

# 20170810\_Kvary\_Migration

September 5, 2017

## 1 Varying the carrying capacity across the landscape matrix

The results here relate to simulations that were run where the carrying capacity was varied across the landscape. The matrix was completely full from the outset and thus there are no colonization dynamics or population bottlenecks. This was done at varying migration rates, as you'll see below. The carrying capacity was varied from 1000 at the "rural" end, declining linearly to a carrying capacity of 10 at the "urban" side. The other parameters in the simulations were as follows:

- Number of simulations: 1000
- Number of generations: 250
- Creation probability: NA
- Bottleneck proportion: NA
- pA and pB: 0.5
- Migration rate: varied from 0 to 0.05

```
In [7]: library(ggplot2)
library(grid)
library(data.table, lib = "~/Rpackages")
library(Rmisc, lib = "~/Rpackages")
library(dplyr)

In [8]: #Working directory for datasets varying migration rate and bottleneck proportion
setwd('/scratch/research/projects/trifolium/SEC_Simulation.Evolutionary.Clines/SEC_Data/
Drift.Migration/1D/Kvary_AllFill')

#Load datasets that will be used for analyses
Kvary_Mig_Summary <- fread('20170831_Kvary_Mig_Summary.csv', header = T)
Kvary_Mig_Coefs <- fread('20170831_FitKvary_Mig_Coef.csv', header = T)

In [9]: Coefs_Cyan_NoMig <- subset(Kvary_Mig_Coefs, id == "Cyan" & Mig_rate == 0)
Coefs_pA <- subset(Kvary_Mig_Coefs, id == "pA" & Mig_rate == 0)
Coefs_pB <- subset(Kvary_Mig_Coefs, id == "pB" & Mig_rate == 0)

In [10]: #Themes used for plotting
ng1=theme(aspect.ratio=0.7,panel.background = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank(),
          panel.border=element_blank(),
          axis.line.x = element_line(color="black",size=1),
          axis.line.y = element_line(color="black",size=1),
          axis.ticks=element_line(color="black"),
          axis.text=element_text(color="black",size=15),
          axis.title=element_text(color="black",size=1),
          axis.title.y=element_text(vjust=2,face="bold",size=15),
          axis.title.x=element_text(vjust=0.1,face="bold",size=15),
          axis.text.x=element_text(size=13),
```

```

axis.text.y=element_text(size=13),
legend.position = "right", legend.direction="vertical",
legend.text=element_text(size=11), legend.key = element_rect(fill = "white"),
legend.title = element_text(size=13,face="bold"),legend.key.size = unit(0.5,
"cm"))

ngl.45=theme(aspect.ratio=0.7,panel.background = element_blank(),
panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),
panel.border=element_blank(),
axis.line.x = element_line(color="black",size=1),
axis.line.y = element_line(color="black",size=1),
axis.ticks=element_line(color="black"),
axis.text=element_text(color="black",size=15),
axis.title=element_text(color="black",size=1),
axis.title.y=element_text(vjust=2,face="bold",size=15),
axis.title.x=element_text(vjust=0.1,face="bold",size=15),
axis.text.x=element_text(size=13,angle=45,hjust=1),
axis.text.y=element_text(size=13),
legend.position = "right", legend.direction="vertical",
legend.text=element_text(size=11), legend.key = element_rect(fill = "white"),
legend.title = element_text(size=13,face="bold"),legend.key.size = unit(0.5,
"cm"))

```

## 1.1 Distribution of slopes for allele and phenotype clines

For each simulation ( $n = 1000$ ), I ran a linear model examining the change in either the frequency of either dominant allele with distance from the starting population or the frequency of HCN with distance. These models have different predictions: for clines in the dominant alleles at either locus, we expect on average half to go up and half to go down whereas for clines in HCN we expect the majority to go down (i.e. negative, loss of HCN across space) due to the epistatic dominance underlying the phenotype.

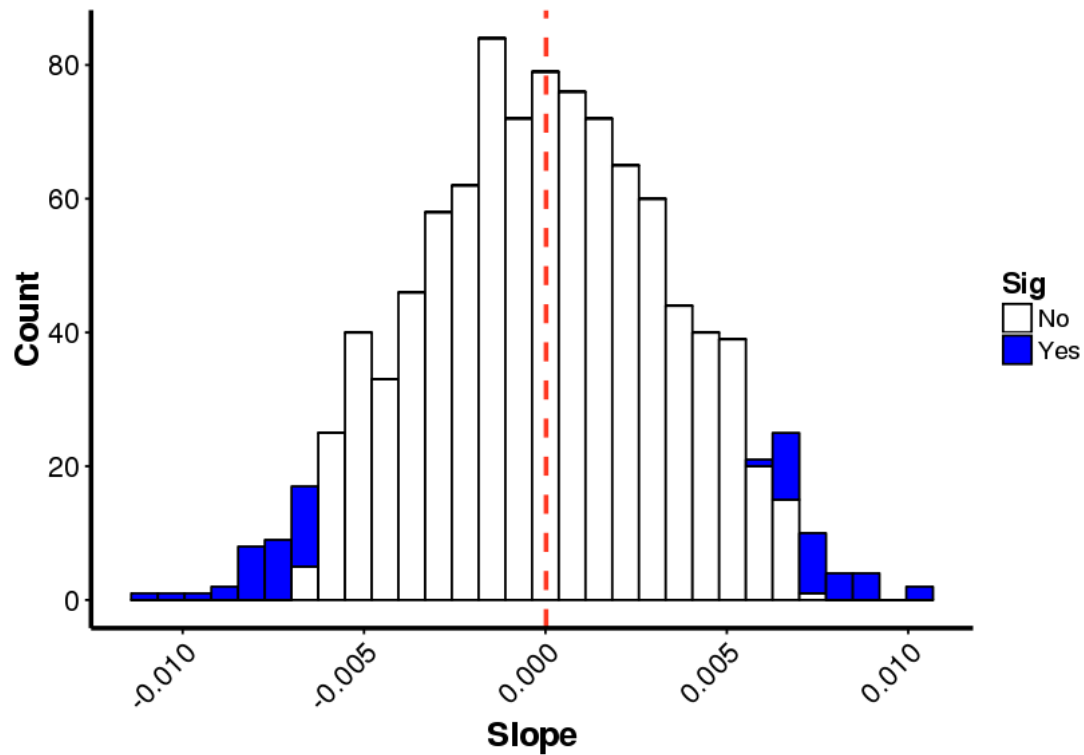
We can start to get at these predictions by looking at the distribution of the slopes from the different models. Note that the distribution of slopes is plotted when migration is 0. **First, we look at the distribution of slopes from models examining the change in the frequency of *Ac* with distance. As predicted, approximately half are positive and half are negative. Blue shading represents significant clines.**

```

In [6]: Coefs_pA <- within(Coefs_pA, {
  Sig = ifelse(p.value < 0.05, "Yes", "No")
})
# Histogram of slopes for 'A' allele with no migration
HistSlopes_pA_NoMig <- ggplot(Coefs_pA, aes(x = estimate, fill = Sig)) +
  ylab("Count") + xlab("Slope") +
  geom_histogram(color = "black") +
  geom_vline(data = Coefs_pA, aes(xintercept = mean(estimate)), size = 1, colour =
"#FF3721", linetype = "dashed") +
  scale_fill_manual(labels = c("No", "Yes"), values=c("white", "blue"))
HistSlopes_pA_NoMig + ngl.45

```

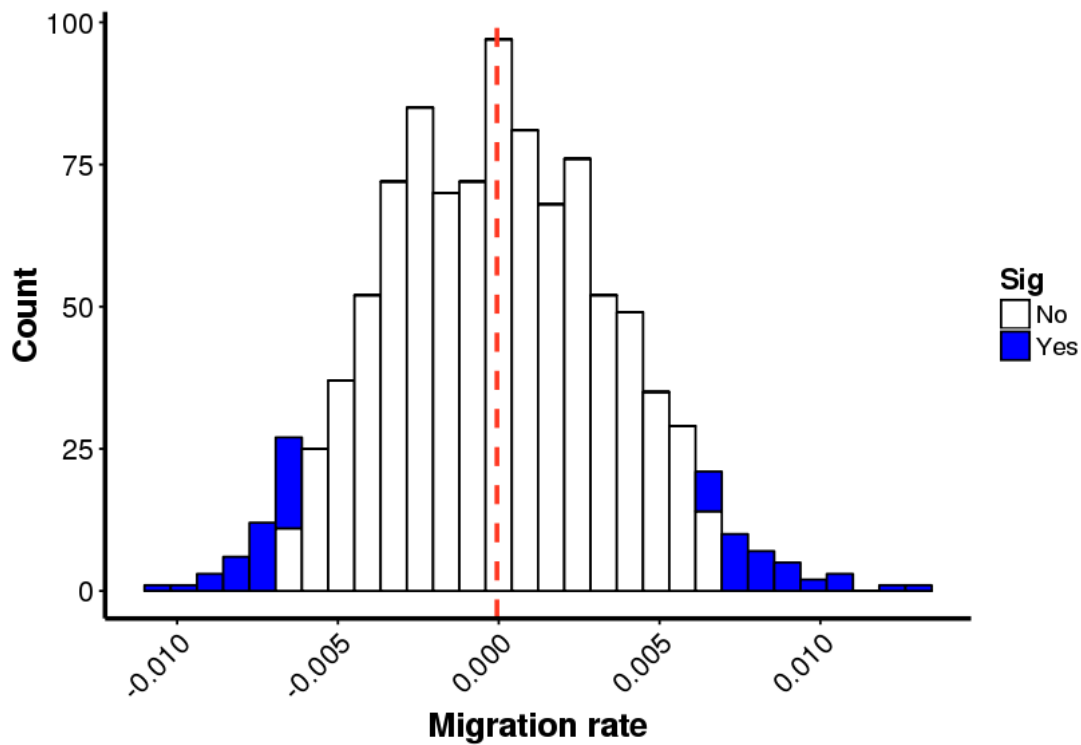
`stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.



We find the same thing for the *Li* allele

```
In [65]: Coefs_pB <- within(Coefs_pB, {
  Sig = ifelse(p.value < 0.05, "Yes", "No")
})
# Histogram of slopes for 'B' allele with no migration
HistSlopes_pB_NoMig <- ggplot(Coefs_pB, aes(x = estimate, fill = Sig)) +
  ylab("Count") + xlab("Migration rate") +
  geom_histogram(color = "black") +
  geom_vline(data = Coefs_pB, aes(xintercept = mean(estimate))), size = 1, colour =
  "#FF3721", linetype = "dashed") +
  scale_fill_manual(labels = c("No", "Yes"), values=c("white", "blue"))
HistSlopes_pB_NoMig + ng1.45
```

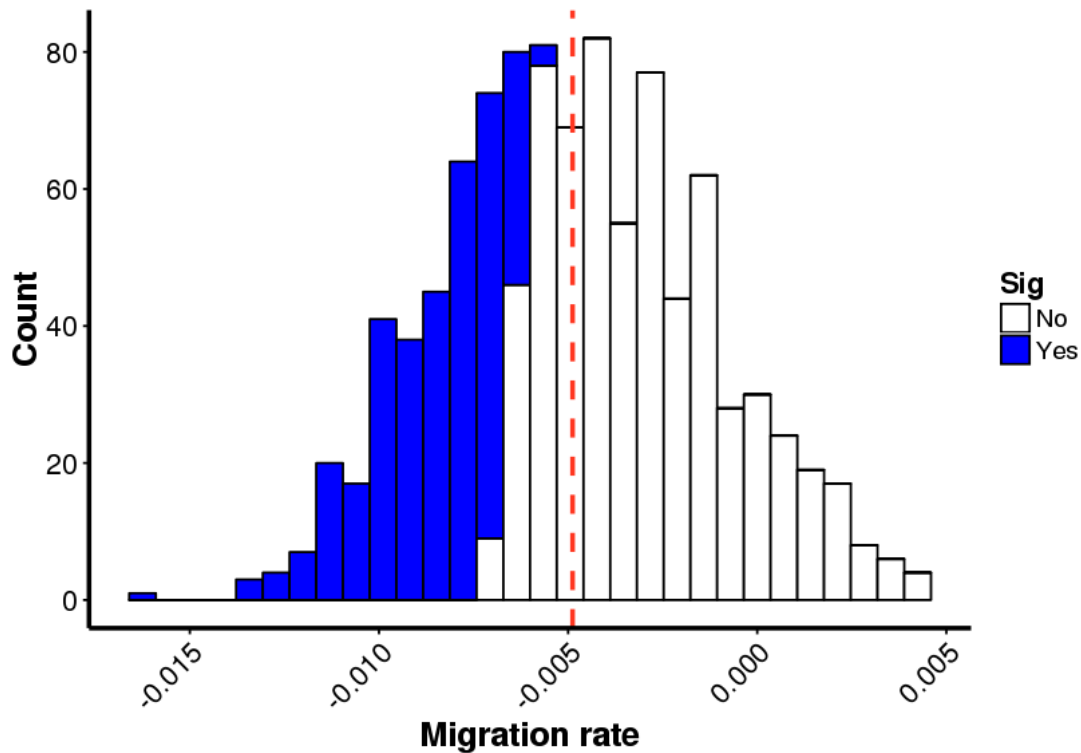
`stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.



For clines in the frequency of HCN, however, the majority of the slopes are negative and there are no significantly positive slopes. The mean slope is also negative

```
In [66]: Coefs_Cyan_NoMig <- within(Coefs_Cyan_NoMig, {
  Sig = ifelse(p.value < 0.05, "Yes", "No")
})
# Histogram of slopes for 'Cyan' allele with no migration
HistSlopes_Cyan_NoMig <- ggplot(Coefs_Cyan_NoMig, aes(x = estimate, fill = Sig)) +
  ylab("Count") + xlab("Migration rate") +
  geom_histogram(color = "black") +
  geom_vline(data = Coefs_Cyan_NoMig, aes(xintercept = mean(estimate)), size = 1,
  colour = "#FF3721", linetype = "dashed") +
  scale_fill_manual(labels = c("No", "Yes"), values=c("white", "blue"))
HistSlopes_Cyan_NoMig + ng1.45
```

`stat\_bin()` using `bins = 30`. Pick better value with `binwidth`.



## 1.2 Mean slope with migration

Here I looked at how the mean slope of allele clines and HCN clines changed with migration.

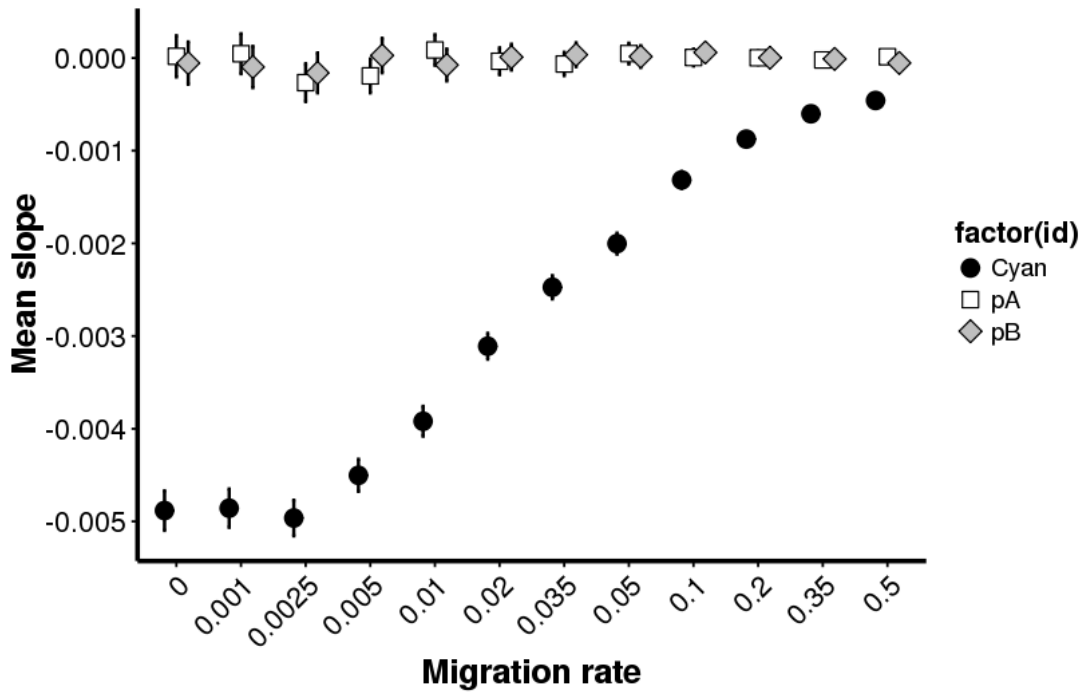
Migration had no effect on the mean slope of clines in *Ac* or *Li*. However, increasing migration resulted in HCN clines with slopes closer to 0. This is consistent with migration homogenizing alleles and flattening out clines.

```
In [42]: #Plot mean slope by migration rate, colored and shaped by phenotype or alleles
MeanSlope_Mig_Type <- ggplot(Kvary_Mig_Summary, aes(x = factor(Mig_rate), y = mean,
  shape = factor(id), fill = factor(id))) +
  geom_errorbar(aes(ymin = mean - ci, ymax = mean + ci), width=0.15, size = 0.7,
  position = position_dodge(width = 0.55)) +
  ylab("Mean slope") + xlab("Migration rate") + geom_point(size = 3.5, color =
  "black",
  position = position_dodge(width = 0.55)) +
  scale_shape_manual(labels = c("Cyan", "pA", "pB"), values=c(21, 22, 23)) +
```

```

scale_fill_manual(labels = c("Cyan", "pA", "pB"), values=c("black", "white",
"grey"))
MeanSlope_Mig_Type + ng1.45

```



### 1.3 Effects of migration on proportion of negative and positive clines

Here I look at how migration affects the proportion of significantly negative and positive clines in the *Ac* and *Li* alleles and in HCN clines.

Increasing migration decreased the proportion of significantly negative clines in HCN, again consistent with the homogenizing effects of migration. In contrast, migration had little effect on the proportion of negative allele clines, although there seems to be a slight increase in the proportion with increasing migration.

```

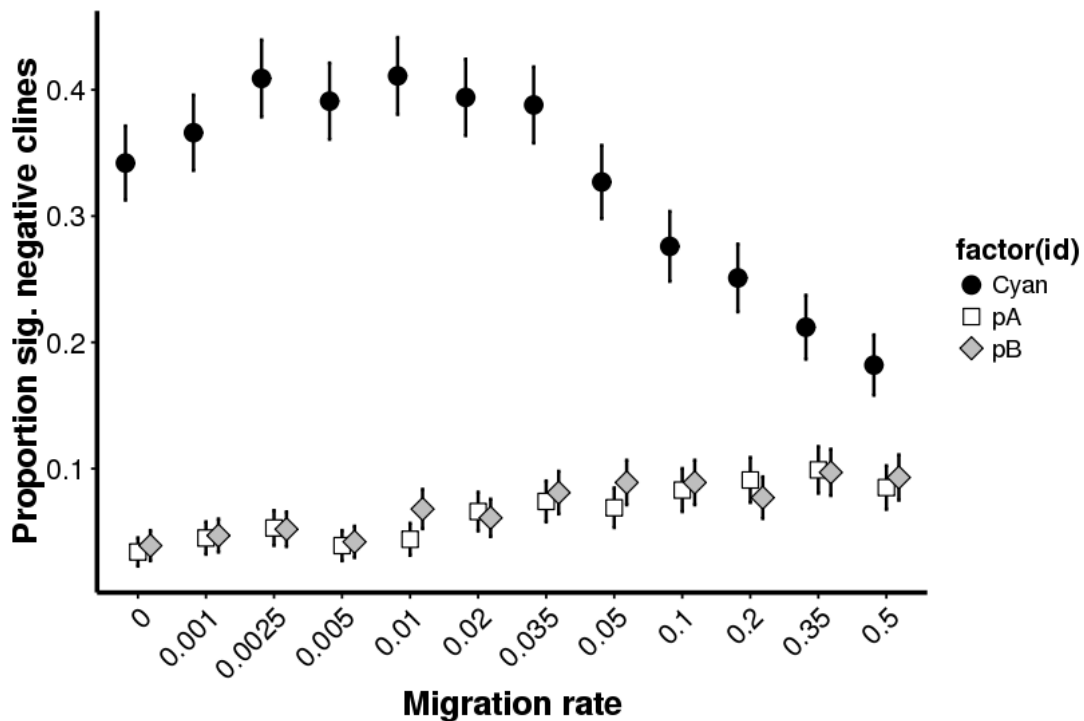
In [11]: #Plot proportion of significantly negative clines by migration rate, colored and shaped
         by id

```

```

NegClines_Mig_Type <- ggplot(Kvary_Mig_Summary, aes(x = factor(Mig_rate), y =
prop_sigNeg,
  shape = factor(id), fill = factor(id))) +
  geom_errorbar(aes(ymin = prop_sigNeg - ci.Neg, ymax = prop_sigNeg + ci.Neg),
width=0.15, size = 0.7,
  position = position_dodge(width = 0.55)) +
  ylab("Proportion sig. negative clines") + xlab("Migration rate") + geom_point(size =
3.5, color = "black",
  position = position_dodge(width = 0.55)) +
  scale_shape_manual(labels = c("Cyan", "pA", "pB"), values=c(21, 22, 23)) +
  scale_fill_manual(labels = c("Cyan", "pA", "pB"), values=c("black", "white",
"grey"))
NegClines_Mig_Type + ng1.45

```



Increasing migration resulted in an increase in the proportion of significantly positive allele clines as well as HCN clines.

In [40]: #Plot proportion of significantly positive clines by migration rate, colored and shaped by id

```

PosClines_Mig_Type <- ggplot(Kvary_Mig_Summary, aes(x = factor(Mig_rate), y =
prop_sigPos,
  shape = factor(id), fill = factor(id))) +
  geom_errorbar(aes(ymin = prop_sigPos - ci.Pos, ymax = prop_sigPos + ci.Pos),
width=0.15, size = 0.7,
  position = position_dodge(width = 0.55)) +
  ylab("Proportion sig. positive clines") + xlab("Migration rate") + geom_point(size =
3.5, color = "black",
  position = position_dodge(width = 0.55)) +
  scale_shape_manual(labels = c("Cyan", "pA", "pB"), values=c(21, 22, 23)) +
  scale_fill_manual(labels = c("Cyan", "pA", "pB"), values=c("black", "white",
"grey"))
PosClines_Mig_Type + ng1.45

```

