

Preliminary genetic analysis for survival in Italian Jersey

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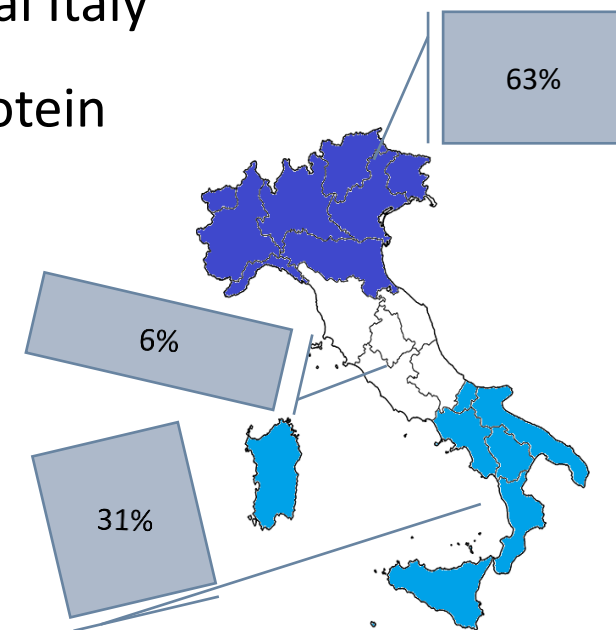
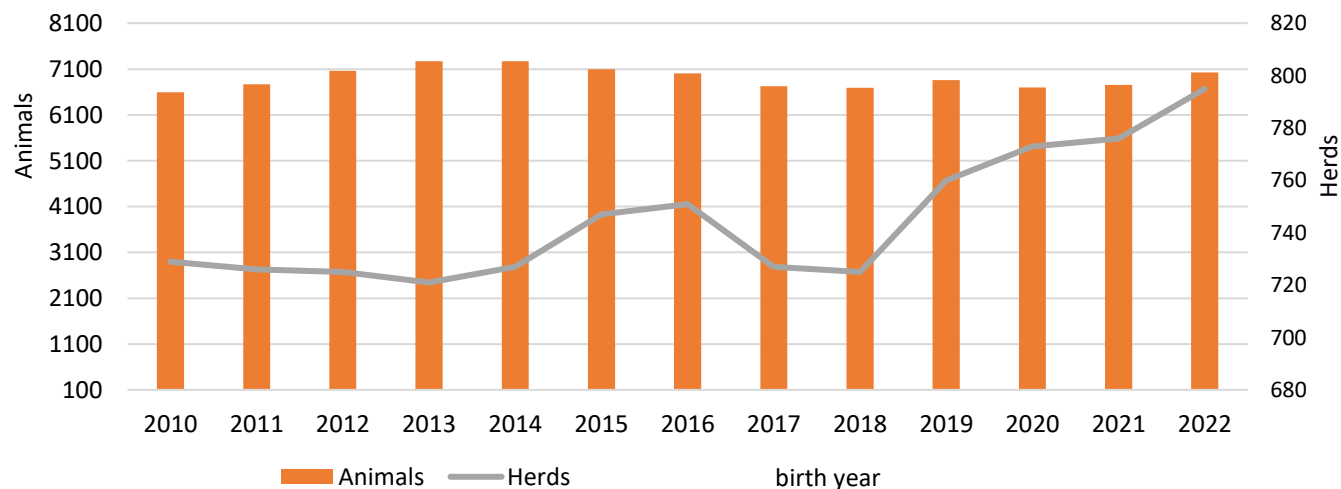
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Italian Jersey – Herd Book and background

- Jersey is farmed in Italy since 1980s
- Jersey Herd Book managed by ANAFIBJ since 1999
- 7025 cows in 795 herds (AIA 2022)
- Herds: 63% in North Italy, 31% in South Italy, 6% in the Central Italy
- Average productions: 7050 kg/lactation, 4.91% fat, 3.92% protein

Trend of Jersey cows and herds in Italy

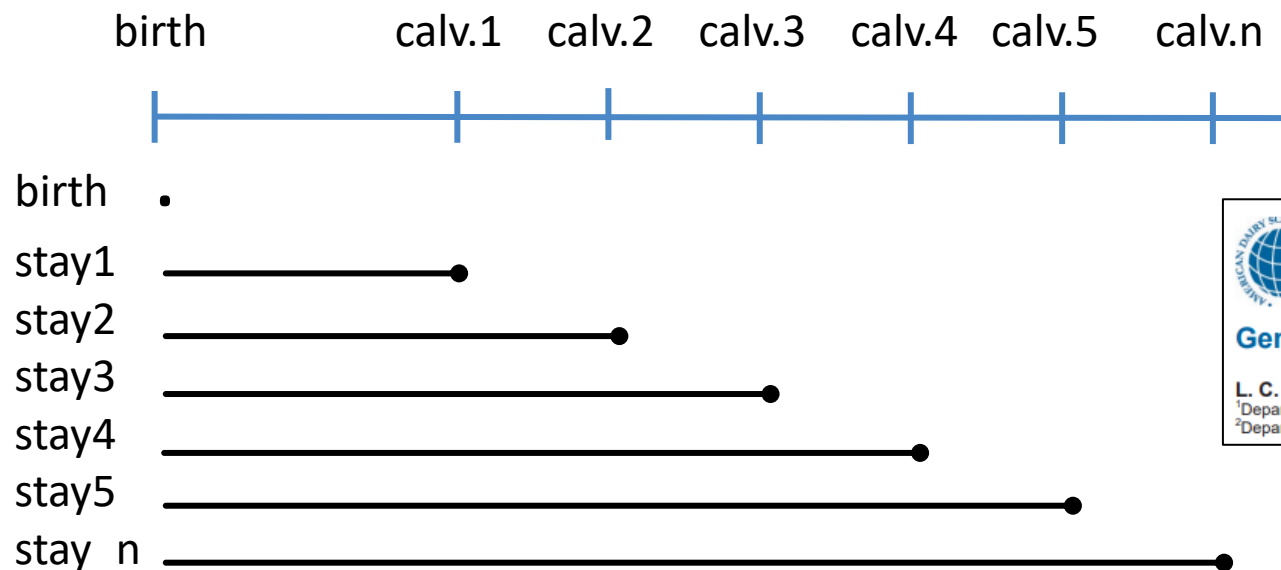


Aim

- LATTEco2 project (PSRN2): ANAFIBJ focused on **animal health and welfare**
- **Jersey longevity breeding value**

Stayability

- Binary trait
- Express the ability of a cow to remain in the herd until a given lactation



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Genetic parameters for stayability of Holsteins in US organic herds

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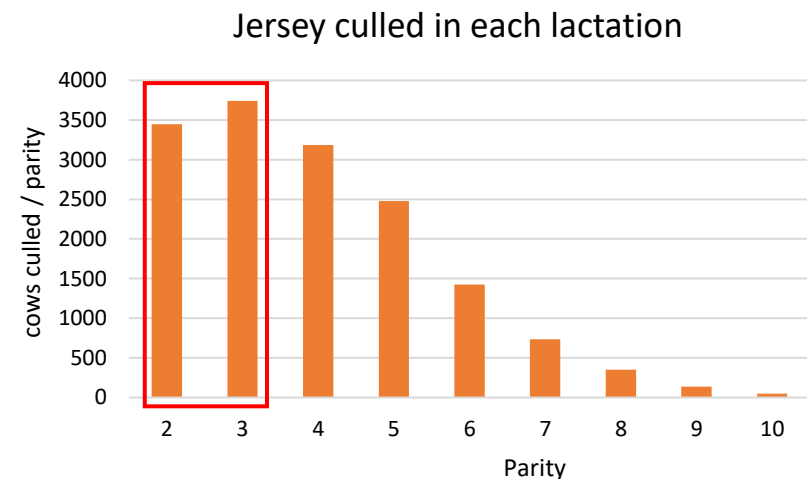
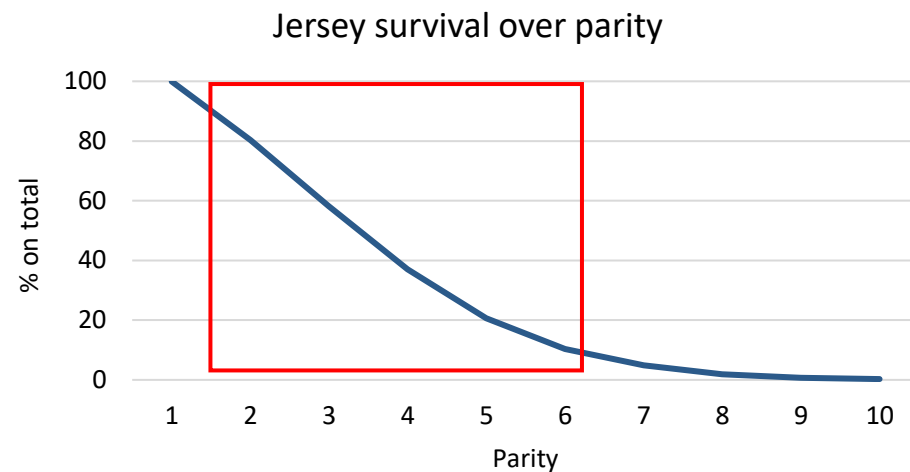
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Editing

- First calving > 31/12/1996
- Birth day < 31/12/2017
- Cows with 1° calving at least, only sequential lactations
- Max 10 parities per cow
- At least 3 daughters/sire, 3 cows/herd and 2 sires/herd → 15881 cows
- Deleted cows that changes herd → 457 sires
- Deleted cows with calving intervals < 240 days or > 700 days → 1015 herds
- Deleted cows with intervals between max event (insemination, calving or td) and last calving > 700 days
- Survival coded as binary trait: 1 as survived at the lactation, 0 not survived

Phenotypic survival rate

Parity	Culled/parity	% of culled/parity	Survived	% on total
1	0	0	15569	100
2	3446	22,1	12123	77,9
3	3744	24,0	8379	53,8
4	3183	20,4	5196	33,4
5	2477	15,9	2719	17,5
6	1426	9,2	1293	8,3
7	736	4,7	557	3,6
8	349	2,2	208	1,3
9	137	0,9	71	0,5
10	48	0,3	23	0,1

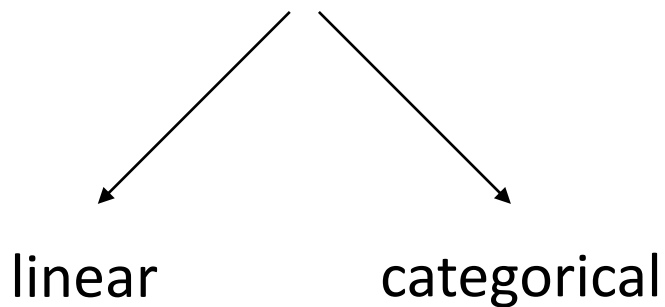


3,05 of average herd life → **Replacement Rate**
 = 1/average herd life
 = **32,8%**

Which model use?

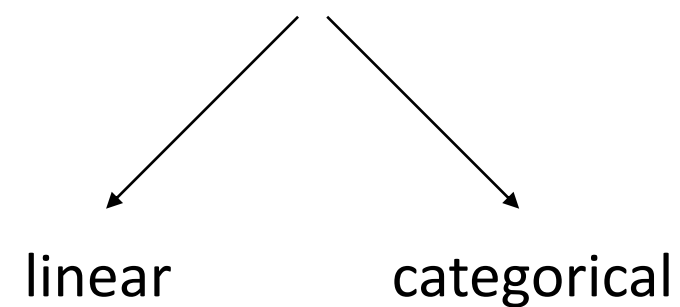
$$y = herd1 + a + e$$

- y = survival from parity 2 to 6
- $herd1$ = random effect of herd of first calving
- a = additive genetic effect
- e = residual error



$$y = herd_year1 + a + e$$

- y = survival from parity 2 to 6
- $herd_year1$ = random effect of herd_year of first calving
- a = additive genetic effect
- e = residual error



First results – stayability 2

Linear model				
	herd1		herd_year1	
	h ² (C.I.)	herd effect (C.I.)	h ² (C.I.)	herd_year effect (C.I.)
stay2	0.051 (0.030; 0.071)	0.050 (0.033; 0.064)	0.022 (0.007; 0.037)	0.125 (0.106; 0.143)

↓
Categorical gives higher h²

↓
Categorical gives higher h²

Categorical model				
	herd1		herd_year1	
	h ² (C.I.)	herd effect (C.I.)	h ² (C.I.)	herd_year effect (C.I.)
stay2	0.112 (0.073; 0.152)	0.097 (0.070; 0.127)	0.051 (0.018; 0.083)	0.231 (0.195; 0.265)

Convergence evaluation: visual inspection of trace plots, effective sample size quantification, Geweke's test

First results, stay3-stay6

	Linear model		Categorical model	
	herd1		herd1	
	h ² (C.I.)	herd effect (C.I.)	h ² (C.I.)	herd effect (C.I.)
stay3	0.099 (0.074; 0.124)	0.081 (0.062; 0.102)	0.159 (0.118; 0.196)	0.137 (0.105; 0.169)
stay4	0.128 (0.100; 0.160)	0.079 (0.058; 0.097)	0.208 (0.165; 0.250)	0.150 (0.112; 0.184)
stay5	0.127 (0.098; 0.152)	0.061 (0.044; 0.079)	0.252 (0.200; 0.301)	0.151 (0.109; 0.192)
stay6	0.105 (0.080; 0.131)	0.045 (0.030; 0.059)	0.274 (0.210; 0.334)	0.147 (0.099; 0.194)

→ Categorical gives higher h²

Convergence evaluation: visual inspection of trace plots, effective sample size quantification, Geweke's test

Rank correlations, stay2-stay6

herd, linear	STAY2	STAY3	STAY4	STAY5	STAY6
STAY2	1	0,86	0,78	0,76	0,62
STAY3		1	0,89	0,82	0,67
STAY4			1	0,92	0,79
STAY5				1	0,94
STAY6					1

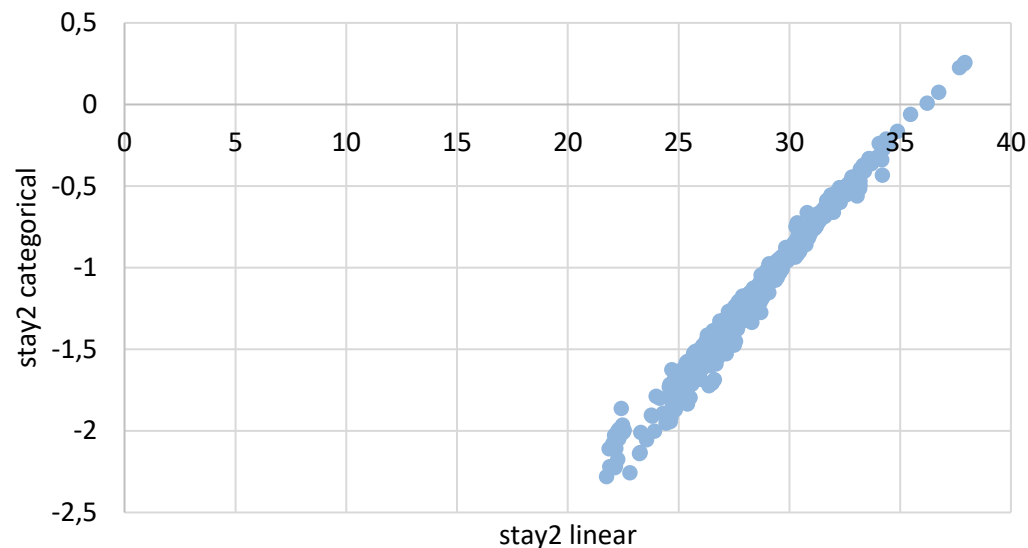
herd, categorical	STAY2	STAY3	STAY4	STAY5	STAY6
STAY2	1	0,87	0,81	0,80	0,69
STAY3		1	0,90	0,79	0,63
STAY4			1	0,88	0,76
STAY5				1	0,94
STAY6					1

herd_year, linear	STAY2	STAY3	STAY4	STAY5	STAY6
STAY2	1	0,73	0,62	0,62	0,51
STAY3		1	0,77	0,66	0,47
STAY4			1	0,85	0,70
STAY5				1	0,91
STAY6					1

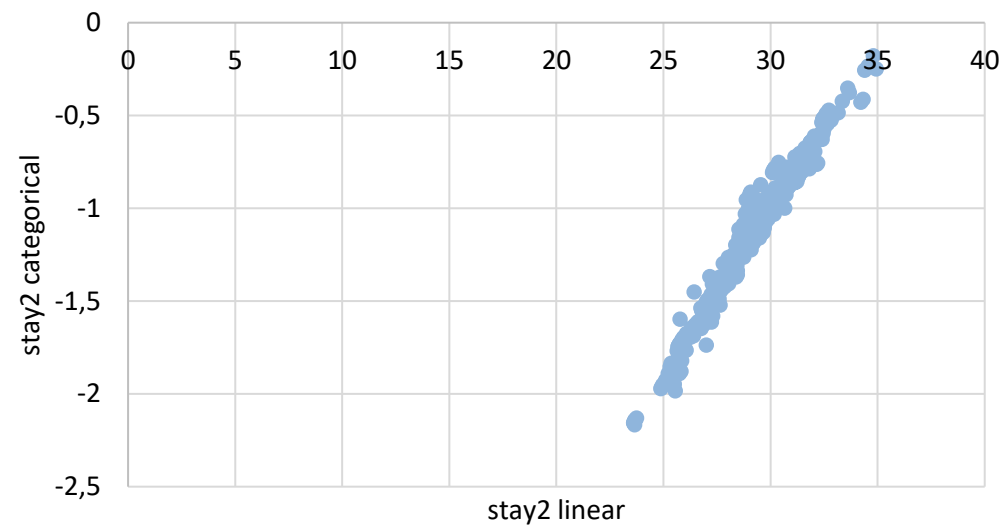
herd_year, categorical	STAY2	STAY3	STAY4	STAY5	STAY6
STAY2	1	0,72	0,62	0,57	0,48
STAY3		1	0,81	0,62	0,43
STAY4			1	0,82	0,68
STAY5				1	0,94
STAY6					1

Models comparison

Rank correlation herd in STAY2, lin vs cat



Rank correlation herd_year in STAY2, lin vs cat



Rank correlation between linear model and categorical model is very high → linear model can be applied

Conclusions

- Heritability is low but there is variance → selection is possible
- High correlation between linear and categorical models → **linear model can be used**
- Still discussing about which model is better
- Evaluation of stayability 4 as breeding objective

- Next... Conformation trait (expected correlation with some udder traits and feet&legs)

Thank you for the attention



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