



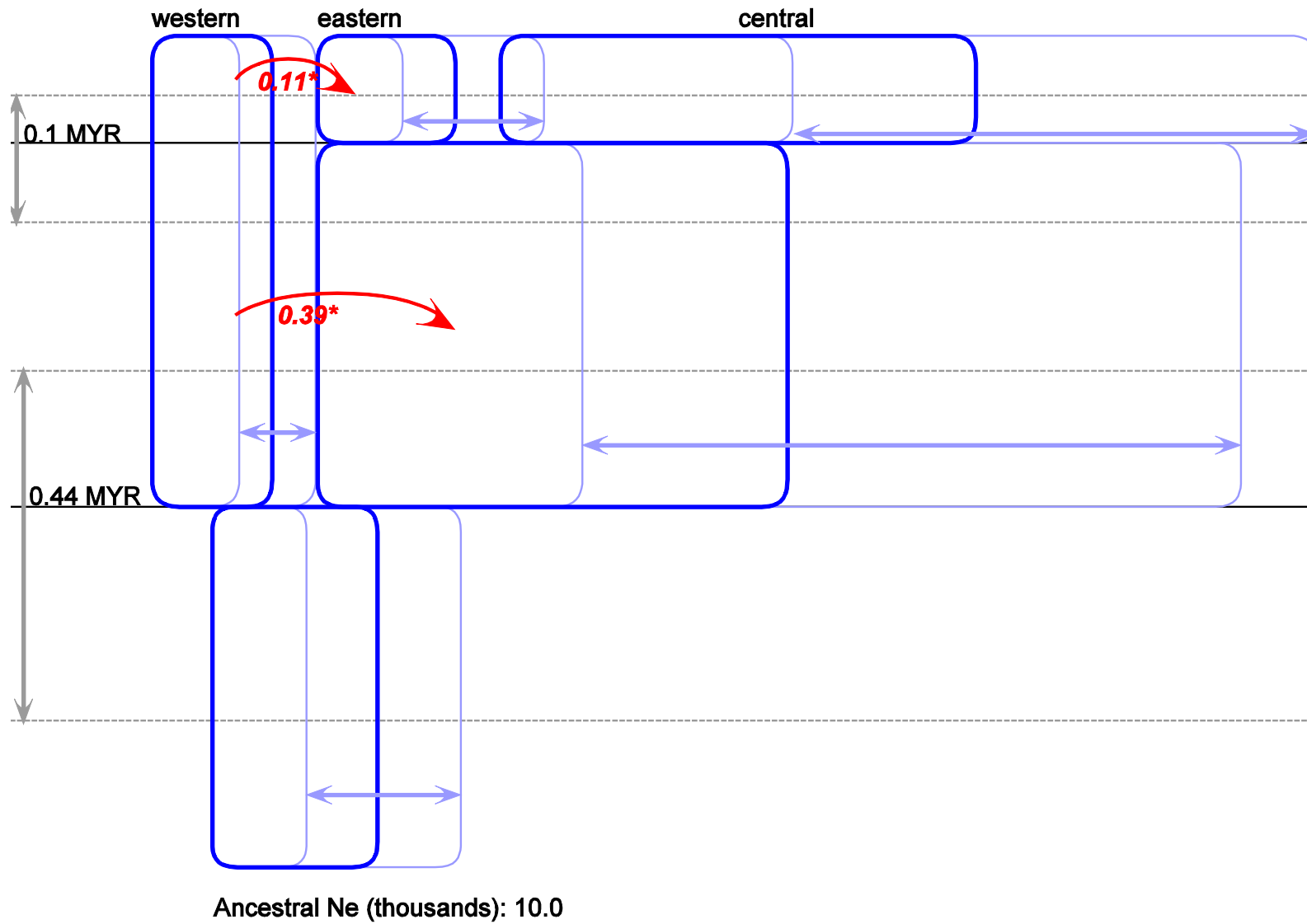
Example demonstrating the use of the `-b` option to alter the width of population boxes to avoid overlapping confidence intervals

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_popspacing.eps -b3.0`



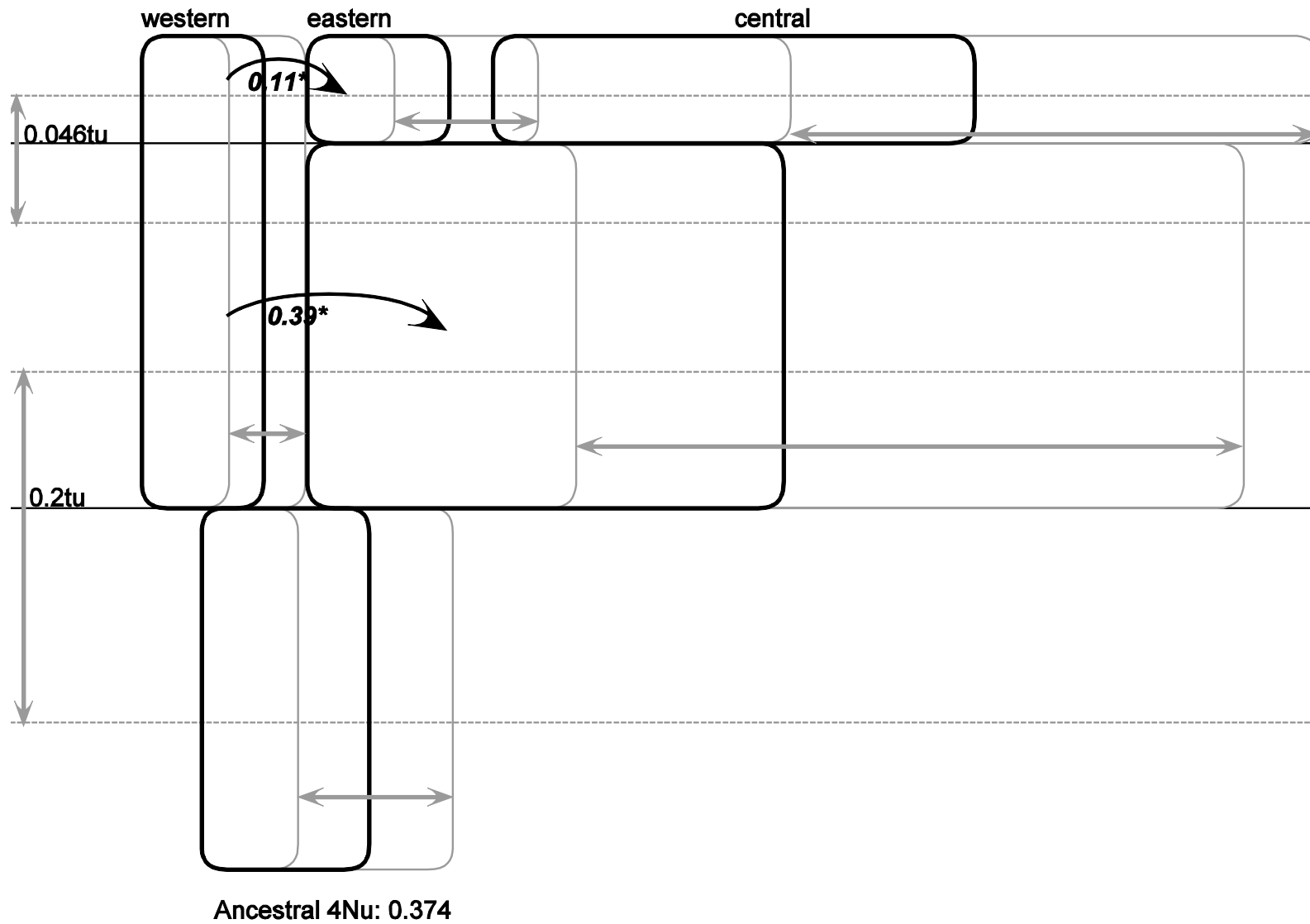
Example demonstrating the use of the `-c` option to print in color

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_color.eps -c`



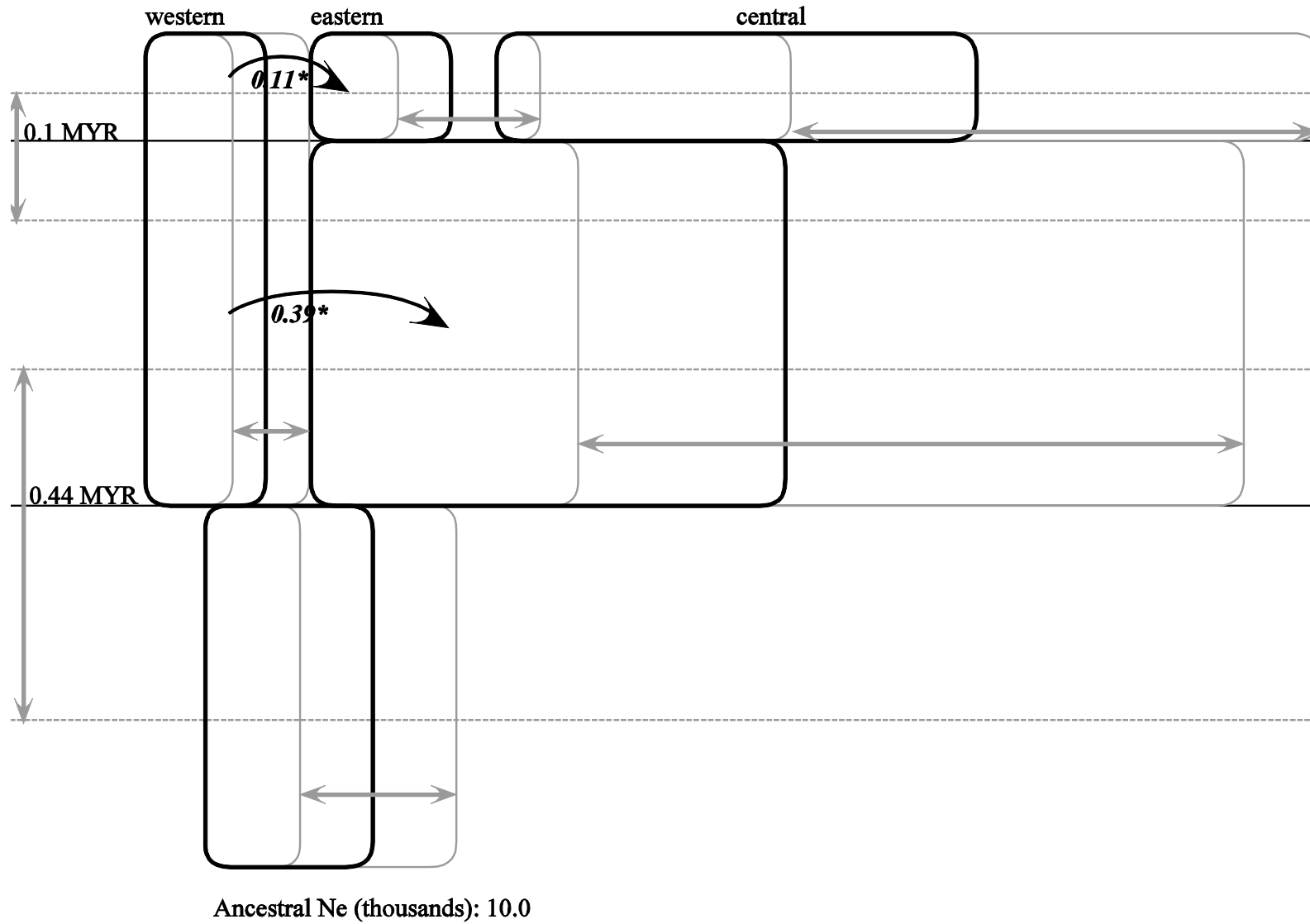
Example demonstrating the use of the `-d` option to use mutation rate scales rather than demographic scales

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_nodemographics.eps -d`



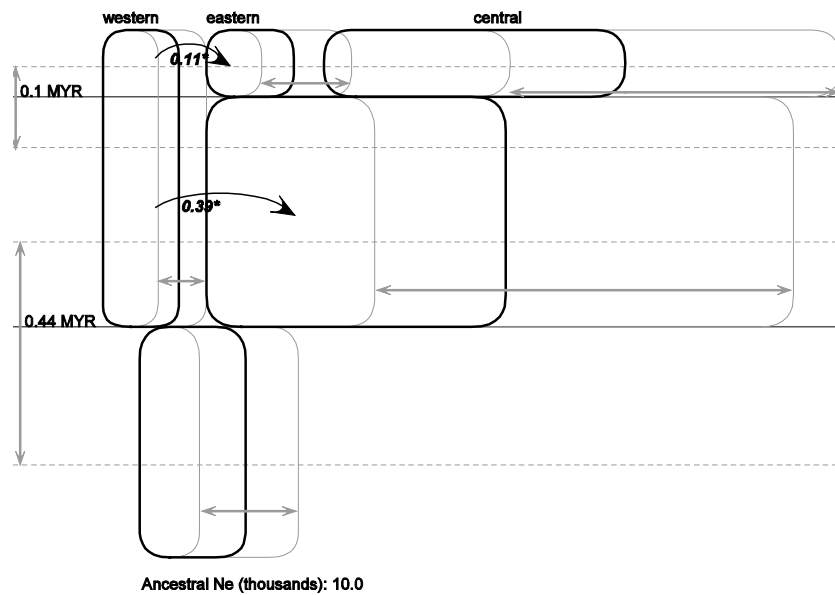
Example demonstrating the use of the `-f` option to use another font

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_fontTimes-roman.eps -fTimes-roman`



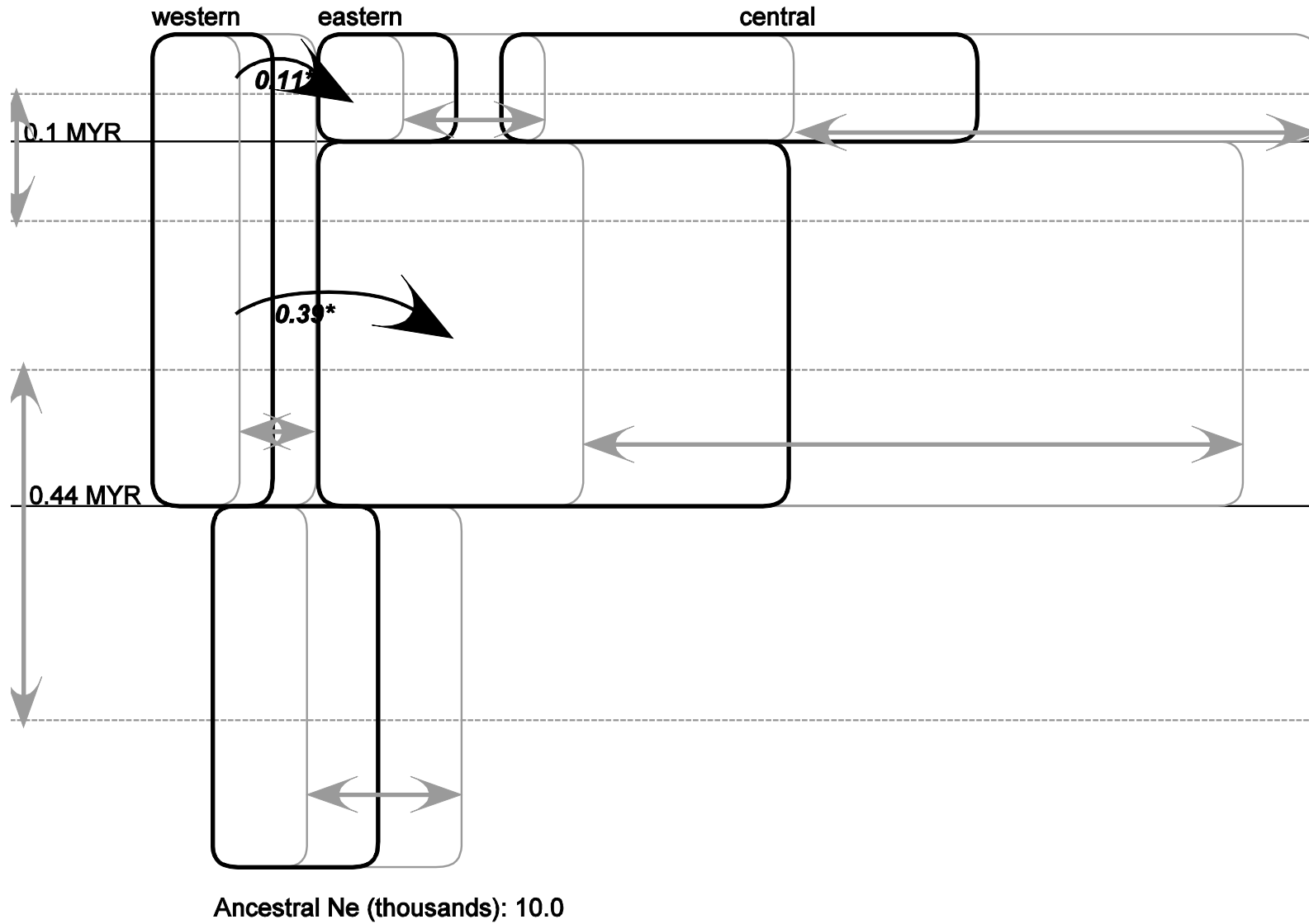
Example demonstrating the use of the `-g` option to rescale the entire plot, in this case a much smaller figure

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_globalscalesmalle.eps -g0.5`



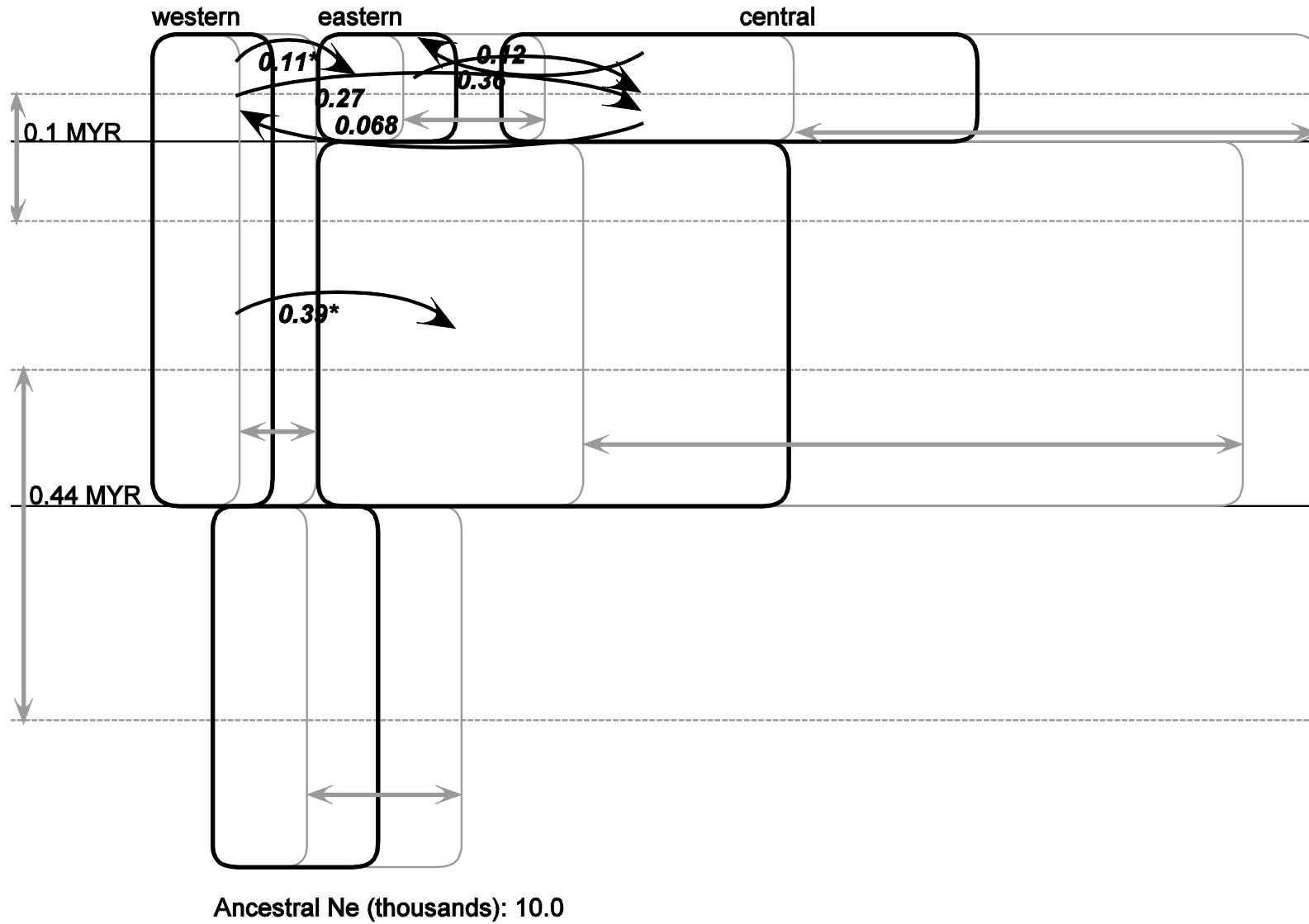
Example demonstrating the use of the `-h` option to increase the width of arrows, useful when rescaling plots

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_widearrows.eps -h2`



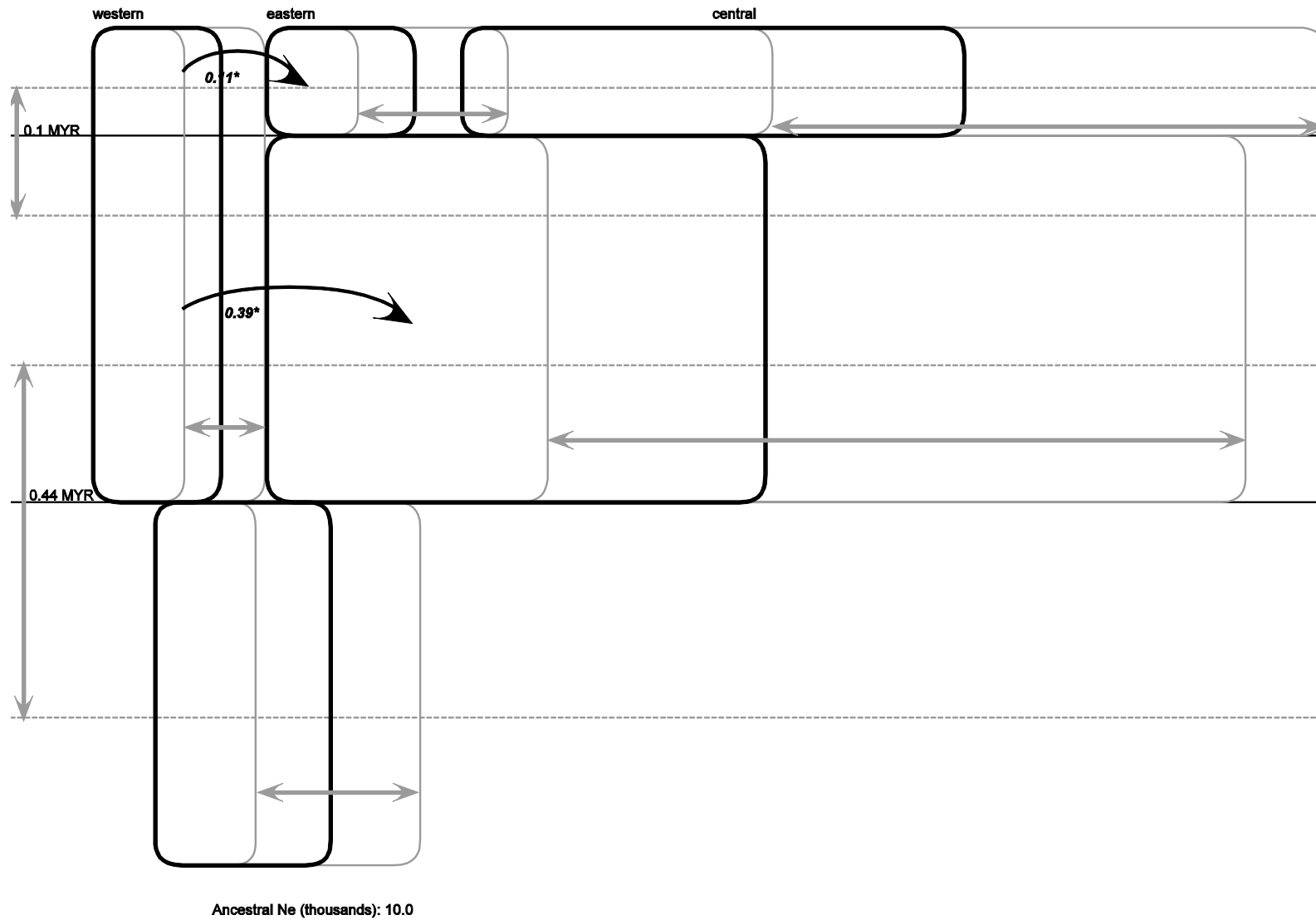
Example demonstrating the use of the `-ma` option to print all arrows for all migration rates where $2NM > 0$

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_m_arrows_all.eps -ma`



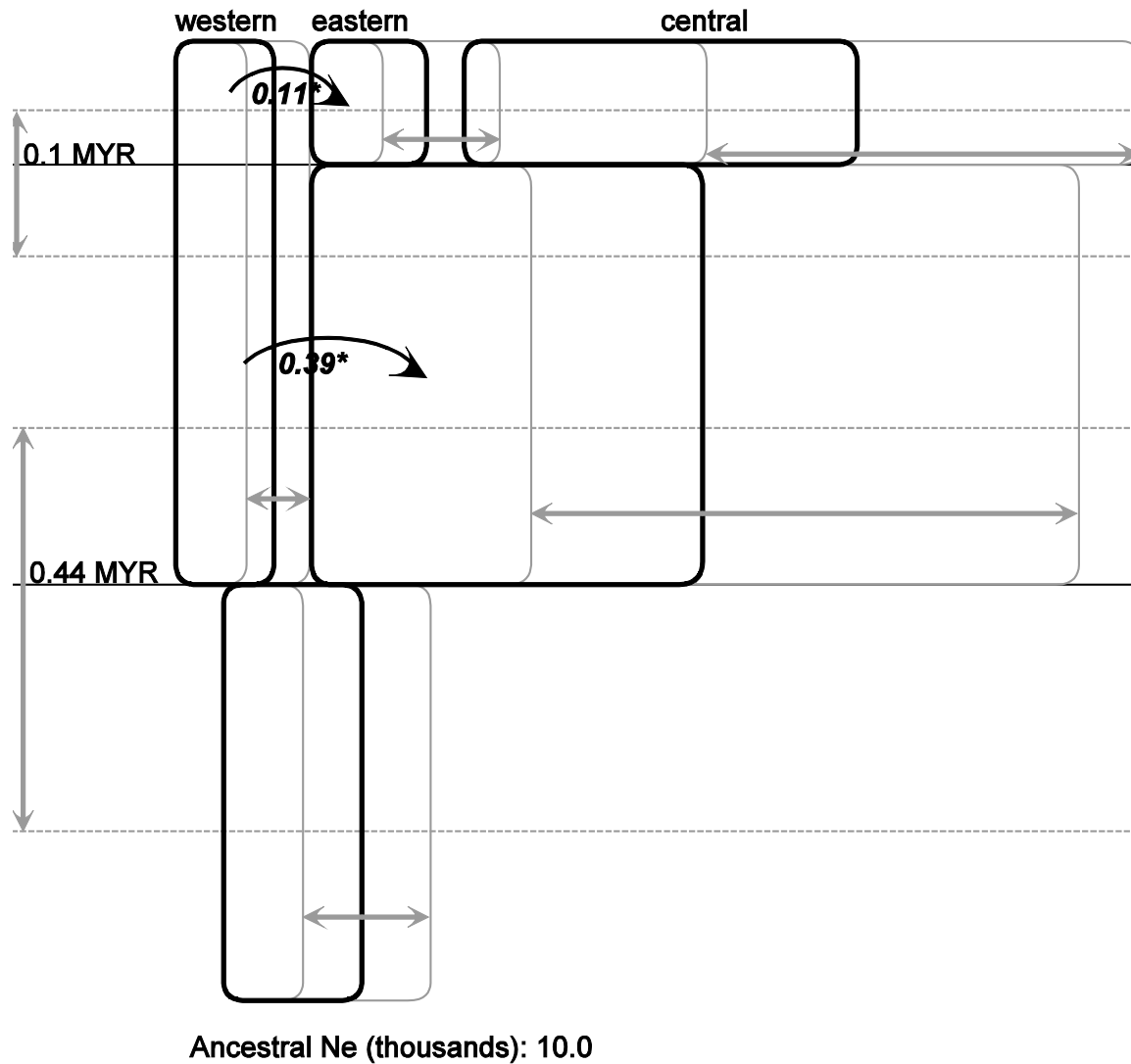
Example demonstrating the use of the `-p` option to change the fontsize, in this example 8 instead of the default of 14

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_smallfont.eps -p8`



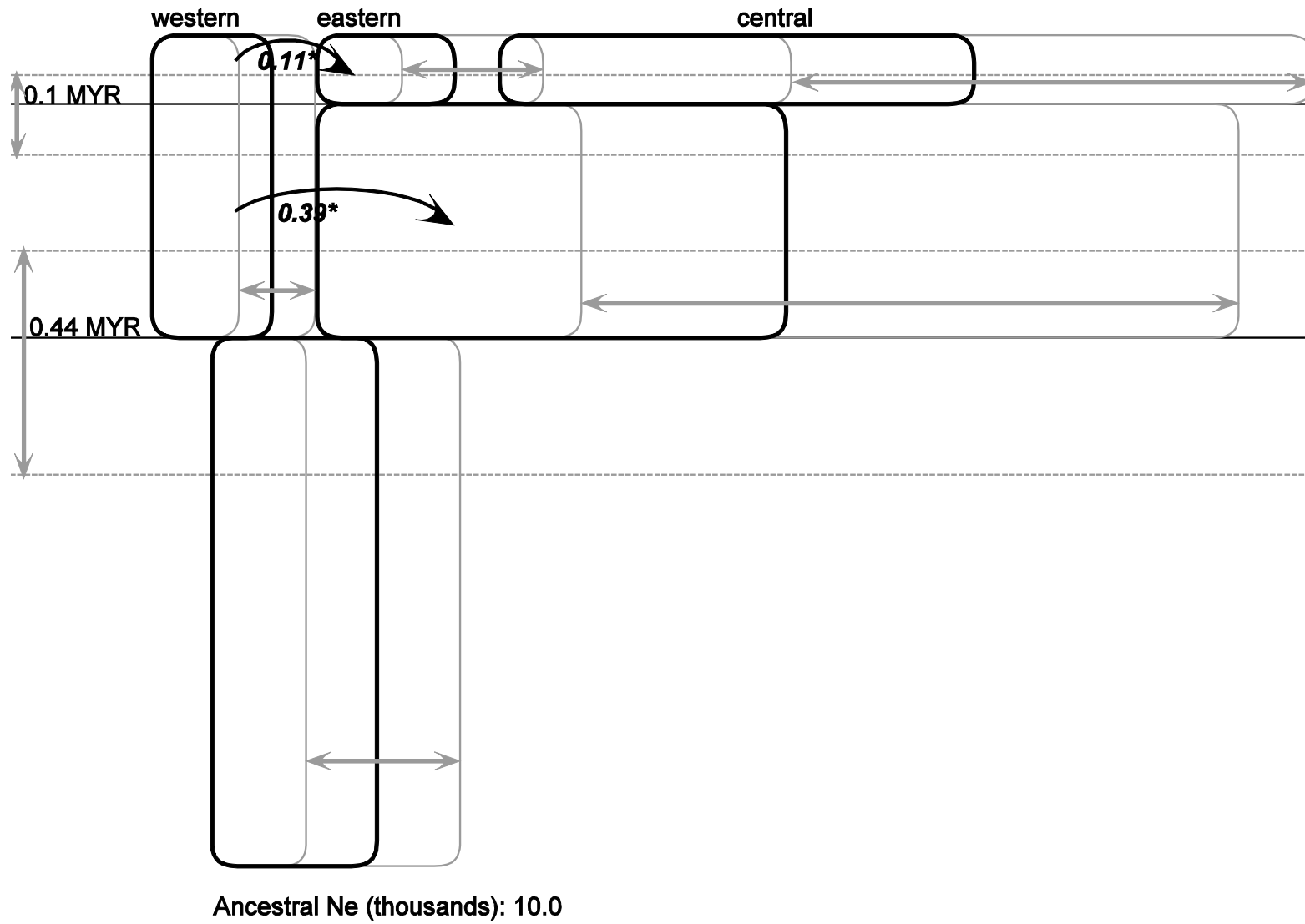
Example demonstrating the use of the `-s` option to print a square plot rather than landscape

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_squareplot.eps -s`



Example demonstrating the use of the `-t` option to set the height of the oldest splittime

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_example_highrelativeheight.eps -t0.5`



Example demonstrating the use of the `-y` option to adjust the height of the splittime relative to the bottom of the figure

Command line: `python IMfig.py -iIMa2_3pop_example.out -oimfig_3pop_exampleSplittimeheight.eps -y0.5`

