Run dmc

Sarah P. Flanagan

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First I'll set up the working environment.

and load the necessary files

```
vcf<-parse.vcf("p4.upd.vcf") #this is the smaller dataset
```

```
vcf$SNP<-paste(vcf$`#CHROM`,vcf$POS,sep=".")
scaffs<-levels(as.factor(vcf[,1]))
scaffs[1:22]<-lgs
scaff.starts<-tapply(vcf$POS,vcf$`#CHROM`,max)
scaff.starts<-data.frame(rbind(cbind(names(scaff.starts),scaff.starts)),stringsAsFactors = F)
locus.info<-c(colnames(vcf[1:9]),"SNP")
```

Now I'll go through the steps outline in https://github.com/kristinmlee/dmc/blob/master/dmc_example.md

Calculate neutral F matrix

For this first step (calculating the neutral variance/covariance matrix, F), I'll use linkage groups that have no or few shared outlier loci. I need to (1) Calculate allele frequencies for each population, (2) specify a vector of sample sizes for each population, and (3) specify a string for filename for output. This step is baseline for all parameter sensitivity analyses.

```
calc.allFreqs<-function(vcf,pop.list, pop.labs){
  allFreqs<-do.call(rbind,lapply(pop.list, function(pop){
    this.vcf<-cbind(vcf[,1:9],vcf$SNP,vcf[,grep(pop,colnames(vcf))])
    afs<-do.call(rbind,apply(this.vcf,1,calc.afs.vcf))
    return(afs$RefFreq)
  }))
  colnames(allFreqs)<-vcf$SNP
  rownames(allFreqs)<-pop.labs
  return(allFreqs)
}
#calculate selected allele frequencies
LG4<-calc.allFreqs(vcf[vcf$`#CHROM` == "LG4" & vcf$POS < 120000,],pop.list,pop.labs)
saveRDS(LG4,"dmc/selectedRegionAlleleFreqs_p4LG4.RDS")
saveRDS(vcf[vcf$`#CHROM`=="LG4","POS"],"dmc/selectedRegionPositions_p4LG4.RDS")

#calculate neutral allele frequencies
allFreqs<-calc.allFreqs(vcf[vcf$`#CHROM` %in%
                              c("LG3","LG5","LG6","LG7","LG8","LG9","LG11","LG15","LG16","LG17","LG19",
                    pop.list,pop.labs)
saveRDS(allFreqs,"dmc/neutralAlleleFreqs_p4LG4.RDS")
```

```
allFreqs<-readRDS("dmc/neutralAlleleFreqs_p4LG4.RDS")
```

Once those are calculated, I can calculate the neutral F matrix, in addition to its determinant and inverse.

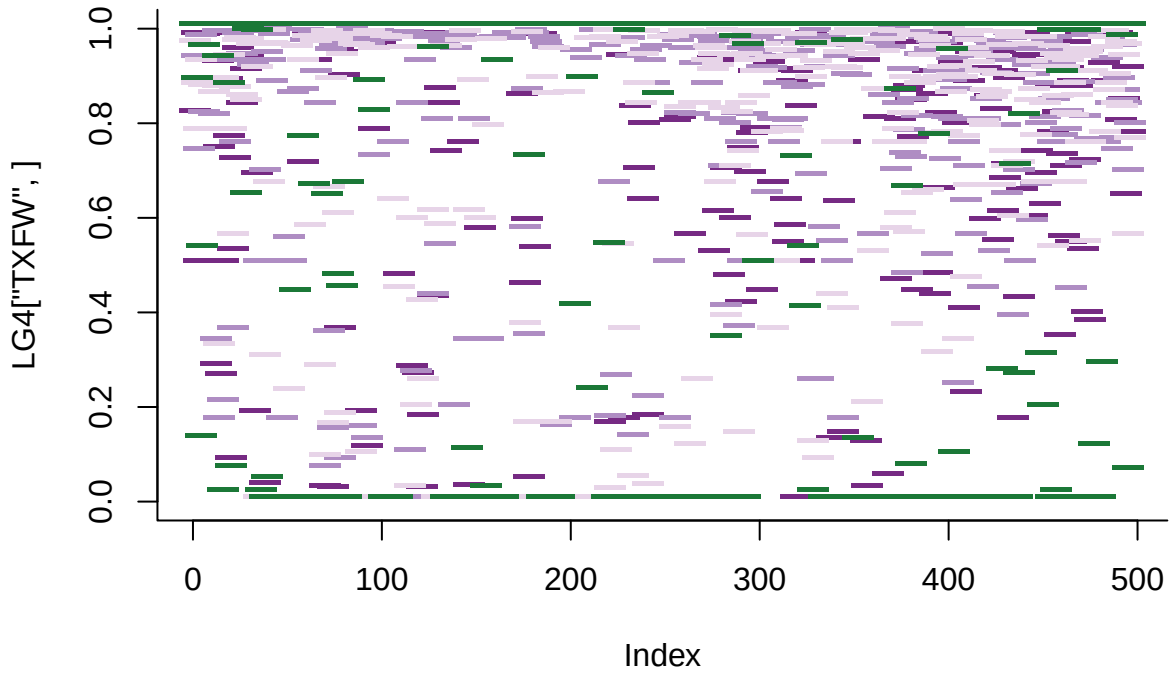
```
sampleSizes<-unlist(lapply(pop.list,function(pop){
  n<-length(grep(pop,colnames(vcf)))
```

```
  return(2*n) }))
numPops<-16

#calculate the neutral F matrix
saveRDS(sampleSizes,"dmc/sampleSizes.RDS")
neutralF_filename<-"dmc/neutralF_p4LG4"
source("../programs/dmc-master/calcNeutralF.R")
F_estimate<-readRDS("dmc/neutralF_p4LG4.RDS")

#calculate the determinant and inverse of the neutral F matrix
M <- numPops
Tmatrix <- matrix(data = rep(-1 / M, (M - 1) * M), nrow = M - 1, ncol = M)
diag(Tmatrix) = (M - 1) / M
sampleErrorMatrix = diag(1/sampleSizes, nrow = numPops, ncol = numPops)
det_FOmegas_neutral = det(Tmatrix %*% (F_estimate + sampleErrorMatrix) %*% t(Tmatrix))
saveRDS(det_FOmegas_neutral, "dmc/det_FOmegas_neutral_p4LG4.RDS")

inv_FOmegas_neutral = ginv(Tmatrix %*% (F_estimate + sampleErrorMatrix) %*% t(Tmatrix))
saveRDS(inv_FOmegas_neutral, "dmc/inv_FOmegas_neutral_p4LG4.RDS")
```

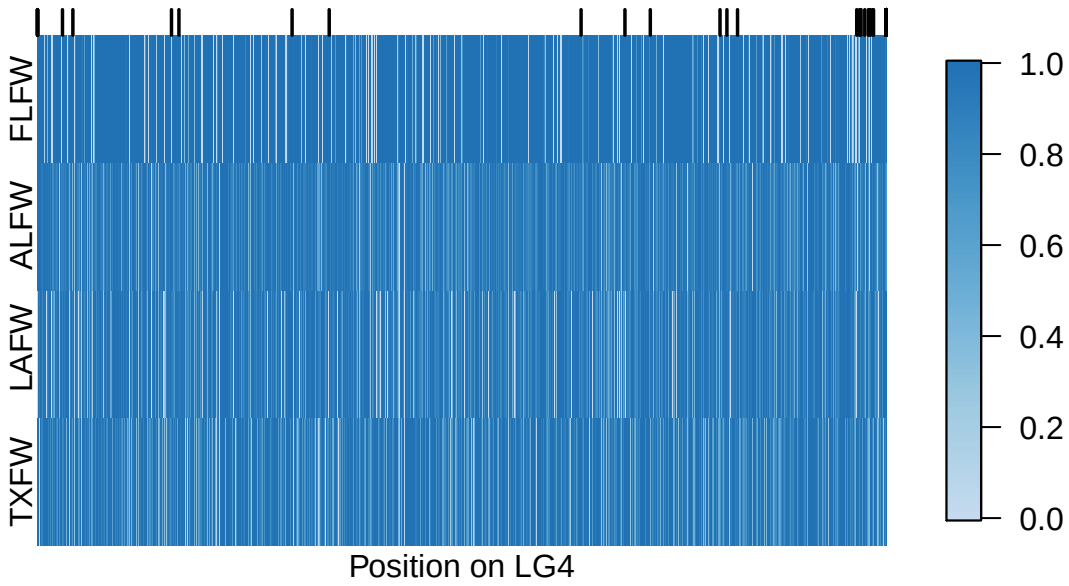
Note: I had to use to allow read/write in the scripts.

Let's look at the allele frequencies on LG4. This will help inform the hypotheses I test with dmc.

```
stacks.sig<-read.delim("p4.stacks.sig.snps.txt")
stacks.sig$SNP<-paste(stacks.sig$Chr,(stacks.sig$BP+1),sep=".")
LG4<-readRDS("dmc/selectedRegionAlleleFreqs_p4LG4.RDS")
allFreqs<-readRDS("dmc/neutralAlleleFreqs_p4LG4.RDS")
# LG4[rownames(LG4) %in% c("FLFW","ALFW","LAFW","TXFW"),colnames(LG4) %in% stacks.sig$SNP]
# LG4[rownames(LG4) %in% c("FLFW","ALFW","LAFW","TXFW"),
#           which(colnames(LG4) %in% stacks.sig$SNP)[1]:
#             which(colnames(LG4) %in% stacks.sig$SNP)[length(which(colnames(LG4) %in% stacks.sig$SNP))]
grp.colors<-c('#762a83','#af8dc3','#e7d4e8','#d9f0d3','#7fbf7b','#1b7837')
plot(LG4["TXFW",],col=grp.colors[1],pch="-",bty="L",lwd=2,cex=2)
points(LG4["LAFW",],col=grp.colors[2],pch="-",bty="L",lwd=2,cex=2)
points(LG4["ALFW",],col=grp.colors[3],pch="-",bty="L",lwd=2,cex=2)
points(LG4["FLFW",],col=grp.colors[6],pch="-",bty="L",lwd=2,cex=2)
```




```
cols<-colorRampPalette(t(brewer.pal(9,name="Blues")[3:7]))(100)

fields::image.plot(t(allFreqs[rownames(allFreqs) %in% c("FLFW","ALFW","LAFW","TXFW"),]),col=cols,
      axes=FALSE)
text(x=-0.02,y=1,"FLFW",srt=90,xpd=TRUE)
text(x=-0.02,y=0.67,"ALFW",srt=90,xpd=TRUE)
text(x=-0.02,y=0.35,"LAFW",srt=90,xpd=TRUE)
text(x=-0.02,y=0,"TXFW",srt=90,xpd=TRUE)
mtext("Position on LG4",1)
axis(3,at =t(LG4[rownames(LG4) %in% c("FLFW","ALFW","LAFW","TXFW"),colnames(LG4) %in% stacks.sig$SNP]),
     labels = FALSE,lwd=0,lwd.ticks = 1.75,tck=-.05)
```



This shows that the FLFW site has somewhat different allele frequencies than the other sites. This suggests that I should test to see whether there was an independent mutation in the FLFW population and the other

three have a single sweep.

Calculate F(S) matrices

We generate matrices for the following five models: *1. All selected pops have independent mutations of beneficial allele* 2. All selected pops share beneficial allele via migration *3. Beneficial allele was standing the ancestor of all selected pops* 4. There was an independent mutation in FLFW and the other three share a sweep. *5. FLFW has an independent mutation and the others share a beneficial allele via standing variation

I've written a giant function to run all five models and calculate their composite likelihoods. The composite likelihoods include knowing how far away we are from the proposed selected site. Therefore, the first step for calculating them is to randomize with respect to the reference allele.

The inverses and determinants generated can be used to calculate the log-likelihood of a site a given distance away from a proposed selected site. To do this, we sum the log-likelihoods across all SNPs in the window to obtain a composite log-likelihood under a given convergence model with a set of parameters for a proposed selected site.

```
run.dmc<-function(F_estimate,out_name,positions, sampleSizes,selSite=NA,nselsites=50,rec =2.17*10^-8,
                  Ne = 8.3*10^6,selPops = c(3,5,7,16),numBins = 1000,numPops = 16,
                  sels = c(1e-4, 1e-3, 0.01, seq(0.02, 0.14, by = 0.01), seq(0.15, 0.3, by = 0.05),
                           seq(0.4, 0.6, by = 0.1)),
                  times = c(0, 5, 25, 50, 100, 500, 1000, 1e4, 1e6),
                  migs = c(10^-(seq(5, 1, by = -2)), 0.5, 1),mod4_sets=list(c(3,5,7),16),
                  mod1=TRUE,mod2=TRUE,mod3=TRUE,mod4=TRUE,mod5=TRUE,complike=TRUE,
                  neutral_det_name="dmc/det_FOmegas_neutral_p4LG4.RDS",
                  neutral_inv_name="dmc/inv_FOmegas_neutral_p4LG4.RDS"){
  #make all the parameters global
  F_estimate<<-F_estimate
  positions<<-positions
  sampleSizes<<-sampleSizes
  Ne<<-Ne
  rec<<-rec
  selPops<<-selPops
  numBins<<-numBins
  numPops<<-numPops
  sels<<-sels
  times<<-times
  migs<<-migs
  neutral_det_name<<-neutral_det_name
  neutral_inv_name<<-neutral_inv_name
  print(paste(neutral_det_name,neutral_inv_name,sep=","))
  #set up parameters
  M <<- numPops
  Tmatrix <<- matrix(data = rep(-1 / M, (M - 1) * M), nrow = M - 1, ncol = M)
  diag(Tmatrix) = (M - 1) / M
  gs<<-c(1/(2*Ne), 10^-(4:1))
  sampleErrorMatrix <<- diag(1/sampleSizes, nrow = numPops, ncol = numPops)
  if(is.na(selSite[1])) selSite=seq(min(positions), max(positions), length.out = nselsites)
  selSite<<-selSite
  sources <<- selPops
  sets<<-mod4_sets
  #save params
  params<-list(F_estimate,out_name,positions, sampleSizes,selSite,rec,
```

```
              Ne,selPops,numBins,numPops,sels,times,gs,migs,mod4_sets)
names(params)<-c("F_estimate","out_name","positions", "sampleSizes","selSite","rec",
                 "Ne","selPops","numBins","numPops","sels","times","gs","migs","mod4_sets")
print(params)
################ calculate F(S) ################
source("../programs/dmc-master/genSelMatrices_individualModes.R")

################ model 1 ################
if(mod1==TRUE){
  FOmegas_ind = lapply(sels, function(sel) {
    calcFOmegas_indSweeps(sel)
  })

  saveRDS(FOmegas_ind, paste("dmc/FOmegas_ind_",out_name,".RDS",sep=""))
  #model 1 determinant
  det_FOmegas_ind = lapply(FOmegas_ind, function(sel) {
    lapply(sel, function(dist) {
      det(dist)
    })
  })
  saveRDS(det_FOmegas_ind, paste("dmc/det_FOmegas_ind_",out_name,".RDS",sep=""))
  #model 1 inverse
  inv_FOmegas_ind = lapply(FOmegas_ind, function(sel) {
    lapply(sel, function(dist) {
      ginv(dist)
    })
  })
  saveRDS(inv_FOmegas_ind, paste("dmc/inv_FOmegas_ind_",out_name,".RDS",sep=""))
}
################ model 2 ################
if(mod2==TRUE){
  FOmegas_mig = lapply(sels ,function(sel) {
    lapply(migs, function(mig) {
      lapply(sources, function(my.source) {
        calcFOmegas_mig(sel, mig, my.source)
      })
    })
  })

  saveRDS(FOmegas_mig, paste("dmc/FOmegas_mig_",out_name,".RDS",sep=""))
  #determinant
  det_FOmegas_mig = lapply(FOmegas_mig, function(sel) {
    lapply(sel, function(mig) {
      lapply(mig, function(source) {
        lapply(source, function(dist) {
          det(dist)
        })
      })
    })
  })
  saveRDS(det_FOmegas_mig, paste("dmc/det_FOmegas_mig_",out_name,".RDS",sep=""))
  #inverse
  inv_FOmegas_mig = lapply(FOmegas_mig, function(sel) {
```

```
    lapply(sel, function(mig) {
      lapply(mig, function(source) {
        lapply(source, function(dist) {
          ginv(dist)
        })
      })
    })
  })
  saveRDS(inv_FOmegas_mig, paste("dmc/inv_FOmegas_mig_",out_name,".RDS",sep=""))
}
############### model 3 ###############
if(mod3==TRUE)
{
  FOmegas_sv = lapply(sels, function(sel) {
    lapply(gs, function(g) {
      lapply(times, function(time) {
        lapply(sources, function(my.source) {
          calcFOmegas_stdVar.source(sel, g, time, my.source)
        })
      })
    })
  })

  saveRDS(FOmegas_sv, paste("dmc/FOmegas_sv_",out_name,".RDS",sep=""))
  #determinant
  det_FOmegas_sv = lapply(FOmegas_sv, function(sel) {
    lapply(sel, function(g) {
      lapply(g, function(time) {
        lapply(time, function(my.source) {
          lapply(my.source, function(dist) {
            det(dist)
          })
        })
      })
    })
  })
  saveRDS(det_FOmegas_sv, paste("dmc/det_FOmegas_sv_",out_name,".RDS",sep=""))
  #inverse
  inv_FOmegas_sv = lapply(FOmegas_sv, function(sel) {
    lapply(sel, function(g) {
      lapply(g, function(time) {
        lapply(time, function(my.source) {
          lapply(my.source, function(dist) {
            ginv(dist)
          })
        })
      })
    })
  })
  saveRDS(inv_FOmegas_sv, paste("dmc/inv_FOmegas_sv_",out_name,".RDS",sep=""))
}
############### model 4 ###############
if(mod4==TRUE){
```

```
  source("../programs/dmc-master/genSelMatrices_multipleModes.R")

  my.modes_migInd=c("mig","ind")

  #the parameters time and g are not involved in the migration model so we only loop over
  ## the first element of these vectors
  FOmegas_mixed_migInd = lapply(sels ,function(sel) {
    lapply(gs[1], function(g) {
      lapply(times[1], function(time) {
        lapply(migs, function(mig) {
          lapply(sources, function(my.source) {
            calcFOmegas_mixed(sel, g, time, mig, my.source, my.modes_migInd)
          })
        })
      })
    })
  })

  saveRDS(FOmegas_mixed_migInd, paste("dmc/FOmegas_mixed_migInd_",out_name,".RDS",sep=""))

  detFOmegas_mixed_migInd = lapply(FOmegas_mixed_migInd, function(sel) {
    lapply(sel, function(g) {
      lapply(g, function(time) {
        lapply(time, function(mig) {
          lapply(mig, function(source) {
            lapply(source, function(dist) {
              det(dist)
            })
          })
        })
      })
    })
  })
  saveRDS(detFOmegas_mixed_migInd, paste("dmc/det_FOmegas_mixed_migInd_",out_name,".RDS",sep=""))

  invFOmegas_mixed_migInd = lapply(FOmegas_mixed_migInd, function(sel) {
    lapply(sel, function(g) {
      lapply(g, function(time) {
        lapply(time, function(mig) {
          lapply(mig, function(source) {
            lapply(source, function(dist) {
              ginv(dist)
            })
          })
        })
      })
    })
  })
  saveRDS(invFOmegas_mixed_migInd, paste("dmc/inv_FOmegas_mixed_migInd_",out_name,".RDS",sep=""))
}
############### model 5 ###############
if(mod5==TRUE){
  my.modes_svInd = c("sv", "ind")
```

```
  #the parameter mig is not involved in the standing variant model so we only loop over
  ## the first element of this vector
  FOmegas_mixed_svInd = lapply(sels ,function(sel) {
    lapply(gs, function(g) {
      lapply(times, function(time) {
        lapply(migs[1], function(mig) {
          lapply(sources, function(my.source) {
            calcFOmegas_mixed(sel, g, time, mig, my.source, my.modes_svInd)
          })
        })
      })
    })
  })

  saveRDS(FOmegas_mixed_svInd, paste("dmc/FOmegas_mixed_svInd_",out_name,".RDS",sep=""))

  detFOmegas_mixed_svInd = lapply(FOmegas_mixed_svInd, function(sel) {
    lapply(sel, function(g) {
      lapply(g, function(time) {
        lapply(time, function(mig) {
          lapply(mig, function(source) {
            lapply(source, function(dist) {
              det(dist)
            })
          })
        })
      })
    })
  })
  saveRDS(detFOmegas_mixed_svInd, paste("dmc/det_FOmegas_mixed_svInd_",out_name,".RDS",sep=""))

  invFOmegas_mixed_svInd = lapply(FOmegas_mixed_svInd, function(sel) {
    lapply(sel, function(g) {
      lapply(g, function(time) {
        lapply(time, function(mig) {
          lapply(mig, function(source) {
            lapply(source, function(dist) {
              ginv(dist)
            })
          })
        })
      })
    })
  })
  saveRDS(invFOmegas_mixed_svInd, paste("dmc/inv_FOmegas_mixed_svInd_",out_name,".RDS",sep=""))
}
################ calculate composite likelihoods ################
if(complike==TRUE){
  #randomize allele freqs
  freqs_notRand = readRDS("dmc/selectedRegionAlleleFreqs_p4LG4.RDS")
  randFreqs = apply(freqs_notRand, 2, function(my.freqs) {
    if(runif(1) < 0.5) {
      my.freqs = 1 - my.freqs
```

```
  }
  my.freqs
})
saveRDS(randFreqs, paste("dmc/selectedRegionAlleleFreqsRand_",out_name,".RDS",sep=""))
freqs<<-randFreqs

#calc the likelihoods
source("../programs/dmc-master/calcCompositeLike.R")

## Neutral model

det_FOmegas_neutral = readRDS(neutral_det_name)
inv_FOmegas_neutral = readRDS(neutral_inv_name)
compLikelihood_neutral = lapply(1 : length(selSite), function(j) {
  calcCompLikelihood_neutral(j, det_FOmegas_neutral, inv_FOmegas_neutral)
})
saveRDS(compLikelihood_neutral, paste("dmc/compLikelihood_neutral_p4LG4.RDS",sep=""))

## Model 1
det_FOmegas_ind = readRDS(paste("dmc/det_FOmegas_ind_",out_name,".RDS",sep=""))
inv_FOmegas_ind = readRDS(paste("dmc/inv_FOmegas_ind_",out_name,".RDS",sep=""))
compLikelihood_ind = lapply(1 : length(selSite), function(j) {
  lapply(1 : length(sels), function(sel) calcCompLikelihood_1par(j, det_FOmegas_ind,
                                                                 inv_FOmegas_ind, sel))
})
saveRDS(compLikelihood_ind, paste("dmc/compLikelihood_ind_",out_name,".RDS",sep=""))

## Model 2
det_FOmegas_mig = readRDS(paste("dmc/det_FOmegas_mig_",out_name,".RDS",sep=""))
inv_FOmegas_mig = readRDS(paste("dmc/inv_FOmegas_mig_",out_name,".RDS",sep=""))
compLikelihood_mig = lapply(1 : length(selSite), function(j) {
  lapply(1 : length(sels), function(sel) {
    lapply(1 : length(migs), function(mig) {
      lapply(1 : length(sources), function(my.source) {
        calcCompLikelihood_3par(j, det_FOmegas_mig, inv_FOmegas_mig, sel, mig,
                                my.source)
      })
    })
  })
})
saveRDS(compLikelihood_mig, paste("dmc/compLikelihood_mig_",out_name,".RDS",sep=""))

## Model 3
det_FOmegas_sv = readRDS(paste("dmc/det_FOmegas_sv_",out_name,".RDS",sep=""))
inv_FOmegas_sv = readRDS(paste("dmc/inv_FOmegas_sv_",out_name,".RDS",sep=""))
compLikelihood_sv = lapply(1 : length(selSite), function(j) {
  lapply(1 : length(sels), function(sel) {
    lapply(1 : length(gs), function(g) {
      lapply(1 : length(times), function(t) {
        lapply(1: length(sources), function(my.source) {
          calcCompLikelihood_4par(j, det_FOmegas_sv, inv_FOmegas_sv, sel, g, t,
                                  my.source)
        })
```

```
      })
    })
  })
})
saveRDS(compLikelihood_sv, paste("dmc/compLikelihood_sv_",out_name,".RDS",sep=""))

## Model 4
det_FOmegas_mixed_migInd = readRDS(paste("dmc/det_FOmegas_mixed_migInd_",out_name,".RDS",sep=""))
inv_FOmegas_mixed_migInd = readRDS(paste("dmc/inv_FOmegas_mixed_migInd_",out_name,".RDS",sep=""))

# same trick as above (the parameters time and g are not involved in the migration
## model so we only loop over the first element of these vectors)
# now save lists for each proposed selected site (may want to do this for other
## models/more elegantly depending on density of parameter space)
for(j in 1 : length(selSite)) {
  compLikelihood_mixed_migInd = lapply(1 : length(sels), function(sel) {
    lapply(1 : length(gs[1]), function(g) {
      lapply(1 : length(times[1]), function(t) {
        lapply(1 : length(migs), function (mig) {
          lapply(1: length(sources), function(my.source) {
            calcCompLikelihood_5par(j, det_FOmegas_mixed_migInd,
                                    inv_FOmegas_mixed_migInd, sel, g, t, mig,
                                    my.source)
          })
        })
      })
    })
  })
  saveRDS(compLikelihood_mixed_migInd,
          paste("dmc/compLikelihood_mixed_migInd_",out_name,"_selSite", j, ".RDS",
                sep = ""))
}

## Model 5
det_FOmegas_mixed_svInd = readRDS(paste("dmc/det_FOmegas_mixed_svInd_",out_name,".RDS",sep=""))
inv_FOmegas_mixed_svInd = readRDS(paste("dmc/inv_FOmegas_mixed_svInd_",out_name,".RDS",sep=""))

#same trick as above (the parameter mig is not involved in the migration model so we
##only loop over the first element of this vector)
# now save lists for each proposed selected site (may want to do this for other
## models/more elegantly depending on density of parameter space)
for(j in 1 : length(selSite)) {
  compLikelihood_mixed_svInd = lapply(1 : length(sels), function(sel) {
    lapply(1 : length(gs), function(g) {
      lapply(1 : length(times), function(t) {
        lapply(1 : length(migs[1]), function (mig) {
          lapply(1: length(sources), function(my.source) {
            calcCompLikelihood_5par(j, det_FOmegas_mixed_svInd,
                                    inv_FOmegas_mixed_svInd, sel, g, t, mig,
                                    my.source)
          })
        })
      })
    })
```

```
        })
      })
      saveRDS(compLikelihood_mixed_svInd,
              paste("dmc/compLikelihood_mixed_svInd_",out_name,"_selSite", j, ".RDS",
                    sep = ""))
    }

    #combine models 4 and 5 output

    ## Model 4
    compLikelihood_mixed_migInd_all = lapply(1: length(selSite), function(i) {
      readRDS(paste("dmc/compLikelihood_mixed_migInd_",out_name,"_selSite", i, ".RDS",
                    sep = ""))
    })

    saveRDS(compLikelihood_mixed_migInd_all, paste("dmc/compLikelihood_mixed_migInd_",out_name,".RDS",s

    ## Model 5
    compLikelihood_mixed_svInd_all = lapply(1: length(selSite), function(i) {
      readRDS(paste("dmc/compLikelihood_mixed_svInd_",out_name,"_selSite", i, ".RDS",
                    sep = ""))
    })

    saveRDS(compLikelihood_mixed_svInd_all, paste("dmc/compLikelihood_mixed_svInd_",out_name,".RDS",sep=
  }
  return(params)
}
```

I have to set some parameters before running the function, including the sets of parameters I want to try different settings for.

```
################ Set parameters ################
positions<-readRDS("dmc/selectedRegionPositions_p4LG4.RDS")
F_estimate<-readRDS("dmc/neutralF_p4LG4.RDS")
sampleSizes<-readRDS("dmc/sampleSizes.RDS")

numPops = 16
numPops <- 16
selPops <- c(3,5,7,16)
numBins <- 1000

selSite = positions[seq(1, length(positions), length.out = 50)]
sels = c(1e-4, 1e-3, 0.01, seq(0.02, 0.14, by = 0.01), seq(0.15, 0.3, by = 0.05),
         seq(0.4, 0.6, by = 0.1))
times = c(0, 5, 25, 50, 100, 500, 1000, 1e4, 1e6)
migs = c(10^-(seq(5, 1, by = -2)), 0.5, 1)
mod4_sets=list(c(3,5,7),16)
```

And I'm going to run it with a variety of effective population sizes and recombination rates to see how robust the models are to that parameter.

```
################ Run the program ################
Nes <- c(8.3*10^3,8.3*10^4,8.3*10^5,8.3*10^6)
rs<-c(2.17*10^-8,2*10^-7,6*10^-6,5.6*10^-6)
```

```
dmc.out<-lapply(rs,function(r){
  rec<-r
  rname<-gsub("(\\d).*(\\d)$","\\1_\\2",as.character(r))
  lapply(Nes, function(ne){
    out_name<-paste("p4LG4_",ne,"_",rname,sep="")
    dir<-getwd()
    print(paste("running",out_name,"in",dir,sep=" "))
    p<-run.dmc(F_estimate = F_estimate,out_name = out_name,positions = positions,sampleSizes = sampleSi
               selSite=selSite,rec =rec,
               Ne = ne,selPops = selPops,numBins = numBins,numPops = numPops,
               sels = sels, times = times,
               migs = migs,mod4_sets=mod4_sets)
    return(p)
  })
})
print("Done running dmc")
```

I'm running this one on abies using `nohup Rscript ~/Projects/popgen/scripts/002_run_dmc.R >> ~/Projects/popgen/dmc_ne.log 2>&1 &`.

Estimate recombination rates

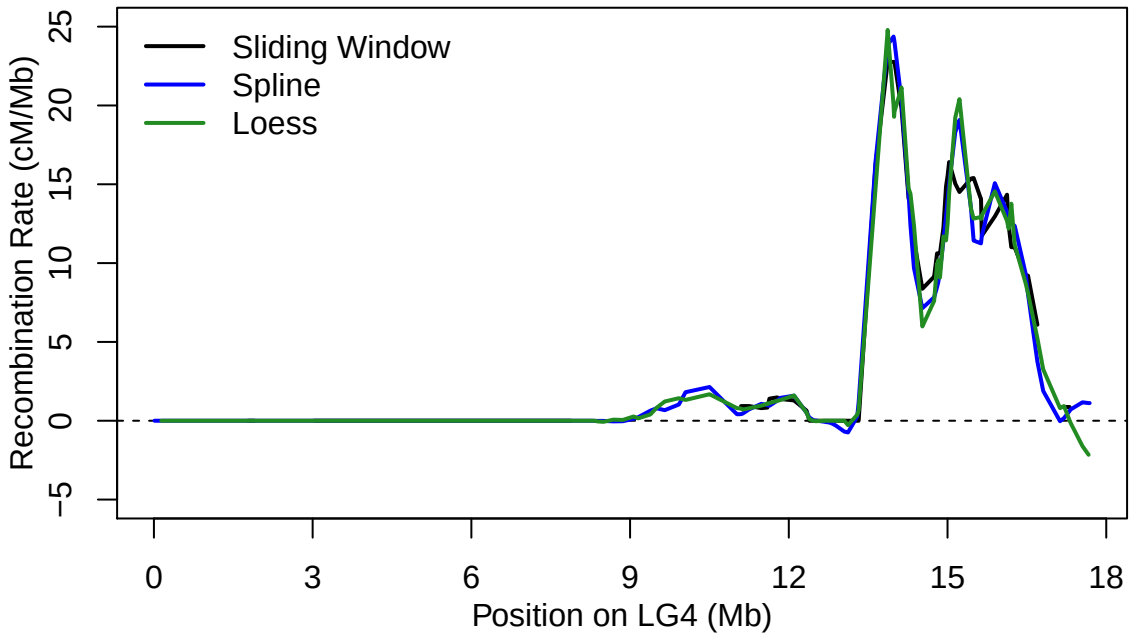
```
ssc.map<-read.delim("../../scovelli_genome/SSC_linkage_map_20160701.txt",header=T)
colnames(ssc.map)<-c("map","mkr","gen","scaffold","scaffold_orientation","scaffold.bp","phys","node")
ssc.map$set<-"Syngnathus.scovelli"
map<-ssc.map[,c("set","map","mkr","phys","gen")]
write.table(map,"../../scovelli_genome/ssc_map.txt",sep=" ",row.names=FALSE, col.names = TRUE)
library(MareyMap)
startMareyMapGUI()
#using the GUI, I ran all three types of recombination rate estimators and saved the MapSet
```

```
ssc.map<-read.delim("../../scovelli_genome/ssc_MareyMap.txt",comment.char = "#",sep=" ")
#genome-wide
r<-data.frame(Genome_wide=c(mean(ssc.map$slidingwindow,na.rm = TRUE)/1000000,
                            mean(ssc.map$spline,na.rm = TRUE)/1000000,
                            mean(ssc.map$loess,na.rm = TRUE)/1000000),
              LG4=c(mean(ssc.map$slidingwindow[ssc.map$map=="LG4"],na.rm = TRUE)/1000000,
                            mean(ssc.map$spline[ssc.map$map=="LG4"],na.rm = TRUE)/1000000,
                            mean(ssc.map$loess[ssc.map$map=="LG4"],na.rm = TRUE)/1000000),
              LG4_first12Mb=c(mean(ssc.map$slidingwindow[ssc.map$map=="LG4" & ssc.map$phys<12*10^6],na.r
                            mean(ssc.map$spline[ssc.map$map=="LG4"& ssc.map$phys<12*10^6],na.rm = TRUE),
                            mean(ssc.map$loess[ssc.map$map=="LG4"& ssc.map$phys<12*10^6],na.rm = TRUE)/1
              row.names = c("Sliding Window","Spline","Loess"))
kable(r,caption="Recombination rate estimates")
```

Table 1: Recombination rate estimates

	Genome_wide	LG4	LG4_first12Mb
Sliding Window	5.8e-06	3.7e-06	2e-07
Spline	5.6e-06	3.0e-06	2e-07
Loess	5.6e-06	3.0e-06	2e-07

```
load("../../scovelli_genome/ssc_map.rda")
#plot LG4
plot(set[["LG4"]]@interpolations$slidingwindow@physicalPositions,
     set[["LG4"]]@interpolations$slidingwindow@rates,type="l",
     ylim=c(-5,25),xlab="",ylab="",xaxt='n',lwd=2)
abline(h=0,lty=2)
axis(1,at=seq(0,1.8*10^7,3*10^6),labels = seq(0,18,3))
mtext("Position on LG4 (Mb)",1,line=2)
mtext("Recombination Rate (cM/Mb)",2,line=2)
lines(set[["LG4"]]@interpolations$spline@physicalPositions,
      set[["LG4"]]@interpolations$spline@rates,type="l",col="blue",lwd=2)
lines(set[["LG4"]]@interpolations$loess@physicalPositions,
      set[["LG4"]]@interpolations$loess@rates,type="l",lwd=2,col="forestgreen")
legend("topleft",bty='n',col=c("black","blue","forestgreen"),lwd=2,c("Sliding Window","Spline","Loess"))
```



Evaluate the output of the initial dmc runs

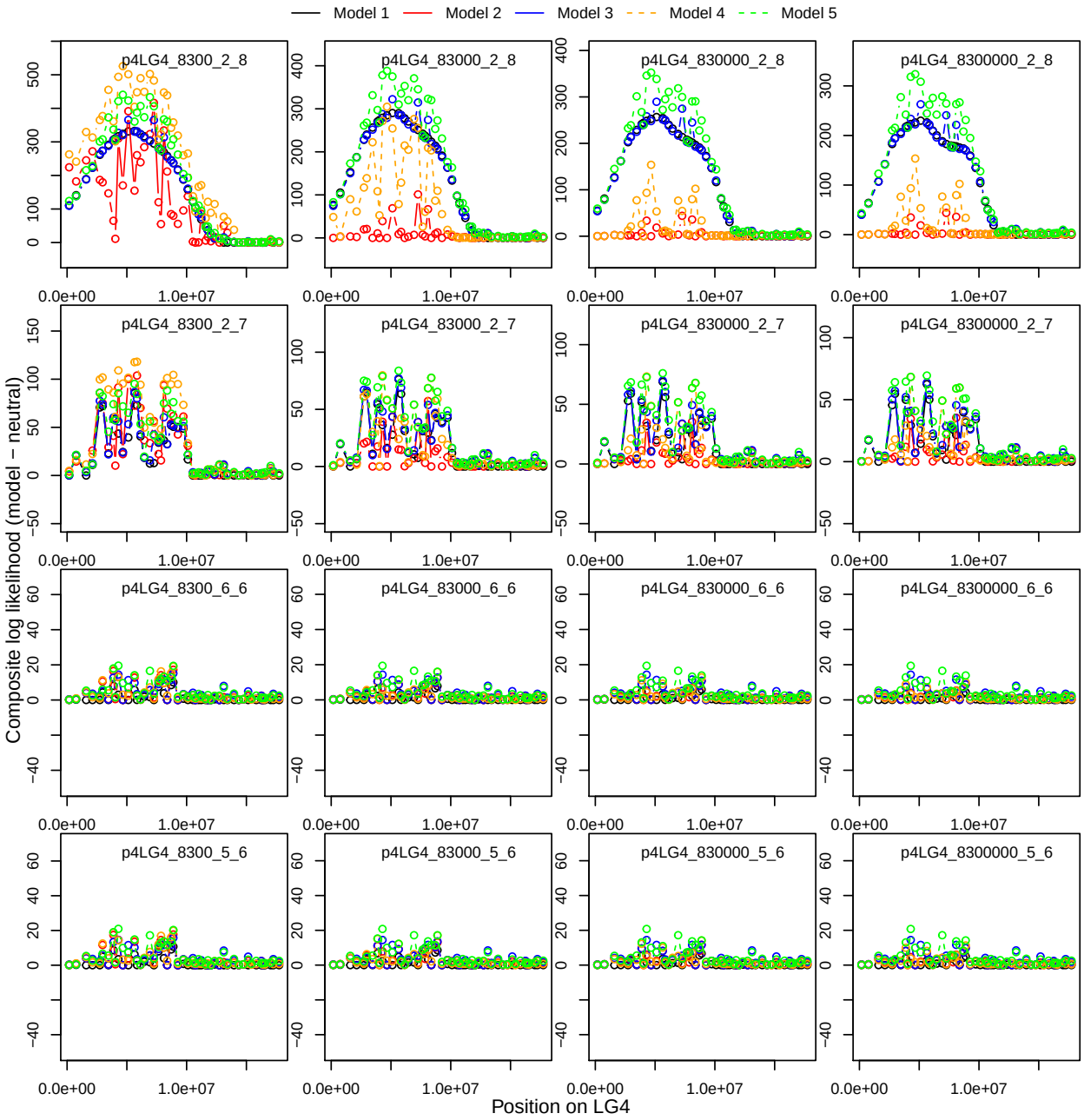
Plot maximum composite likelihood ratios for models over proposed selected sites

```
calc.max.complike<-function(pattern){
  #read in composite likelihood files and calculate max for all proposed selected sites
  compLikelihood_neutral = readRDS("dmc/compLikelihood_neutral_p4LG4.RDS")
  compLikelihood_neutral_site = sapply(1 : length(compLikelihood_neutral), function(i) {
    max(unlist(compLikelihood_neutral[[i]]))
  })

  compLikelihood_ind = readRDS(paste("dmc/compLikelihood_ind_",pattern,".RDS",sep=""))
  compLikelihood_ind_site = sapply(1 : length(selSite), function(i) {
    max(unlist(compLikelihood_ind[[i]]))
  })
```

```
  compLikelihood_mig = readRDS(paste("dmc/compLikelihood_mig_",pattern,".RDS",sep=""))
  compLikelihood_mig_site = sapply(1 : length(selSite), function(i) {
    max(unlist(compLikelihood_mig[[i]]))
  })

  compLikelihood_sv = readRDS(paste("dmc/compLikelihood_sv_",pattern,".RDS",sep=""))
  compLikelihood_sv_site = sapply(1 : length(selSite), function(i) {
    max(unlist(compLikelihood_sv[[i]]))
  })

  compLikelihood_mixed_migInd = readRDS(paste("dmc/compLikelihood_mixed_migInd_",pattern,".RDS",sep=""))
  compLikelihood_mixed_migInd_site = sapply(1 : length(selSite), function(i) {
    max(unlist(compLikelihood_mixed_migInd[[i]]))
  })

  compLikelihood_mixed_svInd = readRDS(paste("dmc/compLikelihood_mixed_svInd_",pattern,".RDS",sep=""))
  compLikelihood_mixed_svInd_site = sapply(1 : length(selSite), function(i) {
    max(unlist(compLikelihood_mixed_svInd[[i]]))
  })
  return(c(ind=(compLikelihood_ind_site - compLikelihood_neutral_site),
           mig=(compLikelihood_mig_site - compLikelihood_neutral_site),
           sv=(compLikelihood_sv_site - compLikelihood_neutral_site),
           migInd=(compLikelihood_mixed_migInd_site - compLikelihood_neutral_site),
           svInd=(compLikelihood_mixed_svInd_site - compLikelihood_neutral_site)))
}

plot.complike<-function(pattern,leg=TRUE,lab=TRUE){
  max.likes<-calc.max.complike(pattern)

  plot_range = range(max.likes)

  if(lab==TRUE){
    x.lab<-"Proposed position selected site"
    y.lab<-"Composite log-likelihood (model - neutral)"
  } else{
    x.lab<-y.lab<-""
  }

  plot(selSite, max.likes[grep("ind",names(max.likes))], type = "b",
       ylim = c(plot_range[1] - 50, plot_range[2] + 50),
       xlab = x.lab,
       ylab = y.lab)
  lines(selSite, max.likes[grep("mig\\d+",names(max.likes))], col = "red",
        type = "b")
  lines(selSite, max.likes[grep("sv\\d+",names(max.likes))], col = "blue",
        type = "b")
  lines(selSite, max.likes[grep("migInd",names(max.likes))],
        col = "orange", lty = 2, type = "b")
  lines(selSite, max.likes[grep("svInd",names(max.likes))],
        col = "green", lty = 2, type = "b")
  legend("top",bty='n',legend = pattern)
  if(isTRUE(leg)){
    legend("topright", col = c("black", "red", "blue", "orange", "green"),
```

```
          lty = c(rep(1, 3), rep(2, 2)), sapply(1 : 5, function(i) paste("Model", i)))
  }
  return(list(max.likes,pattern))
}
```

```
patterns<-c("p4LG4_8300_2_8","p4LG4_83000_2_8","p4LG4_830000_2_8","p4LG4_8300000_2_8",
            "p4LG4_8300_2_7","p4LG4_83000_2_7","p4LG4_830000_2_7","p4LG4_8300000_2_7",
            "p4LG4_8300_6_6","p4LG4_83000_6_6","p4LG4_830000_6_6","p4LG4_8300000_6_6",
            "p4LG4_8300_5_6","p4LG4_83000_5_6","p4LG4_830000_5_6","p4LG4_8300000_5_6")
par(mfrow=c(4,4),mar=c(1.5,1.5,0.5,0.5),oma=c(2,2,2,2))
ne.complikes<-lapply(patterns,plot.complike,leg=FALSE,lab=FALSE)
mtext("Position on LG4",1,outer=TRUE,cex=0.8,line=.5)
mtext("Composite log likelihood (model - neutral)",2,outer=T,cex=0.8,line=.5)
par(fig=c(0,1,0,1),oma=c(0,0,0,0),mar=c(0,0,0,0),new=TRUE)
plot(0,0,type='n',bty='n',xaxt='n',yaxt='n')
legend("top", col = c("black", "red", "blue", "orange", "green"),ncol=5,bty='n',
          lty = c(rep(1, 3), rep(2, 2)), sapply(1 : 5, function(i) paste("Model", i)))
```



Get maximum composite likelihood estimates

```
#These won't work if the parameters aren't specified as above
get.mcle<-function(max.complikes,Ne,rec,selSite= positions[seq(1, length(positions), length.out = 50)],
                   sels = c(1e-4, 1e-3, 0.01, seq(0.02, 0.14, by = 0.01), seq(0.15, 0.3, by = 0.05),
                            seq(0.4, 0.6, by = 0.1)),
                   times = c(0, 5, 25, 50, 100, 500, 1000, 1e4, 1e6),
                   migs = c(10^-(seq(5, 1, by = -2)), 0.5, 1),sources=c(3,5,7,16)){
  Ne<<-Ne
  rec<<-rec
  gs = c(1/(2*Ne), 10^-(4:1))
```

```
  source("../programs/dmc-master/getMCLE.R")

  ## Model 1
  m1<-cbind(getMCLEind(max.complikes[grep("ind",names(max.complikes))], selSite, sels),
            maxG=NA,maxTime=NA,maxSource=NA)

  ## Model 2
  m2<-cbind(getMCLEmig(max.complikes[grep("mig\\d+",names(max.complikes))], selSite, sels, migs, sources
            maxG=NA)

  ## Model 3
  m3<-getMCLEsv_source(max.complikes[grep("sv\\d+",names(max.complikes))], selSite, sels, gs, times, sou

  ## Model 4
  m4<-getMCLEmixed(max.complikes[grep("migInd",names(max.complikes))], selSite, sels, gs[1], times[1], m

  ## Model 5
  m5<-getMCLEmixed(max.complikes[grep("svInd",names(max.complikes))], selSite, sels, gs, times, migs[1]
  mcles<-rbind(m1,m2,m3,m4,m5)
  rownames(mcles)<-c("Model1","Model2","Model3","Model4","Model5")
  return(mcles)
}
```

```
rs<-c("2_8"=2.17*10^-8,"2_7"=2*10^-7,"6_6"=6*10^-6,"5_6"=5.6*10^-6)
ne.mcles<-lapply(ne.complikes, function(max.complikes){
  pattern<-max.complikes[[2]]
  Ne<-as.numeric(gsub("p4LG4_(\\d+)_.*","\\1",pattern))
  r<-gsub("p4LG4_\\d+_(\\d_\\d)","\\1",pattern)
  rec<-rs[r]
  max.complikes<-max.complikes[[1]]
  mcle<-get.mcle(max.complikes,Ne=Ne,rec=rec)
  return(list(mcle,Ne,rec))
})
names(ne.mcles)<-patterns
lapply(ne.mcles,function(mcle){ kable(mcle[[1]]) })
```

```
## $p4LG4_8300_2_8
##
##
##           maxLoc   maxSel       maxG   maxTime   maxSource
## -------  -------  -------  ---------  --------  ----------
## Model1    173302    1e-04         NA        NA          NA
## Model2    173302    1e-04   1.00e-05         3          NA
## Model3    173302    1e-04   6.02e-05         0           3
## Model4    173302    1e-04   6.02e-05         0           3
## Model5    173302    1e-04   6.02e-05         0           3
##
## $p4LG4_83000_2_8
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
## Model2    173302    1e-04   1e-05         3          NA
```

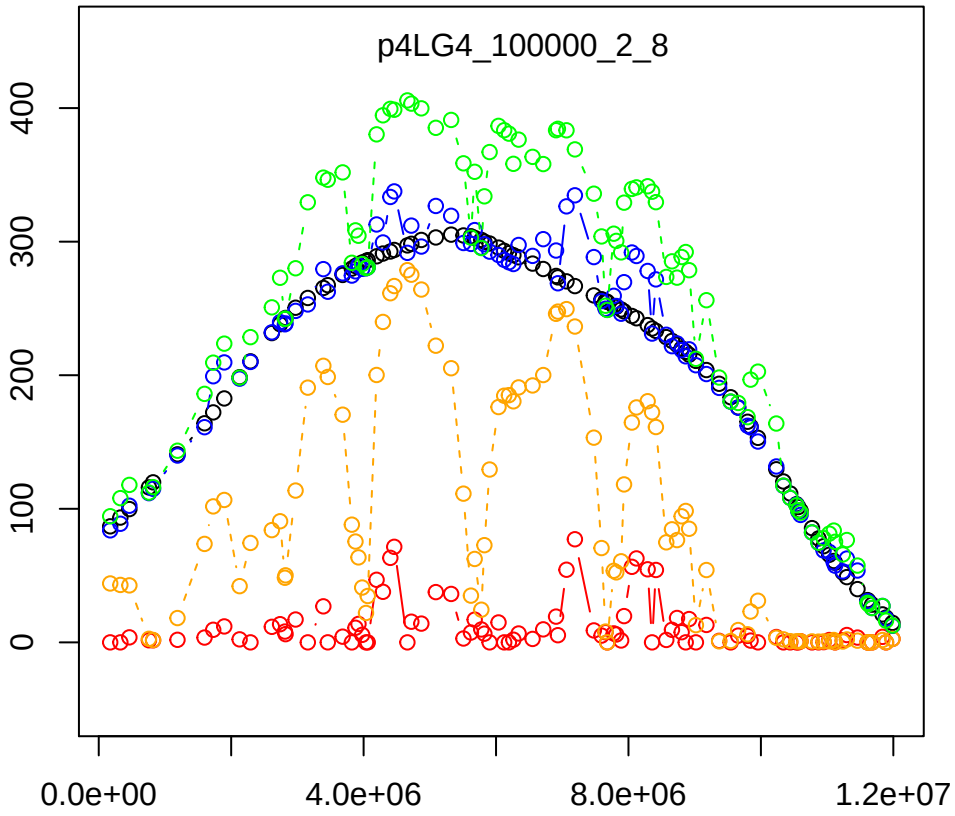
```
## Model3    173302    1e-04   6e-06         0           3
## Model4    173302    1e-04   6e-06         0           3
## Model5    173302    1e-04   6e-06         0           3
##
## $p4LG4_830000_2_8
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
## Model2    173302    1e-04   1e-05         3          NA
## Model3    173302    1e-04   6e-07         0           3
## Model4    173302    1e-04   6e-07         0           3
## Model5    173302    1e-04   6e-07         0           3
##
## $p4LG4_8300000_2_8
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
## Model2    173302    1e-04   1e-05         3          NA
## Model3    173302    1e-04   1e-07         0           3
## Model4    173302    1e-04   1e-07         0           3
## Model5    173302    1e-04   1e-07         0           3
##
## $p4LG4_8300_2_7
##
##
##           maxLoc   maxSel       maxG   maxTime   maxSource
## -------  -------  -------  ---------  --------  ----------
## Model1    173302    1e-04         NA        NA          NA
## Model2    173302    1e-04   1.00e-05         3          NA
## Model3    173302    1e-04   6.02e-05         0           3
## Model4    173302    1e-04   6.02e-05         0           3
## Model5    173302    1e-04   6.02e-05         0           3
##
## $p4LG4_83000_2_7
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
## Model2    173302    1e-04   1e-05         3          NA
## Model3    173302    1e-04   6e-06         0           3
## Model4    173302    1e-04   6e-06         0           3
## Model5    173302    1e-04   6e-06         0           3
##
## $p4LG4_830000_2_7
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
```

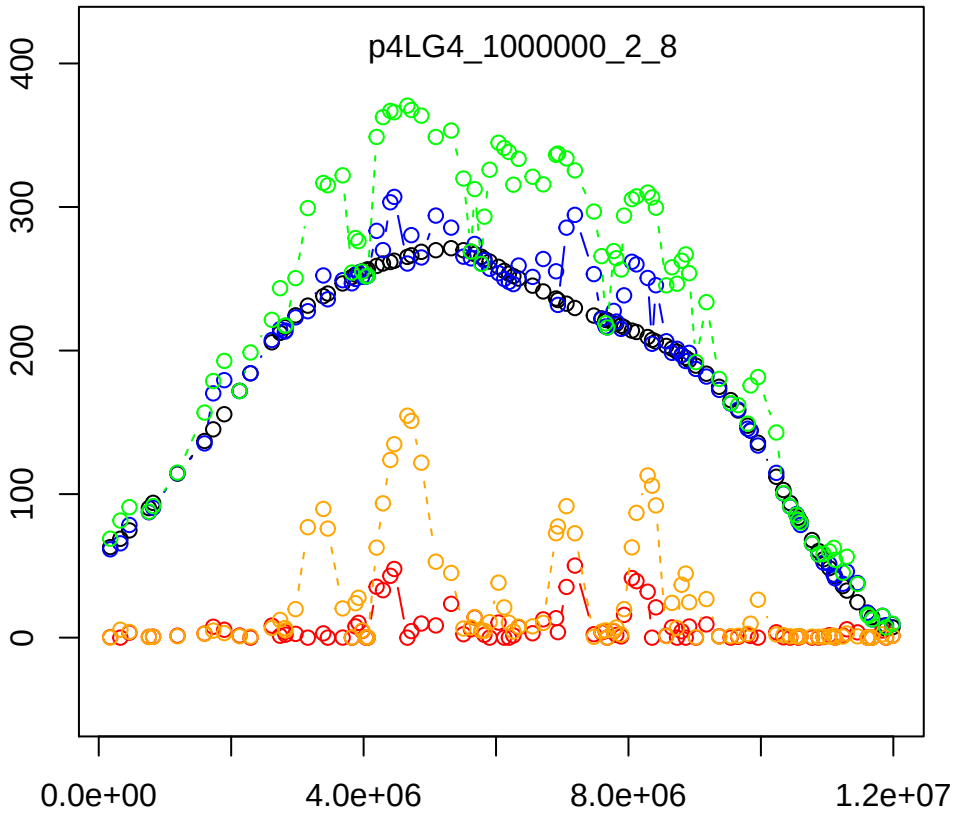
```
## Model2    173302    1e-04   1e-05         3          NA
## Model3    173302    1e-04   6e-07         0           3
## Model4    173302    1e-04   6e-07         0           3
## Model5    173302    1e-04   6e-07         0           3
##
## $p4LG4_8300000_2_7
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
## Model2    173302    1e-04   1e-05         3          NA
## Model3    173302    1e-04   1e-07         0           3
## Model4    173302    1e-04   1e-07         0           3
## Model5    173302    1e-04   1e-07         0           3
##
## $p4LG4_8300_6_6
##
##
##           maxLoc   maxSel       maxG   maxTime   maxSource
## -------  -------  -------  ---------  --------  ----------
## Model1    173302    1e-04         NA        NA          NA
## Model2    173302    1e-04   1.00e-05         3          NA
## Model3    173302    1e-04   6.02e-05         0           3
## Model4    173302    1e-04   6.02e-05         0           3
## Model5    173302    1e-04   6.02e-05         0           3
##
## $p4LG4_83000_6_6
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
## Model2    173302    1e-04   1e-05         3          NA
## Model3    173302    1e-04   6e-06         0           3
## Model4    173302    1e-04   6e-06         0           3
## Model5    173302    1e-04   6e-06         0           3
##
## $p4LG4_830000_6_6
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA        NA          NA
## Model2    173302    1e-04   1e-05         3          NA
## Model3    173302    1e-04   6e-07         0           3
## Model4    173302    1e-04   6e-07         0           3
## Model5    173302    1e-04   6e-07         0           3
##
## $p4LG4_8300000_6_6
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
```

```
## Model1    173302    1e-04      NA         NA          NA
## Model2    173302    1e-04   1e-05          3          NA
## Model3    173302    1e-04   1e-07          0           3
## Model4    173302    1e-04   1e-07          0           3
## Model5    173302    1e-04   1e-07          0           3
##
## $p4LG4_8300_5_6
##
##
##           maxLoc   maxSel       maxG   maxTime   maxSource
## -------  -------  -------  ---------  --------  ----------
## Model1    173302    1e-04         NA         NA          NA
## Model2    173302    1e-04   1.00e-05          3          NA
## Model3    173302    1e-04   6.02e-05          0           3
## Model4    173302    1e-04   6.02e-05          0           3
## Model5    173302    1e-04   6.02e-05          0           3
##
## $p4LG4_83000_5_6
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA         NA          NA
## Model2    173302    1e-04   1e-05          3          NA
## Model3    173302    1e-04   6e-06          0           3
## Model4    173302    1e-04   6e-06          0           3
## Model5    173302    1e-04   6e-06          0           3
##
## $p4LG4_830000_5_6
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA         NA          NA
## Model2    173302    1e-04   1e-05          3          NA
## Model3    173302    1e-04   6e-07          0           3
## Model4    173302    1e-04   6e-07          0           3
## Model5    173302    1e-04   6e-07          0           3
##
## $p4LG4_8300000_5_6
##
##
##           maxLoc   maxSel    maxG   maxTime   maxSource
## -------  -------  -------  ------  --------  ----------
## Model1    173302    1e-04      NA         NA          NA
## Model2    173302    1e-04   1e-05          3          NA
## Model3    173302    1e-04   1e-07          0           3
## Model4    173302    1e-04   1e-07          0           3
## Model5    173302    1e-04   1e-07          0           3
```

Model with chosen parameters

```
selSite = positions[seq(1, length(positions[positions<12000000]), length.out = 100)]
par(mfrow=c(2,1),oma=c(2,2,2,2),mar=c(2,2,2,2))
max.complikes1<-plot.complike("p4LG4_100000_2_8",leg=FALSE)
max.complikes2<-plot.complike("p4LG4_1000000_2_8",leg=FALSE)
```


p4LG4_100000_2_8
0
100
200
300
400
0.0e+00
4.0e+06
8.0e+06
1.2e+07


p4LG4_1000000_2_8
0
100
200
300
400
0.0e+00
4.0e+06
8.0e+06
1.2e+07

```
mcle1<-get.mcle(max.complikes1[[1]],Ne=100000,rec=2*10^-8)
kable(mcle1)
```

	maxLoc	maxSel	maxG	maxTime	maxSource
Model1	757972	1e-04	NA	NA	NA
Model2	173302	1e-04	1e-05	3	NA
Model3	173302	1e-04	5e-06	0	3
Model4	173302	1e-04	5e-06	0	3
Model5	173302	1e-04	5e-06	0	3

```
mcle2<-get.mcle(max.complikes2[[1]],Ne=1000000,rec=2*10^-8)
kable(mcle2)
```

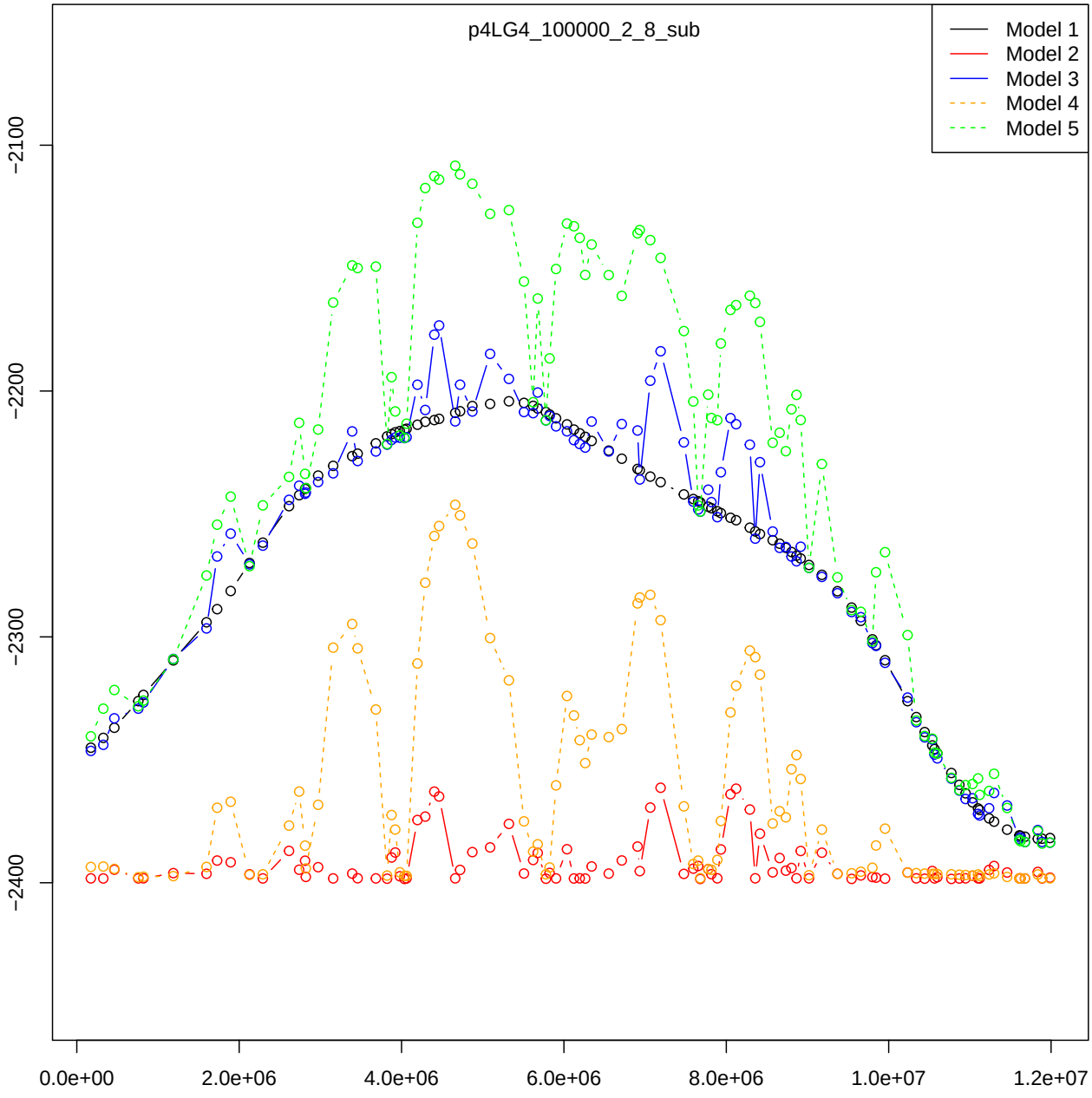
	maxLoc	maxSel	maxG	maxTime	maxSource
Model1	757972	1e-04	NA	NA	NA
Model2	173302	1e-04	1e-05	3	NA
Model3	173302	1e-04	5e-07	0	3
Model4	173302	1e-04	5e-07	0	3
Model5	173302	1e-04	5e-07	0	3

The selection values are still the smallest ones. Kristin Lee indicated that this might occur if there aren't enough neutral SNPs - so I'll try re-calculating neutral SNPS

```
#calculate selected allele frequencies
LG4.sub<-calc.allFreqs(vcf[vcf$`#CHROM` == "LG4" & vcf$POS < 12*10^6,],pop.list,pop.labs)
saveRDS(LG4.sub,"dmc/selectedRegionAlleleFreqs_p4LG4_subset.RDS")
saveRDS(vcf[vcf$`#CHROM`=="LG4"& vcf$POS < 12*10^6,"POS"],"dmc/selectedRegionPositions_p4LG4_subset.RDS

#calculate neutral allele frequencies
all.out<-read.delim("all_outliers.txt",sep='\t',header=TRUE)
allFreqs<-calc.allFreqs(vcf[!vcf$`#CHROM` %in% "LG4" & !vcf$SNP %in% all.out$SNP,],
                  pop.list,pop.labs)
saveRDS(allFreqs,"dmc/neutralAlleleFreqs_p4LG4_notSNPs.RDS")

neutralF_filename<-"dmc/neutralF_p4LG4_subset"
source("../programs/dmc-master/calcNeutralF.R")
F_estimate<-readRDS("dmc/neutralF_p4LG4_subset.RDS")

#calculate the determinant and inverse of the neutral F matrix
M <- numPops
Tmatrix <- matrix(data = rep(-1 / M, (M - 1) * M), nrow = M - 1, ncol = M)
diag(Tmatrix) = (M - 1) / M
sampleErrorMatrix = diag(1/sampleSizes, nrow = numPops, ncol = numPops)
det_FOmegas_neutral = det(Tmatrix %*% (F_estimate + sampleErrorMatrix) %*% t(Tmatrix))
saveRDS(det_FOmegas_neutral, "dmc/det_FOmegas_neutral_p4LG4_subset.RDS")

inv_FOmegas_neutral = ginv(Tmatrix %*% (F_estimate + sampleErrorMatrix) %*% t(Tmatrix))
saveRDS(inv_FOmegas_neutral, "dmc/inv_FOmegas_neutral_p4LG4_subset.RDS")
```

```
positions<-readRDS("dmc/selectedRegionPositions_p4LG4_subset.RDS")
F_estimate<-readRDS("dmc/neutralF_p4LG4_subset.RDS")
```

```
sampleSizes<-readRDS("dmc/sampleSizes.RDS")
neutral_det_name = "dmc/det_FOmegas_neutral_p4LG4_subset.RDS"
neutral_inv_name = "dmc/inv_FOmegas_neutral_p4LG4_subset.RDS"
selSite = positions[seq(1, length(positions[positions<12000000]), length.out = 100)]
par(mfrow=c(1,1),oma=c(2,2,2,2),mar=c(2,2,2,2))
max.complikes1<-plot.complike("p4LG4_100000_2_8_sub",leg=TRUE)
```



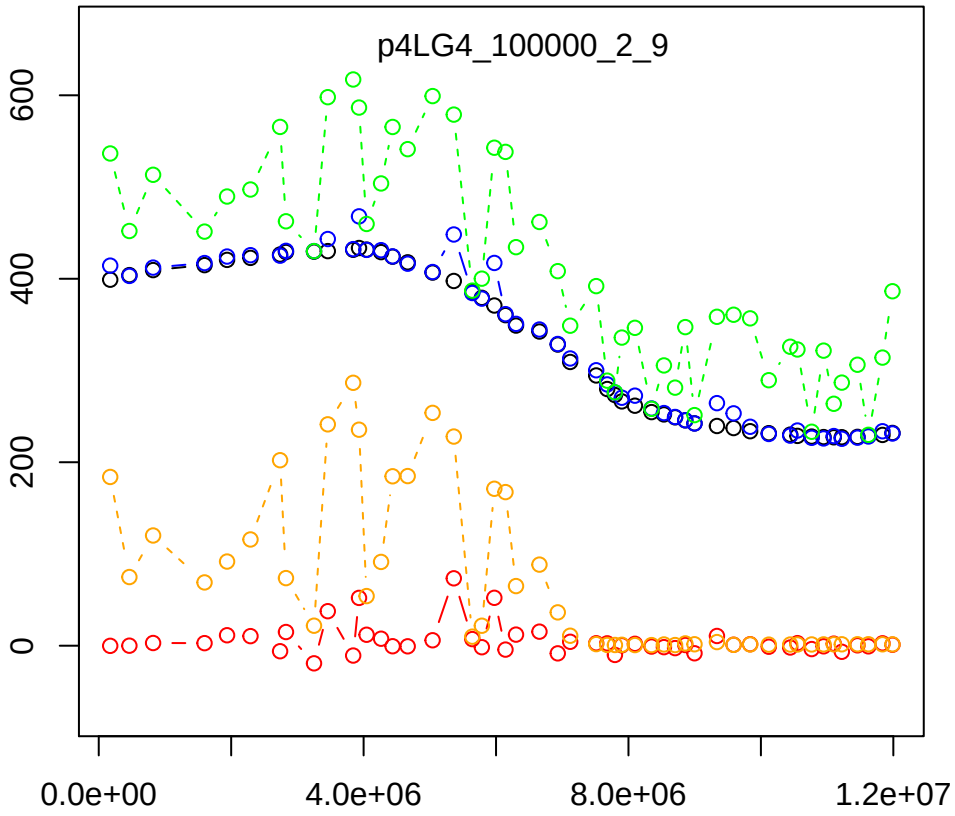

```
mcle.sub<-get.mcle(max.complikes1[[1]],Ne=100000,rec=2*10^-8)
kable(mcle.sub)
```

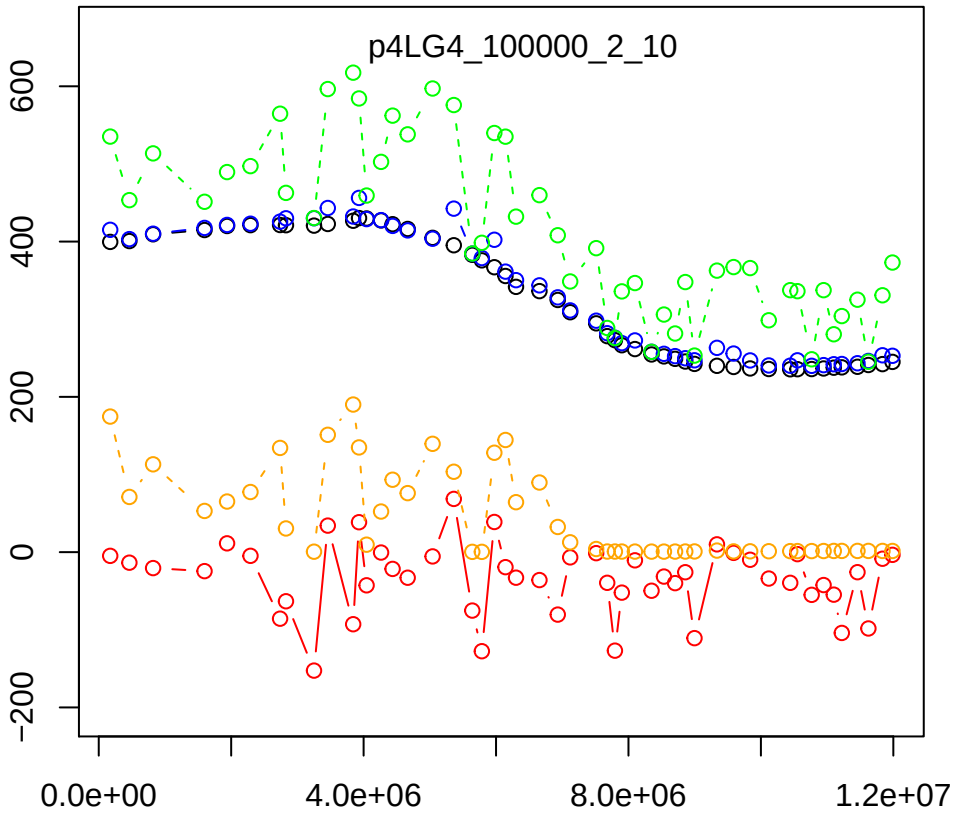
	maxLoc	maxSel	maxG	maxTime	maxSource
Model1	462622	1e-04	NA	NA	NA
Model2	173302	1e-04	1e-05	3	NA
Model3	173302	1e-04	5e-06	0	3

	maxLoc	maxSel	maxG	maxTime	maxSource
Model4	173302	1e-04	5e-06	0	3
Model5	173302	1e-04	5e-06	0	3

Let's try lower recombination rates

```
selSite = positions[seq(1, length(positions), length.out = 50)]
F_estimate<-readRDS("dmc/neutralF_p4LG4.RDS")
sampleSizes<-readRDS("dmc/sampleSizes.RDS")
par(mfrow=c(2,1),oma=c(2,2,2,2),mar=c(2,2,2,2))
max.complikes1<-plot.complike("p4LG4_100000_2_9",leg=FALSE)
max.complikes2<-plot.complike("p4LG4_100000_2_10",leg=FALSE)
```


p4LG4_100000_2_9
600
400
200
0
0.0e+00
4.0e+06
8.0e+06
1.2e+07


p4LG4_100000_2_10
600
400
200
0
−200
0.0e+00
4.0e+06
8.0e+06
1.2e+07

```
mcle1<-get.mcle(max.complikes1[[1]],Ne=100000,rec=2*10^-9)
kable(mcle1)
```

	maxLoc	maxSel	maxG	maxTime	maxSource
Model1	173302	1e-04	NA	NA	NA
Model2	173302	1e-04	1e-05	3	NA
Model3	173302	1e-04	5e-06	0	3
Model4	173302	1e-04	5e-06	0	3
Model5	173302	1e-04	5e-06	0	3

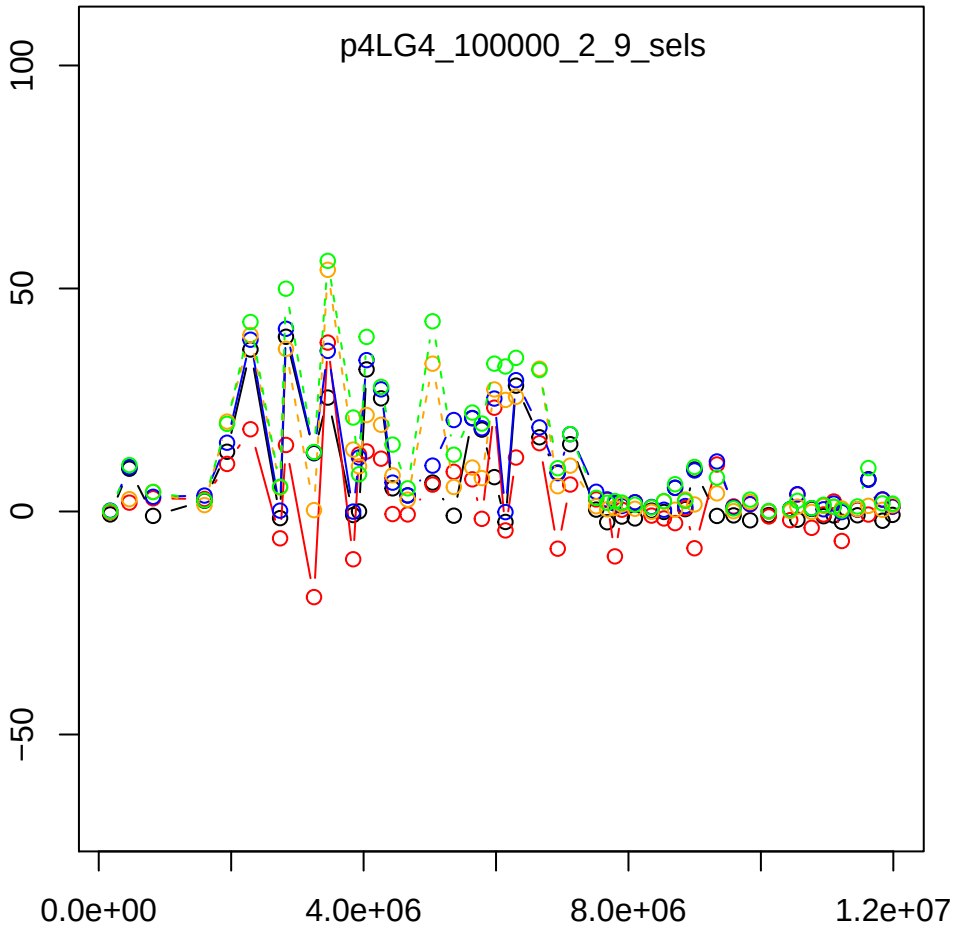
```
mcle2<-get.mcle(max.complikes2[[1]],Ne=100000,rec=2*10^-10)
kable(mcle2)
```

	maxLoc	maxSel	maxG	maxTime	maxSource
Model1	173302	1e-04	NA	NA	NA
Model2	173302	1e-04	1e-05	3	NA
Model3	173302	1e-04	5e-06	0	3
Model4	173302	1e-04	5e-06	0	3
Model5	173302	1e-04	5e-06	0	3

Different selection parameters

Going below 1e-5 (i.e. to 1e-6) caused infinite values to occur

```
sels = c(9e-4,7.5e-4,5e-4, 2.5e-4,1e-4)
par(mfrow=c(1,1),oma=c(2,2,2,2),mar=c(2,2,2,2))
max.complikes.sel<-plot.complike("p4LG4_100000_2_9_sels",leg=FALSE)
```




```
mcle.sel<-get.mcle(max.complikes.sel[[1]],Ne=100000,rec=2*10^-9)
kable(mcle.sel)
```

	maxLoc	maxSel	maxG	maxTime	maxSource
Model1	173302	1e-04	NA	NA	NA
Model2	173302	1e-04	1e-05	3	NA
Model3	173302	1e-04	5e-06	0	3
Model4	173302	1e-04	5e-06	0	3
Model5	173302	1e-04	5e-06	0	3