oneFIll_Bottleneck

December 20, 2017

1 Serial founder events with migration, founder events.

In these simulations, the urban environment was colonized through serial founder events beginning from a single rural population at carrying capcity. We performed simulations under 3 migration rates: 0, 0.01, 0.05. We used 10 fouding proportions: 0.01; 0.02; 0.035; 0.05; 0.075; 0.1; 0.2; 0.5; 0.75; 1.0. The parameter combinations were as follows (all varied parameters crossed factorially, total simulations = 30):

- Number of simulations: 1000
- Number of generations: 500 (following filling of matrix)
- Max Creation probability: 1.0
- Bottleneck proportion: [0.01; 0.02; 0.035; 0.05; 0.075; 0.1; 0.2; 0.5; 0.75; 1.0]
- pA and pB: 0.5
- Migration rate: [0; 0.01; 0.05]
- Maximum *K* (rural): 1000
- Minimum *K* (urban): 1000

```
In [1]: library(plyr)
        library(ggplot2)
        library(data.table, lib="~/Rpackages")
        library(Rmisc, lib = "~/Rpackages")
        library(dplyr)
        library(broom)
```

```
Loading required package: lattice

Attaching package: dplyr

The following objects are masked from package:data.table:

    between, first, last

The following objects are masked from package:plyr:

    arrange, count, desc, failwith, id, mutate, rename, summarise,
    summarize

The following objects are masked from package:stats:

    filter, lag

The following objects are masked from package:base:
```

```
intersect, setdiff, setequal, union
```

```
In [82]: #Working directory for datasets varying migration rate and bottleneck proportion
         setwd('/scratch/research/projects/trifolium/SEC_Simulation.Evolutionary.Clines/SEC_Data
         /drift-migration/1D/Mig_Bot_Vary')

         #Load datasets that will be used for analyses
         datSlopes <- fread('20171106_SlopeSum_Gen_BotMig-Merged_distRev.csv', header = T)
         datFreqFirst <- fread('20171106_FreqFirstGen_BotMig-Merged_distRev.csv', header = T)
         datSlopes$bot <- as.factor(as.character(datSlopes$bot))
         datSlopes$Mig_rate <- as.factor(as.character(datSlopes$Mig_rate))
         datFreqFirst$bot <- as.factor(as.character(datFreqFirst$bot))
         datFreqFirst$Mig_rate <- as.factor(as.character(datFreqFirst$Mig_rate))

         #Data subsets
         datSlopes_GenOne <- subset(datSlopes, seq == "1")
         datSlopes_NoMig <- subset(datSlopes, Mig_rate == "0")
         datSlopes_GenOne_NoMig <- subset(datSlopes, seq == "1" & Mig_rate == "0")
         datFreqFirst_StrongBot_NoMig <- subset(datFreqFirst, bot == "0.01" & Mig_rate == "0")
         datFreqFirst_InterBot_NoMig <- subset(datFreqFirst, bot == "0.2" & Mig_rate == "0")
         datFreqFirst_NoBot_NoMig <- subset(datFreqFirst, bot == "1" & Mig_rate == "0")


         #Proportion of simulations with Cyan lost by distance under strong bottlenecks
         datPropLost_StrongBot_NoMig <- datFreqFirst_StrongBot_NoMig %>%
             group_by(Distance) %>%
             summarize(n = n(),
                       Lost = sum(Cyan == 0) / n,
                       Fixed = sum(Cyan == 1) / n) %>%
             mutate(Founder = "Strong")
         datPropLost_StrongBot_NoMig <- dplyr::select(datPropLost_StrongBot_NoMig, Distance,
                                                   Lost, Founder)


         #Proportion of simulations with Cyan lost by distance under intermediate bottlenecks
         datPropLost_InterBot_NoMig <- datFreqFirst_InterBot_NoMig %>%
             group_by(Distance) %>%
             summarize(n = n(),
                       Lost = sum(Cyan == 0) / n,
                       Fixed = sum(Cyan == 1) / n) %>%
             mutate(Founder = "Intermediate")
         datPropLost_InterBot_NoMig <- dplyr::select(datPropLost_InterBot_NoMig, Distance,
                                                   Lost, Founder)

         #Proportion of simulations with Cyan lost by distance under no bottlenecks
         datPropLost_NoBot_NoMig <- datFreqFirst_NoBot_NoMig %>%
             group_by(Distance) %>%
             summarize(n = n(),
                       Lost = sum(Cyan == 0) / n,
                       Fixed = sum(Cyan == 1) / n) %>%
             mutate(Founder = "None")
         datPropLost_NoBot_NoMig <- dplyr::select(datPropLost_NoBot_NoMig, Distance,
                                                   Lost, Founder)

         # Merge datasets from strong and intermediate bottlenecks above
         datPropLost_merged <- rbind(datPropLost_StrongBot_NoMig, datPropLost_InterBot_NoMig,
         datPropLost_NoBot_NoMig)

         # Calculate mean frequency in first generation across simulations for each distance
         MeanFreqFirstGen_Distance <- datFreqFirst %>%
             group_by(Distance, bot, Mig_rate) %>%
             summarize(Freq = mean(Cyan))

         MeanFreqFirstGen_Distance_StrongBot_NoMig <- subset(MeanFreqFirstGen_Distance, bot ==
         "0.01" & Mig_rate == "0")
         MeanFreqFirstGen_Distance_InterBot_NoMig <- subset(MeanFreqFirstGen_Distance, bot ==
"0.2" & Mig_rate == "0")
MeanFreqFirstGen_Distance_NoBot_NoMig <- subset(MeanFreqFirstGen_Distance, bot == "1" &
Mig_rate == "0")
```

```
Read 1200000 rows and 12 (of 12) columns from 0.046 GB file in 00:00:03
```

In [16]:
```
str(datSlopes)
```

```
Classes data.table and 'data.frame':	15000 obs. of  20 variables:
 $ bot        : Factor w/ 10 levels "0.01","0.025",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ Mig_rate   : Factor w/ 3 levels "0","0.01","0.05": 1 1 1 1 1 1 1 1 1 1 ...
 $ seq        : int  1 2 3 4 5 6 7 8 9 10 ...
 $ mean       : num  0.00151 0.0015 0.0015 0.0015 0.0015 ...
 $ sd         : num  0.00381 0.00381 0.00381 0.0038 0.0038 ...
 $ n          : int  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 ...
 $ se         : num  0.000121 0.00012 0.00012 0.00012 0.00012 ...
 $ ci_mean    : num  0.000236 0.000236 0.000236 0.000236 0.000236 ...
 $ prop_sigPos: num  0.421 0.422 0.42 0.422 0.42 0.42 0.415 0.418 0.419 0.416 ...
 $ prop_pos   : num  0.74 0.74 0.739 0.739 0.739 0.739 0.739 0.739 0.739 0.739 ...
 $ se_pos     : num  0.0139 0.0139 0.0139 0.0139 0.0139 ...
 $ ci_pos     : num  0.0272 0.0272 0.0272 0.0272 0.0272 ...
 $ se_sigPos  : num  0.0156 0.0156 0.0156 0.0156 0.0156 ...
 $ ci_sigPos  : num  0.0306 0.0306 0.0306 0.0306 0.0306 ...
 $ prop_sigNeg: num  0.176 0.177 0.176 0.175 0.175 0.177 0.173 0.17 0.175 0.174 ...
 $ prop_neg   : num  0.241 0.241 0.241 0.241 0.241 0.241 0.241 0.241 0.241 0.241 ...
 $ se_neg     : num  0.0135 0.0135 0.0135 0.0135 0.0135 ...
 $ ci_neg     : num  0.0265 0.0265 0.0265 0.0265 0.0265 ...
 $ se_sigNeg  : num  0.012 0.0121 0.012 0.012 0.012 ...
 $ ci_sigNeg  : num  0.0236 0.0237 0.0236 0.0236 0.0236 ...
 - attr(*, ".internal.selfref")=<externalptr>
```

In [4]:
```
str(datFreqFirst)
```

```
Classes data.table and 'data.frame':	1200000 obs. of  12 variables:
 $ x         : int  0 0 0 0 0 0 0 0 0 0 ...
 $ y         : int  0 0 0 0 0 0 0 0 0 0 ...
 $ bot       : num  0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.01 ...
 $ Sim       : int  0 0 0 1 1 1 2 2 2 3 ...
 $ Generation: int  1 1 1 1 1 1 1 1 1 1 ...
 $ Cyan      : num  0.563 0.563 0.563 0.563 0.563 0.563 0.563 0.563 0.563 0.563 ...
 $ Mat_full  : int  0 0 0 0 0 0 0 0 0 0 ...
 $ Pop_size  : int  1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 ...
 $ Mig_rate  : num  0 0.01 0.05 0 0.01 0.05 0 0.01 0.05 0 ...
 $ pA        : num  0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
 $ pB        : num  0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
 $ Distance  : int  40 40 40 40 40 40 40 40 40 40 ...
 - attr(*, ".internal.selfref")=<externalptr>
```

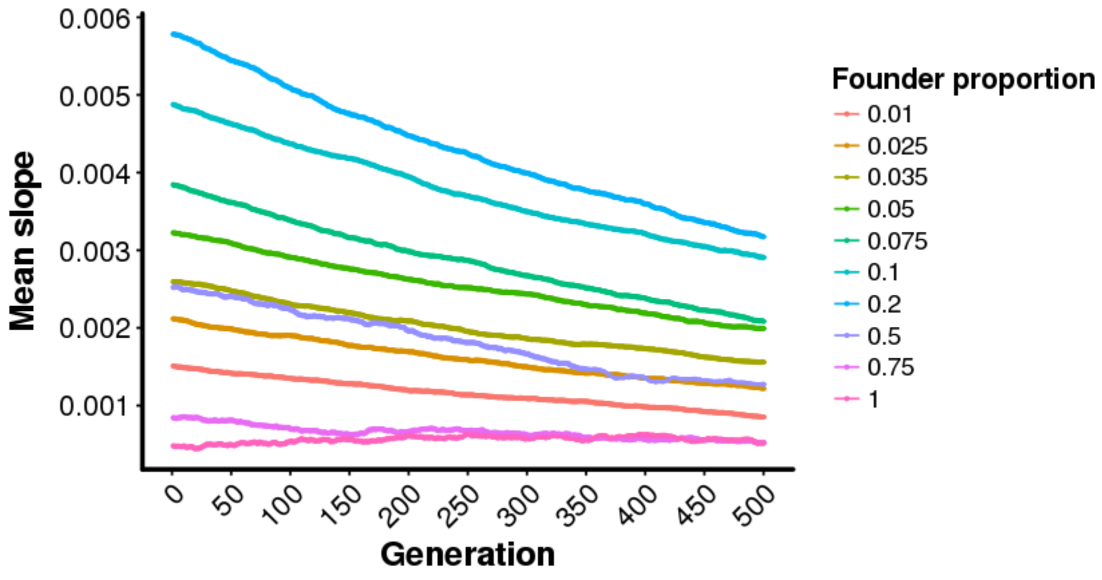
In [5]:
```
#Themes used for plotting
ng1=theme(aspect.ratio=0.7,panel.background = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank(),
          panel.border=element_blank(),
          axis.line.x = element_line(color="black",size=1),
          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"))

         ng1.45=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"))
```

```
In [10]: path = "/scratch/research/projects/trifolium/SEC_Simulation.Evolutionary.Clines/SEC_Sync
         /SEC_Figures/Drift.Migration/Mig_Bot_Vary"

         # ggsave("Mean-slope_BotMig.pdf", plot = MeanSlope_BotMig, device = "pdf", width = 6.0,
         height = 6.0, path = path, dpi = 600)
         # ggsave("PropSigPos_BotMig.pdf", plot = PropSigPos_BotMig, device = "pdf", width = 6.0,
         height = 6.0, path = path, dpi = 600)
         # ggsave("propLost_bot_NoMig.pdf", plot = propLost_bot_NoMig, device = "pdf", width =
         6.0, height = 6.0, path = path, dpi = 600)
         # ggsave("Regression_LostAtGen2_Bot001_NpMig.pdf", plot = LostAt2_bot001_NoMig, device =
         "pdf", width = 6.0, height = 6.0, path = path, dpi = 600)
         # ggsave("Regression_NotLost_Bot02_NoMig.pdf", plot = NotLost_bot02_NoMig, device =
         "pdf", width = 6.0, height = 6.0, path = path, dpi = 600)
         # ggsave("PropNeg_BotMig.pdf", plot = PropNeg_BotMig, device = "pdf", width = 6.0,
         height = 6.0, path = path, dpi = 600)
         ggsave("Mean-slope_Bot_HighMig.pdf", plot = MeanSlope_Bot_HighMig, device = "pdf", width
         = 6.0, height = 6.0, path = path, dpi = 600)
         ggsave("PropSigPos_Bot_HighMig.pdf", plot = PropPos_Bot_HighMig, device = "pdf", width =
         6.0, height = 6.0, path = path, dpi = 600)
```

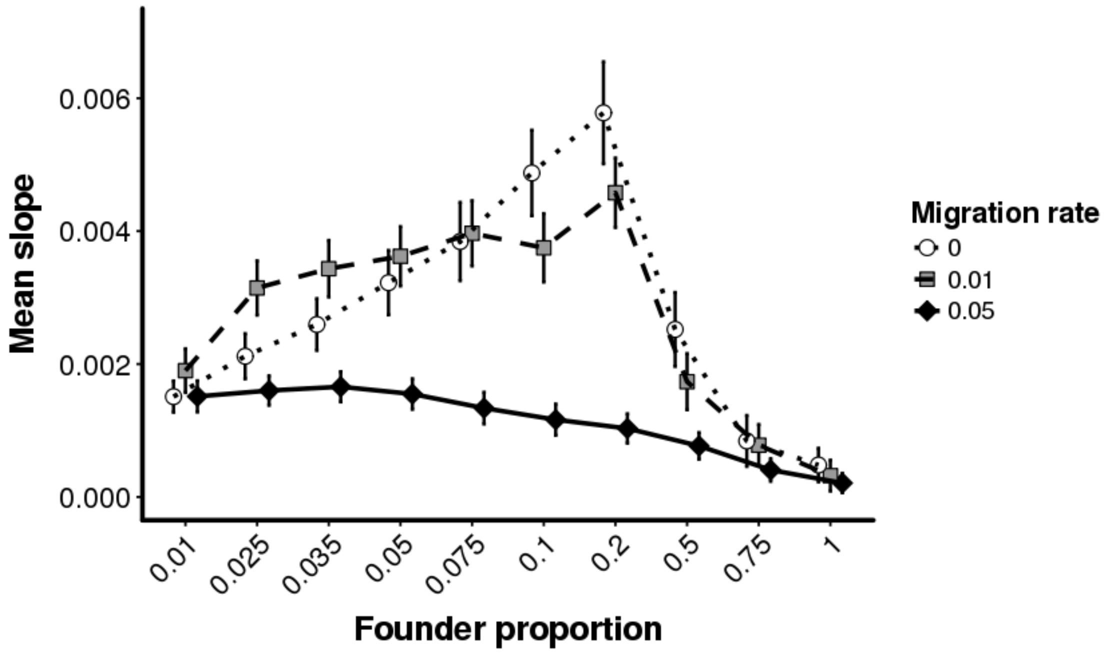
1.1 Mean slope with founder proportion under varying migration rates

Here I look at the mean slope across simulations under varying founding proportions and migration rates. Mean slope is calculated in the first generation following the filling of the landscape matrix. I also plot the change in the mean slope with increasing generations.

```
In [18]: MeanSlope_Cyan_byGen <- ggplot(datSlopes_NoMig, aes(x = seq, y = mean, group = bot,
         color = bot)) +
             ylab("Mean slope") + xlab("Generation") + geom_point(size = 0.5, aes(color = bot)) +
             geom_line(size = 0.5, aes(color = bot)) +
             coord_cartesian(xlim = c(0, 500)) + scale_x_continuous(breaks = seq(from = 0, to =
         500, by = 50)) +
             labs(color = "Founder proportion") + ng1.45
         MeanSlope_Cyan_byGen
```



```
In [9]: MeanSlope_BotMig <- ggplot(datSlopes_GenOne, aes(x = bot, y = mean, group = Mig_rate)) +
            geom_errorbar(aes(ymin = mean - ci_mean, ymax = mean + ci_mean), width=0.15,
        size=0.7,
            position = position_dodge(width = 0.5)) +
            geom_point(size = 3, aes(fill = Mig_rate, shape = Mig_rate), position =
        position_dodge(width = 0.5)) +
            geom_line(size = 1, aes(linetype = Mig_rate), position = position_dodge(width =
        0.5)) +
            scale_shape_manual(labels = c("0", "0.01", "0.05"), values = c(21, 22, 23)) +
            scale_fill_manual(labels = c("0", "0.01", "0.05"), values = c("white", "grey60",
        "black")) +
            scale_linetype_manual(labels = c("0", "0.01", "0.05"), values = c("dotted",
        "dashed", "solid")) +
            coord_cartesian(ylim = c(0, 0.007)) + scale_y_continuous(breaks = seq(from = 0, to =
        0.006, by = 0.002)) +
            ylab("Mean slope") + xlab("Founder proportion") +
            labs(fill = "Migration rate", shape = "Migration rate", linetype = "Migration rate")
        + ng1.45
        MeanSlope_BotMig
```

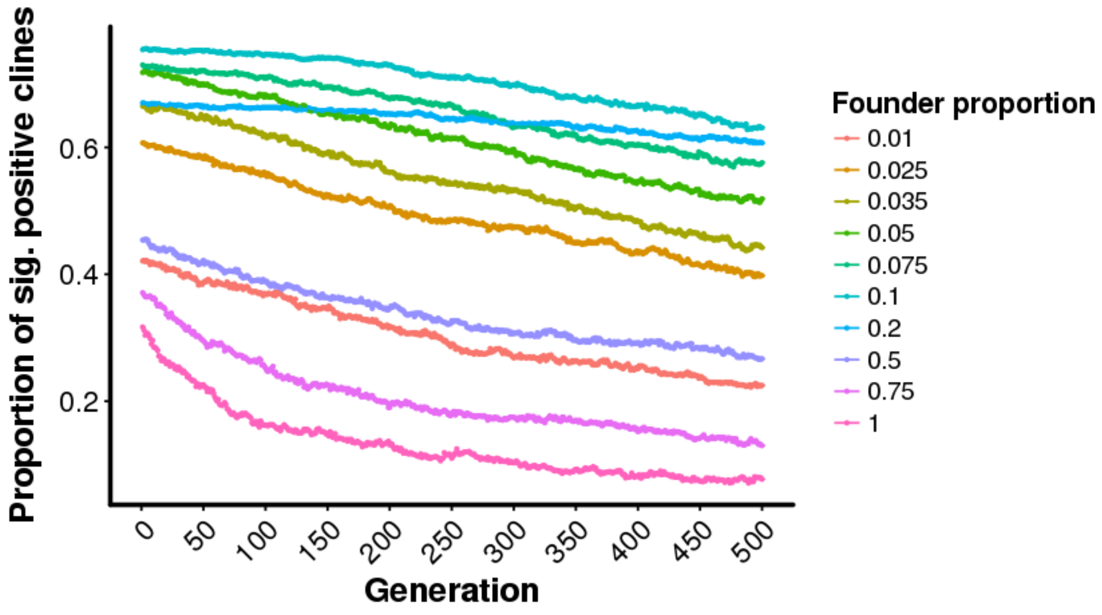


1.2 Effects of founder events and migration on proportion of negative and positive clines

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

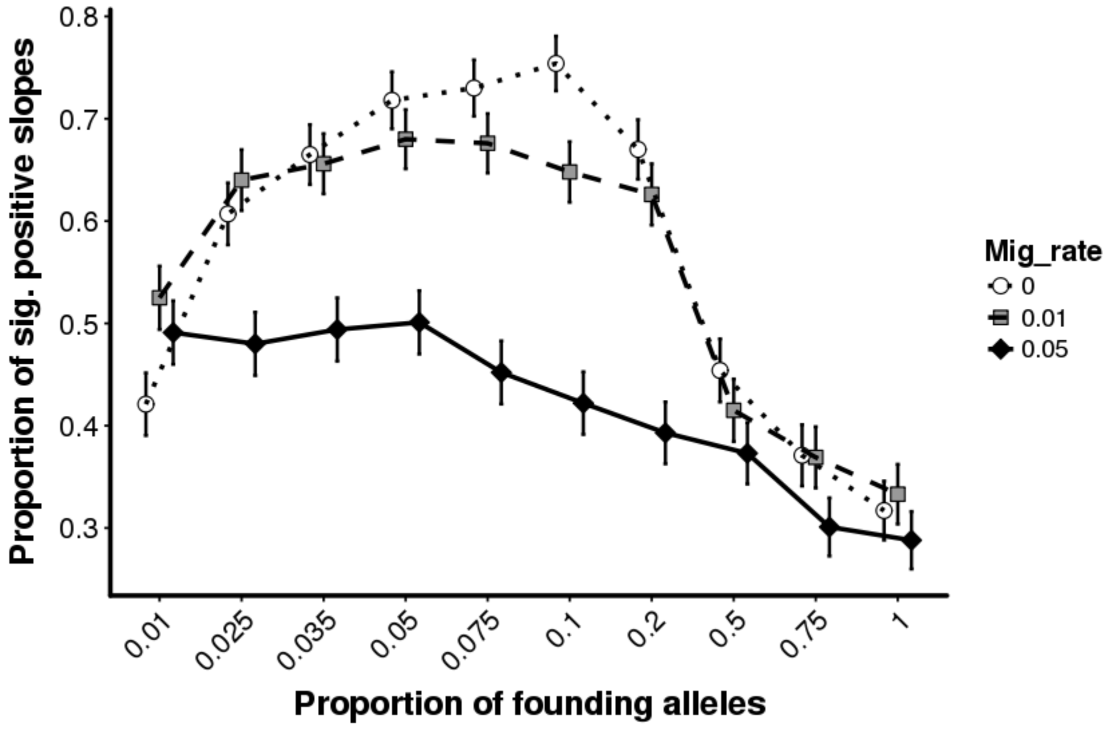
Positive clines: Less HCN in urban environment (i.e. loss of HCN across space)
Negative clines: More HCN in urban environment (i.e. gain in HCN across space)

```
In [21]: PropSigPos_Cyan_byGen <- ggplot(datSlopes_NoMig, aes(x = seq, y = prop_sigPos, group =
         bot, color = bot)) +
             ylab("Proportion of sig. positive clines") + xlab("Generation") + geom_point(size =
         0.5, aes(color = bot)) +
             geom_line(size = 0.5, aes(color = bot)) +
             coord_cartesian(xlim = c(0, 500)) + scale_x_continuous(breaks = seq(from = 0, to =
         500, by = 50)) +
    labs(color = "Founder proportion") + ng1.45
PropSigPos_Cyan_byGen
```



```
In [91]: PropSigPos_BotMig <- ggplot(datSlopes_GenOne, aes(x = bot, y = prop_sigPos, group =
         Mig_rate)) +
             geom_errorbar(aes(ymin = prop_sigPos - ci_sigPos, ymax = prop_sigPos + ci_sigPos),
         width=0.15, size=0.7,
             position = position_dodge(width = 0.5)) +
             geom_point(size = 3, aes(fill = Mig_rate, shape = Mig_rate), position =
         position_dodge(width = 0.5)) +
             geom_line(size = 1, aes(linetype = Mig_rate), position = position_dodge(width =
         0.5)) +
             scale_shape_manual(labels = c("0", "0.01", "0.05"), values = c(21, 22, 23)) +
             scale_fill_manual(labels = c("0", "0.01", "0.05"), values = c("white", "grey60",
         "black")) +
             scale_linetype_manual(labels = c("0", "0.01", "0.05"), values = c("dotted",
         "dashed", "solid")) +
             ylab("Proportion of sig. positive slopes") + xlab("Proportion of founding alleles")
```

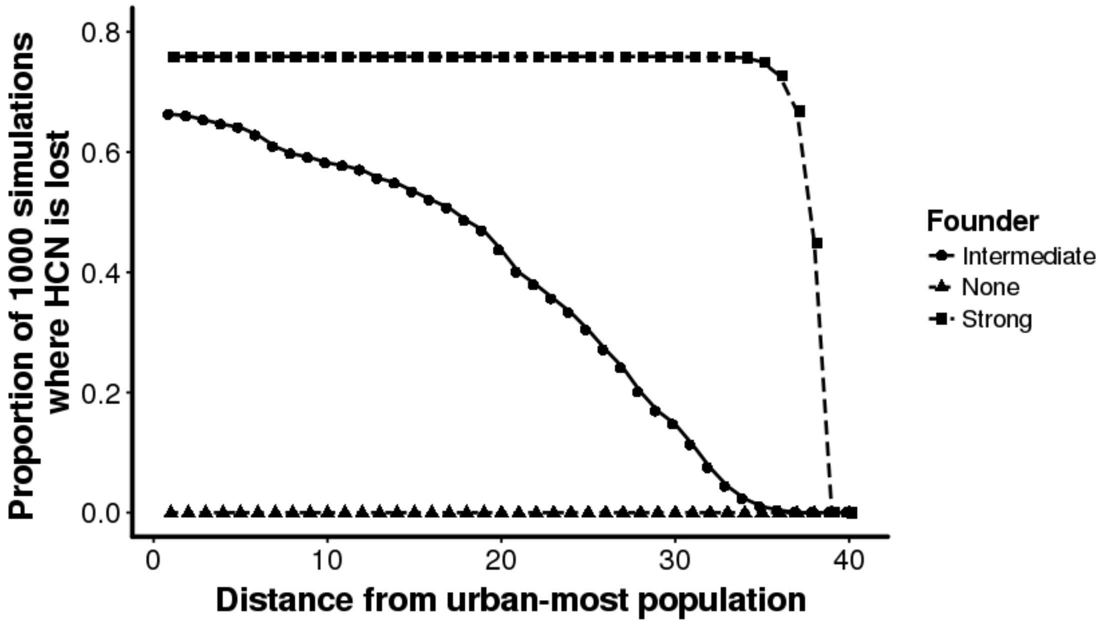
```
+ ng1.45
PropSigPos_BotMig
```



1.3 Dynamics of HCN frequency change during colonization

Here I try to understand the hump-shaped distribution above by exploring how the frequency of HCN changes during the colonization process.

```
In [68]: propLost_bot_NoMig <- ggplot(datPropLost_merged, aes(x = Distance, y = Lost, group =
         Founder)) +
             geom_point(size = 2, aes(fill = Founder, shape = Founder), position =
         position_dodge(width = 0.5)) +
             geom_line(size = 0.75, aes(linetype = Founder)) +
             ylab("Proportion of 1000 simulations
         where HCN is lost") + xlab("Distance from urban-most population") +
             coord_cartesian(ylim = c(0, 0.8)) + scale_y_continuous(breaks = seq(from = 0, to =
0.8, by = 0.2))  + ng1
propLost_bot_NoMig
```

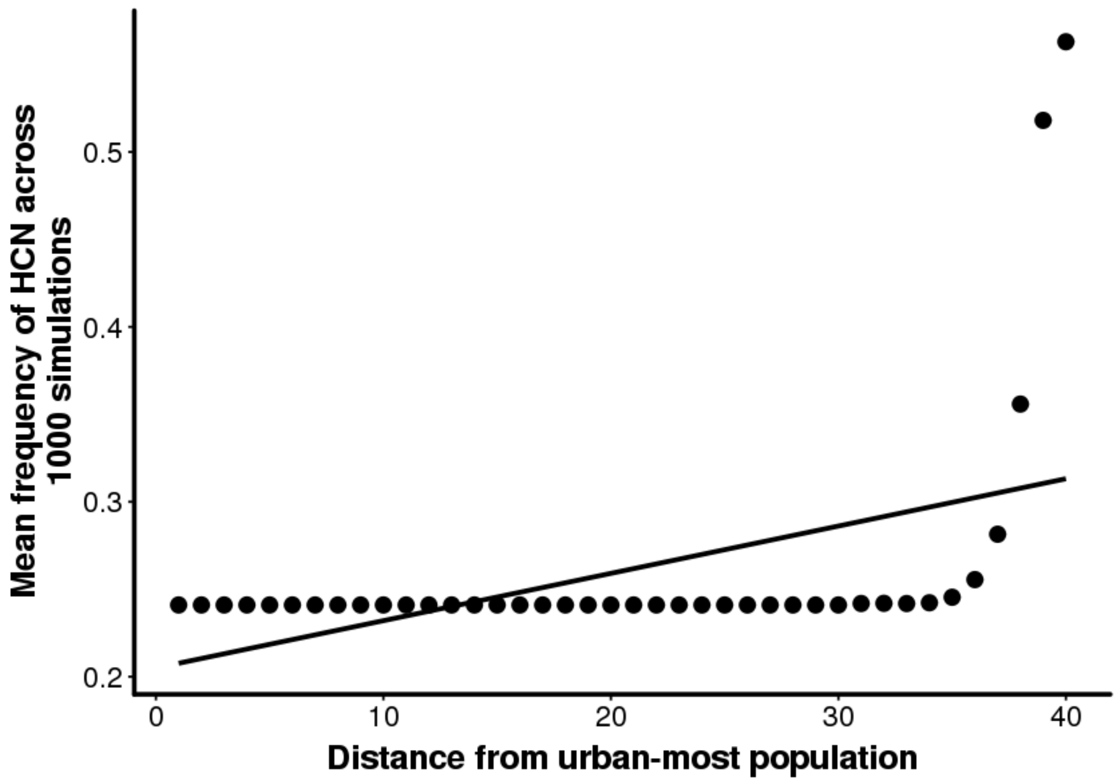


In [72]:
```
lm_FreqFirstGen_StrongBot_NoMig <- lm(Freq ~ Distance, data =
MeanFreqFirstGen_Distance_StrongBot_NoMig)
summary(lm_FreqFirstGen_StrongBot_NoMig)
```

```
Call:
lm(formula = Freq ~ Distance, data = MeanFreqFirstGen_Distance_StrongBot_NoMig)

Residuals:
     Min       1Q   Median       3Q      Max
-0.05468 -0.03498 -0.01131  0.01506  0.24982
```

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.2049757  0.0196579  10.427 1.05e-12 ***
Distance    0.0027050  0.0008356   3.237   0.0025 **
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

Residual standard error: 0.061 on 38 degrees of freedom
Multiple R-squared:  0.2162,Adjusted R-squared:  0.1956
F-statistic: 10.48 on 1 and 38 DF,  p-value: 0.002504
```

```
In [74]: FreqFirstGen_StrongBot_NoMig <- ggplot(MeanFreqFirstGen_Distance_StrongBot_NoMig, aes(x
         = Distance, y = Freq)) +
             geom_point(size = 3) +
             geom_smooth(method = "lm", se = F, colour = "black", size = 1.05) +
             ylab("Mean frequency of HCN across
         1000 simulations") + xlab("Distance from urban-most population") +
             scale_y_continuous(breaks = seq(from = 0, to = 0.5, by = 0.1)) + ng1
         FreqFirstGen_StrongBot_NoMig
```

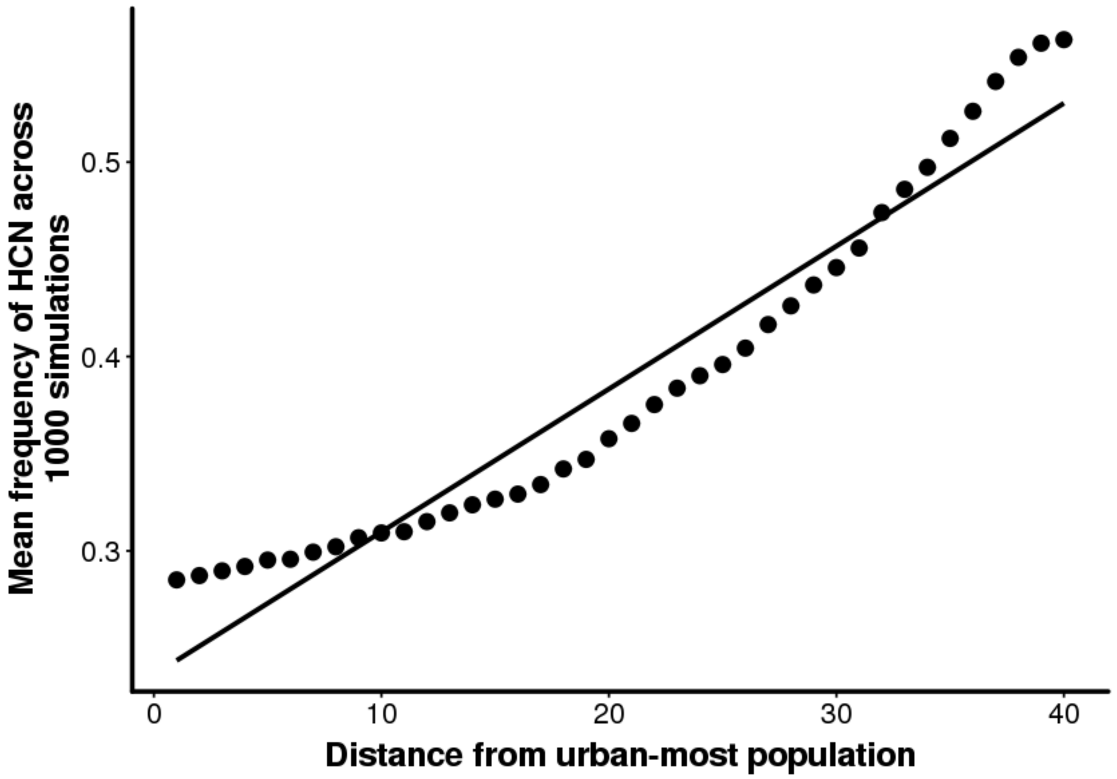


```
In [76]: lm_FreqFirstGen_InterBot_NoMig <- lm(Freq ~ Distance, data =
         MeanFreqFirstGen_Distance_InterBot_NoMig)
         summary(lm_FreqFirstGen_InterBot_NoMig)
```

```
Call:
lm(formula = Freq ~ Distance, data = MeanFreqFirstGen_Distance_InterBot_NoMig)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.028870 -0.021871 -0.007804  0.019546  0.041450 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept) 0.2362970  0.0074957   31.52   <2e-16 ***
Distance    0.0073500  0.0003186   23.07   <2e-16 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

Residual standard error: 0.02326 on 38 degrees of freedom
Multiple R-squared:  0.9334,Adjusted R-squared:  0.9316
F-statistic: 532.2 on 1 and 38 DF,  p-value: < 2.2e-16
```

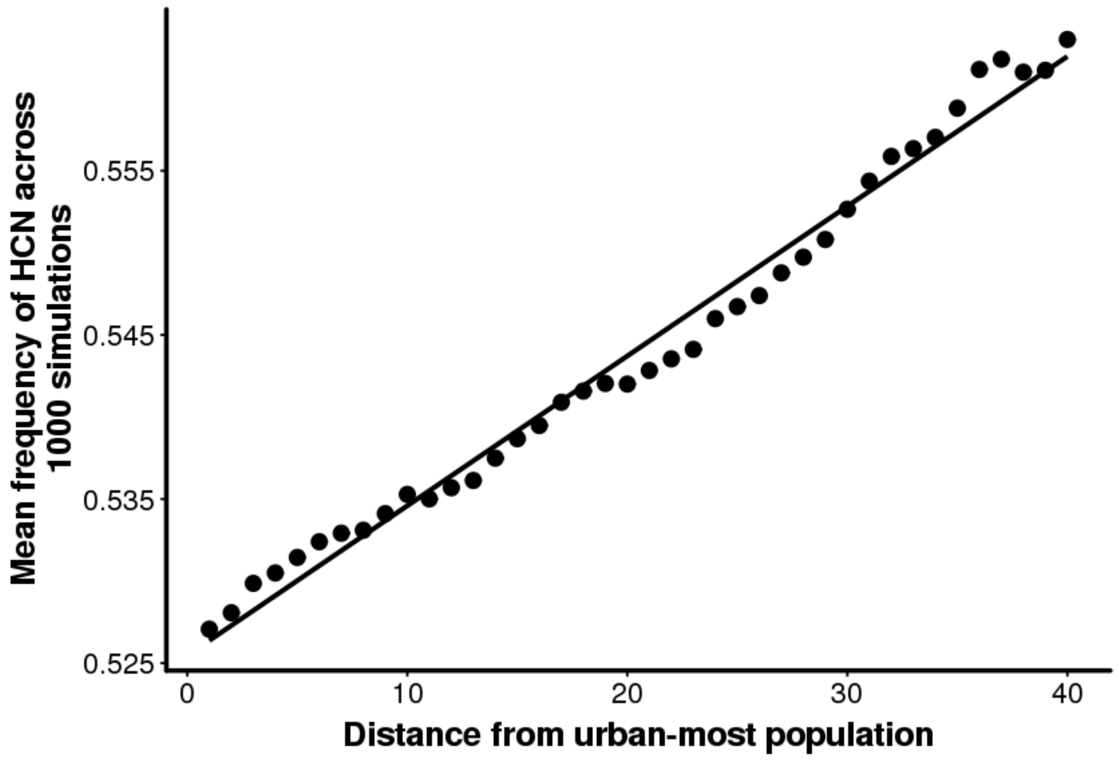
```
In [77]: FreqFirstGen_InterBot_NoMig <- ggplot(MeanFreqFirstGen_Distance_InterBot_NoMig, aes(x =
         Distance, y = Freq)) +
             geom_point(size = 3) +
             geom_smooth(method = "lm", se = F, colour = "black", size = 1.05) +
             ylab("Mean frequency of HCN across
         1000 simulations") + xlab("Distance from urban-most population") + ng1
         FreqFirstGen_InterBot_NoMig + ng1
```



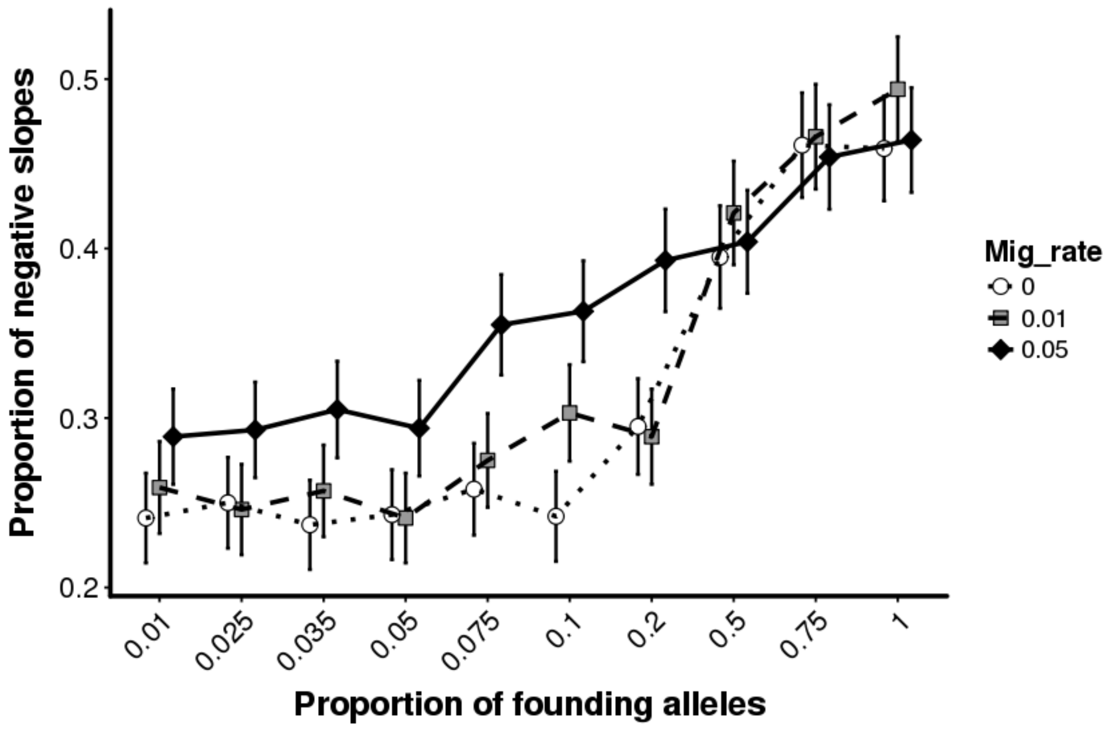
```
In [78]: lm_FreqFirstGen_NoBot_NoMig <- lm(Freq ~ Distance, data =
         MeanFreqFirstGen_Distance_NoBot_NoMig)
         summary(lm_FreqFirstGen_NoBot_NoMig)
```

```
Call:
lm(formula = Freq ~ Distance, data = MeanFreqFirstGen_Distance_NoBot_NoMig)

Residuals:
       Min         1Q     Median         3Q        Max
-2.333e-03 -1.134e-03 -6.130e-06  9.098e-04  2.859e-03

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.5254653  0.0004212 1247.42   <2e-16 ***
Distance    0.0009125  0.0000179   50.96   <2e-16 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1   1

Residual standard error: 0.001307 on 38 degrees of freedom
Multiple R-squared:  0.9856,Adjusted R-squared:  0.9852
F-statistic:  2597 on 1 and 38 DF,  p-value: < 2.2e-16
```

```
In [79]: FreqFirstGen_NoBot_NoMig <- ggplot(MeanFreqFirstGen_Distance_NoBot_NoMig, aes(x =
         Distance, y = Freq)) +
             geom_point(size = 3) +
             geom_smooth(method = "lm", se = F, colour = "black", size = 1.05) +
             ylab("Mean frequency of HCN across
         1000 simulations") + xlab("Distance from urban-most population") + ng1
         FreqFirstGen_NoBot_NoMig + ng1
```



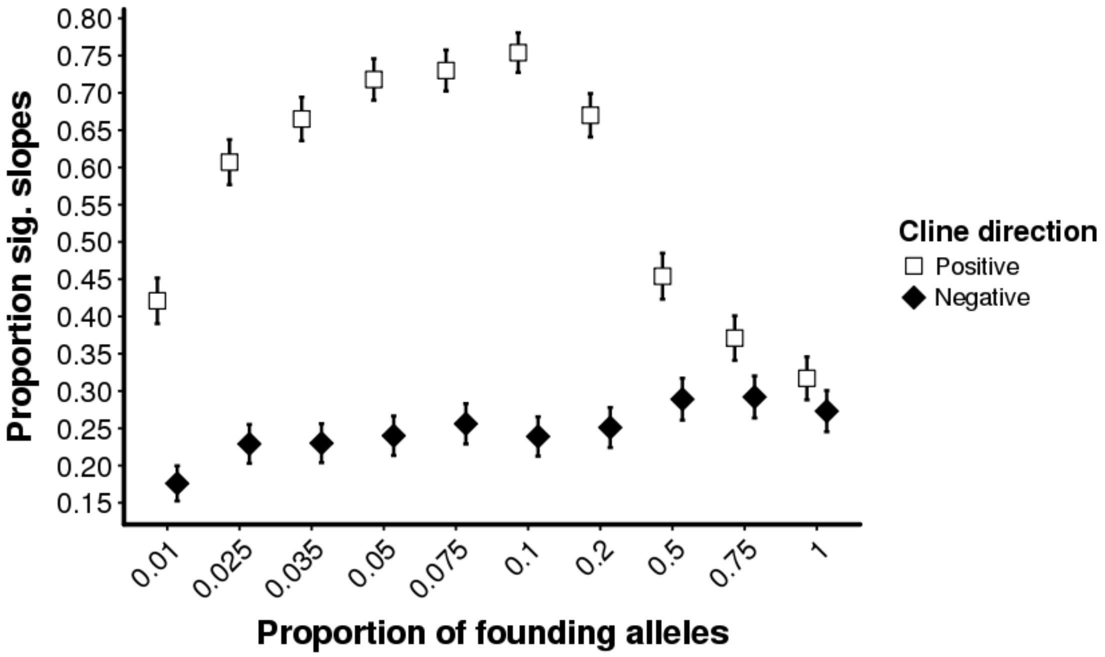
```
In [89]: PropNeg_BotMig <- ggplot(datSlopes_GenOne, aes(x = bot, y = prop_neg, group = Mig_rate))
         +
             geom_errorbar(aes(ymin = prop_neg - ci_neg, ymax = prop_neg + ci_neg), width=0.15,
         size=0.7,
             position = position_dodge(width = 0.5)) +
             geom_point(size = 3, aes(fill = Mig_rate, shape = Mig_rate), position =
         position_dodge(width = 0.5)) +
             geom_line(size = 1, aes(linetype = Mig_rate), position = position_dodge(width =
         0.5)) +
             scale_shape_manual(labels = c("0", "0.01", "0.05"), values = c(21, 22, 23)) +
             scale_fill_manual(labels = c("0", "0.01", "0.05"), values = c("white", "grey60",
         "black")) +
             scale_linetype_manual(labels = c("0", "0.01", "0.05"), values = c("dotted",
         "dashed", "solid")) +
             ylab("Proportion of negative slopes") + xlab("Proportion of founding alleles") +
         ng1.45
         PropNeg_BotMig + ng1.45
```



```
In [87]: #Extra columns that will be used to create melting dataset for plotting proportion of
         positive and negative slopes
         SlopeSum_Melt_NoMig <- dplyr::select(datSlopes_GenOne_NoMig, bot, prop_sigPos,
         ci_sigPos, prop_sigNeg,
           ci_sigNeg)

         #Melt dataframe
         dm1 <- melt(datSlopes_GenOne_NoMig[,c("bot", "prop_sigPos", "ci_sigPos")],
                     id=c("bot", "ci_sigPos"))
         dm2 <- melt(datSlopes_GenOne_NoMig[,c("bot", "prop_sigNeg", "ci_sigNeg")],
                     id=c("bot", "ci_sigNeg"))

         #Rename columns
         setnames(dm1, old = "ci_sigPos", new = "ci")
         setnames(dm2, old = "ci_sigNeg", new = "ci")

         #Merge melted dataframes
         SlopeSum_Melt_NoMig <- rbind(dm1, dm2)
         SlopeSum_Melt_NoMig
```

bot	ci	variable	value
0.01	0.03060106	prop_sigPos	0.421
0.025	0.03027239	prop_sigPos	0.607
0.035	0.02925427	prop_sigPos	0.665
0.05	0.02788964	prop_sigPos	0.718
0.075	0.02751689	prop_sigPos	0.730
0.1	0.02669373	prop_sigPos	0.754
0.2	0.02914409	prop_sigPos	0.670
0.5	0.03085889	prop_sigPos	0.454
0.75	0.02994114	prop_sigPos	0.371
1	0.02884005	prop_sigPos	0.317
0.01	0.02360348	prop_sigNeg	0.176
0.025	0.02604360	prop_sigNeg	0.229
0.035	0.02608347	prop_sigNeg	0.230
0.05	0.02647089	prop_sigNeg	0.240
0.075	0.02704970	prop_sigNeg	0.256
0.1	0.02643305	prop_sigNeg	0.239
0.2	0.02687409	prop_sigNeg	0.251
0.5	0.02809570	prop_sigNeg	0.289
0.75	0.02818150	prop_sigNeg	0.292
1	0.02761243	prop_sigNeg	0.273

```
In [90]: #Plot proportion of significant slopes by migration rate
         PropSig_Bot_NoMig <- ggplot(SlopeSum_Melt_NoMig, aes(x = factor(bot), y = value,
             shape = variable, fill = variable)) +
             geom_errorbar(aes(ymin = value - ci, ymax = value + ci), width=0.15, size = 0.7,
             position = position_dodge(width = 0.55)) +
             ylab("Proportion sig. slopes") + xlab("Proportion of founding alleles") +
         geom_point(size = 3.5, color = "black",
             position = position_dodge(width = 0.55)) +
             scale_shape_manual(labels = c("Positive", "Negative"),values=c(22, 23))+
             scale_fill_manual(labels = c("Positive", "Negative"),values=c("white", "black")) +
             scale_y_continuous(breaks = seq(from = 0, to = 1.0, by = 0.05)) +
             labs(shape = 'Cline direction', fill = 'Cline direction') + ng1.45
         PropSig_Bot_NoMig
```



1.4 Do we need to show what's happening to the individual alleles?