

RITA CASTILHO

WHY BIOGEOGRAPHY MATTERS?



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MARINE BIOGEOGRAPHY AND EVOLUTION

SARDINE'S EVOLUTION



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SARDINE'S EVOLUTION



Case study: sardine evolution A primer

outline

- GEOGRAPHIC DISTRIBUTION
- MOLECULAR DATA
- PHYLOGENETIC ESTIMATION
- HISTORICAL DEMOGRAPHY
- PALEOGEOGRAPHIC EVENTS



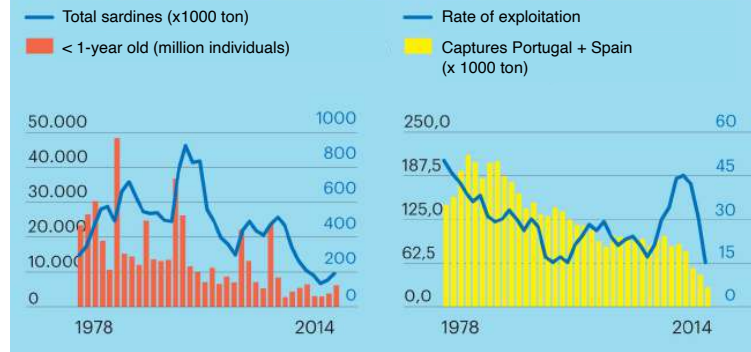
Distribution

Sardina pilchardus is the only sardine species in the Northeastern Atlantic and Mediterranean.



Stock status

Reproduction is declining (left), and captures represent an extremely high effort on the stock (right).



SOURCES
<http://www.fishbase.org/species/sard>
<http://www.earth-touch.com>

SARDINE
SARDINOPS SAGAX

CLEARLY VISIBLE FROM SPOTTER PLANES

MAIN SARDINE SHOAL
 DEPTH ≈ 30M
 MAIN SHOAL CAN BE 7KM LONG OR 25 TIMES THE LENGTH OF THE TITANIC
 WIDTH ≈ 15KM

SARDINES WERE NAMED AFTER THE MEDITERRANEAN ISLAND OF SARDINIA

TIGHTLY PACKED GROUP OF SARDINES = BAITBALL
 DEPTH ≈ 10M
 DIAMETER ≈ 15M
 DOLPHINS CREATE BAITBALLS BY SPLITTING THE MAIN SHOAL & HERDING A SMALLER GROUP OF SARDINES TO THE SURFACE

IDEAL WATER TEMP FOR SARDINES 14-20 °C

SARDINE AVERAGE LENGTH = FOUR AA BATTERIES

SARDINE FEVER
 THE FRANTIC BEHAVIOUR OF PEOPLE INVOLVED IN THE SARDINE RUN

SARDINE RUN BIOMASS COMPARABLE TO SERENGETI MIGRATION

"PACKED LIKE SARDINES IN A CAN" POPULAR IDIOM THAT IMPLIES A TIGHT SQUEEZE



Sardine life-cycle and strategy

CHARACTERISTICS OF K-SELECTED AND r-SELECTED SPECIES

K-selected equilibrium species ← → r-selected opportunist species

population size

time

population size:
 • limited by carrying capacity (K)
 • density dependent
 • relatively stable

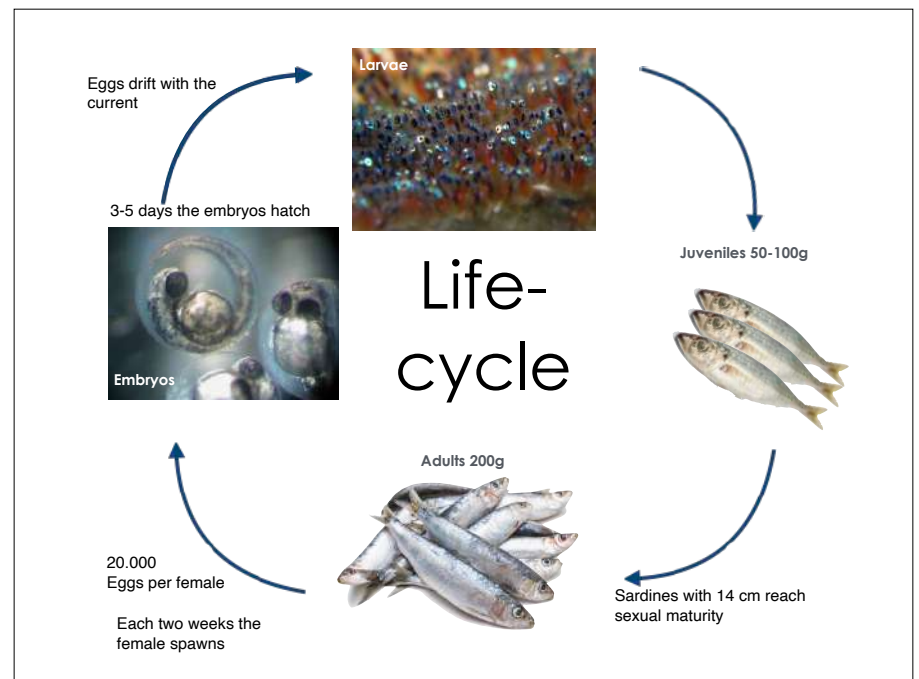
organisms:
 • larger, long lived
 • produce fewer offspring
 • provide greater care for offspring

population size

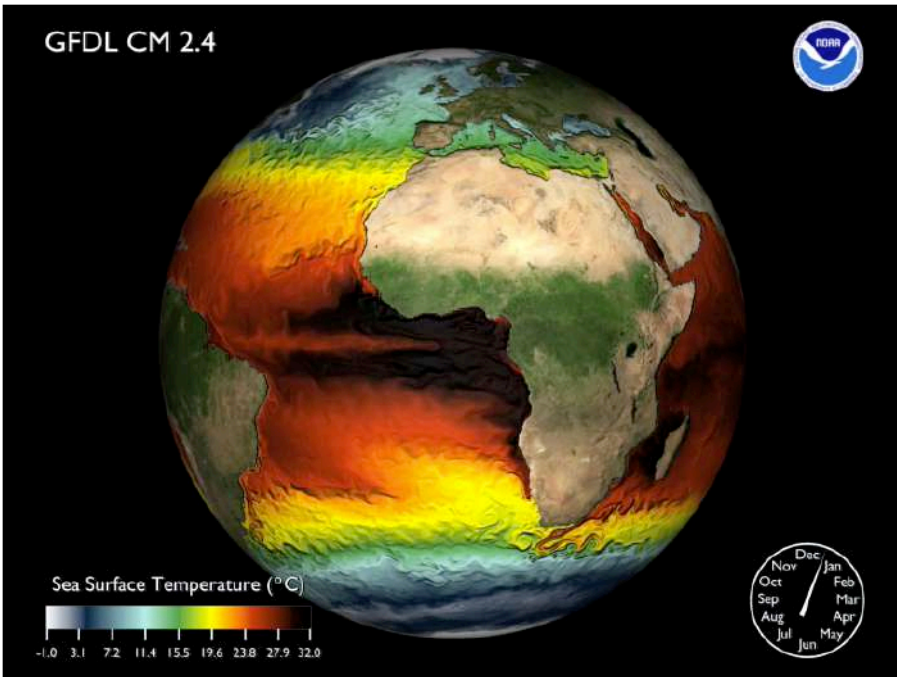
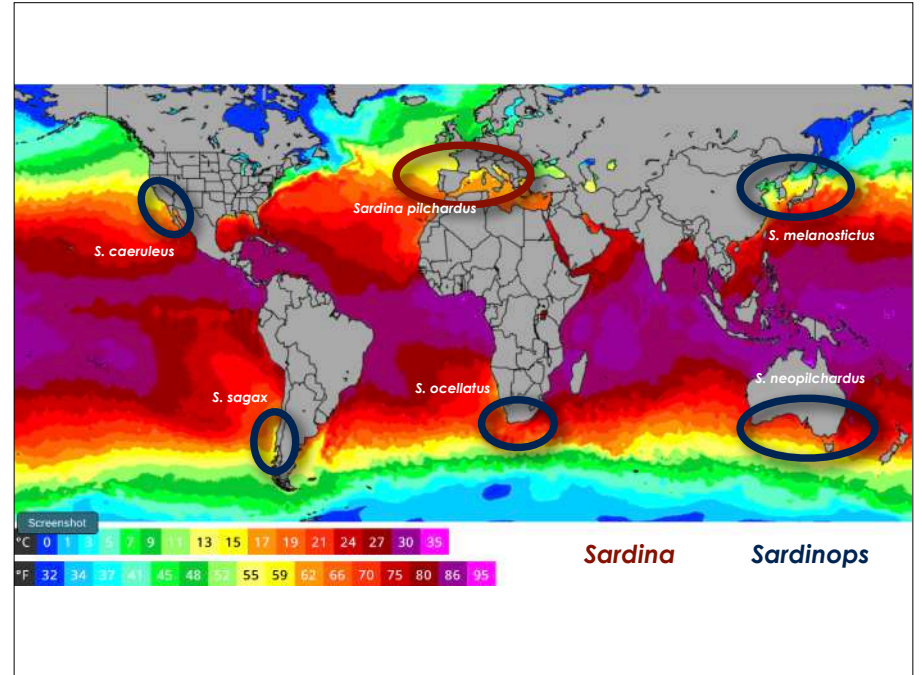
time

population size:
 • limited by reproductive rate (r)
 • density independent
 • relatively unstable

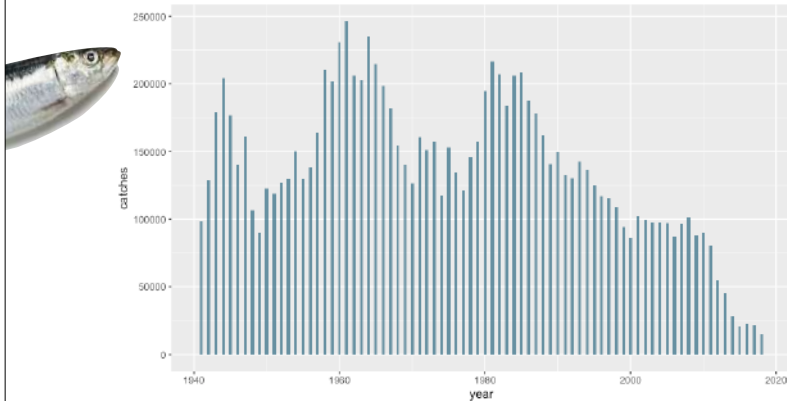
organisms:
 • smaller, short-lived
 • produce many offspring
 • provide no care for offspring



Geographic distribution of sardines



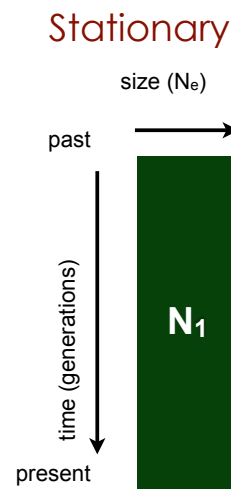
ICES considers that the Iberian sardine stock is in a state of collapse which has resulted in low recruitment for the last decade. This is likely caused by a combination of fisheries and environmental changes.



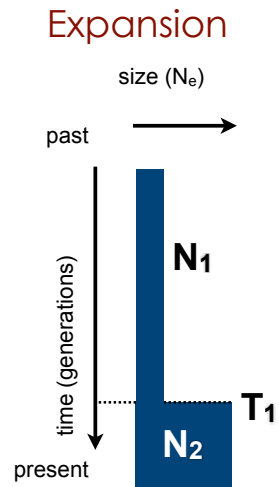
Effects of demographic fluctuations on the genetic make-up of organisms

What happens to the population size over time?

Historical Demography

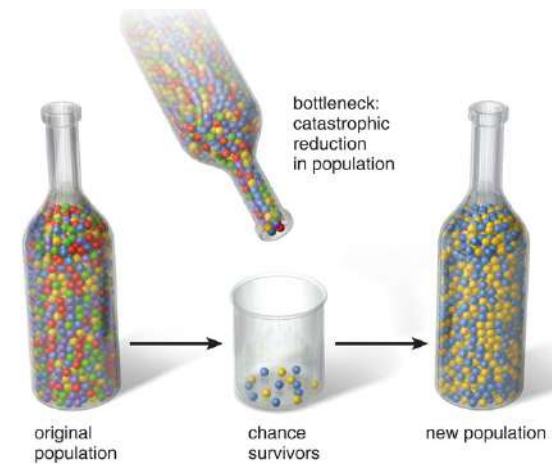
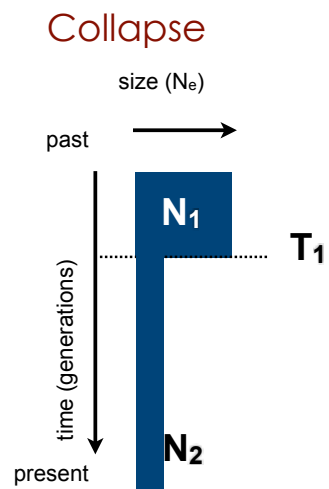


Historical Demography



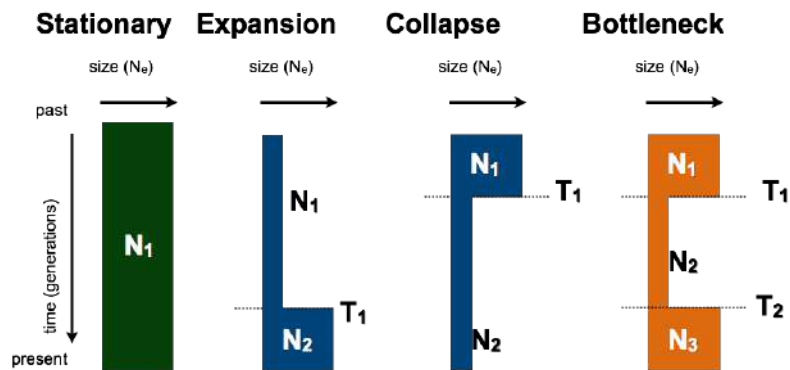
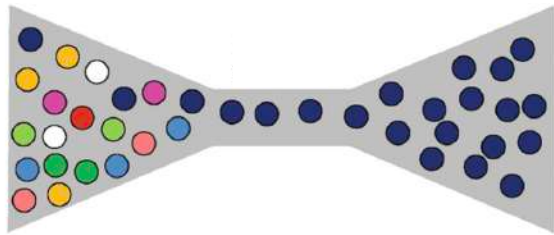
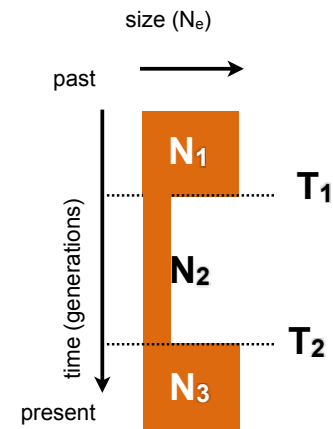
When populations crash,
what happens?

Historical Demography



Historical Demography

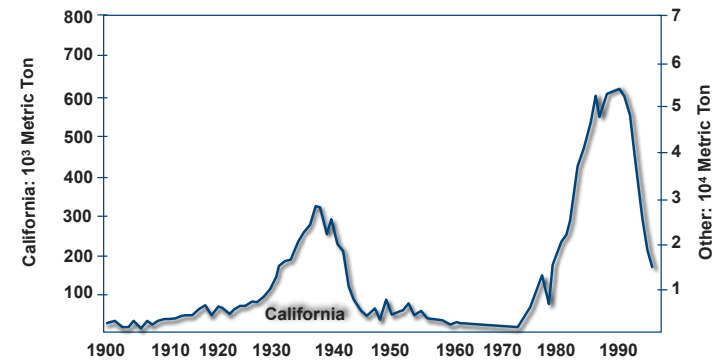
Bottleneck



But can we infer the *past demography* of a species without having a census ?

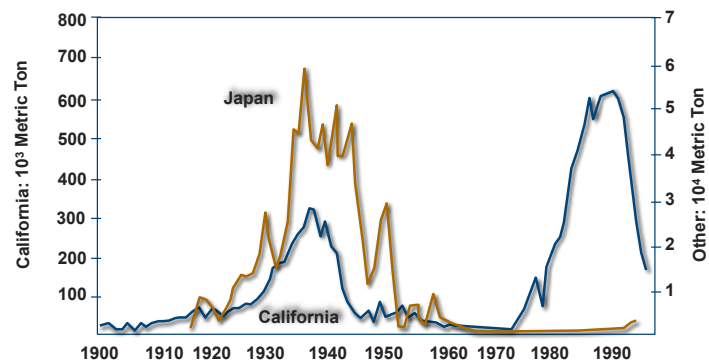
Method I

Apparent oceanwide synchrony in **Pacific** Sardines



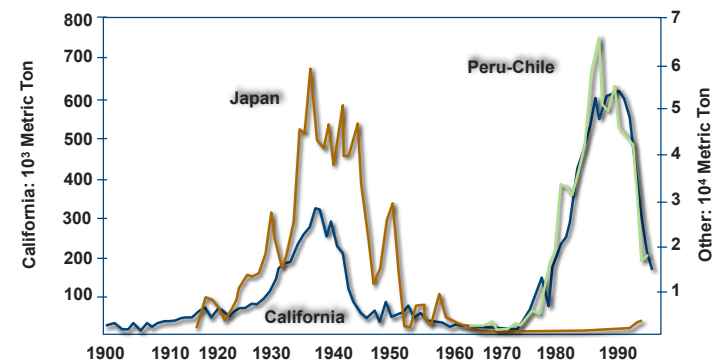
Sources: U.S. GLOBEC, FAO 1998

Apparent oceanwide synchrony in **Pacific** Sardines

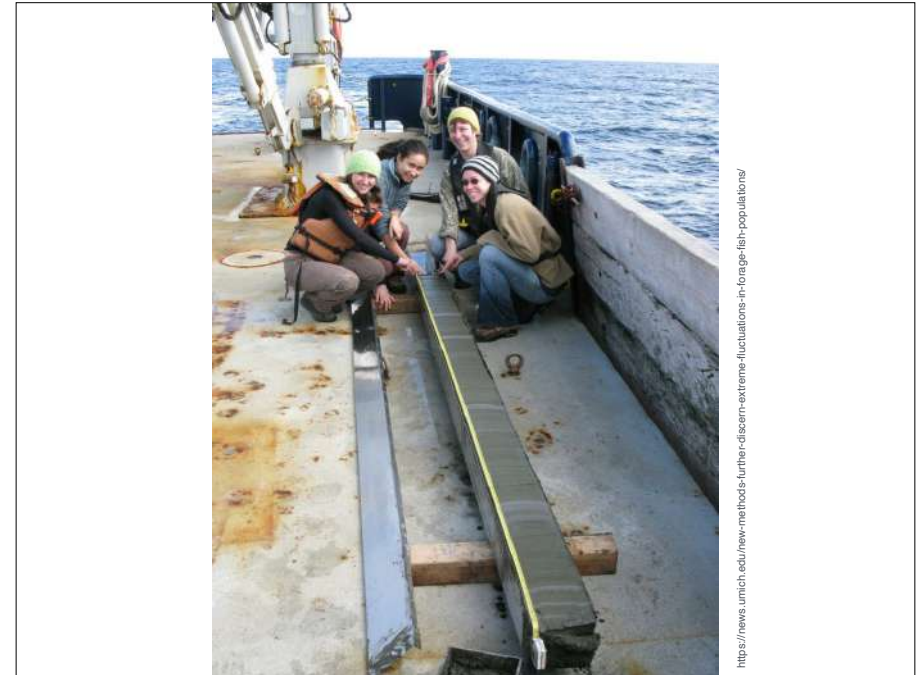
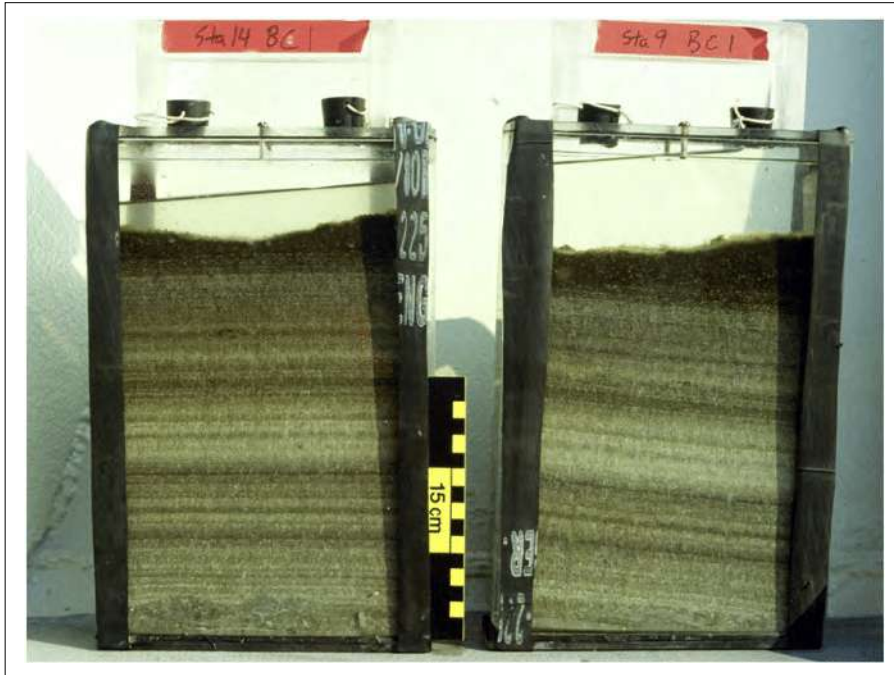


Sources: U.S. GLOBEC, FAO 1998

Apparent oceanwide synchrony in **Pacific** Sardines

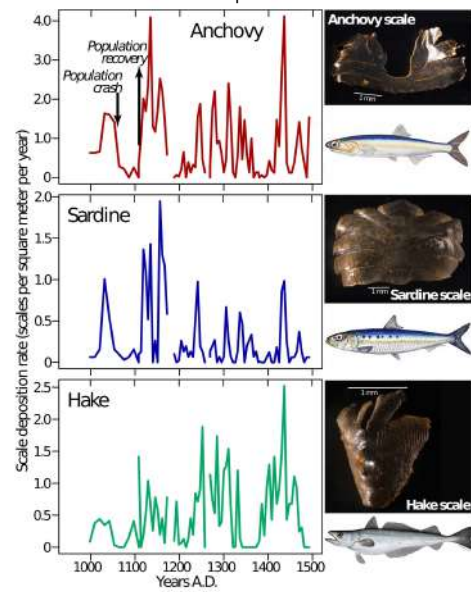


Sources: U.S. GLOBEC, FAO 1998



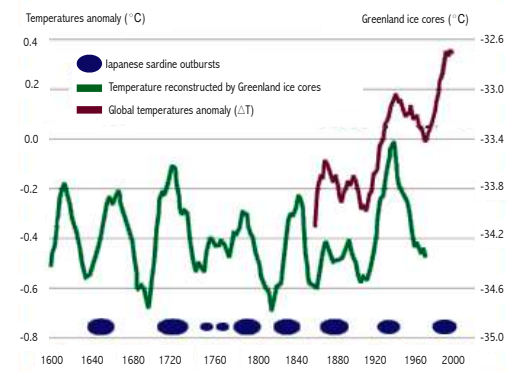
<https://news.umich.edu/new-methods-further-detect-extreme-fluctuations-in-forage-fish-populations/>

Collapse and recovery of forage fish populations prior to commercial exploitation



McClatchie et al. 2017., Geophysical Research Letters

Cyclic temperature fluctuations and Japanese sardine outbursts



Sardine and anchovy populations reconstructed from the data on fish scales in *varved* sediment cores.

Method II

Population size



genetic consequences

haplotype
networks

Haplotypes

Identical sequences from haploid genomes (e.g. mtDNA) are an haplotype

Haplotypes

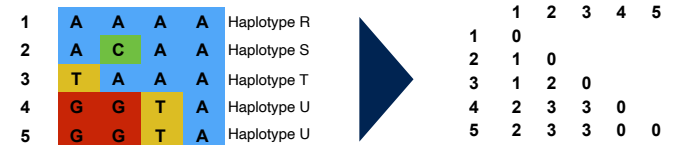
Identical sequences from haploid genomes (e.g. mtDNA) are an haplotype

Several individuals with identical sequences are said to share the same haplotype

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Several individuals with identical sequences are said to share the same haplotype



Haplotype networks

Haplotype network construction is a widely used approach for analysing and visualizing the relationships among DNA sequences within a population or species.

Haplotype networks

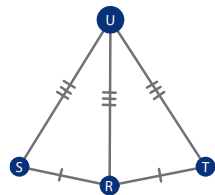
Haplotype network construction is a widely used approach for analysing and visualizing the relationships among DNA sequences within a population or species.

	R	S	T	U
R	0			
S	1	0		
T	1	2	0	
U	2	3	3	0

Haplotype networks

Haplotype network construction is a widely used approach for analysing and visualizing the relationships among DNA sequences within a population or species.

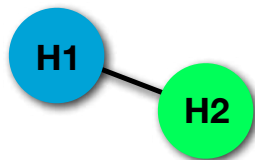
	R	S	T	U
R	0			
S	1	0		
T	1	2	0	
U	2	3	3	0



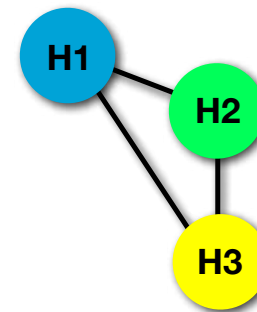
H1 A A **T** G T C G T A



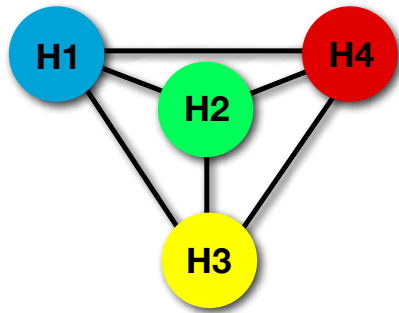
H1 A A **T** G T C G T A
H2 A A **C** G T C G T A



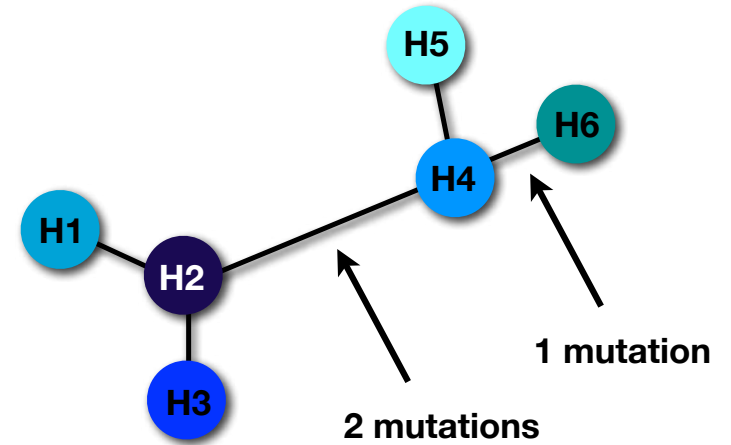
H1 A A **T** G T C G T A
H2 A A **C** G T C G T A
H3 A A **G** G T C G T A



H1 A A T G T C G T A
 H2 A A C G T C G T A
 H3 A A G G T C G T A
 H4 A A A G T C G T A

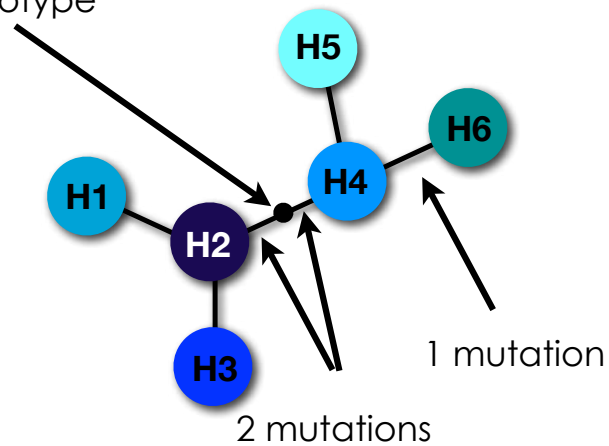


Haplotype networks

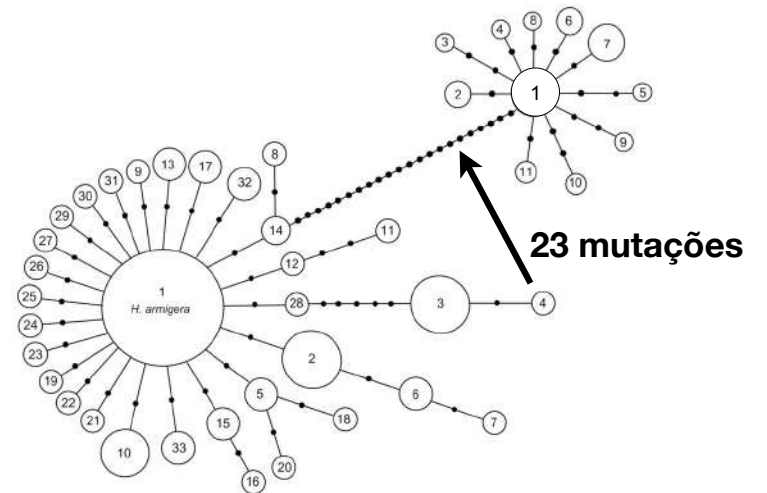


Haplotype networks

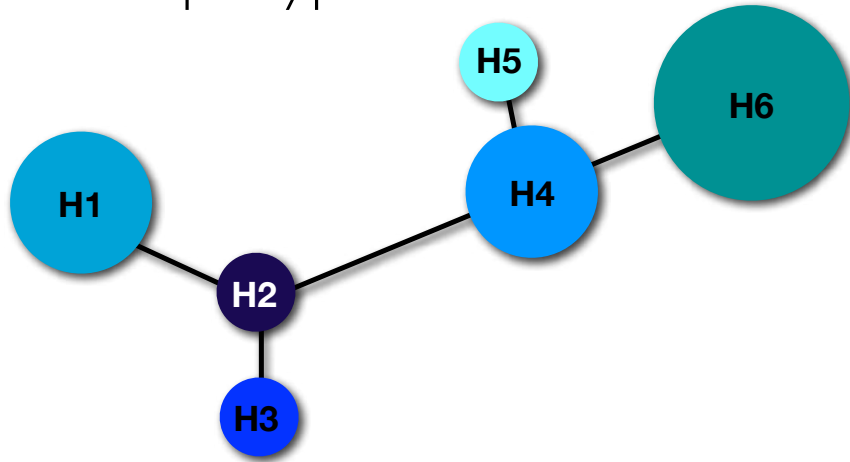
"unkown haplotype"



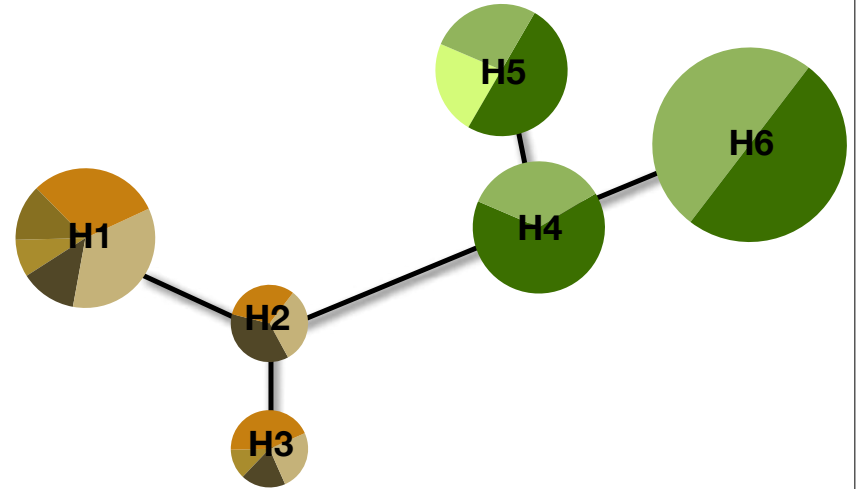
Haplotype networks



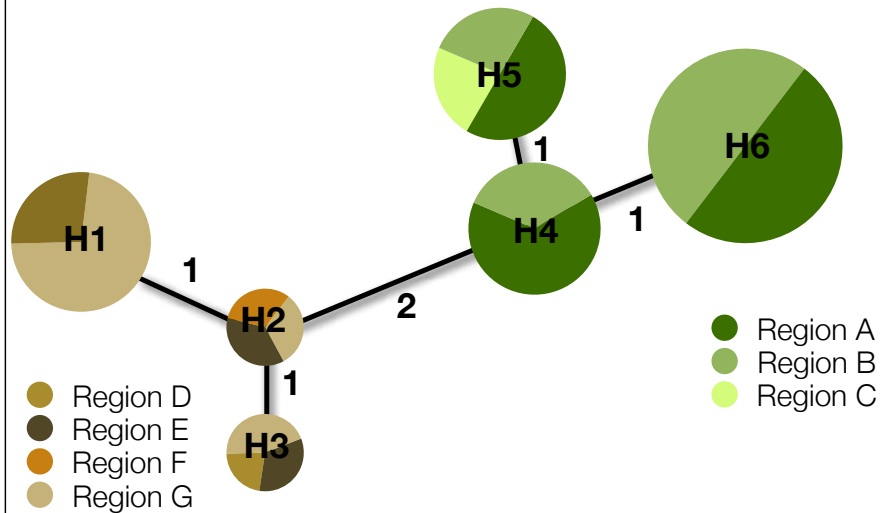
Haplotype networks



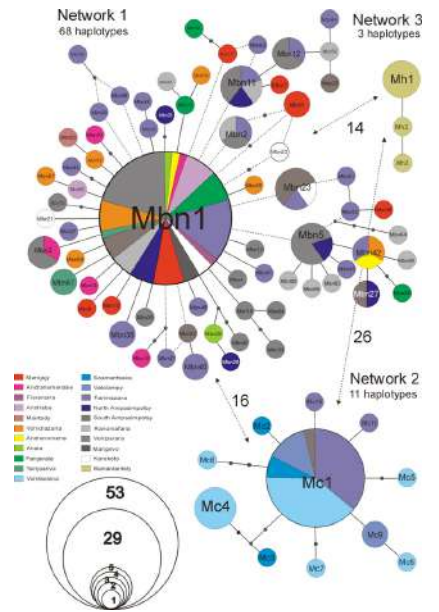
Haplotype networks



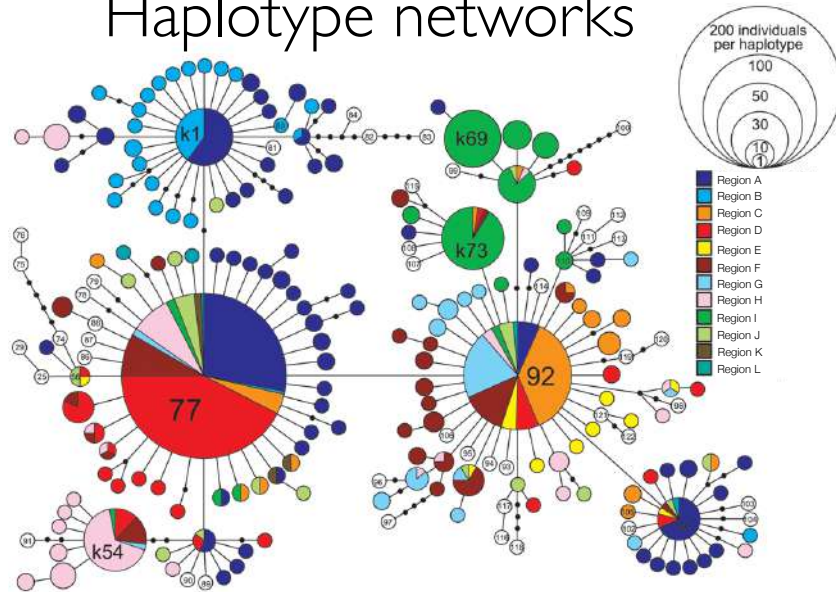
Haplotype networks



Haplotype networks



Haplotype networks



Population size

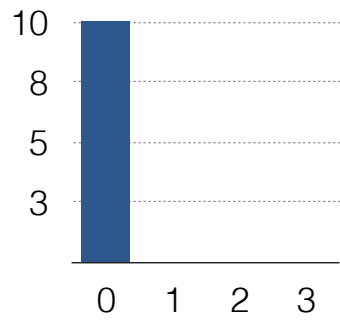


genetic consequences

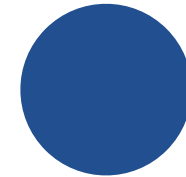
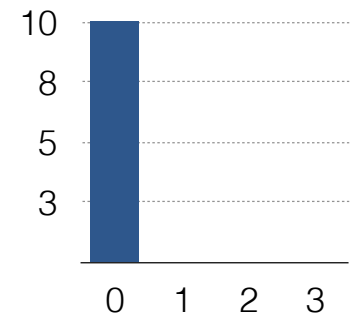
Mismatch analysis
Demography and
Haplotype networks

Number of differences	Counts
0	10
1	0
2	0
3	0

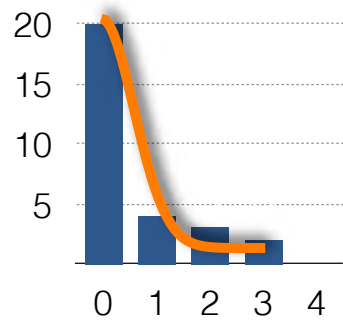
Number of differences	Counts
0	10
1	0
2	0
3	0



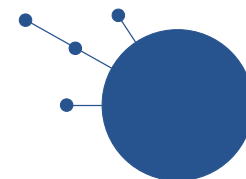
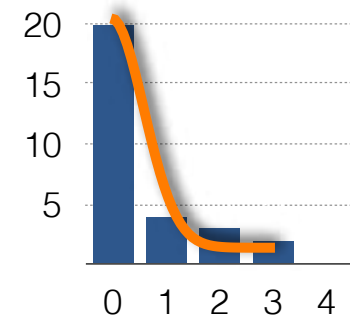
Number of differences	Counts
0	10
1	0
2	0
3	0

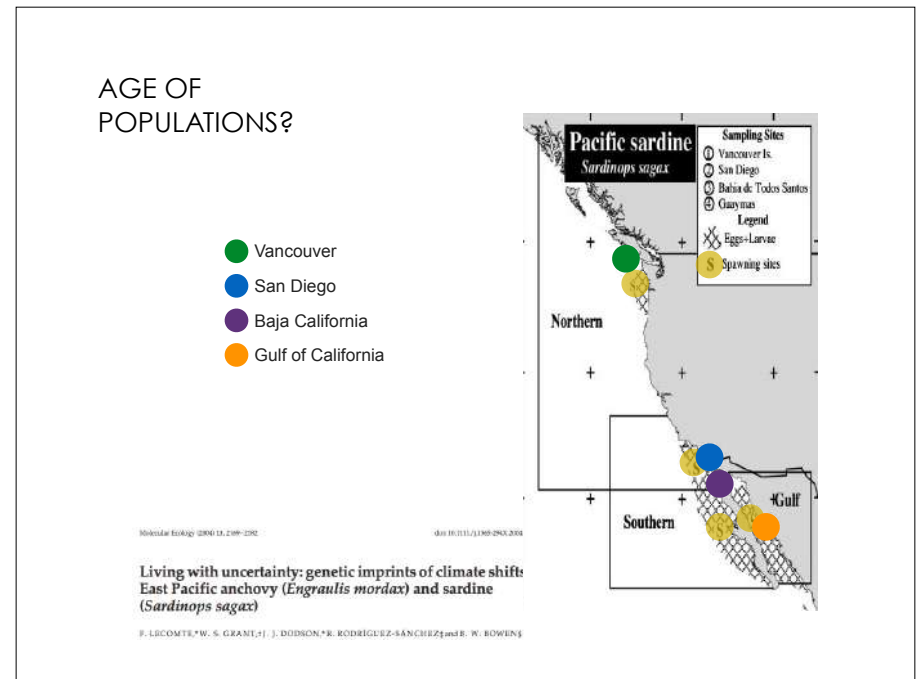
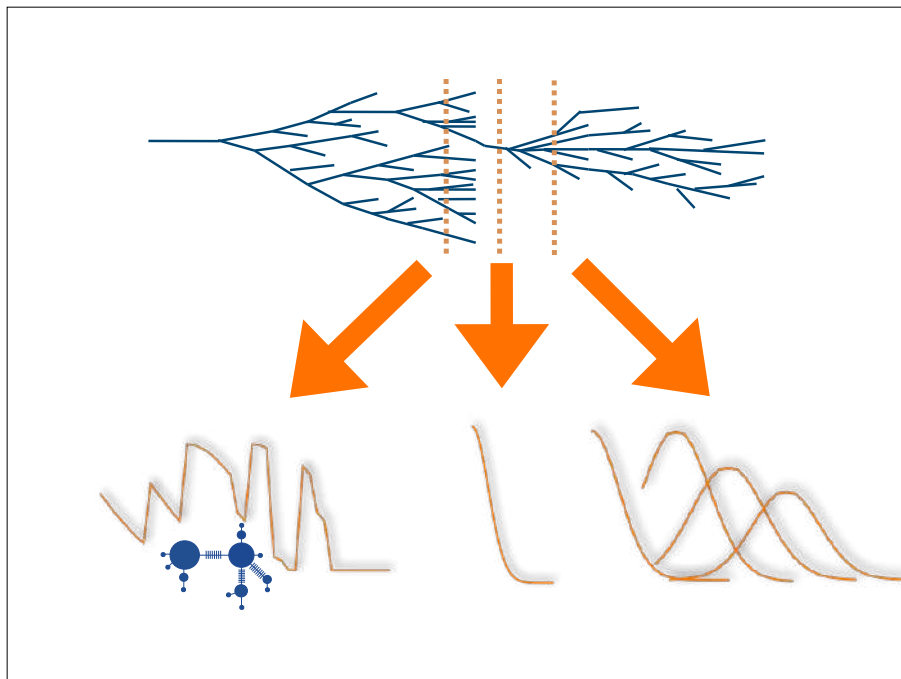
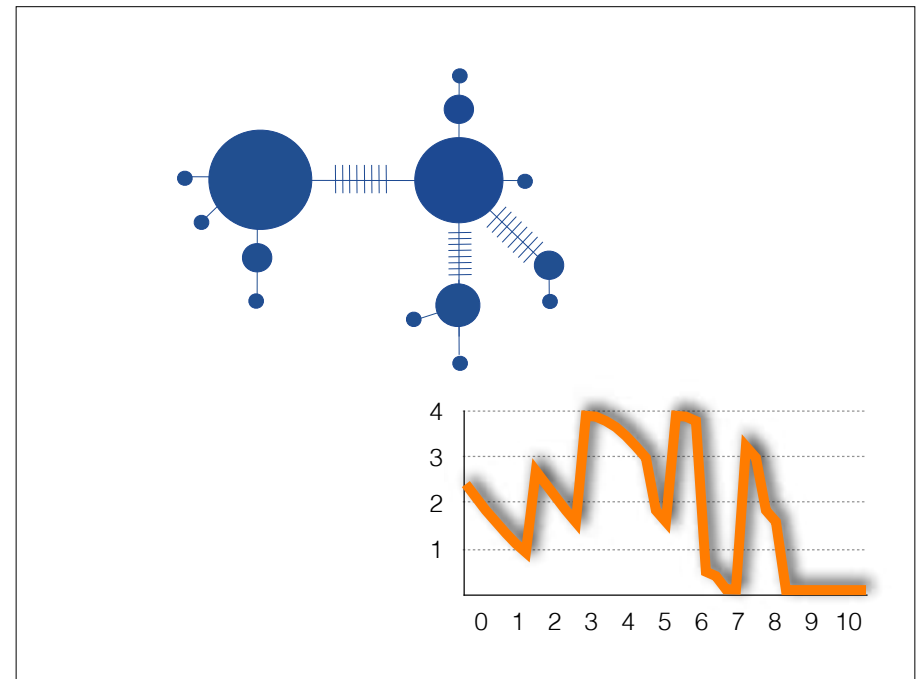
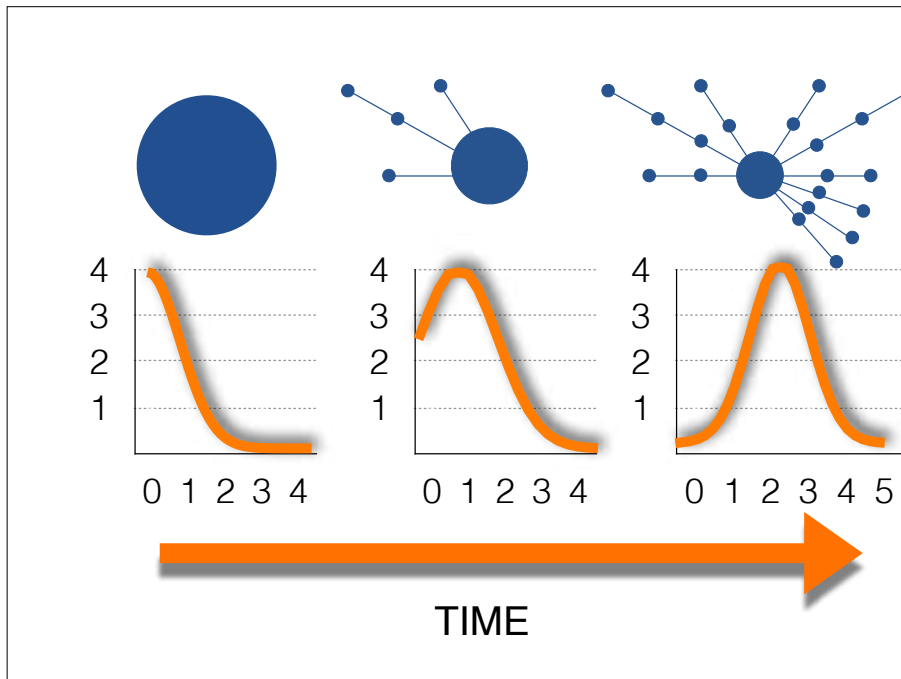


Number of differences	Counts
0	20
1	4
2	3
3	2
4	0

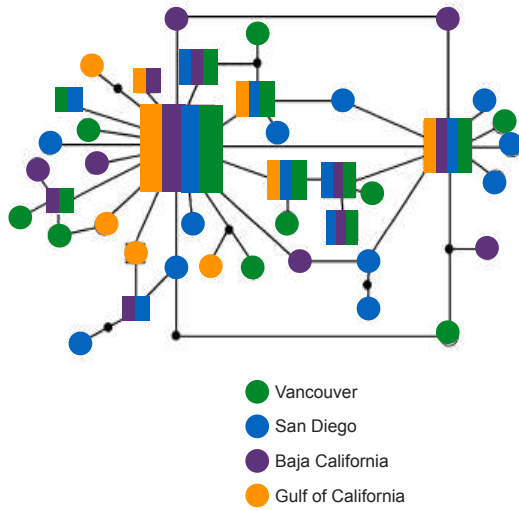
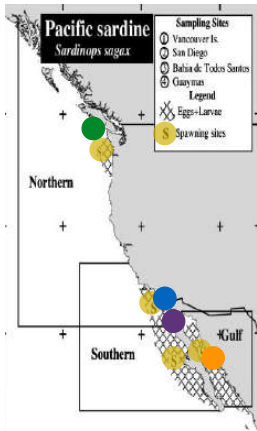


Number of differences	Counts
0	20
1	4
2	3
3	2
4	0



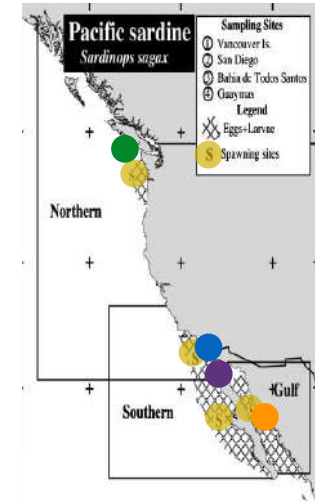
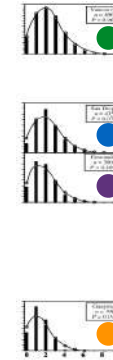


AGE OF POPULATIONS?



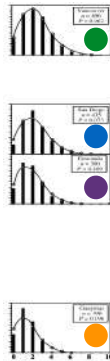
Lecomte et al. (2004)

AGE OF POPULATIONS?

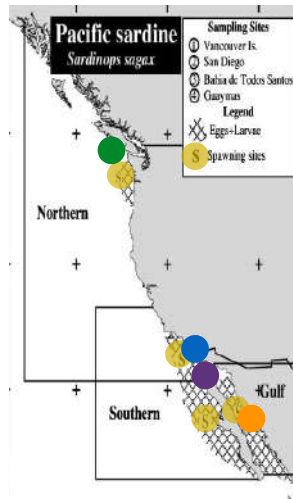


Lecomte et al. (2004)

AGE OF POPULATIONS?

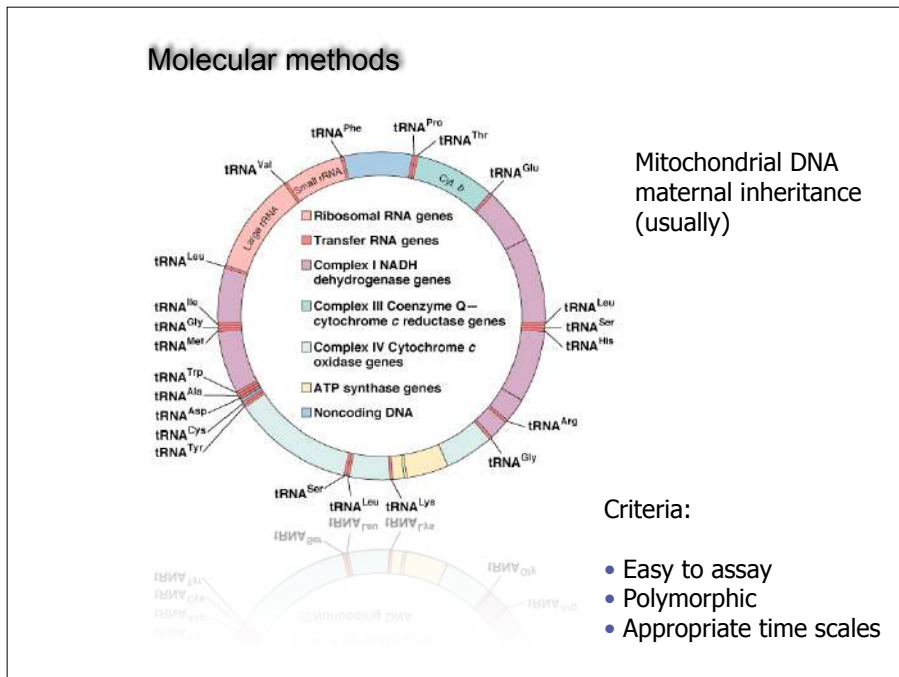
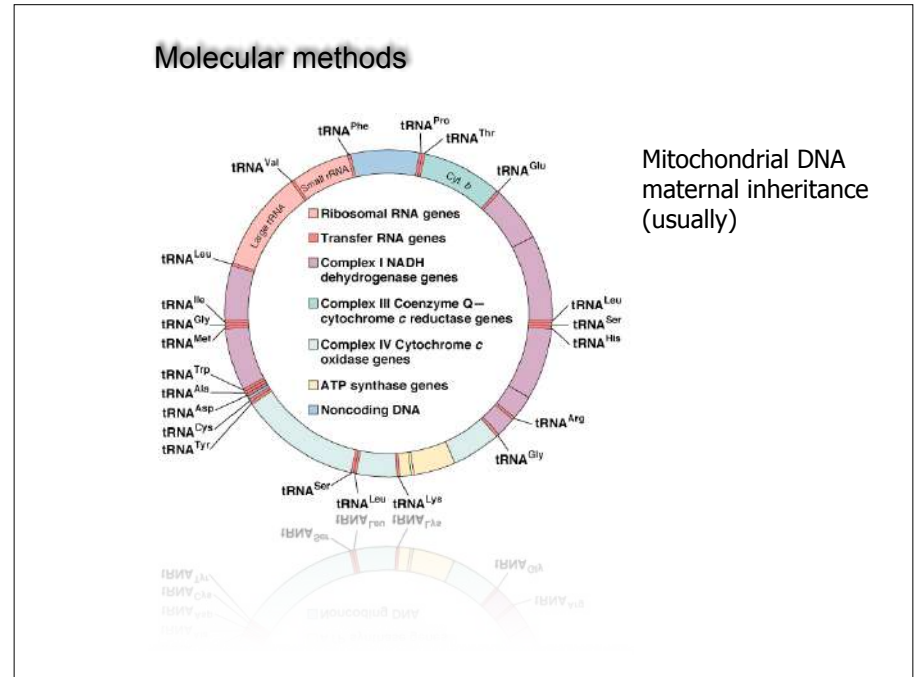
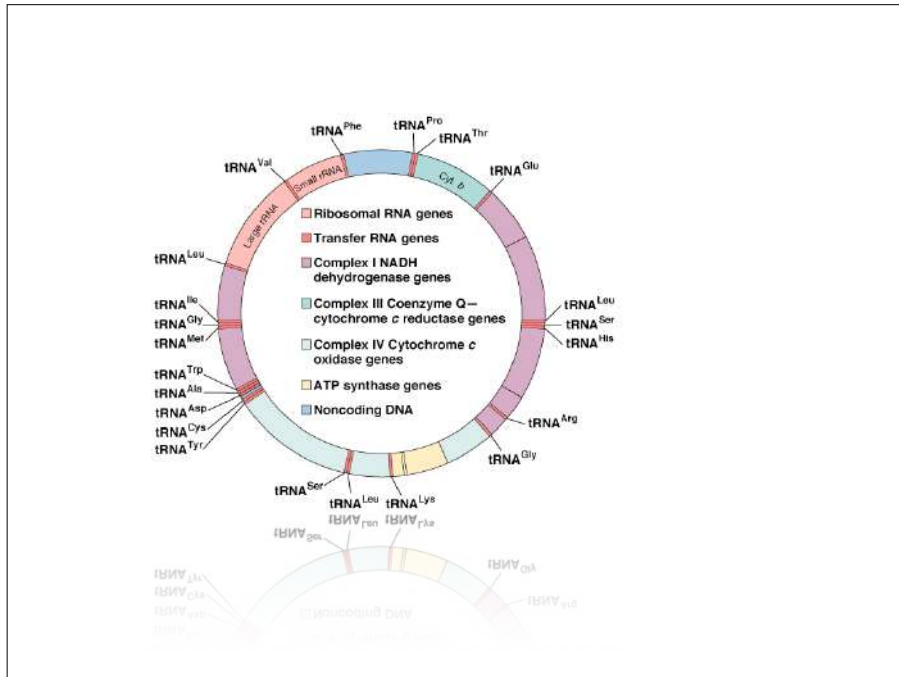


Pacific	Age
Vancouver ●	276 000
San Diego ●	241 000
Baja ●	218 000
Gulf ●	176 000
Global	229 000



Lecomte et al. (2004)

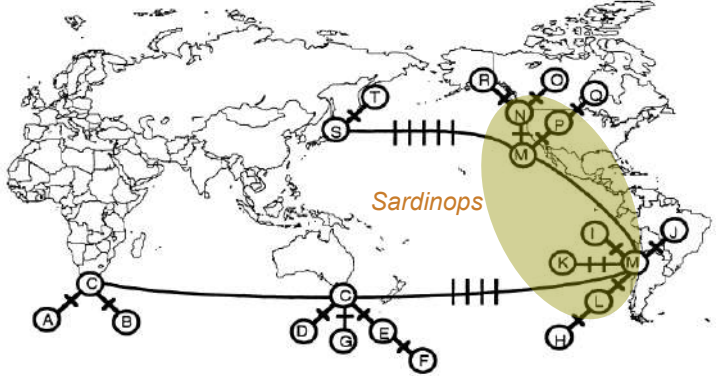
Genetics of sardines



mtDNA Control Region 500 bp - transversions

Haplotype	Position													Location											
	1	11	111	1111	222	2222	2222	2233	333	334	444	4444	4444	SA	AU	CH	CA	JA							
CON	T	T	G	A	G	T	G	T	T	A	T	G	A	C	A	G	C	T	A	A					
A	G	-	-	-	G	-	-	-	A	-	-	-	-	-	-	T	-	-	-	-	1				
B	G	-	-	-	G	-	-	-	A	-	-	-	-	-	-	T	-	-	-	-	1				
C	G	-	-	-	G	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	13	10			
D	G	-	-	-	G	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-		1			
E	G	-	C	-	G	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-		1			
F	G	-	T	-	G	-	-	-	A	-	-	-	-	-	-	G	-	-	-	-		1			
G	G	-	T	-	G	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-		1			
H	G	-	T	-	G	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-			1		
I	G	-	T	-	G	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-			1		
J	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	-				1	
K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				1	
L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				4	
M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				10	
N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				6	5
O	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				1	1
P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				1	1
Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				1	1
R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				1	1
S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					17
T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					1

Bowen & Grant (1997)



Grant & Leslie (1996)

Bowen & Grant (1997)

```

TTGAGTCTGTATGGAACAGCTAAA
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----
G-----G-----A-----T-----

```

Genetic distances (+ standard errors)

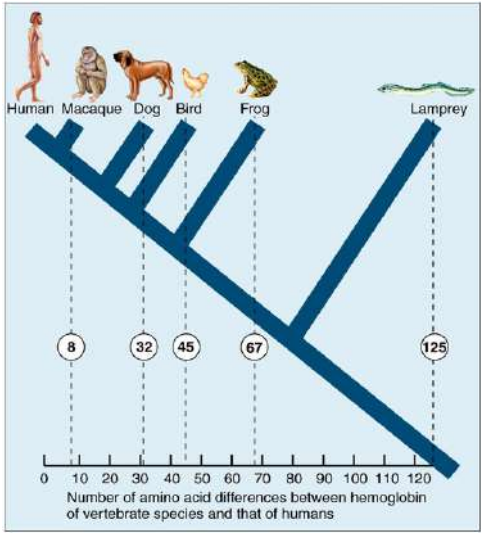
-	0.017	0.183	0.235	0.279	0.292	0.296	0.292
0.003	-	0.185	0.230	0.279	0.292	0.296	0.291
0.698	0.708	-	0.192	0.272	0.293	0.299	0.293
1.069	1.040	0.851	-	0.208	0.196	0.209	0.213
1.311	1.309	1.273	0.911	-	0.013	0.029	0.033
1.356	1.362	1.360	0.852	0.033	-	0.029	0.036
1.414	1.413	1.436	0.967	0.065	0.059	-	0.020
1.388	1.387	1.382	0.969	0.051	0.078	0.049	-

(Grant, Leslie & Bowen 2005)

Molecules reflect evolutionary divergence

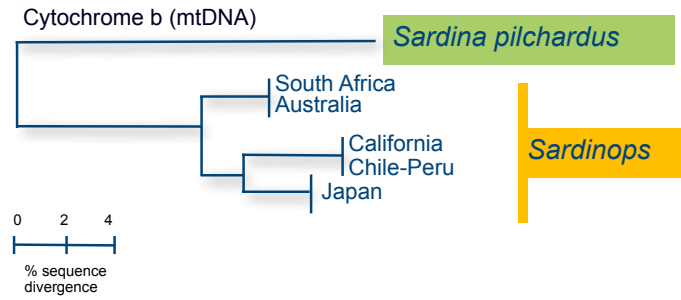


Molecular clock

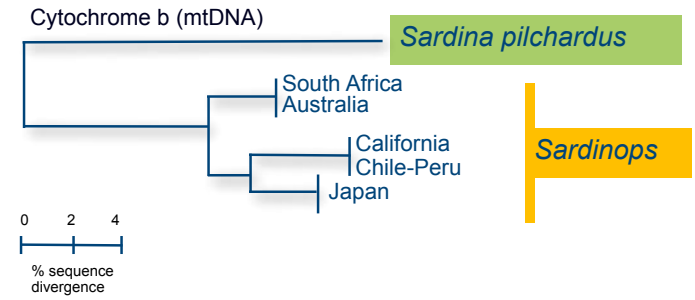


Cytochrome b (mtDNA)



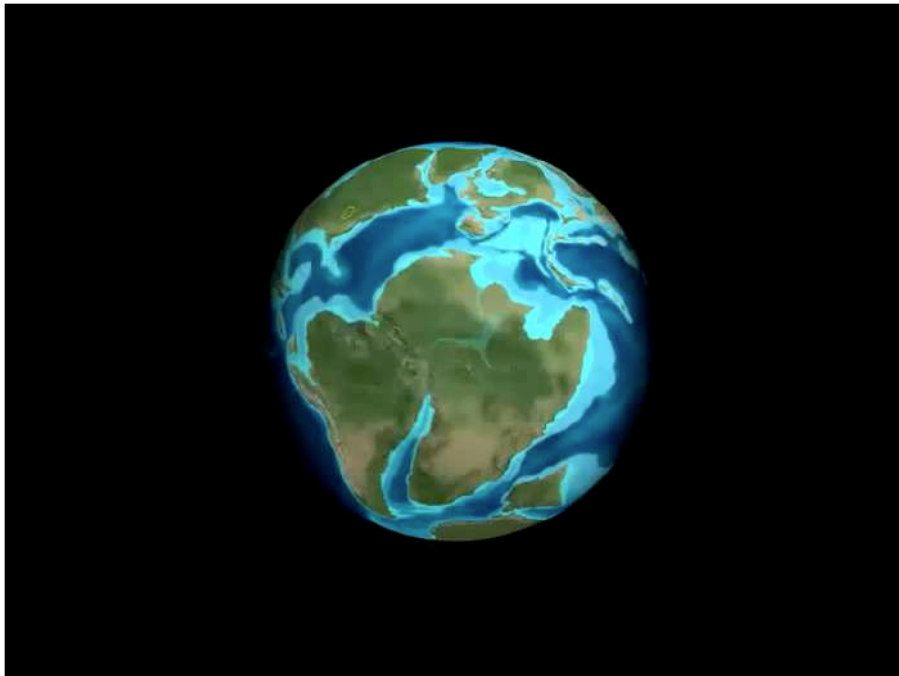


Cytochrome b molecular clock: 1% = 1 MY



Cytochrome b molecular clock: 1% = 1 MY

Distance *Sardinops-Sardina* = ca. 23% = 23MY



Allozyme distances between *Sardina* and *Sardinops* are consistent with 18 MY closure of eastern Tethys Sea

Sardina

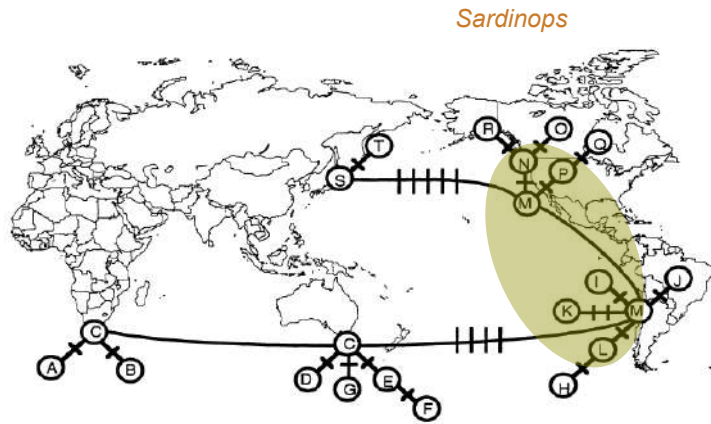
Sardinops



Grant & Leslie (1996)

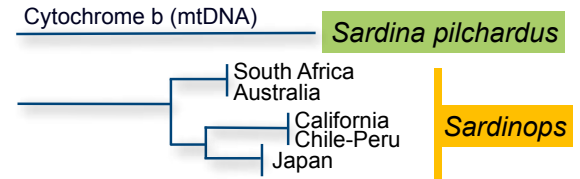
Bowen & Grant (1997)

- 📍 *Sardinops*: mtDNA divergences consistent with Pleistocene dispersal
- 📍 Greatest haplotype diversity in 'center' of distribution



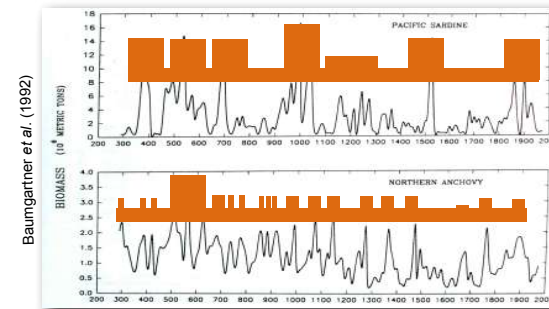
Grant & Leslie (1996)

Bowen & Grant (1997)



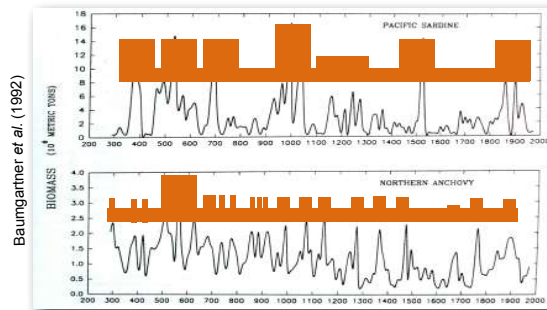
Why is there only shallow population structure in a 18 MY old species?

Why shallow population structure in a 18 MY old species?

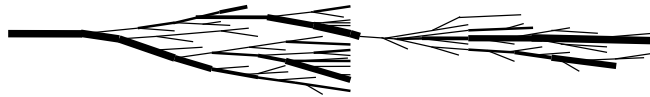


Temporal abundance strong variation

Why shallow population structure in a 18 MY old species?



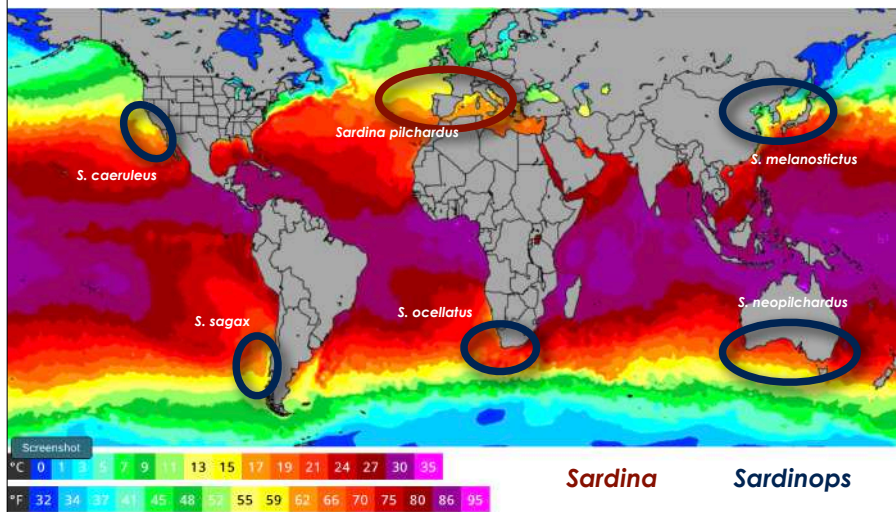
Lineage sorting = lineage extinctions + new mutations



Re-cap

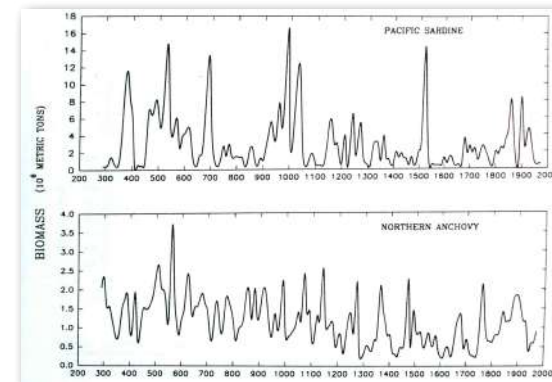
Re-cap

Sardines do not tolerate temperatures below 13 and above 25 degrees celsius



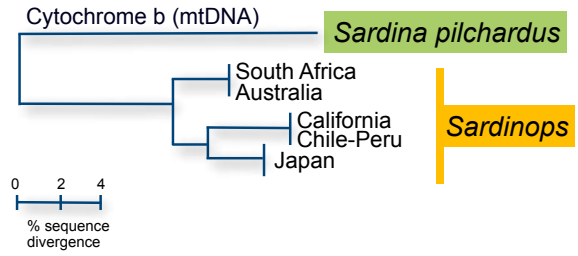
Re-cap

Global scale changes in climate are possibly influencing the abundance of the resource



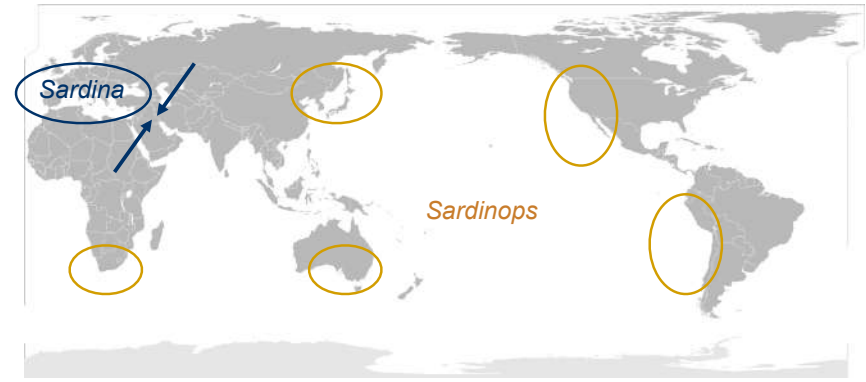
Re-cap

The genetic distances between regional populations (South Africa and Australia, and Chile and California) are small and imply recent divergences between populations



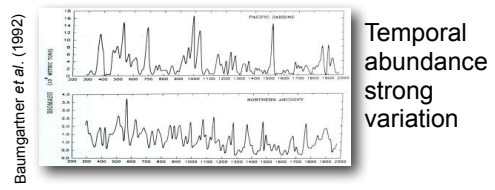
Re-cap

Allozyme distances between *Sardina* and *Sardinops* are consistent with 18 MY closure of eastern Tethys Sea



Re-cap

Shallow population structure in a 18 MY old species because.....



Lineage sorting = lineage extinctions + new mutations

outline

- GEOGRAPHIC DISTRIBUTION
- MOLECULAR DATA
- PHYLOGENETIC ESTIMATION
- HISTORICAL DEMOGRAPHY
- PALEOGEOGRAPHIC EVENTS