Subsampling as an economic consequence of using whole genome sequence data in landscape genomics: how to maximize environmental information from a reduced number of locations?

**Kevin Leempoel**, Sylvie Stucki, Stéphane Joost Laboratory of Geographic Information Systems (LASIG), Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland

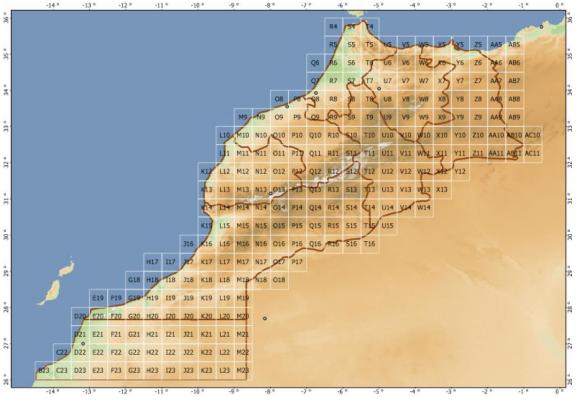
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# **NEXTGEN** project in Morocco

Objectives

- Whole Genome Sequence of sheep and goat
- Identify SNPs under selection
- Assess which environmental variables are significant
- Determine if SNPs under selection occur in the same genes in both species



Stucki 2014

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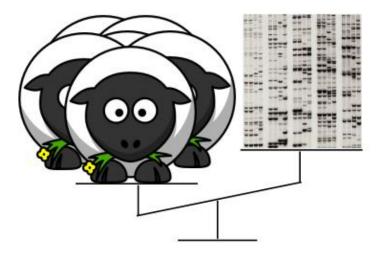
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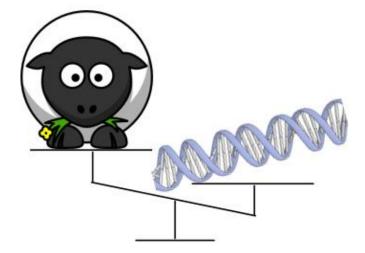
# WGS : a constraint for landscape genomics studies

Genetic markers (ex. AFLP, microsatellites)

Whole Genome Sequencing (WGS)



1000 individuals / 10 - 1000 markers



100 individuals / 10 000 markers

Adapted from Stucki 2014

Requires a careful choice of individuals to sequence



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# Identifying relevant variables and sampling strategy

Sampling on a regular grid

3 farms in each cell, 3 individuals per farm

1283 sheeps and 1412 goats reduce to 164 per species

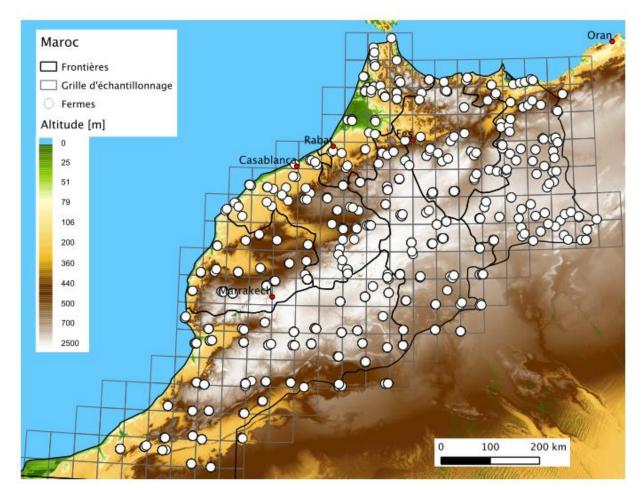
Climatic variables obtained from CRU (resolution : 10')

- Temperature
- Pluviometry

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Solar radiation



Adapted from Stucki 2014

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# A stratified sampling methodology to maximise environmental information

<u>Principal component analysis</u> of the entire set of variables (117)

allows to choose samples as different as possible

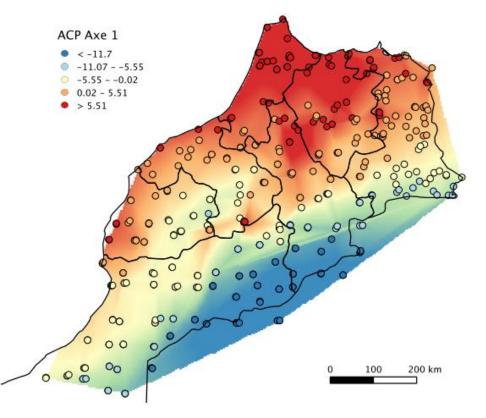
96% of the variance explained by the first 7 axes of the PCA

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Adapted from Stucki 2014



# A stratified sampling methodology to maximise environmental information

Hierarchical agglomerative clustering

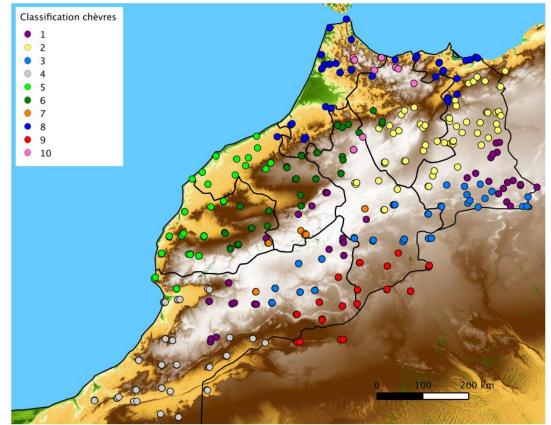
Classification in function of the climatic conditions

Index of spatial distribution to have samples as evenly distributed as possible

Resulted in regroupement based on spatial and altitudinal proximity

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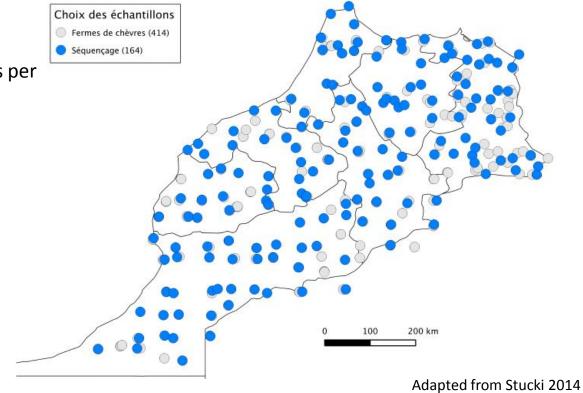


Adapted from Stucki 2014



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### Chosen sheeps



Resulted in a sample of 164 individuals per species.

Representativeness of races was also considered

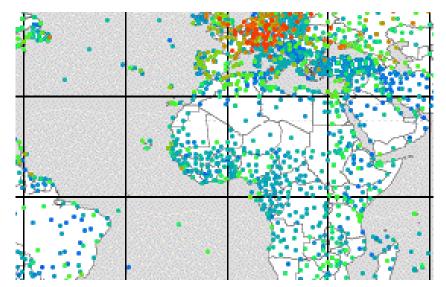
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# Reliability of environmental data in function of scale



Weather stations used in CRU datasets

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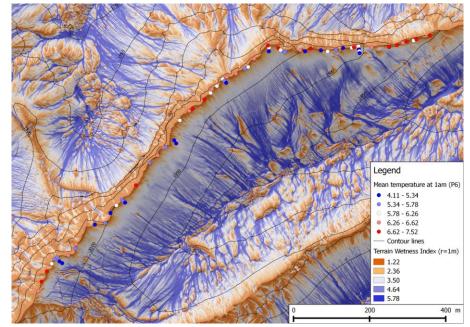
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Relevance of using multi-scale VHR DEM-derived variables in landscape and evolutionary ecology as a surrogate for important climatic variables such as humidity and temperature

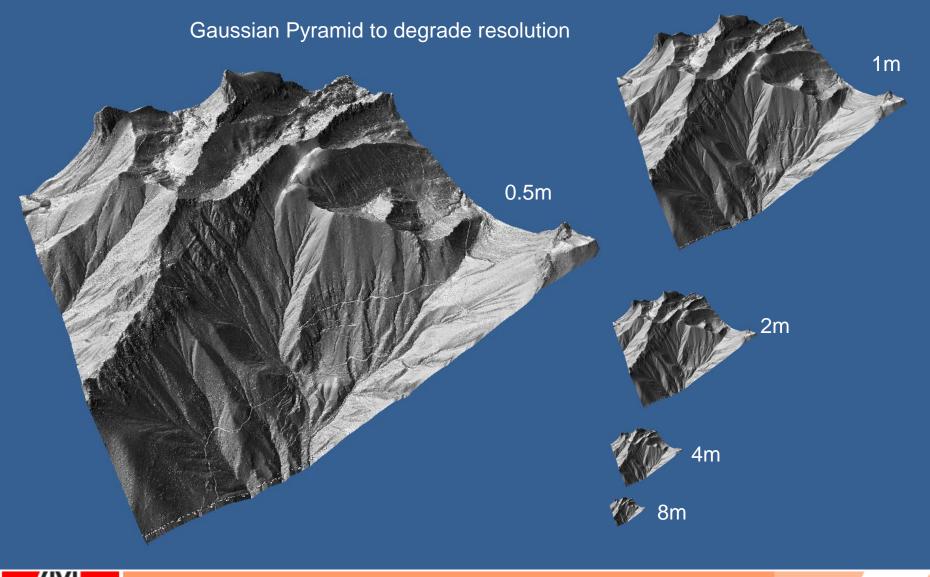
(Leempoel et al., hopefully in 2014)

- Distance to weather stations
- Precision and resolution of DEMs
- Artefacts in remote sensing data



Les Rochers-de-Naye (CH)



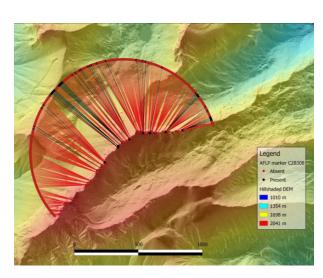




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# <u>At which scale do they matter ?</u>



## Les Rochers-de-Naye

- Local scale (1.5km)
- Alpine plant

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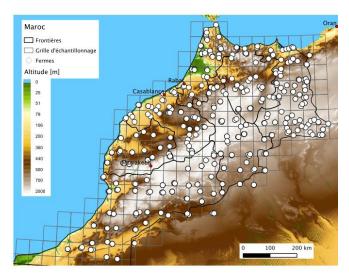
Multi-resolution



Adapted from Lassueur et al. (2007)

### <u>UrbanGene</u>

- Local scale (10x10km) ٠
- Urban plant ٠
- Resolution and window size .



### **NEXTGEN Morocco**

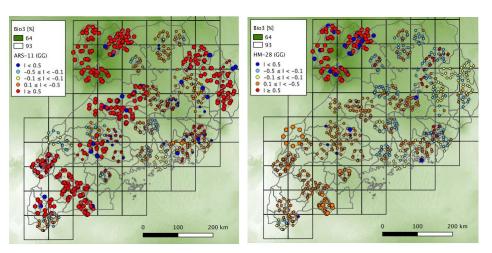
- Regional scale (800x600km)
- Sheeps and Goats
- Resolution and window size

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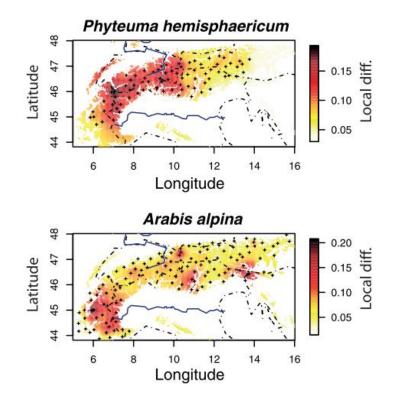
# Exploiting spatial tools to analyse the scale and spatial component

- Local index of spatial association (LISA)
- Geographically weighted regression (GWR)
- LocalDiff



Univariate LISA

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Heatmap of **local genetic differentiation** computed across the Alps

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# Thank you for your attention







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