Challenges to rockfish conservation/management

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General

lifehistory information incomplete
for many insemination/ fertilization/parturition locations unknown

Why?

few fall/winter surveys

physical marking/recovery methods poor
insufficient barotrauma, large numbers

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General

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Genetics

    **statistical and parameter analyses inadequate;
estimates difficult**
      e.g., dispersal rates, gene flow, intrinsic scale, N_e or N_e/N ratio, N_b

  Why?

    modest divergence levels
      large (effective) populations
      long generation times

Geneticists frequently use a value called F_{ST}

F_{ST} is the fixation coefficient

F_{ST} can be a misleading value because it as a relative value, a ratio:

$$F_{ST} = \frac{\sigma^2_{among}}{\sigma^2_{total}}$$

It is not an absolute measure of genetic divergence.

F_{ST} can be used to estimate exchange of individuals among populations

$$F_{ST} \approx \frac{1}{4 N_e m + 1} \qquad N_e m \approx \frac{1}{4 F_{ST}} - \frac{1}{4}$$

That is, at equilibrium between random genetic drift and gene flow

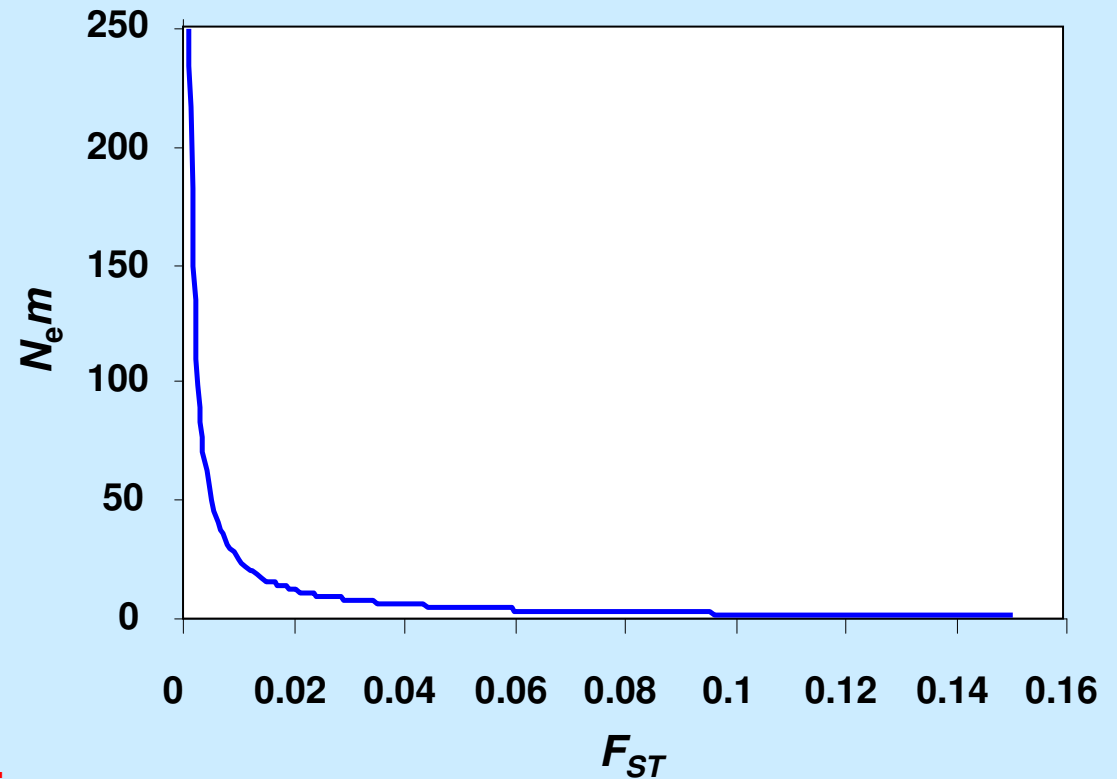**How fast does that equilibrium (for F_{ST}) occur?**

$$t_{1/2} \approx \frac{\ln(2)}{2m + 1/N_e} \qquad \textbf{(Crow and Aoki 1984)}$$

Both the $N_e m$ exchanged and $t_{1/2}$ depend on both effective size (N_e) and proportionate rate of migration (m).

Let's see what kinds of numbers pop out of simple calculations.

First a plot of $N_e m$ versus F_{ST}

There are many migrants at small F_{ST}s

Random drift ↑ divergence
Gene flow ↓ divergence
They are balanced at equilibrium

What do these values mean in a management time-frame?

Let's do some more back-of-the-envelope calculations:

Consider a low F_{ST}:

F_{ST} = 0.0025 corresponds to ~ 100 immigrants ($N_e m$)

N_e	m	$t_{1/2}$
100	1	0.34
1000	0.1	3.45
10000	0.01	34.48
100000	0.001	344.85
1000000	0.0001	3448.49

$t_{1/2}$ is in generations

how long is a rockfish generation?

But wait, there's more!

Often, divergence also reflects historic events

(read post glacial colonization)

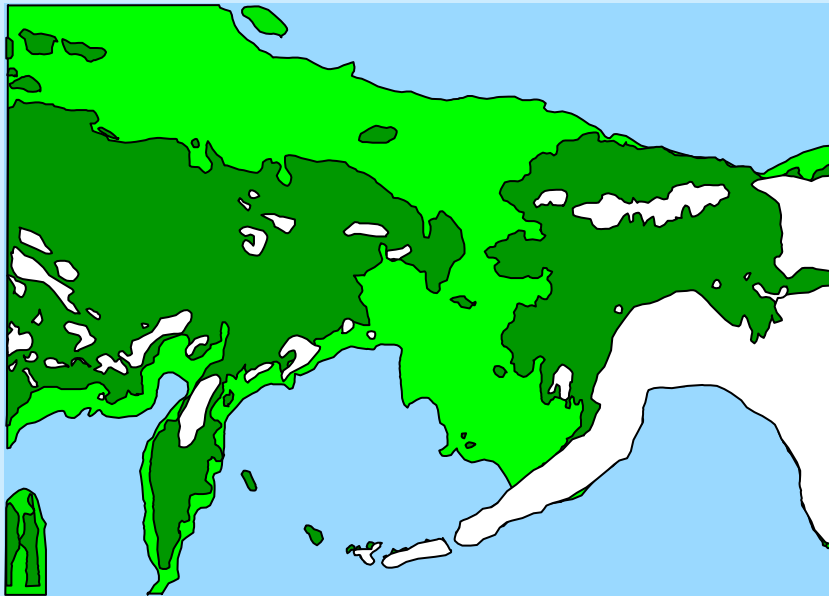**"With marine fishes?" you ask.   "Assuredly!" I reply.**

After colonization from a common source,

divergence might be expected

This means that F_{ST}'s may still be increasing,

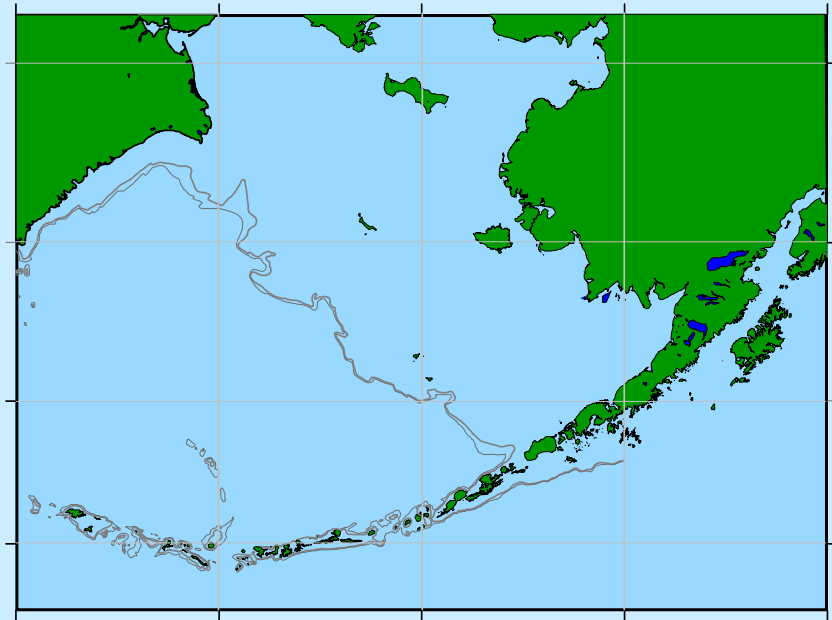**and estimates of $N_e m$'s are inflated.**

Did the glacial advances affect marine species?

Probably. Let's see.

Extent of glaciation and land masses at last glacial maximum

**Sea level was > 100 m lower -- at just about the shelf break**

Any species that depend on the continental shelf for habitat or food would have been depressed or displaced.

16,000 years ago was only 640 generations (25-year generations)

Use study of Northern rockfish (*Sebastes polyspinis*), and example

6 collections (Bering Sea/Aleutian Islands)
two pooled (A2a&b)-- proximity and similarity ($P_{homogeneity}$ = 0.42)
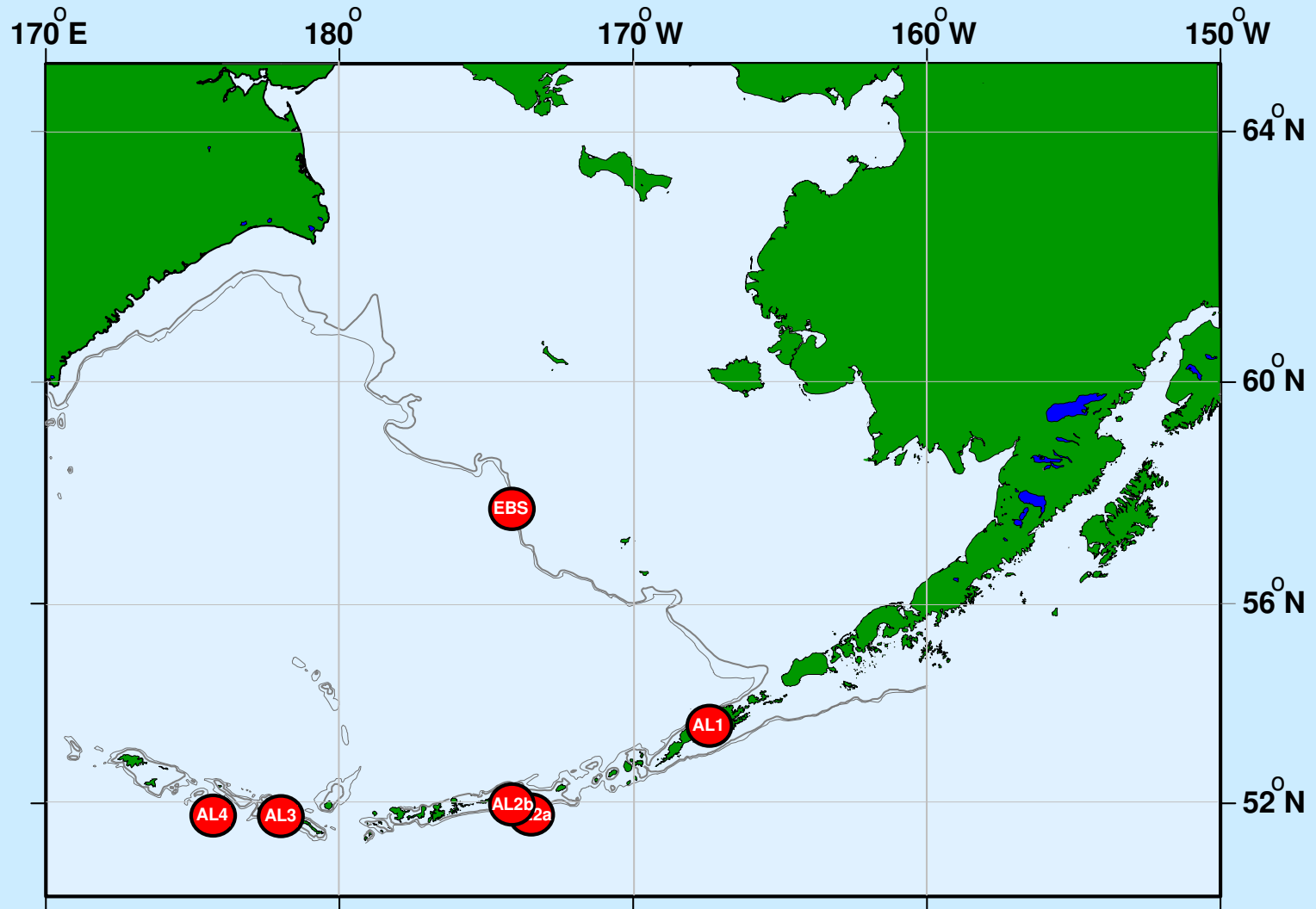
Preliminary analysis

due diligence

11 microsatellite loci -- no LDE or HWE departures (post multiple testing)

Number of alleles (N_a): 8 to 42; average 13.0

Average expected heterozygosity within collections (H_e): 0.79

Average effective # alleles/locus within collections (N_{eff}): 5.9

Homogeneity tests (a variety of approaches):

$P_{homogeneity}$ < 0.001 for aggregate test (all loci)

3 of 11 loci individually significant

but

Fixation coefficient:

not different from zero (F_{ST} = 0.018; P > 0.05)

So what can we do?

Assignment tests:

**Proportion of individuals assigned to their populations of origin
(fish removed from populations for assignment):**

all populations exceeded 40% (20% expected at random).

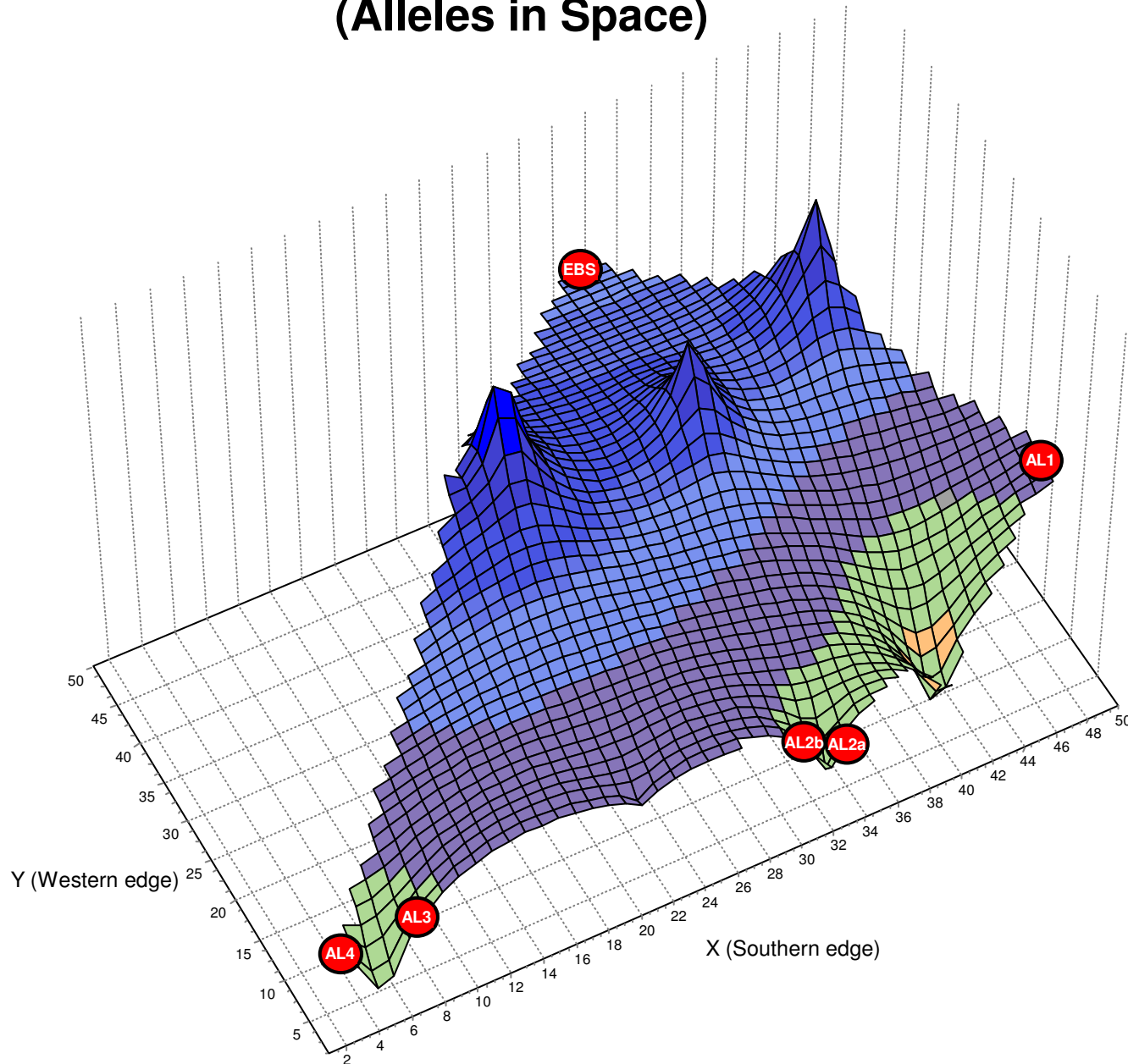| Population	EBS	AI1	AI2	AI3	AI4
EBS	**46.5**	14.9	12.1	13.9	12.7
AI1	15.4	**42.3**	16.7	14.0	11.5
AI2	12.8	15.7	**41.4**	16.2	13.9
AI3	14.1	13.9	14.6	**43.1**	14.3
AI4	12.9	13.1	14.3	14.1	**45.6**

5% allele frequency threshhold

(Geneclass)

Partition heterogeneity by contiguous non significant groups:
Two homogeneous groups of adjacent populations.
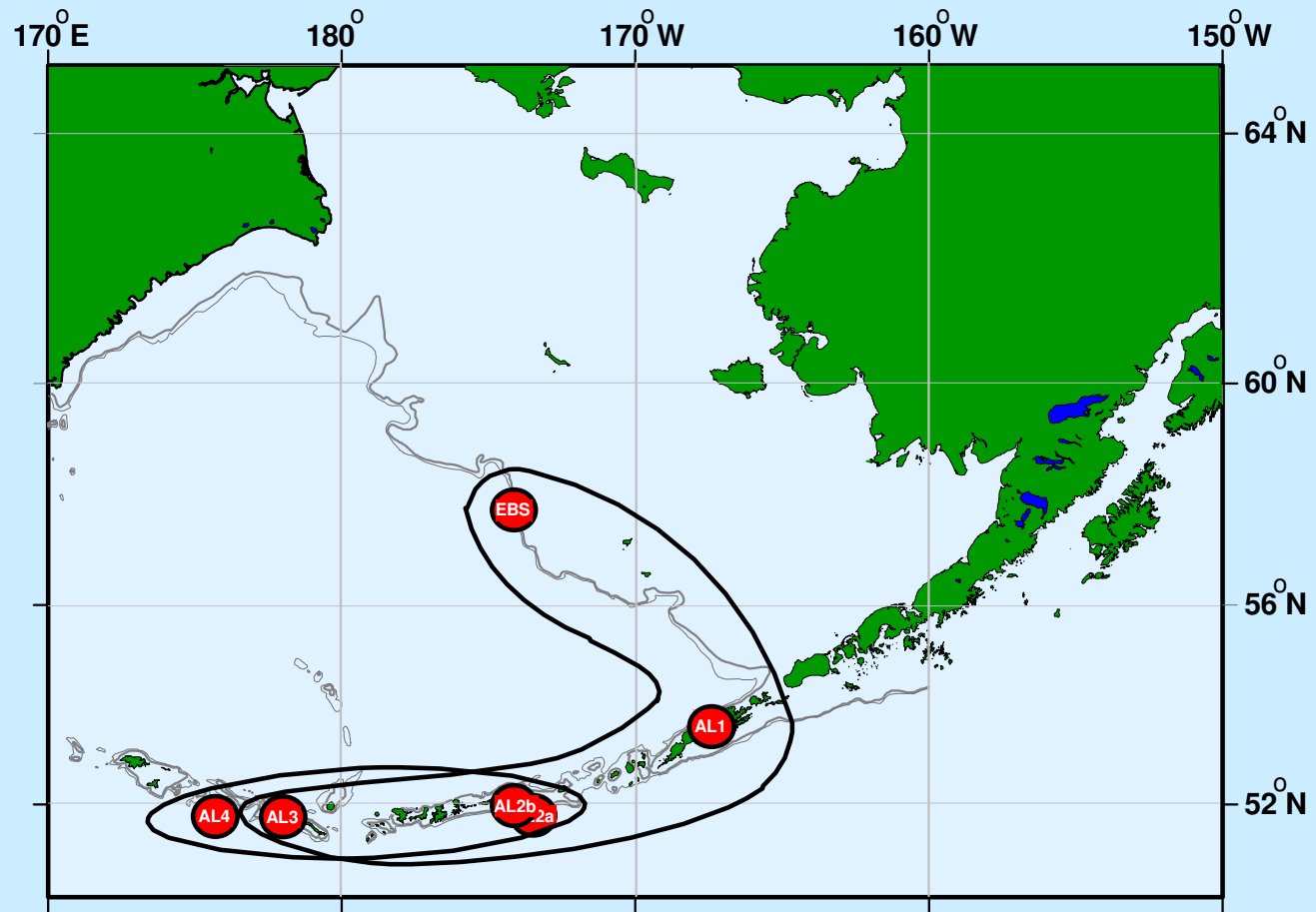
Graphic depiction of gene flow barriers

(Alleles in Space)

**Pairwise estimates of F_{ST} and tests of homogeneity:**

Population	EBS	AL1	AL2	AL3	AL4
EBS		0.0027	0.0032	0.0038	0.0028
AL1	0.1049		0.0007	0.0015	0.0014
AL2	0.0172	0.8106		0.0014	0.0007
AL3	0.0075**	0.0221*	0.1059		0.0007
AL4	0.0003***	0.0113*	0.0910	0.0372*	

fixation index (F_{ST} above diagonal)

$P_{homogeneity}$ between populations (below diagonal)

divergence increased with distance along shelf break.

IBD plot

$\hat{a} = -2.09 * 10^{-5}$

$\hat{b} = 1.9 * 10^{-6}$

$P = 0.017$

$F_{ST}/(1 - F_{ST})$

distance along shelf break (km)
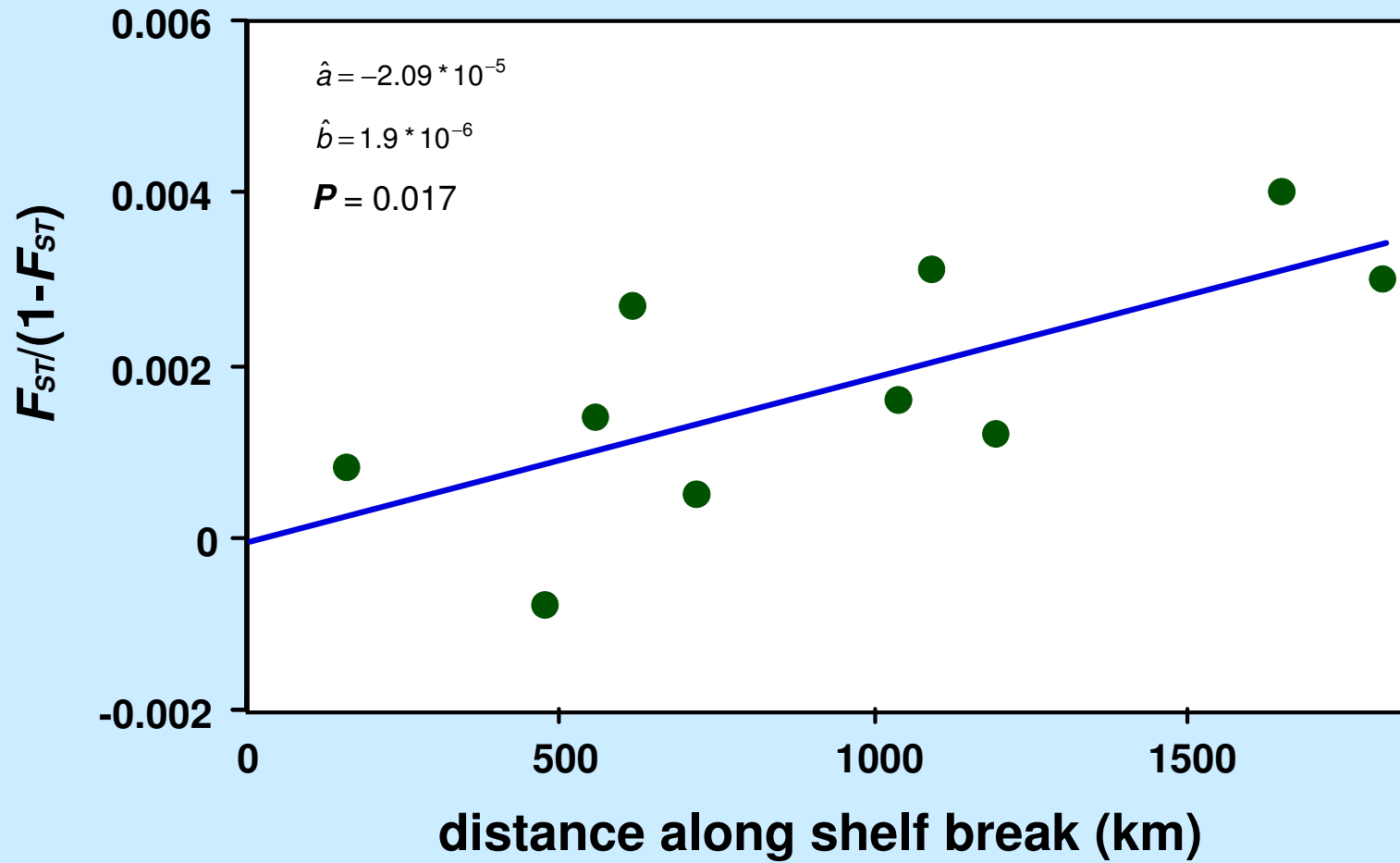
Relationship between $F_{ST}/(1 - F_{ST})$ and distance (d)
(Rousset 1997; for a linearly distributed species):

$$\frac{F_{ST}}{1 - F_{ST}} \approx \frac{A_1}{4 D_e \sigma} + \frac{d}{4 D_e \sigma^2}$$

slope: $1/(4D_e\sigma^2)$

intercept: $A_1/(D_e\sigma)$

D_e **is the effective density – effective number of individuals per unit distance**
or $D*N_e/N$ –- D is density

σ^2 **is variance of average distance of parents from offspring (axial displacement)**
A strip $4\sigma_{axial}^2$ would account for ~95% of parents.

A_1 **is a constant that depends on the distribution of dispersal;**
A_1 **= -0.8238 for a normal distribution**

The geographic scale of the analysis is critical

How can we use this information?

1. We can estimate the density (D);

Northern rockfish ~ 13 years at 50% maturity;

In 2006, ~ 291.5 million fish were 13 years and older in the this area;

⟶ "linear" density of about 136,870 fish/km.

the "line" is about 30 km wide, so this about 4,500/ km^2 in this region.

2. From D we can estimate a set of effective densities (D_e) from a plausible set of N_e/N.

Ne/N	$D_e = D* N_e/N$
0.1	13,687
0.05	6,844
0.01	1,369
0.005	684
0.001	137

3. We can use D_e estimates and the slope to estimate 4σ;

4. We can estimate neighborhood size (N_b) from those results.

N_e/N	$D_e = D^*N_e/N$	$4\sigma = 2^*(1/(4^*\hat{b}^*D_e)1/2$	$D_e^*4\sigma = N_b$
0.1	13,687	12.4	169,751
0.05	6,844	17.5	120,032
0.01	1,369	39.2	53,680
0.005	684	55.5	37,957
0.001	137	124.0	16,975

The estimate of neighborhood size from $\hat{a}$ was 39,416;

-- close to the slope-based estimate (37,957) for an N_e/N ratio of 0.005.

but be very cautious in using the intercept!

Estimate effective population sizes from each of the "populations"

Population	Lower CI	N_e	Upper CI
EBS	450	10,160	∞
AL1	296	896	∞
AL2	468	∞	∞
AL3	353	3,600	∞
AL4	369	1,928	∞

Estimates from the program LDNe;

(linkage disequilibrium for alleles with frequencies of at least 0.05).

Originally, IBD analyses were done from "populations".

(as we showed for northern rockfish)

More recently, Rousset (2000) extend the analysis to individuals.

Genetic divergence between pairs of individuals versus
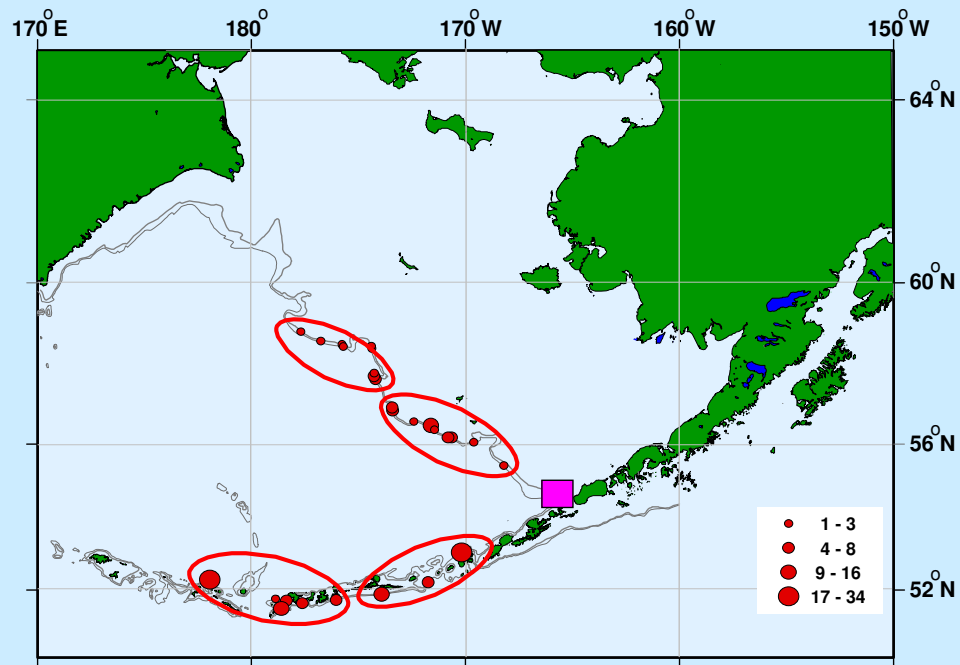**the distance separating them provides considerable power.**

Evaluating autocorrelation between the genotypes of individuals
in different distance classes is another approach

There is now an advantage to more continuous sampling
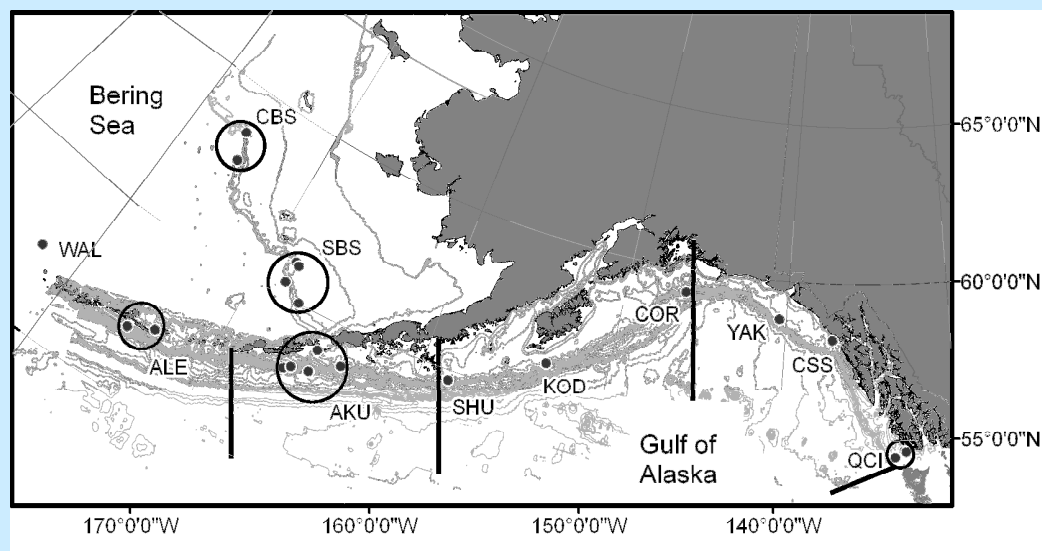
Collections of northern rockfish were taken from 6 sites
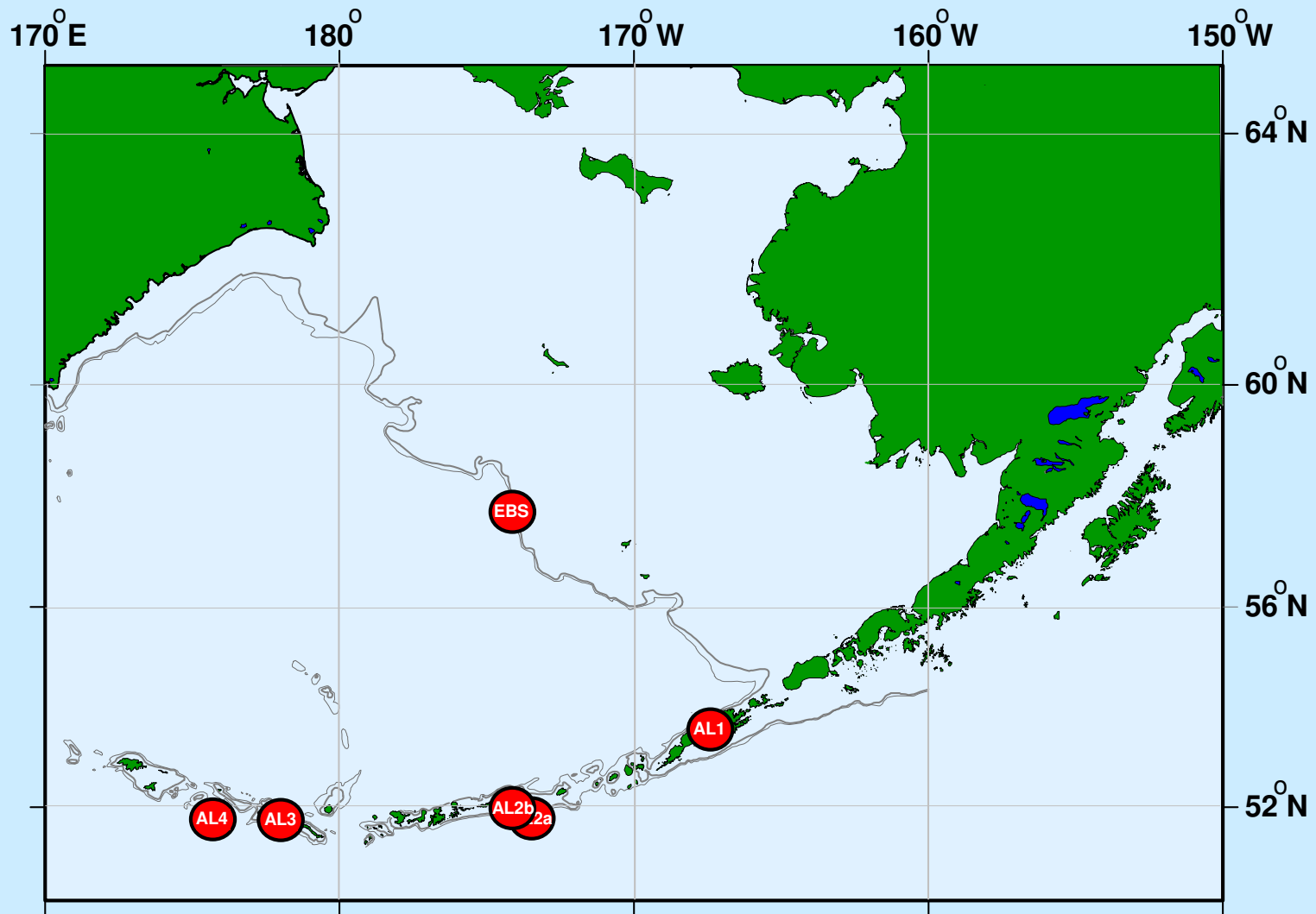
Rougheye rockfish and POP collections were more dispersed

Isolation-by-distance

level of test	species		
	northern	rougheye	POP
n	500	173	499
maximum distance (km)	1820	2076	2056
	P of significant relationship		
groups	0.014	0.250	0.316
individuals (20,000 iterations)	$< 10^{-4}$	0.005	$< 10^{-4}$

(Genepop)

Autocorrelation

Number of distance classes	species		
	northern	rougheye	POP
	P of significant relationship		
4 classes	0.0001	0.841	0.0043
5 classes	0.0002		
6 classes	NA	0.078	0.0063
10 classes	NA	0.033	0.0065
15 classes	NA	0.009	NA

(Alleles in Space)

What can we do?

Generally?

> Obviously, a wide variety of lifehistory information.

Genetics?

> Individual-based genetics analyses and landscape
>
> > genetics methods should improve our
> >
> > understanding of the relationship between
> >
> > population structure and physical factors.
>
> Those analyses will require intensive sampling
>
> > and continued development of analytical methods
> >
> > for data analysis.

Ball's in your court