



# Comparing two techniques for rapid assessment of brown bear abundance in Romania

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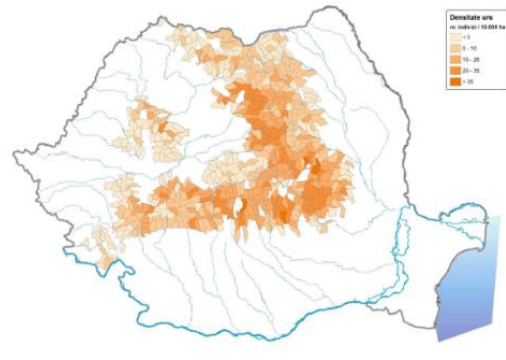




# Bears in Romania



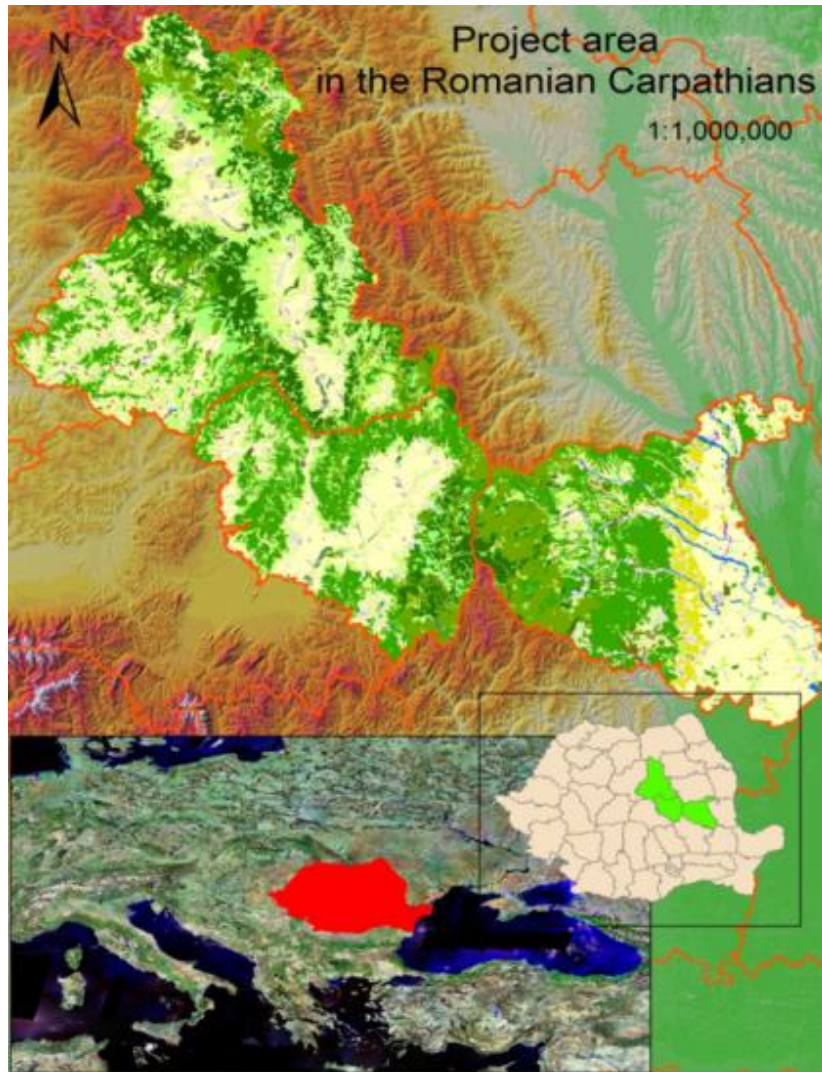
- Species: Brown bear (*Ursus arctos*)
- Distribution area: approx. 69 000 km<sup>2</sup>
- Population size: approx. 6 000 individuals
- Legal status: protected (since 1997)
- Conservation status: LC (IUCN)



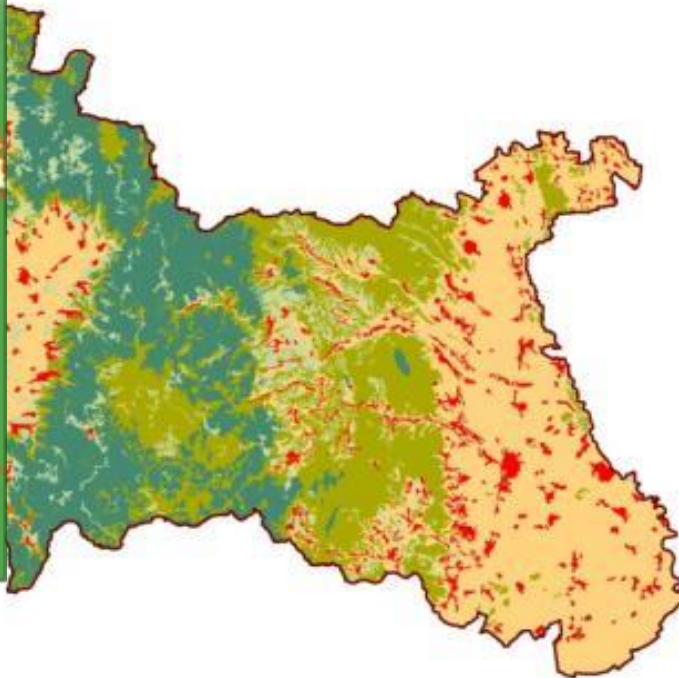




# Study Area



15 196 km<sup>2</sup> - approx. 20% of the estimated total bear distribution area in Romania





# Context of the study

- ❑ high uncertainty around brown bear (*Ursus arctos*) abundance in the Romanian Carpathians,
- ❑ current estimations of abundance do not rely on modern statistical techniques, and lack uncertainty estimates.







# Goal of the study



To test the use of two cost-effective sampling techniques for estimating brown bear abundance from unmarked individuals in an occupancy framework.

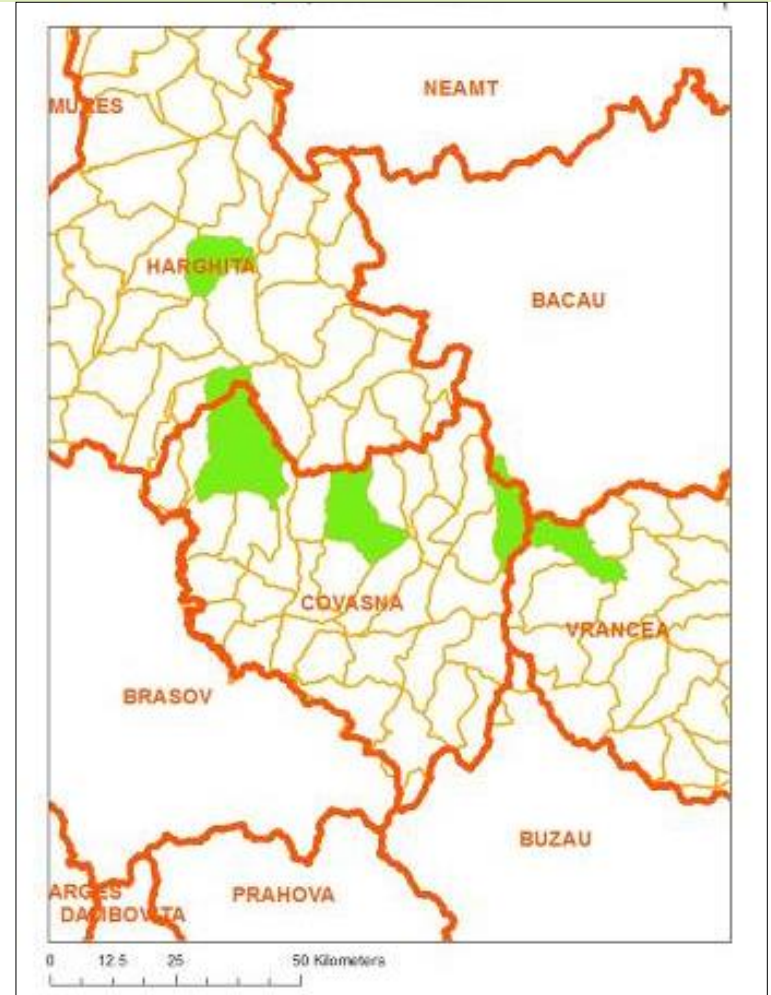




# Study period and Pilot sites

Total surface of the pilot sites 446 sqkm

Season 1 -Spring 2011  
Season 2 - Fall 2011  
Season 3 - Spring 2012





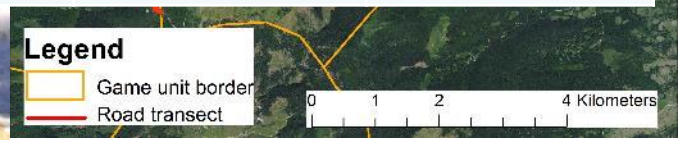
# Methodology

## (1) Track Counts on 2-km forest road segments



Session no.	Transects no.	Visit no./session	Number of total visits	Transect lenght	Km.
I	28	3	84	2	168
II	34	5	170	2	340
III	34	5	170	2	340
<b>Total</b>					848

02/12/2011

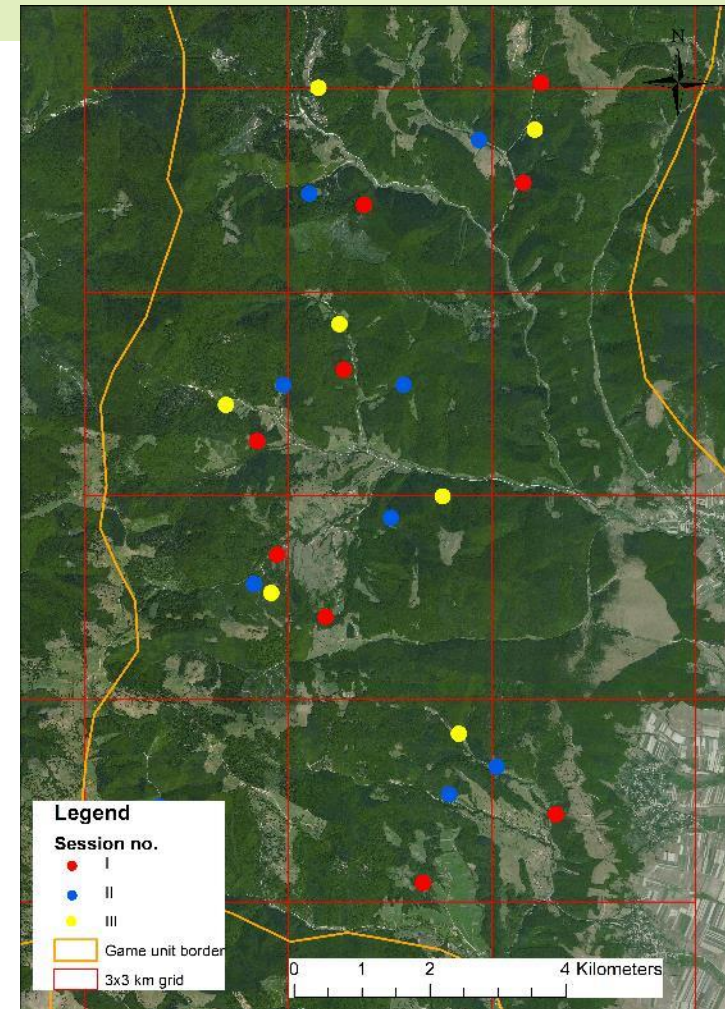
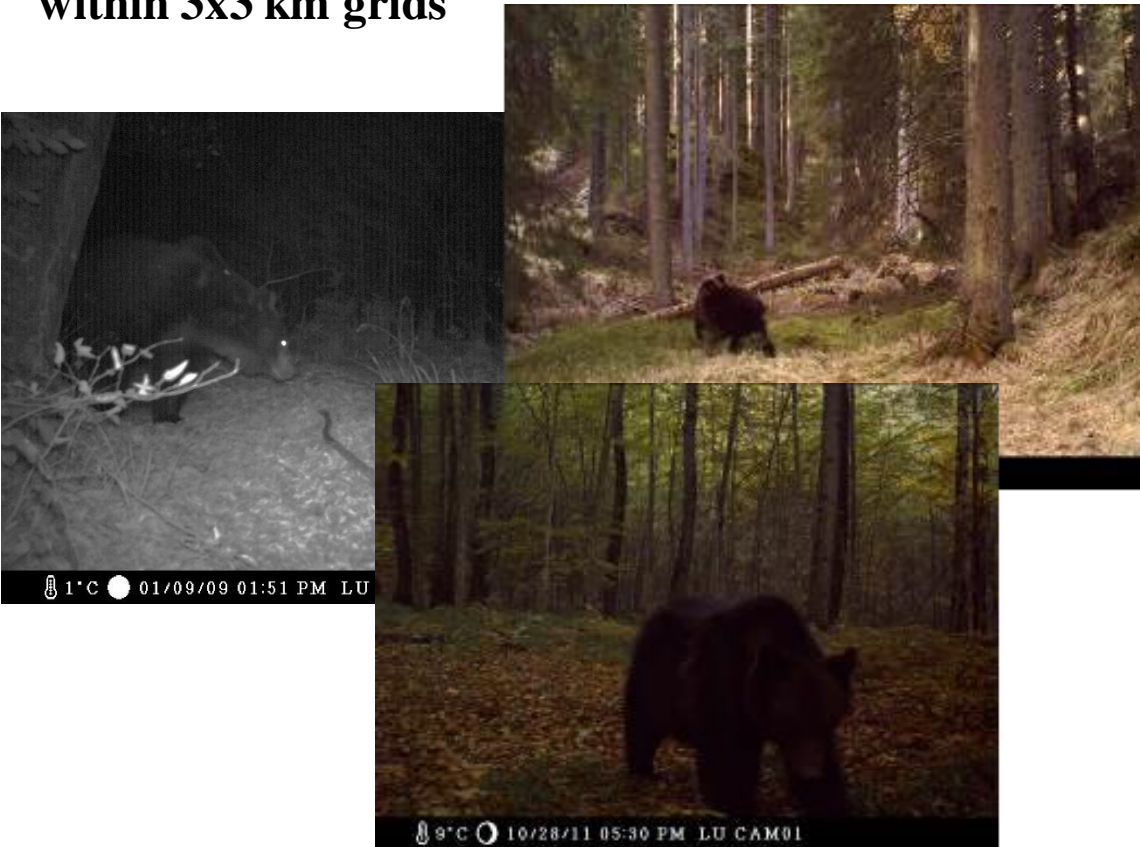






# Methodology

## (2) Detection/Non-detection at camera traps within 3x3 km grids







## R 2.15.2 program, package *unmarked*

- ❑ **Road transect** data - “Royle Biometrics” models for count data (Function *pcount*).
- ❑ **Camera trap** data - “Royle-Nichols” models for binomial data (Function *occuRN*)

Variables for modeling abundance		Variables for modeling detection	
Hunting Management Unit		Julian Day	Day since January 1 <sup>st</sup>
Altitude		Substrate (RT only)	(mud, snow, dry)
Forest Type		Snow Depth (RT only)	
Percent agricultural lands (CT only)		Forest Type (CT only)	
Percent pasture (CT only)		Slope (CT only)	



# Results

## Detection history

Method		Sampling occasions		
		Season 1 - Spring	Season 2 - Autumn	Season 3 - Spring
Camera Traps	# Detections	15	22	25
	# Non-Detections	105	98	94
	Detections %	<b>12.5%</b>	<b>18.3%</b>	<b>21.0%</b>
Road transects	# Detections	55	41	87
	# Non-Detections	25	96	94
	Detections %	<b>68.7%</b>	<b>29.9%</b>	<b>48.1%</b>





# Results

**Variables used to model abundance had low explanatory power.**

## **Example: Transect data Season 2**

Model	K	$\Delta AIC$	AICwt	CumAICWt	R-squared
<b>Abund(ForestType) , p(SnowDepth)</b>	<b>5</b>	<b>0.00</b>	<b>0.4908</b>	<b>0.49</b>	<b>0.133</b>
Abund(1) , p(SnowDepth)	3	1.11	0.2817	0.77	0.000
Abund(MgtUnit) , p(SnowDepth)	5	1.77	0.2027	0.98	0.089
Abund(Altitude) , p(SnowDepth)	4	7.25	0.0130	0.99	0.000
Abund(Altitude+ForestType) , p(SnowDepth)	6	8.14	0.0084	1.00	0.000
Abund(MgtUnit+Altitude) , p(SnowDepth)	6	9.93	0.0034	1.00	0.000



## Bear abundance per transect/camera trap grid

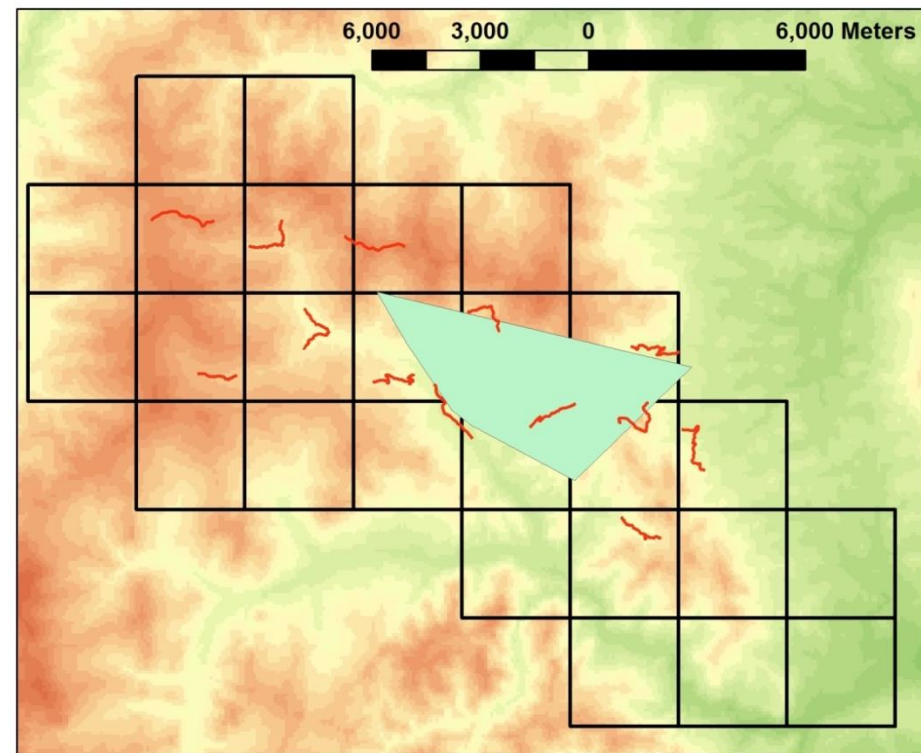
		Spring 2011	Fall/Winter 2011	Spring 2012
<b>Camera Trap data</b>	Mean abundance per camera station	-	<b>1.29</b>	<b>2.78</b>
	90% Credible Interval	-	0.40 – 2.97	0.74 – 5.41
<b>Transect data</b>	Mean abundance per transect	<b>1.34</b>	<b>1.65</b>	<b>1.43</b>
	90% Credible Interval	0.96 – 2.44	0.75 – 3.30	0.88 – 2.56



## Inferring bear densities from transect data

Effective sampling area of each transect unknown, BUT we estimated *post hoc*:

- Seasonal Home Range size from an independent telemetry dataset (10 bears) =  $14 \pm 2.1 \text{ km}^2$  (95% CI = 10 – 18 km<sup>2</sup>) → 1 – 2 grid cells
- There is home range overlap (estimated >1 individual per transect),
- Thus, ADDING UP ABUNDANCES PER TRANSECT IS WRONG





## ASSUMPTION

***Effective sampling area = mean home range size (14 km<sup>2</sup>)***

	Season 1	Season 2	Season 3
<b>Mean abundance per transect (and 90% CI)</b>	1.34 0.96 – 2.44	1.65 0.75 – 3.30	1.43 0.88 – 2.56
	↓	↓	↓
<b>Density per 100 km<sup>2</sup></b>	10 7 – 17	12 5 – 23	10 6 – 18





# Conclusion



Preliminary results as a first step



The following step – DNA methods



***Thank you!***

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