Summary

Deviation from HW

Fitting clines

Plotting clines

Fitting clines: erato

Fitting a descriptive model

WntA: w=34.3, y=54.1, F=0.021

Ro: w=49.1, y=55.7, F=0

Cortex: $p_1 = 0.815$, w=38.0, y=30.4, F=0

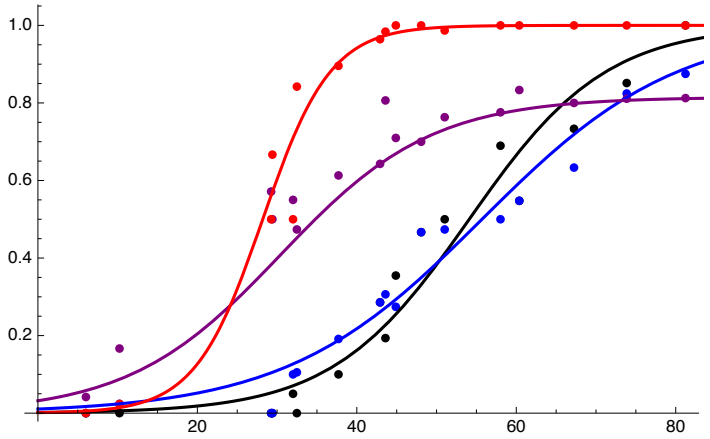
Optix: w=17.0, y=28.2, F=0

Comparing all four clines

WntA and Ro are very close. However, Cortex and Optix differ substantially: Cortex is wider and has $p_1 < 1$

In[427]:=
```
mle[e] = {{0, 1, 34.3, 54.1},
   {0, 1, 49.1, 55.7}, {0, 0.815, 38.0, 30.4}, {0, 1, 17.0, 28.2}};
Show[
 MapThread[ListPlot[Transpose[{x[e], freqs[e][[All, #]]}], PlotStyle → #2] &,
  {{1, 2, 3, 4}, {Black, Blue, Purple, Red}}],
 MapThread[Plot[pCline[#1][x], {x, 0, 90}, PlotStyle → #2] &,
  {mle[e], {Black, Blue, Purple, Red}}]]
```

Out[428]=



Fitting clines: melpomene

WntA: w=35.7, y=50.6, F=0 $p_1 = 0.85$ (ns) w=24.3, y=45.7,

F=0

N: w=36.8, y=34.8, F=0.042

Cortex: w=31.3, y=30.3, F=0

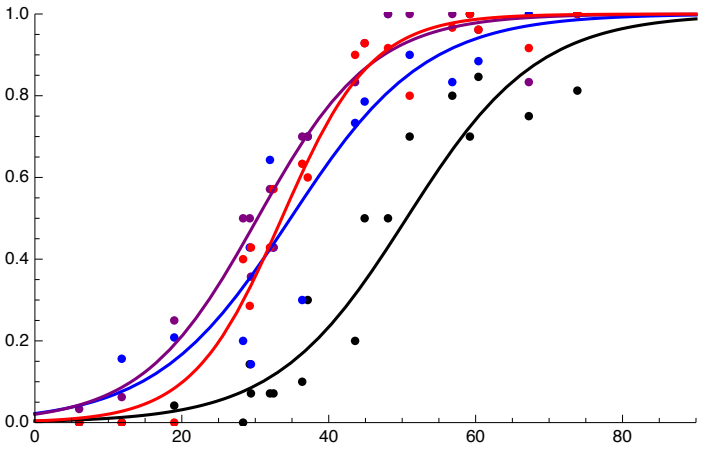
Optix: w=24.5, y=33.6, F=0

Comparing all four clines

N, Cortex and Optix (blue, purple, red) are very close. However, WntA (black) is shifted to the right

In[433]:=
```
mle[m] =
  {{0, 1, 35.7, 50.6}, {0, 1, 36.8, 34.8}, {0, 1, 31.3, 30.3}, {0, 1, 24.5, 33.6}};
Show[
 MapThread[ListPlot[Transpose[{x[m], freqs[m][[All, #]]}], PlotStyle → #2,
    PlotRange → {{0, 90}, {0, 1}}] &, {{1, 2, 3, 4}, {Black, Blue, Purple, Red}}],
 MapThread[Plot[pCline[#1][x], {x, 0, 90}, PlotStyle → #2] &,
  {mle[m], {Black, Blue, Purple, Red}}]]
```

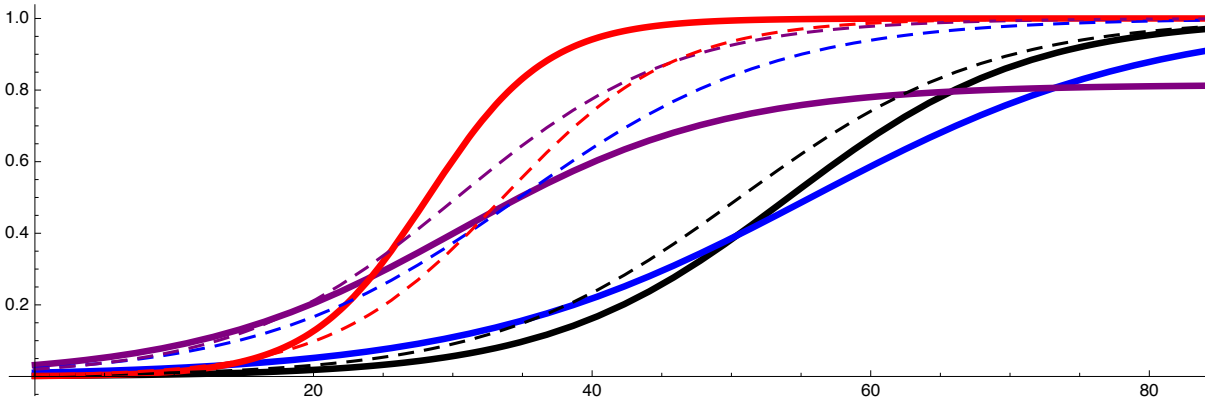
Out[434]=



Comparing erato with melpomene

Thick lines: *erato*, dashed: *melpomene*; WntA, Ro or N, Cortex, Optix (black, blue, purple, red)

Out[446]=



Fitting clines with dominance

Modelling a cline at one locus

The model: h_1, h_2

The model is that fitnesses multiply across loci, and within loci, fitness is $1 - s(P - Q) : 1 + h_1 s(P - Q) : 1 + s(P - Q)$, where $(P - Q) = (p - q) + 2\,pq\,h_2$ assuming HW. Here, the dominance coefficients h_1, h_2 range from -1 to 1. h_1 describes dominance for effects on fitness, whereas h_2 describes dominance for the perceived frequency.

Scaling time to $1/s$, distance to $\sigma \Big/ \sqrt{2\,s}$:

$$\partial_t p = \partial_{x,x} p + ((p - q) + 2\,pq h_2)\,pq\,(1 - h_1\,(p - q)) = \partial_{x,x} p + pq\,f[p]$$

In the special case $h_1 = h_2 = 0$, we have underdominance. If $h_1 = h_2 = 1$:

$$\partial_t p = \partial_{x,x} p + 2\left(1 - 2\,q^2\right) pq^2$$

The cline cannot be pinned by a compensating selection

Travelling wave solution

Fitting clines with dominance: erato

Fitting clines with dominance: melpomene

Summary table

Table 1. Testing for asymmetry of single-locus clines. Linear frequency dependence, with no dominance, maintains a symmetric cline, whereas positive frequency dependence, with full dominance of the lowland alleles, maintains asymmetric clines, with introgression into the lowland population. The table shows the estimated position and width for each locus, in each species, for the best-fitting model. The last row shows the difference in log likelihood between the best-fitting asymmetric vs symmetric models; a positive value favours asymmetry. None of the best-fitting models gave evidence for residual variation (i.e., we estimate $F_{ST} = 0$).

erato	WntA	Ro	Cortex	Optix	*melpomene*	WntA	*N*	Cortex	Optix
width	29.9	47.8	38.0	17.0		32.4	36.8	31.3	14.9
position	47.3	55.7	26.2	28.2		43.5	34.8	30.3	29.8
dominance	+4.38	+0.40	+6.13	−9.28		+2.28	−3.09	−4.56	+4.13

Linkage disequilibrium

D for each site: erato

D for each site: melpomene

Plots of log(L) vs x for all pairs

Estimates of $R = \frac{D}{\sqrt{p_1\,q_1\,p_2\,q_2}}$ for all pairs

Overall estimates

Comparison with Mallet et al 1990

Working for sites with h>0.2

Working for sites with h>0.1

Working for estimates using all populations

Naive approach: marginal significance in *melpomene*, none in *erato*

LD on phenotypes

Simulating clines

In principle, we need to follow haplotype frequencies at up to 4 loci. This should be feasible using the machinery in "Simulations 2019", but requires deciding on many parameters. Following the MS, I focus on WntA and optix. These control the shape of the forewing band, and the size of the red patch & rays, respectively. Since LD is weak, it should be reasonable to focus on just these two loci. Moreover, for both, to a first approximation, the lowland allele is dominant, so we may be able to deal with approximately four phenotypes.

Clines can be shifted for many reasons. LD tends to pull them together, but almost all deviations from symmetry will push them apart.

- independent tension zones (eg +fds or under-dominance acting independently) will drift randomly and in general will be shifted - unless pulled together by LD or by a shared heterogeneous population structure.
- Synergistic costs (eg double heterozygotes being much less fit than expected) can force clines apart - examples from chromosome rearrangements (whwere acrocentrics may also arise)
- Asymmetric selection against recombinants (as in DMI models) cause clines to stagger.
- + ve FDS can lead to establishment of arbitrary hybrid morphs.

We can distinguish neutral vs systematic shifting vs shifts that may occur in any direction.

Qualitatively, shifts tend to increase mean fitness - but there is no exact maximisation principle, even without FDS.

Note that because LD is weak, we can use just the marginal fitnesses of alleles at each locus. However, that will not correctly adress the dynamics, even if it is correct at equilibrium.

Reasonable models could be:

1) Independent FDS on single genes, either additive, or by morph
2) Two-locus models with fixed fitnesses - interaction between heterozygotes, and asymmetric selection against heterozygotes
3) +ve FDS on four morphs, assuming that selection strongly favours the commonest morph, with a power law parameter that favours frequency in synergistic way.
4) Modify this to distinguish heterozygotes etc

One should start both from coincidence and from a staggered initial point (staggering in both directions)

These are all toy models, which should be just illustrative. Next, one needs to fit models more seriously:

- locus by locus looking at evidence of dominance
- two loci, checking how much LD is produced, and whether clines shift as observed

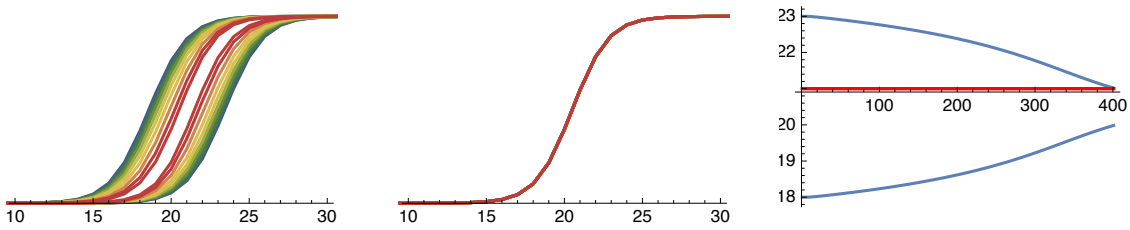
Simple two locus example

Simple two locus examplewith FDS

```
nd = 20; M = makeMendel[{1/2}, {2, 2}]; mig = makeM[0.5, 2 nd + 1];
```

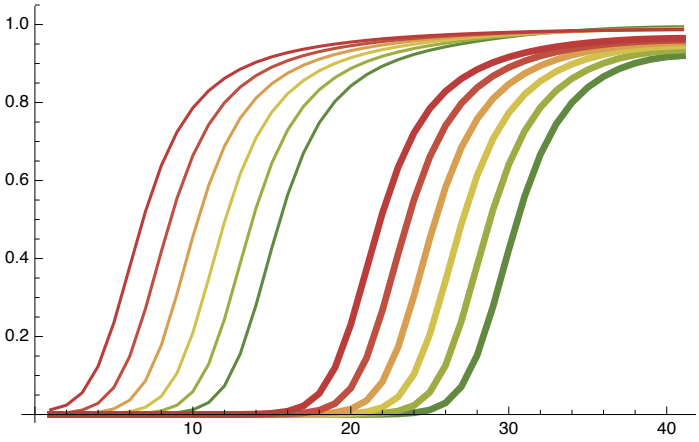
Two loci, +ve selection m=1/2, s=0.2, 20+1+20 demes, starting shifted apart by ±2.5. The clines pull together as a result of LD (blue→red at t=400):

Out[2508]=



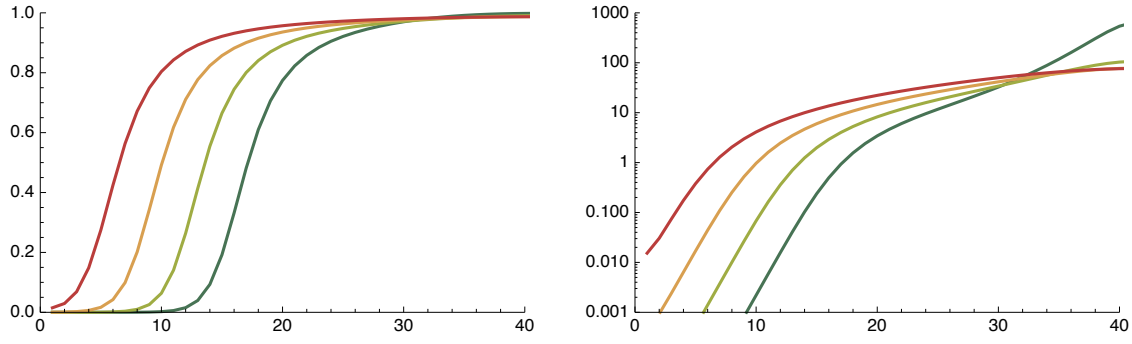
This is with dominance (for both fitness and FDS), s=0.1. The clines move to the left at the same speed, and start too far apart to pull together:

Out[2428]=



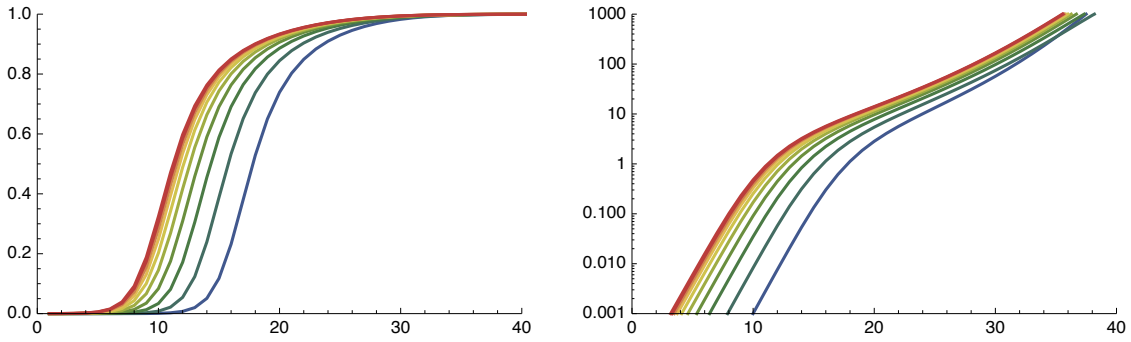
This shows similar simulations, but with the clines coinciding. Selection against the recessive allele is ineffective, so there is an asymmetric tail on the right. This takes time to develop.

Out[2585]=



We would like to find a stable solution. One way to do this is to add a weak selection gradient, so that equilibrium is reached. One would have a selection that increases in strength linearly with position. That is, employ multiplicative fitness against the dominant allele, with linear change in strength. Here, with β=0.001, the clines settle at ~ -11, or counter selection -0.011. This is small relative to the selection 0.1 in the tails - though it will dominate over selection against recessives to the right,

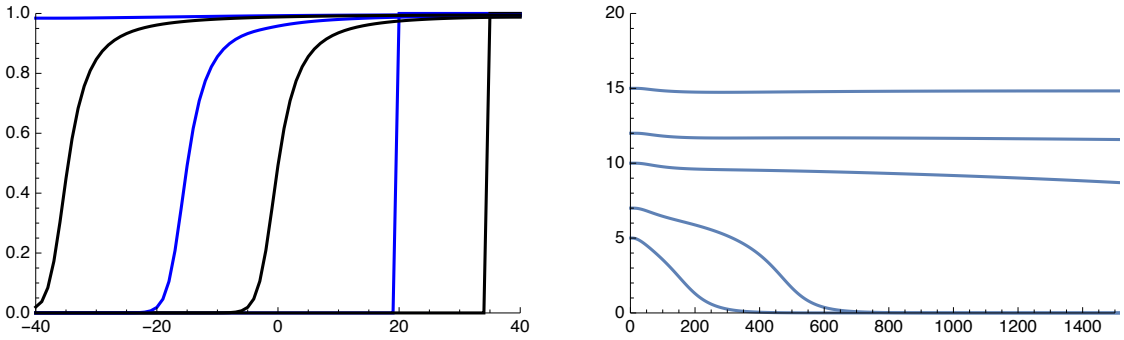
Out[2606]=



Now, try FDS for the four morphs that are expressed with complete dominance. Here, if the clines start far apart (±15, left) they move in parallel and stay shifted. However, if they start closer (<10 apart), they pull together, presumably through a combination of LD and swamping of the hybrid morph. Even when they start apart, they will eventually pull together, but this takes a very long time.

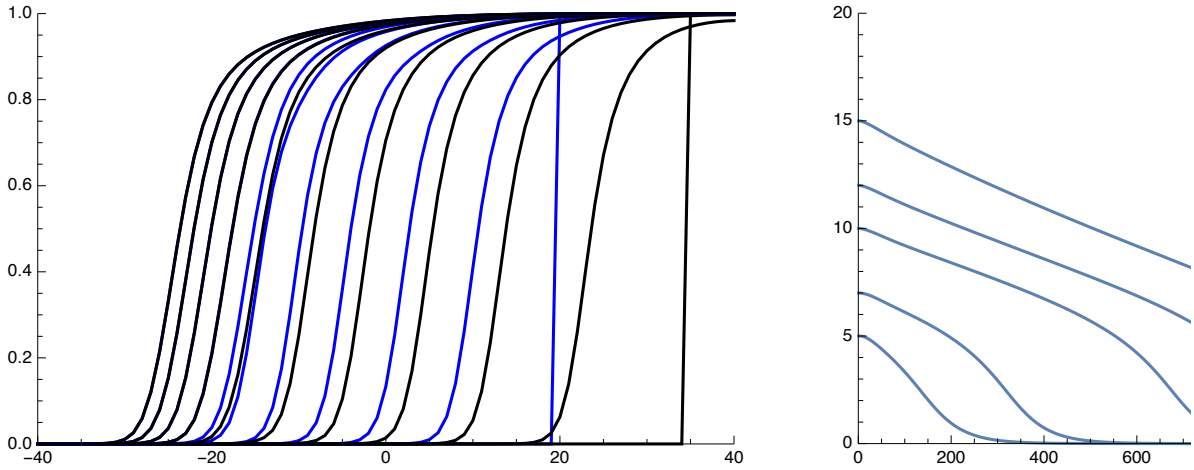
In[560]:=
```
GraphicsRow[
 {makeClineGraph[makePdom[0.1, 0, 40, 2000, {20, 35}], 1000, {Blue, Black}],
  Show[makePosGraph[makePdom[0.1, 0, 40, 2000, {#, 35}],
      PlotRange → {{0, 1500}, {0, 20}}] & /@ {20, 22.5, 25, 27.5, 30}]}]
```

Out[560]=



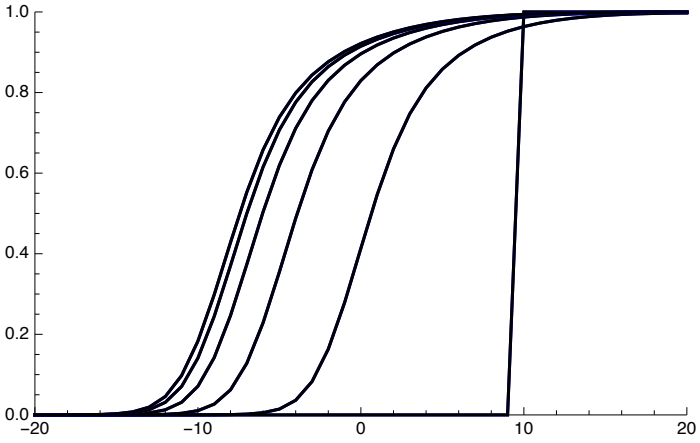
If we impose a weak selection gradient to pin the clines (balancing extrinsic selection against dominance), then the clines are pushed together. After 2000 generations, the cline position has not quite equilibrated, but is consistent with the counter selection $\beta x = 0.011$ identified above

In[2844]:=
```
GraphicsRow[
 {makeClineGraph[makePdom[0.1, 0.00025, 40, 2000, {20, 35}], 200, {Blue, Black}],
  Show[makePosGraph[makePdom[0.1, 0.00025, 40, 2000, {#, 35}],
      PlotRange → {{0, 1500}, {0, 20}}] & /@ {20, 22.5, 25, 27.5, 30}]}]
```



In[387]:=
```
makeClineGraph[makePdom[0.1, 0.001, 20, 1000, {10, 10}], 200, {Blue, Black}]
```

Out[387]=



Relation between R_{max} and s for two-locus models with dominance: R~0.73s

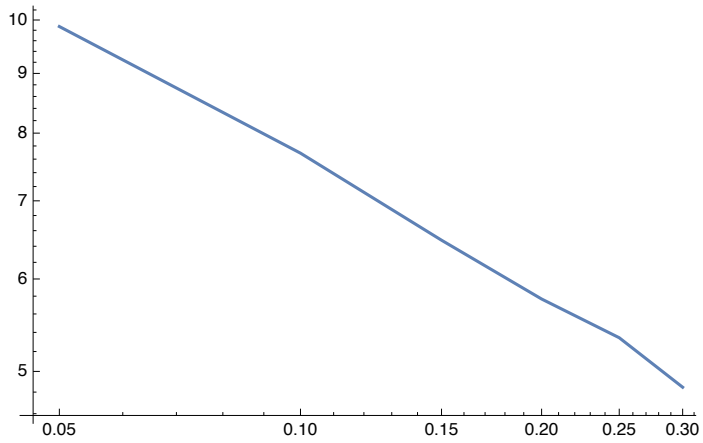
In[594]:=
```
nd = 40;
tt = Table[(gg = makeClineDom[s, 0.001, nd, 1000, {nd - 10, nd - 10}];
pp = makePdom[s, 0.001, nd, 1000, {nd - 10, nd - 10}];
ww = 1 / Max[Drop[pp[[-1, All, 1]], 1] - Drop[pp[[-1, All, 1]], -1]];
    dl = MapThread[(#2[[4]] - #1[[1]]^2) / (#1[[1]] (1 - #1[[1]])) &, Last /@ {pp, gg}];
    intD = Interpolation[dl];
    {s, FindMaximum[intD[x], {x, nd / 2, 1, nd}][[1]], ww}), {s, 0.05, 0.3, 0.05}];
TableForm[Prepend[tt, {"s", "Rmax", "w"}]]
```

Out[596]//TableForm=

s	R_{max}	w
0.05	0.0438807	9.87229
0.1	0.074475	7.69013
0.15	0.104376	6.47688
0.2	0.13307	5.76764
0.25	0.159331	5.34332
0.3	0.185075	4.84646

In[600]:=
```
ListLogLogPlot[tt[[All, {1, 3}]], Joined → True]
Fit[Log[tt[[1 ;; -4, {1, 3}]]], {1, ls}, ls]
```

Out[600]=



Out[601]=
```
1.15178 - 0.381152 ls
```

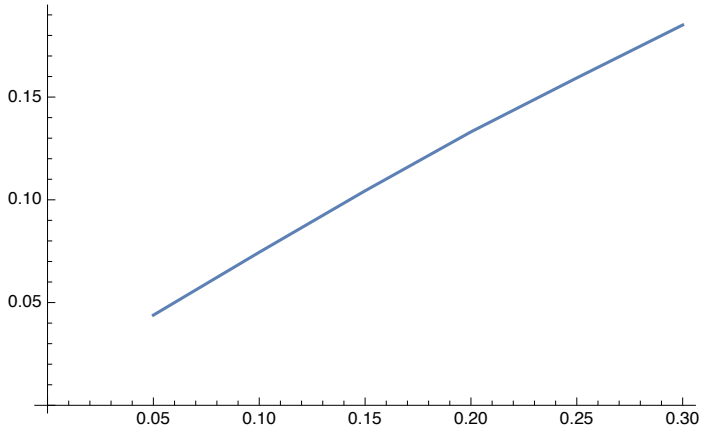
We have that w ~ $2.5\sqrt{s} \sim 3.53\,\sigma\sqrt{s}$ or ~ $\sqrt{12\,\sigma^2/s}$

In[602]:=
```
tt[[All, 3]] √tt[[All, 1]]
```

Out[602]=
```
{2.20751, 2.43183, 2.50848, 2.57937, 2.67166, 2.65451}
```

In[422]:=
```
ListLinePlot[tt]
{Fit[tt, {s}, s], Fit[Drop[tt, -3], {s}, s], Fit[tt // Log, {1, s}, s]}
```

Out[422]=



Out[423]=
```
{0.647328 s, 0.722797 s, -0.721261 + 0.807047 s}
```

Summary so far

It seems that there are several forces acting on clines maintained by +ve FDS:

- dominance causes a systematic movement
- heterogeneous density or adaptation to different environments *at these loci* could pin clines; the former is more likely
- LD will pull overlapping clines together
- A shift will be generated by selection
- FDS can maintain a hybrid morph, but if it is symmetric, there is no force maintaining

Definitions

Raw data

Setting up data: codes, nPops,gen, freqs, x, z

codes

gen, freqs

x, z

In[19]:=
```
x::usage = "x[e] gives the position of the sites along the transect";
x[s : (e | m)] := x[s] = rawLocs[s][[All, 2]];
```

In[21]:=
```
z::usage = "z[e] gives the altitude of the sites";
z[s : (e | m)] := z[s] = rawLocs[s][[All, 3]];
```

nPops, nInds

types, typeArray, genFreqs

Deviations from HW: likHW, Fis

LD: rangeD, rangeR, likD, likR, expG, mleD, likDTable

Phenotype data

Raw data: erato

Processing data

Simulating clines (extensions to "Simulations 2019")

iterateCline

fdsW

fdsW2

This function aims to define, specifically for a system with dominance, +ve FDS that acts equally to favour each of the morphs. We have morph frequencies P_{00}, …, and define the fitnesses of the four morphs as:

$1 + s(P_{00} - Q_{00})$ $1 + s(P_{01} - Q_{01})$
$1 + s(P_{10} - Q_{00})$ $1 + s(P_{11} - Q_{11})$

So, if any morph is common, its fitness will be 1+s, and the others will all be 1-s. If two are equally common (00,01 say) then they each have fitness 1, and the others will be 1-s

In[99]:=
```
fdsW2::usage =
  "fdsW2[s,{{P11,P12},{P21,P22}}] generates a 4×4 matrix giving the
    fitness of every diploid genotype, assuming +ve frequency
    dependence that acts independently at two loci, with
    complete dominance for allele 2, and two alleles. ";
```

In[100]:=
```
fdsW2[s_, {{P11_, P12_}, {P21_, P22_}}] := Module[{j = Length /@ s, hs},
   Outer[
    fdsW2[Transpose[{#1, #2}], s, {{P11, P12}, {P21, P22}}] &,
    haps[{2, 2}], haps[{2, 2}], 1]];
```

In[101]:=
```
fdsW2[{{1, 1}, {1, 1}}, s_, {{P11_, P12_}, {P21_, P22_}}] := 1 + s (2 P11 - 1);
fdsW2[{{1, 1}, {1, 2} | {2, 1} | {2, 2}},
   s_, {{P11_, P12_}, {P21_, P22_}}] := 1 + s (2 P12 - 1);
fdsW2[{{1, 2} | {2, 1} | {2, 2}, {1, 1}}, s_, {{P11_, P12_}, {P21_, P22_}}] :=
  1 + s (2 P21 - 1);
fdsW2[{{1, 2} | {2, 1} | {2, 2}, {1, 2} | {2, 1} | {2, 2}},
   s_, {{P11_, P12_}, {P21_, P22_}}] := 1 + s (2 P22 - 1);
```

makeClineDom

In[105]:=
```
makeClineDom::usage =
  "makeClineDom[s,β,nd,tmax,{y1,y2}] stores a two-locus cline,
    with extrinsic selection gradient βx, initial steps
    at {y0,y1}, on a range {-nd,nd}. Positive FDS s acts
    symmetrically on the four morphs, assuming complete dominance";
```

In[106]:=
```
makeClineDom[s_, β_, nd_, tm_, {y1_, y2_}] :=
  makeClineDom[s, β, nd, tm, {y1, y2}] =
   Module[{M = makeMendel[{1/2}, {2, 2}], mwx, mig, pp, uu},
    mwx[r_] := multW[{{-r, r}, {-r, r}}];
    mig = makeM[0.5, 2 nd + 1];
    NestList[(
       pp = alleleFreqs[#, {2, 2}][[All, 2]] & /@ #;
       uu = {{(1 - #[[1]])^2 (1 - #[[2]])^2, (1 - #[[1]])^2 #[[2]] (2 - #[[2]])},
            {#[[1]] (2 - #[[1]]) (1 - #[[2]])^2, #[[1]] (2 - #[[1]]) #[[2]] (2 - #[[2]])}} & /@ pp;
       wl = MapThread[mwx[β #1] fdsW2[s, #2] &, {Range[-nd, nd], uu}];
       iterateCline[#, wl, M, mig]) &, stepCline[nd, {y1, y2}, tm]];
```

makePdom

In[107]:=
```
makePdom::usage =
  "makePdom[s,β,nd,tmax,{y1,y2}] gives allele frequencies for a
    two-locus cline, with extrinsic selection gradient βx, initial
    steps at {y0,y1}, on a range {-nd,nd}. Positive FDS s acts
    symmetrically on the four morphs, assuming complete dominance";
```

In[108]:=
```
makePdom[s_, β_, nd_, tm_, {y1_, y2_}] := Map[
   alleleFreqs[#, {2, 2}][[All, 2]] &, makeClineDom[s, β, nd, tm, {y1, y2}], {2}];
```

makeClineGraph

posCline

makePosGraph

solnCline

speed

x0