**Bioinformatic scripts included in**

***Genome-wide diversity and global migration patterns in dromedaries follow ancient caravan routes***

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***# Script for Admixture analysis***

Software Version: ADMIXTURE 1.3

<https://bioinformaticshome.com/tools/descriptions/ADMIXTURE.html>

Alexander DH, Lange K (2011) "Enhancements to the ADMIXTURE algorithm for individual ancestry estimation." *BMC Bioinformatics*

<https://doi.org/10.1186/1471-2105-12-246>

# Run Admixture in a loop for K=1-10

# Move to the Applications/admixture folder and copy-paste all input files there

for K in 1 2 3 4 5 6 7 8 9 10;

./admixture --cv filename.ped $K | tee filename\_log${K}.out

# Extract the CV values to see for the best K (with the lowest cv values)

grep -h CV filename\_log\*.out

# Plot Q-estimates in R

filename <-read.table("/Users/Username/path~/file.Q")

par(mfrow=c(3,1))

barplot(t(as.matrix(filename)), col=rainbow(1), border=NA)

**# Plot Admixture on R**

filename <- read.table("/Users/Username/path~/file.Q")

par(mfrow=c(3,1))

barplot(t(as.matrix(filename)), col=rainbow(1), border=NA)

# Add Axis to barplots

axis(1, at = seq(0.6,115.2, 1.2), labels = names, las=2, tck=0, col="white", cex=0.6)

***# R codes for Principal component analysis using adegenet package***

Software Version: *adegenet* R package v. 2.1.3

<https://cran.r-project.org/web/packages/adegenet/index.html>

# Jombart Thibout (2008) adegenet: a R package for the multivariate analysis of genetic markers

Bioinformatics, Volume 24, Issue 11, 1 June 2008, Pages 1403–1405, <https://doi.org/10.1093/bioinformatics/btn129>

library(adegenet)

library(pegas)

DROM95<- read.PLINK("DROM95\_AFAS\_Had\_Ken.raw", parallel=FALSE)

#make a PCA

pcaDROM95 <- glPca(DROM95)

names(pcaDROM95)

#make an s.class plot

myCol <- c("red","blue","cyan3", "orange")

s.class(pcaDROM95$scores, fac=pop(DROM95), col=myCol, xax=1, yax=3)

s.class(pcaDROM95$scores, fac=pop(DROM95),xax=1, yax=3, col=transp(myCol,.6), cstar=0, cpoint=2)

add.scatter.eig(pcaDROM95$eig[1:25],3,1,3, ratio=.3)

title(xlab="PC1", ylab="PC3")

dev.off()

colorplot(pcaDROM95$scores, pcaDROM95$scores)

***# R codes for plotting EEMS results***

Software Version: EEMS (<https://github.com/dipetkov/eems>)

Petkova D, Novembre J and Stephens M (2016) Visualizing spatial population structure with estimated effective migration surfaces. *Nat Genet* 48, 94–100.

<https://doi.org/10.1038/ng.3464>

run <- system.file("./run\_10M/", package = "rEEMSplots")

eems\_results <- file.path(run, " outputs")

name\_figures <- file.path(path.expand("~"), " outputs")

eems.plots(mcmcpath = "./run\_10M/",

       plotpath = "./test\_outputs-default/testoutdeafaults",

       longlat = TRUE,

       add.grid = TRUE,

       col.grid = "gray90",

       lwd.grid = 2,

       add.outline = TRUE,

       col.outline = "black",

       lwd.outline = 2,

       add.demes = TRUE,

       col.demes = "black",

       pch.demes = 5,

          min.cex.demes = 0.5,

       max.cex.demes = 1.5,

       plot.height = 8,

       plot.width = 7,

       res = 600,

       out.pdf = FALSE)

***#BayeScan***

Software Version: BayeScan 2.1

<http://cmpg.unibe.ch/software/BayeScan/>

Foll M and OE Gaggiotti (2008) A genome scan method to identify selected loci appropriate for both dominant and codominant markers: A Bayesian perspective. [*Genetics* 180: 977-993](http://www.genetics.org/cgi/content/abstract/180/2/977), <https://doi.org/10.1534/genetics.108.092221>

# Run BayeScan to look for SNPs putatively under selection between Hadana and the other remaining Saudi Arabian dromedaries

## Step 1 make directories

cd /genetics/elbers

mkdir drom95

## Step 2 get files

### this contains scripts to make BayeScan input

wget http://sfg.stanford.edu/Scripts.zip

unzip Scripts.zip

### These are the ped and map files that still contain the scaffold/contig information

DROM95\_AFAS\_23K.map

DROM95\_AFAS\_23K.ped

## Step 3 modify the ped file and make a copy of the map file

grep -P "SA\w+" DROM95\_AFAS\_23K.ped > hadhana\_23K.ped

cp DROM95\_AFAS\_23K.map hadhana\_23K.map

## Step 4 Make BayeScan input

### use PLINK to convert PED and MAP into VCF

/opt/plink/plink --file hadhana\_23K --recode vcf --out hadhana\_23K --allow-extra-chr

### use PERL to add GQ and get rid of AS\_ at beginnging of sample names in VCF file

perl -pe "s/(GT)/\1:GQ/" hadhana\_23K.vcf | perl -pe "s/(.\/.)/\1:30/g" |perl -pe "s/AS\_//g" > hadhana\_23K-bayescan.vcf

### Use Simple Fool's Guide to RNASeq script to make BayeScan input (make a popfile first)

#####beginning of popfile#####

SA811 hadhana

SA813 hadhana

SA814 hadhana

SA815 hadhana

SA816 hadhana

SA817 hadhana

SA819 hadhana

SA471 RestOfSa

SA473 RestOfSa

SA795A RestOfSa

SA796A RestOfSa

SA797A RestOfSa

SA798A RestOfSa

SA799A RestOfSa

SA800A RestOfSa

#####end of popfile######

### Run script to make BayeScan input

python Scripts\ for\ SFG/make\_bayescan\_input.py hadhana\_23K-bayescan.vcf popfile 30 0 0 1

### population key for BayeScan input (pop 1 is hadhana)

1 hadhana

2 RestOfSa

## Step 5 Run BayeScan

cp /opt/BayeScan2.1/binaries/BayeScan2.1\_linux64bits BayeScan2.1

chmod u+x BayeScan2.1

./BayeScan2.1 bayes\_input.txt -snp -od . -o bayes\_input-results -threads 75 > bayescan.log 2>&1 &

## Step 6 Determine outliers

### Determine outliers using R

R

###source the plot\_R.r script from Bayescan distribution

source("plot\_R.r")

###get outliers corrected with a false discovery rate up to 0.2 for input without low frequency snps

snps\_results <- plot\_bayescan("bayes\_input-results\_fst.txt", FDR=0.15)

snps\_results$outliers

# 10926

### 1 outliers, for FDR between 0.15

snps\_results <- plot\_bayescan("bayes\_input-results\_fst.txt", FDR=0.2)

snps\_results$outliers

# 6311 10926 16918

### 3 outliers, for FDR between 0.2

###save the candidate loci to a text file

write(snps\_results$outliers, file="outlier\_snps.txt", ncolumns=1,append=FALSE)

cp snpkey.txt snpkey.txt2

cp hadhana\_23K.vcf hadhana\_23K.vcf2

#code to create IGV batch file for noMAF loci

while read i;do

perl -pi -e "s/^$i\t(.+)\_(.+)\n/goto \1:\2\n/" snpkey.txt2

done < outlier\_snps.txt

grep 'goto' snpkey.txt2 > outlier\_snps.igv.txt

perl -pe "s/goto (\w+\.\d):(\d+)\n/\1\t\2\n/" outlier\_snps.igv.txt > outlier\_snps.vcf.txt

while read i;do

perl -li -e $i

perl -pi -e "s/(^$i)\t\d+\_\d+\t(.+)\n/\1\tOUTLIER\_SNP\t\2\n/" hadhana\_23K.vcf2

done < outlier\_snps.vcf.txt

grep 'OUTLIER\_SNP\|^#' hadhana\_23K.vcf2 | grep -v "contig" > hadhana\_23K\_outlier\_snps\_fdr\_0.2\_not\_0.05.vcf

***# EBSP: Extended Bayesian Skyline Plot***

Software Version: Beast 2.5.1 (https://github.com/CompEvol/beast2/releases/tag/v2.5.1)

Bouckaert, R. et al. (2019) BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. *PLoS Comput. Biol*. 15, e1006650.

<https://doi.org/10.1371/journal.pcbi.1006650>

## Creating an Extended Bayesian Skyline Plot with ddRAD data from dromedaries

# STEP 1 Get only READ 1 from BAM files

cd /genetics/Burger/DROM\_ddRAD/alignments\_GCA\_000803125/

ls \*.bam |perl -pe "s/.sorted.bam//g" > samples

mkdir ../read-1-only

chmod a+rwx ../read-1-only

while read i;do

samtools view -b -f 64 -F 4 ${i}.sorted.bam > ../read-1-only/${i}.read1.bam

done < samples

# STEP 2 Analyze mapped read 1's

cd /genetics/Burger/DROM\_ddRAD/read-1-only/

ls \*.bam |perl -pe "s/.read1.bam//g" > samples

x=1

while read i;do

pstacks -t bam -p 75 -f ${i}.read1.bam -o ./ -i $x -m 3 >> pstacks.log 2>&1

x=$((x+1))

done < samples &

# STEP 3 Make a catalog of stack loci

cd /genetics/Burger/DROM\_ddRAD/read-1-only/

perl -pe "s/(.+)/\1.read1\tONE/g" samples > popmap.txt

cstacks -P./ -p 75 -n 2 -b 1 \

-M ./popmap.txt > cstacks.log 2>&1 &

# STEP 4 Compare the catalog to each individual's RAD loci

cd /genetics/Burger/DROM\_ddRAD/read-1-only/

sstacks -P./ -p 75 -b 1 \

-M ./popmap.txt > sstacks.log 2>&1 &

# STEP 5 Create VCF and FASTA files

cd /genetics/Burger/DROM\_ddRAD/read-1-only/

# b = Batch ID to examine when exporting from the catalog

# P = path to the directory containing the Stacks files

# p = minimum number of populations a locus must be present in to process a locus

# m = minimum stack depth required for individuals at a locus

# r = minimum percentage of individuals in a population required to process a locus for that population

# --fasta = output fasta sequences

# --vcf = output variant call format file

populations -t 75 -P ./ -b 1 -p 1 \

--max\_obs\_het 0.5 \

-M ./popmap.txt -m 6 -r 0 --vcf --fasta > populations.log 2>&1 &

mv batch\_1.fa batch\_1\_drom\_and\_bactrian.fa

mv batch\_1.vcf batch\_1\_drom\_and\_bactrian.vcf

mv batch\_1.populations.log batch\_1\_drom\_and\_bactrian.populations.log

mv batch\_1.haplotypes.tsv batch\_1\_drom\_and\_bactrian.haplotypes.tsv

mv batch\_1.sumstats\_summary.tsv batch\_1\_drom\_and\_bactrian.sumstats\_summary.tsv

mv batch\_1.hapstats.tsv batch\_1\_drom\_and\_bactrian.hapstats.tsv

mv batch\_1.sumstats.tsv batch\_1\_drom\_and\_bactrian.sumstats.tsv

# STEP 6 Modify and download script to convert STACKS FASTA output to FASTA Files with at least 4 SNPs per locus

cd /genetics/Burger/DROM\_ddRAD/read-1-only/

# STEP 6 Modify and download script to convert STACKS FASTA output to FASTA Files with at least 4 SNPs per locus

cd /genetics/Burger/DROM\_ddRAD/read-1-only/

wget https://raw.githubusercontent.com/jelber2/RAD-Scripts/master/RAD\_Haplotypes.R

## note forked from https://github.com/rcristofari/RAD-Scripts/blob/master/RAD\_Haplotypes.R

chmod u+x RAD\_Haplotypes.R

## edit RAD\_Haplotypes.R to allow for a custom map in the format samplenumber\tsamplename\tpopulation

perl -pe "s/if\(ignore==1\)\{map\[,2\]<-\'ALL\'/if\(ignore==1\)\{map\[,3\]<-\'ALL\'/" RAD\_Haplotypes.R > RAD\_Haplotypes2.R

perl -pi -e "s/as.character\(map\[,1\]\)->Name/as.character\(map\[,1\]\)->Sample/" RAD\_Haplotypes2.R

perl -pi -e "s/as.character\(map\[,2\]\)->Pop/as.character\(map\[,2\]\)->Name/" RAD\_Haplotypes2.R

perl -pi -e "s/seq\(1,length\(Name\),1\)->Sample/as.character\(map\[,3\]\)->Pop/" RAD\_Haplotypes2.R

# STEP 7 Install Required R Packages

### Do these steps to update R to version 3.4.3

# add to /etc/apt/sources.list

deb https://cran.rstudio.org/bin/linux/ubuntu xenial/

sudo apt-get update

sudo apt-get install r-base

sudo apt-get install r-base-dev

###

# Install required packages on Genetics Server

R

install.packages("devtools")

quit()

R -e "require(devtools); install\_version('igraph', version='1.0.1', repos='https://cran.rstudio.org/')"

R

install.packages("adegenet")

install.packages("ape")

install.packages("pegas")

install.packages("seqinr")

install.packages("sqldf")

install.packages("tcltk")

install.packages("ggplot2")

install.packages("gridExtra")

quit()

# STEP 8 CREATE folder of FASTA files and run RAD\_Haplotypes.R

mkdir fasta-drom-and-bactrian

## Need to get sample numbers for all fasta sequences

grep ">" batch\_1\_drom\_and\_bactrian.fa | grep -Po "Sample\_\d+" |grep -Po "\d+" > Samplenumber

## Need to get sample names for all fasta sequences

grep ">" batch\_1\_drom\_and\_bactrian.fa | grep -Po "\[.+;" |perl -pe "s/;|\[//g" > Samplename

## combine samplenames and samplesnumbers into a single file with 2 columns

paste Samplenumber Samplename > map.txt

## retain only unique samplenumber samplename combinations and add a third column with ONE

sort -nu map.txt | perl -pe "s/read1/read1\tONE/g" > map2.txt

## get only loci that have DC156 (bactrian) sequences

### first put header and sequence on a single line

cat batch\_1\_drom\_and\_bactrian.fa |paste - - > batch\_1\_drom\_and\_bactrian.fa.oneline.fa

### next grab the CLocus\_### for all DC156 sequences

grep "DC156.read1" batch\_1\_drom\_and\_bactrian.fa.oneline.fa | grep -Po "CLocus\_\d+\_" |sort -u > bactrian.loci

### finally retain only loci for which the bactrian has sequences then convert them to standard FASTA format

grep -f bactrian.loci batch\_1\_drom\_and\_bactrian.fa.oneline.fa |tr "\t" "\n" > batch\_1\_drom\_and\_bactrian.fa.oneline.fa.only.bactrian.loci.fa

## Get sequences for RAD loci to estimate molecular clock rate

./RAD\_Haplotypes2.R --fasta=batch\_1\_drom\_and\_bactrian.fa.oneline.fa.only.bactrian.loci.fa --map=map2.txt --out=fasta-drom-and-bactrian/. --type='fasta' --nind=2 --min --ploidy=2 --ignore\_pop=1 > RAD\_Haplotypes2-drom-bactrian.log 2>&1 &

# STEP 9 append -1 and -2 to end of each sample's sequences (2 per locus)

cd fasta-drom-and-bactrian/

for file in \*?snps.subset.fa;do

sed -i '1~4s/$/-1/' $file

sed -i '3~4s/$/-2/' $file

done

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

mkdir 7snps && cp \*7snps\* 7snps/.

# STEP 10 Estimate molecular clock rate

## First need to calculate average pairwise differences between dromedary sequences and bactrianr Puma

## Second need to know the age of the most recent common ancestor

## Install R packages

R

source("https://bioconductor.org/biocLite.R")

biocLite("Biostrings")

install.packages("seqinr")

quit()

###calculate-average-number-of-mutations-and-sites-for-RAD-loci.R###

# load packages

suppressPackageStartupMessages(suppressWarnings(library(Biostrings)))

suppressPackageStartupMessages(suppressWarnings(library(seqinr)))

# read in files

files <- list.files(pattern=".fa$")

# make empty loci list

loci <- list()

# read in fasta sequences

for (i in 1:length(files)) {loci[[i]] <- read.fasta(files[i])}

# calculate average number of differences for each locus

locimeans <- integer(0) # make an empty integer

locilength <- integer(0) # make an empty integer

for (i in 1:length(loci)){ # loop through all loci (i.e., each fasta file)

testnames <- names(loci[[i]]) # gets fasta headers minus ">"

locusname <- testnames[[1]] # gets the name of the first sequence in the fasta file

test1name <- paste0(regmatches(locusname,regexpr("Locus\_\\d+\_",locusname,perl=T)),"DC156.read1-1") # looks for Locus\_####\_ (from the header of the first sequence in the fasta file) and then appends DC156.read1-1

test2name <- paste0(regmatches(locusname,regexpr("Locus\_\\d+\_",locusname,perl=T)),"DC156.read1-2") # looks for Locus\_####\_ (from the header of the first sequence in the fasta file) and then appends DC156.read1-2

test1 <- loci[[i]][names(loci[[i]]) %in% c(test1name)] # creates the name of the sequence for Locus\_###\_DC156-read1-1

test1seq <- toupper(c2s(test1[[1]])) # gets only the sequence for Locus\_###\_DC156-read1-1

locilength <- c(locilength,getLength(test1seq))

test2 <- loci[[i]][names(loci[[i]]) %in% c(test2name)] # creates the name of the sequence for Locus\_###\_DC156-read1-2

test2seq <- toupper(c2s(test2[[1]])) # gets only the sequence for Locus\_###\_DC156-read1-1

test3 <- loci[[i]][!names(loci[[i]]) %in% c(test1name,test2name)] # gets all of names of the sequences other than Locus\_###\_DC156-read1-1 and Locus\_###\_DC156-read1-2

test3seq <- character(0) # creates an empty character

for (i in 1:length(test3)){test3seq <- c(test3seq,toupper(c2s(test3[[i]])))} # gets all of the remaning sequences (minus Locus\_###\_DC156-read1-1 and Locus\_###\_DC156-read1-2)

test1seqdif <- integer(0) # creates an empty integer

for (i in 1:length(test3seq)){test1seqdif <- as.integer(c(test1seqdif, nmismatch(pairwiseAlignment(test3seq[[i]], test1seq))))} # calculates the number of differences for all of the sequences compared to Locus\_###\_DC156-read1-1

test2seqdif <- integer(0) # creates and empty integer

for (i in 1:length(test3seq)){test2seqdif <- as.integer(c(test2seqdif, nmismatch(pairwiseAlignment(test3seq[[i]], test2seq))))} # calculates the number of differences for all of the sequences compared to Locus\_###\_DC156-read1-2

locimeans <- c(locimeans,mean(c(mean(test1seqdif),mean(test2seqdif)))) # calculates the mean differences for all sequences versus Locus\_###\_DC156-read1-2 and Locus\_###\_DC156-read1-1

}

cat("\nThere are on average",mean(locimeans),"mutations between dromedary and bactrian for",length(loci), "RAD loci with an average length of",mean(locilength),"nucleotides/sites.\n\n") # calculates the mean number of mutations, number of RAD loci, and average number of sites (length of RAD loci)

###calculate-average-number-of-mutations-and-sites-for-RAD-loci.R###

## Calculate number of mutations and average length of RAD loci

## Do this for RAD loci with 5,6, and 7 snps

cd /genetics/Burger/DROM\_ddRAD/read-1-only/fasta-drom-and-bactrian/5snps

Rscript /genetics/Burger/DROM\_ddRAD/read-1-only/calculate-average-number-of-mutations-and-sites-for-RAD-loci.R

# There are on average 1.689951 mutations between dromedary and bactrian for 132 RAD loci with an average length of 110 nucleotides/sites.

cd /genetics/Burger/DROM\_ddRAD/read-1-only/fasta-drom-and-bactrian/6snps

Rscript /genetics/Burger/DROM\_ddRAD/read-1-only/calculate-average-number-of-mutations-and-sites-for-RAD-loci.R

# There are on average 1.515028 mutations between dromedary and bactrian for 24 RAD loci with an average length of 110 nucleotides/sites.

cd /genetics/Burger/DROM\_ddRAD/read-1-only/fasta-drom-and-bactrian/7snps

Rscript /genetics/Burger/DROM\_ddRAD/read-1-only/calculate-average-number-of-mutations-and-sites-for-RAD-loci.R

# There are on average 2.04964 mutations between dromedary and bactrian for 14 RAD loci with an average length of 110 nucleotides/sites.

###NOTE###

The divergence time between the Bactrian camel and dromedary is ~4.4 Mya. (Wu et al. 2014).

###NOTE###

# To calculate molecular clock rate for BEAST2,

# standard format = mutations/site/million\_years [note time axis is millions of years and assumes generation time of 1 year]

# So, we need to multiply the standard format by dromedary generation time (5 years) and divide by 1 million years to get time axis in years.

# mutations = average number of differences(i.e., mutations) for 5,6, and 7 snp rad loci (i.e., X,Y,Z) between dromedary and bactrian camels = mut = mean(c(1.689951,1.515028,2.04964)) = 1.75154

# site = average length of RAD loci for 5,6,7 snp rad loci = 110

# divergence time between bactrian and dromedary = 4.4

# standard format = mut/site/divergenceTime = 1.75154/110/4.4 = 0.003618884

# standard format is a strict molecular clock with prior with a lognormal distribution with a mean of 0.003618884 and standard deviation so that the minimum is 0.003130223 and the maximum is 0.004234793

# desired format = standard format multiplied by dromedary generation time (5 years) and divided by 1 million years

# desired format mean = (0.003618884\*5)/1000000 = 1.809442e-08

# desired format min = (0.003618884\*5)/1000000 = 1.565111e-08

# desired format max = (0.003618884\*5)/1000000 = 2.117397e-08

# STEP 11 Re-run Steps 5,8,9 without DC156

## STEP 5 Repeated (except without DC156.read1)

grep -v "DC156.read1" popmap.txt > popmap-without-DC156.txt

populations -t 75 -P ./ -b 1 -p 1 \

--max\_obs\_het 0.5 \

-M ./popmap-without-DC156.txt -m 6 -r 0 --vcf --fasta > drom-only-population.log 2>&1 &

## STEP 8 Repeated CREATE folder of FASTA files and run RAD\_Haplotypes.R

mkdir fasta-drom

### Need to get sample numbers for all fasta sequences

grep ">" batch\_1.fa | grep -Po "Sample\_\d+" |grep -Po "\d+" > Samplenumber

### Need to get sample names for all fasta sequences

grep ">" batch\_1.fa | grep -Po "\[.+;" |perl -pe "s/;|\[//g" > Samplename

### combine samplenames and samplesnumbers into a single file with 2 columns

paste Samplenumber Samplename > drommap.txt

cd /genetics/elbers/dromedary-ebsp

mkdir africa-no-kenya

mkdir asia-no-hadhana

### Need to get sample numbers for all fasta sequences

grep ">" batch\_1.fa | grep -Po "Sample\_\d+" |grep -Po "\d+" > Samplenumber

### Need to get sample names for all fasta sequences

grep ">" batch\_1.fa | grep -Po "\[.+;" |perl -pe "s/;|\[//g" > Samplename

### combine samplenames and samplesnumbers into a single file with 2 columns

paste Samplenumber Samplename > drommap.txt

### retain only unique samplenumber samplename combinations and add a third column with ONE

sort -nu drommap.txt | perl -pe "s/read1/read1\tONE/g" > drommap2.txt

cat batch\_1.fa |paste - - |grep -vf list-of-dromedary-samples-to-remove-from-ebsp.txt |tr '\t' '\n' > dromedary-fasta-for-ebsp.fa

grep -vf list-of-dromedary-samples-to-remove-from-ebsp.txt drommap2.txt > drommap3.txt

grep -vf list-of-dromedary-samples-from-africa.txt drommap3.txt |grep -vf list-of-dromedary-samples-from-hadhana.txt > asia-map.txt

grep -vf list-of-dromedary-samples-from-asia.txt drommap3.txt |grep -vf list-of-dromedary-samples-from-kenya.txt > africa-map.txt

cat dromedary-fasta-for-ebsp.fa |paste - - |grep -vf list-of-dromedary-samples-from-asia.txt |grep -vf list-of-dromedary-samples-from-kenya.txt| tr '\t' '\n' > dromedary-fasta-for-africa-ebsp.fa

cat dromedary-fasta-for-ebsp.fa |paste - - |grep -vf list-of-dromedary-samples-from-africa.txt |grep -vf list-of-dromedary-samples-from-hadhana.txt |tr '\t' '\n' > dromedary-fasta-for-asia-ebsp.fa

# Modify and download script to convert STACKS FASTA output to FASTA Files with at least 4 SNPs per locus

wget https://raw.githubusercontent.com/jelber2/RAD-Scripts/master/RAD\_Haplotypes.R

## note forked from https://github.com/rcristofari/RAD-Scripts/blob/master/RAD\_Haplotypes.R

chmod u+x RAD\_Haplotypes.R

## edit RAD\_Haplotypes.R to allow for a custom map in the format samplenumber\tsamplename\tpopulation

perl -pe "s/if\(ignore==1\)\{map\[,2\]<-\'ALL\'/if\(ignore==1\)\{map\[,3\]<-\'ALL\'/" RAD\_Haplotypes.R > RAD\_Haplotypes2.R

perl -pi -e "s/as.character\(map\[,1\]\)->Name/as.character\(map\[,1\]\)->Sample/" RAD\_Haplotypes2.R

perl -pi -e "s/as.character\(map\[,2\]\)->Pop/as.character\(map\[,2\]\)->Name/" RAD\_Haplotypes2.R

perl -pi -e "s/seq\(1,length\(Name\),1\)->Sample/as.character\(map\[,3\]\)->Pop/" RAD\_Haplotypes2.R

### Get sequences for RAD loci to estimate molecular clock rate

### used 75% of sample size for minimum number of individuals per locus to keep a locus

### note that I removed kenya samples from africa and hadhana samples from asia

./RAD\_Haplotypes2.R --fasta=dromedary-fasta-for-ebsp.fa --map=drommap3.txt --out=all/. --type='fasta' --nind=71 --min --ploidy=2 --ignore\_pop=1 > RAD\_Haplotypes2-all.log 2>&1 &

./RAD\_Haplotypes2.R --fasta=dromedary-fasta-for-africa-ebsp.fa --map=africa-map.txt --out=africa-no-kenya/. --type='fasta' --nind=31 --min --ploidy=2 --ignore\_pop=1 > RAD\_Haplotypes2-africa.log 2>&1 &

./RAD\_Haplotypes2.R --fasta=dromedary-fasta-for-asia-ebsp.fa --map=asia-map.txt --out=asia-no-hadhana/. --type='fasta' --nind=34 --min --ploidy=2 --ignore\_pop=1 > RAD\_Haplotypes2-asia.log 2>&1 &

## first number is number of SNPs per locus

## second number is number of loci with at least first number

## ex 4=93, there are 93 RAD loci in the EBSP with at least 4 SNPs per locus

## ideally aiming for 50 RAD loci with at least 5,6,7 SNPs per RAD locus

## but maybe including the RAD loci with 4 SNPs per locus is not so bad

# all asia

#4=93

#5=30

#6=10

# all asia minus hadhana

#4=99

#5=31

#6=8

# all africa

#4=68

#5=22

#6=11

# all africa minus kenya

#4=69

#5=21

#6=11

## STEP 9 Repeated append -1 and -2 to end of each sample's sequences (2 per locus)

/genetics/elbers/dromedary-ebsp/all

rm \*0snps.subset.fa

rm \*1snps.subset.fa

rm \*2snps.subset.fa

rm \*3snps.subset.fa

for file in \*?snps.subset.fa;do

sed -i '1~4s/$/-1/' $file

sed -i '3~4s/$/-2/' $file

done

ls \*4snps.subset.fa|wc -l

ls \*5snps.subset.fa|wc -l

ls \*6snps.subset.fa|wc -l

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

rm \*.fa

cp ?snps/\* .

rm ?snps -r

ls \*.fa > all-all

ls \*.fa |sort -R |head -n 50 > all-random1

mkdir all-random1-seq

cd all-random1-seq

while read i;do cp ../$i .;done < ../all-random1

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

x=1

for i in `ls \*4snps.subset.fa`;do

mv 4snps/${i} 4snps/${x}\_subset.fa

((x++))

done

for i in `ls \*5snps.subset.fa`;do

mv 5snps/${i} 5snps/${x}\_subset.fa

((x++))

done

for i in `ls \*6snps.subset.fa`;do

mv 6snps/${i} 6snps/${x}\_subset.fa

((x++))

done

rm \*.fa

cd africa-no-kenya/

rm \*0snps.subset.fa

rm \*1snps.subset.fa

rm \*2snps.subset.fa

rm \*3snps.subset.fa

for file in \*?snps.subset.fa;do

sed -i '1~4s/$/-1/' $file

sed -i '3~4s/$/-2/' $file

done

ls \*4snps.subset.fa|wc -l

ls \*5snps.subset.fa|wc -l

ls \*6snps.subset.fa|wc -l

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

rm \*.fa

cp ?snps/\* .

rm ?snps -r

ls \*.fa > africa-all

ls \*.fa |sort -R |head -n 50 > africa-random1

ls \*.fa |sort -R |head -n 50 > africa-random2

ls \*.fa |sort -R |head -n 50 > africa-random3

mkdir africa-random1-seq

mkdir africa-random2-seq

mkdir africa-random3-seq

cd africa-random1-seq

while read i;do cp ../$i .;done < ../africa-random1

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

x=1

for i in `ls \*4snps.subset.fa`;do

mv 4snps/${i} 4snps/${x}\_subset.fa

((x++))

done

for i in `ls \*5snps.subset.fa`;do

mv 5snps/${i} 5snps/${x}\_subset.fa

((x++))

done

for i in `ls \*6snps.subset.fa`;do

mv 6snps/${i} 6snps/${x}\_subset.fa

((x++))

done

rm \*.fa

cd ../africa-random2-seq

while read i;do cp ../$i .;done < ../africa-random2

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

x=1

for i in `ls \*4snps.subset.fa`;do

mv 4snps/${i} 4snps/${x}\_subset.fa

((x++))

done

for i in `ls \*5snps.subset.fa`;do

mv 5snps/${i} 5snps/${x}\_subset.fa

((x++))

done

for i in `ls \*6snps.subset.fa`;do

mv 6snps/${i} 6snps/${x}\_subset.fa

((x++))

done

rm \*.fa

cd ../africa-random3-seq

while read i;do cp ../$i .;done < ../africa-random3

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

x=1

for i in `ls \*4snps.subset.fa`;do

mv 4snps/${i} 4snps/${x}\_subset.fa

((x++))

done

for i in `ls \*5snps.subset.fa`;do

mv 5snps/${i} 5snps/${x}\_subset.fa

((x++))

done

for i in `ls \*6snps.subset.fa`;do

mv 6snps/${i} 6snps/${x}\_subset.fa

((x++))

done

rm \*.fa

cd ../../asia-no-hadhana/

rm \*0snps.subset.fa

rm \*1snps.subset.fa

rm \*2snps.subset.fa

rm \*3snps.subset.fa

for file in \*?snps.subset.fa;do

sed -i '1~4s/$/-1/' $file

sed -i '3~4s/$/-2/' $file

done

ls \*4snps.subset.fa|wc -l

ls \*5snps.subset.fa|wc -l

ls \*6snps.subset.fa|wc -l

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

rm \*.fa

cp ?snps/\* .

rm ?snps -r

ls \*.fa > asia-all

ls \*.fa |sort -R |head -n 50 > asia-random1

ls \*.fa |sort -R |head -n 50 > asia-random2

ls \*.fa |sort -R |head -n 50 > asia-random3

mkdir asia-random1-seq

mkdir asia-random2-seq

mkdir asia-random3-seq

cd asia-random1-seq

while read i;do cp ../$i .;done < ../asia-random1

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

x=1

for i in `ls \*4snps.subset.fa`;do

mv 4snps/${i} 4snps/${x}\_subset.fa

((x++))

done

for i in `ls \*5snps.subset.fa`;do

mv 5snps/${i} 5snps/${x}\_subset.fa

((x++))

done

for i in `ls \*6snps.subset.fa`;do

mv 6snps/${i} 6snps/${x}\_subset.fa

((x++))

done

rm \*.fa

cd ../asia-random2-seq

while read i;do cp ../$i .;done < ../asia-random2

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

x=1

for i in `ls \*4snps.subset.fa`;do

mv 4snps/${i} 4snps/${x}\_subset.fa

((x++))

done

for i in `ls \*5snps.subset.fa`;do

mv 5snps/${i} 5snps/${x}\_subset.fa

((x++))

done

for i in `ls \*6snps.subset.fa`;do

mv 6snps/${i} 6snps/${x}\_subset.fa

((x++))

done

rm \*.fa

cd ../asia-random3-seq

while read i;do cp ../$i .;done < ../asia-random3

mkdir 4snps && cp \*4snps\* 4snps/.

mkdir 5snps && cp \*5snps\* 5snps/.

mkdir 6snps && cp \*6snps\* 6snps/.

x=1

for i in `ls \*4snps.subset.fa`;do

mv 4snps/${i} 4snps/${x}\_subset.fa

((x++))

done

for i in `ls \*5snps.subset.fa`;do

mv 5snps/${i} 5snps/${x}\_subset.fa

((x++))

done

for i in `ls \*6snps.subset.fa`;do

mv 6snps/${i} 6snps/${x}\_subset.fa

((x++))

done

rm \*.fa

cd /genetics/elbers

wget https://github.com/CompEvol/beast2/releases/download/v2.5.1/BEAST.v2.5.1.Linux.tgz

tar xzf BEAST.v2.5.1.Linux.tgz

########

MAKE input files

########

cd /genetics/elbers/dromedary-ebsp

#####beginning of beast2-input-formatter.sh#####

#! /bin/bash

POSITIONAL=()

while [[ $# -gt 0 ]]

do

key="$1"

case $key in

-o|--output)

beast2input="$2"

shift # past argument

shift # past value

;;

\*) # unknown option

POSITIONAL+=("$1") # save it in an array for later

shift # past argument

;;

esac

done

set -- "${POSITIONAL[@]}" # restore positional parameters

echo "Saving:$beast2input"

if [[ -n $1 ]]; then

echo "Last line of file specified as non-opt/last argument:"

tail -1 "$1"

fi

ls ?snps/\*.fa |perl -pe "s/\dsnps\///g" |perl -pe "s/.fa//g" > test2

cp ?snps/\*.fa .

snps4="$(ls 4snps/\*.fa|wc -l)"

snps5="$(bc <<< $snps4+1)"

snps5a="$(ls 5snps/\*.fa|wc -l)"

snps6="$(bc <<< $snps4+$snps5a+1)"

echo "<?xml version=\"1.0\" encoding=\"UTF-8\" standalone=\"no\"?><beast beautitemplate='Standard' beautistatus='allowLinking|noAutoUpdateFixMeanSubstRate' namespace=\"beast.core:beast.evolution.alignment:beast.evolution.tree.coalescent:beast.core.util:beast.evolution.nuc:beast.evolution.operators:beast.evolution.sitemodel:beast.evolution.substitutionmodel:beast.evolution.likelihood\" required=\"BEAST v2.5.1\" version=\"2.5\">" >> ${beast2input}

while read file\_name;do

echo "<data id=\"$file\_name\" name=\"alignment\">" >> ${beast2input}

cat ${file\_name}.fa |/opt/seqtk/seqtk seq -l0 |paste - - |perl -pe "s/>(Locus\_\d+\_\w+.read1-\d)\t(\w+)\n/\<sequence id\=\"seq\\_\1\" taxon\=\"\1\" totalcount=\"4\" value\=\"\2\"\/\>\n/" >> ${beast2input}

echo "</data>" >> ${beast2input}

done < test2

echo "<map name=\"Uniform\" >beast.math.distributions.Uniform</map>" >> ${beast2input}

echo "<map name=\"Exponential\" >beast.math.distributions.Exponential</map>" >> ${beast2input}

echo "<map name=\"LogNormal\" >beast.math.distributions.LogNormalDistributionModel</map>" >> ${beast2input}

echo "<map name=\"Normal\" >beast.math.distributions.Normal</map>" >> ${beast2input}

echo "<map name=\"Beta\" >beast.math.distributions.Beta</map>" >> ${beast2input}

echo "<map name=\"Gamma\" >beast.math.distributions.Gamma</map>" >> ${beast2input}

echo "<map name=\"LaplaceDistribution\" >beast.math.distributions.LaplaceDistribution</map>" >> ${beast2input}

echo "<map name=\"prior\" >beast.math.distributions.Prior</map>" >> ${beast2input}

echo "<map name=\"InverseGamma\" >beast.math.distributions.InverseGamma</map>" >> ${beast2input}

echo "<map name=\"OneOnX\" >beast.math.distributions.OneOnX</map>" >> ${beast2input}

echo "<run id=\"mcmc\" spec=\"MCMC\" chainLength=\"30000000\">" >> ${beast2input}

echo "<state id=\"state\" storeEvery=\"5000\">" >> ${beast2input}

echo "<tree id=\"Tree.t:26\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.26\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"26\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:14\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.14\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"14\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:25\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.25\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"25\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:3\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.3\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"3\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:32\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.32\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"32\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:12\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.12\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"12\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:23\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.23\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"23\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:9\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.9\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"9\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:20\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.20\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"20\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:28\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.28\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"28\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:19\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.19\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"19\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:22\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.22\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"22\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:16\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.16\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"16\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:29\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.29\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"29\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:37\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.37\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"37\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:30\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.30\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"30\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:10\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.10\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"10\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:38\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.38\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"38\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:18\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.18\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"18\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:8\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.8\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"8\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:21\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.21\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"21\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:33\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.33\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"33\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:15\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.15\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"15\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:31\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.31\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"31\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:36\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.36\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"36\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:24\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.24\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"24\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:27\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.27\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"27\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:11\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.11\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"11\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:2\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.2\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"2\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:4\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.4\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"4\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:17\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.17\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"17\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:35\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.35\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"35\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:13\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.13\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"13\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:1\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.1\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"1\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:34\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.34\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"34\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:5\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.5\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"5\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:7\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.7\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"7\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:6\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.6\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"6\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:40\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.40\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"40\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:43\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.43\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"43\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:41\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.41\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"41\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:44\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.44\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"44\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:39\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.39\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"39\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

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echo "<taxonset id=\"TaxonSet.45\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"45\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:42\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.42\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"42\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:46\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.46\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"46\_subset\"/>" >> ${beast2input}

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echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:47\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.47\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"47\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:50\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.50\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"50\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:48\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.48\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"48\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<tree id=\"Tree.t:49\_subset\" name=\"stateNode\">" >> ${beast2input}

echo "<taxonset id=\"TaxonSet.49\_subset\" spec=\"TaxonSet\">" >> ${beast2input}

echo "<alignment idref=\"49\_subset\"/>" >> ${beast2input}

echo "</taxonset>" >> ${beast2input}

echo "</tree>" >> ${beast2input}

echo "<parameter id=\"kappa.s:4snps\" lower=\"0.0\" name=\"stateNode\">2.0</parameter>" >> ${beast2input}

echo "<parameter id=\"mutationRate.s:4snps\" name=\"stateNode\">1.0</parameter>" >> ${beast2input}

echo "<parameter id=\"mutationRate.s:5snps\" name=\"stateNode\">1.0</parameter>" >> ${beast2input}

echo "<parameter id=\"mutationRate.s:6snps\" name=\"stateNode\">1.0</parameter>" >> ${beast2input}

echo "<stateNode id=\"indicators.alltrees\" spec=\"parameter.BooleanParameter\">false</stateNode>" >> ${beast2input}

echo "<parameter id=\"populationMean.alltrees\" name=\"stateNode\">1.0</parameter>" >> ${beast2input}

echo "<parameter id=\"popSizes.alltrees\" name=\"stateNode\">1.0</parameter>" >> ${beast2input}

echo "</state>" >> ${beast2input}

echo "<init id=\"RandomTree.t:26\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:26\_subset\" taxa=\"@26\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:26\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:26\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:14\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:14\_subset\" taxa=\"@14\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:14\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:14\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:25\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:25\_subset\" taxa=\"@25\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:25\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:25\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:3\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:3\_subset\" taxa=\"@3\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:3\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:3\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:32\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:32\_subset\" taxa=\"@32\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:32\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:32\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:12\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:12\_subset\" taxa=\"@12\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:12\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:12\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:23\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:23\_subset\" taxa=\"@23\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:23\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:23\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:9\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:9\_subset\" taxa=\"@9\_subset\">" >> ${beast2input}

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echo "<parameter id=\"randomPopSize.t:9\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:20\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:20\_subset\" taxa=\"@20\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:20\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:20\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:28\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:28\_subset\" taxa=\"@28\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:28\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:28\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:19\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:19\_subset\" taxa=\"@19\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:19\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:19\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:22\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:22\_subset\" taxa=\"@22\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:22\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:22\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:16\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:16\_subset\" taxa=\"@16\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:16\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:16\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:29\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:29\_subset\" taxa=\"@29\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:29\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:29\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:37\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:37\_subset\" taxa=\"@37\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:37\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:37\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:30\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:30\_subset\" taxa=\"@30\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:30\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:30\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:10\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:10\_subset\" taxa=\"@10\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:10\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:10\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:38\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:38\_subset\" taxa=\"@38\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:38\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:38\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:18\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:18\_subset\" taxa=\"@18\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:18\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:18\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:8\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:8\_subset\" taxa=\"@8\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:8\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:8\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:21\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:21\_subset\" taxa=\"@21\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:21\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:21\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:33\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:33\_subset\" taxa=\"@33\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:33\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:33\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:15\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:15\_subset\" taxa=\"@15\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:15\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:15\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:31\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:31\_subset\" taxa=\"@31\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:31\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:31\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:36\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:36\_subset\" taxa=\"@36\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:36\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:36\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:24\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:24\_subset\" taxa=\"@24\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:24\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:24\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:27\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:27\_subset\" taxa=\"@27\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:27\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:27\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:11\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:11\_subset\" taxa=\"@11\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:11\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:11\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:2\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:2\_subset\" taxa=\"@2\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:2\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:2\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:4\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:4\_subset\" taxa=\"@4\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:4\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:4\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:17\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:17\_subset\" taxa=\"@17\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:17\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:17\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:35\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:35\_subset\" taxa=\"@35\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:35\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:35\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:13\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:13\_subset\" taxa=\"@13\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:13\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:13\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

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echo "<populationModel id=\"ConstantPopulation0.t:1\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:1\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:34\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:34\_subset\" taxa=\"@34\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:34\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:34\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:5\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:5\_subset\" taxa=\"@5\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:5\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:5\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:7\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:7\_subset\" taxa=\"@7\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:7\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:7\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:6\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:6\_subset\" taxa=\"@6\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:6\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:6\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:40\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:40\_subset\" taxa=\"@40\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:40\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:40\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:43\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:43\_subset\" taxa=\"@43\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:43\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:43\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:41\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:41\_subset\" taxa=\"@41\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:41\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:41\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<init id=\"RandomTree.t:44\_subset\" spec=\"beast.evolution.tree.RandomTree\" estimate=\"false\" initial=\"@Tree.t:44\_subset\" taxa=\"@44\_subset\">" >> ${beast2input}

echo "<populationModel id=\"ConstantPopulation0.t:44\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:44\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

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echo "<populationModel id=\"ConstantPopulation0.t:39\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:39\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

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echo "<populationModel id=\"ConstantPopulation0.t:45\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:45\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

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echo "<populationModel id=\"ConstantPopulation0.t:42\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:42\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

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echo "<parameter id=\"randomPopSize.t:46\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

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echo "<populationModel id=\"ConstantPopulation0.t:47\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:47\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

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echo "<parameter id=\"randomPopSize.t:50\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

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echo "<populationModel id=\"ConstantPopulation0.t:48\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:48\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

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echo "<populationModel id=\"ConstantPopulation0.t:49\_subset\" spec=\"ConstantPopulation\">" >> ${beast2input}

echo "<parameter id=\"randomPopSize.t:49\_subset\" name=\"popSize\">1.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</init>" >> ${beast2input}

echo "<distribution id=\"posterior\" spec=\"util.CompoundDistribution\">" >> ${beast2input}

echo "<distribution id=\"prior\" spec=\"util.CompoundDistribution\">" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:10\_subset\" spec=\"Coalescent\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:10\_subset\" spec=\"ScaledPopulationFunction\">" >> ${beast2input}

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echo "<itree id=\"treeIntervals.t:11\_subset\" spec=\"TreeIntervals\" tree=\"@Tree.t:11\_subset\"/>" >> ${beast2input}

echo "<itree id=\"treeIntervals.t:12\_subset\" spec=\"TreeIntervals\" tree=\"@Tree.t:12\_subset\"/>" >> ${beast2input}

echo "<itree id=\"treeIntervals.t:13\_subset\" spec=\"TreeIntervals\" tree=\"@Tree.t:13\_subset\"/>" >> ${beast2input}

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echo "<itree id=\"treeIntervals.t:27\_subset\" spec=\"TreeIntervals\" tree=\"@Tree.t:27\_subset\"/>" >> ${beast2input}

echo "<itree id=\"treeIntervals.t:28\_subset\" spec=\"TreeIntervals\" tree=\"@Tree.t:28\_subset\"/>" >> ${beast2input}

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echo "<treeIntervals idref=\"treeIntervals.t:10\_subset\"/>" >> ${beast2input}

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echo "<populationModel id=\"scaledDemo.t:11\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.58\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:12\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:12\_subset\">" >> ${beast2input}

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echo "<parameter id=\"RealParameter.59\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:13\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:13\_subset\">" >> ${beast2input}

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echo "</distribution>" >> ${beast2input}

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echo "<parameter id=\"RealParameter.62\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:16\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:16\_subset\">" >> ${beast2input}

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echo "<parameter id=\"RealParameter.63\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

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echo "<distribution id=\"ExtendedBayesianSkyline.t:17\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:17\_subset\">" >> ${beast2input}

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echo "<parameter id=\"RealParameter.68\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

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echo "<populationModel id=\"scaledDemo.t:22\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

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echo "<populationModel id=\"scaledDemo.t:25\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.73\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

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echo "<parameter id=\"RealParameter.74\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

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echo "<populationModel id=\"scaledDemo.t:28\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

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echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:35\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:35\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:35\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.84\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:36\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:36\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:36\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.85\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:37\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:37\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:37\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.106\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:38\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:38\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:38\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.86\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:39\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:39\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:39\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.87\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:3\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:3\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:3\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.88\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:40\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:40\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:40\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.89\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:41\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:41\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:41\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.90\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:42\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:42\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:42\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.91\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:43\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:43\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:43\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.92\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:44\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:44\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:44\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.93\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:45\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:45\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:45\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.94\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:46\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:46\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:46\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.95\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:47\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:47\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:47\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.96\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:48\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:48\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:48\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.97\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:49\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:49\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:49\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.98\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:4\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:4\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:4\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.99\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:50\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:50\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:50\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.100\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:5\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:5\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:5\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.101\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:6\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:6\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:6\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.102\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:7\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:7\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:7\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.103\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:8\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:8\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:8\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.104\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"ExtendedBayesianSkyline.t:9\_subset\" spec=\"Coalescent\" treeIntervals=\"@treeIntervals.t:9\_subset\">" >> ${beast2input}

echo "<populationModel id=\"scaledDemo.t:9\_subset\" spec=\"ScaledPopulationFunction\" population=\"@demographic.alltrees\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.105\" lower=\"0.0\" name=\"factor\" upper=\"0.0\">2.0</parameter>" >> ${beast2input}

echo "</populationModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<prior id=\"indicatorsPrior.alltrees\" name=\"distribution\">" >> ${beast2input}

echo "<x id=\"indsSun.alltrees\" spec=\"util.Sum\">" >> ${beast2input}

echo "<arg idref=\"indicators.alltrees\"/>" >> ${beast2input}

echo "</x>" >> ${beast2input}

echo "<distr id=\"Poisson.EBSP\" spec=\"beast.math.distributions.Poisson\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.57\" estimate=\"false\" name=\"lambda\" upper=\"0.0\">0.69314718056</parameter>" >> ${beast2input}

echo "</distr>" >> ${beast2input}

echo "</prior>" >> ${beast2input}

echo "<prior id=\"KappaPrior.s:4snps\" name=\"distribution\" x=\"@kappa.s:4snps\">" >> ${beast2input}

echo "<LogNormal id=\"LogNormalDistributionModel.0\" name=\"distr\">" >> ${beast2input}

echo "<parameter id=\"RealParameter.50\" estimate=\"false\" name=\"M\">1.0</parameter>" >> ${beast2input}

echo "<parameter id=\"RealParameter.51\" estimate=\"false\" name=\"S\">1.25</parameter>" >> ${beast2input}

echo "</LogNormal>" >> ${beast2input}

echo "</prior>" >> ${beast2input}

echo "<prior id=\"popSizePrior.alltrees\" name=\"distribution\" x=\"@popSizes.alltrees\">" >> ${beast2input}

echo "<Exponential id=\"popPriorDist.EBSP\" mean=\"@populationMean.alltrees\" name=\"distr\"/>" >> ${beast2input}

echo "</prior>" >> ${beast2input}

echo "<prior id=\"populationMeanPrior.alltrees\" name=\"distribution\" x=\"@populationMean.alltrees\">" >> ${beast2input}

echo "<OneOnX id=\"OneOnX.EBSP\" name=\"distr\"/>" >> ${beast2input}

echo "</prior>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<distribution id=\"likelihood\" spec=\"util.CompoundDistribution\" useThreads=\"true\">" >> ${beast2input}

echo "<distribution id=\"treeLikelihood.1\_subset\" spec=\"ThreadedTreeLikelihood\" data=\"@1\_subset\" tree=\"@Tree.t:1\_subset\">" >> ${beast2input}

echo "<siteModel id=\"SiteModel.s:4snps\" spec=\"SiteModel\" gammaCategoryCount=\"4\" mutationRate=\"@mutationRate.s:4snps\">" >> ${beast2input}

echo "<parameter id=\"gammaShape.s:4snps\" estimate=\"false\" name=\"shape\">1.0</parameter>" >> ${beast2input}

echo "<parameter id=\"proportionInvariant.s:4snps\" estimate=\"false\" lower=\"0.0\" name=\"proportionInvariant\" upper=\"1.0\">0.0</parameter>" >> ${beast2input}

echo "<substModel id=\"hky.s:4snps\" spec=\"HKY\" kappa=\"@kappa.s:4snps\">" >> ${beast2input}

echo "<frequencies id=\"empiricalFreqs.s:4snps\" spec=\"Frequencies\" data=\"@1\_subset\"/>" >> ${beast2input}

echo "</substModel>" >> ${beast2input}

echo "</siteModel>" >> ${beast2input}

echo "<branchRateModel id=\"StrictClock.c:common\_clock\" spec=\"beast.evolution.branchratemodel.StrictClockModel\">" >> ${beast2input}

echo "<parameter id=\"clockRate.c:common\_clock\" estimate=\"false\" name=\"clock.rate\">1.809442e-08</parameter>" >> ${beast2input}

echo "</branchRateModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

for i in `seq 2 ${snps4}`;do

echo "<distribution id=\"treeLikelihood.${i}\_subset\" spec=\"ThreadedTreeLikelihood\" branchRateModel=\"@StrictClock.c:common\_clock\" data=\"@${i}\_subset\" siteModel=\"@SiteModel.s:4snps\" tree=\"@Tree.t:${i}\_subset\"/>" >> ${beast2input}

done

echo "<distribution id=\"treeLikelihood.${snps5}\_subset\" spec=\"ThreadedTreeLikelihood\" branchRateModel=\"@StrictClock.c:common\_clock\" data=\"@${snps5}\_subset\" tree=\"@Tree.t:${snps5}\_subset\">" >> ${beast2input}

echo "<siteModel id=\"SiteModel.s:5snps\" spec=\"SiteModel\" gammaCategoryCount=\"4\" mutationRate=\"@mutationRate.s:5snps\">" >> ${beast2input}

echo "<parameter id=\"gammaShape.s:5snps\" estimate=\"false\" name=\"shape\">1.0</parameter>" >> ${beast2input}

echo "<parameter id=\"proportionInvariant.s:5snps\" estimate=\"false\" lower=\"0.0\" name=\"proportionInvariant\" upper=\"1.0\">0.0</parameter>" >> ${beast2input}

echo "<substModel id=\"hky.s:5snps\" spec=\"HKY\" kappa=\"@kappa.s:4snps\">" >> ${beast2input}

echo "<frequencies id=\"empiricalFreqs.s:5snps\" spec=\"Frequencies\" data=\"@${snps5}\_subset\"/>" >> ${beast2input}

echo "</substModel>" >> ${beast2input}

echo "</siteModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

for i in `seq $((snps5+1)) $((snps6-1))`;do

echo "<distribution id=\"treeLikelihood.${i}\_subset\" spec=\"ThreadedTreeLikelihood\" branchRateModel=\"@StrictClock.c:common\_clock\" data=\"@${i}\_subset\" siteModel=\"@SiteModel.s:5snps\" tree=\"@Tree.t:${i}\_subset\"/>" >> ${beast2input}

done

echo "<distribution id=\"treeLikelihood.${snps6}\_subset\" spec=\"ThreadedTreeLikelihood\" branchRateModel=\"@StrictClock.c:common\_clock\" data=\"@${snps6}\_subset\" tree=\"@Tree.t:${snps6}\_subset\">" >> ${beast2input}

echo "<siteModel id=\"SiteModel.s:6snps\" spec=\"SiteModel\" gammaCategoryCount=\"4\" mutationRate=\"@mutationRate.s:6snps\">" >> ${beast2input}

echo "<parameter id=\"gammaShape.s:6snps\" estimate=\"false\" name=\"shape\">1.0</parameter>" >> ${beast2input}

echo "<parameter id=\"proportionInvariant.s:6snps\" estimate=\"false\" lower=\"0.0\" name=\"proportionInvariant\" upper=\"1.0\">0.0</parameter>" >> ${beast2input}

echo "<substModel id=\"hky.s:6snps\" spec=\"HKY\" kappa=\"@kappa.s:4snps\">" >> ${beast2input}

echo "<frequencies id=\"empiricalFreqs.s:6snps\" spec=\"Frequencies\" data=\"@${snps6}\_subset\"/>" >> ${beast2input}

echo "</substModel>" >> ${beast2input}

echo "</siteModel>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

for i in `seq $((snps6+1)) 50`;do

echo "<distribution id=\"treeLikelihood.${i}\_subset\" spec=\"ThreadedTreeLikelihood\" branchRateModel=\"@StrictClock.c:common\_clock\" data=\"@${i}\_subset\" siteModel=\"@SiteModel.s:6snps\" tree=\"@Tree.t:${i}\_subset\"/>" >> ${beast2input}

done

echo "</distribution>" >> ${beast2input}

echo "</distribution>" >> ${beast2input}

echo "<operator id=\"KappaScaler.s:4snps\" spec=\"ScaleOperator\" parameter=\"@kappa.s:4snps\" scaleFactor=\"0.5\" weight=\"0.1\"/>" >> ${beast2input}

echo "<operator id=\"FixMeanMutationRatesOperator\" spec=\"DeltaExchangeOperator\" delta=\"0.75\" weight=\"2.0\">" >> ${beast2input}

echo "<parameter idref=\"mutationRate.s:4snps\"/>" >> ${beast2input}

echo "<parameter idref=\"mutationRate.s:5snps\"/>" >> ${beast2input}

echo "<parameter idref=\"mutationRate.s:6snps\"/>" >> ${beast2input}

echo "<weightvector id=\"weightparameter\" spec=\"parameter.IntegerParameter\" dimension=\"3\" estimate=\"false\" lower=\"0\" upper=\"0\">4180 990 330</weightvector>" >> ${beast2input}

echo "</operator>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:10\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:10\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:10\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:10\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:10\_subset\" spec=\"Uniform\" tree=\"@Tree.t:10\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:10\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:10\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:10\_subset\" spec=\"Exchange\" tree=\"@Tree.t:10\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:10\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:10\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:10\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:10\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:11\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:11\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:11\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:11\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:11\_subset\" spec=\"Uniform\" tree=\"@Tree.t:11\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:11\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:11\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:11\_subset\" spec=\"Exchange\" tree=\"@Tree.t:11\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:11\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:11\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:11\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:11\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:12\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:12\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:12\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:12\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:12\_subset\" spec=\"Uniform\" tree=\"@Tree.t:12\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:12\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:12\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:12\_subset\" spec=\"Exchange\" tree=\"@Tree.t:12\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:12\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:12\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:12\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:12\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:13\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:13\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:13\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:13\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:13\_subset\" spec=\"Uniform\" tree=\"@Tree.t:13\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:13\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:13\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:13\_subset\" spec=\"Exchange\" tree=\"@Tree.t:13\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:13\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:13\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:13\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:13\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:14\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:14\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:14\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:14\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:14\_subset\" spec=\"Uniform\" tree=\"@Tree.t:14\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:14\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:14\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:14\_subset\" spec=\"Exchange\" tree=\"@Tree.t:14\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:14\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:14\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:14\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:14\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:15\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:15\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:15\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:15\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:15\_subset\" spec=\"Uniform\" tree=\"@Tree.t:15\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:15\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:15\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:15\_subset\" spec=\"Exchange\" tree=\"@Tree.t:15\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:15\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:15\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:15\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:15\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:16\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:16\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:16\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:16\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:16\_subset\" spec=\"Uniform\" tree=\"@Tree.t:16\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:16\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:16\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:16\_subset\" spec=\"Exchange\" tree=\"@Tree.t:16\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:16\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:16\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:16\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:16\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:17\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:17\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:17\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:17\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:17\_subset\" spec=\"Uniform\" tree=\"@Tree.t:17\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:17\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:17\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:17\_subset\" spec=\"Exchange\" tree=\"@Tree.t:17\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:17\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:17\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:17\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:17\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:18\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:18\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:18\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:18\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:18\_subset\" spec=\"Uniform\" tree=\"@Tree.t:18\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:18\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:18\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:18\_subset\" spec=\"Exchange\" tree=\"@Tree.t:18\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:18\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:18\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:18\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:18\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:19\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:19\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:19\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:19\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:19\_subset\" spec=\"Uniform\" tree=\"@Tree.t:19\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:19\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:19\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:19\_subset\" spec=\"Exchange\" tree=\"@Tree.t:19\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:19\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:19\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:19\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:19\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:1\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:1\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:1\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:1\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:1\_subset\" spec=\"Uniform\" tree=\"@Tree.t:1\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:1\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:1\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:1\_subset\" spec=\"Exchange\" tree=\"@Tree.t:1\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:1\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:1\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:1\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:1\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:20\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:20\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:20\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:20\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:20\_subset\" spec=\"Uniform\" tree=\"@Tree.t:20\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:20\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:20\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:20\_subset\" spec=\"Exchange\" tree=\"@Tree.t:20\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:20\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:20\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:20\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:20\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:21\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:21\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:21\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:21\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:21\_subset\" spec=\"Uniform\" tree=\"@Tree.t:21\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:21\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:21\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:21\_subset\" spec=\"Exchange\" tree=\"@Tree.t:21\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:21\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:21\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:21\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:21\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:22\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:22\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:22\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:22\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:22\_subset\" spec=\"Uniform\" tree=\"@Tree.t:22\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:22\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:22\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:22\_subset\" spec=\"Exchange\" tree=\"@Tree.t:22\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:22\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:22\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:22\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:22\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:23\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:23\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:23\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:23\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:23\_subset\" spec=\"Uniform\" tree=\"@Tree.t:23\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:23\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:23\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:23\_subset\" spec=\"Exchange\" tree=\"@Tree.t:23\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:23\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:23\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:23\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:23\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:24\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:24\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:24\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:24\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:24\_subset\" spec=\"Uniform\" tree=\"@Tree.t:24\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:24\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:24\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:24\_subset\" spec=\"Exchange\" tree=\"@Tree.t:24\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:24\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:24\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:24\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:24\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:25\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:25\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:25\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:25\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:25\_subset\" spec=\"Uniform\" tree=\"@Tree.t:25\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:25\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:25\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:25\_subset\" spec=\"Exchange\" tree=\"@Tree.t:25\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:25\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:25\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:25\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:25\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:26\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:26\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:26\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:26\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:26\_subset\" spec=\"Uniform\" tree=\"@Tree.t:26\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:26\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:26\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:26\_subset\" spec=\"Exchange\" tree=\"@Tree.t:26\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:26\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:26\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:26\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:26\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:27\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:27\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:27\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:27\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:27\_subset\" spec=\"Uniform\" tree=\"@Tree.t:27\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:27\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:27\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:27\_subset\" spec=\"Exchange\" tree=\"@Tree.t:27\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:27\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:27\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:27\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:27\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:28\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:28\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:28\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:28\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:28\_subset\" spec=\"Uniform\" tree=\"@Tree.t:28\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:28\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:28\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:28\_subset\" spec=\"Exchange\" tree=\"@Tree.t:28\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:28\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:28\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:28\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:28\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:29\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:29\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:29\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:29\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:29\_subset\" spec=\"Uniform\" tree=\"@Tree.t:29\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:29\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:29\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:29\_subset\" spec=\"Exchange\" tree=\"@Tree.t:29\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:29\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:29\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:29\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:29\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:2\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:2\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:2\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:2\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:2\_subset\" spec=\"Uniform\" tree=\"@Tree.t:2\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:2\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:2\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:2\_subset\" spec=\"Exchange\" tree=\"@Tree.t:2\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:2\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:2\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:2\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:2\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"bitflip.alltrees\" spec=\"BitFlipOperator\" parameter=\"@indicators.alltrees\" weight=\"3000.0\"/>" >> ${beast2input}

echo "<operator id=\"indicatorSampler.alltrees\" spec=\"SampleOffValues\" dist=\"@popPriorDist.EBSP\" indicators=\"@indicators.alltrees\" values=\"@popSizes.alltrees\" weight=\"1500.0\"/>" >> ${beast2input}

echo "<operator id=\"indicatorScaler.alltrees\" spec=\"ScaleOperator\" degreesOfFreedom=\"1\" indicator=\"@indicators.alltrees\" parameter=\"@popSizes.alltrees\" scaleFactor=\"0.5\" weight=\"1500.0\"/>" >> ${beast2input}

echo "<operator id=\"EBSPupDownOperator.alltrees\" spec=\"UpDownOperator\" scaleFactor=\"0.7\" weight=\"500.0\">" >> ${beast2input}

echo "<up idref=\"popSizes.alltrees\"/>" >> ${beast2input}

echo "<up idref=\"populationMean.alltrees\"/>" >> ${beast2input}

echo "</operator>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:30\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:30\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:30\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:30\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:30\_subset\" spec=\"Uniform\" tree=\"@Tree.t:30\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:30\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:30\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:30\_subset\" spec=\"Exchange\" tree=\"@Tree.t:30\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:30\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:30\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:30\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:30\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:31\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:31\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:31\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:31\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:31\_subset\" spec=\"Uniform\" tree=\"@Tree.t:31\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:31\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:31\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:31\_subset\" spec=\"Exchange\" tree=\"@Tree.t:31\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:31\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:31\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:31\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:31\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:32\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:32\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:32\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:32\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:32\_subset\" spec=\"Uniform\" tree=\"@Tree.t:32\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:32\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:32\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:32\_subset\" spec=\"Exchange\" tree=\"@Tree.t:32\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:32\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:32\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:32\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:32\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:33\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:33\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:33\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:33\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:33\_subset\" spec=\"Uniform\" tree=\"@Tree.t:33\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:33\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:33\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:33\_subset\" spec=\"Exchange\" tree=\"@Tree.t:33\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:33\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:33\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:33\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:33\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:34\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:34\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:34\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:34\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:34\_subset\" spec=\"Uniform\" tree=\"@Tree.t:34\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:34\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:34\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:34\_subset\" spec=\"Exchange\" tree=\"@Tree.t:34\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:34\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:34\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:34\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:34\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:35\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:35\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:35\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:35\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:35\_subset\" spec=\"Uniform\" tree=\"@Tree.t:35\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:35\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:35\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:35\_subset\" spec=\"Exchange\" tree=\"@Tree.t:35\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:35\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:35\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:35\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:35\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:36\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:36\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:36\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:36\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:36\_subset\" spec=\"Uniform\" tree=\"@Tree.t:36\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:36\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:36\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:36\_subset\" spec=\"Exchange\" tree=\"@Tree.t:36\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:36\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:36\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:36\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:36\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:38\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:38\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:38\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:38\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:38\_subset\" spec=\"Uniform\" tree=\"@Tree.t:38\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:38\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:38\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:38\_subset\" spec=\"Exchange\" tree=\"@Tree.t:38\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:38\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:38\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:38\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:38\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:39\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:39\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:39\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:39\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:39\_subset\" spec=\"Uniform\" tree=\"@Tree.t:39\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:39\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:39\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:39\_subset\" spec=\"Exchange\" tree=\"@Tree.t:39\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:39\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:39\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:39\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:39\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:3\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:3\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:3\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:3\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:3\_subset\" spec=\"Uniform\" tree=\"@Tree.t:3\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:3\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:3\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:3\_subset\" spec=\"Exchange\" tree=\"@Tree.t:3\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:3\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:3\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:3\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:3\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:40\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:40\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:40\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:40\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:40\_subset\" spec=\"Uniform\" tree=\"@Tree.t:40\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:40\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:40\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:40\_subset\" spec=\"Exchange\" tree=\"@Tree.t:40\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:40\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:40\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:40\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:40\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:41\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:41\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:41\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:41\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:41\_subset\" spec=\"Uniform\" tree=\"@Tree.t:41\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:41\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:41\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:41\_subset\" spec=\"Exchange\" tree=\"@Tree.t:41\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:41\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:41\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:41\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:41\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:42\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:42\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:42\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:42\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:42\_subset\" spec=\"Uniform\" tree=\"@Tree.t:42\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:42\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:42\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:42\_subset\" spec=\"Exchange\" tree=\"@Tree.t:42\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:42\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:42\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:42\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:42\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:43\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:43\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:43\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:43\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:43\_subset\" spec=\"Uniform\" tree=\"@Tree.t:43\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:43\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:43\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:43\_subset\" spec=\"Exchange\" tree=\"@Tree.t:43\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:43\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:43\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:43\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:43\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:44\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:44\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:44\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:44\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:44\_subset\" spec=\"Uniform\" tree=\"@Tree.t:44\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:44\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:44\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:44\_subset\" spec=\"Exchange\" tree=\"@Tree.t:44\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:44\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:44\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:44\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:44\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:45\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:45\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:45\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:45\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:45\_subset\" spec=\"Uniform\" tree=\"@Tree.t:45\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:45\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:45\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:45\_subset\" spec=\"Exchange\" tree=\"@Tree.t:45\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:45\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:45\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:45\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:45\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:46\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:46\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:46\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:46\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:46\_subset\" spec=\"Uniform\" tree=\"@Tree.t:46\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:46\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:46\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:46\_subset\" spec=\"Exchange\" tree=\"@Tree.t:46\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:46\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:46\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:46\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:46\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:47\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:47\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:47\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:47\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:47\_subset\" spec=\"Uniform\" tree=\"@Tree.t:47\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:47\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:47\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:47\_subset\" spec=\"Exchange\" tree=\"@Tree.t:47\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:47\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:47\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:47\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:47\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:48\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:48\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:48\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:48\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:48\_subset\" spec=\"Uniform\" tree=\"@Tree.t:48\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:48\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:48\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:48\_subset\" spec=\"Exchange\" tree=\"@Tree.t:48\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:48\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:48\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:48\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:48\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:49\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:49\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:49\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:49\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:49\_subset\" spec=\"Uniform\" tree=\"@Tree.t:49\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:49\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:49\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:49\_subset\" spec=\"Exchange\" tree=\"@Tree.t:49\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:49\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:49\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:49\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:49\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:4\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:4\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:4\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:4\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:4\_subset\" spec=\"Uniform\" tree=\"@Tree.t:4\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:4\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:4\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:4\_subset\" spec=\"Exchange\" tree=\"@Tree.t:4\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:4\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:4\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:4\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:4\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:50\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:50\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:50\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:50\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:50\_subset\" spec=\"Uniform\" tree=\"@Tree.t:50\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:50\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:50\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:50\_subset\" spec=\"Exchange\" tree=\"@Tree.t:50\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:50\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:50\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:50\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:50\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:5\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:5\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:5\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:5\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:5\_subset\" spec=\"Uniform\" tree=\"@Tree.t:5\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:5\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:5\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:5\_subset\" spec=\"Exchange\" tree=\"@Tree.t:5\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:5\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:5\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:5\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:5\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:6\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:6\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:6\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:6\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:6\_subset\" spec=\"Uniform\" tree=\"@Tree.t:6\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:6\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:6\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:6\_subset\" spec=\"Exchange\" tree=\"@Tree.t:6\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:6\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:6\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:6\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:6\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:7\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:7\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:7\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:7\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:7\_subset\" spec=\"Uniform\" tree=\"@Tree.t:7\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:7\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:7\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:7\_subset\" spec=\"Exchange\" tree=\"@Tree.t:7\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:7\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:7\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:7\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:7\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:8\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:8\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:8\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:8\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:8\_subset\" spec=\"Uniform\" tree=\"@Tree.t:8\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:8\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:8\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:8\_subset\" spec=\"Exchange\" tree=\"@Tree.t:8\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:8\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:8\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:8\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:8\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:9\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:9\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:9\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:9\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:9\_subset\" spec=\"Uniform\" tree=\"@Tree.t:9\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:9\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:9\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:9\_subset\" spec=\"Exchange\" tree=\"@Tree.t:9\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:9\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:9\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:9\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:9\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeScaler.t:37\_subset\" spec=\"ScaleOperator\" scaleFactor=\"0.5\" tree=\"@Tree.t:37\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineTreeRootScaler.t:37\_subset\" spec=\"ScaleOperator\" rootOnly=\"true\" scaleFactor=\"0.5\" tree=\"@Tree.t:37\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineUniformOperator.t:37\_subset\" spec=\"Uniform\" tree=\"@Tree.t:37\_subset\" weight=\"30.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineSubtreeSlide.t:37\_subset\" spec=\"SubtreeSlide\" tree=\"@Tree.t:37\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineNarrow.t:37\_subset\" spec=\"Exchange\" tree=\"@Tree.t:37\_subset\" weight=\"15.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWide.t:37\_subset\" spec=\"Exchange\" isNarrow=\"false\" tree=\"@Tree.t:37\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<operator id=\"ExtendedBayesianSkylineWilsonBalding.t:37\_subset\" spec=\"WilsonBalding\" tree=\"@Tree.t:37\_subset\" weight=\"3.0\"/>" >> ${beast2input}

echo "<logger id=\"tracelog\" fileName=\"dromedary-ebsp1-tracer-input.log\" logEvery=\"100000\" model=\"@posterior\" sanitiseHeaders=\"true\" sort=\"smart\">" >> ${beast2input}

echo "<log idref=\"posterior\"/>" >> ${beast2input}

echo "<log idref=\"likelihood\"/>" >> ${beast2input}

echo "<log idref=\"prior\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.26\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:26\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:26\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.14\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:14\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:14\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.25\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:25\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:25\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.3\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:3\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:3\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.32\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:32\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:32\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.12\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:12\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:12\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.23\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:23\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:23\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.9\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:9\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:9\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.20\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:20\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:20\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.28\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:28\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:28\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.19\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:19\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:19\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.22\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:22\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:22\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.16\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:16\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:16\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.29\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:29\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:29\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.37\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:37\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:37\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.30\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:30\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:30\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.10\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:10\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:10\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.38\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:38\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:38\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.18\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:18\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:18\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.8\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:8\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:8\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.21\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:21\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:21\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.33\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:33\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:33\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.15\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:15\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:15\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.31\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:31\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:31\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.36\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:36\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:36\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.24\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:24\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:24\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.27\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:27\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:27\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.11\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:11\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:11\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.2\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:2\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:2\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.4\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:4\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:4\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.17\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:17\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:17\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.35\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:35\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:35\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.13\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:13\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:13\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.1\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:1\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:1\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.34\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:34\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:34\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.5\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:5\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:5\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.7\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:7\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:7\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.6\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:6\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:6\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.40\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:40\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:40\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.43\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:43\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:43\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.41\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:41\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:41\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.44\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:44\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:44\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.39\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:39\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:39\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.45\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:45\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:45\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.42\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:42\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:42\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.46\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:46\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:46\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.47\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:47\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:47\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.50\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:50\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:50\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.48\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:48\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:48\_subset\"/>" >> ${beast2input}

echo "<log idref=\"treeLikelihood.49\_subset\"/>" >> ${beast2input}

echo "<log id=\"TreeHeight.t:49\_subset\" spec=\"beast.evolution.tree.TreeHeightLogger\" tree=\"@Tree.t:49\_subset\"/>" >> ${beast2input}

echo "<log idref=\"kappa.s:4snps\"/>" >> ${beast2input}

echo "<log idref=\"mutationRate.s:4snps\"/>" >> ${beast2input}

echo "<log idref=\"mutationRate.s:5snps\"/>" >> ${beast2input}

echo "<log idref=\"mutationRate.s:6snps\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:10\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:11\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:12\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:13\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:14\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:15\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:16\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:17\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:18\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:19\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:1\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:20\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:21\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:22\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:23\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:24\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:25\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:26\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:27\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:28\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:29\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:2\_subset\"/>" >> ${beast2input}

echo "<log idref=\"indicators.alltrees\"/>" >> ${beast2input}

echo "<log idref=\"populationMean.alltrees\"/>" >> ${beast2input}

echo "<log idref=\"popSizes.alltrees\"/>" >> ${beast2input}

echo "<log id=\"sumIndicators\" spec=\"util.Sum\">" >> ${beast2input}

echo "<arg idref=\"indicators.alltrees\"/>" >> ${beast2input}

echo "</log>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:30\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:31\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:32\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:33\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:34\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:35\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:36\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:38\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:39\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:3\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:40\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:41\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:42\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:43\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:44\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:45\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:46\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:47\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:48\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:49\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:4\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:50\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:5\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:6\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:7\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:8\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:9\_subset\"/>" >> ${beast2input}

echo "<log idref=\"ExtendedBayesianSkyline.t:37\_subset\"/>" >> ${beast2input}

echo "</logger>" >> ${beast2input}

echo "<logger id=\"screenlog\" logEvery=\"100000\">" >> ${beast2input}

echo "<log idref=\"posterior\"/>" >> ${beast2input}

echo "<log id=\"ESS.0\" spec=\"util.ESS\" arg=\"@posterior\"/>" >> ${beast2input}

echo "<log idref=\"likelihood\"/>" >> ${beast2input}

echo "<log idref=\"prior\"/>" >> ${beast2input}

echo "</logger>" >> ${beast2input}

echo "<logger id=\"EBSPLogger\" fileName=\"dromedary-ebsp1-logcombiner-input.log\" logEvery=\"5000\" model=\"@demographic.alltrees\">" >> ${beast2input}

echo "<log idref=\"demographic.alltrees\"/>" >> ${beast2input}

echo "</logger>" >> ${beast2input}

echo "</run>" >> ${beast2input}

echo "</beast>" >> ${beast2input}

rm \*.fa

rm test2

#####end of beast2-input-formatter.sh#####

cd /genetics/elbers/dromedary-ebsp/all/all-random1-seq

bash ../../beast2-input-formatter.sh -o all-random1.xml

cd /genetics/elbers/dromedary-ebsp/asia-no-hadhana/asia-random1-seq

bash ../../beast2-input-formatter.sh -o asia-random1.xml

cd /genetics/elbers/dromedary-ebsp/asia-no-hadhana/asia-random2-seq

bash ../../beast2-input-formatter.sh -o asia-random2.xml

cd /genetics/elbers/dromedary-ebsp/asia-no-hadhana/asia-random3-seq

bash ../../beast2-input-formatter.sh -o asia-random3.xml

cd /genetics/elbers/dromedary-ebsp/africa-no-kenya/africa-random1-seq

bash ../../beast2-input-formatter.sh -o africa-random1.xml

cd /genetics/elbers/dromedary-ebsp/africa-no-kenya/africa-random2-seq

bash ../../beast2-input-formatter.sh -o africa-random2.xml

cd /genetics/elbers/dromedary-ebsp/africa-no-kenya/africa-random3-seq

bash ../../beast2-input-formatter.sh -o africa-random3.xml

cd /genetics/elbers/dromedary-ebsp

seq -w 1 70 > samples

echo -e "/genetics/elbers/beast/bin/logcombiner \\" >> logcombiner.sh

while read i;do

echo -e "-log dromedary-ebsp${i}-tracer-input.log \\" >> logcombiner.sh

done < samples

echo "-o dromedary-ebspcombined-tracer-input.log > dromedary-ebspcombined-logcombiner-log-for-tracer-input.log 2>&1" >> logcombiner.sh

echo -e "/genetics/elbers/beast/bin/logcombiner \\" >> logcombiner2.sh

while read i;do

echo -e "-log dromedary-ebsp${i}-logcombiner-input.log \\" >> logcombiner2.sh

done < samples

echo -e "-o dromedary-ebspcombined-EBSPAnalyser-input.log > dromedary-ebspcombined-logcombiner-log-for-EBSPAnalyser-input.log 2>&1" >> logcombiner2.sh

#####beginning of dromedary-ebsp-stats.R#####

# devtools::install\_github("richelbilderbeek/tracerer")

library(tracerer)

# Parse that log file

beast\_log <- parse\_beast\_log("dromedary-ebspcombined-tracer-input.log")

# Calculates the effective sample sizes of all parameter estimates

esses <- calc\_esses(beast\_log, sample\_interval = 1000)

cat("\n")

paste("There are",length(esses), "EBSP parameters, but",length(esses[esses == "NA"]),"are equal to NA, so there are really",

length(esses),"-",length(esses[esses == "NA"]),"parameters.","There are",length(na.omit(esses[esses < 200])), "parameters that have ESS values less than 200.",

"There are",length(na.omit(esses[esses > 200])),"parameters that have ESS values greater than 200.")

cat("\n")

esses2 <- t(x=esses)

write.table(esses2,"esses.txt",quote=F,sep="\t",eol="\r\n")

#####end of dromedary-ebsp-stats.R#####

#####beginning of plot-ebsp.R#####

plotebsp <- function(filename){

pdf(paste(filename,"-psmc-mut-rate-log.pdf",sep=""))

dat<-scan(paste(filename,sep=""), skip=1)

dat<-matrix(dat,nc=5,byrow=T)

colnames(dat)<-c("times","mean","median","lower95HPD","upper95HPD")

dat<-as.data.frame(dat)

dat$times <- dat$times

time1 <- dat[which.min(dat$median),1]

time2 <- time1/1.64

cat(paste("RAD locus mutation rate, has lowest median population size at",round(time1,digits=0),"years ago."))

cat(paste("PSMC locus mutation rate, has lowest median population size at",round(time2,digits=0),"years ago."))

x<-max(dat$times)

y<-max(dat$upper95HPD)

plot.new()

plot.window(xlim=c(1,1000000), ylim=c(0,y\*1.01), log="x") # back 1,000,000 years ago

lines(dat$median ~ dat$times, new=T)

lines(dat$lower95HPD ~ dat$times, lty=2, new=T)

lines(dat$upper95HPD ~ dat$times, lty=2, new=T)

box()

axis(1);axis(2)

title("Extended Bayesian Skyline Plot going back 1,000,000 years", xlab="time (years before present, 0 = 2018AD,\n left side of x axis = 2018, LOG SCALE!!, using RAD loci mut rate)", ylab="effective scaled population size")

dat$times <- dat$times/1.64

x<-max(dat$times)

y<-max(dat$upper95HPD)

plot.new()

plot.window(xlim=c(1,1000000), ylim=c(0,y\*1.01), log="x") # back 1,000,000 years ago

lines(dat$median ~ dat$times, new=T)

lines(dat$lower95HPD ~ dat$times, lty=2, new=T)

lines(dat$upper95HPD ~ dat$times, lty=2, new=T)

box()

axis(1);axis(2)

title("Extended Bayesian Skyline Plot going back 1,000,000 years", xlab="time (years before present, 0 = 2018AD,\n left side of x axis = 2018, LOG SCALE!!, using psmc mut rate)", ylab="effective scaled population size")

dev.off()

}

plotebsp("dromedary-ddrad-ebspcombined-output-to-graph.txt")

#####end of plot-ebsp.R#####

####beginning of run-ebsp.sh#####

#! /bin/bash

POSITIONAL=()

while [[ $# -gt 0 ]]

do

key="$1"

case $key in

-o|--output)

output="$2"

shift # past argument

shift # past value

;;

\*) # unknown option

POSITIONAL+=("$1") # save it in an array for later

shift # past argument

;;

esac

done

set -- "${POSITIONAL[@]}" # restore positional parameters

echo $(date) " Started running EBSP for ${output}"

seq -w 1 70 > samples

while read i;do

cp \*-random?.xml dromedary-ebsp${i}.xml

perl -pi -e "s/ebsp1/ebsp${i}/g" dromedary-ebsp${i}.xml

/genetics/elbers/beast/bin/beast -beagle\_SSE -overwrite dromedary-ebsp${i}.xml > dromedary-ebsp${i}-stdout-stderr.txt 2>&1 &

done < samples &

until [[ $finished -eq 2100000000 ]]

do

sleep 1h

finished="$(tail -n 1 dromedary-ebsp??-tracer-input.log|grep -v '==>'|cut -f 1 |grep -P "\d+"|awk '{sum+=$1}END{print sum}')"

echo $(date) " " $finished " MCMC chains"

done

echo $(date) " Finished running EBSP"

echo $(date) " Started combining Tracer input"

bash /genetics/elbers/dromedary-ebsp/logcombiner.sh && echo $(date) " Finished combining Tracer input" && echo $(date) " Started Tracer" && Rscript /genetics/elbers/dromedary-ebsp/dromedary-ebsp-stats.R > dromedary-ebsp-stats.log 2>&1 && echo $(date) " Finished Tracer" &

echo $(date) " Started combining EBSP tree logs"

bash /genetics/elbers/dromedary-ebsp/logcombiner2.sh

echo $(date) " Finished combining EBSP tree logs"

echo $(date) " Started EBSPAnalyser"

java -cp /genetics/elbers/beast/lib/beast.jar beast.app.tools.EBSPAnalyser -i dromedary-ebspcombined-EBSPAnalyser-input.log \

-burnin 0 -type linear -o dromedary-ddrad-ebspcombined-output-to-graph.txt > dromedary-ddrad-ebspcombined-output-to-graph.log 2>&1

echo $(date) " Finished EBSPAnalyzer"

echo $(date) " Started plotting EBSP"

Rscript /genetics/elbers/dromedary-ebsp/plot-ebsp.R > plot-ebsp.log 2>&1

echo $(date) " Finished plotting EBSP"

rm dromedary-ebsp??.xml.state

rm dromedary-ebsp??.xml

rm dromedary-ebsp??-tracer-input.log

rm dromedary-ebsp??-logcombiner-input.log

cat dromedary-ebsp??-stdout-stderr.txt > ${output}-stdout-stderr.txt

rm dromedary-ebsp??-stdout-stderr.txt

pigz dromedary-ebspcombined-tracer-input.log

pigz dromedary-ebspcombined-EBSPAnalyser-input.log

mv dromedary-ebspcombined-tracer-input.log.gz ${output}-ebspcombined-tracer-input.log.gz

mv dromedary-ebspcombined-EBSPAnalyser-input.log.gz ${output}-ebspcombined-EBSPAnalyser-input.log.gz

mv dromedary-ddrad-ebspcombined-output-to-graph.txt-psmc-mut-rate-log.pdf ${output}-ebsp-graph.pdf

mv dromedary-ddrad-ebspcombined-output-to-graph.txt ${output}-ebsp-values-to-graph.txt

mv dromedary-ddrad-ebspcombined-output-to-graph.log ${output}-ebsp-values-to-graph.log

mv plot-ebsp.log ${output}-plot-ebsp.log

mv esses.txt ${output}-esses.txt

mv run-ebsp-log.txt ${output}-run-ebsp-log.txt

mv dromedary-ebsp-stats.log ${output}-ebsp-stats.log

mv dromedary-ebspcombined-logcombiner-log-for-EBSPAnalyser-input.log ${output}-ebspcombined-logcombiner-log-for-EBSPAnalyser-input.log

mv dromedary-ebspcombined-logcombiner-log-for-tracer-input.log ${output}-ebspcombined-logcombiner-log-for-tracer-input.log

echo $(date) " Finished all EBSP steps"

#####end of run-ebsp.sh#####

cd /genetics/elbers/dromedary-ebsp/

cd /genetics/elbers/dromedary-ebsp/all/all-random1-seq

bash ../../run-ebsp.sh -o all-random1 > run-ebsp-log.txt 2>&1 &

cd /genetics/elbers/dromedary-ebsp/asia-no-hadhana/asia-random1-seq

bash ../../run-ebsp.sh -o asia-random1 > run-ebsp-log.txt 2>&1 &

cd /genetics/elbers/dromedary-ebsp/asia-no-hadhana/asia-random2-seq

bash ../../run-ebsp.sh -o asia-random2 > run-ebsp-log.txt 2>&1 &

cd /genetics/elbers/dromedary-ebsp/asia-no-hadhana/asia-random3-seq

bash ../../run-ebsp.sh -o asia-random3 > run-ebsp-log.txt 2>&1 &

cd /genetics/elbers/dromedary-ebsp/africa-no-kenya/africa-random1-seq

bash ../../run-ebsp.sh -o africa-random1 > run-ebsp-log.txt 2>&1 &

cd /genetics/elbers/dromedary-ebsp/africa-no-kenya/africa-random2-seq

bash ../../run-ebsp.sh -o africa-random2 > run-ebsp-log.txt 2>&1 &

cd /genetics/elbers/dromedary-ebsp/africa-no-kenya/africa-random3-seq

bash ../../run-ebsp.sh -o africa-random3 > run-ebsp-log.txt 2>&1 &

***# R codes for plotting EBSP results***

## read in the data

data1 <- read.table('all-random1-ebsp-values-to-graph.txt', header = T, sep="\t")

data2 <- read.table('asia-random1-ebsp-values-to-graph.txt', header = T, sep="\t")

data3 <- read.table('asia-random2-ebsp-values-to-graph.txt', header = T, sep="\t")

data4 <- read.table('asia-random3-ebsp-values-to-graph.txt', header = T, sep="\t")

data5 <- read.table('africa-random1-ebsp-values-to-graph.txt', header = T, sep="\t")

data6 <- read.table('africa-random2-ebsp-values-to-graph.txt', header = T, sep="\t")

data7 <- read.table('africa-random3-ebsp-values-to-graph.txt', header = T, sep="\t")

## make a column called "type" in the dataframe, so ggplot2 can plot based on "type" (all,asia1,asia2,asia3,africa1,africa2,africa3)

data1$type <- rep("All",length(data1$time))

data2$type <- rep("Asia1",length(data2$time))

data3$type <- rep("Asia2",length(data3$time))

data4$type <- rep("Asia3",length(data4$time))

data5$type <- rep("Africa1",length(data5$time))

data6$type <- rep("Africa2",length(data6$time))

data7$type <- rep("Africa3",length(data7$time))

## combine the data frames

df <- rbind(data1,data2,data3,data4,data5,data6,data7)

df2 <- df[df$time > 100,]

data1 <- data1[data1$time > 100,]

## load ggplot2

library(ggplot2)

plot1 <- ggplot(df2, aes(time, median)) + # load the dataframe and set the x axis as time and the y axis as median effective scaled population size

geom\_line(aes(color=type), size=1.5) + # make ggplot2 plot lines with different colors for the different "types"

geom\_line(data = df2,mapping =aes(time, X95HPDlower, color=type), linetype=5) +

geom\_line(data = df2,mapping =aes(time, X95HPDupper, color=type), linetype=5) +

theme\_bw() + # make the theme black and white

theme(panel.grid.major.x = element\_blank(),

panel.grid.minor.x = element\_blank(),

panel.grid.major.y = element\_blank(),

panel.grid.minor.y = element\_blank(),

panel.border = element\_blank(),

legend.position = c(0.5, 0.5),

axis.line = element\_line(color="black"),

legend.title = element\_blank(),

axis.text = element\_text(size=11)) +

ylab("Scaled effective population size") + # label the y axis

xlab("Years before present") + # label the x axis

xlim(100,max(df$time)) +

scale\_x\_log10(breaks = c(100,1000,10000,100000,1000000))# make the x axis as log scaled and make breaks every power of 10 (10^0,10^1,10^2,10^3,...,10^6)

cols <- c("Africa1" = "darkred","Africa2" = "red3","Africa3"="firebrick1", "All"="gray18","Asia1"= "blue4","Asia2"="blue", "Asia3"="deepskyblue4")

plot2 <- plot1 + scale\_colour\_manual(values=cols)

plot2

ggsave('ebsp-100ybp-ci.png',plot2,device='png',dpi=300,height=6,width=6)

***# Script for hybrid detection***

conda activate samtools1.10

ls /genetics/Burger/DROM\_ddRAD/alignments\_GCA\_000803125/\*.sorted.bam |perl -pe "s/.sorted.bam//g" |perl -pe "s/^.+\///g" > samples

# Get the Reads from the BAM files

parallel --no-notice --jobs 10 '

samtools fastq -@ 75 /genetics/Burger/DROM\_ddRAD/alignments\_GCA\_000803125/{}.sorted.bam 2>/dev/null | \

/genetics/elbers/bbmap-38.79/repair.sh int=f in=STDIN.fq out={}.fq.gz ow=t 2>/dev/null' :::: samples &

wget ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/767/855/GCF\_000767855.1\_Ca\_bactrianus\_MBC\_1.0/GCF\_000767855.1\_Ca\_bactrianus\_MBC\_1.0\_genomic.fna.gz

wget https://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/000/803/125/GCA\_000803125.2\_CamDro2/GCA\_000803125.2\_CamDro2\_genomic.fna.gz

function mask\_data\_chunk () {

# Removes empty records and performs masking, all in pipes

awk -v RS=">" -v FS="\n" -v ORS="" ' { if ($2) print ">"$0 } ' |\

dustmasker -in - -outfmt fasta |\

sed -e '/^>/!s/[a-z]/x/g'

}

export -f mask\_data\_chunk

dustmasker -version

#dustmasker: 1.0.0

#Package: blast 2.7.1, build Oct 18 2017 19:57:24

zcat GCA\_000803125.2\_CamDro2\_genomic.fna.gz | parallel --no-notice --jobs 75 --pipe --recstart '>' --blocksize 100M mask\_data\_chunk > CamDro2.dustmasker.fa

zcat GCF\_000767855.1\_Ca\_bactrianus\_MBC\_1.0\_genomic.fna.gz | parallel --no-notice --jobs 75 --pipe --recstart '>' --blocksize 100M mask\_data\_chunk > CamBac1.dustmasker.fa

rm -f unambiguous.reads.txt

while read i;do

/genetics/elbers/bbmap-38.79/bbsplit.sh minratio=1.0 -Xmx350g ambiguous=toss ambiguous2=toss threads=75 usejni=t \

ref=CamDro2.dustmasker.fa,CamBac1.dustmasker.fa \

in=${i}.fq.gz \

out=/dev/null refstats=${i}.refstats.log 2> ${i}.bbsplit.log

done < samples &

echo -e "Drom888\nDrom889\nDrom890\nDrom891\nDrom892\nDrom893\nDrom715\nDrom717\nDrom719" > hybrids

while read i;do

/genetics/elbers/bbmap-38.79/bbsplit.sh minratio=1.0 -Xmx350g ambiguous=toss ambiguous2=toss threads=75 usejni=t \

ref=CamDro2.dustmasker.fa,CamBac1.dustmasker.fa \

in=${i}.fq.gz \

out=/dev/null refstats=${i}.refstats2.log 2> ${i}.bbsplit.log

done < hybrids &

ls \*.refstats.log |perl -pe "s/.refstats.log//g" |grep -vf hybrids - |grep -v "DC156" > samples2

rm -f unambiguous.reads7.txt

while read i;do

echo "${i}" >> unambiguous.reads7.txt

grep "^CamDro2" ${i}.refstats.log |cut -f 6 >> unambiguous.reads7.txt

grep "^CamBac1" ${i}.refstats.log |cut -f 6 >> unambiguous.reads7.txt

done < samples2

ls \*.refstats2.log |perl -pe "s/.refstats2.log//g" > samples3

while read i;do

echo "${i}" >> unambiguous.reads7.txt

grep "^CamDro2" ${i}.refstats2.log |cut -f 6 >> unambiguous.reads7.txt

grep "^CamBac1" ${i}.refstats2.log |cut -f 6 >> unambiguous.reads7.txt

done < samples3

echo "DC156" >> unambiguous.reads7.txt

grep "^CamDro2" DC156.refstats.log |cut -f 6 >> unambiguous.reads7.txt

grep "^CamBac1" DC156.refstats.log |cut -f 6 >> unambiguous.reads7.txt

cat unambiguous.reads7.txt|paste - - -|grep -P "\d+" |awk '{a=$2+$3;b=$2/a\*100;c=$3/a\*100;print $1,$2"("b")",$3"("c")";}' OFS='\t' |sed '1i Sample\tunambiguously\_mapped\_reads\_to\_Dromedary(percent)\tunambiguously\_mapped\_reads\_to\_Bactrian(percent)'|column -tx

cat unambiguous.reads7.txt|paste - - -|grep -P "\t\d+" > test

rm -f test2

j=`head -n -10 test| wc -l`

for i in `seq 1 $j`;do

echo "not-hybrid" >> test2

done

j=`cat hybrids| wc -l`

for i in `seq 1 $j`;do

echo "hybrid" >> test2

done

echo "Bactrian" >> test2

paste test test2 |awk '{a=$2+$3;c=$3/a\*100;print $1,$2,$3,c,$4;}' OFS='\t' |sed '1i Sample\tunambiguously\_mapped\_reads\_to\_Dromedary\tunambiguously\_mapped\_reads\_to\_Bactrian\tpercent\_Bactrian\ttype' > percentBactrian.txt

# Hybrid individuals (Just drop the KZ and IR and replace with Drom)

Kazakh (KZ888, KZ889, KZ890, KZ891, KZ892, and KZ893) and Iranian (IR715, IR717, IR719).

perl -pi -e "s/Drom888/KZ888/g" percentBactrian.txt

perl -pi -e "s/Drom889/KZ889/g" percentBactrian.txt

perl -pi -e "s/Drom890/KZ890/g" percentBactrian.txt

perl -pi -e "s/Drom891/KZ891/g" percentBactrian.txt

perl -pi -e "s/Drom892/KZ892/g" percentBactrian.txt

perl -pi -e "s/Drom893/KZ893/g" percentBactrian.txt

perl -pi -e "s/Drom715/IR715/g" percentBactrian.txt

perl -pi -e "s/Drom717/IR717/g" percentBactrian.txt

perl -pi -e "s/Drom719/IR719/g" percentBactrian.txt

R

#install.packages("ggplot2")

#install.packages("dplyr")

library("ggplot2")

library("dplyr")

sessionInfo()

#R version 3.6.3 (2020-02-29)

#Platform: x86\_64-pc-linux-gnu (64-bit)

#Running under: Ubuntu 20.04 LTS

#

#Matrix products: default

#BLAS: /usr/lib/x86\_64-linux-gnu/blas/libblas.so.3.9.0

#LAPACK: /usr/lib/x86\_64-linux-gnu/lapack/liblapack.so.3.9.0

#

#locale:

# [1] LC\_CTYPE=en\_GB.UTF-8 LC\_NUMERIC=C

# [3] LC\_TIME=de\_AT.UTF-8 LC\_COLLATE=en\_GB.UTF-8

# [5] LC\_MONETARY=de\_AT.UTF-8 LC\_MESSAGES=en\_GB.UTF-8

# [7] LC\_PAPER=de\_AT.UTF-8 LC\_NAME=C

# [9] LC\_ADDRESS=C LC\_TELEPHONE=C

#[11] LC\_MEASUREMENT=de\_AT.UTF-8 LC\_IDENTIFICATION=C

#

#attached base packages:

#[1] stats graphics grDevices utils datasets methods base

#

#other attached packages:

#[1] dplyr\_0.8.5 ggplot2\_3.3.0

#

#loaded via a namespace (and not attached):

# [1] Rcpp\_1.0.4 fansi\_0.4.1 digest\_0.6.25 withr\_2.1.2

# [5] crayon\_1.3.4 assertthat\_0.2.1 grid\_3.6.3 R6\_2.4.1

# [9] lifecycle\_0.2.0 gtable\_0.3.0 magrittr\_1.5 scales\_1.1.0

#[13] pillar\_1.4.3 rlang\_0.4.5 cli\_2.0.2 farver\_2.0.3

#[17] vctrs\_0.2.4 ellipsis\_0.3.0 tools\_3.6.3 glue\_1.3.2

#[21] purrr\_0.3.3 munsell\_0.5.0 compiler\_3.6.3 pkgconfig\_2.0.3

#[25] colorspace\_1.4-1 tidyselect\_1.0.0 tibble\_3.0.0

setwd("/home/jelber2/Dropbox/camel\_postdoc/manuscripts/dromedary-ddrad/hybrids/")

data <- read.table("percentBactrian.txt",header=T)

data$names <- rep("",length(data$Sample))

data <- data[data$Sample != "DC156",]

data2 <-

data %>%

group\_by(names) %>%

mutate(outlier = percent\_Bactrian > quantile(data$percent\_Bactrian)[4] + IQR(percent\_Bactrian) \* 3) %>%

ungroup

extreme <- quantile(data$percent\_Bactrian)[4] + IQR(data$percent\_Bactrian) \* 3

summary(data2$percent\_Bactrian)

plot2 <- ggplot(data2) +

aes(x = names, y = percent\_Bactrian, label=Sample) +

geom\_boxplot(outlier.shape = NA) + # NO OUTLIERS

geom\_point(data = function(x) dplyr::filter\_(x, ~ outlier), position = position\_jitter(seed = 6L)) + # Outliers

geom\_text(data = function(x) dplyr::filter\_(x, ~ outlier), position = position\_jitter(seed = 6L), hjust = -0.1, vjust= -0.5) +

labs(y="Percent Bactrian camel", x="ddRAD sequenced individuals") +

theme\_bw() +

theme(panel.grid.major.x = element\_blank(),

panel.grid.minor.x = element\_blank(),

panel.grid.major.y = element\_blank(),

panel.grid.minor.y = element\_blank(),

panel.border = element\_blank(),

axis.line = element\_line(color="black"),

legend.title = element\_blank()) +

geom\_hline(yintercept = extreme, color="blue") +

scale\_y\_continuous(breaks = c(0,5,10,15,20,25,30,35,40,45,50,55,60,65),limits=c(0,65))

plot2

ggsave("box-plot-of-ddRAD-hybrids-verus-non-hybrids.png",height=6,width=6,plot2)