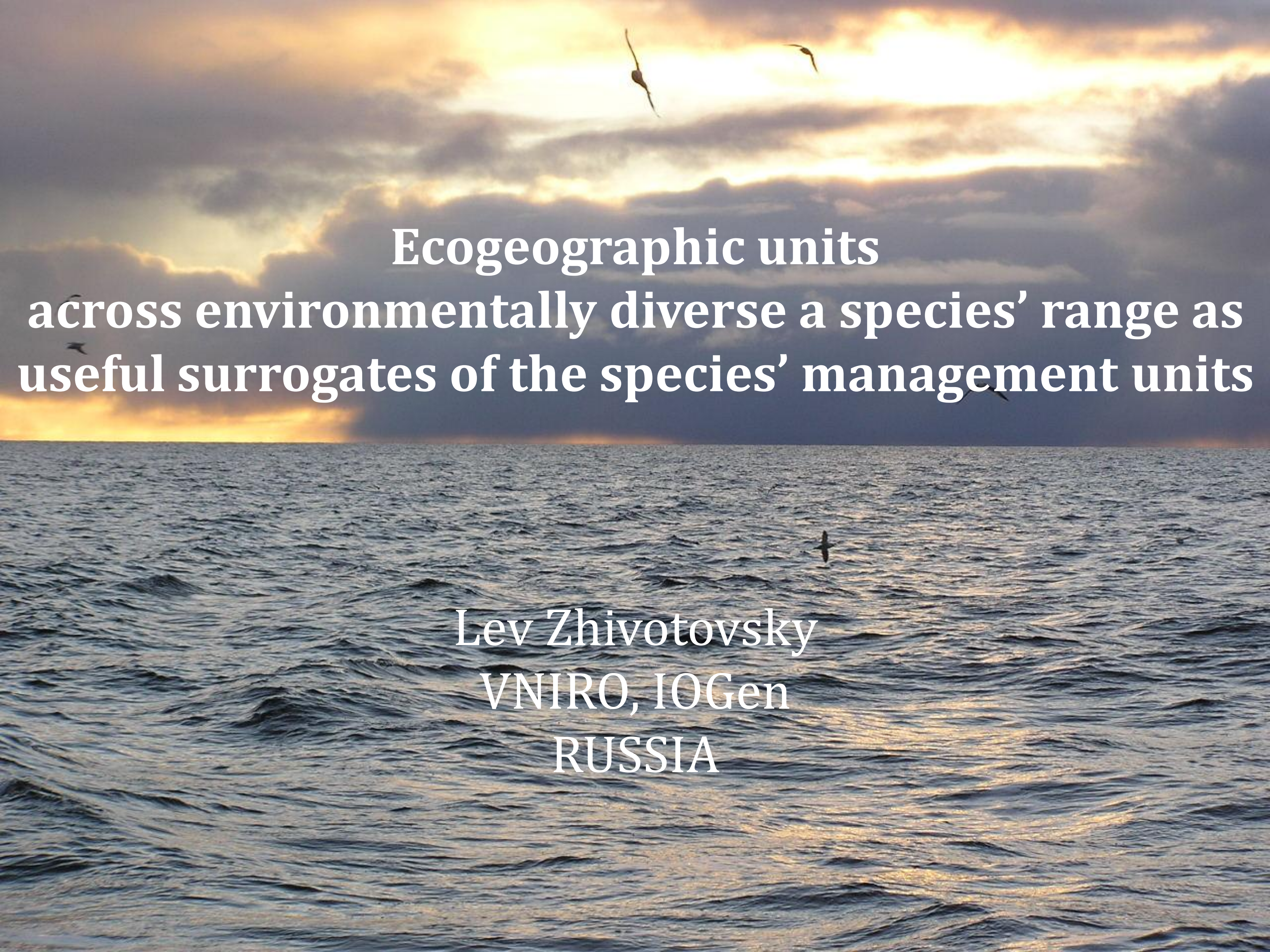


Ecogeographic units across environmentally diverse a species’ range as useful surrogates of the species’ management units

Lev Zhivotovsky
VNIRO, IOGen
RUSSIA

Salmonid fishes of the North Pacific as an example

Environment is a basic, leading power that forces biological species to evolve and fit the surrounding conditions.

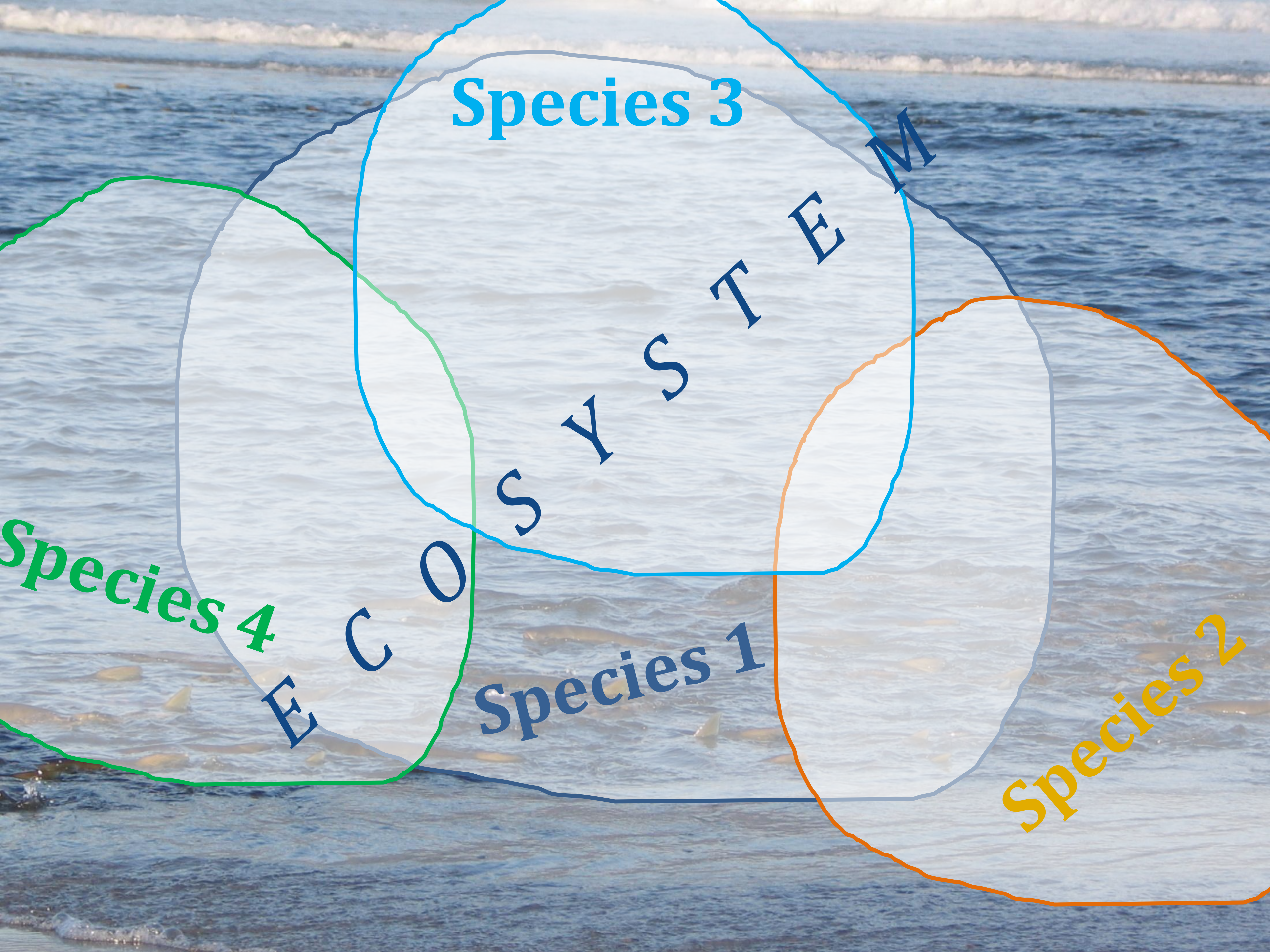
These environmental impacts leave genetic traces in the species' genomes.

Therefore, there exist environmental variables on one hand, and their marks in heritable species' variation on the other hand.

The focus of my talk is how to combine the knowledge of environmental/ecological variables and genetic markers in order to understand the species subdivision into population and other such units.

In the talk, salmonid fishes are used as an example. Although some species are far from the salmonid model, especially those with pelagic eggs and larvae, something might be learned from the salmonid studies.

What is to be managed as a unit?



ECOSYSTEM

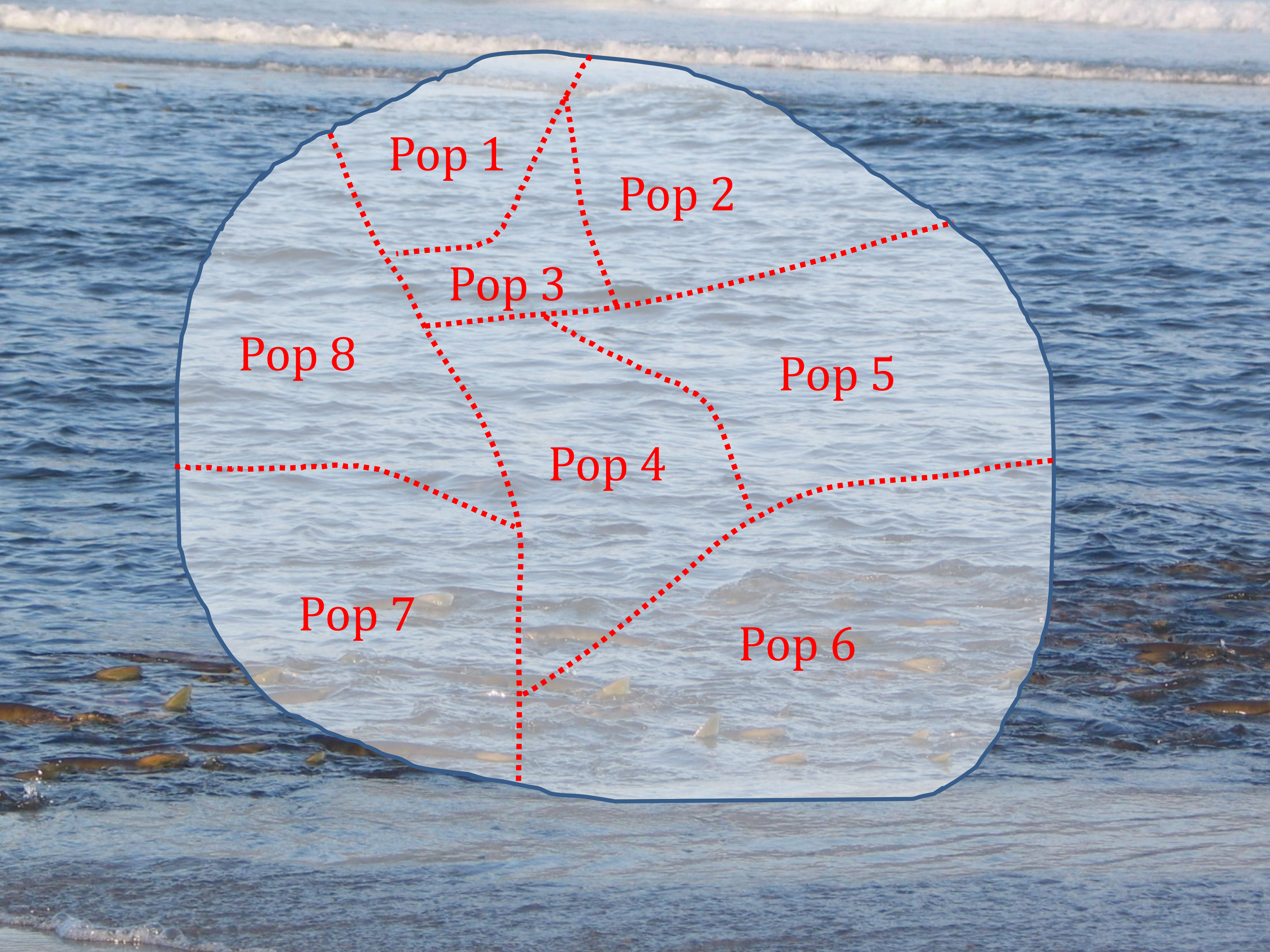
Species 1

Species 2

Species 3

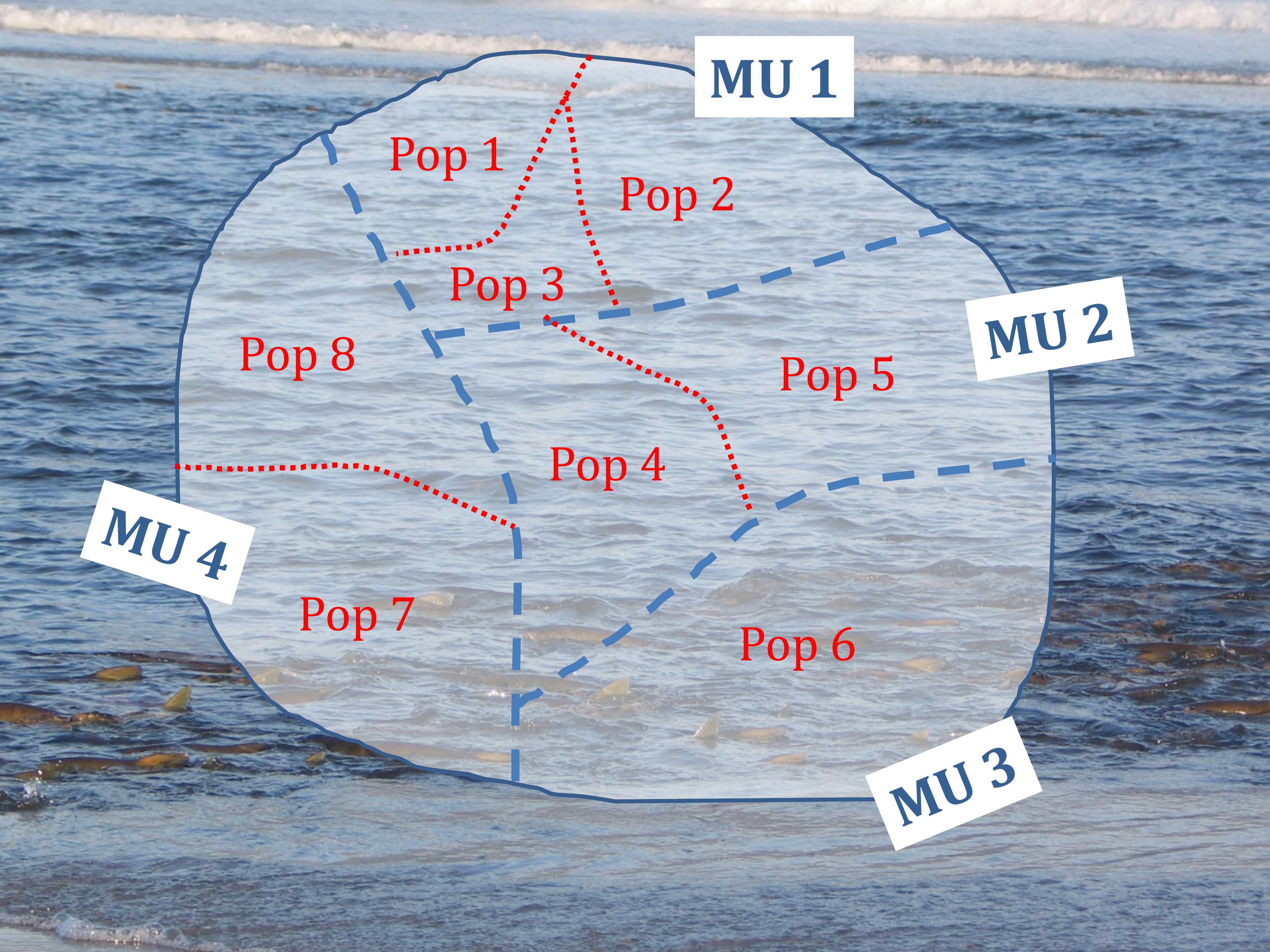
Species 4


Species 1

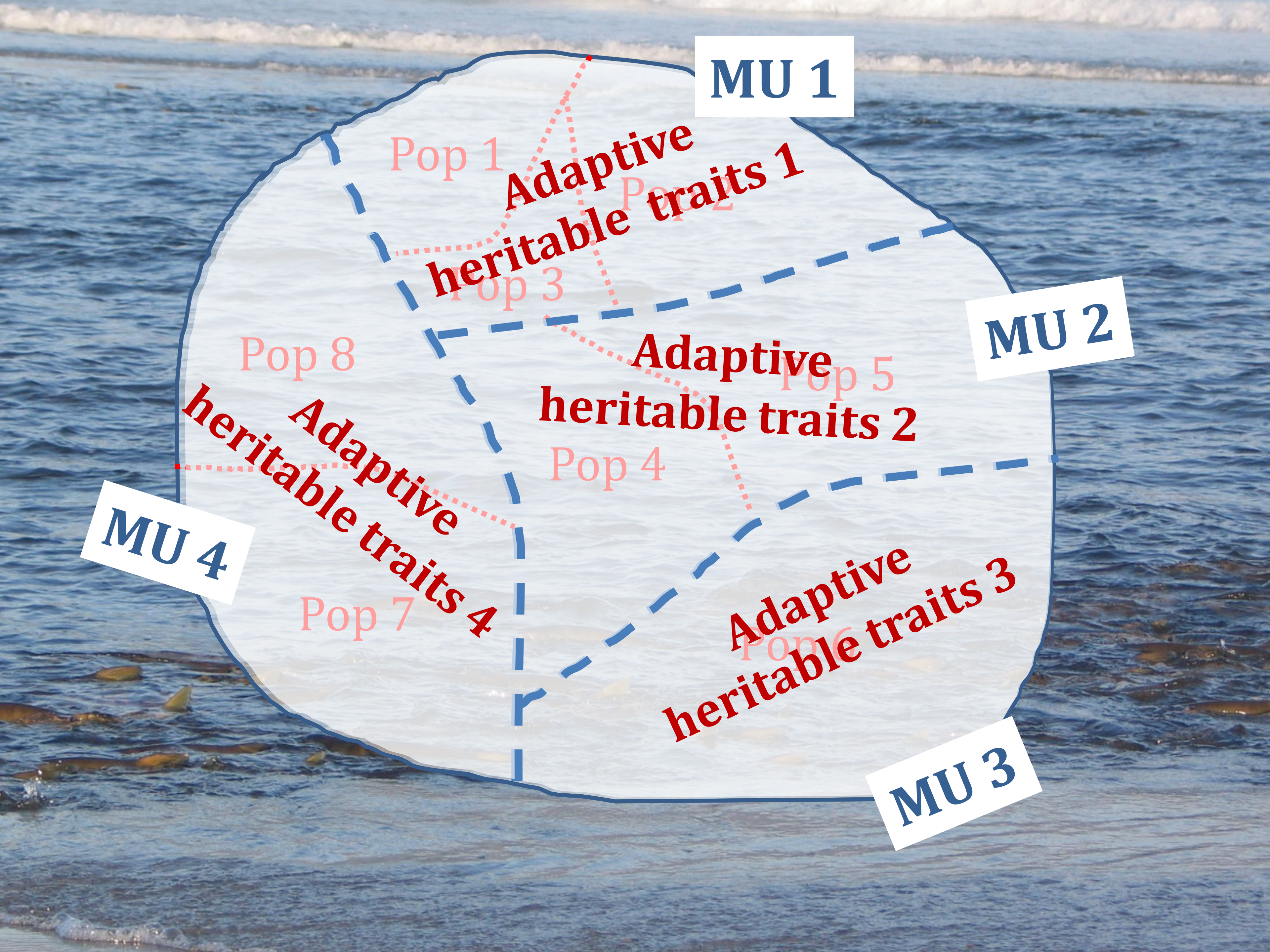

Pop 1
Pop 2
Pop 3
Pop 8
Pop 5
Pop 4
Pop 7
Pop 6

Preliminary definition of ‘management unit’

Management unit (MU), as a biological object, is a set of spatially close populations that have similar biological features, differ and reproductively isolate from the rest of populations of the same species, and thus can be managed independently of other such units.


MU 1
Pop 1
Pop 2
Pop 3
MU 2
Pop 8
Pop 5
Pop 4
MU 4
Pop 7
Pop 6
MU 3

It would be just fantastic to have in hands all those inherited adaptive traits that have provided the populations to fit to their specific environmental conditions, and thus, would help in detecting population and management units.



MU 1

Pop 1

Pop 2

Pop 3

Adaptive heritable traits 1

MU 2

Pop 5

Pop 4

Adaptive heritable traits 2

MU 3

Pop 6

Adaptive heritable traits 3

MU 4

Pop 8

Pop 7

Adaptive heritable traits 4

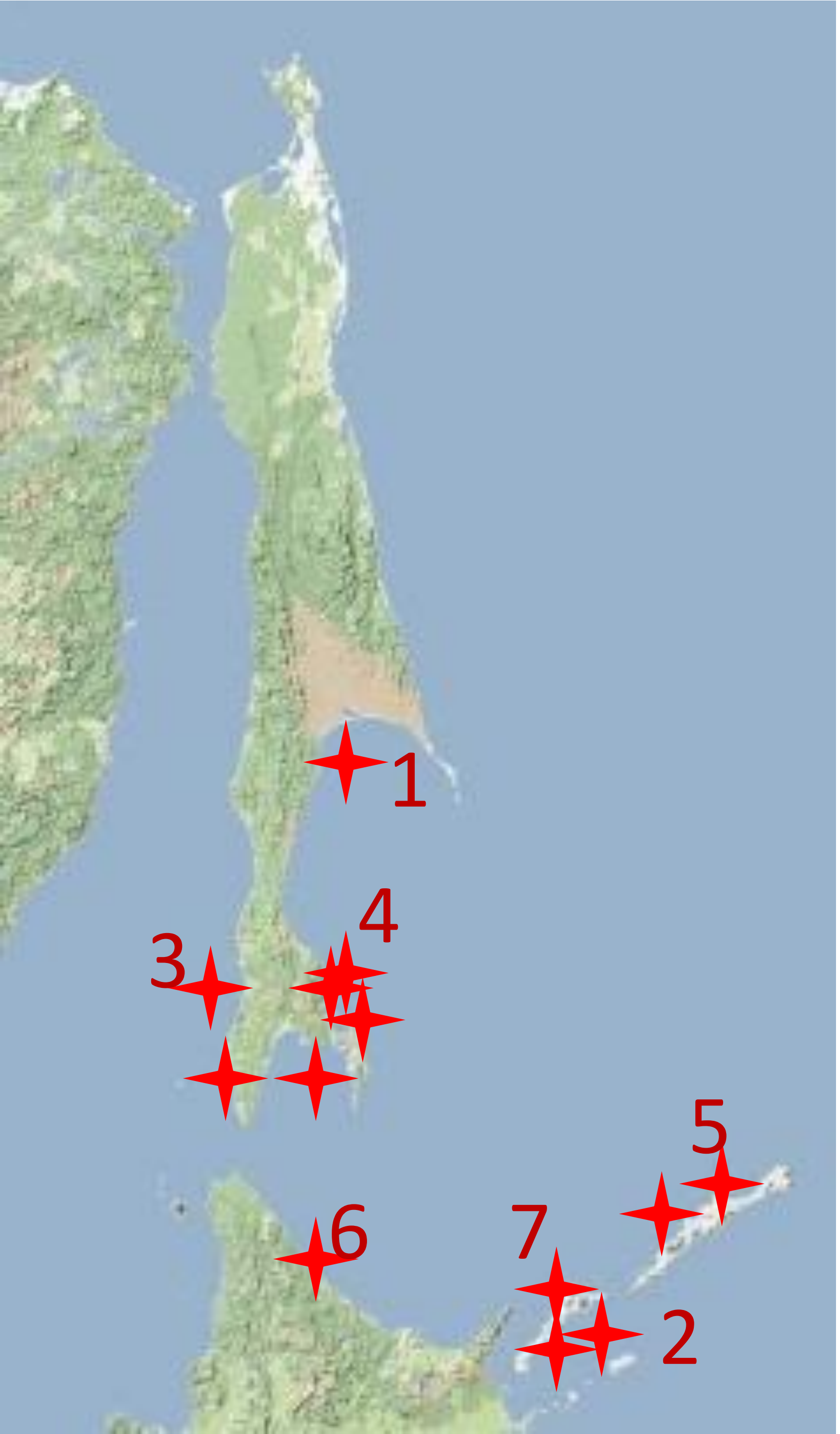
However, too little is known about the genetics of adaptations, even for well studied species.

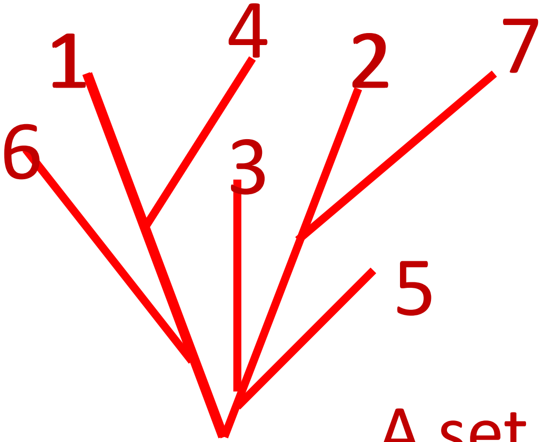
Nevertheless, during the last twenty years, DNA markers are being used more and more extensively in population studies.

Their principal **advantage**:

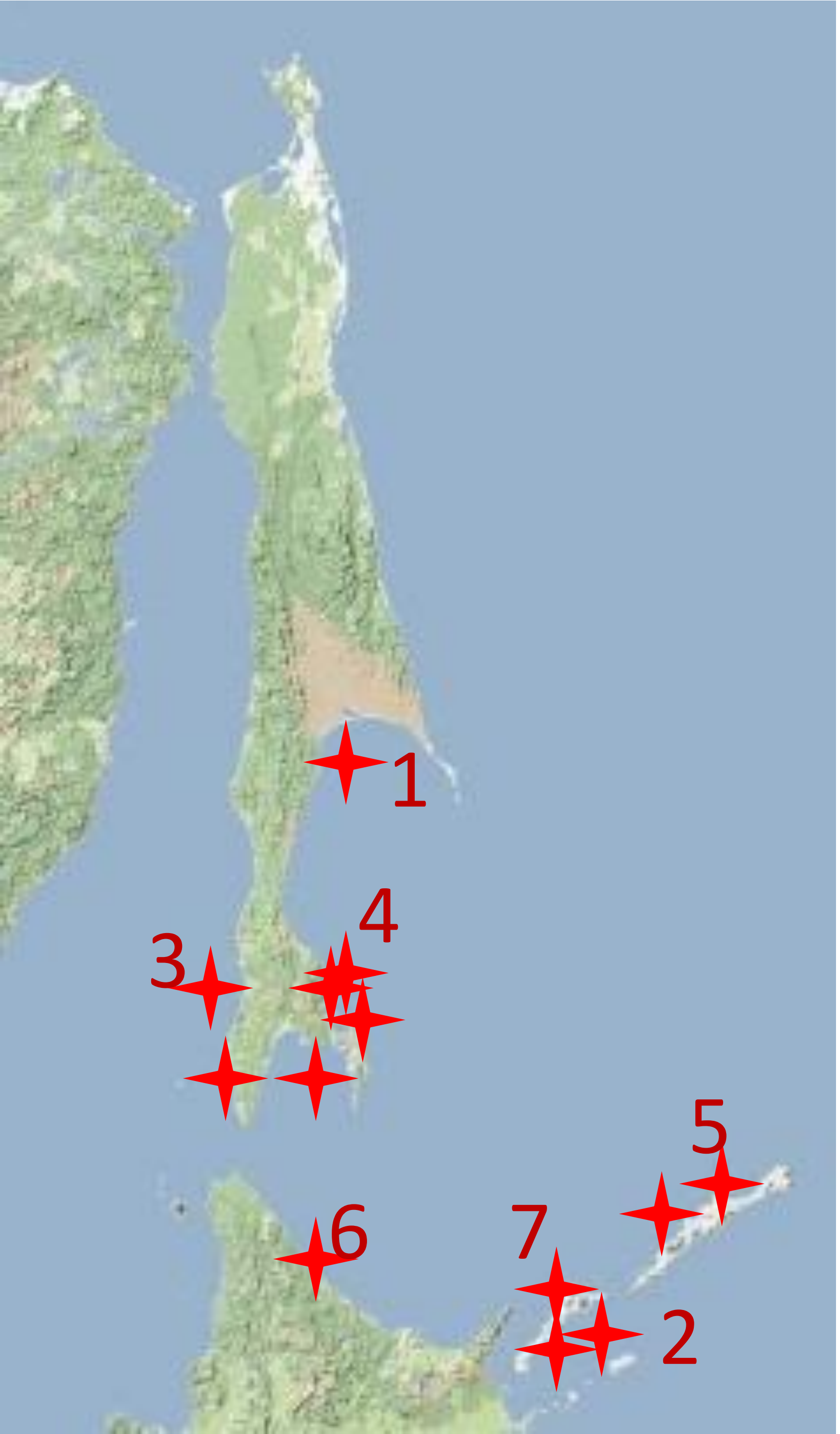
If two populations are reproductively isolated from one another, then, **the more generations have passed since their isolation the more differences between them accumulate at the DNA level**.

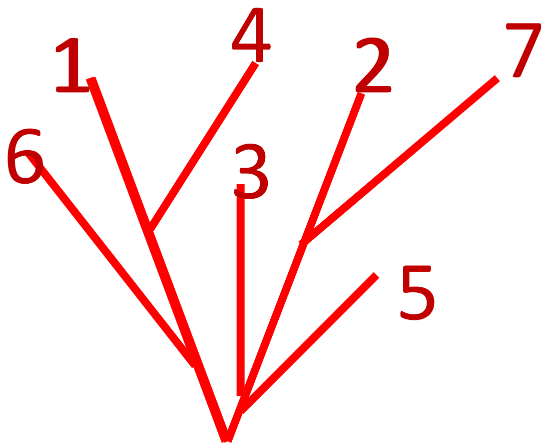
DNA-based estimates have unpredictable components, and thus, may be biased.



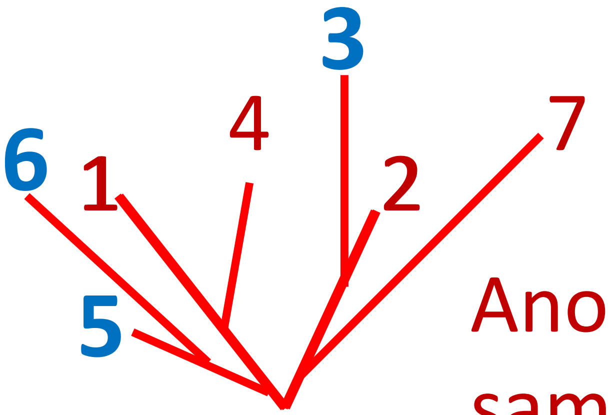


A set of single random samples from different populations forms a genetic tree.





One set of samples



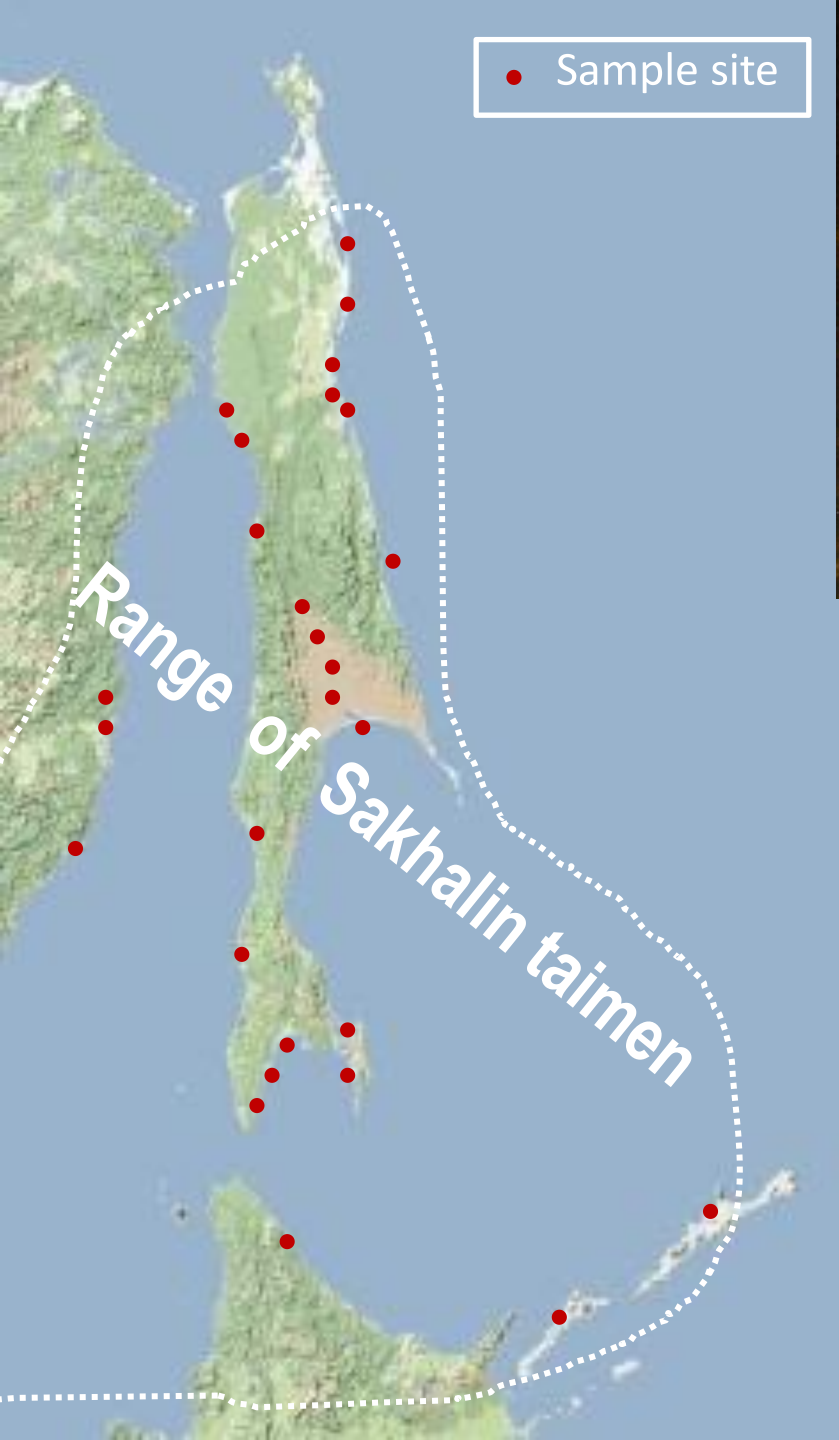
Another set of samples from the same pops

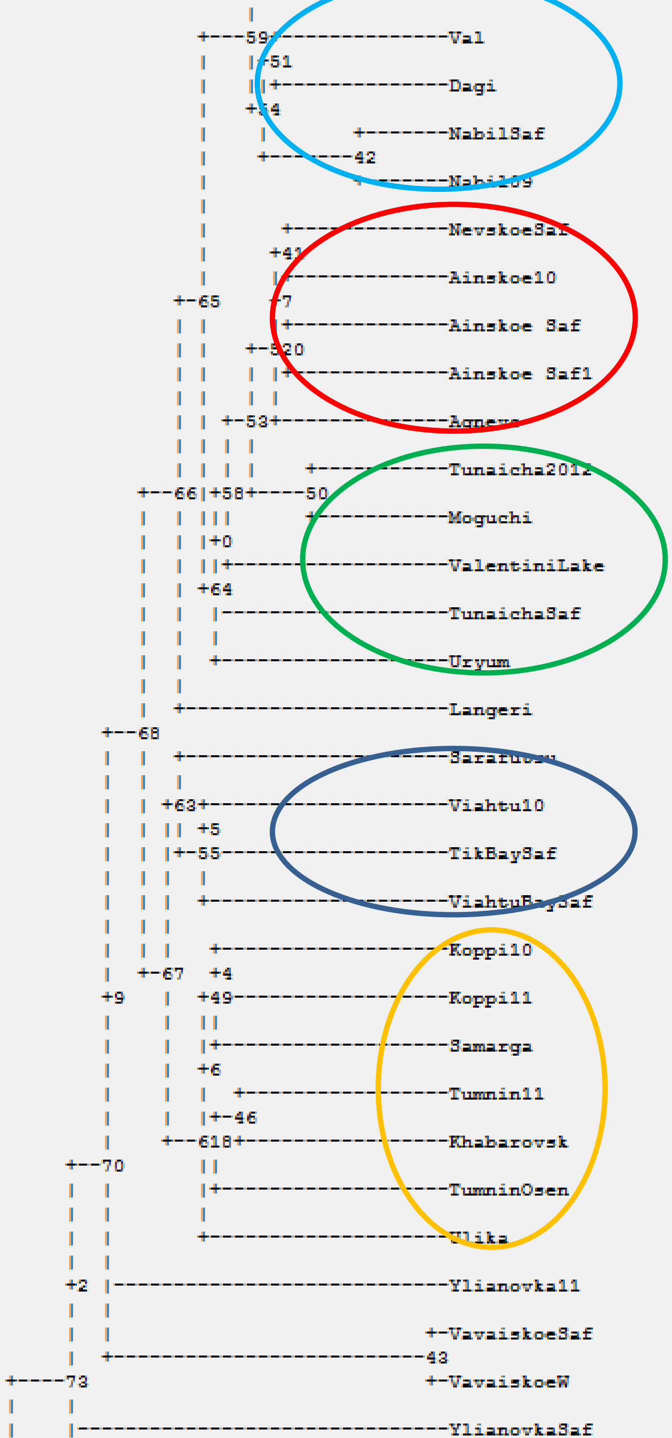
DNA-based figures may be biased due to:

- small sizes of population samples;
- low population sizes (genetic drift);
- small number of DNA markers used;
- small number of population samples across each unit;
- gene flows;
- introduction or artificial reproduction;
- clustering methods.

Therefore, genetic trees and other pictures of population differentiation are not perfect. Say, some genetic clusters may include samples from populations that are quite different geographically/ecologically. The example follows.

Sakhalin taimen
(*Parahucho perryi*)


● Sample site
Range of Sakhalin taimen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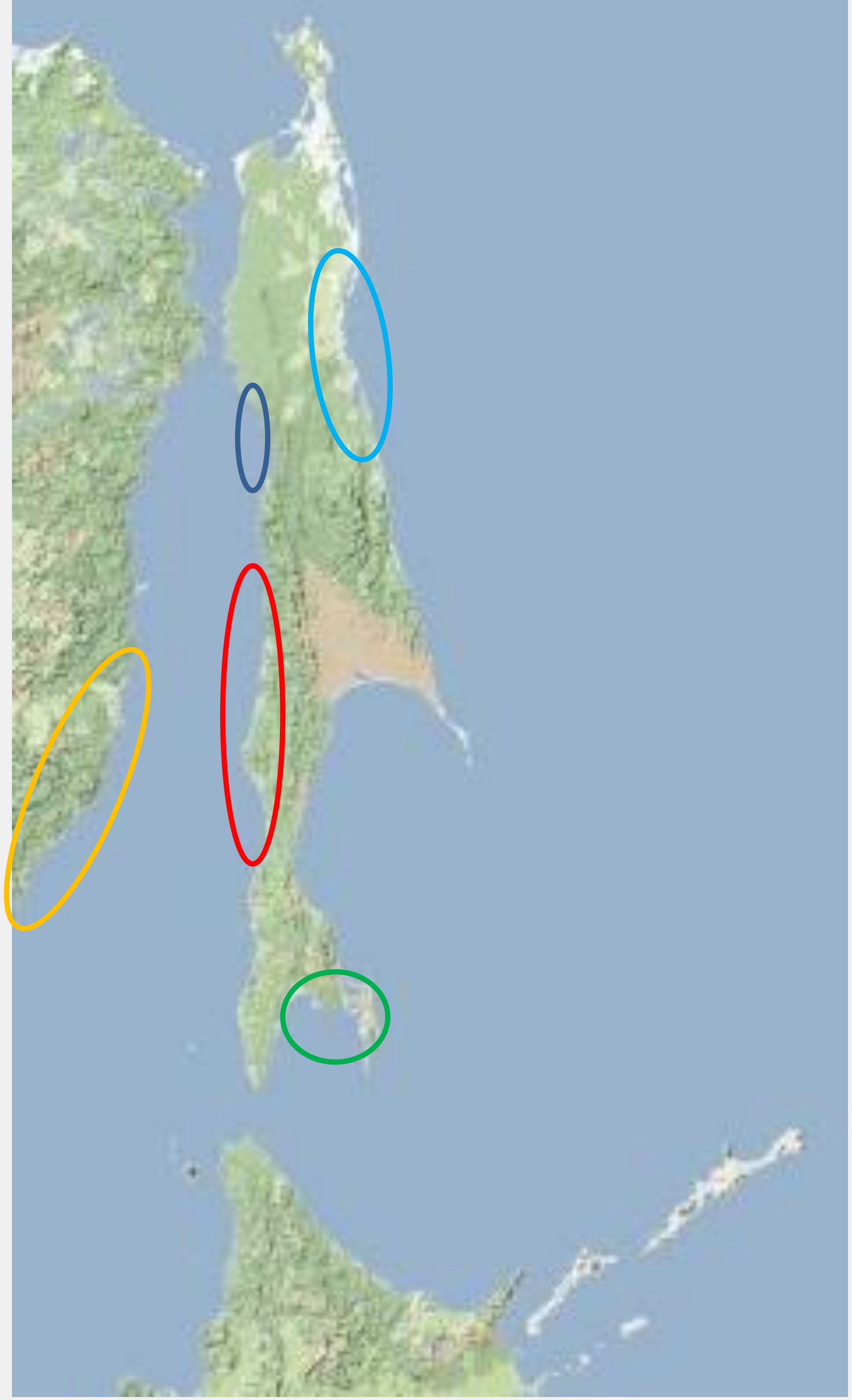
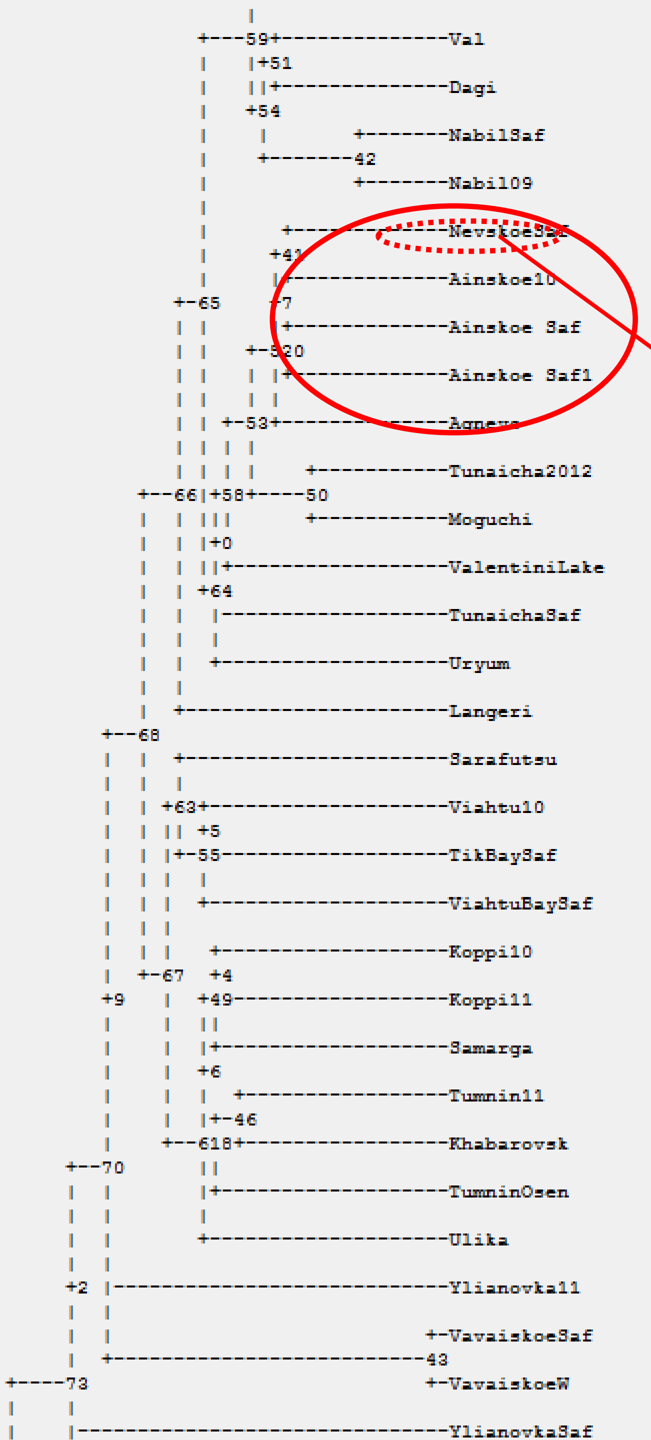
Val
51
Dagi
54
NabilSaf
42
Nabil09
NevskoeSaf
41
Ainskoe10
65
7
Ainskoe Saf
520
Ainskoe Saf1
53
Agneva
Tunaicha2012
66
58
50
Moguchi
0
ValentiniLake
64
TunaichaSaf
Uryum
Langeri
68
Sarafutsu
63
Viahtu10
5
55
TikBaySaf
ViahtuBaySaf
Koppi10
67
4
9
49
Koppi11
Samarga
6
Tumnin11
46
618
Khabarovsk
70
TumninOsen
Ulika
2
Ylianovka11
VavaiskoeSaf
43
73
VavaiskoeW
YlianovkaSaf





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                |   ||+--------------Dagi
                |   +54
                |    |       +-------NabilSaf
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                |            +-------Nabil09
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                |     |+-------------Ainskoe10
              +-65    +7
              | |     |+-------------Ainskoe Saf
              | |   +-520
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              | |   | |
              | | +-53+--------------Agneva
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           |  |  |-------------------TunaichaSaf
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        +--68
        |  |  +----------------------Sarafutsu
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        |  | +63+--------------------Viahtu10
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        |  | |   +-------------------Koppi10
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     |  |       |+-------------------TumninOsen
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|    |-------------------------------YlianovkaSaf
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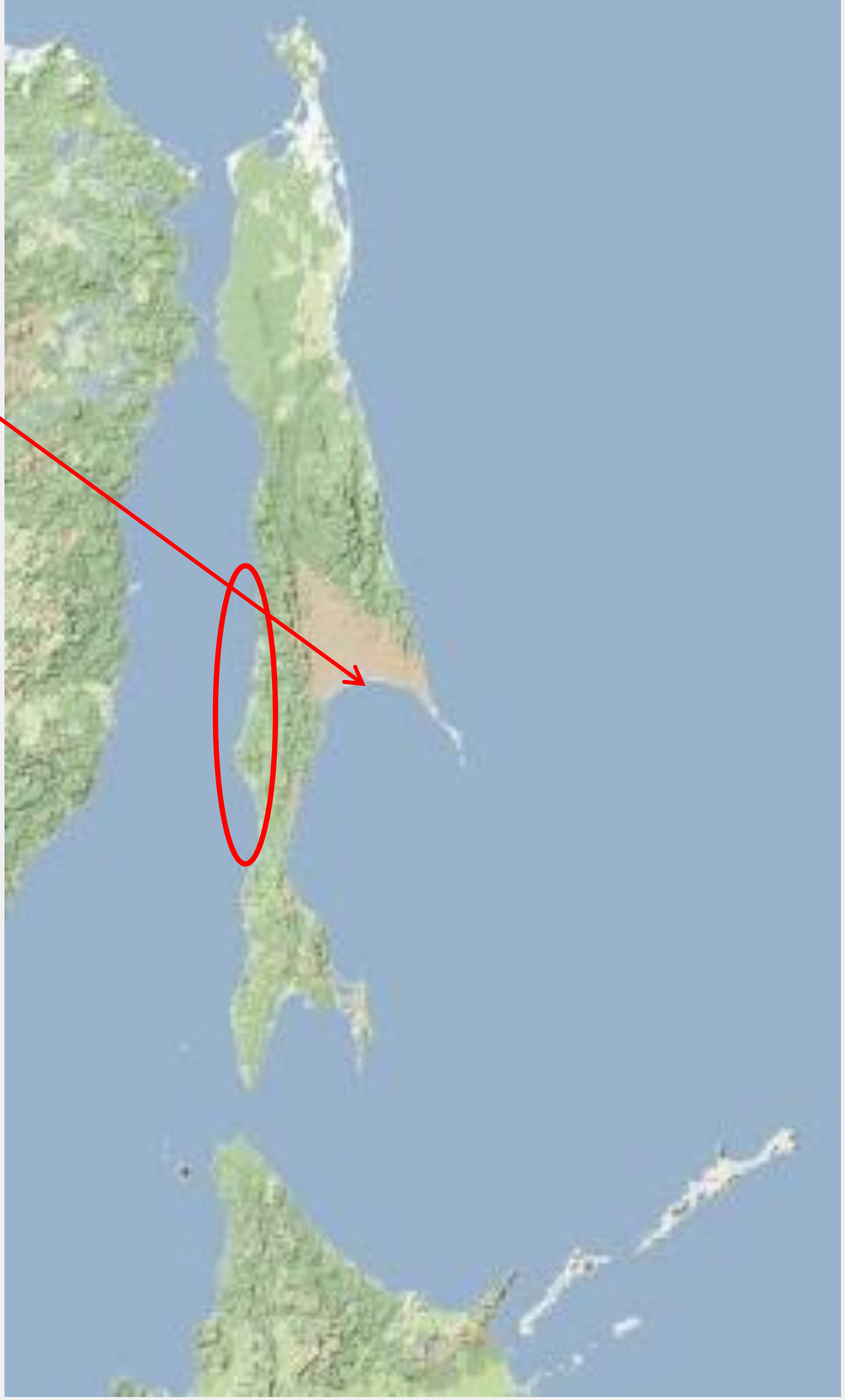

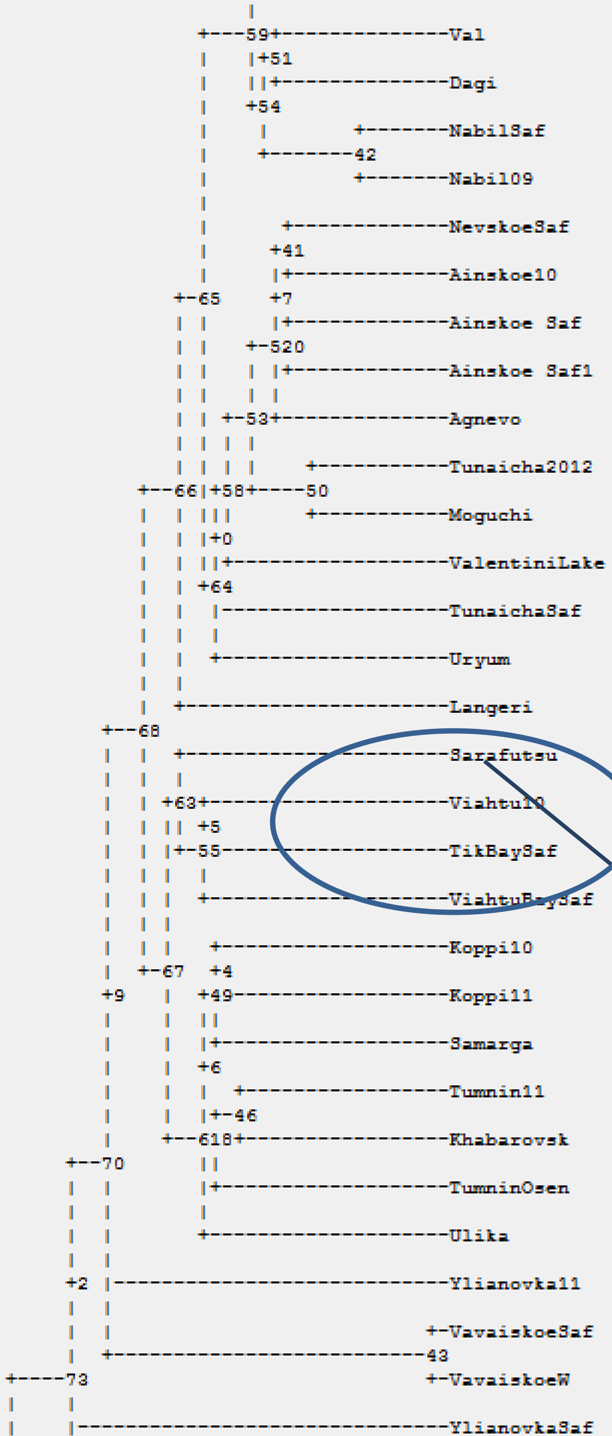

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                |    +-------42
                |            +-------Nabil09
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                |     |+-------------Ainskoe10
              +-65    +7
              | |     |+-------------Ainskoe Saf
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              | |   | |+-------------Ainskoe Saf1
              | |   | |
              | | +-53+--------------Agnevo
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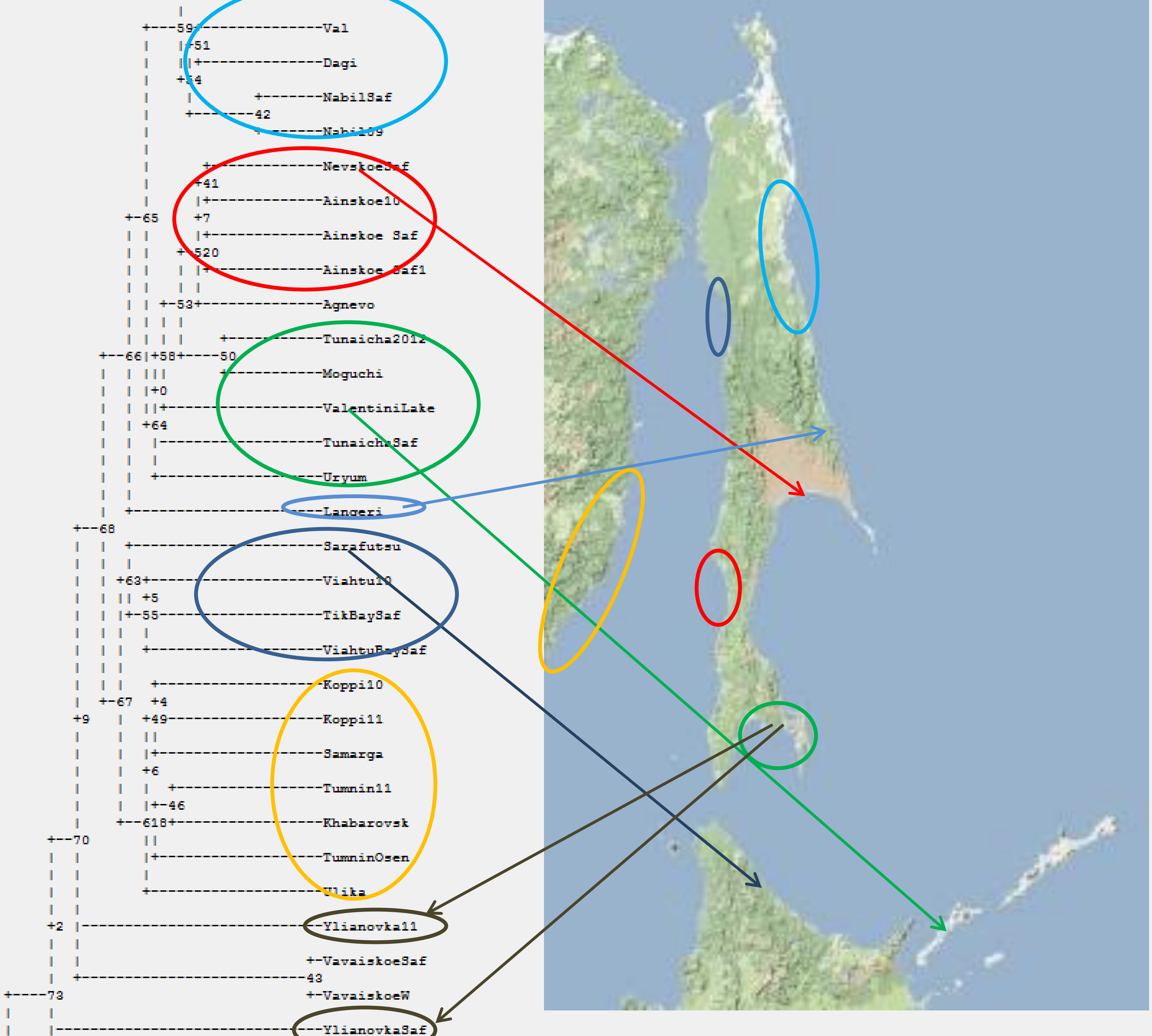

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                |   |+51
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                |     |+-------------Ainskoe10
              +-65    +7
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              | |   | |+-------------Ainskoe Saf1
              | |   | |
              | | +-53+--------------Agnevo
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        |    +--618+-----------------Khabarovsk
     +--70      ||
     |  |       |+-------------------TumninOsen
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+----73                            +-VavaiskoeW
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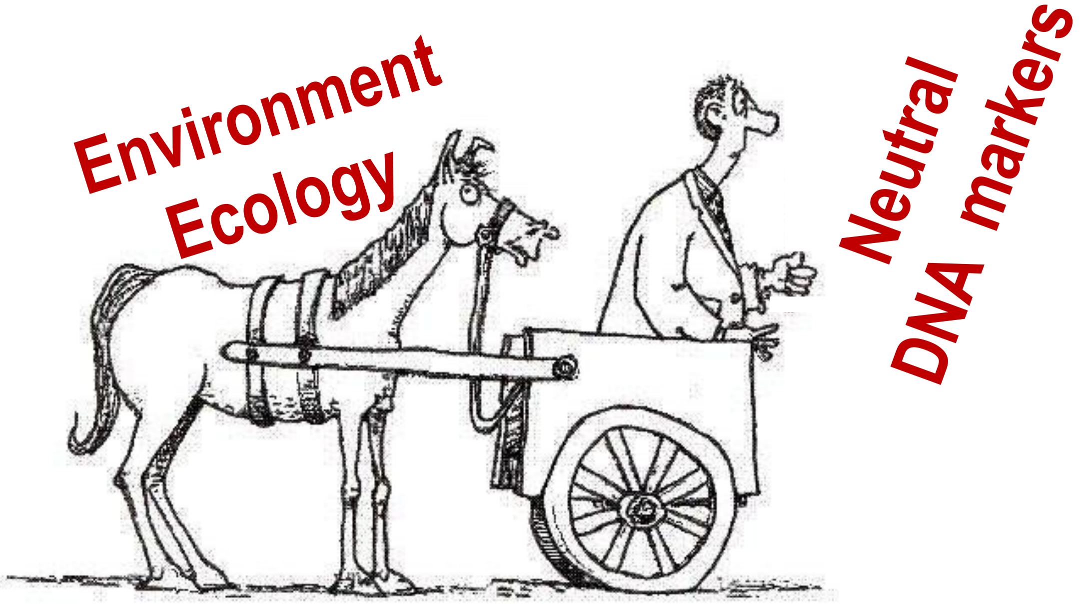
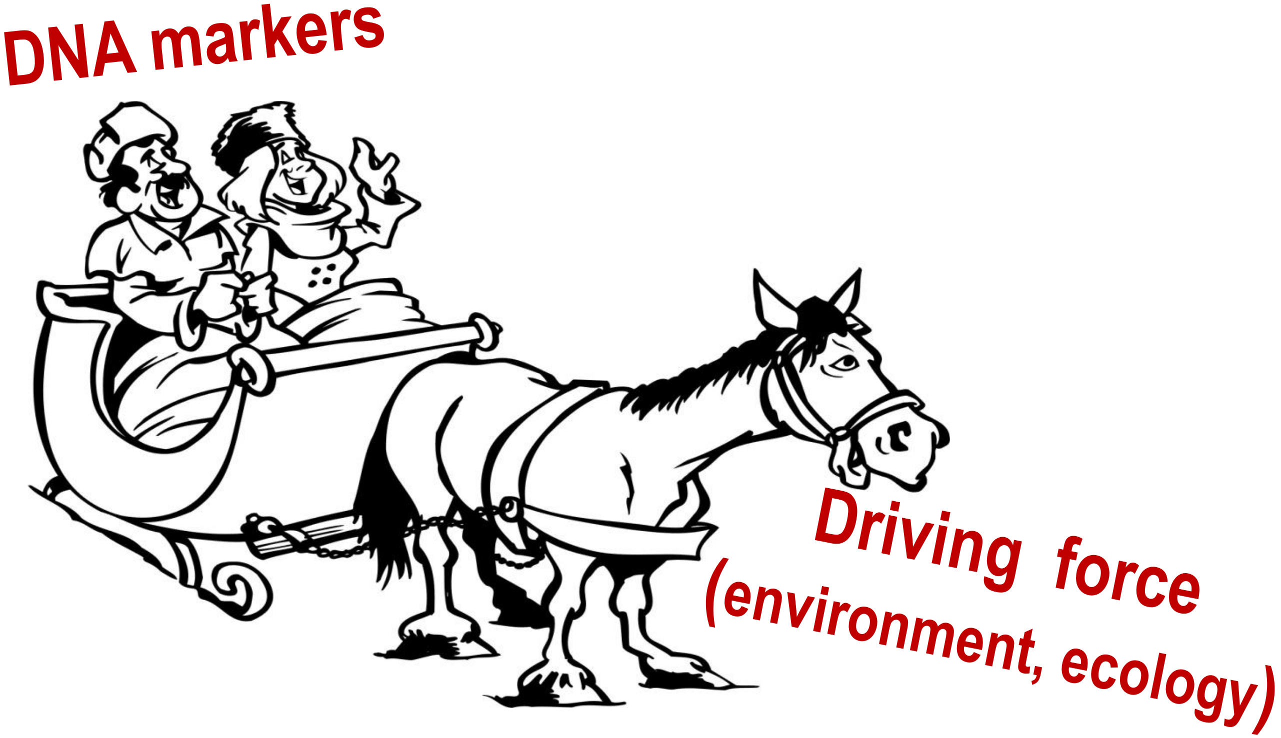
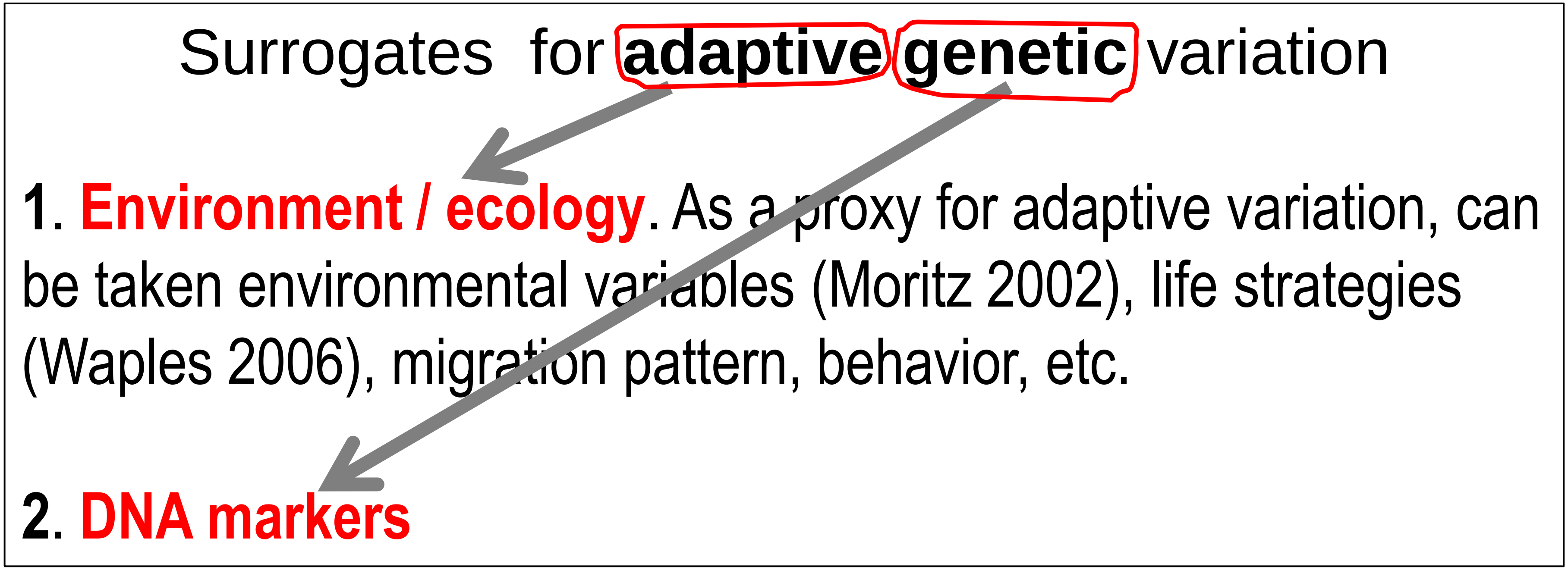


This is why we got the previous figure

This is the unreachable ideal



This is what we can use now!



Surrogates for **adaptive** **genetic** variation

1. **Environment / ecology**. As a proxy for adaptive variation, can be taken environmental variables (Moritz 2002), life strategies (Waples 2006), migration pattern, behavior, etc.

2. **DNA markers**

Surrogates for **adaptive genetic** variation

1. Environment/ecology.

Advantage: they associate with adaptive processes.

Disadvantage: little is known on their genetic associations (in wild nature).

2. DNA markers

Advantage: they represent the genome and can distinguish populations.

Disadvantage: they weakly relate to adaptive variation, i.e., they are almost selectively neutral.

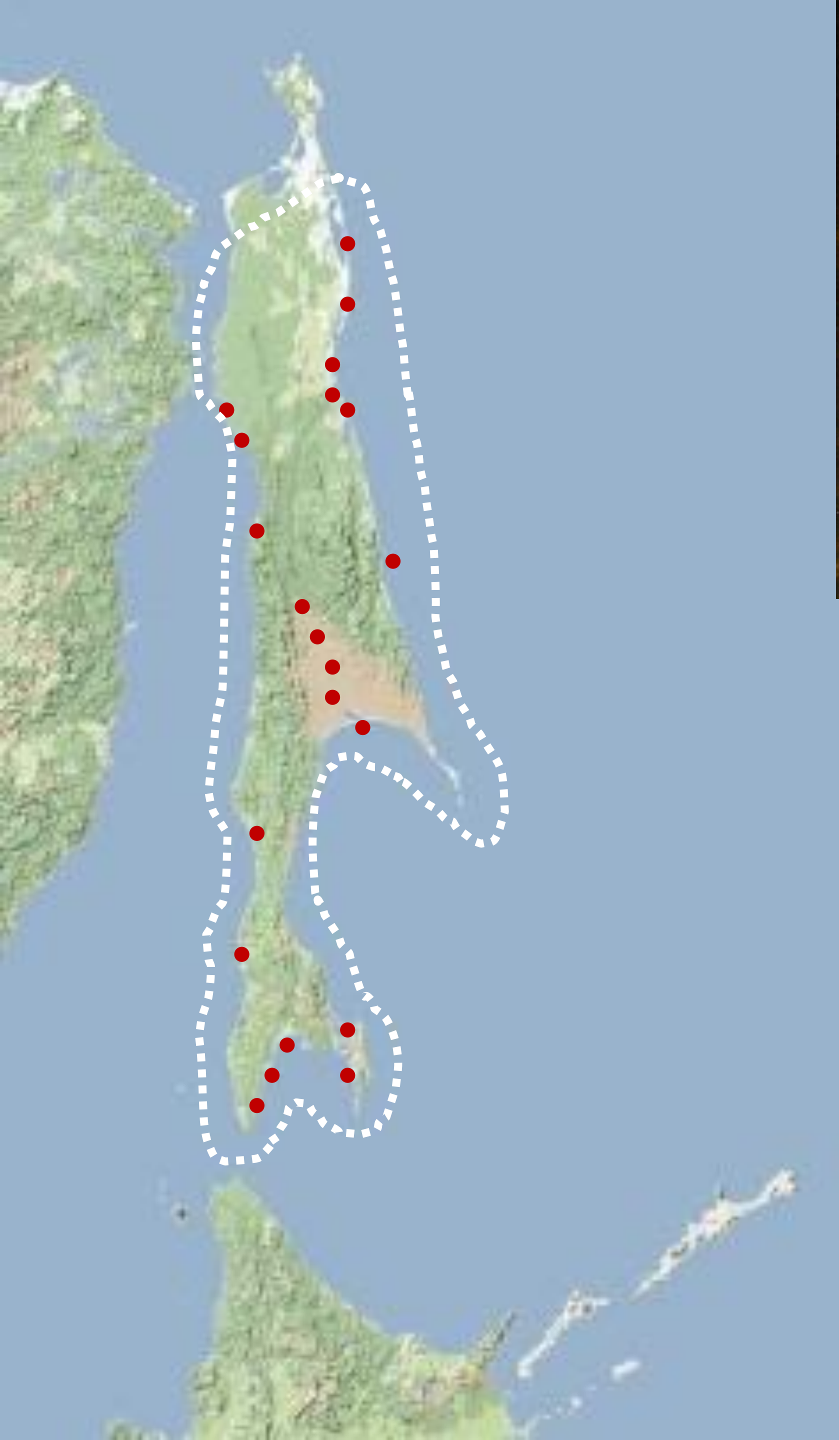
(Whole genome sequencing is able to identify only a modest part of the existing adaptive variation in populations)

The following two-step procedure of population study has been suggested (using the surrogates):

1) Subdividing the studied part of the species into **ecogeographic units** (**EGUs**) based on
    - *geography (environmental variables)*
    - *ecology (behavior, migration pattern, life strategy, etc.)*

2) Testing the relationships between populations within and between the EGUs using *DNA markers*.

Zhivotovsky et al. 2015. *Conservation Genetics* 16: 431-441;
Zhivotovsky 2016. *Russian J. Marine Biol*ogy 42: 373-382.

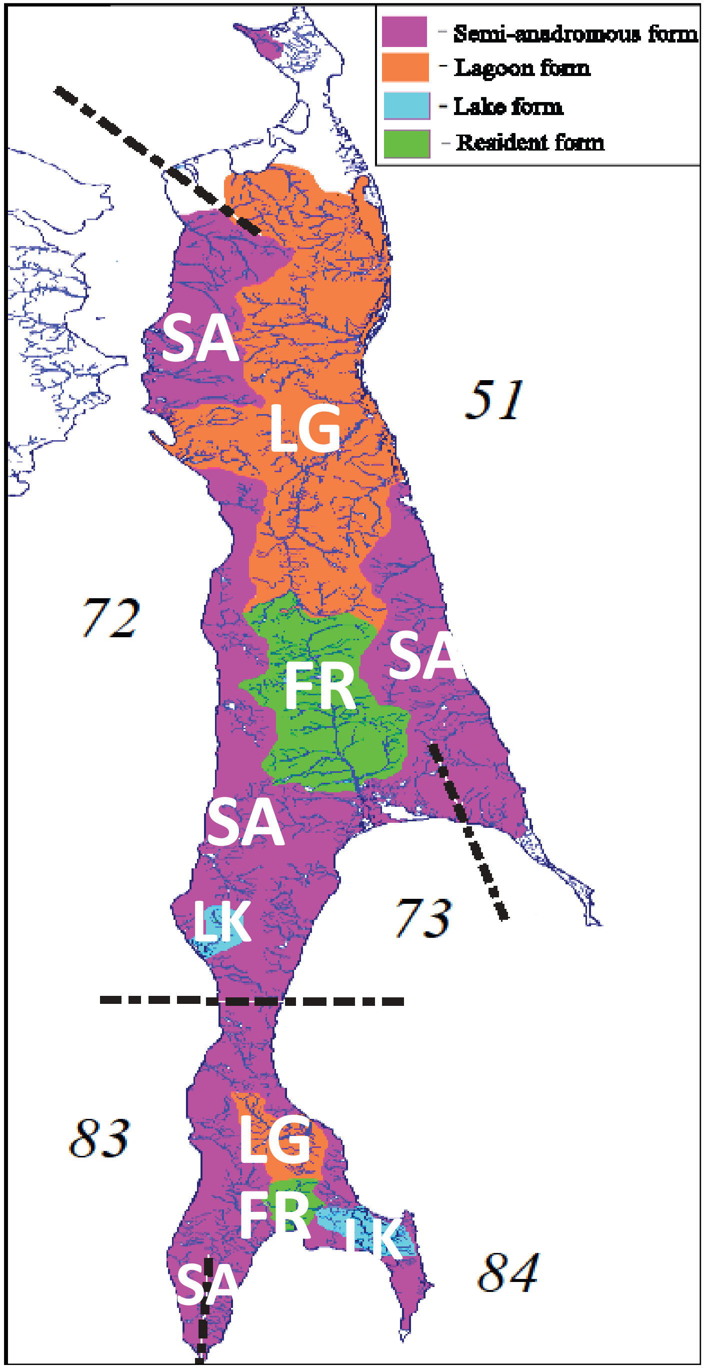


Sakhalin taimen
(*Parahucho perryi*)

Ecogeographic units (EGUs) across the Sakhalin Island's part of the taimen range are composed of both:
(1) **environmental** and (2) **ecological** components:

(1) Subdivision of the species' range into geographic provinces that differ from each other by environment parameters (humidity, temperature, landscape, drainage basins, etc.); denoted with numbers: 51, 72, 73, 83, 84.

(2) Subdivision of the species into behavior/migration forms of the taimen populations: denoted with four colors.

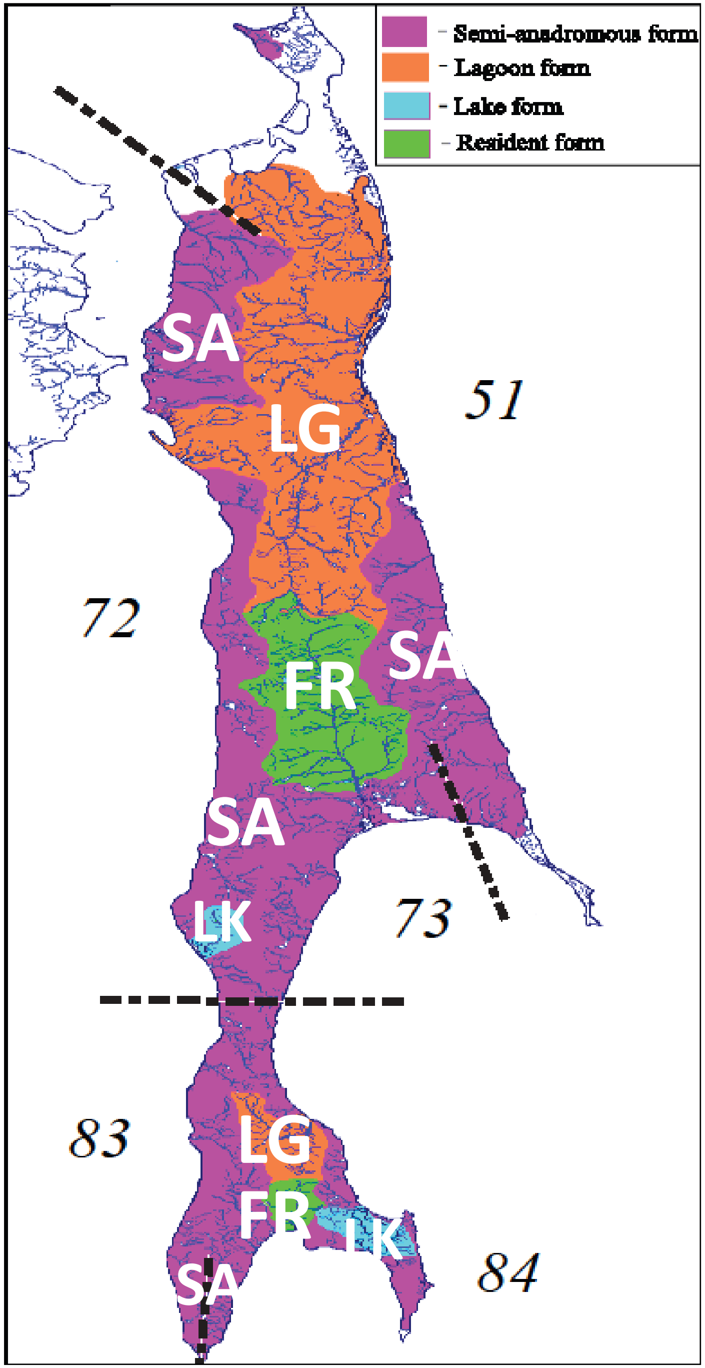


Alltogether, eleven EGUs within Sakhalin Island:
51-LG, 51-SA,
84-LK, 84-LG, 84-FR,
73-FR, 73-SA, etc.

DNA variation:

Total Fst between rivers (pops) = **0.150**

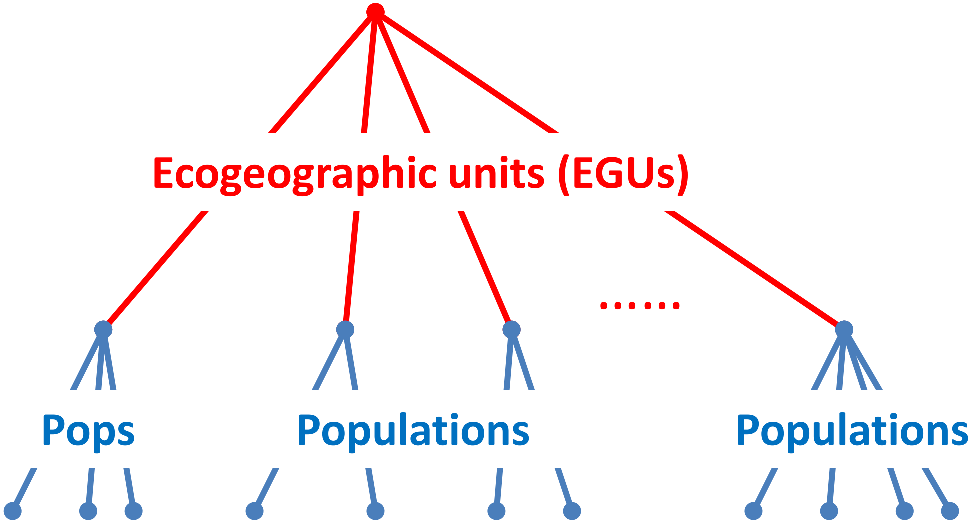
Fst between EGUs= **0.079**



A management unit of a given species, as a biological object, is a single population or a set of spatially close populations that:

- live under similar environmental & ecological conditions different from the rest of the range;
- posses similar biological features and differ in those from other populations of this species;
- reproductively isolated from other populations of the species;
- thus, can be managed with a common strategy of their reproduction, fishery, and conservation.

Two basic levels of hierarchical structure of Sakhalin taimen populations



Ecogeographic units (EGUs)

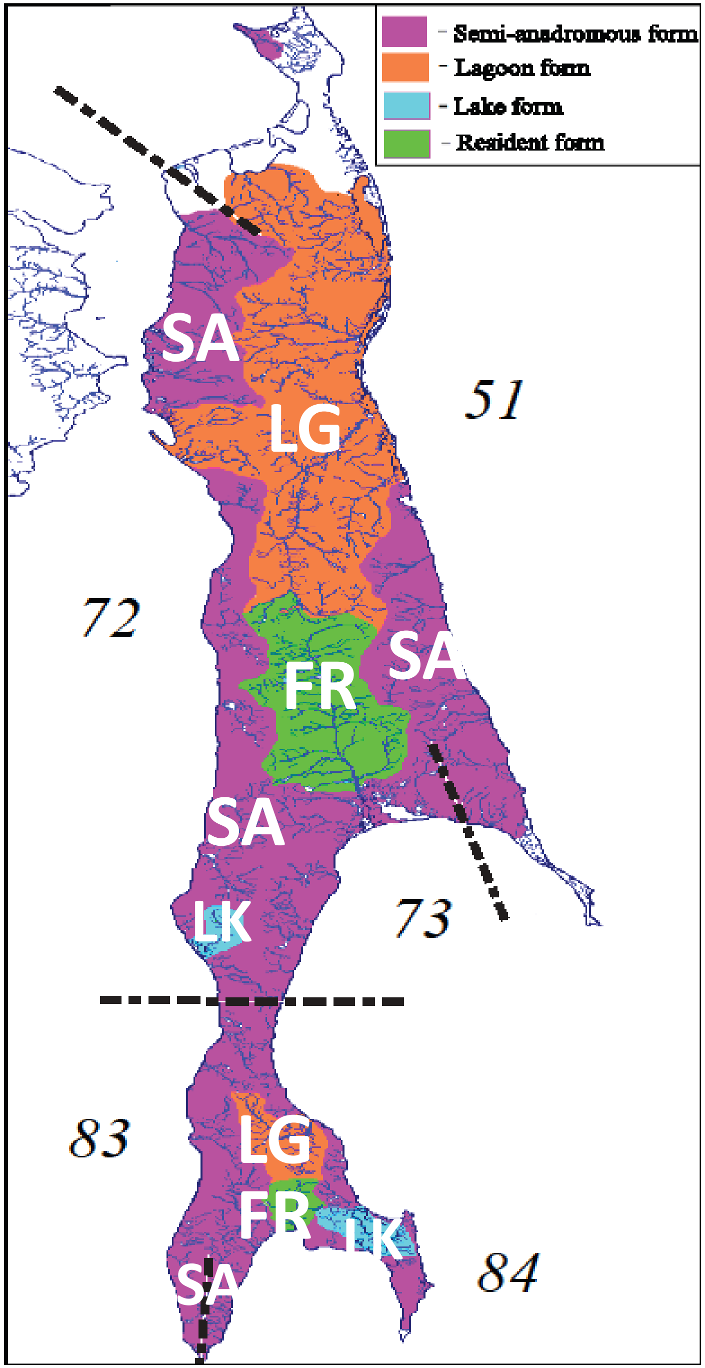
Pops

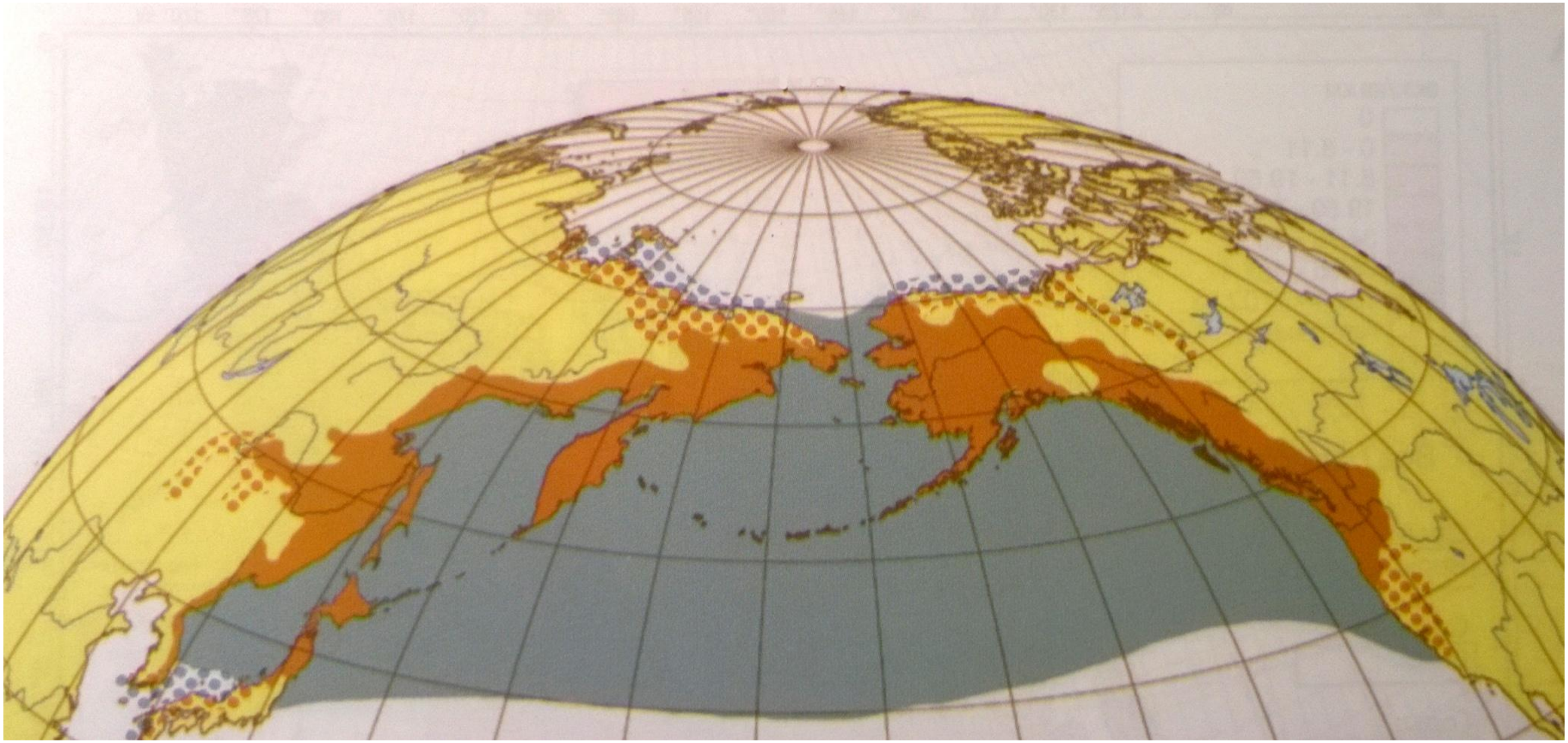
Populations

......

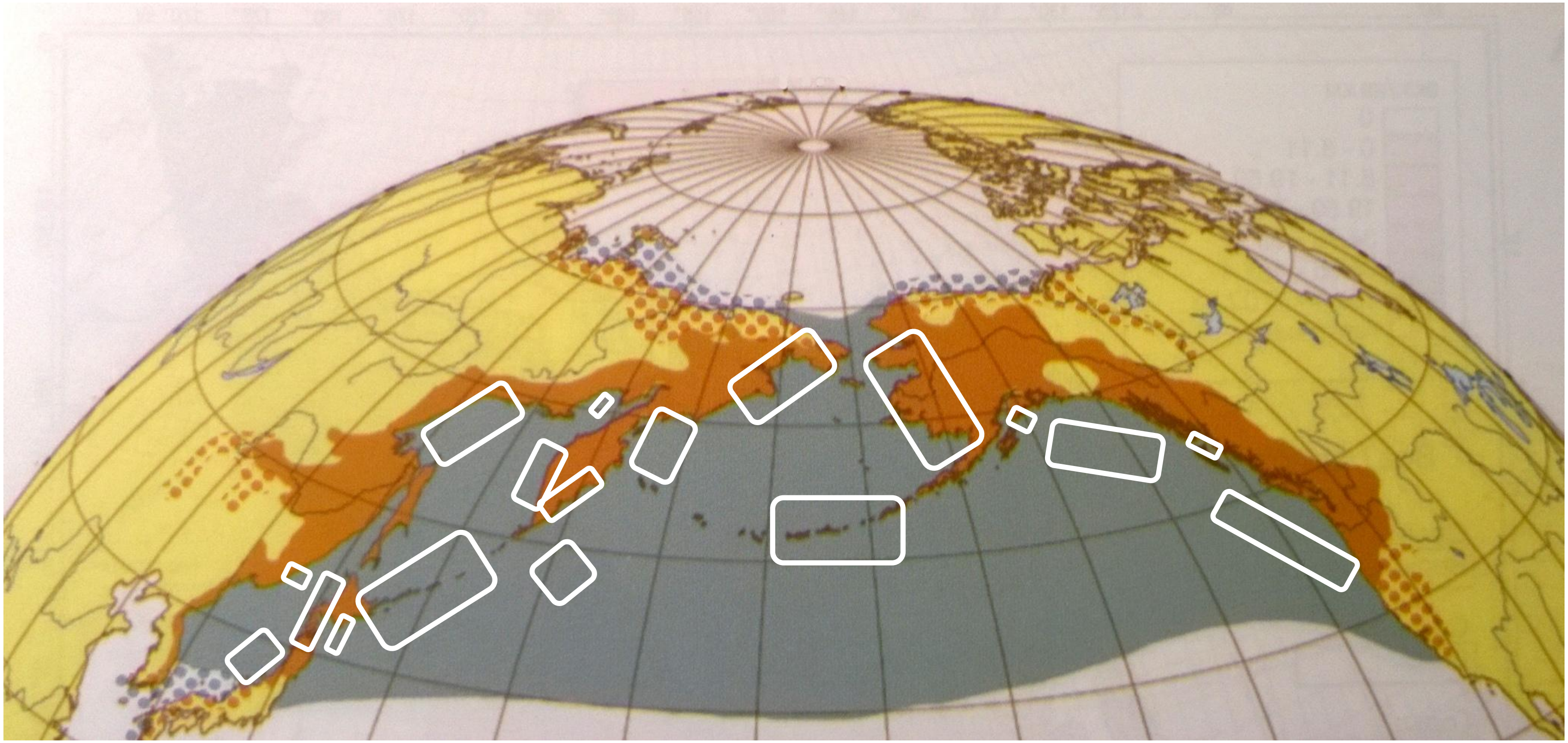
Populations

EGUs can be viewed as management units

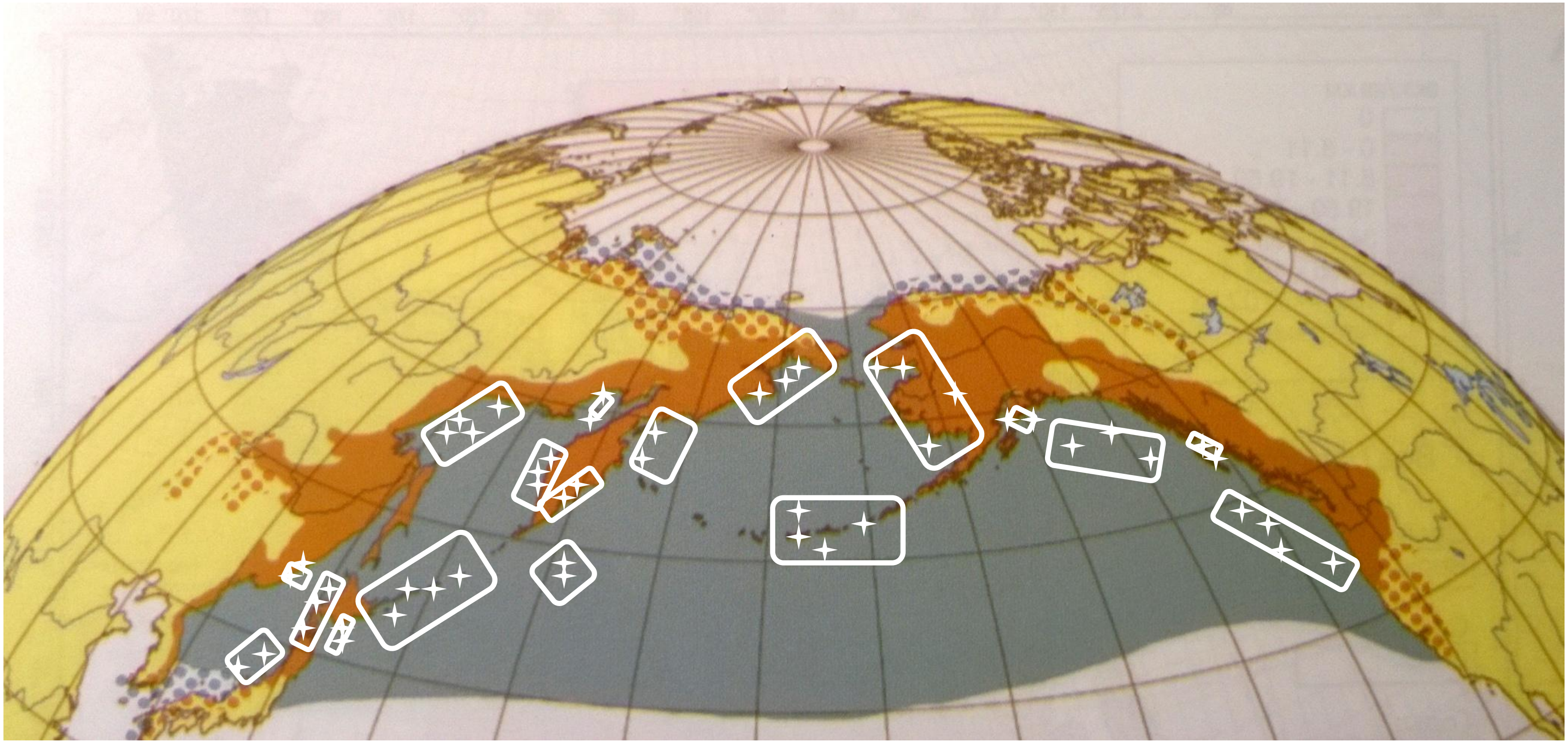




A possible logics for studying
species population structure
and selection of management units
(the dark is a species range):



Step 1. Subdivision of the species range into ecogeographic units (EGUs) based on environmental/ecological variables.



Step 2. Multiple samples (stars) from the EGUs for DNA- and other analyses

Step 3. Interpretation of the results obtained

Where are EGUs (MUs) in the open sea ?

Conclusions

- The biology of reproduction, migration, feeding, etc. should be studied ‘wider’ and ‘deeper’ to understand better the niche structure, i.e. environmental and ecological subdivision, of each key species of marine ecosystems.
- Ecogeographic units (EGUs) as nature’s ‘bodies’, based on environment / ecology features, can be used as proxies for management units.
- DNA data are necessary and important for checking, confirmation and modifying the population context of the management units.

Thank you!