

Simulation of the fractional coalescent with two populations

The simulation code `sintree.py` will be available in our private GitHub [address need to be inserted]. Here, a few examples of the output are shown. The key code is given in the snippet in Figure 1. Figure 2 gives examples for two populations with different α , all histograms were drawn from 5000 independent replicates using the same effective population sizes ($\Theta_1 = 0.01, \Theta_2 = 0.01$) and immigration rates ($M_{2 \rightarrow 1} = 100, M_{1 \rightarrow 2} = 100$), but different α . Each histogram is compared with the standard Kingman coalescent.

```
# generates Mittag-Leffler time interval based on mylambda and alpha
# for each evolutionary force: Theta_1, Theta_2, M_21, M_12
# for the future, I assume this also will work for growth and population divergence
# with the correct lambda
def randommlftime(mylambda, alpha):
    pia = 3.1415926 * alpha
    r1 = np.random.uniform(0,1)
    r2 = np.random.uniform(0,1)
    denoma = 1.0 / alpha
    denomlambda = 1.0 / mylambda
    return -denomlambda**denoma *
           (np.sin(pia)/(np.tan(pia*(1.0-r1)))-np.cos(pia))**denoma *
           np.log(r2)

# creates the time for a migration or coalescent event,
# evaluating the time intervals for each force and picks the smallest
# looping through Y , the alphas vector here needs and entry for every force
# see the function fill_Yalphas()
def randomtime(Y,alphas,t0):
    smallu = 1e100
    for yi,ai in zip(Y,alphas):
        u = randommlftime(yi,ai)
        if u < smallu:
            smallu = u
    return t0 + smallu
```

Figure 1: Key python function to draw new event times using the fractional coalescent with different α per population.

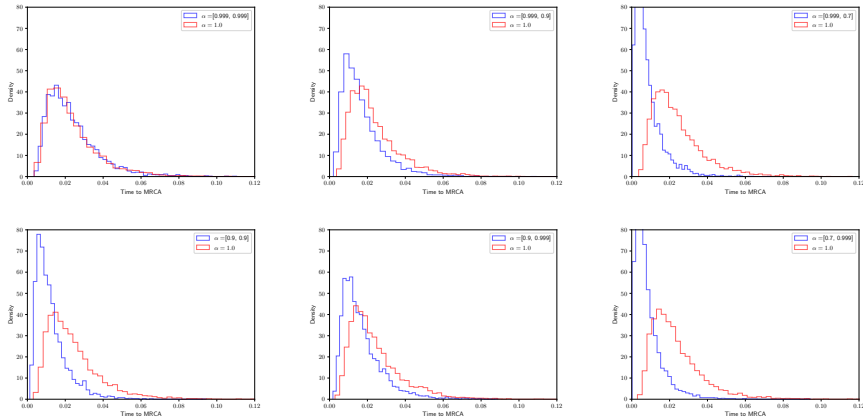


Figure 2: Comparison of six different scenarios for two populations with different α : top left: both populations are essentially following the Kingman coalescent; top middle and right: one population deviates from the Kingman coalescent; bottom left: both populations deviate similarly from Kingman coalescent, bottom middle and right: Same scenario as 'top middle and right' except that the α are reversed.

The script has several options:

usage: simtree.py [-h] [-l LOCI]

[-s SITES]
 [-i INDIVIDUALS]
 [-t THETA]
 [-m MIG]
 [-a ALPHA]
 [-f FILE]
 [-p]

Simulate a tree

optional arguments:

-h, --help show this help message and exit
 -l LOCI, --loci LOCI number of loci
 -s SITES, --sites SITES number of sites
 -i INDIVIDUALS, --individuals INDIVIDUALS Number of samples for each population
 -t THETA, --theta THETA thetas for each population
 -m MIG, --mig MIG migration rate for each population
 -a ALPHA, --alpha ALPHA alpha for each population
 -f FILE, --file FILE treefile to be used with migdata, default is NONE
 -p, --plot 2 which is a placeholder for sys.stdout
 Plots density histogram of TMRCA