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Demographic and evolutionary history of *Abies alba* in the pyrenees

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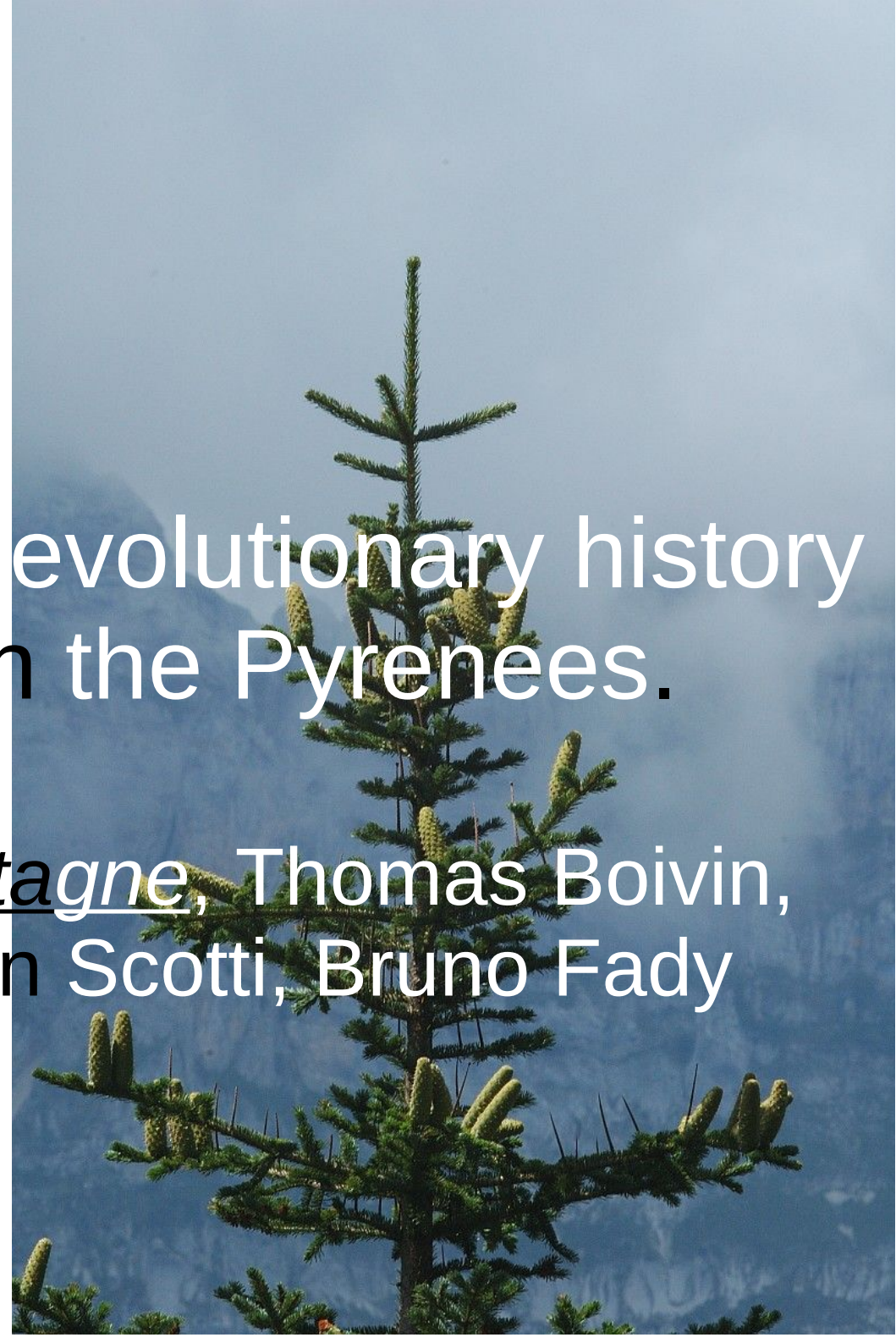
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Demographic and evolutionary history of *Abies alba* in the Pyrenees.

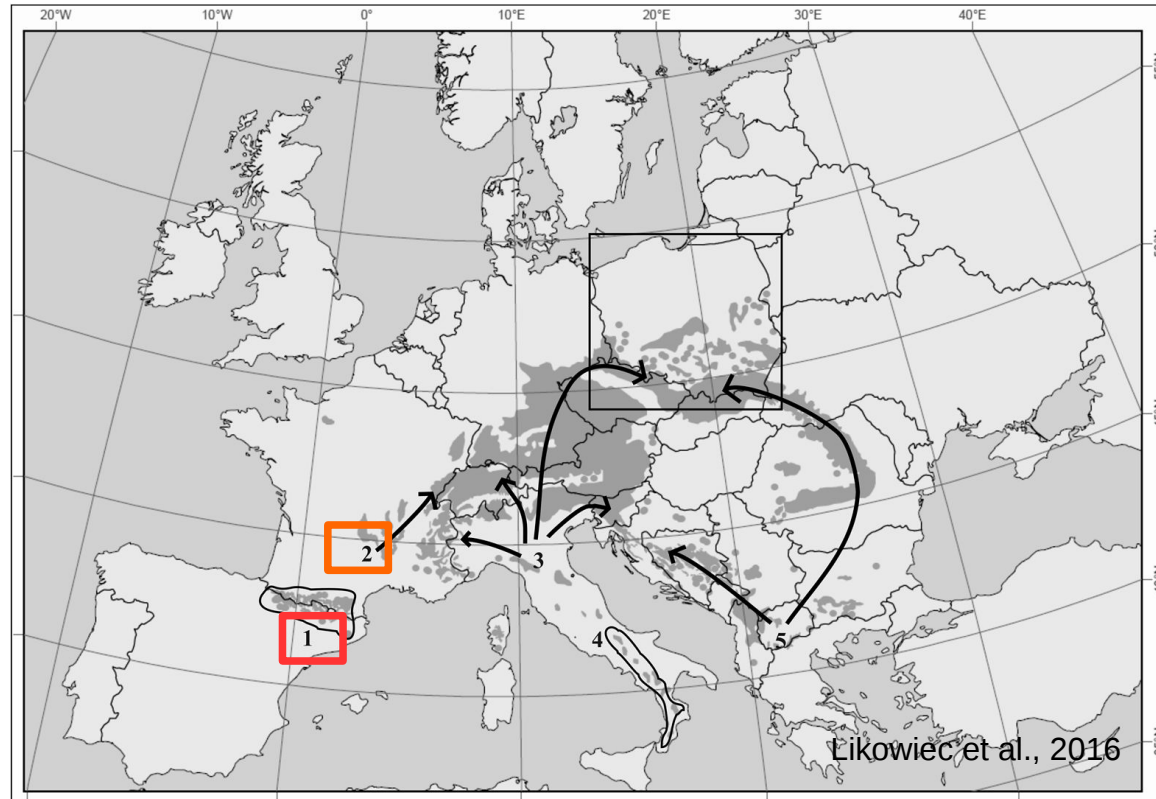
Caroline Scotti-Saintagne, Thomas Boivin,
Brigitte Musch, Ivan Scotti, Bruno Fady

**AFORGEN meeting - Kranjska Gora, Slovenia
21. -23. June 2018**



What do we know ?

Map of the current natural range and the location of hypothetical glacial refugia



1 Iberian Peninsula, Pyrenees; **2 Southwestern France**; 3 Apennine Peninsula, northwestern Italy; 4 Apennine Peninsula, southern Italy-Calabria; 5 Balkan Peninsula, the southern Balkans Massif and the most likely routes of postglacial recolonization (arrows) of Abies Massif in Europe.

Likowiec et al., 2016 (Poland)

Gomory et al., 2004 (Eastern Europe)

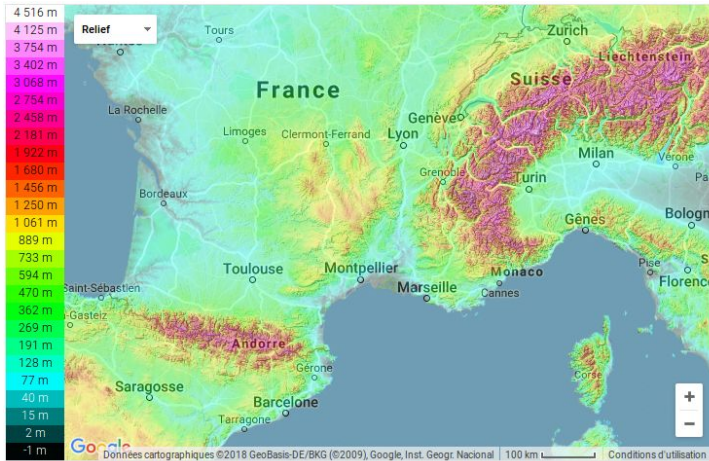
Liepelt et al., 2009 (Europe)

Sancho-Knapik et al., 2014 (Spain)

Belletti et al., 2017 (Italy)

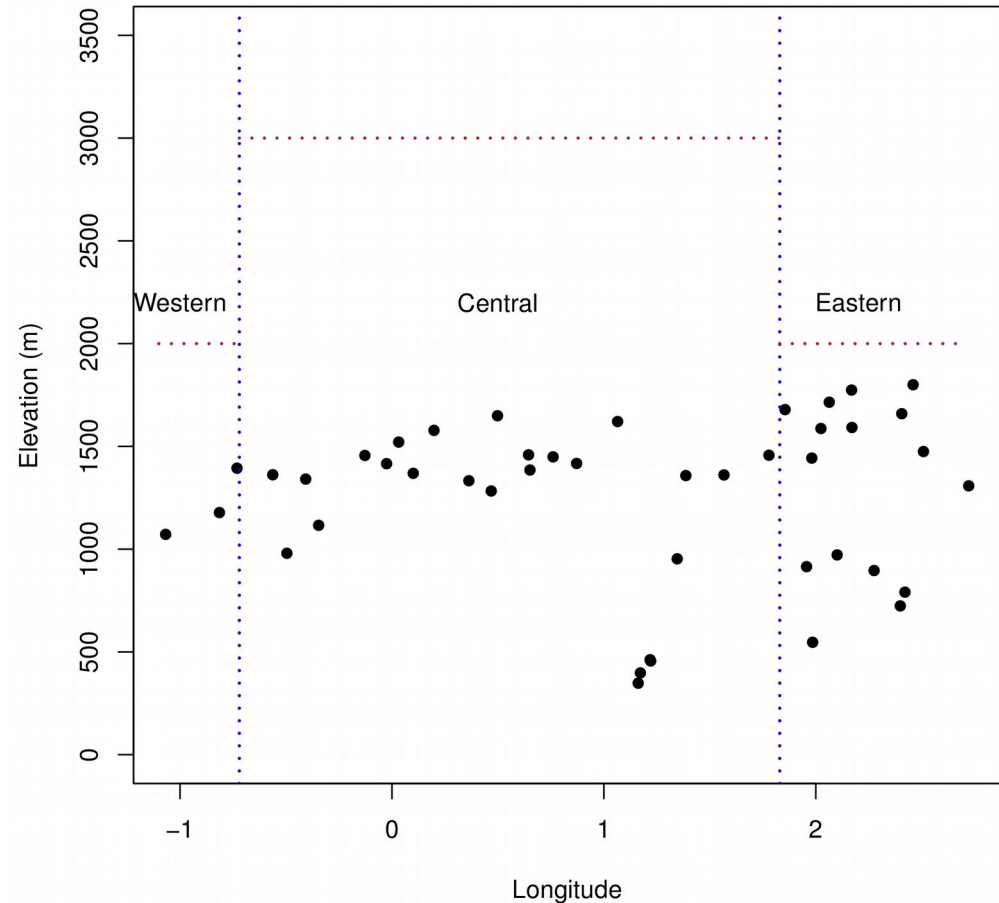
Piotti et al., 2017 (Italy)

Extensive sampling along the Pyrenees

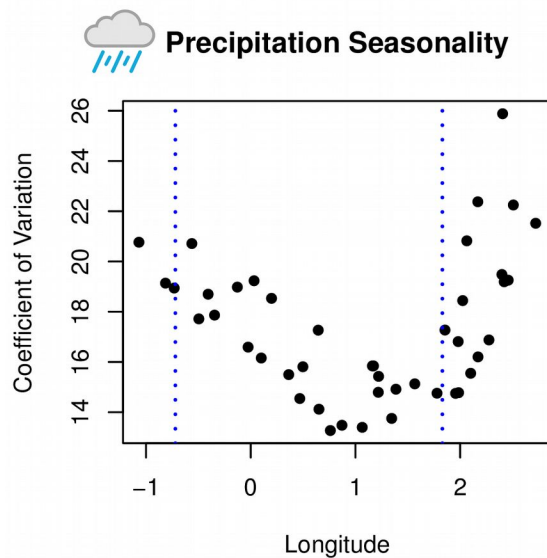
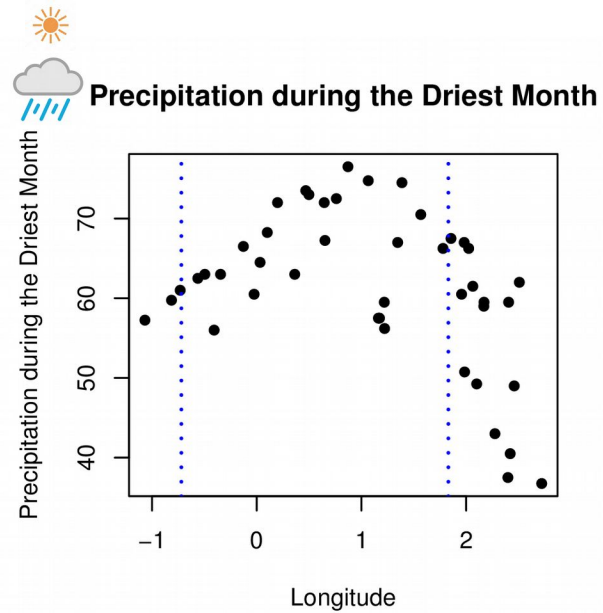
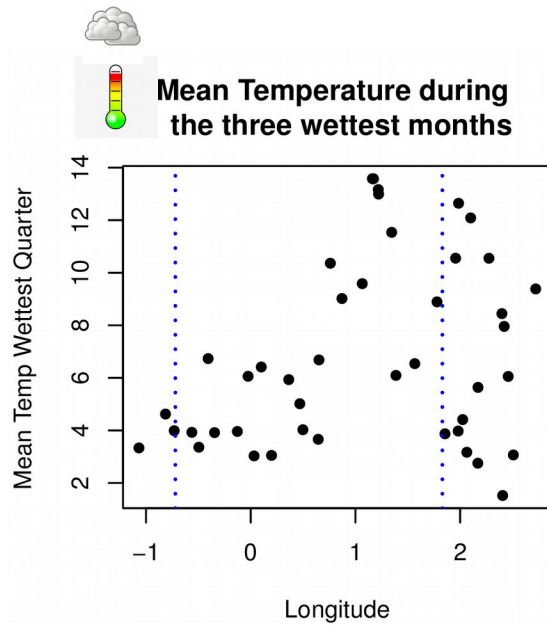


A barrier to south-north recolonization,
A long east-west mountain (450 Km) where
divergence can occur along geomorphological
and altitudinal gradients

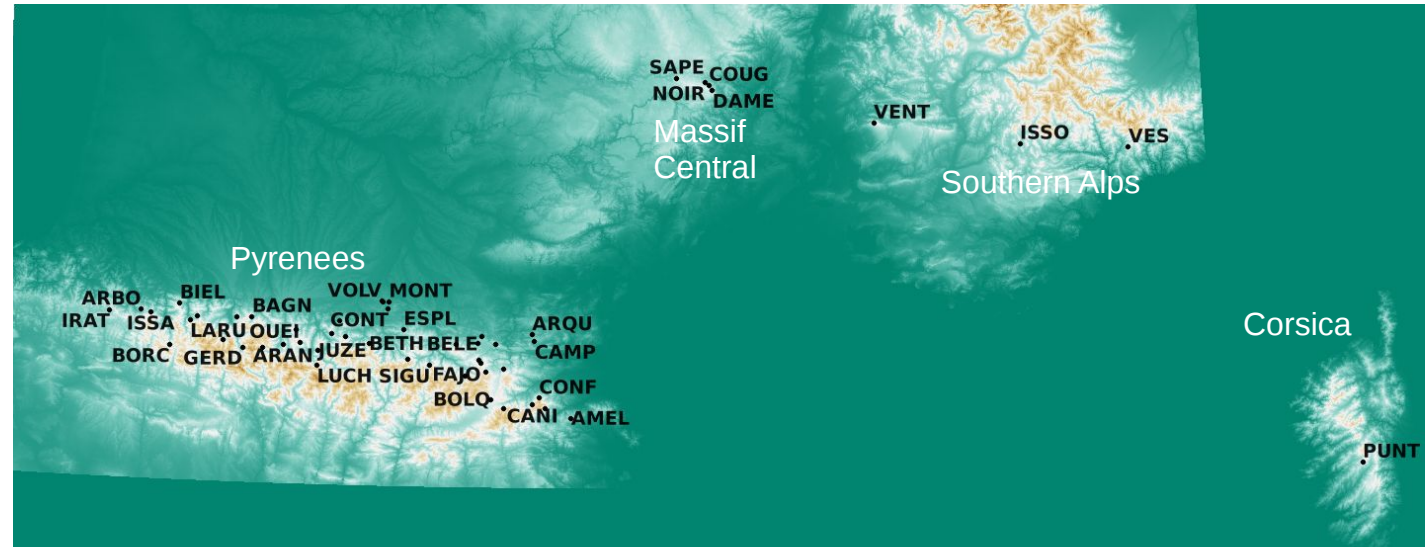
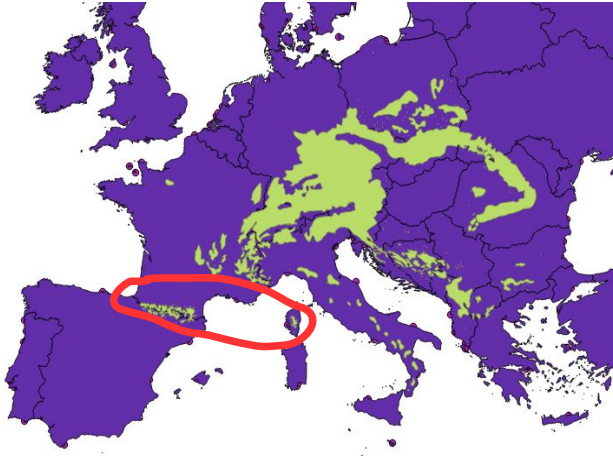
44 natural populations of *Abies alba* in three
geographic area of the Pyrenees



Climatic variation among the populations



Outside references have been added



Pyrenees : 44 natural stands x 30 samples

Central Massif : 4 sites x 30 samples

Southern Alps : 3 sites x 30 samples

Corsica : 1 sites x 30 samples

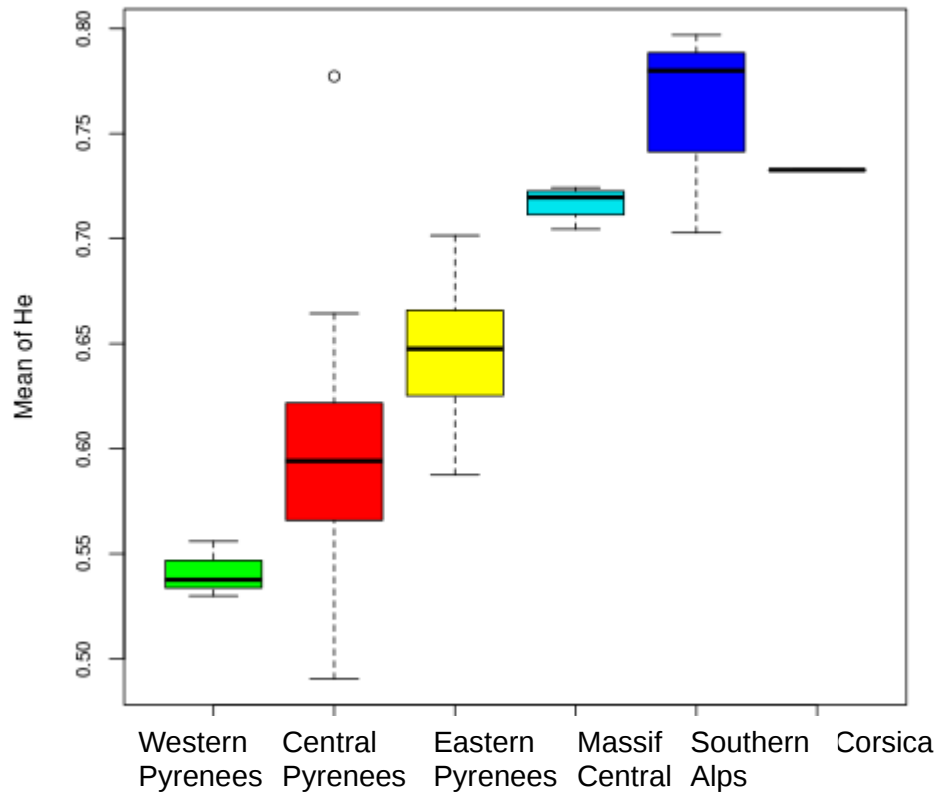
1655 individuals

10 nuclear SSR markers (Cremer et al., 2006, Hensen et al., 2005)
3 chloroplast SSR markers (Liepelt et al., 2001 ; vendramin & Ziegenhagen, 1997)

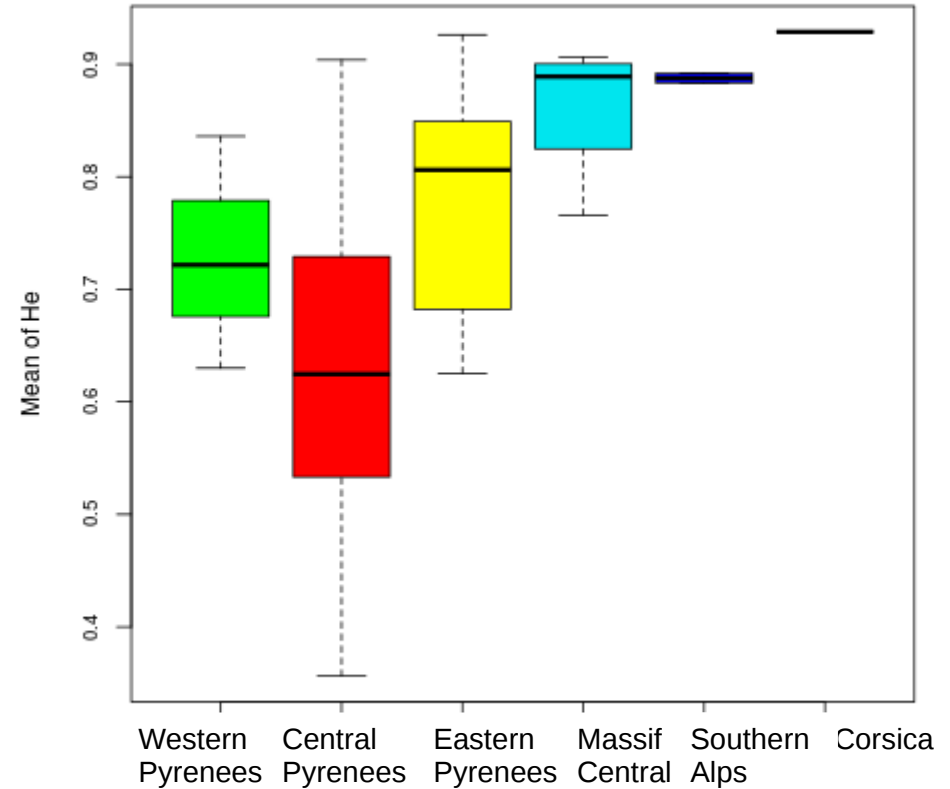


Pattern of Genetic diversity in the South-West *A. alba* distribution

Nuclear SSR



Cp SSR



GENETIC DIVERSITY / ENVIRONMENT

Genetic Diversity

N_a, H_e, H_o, F_i, P, Q

17 response variables

=

f (Environmental variables)

-Longitude, Latitude, Slope, Altitude, Orientation, seismography
-19 bioclimatic Variables (from Worldclim)



Present (0 y BP)

Mid-Holocene (6000 y BP)

Last Glacial maximum (22,000 y BP)

Last inter-glacial (120,000-140,000 y BP)

83 environmental co-variables

Conditional inference trees (see Hothorn et al. 2006 for methodological foundations), *ctree* R package partykit

Why ?

NON-Parametric tree-structure models of regression : applicable to all kinds of regression problems : nominal, ordinal, numeric, censored as well as multivariate response variables and arbitrary measurement scales of the covariate

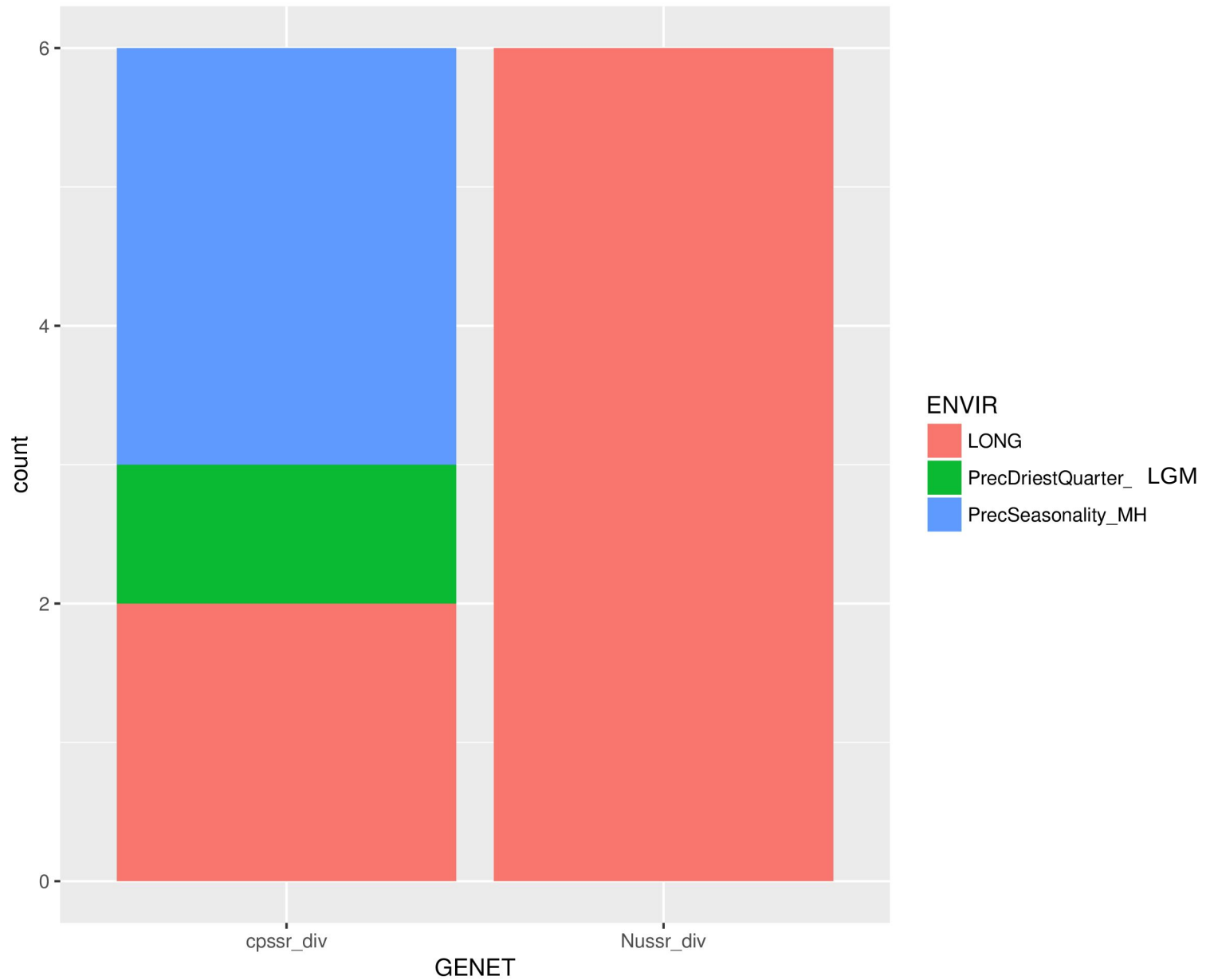
Useful when the sample size is small, but the number of predictors is large

The algorithm also **returns the p-values** that show how confident one can be about every split (permutations)

Stability assessment of variable and cutpoint selection are inspected using stabletree Package stablelearner (Philipp, M., Zeileis, A., and Strobl, C. (2016))

GENETIC DIVERSITY / ENVIRONMENT

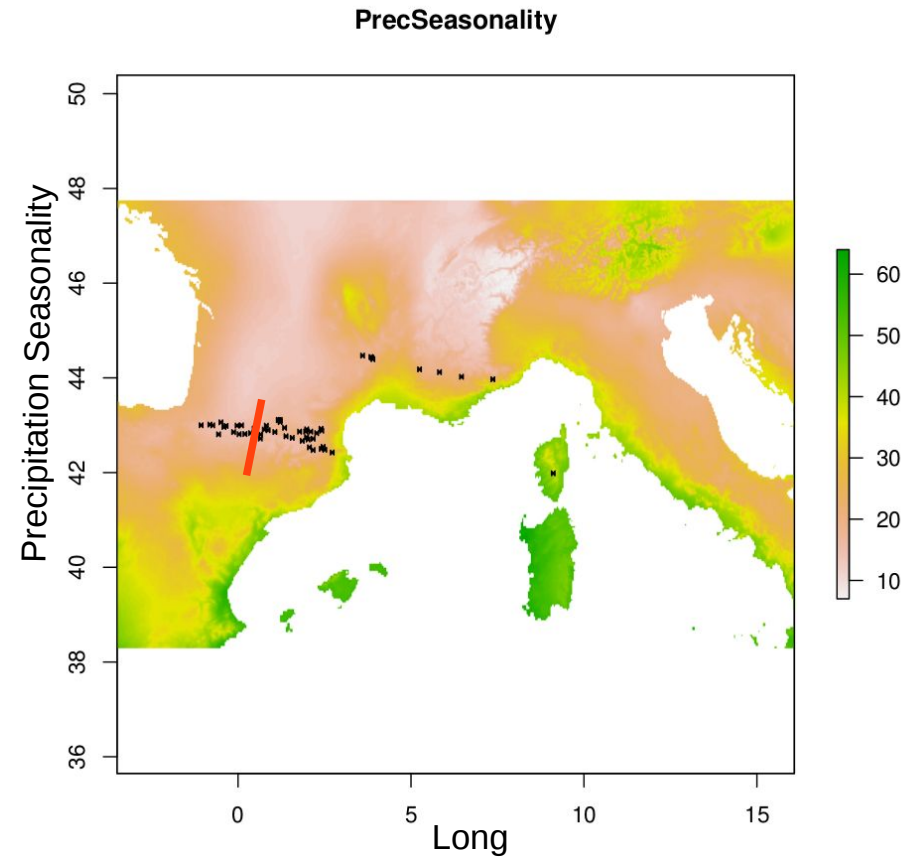
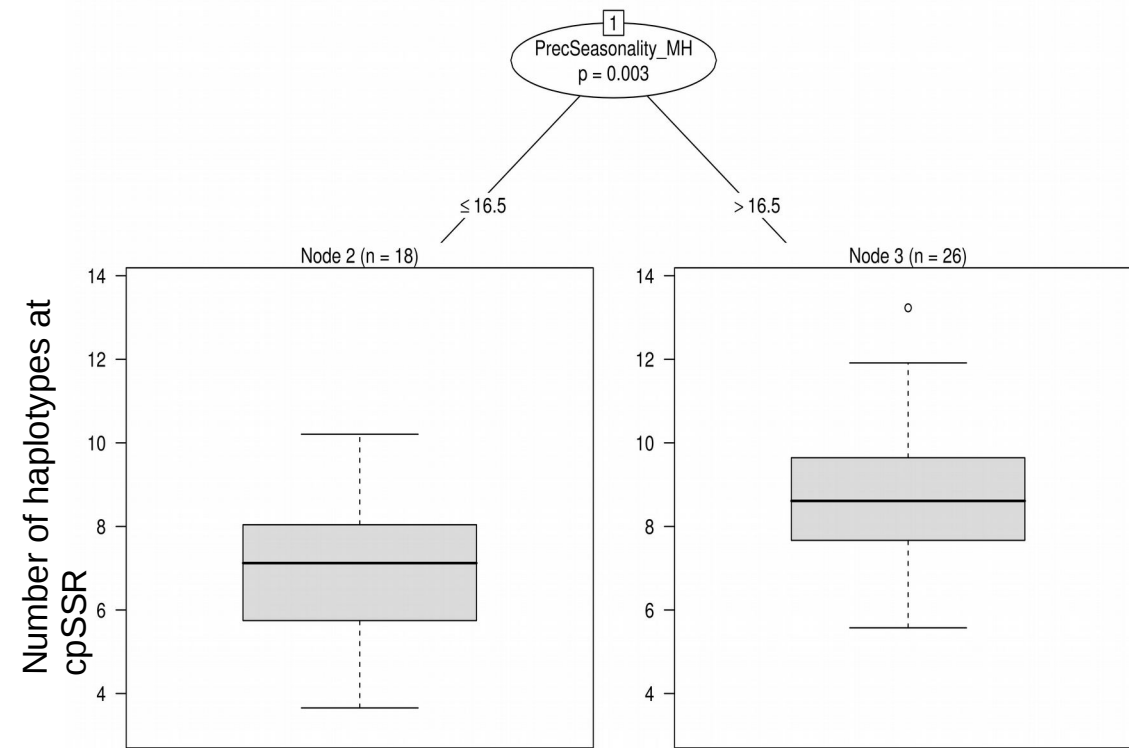
List of the environmental variables (among 83) having significant effect on the genetic variables (17) :
Based on 500 bootstrapping of conditional inference trees (ctree partykit R package; Strobl et al., 2008).



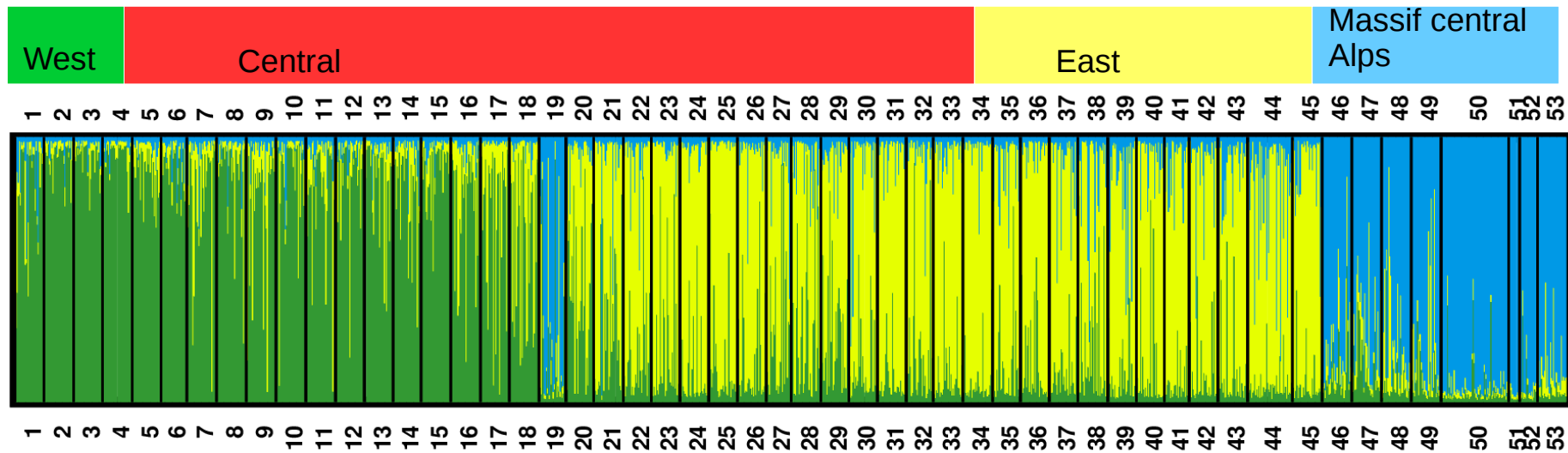
Genetic Diversity = f (Environmental variables)

Number of haplotypes at cpSSR

Precipitation seasonality during the mid holocene (about 6000 years ago)



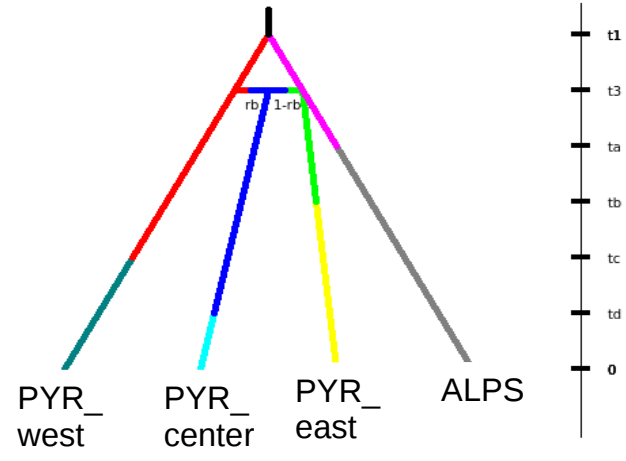
Two genetic cluster in the Pyrenees



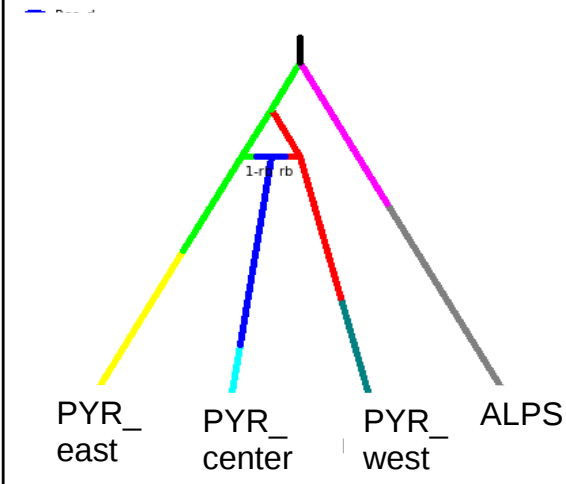
F_{ST}	Cluster	Cluster
Cluster	0.08	
Cluster	0.13	0.11

Which demographic scenario best explains the genetic parameters ?

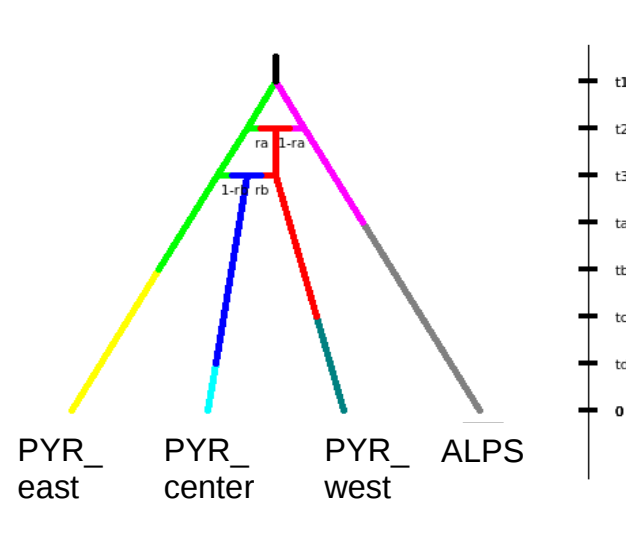
S1 : One split model + one admixture event



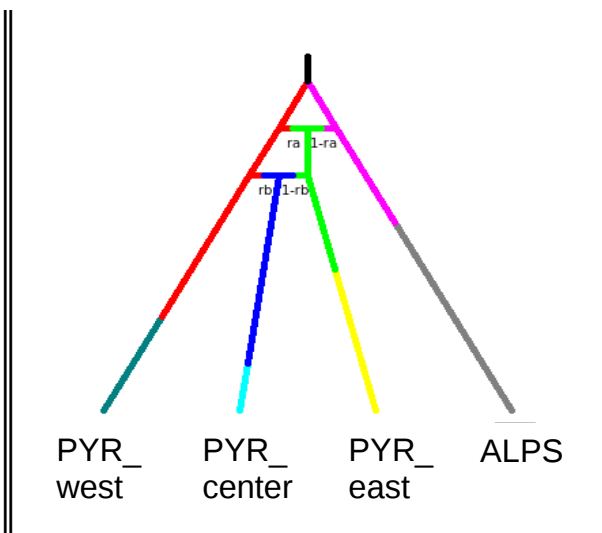
S2: Two split model + one admixture event



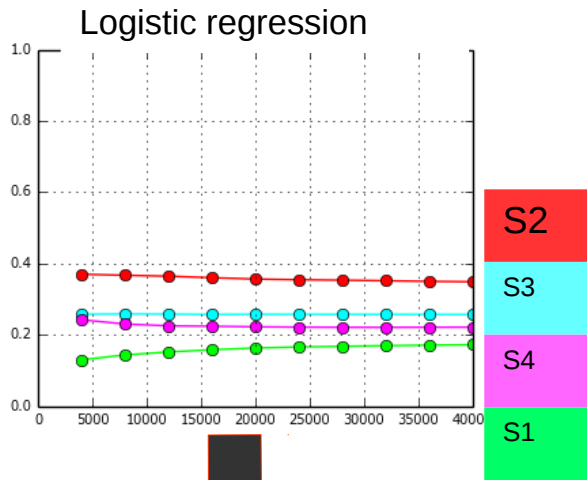
S3 : One Split + two admixture events



S4 : One split + two admixture events



Genetic diversity has been shaped during the mid Quaternary

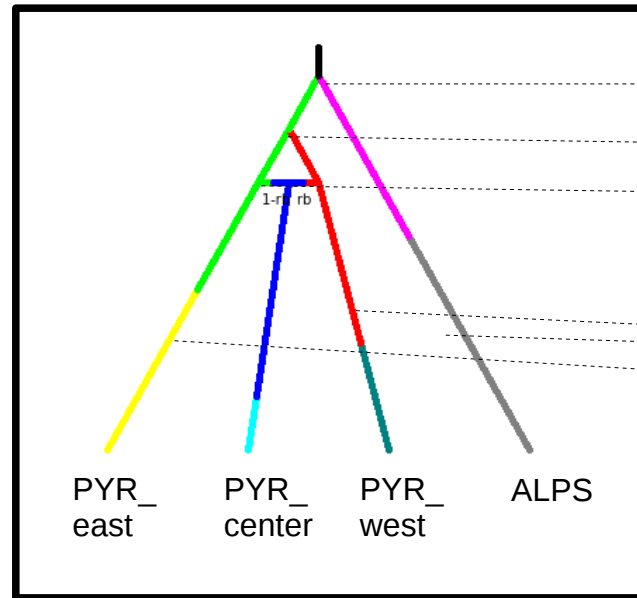


Small differences
But **S2** is the best

S2 : Two split model

+

one admixture event

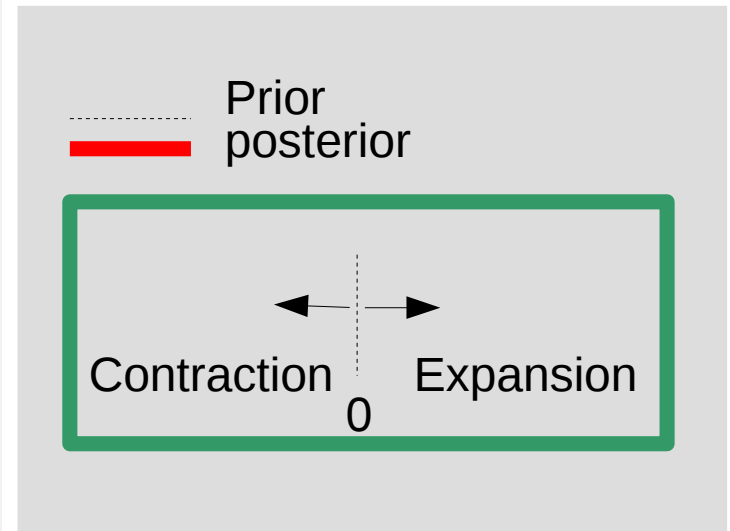
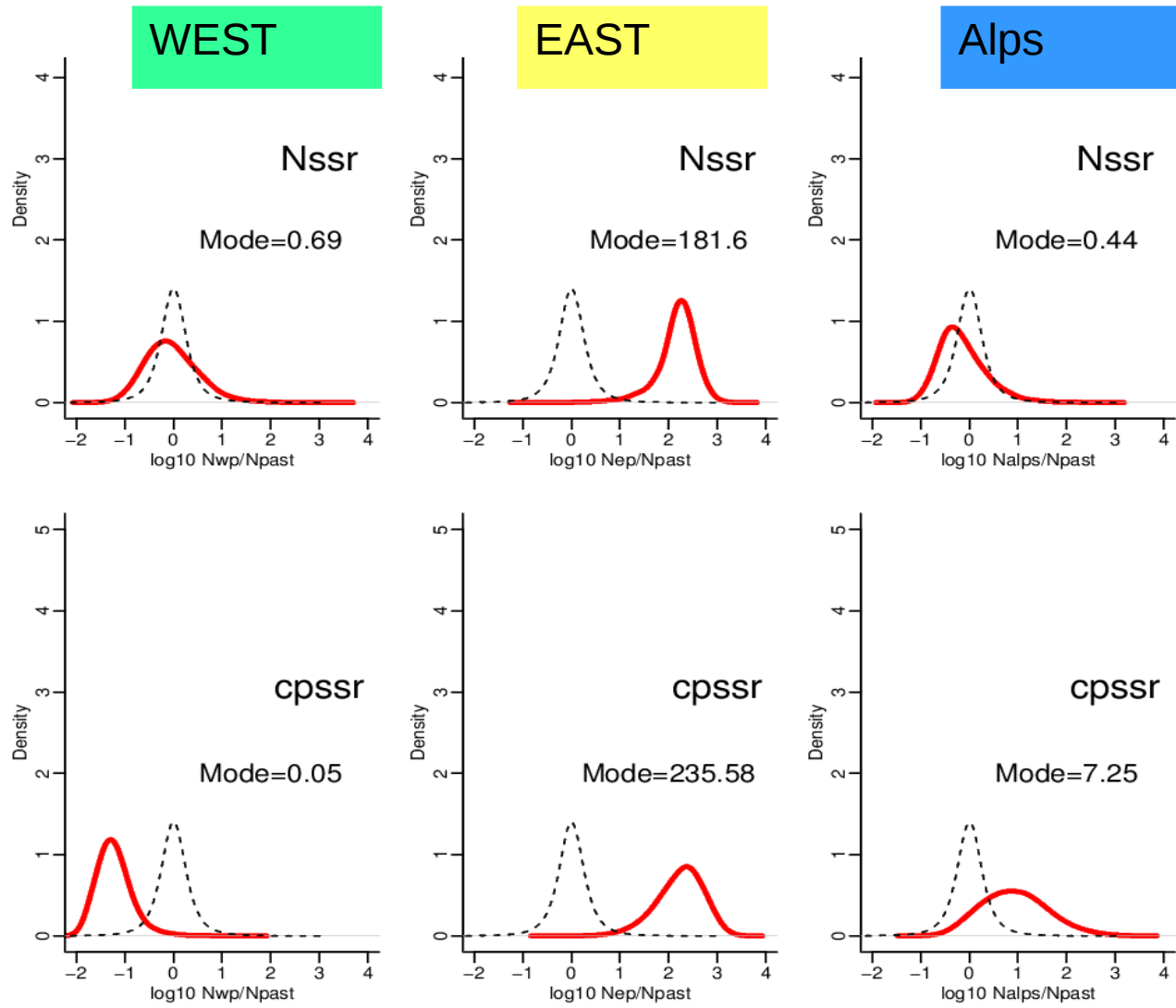


Event	Where ?	When ? generations	When ? millions years*
Split	Alps/Pyr	24253	1.2
Split	Pyr _w /Pyr _e	21909	1.09
merge	Pyr _w /Pyr _e	19936	0.99
Resizing	Pyr _w	14434	0.72
	Alps	13931	0.69
	Pyr _E	13707	0.68

*50 years for one generation

All the events happened over 10 322 generations (516100 years)
Between 0.65 and 1.2 Millions years : Pleistocene / Mid Quaternary

Different demographic signature among regions



Ratio of present-to-past theta :
 correctly represents ratios of effective population sizes.
 if constant mutation rates over time ($\mu_0 = \mu_1$)

$$r_0 = \theta_0 / \theta_1 = N_0 \mu_0 / N_1 \mu_1 = N_0 / N_1 \text{ (see Barthe et al., 2017)}$$

Conclusions



Pays Basque

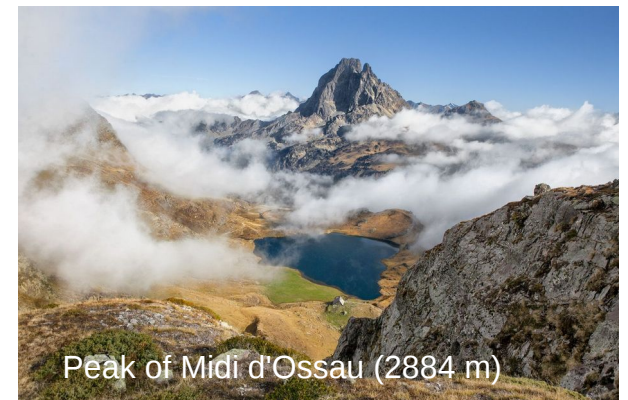
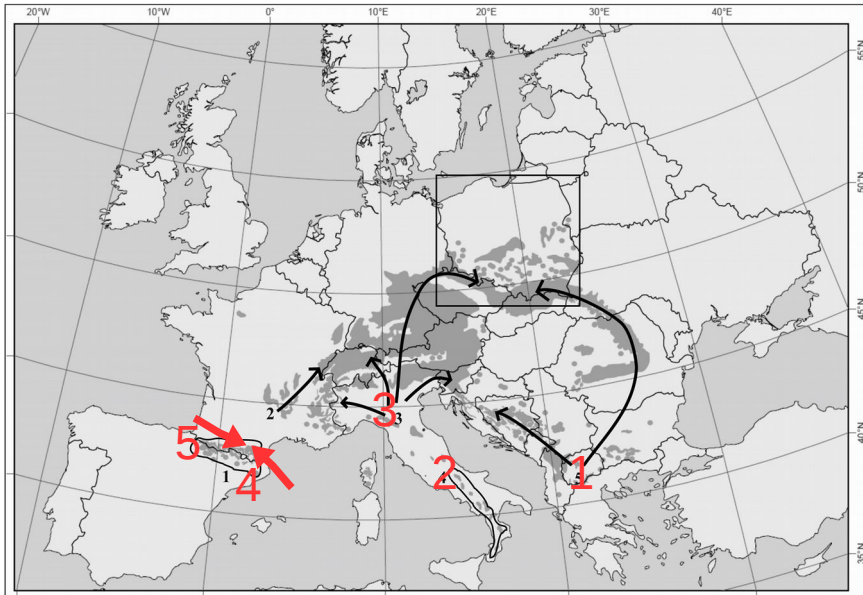
Genetic diversity organized in the Pyrenees according to the longitude and past climate ([precipitation](#) at [mid-holocene/LGM](#))

The split between genetic lineages and the merging events took place during the [Pleistocene](#)

Different demographies between East and West Pyrenees : [Contraction/Expansion](#)

Importance of the Pyrenees as a [refuge](#) : divergence system for European forest tree

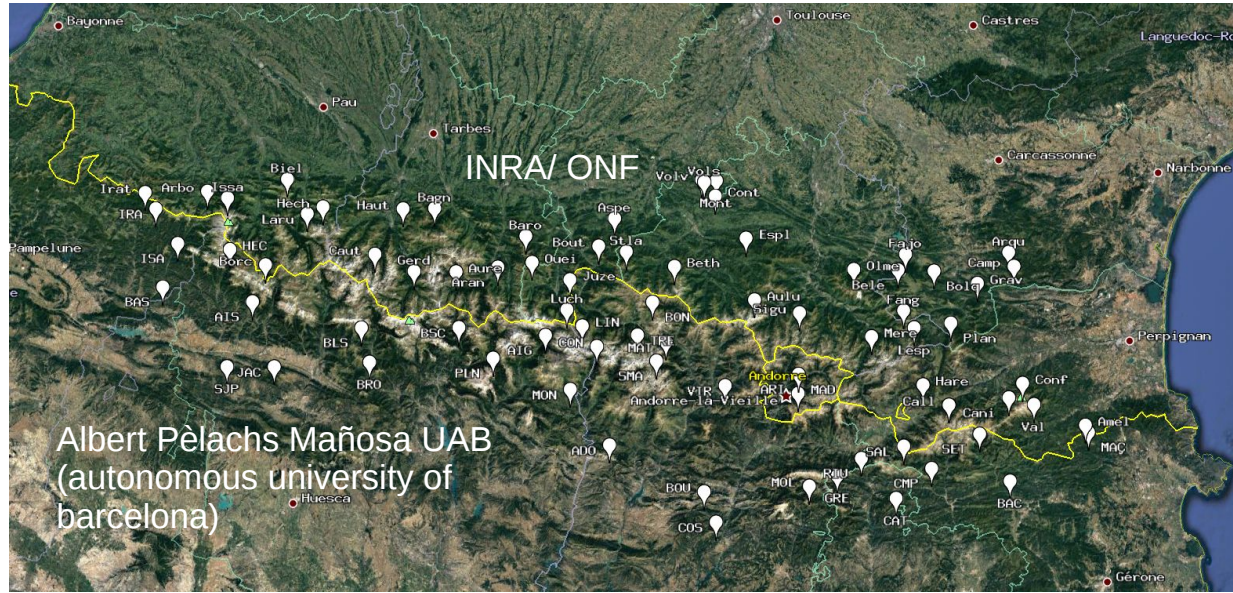
Importance of the Pyrenees as a [secondary contact zone](#) in central Pyrenees



Peak of Midi d'Ossau (2884 m)

Next...

NEXT : Sampling on the north and south faces of the Pyrenees



80 polymorphic SNPs in the Pyrenees (Roschanski et al.,2013, Brousseau et al., 2016; Roschanski et al.,2016)



Genomic -Transcriptomic platform of Bordeaux
Sequenom analysis

Thank you !

