Population demographic history visualization with R package: popdemog

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## Introduction

Demographic history tells about when and where a particular population come from, what is the genetic relationship to each other populations, and how the population size changes along the time. In population genetics studies, demograohic history could be either as the result of un-recorded demograohic inference from genetic data, or the assumption model to conduct simulations for possible hypothesis tests. Both of them need a good way to represent the history, especially when multiple populations involves.

The package *popdemog* is going to give a solution to represent population demographic history. It is originally designed for the simulation software ms and aims to visualize the simulation script. Currently it can support many simulators’ input, such as ms and msa [[1]](#footnote-22), msHot [[2]](#footnote-23), MaCS [[3]](#footnote-24), and Cosi [[4]](#footnote-25). msprime’s simulation script[[5]](#footnote-26) can also be supported by this package since it can be easily translated into ms-compitable commands. More diverse inputs from simulation language will be supported in the future, please check the support list for update.

In this package, we provide three easy-to-use functions: **PlotMS**, **PlotMMig**, and **PlotMig**. **PlotMS** is the main function to capture the demographic information from simulation script or simulation parameter file and output the tree structure of population evolution history and the arrows of migrations between lineages. **PlotMMig** and **PlotMig** are designed to deal with complex migration events. **PlotMMig** gives the overview of migrations over the time while **PlotMig** can only show migrations at one specified time point. However, **PlotMig** has more free variables to adjust and produce finer figure for migration presentation than **PlotMMig**. Besides, we have function **NRuler** to add population size ruler to the plot.

To better understand the examples in this tutorial, user should have a little bit experience in simulation, a little knowledge about effective population size, and the basic skill to generate figures with R. In this tutorial, we will use a demographic model from Cosi as an example to explore the power of *popdemog* in the population history representation. We also attached abundant examples to help user to handle this package.

Format rule in this tutorial: *package*, **function**, option & code.

## Simulator supporting list

|  |  |  |
| --- | --- | --- |
| Simulator | Keyword | Notes |
| Cosi | “cosi” | parameter file as the input |
| ms | “ms” |  |
| msa | “msa” |  |
| msHot | “mshot” |  |
| msprime | “msprime” | need to convert to ms-compatile format as the input |
| MaCS | “macs” |  |
| SCRM | “scrm” |  |

## Install package *popdemog*

Package *popdemog* can always be installed from the source file

install.packages("https://github.com/YingZhou001/popdemog/raw/master/popdemog\_1.0.tar.gz", repos=NULL)

then load it with

library(popdemog)

Now functions from this package are ready to use.

## Plot demographic history with **PlotMS**

The function **PlotMS** requires the input.file or input.cmd, and the type of the input to be specified.

### Script input: input.file, input.cmd, and type

The input.file contains the all information for demographic history, it can be a copy of simulation script or the parameter file from simulation tools.

For example, the script of ms

./ms 1 1 -r 25 250001 -t 2.5 -I 4 50 50 50 60 -n 1 10 -n 2 10 -n 3 10 -n 4 10 -em 0 1 4 0.32 -em 0 4 1 0.32 -em 0 3 4 0.08 -em 0 4 3 0.08 -em 5e-04 2 1 2000 -em 6e-04 2 1 0 -ej 7e-04 2 4 -en 0.02 4 2.4 -en 0.035 1 0.77 -en 0.04 3 0.77 -en 0.1997 4 0.0125 -en 0.1998 3 0.00149253731343284 -en 0.1999 1 0.005 -ej 0.2 3 1 -em 0.1996 1 4 0 -em 0.1995 4 1 0 -em 0.1994 3 4 0 -em 0.1993 4 3 0 -en 0.3499 1 0.00117647058823529 -ej 0.35 1 4 -en 1.7 4 1.25

and the parameter file (from the software Cosi2) of Cosi can be the input.file.

# sample file  
# comments have #s in front of them  
# newlines don't matter.  
  
#-- options that could be uncommented  
#infinite\_sites yes  
#random\_seed 12345 # Specifies a particular random number seed  
  
# in bp.  
length 250000  
  
# per bp per generation  
mutation\_rate 1.5e-8  
  
recomb\_file model.out  
gene\_conversion\_relative\_rate 0.3  
  
# population info  
  
pop\_define 1 european  
pop\_define 3 african-american  
pop\_define 4 asian  
pop\_define 5 african  
  
#european  
pop\_size 1 100000  
sample\_size 1 50  
  
#african american  
pop\_size 3 100000  
sample\_size 3 50  
  
#asian  
pop\_size 4 100000  
sample\_size 4 50  
  
#african  
pop\_size 5 100000  
sample\_size 5 60  
  
pop\_event migration\_rate "afr->eur migration" 5 1 0. .000032  
pop\_event migration\_rate "eur->afr migration" 1 5 0 .000032  
pop\_event migration\_rate "afr->as migration" 5 4 0. .000008  
pop\_event migration\_rate "as->afr migration" 4 5 0 .000008  
pop\_event admix "african american admix" 3 1 5. .2  
pop\_event split "african to aa" 5 3 7.0  
  
pop\_event change\_size "agriculture - african" 5 200 24000  
pop\_event change\_size "agriculture - european" 1 350 7700  
pop\_event change\_size "agriculture - asian" 4 400 7700  
pop\_event bottleneck "african bottleneck" 5 1997 .008  
pop\_event bottleneck "asian bottleneck" 4 1998 .067  
pop\_event bottleneck "european bottleneck" 1 1999 .02  
  
pop\_event split "asian and european split" 1 4 2000  
pop\_event migration\_rate "afr->eur migration" 5 1 1996 0  
pop\_event migration\_rate "eur->afr migration" 1 5 1995 0  
pop\_event migration\_rate "afr->as migration" 5 4 1994 0  
pop\_event migration\_rate "as->afr migration" 4 5 1993 0  
  
pop\_event bottleneck "OoA bottleneck" 1 3499 .085  
pop\_event split "out of Africa" 5 1 3500  
  
pop\_event change\_size "african pop size" 5 17000 12500

We save ms’ script in the “sample.ms.cmd” as the example input further illustration.

For the user who want to use this package to debug their simulation script, we also provide the string input option input.cmd, which allows to paste the command as string input to the plot function. type is to help **PlotMS** to recognize the input.file. Any dis-consistence between the type and the input would lead to the software crash or incorrect output model plot. Please check the supporting list to confirm your simulator is supported and find the right keyword for your simulator.

### Scale population size: N4

Effective population size is a important parameter in simulations with ms-like script (msHot, scrm, and MaCS), it is used to scale the real population size and the time for demographic events. N4 is remained here as the same meaning of in ms, which must be specified properly to give the right times for demographic events and the accurate sizes for populations. In two cases we do not need to care about this parameter: 1) we only want to output the topology plot with pop.scale="topology"; 2) the simulation script do not need to re-scale the population size and time, such as Cosi.

### Ouput the demographic history

Now we can generate our first plot of demographic history from the ms file “sample.ms.cmd” as follow, N4 is 10000 in this case.

PlotMS(input.file="sample.ms.cmd", type="ms", N4=10000)

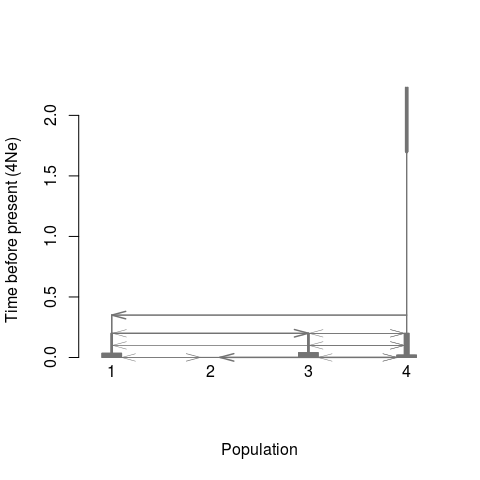


Figure 1: Raw plot of the simple history

Usually, the quick plot is not satisfied. We have enough options to customize the output graph.

1.Adjust the lineage width. Lineage width directly reflects the population size. Here we use logarithm with base of 50 to resale the population size so as the width of lineage, following the function

pop.scale="log", log.base =50

2.Adjust the population position. A vector inpos is used to store the position of each population. inpos[i] for the ith population.

inpos=c(3,6,1,9)

3.Add color to each lineage. col.pop[i] is stored the color for the th population. The color of arrow is the same with the source population by default, or can be reset with ‘col.arrow’.

col.pop=c("blue", "coral3", "gold3", "brown")

4.Add population labels to each lineage. pops[i] is the name for the ith population.

pops=c("European", "African American", "Asian", "African")

add these settings to **PlotMS**, we have:

PlotMS(input.file="sample.ms.cmd", type="ms", N4=10000, pop.scale="log",   
 log.base =50, inpos=c(3,6,1,9),   
 col.pop=c("blue", "coral3", "gold3", "brown"),   
 pops=c("European", "African American", "Asian", "African"))

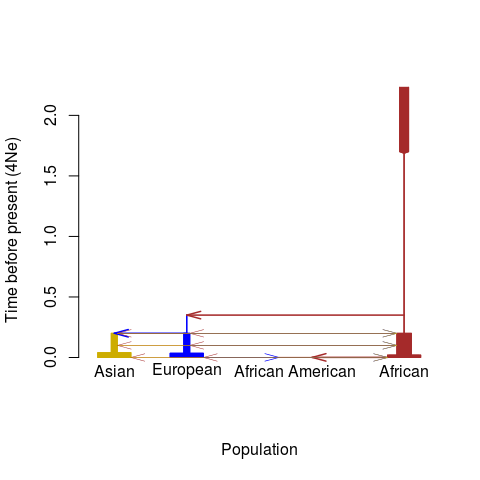


Figure 2: Adjusted plot of the simple history

However, if the recent events should be more fantastic than ancient ones, so we can zoom in them with

time.scale="log10year",

which will result the y-axis as the value of , using default 25 years per generation. The year per generation can be defined with the parameter gen.

We can also only show the topology structure by

pop.scale="topology"

which tells the function to ignore the time and population size but focus on the order of demographic events.  
We can also adjust the font size, axis label size, and the arrow size to fit to diverse plot region.

cex.lab=0.6  
cex.axis=0.6  
length.arrow=0.05

If there are too many background migrations, these events can be masked by

m.adjust=0.05 #mask the migration with per generation rate less than 0.05

Then we have the demographic figures with:

par(mfrow=c(1,2))  
PlotMS(input.file="sample.ms.cmd", type="ms", N4=10000,   
 pop.scale="log", log.base =50, inpos=c(3,6,1,9),   
 col.pop=c("blue", "coral3", "gold3", "brown"),   
 pops=c("European", "African American", "Asian", "African"),   
 time.scale="log10year", cex.lab=0.6, cex.axis=0.6, length.arrow=0.05, m.adjust=0.05)  
title("Zoom in recent events", cex=0.8)  
NRuler("topleft", Nsize=c(1e3, 1e5), Nlab=c("1e3","1e5"), N4=10000, pop.scale="log",log.base=50, lwd=1, cex=0.6)  
PlotMS(input.file="sample.ms.cmd", type="ms", N4=10000,   
 pop.scale="topology", inpos=c(3,6,1,9),   
 col.pop=c("blue", "coral3", "gold3", "brown"),   
 pops=c("European", "African American", "Asian", "African"),   
 cex.lab=0.6, cex.axis=0.6, length.arrow=0.05, ylab="Time before present", m.adjust=0.05)  
title("Topology plot", cex=0.8)

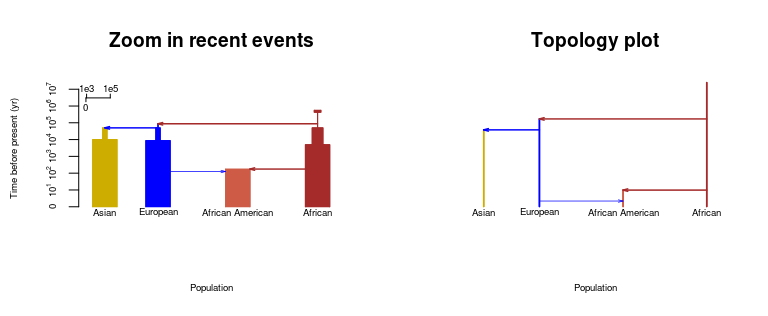


Figure 3: Two types of the simple history plots

## Plot migrations

When multiple migrations exist at a particular time point, arrows in **PlotMS** might cross with the population lineages and overlap with each other. The migration events will be hard to read in this setting, so we use function **PlotMig** to output the migration pattern on the specified time. We also have **PlotMMig** to output the overview of all possible migration patterns among simulated populations. Both of these two migration plot function are based on the output of function **PlotMS** with plot=F.

### Using **PlotMMig** to creat an overview of migrations

**PlotMMig** will automatically output pattern and the duration of each migration. Plot setting would be passed from function **PlotMS** to **PlotMMig** through the output list mig\_par, more information will be found with help(PlotMS) in R.

#output the demograohic information from PlotMS  
out<-PlotMS(input.file="sample.ms.cmd", type="ms", N4=10000, pop.scale="log",   
 log.base =50, col.arrow="black", time.scale="kyear",  
 col.pop=c("blue", "coral3", "gold3", "brown"),   
 pops=c("European", "African American", "Asian", "African"),   
 plot.out=F, demo.out=T,  
 cex.lab=0.5, cex.axis=0.6, length.arrow=0.05)  
#plot the overview of all migrations  
PlotMMig(demograph\_out=out$demograph\_out, mig\_par=out$mig\_par)

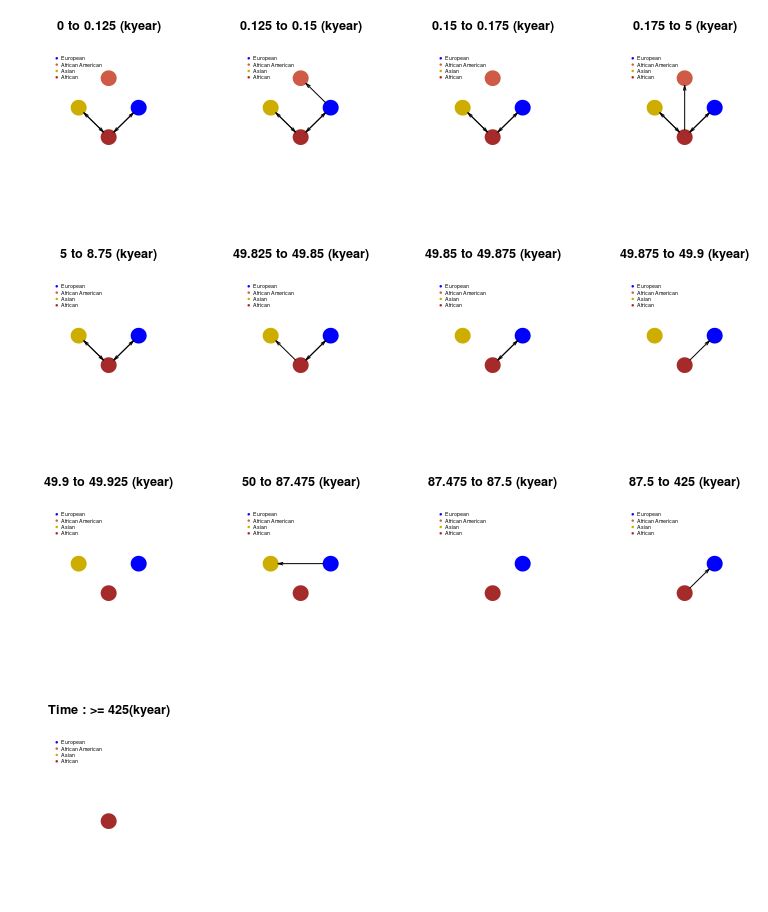


Figure 4: Overview of all migrations

### Using **PlotMig** to creat a fine migration plot

**PlotMig** is designed for the need to show migration at the specified time. We are going to plot all migrations at time 0.0005 (with time\_pt=0.0005) and ignore the population size difference (with pop.scale="topology"). The time point stay the same scale with the setting of time.scale. In this example, time.scale="4Ne" and it gives out the migration at years ago.

out<-PlotMS(input.file="sample.ms.cmd", type="ms", N4=10000, plot.out=F, demo.out=T)  
PlotMig(time\_pt=0.0005, demograph\_out=out$demograph\_out, mig\_par=out$mig\_par,   
 pop.scale="log", col.pop=c("blue", "coral3", "gold3", "brown"),   
 log.base=20, ylim=c(-3, 5));  
NRuler("bottomleft", Nsize=c(1e4, 1e5), Nlab=c("1e4","1e5"), N4=10000, pop.scale="log",log.base=20, lwd=1, cex=0.6)  
legend("topleft", legend=c("European", "African American", "Asian", "African"),   
 pch=20, col=c("blue", "coral3", "gold3", "brown"), bty="n")  
title(paste("Time: 0.0005 (",out$mig\_par$time.scale, ")"))

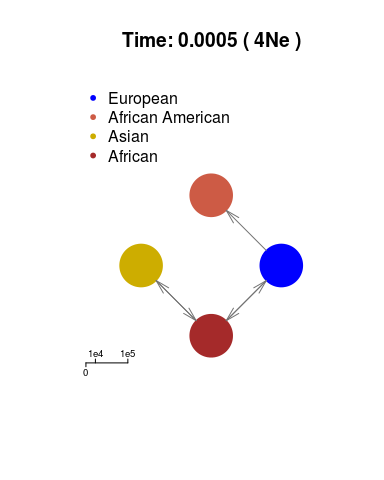


Figure 5: Migration at one time

In the Figure 5, the variable topology.scale=1.4 is used to re-scale the mono population size to 1.4 fold. The color and size of arrows can also be adjusted by the variable col.arrow and the length.arrow, please check the arguments with help(PlotMig) for more information.

### Add migrations to maps

Next, we are going to see an example of adding migration plot to a map. In this example, we need to install the package named maps

install.package("maps")

then load the map and save the latitude and longitude for each population in a matrix as inp.map.pos. We also need to set add=T to let **PlotMS** add plot to other backgrounds. We also set m.adjust=0.01 to avoid minor migrations and set topology.scale=10 to make each population circle large enough to be well distinguished.

library(maps)  
##initate the world map  
map('legacy\_world', fill=T, col="gray45", bg="lightgray", lty=0)  
axis(1);axis(2);  
##the positions for the four populations  
##European 50, 20  
##Asian 36, 112  
##African 7, 23  
##African American 38, -100  
inp.map.pos<-cbind(c(20, -100, 112, 23), c(50, 38, 36, 7))  
  
out<-PlotMS(input.file="sample.ms.cmd", type="ms", N4=10000, plot.out=F, demo.out=T)  
times<-out$mig\_par$time #time points for all events  
times #output times points for all demographic events

## [1] 0.0000 0.0005 0.0006 0.0007 0.0200 0.0350 0.0400 0.1993 0.1994 0.1995  
## [11] 0.1996 0.1997 0.1998 0.1999 0.2000 0.3499 0.3500 1.7000

for(i in times){  
PlotMig(time\_pt=i, demograph\_out=out$demograph\_out, mig\_par=out$mig\_par,   
 pop.scale="topology", col.pop=c("blue", "coral3", "gold3", "brown"),   
 topology.scale=10, add=T, map.pos=inp.map.pos, length.arrow=0.1, m.adjust=0.01,   
 col.arrow=c("blue", "coral3", "gold3", "brown"));  
}  
title("Migrations on the simple history")

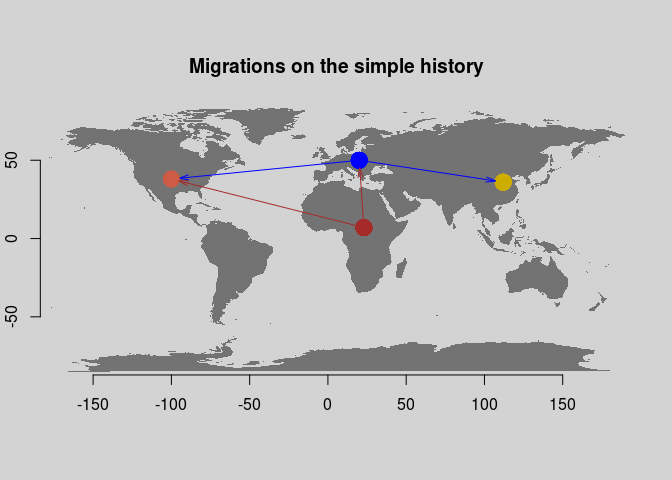


Figure 6: Add migrations to a map

## More examples

### Modified Tennessen’s model with Neanderthal introgression[[6]](#footnote-44)

cat("macs 2025 15000000 -i 10 -r 3.0e-04 -t 0.00069 -T -I 4 10 1006 1008 1 0  
-n 4 0.205 -n 1 58.00274 -n 2 70.041 -n 3 187.55 -eg 0.9e-10 1 482.46  
-eg 1.0e-10 2 570.18 -eg 1.1e-10 3 720.23 -em 1.2e-10 1 2 0.731  
-em 1.3e-10 2 1 0.731 -em 1.4e-10 3 1 0.2281 -em 1.5e-10 1 3 0.2281  
-em 1.6e-10 2 3 0.9094 -em 1.7e-10 3 2 0.9094 -eg 0.007 1 0  
-en 0.007001 1 1.98 -eg 0.007002 2 89.7668 -eg 0.007003 3 113.3896  
-eG 0.031456 0 -en 0.031457 2 0.1412 -en 0.031458 3 0.07579  
-eM 0.031459 0 -ej 0.03146 3 2 -en 0.0314601 2 0.2546  
-em 0.0314602 2 1 4.386 -em 0.0314603 1 2 4.386 -eM 0.0697669 0  
-ej 0.069767 2 1 -en 0.0697671 1 1.98 -en 0.2025 1 1 -ej 0.9575923 4 1  
-em 0.06765 2 4 32 -em 0.06840 2 4 0", file="model-Tennessen.cmd")  
#plot the demographic graph  
par(mfrow=c(1,2))  
PlotMS(input.file="model-Tennessen.cmd", type="macs", N4=30000,   
 pop.scale="log", log.base =50, inpos = c(1,4,7,9), time.scale = "log10year",   
 col.pop=c("brown", "blue", "gold3", "forestgreen"),   
 pops=c("AFR", "EUR", "ASIA", "ARC"), cex.lab=1, cex.axis = 1, xlab="", length.arrow=0.1)  
title("Demographic histoy")  
PlotMS(input.file="model-Tennessen.cmd", type="macs", N4=30000,  
 time.scale = "log10year", plot.out = F, demo.out = T)->out;  
#log10(1000)=3  
PlotMig(time\_pt=3, demograph\_out=out$demograph\_out,  
mig\_par=out$mig\_par, col.pop=c("brown", "blue", "gold3", "forestgreen"), pop.scale="topology");  
legend("topleft", legend=c("AFR", "EUR", "ASIA", "ARC"),   
 col=c("brown", "blue", "gold3", "forestgreen"), pch=20, bty="n")  
title("Migrations at 1000 years ago");unlink("model-Tennessen.cmd")

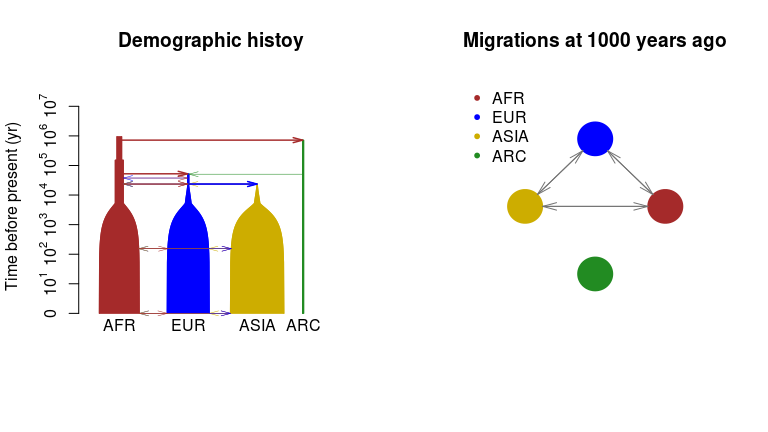


Figure 7: Modified Tennessen’s model

### Archaic introgrssion model [[7]](#footnote-47)

cat("./ms 44 1 -r 20000 50000000 -t 30000 -I 6 20 20 1 1 1 1 -en 0 1 1  
-en 0 2 1 -en 0 3 1e-10 -en 0 4 1e-10 -en 0 5 1e-10 -en 0 6 1e-10  
-es 0.0125 2 0.97 -en 0.02500025 7 0.25 -en 0.02500025 2 1 -ej 0.05 4 3  
-ej 0.05 6 5 -en 0.05000025 3 0.25 -en 0.05000025 5 0.25 -ej 0.0500025 5 3  
-en 0.050005 3 0.25 -ej 0.075 2 1 -en 0.0750025 1 1 -ej 0.1 7 3  
-en 0.1000025 3 0.25 -ej 0.3 3 1 -en 0.3000025 1 1", file="test.1.ms.cmd")  
PlotMS(input.file = "test.1.ms.cmd", type="ms", N4=10000,   
time.scale = "kyear", length.arrow=0.1, inpos=c(1,2,5,4.5,5.5,6,3),   
col.pop=c("brown", "blue", "forestgreen", rainbow(10)[6:9]));unlink("test.1.ms.cmd")

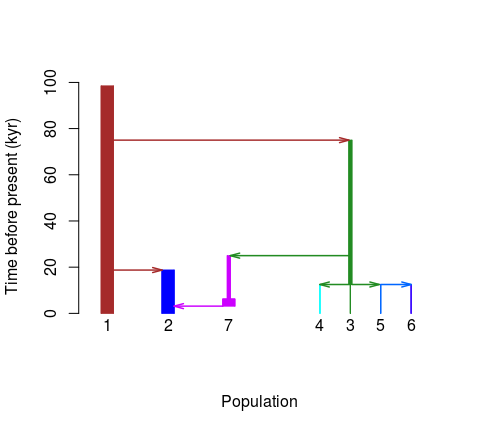


Figure 8: Archaic introgrssion model

### Migration model from ms.

cat("./ms 15 100 -t 3.0 -I 6 0 7 0 0 8 0 -m 1 2 2.5 -m 2 1 2.5 -m 2 3 2.5  
-m 3 2 2.5 -m 4 5 2.5 -m 5 4 2.5 -m 5 6 2.5 -m 6 5 2.5 -em 2.0 3 4 2.5  
-em 2.0 4 3 2.5", file="test.2.ms.cmd")  
PlotMS(input.file = "test.2.ms.cmd", type="ms", N4=10000, col.pop="gray",  
col.arrow="black", length.arrow=0.1, lwd.arrow=2);unlink("test.2.ms.cmd")

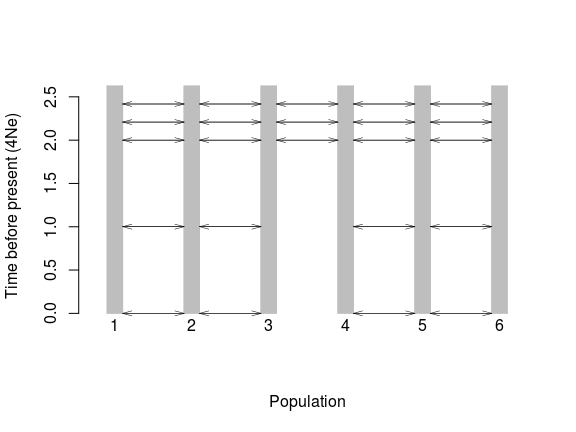


Figure 9: Migration

### Ryan2009’s model[[8]](#footnote-53)

cat("./ms 1 1 -t 1.0 -I 3 10 10 10 -n 1 1.682020 -n 2 3.736830 -n 3 7.292050  
-eg 0 2 116.010723 -eg 0 3 160.246047  
-ma 0 0.881098 0.561966 0.881098 0 2.797460 0.561966 2.797460 0  
-ej 0.028985 3 2 -en 0.028985 2 0.287184  
-ema 0.028985 3 0 7.293140 0 7.293140 0 0 0 0 0 -ej 0.197963 2 1  
-en 0.303501 1 1", file="Ryan2009.cmd")  
PlotMS(input.file = "Ryan2009.cmd", type="ms", N4=35000, pop.scale="log",   
log.base=2, time.scale="kyear",  
pops=c("AFR", "EUR", "ESA"), col.pop=c("brown", "blue", "gold3"));unlink("Ryan2009.cmd")

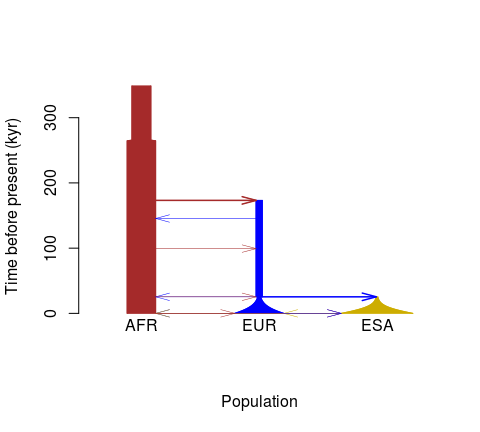


Figure 10: Ryan2009

### Zigzag model

cat("ms 4 1 -t 7156.0000000 -r 2000.0000 10000000 -eN 0 5 -eG 0.000582262 1318.18  
-eG 0.00232905 -329.546 -eG 0.00931619 82.3865 -eG 0.0372648 -20.5966  
-eG 0.149059 5.14916 -eN 0.596236 0.5 -T", file="zigzag.cmd")  
par(mfrow=c(1,2))  
PlotMS(input.file = "zigzag.cmd", type="ms", N4=10000)  
#change the time unit  
PlotMS(input.file = "zigzag.cmd", type="ms", N4=10000, time.scale="log10year");unlink("zigzag.cmd")

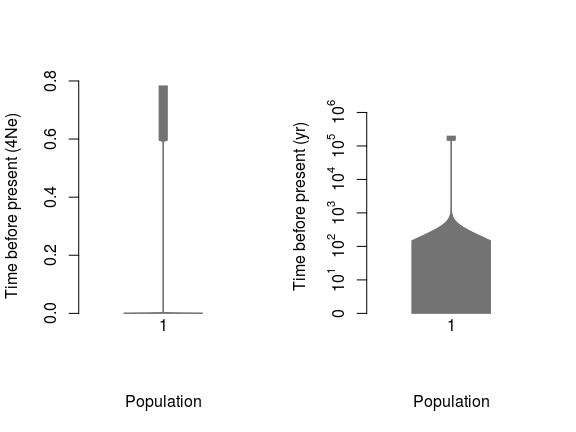


Figure 11: zigzag model

### Demographic plot from msprime’s script

This package is able to extract the demographic information from msprime. For the ms-compatible command, user only need to set the ‘type’ to be “msprime” and copy the command line to input file; for the python scripts, we will use “msprime2ms.py” to translate the simulation script of msprime to ms-compatible command, and then plot them out. Here we give an example to plot the demographic graph from msprime’s script. Suppose msprime has been successfully installed, and the msprime’s scripts of the demographic events are as follow and saved in the file “demo1.py” (copy from the msprime’s online documents[[9]](#footnote-60)):

# First we set out the maximum likelihood values of the various parameters  
N\_A = 7300  
N\_B = 2100  
N\_AF = 12300  
N\_EU0 = 1000  
N\_AS0 = 510  
# Times are provided in years, so we convert into generations.  
generation\_time = 25  
T\_AF = 220e3 / generation\_time  
T\_B = 140e3 / generation\_time  
T\_EU\_AS = 21.2e3 / generation\_time  
# We need to work out the starting (diploid) population sizes based on  
# the growth rates provided for these two populations  
r\_EU = 0.004  
r\_AS = 0.0055  
N\_EU = N\_EU0 / math.exp(-r\_EU \* T\_EU\_AS)  
N\_AS = N\_AS0 / math.exp(-r\_AS \* T\_EU\_AS)  
# Migration rates during the various epochs.  
m\_AF\_B = 25e-5  
m\_AF\_EU = 3e-5  
m\_AF\_AS = 1.9e-5  
m\_EU\_AS = 9.6e-5  
# Population IDs correspond to their indexes in the population  
# configuration array. Therefore, we have 0=YRI, 1=CEU and 2=CHB  
# initially.  
population\_configurations = [  
msprime.PopulationConfiguration(  
 sample\_size=0, initial\_size=N\_AF),  
msprime.PopulationConfiguration(  
 sample\_size=1, initial\_size=N\_EU, growth\_rate=r\_EU),  
msprime.PopulationConfiguration(  
 sample\_size=1, initial\_size=N\_AS, growth\_rate=r\_AS)  
]  
migration\_matrix = [  
[ 0, m\_AF\_EU, m\_AF\_AS],  
[m\_AF\_EU, 0, m\_EU\_AS],  
[m\_AF\_AS, m\_EU\_AS, 0],  
]  
  
demographic\_events = [  
# CEU and CHB merge into B with rate changes at T\_EU\_AS  
msprime.MassMigration(  
 time=T\_EU\_AS, source=2, destination=1, proportion=1.0),  
msprime.MigrationRateChange(time=T\_EU\_AS, rate=0),  
msprime.MigrationRateChange(  
 time=T\_EU\_AS, rate=m\_AF\_B, matrix\_index=(0, 1)),  
msprime.MigrationRateChange(  
 time=T\_EU\_AS, rate=m\_AF\_B, matrix\_index=(1, 0)),  
msprime.PopulationParametersChange(  
 time=T\_EU\_AS, initial\_size=N\_B, growth\_rate=0, population\_id=1),  
# Population B merges into YRI at T\_B  
msprime.MassMigration(  
 time=T\_B, source=1, destination=0, proportion=1.0),  
# Size changes to N\_A at T\_AF  
msprime.PopulationParametersChange(  
 time=T\_AF, initial\_size=N\_A, population\_id=0)  
]

Then we use the “msprime2ms.py” to convert the demographic description into *ms*-compatible format:

python msprime2ms.py demo1.py population\_configurations migration\_matrix demographic\_events

where *population\_configurations* is the name of the variable for population\_configurations, *migration\_matrix* is the name of the variable for migration\_matrix, and *demographic\_events* is the name of the variable for demographic\_events. Save the output to the file named “msprime.demo.cmd”

cat("  
--structure 3 1 1 1  
--population-size 1 0.3075  
--population-size 2 0.7431335886597129  
--population-growth-rate-change 0 2 160.0  
--population-size 3 1.352258276948663  
--population-growth-rate-change 0 3 220.0  
--migration-matrix x 1.2 0.76 1.2 x 3.8400000000000003 0.76 3.8400000000000003 x  
--population-split 0.0212 3 2  
--population-size-change 0.0212 2 0.0525  
--population-growth-rate-change 0.0212 2 0  
--migration-matrix-change 0.0212 3 x 10.0 x 10.0 x x x x x  
--population-split 0.14 2 1  
--population-size-change 0.22 1 0.1825",  
file="msprime.demo.cmd")

Then we can use functions *PlotMS* and *PlotMig* to plot the demographic history.

#plot the demographic graph  
par(mfrow=c(1,2))  
PlotMS(input.file="msprime.demo.cmd", type="msprime", N4=4\*10000,   
 pop.scale="log", log.base=10, inpos = c(1,4,7), time.scale = "log10year",   
 col.pop=c("brown", "blue", "gold3"), pops=c("AFR", "EUR", "ASIA"),   
 cex.lab=1, cex.axis = 1, xlab="", length.arrow=0.1)  
title("Demographic histoy")  
NRuler("topleft", Nsize=c(1e3, 1e5, 1e6), Nlab=c("1e3","1e5", "1e6"), N4=40000, pop.scale="log",log.base=10, lwd=1, cex=0.6)  
PlotMS(input.file="msprime.demo.cmd", type="msprime", N4=4\*10000,  
 time.scale = "log10year", plot.out = F, demo.out = T )->out;  
#log10(100)=2  
PlotMig(time\_pt=2, demograph\_out=out$demograph\_out,  
mig\_par=out$mig\_par, col.pop=c("brown", "blue", "gold3"), pop.scale="topology");  
legend("topleft", legend=c("AFR", "EUR", "ASIA"), col=c("brown", "blue", "gold3"), pch=20, bty="n")  
title("Migrations at 100 years ago");unlink("msprime.demo.cmd")

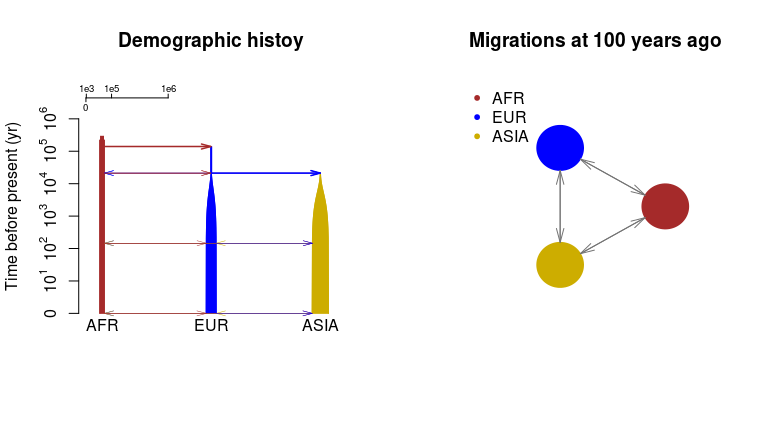


Figure 12: Plot from msprime’s input

### Support for SCRM simulation script

This package can also support the scrm simulation command[[10]](#footnote-64). Here we make an example simulation script that changing -em 5e-04 2 1 2000 -em 6e-04 2 1 0 in the ms style command from the file “sample.ms.cmd” to -eps 5e-04 2 1 0.8.

cat("scrm 1 1 -r 25 250001 -t 2.5 -I 4 50 50 50 60 -n 1 10 -n 2 10  
 -n 3 10 -n 4 10 -em 0 1 4 0.32 -em 0 4 1 0.32 -em 0 3 4 0.08   
 -em 0 4 3 0.08 -eps 5e-04 2 1 0.8 -ej 7e-04 2 4   
 -en 0.02 4 2.4 -en 0.035 1 0.77 -en 0.04 3 0.77 -en 0.1997 4 0.0125   
 -en 0.1998 3 0.00149253731343284 -en 0.1999 1 0.005 -ej 0.2 3 1   
 -em 0.1996 1 4 0 -em 0.1995 4 1 0 -em 0.1994 3 4 0 -em 0.1993 4 3 0   
 -en 0.3499 1 0.00117647058823529 -ej 0.35 1 4 -en 1.7 4 1.25", file="scrm.demo.cmd")  
par(mfrow=c(1,2))  
PlotMS(input.file="scrm.demo.cmd", type="scrm", N4=10000,  
 pop.scale="log", log.base =50, inpos=c(3,6,1,9),  
 col.pop=c("blue", "coral3", "gold3", "brown"),  
 pops=c("European", "African American", "Asian", "African"),  
 time.scale="log10year", cex.lab=0.6, cex.axis=0.6, length.arrow=0.05, m.adjust=0.05)  
title("Zoom in recent events", cex=0.8)  
PlotMS(input.file="scrm.demo.cmd", type="scrm", N4=10000,  
 pop.scale="topology", inpos=c(3,6,1,9),  
 col.pop=c("blue", "coral3", "gold3", "brown"),  
 pops=c("European", "African American", "Asian", "African"),  
 cex.lab=0.6, cex.axis=0.6, length.arrow=0.05, ylab="Time before present", m.adjust=0.05)  
title("Topology plot", cex=0.8);unlink("scrm.demo.cmd")

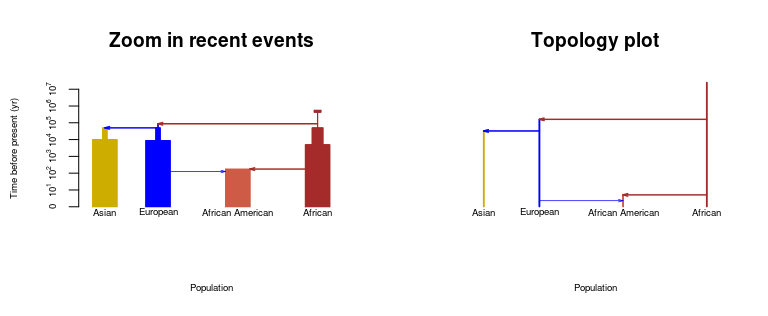


Figure 13: Two types of the simple history plots (repeat of Figure 3 with SCRM input)

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Xiaowen Tian wrote the python script “msprime2ms.py”.

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