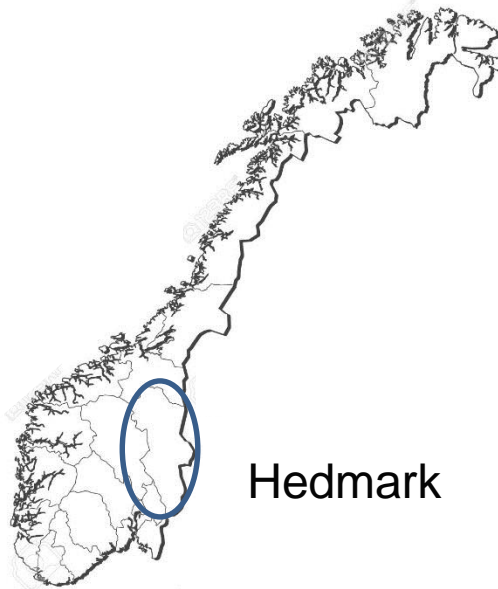


# Use of DNA technology to define moose populations for management

Simen Pedersen, Kjartan Østbye, Kim Præbel and Ole A. Bakmann.

# Background



Hedmark

400 km

# Background

- Migratory moose
- High elevation in summer, move to winter ranges at lower altitude
- Crosses management borders and landowner borders on the way

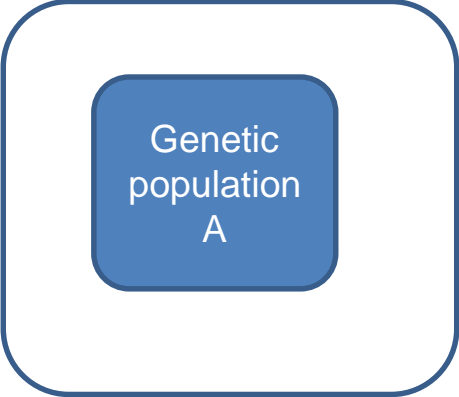


# Background

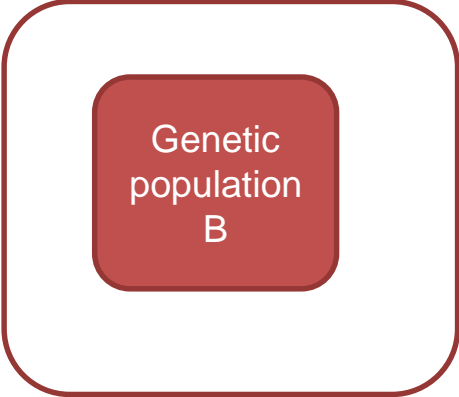
- Biological vs Administrative borders
- Improve cost and benefit sharing among landowners
- GPS collaring may document migration and spatial distribution – but is costly
- Could the use of DNA be a cheap alternative?



# Genetic population vs. management units



Genetic  
population  
A



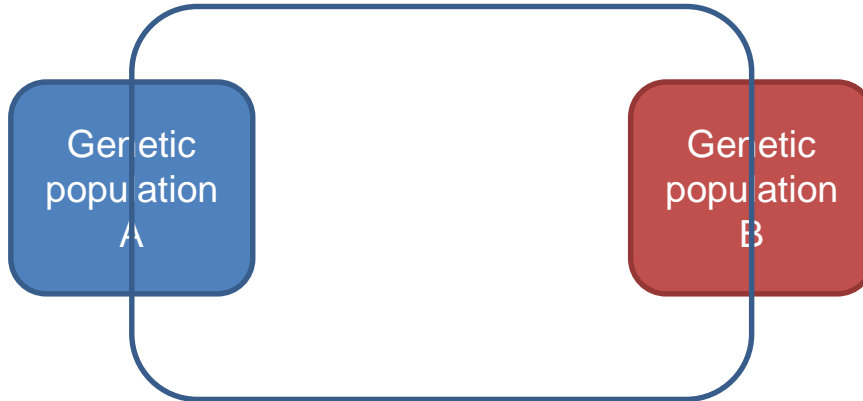
Genetic  
population  
B

# Genetic population vs. management units

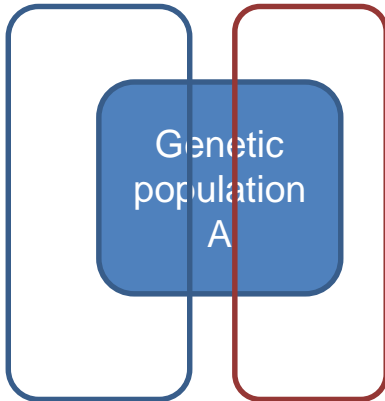
Genetic  
population  
A

Genetic  
population  
B

# Genetic population vs. management units

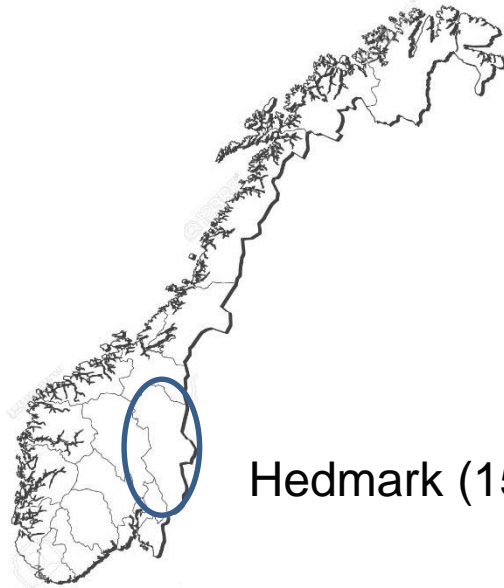


# Genetic population vs. management units



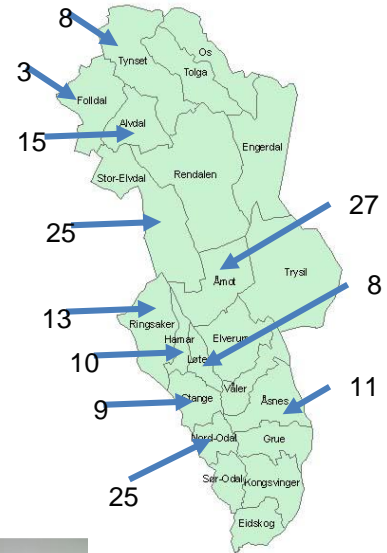


# Methods: Tissue sample collection in 2015



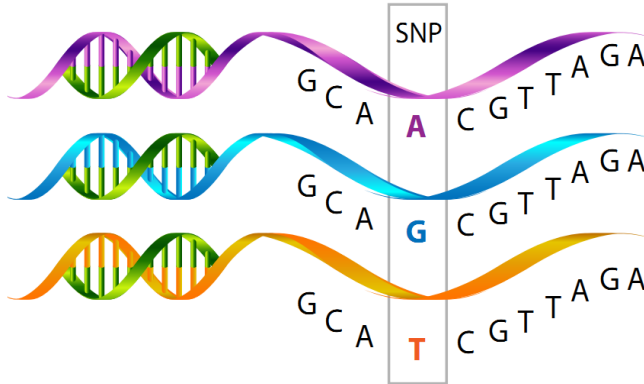
400 km

Hedmark (154 samples)



# Methods

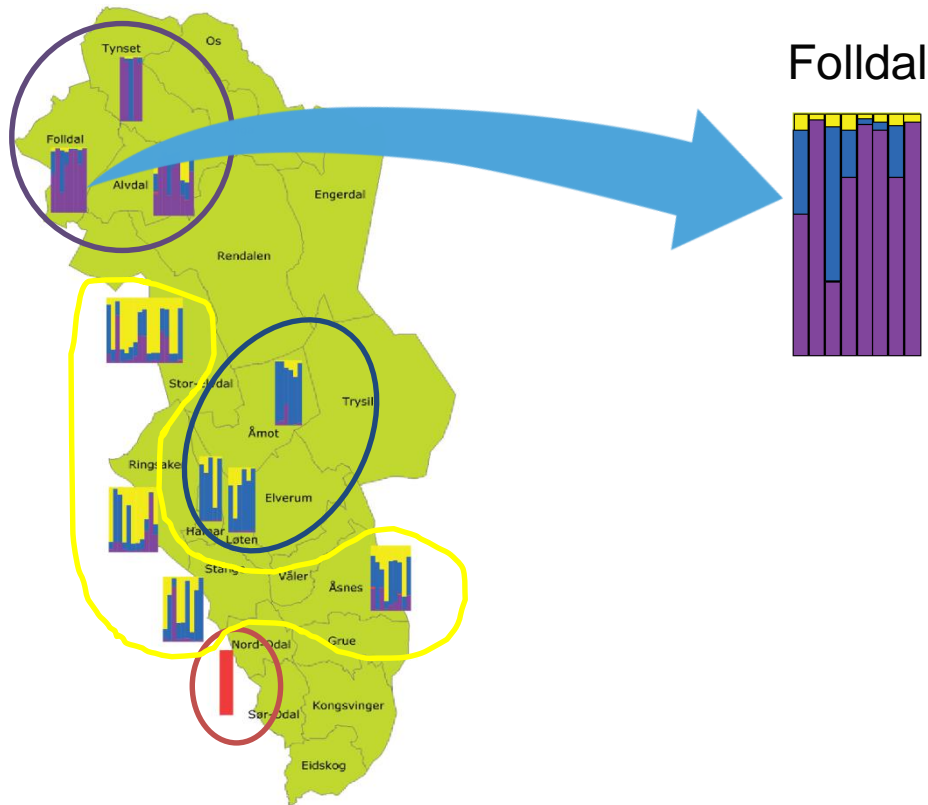
- Single Nucleotide Polymorphism (SNPs)



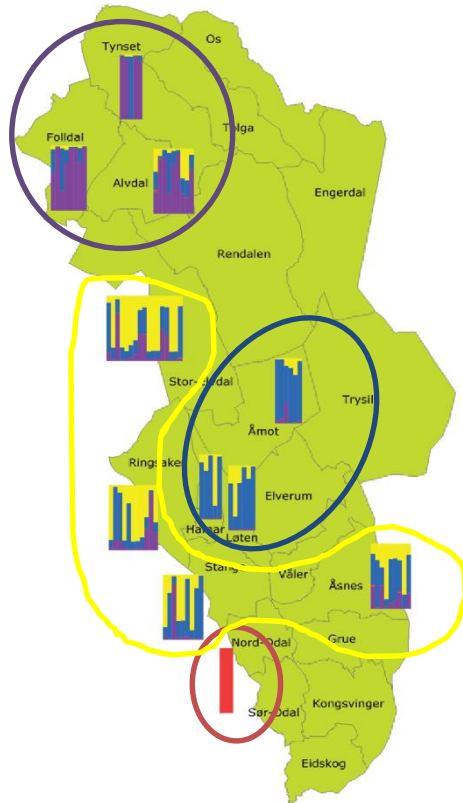
# Methods

- Defining how many populations we have in our sample material (STRUCTURE)
- Defining which population the individual moose belong to

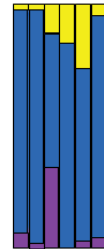
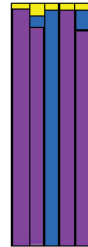
# Results



# Results - immigration

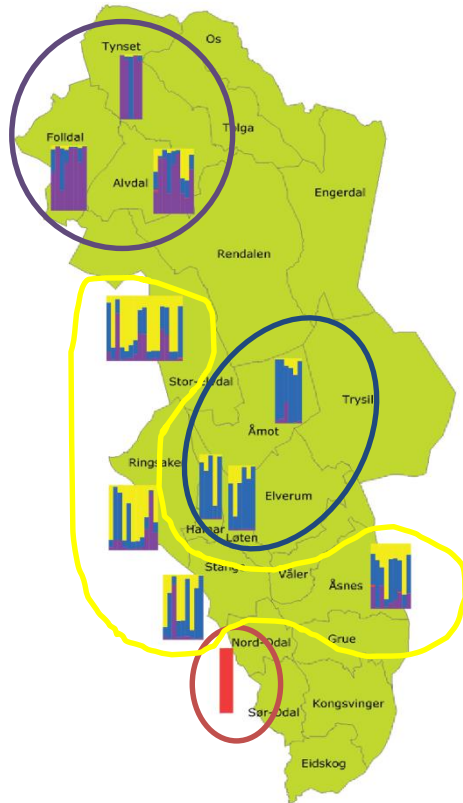


Tynset

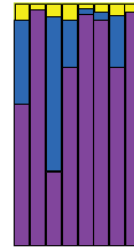


Eastern

# Results - hybridization

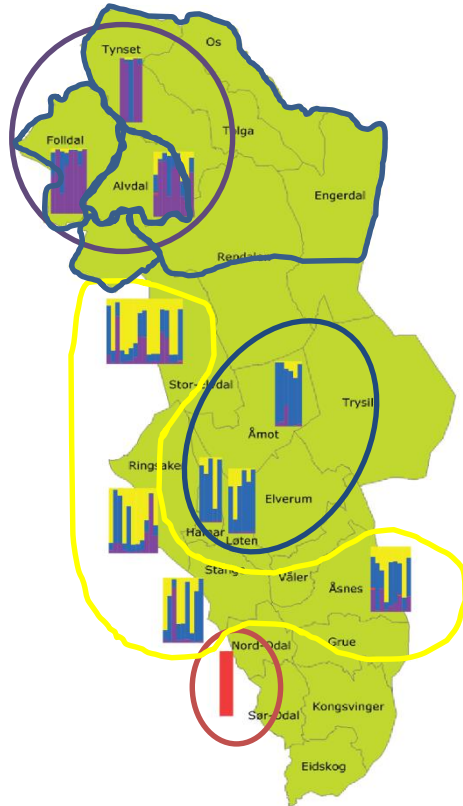


Folldal



F1 Hybrid

# Results – management units



# Discussion

- Cheaper alternative to collaring – maybe interesting for management?
- Higher correspondance between administrative and biological borders
- Better cost/income sharing among landowners?
- A tool for monitoring individual dispersal in relation to Chronic Wasting Disease?





Thank you!

