

# Preliminary results from simulations with n diploids

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## 1 Scenario

All genes have length 500. Population sizes are 100,000 at tips, and at rootward ends of branches, and 200,000 at tipward ends of internal branches and at the root. The root height was 0.042. Full details of node heights are at the end.

The number of genes  $G$  was 5, and the number of individuals  $N$  per species 1. The mutation rates  $T$  was  $8e-8$ . The  $T$  values are in expected substitutions per site per generation. .

Strict clock branch rates assumed in simulation and BEAST.

HKY substitution model assumed in simulation and BEAST. In simulations, the Seq-Gen parameters are  $\kappa=3$ , frequencies .3 A and T, .2 C and G. (Seq-Gen called with `-t3.0 -f0.3,0.2,0.2,0.3`. These are estimated in BEAST.

No site rate heterogeneity assumed within genes in simulation and BEAST.

Genes have the same mutation rate in simulations. Rates are estimated in BEAST.

Priors on population sizes, relative mutation rates of genes, and the ‘event rate’ (something like a diversification rate) for the diploid and tetraploid trees in the network, are all diffuse lognormals.

## 2 Results for ten replicates

- 1 OK
- 2 x0,y0,z0 joins ab not cd
- 3 wrong at the root (just)
- 4 OK
- 5 x1,y1,z1 joins ab not cd, x0,y0,z0 joins ef not efg
- 6 e joins g not f
- 7 x1,y1,z1 joins efgh not efg
- 8 x1,y1,z1 joins ab not cd
- 9 OK (just)
- 10 x1,y1,z1 joins ab not cd

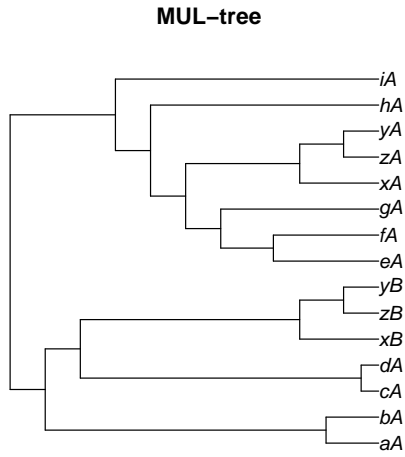


Figure 1: MUL-tree for simulation. 9 diploids a-i, 3 tetraploids x,y,z.

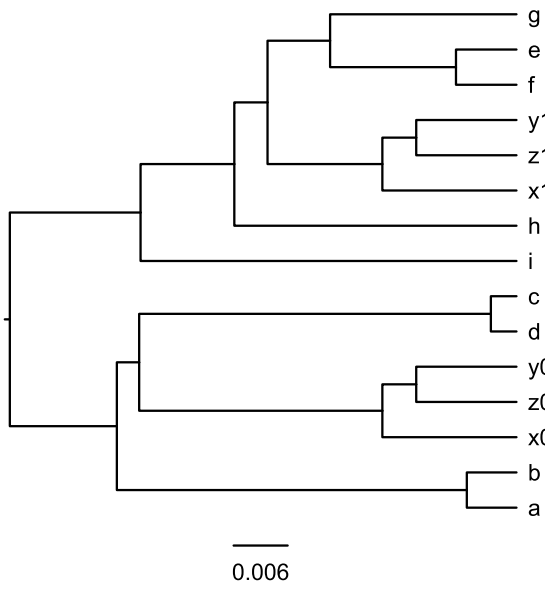


Figure 2: Rep 1

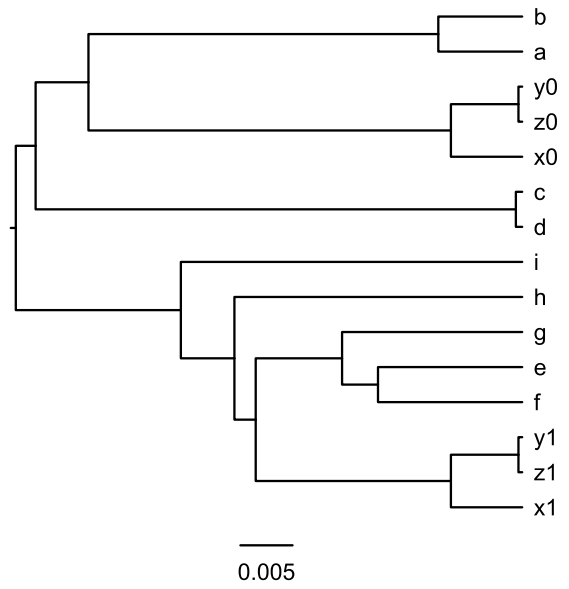


Figure 3: Rep 2

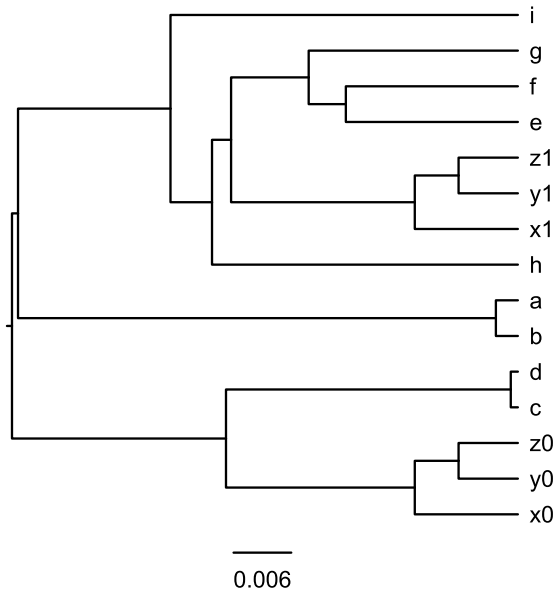


Figure 4: Rep 3

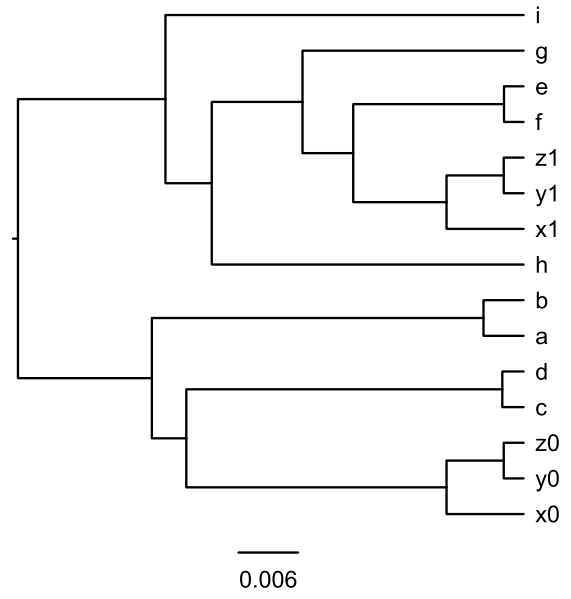


Figure 5: Rep 4

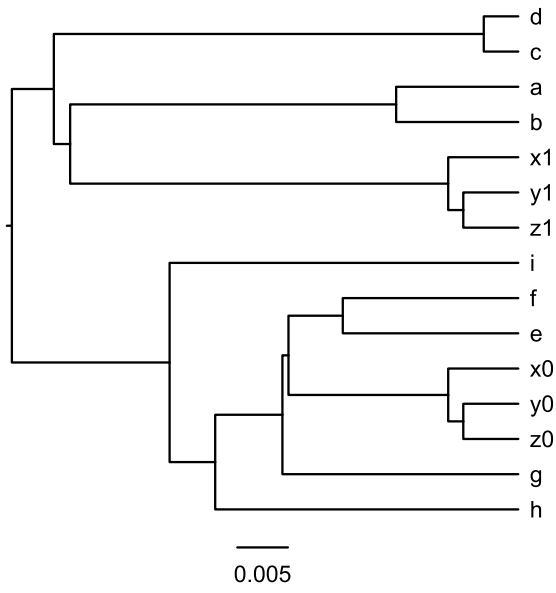


Figure 6: Rep 5

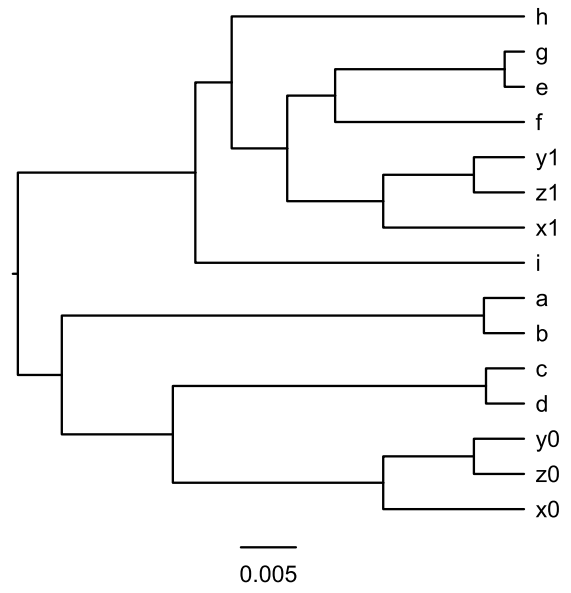


Figure 7: Rep 6

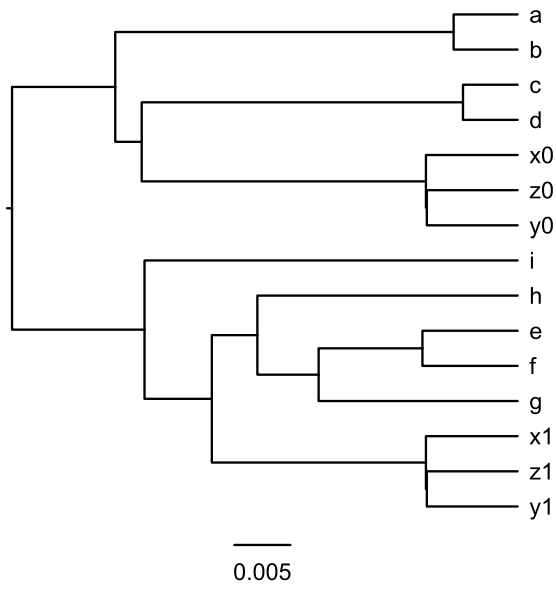


Figure 8: Rep 7

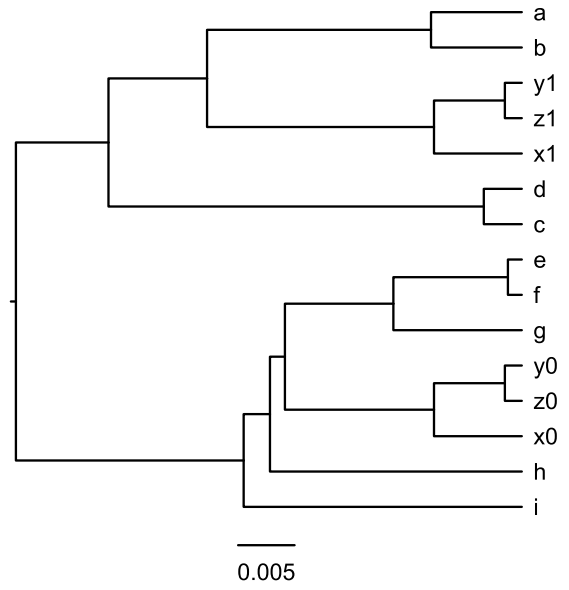


Figure 9: Rep 8

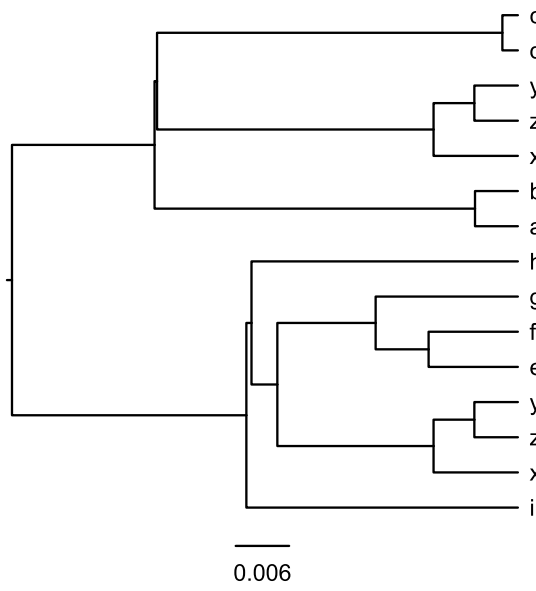


Figure 10: Rep 9

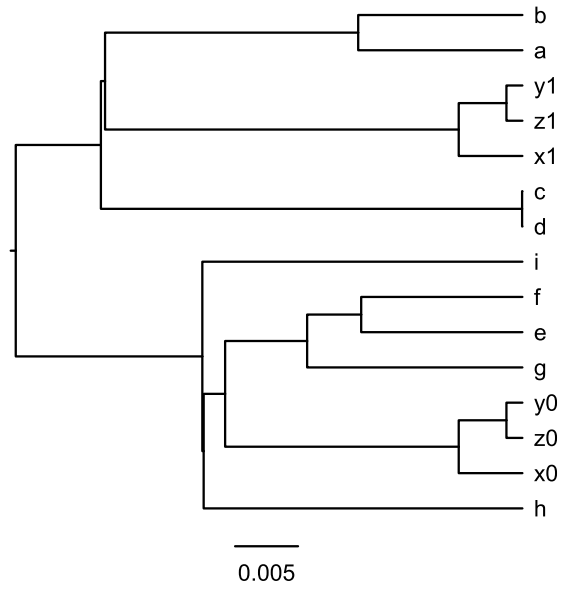


Figure 11: Rep 10

### 3 Configuration file

```
PROGRAMPARAMETERS
beastseed 652989819
beastchainlength 5000000
beastscreen.logevery 10000
beastparams.logevery 1000
beastgtrees.logevery 1000
beastmultree.logevery 1000
beastdbugtune.logevery 10000
treeannburnin 501
SCENARIO
nofGNRT 1
5 1 10 8e-8
noftetratrees 1
genelength 500
ditree ntips 9
a height 0 tippop 100000 prevpop 100000
b height 0 tippop 100000 prevpop 100000
c height 0 tippop 100000 prevpop 100000
d height 0 tippop 100000 prevpop 100000
e height 0 tippop 100000 prevpop 100000
f height 0 tippop 100000 prevpop 100000
g height 0 tippop 100000 prevpop 100000
h height 0 tippop 100000 prevpop 100000
i height 0 tippop 100000 prevpop 100000
(a,b) height 0.006 tippop * prevpop 100000
(c,d) height 0.002 tippop * prevpop 100000
((a,b),(c,d)) height 0.038 tippop * prevpop 100000
(e,f) height 0.012 tippop * prevpop 100000
((e,f),g) height 0.018 tippop * prevpop 100000
(((e,f),g),h) height 0.026 tippop * prevpop 100000
((((e,f),g),h),i) height 0.030 tippop * prevpop 100000
(((a,b),(c,d)),(((e,f),g),h),i)) height 0.042 tippop * prevpop *
tetratree ntips 3
z height 0 tippop 100000 prevpop 100000
y height 0 tippop 100000 prevpop 100000
x height 0 tippop 100000 prevpop 100000
(z,y) height 0.004 tippop * prevpop 100000
(x,(z,y)) height 0.009 tippop * prevpop *
hyb 0.015 100000 join * * foot1 ((e,f),g) .022 100000 foot2 (c,d) .034 100000
```