



Distributions of farms in 2030

A combined Markov Chain and generalized linear model approach

Christiansen, Lasse Engbo

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Distributions of farms in 2030

A combined Markov Chain and
generalized linear model approach



Lasse Engbo Christiansen

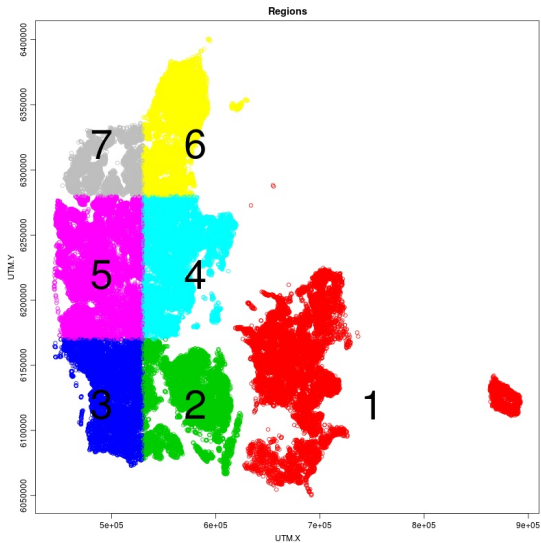
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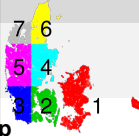
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Overview

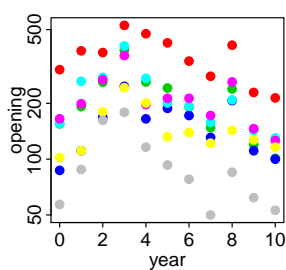
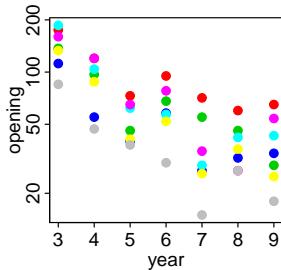
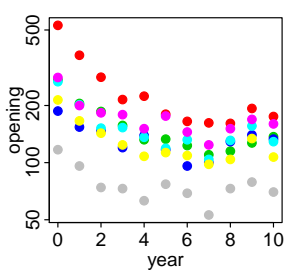
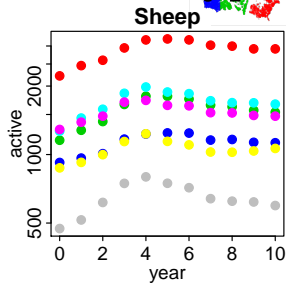
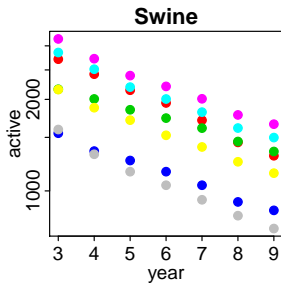
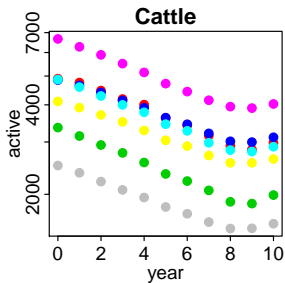
- Looking at data
- Transition probability matrices
- Prediction of new farms
- Results

Data - Definition of regions



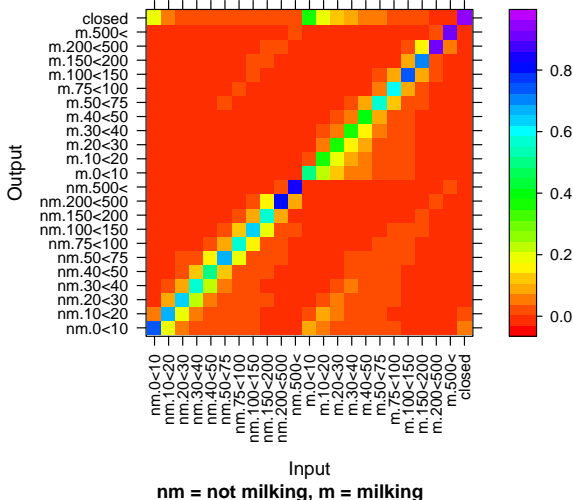


How many farms are there per year and region



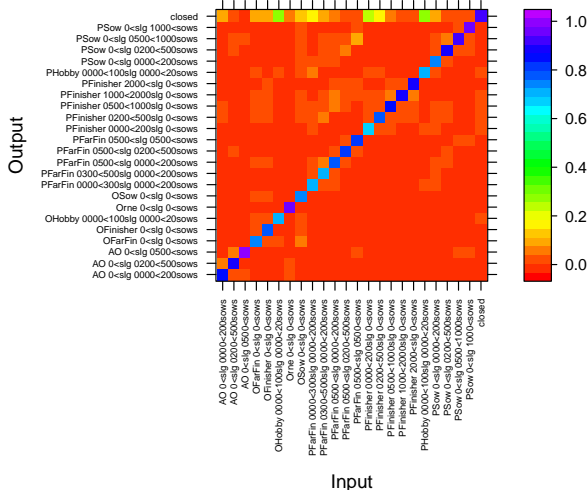
Transition probability matrix (TPM) - An example

1 year transition probability matrix for Cattle



Transition probability matrix (TPM) - Another example

1 year transition probability matrix for Swine



Does TPMs differ between regions?

For each animal species:

- Country wide counts of jumps \rightarrow expected jumps per region.
- χ^2 test was performed using cells where at least 5 jumps were expected in all regions.

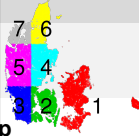
Result:

	Degrees of freedom	Smallest p-value
Cattle	85	$<1e-16$
Swine	90	$5e-11$
Sheep and Goat	58	$3e-8$

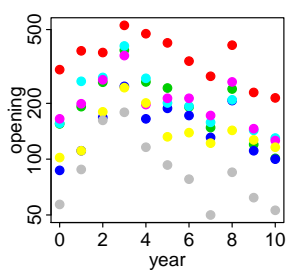
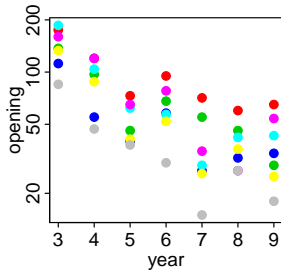
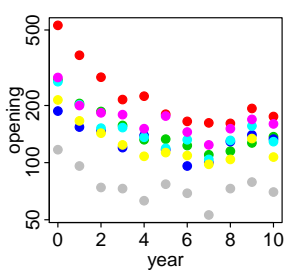
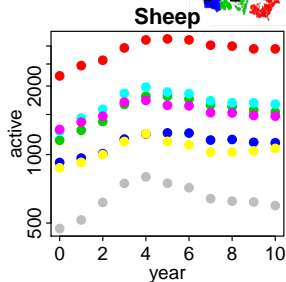
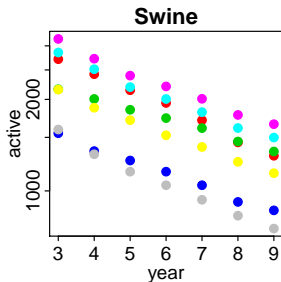
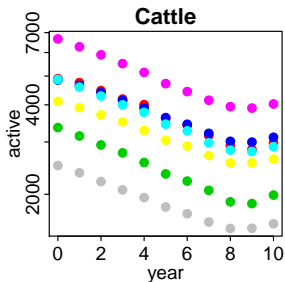
Methods for predicting structural development

First:

- Used regional TPMs for each species.
- Allowed for closed farms to reopen according to the TPM.
- Resulted in too many farms reopening.



How many farms are there per year and region



Subsets

Cattle and swine herds were analyzed the same way :

- A opening = year * region , all years
log-linear per region for all years.
- B opening = region , from 2006
geometric mean per region for year ≥ 2006 .
- C opening = year * region, until 2007
log-linear per region for year ≤ 2007 .

Sheep and goat behave differently:

- FA opening = year * region , all years
log-linear per region for all years.
- FB opening = year * region , from 2002
log-linear per region for year ≥ 2002 .
- FC opening = region
geometric mean per region for all years.

Methods for predicting structural development

First:

- Used regional TPMs for each species.
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Methods for predicting structural development

First:

- Used regional TPMs for each species.
- Allowed for closed farms to reopen according to the TPM.
- Resulted in too many farms reopening.

Now:

- Active farms: Used regional TPMs for each species.
- No. of opening farms were predicted by log-linear regression per region.
- This was repeated using different subsets of the data to give different predictions.

Locations and sizes for new herds

Where are they?

- New herds were randomly assigned to unused CHR numbers within their region.
- This also adds coordinates.

How big are they?

- All herds that change size category had their number of animals sampled among all herds that were in that size category.
- Herds in the largest size categories (Within production types) will likely grow in size.
- A variant was made by scaling the largest farms randomly using expert guestimates of upper bounds.

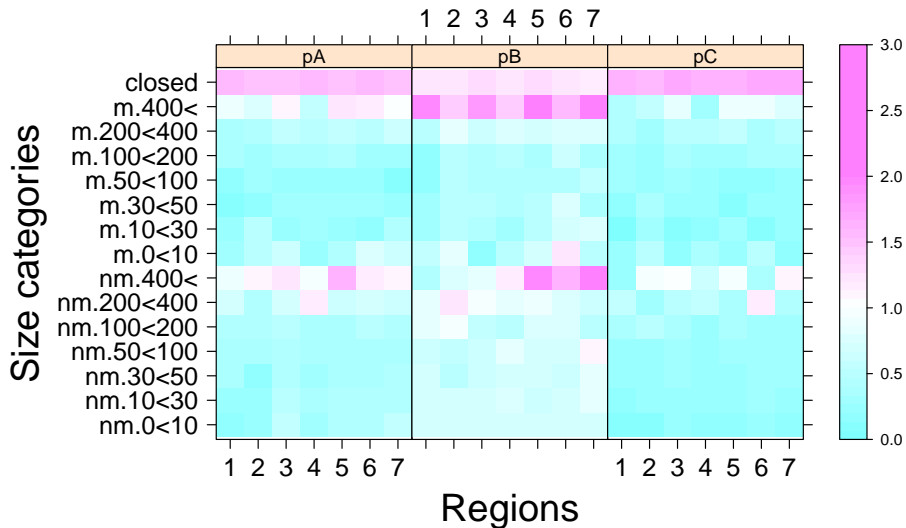
Large differences in predictions

- Predictions are made starting from year 2010 except for swine where we only have data to 2009.
- The TPM are estimated based on the same data as the openings, and is also done by region.

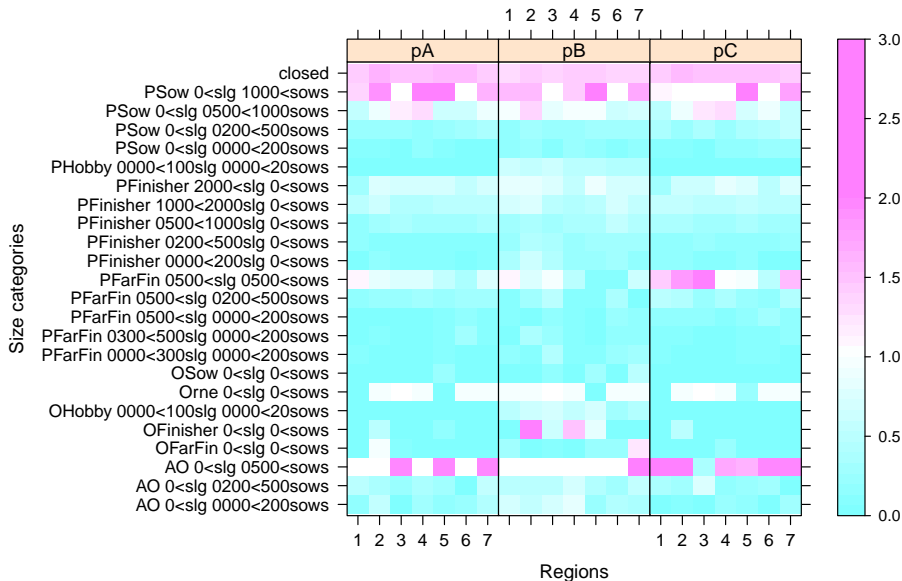
Distribution of herds on species:

	Cattle	Swine	Sheep'n'goat	Total
DADS2007	23550	11473	15830	50853
CHR2010	19218	8568	10379	38165
2030pA-FA	7922	3121	6411	17454
2030pB-FA	13800	4540	6411	24751
2030pC-FA	5307	3448	6411	15166
2030pA-FB	7922	3121	3082	14125
2030pA-FC	7922	3121	11628	22671

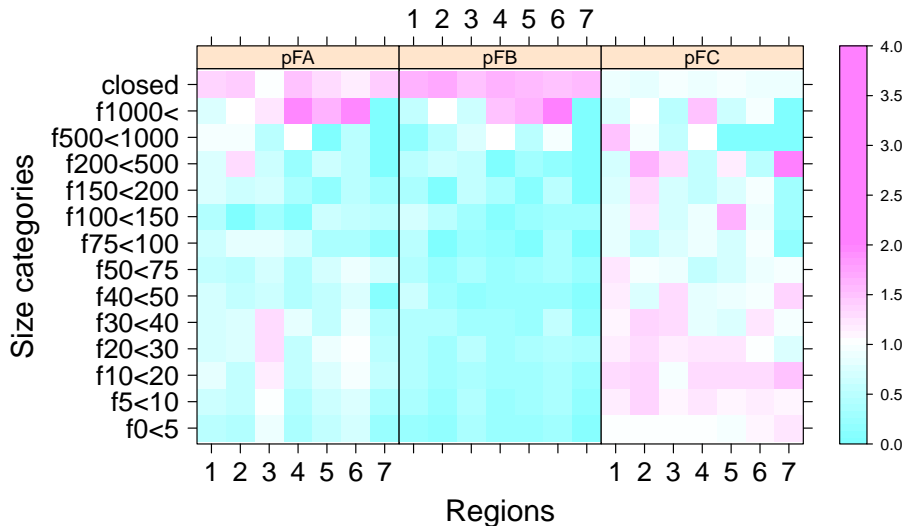
Relative change in distribution of Cattle



Relative change in distribution of Swine



Relative change in distribution of Sheep and goat



End of overview

Comments or questions?