# Supplementary Online Material for: Stable *Heliconius* butterfly hybrid zones are correlated with a local rainfall peak at the edge of the Amazon basin

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### *S1: Genetics of colour patterns*

Specimens were genotyped using their colour pattern phenotypes. The Mendelian genetics of colour patterns in the Amazonian and Andean races of *H. erato* and *H. melpomene* are described in more detail in Mallet (1989) and Mallet et al. (1990) and are merely outlined here.

In *H. erato*, three loci determine the major colour pattern elements. The *D* locus (referred to as $D^{Ry}/d^{rY}$ in Mallet (1989)) determines the presence/absence of proximal forewing patch known as "dennis" as well as hindwing rays, and the yellow versus red colour of the forewing band. *DD* genotypes have dennis, rays and a yellow forewing band, whereas *dd* genotypes have no dennis or rays and a red forewing band. Heterozygotes are recognisable because the red colour elements are expressed; *Dd* heterozygotes have dennis and rays, with a red forewing band. A more or less dominant locus *Sd* determines the width of the forewing band. Recessive homozygotes (*sdsd*) have a broad forewing band, and dominant homozygotes (*SdSd*) and heterozygotes (*Sdsd*) have a narrow forewing band (Mallet 1989). The *Sd* and *Cr* loci interact to produce the yellow hindwing bar of the postman pattern race. Only in *sdsdcrcr* genotypes is the hindwing bar completely expressed. In *Sd- crcr* individuals a weak hindwing bar is expressed (with a narrow forewing band), whereas in *sdsd Cr-* individuals only the tips of the hindwing bar are expressed (with a broad forewing band). *Sd- Cr-* individuals have no hindwing bar expression except for occasional "shadows" on the undersides of *Crcr* genotypes.

In *H. melpomene*, four dominant loci determine colour pattern differences. The *D* locus (called $D^R$/d in Turner (1972) and Mallet (1989)) determines the presence (*D-*) or absence (*dd*) of the dennis and rays. The *Yb* locus determines the presence (*ybyb*) or absence (*Yb-*) of the yellow hind-wing bar. The *N* locus ($N^N/N^B$ in Mallet (1989)), is putatively codominant (Turner 1972), but heterozygotes *Nn* are often hard to distinguish from *NN* homozygotes (Mallet 1989) and so *N* is treated as dominant here. The *N* locus interacts with another locus, *B* to determine the shape and colour of the forewing band; the *N* allele codes for a yellow forewing band, as well as narrowing any red forewing band present. The *B* allele codes for a red forewing band. *bbN-* individuals have a yellow forewing bar, whereas *B-nn* shows full red forewing bar expression. *B-N-* genotypes show a yellow bar, with a narrow red outer rim. Finally, double recessive homozygotes (*bbnn*) have melanic forewings with no band. The *N* and *Yb* loci are tightly linked (with recombination rate, $c \approx 0.005$), and the *B* and *D* loci are thought to be moderately ($c \approx 0.135$) or tightly linked (Sheppard et al. 1985; Mallet 1989; Baxter et al. 2010).

The *H. melpomene N* locus can be difficult to score due to epistatic effects of another locus, *M* (Mallet 1989). *M* has never been mapped but is almost certainly linked to the *B-D* region (Simon Baxter, pers. comm.), and its existence may explain curious features of (apparent) disequilibria measured among mapped loci (see results).

Recent studies confirm that the *N/Yb/Cr* and *B/D* loci are gene regulatory elements in homologous regions of the genomes of *H.erato* and *H. melpomene* (Joron et al. 2006, 2011; Reed et al. 2011). A third locus has now been characterized, which shows similar identity between the *H. erato Sd* and the *H. melpomene Ac* (Martin et al. 2012). However, the *Ac* locus appears to be involved here only in *erato*, and not in the *melpomene* hybrid zone. In spite of the homologous genomic locations of these three genes in the two species, one of the mimetic species, *H. melpomene*, has almost certainly adapted to and recreated the other's colour patterns, as the two species are sufficiently divergent to prevent any possible hybridization and the allelic variants at these loci show no homologies other than genomic location (Supple et al. 2013).

### *S2: R code for iterative solution of multilocus clines and for cline fitting via likelihood*

The model described in the methods section was iterated for 200 generations in a one-dimensional series of 200 demes, each connected to others by migration to obtain appropriate theoretical cline shapes for fitting to the data. This was sufficient as clines stabilized after a few tens of generations at the selection pressures used, and showed no discontinuities; see Fig. 3, top panels). Starting conditions did not affect cline shape; we initiated the model with "secondary contact" between the two pure genotypes, which meet in the middle of the series of demes in an initially abrupt step (see also Mallet and Barton (1989a). In each generation, the order of processes was migration, selection and then reproduction. The proportions of genotypes migrating to other demes was modelled as a binomial function to yield effectively continuous Gaussian migration across the discrete array of demes, as in Mallet and Barton (1989a). Because we know that selection in this system is liable to be high (Mallet and Barton 1989b), we implemented frequency dependent selection of $2s = 0.6$ on each locus.

For each cline, we optimised its position on the transect while simultaneously stretching / compressing the cline width to fit it to a kilometre scale, until we found the maximum likelihood position and width. For the codominant locus *erato D* we estimated the likelihood of the observed number of *D* alleles. Log likelihoods were calculated using the formula:

$$logL = \sum i \ln p + (2n - i)\ln(1 - p) \qquad \text{Equation 1a}$$

where $p$ is the frequency of the dominant allele predicted from the theoretical cline, $i$ is observed number of *D* alleles, and $n$ is sample size of genotypes. Dominant loci *Cr* and *Sd* in *H. erato* as well as all loci in *H. melpomene* were fitted using the expected Hardy-Weinberg phenotype frequency obtained from the theoretical cline:

$$logL = \sum(n - i)\ln(1 - p)^2) + i\ln(p^2 + 2p(1 - p)) \qquad \text{Equation 1b}$$

where $i$ is the observed number of dominant phenotypes. The assumption of Hardy-Weinberg equilibrium was tested and found to hold for the *D* locus in *H. melpomene* (Mallet et al. 1990: p. 926).

### *S3. Implementation of interaction of iterated warning colour cline with a density trough and exogenous cline*

The dominant cline (*A*) was subject to a frequency-dependent selection of $2s = 0.5$, with a migration rate of $\sigma^2 = 30$. In the absence of any other force, the cline moves across the series of demes at a constant rate. To model a density trough across the demes, we used a cosine function in the interval 0 to 2π radians to generate a dip in which density was reduced maximally to 50% relative to the rest of the demes. To model an unlinked cline tied to the environment (i.e. one maintained by exogenous selection), we iterated a dominant allele *E*, favoured on one side of the demic array, relative to allele *e*. The exogenous gradient in selection was modelled using a logistic function:

$$f(x) = \frac{e^{b(x-a)}}{1+e^{b(x-a)}} \qquad \text{Equation 2}$$

where $a$ is the centre of the selection gradient, $b$ is the slope and $x$ is the deme number. Selection on locus $E$ across the series of demes was given by a sigmoid with a centre of 50.5 and a slope -1, with the asymptote rescaled to $s_E = 0.5$. The fitness of $EE$ genotypes was $1 - s_E f(x)$, that of $ee$ was $1 - s_E(1-f(x))$; heterozygotes $Ee$ had intermediate fitness.

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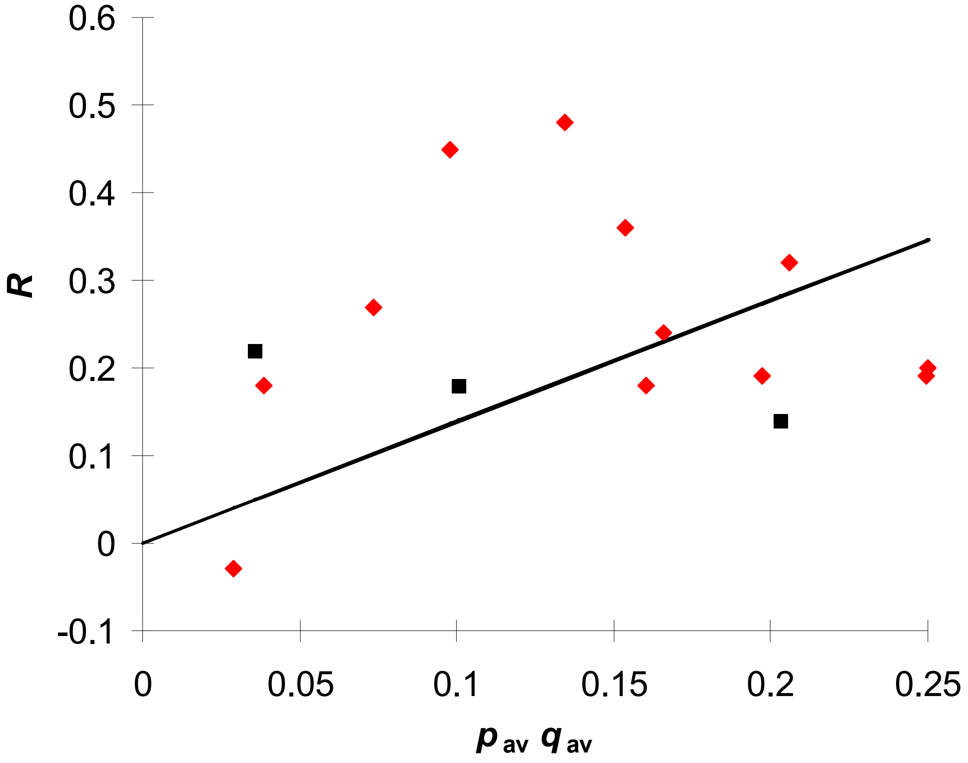

Figure S1. Least squares regression of linkage disequilibrium ($R$) for *H. erato* estimated from all three loci against the product of average allele frequencies, using only sample sizes greater than 20. 1986 values shown in red, 2011 values shown in black. The intercept was constrained to zero, with the slope then estimated as 1.38 (0.82-1.95), giving $R_{max} = 0.35$ (0.20, 0.49) when $p_{av}q_{av} = 0.25$ (the middle of the hybrid zone).

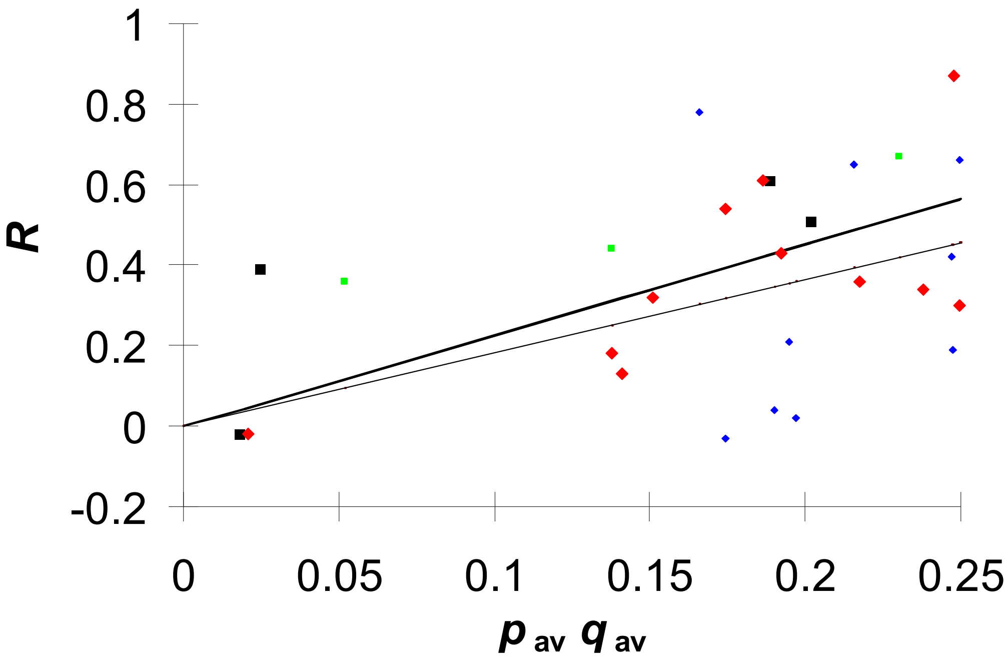

Figure S2. Least squares regression of linkage disequilibrium ($R$) for *H. melpomene* unlinked loci using sample sizes greater than 17. The estimates shown are for unlinked loci $D$ and $Yb$, with 1986 results shown in red, 2011 results shown in black. The fitted regression (heavy line) gives $R_{max} = 0.56$ (0.42-0.71) when $p_{\mathrm{av}}q_{\mathrm{av}} = 0.25$. Also shown are disequilibria between unlinked loci $b$ and $Yb$, with 1986 results in blue, 2011 results in green. Here regression (faint line) gives $R_{max} = 0.45$ (0.22-0.69) when $p_{\mathrm{av}}q_{\mathrm{av}} = 0.25$ (the middle of the hybrid zone).

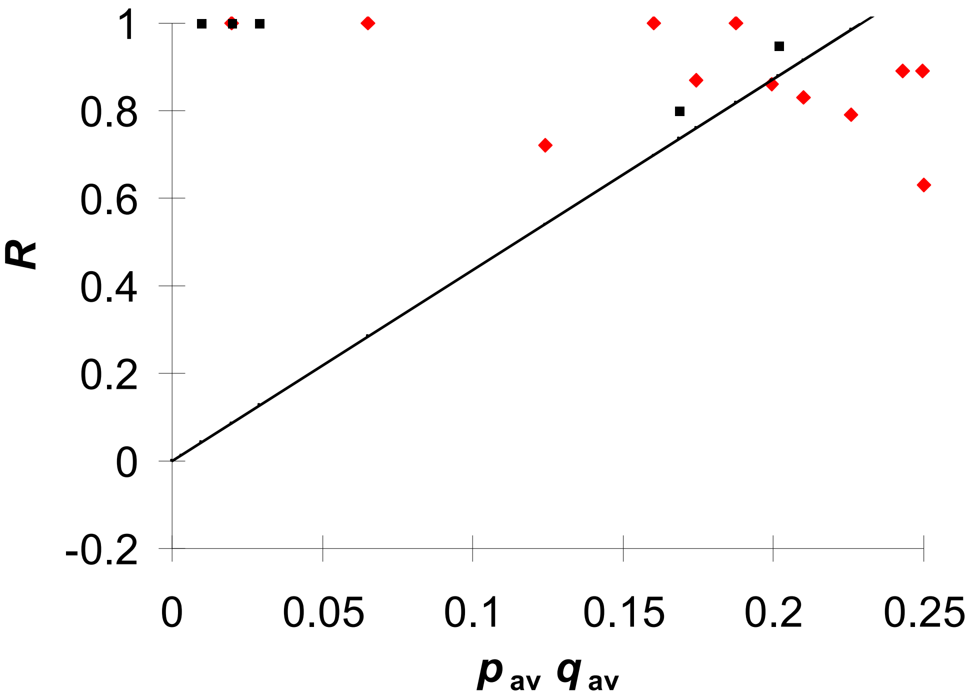

Figure S3. Linkage disequilibrium (*R*) for *H. melpomene* linked loci *N* and *Yb* plotted against the product of the average allele frequencies. 1986 values shown in red, 2011 values shown in black.

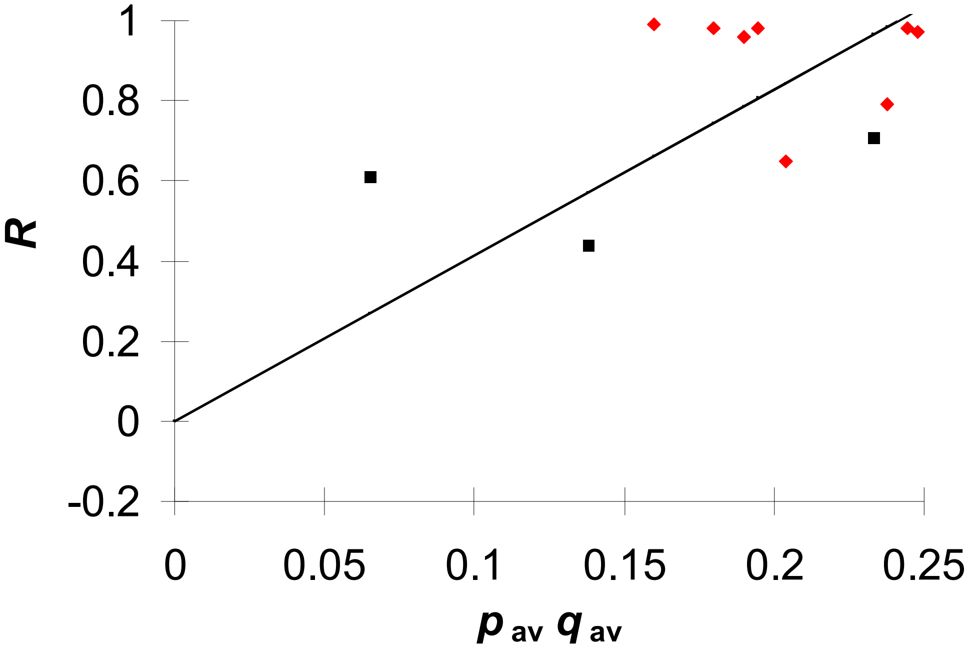

Figure S4. Linkage disequilibrium (*R*) for *H. melpomene* linked loci *b* and *D* plotted against the product of the average allele frequencies. 1986 values shown in red, 2011 values shown in black.

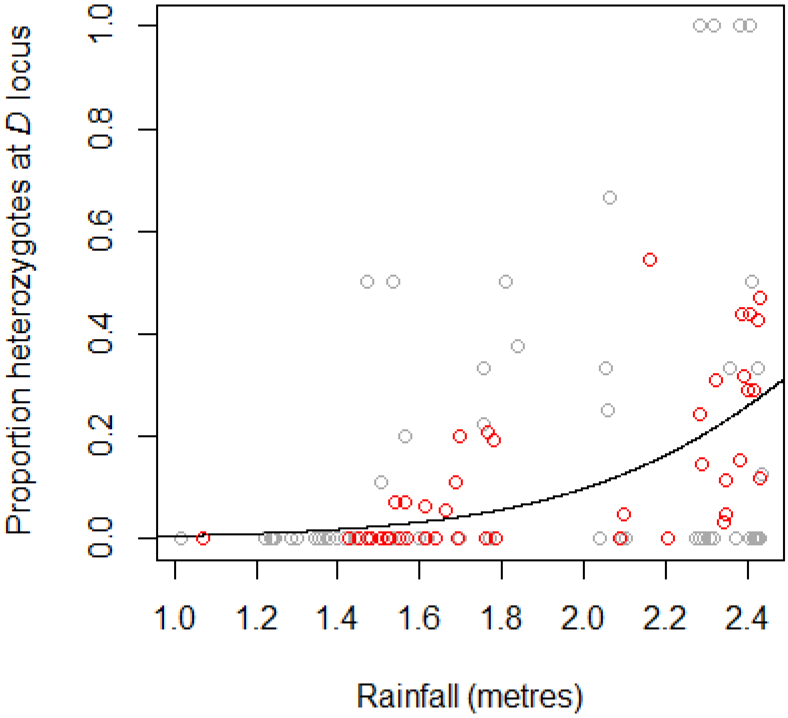

Figure S5. Rainfall plotted against proportions of heterozygotes at the *H. erato D* locus, with model predictions. Populations with sample sizes greater than 10 are shown in red.

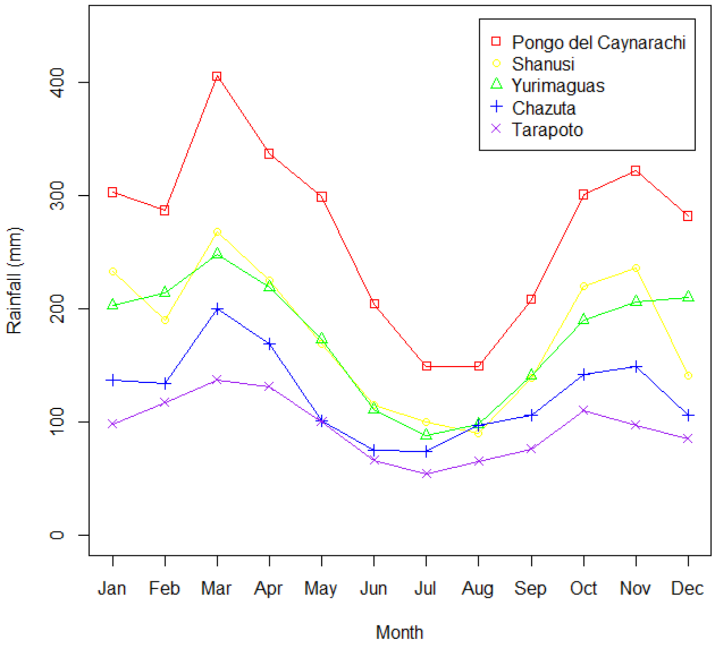

Figure S6. Monthly rainfall data at sites across the hybrid zone. Tarapoto and Chazuta fall on the Andean side of the hybrid zone, Shanusi and Yurimaguas on the Amazonian side and Pongo del Caynarachi falls in the centre of the hybrid zone.

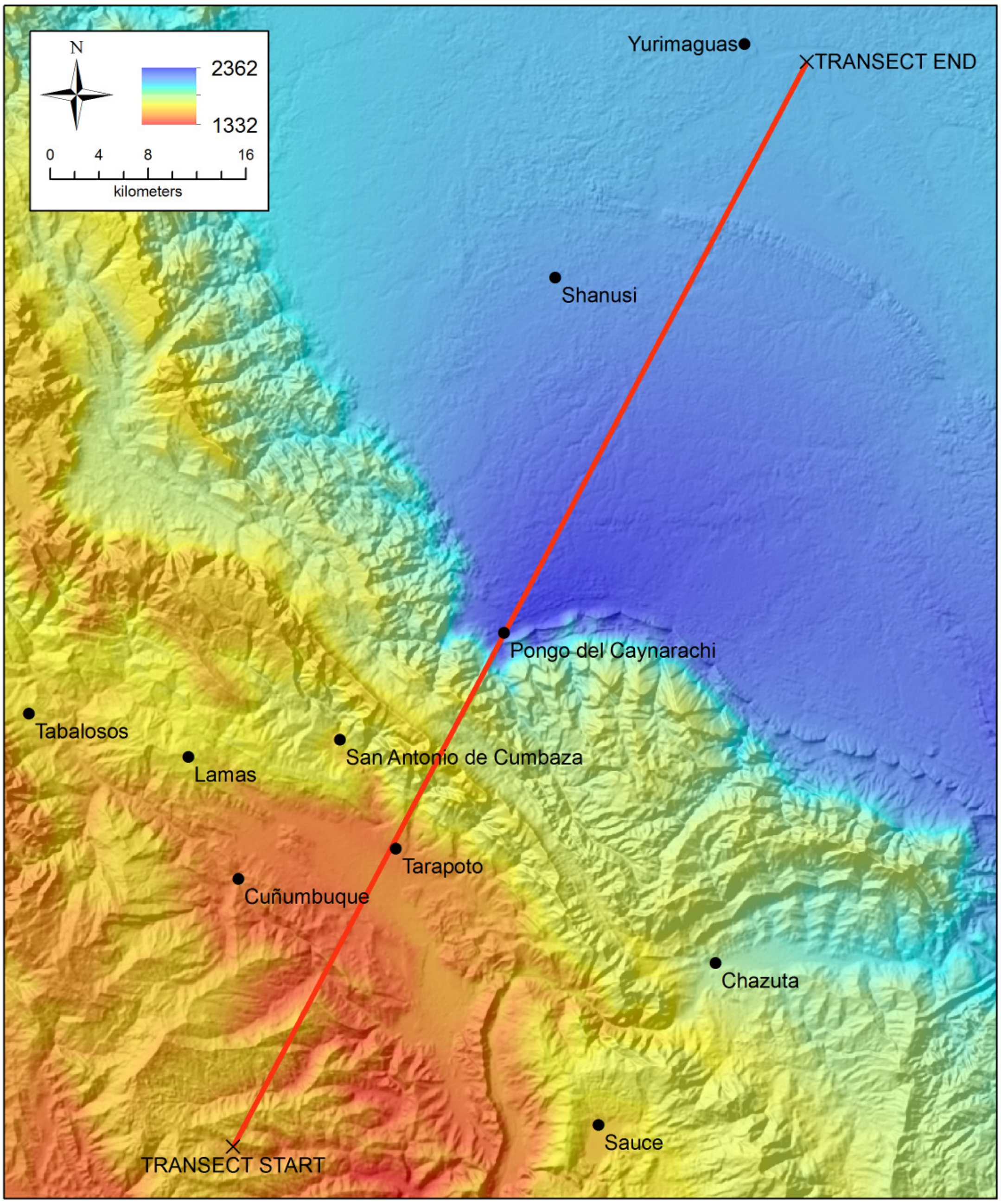

Figure S7. Gridded annual rainfall data overlaid onto a SRTM 90 metre resolution digital elevation model. The transect used in marked in red.

Table S1. Genotypic data for *Heliconius erato*. Exact coordinates: an individual GPS reading was taking for the specimen; approximate coordinate: the coordinates for the specimen were estimated, along with a measure of accuracy.

| General locality | Exact coordinates | Approximate coordinates | Accuracy | D | Cr | Sd |
|---|---|---|---|---|---|---|
| Alianza |  | S6.126642 W76.267197 | ±50m | DD | C- | S- |
| Alto Shilcayo |  | S6.448943 W76.340899 | ±920m | dd | cc | ss |
| Alto Shilcayo |  | S6.448943 W76.340899 | ±920m | dd | cc | ss |
| Alto Shilcayo |  | S6.448943 W76.340899 | ±920m | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52071 W76.28428 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52071 W76.28428 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 |  |  | dd | cc | ss |
| Bello Horizonte a Santa Elena | S6.52062 W76.28385 |  |  | dd | cc | ss |
| Biodiversidad |  | S6.46041 W76.29039 | ±100m | dd | cc | Ss |
| Bonilla | S6.22317 W76.28631 |  |  | Dd | C- | S- |
| Brisas del Paredon | S6.43048 W76.26252 |  |  | Dd | cc | ss |
| Camino a Isla Bonita | S6.45929 W76.37193 |  |  | dd | cc | ss |
| Camino a Isla Bonita | S6.45929 W76.37193 |  |  | dd | cc | ss |
| Camino a Isla Bonita | S6.45929 W76.37193 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Casa de Orlando | S6.442639 W76.335470 |  |  | dd | cc | ss |
| Cataratas de Ahuashiyacu | S6.45402 W76.31108 |  |  | dd | cc | ss |
| Cataratas de Ahuashiyacu | S6.45672 W76.30921 |  |  | dd | cc | ss |
| Cataratas de Ahuashiyacu | S6.45353 W76.31189 |  |  | dd | cc | ss |
| Cataratas de Ahuashiyacu | S6.45353 W76.31189 |  |  | dd | cc | ss |
| Cataratas de Ahuashiyacu | S6.45353 W76.31189 |  |  | dd | cc | ss |
| Cataratas de Ahuashiyacu | S6.45353 W76.31189 |  |  | dd | cc | ss |
| Cataratas de Ahuashiyacu | S6.45353 W76.31189 |  |  | dd | cc | ss |
| Chazuta | S6.56654 W76.12738 |  |  | dd | cc | ss |
| Chazuta | S6.56654 W76.12738 |  |  | dd | cc | ss |

```
# BELOW IS R CODE FOR GENERATING THEORETICAL CLINES, FITTING THOSE CLINES TO OBSERVED DATA
# USING LIKELIHOOD, AND FINDING SUPPORT LIMITS FOR DIFFERENCES IN WIDTH RATIOS BETWEEN
# CLINES.  THE CODE WAS NOT WRITTEN WITH OTHER USERS IN MIND, AND SO IS LIKELY TO BE HARD
# TO DECIPHER. ANY QUERIES SHOULD BE MADE TO NEIL ROSSER.


##################################################
####SIMULATE CLINES FOR HELICONIUS ERATO (3 LOCI)####
##################################################

#!/usr/bin/env Rscript

library(data.table)

#STARTING CONDITIONS
#Vector of demes (should be an even number)
demes<-c(1:100)
#time steps
time_step<-c(1:100)

results<-matrix(ncol=6+length(demes))
colnames(results) <- c("locus","selectionD","selectionC","selectionS","migration","generation",demes)
results<-results[-1,]

#set up the loops for the varying levels of selection /migration you want to test
for (selectionD in c(0.1)){
for (selectionC in seq(0.1,0.8,0.1)){
for (selectionS in seq(0.1,0.8,0.1)){
for (n in c(10,20,30,40)){
print(paste(c("selection =",selectionD,"migration =",n)))

#Specify the loci, gametes and possible genotypes
locus1<-c("D","d")
locus2<-c("C","c")
locus3<-c("S","s")
gametes<-c()
for(i in locus1){
for (j in locus2){
for (k in locus3){
gametes<-append(gametes,paste(i,j,k,sep=""))
}}}
genotypes<-c()
for(i in gametes){
for (j in gametes){
genotypes<-append(genotypes,paste(i,j,sep=""))}}
#starting frequency of alleles
D<-c(rep(0,length(demes)/2),rep(1,length(demes)/2))
d<-1-D
```

```
C<-c(rep(0,length(demes)/2),rep(1,length(demes)/2))
c<-1-C
S<-c(rep(0,length(demes)/2),rep(1,length(demes)/2))
s<-1-S
#selection - see for loop below
#Migration function, for n see for loop below (n is the maximum distance (= deme) that genotypes will
migrate to. k (the number of trials), is 2*n)
a<-0.5
mig<-function(i)
{((factorial(2*n))/((factorial(n-i))*(factorial(n+i))))*(a^(n-i))*((1-a)^(n+i))}

demic_freqsD<-D
demic_freqsC<-C
demic_freqsS<-S

#FOR EACH DEME IN THE VECTOR CALCULATE GENOTYPE FREQUENCIES BASED ON THE ALLELES...
freq_genotypes_demes<-matrix(nrow=length(demes), ncol=length(genotypes))
for (j in demes){
#CALCULATE GENOTYPE FREQUENCIES
genotype_freqs<-c()
for (k in genotypes){
genotype<-unlist(strsplit(k, split=""))
prop_expression<-c()
for (l in 1:length(genotype)){
if (l<length(genotype)){
prop_expression<-paste(prop_expression,genotype[l],"[",j,"]","*")
}else{
prop_expression<-paste(prop_expression,genotype[l],"[",j,"]")}}
genotype_freqs<-append(genotype_freqs,eval(parse(text=prop_expression)))}
freq_genotypes_demes[j,]<-(genotype_freqs)
}

#FOR EACH TIME STEP
for (time in time_step){
print(c("time step =",time))
#MIGRATION...
new_freq_genotypes_demes<-matrix(0,nrow=length(demes), ncol=length(genotypes))

for (i in 1:length(demes)){

#If the first deme in the array
if(i==1){
#Do the prop staying in the deme
for (j in 1:ncol(freq_genotypes_demes)){
new_freq_genotypes_demes[i,j]<-new_freq_genotypes_demes[i,j]+mig(0)*freq_genotypes_demes[i,j]}
#now do the prop migrating to the jth deme away
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
```

```
new_freq_genotypes_demes[i+k,j]<-
new_freq_genotypes_demes[i+k,j]+(mig(k)*freq_genotypes_demes[i,j])}}

#Now do the props migrating in from the imaginary demes
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
for (l in k:n){
new_freq_genotypes_demes[i+k-1,j]<-new_freq_genotypes_demes[i+k-
1,j]+(mig(l)*freq_genotypes_demes[i,j])
}}}}

#If the last deme in the array
else if(i==length(demes)){
#Do the prop staying in the deme
for (j in 1:ncol(freq_genotypes_demes)){
new_freq_genotypes_demes[i,j]<-new_freq_genotypes_demes[i,j]+mig(0)*freq_genotypes_demes[i,j]}
#now do the prop migrating to the jth deme away
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
new_freq_genotypes_demes[i-k,j]<-new_freq_genotypes_demes[i-
k,j]+(mig(k)*freq_genotypes_demes[i,j])}}
#Now do the props migrating in from the imaginary demes
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
for (l in k:n){
new_freq_genotypes_demes[(i+1)-k,j]<-new_freq_genotypes_demes[(i+1)-
k,j]+(mig(l)*freq_genotypes_demes[i,j])
}}}

#Else all other demes...
}else{
#prop staying in deme
for (j in 1:ncol(freq_genotypes_demes)){
new_freq_genotypes_demes[i,j]<-new_freq_genotypes_demes[i,j]+mig(0)*freq_genotypes_demes[i,j]}
#now do the prop migrating to the jth deme away
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
if(i+k<=length(demes)){
new_freq_genotypes_demes[i+k,j]<-
new_freq_genotypes_demes[i+k,j]+(mig(k)*freq_genotypes_demes[i,j])}
if(i-k>=1){
new_freq_genotypes_demes[i-k,j]<-new_freq_genotypes_demes[i-
k,j]+(mig(k)*freq_genotypes_demes[i,j])}}}}}

freq_genotypes_demes<-new_freq_genotypes_demes

#SELECTION
```

```
new_freq_genotypes_demes<-matrix(0,nrow=length(demes), ncol=length(genotypes))

#first calculate the fraction of each genotype that survive
for (j in 1:length(demes)){
for (k in 1:length(genotypes)){

#selection on the D locus
genotype_D<-paste(substr(genotypes[k],1,1),substr(genotypes[k],4,4),sep="")
D_DH_freqs<-c()
D_HET_freqs<-c()
D_RH_freqs<-c()
for (l in 1:length(genotypes)){
if (k != l){
genotypes_D<-c(paste((substr(genotypes[l],1,1)),substr(genotypes[l],4,4),sep=""))
if (genotypes_D=="DD"){
D_DH_freqs<-append(D_DH_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_D=="Dd"|genotypes_D=="dD"){
D_HET_freqs<-append(D_HET_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_D=="dd"){
D_RH_freqs<-append(D_RH_freqs,freq_genotypes_demes[j,l])}

D_DH_freqs<-sum(D_DH_freqs)
D_HET_freqs<-sum(D_HET_freqs)
D_RH_freqs<-sum(D_RH_freqs)

if (genotype_D=="DD"){
W_genD<-1-(selectionD*(D_RH_freqs+0.5*D_HET_freqs))
}else if (genotype_D=="Dd"|genotype_D=="dD"){
W_genD<-1-(selectionD*(0.5*D_DH_freqs+0.5*D_RH_freqs))
}else if (genotype_D=="dd"){
W_genD<-1-(selectionD*(D_DH_freqs+0.5*D_HET_freqs))}
}}

#selection on the C locus
genotype_C<-paste(substr(genotypes[k],2,2),substr(genotypes[k],5,5),sep="")
C_DH_freqs<-c()
C_HET_freqs<-c()
C_RH_freqs<-c()
for (l in 1:length(genotypes)){
if (k != l){
genotypes_C<-c(paste((substr(genotypes[l],2,2)),substr(genotypes[l],5,5),sep=""))
if (genotypes_C=="CC"){
C_DH_freqs<-append(C_DH_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_C=="Cc"|genotypes_C=="cC"){
C_HET_freqs<-append(C_HET_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_C=="cc"){
C_RH_freqs<-append(C_RH_freqs,freq_genotypes_demes[j,l])}
```

```
C_DH_freqs<-sum(C_DH_freqs)
C_HET_freqs<-sum(C_HET_freqs)
C_RH_freqs<-sum(C_RH_freqs)

if (genotype_C=="CC"){
W_genC<-1-(selectionC*(C_RH_freqs))
}else if (genotype_C=="Cc"|genotype_C=="cC"){
W_genC<-1-(selectionC*(C_RH_freqs))
}else if (genotype_C=="cc"){
W_genC<-1-(selectionC*(C_DH_freqs+C_HET_freqs))}
}}

#selection on the S locus
genotype_S<-paste(substr(genotypes[k],3,3),substr(genotypes[k],6,6),sep="")
S_DH_freqs<-c()
S_HET_freqs<-c()
S_RH_freqs<-c()
for (l in 1:length(genotypes)){
if (k != l){
genotypes_S<-c(paste((substr(genotypes[l],3,3)),substr(genotypes[l],6,6),sep=""))
if (genotypes_S=="SS"){
S_DH_freqs<-append(S_DH_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_S=="Ss"|genotypes_S=="sS"){
S_HET_freqs<-append(S_HET_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_S=="ss"){
S_RH_freqs<-append(S_RH_freqs,freq_genotypes_demes[j,l])}

S_DH_freqs<-sum(S_DH_freqs)
S_HET_freqs<-sum(S_HET_freqs)
S_RH_freqs<-sum(S_RH_freqs)

if (genotype_S=="SS"){
W_genS<-1-(selectionS*(S_RH_freqs))
}else if (genotype_S=="Ss"|genotype_S=="sS"){
W_genS<-1-(selectionS*(S_RH_freqs))
}else if (genotype_S=="ss"){
W_genS<-1-(selectionS*(S_DH_freqs+S_HET_freqs))}
}}

#now calculate the proportion surviving given the proportion surviving at each locus
new_freq_genotypes_demes[j,k]<-(W_genD*W_genC*W_genS)*freq_genotypes_demes[j,k]

}}

#Now calculate the new genotype frequencies for each deme
for (j in 1:length(demes)){
total<-sum(new_freq_genotypes_demes[j,])
for (k in 1:length(genotypes)){
```

```
new_freq_genotypes_demes[j,k]<-new_freq_genotypes_demes[j,k]/total
}}

freq_genotypes_demes<-new_freq_genotypes_demes



#calculate gametes frequencies for each deme:
new_freq_genotypes_demes<-matrix(0,nrow=length(demes), ncol=length(genotypes))
for (j in 1:length(demes)){
list_of_gametes<-c()
gamete_frequencies<-c()
for (k in 1:length(genotypes)){
genotype<-unlist(strsplit(genotypes[k],split=""))
#make a vector with all the possible gametes for that genotype..
gametes<-c()
gametes<-append(gametes,paste(genotype[1],genotype[2],genotype[3],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[2],genotype[6],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[5],genotype[3],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[5],genotype[6],sep=""))
gametes<-append(gametes,paste(genotype[4],genotype[2],genotype[3],sep=""))
gametes<-append(gametes,paste(genotype[4],genotype[2],genotype[6],sep=""))
gametes<-append(gametes,paste(genotype[4],genotype[5],genotype[3],sep=""))
gametes<-append(gametes,paste(genotype[4],genotype[5],genotype[6],sep=""))
#now make a list of the probabilities of each gametic type. These probablities are equal with no linkage.
gametic_probs<-rep(0.125,8)
gametic_freqs<-freq_genotypes_demes[j,k]*gametic_probs
list_of_gametes<-append(list_of_gametes,gametes)
gamete_frequencies<-append(gamete_frequencies,gametic_freqs)}
#Use the data.table package to get the list of unique gametes and sum their frequencies...
gamete_table<-data.frame(list_of_gametes,gamete_frequencies)
gamete_table<-data.table(gamete_table)
gamete_table<-
gamete_table[,list(gamete_frequencies=sum(gamete_frequencies)),by='list_of_gametes']

#Now calculate the genotype frequencies generated by these gametes
punnet_square<-matrix(nrow=length(gamete_table$list_of_gametes),
ncol=length(gamete_table$list_of_gametes))
rownames(punnet_square) <- gamete_table$list_of_gametes
colnames(punnet_square) <- gamete_table$list_of_gametes

for (l in 1:length(gamete_table$list_of_gametes)){
for (m in 1:length(gamete_table$list_of_gametes)){
punnet_square[l,m]<-gamete_table$gamete_frequencies[l]*gamete_table$gamete_frequencies[m]}}

colnames(new_freq_genotypes_demes) <- genotypes

for (z in 1:length(genotypes)){
```

```
genotype_freq_from_Punnet<-punnet_square[substr(genotypes[z],1,nchar(genotypes[z])/2),substr(genotypes[z],nchar(genotypes[z])/2+1,nchar(genotypes[z]))]
new_freq_genotypes_demes[j,z]<-genotype_freq_from_Punnet
}}
freq_genotypes_demes<-new_freq_genotypes_demes

#Now save the allele frequencies
newD<-c()
newC<-c()
newS<-c()

for (j in 1:length(demes)){
demicD<-c()
demicC<-c()
demicS<-c()
for (k in 1:length(genotypes)){
genotypeD<-c(paste((substr(genotypes[k],1,1)),substr(genotypes[k],4,4),sep=""))
genotypeC<-c(paste((substr(genotypes[k],2,2)),substr(genotypes[k],5,5),sep=""))
genotypeS<-c(paste((substr(genotypes[k],3,3)),substr(genotypes[k],6,6),sep=""))

if(genotypeD=="DD"){
demicD<-append(demicD,new_freq_genotypes_demes[j,k])}
if(genotypeD=="Dd"|genotypeD=="dD"){
demicD<-append(demicD,new_freq_genotypes_demes[j,k]/2)}

if(genotypeS=="SS"){
demicS<-append(demicS,new_freq_genotypes_demes[j,k])}
if(genotypeS=="Ss"|genotypeS=="sS"){
demicS<-append(demicS,new_freq_genotypes_demes[j,k]/2)}

if(genotypeC=="CC"){
demicC<-append(demicC,new_freq_genotypes_demes[j,k])}
if(genotypeC=="Cc"|genotypeC=="cC"){
demicC<-append(demicC,new_freq_genotypes_demes[j,k]/2)}

}
newD<-append(newD,sum(demicD))
newC<-append(newC,sum(demicC))
newS<-append(newS,sum(demicS))}

D<-newD
d<-1-D
C<-newC
c<-1-C
S<-newS
s<-1-S
```

```
demic_freqsD<-rbind(demic_freqsD,D)
demic_freqsC<-rbind(demic_freqsC,C)
demic_freqsS<-rbind(demic_freqsS,S)

}

results<-rbind(results,c("D",selectionD,selectionC,selectionS,n,max(time),demic_freqsD[max(time)+1,]))
results<-rbind(results,c("C",selectionD,selectionC,selectionS,n,max(time),demic_freqsC[max(time)+1,]))
results<-rbind(results,c("S",selectionD,selectionC,selectionS,n,max(time),demic_freqsS[max(time)+1,]))

}}}}

write.csv(results,paste("results_selectionD_",selectionD,".csv",sep=""))


#########################################################
####SIMULATED CLINES FOR HELICONIUS MELPOMENE (4 LOCI)###
#########################################################

#!/usr/bin/env Rscript

library(data.table)

#STARTING CONDITIONS
#Vector of demes (should be an even number)
demes<-c(1:10)
#time steps
time_step<-c(1:2)

results<-matrix(ncol=9+length(demes))
colnames(results) <-
c("locus","selectionB","selectionD","selectionN","selectionY","migration","recomb_r_BD","recomb_r_N
Y","n_generations",demes)
results<-results[-1,]

#set up the loops for the varying levels of selection /migration you want to test
for (selectionB in seq(0.6,0.7,0.1)){
for (selectionD in seq(0.6,0.7,0.1)){
for (selectionN in seq(0.6,0.7,0.1)){
for (selectionY in seq(0.6,0.7,0.1)){
for (n in c(1,2)){
for (recomb_rate_BD in c(0.03,0.135)){
for (recomb_rate_NY in c(0.03,0.135)){

print(paste(c("selection =",selectionB)))

#calculate the gamete weights for the specified recombination rates
```

```
recomb_at_niether<-((1-recomb_rate_BD)*(1-recomb_rate_NY))/4
recomb_at_BD<-(recomb_rate_BD*(1-recomb_rate_NY))/4
recomb_at_NY<-((1-recomb_rate_BD)*recomb_rate_NY)/4
recomb_at_both<-(recomb_rate_BD*recomb_rate_NY)/4

#Specify the loci, gametes and possible genotypes
locus1<-c("B","b")
locus2<-c("D","d")
locus3<-c("N","n")
locus4<-c("Y","y")
gametes<-c()
for(i in locus1){
for (j in locus2){
for (k in locus3){
for (l in locus4){
gametes<-append(gametes,paste(i,j,k,l,sep=""))
}}}}
genotypes<-c()
for(i in gametes){
for (j in gametes){
genotypes<-append(genotypes,paste(i,j,sep=""))}}
#starting frequency of alleles

B_all<-c(rep(1,length(demes)/2),rep(0,length(demes)/2))
b_all<-1-B_all
D_all<-c(rep(0,length(demes)/2),rep(1,length(demes)/2))
d_all<-1-D_all
N_all<-c(rep(0,length(demes)/2),rep(1,length(demes)/2))
n_all<-1-N_all
Y_all<-c(rep(0,length(demes)/2),rep(1,length(demes)/2))
y_all<-1-Y_all

#Migration function. n is the maximum distance (= deme) that genotypes will migrate to. k (the number of trials), is 2*n
a<-0.5
mig<-function(i)
{((factorial(2*n))/((factorial(n-i))*(factorial(n+i))))*(a^(n-i))*((1-a)^(n+i))}
#Find max slope of simulated cline function
max_slope <- function(x) {
slopes<-c()
for (i in 1:(length(x)-1)){
slopes<-append(slopes,x[i+1]-x[i])}
return(max(slopes))
}

demic_freqsB<-B_all
demic_freqsD<-D_all
demic_freqsN<-N_all
```

```
demic_freqsY<-Y_all

#FOR EACH DEME IN THE VECTOR CALCULATE GENOTYPE FREQUENCIES BASED ON THE ALLELES...
freq_genotypes_demes<-matrix(nrow=length(demes), ncol=length(genotypes))
for (j in demes){
#CALCULATE GENOTYPE FREQUENCIES
genotype_freqs<-c()
for (k in genotypes){
genotype<-unlist(strsplit(k, split=""))
prop_expression<-c()
for (l in 1:length(genotype)){
if (l<length(genotype)){
prop_expression<-paste(prop_expression,genotype[l],"_all","[",j,"]","*",sep="")
}else{
prop_expression<-paste(prop_expression,genotype[l],"_all","[",j,"]",sep="")}}
genotype_freqs<-append(genotype_freqs,eval(parse(text=prop_expression)))}
freq_genotypes_demes[j,]<-(genotype_freqs)
}

#FOR EACH TIME STEP
for (time in time_step){
print(c("time step =",time))
#MIGRATION...
new_freq_genotypes_demes<-matrix(0,nrow=length(demes), ncol=length(genotypes))

for (i in 1:length(demes)){

#If the first deme in the array
if(i==1){
#Do the prop staying in the deme
for (j in 1:ncol(freq_genotypes_demes)){
new_freq_genotypes_demes[i,j]<-new_freq_genotypes_demes[i,j]+mig(0)*freq_genotypes_demes[i,j]}
#now do the prop migrating to the jth deme away
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
new_freq_genotypes_demes[i+k,j]<-
new_freq_genotypes_demes[i+k,j]+(mig(k)*freq_genotypes_demes[i,j])}}

#Now do the props migrating in from the imaginary demes
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
for (l in k:n){
new_freq_genotypes_demes[i+k-1,j]<-new_freq_genotypes_demes[i+k-
1,j]+(mig(l)*freq_genotypes_demes[i,j])
}}}}

#If the last deme in the array
else if(i==length(demes)){
```

```
#Do the prop staying in the deme
for (j in 1:ncol(freq_genotypes_demes)){
new_freq_genotypes_demes[i,j]<-new_freq_genotypes_demes[i,j]+mig(0)*freq_genotypes_demes[i,j]}
#now do the prop migrating to the jth deme away
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
new_freq_genotypes_demes[i-k,j]<-new_freq_genotypes_demes[i-
k,j]+(mig(k)*freq_genotypes_demes[i,j])}}
#Now do the props migrating in from the imaginary demes
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
for (l in k:n){
new_freq_genotypes_demes[(i+1)-k,j]<-new_freq_genotypes_demes[(i+1)-
k,j]+(mig(l)*freq_genotypes_demes[i,j])
}}}

#Else all other demes...
}else{
#prop staying in deme
for (j in 1:ncol(freq_genotypes_demes)){
new_freq_genotypes_demes[i,j]<-new_freq_genotypes_demes[i,j]+mig(0)*freq_genotypes_demes[i,j]}
#now do the prop migrating to the jth deme away
for (j in 1:ncol(freq_genotypes_demes)){
for (k in 1:n){
if(i+k<=length(demes)){
new_freq_genotypes_demes[i+k,j]<-
new_freq_genotypes_demes[i+k,j]+(mig(k)*freq_genotypes_demes[i,j])}
if(i-k>=1){
new_freq_genotypes_demes[i-k,j]<-new_freq_genotypes_demes[i-
k,j]+(mig(k)*freq_genotypes_demes[i,j])}}}}}

freq_genotypes_demes<-new_freq_genotypes_demes

#SELECTION

new_freq_genotypes_demes<-matrix(0,nrow=length(demes), ncol=length(genotypes))

#first calculate the fraction of each genotype that survive
for (j in 1:length(demes)){
for (k in 1:length(genotypes)){

#selection on the B locus
genotype_B<-paste(substr(genotypes[k],1,1),substr(genotypes[k],5,5),sep="")
B_DH_freqs<-c()
B_HET_freqs<-c()
B_RH_freqs<-c()
for (l in 1:length(genotypes)){
if (k != l){
```

```
genotypes_B<-c(paste((substr(genotypes[l],1,1)),substr(genotypes[l],5,5),sep=""))
if (genotypes_B=="BB"){
B_DH_freqs<-append(B_DH_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_B=="Bb"|genotypes_B=="bB"){
B_HET_freqs<-append(B_HET_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_B=="bb"){
B_RH_freqs<-append(B_RH_freqs,freq_genotypes_demes[j,l])}

B_DH_freqs<-sum(B_DH_freqs)
B_HET_freqs<-sum(B_HET_freqs)
B_RH_freqs<-sum(B_RH_freqs)

if (genotype_B=="BB"){
W_genB<-1-(selectionB*(B_RH_freqs))
}else if (genotype_B=="Bb"|genotype_B=="bB"){
W_genB<-1-(selectionB*(B_RH_freqs))
}else if (genotype_B=="bb"){
W_genB<-1-(selectionB*(B_DH_freqs+B_HET_freqs))}
}}

#selection on the D locus
genotype_D<-paste(substr(genotypes[k],2,2),substr(genotypes[k],6,6),sep="")
D_DH_freqs<-c()
D_HET_freqs<-c()
D_RH_freqs<-c()
for (l in 1:length(genotypes)){
if (k != l){
genotypes_D<-c(paste((substr(genotypes[l],2,2)),substr(genotypes[l],6,6),sep=""))
if (genotypes_D=="DD"){
D_DH_freqs<-append(D_DH_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_D=="Dd"|genotypes_D=="dD"){
D_HET_freqs<-append(D_HET_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_D=="dd"){
D_RH_freqs<-append(D_RH_freqs,freq_genotypes_demes[j,l])}

D_DH_freqs<-sum(D_DH_freqs)
D_HET_freqs<-sum(D_HET_freqs)
D_RH_freqs<-sum(D_RH_freqs)

if (genotype_D=="DD"){
W_genD<-1-(selectionD*(D_RH_freqs))
}else if (genotype_D=="Dd"|genotype_D=="dD"){
W_genD<-1-(selectionD*(D_RH_freqs))
}else if (genotype_D=="dd"){
W_genD<-1-(selectionD*(D_DH_freqs+D_HET_freqs))}
}}

#selection on the N locus
```

```
genotype_N<-paste(substr(genotypes[k],3,3),substr(genotypes[k],7,7),sep="")
N_DH_freqs<-c()
N_HET_freqs<-c()
N_RH_freqs<-c()
for (l in 1:length(genotypes)){
if (k != l){
genotypes_N<-c(paste((substr(genotypes[l],3,3)),substr(genotypes[l],7,7),sep=""))
if (genotypes_N=="NN"){
N_DH_freqs<-append(N_DH_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_N=="Nn"|genotypes_N=="nN"){
N_HET_freqs<-append(N_HET_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_N=="nn"){
N_RH_freqs<-append(N_RH_freqs,freq_genotypes_demes[j,l])}

N_DH_freqs<-sum(N_DH_freqs)
N_HET_freqs<-sum(N_HET_freqs)
N_RH_freqs<-sum(N_RH_freqs)

if (genotype_N=="NN"){
W_genN<-1-(selectionN*(N_RH_freqs))
}else if (genotype_N=="Nn"|genotype_N=="nN"){
W_genN<-1-(selectionN*(N_RH_freqs))
}else if (genotype_N=="nn"){
W_genN<-1-(selectionN*(N_DH_freqs+N_HET_freqs))}
}}

#selection on the Y locus
genotype_Y<-paste(substr(genotypes[k],4,4),substr(genotypes[k],8,8),sep="")
Y_DH_freqs<-c()
Y_HET_freqs<-c()
Y_RH_freqs<-c()
for (l in 1:length(genotypes)){
if (k != l){
genotypes_Y<-c(paste((substr(genotypes[l],4,4)),substr(genotypes[l],8,8),sep=""))
if (genotypes_Y=="YY"){
Y_DH_freqs<-append(Y_DH_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_Y=="Yy"|genotypes_Y=="yY"){
Y_HET_freqs<-append(Y_HET_freqs,freq_genotypes_demes[j,l])
}else if (genotypes_Y=="yy"){
Y_RH_freqs<-append(Y_RH_freqs,freq_genotypes_demes[j,l])}

Y_DH_freqs<-sum(Y_DH_freqs)
Y_HET_freqs<-sum(Y_HET_freqs)
Y_RH_freqs<-sum(Y_RH_freqs)

if (genotype_Y=="YY"){
W_genY<-1-(selectionY*(Y_RH_freqs))
}else if (genotype_Y=="Yy"|genotype_Y=="yY"){
```

```
W_genY<-1-(selectionY*(Y_RH_freqs))
}else if (genotype_Y=="yy"){
W_genY<-1-(selectionY*(Y_DH_freqs+Y_HET_freqs))}
}}

#now calculate the proportion surviving given the proportion surviving at each locus
new_freq_genotypes_demes[j,k]<-(W_genB*W_genD*W_genN*W_genY)*freq_genotypes_demes[j,k]

}}

#Now calculate the new genotype frequencies for each deme
for (j in 1:length(demes)){
total<-sum(new_freq_genotypes_demes[j,])
for (k in 1:length(genotypes)){
new_freq_genotypes_demes[j,k]<-new_freq_genotypes_demes[j,k]/total
}}

freq_genotypes_demes<-new_freq_genotypes_demes

#calculate gametes frequencies for each deme:
new_freq_genotypes_demes<-matrix(0,nrow=length(demes), ncol=length(genotypes))
for (j in 1:length(demes)){
list_of_gametes<-c()
gamete_frequencies<-c()
for (k in 1:length(genotypes)){
genotype<-unlist(strsplit(genotypes[k],split=""))
#make a vector with all the possible gametes for that genotype..
gametes<-c()
gametes<-append(gametes,paste(genotype[1],genotype[2],genotype[3],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[2],genotype[3],genotype[8],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[2],genotype[7],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[2],genotype[7],genotype[8],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[6],genotype[3],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[6],genotype[3],genotype[8],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[6],genotype[7],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[1],genotype[6],genotype[7],genotype[8],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[2],genotype[3],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[2],genotype[3],genotype[8],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[2],genotype[7],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[2],genotype[7],genotype[8],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[6],genotype[3],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[6],genotype[3],genotype[8],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[6],genotype[7],genotype[4],sep=""))
gametes<-append(gametes,paste(genotype[5],genotype[6],genotype[7],genotype[8],sep=""))

#now make a list of the probabilities of each gametic type.
genotype_R<-
c(paste(genotype[1],1,sep=""),paste(genotype[2],2,sep=""),paste(genotype[3],3,sep=""),paste(genotype
```

```
[4],4,sep=""),paste(genotype[5],5,sep=""),paste(genotype[6],6,sep=""),paste(genotype[7],7,sep=""),past
e(genotype[8],8,sep=""))
#make a vector with all the possible gametes for that genotype..
gametes_R<-c()
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[2],genotype_R[3],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[2],genotype_R[3],genotype_R[8],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[2],genotype_R[7],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[2],genotype_R[7],genotype_R[8],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[6],genotype_R[3],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[6],genotype_R[3],genotype_R[8],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[6],genotype_R[7],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[1],genotype_R[6],genotype_R[7],genotype_R[8],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[2],genotype_R[3],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[2],genotype_R[3],genotype_R[8],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[2],genotype_R[7],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[2],genotype_R[7],genotype_R[8],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[6],genotype_R[3],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[6],genotype_R[3],genotype_R[8],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[6],genotype_R[7],genotype_R[4],sep=""))
gametes_R<-
append(gametes_R,paste(genotype_R[5],genotype_R[6],genotype_R[7],genotype_R[8],sep=""))

gametic_probs<-c()

genotype_DB_pos1<-paste(genotype_R[1],genotype_R[2],sep="")
genotype_DB_pos2<-paste(genotype_R[5],genotype_R[6],sep="")
genotype_NY_pos1<-paste(genotype_R[3],genotype_R[4],sep="")
genotype_NY_pos2<-paste(genotype_R[7],genotype_R[8],sep="")

for (i in 1:length(gametes_R)){
gamete_split<-unlist(strsplit(gametes_R[i],split=""))
gamete_DB<-paste(gamete_split[1],gamete_split[2],gamete_split[3],gamete_split[4],sep="")
gamete_NY<-paste(gamete_split[5],gamete_split[6],gamete_split[7],gamete_split[8],sep="")
```

```
if ((gamete_DB==genotype_DB_pos1|gamete_DB==genotype_DB_pos2) &
(gamete_NY==genotype_NY_pos1|gamete_NY==genotype_NY_pos2)){
gametic_probs<-append(gametic_probs,recomb_at_niether)
}else if ((gamete_DB!=genotype_DB_pos1|gamete_DB!=genotype_DB_pos2) &
(gamete_NY==genotype_NY_pos1|gamete_NY==genotype_NY_pos2)){
gametic_probs<-append(gametic_probs,recomb_at_BD)
}else if ((gamete_DB==genotype_DB_pos1|gamete_DB==genotype_DB_pos2) &
(gamete_NY!=genotype_NY_pos1|gamete_NY!=genotype_NY_pos2)){
gametic_probs<-append(gametic_probs,recomb_at_NY)
}else if ((gamete_DB!=genotype_DB_pos1|gamete_DB!=genotype_DB_pos2) &
(gamete_NY!=genotype_NY_pos1|gamete_NY!=genotype_NY_pos2)){
gametic_probs<-append(gametic_probs,recomb_at_both)
}}

gametic_freqs<-freq_genotypes_demes[j,k]*gametic_probs
list_of_gametes<-append(list_of_gametes,gametes)
gamete_frequencies<-append(gamete_frequencies,gametic_freqs)}
#Use the data.table package to get the list of unique gametes and sum their frequencies...
gamete_table<-data.frame(list_of_gametes,gamete_frequencies)
gamete_table<-data.table(gamete_table)
gamete_table<-
gamete_table[,list(gamete_frequencies=sum(gamete_frequencies)),by='list_of_gametes']

#Now calculate the genotype frequencies generated by these gametes
punnet_square<-matrix(nrow=length(gamete_table$list_of_gametes),
ncol=length(gamete_table$list_of_gametes))
rownames(punnet_square) <- gamete_table$list_of_gametes
colnames(punnet_square) <- gamete_table$list_of_gametes

for (l in 1:length(gamete_table$list_of_gametes)){
for (m in 1:length(gamete_table$list_of_gametes)){
punnet_square[l,m]<-gamete_table$gamete_frequencies[l]*gamete_table$gamete_frequencies[m]}}

colnames(new_freq_genotypes_demes) <- genotypes

for (z in 1:length(genotypes)){

genotype_freq_from_Punnet<-
punnet_square[substr(genotypes[z],1,nchar(genotypes[z])/2),substr(genotypes[z],nchar(genotypes[z])/2
+1,nchar(genotypes[z]))]
new_freq_genotypes_demes[j,z]<-genotype_freq_from_Punnet
}}
freq_genotypes_demes<-new_freq_genotypes_demes

#Now save the allele frequencies
newB<-c()
newD<-c()
```

```
newN<-c()
newY<-c()

for (j in 1:length(demes)){
demicB<-c()
demicD<-c()
demicN<-c()
demicY<-c()
for (k in 1:length(genotypes)){
genotypeB<-c(paste((substr(genotypes[k],1,1)),substr(genotypes[k],5,5),sep=""))
genotypeD<-c(paste((substr(genotypes[k],2,2)),substr(genotypes[k],6,6),sep=""))
genotypeN<-c(paste((substr(genotypes[k],3,3)),substr(genotypes[k],7,7),sep=""))
genotypeY<-c(paste((substr(genotypes[k],4,4)),substr(genotypes[k],8,8),sep=""))

if(genotypeB=="BB"){
demicB<-append(demicB,new_freq_genotypes_demes[j,k])}
if(genotypeB=="Bb"|genotypeB=="bB"){
demicB<-append(demicB,new_freq_genotypes_demes[j,k]/2)}

if(genotypeD=="DD"){
demicD<-append(demicD,new_freq_genotypes_demes[j,k])}
if(genotypeD=="Dd"|genotypeD=="dD"){
demicD<-append(demicD,new_freq_genotypes_demes[j,k]/2)}

if(genotypeN=="NN"){
demicN<-append(demicN,new_freq_genotypes_demes[j,k])}
if(genotypeN=="Nn"|genotypeN=="nN"){
demicN<-append(demicN,new_freq_genotypes_demes[j,k]/2)}

if(genotypeY=="YY"){
demicY<-append(demicY,new_freq_genotypes_demes[j,k])}
if(genotypeY=="Yy"|genotypeY=="yY"){
demicY<-append(demicY,new_freq_genotypes_demes[j,k]/2)}

}
newB<-append(newB,sum(demicB))
newD<-append(newD,sum(demicD))
newN<-append(newN,sum(demicN))
newY<-append(newY,sum(demicY))}

B_all<-newB
b_all<-1-B_all
D_all<-newD
d_all<-1-D_all
N_all<-newN
n_all<-1-N_all
Y_all<-newY
y_all<-1-Y_all
```

```
demic_freqsB<-rbind(demic_freqsB,B_all)
demic_freqsD<-rbind(demic_freqsD,D_all)
demic_freqsN<-rbind(demic_freqsN,N_all)
demic_freqsY<-rbind(demic_freqsY,Y_all)
}

results<-rbind(results,c("B",selectionB,selectionD,selectionN,selectionY,n,recomb_rate_BD,recomb_rate_NY,max(time),demic_freqsB[max(time)+1,]))
results<-rbind(results,c("D",selectionB,selectionD,selectionN,selectionY,n,recomb_rate_BD,recomb_rate_NY,max(time),demic_freqsD[max(time)+1,]))
results<-rbind(results,c("N",selectionB,selectionD,selectionN,selectionY,n,recomb_rate_BD,recomb_rate_NY,max(time),demic_freqsN[max(time)+1,]))
results<-rbind(results,c("Y",selectionB,selectionD,selectionN,selectionY,n,recomb_rate_BD,recomb_rate_NY,max(time),demic_freqsY[max(time)+1,]))

}}}}}}

write.csv(results,"results_melpomene.csv")


##############################################################################
###USE LIKELIHOOD TO FIT THE SIMULATED ERATO CLINES TO THE OBSERVED  DATA###
##############################################################################

library(akima)

###likelihood functions to calculate the likelihoods for each cline separately;
func_likelihood_ERATO_LIKE_D <- function(x) {
		freqs_D <- aspline((x[2]*pred_D$km)+x[1], pred_D$freq, xout=obs$km, degree=10)
 p_D <- freqs_D$y
 p_D[p_D==0] <- 1e-5
 p_D[p_D==1] <- 1-1e-5
 likelihood<-sum((log(p_D^y_D))+ log((1-p_D)^(k_D-y_D)))
 return(likelihood)
		}

func_likelihood_ERATO_LIKE_C <- function(x) {
		freqs_C <- aspline((x[2]*pred_C$km)+x[1], pred_C$freq, xout=obs$km, degree=10)
 p_C <- ((freqs_C$y*freqs_C$y)+(2*(freqs_C$y*(1-freqs_C$y))))
 p_C[p_C==0] <- 1e-55
 p_C[p_C==1] <- 1-1e-5
 likelihood<-sum((log(p_C^y_C))+ log((1-p_C)^(k_C-y_C)))
 return(likelihood)
```

```
	}

func_likelihood_ERATO_LIKE_S <- function(x) {
	freqs_S <- aspline((x[2]*pred_S$km)+x[1], pred_S$freq, xout=obs$km, degree=10)
  p_S <- ((freqs_S$y*freqs_S$y)+(2*(freqs_S$y*(1-freqs_S$y))))
  p_S[p_S==0] <- 1e-55
  p_S[p_S==1] <- 1-1e-5
  likelihood<-sum((log(p_S^y_S))+ log((1-p_S)^(k_S-y_S)))
  return(likelihood)
	}

# function to calculate the likelihood of the three clines fitted simultanously:

#THIS VERSION ALLOWS THE POSITIONS OF THE CLINES TO MOVE INDEPENDENTLY and the stretch factor to change..

# requires vector x  with SIX values(THREE constants that is added to the km pos of the predicted values to make them match up with the observed data, AND THREE stretch factors),

# and then for each locus need to have the following data loaded up:
# pred_km (vector; km positions (demes) of simulated data), pred_freqs (vector; predicted frequency of dominant PHENOTYPE for demes), obs_km (vector; observed km positions),
# k (vector; n trials in observed data), y (vector; n successes in observed data)

#do it for the D locus, ussing number of D alleles and expected proportion of D alleles

#Find max slope of simulated cline function
max_slope <- function(x) {
slopes<-c()
for (i in 1:(length(x)-1)){
slopes<-append(slopes,x[i+1]-x[i])}
return(max(slopes))
}

#observed data
obsJM <- read.csv("erato1990.csv", header=T, sep=",")
obsNR <- read.csv("erato2011.csv", header=T, sep=",")
combined <- read.csv("erato_combined.csv", header=T, sep=",")
predicted_all_data <- read.csv("erato_sim_results.csv", header=T, sep=",")
predicted_all_data <- subset(predicted_all_data, selectionD==0.6 & selectionC == 0.6 & selectionS == 0.6)

#Approximate point of the middle of the hybrid zone on the transect (this is used as a starting point in the optimization algorithm) (123.57 is Mallet 1990 estimated centre of D cline).
approx_mid_point<-123.57

#change this to the date set you want to analyse
obs<-combined
```

```
obs <- obs[order(obs$km),]

#Subset the D locus
predicted_D<-subset(predicted_all_data, predicted_all_data$locus == "D")
rownames(predicted_D) <- seq(length=nrow(predicted_D))
#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_D<-predicted_D[7:ncol(predicted_D)]
demes<-c(1:ncol(predicted_for_loops_D))

k_D <- obs$total_alleles ## total number of gene copies sampled
y_D <- obs$n_D_alleles  ## number of successes

#Subset the C locus
predicted_C<-subset(predicted_all_data, predicted_all_data$locus == "C")
rownames(predicted_C) <- seq(length=nrow(predicted_C))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_C<-predicted_C[7:ncol(predicted_C)]
demes<-c(1:ncol(predicted_for_loops_C))

k_C <- obs$total_alleles/2 ## total number individuals
y_C <- k_C-(obs$n_cc_individuals)  ## total number of C- individuals

#Subset the S locus
predicted_S<-subset(predicted_all_data, predicted_all_data$locus == "S")
rownames(predicted_S) <- seq(length=nrow(predicted_S))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_S<-predicted_S[7:ncol(predicted_S)]
demes<-c(1:ncol(predicted_for_loops_S))

k_S <- obs$total_alleles/2 ## total number individuals
y_S <- k_S-(obs$n_ss_individuals)  ## total number of C- individuals

#Now loop through all the parameter combinations, calculate the likelihood and return
likelihoods<-c()
likelihoods_D<-c()
likelihoods_C<-c()
likelihoods_S<-c()
positions_D<-c()
positions_C<-c()
positions_S<-c()
stretch_factors_D<-c()
stretch_factors_C<-c()
stretch_factors_S<-c()
```

```
D_centres<-c()
C_centres<-c()
S_centres<-c()
D_cline_widths<-c()
C_cline_widths<-c()
S_cline_widths<-c()
D_max_slope<-c()
C_max_slope<-c()
S_max_slope<-c()

for (i in 1:nrow(predicted_D)){

pred_D <- data.frame(demes,t(predicted_for_loops_D[i,]))
pred_C <- data.frame(demes,t(predicted_for_loops_C[i,]))
pred_S <- data.frame(demes,t(predicted_for_loops_S[i,]))

names(pred_D) <- c("km_D","freq_D")
names(pred_C) <- c("km_C","freq_C")
names(pred_S) <- c("km_S","freq_S")

#optimisation algorithm,
# starting parameters = 1) align the approx middle of the hybrid zone with the middle of the simulated
cline, and 2) using 1 as the stretch factor (i.e. no stretch: less than 1 squeezes the cline together, greater
than 1 pulls it apart).
approx_centre_sim_D<-which.min(abs(pred_D$freq_D-0.5))
starting_param_1<-approx_mid_point-approx_centre_sim_D  #this find the difference between the
observed data and simulated data using the D locus, and uses this as a starting point for each of the loci
likelihood_D <- optim(par = c(starting_param_1,1), func_likelihood_ERATO_LIKE_D, NULL,
control=list(fnscale=-1))
likelihood_C <- optim(par = c(starting_param_1,1), func_likelihood_ERATO_LIKE_C, NULL,
control=list(fnscale=-1))
likelihood_S <- optim(par = c(starting_param_1,1), func_likelihood_ERATO_LIKE_S, NULL,
control=list(fnscale=-1))
likelihood<-sum(likelihood_D$value,likelihood_C$value,likelihood_S$value)
#find middle of clines and widths
#this is a clunky bit to find the centre of the cline; aspline doesn't seem to be able to find the x value for
a given y value, only the other way round, so had to do it like this
interp.dat<-aspline((likelihood_D$par[2]*pred_D$km)+likelihood_D$par[1], pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
D_cline_max_slope<-max_slope(interp.dat$y)
D_cline_width<-(1/D_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)
interp.dat<-aspline((likelihood_C$par[2]*pred_C$km)+likelihood_C$par[1], pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
C_cline_max_slope<-max_slope(interp.dat$y)
```

```
C_cline_width<-(1/C_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in the interp.dat fine scale)
interp.dat<-aspline((likelihood_S$par[2]*pred_S$km)+likelihood_S$par[1], pred_S$freq, xout= seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
S_cline_max_slope<-max_slope(interp.dat$y)
S_cline_width<-(1/S_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in the interp.dat fine scale)

#append results to results vectors..
likelihoods<-append(likelihoods,likelihood)
likelihoods_D<-append(likelihoods_D,likelihood_D$value)
likelihoods_C<-append(likelihoods_C,likelihood_C$value)
likelihoods_S<-append(likelihoods_S,likelihood_S$value)
positions_D<-append(positions_D,likelihood_D$par[1])
positions_C<-append(positions_C,likelihood_C$par[1])
positions_S<-append(positions_S,likelihood_S$par[1])
stretch_factors_D<-append(stretch_factors_D,likelihood_D$par[2])
stretch_factors_C<-append(stretch_factors_C,likelihood_C$par[2])
stretch_factors_S<-append(stretch_factors_S,likelihood_S$par[2])
D_centres<-append(D_centres,D_cline_centre)
C_centres<-append(C_centres,C_cline_centre)
S_centres<-append(S_centres,S_cline_centre)
D_cline_widths<-append(D_cline_widths,D_cline_width)
C_cline_widths<-append(C_cline_widths,C_cline_width)
S_cline_widths<-append(S_cline_widths,S_cline_width)
D_max_slope<-append(D_max_slope,D_cline_max_slope*100)#times 100 to bring on to km scale
C_max_slope<-append(C_max_slope,C_cline_max_slope*100)#times 100 to bring on to km scale
S_max_slope<-append(S_max_slope,S_cline_max_slope*100)#times 100 to bring on to km scale

}

####
#NaNs may be produced - this is OK - its just when the Optimization tests weird starting parameters I think.

#you may need to change 1:4 to get the right columns to paste into the results....
results<-cbind(predicted_D[1:5],likelihoods,positions_D,positions_C,positions_S,stretch_factors_D,stretch_factors_C,stretch_factors_S,D_centres,C_centres,S_centres,D_cline_widths,C_cline_widths,S_cline_widths,D_max_slope,C_max_slope,S_max_slope,likelihoods_D,likelihoods_C,likelihoods_S)

results<-results[order(-results$likelihoods),]

results[1:20,]

#Now extract the best fitting simulated cline for plotting etc (need to centre on zero again).
```

```
pred_D <- data.frame(demes,t(predicted_for_loops_D[row.names(results)[1],]))
pred_C <- data.frame(demes,t(predicted_for_loops_C[row.names(results)[1],]))
pred_S <- data.frame(demes,t(predicted_for_loops_S[row.names(results)[1],]))

names(pred_D) <- c("km_D","freq_D")
names(pred_C) <- c("km_C","freq_C")
names(pred_S) <- c("km_S","freq_S")

par(mfrow=c(3,1))
plot(obs$km,obs$propD)
lines(pred_D$freq ~ I((results[1,10]*pred_D$km)+results[1,7]), col="red")
plot(obs$km,obs$propC)
lines(pred_C$freq ~ I((results[1,11]*pred_C$km)+results[1,8]), col="red")
plot(obs$km,obs$propS)
lines(pred_S$freq ~ I(results[1,12]*(pred_S$km)+results[1,9]), col="red")

# THIS IS FOR FINDING SLOPE SUPPORT LIMITS
#this code plays with the stretch factor increasing (and then decreasing it) until the log likelihoods drop
by -2.
#the code is quite long because each time you play with the stretch factor that moves the position of the
centre of the cline, so you keep
#having to realign the cline and make the centre in the same place it was before.

#do it for the D cline
mid_point_for_pivot<-results[1,13]
positions<-results[1,7]
test.val.upper<-results[1,10]
while(func_likelihood_ERATO_LIKE_D(c(positions,test.val.upper)) > results[1,22] - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
D_cline_width_upper_interval<-(1/D_cline_slope_lower_interval)

mid_point_for_pivot<-results[1,13]
positions<-results[1,7]
test.val.lower<-results[1,10]
while(func_likelihood_ERATO_LIKE_D(c(positions,test.val.lower)) > results[1,22] - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
```

```
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
D_cline_width_lower_interval<-(1/D_cline_slope_upper_interval)

#do it for the C cline
mid_point_for_pivot<-results[1,14]
positions<-results[1,8]
test.val.upper<-results[1,11]
while(func_likelihood_ERATO_LIKE_C(c(positions,test.val.upper)) > results[1,23] - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
C_cline_width_upper_interval<-(1/C_cline_slope_lower_interval)

mid_point_for_pivot<-results[1,14]
positions<-results[1,8]
test.val.lower<-results[1,11]
while(func_likelihood_ERATO_LIKE_C(c(positions,test.val.lower)) > results[1,23] - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
C_cline_width_lower_interval<-(1/C_cline_slope_upper_interval)

#do it for the S cline
mid_point_for_pivot<-results[1,15]
positions<-results[1,9]
```

```
test.val.upper<-results[1,12]
while(func_likelihood_ERATO_LIKE_S(c(positions,test.val.upper)) > results[1,24] - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
S_cline_width_upper_interval<-(1/S_cline_slope_lower_interval)

mid_point_for_pivot<-results[1,15]
positions<-results[1,9]
test.val.lower<-results[1,12]
while(func_likelihood_ERATO_LIKE_S(c(positions,test.val.lower)) > results[1,24] - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
S_cline_width_lower_interval<-(1/S_cline_slope_upper_interval)

# THIS IS FOR FINDING CENTRE SUPPORT LIMITS
#do it for the D cline
test.val.upper<-results[1,7]
while(func_likelihood_ERATO_LIKE_D(c(test.val.upper,results[1,10])) > results[1,22] - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(test.val.upper,results[1,10])),sep=""))
test.val.lower<-results[1,7]
while(func_likelihood_ERATO_LIKE_D(c(test.val.lower,results[1,10])) > results[1,22] - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(test.val.lower,results[1,10])),sep=""))
```

```
interp.dat<-aspline((results[1,10]*pred_D$km)+test.val.upper, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
D_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results[1,10]*pred_D$km)+test.val.lower, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
D_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]

#do it for the C cline
test.val.upper<-results[1,8]
while(func_likelihood_ERATO_LIKE_C(c(test.val.upper,results[1,11])) > results[1,23] - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(test.val.upper,results[1,11])),sep=""))
test.val.lower<-results[1,8]
while(func_likelihood_ERATO_LIKE_C(c(test.val.lower,results[1,11])) > results[1,23] - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(test.val.lower,results[1,11])),sep=""))

interp.dat<-aspline((results[1,11]*pred_C$km)+test.val.upper, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
C_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results[1,11]*pred_C$km)+test.val.lower, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
C_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]

#do it for the S cline
test.val.upper<-results[1,9]
while(func_likelihood_ERATO_LIKE_S(c(test.val.upper,results[1,12])) > results[1,24] - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(test.val.upper,results[1,12])),sep=""))
test.val.lower<-results[1,9]
while(func_likelihood_ERATO_LIKE_S(c(test.val.lower,results[1,12])) > results[1,24] - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(test.val.lower,results[1,12])),sep=""))

interp.dat<-aspline((results[1,12]*pred_S$km)+test.val.upper, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
S_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results[1,12]*pred_S$km)+test.val.lower, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
S_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
```

```
results_for_best_fitting_cline<-results[1,]
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,D_cline_slope_lower_interval,D_cline_slope_upper_interval,D_clin
e_width_lower_interval,D_cline_width_upper_interval)
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,C_cline_slope_lower_interval,C_cline_slope_upper_interval,C_cline
_width_lower_interval,C_cline_width_upper_interval)
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,S_cline_slope_lower_interval,S_cline_slope_upper_interval,S_cline
_width_lower_interval,S_cline_width_upper_interval)
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,D_cline_centre_upper,D_cline_centre_lower,C_cline_centre_upper,
C_cline_centre_lower,S_cline_centre_upper,S_cline_centre_lower)

results_for_best_fitting_cline<-results_for_best_fitting_cline[-(c(1,7:12))]

#FIGURE COMBINED WITH SEPARATE POINTS FOR TIME PERIODS
par(mfrow=c(4,1),mar=c(2.5, 3, 1, 1.5),mgp=c(1.5,0.5,0))
plot(obsJM$km,obsJM$propD,col="white",pch=1,ylab=expression(paste(italic(D),"
frequency")),xlab="Transect position (km)")
legend("topleft",inset=c(0.025,0.05),c("1986","2011"),pch=c(1,4),col=c("blue","red"))
lines(pred_D$freq_D ~ I((results[1,10]*pred_D$km_D)+results[1,7]), col="black")
points(obsJM$km,obsJM$propD,col="blue",pch=1,ylab=expression(paste(italic(D),"
frequency")),xlab="Transect position (km)")
points(obsNR$km,obsNR$propD,col="red",pch=4)
plot(obsJM$km,obsJM$propC,col="white",pch=1,ylab=expression(paste(italic(Cr),"
frequency")),xlab="Transect position (km)")
lines(pred_C$freq_C ~ I((results[1,11]*pred_C$km_C)+results[1,8]), col="black")
points(obsJM$km,obsJM$propC,col="blue",pch=1,ylab=expression(paste(italic(Cr))),xlab="Transect
position (km)")
points(obsNR$km,obsNR$propC,col="red",pch=4)
plot(obsJM$km,obsJM$propS,col="white",pch=1,ylab=expression(paste(italic(Sd),"
frequency")),xlab="Transect position (km)")
lines(pred_S$freq_S ~ I((results[1,12]*pred_S$km_S)+results[1,9]), col="black")
points(obsJM$km,obsJM$propS,col="blue",pch=1,ylab=expression(paste(italic(Sd))),xlab="Transect
position (km)")
points(obsNR$km,obsNR$propS,col="red",pch=4)

#BLUBBLE PLOT FIGURE COMBINED WITH SEPARATE POINTS FOR TIME PERIODS
par(mfrow=c(4,1),mar=c(2.5, 3, 1.5, 1.5),mgp=c(1.5,0.5,0))
plot(obsJM$km,obsJM$propD,col="white",pch=1,ylab=expression(paste(italic(D),"
frequency")),xlab="Transect position (km)",,main="FIGURE 2A")
legend("topleft",inset=c(0.025,0.05),c("1986","2011"),pch=c(1,1),col=c("blue","red"))
```

```
legend("bottomright",inset=c(0.025,0.05),c("1","10","50"),pch=1,pt.cex=c(0.53103,1.53103,2.23),col=c("
black"),title=expression(paste(italic(n))))
lines(pred_D$freq_D ~ I((results[1,10]*pred_D$km_D)+results[1,7]), col="black")
points(obsJM$km,obsJM$propD,col="blue",pch=1,cex=0.23+c(log10(obsJM$total_alleles)))
points(obsNR$km,obsNR$propD,col="red",pch=1,cex=0.23+c(log10(obsNR$total_alleles)))
plot(obsJM$km,obsJM$propC,col="white",pch=1,ylab=expression(paste(italic(Cr),"
frequency")),xlab="Transect position (km)")
lines(pred_C$freq_C ~ I((results[1,11]*pred_C$km_C)+results[1,8]), col="black")
points(obsJM$km,obsJM$propC,col="blue",pch=1,cex=c(0.23+log10(obsJM$total_alleles)))
points(obsNR$km,obsNR$propC,col="red",pch=1,cex=c(0.23+log10(obsNR$total_alleles)))
plot(obsJM$km,obsJM$propS,col="white",pch=1,ylab=expression(paste(italic(Sd),"
frequency")),xlab="Transect position (km)")
lines(pred_S$freq_S ~ I((results[1,12]*pred_S$km_S)+results[1,9]), col="black")
points(obsJM$km,obsJM$propS,col="blue",pch=1,cex=c(0.23+log10(obsJM$total_alleles)))
points(obsNR$km,obsNR$propS,col="red",pch=1,cex=c(0.23+log10(obsNR$total_alleles)))


###############################################################################
###USE LIKELIHOOD TO FIT THE SIMULATED MELPOMENE CLINES TO THE OBSERVED DATA###
###############################################################################

library(akima)

func_likelihood_MELP_B <- function(x) {
            freqs_B <- aspline((x[2]*pred_B$km)+x[1], pred_B$freq, xout=obs$km, degree=10)
  p_B <- ((freqs_B$y*freqs_B$y)+(2*(freqs_B$y*(1-freqs_B$y))))
  p_B[p_B==0] <- 1e-55
  p_B[p_B==1] <- 1-1e-5
  #had to divide likelihood calculation up as R stored very small probabilities as zero (before was coded
as likelihood_B<-sum((log(p_B^y_B))+ log((1-p_B)^(k_B-y_B))) - see erato script)
  part_a<-p_B^y_B
  part_b<-(1-p_B)^(k_B-y_B)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
  return(likelihood)
            }

func_likelihood_MELP_D <- function(x) {
  freqs_D <- aspline((x[2]*pred_D$km)+x[1], pred_D$freq, xout=obs$km, degree=10)
  p_D <- ((freqs_D$y*freqs_D$y)+(2*(freqs_D$y*(1-freqs_D$y))))
  p_D[p_D==0] <- 1e-55
  p_D[p_D==1] <- 1-1e-5
  part_a<-p_D^y_D
  part_b<-(1-p_D)^(k_D-y_D)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
```

```
  return(likelihood)
          }

func_likelihood_MELP_N <- function(x) {
          freqs_N <- aspline((x[2]*pred_N$km)+x[1], pred_N$freq, xout=obs$km, degree=10)
  p_N <- ((freqs_N$y*freqs_N$y)+(2*(freqs_N$y*(1-freqs_N$y))))
  p_N[p_N==0] <- 1e-55
  p_N[p_N==1] <- 1-1e-5
  part_a<-p_N^y_N
  part_b<-(1-p_N)^(k_N-y_N)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
  return(likelihood)
          }

func_likelihood_MELP_Y <- function(x) {
          freqs_Y <- aspline((x[2]*pred_Y$km)+x[1], pred_Y$freq, xout=obs$km, degree=10)
  p_Y <- ((freqs_Y$y*freqs_Y$y)+(2*(freqs_Y$y*(1-freqs_Y$y))))
  p_Y[p_Y==0] <- 1e-55
  p_Y[p_Y==1] <- 1-1e-5
  part_a<-p_Y^y_Y
  part_b<-(1-p_Y)^(k_Y-y_Y)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
  return(likelihood)
          }

#Find max slope of simulated cline function
max_slope <- function(x) {
slopes<-c()
for (i in 1:(length(x)-1)){
slopes<-append(slopes,x[i+1]-x[i])}
return(max(slopes))
}

#observed data
obsJM <- read.csv("melpomene1990.csv", header=T, sep=",")
obsNR <- read.csv("melpomene2011.csv", header=T, sep=",")
combined <- read.csv("melpomene_combined.csv", header=T, sep=",")
predicted_all_data <- read.csv("melp_sim_results.csv", header=T, sep=",")
predicted_all_data<-
subset(predicted_all_data,selectionB==0.6&selectionD==0.6&selectionN==0.6&selectionY==0.6&recomb_r_BD==0.135)

#Approximate point of the middle of the hybrid zone on the transect (this is used as a starting point in the optimization algorithm) (123.57 is Mallet 1990 estimated centre of D cline).
```

```
approx_mid_point<-123.57

#change this to the date set you want to analyse
obs<-combined
obs <- obs[order(obs$km),]

#Subset the B locus
predicted_B<-subset(predicted_all_data, predicted_all_data$locus == "B")
rownames(predicted_B) <- seq(length=nrow(predicted_B))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_B<-predicted_B[10:ncol(predicted_B)]
demes<-c(1:ncol(predicted_for_loops_B))

k_B <- obs$total_alleles/2 ## total number individuals
y_B <- k_B-(obs$n_bb_individuals)  ## total number of B- individuals

#Subset the D locus
predicted_D<-subset(predicted_all_data, predicted_all_data$locus == "D")
rownames(predicted_D) <- seq(length=nrow(predicted_D))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_D<-predicted_D[10:ncol(predicted_D)]
demes<-c(1:ncol(predicted_for_loops_D))

k_D <- obs$total_alleles/2 ## total number individuals
y_D <- k_D-(obs$n_dd_individuals)  ## total number of D- individuals

#Subset the N locus
predicted_N<-subset(predicted_all_data, predicted_all_data$locus == "N")
rownames(predicted_N) <- seq(length=nrow(predicted_N))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_N<-predicted_N[10:ncol(predicted_N)]
demes<-c(1:ncol(predicted_for_loops_N))

k_N <- obs$total_alleles/2 ## total number individuals
y_N <- k_N-(obs$n_nn_individuals)  ## total number of N- individuals

#Subset the Y locus (predicted cline is the same as the N locus assuming very tight linkage)...
predicted_Y<-subset(predicted_all_data, predicted_all_data$locus == "Y")
rownames(predicted_Y) <- seq(length=nrow(predicted_Y))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
```

```
predicted_for_loops_Y<-predicted_Y[10:ncol(predicted_Y)]
demes<-c(1:ncol(predicted_for_loops_Y))

k_Y <- obs$total_alleles/2 ## total number individuals
y_Y <- k_Y-(obs$n_yy_individuals)  ## total number of Y- individuals

#Now loop through all the parameter combinations, calculate the likelihood and return
likelihoods<-c()
likelihoods_B<-c()
likelihoods_D<-c()
likelihoods_N<-c()
likelihoods_Y<-c()
positions_B<-c()
positions_D<-c()
positions_N<-c()
positions_Y<-c()
stretch_factors_B<-c()
stretch_factors_D<-c()
stretch_factors_N<-c()
stretch_factors_Y<-c()
B_centres<-c()
D_centres<-c()
N_centres<-c()
Y_centres<-c()
B_cline_widths<-c()
D_cline_widths<-c()
N_cline_widths<-c()
Y_cline_widths<-c()
B_max_slope<-c()
D_max_slope<-c()
N_max_slope<-c()
Y_max_slope<-c()

for (i in 1:nrow(predicted_B)){

pred_B <- data.frame(demes,t(predicted_for_loops_B[i,]))
pred_D <- data.frame(demes,t(predicted_for_loops_D[i,]))
pred_N <- data.frame(demes,t(predicted_for_loops_N[i,]))
pred_Y <- data.frame(demes,t(predicted_for_loops_Y[i,]))

names(pred_B) <- c("km_B","freq_B")
names(pred_D) <- c("km_D","freq_D")
names(pred_N) <- c("km_N","freq_N")
names(pred_Y) <- c("km_Y","freq_Y")

#optimisation algorithm,
```

```
# starting parameters = 1) align the approx middle of the hybrid zone with the middle of the simulated
cline, and 2) using 1 as the stretch factor (i.e. no stretch: less than 1 squeezes the cline together, greater
than 1 pulls it apart).
approx_centre_sim_D<-which.min(abs(pred_D$freq_D-0.5))
starting_param_1<-approx_mid_point-approx_centre_sim_D  #this find the difference between the
observed data and simulated data using the D locus, and uses this as a starting point
likelihood_B <- optim(par = c(starting_param_1,1), func_likelihood_MELP_B, NULL, control=list(fnscale=-
1))
likelihood_D <- optim(par = c(starting_param_1,1), func_likelihood_MELP_D, NULL,
control=list(fnscale=-1))
likelihood_N <- optim(par = c(starting_param_1,1), func_likelihood_MELP_N, NULL,
control=list(fnscale=-1))
likelihood_Y <- optim(par = c(starting_param_1,1), func_likelihood_MELP_Y, NULL, control=list(fnscale=-
1))
likelihood<-sum(likelihood_B$value,likelihood_D$value,likelihood_N$value,likelihood_Y$value)
#find middle of clines and widths
#this is a clunky bit to find the centre of the cline; the spline doesn't seem to be able to find the x value
for a given y value, only the other way round, so had to do it like this
interp.dat<-aspline((likelihood_B$par[2]*pred_B$km)+likelihood_B$par[1], pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
B_cline_max_slope<-max_slope(1-interp.dat$y)
B_cline_width<-(1/B_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

interp.dat<-aspline((likelihood_D$par[2]*pred_D$km)+likelihood_D$par[1], pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
D_cline_max_slope<-max_slope(interp.dat$y)
D_cline_width<-(1/D_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

interp.dat<-aspline((likelihood_N$par[2]*pred_N$km)+likelihood_N$par[1], pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
N_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
N_cline_max_slope<-max_slope(interp.dat$y)
N_cline_width<-(1/N_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

interp.dat<-aspline((likelihood_Y$par[2]*pred_Y$km)+likelihood_Y$par[1], pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
Y_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
Y_cline_max_slope<-max_slope(interp.dat$y)
Y_cline_width<-(1/Y_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

#append results to results vectors..
likelihoods<-append(likelihoods,likelihood)
```

```
likelihoods_B<-append(likelihoods_B,likelihood_B$value)
likelihoods_D<-append(likelihoods_D,likelihood_D$value)
likelihoods_N<-append(likelihoods_N,likelihood_N$value)
likelihoods_Y<-append(likelihoods_Y,likelihood_Y$value)
positions_B<-append(positions_B,likelihood_B$par[1])
positions_D<-append(positions_D,likelihood_D$par[1])
positions_N<-append(positions_N,likelihood_N$par[1])
positions_Y<-append(positions_Y,likelihood_Y$par[1])
stretch_factors_B<-append(stretch_factors_B,likelihood_B$par[2])
stretch_factors_D<-append(stretch_factors_D,likelihood_D$par[2])
stretch_factors_N<-append(stretch_factors_N,likelihood_N$par[2])
stretch_factors_Y<-append(stretch_factors_Y,likelihood_Y$par[2])
B_centres<-append(B_centres,B_cline_centre)
D_centres<-append(D_centres,D_cline_centre)
N_centres<-append(N_centres,N_cline_centre)
Y_centres<-append(Y_centres,Y_cline_centre)
B_cline_widths<-append(B_cline_widths,B_cline_width)
D_cline_widths<-append(D_cline_widths,D_cline_width)
N_cline_widths<-append(N_cline_widths,N_cline_width)
Y_cline_widths<-append(Y_cline_widths,Y_cline_width)
B_max_slope<-append(B_max_slope,B_cline_max_slope*100)#times 100 to bring on to km scale
D_max_slope<-append(D_max_slope,D_cline_max_slope*100)#times 100 to bring on to km scale
N_max_slope<-append(N_max_slope,N_cline_max_slope*100)#times 100 to bring on to km scale
Y_max_slope<-append(Y_max_slope,Y_cline_max_slope*100)#times 100 to bring on to km scale

}

results<-
cbind(predicted_D[1:9],likelihoods,likelihoods_B,likelihoods_D,likelihoods_N,likelihoods_Y,positions_B,
positions_D,positions_N,positions_Y,stretch_factors_B,stretch_factors_D,stretch_factors_N,stretch_fact
ors_Y,B_centres,D_centres,N_centres,Y_centres,B_cline_widths,D_cline_widths,N_cline_widths,Y_cline
_widths,B_max_slope,D_max_slope,N_max_slope,Y_max_slope)

results<-results[order(-results$likelihoods),]

#put in the row for the most likely selection values here...
pred_B <- data.frame(demes,t(predicted_for_loops_B[row.names(results)[1],]))
pred_D <- data.frame(demes,t(predicted_for_loops_D[row.names(results)[1],]))
pred_N <- data.frame(demes,t(predicted_for_loops_N[row.names(results)[1],]))
pred_Y <- data.frame(demes,t(predicted_for_loops_Y[row.names(results)[1],]))

names(pred_B) <- c("km_B","freq_B")
names(pred_D) <- c("km_D","freq_D")
names(pred_N) <- c("km_N","freq_N")
names(pred_Y) <- c("km_Y","freq_Y")

#FIGURE FOR COMBINED WITH SEPARATE POINTS FOR TIME PERIODS
par(mfrow=c(4,1),mar=c(2.5, 3, 1, 1.5),mgp=c(1.5,0.5,0))
```

```
plot(obsJM$km,obsJM$propB,col="white",pch=1,ylab=expression(paste(italic(b),"
frequency")),xlab="Transect position (km)")
legend("topleft",inset=c(0.025,0.05),c("1986","2011"),pch=c(1,4),col=c("blue","red"))
lines(1-pred_B$freq_B ~ I((results[1,19]*pred_B$km_B)+results[1,15]), col="black")
points(obsNR$km,obsNR$propB,col="red",pch=4)
points(obsJM$km,obsJM$propB,col="blue",pch=1)

plot(obsJM$km,obsJM$propD,col="white",pch=1,ylab=expression(paste(italic(D),"
frequency")),xlab="Transect position (km)")
lines(pred_D$freq_D ~ I((results[1,20]*pred_D$km_D)+results[1,16]), col="black")
points(obsJM$km,obsJM$propD,col="blue",pch=1)
points(obsNR$km,obsNR$propD,col="red",pch=4)

plot(obsJM$km,obsJM$propN,col="white",pch=1,ylab=expression(paste(italic(N),"
frequency")),xlab="Transect position (km)")
lines(pred_N$freq_N ~ I((results[1,21]*pred_N$km_N)+results[1,17]), col="black")
points(obsJM$km,obsJM$propN,col="blue",pch=1)
points(obsNR$km,obsNR$propN,col="red",pch=4)

plot(obsJM$km,obsJM$propY,col="white",pch=1,ylab=expression(paste(italic(Y),"
frequency")),xlab="Transect position (km)")
points(obsJM$km,obsJM$propY,col="blue",pch=1)
points(obsNR$km,obsNR$propY,col="red",pch=4)
lines(pred_Y$freq_Y ~ I((results[1,22]*pred_Y$km_Y)+results[1,18]), col="black")

  #FIGURE FOR COMBINED WITH SEPARATE POINTS FOR TIME PERIODS for the B cline  (slope and and
centres inserted from other data)
par(mfrow=c(4,1),mar=c(2.5, 3, 1, 1.5),mgp=c(1.5,0.5,0))
plot(obsJM$km,obsJM$propB,col="white",pch=1,ylab=expression(paste(italic(b),"
frequency")),xlab="Transect position (km)")
legend("topleft",inset=c(0.025,0.05),c("1986","2011"),pch=c(1,4),col=c("blue","red"))
lines(1-pred_B$freq_B ~ I((2.285966*pred_B$km_B)+-107.30842), col="blue")
lines(1-pred_B$freq_B ~ I((1.377966*pred_B$km_B)+ -16.42842), col="red")
points(obsJM$km,obsJM$propB,col="blue",pch=1)
points(obsNR$km,obsNR$propB,col="red",pch=4)

plot(obsJM$km,obsJM$propD,col="white",pch=1,ylab=expression(paste(italic(D),"
frequency")),xlab="Transect position (km)")
lines(pred_D$freq_D ~ I((results[1,20]*pred_D$km_D)+results[1,16]), col="black")
points(obsJM$km,obsJM$propD,col="blue",pch=1)
points(obsNR$km,obsNR$propD,col="red",pch=4)

plot(obsJM$km,obsJM$propN,col="white",pch=1,ylab=expression(paste(italic(N),"
frequency")),xlab="Transect position (km)")
lines(pred_N$freq_N ~ I((results[1,21]*pred_N$km_N)+results[1,17]), col="black")
points(obsJM$km,obsJM$propN,col="blue",pch=1)
points(obsNR$km,obsNR$propN,col="red",pch=4)
```

```
plot(obsJM$km,obsJM$propY,col="white",pch=1,ylab=expression(paste(italic(Yb),"
frequency")),xlab="Transect position (km)")
lines(pred_Y$freq_Y ~ I((results[1,22]*pred_Y$km_Y)+results[1,18]), col="black")
points(obsJM$km,obsJM$propY,col="blue",pch=1,ylab="Yb frequency",xlab="Transect position (km)")
points(obsNR$km,obsNR$propY,col="red",pch=4)


#BUBBLE PLOT FIGURE FOR COMBINED WITH SEPARATE POINTS FOR TIME PERIODS for the B cline
(slope and and centres inserted from other data)
#0.23 added to cex to make smallest points little circles rather than dots.
par(mfrow=c(4,1),mar=c(2.5, 3, 1.5, 1.5),mgp=c(1.5,0.5,0))
plot(obsJM$km,obsJM$propB,col="white",pch=1,ylab=expression(paste(italic(b),"
frequency")),xlab="Transect position (km)",main="FIGURE 2B")
legend("topleft",inset=c(0.025,0.05),c("1986","2011"),pch=c(1,1),col=c("blue","red"))
legend("bottomright",inset=c(0.025,0.05),c("1","10","50"),pch=1,pt.cex=c(0.53103,1.53103,2.23),col=c("
black"),title=expression(paste(italic(n))))
lines(1-pred_B$freq_B ~ I((2.285966*pred_B$km_B)+-107.30842), col="blue")
lines(1-pred_B$freq_B ~ I((1.377966*pred_B$km_B)+ -16.42842), col="red")
points(obsJM$km,obsJM$propB,col="blue",pch=1,cex=c(0.23+log10(obsJM$total_alleles)))
points(obsNR$km,obsNR$propB,col="red",pch=1,cex=c(0.23+log10(obsNR$total_alleles)))

plot(obsJM$km,obsJM$propD,col="white",pch=1,ylab=expression(paste(italic(D),"
frequency")),xlab="Transect position (km)")
lines(pred_D$freq_D ~ I((results[1,20]*pred_D$km_D)+results[1,16]), col="black")
points(obsJM$km,obsJM$propD,col="blue",pch=1,cex=c(0.23+log10(obsJM$total_alleles)))
points(obsNR$km,obsNR$propD,col="red",pch=1,cex=c(0.23+log10(obsNR$total_alleles)))

plot(obsJM$km,obsJM$propN,col="white",pch=1,ylab=expression(paste(italic(N),"
frequency")),xlab="Transect position (km)")
lines(pred_N$freq_N ~ I((results[1,21]*pred_N$km_N)+results[1,17]), col="black")
points(obsJM$km,obsJM$propN,col="blue",pch=1,cex=c(0.23+log10(obsJM$total_alleles)))
points(obsNR$km,obsNR$propN,col="red",pch=1,cex=c(0.23+log10(obsNR$total_alleles)))

plot(obsJM$km,obsJM$propY,col="white",pch=1,ylab=expression(paste(italic(Yb),"
frequency")),xlab="Transect position (km)")
lines(pred_Y$freq_Y ~ I((results[1,22]*pred_Y$km_Y)+results[1,18]), col="black")
points(obsJM$km,obsJM$propY,col="blue",pch=1,cex=c(0.23+log10(obsJM$total_alleles)))
points(obsNR$km,obsNR$propY,col="red",pch=1,cex=c(0.23+log10(obsNR$total_alleles)))

# THIS IS FOR FINDING SLOPE/ WIDTH /  CENTRE SUPPORT LIMITS FOR THE BEST FITTING CLINE
#this code plays with the stretch factor increasing (and then decreasing it) until the log likelihoods drop
by -2.
#the code is quite long because each time you play with the stretch factor that moves the position of the
centre of the cline, so you keep
#having to realign the cline and make the centre in the same place it was before.

results<-results[1,]
```

```
#do it for the B cline
mid_point_for_pivot<-results$B_centres
positions<-results$positions_B
test.val.upper<-results$stretch_factors_B
best_fit_LL<-func_likelihood_MELP_B(c(positions,results$stretch_factors_B))
while(func_likelihood_MELP_B(c(positions,test.val.upper)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_B$km)+positions, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_B(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_B$km)+positions, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope_lower_interval<-max_slope(1-interp.dat$y)*100  #times by 100 to bring onto km scale
B_cline_width_upper_interval<-(1/B_cline_slope_lower_interval)

mid_point_for_pivot<-results$B_centres
positions<-results$positions_B
test.val.lower<-results$stretch_factors_B
best_fit_LL<-func_likelihood_MELP_B(c(positions,results$stretch_factors_B))
while(func_likelihood_MELP_B(c(positions,test.val.lower)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_B$km)+positions, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_B(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_B$km)+positions, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope_upper_interval<-max_slope(1-interp.dat$y)*100  #times by 100 to bring onto km scale
B_cline_width_lower_interval<-(1/B_cline_slope_upper_interval)

#do it for the D cline
mid_point_for_pivot<-results$D_centres
positions<-results$positions_D
test.val.upper<-results$stretch_factors_D
best_fit_LL<-func_likelihood_MELP_D(c(positions,results$stretch_factors_D))
while(func_likelihood_MELP_D(c(positions,test.val.upper)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
```

```
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_D(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
D_cline_width_upper_interval<-(1/D_cline_slope_lower_interval)

mid_point_for_pivot<-results$D_centres
positions<-results$positions_D
test.val.lower<-results$stretch_factors_D
best_fit_LL<-func_likelihood_MELP_D(c(positions,results$stretch_factors_D))
while(func_likelihood_MELP_D(c(positions,test.val.lower)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_D(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
D_cline_width_lower_interval<-(1/D_cline_slope_upper_interval)

#do it for the N cline
mid_point_for_pivot<-results$N_centres
positions<-results$positions_N
test.val.upper<-results$stretch_factors_N
best_fit_LL<-func_likelihood_MELP_N(c(positions,results$stretch_factors_N))
while(func_likelihood_MELP_N(c(positions,test.val.upper)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_N$km)+positions, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_N(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_N$km)+positions, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
N_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
N_cline_width_upper_interval<-(1/N_cline_slope_lower_interval)

mid_point_for_pivot<-results$N_centres
positions<-results$positions_N
test.val.lower<-results$stretch_factors_N
```

```
best_fit_LL<-func_likelihood_MELP_N(c(positions,results$stretch_factors_N))
while(func_likelihood_MELP_N(c(positions,test.val.lower)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_N$km)+positions, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_N(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_N$km)+positions, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
N_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
N_cline_width_lower_interval<-(1/N_cline_slope_upper_interval)

#do it for the Y cline
mid_point_for_pivot<-results$Y_centres
positions<-results$positions_Y
test.val.upper<-results$stretch_factors_Y
best_fit_LL<-func_likelihood_MELP_Y(c(positions,results$stretch_factors_Y))
while(func_likelihood_MELP_Y(c(positions,test.val.upper)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_Y$km)+positions, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_Y(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_Y$km)+positions, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
Y_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
Y_cline_width_upper_interval<-(1/Y_cline_slope_lower_interval)

mid_point_for_pivot<-results$Y_centres
positions<-results$positions_Y
test.val.lower<-results$stretch_factors_Y
best_fit_LL<-func_likelihood_MELP_Y(c(positions,results$stretch_factors_Y))
while(func_likelihood_MELP_Y(c(positions,test.val.lower)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_Y$km)+positions, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_Y(c(positions,test.val.lower)),sep=""))
```

```
interp.dat<-aspline((test.val.lower*pred_Y$km)+positions, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
Y_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
Y_cline_width_lower_interval<-(1/Y_cline_slope_upper_interval)

# THIS IS FOR FINDING CENTRE SUPPORT LIMITS

#do it for the B cline
test.val.upper<-results$positions_B
best_fit_LL<-func_likelihood_MELP_B(c(results$positions_B,results$stretch_factors_B))
while(func_likelihood_MELP_B(c(test.val.upper,results$stretch_factors_B)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_B(c(test.val.upper,results$stretch_factors_B)),sep=""))
test.val.lower<-results$positions_B
while(func_likelihood_MELP_B(c(test.val.lower,results$stretch_factors_B)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_B(c(test.val.lower,results$stretch_factors_B)),sep=""))

interp.dat<-aspline((results$stretch_factors_B*pred_B$km)+test.val.upper, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
B_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results$stretch_factors_B*pred_B$km)+test.val.lower, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
B_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]

#do it for the D cline
test.val.upper<-results$positions_D
best_fit_LL<-func_likelihood_MELP_D(c(results$positions_D,results$stretch_factors_D))
while(func_likelihood_MELP_D(c(test.val.upper,results$stretch_factors_D)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_D(c(test.val.upper,results$stretch_factors_D)),sep=""))
test.val.lower<-results$positions_D
while(func_likelihood_MELP_D(c(test.val.lower,results$stretch_factors_D)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_D(c(test.val.lower,results$stretch_factors_D)),sep=""))

interp.dat<-aspline((results$stretch_factors_D*pred_D$km)+test.val.upper, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
D_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
```

```
interp.dat<-aspline((results$stretch_factors_D*pred_D$km)+test.val.lower, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
D_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]

#do it for the N cline
test.val.upper<-results$positions_N
best_fit_LL<-func_likelihood_MELP_N(c(results$positions_N,results$stretch_factors_N))
while(func_likelihood_MELP_N(c(test.val.upper,results$stretch_factors_N)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood =
",func_likelihood_MELP_N(c(test.val.upper,results$stretch_factors_N)),sep=""))
test.val.lower<-results$positions_N
while(func_likelihood_MELP_N(c(test.val.lower,results$stretch_factors_N)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_N(c(test.val.lower,results$stretch_factors_N)),sep=""))

interp.dat<-aspline((results$stretch_factors_N*pred_N$km)+test.val.upper, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
N_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results$stretch_factors_N*pred_N$km)+test.val.lower, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
N_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]

#do it for the Y cline
test.val.upper<-results$positions_Y
best_fit_LL<-func_likelihood_MELP_Y(c(results$positions_Y,results$stretch_factors_Y))
while(func_likelihood_MELP_Y(c(test.val.upper,results$stretch_factors_Y)) > best_fit_LL - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_Y(c(test.val.upper,results$stretch_factors_Y)),sep=""))
test.val.lower<-results$positions_Y
while(func_likelihood_MELP_Y(c(test.val.lower,results$stretch_factors_Y)) > best_fit_LL - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_MELP_Y(c(test.val.lower,results$stretch_factors_Y)),sep=""))

interp.dat<-aspline((results$stretch_factors_Y*pred_Y$km)+test.val.upper, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
Y_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results$stretch_factors_Y*pred_Y$km)+test.val.lower, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
Y_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
```

```
results_for_best_fitting_cline<-results[1,]
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,B_cline_slope_lower_interval,B_cline_slope_upper_interval,B_cline
_width_lower_interval,B_cline_width_upper_interval)
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,D_cline_slope_lower_interval,D_cline_slope_upper_interval,D_clin
e_width_lower_interval,D_cline_width_upper_interval)
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,N_cline_slope_lower_interval,N_cline_slope_upper_interval,N_clin
e_width_lower_interval,N_cline_width_upper_interval)
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,Y_cline_slope_lower_interval,Y_cline_slope_upper_interval,Y_cline
_width_lower_interval,Y_cline_width_upper_interval)
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,B_cline_centre_upper,B_cline_centre_lower,D_cline_centre_upper,
D_cline_centre_lower,N_cline_centre_upper,N_cline_centre_lower,Y_cline_centre_upper,Y_cline_centr
e_lower)


##############################################################
###FIND SUPPORT LIMITS FOR WIDTH RATIO BETWEEN ERATO CLINES###
##############################################################

library(akima)

###likelihood functions to calculate the likelihoods for each cline separately;
func_likelihood_ERATO_LIKE_D <- function(x) {
	freqs_D <- aspline((x[2]*pred_D$km)+x[1], pred_D$freq, xout=obs$km, degree=10)
  p_D <- freqs_D$y
  p_D[p_D==0] <- 1e-5
  p_D[p_D==1] <- 1-1e-5
  likelihood<-sum((log(p_D^y_D))+ log((1-p_D)^(k_D-y_D)))
  return(likelihood)
	}

func_likelihood_ERATO_LIKE_C <- function(x) {
	freqs_C <- aspline((x[2]*pred_C$km)+x[1], pred_C$freq, xout=obs$km, degree=10)
  p_C <- ((freqs_C$y*freqs_C$y)+(2*(freqs_C$y*(1-freqs_C$y))))
  p_C[p_C==0] <- 1e-55
  p_C[p_C==1] <- 1-1e-5
  likelihood<-sum((log(p_C^y_C))+ log((1-p_C)^(k_C-y_C)))
  return(likelihood)
	}

func_likelihood_ERATO_LIKE_S <- function(x) {
	freqs_S <- aspline((x[2]*pred_S$km)+x[1], pred_S$freq, xout=obs$km, degree=10)
  p_S <- ((freqs_S$y*freqs_S$y)+(2*(freqs_S$y*(1-freqs_S$y))))
```

```
 p_S[p_S==0] <- 1e-55
 p_S[p_S==1] <- 1-1e-5
 likelihood<-sum((log(p_S^y_S))+ log((1-p_S)^(k_S-y_S)))
 return(likelihood)
          }

# function to calculate the likelihood of the three clines fitted simultanously:

#THIS VERSION ALLOWS THE POSITIONS OF THE CLINES TO MOVE INDEPENDENTLY and the stretch
factor to change..

# requires vector x  with SIX values(THREE constants that is added to the km pos of the predicted values
to make them match up with the observed data, AND THREE stretch factors),

# and then for each locus need to have the following data loaded up:
# pred_km (vector; km positions (demes) of simulated data), pred_freqs (vector; predicted frequency of
dominant PHENOTYPE for demes), obs_km (vector; observed km positions),
# k (vector; n trials in observed data), y (vector; n successes in observed data)

#do it for the D locus, ussing number of D alleles and expected proportion of D alleles
#do it for the D locus, ussing number of D alleles and expected proportion of D alleles

#Find max slope of simulated cline function
max_slope <- function(x) {
slopes<-c()
for (i in 1:(length(x)-1)){
slopes<-append(slopes,x[i+1]-x[i])}
return(max(slopes))
}

#observed data
obsJM <- read.csv("erato1990.csv", header=T, sep=",")
obsNR <- read.csv("erato2011.csv", header=T, sep=",")
combined <- read.csv("erato_combined.csv", header=T, sep=",")
predicted_all_data <- read.csv("erato_sim_results.csv", header=T, sep=",")
predicted_all_data <- subset(predicted_all_data, selectionD==0.6 & selectionC == 0.6 & selectionS ==
0.6)

#Approximate point of the middle of the hybrid zone on the transect (this is used as a starting point in
the optimization algorithm) (123.57 is Mallet 1990 estimated centre of D cline).
approx_mid_point<-123.57

#change this to the date set you want to analyse
obs<-combined
obs <- obs[order(obs$km),]

#Subset the D locus
predicted_D<-subset(predicted_all_data, predicted_all_data$locus == "D")
```

```
rownames(predicted_D) <- seq(length=nrow(predicted_D))
#this predicted for loops is just the allele frequencies without the row details, so you may have to change the "5" depending on the input file
predicted_for_loops_D<-predicted_D[7:ncol(predicted_D)]
demes<-c(1:ncol(predicted_for_loops_D))

k_D <- obs$total_alleles ## total number of gene copies sampled
y_D <- obs$n_D_alleles  ## number of successes

#Subset the C locus
predicted_C<-subset(predicted_all_data, predicted_all_data$locus == "C")
rownames(predicted_C) <- seq(length=nrow(predicted_C))

#this predicted for loops is just the allele frequencies without the row details, so you may have to change the "5" depending on the input file
predicted_for_loops_C<-predicted_C[7:ncol(predicted_C)]
demes<-c(1:ncol(predicted_for_loops_C))

k_C <- obs$total_alleles/2 ## total number individuals
y_C <- k_C-(obs$n_cc_individuals)  ## total number of C- individuals

#Subset the S locus
predicted_S<-subset(predicted_all_data, predicted_all_data$locus == "S")
rownames(predicted_S) <- seq(length=nrow(predicted_S))

#this predicted for loops is just the allele frequencies without the row details, so you may have to change the "5" depending on the input file
predicted_for_loops_S<-predicted_S[7:ncol(predicted_S)]
demes<-c(1:ncol(predicted_for_loops_S))

k_S <- obs$total_alleles/2 ## total number individuals
y_S <- k_S-(obs$n_ss_individuals)  ## total number of C- individuals

#Now loop through all the parameter combinations, calculate the likelihood and return
likelihoods<-c()
likelihoods_D<-c()
likelihoods_C<-c()
likelihoods_S<-c()
positions_D<-c()
positions_C<-c()
positions_S<-c()
stretch_factors_D<-c()
stretch_factors_C<-c()
stretch_factors_S<-c()
D_centres<-c()
C_centres<-c()
S_centres<-c()
D_cline_widths<-c()
```

```
C_cline_widths<-c()
S_cline_widths<-c()
D_max_slope<-c()
C_max_slope<-c()
S_max_slope<-c()

for (i in 1:nrow(predicted_D)){

pred_D <- data.frame(demes,t(predicted_for_loops_D[i,]))
pred_C <- data.frame(demes,t(predicted_for_loops_C[i,]))
pred_S <- data.frame(demes,t(predicted_for_loops_S[i,]))

names(pred_D) <- c("km_D","freq_D")
names(pred_C) <- c("km_C","freq_C")
names(pred_S) <- c("km_S","freq_S")

#optimisation algorithm,
# starting parameters = 1) align the approx middle of the hybrid zone with the middle of the simulated
cline, and 2) using 1 as the stretch factor (i.e. no stretch: less than 1 squeezes the cline together, greater
than 1 pulls it apart).
approx_centre_sim_D<-which.min(abs(pred_D$freq_D-0.5))
starting_param_1<-approx_mid_point-approx_centre_sim_D  #this find the difference between the
observed data and simulated data using the D locus, and uses this as a starting point for each of the loci
likelihood_D <- optim(par = c(starting_param_1,1), func_likelihood_ERATO_LIKE_D, NULL,
control=list(fnscale=-1))
likelihood_C <- optim(par = c(starting_param_1,1), func_likelihood_ERATO_LIKE_C, NULL,
control=list(fnscale=-1))
likelihood_S <- optim(par = c(starting_param_1,1), func_likelihood_ERATO_LIKE_S, NULL,
control=list(fnscale=-1))
likelihood<-sum(likelihood_D$value,likelihood_C$value,likelihood_S$value)
#find middle of clines and widths
#this is a clunky bit to find the centre of the cline; aspline doesn't seem to be able to find the x value for
a given y value, only the other way round, so had to do it like this
interp.dat<-aspline((likelihood_D$par[2]*pred_D$km)+likelihood_D$par[1], pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
D_cline_max_slope<-max_slope(interp.dat$y)
D_cline_width<-(1/D_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)
interp.dat<-aspline((likelihood_C$par[2]*pred_C$km)+likelihood_C$par[1], pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
C_cline_max_slope<-max_slope(interp.dat$y)
C_cline_width<-(1/C_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)
interp.dat<-aspline((likelihood_S$par[2]*pred_S$km)+likelihood_S$par[1], pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
```

```
S_cline_max_slope<-max_slope(interp.dat$y)
S_cline_width<-(1/S_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in the interp.dat fine scale)

#append results to results vectors..
likelihoods<-append(likelihoods,likelihood)
likelihoods_D<-append(likelihoods_D,likelihood_D$value)
likelihoods_C<-append(likelihoods_C,likelihood_C$value)
likelihoods_S<-append(likelihoods_S,likelihood_S$value)
positions_D<-append(positions_D,likelihood_D$par[1])
positions_C<-append(positions_C,likelihood_C$par[1])
positions_S<-append(positions_S,likelihood_S$par[1])
stretch_factors_D<-append(stretch_factors_D,likelihood_D$par[2])
stretch_factors_C<-append(stretch_factors_C,likelihood_C$par[2])
stretch_factors_S<-append(stretch_factors_S,likelihood_S$par[2])
D_centres<-append(D_centres,D_cline_centre)
C_centres<-append(C_centres,C_cline_centre)
S_centres<-append(S_centres,S_cline_centre)
D_cline_widths<-append(D_cline_widths,D_cline_width)
C_cline_widths<-append(C_cline_widths,C_cline_width)
S_cline_widths<-append(S_cline_widths,S_cline_width)
D_max_slope<-append(D_max_slope,D_cline_max_slope*100)#times 100 to bring on to km scale
C_max_slope<-append(C_max_slope,C_cline_max_slope*100)#times 100 to bring on to km scale
S_max_slope<-append(S_max_slope,S_cline_max_slope*100)#times 100 to bring on to km scale

}

####
#NaNs may be produced - this is OK - its just when the Optimization tests weird starting parameters I think.

#you may need to change 1:4 to get the right columns to paste into the results....
results<-cbind(predicted_D[1:5],likelihoods,positions_D,positions_C,positions_S,stretch_factors_D,stretch_factors_C,stretch_factors_S,D_centres,C_centres,S_centres,D_cline_widths,C_cline_widths,S_cline_widths,D_max_slope,C_max_slope,S_max_slope,likelihoods_D,likelihoods_C,likelihoods_S)

results<-results[order(-results$likelihoods),]

results[1:20,]

#Now extract the best fitting simulated cline for plotting etc (need to centre on zero again).

pred_D <- data.frame(demes,t(predicted_for_loops_D[row.names(results)[1],]))
pred_C <- data.frame(demes,t(predicted_for_loops_C[row.names(results)[1],]))
pred_S <- data.frame(demes,t(predicted_for_loops_S[row.names(results)[1],]))

names(pred_D) <- c("km_D","freq_D")
```

```
names(pred_C) <- c("km_C","freq_C")
names(pred_S) <- c("km_S","freq_S")

# THIS IS FOR FINDING THE WIDTH RATIO SUPPORT LIMITS
# basically I widen one cline while simulataneously narrowing the other, until the summed likelihoods of
the two clines drops by -2/
#the code is quite long because each time you play with the stretch factor that moves the position of the
centre of the cline, so you keep
#having to realign the cline and make the centre in the same place it was before.

### DO IT FOR D VERSUS C
#find upper bound
##starting ratio of widths
D.vs.C_ratio<-results$D_cline_widths/results$C_cline_widths

#for the D cline
mid_point_for_pivotD<-results$D_centres
positionsD<-results$positions_D
test.val.D<-results$stretch_factors_D
#for the C cline
mid_point_for_pivotC<-results$C_centres
positionsC<-results$positions_C
test.val.C<-results$stretch_factors_C

starting_likelihood<-func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_C(c(positionsC,test.val.C))

while(func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_C(c(positionsC,test.val.C))  > starting_likelihood - 2 )
{test.val.D<-test.val.D+0.0001
test.val.C<-test.val.C-0.0001
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.C<-aspline((test.val.C*pred_C$km)+positionsC, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.D<-interp.dat.D$x[which.min(abs(interp.dat.D$y-0.5))]
cline_centre.C<-interp.dat.C$x[which.min(abs(interp.dat.C$y-0.5))]
positionsD<-positionsD-(cline_centre.D-mid_point_for_pivotD)
positionsC<-positionsC-(cline_centre.C-mid_point_for_pivotC)
}
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope<-max_slope(interp.dat.D$y)*100  #times by 100 to bring onto km scale
D_cline_width<-(1/D_cline_slope)
interp.dat.C<-aspline((test.val.C*pred_C$km)+positionsC, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_slope<-max_slope(interp.dat.C$y)*100  #times by 100 to bring onto km scale
C_cline_width<-(1/C_cline_slope)
```

```
D.vs.C_ratio.upper<-D_cline_width/C_cline_width

#Find lower bound
#for the D cline
mid_point_for_pivotD<-results$D_centres
positionsD<-results$positions_D
test.val.D<-results$stretch_factors_D
#for the C cline
mid_point_for_pivotC<-results$C_centres
positionsC<-results$positions_C
test.val.C<-results$stretch_factors_C

starting_likelihood<-func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_C(c(positionsC,test.val.C))

while(func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_C(c(positionsC,test.val.C))  > starting_likelihood - 2 )
{test.val.D<-test.val.D-0.0001
test.val.C<-test.val.C+0.0001
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.C<-aspline((test.val.C*pred_C$km)+positionsC, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.D<-interp.dat.D$x[which.min(abs(interp.dat.D$y-0.5))]
cline_centre.C<-interp.dat.C$x[which.min(abs(interp.dat.C$y-0.5))]
positionsD<-positionsD-(cline_centre.D-mid_point_for_pivotD)
positionsC<-positionsC-(cline_centre.C-mid_point_for_pivotC)
}
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope<-max_slope(interp.dat.D$y)*100  #times by 100 to bring onto km scale
D_cline_width<-(1/D_cline_slope)
interp.dat.C<-aspline((test.val.C*pred_C$km)+positionsC, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_slope<-max_slope(interp.dat.C$y)*100  #times by 100 to bring onto km scale
C_cline_width<-(1/C_cline_slope)

D.vs.C_ratio.lower<-D_cline_width/C_cline_width

### DO IT FOR D VERSUS S
#FIND UPPER BOUND
##starting ratio of widths
D.vs.S_ratio<-results$D_cline_widths/results$S_cline_widths
mid_point_for_pivotD<-results$D_centres
positionsD<-results$positions_D
test.val.D<-results$stretch_factors_D
mid_point_for_pivotS<-results$S_centres
```

```
positionsS<-results$positions_S
test.val.S<-results$stretch_factors_S

starting_likelihood<-func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_S(c(positionsS,test.val.S))

while(func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_S(c(positionsS,test.val.S))  > starting_likelihood - 2 )
{test.val.D<-test.val.D+0.0001
test.val.S<-test.val.S-0.0001
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.S<-aspline((test.val.S*pred_S$km)+positionsS, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.D<-interp.dat.D$x[which.min(abs(interp.dat.D$y-0.5))]
cline_centre.S<-interp.dat.S$x[which.min(abs(interp.dat.S$y-0.5))]
positionsD<-positionsD-(cline_centre.D-mid_point_for_pivotD)
positionsS<-positionsS-(cline_centre.S-mid_point_for_pivotS)
}
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope<-max_slope(interp.dat.D$y)*100  #times by 100 to bring onto km scale
D_cline_width<-(1/D_cline_slope)
interp.dat.S<-aspline((test.val.S*pred_S$km)+positionsS, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_slope<-max_slope(interp.dat.S$y)*100  #times by 100 to bring onto km scale
S_cline_width<-(1/S_cline_slope)

D.vs.S_ratio.upper<-D_cline_width/S_cline_width

#FIND lower BOUND
##starting ratio of widths
D.vs.S_ratio<-results$D_cline_widths/results$S_cline_widths

mid_point_for_pivotD<-results$D_centres
positionsD<-results$positions_D
test.val.D<-results$stretch_factors_D
mid_point_for_pivotS<-results$S_centres
positionsS<-results$positions_S
test.val.S<-results$stretch_factors_S

starting_likelihood<-func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_S(c(positionsS,test.val.S))

while(func_likelihood_ERATO_LIKE_D(c(positionsD,test.val.D)) +
func_likelihood_ERATO_LIKE_S(c(positionsS,test.val.S))  > starting_likelihood - 2 )
{test.val.D<-test.val.D-0.0001
test.val.S<-test.val.S+0.0001
```

```
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.S<-aspline((test.val.S*pred_S$km)+positionsS, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.D<-interp.dat.D$x[which.min(abs(interp.dat.D$y-0.5))]
cline_centre.S<-interp.dat.S$x[which.min(abs(interp.dat.S$y-0.5))]
positionsD<-positionsD-(cline_centre.D-mid_point_for_pivotD)
positionsS<-positionsS-(cline_centre.S-mid_point_for_pivotS)
}
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope<-max_slope(interp.dat.D$y)*100  #times by 100 to bring onto km scale
D_cline_width<-(1/D_cline_slope)
interp.dat.S<-aspline((test.val.S*pred_S$km)+positionsS, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_slope<-max_slope(interp.dat.S$y)*100  #times by 100 to bring onto km scale
S_cline_width<-(1/S_cline_slope)

D.vs.S_ratio.lower<-D_cline_width/S_cline_width

while(func_likelihood_ERATO_LIKE_D(c(positions,test.val.upper)) > results[1,22] - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
D_cline_width_upper_interval<-(1/D_cline_slope_lower_interval)

mid_point_for_pivot<-results[1,13]
positions<-results[1,7]
test.val.lower<-results[1,10]
while(func_likelihood_ERATO_LIKE_D(c(positions,test.val.lower)) > results[1,22] - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_D$km)+positions, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
```

```
D_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
D_cline_width_lower_interval<-(1/D_cline_slope_upper_interval)

#do it for the C cline
mid_point_for_pivot<-results[1,14]
positions<-results[1,8]
test.val.upper<-results[1,11]
while(func_likelihood_ERATO_LIKE_C(c(positions,test.val.upper)) > results[1,23] - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
C_cline_width_upper_interval<-(1/C_cline_slope_lower_interval)

mid_point_for_pivot<-results[1,14]
positions<-results[1,8]
test.val.lower<-results[1,11]
while(func_likelihood_ERATO_LIKE_C(c(positions,test.val.lower)) > results[1,23] - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_C$km)+positions, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
C_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
C_cline_width_lower_interval<-(1/C_cline_slope_upper_interval)

#do it for the S cline
mid_point_for_pivot<-results[1,15]
positions<-results[1,9]
test.val.upper<-results[1,12]
while(func_likelihood_ERATO_LIKE_S(c(positions,test.val.upper)) > results[1,24] - 2 )
{test.val.upper<-test.val.upper+0.0001
interp.dat<-aspline((test.val.upper*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
```

```
}
print(paste("stretch upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(positions,test.val.upper)),sep=""))
interp.dat<-aspline((test.val.upper*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_slope_lower_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
S_cline_width_upper_interval<-(1/S_cline_slope_lower_interval)

mid_point_for_pivot<-results[1,15]
positions<-results[1,9]
test.val.lower<-results[1,12]
while(func_likelihood_ERATO_LIKE_S(c(positions,test.val.lower)) > results[1,24] - 2 )
{test.val.lower<-test.val.lower-0.0001
interp.dat<-aspline((test.val.lower*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
positions<-positions-(cline_centre-mid_point_for_pivot)
}
print(paste("stretch lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(positions,test.val.lower)),sep=""))
interp.dat<-aspline((test.val.lower*pred_S$km)+positions, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
S_cline_slope_upper_interval<-max_slope(interp.dat$y)*100  #times by 100 to bring onto km scale
S_cline_width_lower_interval<-(1/S_cline_slope_upper_interval)

# THIS IS FOR FINDING CENTRE SUPPORT LIMITS
#do it for the D cline
test.val.upper<-results[1,7]
while(func_likelihood_ERATO_LIKE_D(c(test.val.upper,results[1,10])) > results[1,22] - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(test.val.upper,results[1,10])),sep=""))
test.val.lower<-results[1,7]
while(func_likelihood_ERATO_LIKE_D(c(test.val.lower,results[1,10])) > results[1,22] - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_D(c(test.val.lower,results[1,10])),sep=""))

interp.dat<-aspline((results[1,10]*pred_D$km)+test.val.upper, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
D_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results[1,10]*pred_D$km)+test.val.lower, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
D_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
```

```
#do it for the C cline
test.val.upper<-results[1,8]
while(func_likelihood_ERATO_LIKE_C(c(test.val.upper,results[1,11])) > results[1,23] - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(test.val.upper,results[1,11])),sep=""))
test.val.lower<-results[1,8]
while(func_likelihood_ERATO_LIKE_C(c(test.val.lower,results[1,11])) > results[1,23] - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_C(c(test.val.lower,results[1,11])),sep=""))

interp.dat<-aspline((results[1,11]*pred_C$km)+test.val.upper, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
C_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results[1,11]*pred_C$km)+test.val.lower, pred_C$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
C_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]

#do it for the S cline
test.val.upper<-results[1,9]
while(func_likelihood_ERATO_LIKE_S(c(test.val.upper,results[1,12])) > results[1,24] - 2 )
{test.val.upper<-test.val.upper+0.0001
}
print(paste("centre upper bound =",test.val.upper,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(test.val.upper,results[1,12])),sep=""))
test.val.lower<-results[1,9]
while(func_likelihood_ERATO_LIKE_S(c(test.val.lower,results[1,12])) > results[1,24] - 2 )
{test.val.lower<-test.val.lower-0.0001
}
print(paste("centre lower bound =",test.val.lower,sep=""))
print(paste("likelihood = ",func_likelihood_ERATO_LIKE_S(c(test.val.lower,results[1,12])),sep=""))

interp.dat<-aspline((results[1,12]*pred_S$km)+test.val.upper, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
S_cline_centre_upper<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
interp.dat<-aspline((results[1,12]*pred_S$km)+test.val.lower, pred_S$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
S_cline_centre_lower<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]

results_for_best_fitting_cline<-results[1,]
results_for_best_fitting_cline<-
cbind(results_for_best_fitting_cline,D_cline_slope_lower_interval,D_cline_slope_upper_interval,D_cline_width_lower_interval,D_cline_width_upper_interval)
```

```
results_for_best_fitting_cline<-cbind(results_for_best_fitting_cline,C_cline_slope_lower_interval,C_cline_slope_upper_interval,C_cline_width_lower_interval,C_cline_width_upper_interval)
results_for_best_fitting_cline<-cbind(results_for_best_fitting_cline,S_cline_slope_lower_interval,S_cline_slope_upper_interval,S_cline_width_lower_interval,S_cline_width_upper_interval)
results_for_best_fitting_cline<-cbind(results_for_best_fitting_cline,D_cline_centre_upper,D_cline_centre_lower,C_cline_centre_upper,C_cline_centre_lower,S_cline_centre_upper,S_cline_centre_lower)

results_for_best_fitting_cline<-results_for_best_fitting_cline[-(c(1,7:12))]


##############################################################
###FIND SUPPORT LIMITS FOR WIDTH RATIO BETWEEN MELPOMENE CLINES###
##############################################################

library(akima)

func_likelihood_MELP_B <- function(x) {
	freqs_B <- aspline((x[2]*pred_B$km)+x[1], pred_B$freq, xout=obs$km, degree=10)
  p_B <- ((freqs_B$y*freqs_B$y)+(2*(freqs_B$y*(1-freqs_B$y))))
  p_B[p_B==0] <- 1e-55
  p_B[p_B==1] <- 1-1e-5
  #had to divide likelihood calculation up as R stored very small probabilities as zero (before was coded as likelihood_B<-sum((log(p_B^y_B))+ log((1-p_B)^(k_B-y_B))) - see erato script)
  part_a<-p_B^y_B
  part_b<-(1-p_B)^(k_B-y_B)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
  return(likelihood)
	}

func_likelihood_MELP_D <- function(x) {
  freqs_D <- aspline((x[2]*pred_D$km)+x[1], pred_D$freq, xout=obs$km, degree=10)
  p_D <- ((freqs_D$y*freqs_D$y)+(2*(freqs_D$y*(1-freqs_D$y))))
  p_D[p_D==0] <- 1e-55
  p_D[p_D==1] <- 1-1e-5
  part_a<-p_D^y_D
  part_b<-(1-p_D)^(k_D-y_D)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
  return(likelihood)
	}

func_likelihood_MELP_N <- function(x) {
```

```
	freqs_N <- aspline((x[2]*pred_N$km)+x[1], pred_N$freq, xout=obs$km, degree=10)
  p_N <- ((freqs_N$y*freqs_N$y)+(2*(freqs_N$y*(1-freqs_N$y))))
  p_N[p_N==0] <- 1e-55
  p_N[p_N==1] <- 1-1e-5
  part_a<-p_N^y_N
  part_b<-(1-p_N)^(k_N-y_N)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
  return(likelihood)
	}

func_likelihood_MELP_Y <- function(x) {
	freqs_Y <- aspline((x[2]*pred_Y$km)+x[1], pred_Y$freq, xout=obs$km, degree=10)
  p_Y <- ((freqs_Y$y*freqs_Y$y)+(2*(freqs_Y$y*(1-freqs_Y$y))))
  p_Y[p_Y==0] <- 1e-55
  p_Y[p_Y==1] <- 1-1e-5
  part_a<-p_Y^y_Y
  part_b<-(1-p_Y)^(k_Y-y_Y)
  part_a[part_a==0] <- 1e-55
  part_b[part_b==0] <- 1e-55
  likelihood<-sum(log(part_a)+log(part_b))
  return(likelihood)
	}

#Find max slope of simulated cline function
max_slope <- function(x) {
slopes<-c()
for (i in 1:(length(x)-1)){
slopes<-append(slopes,x[i+1]-x[i])}
return(max(slopes))
}

#observed data
obsJM <- read.csv("melpomene1990.csv", header=T, sep=",")
obsNR <- read.csv("melpomene2011.csv", header=T, sep=",")
combined <- read.csv("melpomene_combined.csv", header=T, sep=",")
predicted_all_data <- read.csv("melp_sim_results.csv", header=T, sep=",")
predicted_all_data<-
subset(predicted_all_data,selectionB==0.6&selectionD==0.6&selectionN==0.6&selectionY==0.6&recomb_r_BD==0.135)

#Approximate point of the middle of the hybrid zone on the transect (this is used as a starting point in the optimization algorithm) (123.57 is Mallet 1990 estimated centre of D cline).
approx_mid_point<-123.57

#change this to the date set you want to analyse
obs<-combined
```

```
obs <- obs[order(obs$km),]

#Subset the B locus
predicted_B<-subset(predicted_all_data, predicted_all_data$locus == "B")
rownames(predicted_B) <- seq(length=nrow(predicted_B))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_B<-predicted_B[10:ncol(predicted_B)]
demes<-c(1:ncol(predicted_for_loops_B))

k_B <- obs$total_alleles/2 ## total number individuals
y_B <- k_B-(obs$n_bb_individuals)  ## total number of B- individuals

#Subset the D locus
predicted_D<-subset(predicted_all_data, predicted_all_data$locus == "D")
rownames(predicted_D) <- seq(length=nrow(predicted_D))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_D<-predicted_D[10:ncol(predicted_D)]
demes<-c(1:ncol(predicted_for_loops_D))

k_D <- obs$total_alleles/2 ## total number individuals
y_D <- k_D-(obs$n_dd_individuals)  ## total number of D- individuals

#Subset the N locus
predicted_N<-subset(predicted_all_data, predicted_all_data$locus == "N")
rownames(predicted_N) <- seq(length=nrow(predicted_N))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_N<-predicted_N[10:ncol(predicted_N)]
demes<-c(1:ncol(predicted_for_loops_N))

k_N <- obs$total_alleles/2 ## total number individuals
y_N <- k_N-(obs$n_nn_individuals)  ## total number of N- individuals

#Subset the Y locus (predicted cline is the same as the N locus assuming very tight linkage)...
predicted_Y<-subset(predicted_all_data, predicted_all_data$locus == "Y")
rownames(predicted_Y) <- seq(length=nrow(predicted_Y))

#this predicted for loops is just the allele frequencies without the row details, so you may have to
change the "5" depending on the input file
predicted_for_loops_Y<-predicted_Y[10:ncol(predicted_Y)]
demes<-c(1:ncol(predicted_for_loops_Y))

k_Y <- obs$total_alleles/2 ## total number individuals
```

```
y_Y <- k_Y-(obs$n_yy_individuals)  ## total number of Y- individuals

#Now loop through all the parameter combinations, calculate the likelihood and return
likelihoods<-c()
likelihoods_B<-c()
likelihoods_D<-c()
likelihoods_N<-c()
likelihoods_Y<-c()
positions_B<-c()
positions_D<-c()
positions_N<-c()
positions_Y<-c()
stretch_factors_B<-c()
stretch_factors_D<-c()
stretch_factors_N<-c()
stretch_factors_Y<-c()
B_centres<-c()
D_centres<-c()
N_centres<-c()
Y_centres<-c()
B_cline_widths<-c()
D_cline_widths<-c()
N_cline_widths<-c()
Y_cline_widths<-c()
B_max_slope<-c()
D_max_slope<-c()
N_max_slope<-c()
Y_max_slope<-c()

for (i in 1:nrow(predicted_B)){

pred_B <- data.frame(demes,t(predicted_for_loops_B[i,]))
pred_D <- data.frame(demes,t(predicted_for_loops_D[i,]))
pred_N <- data.frame(demes,t(predicted_for_loops_N[i,]))
pred_Y <- data.frame(demes,t(predicted_for_loops_Y[i,]))

names(pred_B) <- c("km_B","freq_B")
names(pred_D) <- c("km_D","freq_D")
names(pred_N) <- c("km_N","freq_N")
names(pred_Y) <- c("km_Y","freq_Y")

#optimisation algorithm,
# starting parameters = 1) align the approx middle of the hybrid zone with the middle of the simulated cline, and 2) using 1 as the stretch factor (i.e. no stretch: less than 1 squeezes the cline together, greater than 1 pulls it apart).
approx_centre_sim_D<-which.min(abs(pred_D$freq_D-0.5))
starting_param_1<-approx_mid_point-approx_centre_sim_D  #this find the difference between the observed data and simulated data using the D locus, and uses this as a starting point
```

```
likelihood_B <- optim(par = c(starting_param_1,1), func_likelihood_MELP_B, NULL, control=list(fnscale=-
1))
likelihood_D <- optim(par = c(starting_param_1,1), func_likelihood_MELP_D, NULL,
control=list(fnscale=-1))
likelihood_N <- optim(par = c(starting_param_1,1), func_likelihood_MELP_N, NULL,
control=list(fnscale=-1))
likelihood_Y <- optim(par = c(starting_param_1,1), func_likelihood_MELP_Y, NULL, control=list(fnscale=-
1))
likelihood<-sum(likelihood_B$value,likelihood_D$value,likelihood_N$value,likelihood_Y$value)
#find middle of clines and widths
#this is a clunky bit to find the centre of the cline; the spline doesn't seem to be able to find the x value
for a given y value, only the other way round, so had to do it like this
interp.dat<-aspline((likelihood_B$par[2]*pred_B$km)+likelihood_B$par[1], pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
B_cline_max_slope<-max_slope(1-interp.dat$y)
B_cline_width<-(1/B_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

interp.dat<-aspline((likelihood_D$par[2]*pred_D$km)+likelihood_D$par[1], pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
D_cline_max_slope<-max_slope(interp.dat$y)
D_cline_width<-(1/D_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

interp.dat<-aspline((likelihood_N$par[2]*pred_N$km)+likelihood_N$par[1], pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
N_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
N_cline_max_slope<-max_slope(interp.dat$y)
N_cline_width<-(1/N_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

interp.dat<-aspline((likelihood_Y$par[2]*pred_Y$km)+likelihood_Y$par[1], pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
Y_cline_centre<-interp.dat$x[which.min(abs(interp.dat$y-0.5))]
Y_cline_max_slope<-max_slope(interp.dat$y)
Y_cline_width<-(1/Y_cline_max_slope)/100 #divide by 100 to bring into km scale (10m was specified in
the interp.dat fine scale)

#append results to results vectors..
likelihoods<-append(likelihoods,likelihood)
likelihoods_B<-append(likelihoods_B,likelihood_B$value)
likelihoods_D<-append(likelihoods_D,likelihood_D$value)
likelihoods_N<-append(likelihoods_N,likelihood_N$value)
likelihoods_Y<-append(likelihoods_Y,likelihood_Y$value)
positions_B<-append(positions_B,likelihood_B$par[1])
positions_D<-append(positions_D,likelihood_D$par[1])
```

```
positions_N<-append(positions_N,likelihood_N$par[1])
positions_Y<-append(positions_Y,likelihood_Y$par[1])
stretch_factors_B<-append(stretch_factors_B,likelihood_B$par[2])
stretch_factors_D<-append(stretch_factors_D,likelihood_D$par[2])
stretch_factors_N<-append(stretch_factors_N,likelihood_N$par[2])
stretch_factors_Y<-append(stretch_factors_Y,likelihood_Y$par[2])
B_centres<-append(B_centres,B_cline_centre)
D_centres<-append(D_centres,D_cline_centre)
N_centres<-append(N_centres,N_cline_centre)
Y_centres<-append(Y_centres,Y_cline_centre)
B_cline_widths<-append(B_cline_widths,B_cline_width)
D_cline_widths<-append(D_cline_widths,D_cline_width)
N_cline_widths<-append(N_cline_widths,N_cline_width)
Y_cline_widths<-append(Y_cline_widths,Y_cline_width)
B_max_slope<-append(B_max_slope,B_cline_max_slope*100)#times 100 to bring on to km scale
D_max_slope<-append(D_max_slope,D_cline_max_slope*100)#times 100 to bring on to km scale
N_max_slope<-append(N_max_slope,N_cline_max_slope*100)#times 100 to bring on to km scale
Y_max_slope<-append(Y_max_slope,Y_cline_max_slope*100)#times 100 to bring on to km scale

}

results<-cbind(predicted_D[1:9],likelihoods,likelihoods_B,likelihoods_D,likelihoods_N,likelihoods_Y,positions_B,positions_D,positions_N,positions_Y,stretch_factors_B,stretch_factors_D,stretch_factors_N,stretch_factors_Y,B_centres,D_centres,N_centres,Y_centres,B_cline_widths,D_cline_widths,N_cline_widths,Y_cline_widths,B_max_slope,D_max_slope,N_max_slope,Y_max_slope)

results<-results[order(-results$likelihoods),]

#put in the row for the most likely selection values here...
pred_B <- data.frame(demes,t(predicted_for_loops_B[row.names(results)[1],]))
pred_D <- data.frame(demes,t(predicted_for_loops_D[row.names(results)[1],]))
pred_N <- data.frame(demes,t(predicted_for_loops_N[row.names(results)[1],]))
pred_Y <- data.frame(demes,t(predicted_for_loops_Y[row.names(results)[1],]))

names(pred_B) <- c("km_B","freq_B")
names(pred_D) <- c("km_D","freq_D")
names(pred_N) <- c("km_N","freq_N")
names(pred_Y) <- c("km_Y","freq_Y")

# THIS IS FOR FINDING THE WIDTH RATIO SUPPORT LIMITS
# basically I widen one cline while simulataneously narrowing the other, until the summed likelihoods of the two clines drops by -2/
#the code is quite long because each time you play with the stretch factor that moves the position of the centre of the cline, so you keep
#having to realign the cline and make the centre in the same place it was before.

### DO IT FOR D VERSUS B
```

```
#Find the upper bound
##starting ratio of widths
D.vs.B_ratio<-results$D_cline_widths/results$B_cline_widths

#for the D cline
mid_point_for_pivotD<-results$D_centres
positionsD<-results$positions_D
test.val.D<-results$stretch_factors_D
#for the B cline
mid_point_for_pivotB<-results$B_centres
positionsB<-results$positions_B
test.val.B<-results$stretch_factors_B

starting_likelihood<-func_likelihood_MELP_D(c(positionsD,test.val.D)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))

while(func_likelihood_MELP_D(c(positionsD,test.val.D)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))  > starting_likelihood - 2 )
{test.val.D<-test.val.D+0.0001
test.val.B<-test.val.B-0.0001
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.D<-interp.dat.D$x[which.min(abs(interp.dat.D$y-0.5))]
cline_centre.B<-interp.dat.B$x[which.min(abs(interp.dat.B$y-0.5))]
positionsD<-positionsD-(cline_centre.D-mid_point_for_pivotD)
positionsB<-positionsB-(cline_centre.B-mid_point_for_pivotB)
}
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope<-max_slope(interp.dat.D$y)*100  #times by 100 to bring onto km scale
D_cline_width<-(1/D_cline_slope)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope<-max_slope(1-interp.dat.B$y)*100  #times by 100 to bring onto km scale
B_cline_width<-(1/B_cline_slope)

D.vs.B_ratio.upper<-D_cline_width/B_cline_width

#Find the lower bound
##starting ratio of widths
D.vs.B_ratio<-results$D_cline_widths/results$B_cline_widths

#for the D cline
mid_point_for_pivotD<-results$D_centres
positionsD<-results$positions_D
test.val.D<-results$stretch_factors_D
```

```
#for the B cline
mid_point_for_pivotB<-results$B_centres
positionsB<-results$positions_B
test.val.B<-results$stretch_factors_B

starting_likelihood<-func_likelihood_MELP_D(c(positionsD,test.val.D)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))

while(func_likelihood_MELP_D(c(positionsD,test.val.D)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))  > starting_likelihood - 2 )
{test.val.D<-test.val.D-0.0001
test.val.B<-test.val.B+0.0001
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.D<-interp.dat.D$x[which.min(abs(interp.dat.D$y-0.5))]
cline_centre.B<-interp.dat.B$x[which.min(abs(interp.dat.B$y-0.5))]
positionsD<-positionsD-(cline_centre.D-mid_point_for_pivotD)
positionsB<-positionsB-(cline_centre.B-mid_point_for_pivotB)
}
interp.dat.D<-aspline((test.val.D*pred_D$km)+positionsD, pred_D$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
D_cline_slope<-max_slope(interp.dat.D$y)*100  #times by 100 to bring onto km scale
D_cline_width<-(1/D_cline_slope)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope<-max_slope(1-interp.dat.B$y)*100  #times by 100 to bring onto km scale
B_cline_width<-(1/B_cline_slope)

D.vs.B_ratio.lower<-D_cline_width/B_cline_width

### DO IT FOR N VERSUS B
#Find the upper bound
##starting ratio of widths
N.vs.B_ratio<-results$N_cline_widths/results$B_cline_widths

#for the N cline
mid_point_for_pivotN<-results$N_centres
positionsN<-results$positions_N
test.val.N<-results$stretch_factors_N
#for the B cline
mid_point_for_pivotB<-results$B_centres
positionsB<-results$positions_B
test.val.B<-results$stretch_factors_B

starting_likelihood<-func_likelihood_MELP_N(c(positionsN,test.val.N)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))
```

```
while(func_likelihood_MELP_N(c(positionsN,test.val.N)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))  > starting_likelihood - 2 )
{test.val.N<-test.val.N+0.0001
test.val.B<-test.val.B-0.0001
interp.dat.N<-aspline((test.val.N*pred_N$km)+positionsN, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.N<-interp.dat.N$x[which.min(abs(interp.dat.N$y-0.5))]
cline_centre.B<-interp.dat.B$x[which.min(abs(interp.dat.B$y-0.5))]
positionsN<-positionsN-(cline_centre.N-mid_point_for_pivotN)
positionsB<-positionsB-(cline_centre.B-mid_point_for_pivotB)
}
interp.dat.N<-aspline((test.val.N*pred_N$km)+positionsN, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
N_cline_slope<-max_slope(interp.dat.N$y)*100  #times by 100 to bring onto km scale
N_cline_width<-(1/N_cline_slope)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope<-max_slope(1-interp.dat.B$y)*100  #times by 100 to bring onto km scale
B_cline_width<-(1/B_cline_slope)

N.vs.B_ratio.upper<-N_cline_width/B_cline_width

#Find the lower bound
##starting ratio of widths
N.vs.B_ratio<-results$N_cline_widths/results$B_cline_widths

#for the N cline
mid_point_for_pivotN<-results$N_centres
positionsN<-results$positions_N
test.val.N<-results$stretch_factors_N
#for the B cline
mid_point_for_pivotB<-results$B_centres
positionsB<-results$positions_B
test.val.B<-results$stretch_factors_B

starting_likelihood<-func_likelihood_MELP_N(c(positionsN,test.val.N)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))

while(func_likelihood_MELP_N(c(positionsN,test.val.N)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))  > starting_likelihood - 2 )
{test.val.N<-test.val.N-0.0001
test.val.B<-test.val.B+0.0001
interp.dat.N<-aspline((test.val.N*pred_N$km)+positionsN, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
```

```
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.N<-interp.dat.N$x[which.min(abs(interp.dat.N$y-0.5))]
cline_centre.B<-interp.dat.B$x[which.min(abs(interp.dat.B$y-0.5))]
positionsN<-positionsN-(cline_centre.N-mid_point_for_pivotN)
positionsB<-positionsB-(cline_centre.B-mid_point_for_pivotB)
}
interp.dat.N<-aspline((test.val.N*pred_N$km)+positionsN, pred_N$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
N_cline_slope<-max_slope(interp.dat.N$y)*100  #times by 100 to bring onto km scale
N_cline_width<-(1/N_cline_slope)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope<-max_slope(1-interp.dat.B$y)*100  #times by 100 to bring onto km scale
B_cline_width<-(1/B_cline_slope)

N.vs.B_ratio.lower<-N_cline_width/B_cline_width

### DO IT FOR Y VERSUS B
#Find the upper bound
##starting ratio of widths
Y.vs.B_ratio<-results$Y_cline_widths/results$B_cline_widths

#for the Y cline
mid_point_for_pivotY<-results$Y_centres
positionsY<-results$positions_Y
test.val.Y<-results$stretch_factors_Y
#for the B cline
mid_point_for_pivotB<-results$B_centres
positionsB<-results$positions_B
test.val.B<-results$stretch_factors_B

starting_likelihood<-func_likelihood_MELP_Y(c(positionsY,test.val.Y)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))

while(func_likelihood_MELP_Y(c(positionsY,test.val.Y)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))  > starting_likelihood - 2 )
{test.val.Y<-test.val.Y+0.0001
test.val.B<-test.val.B-0.0001
interp.dat.Y<-aspline((test.val.Y*pred_Y$km)+positionsY, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.Y<-interp.dat.Y$x[which.min(abs(interp.dat.Y$y-0.5))]
cline_centre.B<-interp.dat.B$x[which.min(abs(interp.dat.B$y-0.5))]
positionsY<-positionsY-(cline_centre.Y-mid_point_for_pivotY)
positionsB<-positionsB-(cline_centre.B-mid_point_for_pivotB)
}
```

```
interp.dat.Y<-aspline((test.val.Y*pred_Y$km)+positionsY, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
Y_cline_slope<-max_slope(interp.dat.Y$y)*100  #times by 100 to bring onto km scale
Y_cline_width<-(1/Y_cline_slope)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope<-max_slope(1-interp.dat.B$y)*100  #times by 100 to bring onto km scale
B_cline_width<-(1/B_cline_slope)

Y.vs.B_ratio.upper<-Y_cline_width/B_cline_width

#Find the lower bound
##starting ratio of widths
Y.vs.B_ratio<-results$Y_cline_widths/results$B_cline_widths

#for the Y cline
mid_point_for_pivotY<-results$Y_centres
positionsY<-results$positions_Y
test.val.Y<-results$stretch_factors_Y
#for the B cline
mid_point_for_pivotB<-results$B_centres
positionsB<-results$positions_B
test.val.B<-results$stretch_factors_B

starting_likelihood<-func_likelihood_MELP_Y(c(positionsY,test.val.Y)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))

while(func_likelihood_MELP_Y(c(positionsY,test.val.Y)) +
func_likelihood_MELP_B(c(positionsB,test.val.B))  > starting_likelihood - 2 )
{test.val.Y<-test.val.Y-0.0001
test.val.B<-test.val.B+0.0001
interp.dat.Y<-aspline((test.val.Y*pred_Y$km)+positionsY, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10)
cline_centre.Y<-interp.dat.Y$x[which.min(abs(interp.dat.Y$y-0.5))]
cline_centre.B<-interp.dat.B$x[which.min(abs(interp.dat.B$y-0.5))]
positionsY<-positionsY-(cline_centre.Y-mid_point_for_pivotY)
positionsB<-positionsB-(cline_centre.B-mid_point_for_pivotB)
}
interp.dat.Y<-aspline((test.val.Y*pred_Y$km)+positionsY, pred_Y$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
Y_cline_slope<-max_slope(interp.dat.Y$y)*100  #times by 100 to bring onto km scale
Y_cline_width<-(1/Y_cline_slope)
interp.dat.B<-aspline((test.val.B*pred_B$km)+positionsB, pred_B$freq, xout=
seq(min(obs$km),max(obs$km),0.01), degree=10) #generate interpolated values at a fine scale (to 10m)
B_cline_slope<-max_slope(1-interp.dat.B$y)*100  #times by 100 to bring onto km scale
B_cline_width<-(1/B_cline_slope)
```

```
Y.vs.B_ratio.lower<-Y_cline_width/B_cline_width
```

| | | | | |
|---|---|---|---|---|
| Chazuta | S6.56654 W76.12738 | dd | cc | ss |
| Chazuta | S6.56156 W76.12345 | dd | cc | ss |
| Chazuta | S6.55604 W76.12113 | dd | cc | ss |
| Chazuta | S6.56654 W76.12749 | dd | cc | ss |
| Chazuta | S6.56654 W76.12749 | dd | cc | ss |
| Chazuta | S6.56654 W76.12749 | dd | cc | ss |
| Chazuta | S6.56658 W76.12732 | dd | cc | ss |
| Chazuta | S6.56380 W76.12621 | dd | cc | ss |
| Chazuta | S6.56380 W76.12621 | dd | cc | ss |
| Chazuta | S6.56345 W76.12596 | dd | cc | ss |
| Chazuta | S6.56311 W76.12593 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56654 W76.12749 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.55865 W76.12026 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56532 W76.12724 | dd | cc | ss |
| Chazuta | S6.56532 W76.12724 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Chazuta | S6.56379 W76.12296 | dd | cc | ss |
| Davicillo | S6.25082 W76.26954 | DD | cc | S- |
| Davicillo | S6.24880 W76.26436 | DD | C- | Ss |
| Davicillo | S6.25061 W76.26853 | DD | C- | S- |
| Davicillo | S6.25080 W76.26948 | DD | C- | S- |
| Davicillo | S6.25080 W76.26948 | DD | C- | S- |
| Davicillo | S6.25080 W76.26948 | DD | C- | S- |
| Davicillo | S6.25080 W76.26948 | DD | C- | S- |
| Davicillo | S6.25080 W76.26948 | Dd | C- | SS |
| Davicillo | S6.25080 W76.26948 | DD | C- | S- |
| Davicillo | S6.25087 W76.26925 | DD | C- | S- |
| Davicillo | S6.25135 W76.26749 | DD | C- | S- |
| Davicillo | S6.25135 W76.26749 | Dd | C- | SS |

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| Davicillo | S6.24880 W76.26441 | | | DD | C- | S- |
| Davicillo | S6.25135 W76.26749 | | | DD | C- | S- |
| Davicillo | S6.24880 W76.26441 | | | DD | C- | S- |
| Davicillo | S6.24880 W76.26441 | | | DD | C- | S- |
| Davicillo | S6.24880 W76.26441 | | | DD | C- | S- |
| Davicillo | S6.24880 W76.26441 | | | DD | C- | S- |
| Davicillo | S6.24880 W76.26441 | | | DD | C- | S- |
| Davicillo | S6.25080 W76.26986 | | | DD | C- | S- |
| Davicillo | S6.25135 W76.26749 | | | DD | C- | S- |
| Davicillo | S6.25135 W76.26749 | | | DD | C- | S- |
| Davicillo | | S6.248668 W76.264448 | ±150m | DD | C- | S- |
| Davicillo | | S6.248668 W76.264448 | ±150m | DD | C- | S- |
| Davicillo | | S6.248668 W76.264448 | ±150m | DD | C- | S- |
| Davicillo | S6.24886 W76.26434 | | | DD | C- | S- |
| Davicillo | S6.24886 W76.26434 | | | DD | C- | S- |
| Davicillo | S6.24886 W76.26434 | | | DD | C- | S- |
| Davicillo | S6.24886 W76.26434 | | | DD | C- | S- |
| Davicillo | S6.24886 W76.26434 | | | DD | C- | S- |
| Davicillo | | S6.248668 W76.264448 | ±150m | DD | C- | S- |
| Davicillo | S6.25127 W76.26755 | | | DD | C- | S- |
| Davicillo | S6.25127 W76.26755 | | | DD | C- | S- |
| Davicillo | S6.25127 W76.26755 | | | DD | C- | S- |
| Davicillo | S6.25127 W76.26755 | | | DD | C- | S- |
| Davicillo | S6.25061 W76.26843 | | | Dd | C- | S- |
| Davicillo | S6.25061 W76.26843 | | | DD | C- | S- |
| Davicillo | S6.25061 W76.26843 | | | DD | C- | S- |
| Davicillo | S6.25061 W76.26843 | | | DD | C- | S- |
| Davicillo | S6.25061 W76.26843 | | | DD | C- | S- |
| Davicillo | S6.25061 W76.26843 | | | DD | C- | S- |
| Davicillo | S6.25061 W76.26843 | | | DD | C- | S- |
| Davicillo | S6.249882 W76.266064 | | | DD | C- | S- |
| Davicillo | S6.249882 W76.266064 | | | DD | C- | S- |
| Davicillo | S6.24881 W76.26441 | | | Dd | C- | S- |
| Davicillo | S6.24881 W76.26441 | | | DD | C- | S- |
| Davicillo | S6.24871 W76.26431 | | | DD | C- | S- |
| El pongo del Cainarachi | | S6.338617 W76.288283 | ±50m | dd | C- | S- |
| El Tunel | S6.44850 W76.28728 | | | dd | cc | ss |
| El Tunel | S6.45423 W76.28515 | | | dd | cc | Ss |
| El Tunel | S6.45551 W76.28430 | | | dd | cc | ss |
| El Tunel | S6.45551 W76.28430 | | | dd | cc | ss |
| El Tunel | | S6.453253 W76.287319 | ±100m | dd | cc | ss |
| El Tunel | S6.45289 W76.28637 | | | dd | cc | ss |
| El Tunel | S6.45359 W76.28789 | | | dd | cc | ss |
| El Tunel | S6.45396 W76.28547 | | | dd | cc | ss |
| El Tunel | S6.45396 W76.28547 | | | dd | cc | Ss |
| El Tunel | S6.45396 W76.28547 | | | dd | cc | ss |

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| El Tunel | S6.45396 W76.28547 | | | dd | cc | ss |
| El Tunel | S6.45673 W76.28439 | | | dd | cc | ss |
| El Tunel | S6.45673 W76.28439 | | | dd | cc | ss |
| El Tunel | S6.45673 W76.28439 | | | dd | cc | Ss |
| El Tunel | S6.45673 W76.28439 | | | dd | cc | ss |
| El Tunel | S6.45673 W76.28439 | | | dd | cc | ss |
| El Tunel | S6.45785 W76.28507 | | | dd | cc | ss |
| El Tunel | S6.45785 W76.28507 | | | dd | cc | ss |
| El Tunel | S6.45785 W76.28507 | | | dd | cc | ss |
| El Tunel | S6.45785 W76.28507 | | | Dd | cc | Ss |
| El Tunel | S6.45669 W76.28441 | | | dd | cc | ss |
| El Tunel | S6.45588 W76.28398 | | | dd | cc | ss |
| El Tunel | S6.45588 W76.28398 | | | dd | cc | ss |
| El Tunel | | S6.454000 W76.285439 | ±150m | dd | cc | ss |
| El Tunel | S6.45277 W76.28632 | | | dd | cc | ss |
| El Tunel - km32.5 trail | S6.44894 W76.28132 | | | dd | cc | ss |
| El Tunel - km32.5 trail | S6.45628 W76.27714 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | S6.26930 W76.75069 | | | dd | cc | ss |
| Florida | | S6.267960 W76.749276 | ±300m | dd | cc | ss |
| Florida | | S6.267960 W76.749276 | ±300m | dd | cc | ss |
| Florida | | S6.267960 W76.749276 | ±300m | dd | cc | ss |
| Florida | S6.266642 W76.74789 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.47669 W76.35183 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.47668 W76.35199 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | | S6.47622 W76.35176 | ±150m | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.47617 W76.35177 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.47730 W76.35170 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.47676 W76.35184 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.47234 W76.35004 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.46992 W76.34619 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.46992 W76.34619 | | | dd | cc | ss |
| Fraser's Pardalinus Trail | S6.47045 W76.34783 | | | dd | cc | ss |
| Jepelacio | S6.10206 W76.94178 | | | dd | cc | ss |
| La Antena | S6.45468 W76.29933 | | | dd | cc | ss |
| La Antena | S6.45468 W76.29933 | | | dd | cc | ss |
| La Antena | S6.454679 W76.299326 | | | dd | cc | ss |

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|---|---|---|---|---|---|---|
| La Antena | S6.45431 W76.29889 | | | dd | cc | ss |
| La Antena | S06.45431 W076.29889 | | | dd | cc | ss |
| La Carachamera | S6.43152 W76.25316 | | | dd | cc | ss |
| La Carachamera | S6.43166 W76.25295 | | | dd | cc | ss |
| Micaela Bastida km6.1 | S5.94594 W76.24637 | | | DD | C- | S- |
| Micaela Bastida km6.1 | S5.94582 W76.24720 | | | DD | C- | S- |
| Micaela Bastida km6.1 | S5.94576 W76.24687 | | | DD | C- | S- |
| Micaela Bastida km6.1 | S5.94583 W76.24658 | | | DD | C- | S- |
| Micaela Bastida km6.1 | S5.94583 W76.24658 | | | DD | C- | S- |
| Micaela Ba-tida km 4.8 | S5.960674 W76.244929 | | | DD | C- | S- |
| Micaela Ba-tida km 4.8 | S5.954868 W76.239834 | | | DD | C- | S- |
| Micaela Ba-tida km 6.1 | S5.9458 W76.24552 | | | DD | C- | S- |
| Micaela Ba-tida km 6.1 | S5.94587 W76.24526 | | | DD | C- | S- |
| Micaela Ba-tida km 6.1 | S5.94587 W76.24526 | | | DD | C- | S- |
| Micaela Ba-tida km 6.1 | S5.945549 W76.245444 | | | DD | C- | S- |
| Micaela Ba-tida km 6.1 | S5.9456 W76.24495 | | | DD | C- | S- |
| Moyobamba Antenna | S6.09736 W76.98174 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09736 W76.98174 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09701 W76.98145 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09736 W76.98174 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09736 W76.98174 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09588 W76.97728 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09602 W76.97742 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09428 W76.97146 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09512 W76.97936 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09588 W76.97728 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09512 W76.97936 | | | dd | cc | ss |
| Moyobamba Antenna | S6.09445 W76.97080 | | | dd | cc | ss |
| Pongo | S06.29917 W076.23529 | | | DD | C- | S- |
| Pongo - Barranquita km3.5 | S6.31371 W76.25829 | | | DD | C- | S- |
| Pongo - Barranquita km3.5 | S6.30868 W76.25721 | | | Dd | C- | S- |
| Pongo - Barranquita km3.5 | S6.30868 W76.25721 | | | DD | C- | S- |
| Pongo - Barranquitas km6 | S6.29990 W76.23557 | | | DD | C- | S- |
| Pongo - Barranquitas km6.3 | S6.297089 W76.235164 | | | DD | C- | S- |
| Pongo - Barranquitas: either km 6.3 or km7.2 | S6.290752 W76.235435 | | | DD | C- | Ss |
| Pongo Cataratas | S6.35276 W76.30186 | | | dd | C- | Ss |
| Pongo Cataratas | S6.34888 W76.30000 | | | dd | Cc | ss |
| Pongo Cataratas | S6.35044 W76.30023 | | | dd | cc | ss |
| Pongo Cataratas | S6.34950 W76.30008 | | | dd | Cc | ss |
| Pongo Cataratas | S6.34950 W76.30008 | | | Dd | C- | Ss |
| Pongo Cataratas | S6.34947 W76.29986 | | | Dd | C- | SS |
| Pongo Cataratas | S6.34947 W76.29986 | | | DD | cc | ss |
| Pongo Cataratas | S6.34947 W76.29986 | | | dd | Cc | ss |
| Pongo Cataratas | S6.35254 W76.30157 | | | dd | Cc | ss |
| Pongo Cataratas | S6.35018 W76.30008 | | | Dd | C- | Ss |
| Pongo Cataratas | | S6.348430 W76.302170 | ±50m | Dd | C- | S- |

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| Pongo Cataratas | | S6.348430 W76.302170 | ±50m | dd | Cc | ss |
| Pongo Cataratas | | S6.348430 W76.302170 | ±50m | Dd | cc | Ss |
| Pongo Cataratas | | S6.348430 W76.302170 | ±50m | dd | cc | S- |
| Pongo Cataratas | | S6.348430 W76.302170 | ±50m | dd | C- | S- |
| Pongo Cataratas | S6.35114 W76.30119 | | | Dd | Cc | ss |
| Pongo Cataratas | S6.35081 W76.30034 | | | Dd | cc | ss |
| Pongo de Cainarache | S6.33628 W76.27858 | | | DD | C- | Ss |
| Pongo de Cainarache, south of | S6.33903 W76.28200 | | | DD | C- | Ss |
| Pongo-Barranquitas km5.9 | S6.30507 W76.23275 | | | DD | C- | Ss |
| Pongo-Barranquitas km5.9 | S6.30575 W76.23215 | | | Dd | C- | Ss |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | Dd | C- | SS |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30615 W76.22977 | | | DD | C- | Ss |
| Pongo-Barranquitas km5.9 | S6.30531 W76.23254 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30355 W76.23367 | | | dd | C- | Ss |
| Pongo-Barranquitas km5.9 | S6.30079 W76.23603 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30272 W76.23368 | | | DD | cc | S- |
| Pongo-Barranquitas km5.9 | S6.30079 W76.23603 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30282 W76.23377 | | | Dd | C- | Ss |
| Pongo-Barranquitas km5.9 | S6.30282 W76.23377 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.302929 W76.234025 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30472 W76.23311 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30347 W76.23379 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.306407 W76.230117 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30711 W76.22987 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30527 W76.23254 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30527 W76.23254 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.306407 W76.230117 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30489 W76.23293 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | DD | C- | S- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | DD | C- | S- |
| Pongo-Barranquitas km6 | S6.29990 W76.23557 | | | DD | C- | S- |
| Pongo-Barranquitas km6 | | S6.298590 W76.237088 | ±200m | DD | C- | Ss |
| Pongo-Barranquitas km6 | | S6.298590 W76.237088 | ±200m | DD | C- | S- |
| Pongo-Barranquitas km6 | S6.29960 W76.23534 | | | DD | C- | S- |
| Pongo-Barranquitas km6.3 | | | | DD | C- | S- |
| Pongo-Barranquitas km6.3 | | | | DD | C- | S- |
| Rancho Vista | S6.46147 W76.35926 | | | dd | cc | ss |
| Rancho Vista | S6.46002 W76.35941 | | | dd | cc | ss |
| Rancho Vista | S6.45500 W76.35906 | | | dd | cc | ss |
| Rancho Vista | S6.45635 W76.35852 | | | dd | cc | ss |
| Rancho Vista | S6.45827 W76.35914 | | | dd | cc | ss |
| Rancho Vista | S6.45657 W76.35836 | | | dd | cc | ss |
| Rancho Vista | S6.45812 W76.35931 | | | dd | cc | ss |

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| Rancho Vista | S6.45812 W76.35931 | | | dd | cc | ss |
| Rancho Vista | S6.45515 W76.35909 | | | dd | cc | ss |
| Rancho Vista | S6.45159 W76.35851 | | | dd | cc | ss |
| Rancho Vista | S6.45160 W76.35849 | | | dd | cc | ss |
| Rancho Vista | | S6.45515 W76.35909 | ±700m | dd | cc | ss |
| Rio Shilcayo | S6.45599 W76.34688 | | | dd | cc | ss |
| Rio Shilcayo | S6.45508 W76.34611 | | | dd | cc | ss |
| Rio Shilcayo | S6.45508 W76.34611 | | | dd | cc | ss |
| Rio Shilcayo | S6.45508 W76.34611 | | | dd | cc | ss |
| Rio Shilcayo | S6.45508 W76.34611 | | | dd | cc | ss |
| Rio Shilcayo | S6.45508 W76.34611 | | | dd | cc | ss |
| Rio Shilcayo | S6.45539 W76.34479 | | | dd | cc | ss |
| Rio Shilcayo | S6.46708 W76.35302 | | | dd | cc | ss |
| Rio Shilcayo | S6.45165 W76.34596 | | | dd | cc | ss |
| Rio Shilcayo | S6.45508 W76.34611 | | | dd | cc | ss |
| Rio Shilcayo | S6.45508 W76.34611 | | | dd | cc | ss |
| Rio Shilcayo | S6.46402 W76.35125 | | | dd | cc | ss |
| Rio Shilcayo | S6.45849 W76.34896 | | | dd | cc | ss |
| Rio Shilcayo | S6.46913 W76.35440 | | | dd | cc | ss |
| Rio Shilcayo | S6.46575 W76.35265 | | | dd | cc | ss |
| Rio Shilcayo | S6.47382 W76.35425 | | | dd | cc | ss |
| Rio Shilcayo | | S6.46708 W76.35302 | ±150m | dd | cc | ss |
| Rio Shilcayo | S6.45735 W76.35266 | | | dd | cc | ss |
| Rio Shilcayo | S6.45929 W76.35248 | | | dd | cc | ss |
| Rio Shilcayo | S6.46001 W76.35054 | | | dd | cc | ss |
| Rio Shilcayo | S6.45716 W76.35261 | | | dd | cc | ss |
| Rio Shilcayo | S6.45658 W76.35249 | | | dd | cc | ss |
| Rio Shilcayo | S6.45574 W76.35156 | | | dd | cc | ss |
| Rio Shilcayo | S6.45574 W76.35156 | | | dd | cc | ss |
| Rio Shilcayo | S6.45577 W76.35130 | | | dd | cc | ss |
| Rio Shilcayo | S6.45453 W76.35068 | | | dd | cc | ss |
| Rio Shilcayo | S6.45339 W76.34019 | | | dd | cc | ss |
| Rio Shilcayo | S6.45417 W76.34190 | | | dd | cc | ss |
| Rio Shilcayo | S6.45534 W76.34423 | | | dd | cc | ss |
| Rio Shilcayo | S6.45271 W76.34011 | | | dd | cc | ss |
| Rio Shilcayo | S6.45271 W76.34011 | | | dd | cc | ss |
| Rio Shilcayo | S6.45271 W76.34011 | | | dd | cc | ss |
| Rio Shilcayo | S6.44830 W76.34538 | | | Dd | cc | ss |
| Rio Shilcayo | S6.44830 W76.34538 | | | dd | cc | ss |
| Rio Shilcayo, east bank | S6.47451 W76.35384 | | | dd | cc | ss |
| Rio Shilcayo, east bank | S6.46839 W76.35114 | | | dd | cc | ss |
| Rio Shilcayo, east bank | S6.47451 W76.35384 | | | dd | cc | ss |
| Rio Shilcayo, east bank | S6.46560 W76.34767 | | | Dd | cc | ss |
| Rumipata | S6.07788 W76.96931 | | | dd | cc | ss |
| Sachawawa | | S6.268356 W76.299331 | ±50m | DD | Cc | ss |
| San Antonio de Cumbaza | S6.40201 W76.39571 | | | dd | cc | ss |

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| San Antonio de Cumbaza | S6.40779 W76.40247 | | | dd | cc | ss |
| San Antonio de Cumbaza | S6.40465 W76.39723 | | | dd | cc | ss |
| Tangarana | S6.32515 W76.69459 | | | dd | cc | ss |
| Tangarana | S6.32159 W76.69527 | | | dd | cc | ss |
| Tangarana | S6.32753 W76.69411 | | | dd | cc | ss |
| Tangarana | S6.32159 W76.69527 | | | dd | cc | ss |
| Tangarana | | | | dd | cc | ss |
| Tangarana | | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46713 W76.33475 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46713 W76.33475 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46713 W76.33475 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46202 W76.33473 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46716 W76.33639 | | | dd | cc | ss |
| Tarapoto - Uruahasha | | S6.463401 W76.334952 | ±400m | dd | cc | ss |
| Tarapoto - Uruahasha | S6.47588 W76.34748 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.47292 W76.34485 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.47182 W76.34204 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.47175 W76.34043 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46867 W76.33675 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46773 W76.33631 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46773 W76.33631 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46718 W76.33637 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46718 W76.33637 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46595 W76.33492 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46705 W76.33477 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46705 W76.33477 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46699 W76.33473 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46699 W76.33473 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46649 W76.33431 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46632 W76.33398 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46587 W76.33240 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46278 W76.33546 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46161 W76.33429 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.47213 W76.34123 | | | dd | cc | ss |
| Tarapoto - Uruahasha | | S6.466808 W76.339537 | ±350m | dd | cc | ss |
| Tarapoto - Uruahasha | | S6.466808 W76.339537 | ±350m | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46922 W76.34145 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46922 W76.34145 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46080 W76.33346 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45661 W76.32987 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46904 W76.33703 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46857 W76.33663 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46857 W76.33663 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46780 W76.33633 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46768 W76.33639 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46768 W76.33639 | | | dd | cc | ss |

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|---|---|---|---|---|---|---|
| Tarapoto - Uruahasha | S6.46690 W76.33641 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46690 W76.33641 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46690 W76.33641 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46148 W76.33415 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45661 W76.32987 | | | Dd | cc | ss |
| Tarapoto - Uruahasha | S6.45661 W76.32987 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46220 W76.33501 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46276 W76.33602 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46276 W76.33602 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.46429 W76.33629 | | | dd | cc | ss |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | dd | cc | ss |
| Tarapoto - Yurimaguas (km 68) | | S6.233789 W76.277508 | ±400m | Dd | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.28891 W76.26358 | | | Dd | CC | SS |
| Tarapoto - Yurimaguas km 59.3 | S6.29829 W76.28022 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29808 W76.28087 | | | DD | cc | Ss |
| Tarapoto - Yurimaguas km 59.3 | S6.29824 W76.27996 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29815 W76.27898 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29860 W76.27592 | | | DD | cc | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29860 W76.27592 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29860 W76.27592 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29860 W76.27592 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29860 W76.27592 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29831 W76.28007 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29287 W76.28942 | | | DD | Cc | Ss |
| Tarapoto - Yurimaguas km 59.3 | S6.29417 W76.29009 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29417 W76.29009 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29826 W76.28058 | | | DD | C- | Ss |
| Tarapoto - Yurimaguas km 59.3 | S6.29829 W76.28022 | | | DD | cc | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29829 W76.28022 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29829 W76.28022 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29817 W76.27910 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29814 W76.28053 | | | Dd | Cc | Ss |
| Tarapoto - Yurimaguas km 59.3 | S6.29835 W76.28033 | | | dd | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29812 W76.28049 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29812 W76.28049 | | | DD | C- | Ss |
| Tarapoto - Yurimaguas km 59.3 | S6.29835 W76.28033 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | | S6.298124 W76.276972 | ±100m | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29647 W76.27267 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 59.3 | S6.29856 W76.27596 | | | Dd | C- | Ss |
| Tarapoto - Yurimaguas km 61.1 | S6.28633 W76.27614 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km 68.2 | S6.23225 W76.27182 | | | DD | cc | S- |

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|---|---|---|---|---|---|---|
| Tarapoto - Yurimaguas km 68.2 | S6.23006 W76.29049 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19115 W76.26257 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19115 W76.26257 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19213 W76.26287 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19213 W76.26287 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19256 W76.26290 | | | DD | CC | Ss |
| Tarapoto - Yurimaguas km 73.3 | S6.19115 W76.26257 | | | DD | Cc | Ss |
| Tarapoto - Yurimaguas km 73.3 | S6.19115 W76.26257 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19115 W76.26257 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19115 W76.26257 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km 73.3 | S6.19252 W76.26296 | | | DD | C- | Ss |
| Tarapoto - Yurimaguas km 73.3 | | S6.19120 W76.26254 | ±100m | DD | C- | S- |
| Tarapoto - Yurimaguas km25 | S6.41067 W76.32610 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km25 | S6.41066 W76.32611 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km47.5 | S6.37721 W76.28881 | | | dd | cc | Ss |
| Tarapoto - Yurimaguas km47.5 | S6.37670 W76.28859 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 | S6.37785 W76.28940 | | | Dd | cc | ss |
| Tarapoto - Yurimaguas km49 | S6.37308 W76.28523 | | | Dd | cc | ss |
| Tarapoto - Yurimaguas km49 | S6.37785 W76.28940 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 | S6.37785 W76.28940 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 | S6.37785 W76.28940 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 | | S6.376850 W76.288282 | ±50m | dd | cc | ss |
| Tarapoto - Yurimaguas km49 | | S6.372729 W76.284959 | ±100m | dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37027 W76.29170 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37027 W76.29170 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36837 W76.29188 | | | dd | cc | SS |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37005 W76.29147 | | | dd | cc | Ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37005 W76.29147 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36826 W76.29173 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36825 W76.29183 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37178 W76.29251 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | Dd | Cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37036 W76.29160 | | | dd | cc | Ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37039 W76.29160 | | | Dd | Cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36826 W76.29173 | | | Dd | cc | ss |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36826 W76.29173 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km49.5 | S6.36634 W76.29204 | | | dd | cc | Ss |
| Tarapoto - Yurimaguas km49.5 | S6.36631 W76.29191 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29433 | | | Dd | C- | Ss |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29433 | | | dd | cc | SS |
| Tarapoto - Yurimaguas km50 | S6.36249 W76.29431 | | | dd | cc | Ss |
| Tarapoto - Yurimaguas km50 | S6.36249 W76.29431 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km50 | S6.36249 W76.29431 | | | dd | cc | ss |
| Tarapoto - Yurimaguas km50 | S6.36249 W76.29431 | | | dd | C- | Ss |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | | | Dd | Cc | ss |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | | | dd | cc | ss |

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|---|---|---|---|---|---|---|
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32174 W76.28149 | | | Dd | Cc | ss |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32064 W76.28068 | | | dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32118 W76.28120 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32174 W76.28152 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.31510 W76.27191 | | | DD | Cc | Ss |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.31539 W76.28124 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.31510 W76.27191 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.31590 W76.28014 | | | DD | C- | Ss |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.31691 W76.27428 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | dd | Cc | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | DD | cc | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32049 W76.27571 | | | DD | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32140 W76.28282 | | | Dd | C- | ss |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32145 W76.28166 | | | Dd | C- | Ss |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32170 W76.28155 | | | dd | Cc | ss |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32152 W76.28169 | | | Dd | C- | S- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32152 W76.28169 | | | DD | C- | Ss |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32152 W76.28169 | | | DD | Cc | Ss |
| Tarapoto - Yurimaguas km73.3 | S6.19198 W76.26285 | | | DD | C- | Ss |
| Tarapoto - Yurimaguas km73.3 | | S6.191905 W76.261480 | ±150m | DD | C- | Ss |
| Tarapoto - Yurimaguas km73.3 | | S6.191905 W76.261480 | ±150m | DD | C- | S- |
| Tarapoto-Yurimagua- km 47.5 Trail to pylon- | S6.37773 W76.28932 | | | dd | cc | ss |
| Tarapoto-Yurimagua- km 47.5 Trail to pylon- | S6.37773 W76.28932 | | | dd | cc | ss |
| Tarapoto-Yurimagua- km 47.5 Trail to pylon- | S6.37773 W76.28932 | | | Dd | cc | ss |
| Tioyacu | S5.99243 W77.28818 | | | dd | cc | ss |
| Tunel | S06.45673 W076.28445 | | | dd | cc | ss |
| Tunel | S06.45551 W076.28430 | | | dd | cc | ss |
| Tunel | S06.45551 W076.28430 | | | dd | cc | ss |
| Tunel | S06.45551 W076.28430 | | | Dd | C- | ss |
| Urahuasha | S6.46697 W76.33475 | | | dd | cc | ss |
| Urahuasha | S6.46697 W76.33475 | | | dd | cc | ss |
| Urahuasha | S6.46697 W76.33475 | | | dd | cc | ss |
| Urahuasha | S6.46697 W76.33475 | | | dd | cc | ss |
| Urahuasha | S6.46697 W76.33475 | | | dd | cc | ss |
| Urahuasha | S06.47588 W076.34748 | | | dd | cc | ss |
| Urahuasha | S06.47588 W076.34748 | | | dd | cc | ss |
| Waqanki | S06.08715 W076.98433 | | | dd | cc | ss |
| Waqanki | S06.08800 W076.98580 | | | dd | cc | ss |

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|---|---|---|---|---|---|---|
| Waqanki | S06.08715 W076.98433 | | | dd | cc | ss |
| Waqanki | S06.08715 W076.98433 | | | dd | cc | ss |
| Waqanki | S06.08800 W076.98580 | | | dd | cc | ss |

## Table S2. Genotypic data for *Heliconius melpomene*.

| General locality | Exact coordinates | Approximate coordinates | Accuracy | B | D | N | Yb |
|---|---|---|---|---|---|---|---|
| Alto Ahuashiyacu | | S6.454188 W76.308123 | accuracy unclear | B- | dd | nn | yy |
| Alto Shilcayo | | S6.448943 W76.340899 | ±920m | B- | dd | nn | yy |
| Alto Shilcayo | | S6.448943 W76.340899 | ±920m | B- | dd | nn | yy |
| Alto Shilcayo | | S6.448943 W76.340899 | ±920m | B- | dd | nn | yy |
| Alto Shilcayo | | S6.448943 W76.340899 | ±920m | B- | dd | nn | yy |
| Alto Shilcayo | | S6.448943 W76.340899 | ±920m | B- | dd | nn | yy |
| Alto Shilcayo | | S6.448943 W76.340899 | ±920m | B- | dd | nn | yy |
| Alto Shilcayo | | S6.448943 W76.340899 | ±920m | B- | dd | nn | yy |
| Antonio_Cumbaza | S06.40465 W076.39723 | | | B- | dd | nn | yy |
| Antonio_Cumbaza | S06.40465 W076.39723 | | | B- | dd | nn | yy |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 | | | B- | dd | nn | yy |
| Bello Horizonte a Santa Elena | S6.52232 W76.28278 | | | B- | dd | nn | yy |
| Bello Horizonte a Santa Elena | S6.52089 W76.28137 | | | B- | dd | nn | yy |
| Bello Horizonte a Santa Elena | S6.52062 W76.28385 | | | B- | dd | nn | yy |
| Biodiversidad | S6.458949 W76.288239 | | | B- | dd | nn | yy |
| Camino a Isla Bonita | S6.45773 W76.37474 | | | B- | dd | nn | yy |
| Camino a Isla Bonita | S6.45929 W76.37193 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | Nn | Yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.442639 W76.335470 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.44271 W76.33541 | | | B- | dd | nn | yy |

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|---|---|---|---|---|---|---|---|
| Casa de Orlando | S6.44280 W76.33571 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.44280 W76.33571 | | | B- | dd | nn | yy |
| Casa de Orlando | S6.44280 W76.33571 | | | B- | dd | nn | yy |
| Cesar_trail | S06.45690 W076.30921 | | | B- | dd | nn | yy |
| Chazuta | S6.55324 W76.12083 | | | B- | dd | nn | yy |
| Chazuta | S6.56654 W76.12749 | | | B- | dd | nn | yy |
| Chazuta | S6.55908 W76.12574 | | | B- | dd | nn | yy |
| Chazuta | S6.56417 W76.12629 | | | B- | dd | nn | yy |
| Chazuta | S6.56654 W76.12749 | | | B- | dd | nn | yy |
| Chazuta | S6.56654 W76.12749 | | | B- | dd | nn | yy |
| Davicillo | S6.24880 W76.26441 | | | bb | D- | N- | Y- |
| El Tunel | S6.45289 W76.28637 | | | B- | dd | nn | yy |
| El Tunel | S6.45289 W76.28637 | | | B- | D- | nn | yy |
| El Tunel | S6.45314 W76.28763 | | | B- | D- | nn | yy |
| El Tunel | S6.45544 W76.28453 | | | B- | dd | nn | yy |
| El Tunel | S6.45277 W76.28632 | | | B- | dd | nn | yy |
| El Tunel | | S6.454222 W76.285140 | ±200m | B- | dd | nn | yy |
| El Tunel | S6.45289 W76.28637 | | | B- | dd | nn | yy |
| El Tunel | S6.45289 W76.28637 | | | B- | dd | nn | yy |
| El Tunel | S6.45289 W76.28637 | | | B- | dd | nn | yy |
| El Tunel | S6.45289 W76.28637 | | | B- | dd | nn | yy |
| El Tunel | S6.45289 W76.28637 | | | B- | dd | nn | yy |
| El Tunel | S6.45277 W76.28632 | | | B- | dd | nn | yy |
| El Tunel | S6.45277 W76.28632 | | | B- | dd | nn | yy |
| El Tunel | S6.45277 W76.28632 | | | B- | dd | nn | yy |
| El Tunel | S6.45359 W76.28789 | | | B- | dd | nn | yy |
| El Tunel | | S6.453253 W76.287319 | ±100m | B- | dd | nn | yy |
| El Tunel | | S6.453253 W76.287319 | ±100m | B- | dd | nn | yy |
| El Tunel | S6.45338 W76.28758 | | | B- | dd | nn | yy |
| El Tunel | S6.45359 W76.28789 | | | B- | dd | nn | yy |
| El Tunel | S6.45355 W76.28778 | | | B- | dd | nn | yy |
| El Tunel | S6.45396 W76.28547 | | | B- | dd | nn | yy |
| El Tunel | S6.45396 W76.28547 | | | B- | dd | nn | yy |
| El Tunel | S6.45396 W76.28547 | | | B- | dd | nn | yy |
| El Tunel | S6.45277 W76.28632 | | | B- | dd | nn | yy |
| El Tunel | S6.45314 W76.28768 | | | B- | dd | nn | yy |
| El Tunel | S6.45351 W76.28763 | | | B- | dd | nn | yy |
| El Tunel | S6.45351 W76.28763 | | | B- | dd | nn | yy |
| El Tunel | S6.45673 W76.28439 | | | bb | D- | N- | Y- |
| El Tunel | S6.45673 W76.28439 | | | B- | dd | nn | yy |
| El Tunel | S6.45673 W76.28439 | | | B- | dd | nn | yy |
| El Tunel | S6.45689 W76.28453 | | | B- | dd | nn | yy |
| El Tunel | S6.45673 W76.28439 | | | B- | D- | nn | yy |
| El Tunel | | S6.453110 W76.287176 | ±100m | B- | dd | nn | yy |
| El Tunel | S6.45669 W76.28441 | | | B- | D- | nn | yy |
| El Tunel | S6.45588 W76.28398 | | | B- | dd | nn | yy |

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|---|---|---|---|---|---|---|---|
| El Tunel | S6.45669 W76.28441 | | | B- | dd | nn | yy |
| El Tunel | S6.45629 W76.28430 | | | B- | dd | nn | yy |
| El Tunel | S6.45629 W76.28430 | | | B- | dd | nn | yy |
| El Tunel | S6.45629 W76.28430 | | | B- | dd | nn | yy |
| El Tunel | S6.45502 W76.28477 | | | B- | dd | nn | yy |
| El Tunel | S6.45399 W76.28540 | | | B- | dd | nn | yy |
| El Tunel | S6.45327 W76.28603 | | | B- | D- | nn | yy |
| El Tunel - km32.5 trail | S6.44850 W76.28151 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.45412 W76.27756 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44894 W76.28132 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44894 W76.28132 | | | B- | dd | N- | Y- |
| El Tunel - km32.5 trail | S6.45437 W76.27739 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.45437 W76.27739 | | | B- | D- | N- | Yy |
| El Tunel - km32.5 trail | S6.45437 W76.27739 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44804 W76.27225 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.43741 W76.27770 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44880 W76.28139 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44880 W76.28139 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44880 W76.28139 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44880 W76.28139 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.44880 W76.28139 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.45399 W76.27764 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.45399 W76.27764 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.45434 W76.27728 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.45434 W76.27728 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.45434 W76.27728 | | | B- | dd | nn | yy |
| El Tunel - km32.5 trail | S6.43905 W76.27452 | | | B- | dd | nn | yy |
| Escalera_Cesar'sTrail | S6.45353 W76.31189 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47668 W76.35199 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | | S6.47622 W76.35176 | ±150m | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | | S6.47622 W76.35176 | ±150m | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | | S6.47622 W76.35176 | ±150m | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47693 W76.35100 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47620 W76.35179 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47490 W76.35118 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47234 W76.35004 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47034 W76.34725 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47019 W76.34672 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.46862 W76.34629 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.46968 W76.34640 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.46992 W76.34619 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.46992 W76.34619 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.46992 W76.34619 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.46992 W76.34619 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.46992 W76.34619 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47310 W76.35034 | | | B- | dd | nn | yy |

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|---|---|---|---|---|---|---|---|
| Fraser's Pardalinus Trail | S6.47221 W76.34998 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47310 W76.35034 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47339 W76.35055 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47310 W76.35034 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47339 W76.35055 | | | B- | dd | nn | yy |
| Fraser's Pardalinus Trail | S6.47339 W76.35055 | | | B- | dd | nn | yy |
| La Antena | S06.45474 W076.29936 | | | B- | dd | nn | yy |
| La Antena | S6.45714 W76.29847 | | | B- | dd | nn | yy |
| La Antena | | S6.45468 W76.29933 | accuracy unclear | B- | dd | nn | yy |
| La Antena | S06.45431 W076.29889 | | | B- | dd | nn | yy |
| La Antena | S06.45431 W076.29889 | | | B- | dd | nn | yy |
| La Antena | S06.45431 W076.29889 | | | B- | dd | nn | yy |
| La Antena | S6.455593 W76.299112 | | | B- | dd | nn | yy |
| La Carachamera | S6.43188 W76.25192 | | | B- | dd | nn | yy |
| La Carachamera | S6.43188 W76.25192 | | | B- | dd | nn | yy |
| La Carachamera | S6.43188 W76.25192 | | | B- | dd | nn | yy |
| La Carachamera | S6.43782 W76.24503 | | | B- | dd | nn | yy |
| La Carachamera | S6.43782 W76.24503 | | | B- | dd | nn | yy |
| La Carachamera | S6.43802 W76.24488 | | | B- | dd | nn | yy |
| La Carachamera | S6.43782 W76.24503 | | | B- | dd | nn | yy |
| La Carachamera | | S6.434777 W76.248140 | ±700m | B- | dd | nn | yy |
| La Carachamera | S6.43732 W76.24551 | | | B- | dd | nn | yy |
| Micaela Bastida km6.1 | | S05.943371 W76.245272 | ±200m | bb | D- | N- | Y- |
| Micaela Bastida km6.1 | | S05.943371 W76.245272 | ±200m | bb | D- | N- | Y- |
| Micaela Bastida km6.1 | S5.94577 W76.24530 | | | bb | D- | N- | Y- |
| Micaela Bastida km6.1 | S5.94583 W76.24658 | | | bb | D- | N- | Y- |
| Micaela Ba-tida km 6.1 | S5.9458 W76.24552 | | | bb | D- | N- | Y- |
| Micaela Ba-tida km 6.1 | S5.9458 W76.24552 | | | bb | D- | N- | Y- |
| Micaela Ba-tida km 6.2 | S5.945549 W76.245444 | | | bb | D- | N- | Y- |
| Moyobamba Antenna | S6.09602 W76.97742 | | | B- | dd | nn | yy |
| Pongo - Barranquita km3.5 | S6.31371 W76.25829 | | | bb | D- | N- | yy |
| Pongo - Barranquita km3.5 | S6.31371 W76.25829 | | | B- | D- | N- | Y- |
| Pongo - Barranquita km3.5 | S6.31371 W76.25829 | | | bb | D- | N- | Y- |
| Pongo - Barranquita km3.5 | S6.30868 W76.25721 | | | bb | D- | N- | Y- |
| Pongo - Barranquita km3.5 | S6.30868 W76.25721 | | | bb | D- | N- | Y- |
| Pongo - Barranquita km3.5 | S6.30868 W76.25721 | | | bb | D- | N- | Y- |
| Pongo - Barranquita km3.5 | S6.30773 W76.25783 | | | bb | D- | N- | Y- |
| Pongo - Barranquita km3.5 | S6.30330 W76.25782 | | | bb | D- | N- | Y- |
| Pongo - Barranquitas km7.2 | S6.287826 W76.230743 | | | bb | D- | N- | Y- |
| Pongo Cataratas | S6.34870 W76.30000 | | | B- | dd | N- | Yy |
| Pongo Cataratas | S6.34870 W76.30000 | | | bb | D- | N- | Y- |
| Pongo Cataratas | S6.34947 W76.29986 | | | B- | D- | N- | Y- |
| Pongo Cataratas | S6.34870 W76.30000 | | | B- | D- | nn | yy |
| Pongo Cataratas | S6.34857 W76.29997 | | | bb | D- | Nn | Yy |
| Pongo Cataratas | S6.34857 W76.29997 | | | B- | D- | N- | Yy |
| Pongo Cataratas | S6.34857 W76.29997 | | | B- | dd | nn | yy |

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|---|---|---|---|---|---|---|---|
| Pongo Cataratas | S6.35361 W76.30237 | | | bb | D- | N- | Y- |
| Pongo Cataratas | | S6.354520 W76.302640 | ±50m | B- | dd | nn | yy |
| Pongo Cataratas | S6.35028 W76.30017 | | | B- | D- | N- | Yy |
| Pongo Cataratas | S6.35307 W76.30199 | | | B- | D- | N- | yy |
| Pongo de Cainarache | S6.32625 W76.27248 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30733 W76.22989 | | | B- | dd | nn | yy |
| Pongo-Barranquitas km5.9 | S6.30531 W76.23254 | | | B- | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30531 W76.23254 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30531 W76.23254 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30158 W76.23505 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30382 W76.23355 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30288 W76.23390 | | | bb | D- | N- | yy |
| Pongo-Barranquitas km5.9 | S6.30282 W76.23377 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30282 W76.23377 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30527 W76.23254 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30622 W76.23166 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30711 W76.22987 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30711 W76.22987 | | | B- | D- | N- | Yy |
| Pongo-Barranquitas km5.9 | S6.30711 W76.22987 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.306407 W76.230117 | | | B- | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30499 W76.23290 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | | S06.304314 W76.233089 | ±500m | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30387 W76.23347 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30079 W76.23603 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | B- | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | bb | dd | N- | Yy |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30716 W76.22979 | | | bb | D- | N- | Y- |
| Pongo-Barranquitas km5.9 | S6.30513 W76.23262 | | | bb | D- | N- | Y- |
| Rancho Vista | S6.45131 W76.35851 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45238 W76.35845 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45238 W76.35845 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45680 W76.35904 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45144 W76.35844 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45144 W76.35844 | | | B- | dd | nn | yy |
| Rancho Vista | S6.46147 W76.35926 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45500 W76.35906 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45657 W76.35836 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45812 W76.35931 | | | B- | dd | nn | yy |

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|---|---|---|---|---|---|---|---|
| Rancho Vista | S6.45812 W76.35931 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45812 W76.35931 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45635 W76.35852 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45812 W76.35931 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45997 W76.35946 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45609 W76.35854 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45160 W76.35849 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45160 W76.35849 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45160 W76.35849 | | | B- | dd | nn | yy |
| Rancho Vista | S6.45160 W76.35849 | | | B- | dd | nn | yy |
| Rancho Vista | | S6.45515 W76.35909 | ±700m | B- | dd | nn | yy |
| Rancho Vista | | S6.45515 W76.35909 | ±700m | B- | dd | nn | yy |
| Rancho Vista | | S6.45515 W76.35909 | ±700m | B- | dd | nn | yy |
| Rancho Vista | | S6.45515 W76.35909 | ±700m | B- | dd | nn | yy |
| Rancho Vista | | S6.45515 W76.35909 | ±700m | B- | dd | nn | yy |
| Rancho Vista | | S6.45515 W76.35909 | ±700m | B- | dd | nn | yy |
| Rancho_vista | | S6.45515 W76.35909 | ±700m | B- | dd | nn | yy |
| Rancho_vista | | S6.45515 W76.35910 | ±700m | B- | dd | nn | yy |
| Rancho_vista | | S6.45515 W76.35911 | ±700m | B- | dd | nn | yy |
| Rancho_vista | | S6.45515 W76.35912 | ±700m | B- | dd | nn | yy |
| Rancho_vista | | S6.45515 W76.35913 | ±700m | B- | dd | nn | yy |
| Rancho_vista | | S6.45515 W76.35913 | ±700m | B- | dd | nn | yy |
| Rio Shilcayo | S6.46336 W76.35129 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45508 W76.34611 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45638 W76.34716 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45508 W76.34611 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45514 W76.34578 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45415 W76.34200 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45539 W76.34479 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45539 W76.34479 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45508 W76.34611 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45508 W76.34611 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.46336 W76.35129 | | | B- | dd | nn | yy |
| Rio Shilcayo | | S6.462348 W76.351388 | ±250m | B- | dd | nn | yy |
| Rio Shilcayo | S6.45658 W76.34748 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45508 W76.34611 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.460240 W76.350249 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.46848 W76.35334 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45658 W76.34748 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45627 W76.34692 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45652 W76.34740 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45652 W76.34740 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.46251 W76.35139 | | | B- | D- | nn | yy |
| Rio Shilcayo | S6.46505 W76.35161 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.46376 W76.35125 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45575 W76.35159 | | | B- | dd | nn | yy |

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|---|---|---|---|---|---|---|---|
| Rio Shilcayo | S6.45607 W76.34612 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.44863 W76.33520 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45420 W76.33983 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45420 W76.33983 | | | B- | dd | nn | yy |
| Rio Shilcayo | S6.45534 W76.34423 | | | B- | dd | nn | yy |
| Rio Shilcayo, east bank | S6.46684 W76.34876 | | | B- | dd | nn | yy |
| Rio Shilcayo, east bank | S6.46743 W76.35009 | | | B- | dd | nn | yy |
| Rio Shilcayo, east bank | S6.46743 W76.35009 | | | B- | dd | nn | yy |
| Rio Shilcayo, east bank | S6.46780 W76.35045 | | | B- | dd | nn | yy |
| Rio Shilcayo, east bank | S6.47086 W76.35202 | | | B- | dd | nn | yy |
| Rio Shilcayo, east bank | S6.47086 W76.35202 | | | B- | dd | nn | yy |
| Rio Shilcayo, east bank | S6.47086 W76.35202 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45746 W76.34879 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.46251 W76.35139 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.46402 W76.35125 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45322 W76.34677 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45652 W76.34740 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45658 W76.34748 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45658 W76.34748 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45658 W76.34748 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45658 W76.34748 | | | B- | dd | nn | yy |
| Rio_Shilcayo | S6.45658 W76.34748 | | | B- | dd | nn | yy |
| San Antonio de Cumbaza | S6.407227 W76.401707 | | | B- | dd | Nn | Yy |
| San Roque de Cumbaza | S6.38569 W76.44278 | | | B- | dd | nn | yy |
| San Roque de Cumbaza | S6.38569 W76.44278 | | | B- | dd | nn | yy |
| San Roque de Cumbaza | S6.38332 W76.44091 | | | B- | dd | nn | yy |
| San Roque de Cumbaza | S6.38332 W76.44091 | | | B- | dd | nn | yy |
| San_Antonio | S6.40779 W76.40247 | | | B- | dd | nn | yy |
| San_Antonio | S06.40318 W076.39610 | | | B- | dd | nn | yy |
| San_Antonio | S6.40416 W76.39639 | | | B- | dd | nn | yy |
| San_Antonio | S6.40308 W76.39574 | | | B- | dd | nn | yy |
| San_Antonio | S6.40308 W76.39597 | | | B- | dd | nn | yy |
| San_Antonio | S6.40440 W76.39606 | | | B- | dd | nn | yy |
| San_Antonio | S6.40723 W76.40171 | | | B- | dd | nn | yy |
| San_Antonio | S6.40723 W76.40171 | | | B- | dd | nn | yy |
| San_Antonio | S6.40362 W76.39261 | | | B- | dd | nn | yy |
| San_Antonio | S6.40362 W76.39261 | | | B- | dd | nn | yy |
| San_Antonio | S6.40735 W76.40174 | | | B- | dd | nn | yy |
| San_Antonio | S6.40475 W76.39789 | | | B- | dd | nn | yy |
| San_Antonio | S6.40277 W76.39563 | | | B- | dd | nn | yy |
| San_Antonio | S6.40420 W76.39485 | | | B- | dd | nn | yy |
| San_Antonio | S6.40420 W76.39485 | | | B- | dd | nn | yy |
| San_Antonio | S6.40420 W76.39485 | | | B- | dd | nn | yy |
| San_Antonio | S6.40420 W76.39485 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | | S6.463401 W76.334952 | ±400m | B- | dd | nn | yy |
| Tarapoto - Uruahasha | | S6.463401 W76.334952 | ±400m | B- | dd | nn | yy |

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| Tarapoto - Uruahasha | S6.47187 W76.34263 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.47175 W76.34043 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46867 W76.33675 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46773 W76.33631 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46718 W76.33637 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46624 W76.33386 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46616 W76.33205 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46635 W76.33182 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46587 W76.33240 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46541 W76.33561 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46162 W76.33424 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | | S6.466808 W76.339537 | ±350m | B- | dd | nn | yy |
| Tarapoto - Uruahasha | | S6.466808 W76.339537 | ±350m | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46037 W76.33297 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.47160 W76.33838 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46919 W76.33763 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46768 W76.33639 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46768 W76.33639 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46690 W76.33641 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.46690 W76.33641 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.45678 W76.33040 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | B- | dd | nn | yy |
| Tarapoto - Uruahasha | S6.45753 W76.33072 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km 59.3 | S6.29417 W76.29009 | | | B- | D- | N- | Y- |
| Tarapoto - Yurimaguas km 59.3 | S6.29287 W76.28942 | | | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km 59.3 | S6.29284 W76.28943 | | | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km 59.3 | S6.29417 W76.29009 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41324 W76.31994 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41293 W76.31986 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41293 W76.31986 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41293 W76.31986 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | Nn | Yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |

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| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | D- | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41247 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41244 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41244 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km25 | S6.41244 W76.31773 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km36.7 | S6.42957 W76.25994 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km36.7 | S6.42899 W76.25901 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km38 | S6.42550 W76.25338 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km42 | S6.40477 W76.26779 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km42 | S6.40456 W76.26789 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km42 | S6.40477 W76.26779 | | | B- | dd | N- | Yy |
| Tarapoto - Yurimaguas km42 | S6.40395 W76.26796 | | | B- | dd | N- | Yy |
| Tarapoto - Yurimaguas km47.5 | S6.37284 W76.28488 | | | B- | D- | N- | Y- |
| Tarapoto - Yurimaguas km49 | | S6.374566 W76.287069 | ±400m | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km49 | | S6.374566 W76.287069 | ±400m | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37027 W76.29170 | | | B- | D- | N- | Y- |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36826 W76.29173 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36826 W76.29173 | | | B- | dd | N- | Yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36825 W76.29183 | | | B- | D- | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37046 W76.29162 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | D- | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | dd | N- | Yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | D- | N- | Yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | bb | D- | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | D- | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | D- | N- | Y- |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.37093 W76.29245 | | | B- | D- | nn | yy |
| Tarapoto - Yurimaguas km49 (Puente Sisayacu) | S6.36826 W76.29173 | | | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km49.5 | S6.36634 W76.29204 | | | B- | D- | N- | Yy |
| Tarapoto - Yurimaguas km49.5 | S6.36634 W76.29204 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km49.5 | S6.36631 W76.29191 | | | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km49.5 | S6.36631 W76.29191 | | | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km49.5 | S6.36630 W76.29190 | | | B- | D- | N- | Yy |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29433 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km50 | S6.36471 W76.29292 | | | B- | dd | Nn | yy |
| Tarapoto - Yurimaguas km50 | S6.36249 W76.29431 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km50 | S6.36249 W76.29431 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | | | B- | dd | N- | Yy |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | | | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | | | bb | D- | Nn | Y- |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | | | B- | dd | N- | Y- |

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| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km50 | S6.36250 W76.29422 | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.31543 W76.28149 | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32220 W76.27905 | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32220 W76.27905 | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32220 W76.27905 | bb | D- | N- | Yy |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32693 W76.28107 | B- | dd | nn | yy |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32140 W76.28282 | B- | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32140 W76.28282 | B- | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32140 W76.28282 | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32140 W76.28282 | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32145 W76.28166 | bb | D- | N- | Y- |
| Tarapoto - Yurimaguas km56.8 (Puente Yurayacu) | S6.32145 W76.28166 | B- | D- | N- | Y- |
| Tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45551 W076.28430 | B- | D- | nn | yy |
| Tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| Tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| Tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| Tunel | S06.45673 W076.28445 | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | B- | dd | nn | yy |
| Tunel | S06.45330 W076.28609 | B- | dd | nn | yy |
| Tunel | S6.45344  W76.28764 | B- | dd | nn | yy |
| Tunel | S6.45289 W76.28637 | B- | dd | nn | yy |
| Tunel | S6.45289 W76.28637 | B- | dd | nn | yy |
| Tunel | S6.45289 W76.28637 | B- | dd | nn | yy |
| Tunel | S6.45289 W76.28637 | B- | dd | nn | yy |
| Tunel | S6.45289 W76.28637 | B- | dd | nn | yy |
| Tunel | S06.45288 W076.28638 | B- | dd | nn | yy |
| Tunel | S06.45288 W076.28638 | B- | dd | nn | yy |
| Tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| Tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| Tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| tunel | S06.45551 W076.28430 | B- | dd | nn | yy |
| Tunel | S6.45629 W76.28430 | B- | dd | nn | yy |
| Tunel | S6.45588 W76.28398 | B- | dd | nn | yy |

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| Tunel | S06.45330 W076.28609 | | | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | | | B- | dd | nn | yy |
| Tunel | S06.45330 W076.28609 | | | B- | dd | nn | yy |
| Tunel | S06.45330 W076.28609 | | | B- | dd | nn | yy |
| Tunel | S06.45330 W076.28609 | | | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | | | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | | | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | | | B- | dd | nn | yy |
| Tunel | S06.45464 W076.28688 | | | B- | dd | nn | yy |
| Urahuasha | S06.46234 W076.33530 | | | B- | dd | nn | yy |
| Urahuasha | S06.46234 W076.33530 | | | B- | dd | nn | yy |
| Urahuasha | S06.46234 W076.33530 | | | B- | dd | nn | yy |
| Urahuasha | S06.46234 W076.33530 | | | B- | dd | nn | yy |
| Urahuasha | S06.47588 W076.34748 | | | B- | dd | nn | yy |
| Urahuasha | | S06.465440 W076.335373 | ±500m | B- | dd | nn | yy |
| Urahuasha | | S06.465440 W076.335373 | ±500m | B- | dd | nn | yy |
| Urahuasha | | S06.465440 W076.335373 | ±500m | B- | dd | nn | yy |